



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:38 PM GMT

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

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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

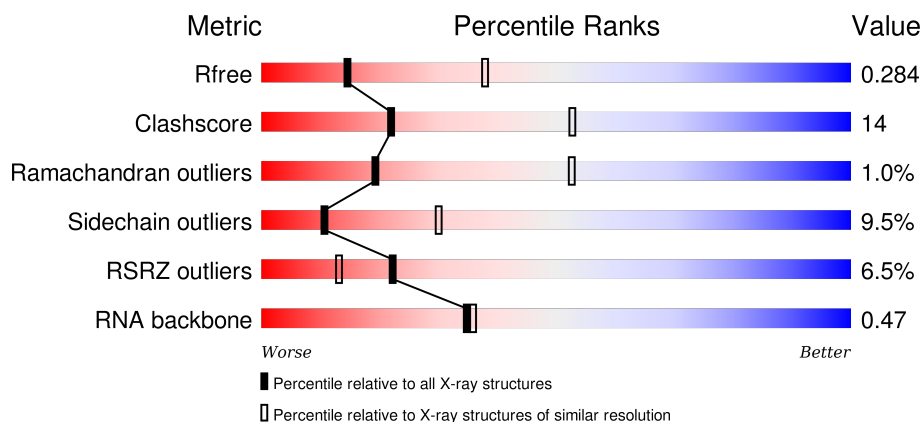
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)
RNA backbone	2183	1091 (3.20-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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>38%</div> <div>43%</div> <div>16%</div> <div>..</div> </div>
1	CA	1521	<div> <div>2%</div> <div>33%</div> <div>47%</div> <div>17%</div> <div>..</div> </div>
2	AB	256	<div> <div>6%</div> <div>50%</div> <div>32%</div> <div>8%</div> <div>10%</div> </div>
2	CB	256	<div> <div>43%</div> <div>49%</div> <div>32%</div> <div>8%</div> <div>10%</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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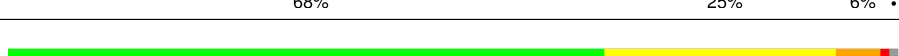

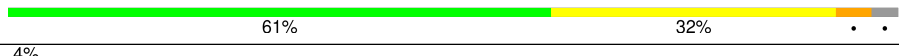


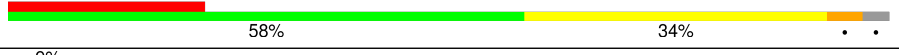

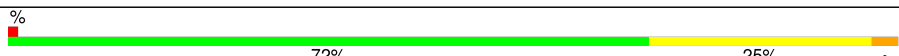

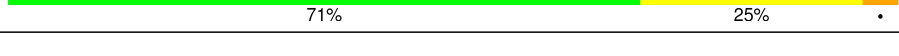
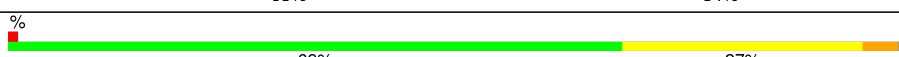





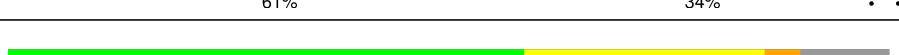



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Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AW	3	
23	CW	3	
24	AX	77	
24	CX	77	
25	AY	76	
25	CY	76	
26	BA	2915	
26	DA	2915	
27	BB	121	
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	

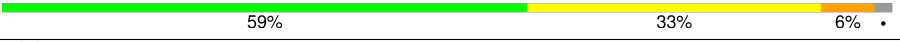




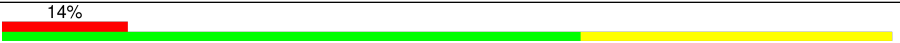
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Mol	Chain	Length	Quality of chain
40	DT	146	
41	BU	118	
41	DU	118	
42	BV	101	
42	DV	101	
43	BW	113	
43	DW	113	
44	BX	96	
44	DX	96	
45	BY	110	
45	DY	110	
46	BZ	206	
46	DZ	206	
47	B0	85	
47	D0	85	
48	B1	98	
48	D1	98	
49	B2	72	
49	D2	72	
50	B3	60	
50	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
57	MG	AA	3024	-	-	-	X
57	MG	AA	3030	-	-	-	X
57	MG	AA	3055	-	-	-	X
57	MG	AA	3074	-	-	-	X
57	MG	AA	3083	-	-	-	X
57	MG	AA	3089	-	-	-	X
57	MG	AA	3090	-	-	-	X
57	MG	AA	3091	-	-	-	X
57	MG	AA	3113	-	-	-	X
57	MG	AA	3116	-	-	-	X
57	MG	AA	3144	-	-	-	X
57	MG	AA	3155	-	-	-	X
57	MG	AA	3172	-	-	-	X
57	MG	AA	3204	-	-	-	X
57	MG	AX	3007	-	-	-	X
57	MG	B7	102	-	-	-	X
57	MG	BA	3026	-	-	-	X
57	MG	BA	3027	-	-	-	X
57	MG	BA	3036	-	-	-	X
57	MG	BA	3041	-	-	-	X
57	MG	BA	3053	-	-	-	X
57	MG	BA	3054	-	-	-	X
57	MG	BA	3067	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	BA	3101	-	-	-	X
57	MG	BA	3105	-	-	-	X
57	MG	BA	3111	-	-	-	X
57	MG	BA	3114	-	-	-	X
57	MG	BA	3118	-	-	-	X
57	MG	BA	3125	-	-	-	X
57	MG	BA	3131	-	-	-	X
57	MG	BA	3133	-	-	-	X
57	MG	BA	3148	-	-	-	X
57	MG	BA	3150	-	-	-	X
57	MG	BA	3152	-	-	-	X
57	MG	BA	3160	-	-	-	X
57	MG	BA	3183	-	-	-	X
57	MG	BA	3185	-	-	-	X
57	MG	BA	3190	-	-	-	X
57	MG	BA	3193	-	-	-	X
57	MG	BA	3200	-	-	-	X
57	MG	BA	3212	-	-	-	X
57	MG	BA	3226	-	-	-	X
57	MG	BA	3244	-	-	-	X
57	MG	BA	3245	-	-	-	X
57	MG	BA	3246	-	-	-	X
57	MG	BA	3253	-	-	-	X
57	MG	BA	3257	-	-	-	X
57	MG	BA	3259	-	-	-	X
57	MG	BA	3267	-	-	-	X
57	MG	BA	3271	-	-	-	X
57	MG	BA	3277	-	-	-	X
57	MG	BA	3281	-	-	-	X
57	MG	BA	3283	-	-	-	X
57	MG	BA	3294	-	-	-	X
57	MG	BA	3303	-	-	-	X
57	MG	BA	3310	-	-	-	X
57	MG	BA	3314	-	-	-	X
57	MG	BA	3366	-	-	-	X
57	MG	BA	3384	-	-	-	X
57	MG	BA	3385	-	-	-	X
57	MG	BA	3391	-	-	-	X
57	MG	BA	3396	-	-	-	X
57	MG	BA	3401	-	-	-	X
57	MG	BA	3403	-	-	-	X
57	MG	BA	3405	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	BA	3412	-	-	-	X
57	MG	BA	3423	-	-	-	X
57	MG	BA	3431	-	-	-	X
57	MG	BA	3432	-	-	-	X
57	MG	BA	3436	-	-	-	X
57	MG	BA	3437	-	-	-	X
57	MG	BA	3443	-	-	-	X
57	MG	BA	3461	-	-	-	X
57	MG	BA	3490	-	-	-	X
57	MG	BA	3498	-	-	-	X
57	MG	BA	3508	-	-	-	X
57	MG	BA	3509	-	-	-	X
57	MG	BA	3514	-	-	-	X
57	MG	BA	3529	-	-	-	X
57	MG	BA	3530	-	-	-	X
57	MG	BA	3532	-	-	-	X
57	MG	BA	3533	-	-	-	X
57	MG	BA	3534	-	-	-	X
57	MG	BA	3545	-	-	-	X
57	MG	BA	3546	-	-	-	X
57	MG	BA	3602	-	-	-	X
57	MG	BA	3651	-	-	-	X
57	MG	BA	3663	-	-	-	X
57	MG	BA	3677	-	-	-	X
57	MG	BA	3686	-	-	-	X
57	MG	BA	3698	-	-	-	X
57	MG	BA	3705	-	-	-	X
57	MG	BA	3706	-	-	-	X
57	MG	BA	3707	-	-	-	X
57	MG	BA	3709	-	-	-	X
57	MG	BD	301	-	-	-	X
57	MG	BD	303	-	-	-	X
57	MG	BD	306	-	-	-	X
57	MG	BD	308	-	-	-	X
57	MG	BD	310	-	-	-	X
57	MG	BD	311	-	-	-	X
57	MG	BE	3001	-	-	-	X
57	MG	BE	3002	-	-	-	X
57	MG	BF	304	-	-	-	X
57	MG	BF	307	-	-	-	X
57	MG	BN	3001	-	-	-	X
57	MG	BN	3004	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	BN	3006	-	-	-	X
57	MG	BP	3001	-	-	-	X
57	MG	BQ	3001	-	-	-	X
57	MG	BQ	3002	-	-	-	X
57	MG	BQ	3003	-	-	-	X
57	MG	BR	203	-	-	-	X
57	MG	BU	204	-	-	-	X
57	MG	BU	206	-	-	-	X
57	MG	BU	208	-	-	-	X
57	MG	BW	202	-	-	-	X
57	MG	CA	3017	-	-	-	X
57	MG	CA	3047	-	-	-	X
57	MG	CA	3054	-	-	-	X
57	MG	CA	3058	-	-	-	X
57	MG	CA	3070	-	-	-	X
57	MG	CA	3074	-	-	-	X
57	MG	CA	3095	-	-	-	X
57	MG	CA	3097	-	-	-	X
57	MG	CA	3116	-	-	-	X
57	MG	CA	3126	-	-	-	X
57	MG	DA	3001	-	-	-	X
57	MG	DA	3004	-	-	-	X
57	MG	DA	3015	-	-	-	X
57	MG	DA	3017	-	-	-	X
57	MG	DA	3020	-	-	-	X
57	MG	DA	3023	-	-	-	X
57	MG	DA	3030	-	-	-	X
57	MG	DA	3039	-	-	-	X
57	MG	DA	3042	-	-	-	X
57	MG	DA	3044	-	-	-	X
57	MG	DA	3058	-	-	-	X
57	MG	DA	3059	-	-	-	X
57	MG	DA	3061	-	-	-	X
57	MG	DA	3096	-	-	-	X
57	MG	DA	3100	-	-	-	X
57	MG	DA	3103	-	-	-	X
57	MG	DA	3106	-	-	-	X
57	MG	DA	3116	-	-	-	X
57	MG	DA	3119	-	-	-	X
57	MG	DA	3127	-	-	-	X
57	MG	DA	3141	-	-	-	X
57	MG	DA	3145	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	DA	3152	-	-	-	X
57	MG	DA	3161	-	-	-	X
57	MG	DA	3162	-	-	-	X
57	MG	DA	3166	-	-	-	X
57	MG	DA	3170	-	-	-	X
57	MG	DA	3171	-	-	-	X
57	MG	DA	3173	-	-	-	X
57	MG	DA	3174	-	-	-	X
57	MG	DA	3177	-	-	-	X
57	MG	DA	3183	-	-	-	X
57	MG	DA	3185	-	-	-	X
57	MG	DA	3192	-	-	-	X
57	MG	DA	3207	-	-	-	X
57	MG	DA	3210	-	-	-	X
57	MG	DA	3216	-	-	-	X
57	MG	DA	3228	-	-	-	X
57	MG	DA	3230	-	-	-	X
57	MG	DA	3234	-	-	-	X
57	MG	DA	3238	-	-	-	X
57	MG	DA	3242	-	-	-	X
57	MG	DA	3243	-	-	-	X
57	MG	DA	3251	-	-	-	X
57	MG	DA	3255	-	-	-	X
57	MG	DA	3257	-	-	-	X
57	MG	DA	3258	-	-	-	X
57	MG	DA	3267	-	-	-	X
57	MG	DA	3274	-	-	-	X
57	MG	DA	3277	-	-	-	X
57	MG	DA	3291	-	-	-	X
57	MG	DA	3307	-	-	-	X
57	MG	DA	3312	-	-	-	X
57	MG	DA	3319	-	-	-	X
57	MG	DA	3348	-	-	-	X
57	MG	DA	3350	-	-	-	X
57	MG	DA	3351	-	-	-	X
57	MG	DA	3363	-	-	-	X
57	MG	DA	3369	-	-	-	X
57	MG	DA	3371	-	-	-	X
57	MG	DA	3373	-	-	-	X
57	MG	DA	3376	-	-	-	X
57	MG	DA	3382	-	-	-	X
57	MG	DA	3387	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	DA	3410	-	-	-	X
57	MG	DA	3417	-	-	-	X
57	MG	DA	3426	-	-	-	X
57	MG	DA	3430	-	-	-	X
57	MG	DA	3440	-	-	-	X
57	MG	DA	3441	-	-	-	X
57	MG	DA	3444	-	-	-	X
57	MG	DA	3448	-	-	-	X
57	MG	DA	3453	-	-	-	X
57	MG	DA	3456	-	-	-	X
57	MG	DA	3462	-	-	-	X
57	MG	DA	3466	-	-	-	X
57	MG	DA	3471	-	-	-	X
57	MG	DA	3473	-	-	-	X
57	MG	DA	3474	-	-	-	X
57	MG	DA	3475	-	-	-	X
57	MG	DA	3483	-	-	-	X
57	MG	DA	3501	-	-	-	X
57	MG	DA	3533	-	-	-	X
57	MG	DA	3537	-	-	-	X
57	MG	DA	3538	-	-	-	X
57	MG	DA	3552	-	-	-	X
57	MG	DA	3559	-	-	-	X
57	MG	DA	3579	-	-	-	X
57	MG	DA	3594	-	-	-	X
57	MG	DA	3602	-	-	-	X
57	MG	DA	3609	-	-	-	X
57	MG	DA	3614	-	-	-	X
57	MG	DA	3619	-	-	-	X
57	MG	DA	3621	-	-	-	X
57	MG	DA	3624	-	-	-	X
57	MG	DA	3628	-	-	-	X
57	MG	DB	3005	-	-	-	X
57	MG	DD	303	-	-	-	X
57	MG	DD	305	-	-	-	X
57	MG	DD	306	-	-	-	X
57	MG	DE	302	-	-	-	X
57	MG	DF	3004	-	-	-	X
57	MG	DP	202	-	-	-	X
57	MG	DU	3001	-	-	-	X
57	MG	DV	201	-	-	-	X



## 2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 290205 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	1498	Total	C	N	O	P	0	0	0
			32205	14333	5970	10404	1498			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

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

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

- Molecule 7 is a protein called 30S ribosomal protein S7.

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

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

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

- Molecule 11 is a protein called 30S ribosomal protein S11.

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

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

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

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

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

- Molecule 19 is a protein called 30S ribosomal protein S19.

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

- Molecule 20 is a protein called 30S ribosomal protein S20.

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

- Molecule 21 is a protein called 30S ribosomal protein Thx.

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

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
22	CV	6	Total	C	N	O	P	0	0	0
			129	58	24	41	6			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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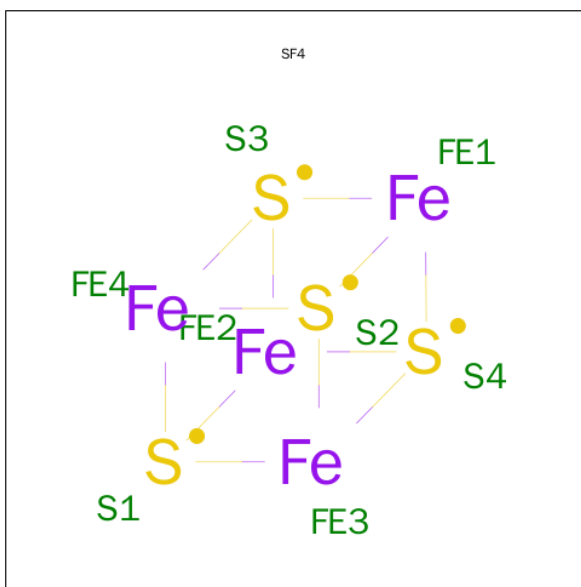
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	B2	1	Total 1	Mg 1	0	0
57	AA	207	Total 207	Mg 207	0	0
57	BQ	5	Total 5	Mg 5	0	0
57	CX	2	Total 2	Mg 2	0	0
57	DV	2	Total 2	Mg 2	0	0
57	AM	1	Total 1	Mg 1	0	0
57	BU	8	Total 8	Mg 8	0	0
57	DR	2	Total 2	Mg 2	0	0
57	AD	2	Total 2	Mg 2	0	0
57	BN	6	Total 6	Mg 6	0	0
57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

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

- Molecule 58 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



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

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

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

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

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

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

- Molecule 61 is water.

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

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

*Continued on next page...*

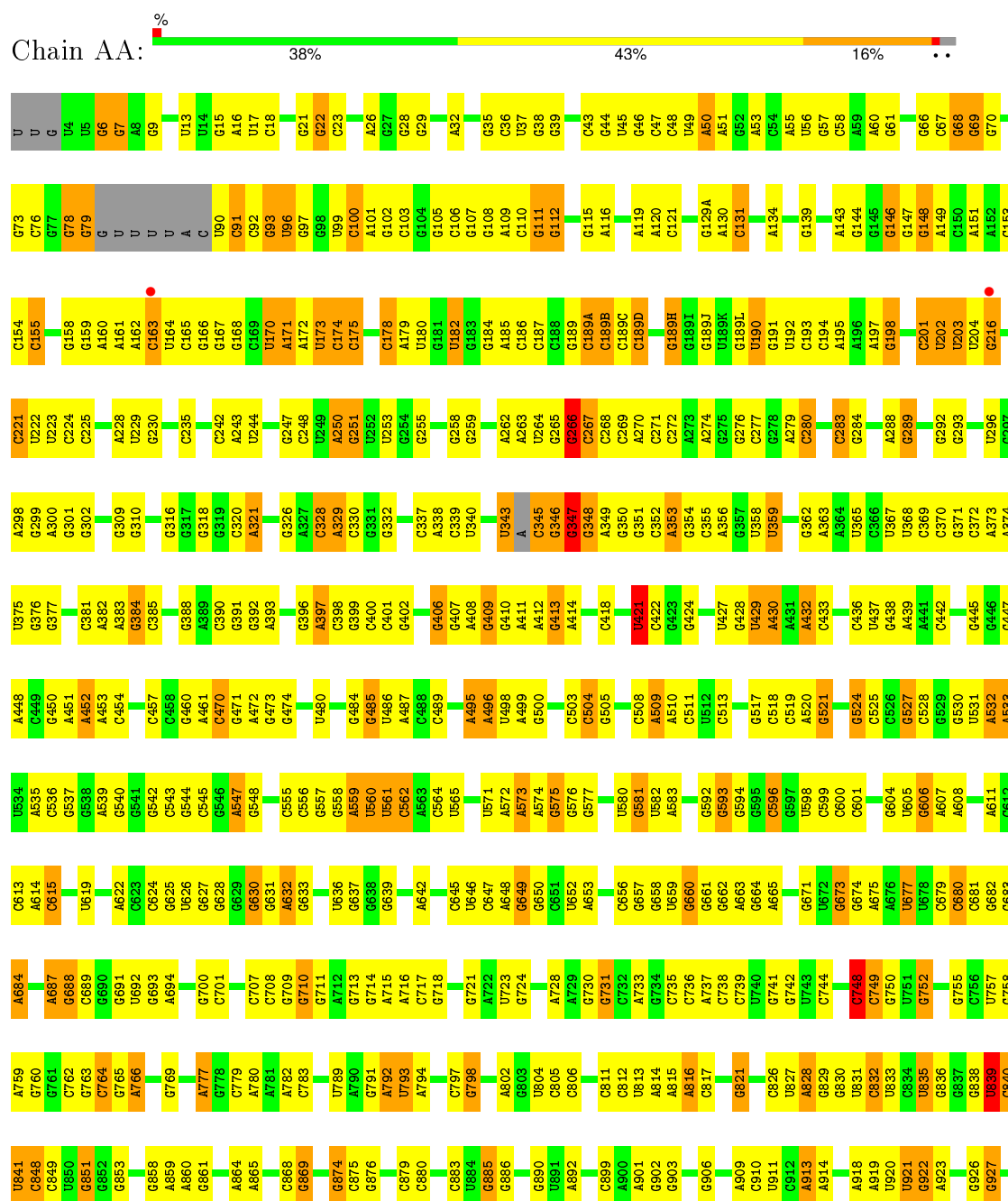
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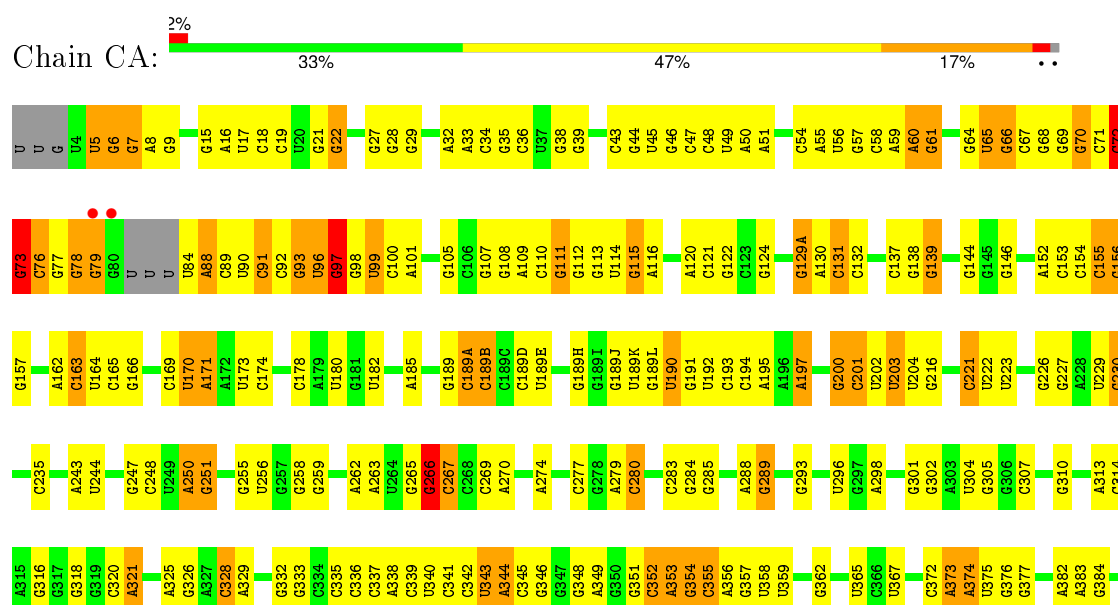
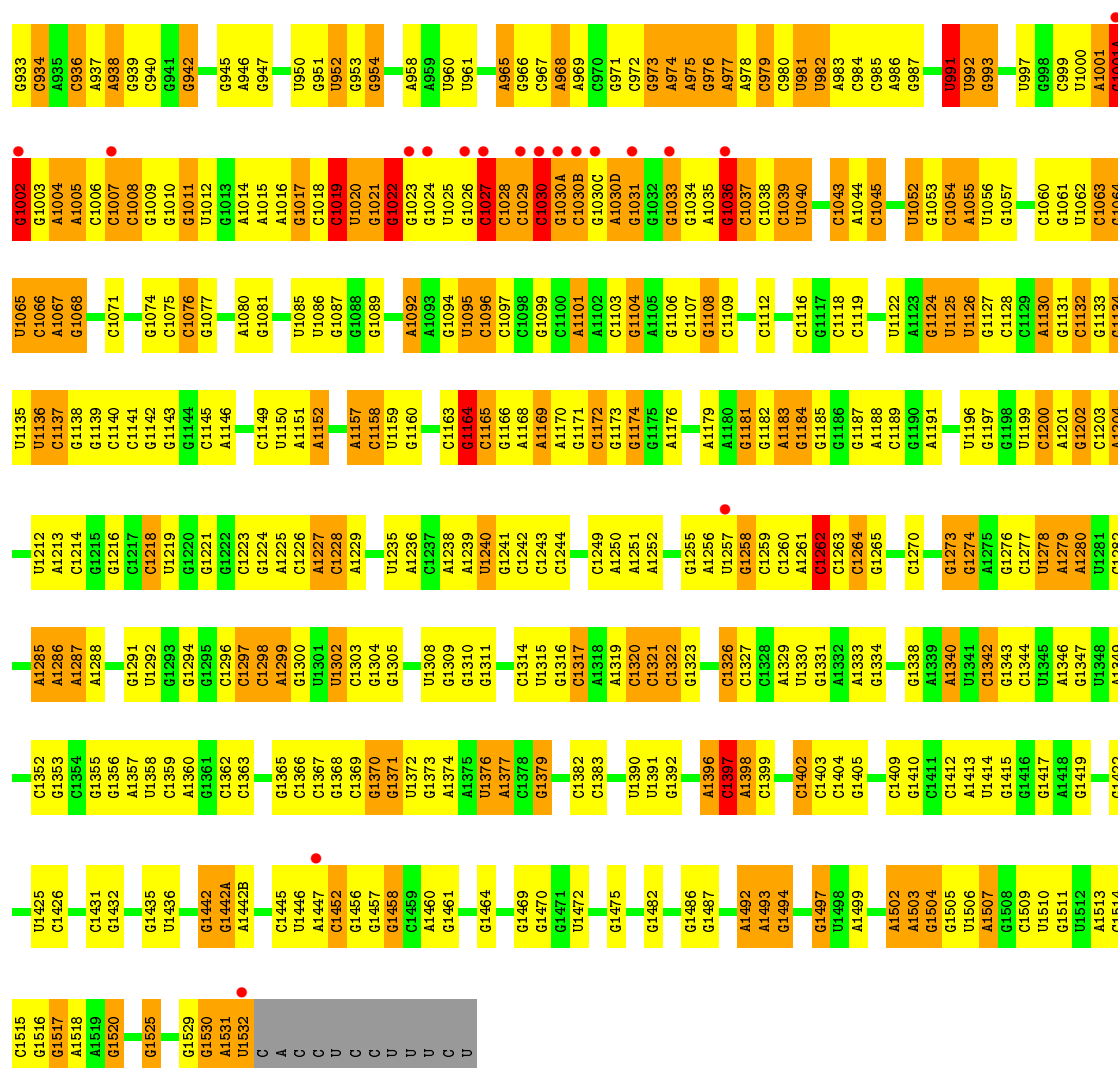
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
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			1	1		
61	CX	1	Total	O	0	0
			1	1		
61	DA	767	Total	O	0	0
			767	767		
61	DB	9	Total	O	0	0
			9	9		
61	DD	9	Total	O	0	0
			9	9		
61	DE	5	Total	O	0	0
			5	5		
61	DF	6	Total	O	0	0
			6	6		
61	DN	2	Total	O	0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

### 3 Residue-property plots

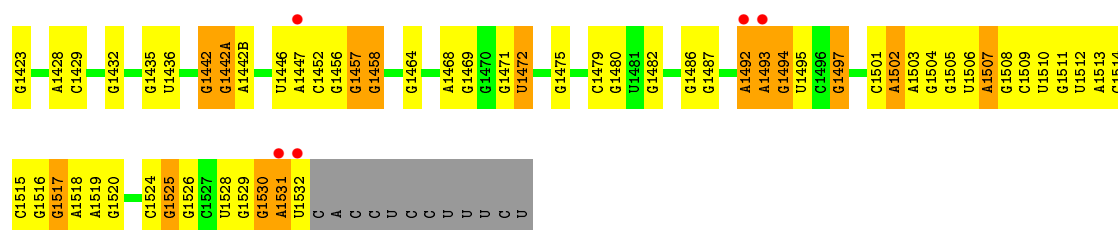
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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



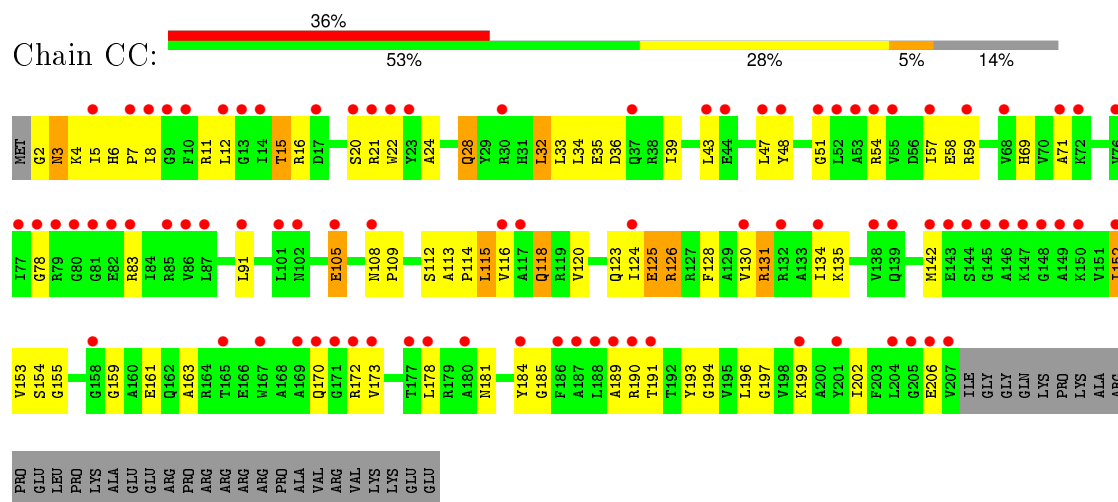


A1357	G1293	C1226	G1160	G1034	C979	G829	U751	A684	G544	G460	U387
U1358	G1294	A1227	G1161	A1035	C980	G830	G752	G685	C545	A461	C390
C1359	G1295	C1228	G1162	G1036	U981	U831	U686	U686	G546	C470	C391
A1360	C1296	A1229	G1163	A1037	U982	C832	C754	A687	G547	G471	G392
G1361	G1297	G1230	G1104	G1038	A983	U833	G755	G688	G548	A472	A393
C1362	C1298	G1231	G1105	C1039	C984	C834	G756	C689	C549	G473	
G1363	A1299		U1040	U1040	C985	U835	U757	G690	C550	G474	
A1363A	G1300	U1235	A1170	A1041	A986	G836	G758	G691	U551	G475	A397
U1364	U1301	A1236	G1171	G1042	G987	G837	A759	U692	U552	G476	C398
G1365	U1302	C1237	C1172	C1043	C988	U838	G760	G693			G399
C1366	G1303	A1238	A1109	A1044	C989	U839	G761	A694	C556	G484	C400
G1367	G1304	A1239	G1174	C1045	C990	C840	G762	A695		G485	C401
C1368	G1305	U1240	A1175	A1046	U991	U841	G763	A696	U559	U486	
C1369	A1176		G1047	U992	U992	C848	C764	U697	U560	A487	
G1370	G1177			A923	G993	C849	G765	G698	C629	C488	U405
G1371	G1309	C1244	U1052	G1053	A994	U850	A766	C699	C630	G407	G406
U1372	G1310	A1245	G1115	C1054	C995	G851	A767	G700	G631	U498	A408
G1373	G1311	A1180	G1117	U1055	A996	G852	A768	C701	U567	U494	A409
A1374	G1312	G1181	C1118	A1056	U997	G853	G769	A702	G568	A495	C410
G1375	U1313	G1182	C1119	U1056	C998		G775	C707		A496	A411
U1376	C1314	A1183	G1120	G1057	C999	C857	G776	C708	U571	U498	A412
A1377	U1315	G1184	U1121	C1058	U1000	G858	A777	C709	A572	A499	G413
C1378	G1316	G1185	U1122	C1059	A1001	A859	G778	G710	A573	G500	A414
G1379	C1317	G1186	A1123	G1060	G1001A	A860	G779	G711	C574	C501	
U1380	A1318	G1187	G1124	G1061	G1002	G861	A780	A712	G575	G502	C417
U1381	A1319		U1125	U1062	G1003				C576	C503	G418
C1382	C1320	G1190	U1126	C1063	A1004	A864	G786	G713	C577	C504	C419
C1383	C1321	A1191	G1127	G1064	A1005	A865		G714	C578	U505	U420
	C1322		U1194	U1065	C1006	C866	U789	A715	C645	C508	U421
G1386			G1195	C1066	C1007	G867	U790	A716	U580	A509	G423
G1392	C1325	C1262	C1263	A1067	G1008	C868	G791	C717	U582	A510	G424
U1393	C1327	G1264	U1197	G1068		U870	A792	C719	C511	C512	
A1394	C1328	G1265	G1133	U1073	C948	U871	U793	C720	U512	U428	
C1395	A1329	G1266	G1134	G1074	A872	A873	A794	C721	C514	U429	
A1396	U1330		U1135	C1075	A874			A722	C515	A430	
G1397	G1331		C1137	C1076	U952	G874	G797	U723	U516	A431	
A1398	A1332	C1270	G1202	G1077	C877		G798	G724	G592	A432	
C1399	A1333	G1271	C1203	U1078	G878		G800	A728	C518	C433	
C1400	G1334	G1272	G1139	G1079	C879		U801	A729	C519	U434	
G1401		U1205	C1140	A1080	C880	G881	G803	G730	C520	C435	
C1402	G1338	G1273	C1141	G1081	A958		U804	G731	G596	G521	C436
A1403	A1339	A1275	G1142	G1082	U1020		C805	G732	C597	C522	U437
C1404	A1340	G1276	G1143	U1083	G1021		C806	A733	U598	A523	G438
G1405	U1341	C1277	G1144	U1084	G1022	G885	C811	C736	C600	C524	A439
U1406	G1342	U1278	C1145	U1085	G1023	G886	C812	G737	A602	C526	C442
	G1343	A1279	A1146	U1086	U1024	G887	U813	C738	U603	C527	C443
	C1344	U1212	U1211	G1087	G1025		A814		U605	C528	C444
	U1345	U1281	A1213	G1088	G1026	G890	A815	G741	U606	U531	G445
G1409	A1346	C1282	C1214	U1089	G1027	U891	A816	G742	G607	A532	G447
C1410	G1347	G1283	G1215	U1090	C1028	A892	C817	G745	A608	A533	A448
C1411	U1348	C1284	G1216	U1091	C1029	C893		A746	A609	G538	A452
A1412	A1349	A1285	C1217	A1092	C1030	G894	A817	C747	G610	A539	
U1414	A1350	A1286	G1218	A1093	C972	G895	C817	C748	A611	A541	C456
G1415	U1351	A1287	G1154	G1094	G1030A			C749	C612	G542	
G1416	C1352	A1288	G1155	U1095	G1030B	C899	G821		G613		
U1417	U1353	A1289	G1156	C1096	G1030C	A900	C826		C680	G457	
A1418	G1354	G1290	A1157	C1097	G1031	A901	U827				
G1419	C1355	C1223	C1158	U1098	G1032	G902	U827				
			U1159	G1099	G1033	G903	A828				
G1422		U1292									

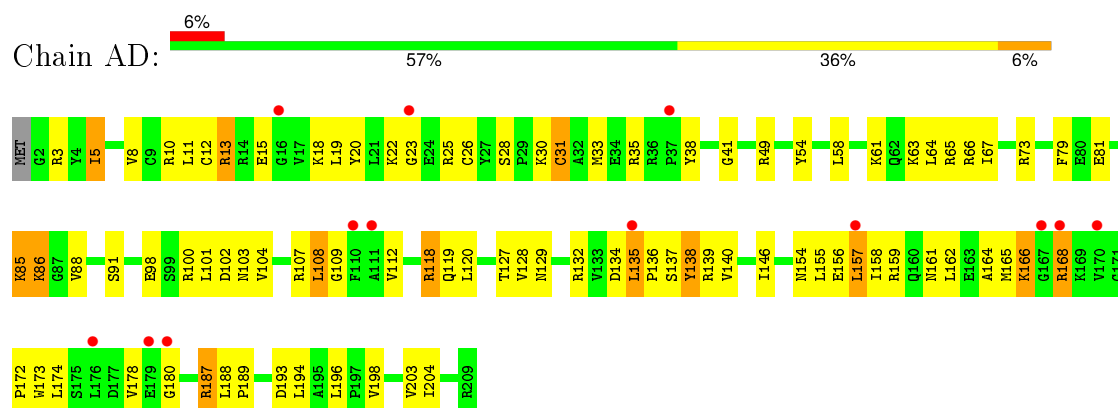


PRO  
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ALA  
ARG  
PRO  
GLU  
LEU  
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LYS  
ALA  
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GLU

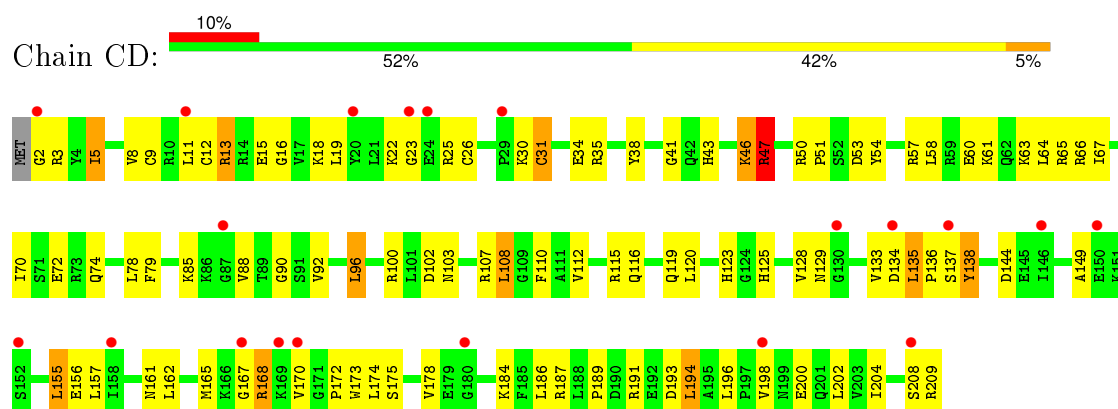
- Molecule 3: 30S ribosomal protein S3



- Molecule 4: 30S ribosomal protein S4

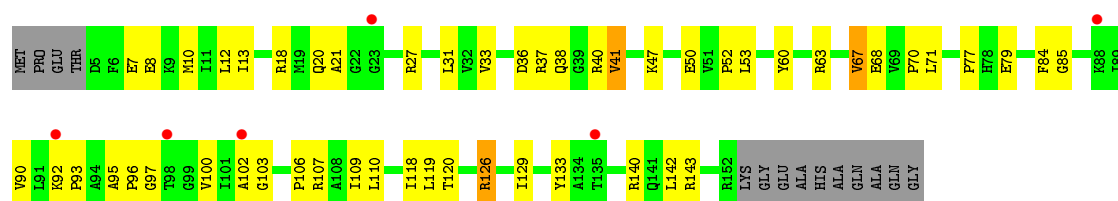


- Molecule 4: 30S ribosomal protein S4

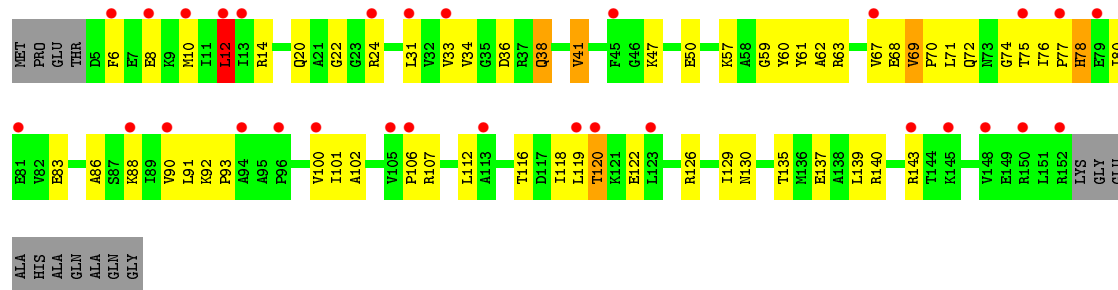


- Molecule 5: 30S ribosomal protein S5

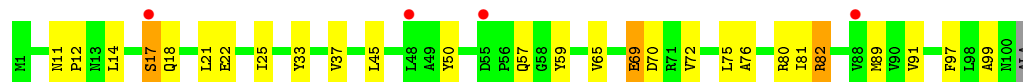
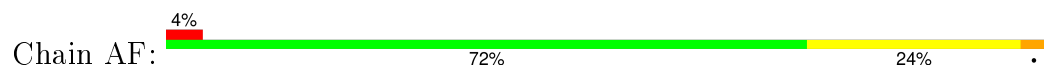




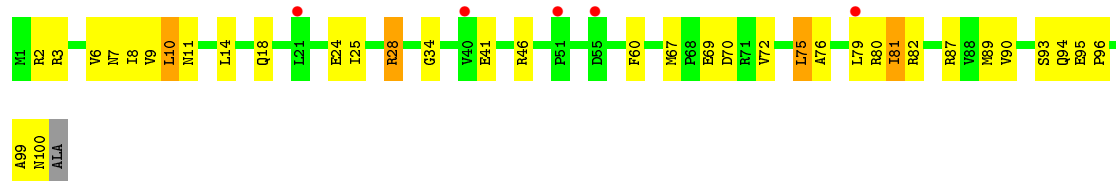
• Molecule 5: 30S ribosomal protein S5



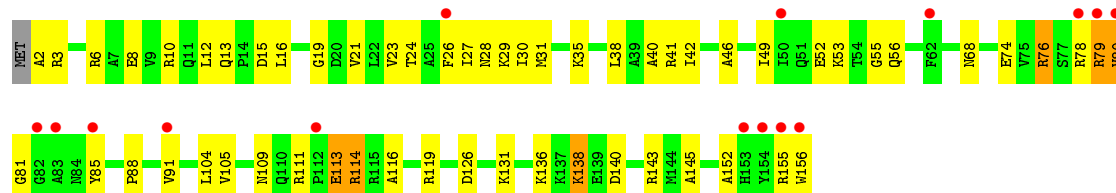
• Molecule 6: 30S ribosomal protein S6



• Molecule 6: 30S ribosomal protein S6



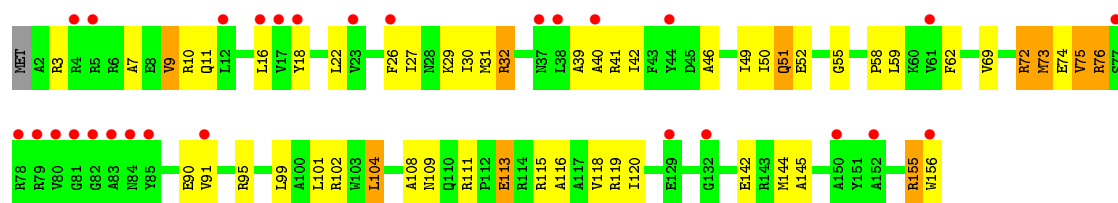
• Molecule 7: 30S ribosomal protein S7



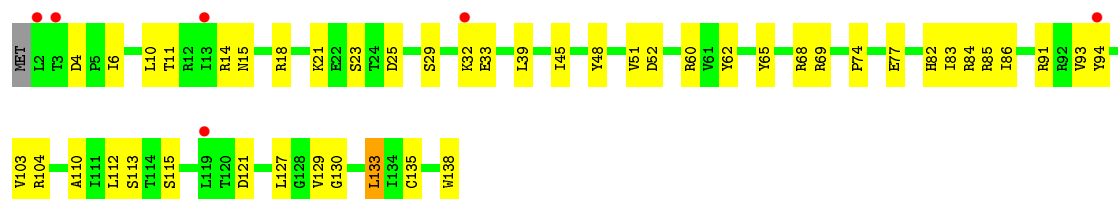
• Molecule 7: 30S ribosomal protein S7



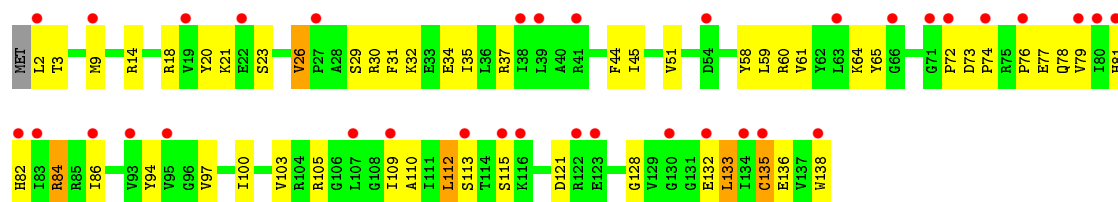




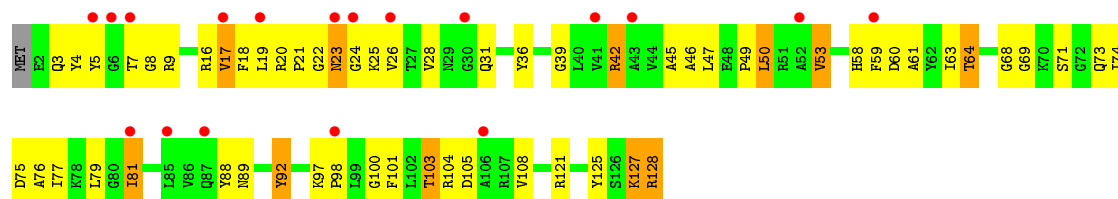
• Molecule 8: 30S ribosomal protein S8



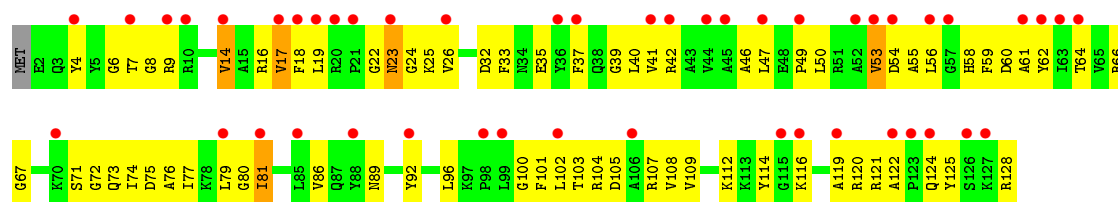
• Molecule 8: 30S ribosomal protein S8



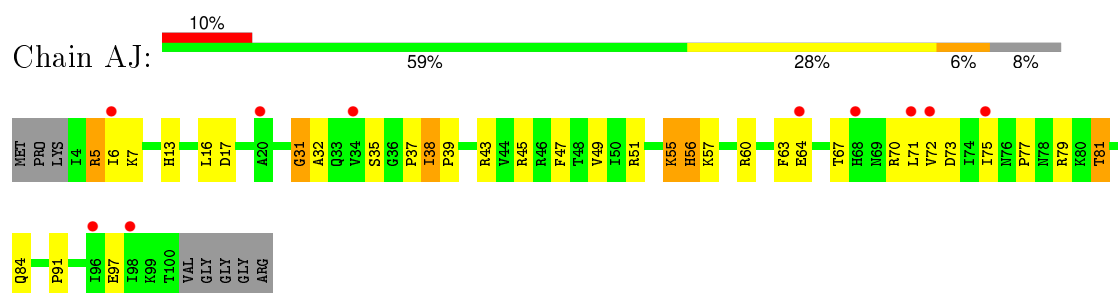
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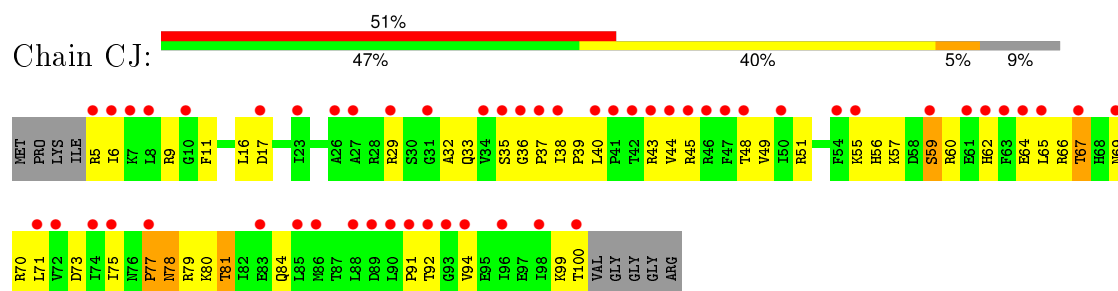
• Molecule 9: 30S ribosomal protein S9



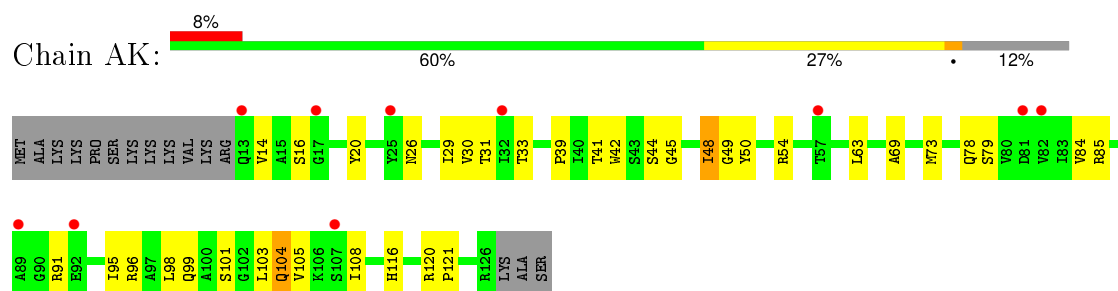
• Molecule 10: 30S ribosomal protein S10



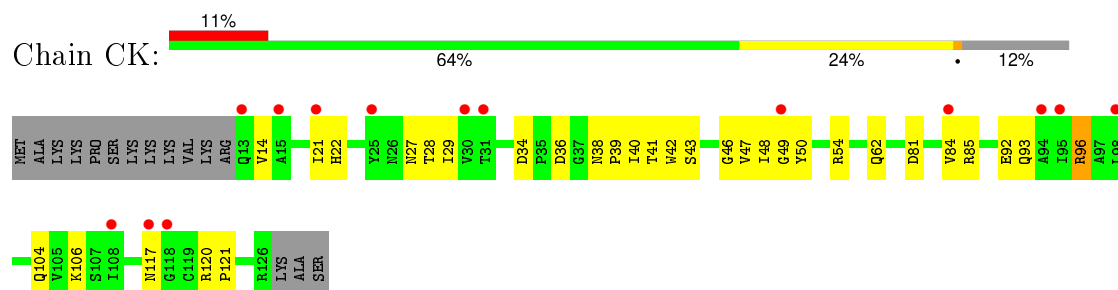
- Molecule 10: 30S ribosomal protein S10



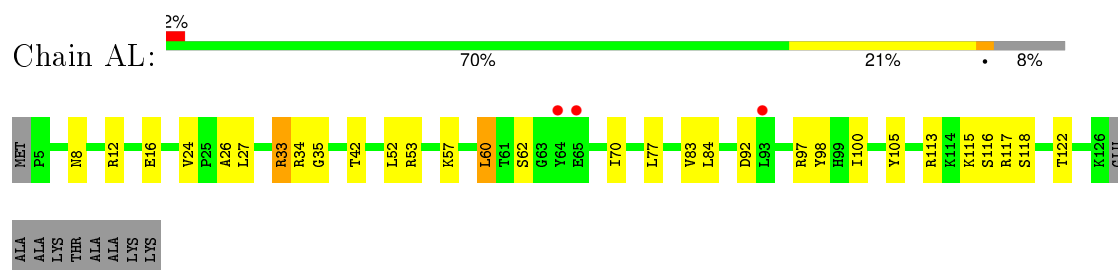
- Molecule 11: 30S ribosomal protein S11



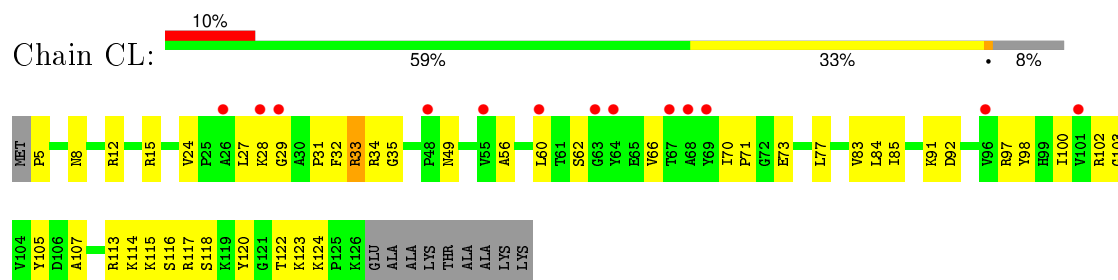
- Molecule 11: 30S ribosomal protein S11



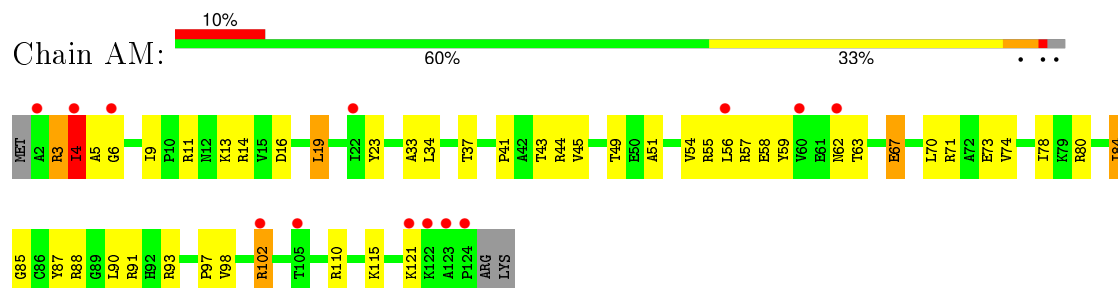
- Molecule 12: 30S ribosomal protein S12



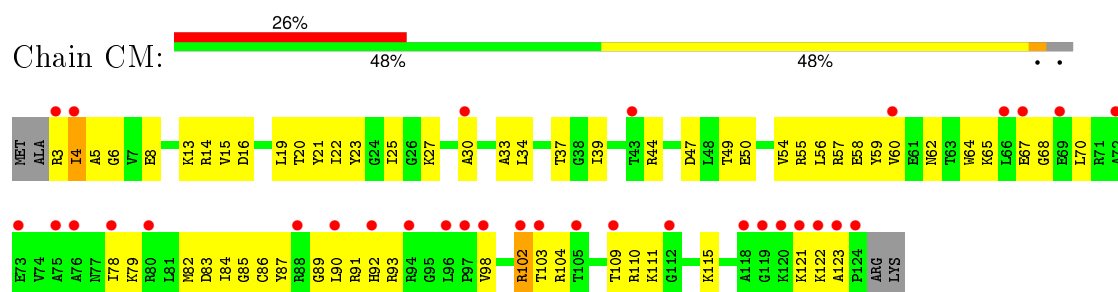
- Molecule 12: 30S ribosomal protein S12



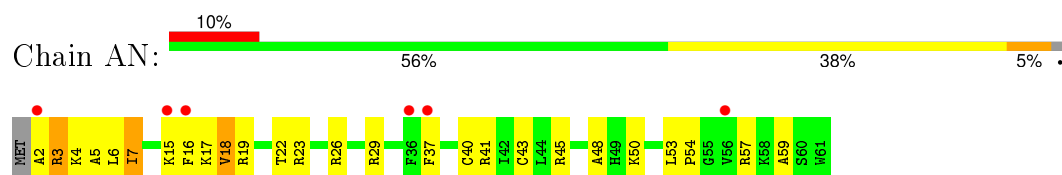
- Molecule 13: 30S ribosomal protein S13



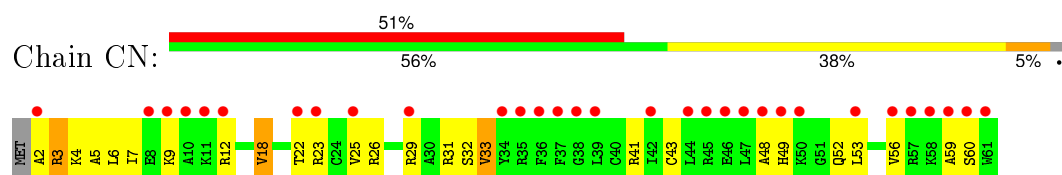
- Molecule 13: 30S ribosomal protein S13



- Molecule 14: 30S ribosomal protein S14 type Z



- Molecule 14: 30S ribosomal protein S14 type Z

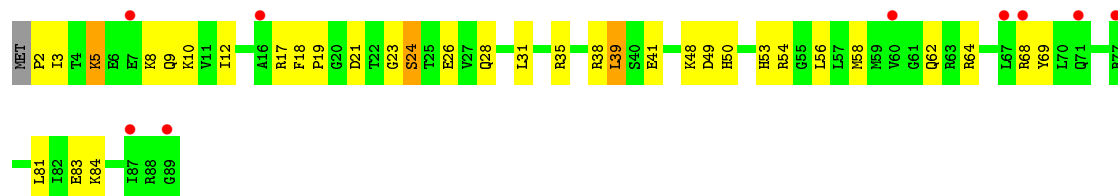


- Molecule 15: 30S ribosomal protein S15

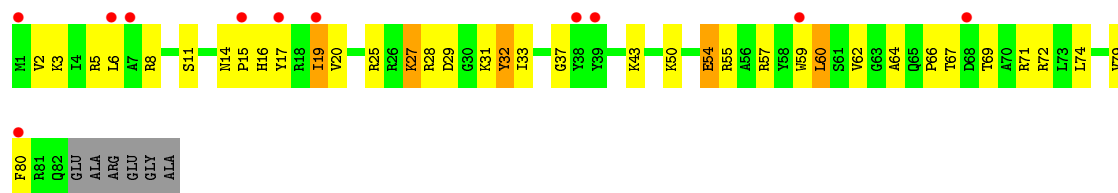




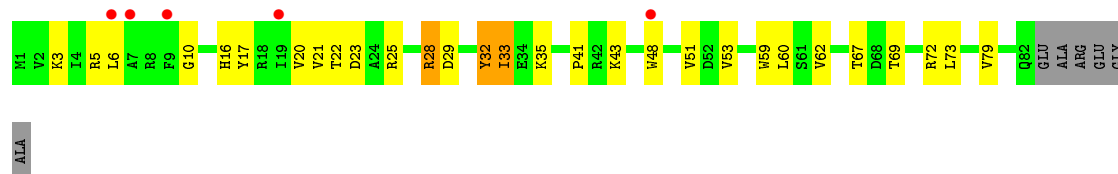
- Molecule 15: 30S ribosomal protein S15



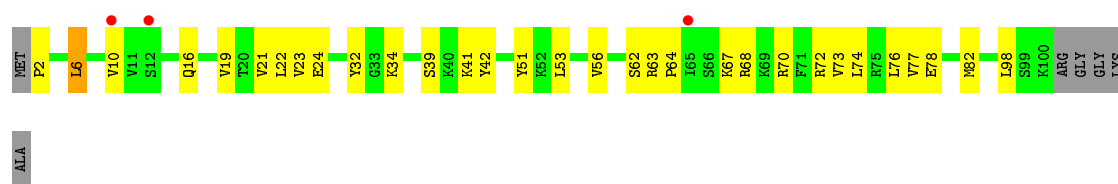
- Molecule 16: 30S ribosomal protein S16



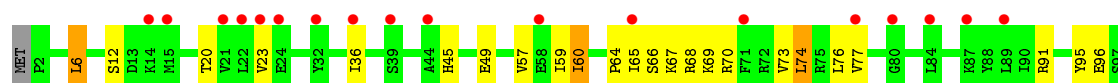
- Molecule 16: 30S ribosomal protein S16

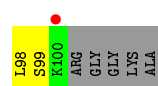


- Molecule 17: 30S ribosomal protein S17

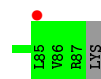
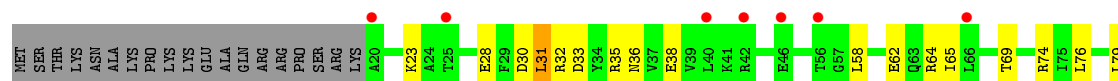


- Molecule 17: 30S ribosomal protein S17

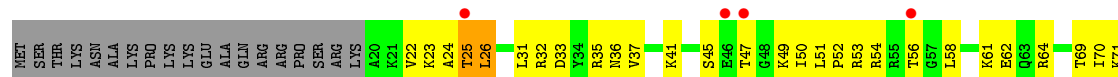
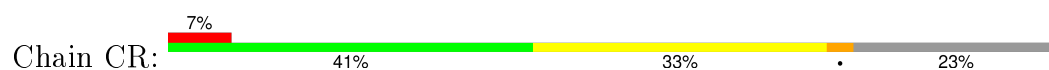




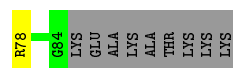
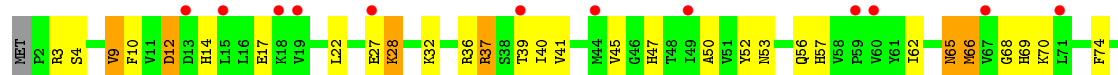
- Molecule 18: 30S ribosomal protein S18



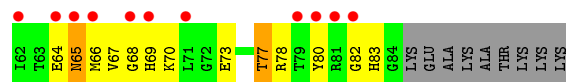
- Molecule 18: 30S ribosomal protein S18



- Molecule 19: 30S ribosomal protein S19

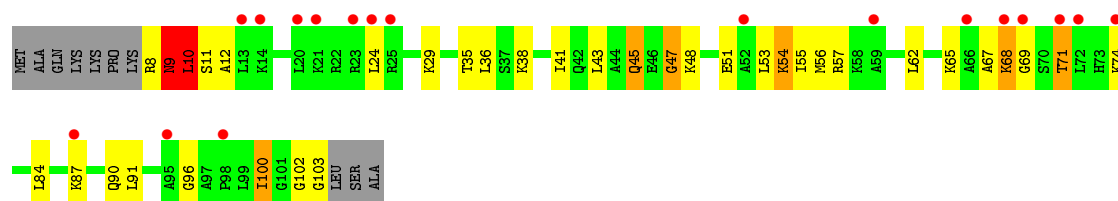


- Molecule 19: 30S ribosomal protein S19

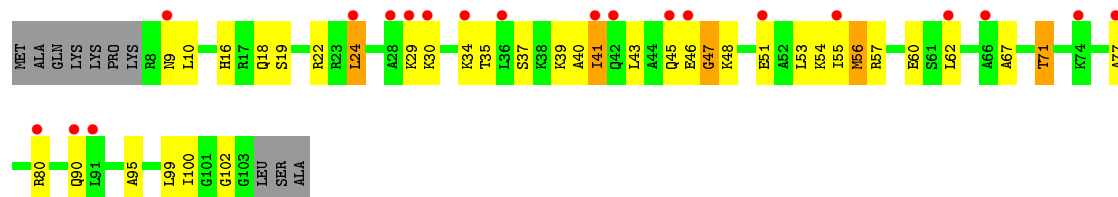


- Molecule 20: 30S ribosomal protein S20

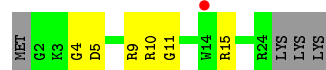




• Molecule 20: 30S ribosomal protein S20



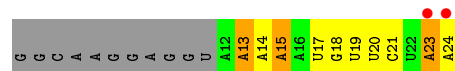
• Molecule 21: 30S ribosomal protein Thx



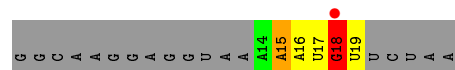
• Molecule 21: 30S ribosomal protein Thx



• Molecule 22: mRNA



• Molecule 22: mRNA



• Molecule 23: Cytidine-Puromycin





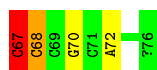
- Molecule 23: Cytidine-Puromycin

Chain CW: 33% 67%



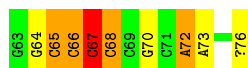
- Molecule 24: P-site tRNA

Chain AX: 32% 45% 19% ..



- Molecule 24: P-site tRNA

Chain CX: 22% 43% 31% ..



- Molecule 25: E-site tRNA

Chain AY: 93%



- Molecule 25: E-site tRNA

Chain CY: 5% 93%



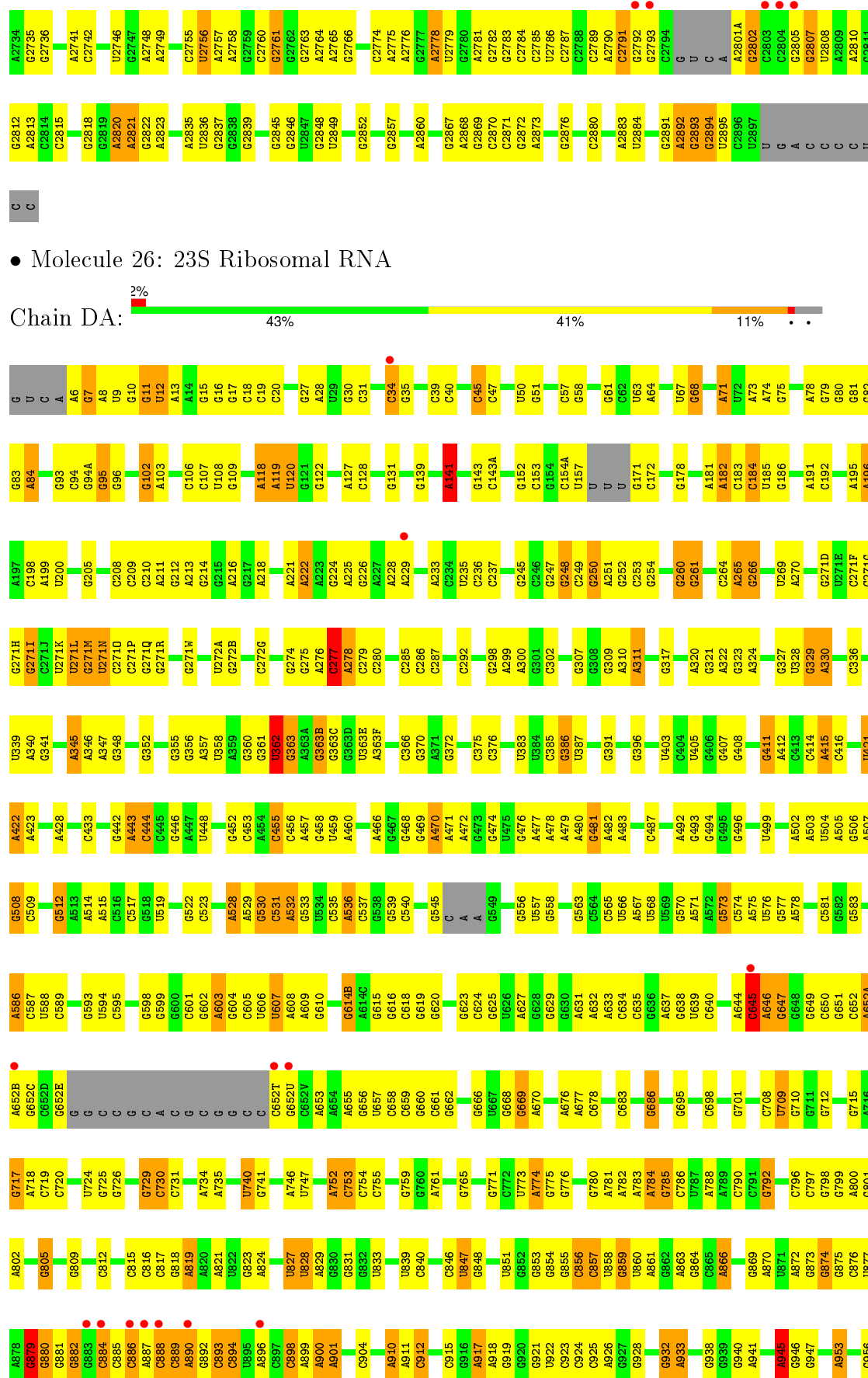
- Molecule 26: 23S Ribosomal RNA

Chain BA: 51% 36% 9% ..

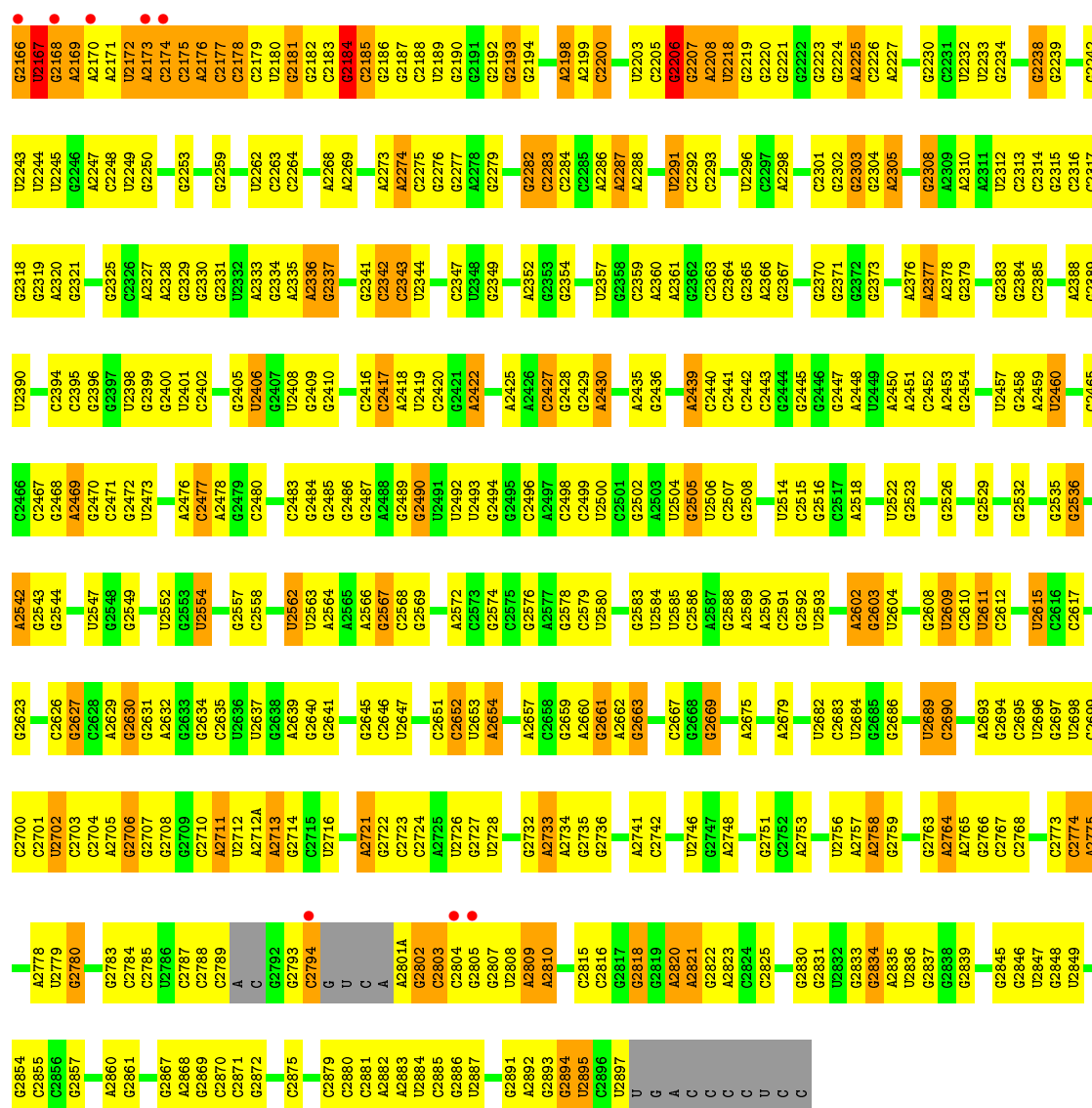






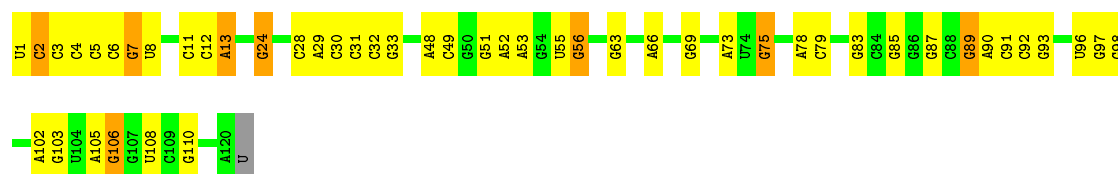






## • Molecule 27: 5S Ribosomal RNA

Chain BB: 59% 34% 7%



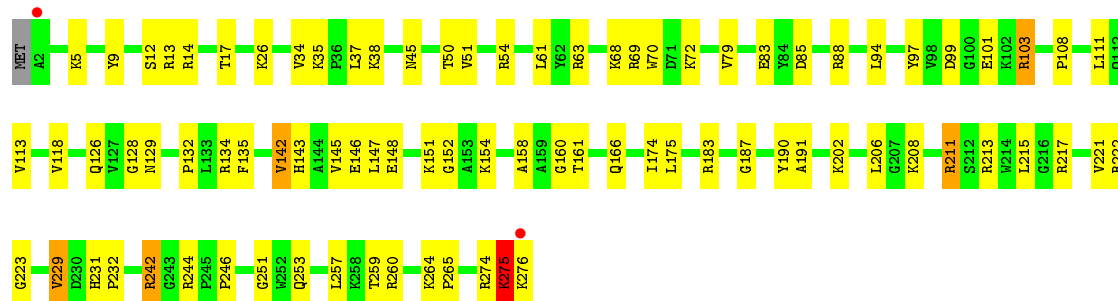
## • Molecule 27: 5S Ribosomal RNA

Chain DB: 26% 55% 17%

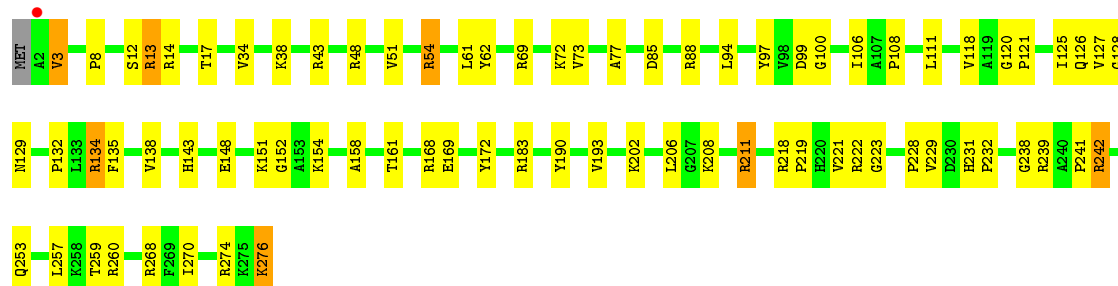




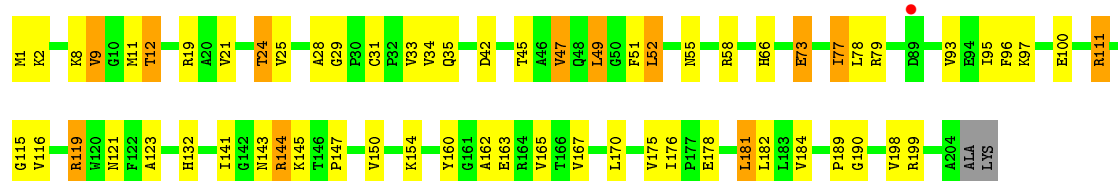
- Molecule 28: 50S ribosomal protein L2



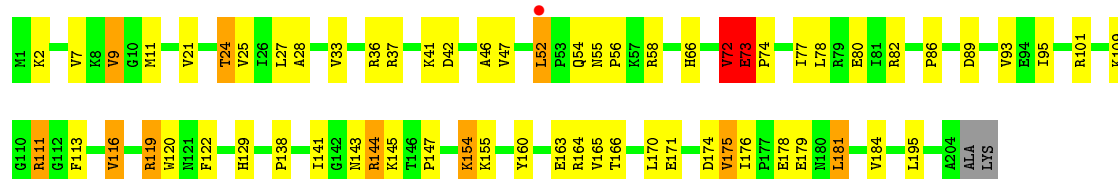
- Molecule 28: 50S ribosomal protein L2



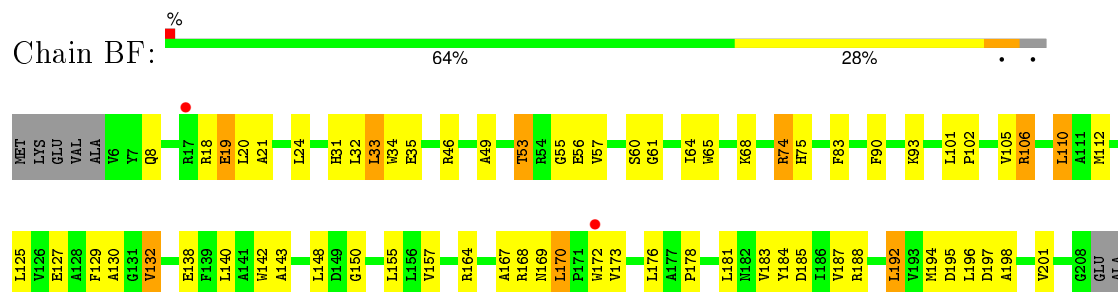
- Molecule 29: 50S ribosomal protein L3



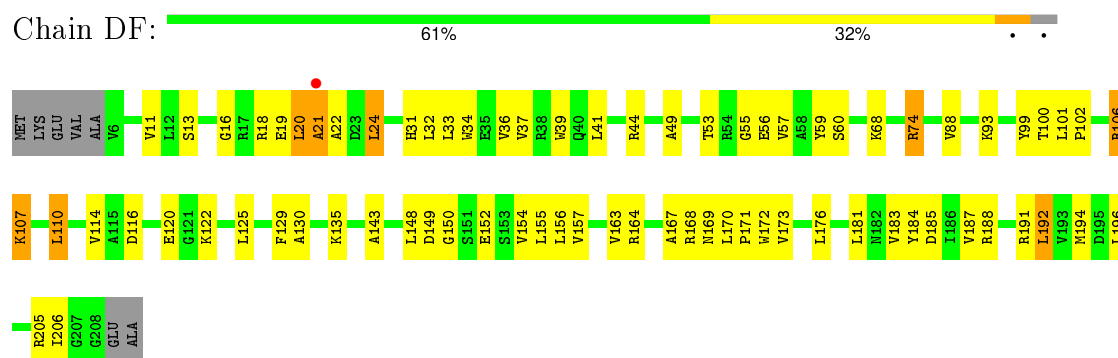
- Molecule 29: 50S ribosomal protein L3



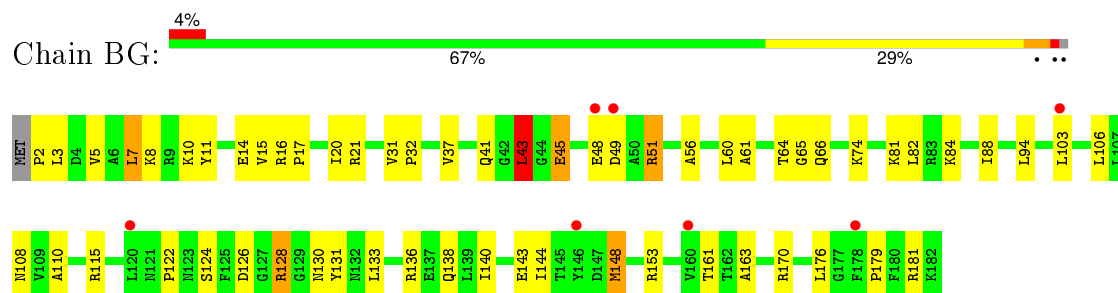
- Molecule 30: 50S ribosomal protein L4



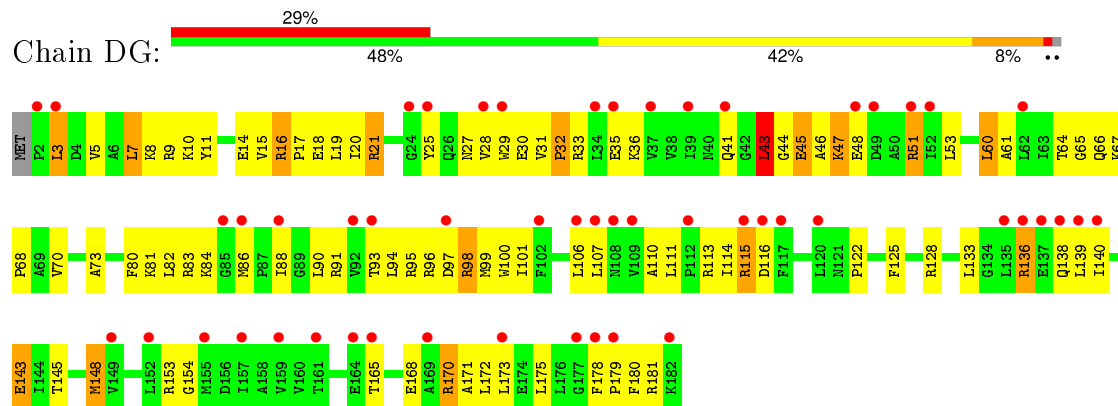
- Molecule 30: 50S ribosomal protein L4



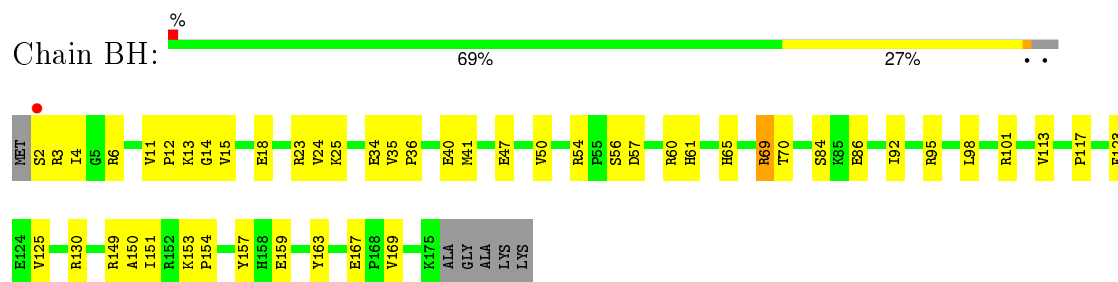
- Molecule 31: 50S ribosomal protein L5



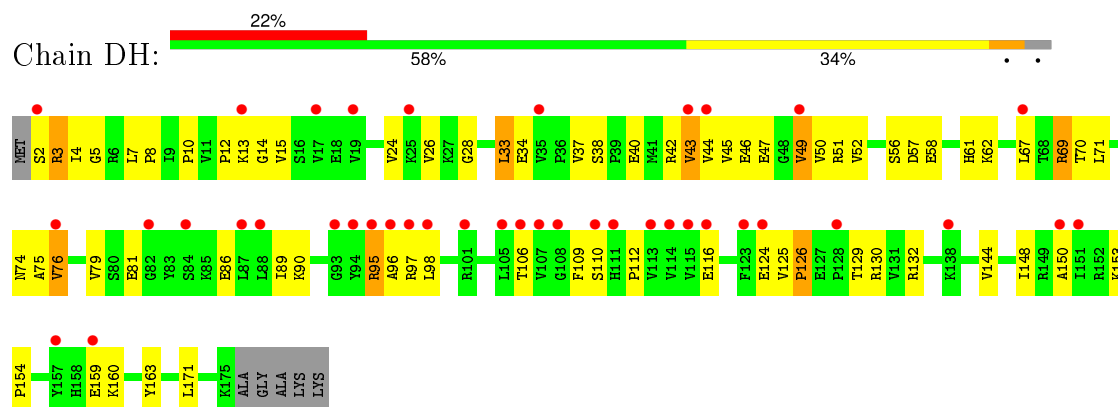
- Molecule 31: 50S ribosomal protein L5



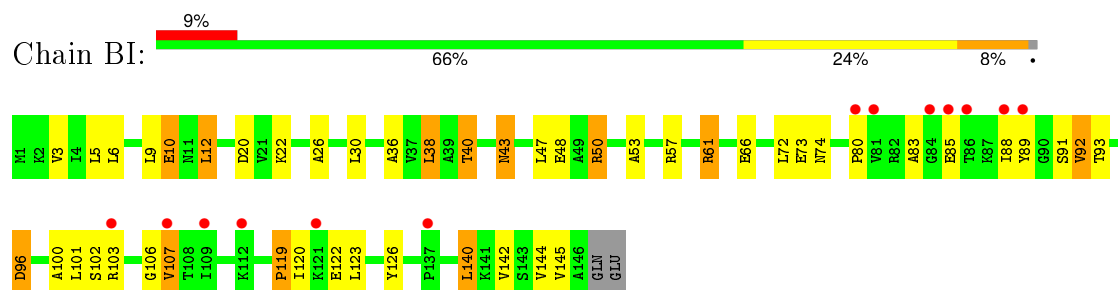
- Molecule 32: 50S ribosomal protein L6



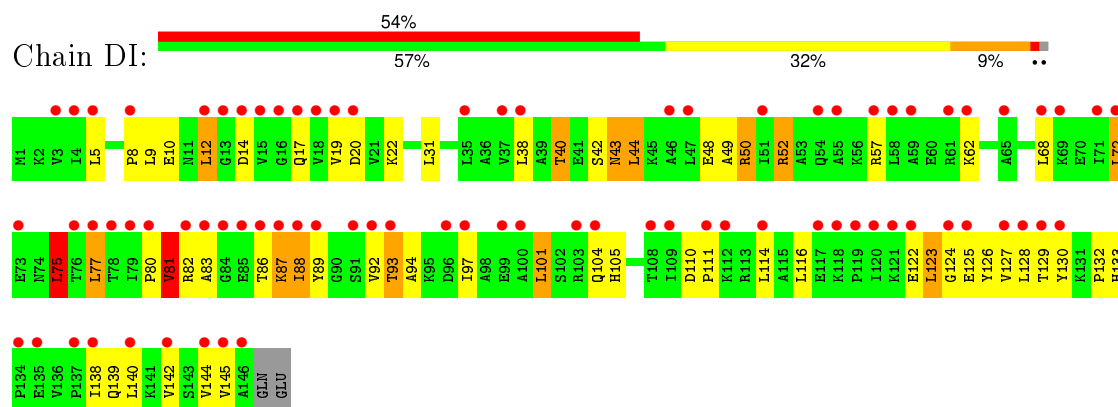
• Molecule 32: 50S ribosomal protein L6



• Molecule 33: 50S ribosomal protein L9

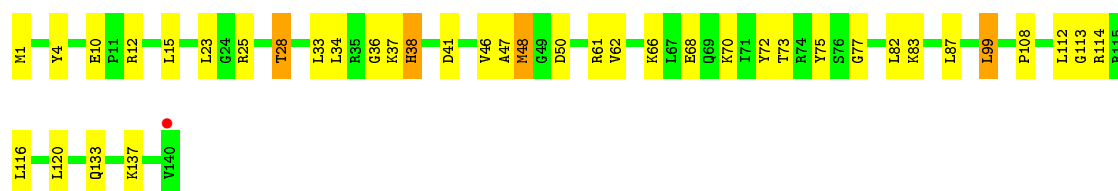


• Molecule 33: 50S ribosomal protein L9

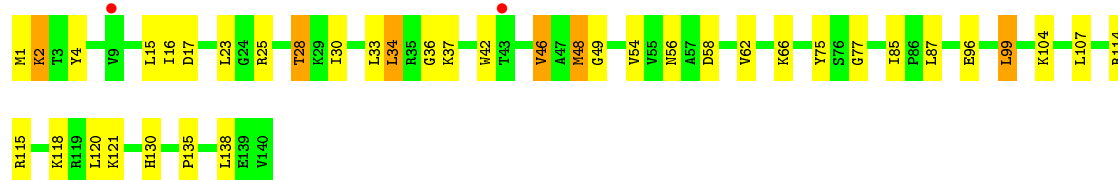
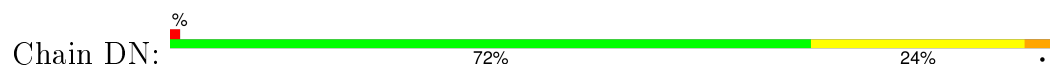


• Molecule 34: 50S ribosomal protein L13

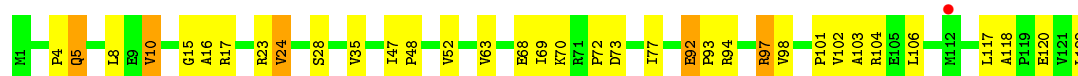
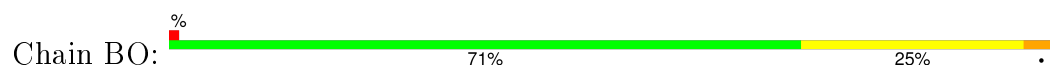




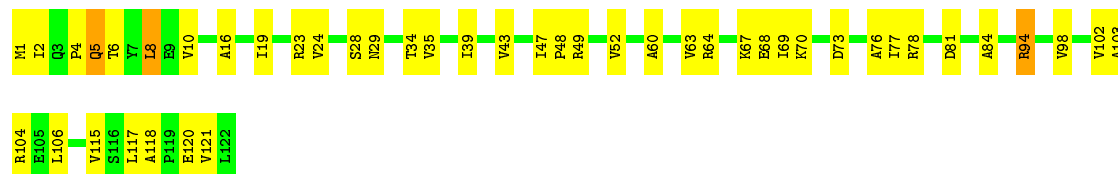
- Molecule 34: 50S ribosomal protein L13



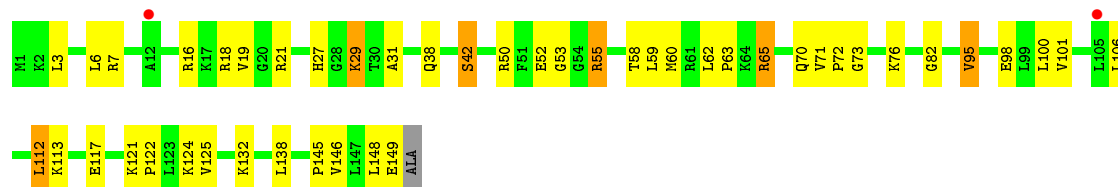
- Molecule 35: 50S ribosomal protein L14



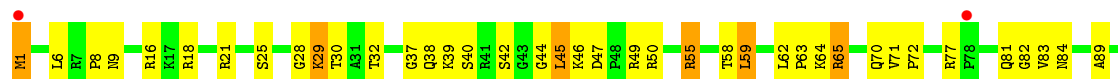
- Molecule 35: 50S ribosomal protein L14



- Molecule 36: 50S ribosomal protein L15



- Molecule 36: 50S ribosomal protein L15

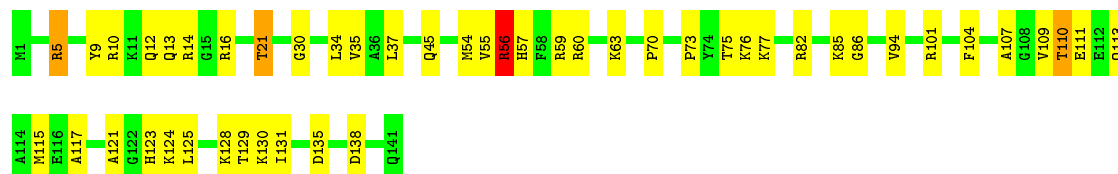






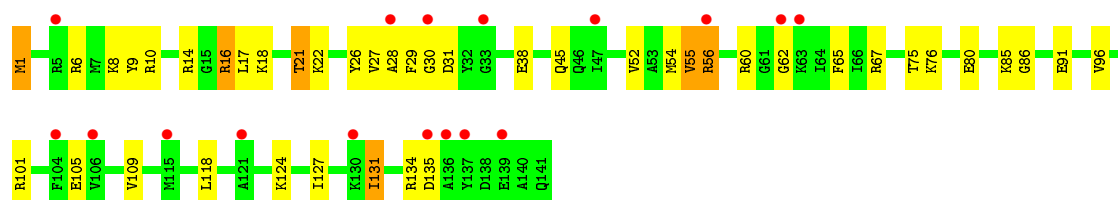
- Molecule 37: 50S ribosomal protein L16

Chain BQ: 66% 31% ..



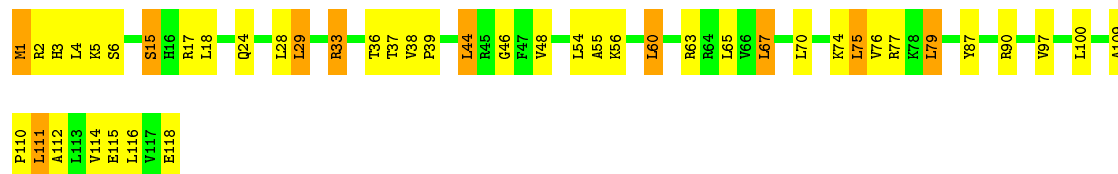
- Molecule 37: 50S ribosomal protein L16

Chain DQ: 12% 70% 26% .



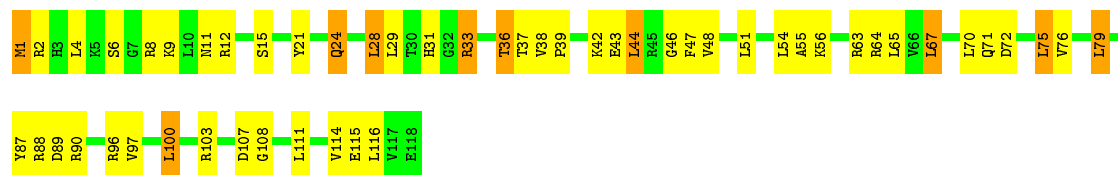
- Molecule 38: 50S ribosomal protein L17

Chain BR: 62% 30% 8%



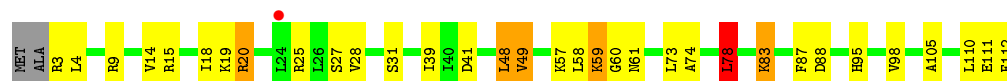
- Molecule 38: 50S ribosomal protein L17

Chain DR: 55% 36% 8%

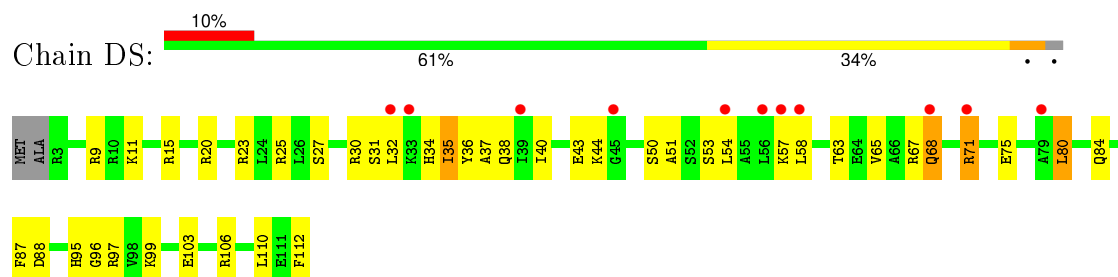


- Molecule 39: 50S ribosomal protein L18

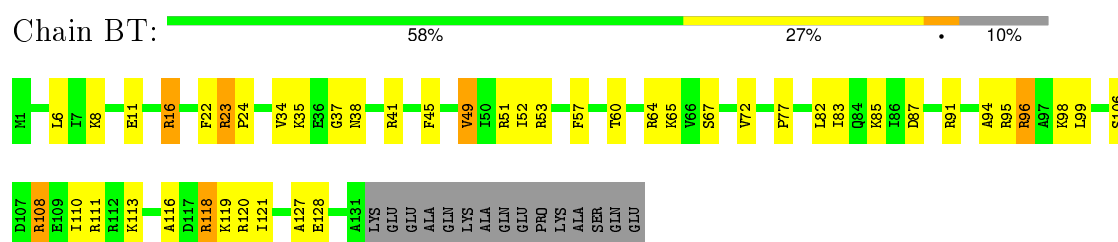
Chain BS: 69% 24% . . .



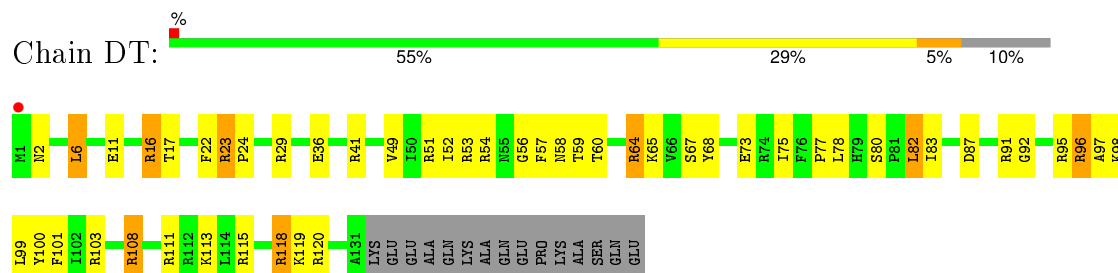
- Molecule 39: 50S ribosomal protein L18



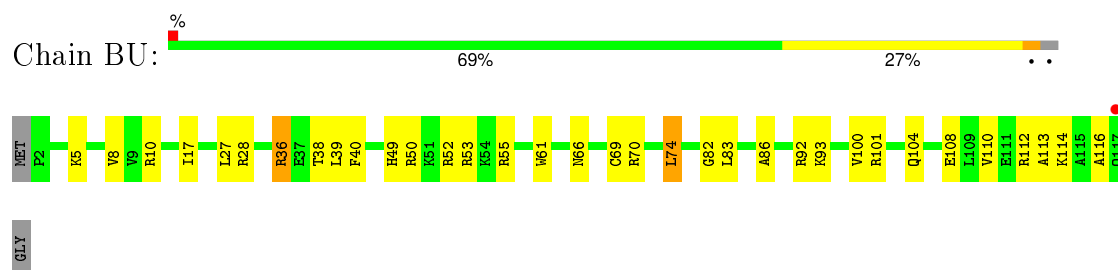
- Molecule 40: 50S ribosomal protein L19



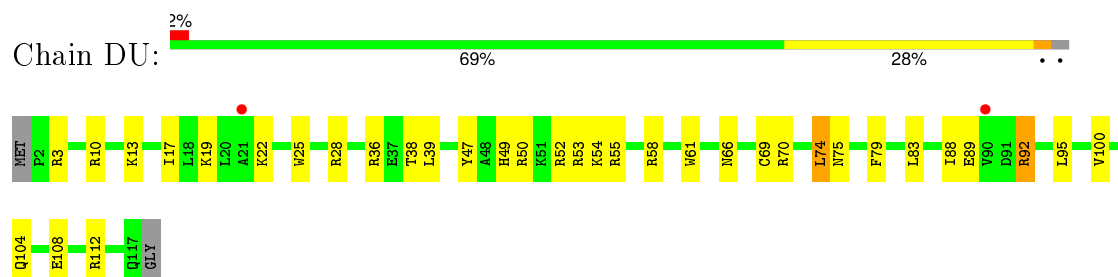
- Molecule 40: 50S ribosomal protein L19



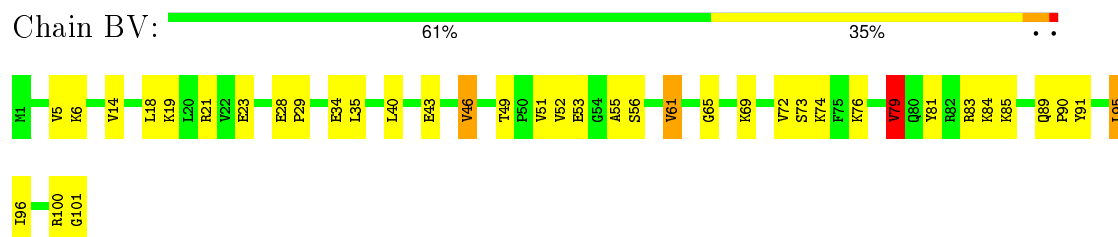
- Molecule 41: 50S ribosomal protein L20



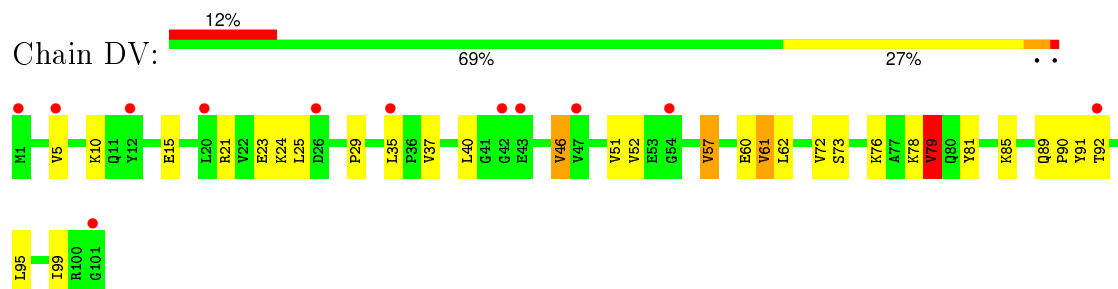
- Molecule 41: 50S ribosomal protein L20



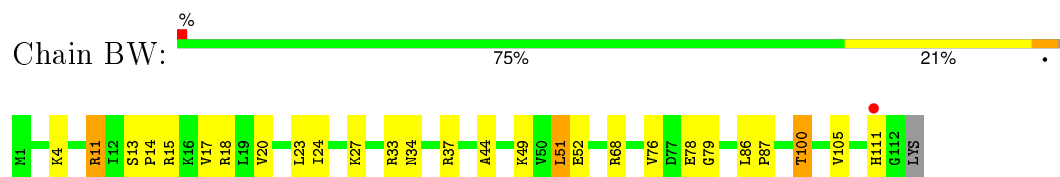
- Molecule 42: 50S ribosomal protein L21



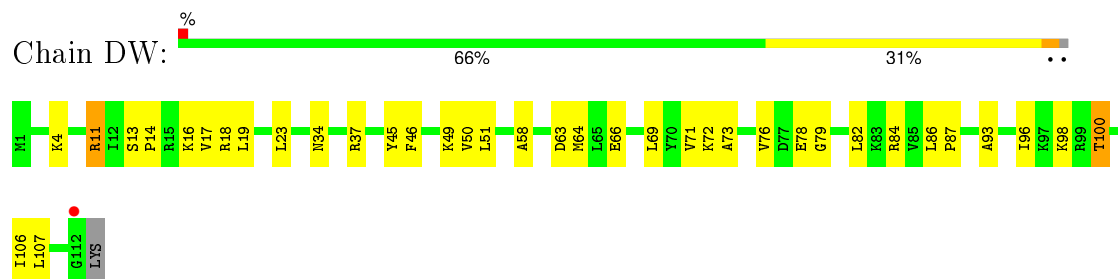
- Molecule 42: 50S ribosomal protein L21



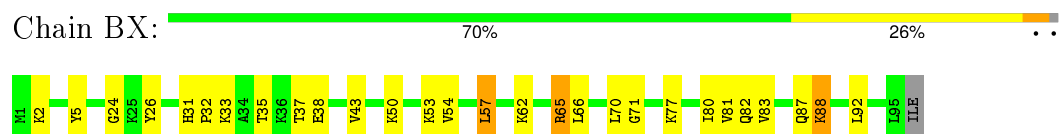
- Molecule 43: 50S ribosomal protein L22



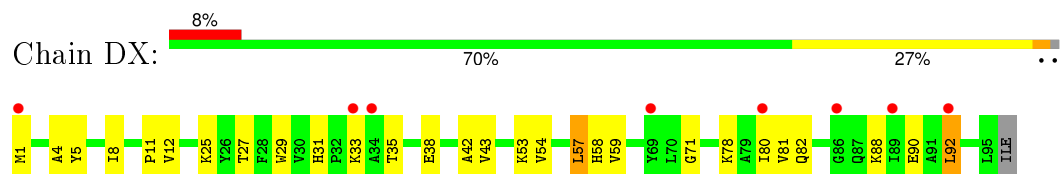
- Molecule 43: 50S ribosomal protein L22



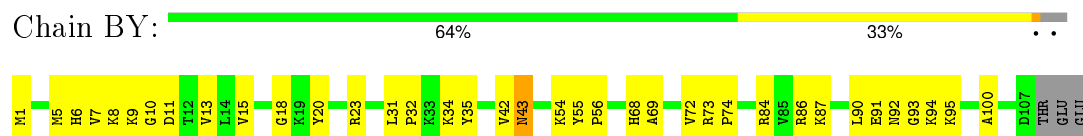
- Molecule 44: 50S ribosomal protein L23



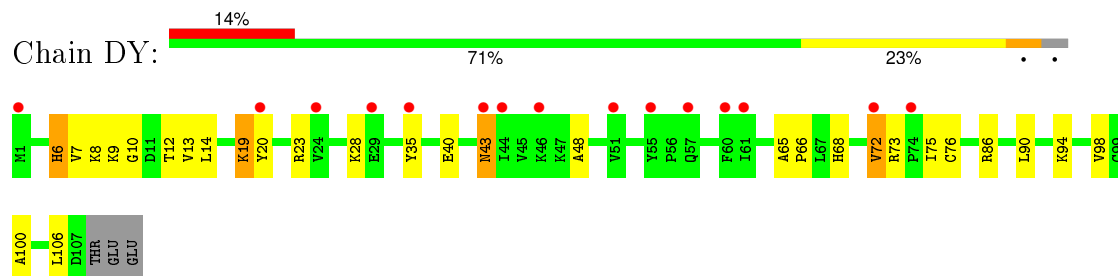
- Molecule 44: 50S ribosomal protein L23



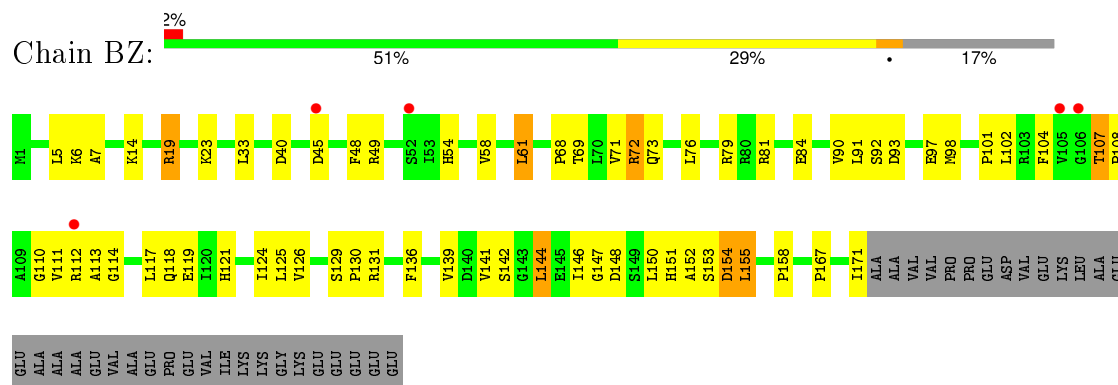
- Molecule 45: 50S ribosomal protein L24



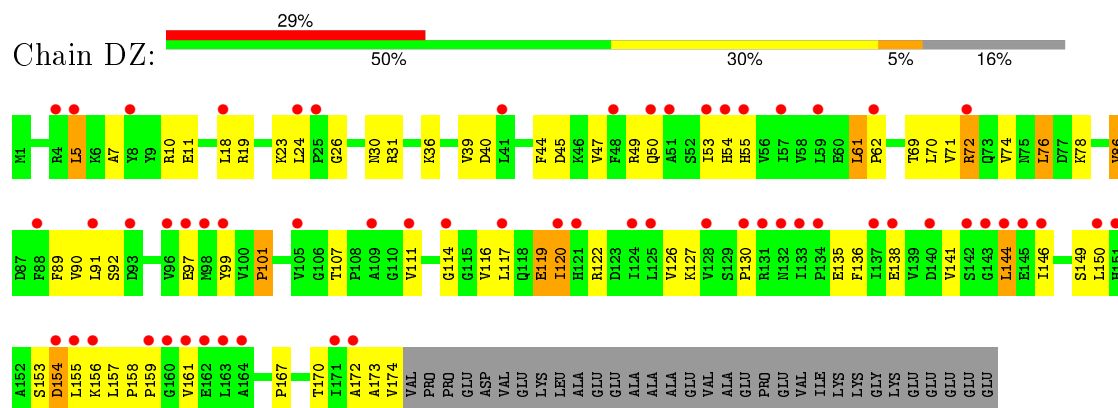
- Molecule 45: 50S ribosomal protein L24



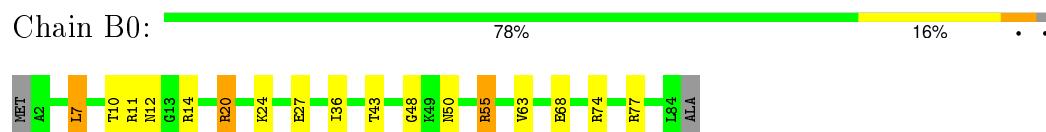
- Molecule 46: 50S ribosomal protein L25



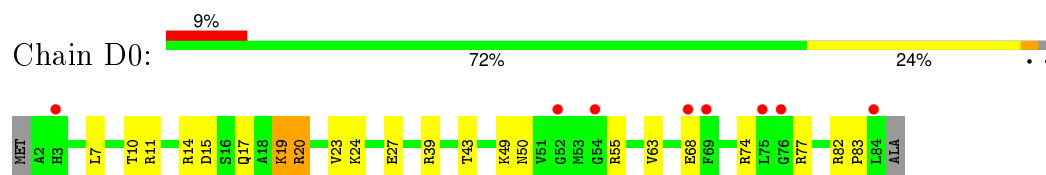
- Molecule 46: 50S ribosomal protein L25



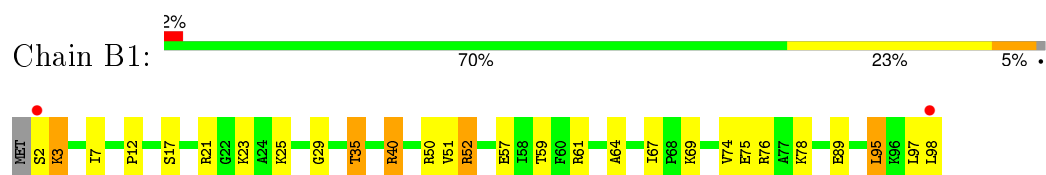
- Molecule 47: 50S ribosomal protein L27



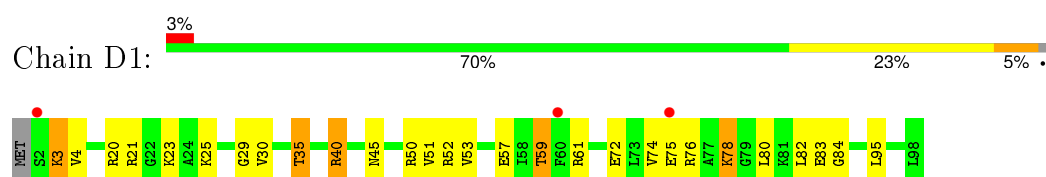
- Molecule 47: 50S ribosomal protein L27



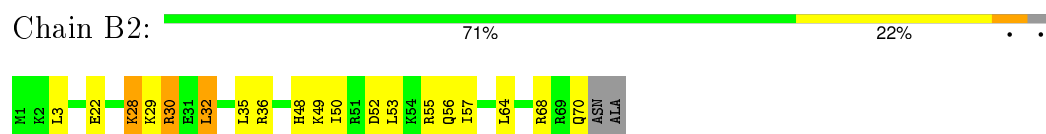
- Molecule 48: 50S ribosomal protein L28



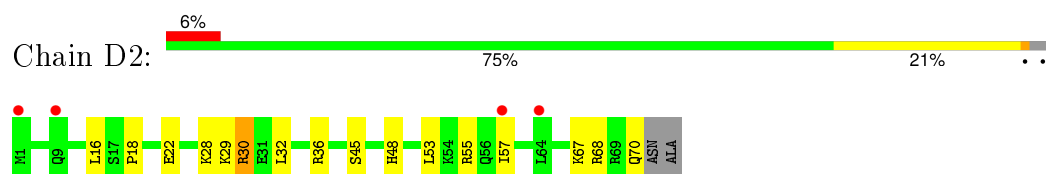
- Molecule 48: 50S ribosomal protein L28



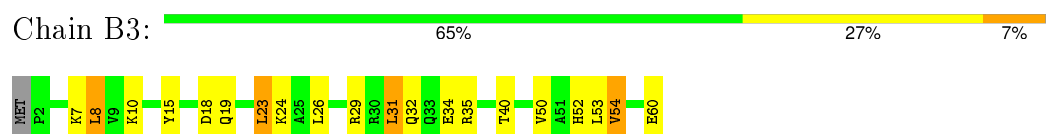
- Molecule 49: 50S ribosomal protein L29



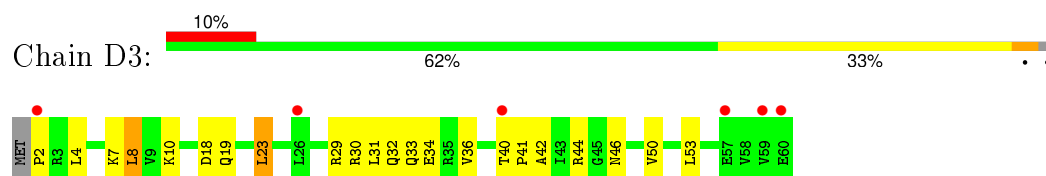
- Molecule 49: 50S ribosomal protein L29



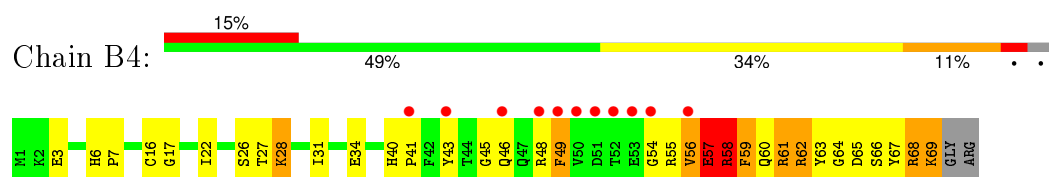
- Molecule 50: 50S ribosomal protein L30



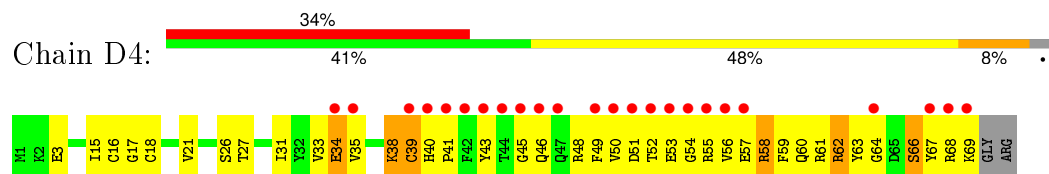
- Molecule 50: 50S ribosomal protein L30



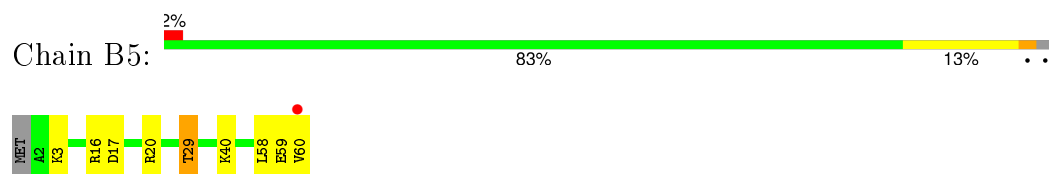
- Molecule 51: 50S ribosomal protein L31



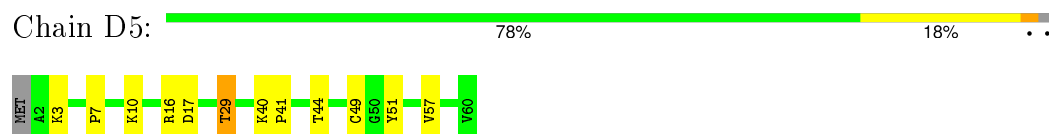
- Molecule 51: 50S ribosomal protein L31



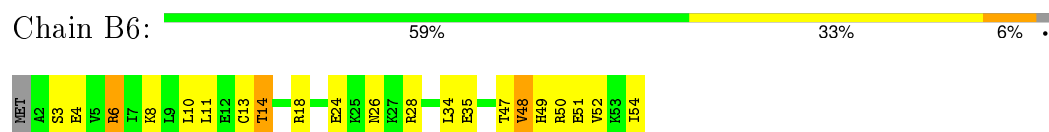
- Molecule 52: 50S ribosomal protein L32



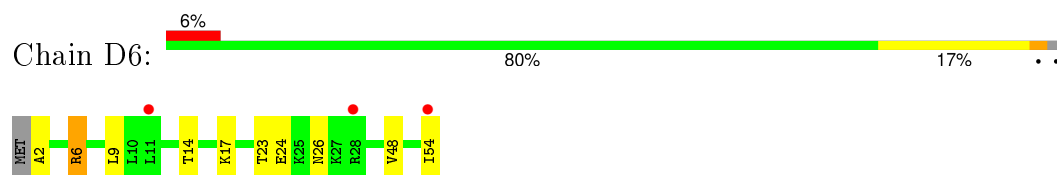
- Molecule 52: 50S ribosomal protein L32



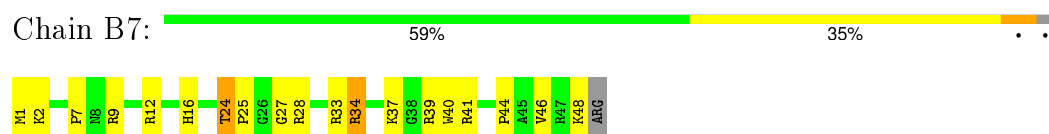
- Molecule 53: 50S ribosomal protein L33



- Molecule 53: 50S ribosomal protein L33

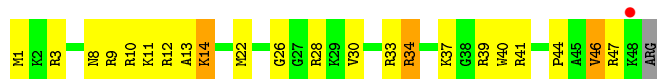


- Molecule 54: 50S ribosomal protein L34



- Molecule 54: 50S ribosomal protein L34

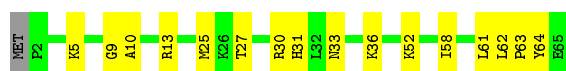
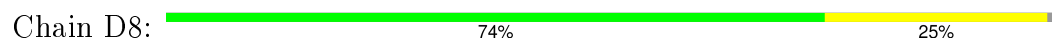




- Molecule 55: 50S ribosomal protein L35



- 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, $\alpha$ , $\beta$ , $\gamma$	207.56Å 444.23Å 613.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	150.38 – 2.80 150.38 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.0 (150.38-2.80) 98.0 (150.38-2.80)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.29 (at 2.82Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.234 , 0.280 0.239 , 0.284	Depositor DCC
$R_{free}$ test set	67651 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	50.1	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 62.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 1345521 reflections	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	290205	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, MG, PPU, K, ZN, 31H, 5MC, 4SU, SF4, PSU

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

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

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

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

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	1
7	AG	0	1
20	AT	0	1
29	DE	0	1
33	DI	0	1
39	BS	0	1
46	BZ	0	1
51	B4	0	2
51	D4	0	1
All	All	0	10

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	1154	G	C6-N1	-12.37	1.30	1.39
1	AA	1172	C	N3-C4	-10.50	1.26	1.33
1	CA	1154	G	N1-C2	-10.41	1.29	1.37
1	AA	1172	C	C2-N3	-8.49	1.28	1.35
1	AA	1164	G	N1-C2	-6.91	1.32	1.37
1	CA	1154	G	N7-C5	-6.70	1.35	1.39
1	AA	1164	G	C6-N1	-6.60	1.34	1.39
22	CV	18	G	N9-C4	6.02	1.42	1.38
1	CA	1154	G	C8-N7	-5.99	1.27	1.30
22	CV	18	G	C5-C6	5.82	1.48	1.42
1	CA	1119	C	N1-C2	5.59	1.45	1.40
26	BA	1142(A)	A	N9-C4	-5.56	1.34	1.37
26	BA	945	A	N9-C4	-5.52	1.34	1.37
1	CA	1154	G	C5-C4	5.47	1.42	1.38
22	CV	18	G	N3-C4	-5.46	1.31	1.35
1	CA	1119	C	N3-C4	-5.44	1.30	1.33
24	AX	22	G	N7-C5	5.24	1.42	1.39
26	BA	528	A	N9-C4	-5.24	1.34	1.37
26	BA	330	A	N9-C4	-5.17	1.34	1.37
24	AX	14	A	N7-C5	-5.08	1.36	1.39

All (455) bond angle outliers are listed below:

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

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1154	G	N3-C2-N2	23.20	136.14	119.90
1	AA	1172	C	C2-N3-C4	20.22	130.01	119.90
22	CV	18	G	C2-N3-C4	19.75	121.78	111.90
1	CA	1119	C	N3-C2-O2	-17.59	109.59	121.90
22	CV	18	G	N9-C4-C5	17.52	112.41	105.40
1	AA	1172	C	N3-C4-N4	-16.25	106.62	118.00
1	AA	1172	C	C5-C4-N4	16.18	131.53	120.20
1	CA	1119	C	C2-N1-C1'	15.95	136.34	118.80
22	CV	18	G	N3-C4-C5	-15.80	120.70	128.60
22	CV	18	G	C8-N9-C4	-15.55	100.18	106.40
22	CV	18	G	N1-C6-O6	-15.53	110.58	119.90
1	CA	1119	C	C2-N3-C4	15.35	127.57	119.90
1	CA	72	C	N1-C2-O2	14.13	127.38	118.90
22	CV	18	G	C4-C5-N7	-13.80	105.28	110.80
1	CA	1154	G	C5-C6-N1	-13.29	104.85	111.50
1	CA	1154	G	N1-C6-O6	-13.15	112.01	119.90
1	CA	1154	G	C2-N3-C4	-11.85	105.98	111.90
1	CA	1119	C	C6-N1-C1'	-11.84	106.59	120.80
26	DA	2139	C	C2-N1-C1'	11.43	131.37	118.80
1	AA	1172	C	C4-C5-C6	-11.42	111.69	117.40
1	CA	1004	A	O4'-C1'-N9	11.33	117.26	108.20
1	AA	1172	C	C5-C6-N1	11.23	126.62	121.00
27	DB	30	C	C6-N1-C2	-11.19	115.83	120.30
26	DA	1507	A	C5-C6-N1	-11.18	112.11	117.70
1	CA	1119	C	C6-N1-C2	-11.11	115.86	120.30
26	DA	2139	C	N1-C2-O2	10.94	125.47	118.90
1	CA	1154	G	C6-N1-C2	10.77	131.56	125.10
24	AX	46	G	C6-N1-C2	-10.63	118.72	125.10
1	CA	1154	G	C4-N9-C1'	10.51	140.16	126.50
1	CA	97	G	C6-N1-C2	10.34	131.30	125.10
26	BA	2061	G	O5'-P-OP2	-10.00	96.70	105.70
24	AX	14	A	C4-C5-C6	9.98	121.99	117.00
1	AA	359	U	O5'-P-OP1	-9.90	96.79	105.70
1	CA	1281	U	O4'-C1'-N1	-9.83	100.34	108.20
1	AA	1172	C	C6-N1-C2	-9.81	116.38	120.30
1	AA	1172	C	C2-N1-C1'	9.73	129.51	118.80
1	CA	1119	C	C5-C6-N1	9.70	125.85	121.00
22	CV	18	G	C5-C6-O6	9.69	134.41	128.60
26	DA	2139	C	C6-N1-C1'	-9.57	109.31	120.80
26	DA	2136	C	N1-C2-O2	9.53	124.62	118.90
1	CA	93	G	O4'-C1'-N9	9.48	115.78	108.20
1	AA	148	G	N3-C4-N9	-9.46	120.33	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1398	A	O5'-P-OP1	-9.41	97.23	105.70
26	DA	1482	G	C2-N3-C4	-9.37	107.22	111.90
26	DA	2155	G	N3-C2-N2	9.31	126.42	119.90
26	DA	1507	A	C2-N3-C4	-9.26	105.97	110.60
22	CV	18	G	C6-C5-N7	9.08	135.85	130.40
1	AA	1172	C	N1-C2-N3	-9.04	112.87	119.20
2	CB	23	ARG	NE-CZ-NH1	-9.02	115.79	120.30
26	BA	512	G	O4'-C1'-N9	9.02	115.42	108.20
1	CA	1400	C	N1-C2-O2	8.90	124.24	118.90
27	DB	30	C	N3-C2-O2	-8.87	115.69	121.90
24	CX	34	C	C2-N3-C4	-8.79	115.50	119.90
26	DA	2152	G	N1-C6-O6	8.79	125.17	119.90
1	CA	1154	G	C8-N9-C1'	-8.65	115.76	127.00
1	CA	99	U	N1-C2-O2	-8.57	116.80	122.80
1	AA	1030(B)	C	C2-N1-C1'	8.56	128.21	118.80
24	CX	34	C	C4-C5-C6	8.48	121.64	117.40
1	CA	407	G	C6-C5-N7	8.42	135.45	130.40
26	BA	1614	A	O5'-P-OP1	-8.40	98.14	105.70
26	BA	2189	U	N1-C2-O2	8.36	128.66	122.80
1	CA	407	G	N3-C4-C5	8.34	132.77	128.60
1	CA	1256	A	N1-C6-N6	8.32	123.59	118.60
1	AA	1030(B)	C	C6-N1-C2	-8.29	116.98	120.30
1	AA	1007	C	C2-N3-C4	8.27	124.03	119.90
1	CA	407	G	C4-N9-C1'	-8.26	115.77	126.50
1	CA	1154	G	N1-C2-N3	8.23	128.84	123.90
27	DB	30	C	C4-C5-C6	8.20	121.50	117.40
24	AX	14	A	C5-N7-C8	8.16	107.98	103.90
26	DA	2137	C	C5-C6-N1	8.14	125.07	121.00
24	CX	14	A	C4-C5-C6	8.12	121.06	117.00
1	CA	407	G	N3-C4-N9	-8.09	121.15	126.00
26	BA	2140	C	C2-N1-C1'	8.07	127.68	118.80
1	CA	1125	U	C5-C6-N1	8.06	126.73	122.70
1	CA	1009	G	C5-C6-O6	8.04	133.42	128.60
26	BA	330	A	C2-N3-C4	-8.03	106.58	110.60
1	CA	1400	C	C2-N1-C1'	8.02	127.63	118.80
26	DA	2152	G	C5-C6-O6	-7.99	123.81	128.60
24	AX	67	C	C2-N1-C1'	7.98	127.58	118.80
1	AA	1007	C	N1-C2-O2	7.96	123.68	118.90
1	AA	1030(B)	C	N1-C2-O2	7.88	123.63	118.90
26	DA	2121	G	N1-C6-O6	7.87	124.62	119.90
1	CA	1009	G	O5'-P-OP2	-7.83	98.65	105.70
22	CV	18	G	C6-N1-C2	-7.79	120.43	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	70	G	C5-C6-O6	7.71	133.23	128.60
1	AA	1030(B)	C	N3-C2-O2	-7.69	116.52	121.90
24	AX	22	G	N1-C6-O6	-7.67	115.30	119.90
1	CA	1009	G	N1-C6-O6	-7.62	115.33	119.90
1	CA	1400	C	C6-N1-C2	-7.59	117.26	120.30
1	CA	1007	C	C5-C6-N1	7.58	124.79	121.00
1	CA	1119	C	C5-C4-N4	7.49	125.44	120.20
1	CA	407	G	C4-C5-C6	-7.48	114.31	118.80
1	CA	97	G	N3-C4-C5	7.46	132.33	128.60
24	AX	22	G	C4-C5-C6	-7.45	114.33	118.80
26	DA	2152	G	C6-C5-N7	-7.45	125.93	130.40
1	CA	72	C	N3-C2-O2	-7.44	116.69	121.90
27	BB	89	G	O5'-P-OP2	-7.43	99.01	105.70
1	CA	1001(A)	G	N3-C4-N9	7.39	130.44	126.00
24	CX	67	C	C2-N1-C1'	7.38	126.91	118.80
26	DA	2121	G	C5-C6-O6	-7.37	124.18	128.60
26	BA	1653	G	P-O3'-C3'	7.35	128.52	119.70
24	CX	67	C	N1-C2-O2	7.30	123.28	118.90
1	CA	97	G	C5-C6-N1	-7.26	107.87	111.50
26	DA	512	G	O4'-C1'-N9	7.25	114.00	108.20
1	AA	1022	G	N3-C2-N2	7.22	124.95	119.90
1	CA	1125	U	C2-N1-C1'	7.21	126.36	117.70
26	BA	1108	U	N1-C2-O2	7.21	127.85	122.80
1	CA	1154	G	C4-C5-C6	7.20	123.12	118.80
26	BA	1022	G	N3-C4-N9	-7.18	121.69	126.00
27	DB	30	C	C2-N1-C1'	7.18	126.70	118.80
1	CA	1002	G	C5-C6-O6	7.18	132.91	128.60
1	CA	407	G	N1-C2-N2	7.18	122.66	116.20
27	DB	30	C	N3-C4-C5	-7.16	119.03	121.90
1	CA	1256	A	C5-C6-N6	-7.13	118.00	123.70
24	AX	22	G	C5-N7-C8	-7.10	100.75	104.30
26	BA	1108	U	C2-N1-C1'	7.08	126.19	117.70
26	DA	2139	C	N3-C2-O2	-7.02	116.99	121.90
22	CV	18	G	C5-C6-N1	7.00	115.00	111.50
26	DA	2136	C	N3-C2-O2	-6.96	117.03	121.90
26	BA	2140	C	C6-N1-C2	-6.93	117.53	120.30
26	BA	1108	U	N3-C2-O2	-6.91	117.36	122.20
1	CA	992	U	P-O3'-C3'	6.87	127.95	119.70
1	AA	198	G	C4-N9-C1'	6.86	135.42	126.50
1	CA	1119	C	N3-C4-C5	-6.86	119.16	121.90
1	CA	1400	C	C5-C6-N1	6.86	124.43	121.00
26	BA	330	A	N1-C2-N3	6.83	132.72	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	1021	A	C2-N3-C4	-6.81	107.19	110.60
24	CX	46	G	C6-N1-C2	-6.79	121.03	125.10
26	DA	2206	G	C4-N9-C1'	-6.76	117.71	126.50
37	BQ	56	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	CA	1001(A)	G	C4-N9-C1'	6.75	135.28	126.50
1	CA	407	G	C8-N9-C1'	6.72	135.74	127.00
1	AA	148	G	C4-N9-C1'	-6.72	117.76	126.50
1	AA	148	G	C8-N9-C1'	6.68	135.68	127.00
1	AA	1001	A	C5-C6-N6	6.67	129.04	123.70
26	DA	645	C	C2-N1-C1'	6.66	126.12	118.80
26	BA	528	A	C2-N3-C4	-6.65	107.28	110.60
26	BA	1654	A	O5'-P-OP1	-6.64	99.72	105.70
26	BA	2189	U	N3-C2-O2	-6.64	117.55	122.20
1	CA	76	C	N1-C2-O2	6.64	122.88	118.90
26	DA	2177	C	C2-N1-C1'	6.61	126.07	118.80
26	DA	2206	G	C8-N9-C1'	6.60	135.58	127.00
35	DO	8	LEU	CA-CB-CG	6.57	130.41	115.30
24	AX	22	G	N3-C4-N9	-6.56	122.07	126.00
1	AA	421	U	N1-C2-O2	6.55	127.39	122.80
26	BA	1992	G	P-O3'-C3'	6.54	127.55	119.70
26	DA	2167	U	C2-N1-C1'	6.54	125.55	117.70
26	BA	887	A	O4'-C1'-N9	6.53	113.43	108.20
26	DA	2137	C	C6-N1-C2	-6.53	117.69	120.30
1	AA	1011	G	N3-C4-C5	-6.51	125.35	128.60
1	CA	1154	G	N3-C4-N9	6.48	129.89	126.00
1	CA	1034	G	N7-C8-N9	6.47	116.34	113.10
1	AA	1019	C	C5-C6-N1	6.47	124.23	121.00
1	CA	1001(A)	G	C8-N9-C1'	-6.47	118.59	127.00
26	DA	645	C	N1-C2-O2	6.46	122.78	118.90
26	DA	2140	C	N3-C2-O2	-6.45	117.38	121.90
24	AX	67	C	C6-N1-C1'	-6.45	113.06	120.80
26	DA	2152	G	N3-C4-N9	6.44	129.87	126.00
24	CX	44	A	N1-C6-N6	6.44	122.46	118.60
24	AX	14	A	C5-C6-N1	-6.43	114.49	117.70
26	DA	2177	C	N1-C2-O2	6.43	122.75	118.90
26	DA	2167	U	N1-C2-O2	6.39	127.28	122.80
1	CA	1150	U	C5-C4-O4	6.39	129.73	125.90
26	DA	2155	G	C6-N1-C2	6.39	128.93	125.10
1	AA	148	G	N3-C4-C5	6.37	131.79	128.60
1	CA	72	C	C4-C5-C6	-6.35	114.22	117.40
1	CA	1119	C	N1-C2-N3	-6.33	114.77	119.20
1	CA	1036	G	N3-C4-N9	6.32	129.79	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	148	G	C6-C5-N7	6.30	134.18	130.40
1	CA	1018	C	C2-N1-C1'	6.28	125.71	118.80
26	DA	1507	A	C4-C5-C6	6.27	120.14	117.00
26	BA	1142(A)	A	C2-N3-C4	-6.26	107.47	110.60
24	AX	46	G	N1-C2-N3	6.26	127.66	123.90
24	CX	34	C	N1-C2-N3	6.26	123.58	119.20
1	CA	1003	G	N7-C8-N9	6.25	116.23	113.10
1	CA	754	C	C2-N1-C1'	6.25	125.68	118.80
1	AA	421	U	N3-C2-O2	-6.25	117.83	122.20
24	AX	14	A	C8-N9-C1'	-6.22	116.50	127.70
24	AX	46	G	C5-C6-N1	6.22	114.61	111.50
1	CA	1031	G	N3-C4-N9	6.22	129.73	126.00
1	CA	1308	U	C5-C4-O4	6.22	129.63	125.90
1	AA	1011	G	N3-C4-N9	6.21	129.73	126.00
26	DA	2137	C	C2-N1-C1'	6.21	125.63	118.80
1	AA	148	G	N9-C4-C5	6.20	107.88	105.40
26	BA	12	U	C2-N1-C1'	6.20	125.14	117.70
26	DA	1699	G	N1-C6-O6	6.16	123.59	119.90
1	CA	1229	A	C6-N1-C2	6.13	122.28	118.60
1	AA	1172	C	C6-N1-C1'	-6.13	113.45	120.80
26	BA	945	A	C2-N3-C4	-6.12	107.54	110.60
1	CA	1126	U	C2-N1-C1'	6.12	125.05	117.70
26	DA	2700	C	C6-N1-C2	6.12	122.75	120.30
26	DA	2152	G	C4-N9-C1'	6.12	134.45	126.50
1	CA	93	G	C8-N9-C1'	6.12	134.95	127.00
26	DA	2160	G	N3-C4-N9	6.10	129.66	126.00
26	DA	1507	A	N1-C2-N3	6.10	132.35	129.30
24	AX	22	G	C6-C5-N7	6.09	134.05	130.40
27	DB	20	C	C2-N1-C1'	6.09	125.50	118.80
26	DA	2167	U	N3-C2-O2	-6.09	117.94	122.20
26	DA	898	C	C6-N1-C2	-6.08	117.87	120.30
1	CA	988	G	N3-C4-N9	6.08	129.65	126.00
1	CA	992	U	OP2-P-O3'	6.08	118.58	105.20
1	AA	93	G	C6-N1-C2	6.08	128.75	125.10
26	DA	2152	G	C8-N9-C1'	-6.08	119.10	127.00
26	DA	2133	G	C2-N3-C4	-6.07	108.86	111.90
1	AA	1262	C	C2-N3-C4	6.07	122.94	119.90
26	BA	1175	U	P-O3'-C3'	6.06	126.97	119.70
1	CA	1034	G	C8-N9-C4	-6.06	103.98	106.40
1	AA	1001	A	N1-C6-N6	-6.05	114.97	118.60
1	CA	1400	C	N3-C2-O2	-6.05	117.67	121.90
1	CA	1064	G	P-O3'-C3'	6.04	126.95	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1154	G	C8-N9-C4	-6.04	103.98	106.40
1	CA	1012	U	N1-C2-N3	6.04	118.52	114.90
26	DA	2152	G	N9-C4-C5	-6.04	102.99	105.40
1	AA	921	U	C2-N3-C4	6.01	130.61	127.00
1	CA	99	U	N3-C2-O2	6.01	126.41	122.20
1	CA	1154	G	N3-C4-C5	-6.01	125.60	128.60
1	AA	421	U	C2-N1-C1'	6.00	124.90	117.70
1	AA	1396	A	C6-N1-C2	5.98	122.19	118.60
1	CA	1027	C	N1-C2-O2	5.97	122.48	118.90
26	DA	893	C	C2-N1-C1'	5.94	125.34	118.80
26	DA	2150	U	N3-C2-O2	-5.94	118.04	122.20
1	CA	1355	G	N1-C6-O6	5.94	123.46	119.90
26	DA	1482	G	N1-C2-N3	5.93	127.46	123.90
26	BA	2174	C	N1-C2-O2	5.93	122.46	118.90
1	CA	1125	U	O4'-C1'-N1	5.93	112.94	108.20
24	AX	14	A	C4-N9-C1'	5.91	136.94	126.30
24	AX	14	A	N1-C6-N6	5.87	122.12	118.60
1	CA	435	C	N1-C2-O2	-5.87	115.38	118.90
1	CA	457	C	C2-N1-C1'	5.87	125.25	118.80
1	CA	1355	G	C5-C6-O6	-5.87	125.08	128.60
1	AA	198	G	C8-N9-C1'	-5.86	119.38	127.00
1	CA	1036	G	C5-C6-O6	-5.86	125.08	128.60
26	BA	1022	G	N3-C2-N2	-5.82	115.83	119.90
24	AX	22	G	C5-C6-N1	5.81	114.41	111.50
26	BA	1022	G	C4-N9-C1'	-5.81	118.95	126.50
1	AA	198	G	O4'-C1'-N9	5.80	112.84	108.20
1	CA	1216	G	N3-C4-C5	5.79	131.50	128.60
1	CA	1009	G	N9-C4-C5	5.79	107.72	105.40
1	AA	345	C	N1-C2-O2	5.79	122.37	118.90
1	CA	93	G	C4-N9-C1'	-5.78	118.98	126.50
24	CX	44	A	C5-C6-N6	-5.78	119.07	123.70
26	BA	1021	A	N1-C2-N3	5.78	132.19	129.30
1	CA	950	U	N1-C2-O2	5.78	126.84	122.80
26	BA	945	A	N1-C6-N6	5.77	122.06	118.60
26	BA	2175	C	N1-C2-O2	5.77	122.36	118.90
26	DA	1699	G	C5-C6-O6	-5.76	125.15	128.60
26	DA	893	C	N1-C2-O2	5.75	122.35	118.90
26	BA	845	G	O4'-C1'-N9	5.75	112.80	108.20
26	DA	2177	C	C6-N1-C1'	-5.75	113.90	120.80
26	BA	2100	G	C5-C6-O6	-5.72	125.17	128.60
1	CA	1273	G	C5-C6-O6	-5.72	125.17	128.60
26	DA	2178	C	C2-N1-C1'	5.71	125.08	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	DI	123	LEU	CA-CB-CG	5.70	128.41	115.30
26	DA	2152	G	C4-C5-N7	5.69	113.08	110.80
1	CA	407	G	N3-C2-N2	-5.69	115.92	119.90
26	DA	2711	A	C8-N9-C4	5.69	108.08	105.80
1	CA	97	G	N1-C2-N3	-5.68	120.49	123.90
26	BA	1530	C	P-O3'-C3'	5.68	126.51	119.70
26	DA	141	A	N7-C8-N9	5.68	116.64	113.80
26	BA	2189	U	C2-N1-C1'	5.67	124.50	117.70
26	BA	1993	U	O5'-P-OP1	-5.67	100.60	105.70
24	CX	67	C	C6-N1-C1'	-5.67	114.00	120.80
1	AA	1067	A	P-O3'-C3'	5.66	126.50	119.70
26	BA	2140	C	N1-C2-O2	5.66	122.30	118.90
26	BA	1313	U	C2-N1-C1'	5.66	124.49	117.70
1	CA	1183	A	P-O3'-C3'	5.65	126.48	119.70
24	AX	46	G	C5-C6-O6	-5.64	125.22	128.60
1	CA	1123	A	C5-C6-N6	5.63	128.21	123.70
1	AA	913	A	P-O3'-C3'	5.63	126.45	119.70
1	CA	927	G	C5-C6-O6	5.62	131.97	128.60
27	DB	20	C	C6-N1-C1'	-5.62	114.05	120.80
26	DA	945	A	O4'-C1'-N9	5.62	112.69	108.20
26	BA	2164	C	N1-C2-O2	-5.61	115.53	118.90
1	CA	1003	G	C4-N9-C1'	5.60	133.78	126.50
26	DA	1482	G	C5-C6-N1	-5.60	108.70	111.50
27	DB	8	U	C5-C6-N1	5.60	125.50	122.70
26	DA	2155	G	C5-C6-O6	5.59	131.96	128.60
27	BB	89	G	O5'-P-OP1	5.59	117.40	110.70
24	AX	22	G	C8-N9-C1'	5.58	134.25	127.00
26	DA	1531	C	C2-N1-C1'	5.58	124.94	118.80
1	CA	266	G	C4-N9-C1'	5.58	133.75	126.50
1	CA	1038	C	C2-N3-C4	5.57	122.69	119.90
1	AA	1329	A	C6-N1-C2	5.56	121.94	118.60
1	CA	1094	G	O4'-C1'-N9	5.56	112.65	108.20
26	DA	2140	C	C6-N1-C2	-5.56	118.08	120.30
1	AA	347	G	OP1-P-O3'	5.56	117.43	105.20
1	CA	1220	G	N3-C4-N9	-5.55	122.67	126.00
26	BA	2128	C	N1-C2-O2	-5.54	115.57	118.90
26	BA	2286	A	N7-C8-N9	5.53	116.57	113.80
24	CX	14	A	C4-N9-C1'	5.53	136.26	126.30
1	CA	997	U	C5-C4-O4	5.53	129.22	125.90
26	BA	528	A	C5-N7-C8	-5.52	101.14	103.90
1	AA	343	U	O4'-C1'-N1	5.52	112.62	108.20
26	DA	1647	G	O4'-C1'-N9	-5.52	103.78	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1158	C	N1-C2-O2	5.50	122.20	118.90
26	DA	1021	A	C2-N3-C4	-5.50	107.85	110.60
1	CA	1001(A)	G	N3-C4-C5	-5.49	125.85	128.60
26	DA	34	C	N1-C2-O2	5.49	122.19	118.90
24	AX	67	C	C5-C6-N1	5.48	123.74	121.00
1	CA	1256	A	C4-C5-N7	5.48	113.44	110.70
26	DA	1653	G	C4-N9-C1'	5.48	133.62	126.50
1	CA	1256	A	C6-C5-N7	-5.48	128.47	132.30
24	AX	46	G	N3-C4-C5	-5.47	125.86	128.60
39	BS	78	LEU	CA-CB-CG	5.47	127.88	115.30
26	BA	1372	U	N3-C4-O4	5.46	123.22	119.40
26	BA	1022	G	C8-N9-C1'	5.46	134.10	127.00
1	CA	1154	G	C6-C5-N7	-5.46	127.13	130.40
26	DA	1022	G	N3-C2-N2	-5.45	116.08	119.90
26	DA	2139	C	C5-C6-N1	5.45	123.73	121.00
1	AA	1030(B)	C	O4'-C1'-N1	5.45	112.56	108.20
24	CX	44	A	C6-C5-N7	-5.44	128.49	132.30
26	DA	1882	C	C5-C6-N1	5.44	123.72	121.00
1	AA	1040	U	C5-C4-O4	5.43	129.16	125.90
1	CA	1126	U	N1-C2-O2	5.43	126.60	122.80
26	BA	2140	C	N3-C2-O2	-5.42	118.10	121.90
1	CA	1036	G	N3-C4-C5	-5.41	125.89	128.60
26	BA	1173	G	O4'-C1'-N9	5.41	112.53	108.20
33	DI	72	LEU	CA-CB-CG	5.41	127.73	115.30
1	CA	84	U	C2-N1-C1'	5.40	124.18	117.70
1	CA	76	C	N3-C2-O2	-5.40	118.12	121.90
26	BA	2126	A	O4'-C1'-N9	-5.39	103.89	108.20
1	CA	1135	U	O4'-C1'-N1	5.38	112.51	108.20
26	BA	2158	A	P-O3'-C3'	5.38	126.16	119.70
1	AA	1030	C	C2-N1-C1'	5.38	124.72	118.80
1	CA	1003	G	N3-C4-C5	-5.37	125.92	128.60
26	BA	1297	C	OP1-P-O3'	5.37	117.01	105.20
26	DA	277	C	N1-C2-O2	5.37	122.12	118.90
26	BA	1380	G	O5'-P-OP2	-5.36	100.87	105.70
1	CA	73	G	N9-C1'-C2'	-5.36	106.10	112.00
26	DA	2121	G	C6-C5-N7	-5.36	127.18	130.40
26	BA	2127	G	N9-C1'-C2'	-5.36	106.10	112.00
1	AA	1040	U	C2-N3-C4	5.36	130.22	127.00
26	BA	114	U	C2-N1-C1'	5.36	124.13	117.70
26	BA	645	C	C2-N1-C1'	5.35	124.69	118.80
1	CA	1067	A	P-O3'-C3'	5.35	126.12	119.70
22	CV	18	G	C5-N7-C8	5.34	106.97	104.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	457	C	C6-N1-C1'	-5.34	114.39	120.80
1	CA	1329	A	C5-C6-N6	5.34	127.97	123.70
1	CA	1001(A)	G	C6-C5-N7	-5.34	127.20	130.40
1	AA	1001(A)	G	C4-N9-C1'	5.34	133.44	126.50
44	DX	57	LEU	CA-CB-CG	5.33	127.57	115.30
1	CA	1355	G	C6-C5-N7	-5.33	127.20	130.40
26	DA	879	G	C4-N9-C1'	5.33	133.43	126.50
24	CX	67	C	N3-C2-O2	-5.32	118.18	121.90
26	DA	2122	U	C5-C4-O4	-5.32	122.71	125.90
1	CA	97	G	C4-N9-C1'	-5.31	119.60	126.50
1	AA	76	C	C2-N3-C4	5.31	122.55	119.90
1	AA	347	G	P-O3'-C3'	5.30	126.06	119.70
26	BA	2135	A	N1-C6-N6	5.30	121.78	118.60
22	AV	17	U	C5-C4-O4	5.30	129.08	125.90
1	AA	991	U	OP2-P-O3'	5.29	116.84	105.20
26	BA	1022	G	N3-C4-C5	5.29	131.25	128.60
1	CA	1128	C	P-O3'-C3'	5.29	126.05	119.70
1	CA	78	G	C8-N9-C1'	5.29	133.87	127.00
26	BA	2135	A	C5-C6-N6	-5.28	119.48	123.70
5	CE	12	LEU	CA-CB-CG	5.28	127.44	115.30
24	CX	44	A	N7-C8-N9	5.28	116.44	113.80
1	AA	839	U	P-O3'-C3'	5.27	126.03	119.70
26	BA	528	A	N3-C4-N9	-5.26	123.19	127.40
26	DA	1992	G	P-O3'-C3'	5.26	126.01	119.70
1	CA	1220	G	N9-C4-C5	5.26	107.50	105.40
1	AA	921	U	C5-C4-O4	5.25	129.05	125.90
1	CA	1011	G	C4-N9-C1'	5.24	133.32	126.50
1	CA	1256	A	O4'-C1'-N9	-5.24	104.00	108.20
1	CA	1003	G	C8-N9-C4	-5.24	104.31	106.40
1	CA	1400	C	C2-N3-C4	5.23	122.52	119.90
26	DA	362	U	C5-C6-N1	5.23	125.31	122.70
1	CA	1020	U	C2-N3-C4	-5.23	123.86	127.00
26	DA	269	U	C2-N1-C1'	5.23	123.97	117.70
1	AA	1002	G	N3-C4-N9	5.22	129.13	126.00
1	CA	1400	C	O5'-P-OP2	5.22	116.96	110.70
24	AX	22	G	N7-C8-N9	5.22	115.71	113.10
24	CX	59	A	O4'-C1'-N9	5.21	112.37	108.20
1	CA	189(J)	G	O4'-C1'-N9	5.21	112.37	108.20
26	DA	277	C	P-O3'-C3'	5.21	125.95	119.70
1	CA	1002	G	N1-C6-O6	-5.20	116.78	119.90
1	AA	1030(B)	C	C6-N1-C1'	-5.20	114.56	120.80
1	CA	78	G	N9-C1'-C2'	-5.19	106.29	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	DA	2121	G	N9-C4-C5	-5.19	103.33	105.40
24	AX	14	A	N3-C4-N9	5.18	131.55	127.40
26	BA	2060	A	C8-N9-C4	5.18	107.87	105.80
24	CX	34	C	C6-N1-C2	-5.18	118.23	120.30
1	CA	1035	A	N9-C1'-C2'	-5.17	106.31	112.00
26	DA	2121	G	N3-C4-N9	5.17	129.10	126.00
1	AA	198	G	N7-C8-N9	5.17	115.69	113.10
1	AA	748	C	P-O3'-C3'	5.16	125.90	119.70
24	CX	14	A	C8-N9-C1'	-5.16	118.42	127.70
26	DA	1314	C	C2-N1-C1'	5.16	124.47	118.80
26	BA	729	G	C5-C6-O6	-5.15	125.51	128.60
29	DE	72	VAL	C-N-CA	5.14	134.55	121.70
26	BA	1265	A	O5'-P-OP2	-5.13	101.08	105.70
26	DA	2473	U	C2-N1-C1'	5.13	123.86	117.70
1	CA	1154	G	N7-C8-N9	5.13	115.67	113.10
26	BA	2712	U	O4'-C1'-N1	5.12	112.30	108.20
1	AA	1007	C	C5-C6-N1	5.12	123.56	121.00
1	CA	1213	A	O4'-C1'-N9	5.11	112.29	108.20
24	CX	59	A	C4-N9-C1'	-5.11	117.11	126.30
1	CA	1395	C	N1-C2-O2	5.11	121.96	118.90
2	CB	98	LEU	CA-CB-CG	5.11	127.05	115.30
26	BA	1176	G	P-O3'-C3'	5.10	125.82	119.70
26	BA	2135	A	N9-C4-C5	-5.10	103.76	105.80
26	DA	2184	G	C8-N9-C1'	-5.10	120.37	127.00
1	AA	1340	A	C6-N1-C2	5.10	121.66	118.60
1	AA	1036	G	N3-C2-N2	-5.09	116.33	119.90
26	DA	1313	U	C2-N1-C1'	5.09	123.81	117.70
26	DA	2140	C	C2-N1-C1'	5.09	124.40	118.80
1	CA	985	C	N1-C2-O2	-5.09	115.84	118.90
26	BA	1394	U	O5'-P-OP1	-5.09	101.12	105.70
26	BA	383	U	C2-N1-C1'	-5.08	111.60	117.70
1	CA	1018	C	C5-C6-N1	5.08	123.54	121.00
26	DA	2593	U	N3-C4-O4	-5.08	115.84	119.40
1	CA	1038	C	N3-C4-C5	-5.08	119.87	121.90
33	DI	75	LEU	CA-CB-CG	5.08	126.98	115.30
26	DA	1963	U	C2-N1-C1'	5.08	123.79	117.70
1	AA	1172	C	O4'-C1'-N1	5.08	112.26	108.20
26	BA	528	A	N3-C4-C5	5.07	130.35	126.80
26	DA	932	G	C4-N9-C1'	-5.07	119.90	126.50
1	AA	1397	C	C2-N1-C1'	5.07	124.38	118.80
1	CA	1231	G	C5-C6-O6	-5.07	125.56	128.60
26	BA	527	C	C6-N1-C2	-5.07	118.27	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	BX	57	LEU	CA-CB-CG	5.07	126.95	115.30
26	DA	2184	G	N3-C4-N9	5.07	129.04	126.00
1	AA	1027	C	C2-N3-C4	5.06	122.43	119.90
1	CA	72	C	C2-N3-C4	5.06	122.43	119.90
26	DA	2133	G	C5-C6-N1	-5.06	108.97	111.50
1	CA	1120	G	N7-C8-N9	5.06	115.63	113.10
1	CA	1256	A	N9-C4-C5	-5.05	103.78	105.80
1	CA	1273	G	N3-C4-N9	5.05	129.03	126.00
1	CA	1003	G	N3-C4-N9	5.05	129.03	126.00
26	BA	1936	A	O4'-C1'-N9	5.04	112.23	108.20
1	AA	1027	C	N3-C4-C5	-5.04	119.89	121.90
26	BA	887	A	P-O3'-C3'	5.04	125.75	119.70
26	BA	548	A	P-O3'-C3'	5.04	125.74	119.70
1	CA	1011	G	C8-N9-C1'	-5.03	120.46	127.00
26	BA	2140	C	C6-N1-C1'	-5.03	114.76	120.80
52	B5	58	LEU	CA-CB-CG	5.03	126.86	115.30
24	CX	22	G	C5-N7-C8	-5.03	101.79	104.30
1	AA	175	C	C5-C6-N1	5.03	123.51	121.00
26	DA	1507	A	N1-C6-N6	5.02	121.61	118.60
1	CA	1355	G	N3-C4-N9	5.02	129.01	126.00
33	DI	88	ILE	CB-CA-C	-5.02	101.56	111.60
1	AA	1033	G	O4'-C1'-N9	5.01	112.21	108.20
26	DA	528	A	C2-N3-C4	-5.01	108.10	110.60
1	AA	1308	U	C2-N3-C4	5.01	130.00	127.00
2	CB	187	LEU	CA-CB-CG	5.01	126.82	115.30
26	DA	2689	U	P-O3'-C3'	5.01	125.71	119.70
1	AA	266	G	P-O3'-C3'	5.01	125.71	119.70
26	BA	2109	U	C2-N1-C1'	5.01	123.71	117.70
26	DA	2122	U	C2-N3-C4	-5.00	124.00	127.00
26	DA	2176	A	C5-C6-N6	-5.00	119.70	123.70

There are no chirality outliers.

All (10) planarity outliers are listed below:

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

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Mol	Chain	Res	Type	Group
51	D4	66	SER	Peptide
29	DE	72	VAL	Peptide
33	DI	81	VAL	Peptide

## 5.2 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	32205	0	16255	743	1
1	CA	32312	0	16307	964	1
2	AB	1846	0	1867	74	0
2	CB	1825	0	1828	76	0
3	AC	1552	0	1546	49	0
3	CC	1542	0	1517	58	0
4	AD	1659	0	1676	74	0
4	CD	1674	0	1714	83	0
5	AE	1129	0	1184	33	0
5	CE	1133	0	1191	39	0
6	AF	806	0	793	16	0
6	CF	816	0	808	23	0
7	AG	1231	0	1238	37	0
7	CG	1235	0	1249	38	0
8	AH	1088	0	1126	35	0
8	CH	1088	0	1126	40	0
9	AI	983	0	986	48	0
9	CI	978	0	966	53	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	38	0
11	AK	829	0	825	23	0
11	CK	833	0	836	20	0
12	AL	930	0	980	21	0
12	CL	930	0	980	33	0
13	AM	958	0	1002	37	0
13	CM	950	0	988	47	0
14	AN	492	0	529	27	0
14	CN	492	0	529	23	0
15	AO	728	0	760	22	0
15	CO	728	0	760	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	AP	681	0	697	27	0
16	CP	677	0	686	26	0
17	AQ	823	0	891	23	0
17	CQ	823	0	891	18	0
18	AR	555	0	618	11	0
18	CR	555	0	618	23	0
19	AS	652	0	662	29	0
19	CS	646	0	644	40	0
20	AT	728	0	798	27	0
20	CT	727	0	796	23	0
21	AU	199	0	208	5	0
21	CU	199	0	208	8	0
22	AV	277	0	140	7	0
22	CV	129	0	65	16	0
23	AW	74	0	51	5	0
23	CW	74	0	51	11	0
24	AX	1633	0	836	35	0
24	CX	1635	0	838	83	0
25	AY	104	0	56	3	0
25	CY	104	0	56	2	0
26	BA	60729	0	30620	950	0
26	DA	60311	0	30412	1223	1
27	BB	2573	0	1306	32	0
27	DB	2573	0	1306	87	0
28	BD	2136	0	2218	67	0
28	DD	2136	0	2218	74	0
29	BE	1559	0	1618	43	0
29	DE	1559	0	1618	56	0
30	BF	1584	0	1625	49	0
30	DF	1580	0	1619	55	0
31	BG	1425	0	1443	37	0
31	DG	1424	0	1434	73	0
32	BH	1330	0	1407	29	0
32	DH	1330	0	1407	44	0
33	BI	1085	0	1114	28	1
33	DI	1061	0	1080	50	0
34	BN	1117	0	1184	21	0
34	DN	1117	0	1184	29	0
35	BO	933	0	996	27	0
35	DO	933	0	996	38	0
36	BP	1135	0	1212	53	0
36	DP	1135	0	1212	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	BQ	1122	0	1179	38	0
37	DQ	1122	0	1179	33	0
38	BR	968	0	1033	26	1
38	DR	968	0	1033	36	0
39	BS	877	0	938	28	0
39	DS	870	0	923	29	0
40	BT	1091	0	1151	37	0
40	DT	1083	0	1136	39	0
41	BU	959	0	1019	24	0
41	DU	959	0	1018	29	0
42	BV	771	0	830	21	1
42	DV	771	0	830	24	0
43	BW	886	0	940	15	0
43	DW	886	0	940	20	0
44	BX	750	0	814	24	0
44	DX	750	0	814	19	0
45	BY	806	0	881	24	0
45	DY	806	0	881	19	0
46	BZ	1349	0	1355	38	0
46	DZ	1360	0	1363	47	0
47	B0	653	0	674	20	0
47	D0	653	0	674	19	0
48	B1	755	0	826	19	0
48	D1	755	0	826	20	0
49	B2	588	0	643	8	0
49	D2	588	0	643	9	0
50	B3	469	0	518	15	0
50	D3	464	0	514	15	0
51	B4	552	0	533	32	0
51	D4	532	0	503	28	0
52	B5	455	0	465	8	0
52	D5	455	0	465	10	0
53	B6	453	0	473	13	0
53	D6	449	0	469	6	0
54	B7	418	0	467	19	0
54	D7	418	0	467	15	0
55	B8	511	0	571	29	0
55	D8	517	0	582	14	0
56	B9	307	0	335	8	0
56	D9	307	0	335	10	0
57	AA	207	0	0	0	0
57	AD	2	0	0	0	0

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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	CX	2	0	0	0	0
57	D3	1	0	0	0	0
57	D5	1	0	0	0	0
57	D8	2	0	0	0	0
57	DA	629	0	0	0	0
57	DB	10	0	0	0	0
57	DD	7	0	0	0	0
57	DE	4	0	0	0	0
57	DF	4	0	0	0	0
57	DG	1	0	0	0	0
57	DN	1	0	0	0	0
57	DO	1	0	0	0	0
57	DP	2	0	0	0	0
57	DQ	3	0	0	0	0
57	DR	2	0	0	0	0
57	DU	4	0	0	0	0
57	DV	2	0	0	0	0
57	DW	2	0	0	0	0
57	DY	1	0	0	0	0
58	AD	8	0	0	1	0
58	CD	8	0	0	1	0
59	AN	1	0	0	0	0
59	B4	1	0	0	0	0
59	B5	1	0	0	0	0
59	B6	1	0	0	0	0
59	B9	1	0	0	0	0
59	BY	1	0	0	0	0
59	CN	1	0	0	0	0
59	D4	1	0	0	0	0
59	D5	1	0	0	0	0
59	D6	1	0	0	0	0
59	D9	1	0	0	0	0
59	DY	1	0	0	0	0
60	AX	1	0	0	0	0
60	CX	1	0	0	0	0
61	AA	170	0	0	16	0
61	AL	2	0	0	1	0
61	AO	1	0	0	0	0
61	AU	1	0	0	1	0
61	AV	2	0	0	0	0
61	AW	3	0	0	0	0
61	B0	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	B1	1	0	0	0	0
61	B3	1	0	0	0	0
61	B5	5	0	0	0	0
61	B7	1	0	0	1	0
61	B8	7	0	0	0	0
61	BA	1102	0	0	59	0
61	BB	36	0	0	1	0
61	BD	8	0	0	1	0
61	BE	13	0	0	5	0
61	BF	4	0	0	0	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BP	15	0	0	1	0
61	BQ	3	0	0	0	0
61	BR	1	0	0	1	0
61	BS	1	0	0	0	0
61	BT	3	0	0	0	0
61	BU	1	0	0	1	0
61	BV	4	0	0	0	0
61	BW	2	0	0	0	0
61	BX	2	0	0	0	0
61	CA	130	0	0	8	0
61	CE	1	0	0	0	0
61	CJ	2	0	0	0	0
61	CN	1	0	0	0	0
61	CT	1	0	0	0	0
61	CV	1	0	0	0	0
61	CW	1	0	0	0	0
61	CX	1	0	0	1	0
61	D0	5	0	0	1	0
61	D1	1	0	0	0	0
61	D3	2	0	0	0	0
61	D7	1	0	0	0	0
61	D8	4	0	0	0	0
61	DA	767	0	0	55	0
61	DB	9	0	0	0	0
61	DD	9	0	0	3	0
61	DE	5	0	0	0	0
61	DF	6	0	0	0	0
61	DN	2	0	0	0	0
61	DP	12	0	0	3	0
61	DR	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	DT	1	0	0	0	0
61	DU	2	0	0	0	0
61	DV	1	0	0	1	0
61	DX	2	0	0	0	0
61	DY	1	0	0	1	0
All	All	290205	0	193167	6242	3

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 14.

All (6242) 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)
1:CA:1002:G:H1	1:CA:1038:C:N4	1.48	1.11
26:DA:2121:G:H1	26:DA:2177:C:N4	1.52	1.06
1:AA:1164:G:N2	1:AA:1165:C:C5	2.24	1.06
1:CA:72:C:N4	1:CA:97:G:N1	2.04	1.05
26:DA:2139:C:N4	26:DA:2152:G:H1	1.55	1.04
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.40	1.03
1:CA:1162:C:N4	1:CA:1174:G:H1	1.56	1.03
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.20	1.03
26:DA:2137:C:N4	26:DA:2154:G:H1	1.55	1.02
1:CA:1245:A:H61	1:CA:1292:U:H3	1.07	1.02
1:CA:1244:C:N4	1:CA:1293:G:H1	1.56	1.02
1:CA:76:C:C4	1:CA:93:G:N1	2.28	1.01
1:CA:1114:C:N4	1:CA:1186:G:H1	1.57	1.01
22:CV:18:G:N2	24:CX:34:C:N3	2.07	1.01
1:CA:1355:G:H1	1:CA:1367:C:H42	1.04	1.00
26:DA:2104:G:H1	26:DA:2185:C:N4	1.58	1.00
1:CA:985:C:N4	1:CA:1220:G:H1	1.60	0.99
1:CA:76:C:N4	1:CA:93:G:C6	2.31	0.99
22:CV:18:G:H1	24:CX:34:C:N4	1.60	0.99
1:AA:1164:G:N2	1:AA:1165:C:C6	2.31	0.99
26:BA:2138:C:H42	26:BA:2153:G:H1	1.04	0.99
1:CA:1000:U:H3	1:CA:1041:A:N6	1.61	0.98
26:BA:2102:U:H3	26:BA:2187:G:H1	1.11	0.98
1:CA:1000:U:H3	1:CA:1041:A:H61	0.98	0.97
24:CX:30:G:H1	24:CX:40:C:H42	1.00	0.97
1:CA:1133:G:H1	1:CA:1141:C:H42	1.10	0.97
1:AA:1089:G:H1	1:AA:1096:C:N4	1.62	0.97
1:CA:76:C:N4	1:CA:93:G:N1	2.13	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CX:49:G:N1	24:CX:65:C:N4	2.12	0.96
1:CA:72:C:N3	1:CA:97:G:N2	2.14	0.96
24:CX:49:G:N2	24:CX:65:C:N3	2.13	0.95
26:DA:2141:G:O6	26:DA:2150:U:O2	1.86	0.94
26:BA:2096:U:H3	26:BA:2193:G:H1	1.00	0.94
1:CA:999:C:N3	1:CA:1042:G:N2	2.16	0.94
1:CA:989:C:N3	1:CA:1216:G:N1	2.15	0.93
1:CA:1262:C:H42	1:CA:1273:G:H1	1.13	0.93
24:AX:49:G:H1	24:AX:65:C:H42	1.16	0.93
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.48	0.93
47:B0:11:ARG:O	47:B0:14:ARG:NH2	2.00	0.93
1:CA:70:G:H1	1:CA:99:U:H3	1.17	0.93
40:BT:16:ARG:NH2	40:BT:83:ILE:O	2.02	0.93
1:AA:1502:A:H2	1:AA:1505:G:H1	1.16	0.93
23:CW:76:PPU:H5''	23:CW:76:PPU:H8	1.49	0.92
26:BA:2103:C:H42	26:BA:2186:G:H1	1.11	0.92
26:DA:2141:G:C6	26:DA:2150:U:O2	2.23	0.92
1:CA:407:G:OP1	4:CD:115:ARG:NH2	2.03	0.91
31:DG:41:GLN:HE22	31:DG:153:ARG:HB3	1.35	0.91
22:CV:17:U:H3	24:CX:35:A:H61	1.08	0.91
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.51	0.91
46:BZ:153:SER:HB3	46:BZ:167:PRO:HB3	1.53	0.91
1:CA:1133:G:H1	1:CA:1141:C:N4	1.69	0.91
26:BA:1176:G:H1'	26:BA:1177:A:H5'	1.53	0.91
22:CV:17:U:H3	24:CX:35:A:N6	1.70	0.90
24:AX:28:C:H42	24:AX:42:G:H1	1.19	0.90
26:DA:2139:C:N4	26:DA:2152:G:N1	2.17	0.90
1:CA:1002:G:N2	1:CA:1038:C:N3	2.18	0.89
1:CA:1027:C:C2	1:CA:1034:G:N2	2.40	0.89
26:DA:1607:C:N4	26:DA:1622:G:OP2	2.04	0.89
1:CA:999:C:N4	1:CA:1042:G:N1	2.21	0.89
22:CV:18:G:H1	24:CX:34:C:H42	0.93	0.88
26:BA:2136:C:H42	26:BA:2155:G:H1	1.12	0.88
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.53	0.88
26:DA:2121:G:N1	26:DA:2177:C:N4	2.16	0.88
24:AX:5:G:H1	24:AX:68:C:H42	1.20	0.88
1:AA:1089:G:H1	1:AA:1096:C:H42	0.91	0.88
23:AW:76:PPU:H8	23:AW:76:PPU:H5''	1.53	0.88
26:BA:2140:C:C2	26:BA:2151:G:N2	2.41	0.88
1:CA:1244:C:N3	1:CA:1293:G:N2	2.22	0.87
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.54	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1169:G:H1	26:DA:1180:C:H42	1.14	0.87
24:CX:43:A:H2'	24:CX:44:A:H8	1.39	0.87
26:DA:1689:A:H62	26:DA:1698:A:H2	1.23	0.87
26:BA:2124:G:H1	26:BA:2174:C:H42	1.22	0.87
24:CX:30:G:H1	24:CX:40:C:N4	1.71	0.87
26:BA:993:G:OP1	41:BU:50:ARG:NH2	2.06	0.86
27:DB:32:C:H1'	27:DB:51:G:H22	1.39	0.86
24:CX:49:G:H1	24:CX:65:C:N4	1.72	0.86
26:DA:2121:G:N2	26:DA:2177:C:N3	2.23	0.86
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.11	0.85
1:AA:1007:C:H2'	1:AA:1008:C:H5''	1.56	0.85
1:AA:677:U:H3	1:AA:713:G:H22	1.24	0.85
35:DO:35:VAL:HG11	35:DO:103:ALA:HB3	1.58	0.85
46:DZ:138:GLU:H	46:DZ:156:LYS:HE2	1.40	0.85
1:AA:78:G:N2	1:AA:91:C:N3	2.25	0.85
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.09	0.85
26:BA:2445:G:OP1	30:BF:74:ARG:NH2	2.10	0.85
26:BA:1993:U:OP2	61:BA:4878:HOH:O	1.93	0.85
1:AA:1164:G:O6	1:AA:1173:G:C4	2.30	0.85
1:CA:985:C:H42	1:CA:1220:G:H1	0.87	0.85
1:AA:1158:C:H5	1:AA:1181:G:H1	1.19	0.85
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.09	0.85
32:DH:46:GLU:HB2	32:DH:49:VAL:HG12	1.59	0.85
26:DA:2127:G:O6	26:DA:2161:C:N3	2.10	0.84
26:DA:1604:C:OP1	61:DA:3949:HOH:O	1.95	0.84
51:D4:51:ASP:HA	51:D4:53:GLU:HG2	1.57	0.84
26:BA:2157:G:N3	26:BA:2158:A:N6	2.24	0.84
1:CA:1047:G:HO2'	1:CA:1215:G:HO2'	1.14	0.84
26:DA:2793:G:O6	26:DA:2803:C:N4	2.10	0.84
26:BA:2100:G:H1	26:BA:2189:U:H3	1.25	0.84
26:DA:1772:G:OP1	61:DA:4123:HOH:O	1.95	0.84
35:BO:35:VAL:HG11	35:BO:103:ALA:HB3	1.58	0.84
1:CA:76:C:N3	1:CA:93:G:N2	2.27	0.83
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.58	0.83
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.60	0.83
26:DA:994:C:OP1	41:DU:53:ARG:NH2	2.10	0.83
1:CA:76:C:C4	1:CA:93:G:C2	2.66	0.83
24:CX:76:31H:OP1	26:DA:2439:A:N6	2.12	0.83
26:DA:731:C:OP1	61:DA:4214:HOH:O	1.94	0.83
26:BA:2120:G:H1	26:BA:2178:C:H42	1.22	0.83
1:CA:1162:C:N3	1:CA:1174:G:N2	2.25	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1162:C:H42	1:CA:1174:G:H1	0.85	0.82
1:CA:1114:C:H42	1:CA:1186:G:H1	0.85	0.82
26:BA:2849:U:O4	40:BT:23:ARG:NH2	2.13	0.82
1:CA:692:U:O2'	1:CA:694:A:N7	2.12	0.82
1:CA:985:C:N3	1:CA:1220:G:N2	2.26	0.82
46:BZ:151:HIS:O	46:BZ:153:SER:N	2.13	0.82
26:DA:1918:A:O2'	26:DA:1920:C:N4	2.11	0.82
26:DA:652(E):G:N2	26:DA:652(T):C:O2	2.12	0.82
26:DA:2137:C:N3	26:DA:2154:G:N2	2.25	0.82
26:DA:2114:A:N1	26:DA:2117:A:N6	2.28	0.82
45:BY:92:ASN:HB3	45:BY:94:LYS:H	1.44	0.82
1:AA:982:U:H5''	14:AN:6:LEU:HD21	1.62	0.82
26:DA:2139:C:N3	26:DA:2152:G:N2	2.26	0.82
26:DA:2104:G:H1	26:DA:2185:C:H42	0.83	0.82
26:BA:2138:C:N4	26:BA:2153:G:H1	1.76	0.82
1:AA:78:G:N1	1:AA:91:C:N4	2.28	0.81
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.13	0.81
26:DA:2206:G:H3'	26:DA:2207:G:C8	2.14	0.81
1:CA:1355:G:H1	1:CA:1367:C:N4	1.76	0.81
1:CA:1366:C:O2'	10:CJ:60:ARG:NH2	2.12	0.81
26:BA:2136:C:N4	26:BA:2155:G:H1	1.79	0.81
1:CA:1029:C:N3	1:CA:1032:G:N2	2.28	0.81
1:AA:624:C:H2'	1:AA:625:G:H8	1.45	0.81
26:DA:1039:G:O6	26:DA:1116:C:N4	2.13	0.81
29:BE:121:ASN:ND2	61:BE:3108:HOH:O	2.14	0.81
2:CB:178:ARG:HE	8:CH:74:PRO:HG3	1.44	0.81
54:B7:24:THR:HG22	54:B7:27:GLY:H	1.45	0.81
26:DA:879:G:H3'	26:DA:880:G:H8	1.46	0.81
13:AM:6:GLY:O	31:BG:115:ARG:NH2	2.14	0.81
47:D0:11:ARG:O	47:D0:14:ARG:NH2	2.13	0.81
1:AA:997:U:H3	1:AA:1044:A:H61	1.28	0.81
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.13	0.81
1:CA:36:C:OP1	12:CL:123:LYS:NZ	2.14	0.80
26:BA:2103:C:N4	26:BA:2186:G:H1	1.79	0.80
1:CA:1245:A:N6	1:CA:1292:U:H3	1.79	0.80
26:BA:453:C:OP1	61:BA:4156:HOH:O	1.98	0.80
24:CX:43:A:H2'	24:CX:44:A:C8	2.15	0.80
26:BA:2285:C:OP2	53:B6:6:ARG:NH1	2.13	0.80
1:CA:1507:A:N6	1:CA:1528:U:O4	2.13	0.80
27:DB:8:U:H3	27:DB:113:G:H1	1.29	0.80
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2137:C:H42	26:DA:2154:G:H1	0.84	0.80
26:BA:301:G:OP2	45:BY:84:ARG:NH2	2.15	0.80
1:CA:1228:C:OP1	13:CM:115:LYS:N	2.13	0.80
26:BA:2822:G:OP2	61:BA:4874:HOH:O	1.97	0.80
26:DA:2104:G:N2	26:DA:2185:C:N3	2.27	0.80
1:CA:1502:A:H2	1:CA:1505:G:H1	1.28	0.79
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.64	0.79
26:DA:1533:G:N2	26:DA:1536:C:O2	2.16	0.79
27:DB:20:C:N4	27:DB:63:G:O6	2.14	0.79
26:DA:631:A:OP1	36:DP:65:ARG:NH1	2.15	0.79
26:BA:1338:G:N7	44:BX:62:LYS:NZ	2.29	0.79
1:AA:624:C:H2'	1:AA:625:G:C8	2.18	0.79
40:DT:65:LYS:HE2	40:DT:67:SER:HB2	1.65	0.79
1:CA:316:G:OP2	1:CA:351:G:O2'	2.01	0.79
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.15	0.79
27:DB:86:G:O6	27:DB:91:C:N4	2.13	0.79
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.16	0.79
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.65	0.79
26:BA:303:U:O4	61:BA:4502:HOH:O	2.01	0.79
26:BA:2789:C:O2	26:BA:2894:G:N1	2.14	0.79
1:CA:1400:C:H42	24:CX:34:C:H2'	1.48	0.78
26:BA:2140:C:C4	26:BA:2151:G:N1	2.51	0.78
26:DA:2166:G:H3'	26:DA:2167:U:H5''	1.63	0.78
26:DA:182:A:N3	26:DA:433:C:O2'	2.17	0.78
1:AA:1164:G:O6	1:AA:1173:G:C5	2.35	0.78
26:BA:631:A:OP1	36:BP:65:ARG:NH1	2.17	0.78
26:DA:1250:G:OP2	36:DP:21:ARG:NH1	2.16	0.78
26:DA:847:U:O4	26:DA:933:A:N6	2.17	0.78
26:BA:2142:C:N3	26:BA:2149:G:O6	2.16	0.78
26:BA:1530:C:O2'	26:BA:1531:C:O5'	2.00	0.78
26:DA:1532:C:N4	26:DA:1537:G:O6	2.14	0.78
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.17	0.78
26:DA:120:U:OP2	61:DA:3738:HOH:O	2.00	0.78
1:CA:1007:C:N3	1:CA:1022:G:O6	2.17	0.78
1:CA:1262:C:N4	1:CA:1273:G:H1	1.81	0.78
1:AA:1252:A:H61	1:AA:1285:A:H61	1.28	0.78
26:BA:1434:A:H61	26:BA:1558:A:H62	1.32	0.78
1:AA:765:G:H1	1:AA:812:C:HO2'	1.30	0.78
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.02	0.77
1:AA:347:G:O2'	1:AA:348:G:OP1	2.00	0.77
7:AG:16:LEU:HD11	9:AI:45:ALA:HB2	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2763:G:OP2	61:BA:4535:HOH:O	2.02	0.77
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.18	0.77
26:BA:2746:U:OP2	61:BA:3988:HOH:O	2.00	0.77
22:CV:18:G:N1	24:CX:34:C:N4	2.29	0.77
1:CA:446:G:H1	1:CA:488:C:H42	1.33	0.77
30:BF:53:THR:HG23	30:BF:55:GLY:H	1.49	0.77
1:CA:838:G:O6	1:CA:848:C:N4	2.18	0.77
26:DA:2116:G:N7	26:DA:2166:G:N2	2.32	0.77
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.67	0.77
46:BZ:72:ARG:NH2	46:BZ:97:GLU:O	2.17	0.77
1:CA:373:A:H61	1:CA:391:G:H1'	1.48	0.77
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.18	0.77
13:CM:6:GLY:O	31:DG:115:ARG:NH2	2.18	0.77
12:AL:117:ARG:HB3	12:AL:122:THR:HB	1.67	0.77
1:CA:401:C:O2'	1:CA:621:A:N3	2.16	0.77
33:BI:92:VAL:HG13	33:BI:120:ILE:HB	1.66	0.77
26:DA:2126:A:N6	26:DA:2162:G:O2'	2.18	0.77
26:BA:1817:G:OP1	28:BD:88:ARG:NH2	2.18	0.77
1:CA:1114:C:N3	1:CA:1186:G:N2	2.31	0.77
24:CX:6:G:H1	24:CX:67:C:H42	1.30	0.77
1:CA:1029:C:N4	1:CA:1032:G:N1	2.32	0.77
15:CO:17:ARG:HD3	15:CO:26:GLU:HG3	1.66	0.77
1:CA:954:G:H21	1:CA:1227:A:H62	1.32	0.77
1:CA:1256:A:N6	1:CA:1278:U:H1'	1.98	0.76
26:BA:2308:G:O6	26:BA:2311:A:N6	2.15	0.76
1:CA:1183:A:O2'	1:CA:1185:G:OP2	2.01	0.76
27:DB:5:C:OP1	27:DB:61:G:O2'	2.01	0.76
26:DA:2141:G:O6	26:DA:2150:U:C2	2.37	0.76
30:BF:185:ASP:HA	30:BF:188:ARG:HD3	1.68	0.76
28:DD:238:GLY:O	61:DD:405:HOH:O	2.03	0.76
26:BA:1689:A:H62	26:BA:1698:A:H2	1.30	0.76
1:AA:1089:G:N2	1:AA:1096:C:N3	2.32	0.76
24:CX:3:C:H2'	24:CX:4:G:H5''	1.67	0.76
28:DD:69:ARG:NH2	28:DD:128:GLY:O	2.18	0.76
28:BD:17:THR:O	28:BD:211:ARG:NH2	2.19	0.76
1:CA:1378:C:O2	7:CG:76:ARG:NH2	2.17	0.76
1:AA:184:G:H2'	1:AA:185:A:H8	1.51	0.76
6:CF:25:ILE:HD13	6:CF:82:ARG:HE	1.50	0.76
26:DA:2183:C:H2'	26:DA:2184:G:H8	1.50	0.76
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.66	0.76
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.31	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1470:G:N2	26:DA:1520:G:OP2	2.17	0.76
26:DA:2151:G:H2'	26:DA:2152:G:H8	1.50	0.76
1:CA:1356:G:H1	1:CA:1366:C:H42	1.33	0.76
1:AA:766:A:N6	1:AA:813:U:O2	2.18	0.76
16:CP:28:ARG:NH1	16:CP:29:ASP:OD2	2.19	0.76
26:DA:1143:A:OP1	34:DN:25:ARG:NH2	2.19	0.76
26:DA:586:A:N1	26:DA:809:G:O2'	2.19	0.76
1:CA:1422:G:H5''	35:DO:48:PRO:HB3	1.66	0.76
26:DA:2162:G:H4'	26:DA:2172:U:H2'	1.66	0.76
13:CM:84:ILE:O	13:CM:86:CYS:N	2.19	0.76
9:AI:71:SER:HA	9:AI:74:ILE:HD12	1.67	0.76
26:BA:652(F):G:N2	26:BA:652(S):C:O2	2.19	0.76
26:BA:2142:C:O2	26:BA:2149:G:N1	2.18	0.75
27:DB:32:C:H1'	27:DB:51:G:N2	2.00	0.75
28:DD:85:ASP:OD2	28:DD:88:ARG:NH1	2.19	0.75
1:CA:457:C:N4	1:CA:474:G:O6	2.19	0.75
2:CB:16:HIS:HB3	2:CB:210:SER:HB2	1.68	0.75
1:CA:1359:C:O2'	1:CA:1361:G:N7	2.20	0.75
26:BA:2140:C:O2'	26:BA:2152:G:N2	2.19	0.75
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.66	0.75
1:AA:1422:G:H5''	35:BO:48:PRO:HB3	1.68	0.75
26:BA:1153:C:OP2	61:BA:4487:HOH:O	2.04	0.75
40:DT:16:ARG:NH2	40:DT:83:ILE:O	2.19	0.75
31:DG:80:PHE:O	31:DG:82:LEU:N	2.20	0.75
26:BA:2386:C:O2'	61:BA:4897:HOH:O	2.03	0.75
26:BA:1602:U:O4	61:BA:4096:HOH:O	2.04	0.75
31:DG:43:LEU:HD12	31:DG:45:GLU:HG3	1.67	0.75
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.68	0.75
29:DE:28:ALA:HB3	29:DE:93:VAL:HG12	1.66	0.75
26:DA:2314:C:H2'	26:DA:2315:G:C8	2.21	0.75
26:BA:2287:A:H62	26:BA:2344:U:H3	1.34	0.75
1:CA:1026:G:O6	1:CA:1036:G:N2	2.19	0.75
26:DA:1600:C:OP1	44:DX:58:HIS:NE2	2.17	0.75
26:DA:1530:C:O2'	26:DA:1531:C:O5'	2.03	0.75
26:DA:712:G:N2	26:DA:719:C:O2	2.17	0.75
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.68	0.75
30:BF:18:ARG:NH2	30:BF:127:GLU:OE1	2.20	0.75
51:D4:38:LYS:O	51:D4:40:HIS:N	2.19	0.75
26:BA:2296:U:OP2	39:BS:9:ARG:NH2	2.20	0.75
15:CO:64:ARG:NH2	26:DA:715:G:OP1	2.20	0.75
1:AA:1006:C:H42	1:AA:1023:G:H1	1.32	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:627:G:H2'	1:CA:628:G:H8	1.52	0.75
1:AA:1303:C:OP1	61:AA:4108:HOH:O	2.04	0.75
27:DB:36:C:N4	27:DB:49:C:O2	2.19	0.74
26:BA:279:C:H42	26:BA:361:G:H1	1.35	0.74
26:DA:2430:A:OP2	61:DA:4174:HOH:O	2.04	0.74
26:BA:1021:A:H62	26:BA:1141:U:H3	1.34	0.74
26:DA:2793:G:H22	26:DA:2804:C:H1'	1.51	0.74
49:D2:18:PRO:HB3	49:D2:68:ARG:HH12	1.52	0.74
26:BA:65:C:O2	26:BA:456:C:N4	2.19	0.74
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.19	0.74
1:AA:78:G:N2	1:AA:92:C:N3	2.35	0.74
26:BA:2120:G:H1	26:BA:2178:C:N4	1.84	0.74
2:CB:87:ARG:HD3	2:CB:234:PRO:HD2	1.70	0.74
1:AA:1243:C:H42	1:AA:1294:G:H1	1.33	0.74
26:DA:678:C:N4	26:DA:799:G:O6	2.11	0.74
36:BP:59:LEU:HD21	55:B8:10:ALA:HA	1.67	0.74
26:DA:2138:C:H42	26:DA:2153:G:H1	1.34	0.74
26:DA:2126:A:H61	26:DA:2162:G:HO2'	1.32	0.74
1:AA:448:A:O5'	1:AA:485:G:N2	2.20	0.74
26:BA:1798:U:H5'	28:BD:259:THR:HG22	1.70	0.74
26:BA:568:U:H5'	26:BA:945:A:N1	2.01	0.74
26:BA:9:U:H3	26:BA:2629:A:H2	1.33	0.74
1:CA:44:G:H1	1:CA:398:C:H42	1.35	0.74
26:BA:887:A:O2'	26:BA:888:C:OP2	2.04	0.74
26:DA:1204:A:H2	26:DA:1241:A:H62	1.33	0.74
26:BA:1371:G:N7	61:BA:4204:HOH:O	2.21	0.74
1:AA:642:A:N3	8:AH:113:SER:OG	2.20	0.74
29:BE:55:ASN:HB3	29:BE:58:ARG:HG3	1.69	0.74
26:DA:792:G:O6	61:DA:4068:HOH:O	2.03	0.74
1:CA:1366:C:HO2'	10:CJ:60:ARG:HH22	1.35	0.74
29:BE:28:ALA:HB3	29:BE:93:VAL:HG12	1.69	0.74
48:D1:51:VAL:HG11	48:D1:74:VAL:HG21	1.69	0.74
24:CX:31:G:H3'	24:CX:32:5MC:HM51	1.69	0.73
24:AX:49:G:H1	24:AX:65:C:N4	1.86	0.73
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.68	0.73
26:DA:1335:U:O4	61:DA:3860:HOH:O	2.04	0.73
26:BA:2683:C:O2	35:BO:70:LYS:NZ	2.21	0.73
26:DA:272(G):C:H42	26:DA:363(C):G:H1	1.36	0.73
26:BA:789:A:OP1	61:BA:4147:HOH:O	2.05	0.73
1:CA:532:A:O2'	1:CA:533:A:OP1	2.05	0.73
26:DA:2126:A:N6	26:DA:2162:G:HO2'	1.86	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1997:G:OP2	61:DA:4145:HOH:O	2.04	0.73
9:CI:17:VAL:HG11	9:CI:81:ILE:HA	1.71	0.73
3:CC:120:VAL:HA	3:CC:123:GLN:HE21	1.53	0.73
1:AA:279:A:H4'	1:AA:280:C:H5''	1.69	0.73
26:DA:2118:U:C4	26:DA:2149:G:H1'	2.23	0.73
1:CA:1133:G:N2	1:CA:1141:C:N3	2.36	0.73
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.11	0.73
1:CA:1103:C:H5''	2:CB:98:LEU:HD12	1.70	0.73
1:CA:1244:C:H42	1:CA:1293:G:H1	0.80	0.73
1:CA:1126:U:H1'	1:CA:1281:U:C2	2.23	0.73
26:BA:517:C:OP1	52:B5:16:ARG:NH2	2.20	0.73
33:DI:48:GLU:O	33:DI:52:ARG:NH1	2.21	0.73
36:BP:59:LEU:HD11	55:B8:10:ALA:HB2	1.71	0.73
38:DR:67:LEU:HD13	38:DR:76:VAL:HG21	1.69	0.73
26:DA:1171:G:H22	26:DA:1178:C:H42	1.35	0.73
26:BA:422:A:OP2	61:BA:3938:HOH:O	2.05	0.73
25:CY:76:A:O2'	26:DA:2394:C:N3	2.22	0.73
1:CA:1027:C:C4	1:CA:1034:G:N1	2.56	0.73
26:DA:2576:G:O2'	26:DA:2579:C:OP2	2.07	0.73
26:DA:2794:C:N4	26:DA:2802:G:O6	2.17	0.73
1:AA:596:C:OP2	61:AA:4068:HOH:O	2.06	0.73
31:DG:64:THR:HB	31:DG:94:LEU:HD21	1.69	0.73
1:AA:974:A:OP2	14:AN:29:ARG:NH2	2.22	0.73
28:BD:69:ARG:NH2	28:BD:128:GLY:O	2.21	0.73
19:AS:65:ASN:O	51:B4:58:ARG:NH1	2.21	0.73
1:CA:73:G:H1	1:CA:96:U:H3	1.37	0.72
26:DA:2683:C:OP1	40:DT:53:ARG:NH2	2.21	0.72
1:CA:1053:G:N7	1:CA:1200:C:H5''	2.04	0.72
4:CD:31:CYS:HB2	58:CD:501:SF4:S3	2.29	0.72
4:CD:18:LYS:NZ	4:CD:31:CYS:SG	2.62	0.72
26:DA:1970:A:OP1	61:DA:3907:HOH:O	2.07	0.72
46:BZ:69:THR:HG22	46:BZ:90:VAL:HA	1.71	0.72
26:BA:1019:U:HO2'	26:BA:1021:A:H2	1.35	0.72
26:DA:1653:G:H3'	38:DR:2:ARG:HD3	1.71	0.72
37:DQ:22:LYS:O	46:DZ:78:LYS:NZ	2.21	0.72
26:DA:1316:U:H2'	26:DA:1317:A:H8	1.55	0.72
1:CA:72:C:N4	1:CA:97:G:H1	1.85	0.72
1:CA:76:C:N3	1:CA:93:G:C2	2.57	0.72
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.07	0.72
26:BA:743:G:N7	61:BA:4318:HOH:O	2.22	0.72
42:BV:40:LEU:HB2	42:BV:46:VAL:HG13	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BW:34:ASN:OD1	43:BW:37:ARG:NH1	2.23	0.72
26:DA:1851:U:O4	61:DA:4296:HOH:O	2.06	0.72
12:CL:70:ILE:HG12	12:CL:100:ILE:HD12	1.72	0.72
46:BZ:107:THR:HG21	46:BZ:112:ARG:HH21	1.55	0.72
1:CA:662:G:O2'	1:CA:836:G:OP1	2.07	0.72
47:B0:27:GLU:HG3	47:B0:68:GLU:HA	1.70	0.72
1:CA:839:U:H5''	1:CA:840:C:H5	1.55	0.72
1:CA:839:U:OP2	1:CA:840:C:N4	2.23	0.72
26:DA:2130:U:H4'	26:DA:2133:G:H4'	1.71	0.72
1:AA:45:U:H2'	1:AA:46:G:C8	2.25	0.72
16:CP:59:TRP:HA	16:CP:62:VAL:HG12	1.70	0.72
26:DA:1359:A:C6	26:DA:1372:U:C4	2.77	0.72
8:AH:29:SER:HB2	8:AH:32:LYS:HG3	1.72	0.72
27:DB:29:A:C2	27:DB:30:C:H5	2.06	0.72
26:DA:2447:G:N2	26:DA:2450:A:OP2	2.23	0.72
42:BV:76:LYS:HB2	42:BV:81:TYR:HB3	1.69	0.72
1:CA:72:C:N4	1:CA:97:G:C6	2.57	0.72
1:CA:989:C:O2	1:CA:1216:G:N2	2.19	0.72
28:DD:148:GLU:HB2	28:DD:151:LYS:HD2	1.70	0.72
1:CA:1414:U:H3	1:CA:1486:G:H1	1.37	0.72
24:CX:19:G:N2	24:CX:56:C:N3	2.37	0.71
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.72	0.71
1:AA:1305:G:H5''	21:AU:4:GLY:HA3	1.70	0.71
27:BB:8:U:O3'	39:BS:25:ARG:NH2	2.20	0.71
26:BA:2336:A:H61	47:B0:43:THR:HG22	1.55	0.71
26:DA:2127:G:N1	26:DA:2161:C:O2	2.22	0.71
1:AA:978:A:O2'	1:AA:1322:C:N3	2.22	0.71
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.24	0.71
27:DB:3:C:H2'	27:DB:4:C:C6	2.25	0.71
36:BP:42:SER:O	61:BP:3102:HOH:O	2.06	0.71
26:DA:2287:A:H62	26:DA:2344:U:H3	1.39	0.71
26:DA:2526:G:O2'	56:D9:1:MET:N	2.20	0.71
1:AA:708:C:OP1	11:AK:85:ARG:NH2	2.23	0.71
31:DG:47:LYS:HE2	31:DG:48:GLU:H	1.56	0.71
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.71	0.71
26:BA:1174:A:H1'	26:BA:1175:U:H5''	1.73	0.71
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.24	0.71
1:AA:664:G:H22	1:AA:741:G:H1	1.38	0.71
26:BA:2815:C:H5'	52:B5:29:THR:HG21	1.71	0.71
27:BB:48:A:H4'	39:BS:95:HIS:HD2	1.55	0.71
51:B4:64:GLY:O	51:B4:66:SER:N	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:71:SER:HA	9:CI:74:ILE:HD12	1.72	0.71
26:DA:1637:A:OP2	61:DA:4392:HOH:O	2.07	0.71
39:BS:15:ARG:O	39:BS:19:LYS:HG2	1.91	0.71
24:CX:19:G:H1	24:CX:56:C:H42	1.39	0.71
1:CA:156:G:N2	1:CA:165:C:O2	2.19	0.71
46:DZ:23:LYS:NZ	46:DZ:40:ASP:OD1	2.23	0.71
1:CA:1027:C:N3	1:CA:1034:G:C2	2.59	0.70
1:CA:1399:C:H4'	1:CA:1400:C:H5''	1.73	0.70
1:CA:708:C:H2'	1:CA:709:G:H8	1.55	0.70
9:CI:42:ARG:NH1	9:CI:75:ASP:OD1	2.24	0.70
26:BA:245:G:O6	55:B8:8:LYS:NZ	2.22	0.70
26:DA:587:C:OP2	36:DP:21:ARG:NH2	2.23	0.70
1:AA:1304:G:OP2	61:AA:4108:HOH:O	2.09	0.70
46:DZ:55:HIS:HE1	46:DZ:135:GLU:HG3	1.57	0.70
26:BA:2124:G:H1	26:BA:2174:C:N4	1.88	0.70
3:AC:11:ARG:HB3	3:AC:15:THR:HB	1.72	0.70
1:AA:221:C:H2'	1:AA:222:U:H6	1.57	0.70
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.73	0.70
1:CA:138:G:H2'	1:CA:139:G:H5''	1.74	0.70
1:CA:76:C:C2	1:CA:93:G:N2	2.60	0.70
1:AA:159:G:O2'	1:AA:161:A:N7	2.24	0.70
4:AD:13:ARG:NH1	4:AD:38:TYR:O	2.24	0.70
50:D3:7:LYS:HG3	50:D3:34:GLU:HG3	1.73	0.70
1:AA:560:U:O2'	1:AA:561:U:OP2	2.10	0.70
30:DF:122:LYS:NZ	30:DF:152:GLU:OE2	2.24	0.70
1:AA:242:C:N4	1:AA:284:G:O6	2.20	0.70
26:BA:187:G:OP2	61:BA:4313:HOH:O	2.08	0.70
1:AA:316:G:OP2	1:AA:351:G:O2'	2.09	0.70
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.56	0.70
26:BA:1551:C:OP2	61:BA:4322:HOH:O	2.08	0.70
1:AA:60:A:N1	1:AA:107:G:O2'	2.21	0.70
26:BA:2618:G:H21	29:BE:150:VAL:HG21	1.56	0.70
26:DA:1417:C:OP2	61:DA:4033:HOH:O	2.08	0.70
38:DR:103:ARG:NH1	38:DR:108:GLY:O	2.24	0.70
1:AA:363:A:OP2	12:AL:34:ARG:NH1	2.24	0.70
7:CG:109:ASN:HA	7:CG:119:ARG:HH21	1.55	0.70
1:AA:1464:G:OP2	40:BT:111:ARG:NH2	2.23	0.70
7:CG:99:LEU:HD23	7:CG:102:ARG:HH12	1.56	0.70
8:AH:21:LYS:O	8:AH:65:TYR:OH	2.08	0.70
1:AA:1288:A:N3	1:AA:1352:C:O2'	2.22	0.70
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2107:C:H42	26:DA:2182:G:H1	1.40	0.70
26:DA:827:U:OP1	61:DA:4174:HOH:O	2.10	0.70
1:AA:661:G:H1	1:AA:744:C:H42	1.39	0.70
26:DA:1183:G:O3'	50:D3:29:ARG:NH1	2.24	0.70
26:BA:2107:C:H42	26:BA:2182:G:H1	1.40	0.70
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.36	0.70
20:AT:9:ASN:HD22	20:AT:10:LEU:H	1.40	0.70
1:CA:1034:G:H8	1:CA:1034:G:O5'	1.73	0.70
31:DG:41:GLN:HG3	31:DG:60:LEU:HD21	1.74	0.70
1:AA:1012:U:O2	1:AA:1017:G:O6	2.10	0.70
26:DA:1269:A:N7	61:DA:4369:HOH:O	2.25	0.70
26:DA:1300:U:H4'	26:DA:1301:A:H5''	1.74	0.70
1:CA:977:A:O2'	1:CA:981:U:N3	2.25	0.70
1:AA:1097:C:O2'	1:AA:1169:A:N3	2.20	0.70
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.74	0.70
24:AX:5:G:H1	24:AX:68:C:N4	1.89	0.69
33:BI:38:LEU:HD13	33:BI:40:THR:HG22	1.72	0.69
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.73	0.69
26:BA:1786:A:H1'	26:BA:1938:A:N6	2.07	0.69
26:DA:2659:G:O2'	26:DA:2661:G:N7	2.25	0.69
38:BR:15:SER:OG	61:BR:301:HOH:O	2.08	0.69
1:CA:1120:G:O6	1:CA:1154:G:N2	2.25	0.69
1:CA:1030(C):G:H2'	1:CA:1030(D):A:C8	2.27	0.69
26:DA:1803:A:O2'	28:DD:259:THR:HG21	1.92	0.69
26:DA:1314:C:OP1	61:DA:4077:HOH:O	2.10	0.69
27:DB:3:C:H2'	27:DB:4:C:H6	1.55	0.69
26:BA:271(A):A:N7	26:BA:271(W):G:N2	2.40	0.69
26:BA:331:A:N1	61:BA:4015:HOH:O	2.25	0.69
2:AB:15:VAL:O	2:AB:16:HIS:ND1	2.24	0.69
1:AA:78:G:C2	1:AA:91:C:N3	2.60	0.69
26:DA:1333:C:OP2	61:DA:3859:HOH:O	2.10	0.69
26:BA:2756:U:O2'	61:BA:4010:HOH:O	2.10	0.69
26:DA:2198:A:O2'	26:DA:2224:G:N2	2.26	0.69
33:DI:129:THR:HG22	33:DI:139:GLN:HE22	1.57	0.69
1:AA:148:G:O6	1:AA:174:C:N4	2.25	0.69
26:BA:400:G:N7	61:BA:4780:HOH:O	2.24	0.69
26:BA:2187:G:O2'	26:BA:2188:C:OP1	2.10	0.69
1:AA:1009:G:H1	1:AA:1020:U:H3	0.76	0.69
26:DA:574:C:N3	29:DE:145:LYS:NZ	2.40	0.69
1:AA:1086:U:H3	1:AA:1099:G:H22	1.39	0.69
31:DG:43:LEU:HD21	31:DG:153:ARG:HG2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BE:52:LEU:HD12	29:BE:77:ILE:HD11	1.73	0.69
19:AS:12:ASP:OD2	19:AS:37:ARG:NH1	2.24	0.69
26:DA:2227:A:OP2	61:DA:4135:HOH:O	2.10	0.69
1:AA:148:G:N2	1:AA:175:C:C2	2.61	0.69
12:AL:34:ARG:NH2	61:AL:201:HOH:O	2.26	0.69
1:CA:701:C:OP1	1:CA:702:A:O2'	2.10	0.69
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.25	0.69
8:AH:86:ILE:HG21	8:AH:133:LEU:HD13	1.75	0.69
48:D1:50:ARG:HG2	48:D1:59:THR:HB	1.72	0.69
24:AX:28:C:N4	24:AX:42:G:H1	1.88	0.69
26:BA:2156:G:N2	26:BA:2158:A:H62	1.90	0.69
46:DZ:126:VAL:HG11	46:DZ:161:VAL:HG23	1.73	0.69
1:CA:870:U:OP2	61:CA:4089:HOH:O	2.10	0.69
49:B2:28:LYS:NZ	49:B2:56:GLN:OE1	2.26	0.69
23:CW:76:PPU:HN1	24:CX:76:31H:HN3'	1.39	0.69
26:BA:833:U:O2	36:BP:55:ARG:NH2	2.26	0.69
26:BA:548:A:O2'	26:BA:549:G:OP1	2.11	0.69
28:BD:108:PRO:HB3	28:BD:143:HIS:CE1	2.28	0.69
1:CA:437:U:H5'	4:CD:155:LEU:HD21	1.75	0.69
1:CA:1400:C:O4'	22:CV:18:G:N3	2.27	0.68
47:D0:14:ARG:NH1	61:D0:102:HOH:O	2.26	0.68
30:DF:110:LEU:HD21	30:DF:181:LEU:HG	1.75	0.68
29:BE:143:ASN:HD22	29:BE:147:PRO:HD3	1.57	0.68
1:AA:1311:G:H1	1:AA:1326:C:H42	1.42	0.68
26:DA:2313:C:H2'	26:DA:2314:C:H6	1.58	0.68
26:DA:2136:C:O2'	26:DA:2137:C:H6	1.76	0.68
1:AA:78:G:H1	1:AA:91:C:N4	1.91	0.68
26:DA:2128:C:H5'	26:DA:2173:A:C2	2.27	0.68
26:DA:2445:G:OP1	30:DF:74:ARG:NH2	2.27	0.68
26:BA:2406:U:OP1	61:BA:4116:HOH:O	2.11	0.68
13:AM:11:ARG:HA	13:AM:45:VAL:HB	1.73	0.68
5:AE:102:ALA:O	5:AE:107:ARG:NH1	2.26	0.68
1:CA:72:C:C4	1:CA:97:G:N1	2.56	0.68
13:CM:4:ILE:HG23	13:CM:22:ILE:HD11	1.75	0.68
26:DA:1406:U:O4	26:DA:1596:A:N6	2.18	0.68
26:DA:2376:A:N3	39:DS:106:ARG:NH2	2.41	0.68
31:DG:114:ILE:HG23	31:DG:136:ARG:HH22	1.58	0.68
1:CA:376:G:H1	1:CA:387:U:H3	1.41	0.68
26:BA:1371:G:H2'	26:BA:1372:U:H5	1.59	0.68
1:AA:253:U:OP1	17:AQ:67:LYS:NZ	2.26	0.68
36:BP:121:LYS:HG2	36:BP:122:PRO:HD2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2400:G:O6	61:BA:4049:HOH:O	2.09	0.68
1:AA:789:U:O2'	1:AA:791:G:N7	2.21	0.68
19:AS:9:VAL:HG21	51:B4:61:ARG:HH21	1.58	0.68
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.57	0.68
2:AB:19:HIS:NE2	2:AB:206:ASP:OD2	2.26	0.68
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.27	0.68
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.27	0.68
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.75	0.68
38:DR:33:ARG:NH1	38:DR:115:GLU:OE2	2.26	0.68
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.10	0.68
1:CA:1256:A:H61	1:CA:1278:U:C1'	2.04	0.68
26:BA:370:G:OP2	61:BA:3938:HOH:O	2.12	0.68
1:CA:154:C:C2'	1:CA:155:C:H5'	2.23	0.68
26:BA:271(R):G:H2'	26:BA:271(S):G:H5''	1.74	0.68
26:BA:2111:C:OP2	26:BA:2145:C:N4	2.26	0.68
16:CP:53:VAL:HG13	16:CP:79:VAL:HG22	1.76	0.68
17:CQ:60:ILE:HD12	17:CQ:74:LEU:HG	1.76	0.68
28:DD:232:PRO:O	61:DD:402:HOH:O	2.12	0.68
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.59	0.68
26:DA:1169:G:N2	26:DA:1180:C:N3	2.40	0.68
26:BA:2791:C:N3	26:BA:2805:G:N2	2.36	0.68
1:AA:159:G:N2	1:AA:162:A:OP2	2.26	0.68
46:BZ:45:ASP:OD2	46:BZ:49:ARG:NH1	2.27	0.68
4:CD:172:PRO:HB2	4:CD:187:ARG:HH21	1.58	0.68
12:CL:71:PRO:O	12:CL:102:ARG:NH1	2.23	0.68
46:DZ:72:ARG:NH2	46:DZ:97:GLU:O	2.27	0.68
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.28	0.68
1:CA:1400:C:OP2	22:CV:18:G:N1	2.26	0.67
1:AA:993:G:O6	1:AA:1045:C:N4	2.23	0.67
37:BQ:110:THR:HG23	37:BQ:113:GLN:HB2	1.77	0.67
28:DD:228:PRO:O	61:DD:401:HOH:O	2.12	0.67
26:BA:2810:A:N6	26:BA:2891:G:O2'	2.26	0.67
26:BA:1204:A:H2	26:BA:1241:A:H62	1.40	0.67
1:CA:72:C:N4	1:CA:73:G:C6	2.62	0.67
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.27	0.67
26:DA:2805:G:H2'	26:DA:2807:G:C8	2.29	0.67
37:BQ:30:GLY:HA2	37:BQ:107:ALA:HB2	1.75	0.67
33:DI:40:THR:HG23	33:DI:43:ASN:HD21	1.59	0.67
36:DP:96:THR:H	36:DP:99:LEU:HD21	1.59	0.67
26:DA:1695:G:N7	28:DD:14:ARG:NH2	2.43	0.67
26:BA:2120:G:N2	26:BA:2178:C:N3	2.41	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:801:G:O6	30:BF:53:THR:OG1	2.12	0.67
1:CA:1055:A:N7	1:CA:1200:C:N4	2.42	0.67
26:BA:330:A:H2	26:BA:1210:A:HO2'	1.40	0.67
19:CS:53:ASN:HB2	19:CS:77:THR:HA	1.76	0.67
33:BI:106:GLY:HA2	33:BI:107:VAL:HG22	1.76	0.67
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.27	0.67
1:AA:707:C:OP1	11:AK:85:ARG:NH1	2.28	0.67
26:BA:2239:G:OP2	28:BD:244:ARG:NH1	2.22	0.67
26:DA:1670:C:O2	29:DE:129:HIS:NE2	2.27	0.67
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.30	0.67
1:AA:184:G:H2'	1:AA:185:A:C8	2.28	0.67
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.42	0.67
26:DA:2659:G:N2	26:DA:2662:A:OP2	2.27	0.67
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.09	0.67
26:BA:1333:C:OP2	61:BA:4097:HOH:O	2.13	0.67
26:BA:2141:G:C2	26:BA:2142:C:H1'	2.30	0.67
10:AJ:5:ARG:NH2	10:AJ:73:ASP:OD2	2.28	0.67
27:DB:49:C:OP1	39:DS:97:ARG:N	2.27	0.67
1:AA:975:A:H5'	1:AA:975:A:H8	1.60	0.67
1:AA:661:G:N2	1:AA:744:C:N3	2.40	0.67
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.59	0.67
26:BA:740:U:OP2	61:BA:4541:HOH:O	2.12	0.67
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.27	0.67
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.26	0.67
26:DA:2136:C:O2'	26:DA:2137:C:O4'	2.11	0.67
40:BT:65:LYS:HE2	40:BT:67:SER:HB2	1.77	0.67
20:AT:56:MET:HG3	20:AT:84:LEU:HD22	1.76	0.67
1:AA:1456:G:O6	20:AT:54:LYS:NZ	2.28	0.67
26:BA:2334:G:O6	47:B0:74:ARG:NH2	2.28	0.67
32:DH:124:GLU:HB2	32:DH:132:ARG:HB3	1.77	0.67
26:BA:1250:G:OP2	36:BP:21:ARG:NH1	2.27	0.67
36:BP:62:LEU:O	55:B8:13:ARG:HD3	1.95	0.67
26:BA:962:G:OP1	61:BA:4651:HOH:O	2.13	0.67
26:DA:2651:C:H42	26:DA:2669:G:H1	1.43	0.67
30:DF:21:ALA:HB3	30:DF:22:ALA:HA	1.75	0.67
1:AA:103:C:O2'	1:AA:172:A:N1	2.27	0.67
1:AA:692:U:O2'	1:AA:694:A:N7	2.24	0.67
26:BA:2722:G:OP2	61:BA:3994:HOH:O	2.12	0.67
26:DA:1038:C:H42	26:DA:1117:G:H1	1.43	0.67
26:DA:82:G:N1	26:DA:103:A:OP2	2.23	0.67
1:CA:601:C:H2'	1:CA:602:A:C8	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1153:C:H42	1:CA:1154:G:H21	1.41	0.66
1:AA:598:U:O4	61:AA:4068:HOH:O	2.09	0.66
1:AA:975:A:H4'	1:AA:976:G:H5''	1.77	0.66
26:BA:154:G:O6	26:BA:172:C:N4	2.18	0.66
25:AY:76:A:N6	26:BA:2422:A:O4'	2.28	0.66
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.23	0.66
1:AA:652:U:O4	1:AA:752:G:O2'	2.10	0.66
1:AA:757:U:O2'	1:AA:879:C:O2	2.13	0.66
1:CA:642:A:N3	8:CH:113:SER:OG	2.28	0.66
1:CA:1255:G:OP2	10:CJ:45:ARG:NH2	2.27	0.66
26:BA:2176:A:H2'	26:BA:2177:C:C6	2.30	0.66
52:D5:16:ARG:NH1	52:D5:17:ASP:OD1	2.28	0.66
1:AA:346:G:OP1	40:BT:41:ARG:NH1	2.28	0.66
1:CA:21:G:OP1	61:CA:4042:HOH:O	2.13	0.66
13:CM:90:LEU:HA	13:CM:93:ARG:HD2	1.77	0.66
1:CA:864:A:H5'	5:CE:86:ALA:HB2	1.77	0.66
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.78	0.66
1:CA:673:G:H2'	1:CA:674:G:C8	2.30	0.66
26:BA:243:U:OP1	55:B8:6:THR:OG1	2.11	0.66
1:AA:56:U:H2'	1:AA:57:G:C8	2.29	0.66
1:AA:6:G:H4'	1:AA:298:A:H4'	1.77	0.66
2:CB:71:VAL:HG12	2:CB:170:GLU:HG2	1.78	0.66
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.77	0.66
46:DZ:111:VAL:HG21	46:DZ:117:LEU:HB2	1.77	0.66
26:DA:2504:U:OP2	61:DA:4075:HOH:O	2.12	0.66
44:DX:8:ILE:O	49:D2:36:ARG:NH2	2.27	0.66
26:BA:2779:U:OP1	61:BA:4671:HOH:O	2.13	0.66
26:DA:2494:G:OP2	61:DA:4386:HOH:O	2.13	0.66
26:BA:800:A:H8	26:BA:800:A:OP1	1.78	0.66
26:BA:2125:G:N1	26:BA:2172:U:OP1	2.29	0.66
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.77	0.66
49:D2:22:GLU:OE2	49:D2:68:ARG:NH2	2.28	0.66
3:AC:16:ARG:NH2	3:AC:183:ASP:OD1	2.29	0.66
29:BE:123:ALA:O	61:BE:3101:HOH:O	2.13	0.66
26:DA:2123:G:H1	26:DA:2175:C:H42	1.43	0.66
1:CA:70:G:N2	1:CA:99:U:O2	2.21	0.66
26:DA:2141:G:O4'	26:DA:2151:G:N2	2.29	0.66
1:AA:574:A:OP2	61:AA:4006:HOH:O	2.12	0.66
26:DA:468:G:N7	54:D7:39:ARG:NH2	2.40	0.66
35:BO:63:VAL:HG12	35:BO:106:LEU:HD11	1.76	0.66
42:DV:72:VAL:HG22	42:DV:85:LYS:HB3	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BE:8:LYS:NZ	29:BE:190:GLY:O	2.24	0.66
1:AA:1309:G:OP1	13:AM:88:ARG:NH1	2.29	0.66
31:DG:171:ALA:O	31:DG:175:LEU:N	2.23	0.66
36:BP:50:ARG:HH21	55:B8:7:HIS:HD2	1.42	0.66
19:AS:68:GLY:N	51:B4:58:ARG:HH21	1.94	0.66
26:DA:1993:U:OP2	61:DA:4451:HOH:O	2.13	0.66
26:DA:1665:A:OP2	61:DA:4367:HOH:O	2.14	0.66
26:DA:2736:G:N2	26:DA:2768:C:O2	2.15	0.66
26:BA:2155:G:H2'	26:BA:2156:G:O4'	1.95	0.66
27:DB:22:U:H3	27:DB:61:G:H1	1.44	0.66
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.60	0.66
26:DA:336:C:O2'	45:DY:35:TYR:OH	2.12	0.66
26:BA:963:U:OP1	61:BA:3878:HOH:O	2.13	0.66
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.08	0.66
40:DT:51:ARG:HG3	40:DT:98:LYS:HD2	1.78	0.66
1:CA:1400:C:C6	22:CV:18:G:N3	2.64	0.66
1:CA:1154:G:N7	1:CA:1155:G:C8	2.64	0.66
26:DA:2313:C:H2'	26:DA:2314:C:C6	2.31	0.66
1:AA:976:G:H5'	1:AA:1358:U:O2'	1.96	0.66
26:DA:271(L):U:OP1	33:DI:50:ARG:NH2	2.28	0.66
26:BA:1324:G:N7	61:BA:4100:HOH:O	2.29	0.66
13:CM:13:LYS:NZ	13:CM:21:TYR:OH	2.25	0.66
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.77	0.65
27:DB:54:G:H21	31:DG:29:TRP:HZ2	1.42	0.65
26:DA:2815:C:H5'	52:D5:29:THR:HG21	1.76	0.65
5:CE:78:HIS:HA	8:CH:105:ARG:HG3	1.77	0.65
32:DH:8:PRO:HB3	32:DH:51:ARG:HG2	1.78	0.65
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.29	0.65
26:BA:247:G:OP2	26:BA:249:C:N4	2.28	0.65
29:BE:79:ARG:NE	61:BE:3113:HOH:O	2.19	0.65
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.78	0.65
24:CX:76:31H:OP2	61:CX:3101:HOH:O	2.14	0.65
38:DR:56:LYS:NZ	38:DR:90:ARG:O	2.29	0.65
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.78	0.65
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.95	0.65
26:BA:1342:A:OP2	61:BA:4096:HOH:O	2.13	0.65
7:AG:126:ASP:OD1	7:AG:131:LYS:NZ	2.29	0.65
13:AM:67:GLU:OE2	13:AM:71:ARG:NH2	2.28	0.65
38:BR:67:LEU:HD13	38:BR:76:VAL:HG21	1.77	0.65
26:DA:746:A:N7	61:DA:4449:HOH:O	2.29	0.65
1:CA:975:A:H5'	1:CA:975:A:H8	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1014:A:H1'	19:CS:34:TRP:HB2	1.79	0.65
20:AT:9:ASN:HD22	20:AT:10:LEU:N	1.93	0.65
1:AA:1262:C:N3	1:AA:1273:G:O6	2.29	0.65
26:BA:885:C:H3'	26:BA:886:C:H5''	1.77	0.65
26:BA:356:G:H2'	26:BA:357:A:H8	1.61	0.65
1:CA:753:A:OP1	15:CO:69:TYR:OH	2.12	0.65
26:DA:1031:G:H21	56:D9:36:GLN:HE22	1.43	0.65
28:BD:132:PRO:HD3	28:BD:190:TYR:CZ	2.32	0.65
26:BA:278:A:O2'	26:BA:279:C:OP1	2.14	0.65
26:BA:1184:G:H5'	50:B3:29:ARG:HH11	1.60	0.65
26:BA:2852:G:OP1	61:BA:4891:HOH:O	2.13	0.65
1:CA:903:G:OP1	61:CA:4008:HOH:O	2.14	0.65
26:DA:2698:U:H2'	26:DA:2699:C:C6	2.32	0.65
32:BH:149:ARG:NH1	32:BH:167:GLU:OE2	2.29	0.65
24:CX:31:G:C8	24:CX:32:5MC:HM52	2.32	0.65
1:CA:1190:G:OP1	3:CC:5:ILE:N	2.25	0.65
19:CS:9:VAL:HB	51:D4:67:TYR:HD2	1.60	0.65
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.78	0.65
1:CA:1012:U:O2	1:CA:1017:G:O6	2.14	0.65
1:AA:1261:A:H3'	1:AA:1262:C:H6	1.61	0.65
21:AU:5:ASP:OD2	61:AU:101:HOH:O	2.14	0.65
24:CX:48:C:O2'	24:CX:59:A:H1'	1.97	0.65
29:DE:56:PRO:HG3	29:DE:74:PRO:HG2	1.77	0.65
1:AA:580:U:OP2	61:AA:4021:HOH:O	2.14	0.65
1:AA:966:G:H21	9:AI:127:LYS:HZ1	1.45	0.65
4:CD:53:ASP:HB3	4:CD:57:ARG:HH12	1.62	0.65
51:B4:68:ARG:HD2	51:B4:69:LYS:H	1.62	0.65
26:BA:1187:G:H5''	42:BV:81:TYR:CE1	2.31	0.65
32:DH:90:LYS:HD3	32:DH:159:GLU:HG2	1.79	0.65
3:AC:8:ILE:HD13	3:AC:184:TYR:HB3	1.78	0.65
13:CM:65:LYS:HB3	51:D4:50:VAL:HG11	1.77	0.65
55:D8:33:ASN:HA	55:D8:36:LYS:HD2	1.79	0.65
1:AA:1030:C:H3'	1:AA:1030(A):G:H4'	1.79	0.65
4:AD:23:GLY:HA3	4:AD:112:VAL:HG12	1.79	0.65
13:AM:58:GLU:O	13:AM:62:ASN:ND2	2.30	0.65
2:AB:69:LEU:HD13	2:AB:91:PRO:HB2	1.79	0.65
50:B3:10:LYS:NZ	50:B3:15:TYR:OH	2.28	0.64
9:CI:121:ARG:NH1	9:CI:122:ALA:O	2.31	0.64
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.32	0.64
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.79	0.64
9:CI:112:LYS:NZ	9:CI:116:LYS:O	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DO:19:ILE:HG22	35:DO:43:VAL:HA	1.80	0.64
26:BA:529:A:OP2	34:BN:114:ARG:NH2	2.29	0.64
32:BH:98:LEU:HD13	32:BH:125:VAL:HG23	1.79	0.64
26:DA:458:G:O2'	26:DA:469:G:O6	2.13	0.64
1:CA:405:U:O4	4:CD:2:GLY:N	2.30	0.64
26:DA:1169:G:H1	26:DA:1180:C:N4	1.92	0.64
13:CM:93:ARG:HD3	26:DA:888:C:OP1	1.97	0.64
26:DA:2363:C:O2	47:D0:39:ARG:NH2	2.29	0.64
1:CA:827:U:H2'	1:CA:859:A:H61	1.62	0.64
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.80	0.64
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.20	0.64
26:BA:1823:G:OP1	28:BD:54:ARG:NH1	2.31	0.64
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.97	0.64
23:AW:76:PPU:H103	26:BA:2584:U:H5'	1.78	0.64
27:DB:86:G:N1	27:DB:91:C:N3	2.34	0.64
26:DA:514:A:N3	26:DA:581:C:O2'	2.26	0.64
26:DA:2779:U:H4'	26:DA:2780:G:H5''	1.78	0.64
36:DP:42:SER:O	61:DP:302:HOH:O	2.15	0.64
26:BA:1252:G:OP1	41:BU:36:ARG:NH2	2.30	0.64
26:DA:1971:A:N1	61:DA:3924:HOH:O	2.30	0.64
24:CX:6:G:H1	24:CX:67:C:N4	1.94	0.64
26:BA:2158:A:H2'	26:BA:2158:A:N3	2.12	0.64
1:CA:600:C:H2'	1:CA:601:C:C6	2.33	0.64
27:BB:102:A:N7	61:BB:4020:HOH:O	2.30	0.64
2:AB:121:LEU:HD13	2:AB:126:GLU:HG2	1.80	0.64
26:BA:2151:G:H2'	26:BA:2152:G:C8	2.32	0.64
1:AA:1392:G:N2	1:AA:1502:A:H8	1.95	0.64
26:BA:1815:A:OP2	28:BD:54:ARG:NH2	2.31	0.64
1:AA:377:G:OP1	16:AP:3:LYS:HD2	1.97	0.64
26:BA:1769:G:O2'	26:BA:1958:C:OP1	2.09	0.64
24:AX:55:PSU:O2'	24:AX:57:A:N7	2.24	0.64
26:DA:2408:U:H2'	26:DA:2409:G:C8	2.32	0.64
26:BA:11:G:H2'	26:BA:12:U:H5''	1.78	0.64
1:CA:76:C:N4	1:CA:93:G:C2	2.66	0.64
1:CA:582:U:OP1	15:CO:68:ARG:NH1	2.29	0.64
26:BA:252:G:P	36:BP:50:ARG:HH12	2.21	0.64
3:CC:11:ARG:HB3	3:CC:15:THR:HB	1.79	0.64
26:DA:1276:A:O2'	38:DR:12:ARG:NH2	2.26	0.64
26:BA:1800:C:OP2	28:BD:183:ARG:NH2	2.31	0.64
26:DA:1005:C:H2'	26:DA:1006:C:C6	2.32	0.64
14:AN:3:ARG:HH21	14:AN:3:ARG:HB3	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2741:A:OP1	56:B9:22:ARG:NH2	2.27	0.64
27:BB:33:G:H5'	31:BG:2:PRO:HD3	1.79	0.64
37:DQ:65:PHE:HB2	37:DQ:105:GLU:HB2	1.80	0.64
26:DA:362:U:H1'	26:DA:363:G:H5''	1.80	0.64
26:DA:910:A:N3	26:DA:2264:C:O2'	2.26	0.64
26:BA:2113:U:H3	26:BA:2170:A:H61	1.44	0.64
1:CA:1277:C:HO2'	1:CA:1279:A:H1'	1.63	0.64
1:CA:1395:C:O2	1:CA:1398:A:O2'	2.16	0.64
31:DG:20:ILE:HA	31:DG:25:TYR:HD1	1.63	0.64
46:DZ:53:ILE:HD13	46:DZ:99:TYR:HB2	1.80	0.64
1:CA:975:A:N6	1:CA:1367:C:O4'	2.26	0.63
1:AA:709:G:H2'	1:AA:710:G:H5'	1.80	0.63
26:BA:1250:G:N7	36:BP:18:ARG:NH2	2.46	0.63
1:CA:302:G:O2'	1:CA:556:C:H5''	1.98	0.63
8:CH:135:CYS:SG	8:CH:136:GLU:N	2.71	0.63
26:DA:1385:G:O2'	26:DA:1396:U:O2	2.15	0.63
1:CA:967:C:H3'	1:CA:968:A:H2'	1.79	0.63
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.63	0.63
1:AA:175:C:O5'	1:AA:175:C:H6	1.82	0.63
1:AA:709:G:C2'	1:AA:710:G:H5'	2.27	0.63
1:CA:708:C:OP1	11:CK:85:ARG:NH2	2.27	0.63
26:BA:2384:G:OP2	47:B0:55:ARG:NH1	2.26	0.63
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.81	0.63
26:BA:1676:A:N7	61:BA:4171:HOH:O	2.30	0.63
1:CA:1120:G:C6	1:CA:1154:G:N2	2.67	0.63
1:AA:1366:C:O2'	10:AJ:60:ARG:NH2	2.31	0.63
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.32	0.63
6:CF:11:ASN:HB3	6:CF:14:LEU:HG	1.79	0.63
26:DA:1019:U:OP1	26:DA:1035:U:O2'	2.15	0.63
28:BD:148:GLU:HB2	28:BD:151:LYS:HD2	1.79	0.63
26:BA:71:A:OP2	26:BA:71:A:H3'	1.98	0.63
15:AO:5:LYS:HD2	15:AO:5:LYS:H	1.63	0.63
1:AA:600:C:H2'	1:AA:601:C:H6	1.63	0.63
26:BA:2181:G:O2'	26:BA:2182:G:OP1	2.16	0.63
16:CP:17:TYR:HE2	16:CP:41:PRO:HG3	1.62	0.63
26:BA:1721:G:H2'	26:BA:1740:G:O6	1.99	0.63
46:DZ:10:ARG:NH2	46:DZ:26:GLY:O	2.30	0.63
26:DA:1356:G:OP1	61:DA:4383:HOH:O	2.16	0.63
1:CA:1011:G:H1	1:CA:1018:C:H42	1.47	0.63
1:AA:96:U:O2'	1:AA:97:G:O4'	2.15	0.63
26:DA:1359:A:C6	26:DA:1360:A:C5	2.87	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:521:G:H4'	12:CL:73:GLU:HG2	1.80	0.63
29:DE:72:VAL:HA	29:DE:73:GLU:HB3	1.80	0.63
1:AA:545:C:OP2	4:AD:65:ARG:NH2	2.31	0.63
26:DA:588:U:OP2	61:DA:3879:HOH:O	2.16	0.63
26:DA:2138:C:H2'	26:DA:2139:C:H6	1.64	0.63
26:BA:2141:G:N7	26:BA:2151:G:N2	2.47	0.63
61:BA:4874:HOH:O	38:BR:3:HIS:NE2	2.30	0.63
26:DA:2801(A):A:N3	26:DA:2895:U:H1'	2.13	0.63
41:DU:83:LEU:HD12	41:DU:88:ILE:HB	1.81	0.63
1:CA:419:C:OP1	1:CA:513:C:O2'	2.12	0.63
26:DA:709:U:H2'	26:DA:710:G:C8	2.34	0.63
26:BA:2518:A:OP2	61:BA:4227:HOH:O	2.15	0.63
31:BG:37:VAL:HG21	31:BG:103:LEU:HD21	1.80	0.63
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.39	0.63
26:DA:2136:C:HO2'	26:DA:2137:C:H6	1.47	0.63
1:AA:1125:U:H4'	10:AJ:5:ARG:HH22	1.64	0.63
36:DP:126:VAL:HG12	36:DP:148:LEU:HD22	1.80	0.63
26:DA:2193:G:H2'	26:DA:2194:G:H8	1.64	0.63
1:AA:148:G:N1	1:AA:175:C:N3	2.47	0.63
1:AA:835:U:H3	1:AA:851:G:H1	1.47	0.63
35:DO:102:VAL:HB	35:DO:106:LEU:HD12	1.81	0.63
1:CA:60:A:OP1	1:CA:111:G:N2	2.30	0.63
30:BF:157:VAL:HB	30:BF:194:MET:HG2	1.79	0.63
4:CD:60:GLU:HG3	4:CD:198:VAL:HG13	1.80	0.63
26:BA:1798:U:OP2	28:BD:274:ARG:NH2	2.32	0.62
26:BA:249:C:O2	55:B8:12:LYS:NZ	2.29	0.62
31:DG:122:PRO:HG3	31:DG:180:PHE:HB3	1.79	0.62
31:DG:3:LEU:HD12	31:DG:5:VAL:HG12	1.81	0.62
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.81	0.62
27:DB:24:G:H5'	27:DB:25:A:H62	1.62	0.62
1:AA:826:C:O2	8:AH:15:ASN:ND2	2.32	0.62
26:DA:1429:G:H1'	26:DA:1568:G:H1'	1.81	0.62
1:CA:657:G:H4'	15:CO:28:GLN:HG2	1.81	0.62
26:BA:1243:G:O2'	36:BP:7:ARG:NH2	2.32	0.62
30:DF:184:TYR:CE2	30:DF:188:ARG:HD2	2.33	0.62
28:DD:108:PRO:HB3	28:DD:143:HIS:HE1	1.63	0.62
1:CA:890:G:O2'	1:CA:906:G:O6	2.15	0.62
26:BA:2319:G:N2	39:BS:3:ARG:HA	2.15	0.62
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.79	0.62
26:DA:2590:A:OP2	28:DD:238:GLY:HA2	1.99	0.62
26:DA:1817:G:OP1	28:DD:88:ARG:NH2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1316:U:H2'	26:DA:1317:A:C8	2.34	0.62
2:AB:185:ILE:HG23	2:AB:199:TYR:HB2	1.82	0.62
26:DA:2831:G:OP1	29:DE:58:ARG:NH2	2.29	0.62
30:DF:53:THR:HG23	30:DF:55:GLY:H	1.63	0.62
31:BG:64:THR:HB	31:BG:94:LEU:HD21	1.82	0.62
1:AA:946:A:H2'	1:AA:947:G:C8	2.35	0.62
18:CR:25:THR:O	18:CR:25:THR:OG1	2.15	0.62
9:AI:17:VAL:HG11	9:AI:81:ILE:HA	1.82	0.62
27:DB:17:C:O2	27:DB:67:G:N2	2.21	0.62
26:BA:1314:C:OP1	61:BA:4479:HOH:O	2.15	0.62
44:DX:53:LYS:HB3	44:DX:82:GLN:HB3	1.81	0.62
26:BA:1713:U:H2'	26:BA:1714:G:H8	1.63	0.62
1:CA:1362:C:H2'	1:CA:1363:C:H5''	1.82	0.62
24:CX:42:G:H2'	24:CX:43:A:H8	1.64	0.62
26:DA:1021:A:H62	26:DA:1141:U:H3	1.48	0.62
27:BB:91:C:OP2	37:BQ:16:ARG:NH1	2.32	0.62
26:BA:2303:G:O6	61:BA:3888:HOH:O	2.14	0.62
37:BQ:138:ASP:OD2	46:BZ:81:ARG:NH1	2.32	0.62
4:CD:162:LEU:HA	4:CD:165:MET:HB2	1.81	0.62
26:DA:1370:C:HO2'	26:DA:1811:G:HO2'	1.42	0.62
1:CA:975:A:H4'	1:CA:976:G:H5''	1.82	0.62
24:CX:60:U:H5'	24:CX:61:C:H5	1.63	0.62
26:DA:1230:C:H2'	26:DA:1231:G:H8	1.65	0.62
7:AG:80:VAL:HB	7:AG:85:TYR:HE2	1.63	0.62
27:BB:28:C:OP1	39:BS:31:SER:OG	2.11	0.62
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.14	0.62
54:B7:33:ARG:NH2	61:B7:201:HOH:O	2.26	0.62
26:DA:2001:A:H2'	26:DA:2002:G:C8	2.34	0.62
31:DG:7:LEU:HD23	31:DG:100:TRP:HE3	1.65	0.62
26:BA:2127:G:C6	26:BA:2162:G:N1	2.68	0.62
27:DB:56:G:OP1	31:DG:27:ASN:ND2	2.33	0.62
1:AA:662:G:H2'	1:AA:663:A:C8	2.34	0.62
27:DB:55:U:H4'	31:DG:28:VAL:HG22	1.82	0.62
9:AI:49:PRO:HG2	9:AI:81:ILE:HG23	1.81	0.62
28:BD:12:SER:HB3	28:BD:208:LYS:HB3	1.81	0.62
1:AA:1297:C:O2'	7:AG:114:ARG:NH2	2.31	0.62
25:AY:74:C:H4'	48:B1:23:LYS:HB2	1.81	0.62
26:DA:1857:G:O2'	26:DA:1885:A:N6	2.32	0.62
26:DA:1489:U:HO2'	26:DA:1490:A:H8	1.47	0.62
32:DH:97:ARG:HA	32:DH:125:VAL:HG11	1.81	0.62
1:CA:977:A:HO2'	1:CA:981:U:H3	1.44	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:958:U:OP2	37:BQ:14:ARG:NH1	2.33	0.62
37:DQ:135:ASP:OD2	46:DZ:49:ARG:NH2	2.31	0.62
1:CA:1240:U:C2	7:CG:32:ARG:HD3	2.34	0.62
1:AA:997:U:H3	1:AA:1044:A:N6	1.98	0.62
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.63	0.62
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.15	0.62
26:BA:1379:A:H4'	26:BA:1380:G:OP2	1.99	0.62
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.48	0.62
32:DH:4:ILE:HG22	32:DH:69:ARG:HG2	1.81	0.62
26:DA:953:A:OP1	37:DQ:18:LYS:NZ	2.33	0.62
26:DA:2074:U:H2'	26:DA:2075:U:C6	2.35	0.62
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.00	0.62
1:CA:1120:G:H8	1:CA:1120:G:O5'	1.82	0.62
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.82	0.62
28:DD:108:PRO:HB3	28:DD:143:HIS:CE1	2.35	0.62
26:DA:2857:G:N2	26:DA:2860:A:OP2	2.31	0.62
38:BR:55:ALA:HB2	38:BR:79:LEU:HD13	1.82	0.62
30:DF:101:LEU:O	30:DF:106:ARG:NH1	2.28	0.62
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.33	0.62
31:BG:144:ILE:HA	31:BG:148:MET:HE1	1.80	0.62
26:DA:195:A:OP1	36:DP:46:LYS:NZ	2.31	0.62
18:CR:74:ARG:HG3	18:CR:79:LEU:HB2	1.82	0.62
26:DA:570:G:H2'	26:DA:2030:A:C5	2.35	0.62
1:AA:346:G:C4	1:AA:347:G:H1'	2.35	0.61
26:DA:2302:G:H2'	26:DA:2303:G:H5'	1.82	0.61
26:DA:2203:U:H2'	26:DA:2205:C:C6	2.35	0.61
1:AA:1261:A:H3'	1:AA:1262:C:C6	2.35	0.61
30:DF:53:THR:HG22	30:DF:56:GLU:HG3	1.82	0.61
13:AM:37:THR:O	13:AM:55:ARG:NH1	2.31	0.61
9:CI:53:VAL:O	9:CI:55:ALA:N	2.27	0.61
30:DF:143:ALA:HB1	30:DF:148:LEU:HB2	1.81	0.61
7:AG:46:ALA:HA	7:AG:49:ILE:HD12	1.82	0.61
12:AL:53:ARG:NH1	12:AL:92:ASP:OD2	2.30	0.61
1:AA:1243:C:N4	1:AA:1294:G:H1	1.98	0.61
26:DA:307:G:N7	61:DA:3912:HOH:O	2.31	0.61
1:CA:592:G:H1	1:CA:647:C:N4	1.97	0.61
26:BA:1427:A:H4'	26:BA:1428:C:O5'	2.01	0.61
1:CA:1002:G:H1	1:CA:1038:C:H42	0.71	0.61
2:AB:204:ASN:OD1	2:AB:206:ASP:N	2.28	0.61
26:DA:2831:G:P	29:DE:58:ARG:HH21	2.23	0.61
46:DZ:45:ASP:OD1	46:DZ:49:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:831:G:O2'	36:BP:38:GLN:NE2	2.33	0.61
26:DA:2839:G:H5'	38:DR:46:GLY:HA2	1.83	0.61
39:DS:27:SER:HA	39:DS:88:ASP:HB3	1.82	0.61
26:DA:30:G:H2'	26:DA:31:C:C6	2.35	0.61
1:CA:659:U:C2'	1:CA:660:G:H5'	2.30	0.61
38:DR:28:LEU:HD12	38:DR:48:VAL:HG21	1.82	0.61
6:AF:37:VAL:HA	6:AF:65:VAL:HG12	1.82	0.61
26:DA:2142:C:H2'	26:DA:2143:C:C6	2.35	0.61
23:CW:75:C:C5	23:CW:76:PPU:H93	2.36	0.61
1:AA:958:A:N3	1:AA:985:C:O2'	2.28	0.61
1:CA:1458:G:OP1	20:CT:35:THR:OG1	2.12	0.61
26:DA:1528:A:OP2	26:DA:1542:A:N6	2.33	0.61
10:CJ:81:THR:HA	10:CJ:84:GLN:HB3	1.82	0.61
33:DI:87:LYS:HB3	33:DI:122:GLU:HA	1.83	0.61
38:DR:88:ARG:NH2	38:DR:89:ASP:OD1	2.32	0.61
1:CA:411:A:OP2	4:CD:25:ARG:NH2	2.28	0.61
3:CC:126:ARG:HG2	3:CC:126:ARG:HH11	1.65	0.61
1:CA:975:A:N6	10:CJ:60:ARG:HH12	1.99	0.61
26:BA:1992:G:N7	61:BA:4265:HOH:O	2.31	0.61
1:AA:147:G:H1	1:AA:148:G:N2	1.99	0.61
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.32	0.61
26:DA:1840:G:OP2	61:DA:4276:HOH:O	2.16	0.61
31:DG:83:ARG:N	31:DG:86:MET:SD	2.70	0.61
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.83	0.61
40:DT:60:THR:HG22	40:DT:77:PRO:HA	1.83	0.61
1:CA:1356:G:H1	1:CA:1366:C:N4	1.97	0.61
39:DS:34:HIS:O	39:DS:97:ARG:NH2	2.34	0.61
1:AA:600:C:H2'	1:AA:601:C:C6	2.35	0.61
33:DI:87:LYS:HA	33:DI:123:LEU:H	1.65	0.61
43:DW:73:ALA:HB3	43:DW:106:ILE:HD12	1.82	0.61
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.11	0.61
26:DA:2836:U:H2'	26:DA:2837:G:C8	2.35	0.61
26:BA:1025:G:C4	26:BA:1135:C:H1'	2.36	0.61
35:DO:76:ALA:HB3	40:DT:75:ILE:HB	1.81	0.61
1:CA:1036:G:N7	1:CA:1037:C:C2	2.68	0.61
1:CA:1229:A:O2'	24:CX:30:G:OP1	2.16	0.61
1:AA:757:U:H2'	1:AA:758:G:O4'	2.00	0.61
26:BA:1183:G:O2'	50:B3:29:ARG:NH1	2.34	0.61
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.36	0.61
9:AI:22:GLY:N	9:AI:58:HIS:O	2.30	0.61
26:BA:372:G:OP2	48:B1:69:LYS:HE2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:73:PRO:HB3	3:AC:103:VAL:HG11	1.82	0.61
26:BA:2377:A:H2'	26:BA:2378:A:C8	2.36	0.61
26:BA:2150:U:H2'	26:BA:2151:G:C8	2.36	0.61
1:CA:1423:G:OP1	35:DO:49:ARG:NH2	2.26	0.61
26:DA:881:G:H2'	26:DA:882:G:O4'	2.00	0.61
19:AS:9:VAL:HG21	51:B4:61:ARG:NH2	2.16	0.61
51:B4:61:ARG:NH1	51:B4:62:ARG:O	2.33	0.61
26:BA:1315:C:OP2	61:BA:4479:HOH:O	2.16	0.61
26:BA:228:A:H8	26:BA:229:A:H5'	1.66	0.61
9:CI:37:PHE:HD1	9:CI:40:LEU:HD12	1.66	0.61
26:BA:2454:G:O6	61:BA:4327:HOH:O	2.10	0.61
1:AA:627:G:H2'	1:AA:628:G:H8	1.66	0.61
26:BA:1693:U:O2'	28:BD:14:ARG:NH2	2.33	0.61
26:BA:528:A:N1	26:BA:2042:A:H2'	2.16	0.61
26:DA:2223:G:OP1	28:DD:172:TYR:OH	2.17	0.61
1:AA:171:A:H2'	1:AA:172:A:C8	2.36	0.61
4:CD:64:LEU:HB2	4:CD:198:VAL:HG21	1.83	0.61
26:BA:196:A:H62	36:BP:38:GLN:HE22	1.49	0.61
33:DI:86:THR:O	33:DI:123:LEU:HB2	2.01	0.61
5:AE:18:ARG:HE	5:AE:27:ARG:HH21	1.48	0.61
26:DA:889:C:O2'	26:DA:890:A:O5'	2.18	0.61
26:DA:1324:G:N7	61:DA:3861:HOH:O	2.31	0.61
26:BA:184:C:H2'	26:BA:185:U:C6	2.36	0.61
26:DA:1378:A:OP1	54:D7:10:ARG:NH2	2.33	0.61
1:AA:1317:C:OP1	14:AN:17:LYS:HG2	2.01	0.61
26:DA:1632:A:N7	61:DA:4171:HOH:O	2.31	0.61
53:B6:35:GLU:OE2	53:B6:50:ARG:NH1	2.33	0.61
1:AA:890:G:O2'	1:AA:906:G:O6	2.17	0.61
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.16	0.60
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.34	0.60
26:DA:659:C:H2'	26:DA:660:G:H8	1.66	0.60
26:DA:1587:A:H2'	26:DA:1588:C:C6	2.35	0.60
24:AX:16:C:O2'	24:AX:61:C:OP1	2.15	0.60
13:AM:90:LEU:HA	13:AM:93:ARG:HD2	1.83	0.60
26:DA:2562:U:H1'	35:DO:23:ARG:HH11	1.65	0.60
8:CH:29:SER:HB3	8:CH:32:LYS:HG3	1.82	0.60
1:CA:923:A:O2'	1:CA:1399:C:OP2	2.13	0.60
26:BA:1175:U:HO2'	26:BA:1176:G:P	2.23	0.60
27:DB:30:C:H3'	27:DB:30:C:O2	2.01	0.60
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.83	0.60
37:BQ:77:LYS:NZ	37:BQ:86:GLY:O	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1973:G:OP1	61:DA:4133:HOH:O	2.16	0.60
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.34	0.60
4:AD:172:PRO:HB2	4:AD:187:ARG:HH22	1.66	0.60
36:DP:50:ARG:HG2	55:D8:61:LEU:HD11	1.83	0.60
42:DV:60:GLU:HB3	42:DV:95:LEU:HB3	1.82	0.60
26:BA:1816:G:O6	28:BD:35:LYS:NZ	2.34	0.60
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.32	0.60
56:D9:25:VAL:HB	56:D9:34:GLN:HB2	1.82	0.60
31:BG:41:GLN:HE22	31:BG:153:ARG:HB3	1.66	0.60
1:CA:1275:A:H2'	1:CA:1276:G:O4'	2.01	0.60
1:CA:407:G:N2	1:CA:436:C:C2	2.66	0.60
1:CA:1123:A:H4'	10:CJ:36:GLY:HA3	1.83	0.60
1:AA:347:G:H2'	1:AA:348:G:O4'	2.00	0.60
26:DA:1012:U:OP1	41:DU:75:ASN:ND2	2.31	0.60
28:BD:132:PRO:HG2	28:BD:135:PHE:CD2	2.36	0.60
4:AD:162:LEU:HA	4:AD:165:MET:HB2	1.83	0.60
1:AA:309:G:O2'	1:AA:607:A:N1	2.33	0.60
5:AE:8:GLU:OE2	5:AE:63:ARG:NH2	2.34	0.60
26:BA:1986:A:OP1	61:BA:4252:HOH:O	2.15	0.60
1:CA:986:A:O2'	19:CS:55:LYS:O	2.18	0.60
24:CX:30:G:N2	24:CX:40:C:N3	2.40	0.60
19:AS:32:LYS:HA	19:AS:50:ALA:HB3	1.83	0.60
26:DA:2313:C:H4'	31:DG:91:ARG:HG3	1.84	0.60
26:DA:1539:G:H2'	26:DA:1540:U:O4'	2.01	0.60
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.01	0.60
42:BV:19:LYS:HG2	42:BV:95:LEU:HD23	1.84	0.60
30:DF:20:LEU:HD13	30:DF:125:LEU:HD13	1.82	0.60
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.83	0.60
37:DQ:85:LYS:HD3	47:D0:7:LEU:HD12	1.84	0.60
2:CB:76:GLN:HG3	2:CB:206:ASP:O	2.00	0.60
1:CA:757:U:O2'	1:CA:879:C:O2	2.18	0.60
32:DH:98:LEU:HD13	32:DH:125:VAL:HG23	1.84	0.60
1:AA:649:G:H2'	1:AA:650:G:H8	1.66	0.60
1:AA:918:A:H2'	1:AA:919:A:C8	2.36	0.60
36:DP:29:LYS:HG3	36:DP:30:THR:H	1.64	0.60
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.36	0.60
26:BA:2531:A:H5'	32:BH:157:TYR:CZ	2.36	0.60
18:CR:45:SER:HB3	18:CR:51:LEU:HD21	1.81	0.60
36:DP:82:GLY:HA2	36:DP:113:LYS:O	2.01	0.60
26:BA:1495:A:H2'	26:BA:1496:A:C8	2.36	0.60
26:BA:957:A:H5'	37:BQ:76:LYS:HG3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:64:G:H4'	1:CA:65:U:H3'	1.83	0.60
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.83	0.60
36:DP:63:PRO:HD3	55:D8:27:THR:HG22	1.84	0.60
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.60
1:CA:1226:C:H2'	13:CM:103:THR:HB	1.83	0.60
30:DF:185:ASP:HA	30:DF:188:ARG:HD3	1.83	0.60
1:AA:473:G:H2'	1:AA:474:G:C8	2.37	0.60
1:CA:933:G:O6	7:CG:3:ARG:NH2	2.34	0.60
1:CA:1223:C:OP2	19:CS:78:ARG:NH2	2.34	0.60
1:AA:67:C:H2'	1:AA:68:G:C8	2.37	0.60
1:CA:1304:G:OP1	21:CU:2:GLY:N	2.35	0.60
26:DA:20:C:OP1	41:DU:22:LYS:NZ	2.28	0.60
46:DZ:7:ALA:HB3	46:DZ:61:LEU:HD12	1.83	0.60
31:BG:48:GLU:HA	31:BG:51:ARG:HG3	1.83	0.60
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.02	0.60
26:BA:1175:U:O2'	26:BA:1176:G:O5'	2.07	0.60
2:AB:76:GLN:NE2	2:AB:206:ASP:OD1	2.35	0.60
27:DB:49:C:H2'	27:DB:50:G:C8	2.36	0.60
26:BA:822:U:O4	26:BA:944:G:H1'	2.01	0.60
1:AA:1223:C:P	19:AS:78:ARG:HH21	2.25	0.60
31:BG:161:THR:HG22	31:BG:163:ALA:H	1.66	0.60
40:BT:85:LYS:NZ	40:BT:87:ASP:OD2	2.31	0.60
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.10	0.60
46:BZ:23:LYS:NZ	46:BZ:40:ASP:OD1	2.33	0.60
19:AS:27:GLU:HG2	19:AS:47:HIS:NE2	2.17	0.60
26:DA:2736:G:N1	26:DA:2768:C:N3	2.38	0.60
29:DE:55:ASN:HB3	29:DE:58:ARG:HG3	1.84	0.60
4:AD:166:LYS:HA	4:AD:178:VAL:HG21	1.83	0.60
1:AA:1003:G:C2	1:AA:1004:A:N3	2.70	0.60
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.01	0.60
26:BA:414:C:H2'	26:BA:415:A:C8	2.37	0.60
26:BA:1165:U:H2'	26:BA:1166:C:C6	2.36	0.60
1:CA:999:C:N4	1:CA:1042:G:H1	1.95	0.60
26:DA:2305:A:H61	31:DG:43:LEU:HD13	1.67	0.60
36:DP:63:PRO:HG2	55:D8:25:MET:HB2	1.83	0.60
1:AA:662:G:O2'	1:AA:836:G:OP1	2.20	0.60
31:DG:5:VAL:HG22	31:DG:8:LYS:H	1.66	0.60
33:BI:50:ARG:HA	33:BI:53:ALA:HB3	1.83	0.60
31:DG:96:ARG:O	31:DG:99:MET:HB3	2.01	0.60
26:BA:2086:U:H2'	26:BA:2087:G:C8	2.37	0.60
4:AD:101:LEU:HB2	4:AD:138:TYR:HB3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1028:A:N6	26:DA:1125:G:H2'	2.17	0.60
26:DA:1842:G:O2'	28:DD:253:GLN:NE2	2.28	0.60
1:CA:27:G:H2'	1:CA:28:G:H8	1.66	0.60
26:DA:1688:U:O2	26:DA:1700:A:H5'	2.02	0.60
26:DA:918:A:O2'	27:DB:97:G:N2	2.33	0.60
26:BA:1225:G:OP1	42:BV:69:LYS:NZ	2.24	0.60
1:AA:804:U:H5''	1:AA:805:C:OP2	2.02	0.60
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.02	0.60
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.67	0.59
26:DA:2820:A:O2'	26:DA:2821:A:OP1	2.20	0.59
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.84	0.59
26:DA:1971:A:OP2	28:DD:242:ARG:NH2	2.35	0.59
26:BA:1695:G:N7	28:BD:14:ARG:NH2	2.46	0.59
4:AD:166:LYS:HB2	4:AD:168:ARG:HH12	1.65	0.59
26:DA:2180:U:H2'	26:DA:2181:G:O4'	2.02	0.59
26:DA:2630:G:H2'	26:DA:2631:G:C8	2.37	0.59
39:DS:99:LYS:HE2	39:DS:103:GLU:OE2	2.02	0.59
26:BA:668:G:H5'	26:BA:669:G:OP2	2.02	0.59
9:CI:96:LEU:HD22	9:CI:101:PHE:HB2	1.84	0.59
1:CA:1129:C:OP1	9:CI:16:ARG:NH1	2.35	0.59
26:DA:647:G:H8	26:DA:647:G:O5'	1.85	0.59
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.24	0.59
37:BQ:56:ARG:HH11	37:BQ:56:ARG:CG	2.15	0.59
26:BA:1176:G:H1'	26:BA:1177:A:C5'	2.29	0.59
29:DE:111:ARG:HA	38:DR:1:MET:HE3	1.84	0.59
1:AA:1075:C:H2'	1:AA:1076:C:H5'	1.83	0.59
44:BX:31:HIS:CD2	44:BX:33:LYS:H	2.19	0.59
1:AA:1191:A:H5''	3:AC:4:LYS:HZ2	1.65	0.59
26:DA:271(M):G:H4'	26:DA:271(N):U:OP1	2.01	0.59
43:DW:14:PRO:HG2	43:DW:78:GLU:HG2	1.84	0.59
26:DA:657:U:H2'	26:DA:658:C:C6	2.36	0.59
40:DT:59:THR:HG23	40:DT:78:LEU:HB3	1.83	0.59
24:AX:4:G:H2'	24:AX:5:G:C8	2.37	0.59
1:AA:148:G:N2	1:AA:175:C:O2	2.35	0.59
26:DA:2394:C:OP2	55:D8:30:ARG:NH1	2.35	0.59
26:BA:271(R):G:OP1	48:B1:76:ARG:NH2	2.35	0.59
26:BA:1239:G:OP1	61:BA:4617:HOH:O	2.17	0.59
36:DP:99:LEU:HD23	36:DP:99:LEU:H	1.65	0.59
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.84	0.59
26:DA:2408:U:H2'	26:DA:2409:G:H8	1.67	0.59
54:B7:34:ARG:NH1	54:B7:41:ARG:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:609:A:H2'	1:CA:610:G:H5'	1.84	0.59
18:AR:31:LEU:HD12	18:AR:65:ILE:HB	1.84	0.59
26:DA:1453:U:O2'	26:DA:1455:G:N7	2.33	0.59
1:AA:1228:C:OP1	13:AM:115:LYS:N	2.27	0.59
1:CA:730:G:C5	1:CA:731:G:H1'	2.36	0.59
33:BI:61:ARG:HA	33:BI:61:ARG:HH11	1.68	0.59
26:BA:2732:G:H3'	26:BA:2733:A:O4'	2.02	0.59
29:DE:47:VAL:HG11	29:DE:86:PRO:HD2	1.84	0.59
1:AA:339:C:OP2	35:BO:97:ARG:NH1	2.34	0.59
1:CA:92:C:C2'	1:CA:93:G:H5'	2.33	0.59
23:CW:75:C:C4	23:CW:76:PPU:H93	2.37	0.59
26:BA:1371:G:H2'	26:BA:1372:U:C5	2.37	0.59
1:CA:958:A:H61	19:CS:77:THR:HG23	1.65	0.59
1:CA:545:C:OP2	4:CD:65:ARG:NH2	2.34	0.59
26:DA:1005:C:H2'	26:DA:1006:C:H6	1.68	0.59
30:BF:33:LEU:HB3	36:BP:6:LEU:HD21	1.84	0.59
26:DA:1914:C:H2'	26:DA:1915:U:C6	2.38	0.59
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.83	0.59
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.84	0.59
3:CC:3:ASN:N	3:CC:3:ASN:OD1	2.36	0.59
26:DA:84:A:H5''	45:DY:8:LYS:HG2	1.84	0.59
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.35	0.59
1:AA:763:G:C2'	1:AA:764:C:H5'	2.32	0.59
1:CA:1068:G:OP2	1:CA:1068:G:H8	1.86	0.59
26:DA:2012:G:OP2	43:DW:16:LYS:NZ	2.32	0.59
1:CA:107:G:OP1	1:CA:325:A:N6	2.34	0.59
1:AA:1241:G:OP1	7:AG:35:LYS:NZ	2.33	0.59
26:DA:956:G:OP2	37:DQ:14:ARG:NH2	2.35	0.59
1:CA:792:A:H4'	1:CA:793:U:H5''	1.83	0.59
1:CA:696:A:N3	1:CA:786:G:O2'	2.29	0.59
26:DA:2136:C:O2'	26:DA:2137:C:O5'	2.21	0.59
1:AA:448:A:OP2	1:AA:485:G:N1	2.22	0.59
1:AA:977:A:H2'	1:AA:978:A:H5''	1.85	0.59
26:DA:2834:G:O2'	26:DA:2883:A:N6	2.34	0.59
42:BV:34:GLU:HB3	42:BV:56:SER:HB2	1.85	0.59
1:AA:1392:G:H21	1:AA:1502:A:H8	1.49	0.59
36:DP:37:GLY:O	36:DP:40:SER:OG	2.21	0.59
46:DZ:24:LEU:N	46:DZ:39:VAL:O	2.35	0.59
43:DW:71:VAL:HA	43:DW:107:LEU:HD12	1.83	0.59
1:CA:284:G:H2'	1:CA:285:G:H8	1.68	0.59
9:CI:105:ASP:HB2	9:CI:107:ARG:HG3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:588:G:H4'	8:CH:2:LEU:HD12	1.83	0.59
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.02	0.59
26:DA:2163:C:OP1	26:DA:2165:G:N1	2.36	0.59
26:DA:2166:G:O6	26:DA:2171:A:N6	2.36	0.59
30:BF:184:TYR:CE2	30:BF:188:ARG:HD2	2.37	0.59
26:DA:892:G:H8	26:DA:892:G:O5'	1.86	0.59
26:DA:1301:A:H2	26:DA:1626:G:N3	2.01	0.59
26:DA:1798:U:H5'	28:DD:259:THR:HG22	1.85	0.59
35:DO:68:GLU:HB3	35:DO:78:ARG:HB2	1.83	0.59
35:BO:104:ARG:CZ	40:BT:34:VAL:HG21	2.33	0.59
1:AA:201:C:H42	1:AA:216:G:H1	1.50	0.59
4:AD:107:ARG:HH22	4:AD:194:LEU:HD22	1.68	0.59
26:DA:276:A:H5''	26:DA:277:C:H5'	1.84	0.59
26:DA:578:A:OP2	61:DA:3804:HOH:O	2.16	0.59
44:DX:43:VAL:HG21	44:DX:81:VAL:HG11	1.84	0.59
33:DI:94:ALA:HA	33:DI:97:ILE:HB	1.84	0.59
31:BG:11:TYR:CZ	31:BG:16:ARG:HD3	2.38	0.59
26:DA:861:A:N3	27:DB:79:C:O2'	2.35	0.59
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.36	0.59
24:CX:49:G:C6	24:CX:65:C:N4	2.71	0.59
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.38	0.59
26:BA:886:C:H4'	26:BA:886:C:OP1	2.01	0.59
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.68	0.59
18:CR:22:VAL:HB	18:CR:56:THR:HA	1.85	0.59
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.84	0.59
26:BA:1173:G:O2'	26:BA:1174:A:O5'	2.21	0.59
26:BA:2893:G:H4'	26:BA:2894:G:O5'	2.01	0.59
46:DZ:55:HIS:CE1	46:DZ:135:GLU:HG3	2.38	0.59
26:DA:336:C:HO2'	45:DY:35:TYR:HH	1.49	0.59
24:CX:47:U:H3'	24:CX:48:C:C5'	2.32	0.59
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.85	0.59
26:DA:309:G:N3	26:DA:329:G:O2'	2.35	0.59
7:AG:15:ASP:OD1	7:AG:19:GLY:N	2.36	0.59
26:DA:2572:A:N7	29:DE:144:ARG:HD2	2.18	0.59
26:DA:857:C:OP2	47:D0:77:ARG:NH2	2.36	0.59
26:BA:1019:U:O2'	26:BA:1021:A:H2	1.86	0.58
26:DA:2454:G:O6	61:DA:3985:HOH:O	2.15	0.58
26:DA:171:G:H2'	26:DA:172:C:C6	2.37	0.58
26:DA:479:A:N3	26:DA:481:G:H5''	2.18	0.58
42:DV:76:LYS:HB2	42:DV:81:TYR:HB3	1.85	0.58
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.30	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1860:G:H1	26:DA:1882:C:H42	1.50	0.58
53:B6:34:LEU:HB2	53:B6:51:GLU:HB2	1.84	0.58
1:CA:1126:U:H1'	1:CA:1281:U:N3	2.18	0.58
26:DA:879:G:H3'	26:DA:880:G:C8	2.34	0.58
1:AA:1352:C:N4	61:AA:4166:HOH:O	2.33	0.58
1:AA:191:G:N2	20:AT:103:GLY:HA2	2.17	0.58
26:BA:356:G:H2'	26:BA:357:A:C8	2.37	0.58
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.38	0.58
33:BI:26:ALA:HA	33:BI:30:LEU:HB2	1.85	0.58
51:D4:46:GLN:O	51:D4:48:ARG:N	2.32	0.58
38:DR:11:ASN:ND2	61:DR:3101:HOH:O	2.34	0.58
26:BA:2687:U:H2'	26:BA:2688:U:O4'	2.03	0.58
26:BA:2869:G:H2'	26:BA:2870:C:O4'	2.03	0.58
26:DA:668:G:H5'	26:DA:669:G:OP2	2.01	0.58
43:BW:18:ARG:NH1	43:BW:76:VAL:O	2.37	0.58
1:CA:1004:A:C6	1:CA:1037:C:C2	2.91	0.58
1:CA:978:A:OP1	1:CA:1361:G:N2	2.35	0.58
7:CG:99:LEU:HD23	7:CG:102:ARG:NH1	2.17	0.58
26:BA:330:A:H2	26:BA:1210:A:H2'	1.67	0.58
26:DA:1019:U:H3	26:DA:1142(A):A:H62	1.49	0.58
50:D3:8:LEU:HD13	50:D3:31:LEU:HD23	1.84	0.58
29:BE:47:VAL:HG13	29:BE:49:LEU:HD13	1.84	0.58
1:CA:1530:G:H2'	1:CA:1531:A:O4'	2.03	0.58
6:AF:50:TYR:OH	18:AR:74:ARG:O	2.15	0.58
26:DA:1166:C:H2'	26:DA:1167:U:C6	2.37	0.58
26:DA:2626:C:H2'	26:DA:2627:G:O4'	2.03	0.58
26:BA:1593:G:H2'	26:BA:1594:G:C8	2.38	0.58
1:CA:92:C:H2'	1:CA:93:G:H5'	1.83	0.58
26:BA:2155:G:H3'	26:BA:2156:G:H8	1.68	0.58
26:DA:1420:U:O2'	26:DA:1421:G:OP1	2.21	0.58
5:AE:90:VAL:O	5:AE:120:THR:HA	2.04	0.58
26:DA:1149:G:H2'	26:DA:1150:C:C6	2.38	0.58
9:AI:42:ARG:NH1	9:AI:75:ASP:OD1	2.37	0.58
1:CA:1091:U:N3	1:CA:1094:G:OP2	2.25	0.58
1:CA:1058:G:H1	1:CA:1199:U:H3	1.52	0.58
1:AA:613:C:H2'	1:AA:614:A:C8	2.38	0.58
24:AX:64:G:O2'	37:BQ:10:ARG:NH2	2.37	0.58
41:DU:49:HIS:HA	41:DU:52:ARG:HB3	1.84	0.58
1:CA:1428:A:H2'	1:CA:1429:C:C6	2.38	0.58
1:CA:1356:G:H2'	1:CA:1357:A:C8	2.38	0.58
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1531:C:H42	26:DA:1538:G:H1	1.50	0.58
1:AA:448:A:P	1:AA:485:G:H22	2.26	0.58
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	1.85	0.58
30:DF:101:LEU:HD12	30:DF:102:PRO:HD2	1.86	0.58
28:DD:34:VAL:HB	28:DD:61:LEU:HD12	1.85	0.58
28:DD:218:ARG:HB3	28:DD:219:PRO:HD2	1.86	0.58
43:DW:18:ARG:HG3	43:DW:76:VAL:HB	1.85	0.58
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.84	0.58
1:CA:953:G:H5'	1:CA:965:A:N6	2.19	0.58
32:DH:3:ARG:NH1	32:DH:3:ARG:HB3	2.18	0.58
30:BF:164:ARG:O	30:BF:168:ARG:HB2	2.03	0.58
26:BA:2332:U:O4	61:BA:4724:HOH:O	2.17	0.58
48:B1:51:VAL:HG11	48:B1:74:VAL:HG21	1.86	0.58
33:BI:96:ASP:N	33:BI:96:ASP:OD1	2.36	0.58
2:CB:120:ALA:O	2:CB:122:PHE:N	2.35	0.58
52:B5:59:GLU:HG2	52:B5:60:VAL:N	2.19	0.58
2:AB:210:SER:O	2:AB:214:ILE:HG12	2.03	0.58
13:AM:80:ARG:NH2	51:B4:58:ARG:HD2	2.18	0.58
26:DA:528:A:OP2	34:DN:114:ARG:NH1	2.37	0.58
1:AA:1150:U:O4	1:AA:1151:A:N6	2.37	0.58
1:CA:592:G:H1	1:CA:647:C:H42	1.50	0.58
37:BQ:86:GLY:HA3	47:B0:10:THR:HG23	1.85	0.58
26:DA:2263:C:N4	47:D0:15:ASP:OD1	2.36	0.58
26:DA:322:A:OP2	30:DF:169:ASN:HB2	2.03	0.58
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.86	0.58
26:DA:1427:A:H4'	26:DA:1428:C:O5'	2.04	0.58
26:BA:2820:A:OP2	38:BR:2:ARG:NH2	2.36	0.58
26:DA:251:A:C5	26:DA:252:G:H1'	2.37	0.58
26:DA:2637:U:H5''	29:DE:82:ARG:HH21	1.68	0.58
48:D1:3:LYS:HB2	48:D1:61:ARG:NH1	2.19	0.58
31:DG:113:ARG:NH1	31:DG:139:LEU:O	2.37	0.58
27:BB:75:G:H8	27:BB:75:G:H5''	1.69	0.58
1:AA:13:U:OP1	61:AA:4121:HOH:O	2.17	0.58
11:AK:84:VAL:HG21	11:AK:95:ILE:HD11	1.85	0.58
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.36	0.58
1:AA:35:G:O2'	12:AL:118:SER:O	2.17	0.58
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.31	0.58
33:DI:49:ALA:HA	33:DI:52:ARG:HH22	1.68	0.58
1:CA:157:G:H1	1:CA:164:U:H3	1.50	0.58
1:CA:708:C:H2'	1:CA:709:G:C8	2.36	0.58
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:557:G:OP1	61:AA:4060:HOH:O	2.17	0.58
26:BA:2748:A:H5'	32:BH:4:ILE:HD12	1.84	0.58
9:AI:28:VAL:HG22	9:AI:63:ILE:HB	1.86	0.58
26:DA:2000:G:N7	61:DA:4004:HOH:O	2.32	0.58
2:CB:186:ALA:O	2:CB:201:ILE:N	2.37	0.58
26:BA:220:G:O2'	26:BA:233:A:N3	2.34	0.58
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.32	0.58
24:CX:23:C:H2'	24:CX:24:U:C6	2.39	0.58
17:AQ:6:LEU:HG	17:AQ:23:VAL:HG11	1.86	0.58
42:BV:72:VAL:HG22	42:BV:85:LYS:HB3	1.84	0.58
26:DA:2079:U:O3'	48:D1:35:THR:OG1	2.21	0.58
1:AA:1287:A:N1	1:AA:1370:G:N2	2.48	0.58
1:AA:1352:C:H2'	1:AA:1353:G:C8	2.39	0.58
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.85	0.58
4:CD:162:LEU:HD22	4:CD:178:VAL:HG13	1.86	0.58
1:AA:984:C:H2'	1:AA:985:C:H6	1.67	0.58
1:AA:1216:G:OP1	14:AN:2:ALA:HA	2.03	0.58
33:BI:93:THR:OG1	33:BI:96:ASP:OD1	2.14	0.58
54:B7:12:ARG:NH2	54:B7:44:PRO:HB3	2.19	0.58
44:BX:50:LYS:N	44:BX:87:GLN:OE1	2.33	0.58
8:CH:51:VAL:HG11	8:CH:60:ARG:HH12	1.67	0.58
46:BZ:117:LEU:HD11	46:BZ:144:LEU:HD13	1.86	0.58
26:BA:1954:G:O2'	26:BA:1956:U:O4	2.13	0.58
1:CA:835:U:H3	1:CA:851:G:H1	1.52	0.58
26:DA:2586:C:OP2	26:DA:2608:G:N1	2.35	0.58
26:DA:1169:G:H2'	26:DA:1170:G:C8	2.38	0.58
26:DA:2301:C:H2'	26:DA:2302:G:H8	1.69	0.58
1:CA:516:U:O2'	1:CA:519:C:N3	2.32	0.58
29:DE:111:ARG:HG3	29:DE:160:TYR:CD2	2.39	0.58
1:CA:21:G:H2'	1:CA:22:G:C8	2.39	0.58
36:BP:50:ARG:HH21	55:B8:7:HIS:CD2	2.21	0.58
1:AA:1028:C:H2'	1:AA:1029:C:O4'	2.04	0.58
1:CA:27:G:H2'	1:CA:28:G:C8	2.39	0.58
1:AA:613:C:H2'	1:AA:614:A:H8	1.69	0.58
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.19	0.58
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.85	0.58
26:DA:1514:U:H2'	26:DA:1515:G:H8	1.69	0.58
1:CA:814:A:H2'	1:CA:816:A:H5''	1.85	0.58
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.86	0.58
41:DU:108:GLU:O	41:DU:112:ARG:HG2	2.03	0.58
39:BS:28:VAL:HG11	39:BS:98:VAL:HG13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CX:64:G:H4'	37:DQ:10:ARG:NH2	2.19	0.58
26:BA:1747(A):G:H2'	26:BA:1748:G:H5''	1.85	0.58
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.86	0.58
7:CG:27:ILE:HD12	7:CG:40:ALA:HA	1.86	0.58
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.86	0.58
1:CA:1003:G:H2'	1:CA:1004:A:H1'	1.86	0.57
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.18	0.57
26:DA:678:C:N3	26:DA:799:G:N1	2.42	0.57
26:DA:2233:U:H2'	26:DA:2234:G:C8	2.39	0.57
26:BA:309:G:N3	26:BA:329:G:O2'	2.36	0.57
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.33	0.57
1:CA:600:C:H2'	1:CA:601:C:H6	1.69	0.57
36:DP:29:LYS:HG3	36:DP:30:THR:N	2.18	0.57
2:AB:87:ARG:NE	2:AB:233:SER:HB3	2.19	0.57
26:DA:271(P):C:O3'	33:DI:42:SER:OG	2.18	0.57
26:BA:1300:U:H4'	26:BA:1301:A:C5'	2.33	0.57
8:CH:82:HIS:NE2	8:CH:84:ARG:HG2	2.19	0.57
1:CA:406:G:N3	4:CD:119:GLN:NE2	2.50	0.57
1:CA:1027:C:N3	1:CA:1035:A:C2	2.72	0.57
1:CA:999:C:N4	1:CA:1042:G:C6	2.71	0.57
39:BS:15:ARG:NE	39:BS:88:ASP:OD2	2.35	0.57
26:DA:528:A:C2	26:DA:2042:A:H2'	2.39	0.57
1:AA:154:C:C2'	1:AA:155:C:H5'	2.33	0.57
40:BT:11:GLU:OE1	40:BT:57:PHE:HB3	2.04	0.57
28:DD:206:LEU:O	28:DD:211:ARG:NE	2.34	0.57
26:BA:2207:G:O2'	26:BA:2208:A:OP1	2.18	0.57
26:DA:1014:U:H2'	26:DA:1015:G:C8	2.39	0.57
26:DA:1014:U:H2'	26:DA:1015:G:H8	1.69	0.57
36:DP:44:GLY:CA	36:DP:45:LEU:HB2	2.34	0.57
26:DA:2384:G:OP2	47:D0:55:ARG:NH2	2.37	0.57
1:AA:224:C:H2'	1:AA:225:C:C6	2.40	0.57
20:CT:43:LEU:HD13	20:CT:51:GLU:HB3	1.85	0.57
9:AI:19:LEU:HB3	9:AI:59:PHE:CD1	2.38	0.57
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.40	0.57
26:BA:1021:A:H3'	26:BA:1021:A:C8	2.38	0.57
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.37	0.57
1:CA:880:C:OP1	12:CL:8:ASN:ND2	2.37	0.57
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.87	0.57
1:CA:677:U:H3	1:CA:713:G:H22	1.52	0.57
1:CA:279:A:H4'	1:CA:280:C:H5''	1.85	0.57
27:DB:42:C:O2'	31:DG:67:LYS:O	2.10	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DO:120:GLU:HB2	40:DT:68:TYR:HE2	1.70	0.57
43:BW:79:GLY:HA3	43:BW:100:THR:HG22	1.86	0.57
44:DX:31:HIS:CD2	44:DX:33:LYS:HB2	2.39	0.57
26:DA:1814:G:H4'	28:DD:51:VAL:HG21	1.86	0.57
1:CA:72:C:N4	1:CA:73:G:C5	2.72	0.57
2:CB:207:ALA:O	2:CB:210:SER:HB3	2.04	0.57
1:CA:1029:C:N4	1:CA:1032:G:H1	2.02	0.57
1:AA:170:U:O2'	1:AA:171:A:H5'	2.05	0.57
26:BA:848:G:H2'	26:BA:849:A:C8	2.40	0.57
1:CA:107:G:H2'	1:CA:108:G:O4'	2.05	0.57
4:AD:104:VAL:HG11	4:AD:146:ILE:HD13	1.85	0.57
26:BA:2108:C:H2'	26:BA:2109:U:H6	1.69	0.57
42:DV:78:LYS:HB3	61:DV:301:HOH:O	2.04	0.57
13:AM:34:LEU:HD13	13:AM:41:PRO:HA	1.85	0.57
26:BA:1833:U:O2'	26:BA:1969:A:N1	2.29	0.57
34:DN:121:LYS:HG2	34:DN:130:HIS:NE2	2.20	0.57
1:CA:1024:G:H2'	1:CA:1025:U:H5''	1.87	0.57
26:BA:2138:C:C2	26:BA:2154:G:C2	2.93	0.57
27:DB:50:G:OP1	39:DS:63:THR:N	2.37	0.57
1:AA:160:A:N6	1:AA:345:C:OP2	2.37	0.57
26:DA:2630:G:N2	26:DA:2788:C:O2	2.30	0.57
27:BB:29:A:H2'	27:BB:30:C:C6	2.38	0.57
26:DA:57:C:H2'	26:DA:58:G:O4'	2.05	0.57
9:CI:23:ASN:ND2	9:CI:60:ASP:OD2	2.37	0.57
1:CA:54:C:N4	1:CA:353:A:OP2	2.37	0.57
1:CA:1027:C:C4	1:CA:1034:G:C2	2.93	0.57
1:CA:1148:U:H2'	1:CA:1149:C:O4'	2.04	0.57
26:DA:1171:G:N2	26:DA:1178:C:H42	2.03	0.57
33:DI:87:LYS:HA	33:DI:122:GLU:HA	1.86	0.57
1:CA:559:A:H4'	1:CA:560:U:H5''	1.87	0.57
26:DA:1794:U:H2'	26:DA:1795:C:C6	2.39	0.57
26:DA:2284:C:OP2	53:D6:2:ALA:N	2.38	0.57
26:BA:2243:U:H2'	26:BA:2244:U:C6	2.39	0.57
26:BA:1405:U:H2'	26:BA:1406:U:C6	2.39	0.57
1:AA:532:A:O2'	1:AA:533:A:OP1	2.16	0.57
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.03	0.57
26:DA:2136:C:H42	26:DA:2156:G:H1'	1.68	0.57
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.85	0.57
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.29	0.57
1:AA:1125:U:O2'	1:AA:1126:U:H5''	2.04	0.57
26:BA:994:C:OP1	41:BU:53:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:29:A:C2	27:DB:30:C:C5	2.91	0.57
26:DA:2206:G:H3'	26:DA:2207:G:N7	2.18	0.57
26:DA:2741:A:H61	26:DA:2763:G:H1'	1.69	0.57
36:BP:52:GLU:OE1	36:BP:55:ARG:NH1	2.33	0.57
1:CA:1343:G:O2'	9:CI:121:ARG:HD2	2.04	0.57
1:AA:984:C:H2'	1:AA:985:C:C6	2.40	0.57
26:BA:1300:U:H4'	26:BA:1301:A:H5''	1.85	0.57
32:BH:86:GLU:OE2	32:BH:130:ARG:NH1	2.38	0.57
9:AI:23:ASN:HB2	9:AI:25:LYS:HE3	1.86	0.57
34:BN:70:LYS:HE3	34:BN:72:TYR:CZ	2.39	0.57
26:DA:2138:C:H2'	26:DA:2139:C:C6	2.40	0.57
1:AA:78:G:N2	1:AA:91:C:C2	2.73	0.57
26:DA:1532:C:N3	26:DA:1537:G:N1	2.40	0.57
9:CI:22:GLY:N	9:CI:58:HIS:O	2.34	0.57
2:CB:122:PHE:HA	2:CB:127:ILE:HD12	1.86	0.57
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.05	0.57
1:AA:839:U:H4'	1:AA:840:C:OP2	2.04	0.57
26:DA:2646:C:OP2	26:DA:2732:G:O2'	2.20	0.57
9:AI:8:GLY:HA3	9:AI:76:ALA:O	2.05	0.57
26:DA:992:C:OP1	41:DU:47:TYR:OH	2.11	0.57
49:B2:22:GLU:OE2	49:B2:68:ARG:NH2	2.38	0.57
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.86	0.57
1:AA:1229:A:O2'	24:AX:30:G:OP1	2.23	0.57
1:AA:250:A:H4'	1:AA:251:G:O5'	2.05	0.57
26:DA:530:G:C5	26:DA:2022:U:H5''	2.39	0.57
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.86	0.57
28:DD:51:VAL:HG11	28:DD:54:ARG:HH11	1.69	0.57
26:BA:644:A:H4'	26:BA:645:C:H5	1.70	0.57
1:AA:953:G:H5'	1:AA:965:A:H61	1.69	0.57
1:AA:1036:G:N3	1:AA:1036:G:H2'	2.19	0.57
26:DA:477:A:H2'	26:DA:478:A:C8	2.40	0.57
34:BN:12:ARG:NH1	34:BN:50:ASP:OD2	2.38	0.57
31:DG:47:LYS:HG2	31:DG:48:GLU:N	2.19	0.57
36:BP:63:PRO:HG2	55:B8:25:MET:HB2	1.87	0.57
1:CA:473:G:H2'	1:CA:474:G:C8	2.40	0.57
15:CO:64:ARG:HD3	15:CO:68:ARG:NH2	2.20	0.57
26:DA:827:U:O2'	61:DA:4222:HOH:O	2.18	0.57
26:BA:1019:U:H3	26:BA:1142(A):A:H62	1.51	0.57
26:DA:1991:U:H2'	26:DA:1992:G:H5''	1.87	0.57
1:CA:1492:A:H2'	1:CA:1493:A:C4	2.40	0.57
26:DA:277:C:O2'	26:DA:278:A:OP1	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:269:C:H2'	1:AA:270:A:C8	2.39	0.57
26:BA:2023:G:H5'	26:BA:2617:C:H4'	1.86	0.57
1:AA:438:G:N1	1:AA:495:A:OP2	2.29	0.57
26:BA:839:U:H2'	26:BA:840:C:C6	2.39	0.57
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.87	0.57
1:CA:920:U:H2'	1:CA:921:U:C6	2.40	0.57
26:BA:1859:A:N6	26:BA:1883:G:O2'	2.37	0.57
26:DA:286:C:H2'	26:DA:287:C:H6	1.69	0.57
30:BF:195:ASP:HB3	30:BF:198:ALA:H	1.70	0.57
1:AA:330:C:O2	61:AA:4093:HOH:O	2.15	0.57
26:DA:2103:C:C2'	26:DA:2104:G:H5'	2.35	0.56
26:BA:1174:A:H4'	26:BA:1175:U:OP1	2.05	0.56
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.51	0.56
36:DP:39:LYS:HB2	36:DP:45:LEU:HG	1.87	0.56
1:AA:1372:U:H2'	1:AA:1373:G:O4'	2.05	0.56
11:AK:48:ILE:O	11:AK:50:TYR:N	2.35	0.56
26:DA:536:A:H2'	26:DA:537:C:C6	2.40	0.56
26:BA:2438:U:O2'	26:BA:2440:C:OP1	2.19	0.56
36:DP:64:LYS:HA	55:D8:13:ARG:HB3	1.85	0.56
13:CM:68:GLY:HA3	31:DG:116:ASP:OD1	2.05	0.56
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.87	0.56
26:DA:740:U:H2'	26:DA:741:G:C8	2.40	0.56
26:DA:387:U:OP2	48:D1:20:ARG:NH1	2.32	0.56
2:AB:167:PRO:HG3	2:AB:186:ALA:HB1	1.85	0.56
26:DA:662:G:H5''	36:DP:16:ARG:HG2	1.86	0.56
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.03	0.56
26:DA:888:C:H2'	26:DA:889:C:C4	2.40	0.56
26:DA:889:C:O2'	26:DA:890:A:H8	1.88	0.56
61:BA:3834:HOH:O	54:B7:34:ARG:NH2	2.38	0.56
26:BA:831:G:N2	36:BP:53:GLY:O	2.38	0.56
1:AA:153:C:H42	1:AA:168:G:H1	1.53	0.56
26:BA:36:G:N3	26:BA:450:G:O2'	2.37	0.56
45:BY:35:TYR:CE2	45:BY:69:ALA:HB3	2.40	0.56
9:AI:16:ARG:HB2	9:AI:64:THR:HB	1.87	0.56
26:DA:2774:C:H2'	26:DA:2775:A:O4'	2.06	0.56
26:BA:1788:C:OP1	28:BD:222:ARG:NH2	2.37	0.56
27:DB:12:C:O2'	47:D0:74:ARG:HG2	2.05	0.56
40:BT:95:ARG:HG2	40:BT:95:ARG:HH11	1.71	0.56
4:CD:155:LEU:HD22	4:CD:157:LEU:H	1.70	0.56
26:BA:1239:G:H2'	26:BA:1240:U:O4'	2.05	0.56
26:BA:1252:G:O6	41:BU:36:ARG:HG2	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:71:A:N7	44:BX:31:HIS:HE1	2.03	0.56
30:BF:192:LEU:HD13	30:BF:194:MET:HE2	1.87	0.56
30:DF:11:VAL:HG22	30:DF:125:LEU:HB2	1.86	0.56
26:BA:531:C:OP2	61:BA:4510:HOH:O	2.17	0.56
20:AT:57:ARG:HH22	20:AT:100:ILE:HD11	1.70	0.56
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.05	0.56
26:DA:752:A:H4'	26:DA:753:C:H5'	1.87	0.56
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.70	0.56
50:B3:7:LYS:HG3	50:B3:34:GLU:HG3	1.86	0.56
32:BH:40:GLU:OE1	32:BH:60:ARG:NH1	2.38	0.56
45:BY:86:ARG:NH1	45:BY:100:ALA:O	2.38	0.56
6:CF:2:ARG:HH22	15:CO:2:PRO:HD2	1.71	0.56
26:DA:860:U:H1'	26:DA:2268:A:H5'	1.87	0.56
26:BA:2483:C:N3	37:BQ:124:LYS:NZ	2.48	0.56
7:CG:9:VAL:O	7:CG:11:GLN:NE2	2.38	0.56
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.41	0.56
6:CF:81:ILE:HD11	28:DD:125:ILE:HB	1.87	0.56
1:CA:1326:C:H5''	21:CU:18:TYR:O	2.06	0.56
1:AA:376:G:O2'	16:AP:5:ARG:NH2	2.38	0.56
1:CA:93:G:H2'	1:CA:96:U:H6	1.71	0.56
26:BA:2138:C:N3	26:BA:2153:G:N2	2.45	0.56
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.05	0.56
26:BA:2159:G:H2'	26:BA:2160:G:C8	2.41	0.56
26:DA:2166:G:H3'	26:DA:2167:U:C5'	2.33	0.56
1:CA:1030:C:N4	1:CA:1032:G:O6	2.38	0.56
26:DA:885:C:H3'	26:DA:886:C:H5''	1.87	0.56
26:DA:2224:G:OP1	28:DD:268:ARG:NE	2.39	0.56
26:BA:2648:C:H2'	26:BA:2649:U:C6	2.41	0.56
26:DA:1794:U:H2'	26:DA:1795:C:H6	1.69	0.56
1:AA:193:C:H2'	1:AA:194:C:H6	1.71	0.56
3:CC:54:ARG:HB3	3:CC:54:ARG:NH1	2.21	0.56
26:DA:829:A:N7	26:DA:2248:C:H5'	2.21	0.56
1:CA:93:G:O2'	1:CA:96:U:H5'	2.05	0.56
26:DA:880:G:C2	26:DA:898:C:O2	2.59	0.56
26:DA:2301:C:H2'	26:DA:2302:G:C8	2.40	0.56
24:CX:15:G:H2'	24:CX:59:A:N6	2.21	0.56
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.20	0.56
26:DA:1131:G:O6	26:DA:2040:C:H1'	2.05	0.56
1:AA:858:G:O6	1:AA:869:G:H3'	2.06	0.56
1:CA:250:A:H4'	1:CA:251:G:O5'	2.04	0.56
31:DG:19:LEU:HD13	31:DG:32:PRO:HG2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DG:46:ALA:HB2	31:DG:53:LEU:HD12	1.88	0.56
43:DW:11:ARG:HD2	43:DW:82:LEU:HD12	1.86	0.56
1:AA:21:G:H2'	1:AA:22:G:C8	2.40	0.56
26:BA:1432:C:H2'	26:BA:1433:U:O4'	2.05	0.56
1:AA:277:C:H5''	17:AQ:68:ARG:NH2	2.19	0.56
1:CA:1399:C:H4'	1:CA:1400:C:C5'	2.35	0.56
26:DA:2103:C:H2'	26:DA:2104:G:H5'	1.87	0.56
26:BA:2125:G:H22	26:BA:2172:U:P	2.29	0.56
48:D1:53:VAL:HG22	48:D1:74:VAL:HG13	1.86	0.56
26:DA:517:C:OP1	52:D5:16:ARG:NH2	2.39	0.56
26:BA:2495:G:H5''	37:BQ:82:ARG:HG2	1.85	0.56
26:BA:2000:G:OP1	38:BR:5:LYS:NZ	2.38	0.56
35:BO:16:ALA:HB2	35:BO:52:VAL:HG21	1.87	0.56
48:B1:3:LYS:O	48:B1:12:PRO:HD3	2.06	0.56
26:BA:1028:A:H61	26:BA:1125:G:H2'	1.70	0.56
26:BA:1865:G:OP1	61:BA:4699:HOH:O	2.17	0.56
26:DA:922:U:H2'	26:DA:923:C:C6	2.40	0.56
24:AX:8:4SU:H6	24:AX:8:4SU:O5'	2.04	0.56
29:DE:143:ASN:HD22	29:DE:147:PRO:HD3	1.71	0.56
29:BE:97:LYS:N	29:BE:100:GLU:OE1	2.29	0.56
1:AA:542:G:H5'	4:AD:41:GLY:HA3	1.86	0.56
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.86	0.56
27:DB:2:C:O2'	27:DB:3:C:H5'	2.06	0.56
1:CA:757:U:H2'	1:CA:758:G:O4'	2.05	0.56
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.41	0.56
1:CA:601:C:H2'	1:CA:602:A:H8	1.71	0.56
1:AA:545:C:OP1	4:AD:61:LYS:NZ	2.37	0.56
33:DI:97:ILE:O	33:DI:101:LEU:HB2	2.05	0.56
26:BA:1865:G:N2	26:BA:1877:A:OP2	2.34	0.56
34:BN:15:LEU:HD12	34:BN:137:LYS:HG2	1.87	0.56
26:BA:411:G:C5	36:BP:72:PRO:HB3	2.40	0.56
30:DF:107:LYS:HD3	30:DF:206:ILE:HA	1.88	0.56
26:DA:1366:A:H2'	26:DA:1367:A:O4'	2.06	0.56
50:B3:23:LEU:HD13	50:B3:50:VAL:HG11	1.88	0.56
36:DP:121:LYS:HB3	36:DP:123:LEU:HG	1.87	0.56
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.40	0.56
26:BA:875:G:H2'	26:BA:876:C:O4'	2.06	0.56
26:BA:2690:C:OP1	38:BR:17:ARG:NH1	2.37	0.56
29:BE:111:ARG:HG3	29:BE:160:TYR:CD2	2.41	0.56
26:BA:577:G:O2'	26:BA:1254:A:OP1	2.23	0.56
26:BA:253:C:O2'	61:BA:4683:HOH:O	2.17	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2135:A:N6	26:BA:2156:G:N2	2.54	0.56
25:CY:76:A:N6	26:DA:2422:A:O4'	2.39	0.56
27:DB:1:U:O2'	27:DB:2:C:O5'	2.20	0.56
33:DI:129:THR:HG22	33:DI:139:GLN:NE2	2.20	0.56
26:DA:1022:G:N7	34:DN:66:LYS:HE2	2.21	0.56
1:CA:953:G:H5'	1:CA:965:A:H61	1.69	0.56
26:BA:2291:U:H2'	26:BA:2292:C:C6	2.41	0.56
26:BA:630:G:N2	26:BA:633:A:OP2	2.30	0.56
1:CA:1417:G:O6	61:CA:4029:HOH:O	2.18	0.56
40:BT:96:ARG:CZ	40:BT:96:ARG:HB3	2.35	0.56
1:CA:598:U:H2'	1:CA:599:C:C6	2.41	0.56
26:DA:583:G:OP2	41:DU:10:ARG:NH1	2.36	0.56
2:AB:204:ASN:O	2:AB:210:SER:OG	2.14	0.56
9:CI:49:PRO:HG2	9:CI:81:ILE:HG23	1.88	0.56
32:DH:86:GLU:OE2	32:DH:132:ARG:NH2	2.39	0.56
2:AB:105:PHE:CE1	2:AB:155:LEU:HD12	2.40	0.56
4:CD:64:LEU:HA	4:CD:67:ILE:HD12	1.87	0.56
9:CI:53:VAL:HG21	9:CI:92:TYR:CZ	2.41	0.56
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.05	0.56
26:DA:11:G:H2'	26:DA:12:U:H5''	1.87	0.56
26:DA:323:G:C8	30:DF:171:PRO:HG3	2.41	0.56
46:DZ:146:ILE:HA	46:DZ:174:VAL:HG11	1.88	0.56
26:BA:443:A:H1'	26:BA:1201:C:O4'	2.06	0.56
36:DP:95:VAL:HG13	36:DP:125:VAL:HA	1.87	0.56
14:AN:4:LYS:HA	14:AN:7:ILE:HG22	1.88	0.56
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.24	0.56
32:BH:24:VAL:HG22	32:BH:35:VAL:HB	1.87	0.56
26:DA:2135:A:N6	26:DA:2156:G:C2	2.74	0.56
26:BA:2286:A:H4'	26:BA:2287:A:O4'	2.06	0.56
1:AA:1006:C:N4	1:AA:1023:G:H1	2.01	0.56
52:B5:16:ARG:NH1	52:B5:17:ASP:OD1	2.38	0.56
52:B5:16:ARG:HD2	52:B5:20:ARG:NH1	2.21	0.56
26:BA:2074:U:H2'	26:BA:2075:U:C6	2.41	0.56
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.86	0.56
28:DD:132:PRO:HG2	28:DD:135:PHE:CD2	2.41	0.56
26:BA:583:G:OP2	41:BU:10:ARG:HD2	2.06	0.56
12:AL:33:ARG:HD3	12:AL:62:SER:HB3	1.88	0.56
26:DA:2051:A:H5'	26:DA:2578:G:O4'	2.05	0.56
26:BA:784:A:C6	28:BD:229:VAL:HG11	2.41	0.56
1:CA:976:G:H22	1:CA:1363(A):A:H2'	1.71	0.55
26:DA:2206:G:H3'	26:DA:2207:G:H8	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1320:C:H5'	19:AS:70:LYS:HG3	1.87	0.55
1:AA:147:G:N1	1:AA:148:G:C2	2.74	0.55
15:CO:17:ARG:HH11	15:CO:17:ARG:HG3	1.71	0.55
33:DI:52:ARG:H	33:DI:52:ARG:NH1	2.05	0.55
1:AA:1202:G:H1'	14:AN:29:ARG:HD2	1.88	0.55
10:AJ:55:LYS:HE3	10:AJ:56:HIS:CE1	2.40	0.55
3:CC:8:ILE:HG22	14:CN:49:HIS:O	2.07	0.55
26:DA:1037:G:H1	26:DA:1118:C:H42	1.54	0.55
12:AL:70:ILE:HD13	12:AL:77:LEU:HD12	1.88	0.55
29:DE:72:VAL:CA	29:DE:73:GLU:HB3	2.36	0.55
1:AA:473:G:H2'	1:AA:474:G:H8	1.71	0.55
26:DA:1710:C:H2'	26:DA:1711:C:C6	2.41	0.55
1:AA:1106:G:H5''	3:AC:172:ARG:HG2	1.88	0.55
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.05	0.55
27:BB:11:C:H3'	27:BB:12:C:H6	1.69	0.55
26:DA:1010:A:H1'	26:DA:1153:C:H1'	1.86	0.55
45:DY:28:LYS:HD2	45:DY:40:GLU:HG3	1.86	0.55
26:BA:2304:G:H22	26:BA:2312:U:H3	1.54	0.55
8:CH:86:ILE:HG21	8:CH:133:LEU:HD13	1.88	0.55
33:BI:72:LEU:C	33:BI:74:ASN:H	2.10	0.55
26:BA:648:G:O2'	26:BA:2351:G:OP1	2.19	0.55
26:DA:2682:U:O2'	40:DT:58:ASN:ND2	2.39	0.55
26:BA:2116:G:H22	26:BA:2162:G:P	2.30	0.55
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.41	0.55
26:DA:2802:G:H2'	26:DA:2803:C:O4'	2.06	0.55
26:BA:2839:G:H5'	38:BR:46:GLY:HA2	1.87	0.55
26:BA:2529:G:O6	56:B9:31:LYS:NZ	2.39	0.55
26:BA:657:U:H2'	26:BA:658:C:C6	2.41	0.55
26:BA:1012:U:C5	34:BN:28:THR:HG21	2.41	0.55
34:DN:17:ASP:OD1	34:DN:56:ASN:ND2	2.28	0.55
1:AA:1053:G:N7	1:AA:1200:C:H5''	2.21	0.55
10:CJ:64:GLU:OE2	10:CJ:66:ARG:NH1	2.39	0.55
22:AV:15:A:O5'	22:AV:15:A:H8	1.89	0.55
26:BA:607:U:OP1	30:BF:102:PRO:HA	2.06	0.55
1:AA:636:U:H2'	1:AA:637:G:H8	1.70	0.55
1:AA:1163:C:H2'	1:AA:1164:G:H5''	1.87	0.55
1:CA:1124:G:H5''	10:CJ:35:SER:OG	2.07	0.55
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.89	0.55
1:AA:1458:G:OP1	20:AT:35:THR:OG1	2.12	0.55
1:AA:975:A:N6	10:AJ:60:ARG:HH12	2.04	0.55
26:BA:2393:A:O2'	55:B8:13:ARG:NH1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:912:C:OP1	37:DQ:8:LYS:NZ	2.36	0.55
8:CH:86:ILE:HG13	8:CH:133:LEU:HD22	1.86	0.55
26:BA:1638:C:O3'	26:BA:2709:G:N2	2.39	0.55
26:DA:2552:U:H2'	26:DA:2554:U:OP2	2.06	0.55
26:DA:618:C:H2'	26:DA:619:G:O4'	2.06	0.55
16:CP:72:ARG:HH21	16:CP:73:LEU:HD21	1.71	0.55
26:BA:1385:G:O2'	26:BA:1396:U:O2	2.15	0.55
26:BA:488:G:O2'	43:BW:49:LYS:NZ	2.35	0.55
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.35	0.55
38:BR:56:LYS:NZ	38:BR:90:ARG:O	2.40	0.55
26:DA:874:G:H8	26:DA:874:G:H5'	1.72	0.55
1:CA:877:C:O2	8:CH:3:THR:OG1	2.24	0.55
28:DD:127:VAL:HA	28:DD:193:VAL:HG22	1.88	0.55
1:CA:93:G:H2'	1:CA:96:U:C6	2.41	0.55
24:CX:41:C:H2'	24:CX:42:G:H8	1.71	0.55
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.06	0.55
26:BA:1021:A:H8	26:BA:1021:A:H3'	1.72	0.55
24:CX:16:C:H3'	24:CX:17:C:O2	2.06	0.55
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.06	0.55
26:BA:1204:A:N6	26:BA:1240:U:H2'	2.21	0.55
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.87	0.55
4:AD:109:GLY:HA3	4:AD:165:MET:HG3	1.88	0.55
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.21	0.55
1:CA:406:G:O2'	4:CD:3:ARG:NH2	2.40	0.55
26:DA:2869:G:H2'	26:DA:2870:C:O4'	2.05	0.55
7:CG:115:ARG:HG2	7:CG:118:VAL:HG23	1.89	0.55
35:DO:64:ARG:NH1	35:DO:81:ASP:OD2	2.40	0.55
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.05	0.55
5:CE:8:GLU:OE2	5:CE:63:ARG:NH2	2.40	0.55
1:CA:1024:G:C2'	1:CA:1025:U:H5''	2.36	0.55
24:CX:66:C:H5''	24:CX:67:C:OP2	2.06	0.55
23:CW:76:PPU:O	23:CW:76:PPU:H5'	2.05	0.55
26:BA:1173:G:N2	26:BA:1177:A:OP2	2.34	0.55
1:CA:1065:U:P	1:CA:1190:G:H22	2.29	0.55
28:DD:242:ARG:N	28:DD:242:ARG:HD3	2.20	0.55
1:CA:991:U:H3'	1:CA:1212:U:N3	2.21	0.55
9:AI:50:LEU:HD23	9:AI:81:ILE:HD11	1.87	0.55
1:AA:562:C:N3	12:AL:16:GLU:HB3	2.22	0.55
26:DA:1188:U:H4'	42:DV:79:VAL:HG22	1.88	0.55
26:BA:651:G:OP1	55:B8:19:SER:OG	2.21	0.55
36:DP:55:ARG:HA	61:DP:307:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2296:U:OP2	39:DS:9:ARG:NH2	2.37	0.55
1:AA:70:G:H1	1:AA:99:U:H3	1.55	0.55
41:BU:17:ILE:HG23	41:BU:39:LEU:HD12	1.87	0.55
28:BD:118:VAL:N	28:BD:129:ASN:OD1	2.35	0.55
26:DA:2176:A:H2'	26:DA:2177:C:C5	2.42	0.55
1:CA:96:U:O2'	1:CA:97:G:O4'	2.24	0.55
1:CA:971:G:N2	1:CA:1363(A):A:OP2	2.34	0.55
26:BA:1173:G:H22	26:BA:1177:A:P	2.28	0.55
26:DA:892:G:H2'	26:DA:893:C:O4'	2.07	0.55
26:DA:1803:A:H4'	28:DD:259:THR:HG23	1.89	0.55
31:DG:16:ARG:O	31:DG:20:ILE:HG13	2.07	0.55
26:BA:1721:G:H8	26:BA:1741:A:H62	1.53	0.55
1:CA:113:G:N3	1:CA:353:A:O2'	2.38	0.55
27:DB:40:U:N3	27:DB:44:G:OP2	2.38	0.55
26:DA:796:C:H2'	26:DA:797:C:C6	2.41	0.55
26:DA:1939:U:OP1	26:DA:2604:U:O2'	2.20	0.55
46:BZ:102:LEU:HD23	46:BZ:139:VAL:HG21	1.89	0.55
44:BX:43:VAL:HG21	44:BX:81:VAL:HG11	1.89	0.55
1:AA:673:G:H2'	1:AA:674:G:C8	2.42	0.55
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.88	0.55
24:AX:53:G:H3'	24:AX:54:5MU:H71	1.88	0.55
1:AA:539:A:OP2	12:AL:115:LYS:NZ	2.40	0.55
26:DA:2102:U:H3	26:DA:2187:G:H1	1.55	0.55
1:CA:1099:G:C6	1:CA:1100:C:N3	2.75	0.55
26:DA:2820:A:C6	38:DR:4:LEU:HD11	2.42	0.55
4:CD:161:ASN:O	4:CD:165:MET:N	2.39	0.55
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.40	0.55
33:BI:93:THR:HG22	33:BI:119:PRO:HB3	1.88	0.55
26:BA:645:C:H5'	26:BA:646:A:OP2	2.06	0.55
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.89	0.55
1:AA:28:G:O2'	1:AA:296:U:OP1	2.20	0.55
33:DI:12:LEU:HD22	33:DI:19:VAL:HG21	1.89	0.55
26:BA:463:G:N7	61:BA:4346:HOH:O	2.33	0.55
32:DH:89:ILE:O	32:DH:129:THR:HG23	2.07	0.55
26:DA:800:A:OP1	26:DA:800:A:H8	1.90	0.55
26:BA:684:G:OP1	54:B7:16:HIS:ND1	2.38	0.55
26:BA:1253:A:N6	61:BA:4106:HOH:O	2.19	0.55
1:CA:1277:C:HO2'	1:CA:1279:A:H8	1.54	0.55
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	1.88	0.55
26:DA:1497:U:H5''	26:DA:1498:C:H5	1.71	0.55
49:D2:18:PRO:HB3	49:D2:68:ARG:NH1	2.20	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:880:G:N2	26:BA:898:C:C2	2.75	0.55
26:DA:298:G:H5''	26:DA:299:A:OP1	2.07	0.55
1:AA:838:G:H1	1:AA:848:C:H42	1.55	0.55
1:AA:1036:G:H21	1:AA:1037:C:H1'	1.70	0.55
26:BA:784:A:H5'	26:BA:785:G:OP1	2.07	0.55
30:BF:101:LEU:O	30:BF:106:ARG:NH1	2.39	0.55
1:AA:69:G:H2'	1:AA:70:G:C8	2.41	0.55
26:DA:2867:G:OP2	40:DT:119:LYS:NZ	2.39	0.55
17:CQ:6:LEU:HG	17:CQ:23:VAL:HG11	1.88	0.55
26:DA:729:G:H5'	26:DA:730:C:O5'	2.07	0.55
5:AE:7:GLU:OE1	5:AE:37:ARG:NH2	2.39	0.55
1:AA:17:U:H2'	1:AA:18:C:C6	2.42	0.55
9:AI:31:GLN:HE21	9:AI:36:TYR:HA	1.71	0.55
1:CA:1004:A:H5''	1:CA:1025:U:C5	2.42	0.55
1:CA:97:G:O2'	1:CA:98:G:O4'	2.19	0.55
26:BA:2156:G:H21	26:BA:2158:A:H62	1.54	0.55
26:DA:2723:C:OP2	29:DE:109:LYS:NZ	2.40	0.55
20:AT:9:ASN:O	20:AT:10:LEU:HB2	2.05	0.55
1:AA:1027:C:N3	1:AA:1034:G:C2	2.74	0.55
1:CA:1250:A:H2'	1:CA:1251:A:C8	2.42	0.55
26:BA:582:G:H2'	26:BA:583:G:C8	2.42	0.55
3:CC:43:LEU:HD21	3:CC:91:LEU:HD13	1.89	0.55
1:AA:659:U:C2'	1:AA:660:G:H5'	2.36	0.55
17:AQ:53:LEU:HD23	17:AQ:82:MET:HE1	1.88	0.55
26:DA:1434:A:H61	26:DA:1558:A:N6	2.05	0.55
44:DX:11:PRO:HB3	44:DX:92:LEU:HD11	1.88	0.55
3:CC:47:LEU:O	3:CC:51:GLY:N	2.40	0.55
6:CF:70:ASP:OD1	6:CF:70:ASP:N	2.37	0.55
27:DB:19:G:H2'	27:DB:20:C:O4'	2.06	0.55
1:CA:627:G:H2'	1:CA:628:G:C8	2.39	0.55
26:DA:784:A:C5	28:DD:229:VAL:HG21	2.41	0.55
26:BA:330:A:H2	26:BA:1210:A:C2'	2.20	0.55
2:AB:127:ILE:HD12	2:AB:130:ARG:HD3	1.88	0.55
1:AA:737:A:H2'	1:AA:738:C:C6	2.42	0.55
1:CA:804:U:H5''	1:CA:805:C:OP2	2.07	0.55
1:CA:277:C:H5''	17:CQ:68:ARG:NH2	2.22	0.55
26:DA:480:A:N3	26:DA:499:U:O2'	2.33	0.55
3:AC:100:ALA:O	3:AC:102:ASN:ND2	2.40	0.55
1:AA:1131:G:H2'	1:AA:1132:C:C6	2.42	0.55
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.05	0.55
46:BZ:19:ARG:NH1	46:BZ:84:GLU:O	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DI:52:ARG:H	33:DI:52:ARG:HH11	1.53	0.54
1:CA:979:C:H2'	1:CA:980:C:H5'	1.89	0.54
36:DP:89:ALA:O	36:DP:121:LYS:NZ	2.29	0.54
36:BP:100:LEU:HD12	36:BP:112:LEU:HD11	1.89	0.54
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.43	0.54
1:AA:954:G:H21	1:AA:1227:A:H62	1.55	0.54
26:BA:1899:G:H2'	26:BA:1899:G:N3	2.22	0.54
26:DA:2507:C:H2'	26:DA:2508:G:O4'	2.07	0.54
2:AB:78:GLN:O	2:AB:94:ASN:ND2	2.40	0.54
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.88	0.54
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.07	0.54
1:AA:527:G:O2'	1:AA:535:A:N1	2.37	0.54
26:DA:2183:C:H2'	26:DA:2184:G:C8	2.39	0.54
24:AX:4:G:H2'	24:AX:5:G:H8	1.72	0.54
26:BA:1557:C:OP2	26:BA:1558:A:O2'	2.21	0.54
27:DB:28:C:OP1	39:DS:31:SER:OG	2.17	0.54
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.07	0.54
1:AA:1086:U:H2'	1:AA:1087:G:H8	1.72	0.54
36:BP:121:LYS:HG3	50:D3:2:PRO:HG3	1.88	0.54
26:DA:1038:C:N4	26:DA:1117:G:H1	2.05	0.54
1:AA:1030:C:H5''	1:AA:1030(A):G:O5'	2.07	0.54
1:AA:537:G:H5''	12:AL:113:ARG:NH1	2.23	0.54
26:DA:299:A:N1	26:DA:322:A:O2'	2.32	0.54
1:AA:139:G:N2	1:AA:224:C:O2	2.40	0.54
31:DG:32:PRO:HB3	31:DG:172:LEU:HD22	1.90	0.54
37:DQ:26:TYR:O	37:DQ:67:ARG:NH1	2.35	0.54
26:DA:1753:G:OP2	40:DT:115:ARG:NH2	2.41	0.54
26:BA:2572:A:N7	29:BE:144:ARG:HD2	2.21	0.54
1:CA:49:U:O4	1:CA:365:U:H5	1.90	0.54
26:BA:687:C:H5''	54:B7:2:LYS:HE2	1.89	0.54
1:CA:1202:G:O4'	14:CN:29:ARG:NH1	2.41	0.54
26:BA:2364:C:H2'	26:BA:2365:G:O4'	2.07	0.54
1:CA:72:C:N4	1:CA:97:G:C2	2.73	0.54
24:CX:17:C:OP1	24:CX:60:U:O2'	2.24	0.54
26:DA:515:A:H1'	26:DA:581:C:H1'	1.89	0.54
1:AA:1149:C:P	9:AI:9:ARG:HH21	2.30	0.54
26:BA:2531:A:H5'	32:BH:157:TYR:CE1	2.42	0.54
26:BA:636:G:OP1	36:BP:132:LYS:HE2	2.07	0.54
26:BA:637:A:H5''	36:BP:117:GLU:HG2	1.89	0.54
26:BA:2441:C:OP2	26:BA:2586:C:O2'	2.23	0.54
26:DA:2635:C:O2'	29:DE:80:GLU:OE1	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:85:LYS:HG3	4:AD:86:LYS:H	1.73	0.54
1:CA:944:G:O2'	1:CA:1339:A:N6	2.41	0.54
26:DA:695:G:H4'	26:DA:1380:G:H5'	1.88	0.54
1:CA:1220:G:H5'	19:CS:34:TRP:O	2.07	0.54
1:CA:1000:U:H2'	1:CA:1001:A:C8	2.43	0.54
13:CM:87:TYR:N	19:CS:73:GLU:O	2.40	0.54
29:BE:29:GLY:HA3	61:BE:3106:HOH:O	2.07	0.54
26:DA:1023:U:OP2	61:DA:4207:HOH:O	2.18	0.54
34:BN:36:GLY:HA2	34:BN:38:HIS:CE1	2.43	0.54
26:DA:740:U:H2'	26:DA:741:G:H8	1.72	0.54
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.42	0.54
46:BZ:54:HIS:ND1	46:BZ:101:PRO:HG3	2.23	0.54
26:DA:2695:C:H2'	26:DA:2696:U:C6	2.43	0.54
26:DA:2370:G:H2'	26:DA:2371:G:C8	2.42	0.54
38:BR:33:ARG:NH1	38:BR:115:GLU:OE2	2.35	0.54
26:BA:1939:U:OP1	26:BA:2604:U:O2'	2.21	0.54
1:CA:562:C:H1'	12:CL:15:ARG:HD2	1.90	0.54
50:B3:18:ASP:OD1	50:B3:18:ASP:N	2.41	0.54
26:BA:1791:A:H5'	28:BD:206:LEU:HD12	1.88	0.54
40:DT:99:LEU:O	40:DT:101:PHE:N	2.40	0.54
1:CA:109:A:C6	1:CA:326:G:C6	2.95	0.54
30:DF:167:ALA:HB1	30:DF:173:VAL:HG11	1.87	0.54
1:AA:1055:A:H8	1:AA:1055:A:H5'	1.72	0.54
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.75	0.54
26:DA:1889:A:H2'	26:DA:1890:A:C8	2.42	0.54
26:BA:330:A:HO2'	26:BA:331:A:H8	1.55	0.54
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.23	0.54
4:AD:102:ASP:OD1	4:AD:103:ASN:N	2.41	0.54
26:BA:642:G:N2	26:BA:645:C:OP2	2.41	0.54
1:AA:636:U:H2'	1:AA:637:G:C8	2.42	0.54
26:DA:2478:A:O2'	26:DA:2536:G:N2	2.40	0.54
26:DA:2818:G:OP2	38:DR:42:LYS:NZ	2.39	0.54
26:BA:39:C:O2	30:BF:46:ARG:NH2	2.41	0.54
7:CG:69:VAL:HG21	7:CG:104:LEU:HD11	1.89	0.54
46:DZ:154:ASP:N	46:DZ:154:ASP:OD1	2.41	0.54
40:DT:24:PRO:HA	40:DT:49:VAL:HG22	1.89	0.54
20:CT:16:HIS:O	20:CT:19:SER:OG	2.21	0.54
45:BY:15:VAL:HG21	45:BY:42:VAL:HG11	1.89	0.54
26:DA:993:G:N2	42:DV:23:GLU:OE2	2.39	0.54
53:B6:6:ARG:NH1	53:B6:26:ASN:HB2	2.23	0.54
5:CE:31:LEU:HD11	5:CE:129:ILE:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DD:108:PRO:HG2	28:DD:111:LEU:HB2	1.89	0.54
29:DE:54:GLN:OE1	29:DE:55:ASN:N	2.40	0.54
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.33	0.54
28:DD:77:ALA:HA	28:DD:97:TYR:HA	1.88	0.54
26:BA:1796:U:H2'	26:BA:1797:C:C6	2.43	0.54
51:B4:55:ARG:N	51:B4:56:VAL:HA	2.23	0.54
1:CA:1403:C:N4	22:CV:18:G:OP1	2.41	0.54
1:CA:1118:C:N3	1:CA:1156:G:N2	2.56	0.54
26:DA:2126:A:N3	26:DA:2127:G:H1'	2.22	0.54
26:DA:93:G:H2'	26:DA:94:C:C6	2.43	0.54
1:AA:1460:A:H2'	1:AA:1461:G:O4'	2.07	0.54
26:BA:2532:G:O2'	26:BA:2657:A:N1	2.38	0.54
11:AK:33:THR:HG22	11:AK:39:PRO:HA	1.90	0.54
5:CE:137:GLU:HA	5:CE:140:ARG:HB3	1.89	0.54
3:CC:172:ARG:NH2	3:CC:206:GLU:OE1	2.40	0.54
1:CA:664:G:H22	1:CA:741:G:H1	1.56	0.54
26:DA:492:A:H2'	26:DA:493:G:O4'	2.07	0.54
44:DX:35:THR:HG22	44:DX:38:GLU:HB2	1.90	0.54
1:CA:1027:C:N4	1:CA:1034:G:C6	2.76	0.54
26:DA:2138:C:N4	26:DA:2153:G:H1	2.03	0.54
1:CA:1262:C:N3	1:CA:1273:G:N2	2.49	0.54
10:CJ:38:ILE:O	10:CJ:38:ILE:HG13	2.07	0.54
26:DA:2544:G:H1'	26:DA:2646:C:H4'	1.89	0.54
26:BA:468:G:OP2	54:B7:37:LYS:NZ	2.41	0.54
40:BT:24:PRO:HA	40:BT:49:VAL:HG22	1.89	0.54
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.42	0.54
3:AC:153:VAL:HA	3:AC:197:GLY:O	2.08	0.54
1:CA:1000:U:H2'	1:CA:1001:A:H8	1.70	0.54
1:CA:1120:G:N1	1:CA:1154:G:N3	2.55	0.54
26:DA:880:G:H2'	26:DA:880:G:N3	2.23	0.54
26:BA:2791:C:C2	26:BA:2805:G:N2	2.76	0.54
1:AA:975:A:C8	1:AA:975:A:H5'	2.41	0.54
1:AA:791:G:N2	1:AA:1497:G:O3'	2.39	0.54
27:DB:105:A:OP1	46:DZ:72:ARG:NH1	2.41	0.54
26:BA:1268:A:H2'	26:BA:1269:A:O4'	2.08	0.54
36:BP:82:GLY:HA2	36:BP:113:LYS:O	2.08	0.54
13:CM:34:LEU:HD22	13:CM:39:ILE:HB	1.90	0.54
26:BA:1107:G:H2'	26:BA:1107:G:N3	2.22	0.54
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.41	0.54
45:BY:20:TYR:CE1	45:BY:43:ASN:HA	2.43	0.54
26:DA:2405:G:OP1	36:DP:77:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.72	0.54
1:AA:165:C:H2'	1:AA:166:G:C8	2.43	0.54
18:AR:32:ARG:HA	18:AR:69:THR:HG21	1.90	0.54
26:DA:2135:A:H2'	26:DA:2136:C:C6	2.42	0.54
26:BA:2137:C:N3	26:BA:2154:G:O6	2.41	0.54
1:AA:1285:A:H4'	1:AA:1286:A:O5'	2.08	0.54
36:DP:99:LEU:HA	36:DP:102:ARG:HB3	1.90	0.54
26:BA:587:C:OP2	36:BP:21:ARG:NH2	2.41	0.54
1:CA:501:C:H2'	1:CA:502:G:H8	1.72	0.54
1:AA:1151:A:O2'	1:AA:1152:A:H8	1.91	0.54
26:BA:956:G:OP2	37:BQ:14:ARG:NH2	2.40	0.54
44:BX:54:VAL:HG22	44:BX:81:VAL:HG12	1.89	0.54
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.72	0.54
3:AC:120:VAL:HA	3:AC:123:GLN:HE21	1.73	0.54
51:D4:17:GLY:N	51:D4:33:VAL:O	2.41	0.54
42:BV:74:LYS:HB2	42:BV:83:ARG:HB2	1.88	0.54
26:DA:1966:A:H4'	26:DA:1967:C:OP1	2.08	0.54
22:CV:18:G:N2	24:CX:34:C:C2	2.75	0.53
1:CA:999:C:N3	1:CA:1042:G:C2	2.76	0.53
1:AA:1505:G:O2'	22:AV:13:A:O2'	1.94	0.53
26:DA:2162:G:H5''	26:DA:2172:U:C6	2.43	0.53
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.20	0.53
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.41	0.53
26:BA:885:C:H3'	26:BA:886:C:C5'	2.38	0.53
27:DB:54:G:N2	31:DG:29:TRP:HZ2	2.04	0.53
27:DB:13:A:C2	27:DB:16:G:H1'	2.43	0.53
15:AO:24:SER:HB3	15:AO:27:VAL:HG23	1.89	0.53
1:CA:792:A:H4'	1:CA:793:U:C5'	2.39	0.53
26:BA:747:U:O2	26:BA:2014:A:H1'	2.08	0.53
26:BA:2267:A:H5''	26:BA:2268:A:H5'	1.90	0.53
35:BO:23:ARG:HG3	35:BO:24:VAL:N	2.23	0.53
40:BT:53:ARG:NH1	40:BT:53:ARG:HB3	2.23	0.53
26:DA:2505:G:OP1	61:DA:3855:HOH:O	2.18	0.53
39:DS:58:LEU:HD12	39:DS:65:VAL:HG22	1.89	0.53
1:CA:154:C:H2'	1:CA:155:C:H5'	1.88	0.53
36:DP:99:LEU:O	36:DP:103:ALA:N	2.39	0.53
19:AS:27:GLU:HB3	19:AS:28:LYS:HB3	1.89	0.53
26:BA:2646:C:H2'	26:BA:2647:U:O4'	2.08	0.53
26:DA:71:A:N7	44:DX:31:HIS:HE1	2.06	0.53
32:BH:3:ARG:HD3	32:BH:54:ARG:HH12	1.74	0.53
26:BA:7:G:H2'	26:BA:8:A:O4'	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1047:G:N2	26:BA:1110:G:O2'	2.41	0.53
2:AB:16:HIS:CB	2:AB:204:ASN:HB3	2.33	0.53
1:AA:148:G:C2	1:AA:175:C:N3	2.77	0.53
13:CM:62:ASN:HA	51:D4:49:PHE:HD2	1.73	0.53
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	1.89	0.53
1:AA:1149:C:O2'	1:AA:1280:A:N1	2.31	0.53
26:DA:307:G:H21	26:DA:330:A:H62	1.55	0.53
26:DA:1588:C:H2'	26:DA:1589:C:H6	1.74	0.53
1:AA:841:U:C5	1:AA:848:C:H1'	2.43	0.53
26:DA:2023:G:H1	26:DA:2040:C:H42	1.56	0.53
26:DA:2247:A:H2'	26:DA:2248:C:C6	2.44	0.53
26:DA:1239:G:H2'	26:DA:1240:U:O4'	2.08	0.53
26:BA:2801(A):A:H5''	26:BA:2802:G:C8	2.43	0.53
1:CA:636:U:H2'	1:CA:637:G:H8	1.73	0.53
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.07	0.53
26:BA:2337:G:OP1	61:BA:4006:HOH:O	2.18	0.53
26:DA:1009:A:OP2	34:DN:37:LYS:NZ	2.29	0.53
38:DR:55:ALA:HB2	38:DR:79:LEU:HD13	1.90	0.53
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.90	0.53
1:CA:229:U:O2'	16:CP:23:ASP:OD2	2.25	0.53
19:CS:27:GLU:HB3	19:CS:28:LYS:HB3	1.90	0.53
1:CA:709:G:C2'	1:CA:710:G:H5'	2.38	0.53
26:BA:467:G:OP1	54:B7:33:ARG:NH1	2.41	0.53
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.24	0.53
1:AA:805:C:OP2	61:AA:4031:HOH:O	2.19	0.53
20:AT:65:LYS:HA	20:AT:68:LYS:HD3	1.89	0.53
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.43	0.53
26:DA:1933:G:H2'	26:DA:1934:C:O4'	2.08	0.53
1:AA:460:G:N1	1:AA:470:C:H5'	2.23	0.53
27:DB:98:G:H2'	27:DB:99:G:O4'	2.08	0.53
1:CA:377:G:OP1	16:CP:3:LYS:HD2	2.07	0.53
26:BA:2782:G:OP2	61:BA:4674:HOH:O	2.18	0.53
26:DA:1639:U:H2'	26:DA:1640:C:H5''	1.88	0.53
26:DA:698:C:O2'	26:DA:734:A:N6	2.42	0.53
11:CK:43:SER:HA	11:CK:47:VAL:HG21	1.91	0.53
1:AA:797:C:C2'	1:AA:798:G:H5'	2.38	0.53
46:DZ:70:LEU:O	46:DZ:89:PHE:N	2.32	0.53
1:AA:358:U:H2'	1:AA:359:U:C6	2.43	0.53
46:DZ:120:ILE:HD12	46:DZ:120:ILE:H	1.72	0.53
26:DA:1876:A:H2'	26:DA:1877:A:C8	2.44	0.53
26:BA:1175:U:H1'	26:BA:1176:G:OP1	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:29:A:C2	27:DB:56:G:C2	2.97	0.53
4:CD:173:TRP:CD2	4:CD:189:PRO:HG3	2.43	0.53
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.23	0.53
26:DA:2247:A:H2'	26:DA:2248:C:H6	1.73	0.53
1:CA:1178:G:N2	1:CA:1180:A:H3'	2.23	0.53
26:BA:1009:A:OP2	34:BN:37:LYS:NZ	2.29	0.53
26:DA:623:G:H2'	26:DA:624:C:C6	2.44	0.53
26:DA:1278:A:OP1	38:DR:36:THR:HG23	2.09	0.53
26:DA:2849:U:OP2	40:DT:95:ARG:NH1	2.41	0.53
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.89	0.53
37:DQ:52:VAL:O	37:DQ:56:ARG:HB2	2.07	0.53
36:DP:100:LEU:HD12	36:DP:112:LEU:HD11	1.89	0.53
17:CQ:59:ILE:HG22	17:CQ:73:VAL:HA	1.89	0.53
26:DA:839:U:H2'	26:DA:840:C:C6	2.43	0.53
33:DI:81:VAL:O	33:DI:82:ARG:HG3	2.08	0.53
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.73	0.53
1:AA:392:G:H2'	1:AA:393:A:H8	1.73	0.53
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.08	0.53
7:AG:29:LYS:HB3	7:AG:105:VAL:HG21	1.90	0.53
3:AC:7:PRO:O	3:AC:11:ARG:NH1	2.42	0.53
26:DA:2659:G:N2	26:DA:2661:G:H5''	2.23	0.53
1:AA:947:G:N2	1:AA:1235:U:O2	2.42	0.53
26:DA:1750:G:N3	26:DA:2860:A:H2	2.06	0.53
33:DI:124:GLY:O	33:DI:144:VAL:HB	2.08	0.53
26:BA:414:C:H2'	26:BA:415:A:H8	1.73	0.53
1:AA:1499:A:H1'	1:AA:1520:G:H5'	1.91	0.53
24:CX:12:G:H4'	26:DA:1908:C:O2	2.08	0.53
26:DA:2086:U:H2'	26:DA:2087:G:C8	2.44	0.53
9:CI:24:GLY:HA2	9:CI:59:PHE:O	2.09	0.53
2:AB:231:GLU:HB2	2:AB:232:PRO:HD3	1.91	0.53
26:BA:2031:A:C6	26:BA:2498:C:H1'	2.43	0.53
7:CG:72:ARG:NE	7:CG:142:GLU:OE2	2.42	0.53
1:CA:723:U:HO2'	1:CA:724:G:C5'	2.21	0.53
36:DP:84:ASN:OD1	36:DP:117:GLU:HB2	2.09	0.53
11:AK:98:LEU:O	11:AK:101:SER:OG	2.15	0.53
26:DA:1833:U:O2'	26:DA:1969:A:N1	2.35	0.53
26:BA:2308:G:O2'	26:BA:2310:A:N7	2.41	0.53
1:AA:1456:G:H22	20:AT:43:LEU:HD11	1.74	0.53
1:AA:1030(D):A:N6	1:AA:1031:G:H21	2.07	0.53
26:DA:2522:U:O2'	26:DA:2647:U:OP1	2.16	0.53
24:AX:8:4SU:O2	24:AX:21:A:H2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:122:LYS:HD3	13:CM:123:ALA:H	1.73	0.53
10:CJ:78:ASN:O	10:CJ:80:LYS:N	2.41	0.53
26:DA:18:C:H2'	26:DA:19:C:H6	1.73	0.53
53:D6:9:LEU:HA	53:D6:54:ILE:HB	1.89	0.53
26:BA:1587:A:H2'	26:BA:1588:C:C6	2.43	0.53
45:DY:14:LEU:N	45:DY:73:ARG:O	2.36	0.53
26:BA:1607:C:H4'	26:BA:1608:A:O5'	2.08	0.53
1:CA:1003:G:O3'	1:CA:1004:A:H4'	2.09	0.53
1:CA:1027:C:N3	1:CA:1034:G:N2	2.57	0.53
26:BA:1359:A:N6	26:BA:1372:U:C2	2.76	0.53
45:BY:92:ASN:N	45:BY:93:GLY:HA2	2.23	0.53
26:DA:2312:U:H5'	31:DG:88:ILE:HD11	1.89	0.53
26:BA:826:U:H4'	36:BP:55:ARG:HB2	1.90	0.53
38:DR:33:ARG:NH2	52:D5:57:VAL:O	2.37	0.53
33:BI:102:SER:HA	33:BI:106:GLY:HA3	1.91	0.53
26:BA:2239:G:H5'	28:BD:251:GLY:HA3	1.90	0.53
26:BA:884:C:H2'	26:BA:885:C:O4'	2.08	0.53
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.07	0.53
26:DA:1514:U:H2'	26:DA:1515:G:C8	2.44	0.53
1:AA:828:A:H2'	1:AA:829:G:O4'	2.09	0.53
1:AA:542:G:P	4:AD:10:ARG:HH22	2.32	0.53
26:DA:1212:G:H1'	26:DA:1236:G:N2	2.24	0.53
26:DA:143:G:H2'	26:DA:143(A):C:C6	2.43	0.53
30:DF:192:LEU:HD13	30:DF:194:MET:HE2	1.89	0.53
26:BA:2695:C:H2'	26:BA:2696:U:H6	1.74	0.53
1:CA:1297:C:H4'	1:CA:1298:C:H5''	1.91	0.53
33:BI:80:PRO:HA	33:BI:145:VAL:O	2.08	0.53
17:AQ:21:VAL:N	17:AQ:42:TYR:O	2.36	0.53
1:AA:713:G:H2'	1:AA:714:G:C8	2.43	0.53
1:CA:390:C:H2'	1:CA:391:G:C8	2.44	0.53
1:AA:1189:C:H5''	3:AC:5:ILE:HD12	1.91	0.53
1:CA:501:C:H2'	1:CA:502:G:C8	2.43	0.53
26:DA:307:G:N1	26:DA:310:A:OP2	2.38	0.53
18:CR:47:THR:HG23	18:CR:49:LYS:HG3	1.90	0.53
26:DA:656:G:H2'	26:DA:657:U:O4'	2.09	0.53
43:DW:18:ARG:NH1	43:DW:76:VAL:O	2.42	0.53
27:BB:30:C:H2'	27:BB:31:C:H5'	1.91	0.53
1:AA:1025:U:C2	1:AA:1036:G:O6	2.62	0.53
34:DN:46:VAL:HG23	34:DN:48:MET:HG2	1.91	0.53
6:CF:100:ASN:HD21	18:CR:23:LYS:HG2	1.74	0.53
17:AQ:56:VAL:HB	17:AQ:78:GLU:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CH:103:VAL:HG21	8:CH:110:ALA:HB2	1.89	0.53
26:DA:531:C:H4'	26:DA:532:A:H5''	1.91	0.53
1:AA:1125:U:C4'	10:AJ:5:ARG:HH22	2.21	0.53
13:AM:80:ARG:HH21	51:B4:58:ARG:NH1	2.07	0.53
19:AS:69:HIS:H	51:B4:58:ARG:HH21	1.57	0.53
26:BA:1786:A:H1'	26:BA:1938:A:H61	1.74	0.53
13:CM:4:ILE:HD11	13:CM:60:VAL:HG11	1.91	0.53
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.39	0.53
26:DA:459:U:H5''	54:D7:40:TRP:CD2	2.44	0.53
26:DA:2193:G:H2'	26:DA:2194:G:C8	2.44	0.53
4:AD:162:LEU:HB3	4:AD:178:VAL:HG13	1.90	0.53
32:DH:3:ARG:NH2	32:DH:5:GLY:H	2.07	0.53
26:BA:1792:G:O2'	26:BA:1830:C:OP1	2.22	0.53
1:AA:401:C:OP2	4:AD:73:ARG:NH1	2.42	0.53
32:BH:101:ARG:NH2	32:BH:117:PRO:HB2	2.24	0.53
2:CB:19:HIS:CG	2:CB:20:GLU:H	2.27	0.53
26:BA:2405:G:O2'	26:BA:2411:A:N6	2.41	0.53
26:BA:667:U:O2	55:B8:2:PRO:HD2	2.09	0.53
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.08	0.53
39:BS:83:LYS:HD2	39:BS:111:GLU:OE1	2.09	0.53
26:DA:2667:C:H1'	32:DH:109:PHE:CD1	2.44	0.53
26:DA:1292:U:H2'	26:DA:1293:C:C6	2.44	0.53
1:CA:97:G:C2	1:CA:98:G:C4	2.97	0.52
26:DA:2167:U:H2'	26:DA:2168:G:H21	1.74	0.52
27:BB:105:A:OP1	46:BZ:72:ARG:NH1	2.42	0.52
26:BA:2630:G:H2'	26:BA:2631:G:C8	2.44	0.52
14:AN:29:ARG:HD3	14:AN:40:CYS:SG	2.49	0.52
26:DA:571:A:N6	26:DA:2499:C:O3'	2.41	0.52
26:DA:470:A:OP1	30:DF:59:TYR:HE1	1.91	0.52
26:DA:1022:G:H22	26:DA:1142(A):A:H2	1.54	0.52
1:CA:284:G:H2'	1:CA:285:G:C8	2.44	0.52
8:CH:23:SER:HB2	8:CH:60:ARG:HG2	1.91	0.52
1:AA:390:C:H2'	1:AA:391:G:C8	2.43	0.52
42:DV:5:VAL:HG11	42:DV:57:VAL:HG21	1.91	0.52
36:BP:95:VAL:HG13	36:BP:125:VAL:HG12	1.91	0.52
1:AA:581:G:N2	1:AA:760:G:N7	2.56	0.52
31:DG:73:ALA:HB3	31:DG:84:LYS:HA	1.91	0.52
43:DW:34:ASN:OD1	43:DW:37:ARG:NH2	2.42	0.52
39:BS:14:VAL:O	39:BS:18:ILE:HG12	2.09	0.52
1:CA:1002:G:H2'	1:CA:1003:G:H8	1.73	0.52
26:DA:363(B):G:H2'	26:DA:363(C):G:C8	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1055:A:O2'	3:CC:161:GLU:O	2.24	0.52
26:BA:1570:A:H2'	26:BA:1571:A:C8	2.43	0.52
37:DQ:85:LYS:HD2	37:DQ:85:LYS:N	2.24	0.52
1:AA:1191:A:H5''	3:AC:4:LYS:NZ	2.23	0.52
26:BA:1035:U:H2'	26:BA:1036:G:C8	2.44	0.52
26:BA:34:C:H41	26:BA:447:A:H61	1.56	0.52
26:DA:1503:U:H2'	26:DA:1504:C:C6	2.45	0.52
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.45	0.52
1:AA:396:G:O6	61:AA:4041:HOH:O	2.18	0.52
51:D4:60:GLN:H	51:D4:62:ARG:HE	1.57	0.52
26:BA:2224:G:H4'	26:BA:2226:C:C2	2.44	0.52
26:DA:900:A:H2'	26:DA:901:A:O4'	2.08	0.52
45:DY:86:ARG:NH1	45:DY:100:ALA:O	2.42	0.52
26:DA:2523:G:N3	26:DA:2764:A:O2'	2.42	0.52
27:DB:41:U:O4	31:DG:70:VAL:HB	2.09	0.52
33:DI:77:LEU:HA	33:DI:104:GLN:OE1	2.09	0.52
34:DN:58:ASP:OD1	34:DN:58:ASP:N	2.39	0.52
47:D0:50:ASN:HB3	47:D0:63:VAL:HG22	1.91	0.52
1:AA:524:G:H2'	1:AA:525:C:C6	2.44	0.52
26:BA:1688:U:O2	26:BA:1700:A:H5'	2.09	0.52
26:DA:2343:C:H4'	26:DA:2373:G:O3'	2.09	0.52
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.09	0.52
1:AA:1164:G:N2	1:AA:1165:C:C4	2.75	0.52
1:CA:1216:G:H5''	14:CN:5:ALA:CB	2.39	0.52
1:CA:662:G:H2'	1:CA:663:A:C8	2.44	0.52
30:DF:11:VAL:HB	30:DF:18:ARG:HB3	1.91	0.52
1:AA:154:C:H2'	1:AA:155:C:H5'	1.90	0.52
28:DD:17:THR:O	28:DD:211:ARG:NH2	2.42	0.52
26:DA:537:C:OP1	34:DN:2:LYS:NZ	2.43	0.52
1:AA:167:G:H2'	1:AA:168:G:H8	1.73	0.52
16:CP:23:ASP:OD1	16:CP:25:ARG:HD3	2.09	0.52
45:BY:54:LYS:H	45:BY:56:PRO:HD3	1.73	0.52
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.45	0.52
1:CA:1370:G:N7	9:CI:109:VAL:HG11	2.24	0.52
26:BA:2679:A:H4'	29:BE:165:VAL:HG11	1.92	0.52
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.44	0.52
1:AA:530:G:O6	22:AV:21:C:H1'	2.10	0.52
1:CA:34:C:H2'	1:CA:35:G:H8	1.73	0.52
28:DD:152:GLY:O	28:DD:154:LYS:HG2	2.10	0.52
26:BA:1952:A:N3	26:BA:2560:C:O2'	2.40	0.52
26:DA:2035:G:P	26:DA:2036:C:H41	2.32	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2199:A:OP2	26:BA:2200:C:H5	1.92	0.52
45:DY:13:VAL:HB	45:DY:72:VAL:HG13	1.92	0.52
26:BA:2135:A:H61	26:BA:2156:G:N2	2.07	0.52
26:DA:1604:C:O2'	26:DA:1610:A:N1	2.34	0.52
1:CA:43:C:H2'	1:CA:44:G:O4'	2.10	0.52
26:BA:1315:C:O2'	26:BA:1392:A:N3	2.34	0.52
26:BA:796:C:H2'	26:BA:797:C:C6	2.45	0.52
1:CA:1305:G:H5''	21:CU:4:GLY:HA3	1.90	0.52
26:DA:275:G:H2'	26:DA:276:A:O4'	2.08	0.52
26:DA:1512:U:H2'	26:DA:1513:C:C6	2.44	0.52
26:BA:2312:U:H5'	31:BG:88:ILE:HD11	1.91	0.52
26:BA:1047:G:O2'	26:BA:1109:C:N4	2.42	0.52
35:DO:2:ILE:HD12	35:DO:6:THR:HG21	1.91	0.52
26:DA:253:C:OP2	55:D8:5:LYS:NZ	2.28	0.52
1:CA:632:A:H5'	1:CA:633:G:OP2	2.09	0.52
14:AN:26:ARG:HD3	14:AN:43:CYS:SG	2.50	0.52
1:AA:299:G:H2'	1:AA:300:A:C8	2.45	0.52
26:BA:302:C:OP2	45:BY:73:ARG:NH2	2.41	0.52
1:AA:792:A:H4'	1:AA:793:U:H5''	1.92	0.52
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.91	0.52
22:CV:15:A:H8	22:CV:15:A:O5'	1.92	0.52
1:CA:1035:A:C2	1:CA:1036:G:N7	2.78	0.52
1:CA:1014:A:OP1	19:CS:18:LYS:NZ	2.33	0.52
46:BZ:121:HIS:HB2	46:BZ:171:ILE:HG22	1.92	0.52
1:CA:1029:C:N4	1:CA:1032:G:C6	2.76	0.52
2:CB:96:ARG:CZ	2:CB:98:LEU:HD13	2.40	0.52
26:DA:529:A:OP2	34:DN:114:ARG:NH2	2.41	0.52
1:CA:1011:G:H1	1:CA:1018:C:N4	2.08	0.52
26:DA:1779:U:H2'	61:DA:4364:HOH:O	2.09	0.52
28:DD:51:VAL:HG11	28:DD:54:ARG:NH1	2.24	0.52
1:AA:269:C:H2'	1:AA:270:A:H8	1.75	0.52
8:CH:112:LEU:HB3	8:CH:133:LEU:HA	1.90	0.52
16:AP:57:ARG:HH21	16:AP:79:VAL:HA	1.75	0.52
12:AL:84:LEU:HB2	12:AL:105:TYR:CE2	2.45	0.52
43:BW:14:PRO:HG2	43:BW:78:GLU:CD	2.30	0.52
26:DA:1717:G:N2	26:DA:1745:C:O2	2.43	0.52
28:BD:34:VAL:HG12	28:BD:63:ARG:HG3	1.91	0.52
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.45	0.52
1:CA:989:C:N4	1:CA:1216:G:O6	2.43	0.52
23:AW:76:PPU:O	23:AW:76:PPU:H5'	2.10	0.52
1:CA:1124:G:H4'	1:CA:1125:U:O2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.10	0.52
26:BA:1359:A:N1	26:BA:1372:U:C4	2.76	0.52
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.91	0.52
19:AS:69:HIS:H	51:B4:58:ARG:NH2	2.08	0.52
1:AA:1224:G:O2'	1:AA:1322:C:OP1	2.21	0.52
1:AA:1169:A:OP2	1:AA:1169:A:H8	1.92	0.52
26:DA:1405:U:H2'	26:DA:1406:U:C6	2.45	0.52
38:DR:44:LEU:HD22	38:DR:48:VAL:HG23	1.92	0.52
33:DI:88:ILE:HG22	33:DI:123:LEU:HD23	1.92	0.52
1:CA:1493:A:H5'	1:CA:1494:G:OP2	2.10	0.52
1:CA:789:U:O2'	1:CA:791:G:N7	2.34	0.52
26:DA:781:A:C8	28:DD:219:PRO:HG3	2.44	0.52
26:DA:2773:C:OP1	29:DE:166:THR:OG1	2.27	0.52
1:AA:911:U:OP2	12:AL:97:ARG:NH1	2.42	0.52
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.73	0.52
26:DA:2364:C:H2'	26:DA:2365:G:O4'	2.09	0.52
39:BS:39:ILE:HB	39:BS:49:VAL:HG13	1.91	0.52
26:BA:2114:A:H2'	26:BA:2115:G:O4'	2.09	0.52
26:BA:1826:G:H4'	28:BD:242:ARG:CZ	2.39	0.52
1:CA:745:C:OP1	1:CA:852:G:H5'	2.10	0.52
1:CA:382:A:H2'	1:CA:383:A:C8	2.44	0.52
1:AA:861:G:HO2'	1:AA:874:G:HO2'	1.48	0.52
1:CA:1107:C:OP1	3:CC:173:VAL:N	2.42	0.52
26:DA:1032:A:O2'	26:DA:1034:G:OP2	2.24	0.52
30:DF:155:LEU:HD11	30:DF:176:LEU:HD12	1.90	0.52
1:CA:1002:G:N3	1:CA:1003:G:H8	2.07	0.52
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.27	0.52
1:AA:1009:G:O6	1:AA:1020:U:O4	2.27	0.52
26:BA:2805:G:H2'	26:BA:2807:G:H8	1.74	0.52
1:CA:540:G:H2'	1:CA:541:G:O4'	2.10	0.52
26:BA:271(A):A:N1	26:BA:272(D):G:O2'	2.30	0.52
1:AA:966:G:H21	9:AI:127:LYS:NZ	2.07	0.52
31:DG:17:PRO:HA	31:DG:20:ILE:HD12	1.91	0.52
26:BA:528:A:C2	26:BA:2042:A:H2'	2.45	0.52
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.09	0.52
26:DA:1815:A:OP2	28:DD:54:ARG:NH2	2.41	0.52
1:CA:109:A:H2'	1:CA:326:G:N2	2.24	0.52
45:DY:86:ARG:HB2	45:DY:98:VAL:HG23	1.92	0.52
50:D3:10:LYS:HB3	50:D3:53:LEU:HA	1.91	0.52
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.24	0.52
34:DN:16:ILE:HB	34:DN:54:VAL:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2366:A:H2'	26:DA:2367:G:O4'	2.09	0.52
5:CE:83:GLU:HG2	5:CE:88:LYS:HG3	1.91	0.52
1:AA:119:A:H4'	1:AA:120:A:C8	2.45	0.52
1:CA:190:U:H2'	1:CA:191:G:C8	2.45	0.52
35:DO:115:VAL:HG13	35:DO:121:VAL:HG21	1.91	0.52
1:CA:197:A:C6	1:CA:221:C:H4'	2.45	0.52
1:AA:178:C:H2'	1:AA:179:A:H8	1.75	0.52
26:DA:686:G:N2	26:DA:788:A:H61	2.06	0.52
1:CA:604:G:H2'	1:CA:605:U:O4'	2.10	0.52
1:CA:1278:U:H5'	1:CA:1279:A:O4'	2.09	0.52
1:CA:1367:C:HO2'	10:CJ:48:THR:HG1	1.56	0.52
1:AA:663:A:O3'	18:AR:64:ARG:NH2	2.43	0.52
26:DA:2572:A:C8	29:DE:144:ARG:HD2	2.44	0.52
1:AA:1005:A:C1'	1:AA:1036:G:H22	2.23	0.52
1:AA:276:G:O3'	17:AQ:68:ARG:NH1	2.43	0.52
4:CD:128:VAL:HG12	4:CD:129:ASN:HD22	1.75	0.52
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.92	0.52
28:BD:158:ALA:O	28:BD:161:THR:OG1	2.16	0.52
1:AA:683:G:H2'	1:AA:684:A:C8	2.44	0.52
56:B9:7:VAL:HG12	56:B9:34:GLN:HB3	1.91	0.52
4:CD:19:LEU:HD21	4:CD:63:LYS:HG3	1.90	0.52
11:CK:21:ILE:HD12	11:CK:84:VAL:HG22	1.92	0.52
2:CB:137:ARG:O	2:CB:141:GLU:N	2.37	0.52
1:CA:1399:C:C2	1:CA:1502:A:N6	2.78	0.52
26:DA:607:U:OP1	30:DF:102:PRO:HA	2.09	0.52
39:DS:25:ARG:NE	39:DS:88:ASP:OD2	2.29	0.52
40:DT:24:PRO:HD3	40:DT:52:ILE:HD12	1.92	0.52
26:DA:18:C:H2'	26:DA:19:C:C6	2.45	0.52
1:AA:1371:G:O3'	9:AI:69:GLY:HA3	2.10	0.52
29:DE:2:LYS:HB2	29:DE:95:ILE:HD12	1.92	0.52
1:CA:152:A:N6	1:CA:169:C:N3	2.56	0.52
26:BA:271(M):G:H4'	26:BA:271(N):U:OP1	2.10	0.52
1:CA:811:C:O2'	1:CA:901:A:N1	2.39	0.52
6:CF:7:ASN:HB2	6:CF:89:MET:HB3	1.92	0.52
5:CE:143:ARG:NH1	8:CH:77:GLU:OE2	2.43	0.52
31:DG:106:LEU:HA	31:DG:110:ALA:HB3	1.90	0.52
28:BD:26:LYS:HB3	28:BD:83:GLU:HG2	1.91	0.52
48:D1:23:LYS:HB3	48:D1:29:GLY:HA3	1.92	0.52
26:BA:764:A:O4'	28:BD:213:ARG:HG3	2.10	0.52
5:CE:6:PHE:HB2	5:CE:34:VAL:HG22	1.91	0.52
2:CB:16:HIS:HB3	2:CB:210:SER:CB	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1114:C:O2'	14:CN:60:SER:O	2.14	0.52
26:DA:2160:G:H2'	26:DA:2161:C:O4'	2.09	0.52
4:AD:157:LEU:HD22	4:AD:161:ASN:HD21	1.75	0.52
26:BA:278:A:H2'	26:BA:279:C:C6	2.45	0.52
26:DA:2805:G:C6	26:DA:2807:G:C6	2.98	0.52
26:DA:362:U:H4'	26:DA:363:G:OP1	2.10	0.52
26:BA:2278:A:H5''	47:B0:12:ASN:HD21	1.75	0.52
3:AC:150:LYS:HD3	3:AC:152:ILE:HD11	1.92	0.52
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.40	0.52
26:BA:1653:G:H3'	38:BR:2:ARG:HD3	1.91	0.52
26:DA:817:C:H2'	26:DA:818:G:O4'	2.09	0.52
33:DI:104:GLN:O	33:DI:105:HIS:ND1	2.43	0.52
1:CA:35:G:O2'	12:CL:118:SER:O	2.20	0.52
4:CD:79:PHE:HE1	4:CD:204:ILE:HD13	1.74	0.52
26:BA:1266:G:O5'	43:BW:15:ARG:NH2	2.43	0.52
24:CX:55:PSU:N3	24:CX:58:A:OP2	2.33	0.52
1:AA:1179:A:O3'	9:AI:103:THR:HB	2.09	0.52
26:DA:2360:A:H2'	26:DA:2361:A:O4'	2.10	0.52
32:DH:56:SER:HB3	32:DH:61:HIS:ND1	2.24	0.52
3:CC:33:LEU:HD11	14:CN:52:GLN:O	2.10	0.52
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.92	0.52
26:BA:2116:G:H2'	26:BA:2117:A:C5	2.45	0.51
36:BP:63:PRO:HD3	55:B8:27:THR:HG22	1.93	0.51
13:AM:33:ALA:O	13:AM:37:THR:OG1	2.13	0.51
26:DA:2645:G:N2	26:DA:2767:C:OP2	2.44	0.51
26:DA:833:U:O2	36:DP:55:ARG:NH2	2.43	0.51
26:DA:94(A):G:H2'	26:DA:95:G:O4'	2.10	0.51
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.44	0.51
56:B9:16:VAL:HG22	56:B9:25:VAL:HG22	1.92	0.51
26:BA:2627:G:O2'	26:BA:2781:A:N1	2.35	0.51
24:AX:18:G:O2'	24:AX:19:G:H5'	2.09	0.51
26:DA:271(Q):G:H2'	26:DA:271(R):G:C8	2.45	0.51
41:BU:49:HIS:HA	41:BU:52:ARG:HB3	1.90	0.51
1:CA:200:G:H2'	1:CA:201:C:O4'	2.09	0.51
1:CA:79:G:OP2	1:CA:79:G:H8	1.92	0.51
26:DA:2515:C:H2'	26:DA:2516:G:H8	1.75	0.51
26:DA:2249:U:N3	26:DA:2253:G:OP2	2.35	0.51
1:CA:1153:C:H42	1:CA:1154:G:N2	2.08	0.51
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.76	0.51
37:DQ:16:ARG:HG2	37:DQ:18:LYS:HE2	1.91	0.51
9:CI:53:VAL:C	9:CI:55:ALA:H	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:660:G:H5'	30:DF:99:TYR:CE2	2.46	0.51
1:CA:1191:A:OP1	3:CC:4:LYS:HG3	2.10	0.51
26:DA:7:G:H2'	26:DA:8:A:H8	1.74	0.51
1:AA:1277:C:H1'	1:AA:1282:C:C2	2.46	0.51
27:BB:11:C:H3'	27:BB:12:C:C6	2.44	0.51
4:CD:100:ARG:NH1	4:CD:137:SER:OG	2.39	0.51
5:AE:10:MET:HB2	5:AE:13:ILE:HD11	1.91	0.51
26:DA:539:G:H2'	26:DA:540:C:C6	2.44	0.51
39:BS:74:ALA:O	39:BS:78:LEU:HD23	2.11	0.51
4:AD:128:VAL:HG12	4:AD:129:ASN:HD22	1.75	0.51
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.93	0.51
26:DA:2139:C:N4	26:DA:2152:G:C6	2.79	0.51
26:DA:2104:G:O2'	26:DA:2105:C:O5'	2.26	0.51
31:DG:41:GLN:NE2	31:DG:154:GLY:O	2.23	0.51
27:DB:33:G:C2	27:DB:50:G:C2	2.98	0.51
1:CA:352:C:O2'	1:CA:354:G:OP1	2.18	0.51
1:AA:649:G:H2'	1:AA:650:G:C8	2.44	0.51
37:BQ:86:GLY:HA3	47:B0:10:THR:CG2	2.41	0.51
4:CD:129:ASN:HD21	4:CD:144:ASP:CG	2.13	0.51
33:BI:6:LEU:HG	33:BI:36:ALA:HA	1.93	0.51
4:CD:133:VAL:HG11	4:CD:138:TYR:HD2	1.76	0.51
26:BA:2593:U:H2'	26:BA:2594:C:C6	2.45	0.51
26:DA:2471:C:H2'	26:DA:2472:G:O4'	2.11	0.51
7:CG:116:ALA:O	7:CG:120:ILE:HG13	2.10	0.51
1:CA:56:U:H2'	1:CA:57:G:C8	2.45	0.51
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.45	0.51
26:BA:2362:G:OP1	55:B8:44:LYS:NZ	2.36	0.51
39:DS:68:GLN:O	39:DS:71:ARG:HG3	2.11	0.51
26:BA:2134:A:N3	26:BA:2134:A:H2'	2.25	0.51
1:CA:1348:U:H5''	9:CI:119:ALA:HB3	1.93	0.51
1:AA:1061:G:H1'	10:AJ:56:HIS:CE1	2.46	0.51
1:CA:165:C:H2'	1:CA:166:G:C8	2.46	0.51
26:BA:2182:G:H2'	26:BA:2183:C:C6	2.45	0.51
1:CA:1511:G:H2'	1:CA:1512:U:O4'	2.11	0.51
13:CM:5:ALA:HB3	13:CM:22:ILE:HD12	1.91	0.51
37:BQ:110:THR:OG1	37:BQ:111:GLU:N	2.44	0.51
1:AA:406:G:H21	4:AD:119:GLN:HE22	1.58	0.51
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.43	0.51
26:DA:1783:A:N7	61:DA:4364:HOH:O	2.34	0.51
1:CA:1417:G:N2	1:CA:1482:G:H2'	2.25	0.51
1:CA:1516:G:N2	1:CA:1519:A:OP2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:523:A:C2	12:CL:91:LYS:HB3	2.45	0.51
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.43	0.51
26:DA:1155:A:H5''	41:DU:55:ARG:HD3	1.92	0.51
30:DF:34:TRP:CE2	36:DP:8:PRO:HG3	2.45	0.51
26:BA:2408:U:H2'	26:BA:2409:G:C8	2.45	0.51
26:DA:1899:G:H2'	26:DA:1899:G:N3	2.25	0.51
38:BR:70:LEU:HD13	38:BR:75:LEU:HD13	1.91	0.51
26:BA:1418:G:O2'	26:BA:1580:A:N6	2.42	0.51
30:BF:155:LEU:HD11	30:BF:176:LEU:HD12	1.92	0.51
26:DA:747:U:O2	26:DA:2014:A:H1'	2.11	0.51
26:DA:383:U:H2'	26:DA:385:C:H5	1.75	0.51
26:BA:862:G:O2'	27:BB:78:A:N3	2.40	0.51
31:DG:145:THR:H	31:DG:148:MET:HE3	1.75	0.51
26:BA:2127:G:C6	26:BA:2162:G:C2	2.99	0.51
26:DA:1448:G:O2'	26:DA:1528(A):A:N1	2.34	0.51
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.46	0.51
52:B5:16:ARG:HG2	52:B5:16:ARG:HH11	1.74	0.51
1:AA:682:G:H1	1:AA:708:C:H42	1.57	0.51
1:CA:427:U:H5'	4:CD:41:GLY:HA2	1.92	0.51
33:DI:122:GLU:HB2	33:DI:126:TYR:OH	2.10	0.51
26:DA:646:A:H2'	26:DA:647:G:O4'	2.10	0.51
32:BH:69:ARG:HG3	32:BH:70:THR:N	2.26	0.51
26:BA:222:A:N1	26:BA:233:A:H5''	2.25	0.51
1:AA:270:A:H2'	1:AA:271:C:C6	2.46	0.51
26:DA:752:A:P	54:D7:3:ARG:HH22	2.34	0.51
26:BA:565:C:H4'	26:BA:1253:A:C6	2.46	0.51
9:AI:20:ARG:O	9:AI:60:ASP:N	2.32	0.51
30:DF:183:VAL:O	30:DF:187:VAL:HG23	2.10	0.51
26:BA:1257:C:H5'	30:BF:75:HIS:CE1	2.45	0.51
2:CB:115:LEU:HD11	2:CB:153:ARG:CZ	2.41	0.51
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.91	0.51
26:BA:1506:C:C2'	26:BA:1507:A:H5'	2.41	0.51
26:DA:375:C:H2'	26:DA:376:C:C6	2.46	0.51
40:DT:64:ARG:NH1	40:DT:103:ARG:HA	2.25	0.51
26:DA:2602:A:H4'	26:DA:2603:G:O5'	2.09	0.51
49:D2:29:LYS:HG2	49:D2:57:ILE:HD13	1.91	0.51
1:CA:1243:C:H2'	1:CA:1244:C:C6	2.45	0.51
27:DB:8:U:H6	27:DB:8:U:H5''	1.75	0.51
19:AS:68:GLY:H	51:B4:58:ARG:HE	1.59	0.51
50:D3:29:ARG:N	50:D3:33:GLN:OE1	2.39	0.51
1:AA:517:G:N2	1:AA:533:A:OP2	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1276:G:H2'	1:AA:1277:C:H6	1.75	0.51
26:BA:530:G:C5	26:BA:2022:U:H5''	2.45	0.51
1:AA:193:C:H2'	1:AA:194:C:C6	2.45	0.51
1:CA:432:A:H5''	1:CA:433:C:OP2	2.11	0.51
26:DA:2343:C:O2'	26:DA:2373:G:O2'	2.15	0.51
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	1.93	0.51
7:AG:78:ARG:HE	7:AG:156:TRP:HE3	1.57	0.51
13:CM:91:ARG:HB2	13:CM:98:VAL:HG13	1.92	0.51
11:CK:34:ASP:OD1	11:CK:36:ASP:N	2.44	0.51
26:BA:1026:U:H4'	26:BA:1027:A:OP1	2.10	0.51
1:CA:448:A:O5'	1:CA:485:G:N2	2.34	0.51
26:BA:788:A:OP1	26:BA:791:C:N4	2.40	0.51
1:AA:189(D):C:O2	1:AA:189(H):G:N1	2.44	0.51
34:BN:75:TYR:CE2	34:BN:77:GLY:HA2	2.46	0.51
1:AA:1172:C:N4	1:AA:1173:G:O6	2.44	0.51
1:CA:376:G:H4'	16:CP:5:ARG:HD3	1.91	0.51
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.46	0.51
26:DA:1469:A:H2'	26:DA:1470:G:O4'	2.10	0.51
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.41	0.51
26:DA:2080:G:O2'	26:DA:2081:C:H5'	2.10	0.51
26:DA:2023:G:H5'	26:DA:2617:C:H4'	1.93	0.51
26:BA:271(E):U:H2'	26:BA:271(F):C:C6	2.45	0.51
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.91	0.51
26:BA:1671:U:HO2'	26:BA:1673:U:H5	1.57	0.51
1:AA:1136:U:H5''	1:AA:1137:C:N3	2.25	0.51
20:CT:29:LYS:HD2	20:CT:71:THR:HG21	1.93	0.51
17:AQ:22:LEU:HD13	17:AQ:41:LYS:HG3	1.91	0.51
1:CA:1006:C:H2'	1:CA:1007:C:C6	2.45	0.51
26:DA:2118:U:OP1	26:DA:2148:G:O2'	2.16	0.51
1:CA:1340:A:O2'	24:CX:31:G:O2'	2.14	0.51
1:AA:731:G:H5'	1:AA:766:A:H4'	1.93	0.51
30:BF:53:THR:HG22	30:BF:56:GLU:HG3	1.93	0.51
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.11	0.51
1:AA:975:A:H4'	1:AA:976:G:C5'	2.38	0.51
1:AA:57:G:H2'	1:AA:58:C:C6	2.46	0.51
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.45	0.51
30:DF:125:LEU:HD22	30:DF:196:LEU:HD23	1.93	0.51
46:DZ:7:ALA:O	46:DZ:62:PRO:HD3	2.10	0.51
1:CA:793:U:C4	1:CA:1517:G:H5''	2.46	0.51
26:DA:1186:G:C2	26:DA:1187:G:H1'	2.46	0.51
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:735:C:H2'	1:AA:736:C:H6	1.76	0.51
26:DA:817:C:O2'	26:DA:839:U:OP1	2.25	0.51
26:BA:1178:C:H2'	26:BA:1179:C:C6	2.46	0.51
15:CO:18:PHE:HB2	15:CO:19:PRO:HD2	1.93	0.51
20:AT:38:LYS:HA	20:AT:41:ILE:HD12	1.93	0.51
32:BH:113:VAL:HG11	32:BH:151:ILE:HD13	1.93	0.51
26:BA:2857:G:N2	26:BA:2860:A:OP2	2.37	0.51
26:DA:632:A:H2'	26:DA:633:A:C8	2.46	0.51
7:CG:74:GLU:HG2	7:CG:91:VAL:HG22	1.92	0.51
26:BA:121:G:H4'	26:BA:149:A:H5'	1.93	0.51
26:DA:2218:U:O2	48:D1:52:ARG:NH2	2.44	0.51
34:BN:47:ALA:HB2	34:BN:112:LEU:HD11	1.93	0.51
1:AA:1125:U:H4'	10:AJ:5:ARG:HH12	1.76	0.51
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.42	0.51
1:CA:1321:C:H5''	1:CA:1322:C:H2'	1.91	0.51
1:AA:1311:G:H1	1:AA:1326:C:N4	2.09	0.51
1:AA:7:G:H5'	1:AA:298:A:O4'	2.11	0.51
26:DA:2330:G:H2'	26:DA:2331:G:O4'	2.11	0.51
26:DA:1035:U:H2'	26:DA:1036:G:C8	2.45	0.51
26:BA:910:A:N1	26:BA:2277:G:H1'	2.25	0.51
26:DA:1710:C:H2'	26:DA:1711:C:H6	1.75	0.51
15:AO:56:LEU:HD21	26:BA:715:G:C2	2.46	0.51
26:BA:1028:A:N6	26:BA:1125:G:H2'	2.25	0.51
1:AA:369:C:H42	1:AA:392:G:H1	1.59	0.51
1:CA:1288:A:N1	1:CA:1371:G:H1'	2.25	0.51
26:DA:1011:G:OP2	41:DU:66:ASN:ND2	2.37	0.51
48:D1:80:LEU:HB3	48:D1:82:LEU:HG	1.93	0.51
1:CA:567:G:O6	12:CL:5:PRO:HD3	2.11	0.51
18:CR:58:LEU:HB3	18:CR:62:GLU:HG3	1.93	0.51
35:DO:98:VAL:HG13	35:DO:117:LEU:HB3	1.93	0.51
26:BA:2433:A:OP2	61:BA:4119:HOH:O	2.19	0.51
1:AA:407:G:OP1	4:AD:3:ARG:NH1	2.43	0.51
26:DA:2262:U:H4'	26:DA:2328:A:C2	2.46	0.51
29:DE:179:GLU:HB3	29:DE:181:LEU:HD22	1.93	0.51
1:CA:1187:G:N2	14:CN:60:SER:OG	2.36	0.51
31:DG:138:GLN:HB3	31:DG:153:ARG:O	2.11	0.51
1:AA:765:G:N1	1:AA:812:C:O2'	2.36	0.51
1:AA:345:C:H4'	1:AA:346:G:C4	2.46	0.51
1:CA:1422:G:O3'	35:DO:49:ARG:NH1	2.40	0.51
26:DA:2728:U:H5'	35:DO:70:LYS:HZ3	1.76	0.51
1:CA:1206:G:O4'	3:CC:194:GLY:HA2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.10	0.51
1:CA:413:G:N2	1:CA:428:G:H1'	2.26	0.51
1:CA:1046:A:H61	1:CA:1213:A:N6	2.09	0.51
1:AA:923:A:OP1	5:AE:21:ALA:HB2	2.11	0.51
1:AA:979:C:H2'	1:AA:980:C:H5'	1.93	0.51
1:CA:406:G:H21	4:CD:119:GLN:HE22	1.59	0.51
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.46	0.51
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.25	0.51
24:CX:8:4SU:H6	24:CX:8:4SU:O5'	2.11	0.51
29:DE:9:VAL:HG13	29:DE:25:VAL:O	2.11	0.51
1:CA:1269:A:H2	1:CA:1312:G:N3	2.09	0.51
2:AB:115:LEU:HD13	2:AB:145:LEU:HB3	1.93	0.51
26:DA:2615:U:C2	52:D5:7:PRO:HA	2.46	0.51
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.10	0.51
41:DU:17:ILE:HG23	41:DU:39:LEU:HD12	1.92	0.51
49:D2:16:LEU:O	49:D2:67:LYS:NZ	2.31	0.51
32:BH:159:GLU:HG3	32:BH:169:VAL:HG11	1.93	0.51
26:DA:208:C:H2'	26:DA:209:C:C6	2.46	0.51
24:AX:66:C:H2'	24:AX:67:C:O4'	2.10	0.51
1:CA:1014:A:P	19:CS:18:LYS:HZ1	2.34	0.50
26:DA:2171:A:H1'	26:DA:2172:U:O4'	2.11	0.50
1:CA:839:U:H5''	1:CA:840:C:C5	2.42	0.50
13:CM:82:MET:HE3	13:CM:92:HIS:HB3	1.91	0.50
1:AA:1291:G:O3'	7:AG:41:ARG:NH2	2.44	0.50
1:AA:1255:G:H1	1:AA:1282:C:H42	1.58	0.50
26:DA:2022:U:O2'	26:DA:2617:C:H5'	2.12	0.50
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.92	0.50
42:DV:35:LEU:HB2	42:DV:57:VAL:HG23	1.92	0.50
1:CA:1288:A:H2'	1:CA:1289:A:C8	2.46	0.50
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HG2	1.92	0.50
35:BO:10:VAL:HG13	35:BO:17:ARG:C	2.31	0.50
26:DA:39:C:H2'	26:DA:40:C:C6	2.46	0.50
26:BA:217:G:OP2	61:BA:4821:HOH:O	2.19	0.50
1:CA:899:C:O5'	1:CA:899:C:H6	1.94	0.50
26:BA:143:G:H1'	44:BX:37:THR:HG21	1.93	0.50
1:CA:495:A:H4'	1:CA:496:A:OP1	2.12	0.50
26:BA:1000:A:H62	26:BA:1154:G:H2'	1.77	0.50
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.11	0.50
26:BA:2611:U:C4	52:B5:3:LYS:HG2	2.45	0.50
26:DA:2148:G:H2'	26:DA:2149:G:C8	2.46	0.50
1:AA:1164:G:N7	1:AA:1173:G:N3	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1000:U:O2	1:CA:1041:A:N1	2.45	0.50
26:DA:2162:G:H4'	26:DA:2172:U:C2'	2.39	0.50
26:DA:2315:G:H2'	26:DA:2316:C:C6	2.46	0.50
26:DA:1417:C:H2'	26:DA:1418:G:O4'	2.10	0.50
4:CD:67:ILE:HD13	4:CD:196:LEU:HD23	1.94	0.50
1:AA:339:C:H2'	1:AA:340:U:C6	2.46	0.50
1:CA:790:A:H2'	1:CA:791:G:C8	2.46	0.50
1:AA:130:A:O2'	1:AA:131:C:O5'	2.25	0.50
2:CB:51:LEU:HD23	2:CB:201:ILE:HD12	1.92	0.50
44:DX:31:HIS:CD2	44:DX:33:LYS:H	2.29	0.50
27:DB:45:A:O4'	31:DG:95:ARG:NH1	2.44	0.50
1:CA:763:G:C2'	1:CA:764:C:H5'	2.41	0.50
1:CA:438:G:OP1	4:CD:125:HIS:NE2	2.30	0.50
26:BA:1453:U:O2'	26:BA:1455:G:N7	2.41	0.50
26:DA:1523:U:H2'	26:DA:1524:G:O4'	2.11	0.50
28:BD:97:TYR:CE1	28:BD:103:ARG:HG3	2.45	0.50
26:DA:1130:U:O2	26:DA:2025:C:H5''	2.12	0.50
34:DN:15:LEU:HB2	34:DN:135:PRO:HB2	1.94	0.50
54:D7:9:ARG:HH21	54:D7:47:ARG:HD2	1.77	0.50
1:AA:1142:G:H2'	1:AA:1143:G:O4'	2.11	0.50
30:BF:167:ALA:HB1	30:BF:173:VAL:HG11	1.91	0.50
1:CA:1310:G:H1	1:CA:1327:C:H42	1.59	0.50
26:DA:1592:C:H2'	26:DA:1593:G:H8	1.76	0.50
31:DG:44:GLY:O	31:DG:47:LYS:HB3	2.12	0.50
26:BA:2127:G:O6	26:BA:2162:G:N1	2.43	0.50
19:AS:32:LYS:HE3	19:AS:57:HIS:CD2	2.46	0.50
1:AA:631:G:H2'	1:AA:632:A:C8	2.45	0.50
1:CA:791:G:C6	1:CA:792:A:N7	2.79	0.50
26:BA:1493:C:C5	26:BA:2206:G:H1'	2.46	0.50
35:BO:73:ASP:HB2	40:BT:82:LEU:HD13	1.93	0.50
4:AD:12:CYS:SG	4:AD:19:LEU:HB2	2.52	0.50
1:CA:170:U:O2'	1:CA:171:A:H5'	2.11	0.50
7:CG:16:LEU:HD23	9:CI:41:VAL:HG12	1.93	0.50
26:BA:1666:G:C2'	26:BA:1667:G:H5'	2.40	0.50
26:BA:574:C:N4	26:BA:2034:U:OP1	2.36	0.50
6:CF:99:ALA:HB2	18:CR:31:LEU:HD21	1.92	0.50
26:DA:1375:C:H2'	26:DA:1376:C:H6	1.76	0.50
26:BA:2245:U:H5''	26:BA:2246:G:H5'	1.92	0.50
10:CJ:5:ARG:N	10:CJ:99:LYS:O	2.44	0.50
26:DA:2175:C:H2'	26:DA:2176:A:O4'	2.12	0.50
1:AA:79:G:C2	1:AA:90:U:O2	2.64	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2203:U:H4'	28:DD:151:LYS:HG2	1.91	0.50
1:CA:1009:G:C2	1:CA:1010:G:C8	2.99	0.50
26:DA:12:U:O2	26:DA:2626:C:H4'	2.12	0.50
46:BZ:144:LEU:HD23	46:BZ:148:ASP:HB2	1.92	0.50
9:CI:18:PHE:HD2	9:CI:62:TYR:HD2	1.59	0.50
27:BB:13:A:N1	27:BB:69:G:O2'	2.33	0.50
26:DA:1796:U:H2'	26:DA:1797:C:C6	2.46	0.50
31:BG:106:LEU:HA	31:BG:110:ALA:HB3	1.93	0.50
27:DB:95:C:H2'	27:DB:96:U:C6	2.47	0.50
1:AA:1095:U:H5''	1:AA:1109:C:O2	2.12	0.50
26:BA:2685:G:H5'	35:BO:68:GLU:OE1	2.11	0.50
38:DR:47:PHE:O	38:DR:51:LEU:HG	2.11	0.50
10:CJ:55:LYS:HG3	10:CJ:56:HIS:H	1.75	0.50
26:BA:1124:C:H1'	56:B9:36:GLN:NE2	2.27	0.50
50:B3:8:LEU:HD13	50:B3:31:LEU:HD23	1.93	0.50
26:BA:1784:A:H4'	26:BA:1785:A:O5'	2.12	0.50
13:CM:16:ASP:HB2	13:CM:30:ALA:HB1	1.93	0.50
1:AA:432:A:H5''	1:AA:433:C:OP2	2.10	0.50
27:BB:92:C:OP1	46:BZ:79:ARG:NH1	2.43	0.50
1:AA:264:U:O2'	17:AQ:64:PRO:O	2.26	0.50
33:DI:110:ASP:HB3	33:DI:130:TYR:OH	2.12	0.50
1:AA:903:G:OP1	61:AA:4029:HOH:O	2.19	0.50
26:BA:2805:G:H2'	26:BA:2807:G:C8	2.46	0.50
1:CA:1321:C:H4'	13:CM:87:TYR:CE2	2.47	0.50
39:BS:27:SER:HA	39:BS:88:ASP:HB3	1.92	0.50
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.77	0.50
1:AA:521:G:O6	12:AL:53:ARG:NH2	2.44	0.50
26:BA:222:A:H3'	26:BA:421:U:H5'	1.93	0.50
9:CI:26:VAL:HG22	9:CI:61:ALA:HB3	1.93	0.50
26:BA:2626:C:H2'	26:BA:2627:G:O4'	2.11	0.50
1:AA:189(C):C:H42	1:AA:189(H):G:H1	1.58	0.50
1:CA:613:C:H2'	1:CA:614:A:H8	1.75	0.50
1:CA:620:C:C2	4:CD:135:LEU:HG	2.46	0.50
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.77	0.50
34:BN:4:TYR:HB2	41:BU:101:ARG:NH1	2.27	0.50
27:DB:106:G:H5''	46:DZ:31:ARG:HG2	1.93	0.50
26:BA:1518:U:H2'	26:BA:1519:G:O4'	2.11	0.50
3:CC:113:ALA:HB2	3:CC:202:ILE:HG13	1.92	0.50
51:D4:15:ILE:HG23	51:D4:21:VAL:HG22	1.92	0.50
26:DA:2128:C:H5'	26:DA:2173:A:H2	1.75	0.50
13:CM:60:VAL:HG23	13:CM:64:TRP:HZ3	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2807:G:C6	26:DA:2808:U:C4	3.00	0.50
1:AA:1493:A:H5''	1:AA:1494:G:OP2	2.11	0.50
27:DB:24:G:H4'	27:DB:25:A:N7	2.26	0.50
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.47	0.50
26:BA:1364:G:P	48:B1:3:LYS:HG3	2.51	0.50
30:BF:102:PRO:HB2	30:BF:105:VAL:HG23	1.92	0.50
46:DZ:120:ILE:HD11	46:DZ:173:ALA:HB3	1.94	0.50
33:DI:130:TYR:CE2	33:DI:132:PRO:HB3	2.46	0.50
4:AD:154:ASN:HA	4:AD:159:ARG:HH21	1.77	0.50
26:DA:1507:A:O2'	26:DA:1508:A:O5'	2.25	0.50
26:BA:817:C:OP1	61:BA:4091:HOH:O	2.19	0.50
1:AA:451:A:N6	1:AA:480:U:H2'	2.26	0.50
26:DA:995:C:OP2	41:DU:54:LYS:NZ	2.36	0.50
38:DR:21:TYR:OH	38:DR:43:GLU:HG2	2.12	0.50
1:AA:202:U:O2'	1:AA:203:U:O5'	2.25	0.50
2:CB:24:TRP:CZ3	2:CB:26:PRO:HA	2.46	0.50
45:DY:76:CYS:HA	45:DY:106:LEU:HD22	1.93	0.50
26:DA:2396:G:OP1	48:D1:25:LYS:NZ	2.29	0.50
1:CA:1367:C:O2'	10:CJ:62:HIS:HE1	1.94	0.50
26:DA:1800:C:OP2	28:DD:183:ARG:NH2	2.45	0.50
26:BA:2684:U:H1'	35:BO:70:LYS:HD2	1.94	0.50
33:BI:3:VAL:HG12	33:BI:38:LEU:HA	1.93	0.50
1:CA:828:A:H2'	1:CA:829:G:O4'	2.12	0.50
26:DA:912:C:OP1	37:DQ:9:TYR:OH	2.19	0.50
26:DA:2001:A:OP1	38:DR:9:LYS:NZ	2.33	0.50
32:DH:69:ARG:HG3	32:DH:70:THR:N	2.26	0.50
26:BA:2680:C:OP2	29:BE:111:ARG:NH2	2.44	0.50
1:CA:137:C:C2	1:CA:227:G:C2	3.00	0.50
1:CA:1201:A:H4'	1:CA:1202:G:O5'	2.12	0.50
34:BN:73:THR:OG1	34:BN:82:LEU:HD11	2.11	0.50
26:DA:1786:A:H1'	26:DA:1938:A:N6	2.27	0.50
30:BF:143:ALA:HB1	30:BF:148:LEU:HB2	1.92	0.50
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.11	0.50
37:DQ:27:VAL:HG21	37:DQ:134:ARG:HA	1.93	0.50
15:CO:8:LYS:O	15:CO:12:ILE:HG13	2.12	0.50
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.42	0.50
26:DA:2130:U:O2	26:DA:2134:A:O2'	2.30	0.50
1:CA:1162:C:N4	1:CA:1174:G:N1	2.35	0.50
1:CA:1400:C:N4	24:CX:35:A:C8	2.79	0.50
1:CA:407:G:H5''	4:CD:115:ARG:HB3	1.93	0.50
1:AA:1007:C:C2'	1:AA:1008:C:H5''	2.34	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:338:A:H2	1:CA:351:G:H22	1.60	0.50
26:DA:1449:A:HO2'	26:DA:1529:G:H21	1.55	0.50
1:CA:501:C:H1'	1:CA:549:C:H1'	1.94	0.50
26:BA:1184:G:H5'	50:B3:29:ARG:NH1	2.26	0.50
1:CA:1493:A:H2'	26:DA:1913:A:H61	1.76	0.50
26:DA:781:A:P	28:DD:218:ARG:HH22	2.34	0.50
26:BA:1877:A:H5'	26:BA:1878:G:OP2	2.12	0.50
26:BA:1296:G:OP1	26:BA:2709:G:O2'	2.21	0.50
1:CA:613:C:H2'	1:CA:614:A:C8	2.47	0.50
26:DA:2070:G:H2'	26:DA:2071:A:C8	2.47	0.50
36:DP:25:SER:N	61:DP:311:HOH:O	2.40	0.50
29:DE:7:VAL:HG13	29:DE:27:LEU:HB3	1.94	0.50
1:CA:17:U:H2'	1:CA:18:C:C6	2.47	0.50
26:DA:1756:G:H4'	26:DA:1758:G:O4'	2.12	0.50
29:DE:77:ILE:HD12	29:DE:195:LEU:HD13	1.93	0.50
26:DA:366:C:H5''	26:DA:370:G:H5'	1.92	0.50
26:DA:271(W):G:O6	61:DA:4210:HOH:O	2.14	0.50
26:DA:184:C:H2'	26:DA:185:U:C6	2.47	0.50
24:AX:50:U:H2'	24:AX:51:C:C6	2.46	0.50
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.47	0.50
20:CT:67:ALA:HB2	20:CT:77:ALA:HB2	1.92	0.50
1:CA:91:C:H2'	1:CA:92:C:C6	2.47	0.50
1:CA:1502:A:H2	1:CA:1505:G:N1	2.03	0.50
24:CX:65:C:C4	24:CX:66:C:C4	3.00	0.50
27:DB:7:G:N3	39:DS:38:GLN:NE2	2.38	0.50
26:DA:2684:U:H1'	35:DO:70:LYS:HD2	1.94	0.50
26:DA:1889:A:N1	26:DA:2234:G:H1'	2.26	0.50
26:DA:2377:A:H2'	26:DA:2378:A:C8	2.47	0.50
26:DA:2809:A:H2'	26:DA:2810:A:C8	2.47	0.50
26:DA:469:G:C2'	26:DA:470:A:H5''	2.42	0.50
26:DA:588:U:H2'	26:DA:589:C:C6	2.47	0.50
29:DE:36:ARG:HG2	29:DE:47:VAL:HG12	1.93	0.50
26:DA:2079:U:H2'	26:DA:2080:G:O4'	2.12	0.50
26:DA:1153:C:H2'	26:DA:1154:G:O4'	2.12	0.50
28:DD:72:LYS:HD3	28:DD:97:TYR:CE2	2.47	0.50
26:DA:1987:G:H2'	26:DA:1988:C:C6	2.46	0.50
26:BA:2028:U:H2'	26:BA:2029:G:O4'	2.11	0.50
19:CS:68:GLY:H	51:D4:58:ARG:NH1	2.10	0.50
33:BI:100:ALA:HA	33:BI:103:ARG:HG2	1.93	0.50
44:BX:26:TYR:HB3	44:BX:92:LEU:HD22	1.93	0.50
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:41:VAL:HG23	5:AE:67:VAL:HG12	1.92	0.50
26:BA:588:U:H1'	30:BF:90:PHE:CG	2.47	0.50
1:CA:1104:G:H4'	2:CB:111:ARG:HD2	1.94	0.50
18:CR:50:ILE:HG12	18:CR:70:ILE:HG21	1.93	0.50
26:DA:1581:G:H2'	26:DA:1582:C:O4'	2.11	0.50
26:BA:601:C:O2'	26:BA:605:C:H5''	2.11	0.50
26:BA:614:U:H5'	26:BA:614(C):A:N6	2.27	0.50
24:AX:49:G:N2	24:AX:65:C:N3	2.50	0.49
1:CA:1227:A:N3	19:CS:83:HIS:HB3	2.27	0.49
27:DB:27:C:C4	27:DB:28:C:C4	3.00	0.49
26:BA:2386:C:H2'	26:BA:2387:U:C6	2.47	0.49
26:DA:718:A:H3'	26:DA:719:C:H6	1.77	0.49
31:DG:179:PRO:HG3	51:D4:43:TYR:OH	2.12	0.49
1:AA:664:G:P	18:AR:64:ARG:HH21	2.35	0.49
26:BA:729:G:C6	28:BD:208:LYS:HB2	2.47	0.49
1:CA:696:A:H8	1:CA:696:A:O5'	1.95	0.49
26:DA:857:C:H4'	47:D0:23:VAL:HG21	1.94	0.49
32:DH:3:ARG:HH22	32:DH:5:GLY:H	1.60	0.49
1:CA:406:G:N2	4:CD:119:GLN:HE22	2.10	0.49
26:DA:831:G:O2'	36:DP:38:GLN:NE2	2.45	0.49
26:DA:71:A:H5''	26:DA:73:A:C8	2.47	0.49
11:AK:48:ILE:HG21	11:AK:63:LEU:HB3	1.93	0.49
26:BA:1047:G:H1'	26:BA:1110:G:N2	2.27	0.49
1:CA:1516:G:H2'	1:CA:1518:A:OP2	2.12	0.49
26:BA:2611:U:H6	26:BA:2611:U:H5'	1.77	0.49
1:AA:302:G:O2'	1:AA:556:C:H5''	2.11	0.49
26:BA:26:G:C6	26:BA:27:G:N1	2.80	0.49
26:DA:1163:G:OP1	42:DV:24:LYS:NZ	2.34	0.49
26:BA:1143:A:OP1	34:BN:25:ARG:NH2	2.45	0.49
32:BH:12:PRO:O	32:BH:15:VAL:HG13	2.12	0.49
4:AD:64:LEU:HA	4:AD:67:ILE:HD12	1.94	0.49
26:BA:2563:U:H4'	35:BO:28:SER:HA	1.94	0.49
2:CB:200:ILE:H	2:CB:200:ILE:HD13	1.77	0.49
23:CW:76:PPU:HM2	26:DA:2452:C:N3	2.27	0.49
26:DA:2165:G:O6	26:DA:2171:A:H8	1.95	0.49
7:CG:76:ARG:HB3	7:CG:156:TRP:HH2	1.77	0.49
26:BA:2107:C:N4	26:BA:2182:G:H1	2.07	0.49
1:CA:958:A:N6	19:CS:77:THR:O	2.45	0.49
10:AJ:39:PRO:HA	10:AJ:70:ARG:HD3	1.93	0.49
26:BA:2086:U:H2'	26:BA:2087:G:H8	1.78	0.49
26:DA:781:A:OP1	28:DD:218:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2206:G:H5'	26:BA:2207:G:N7	2.27	0.49
8:CH:20:TYR:CE1	8:CH:76:PRO:HG2	2.48	0.49
26:BA:10:G:N2	26:BA:2802:G:OP1	2.31	0.49
37:DQ:31:ASP:OD1	37:DQ:134:ARG:NH1	2.44	0.49
15:CO:81:LEU:O	15:CO:84:LYS:HG2	2.13	0.49
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.45	0.49
26:BA:403:U:H4'	26:BA:404:C:H5'	1.93	0.49
1:AA:362:G:N1	1:AA:365:U:OP2	2.45	0.49
1:CA:89:C:H2'	1:CA:90:U:O4'	2.12	0.49
1:CA:1029:C:N3	1:CA:1032:G:C2	2.80	0.49
28:BD:85:ASP:OD2	28:BD:88:ARG:NH1	2.44	0.49
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	1.94	0.49
40:BT:45:PHE:CE2	40:BT:65:LYS:HD3	2.47	0.49
24:CX:47:U:H3'	24:CX:48:C:H5'	1.93	0.49
26:DA:330:A:H2	26:DA:1210:A:H2'	1.78	0.49
1:AA:1024:G:C2'	1:AA:1025:U:H5'	2.41	0.49
26:BA:2022:U:O2'	26:BA:2617:C:H5'	2.11	0.49
26:BA:1012:U:H5	34:BN:28:THR:HG21	1.77	0.49
26:DA:1212:G:O2'	26:DA:1235:G:O6	2.30	0.49
26:DA:2035:G:H4'	61:DA:4092:HOH:O	2.11	0.49
26:DA:1790:C:H5''	26:DA:1791:A:OP1	2.12	0.49
26:BA:2867:G:OP2	40:BT:119:LYS:NZ	2.45	0.49
52:D5:41:PRO:O	52:D5:44:THR:OG1	2.24	0.49
26:DA:2458:G:O2'	26:DA:2460:U:O4	2.21	0.49
26:DA:2557:G:H2'	26:DA:2558:C:H6	1.76	0.49
45:DY:94:LYS:NZ	61:DY:601:HOH:O	2.44	0.49
16:AP:19:ILE:N	16:AP:37:GLY:O	2.45	0.49
2:CB:97:TRP:CZ3	2:CB:101:MET:HB2	2.48	0.49
1:AA:353:A:H8	1:AA:353:A:H5'	1.76	0.49
26:DA:2123:G:H1	26:DA:2175:C:N4	2.10	0.49
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.30	0.49
23:AW:76:PPU:H2'	26:BA:2584:U:O2'	2.13	0.49
1:AA:36:C:O2'	12:AL:117:ARG:NH2	2.45	0.49
26:DA:1798:U:OP2	28:DD:274:ARG:NH2	2.45	0.49
26:DA:469:G:H2'	26:DA:470:A:H5''	1.95	0.49
31:DG:14:GLU:O	31:DG:17:PRO:HD2	2.12	0.49
3:AC:134:ILE:HG22	3:AC:168:ALA:HB3	1.95	0.49
31:DG:98:ARG:HA	31:DG:101:ILE:HB	1.93	0.49
1:AA:1068:G:N2	1:AA:1191:A:N3	2.56	0.49
41:DU:92:ARG:HA	41:DU:95:LEU:HB2	1.93	0.49
26:BA:637:A:H8	36:BP:117:GLU:HG3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:224:G:H2'	26:BA:225:A:O4'	2.12	0.49
26:BA:2661:G:H2'	26:BA:2662:A:C8	2.47	0.49
31:BG:74:LYS:O	31:BG:84:LYS:NZ	2.42	0.49
28:DD:118:VAL:N	28:DD:129:ASN:OD1	2.41	0.49
29:BE:11:MET:HG2	29:BE:24:THR:HB	1.93	0.49
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.12	0.49
40:BT:51:ARG:HG3	40:BT:98:LYS:HD2	1.95	0.49
17:CQ:57:VAL:HG12	17:CQ:76:LEU:HA	1.93	0.49
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.12	0.49
7:AG:38:LEU:O	7:AG:42:ILE:HG13	2.12	0.49
1:AA:158:G:N2	1:AA:163:C:O2	2.39	0.49
26:DA:568:U:H5'	26:DA:945:A:N1	2.26	0.49
27:BB:89:G:O6	27:BB:90:A:N6	2.46	0.49
26:DA:774:A:N3	26:DA:774:A:H2'	2.27	0.49
17:CQ:12:SER:HB3	17:CQ:20:THR:HB	1.95	0.49
26:DA:2783:G:H2'	26:DA:2784:C:C6	2.47	0.49
1:CA:407:G:N1	1:CA:436:C:N3	2.37	0.49
26:BA:1357:U:H2'	26:BA:1358:G:O4'	2.13	0.49
4:CD:108:LEU:HD13	4:CD:174:LEU:HD13	1.95	0.49
1:CA:1376:U:H2'	1:CA:1377:A:H8	1.72	0.49
26:DA:2808:U:H5''	26:DA:2891:G:O6	2.12	0.49
1:AA:1494:G:H4'	26:BA:1913:A:C8	2.47	0.49
2:AB:162:ILE:O	2:AB:185:ILE:HG13	2.13	0.49
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.95	0.49
8:CH:82:HIS:HB3	8:CH:138:TRP:NE1	2.26	0.49
30:DF:32:LEU:O	30:DF:36:VAL:HG23	2.12	0.49
26:DA:1411:C:H2'	26:DA:1412:A:C8	2.47	0.49
29:BE:2:LYS:HB2	29:BE:95:ILE:HD12	1.93	0.49
46:BZ:7:ALA:HB3	46:BZ:61:LEU:HD12	1.95	0.49
26:BA:2597:G:OP1	61:BA:4695:HOH:O	2.20	0.49
20:AT:67:ALA:C	20:AT:69:GLY:H	2.16	0.49
37:BQ:85:LYS:HD2	37:BQ:85:LYS:N	2.27	0.49
26:DA:644:A:H4'	26:DA:645:C:C5	2.46	0.49
20:CT:46:GLU:O	20:CT:46:GLU:HG2	2.11	0.49
16:CP:20:VAL:HG22	16:CP:35:LYS:HA	1.94	0.49
7:AG:68:ASN:O	7:AG:138:LYS:HE2	2.11	0.49
26:BA:1226:A:OP1	42:BV:84:LYS:HE2	2.13	0.49
28:BD:9:TYR:CZ	28:BD:13:ARG:HG2	2.48	0.49
1:CA:1004:A:N6	1:CA:1037:C:C2	2.81	0.49
26:DA:2158:A:H4'	26:DA:2159:G:OP1	2.12	0.49
26:BA:2849:U:H4'	26:BA:2868:A:C2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:6:C:C2	27:DB:116:G:N2	2.81	0.49
24:CX:3:C:C2'	24:CX:4:G:H5''	2.40	0.49
13:AM:80:ARG:HH21	51:B4:58:ARG:HH11	1.59	0.49
26:DA:2041:U:H2'	26:DA:2042:A:C8	2.46	0.49
26:BA:1713:U:H2'	26:BA:1714:G:C8	2.46	0.49
32:DH:70:THR:O	32:DH:74:ASN:N	2.39	0.49
26:BA:226:G:H21	26:BA:228:A:H62	1.59	0.49
1:CA:609:A:C2'	1:CA:610:G:H5'	2.42	0.49
1:AA:201:C:H42	1:AA:216:G:H22	1.59	0.49
26:DA:286:C:H2'	26:DA:287:C:C6	2.47	0.49
26:DA:729:G:C6	28:DD:208:LYS:HB2	2.48	0.49
16:CP:22:THR:HA	16:CP:33:ILE:HG12	1.94	0.49
17:CQ:76:LEU:HD12	17:CQ:77:VAL:H	1.78	0.49
30:BF:110:LEU:HD21	30:BF:181:LEU:HG	1.93	0.49
26:DA:2291:U:H2'	26:DA:2292:C:C6	2.48	0.49
26:DA:443:A:H1'	26:DA:1201:C:O4'	2.12	0.49
3:AC:52:LEU:HD21	3:AC:55:VAL:HG23	1.95	0.49
1:AA:1038:C:H2'	1:AA:1039:C:C6	2.48	0.49
24:AX:40:C:C2'	24:AX:41:C:H5'	2.43	0.49
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	1.93	0.49
1:CA:1237:C:H5''	1:CA:1238:A:O4'	2.12	0.49
26:DA:2121:G:C6	26:DA:2177:C:N4	2.80	0.49
26:DA:2104:G:H2'	26:DA:2105:C:C6	2.48	0.49
26:DA:2107:C:N4	26:DA:2182:G:H1	2.07	0.49
26:BA:2150:U:H2'	26:BA:2151:G:H8	1.77	0.49
26:DA:2117:A:N1	26:DA:2171:A:N1	2.60	0.49
1:CA:1015:A:H1'	1:CA:1219:U:H5'	1.94	0.49
1:CA:539:A:H2'	1:CA:540:G:C8	2.48	0.49
26:BA:1692:U:H2'	26:BA:1694:C:C5	2.48	0.49
1:AA:270:A:H2'	1:AA:271:C:H6	1.78	0.49
1:AA:1200:C:OP1	61:AA:4099:HOH:O	2.20	0.49
1:AA:49:U:O4	1:AA:365:U:H5	1.95	0.49
26:BA:542:C:H2'	26:BA:543:C:C6	2.48	0.49
26:BA:30:G:H2'	26:BA:31:C:C6	2.47	0.49
4:AD:20:TYR:CD2	4:AD:26:CYS:HB3	2.48	0.49
26:DA:1754:C:OP1	40:DT:96:ARG:HD2	2.13	0.49
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.93	0.49
26:DA:1570:A:H2'	26:DA:1571:A:C8	2.47	0.49
38:BR:37:THR:HA	38:BR:111:LEU:HD12	1.95	0.49
47:D0:17:GLN:O	47:D0:19:LYS:NZ	2.45	0.49
26:BA:947:G:H2'	26:BA:948:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1394:A:N6	1:CA:1501:C:H5'	2.28	0.49
3:CC:48:TYR:HE1	3:CC:118:GLN:HB2	1.77	0.49
1:AA:1258:G:H2'	1:AA:1259:C:C6	2.47	0.49
30:DF:13:SER:OG	30:DF:16:GLY:O	2.24	0.49
26:DA:2259:G:H1'	26:DA:2427:C:H2'	1.93	0.49
26:DA:2185:C:H2'	26:DA:2186:G:O4'	2.13	0.49
1:CA:999:C:C4	1:CA:1042:G:N1	2.81	0.49
26:BA:2127:G:H21	26:BA:2173:A:H1'	1.77	0.49
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.42	0.49
26:DA:2173:A:C2	26:DA:2174:C:H1'	2.48	0.49
26:BA:2807:G:H2'	26:BA:2808:U:O4'	2.12	0.49
1:CA:22:G:H4'	1:CA:885:G:C8	2.48	0.49
26:DA:1665:A:H4'	35:DO:67:LYS:HB2	1.94	0.49
13:CM:33:ALA:O	13:CM:37:THR:OG1	2.19	0.49
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.47	0.49
26:DA:2646:C:H2'	26:DA:2647:U:O4'	2.12	0.49
26:DA:610:G:N2	26:DA:619:G:H1'	2.27	0.49
1:CA:460:G:N1	1:CA:470:C:H5'	2.28	0.49
26:BA:458:G:C8	54:B7:37:LYS:HG2	2.48	0.49
5:CE:69:VAL:HG22	5:CE:71:LEU:HD12	1.94	0.49
43:DW:58:ALA:HB1	43:DW:64:MET:HB2	1.95	0.49
26:BA:1820:U:C2	28:BD:202:LYS:HD3	2.47	0.49
44:BX:53:LYS:HB3	44:BX:82:GLN:HB3	1.94	0.49
29:DE:116:VAL:HG13	29:DE:122:PHE:HB2	1.95	0.49
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.93	0.49
48:B1:50:ARG:HG2	48:B1:59:THR:HB	1.94	0.49
26:BA:518:G:H2'	26:BA:519:U:C6	2.47	0.49
28:DD:43:ARG:HA	28:DD:48:ARG:O	2.13	0.49
39:DS:87:PHE:HB2	39:DS:112:PHE:CE2	2.48	0.49
26:DA:2103:C:C2	26:DA:2187:G:C2	3.01	0.49
1:CA:1154:G:N7	1:CA:1155:G:N7	2.61	0.49
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.36	0.49
26:BA:2727:G:O2'	35:BO:70:LYS:NZ	2.43	0.49
4:CD:108:LEU:HD23	4:CD:110:PHE:CZ	2.47	0.49
26:DA:468:G:H5''	30:DF:60:SER:HB2	1.95	0.49
26:DA:1788:C:OP1	28:DD:222:ARG:NH2	2.45	0.49
1:CA:1235:U:O2'	1:CA:1305:G:OP1	2.28	0.49
1:CA:1314:C:H2'	1:CA:1315:U:C6	2.48	0.49
36:DP:38:GLN:HG2	36:DP:45:LEU:H	1.76	0.49
1:CA:713:G:H2'	1:CA:714:G:C8	2.46	0.49
26:DA:997:G:OP1	41:DU:92:ARG:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DN:42:TRP:HA	34:DN:48:MET:HE1	1.95	0.49
1:AA:555:C:H2'	1:AA:556:C:C6	2.47	0.49
43:DW:45:TYR:CZ	43:DW:49:LYS:HE3	2.47	0.49
40:BT:116:ALA:HB1	40:BT:121:ILE:HD11	1.94	0.49
1:CA:715:A:H2'	1:CA:716:A:C8	2.47	0.49
26:DA:2734:A:H2'	26:DA:2735:G:O4'	2.13	0.49
36:BP:124:LYS:HE3	36:BP:146:VAL:HG21	1.93	0.49
26:BA:484:C:H2'	26:BA:485:C:C6	2.48	0.49
1:AA:509:A:N3	1:AA:543:C:O2'	2.35	0.49
1:AA:933:G:O6	7:AG:3:ARG:NH2	2.46	0.49
43:BW:68:ARG:HD3	43:BW:111:HIS:HA	1.95	0.49
27:DB:48:A:P	39:DS:30:ARG:HH12	2.36	0.49
1:CA:1260:C:OP1	1:CA:1284:C:O2'	2.26	0.49
26:DA:2207:G:H3'	26:DA:2208:A:H5''	1.95	0.49
30:BF:184:TYR:HE1	36:BP:3:LEU:HD21	1.77	0.49
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.39	0.49
37:BQ:135:ASP:OD2	46:BZ:49:ARG:NH2	2.45	0.49
30:DF:21:ALA:CB	30:DF:22:ALA:HA	2.42	0.49
1:AA:1027:C:H2'	1:AA:1028:C:C6	2.48	0.49
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.30	0.49
26:DA:1688:U:H1'	26:DA:1701:A:C6	2.47	0.49
18:AR:74:ARG:HG3	18:AR:79:LEU:HB2	1.94	0.49
7:CG:31:MET:HA	7:CG:39:ALA:HB2	1.95	0.49
26:DA:1752:C:H2'	26:DA:1753:G:C8	2.48	0.49
26:BA:2572:A:C8	29:BE:144:ARG:HD2	2.47	0.49
4:CD:12:CYS:O	4:CD:16:GLY:N	2.46	0.49
32:DH:40:GLU:OE1	32:DH:61:HIS:NE2	2.46	0.49
26:BA:2570:G:H2'	26:BA:2571:C:O4'	2.13	0.49
26:BA:735:A:N7	26:BA:761:A:H2	2.11	0.49
37:BQ:63:LYS:HE2	46:BZ:118:GLN:NE2	2.27	0.49
46:DZ:69:THR:HG22	46:DZ:90:VAL:HA	1.95	0.49
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.94	0.49
26:DA:1445(A):C:H2'	26:DA:1446:C:H6	1.77	0.49
1:CA:392:G:H2'	1:CA:393:A:C8	2.47	0.49
28:DD:13:ARG:HD2	28:DD:13:ARG:HA	1.59	0.49
33:DI:62:LYS:HE2	33:DI:133:HIS:CD2	2.47	0.49
26:DA:127:A:H5''	26:DA:128:C:O4'	2.13	0.49
1:AA:337:C:H2'	1:AA:338:A:C8	2.48	0.49
1:CA:1006:C:OP1	1:CA:1037:C:O2'	2.31	0.48
1:CA:1244:C:N4	1:CA:1293:G:N1	2.34	0.48
1:CA:1355:G:H2'	1:CA:1356:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1529:G:C6	26:DA:1530:C:N4	2.81	0.48
26:DA:2579:C:H2'	26:DA:2580:U:O4'	2.13	0.48
26:DA:1652:A:OP1	38:DR:8:ARG:NH1	2.41	0.48
28:BD:108:PRO:HB3	28:BD:143:HIS:HE1	1.75	0.48
26:DA:1019:U:O2'	26:DA:1021:A:H2	1.95	0.48
26:DA:709:U:H2'	26:DA:710:G:H8	1.77	0.48
26:BA:644:A:H4'	26:BA:645:C:C5	2.48	0.48
30:BF:101:LEU:HD12	30:BF:102:PRO:HD2	1.95	0.48
26:BA:2749:A:P	32:BH:3:ARG:HH21	2.36	0.48
1:AA:401:C:H2'	1:AA:402:G:C8	2.48	0.48
40:DT:64:ARG:HB2	40:DT:73:GLU:HG2	1.94	0.48
1:AA:1063:C:OP2	1:AA:1064:G:O2'	2.14	0.48
2:CB:142:LEU:HD21	2:CB:146:GLN:HE21	1.78	0.48
26:BA:2037:G:H2'	26:BA:2038:G:C8	2.48	0.48
26:BA:1018:C:O3'	26:BA:1120:G:N2	2.46	0.48
26:DA:2398:U:H2'	26:DA:2399:G:H8	1.77	0.48
1:CA:88:A:H4'	1:CA:89:C:O5'	2.13	0.48
26:BA:2136:C:N3	26:BA:2155:G:N2	2.53	0.48
26:DA:1421:G:C2	26:DA:1422:G:N7	2.81	0.48
26:BA:944:G:H5''	26:BA:945:A:O5'	2.13	0.48
26:DA:2723:C:H5''	38:DR:1:MET:HE2	1.95	0.48
1:AA:1015:A:N3	1:AA:1218:C:O2'	2.44	0.48
26:BA:548:A:H61	42:BV:19:LYS:H	1.61	0.48
1:CA:578:C:OP1	61:CA:4037:HOH:O	2.20	0.48
1:AA:1002:G:C6	1:AA:1003:G:C2	3.02	0.48
26:DA:1860:G:C2	26:DA:1861:G:C8	3.01	0.48
1:AA:189:G:C6	1:AA:189(L):G:C6	3.01	0.48
1:AA:153:C:N4	1:AA:168:G:H1	2.10	0.48
26:DA:1434:A:H61	26:DA:1558:A:H62	1.60	0.48
1:CA:189(A):C:H2'	1:CA:189(B):C:H5'	1.94	0.48
1:CA:130:A:O2'	1:CA:131:C:O5'	2.29	0.48
1:CA:665:A:H1'	1:CA:733:A:O4'	2.13	0.48
26:BA:1949:G:C6	26:BA:1950:G:C6	3.01	0.48
1:CA:16:A:C2'	1:CA:17:U:H5'	2.44	0.48
1:AA:619:U:N3	4:AD:134:ASP:OD1	2.32	0.48
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.48	0.48
26:DA:218:A:C2	26:DA:235:U:H4'	2.49	0.48
26:BA:2012:G:OP1	43:BW:11:ARG:NH2	2.43	0.48
9:AI:26:VAL:HG13	9:AI:61:ALA:HB3	1.94	0.48
41:BU:82:GLY:HA3	41:BU:113:ALA:HB1	1.95	0.48
26:BA:1568:G:N7	61:BD:401:HOH:O	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:27:G:N2	26:DA:512:G:H1'	2.29	0.48
29:BE:176:ILE:HB	29:BE:181:LEU:HB2	1.94	0.48
1:AA:413:G:N2	1:AA:428:G:H1'	2.28	0.48
48:B1:64:ALA:HA	48:B1:67:ILE:HG13	1.95	0.48
1:CA:800:G:H8	1:CA:800:G:O5'	1.96	0.48
26:DA:968:G:H2'	26:DA:969:U:C6	2.48	0.48
26:DA:968:G:H2'	26:DA:969:U:H6	1.78	0.48
1:CA:1038:C:H2'	1:CA:1039:C:H6	1.78	0.48
1:CA:1355:G:N2	1:CA:1367:C:N3	2.53	0.48
1:CA:975:A:C8	1:CA:975:A:H5'	2.46	0.48
1:CA:975:A:H4'	1:CA:976:G:C5'	2.43	0.48
1:CA:1263:C:H2'	1:CA:1264:C:C6	2.48	0.48
26:BA:2127:G:N2	26:BA:2128:C:O2	2.46	0.48
2:AB:15:VAL:HG11	2:AB:209:ARG:HG2	1.95	0.48
26:DA:993:G:OP1	41:DU:50:ARG:NH2	2.47	0.48
1:CA:692:U:H2'	1:CA:694:A:OP2	2.12	0.48
26:DA:1422:G:H4'	26:DA:1493:C:OP1	2.13	0.48
1:AA:346:G:C5	1:AA:347:G:H1'	2.47	0.48
27:DB:5:C:O2'	27:DB:27:C:O2	2.31	0.48
1:AA:447:G:O6	1:AA:485:G:O2'	2.27	0.48
30:DF:120:GLU:HB3	30:DF:122:LYS:HG2	1.95	0.48
24:CX:15:G:H2'	24:CX:59:A:H61	1.78	0.48
18:CR:37:VAL:HG23	18:CR:79:LEU:HD23	1.94	0.48
1:CA:1223:C:P	19:CS:78:ARG:HH21	2.36	0.48
26:BA:565:C:H4'	26:BA:1253:A:N6	2.28	0.48
1:CA:1288:A:N3	1:CA:1352:C:O2'	2.42	0.48
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.94	0.48
1:CA:1080:A:H5'	5:CE:14:ARG:NH2	2.28	0.48
26:BA:1354:A:H5''	28:BD:38:LYS:HD3	1.95	0.48
26:DA:1297:C:OP1	26:DA:2710:C:H4'	2.13	0.48
1:CA:993:G:H2'	1:CA:995:C:H41	1.78	0.48
54:B7:46:VAL:HG13	54:B7:48:LYS:HE3	1.95	0.48
1:AA:749:C:H2'	1:AA:750:G:H8	1.78	0.48
5:CE:80:ILE:HG22	5:CE:91:LEU:HB2	1.95	0.48
26:DA:345:A:N3	26:DA:347:A:N6	2.60	0.48
26:DA:2282:G:H4'	26:DA:2389:G:O2'	2.13	0.48
5:AE:68:GLU:OE1	5:AE:70:PRO:HG3	2.12	0.48
26:BA:1509(B):A:H2'	26:BA:1510:G:O4'	2.13	0.48
1:AA:728:A:C5	15:AO:54:ARG:HD2	2.49	0.48
26:BA:1188:U:H4'	42:BV:79:VAL:HG22	1.96	0.48
35:DO:34:THR:OG1	35:DO:35:VAL:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2126:A:N6	26:DA:2163:C:O4'	2.47	0.48
41:DU:50:ARG:HH12	42:DV:72:VAL:HA	1.79	0.48
1:CA:255:G:OP1	17:CQ:69:LYS:NZ	2.39	0.48
1:AA:763:G:H2'	1:AA:764:C:H5'	1.95	0.48
29:BE:12:THR:HG21	40:BT:11:GLU:HG2	1.95	0.48
26:DA:1754:C:N3	26:DA:2716:U:O2'	2.44	0.48
26:BA:2130:U:C2'	26:BA:2131:G:H21	2.26	0.48
1:CA:735:C:H2'	1:CA:736:C:H6	1.77	0.48
26:DA:2238:G:N3	26:DA:2238:G:H2'	2.29	0.48
26:BA:1794:U:H2'	26:BA:1795:C:C6	2.48	0.48
1:CA:1316:G:N2	1:CA:1319:A:OP2	2.42	0.48
26:BA:918:A:H5''	27:BB:98:G:O2'	2.14	0.48
26:DA:598:G:H2'	26:DA:599:G:O4'	2.13	0.48
26:DA:2133:G:C2	26:DA:2157:G:N3	2.81	0.48
1:CA:1262:C:H2'	1:CA:1263:C:H5'	1.95	0.48
26:BA:2162:G:H4'	26:BA:2172:U:H2'	1.95	0.48
1:CA:1227:A:OP1	19:CS:80:TYR:OH	2.26	0.48
26:DA:1012:U:OP2	41:DU:70:ARG:NH2	2.33	0.48
26:DA:1449:A:O2'	26:DA:1529:G:N2	2.36	0.48
26:DA:2741:A:H2'	26:DA:2742:C:O4'	2.13	0.48
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.94	0.48
8:AH:86:ILE:HG22	8:AH:93:VAL:HG21	1.94	0.48
20:AT:43:LEU:O	20:AT:47:GLY:N	2.46	0.48
1:CA:1212:U:H4'	1:CA:1213:A:O5'	2.13	0.48
27:BB:2:C:H2'	27:BB:3:C:C6	2.48	0.48
26:DA:7:G:H5''	34:DN:130:HIS:HE1	1.78	0.48
1:AA:657:G:C2	1:AA:658:G:C8	3.02	0.48
26:BA:1588:C:H2'	26:BA:1589:C:H6	1.78	0.48
46:DZ:153:SER:HB3	46:DZ:167:PRO:HB3	1.96	0.48
19:CS:12:ASP:OD2	19:CS:35:SER:HB3	2.12	0.48
1:CA:444:C:H2'	1:CA:445:G:H8	1.79	0.48
1:AA:109:A:C6	1:AA:326:G:C6	3.01	0.48
50:B3:19:GLN:OE1	50:B3:52:HIS:NE2	2.45	0.48
1:AA:779:C:OP2	61:AA:4019:HOH:O	2.20	0.48
1:CA:938:A:C6	1:CA:939:G:C5	3.02	0.48
44:DX:5:TYR:CZ	49:D2:30:ARG:HB2	2.48	0.48
26:DA:1025:G:C4	26:DA:1135:C:H1'	2.48	0.48
26:DA:2182:G:H2'	26:DA:2183:C:C6	2.49	0.48
1:CA:984:C:H2'	1:CA:985:C:H6	1.79	0.48
1:AA:1392:G:N2	1:AA:1502:A:C8	2.77	0.48
1:AA:161:A:O5'	1:AA:161:A:H8	1.97	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BI:92:VAL:HG22	33:BI:120:ILE:HD12	1.95	0.48
13:CM:86:CYS:SG	13:CM:89:GLY:N	2.87	0.48
1:CA:1320:C:OP1	19:CS:70:LYS:HE3	2.12	0.48
26:BA:568:U:H5'	26:BA:945:A:C6	2.49	0.48
26:DA:1204:A:H2	26:DA:1241:A:N6	2.06	0.48
26:DA:2727:G:O2'	35:DO:70:LYS:NZ	2.45	0.48
26:DA:1652:A:C2'	26:DA:1653:G:H5'	2.43	0.48
26:DA:1798:U:H5'	28:DD:259:THR:CG2	2.43	0.48
5:AE:102:ALA:HB1	5:AE:106:PRO:HG2	1.94	0.48
46:DZ:97:GLU:HA	46:DZ:127:LYS:HA	1.94	0.48
1:AA:1356:G:H2'	1:AA:1357:A:H8	1.76	0.48
41:DU:79:PHE:CZ	41:DU:83:LEU:HD21	2.48	0.48
1:AA:1239:A:H62	1:AA:1299:A:N6	2.12	0.48
50:B3:50:VAL:O	50:B3:54:VAL:HB	2.14	0.48
1:CA:762:C:H2'	1:CA:763:G:H8	1.78	0.48
1:AA:797:C:H2'	1:AA:798:G:H5'	1.94	0.48
1:AA:392:G:H2'	1:AA:393:A:C8	2.49	0.48
37:DQ:30:GLY:O	37:DQ:134:ARG:HD3	2.14	0.48
46:DZ:119:GLU:HG3	46:DZ:122:ARG:HH12	1.78	0.48
26:BA:1812:A:O2'	28:BD:45:ASN:N	2.41	0.48
1:CA:1075:C:H2'	1:CA:1076:C:H5'	1.95	0.48
1:CA:1078:U:H1'	5:CE:130:ASN:OD1	2.13	0.48
26:BA:84:A:C5'	45:BY:8:LYS:HG2	2.44	0.48
1:AA:1349:A:H5''	9:AI:121:ARG:HB2	1.96	0.48
8:CH:97:VAL:HG21	8:CH:128:GLY:HA2	1.96	0.48
1:AA:186:C:H2'	1:AA:187:C:C6	2.48	0.48
23:CW:76:PPU:H102	26:DA:2584:U:C5'	2.44	0.48
26:BA:2156:G:N2	26:BA:2158:A:N6	2.60	0.48
26:BA:2584:U:H2'	26:BA:2585:U:C6	2.49	0.48
27:DB:31:C:N4	27:DB:51:G:O6	2.47	0.48
1:AA:1116:C:N3	1:AA:1184:G:O6	2.46	0.48
1:AA:44:G:C2	1:AA:45:U:H1'	2.49	0.48
26:DA:2690:C:N4	26:DA:2713:A:H1'	2.28	0.48
1:AA:1452:C:O2'	1:AA:1456:G:H5''	2.13	0.48
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.13	0.48
26:BA:1720:U:H2'	26:BA:1721:G:O4'	2.13	0.48
1:CA:953:G:H8	1:CA:953:G:O5'	1.96	0.48
26:DA:1815:A:H8	26:DA:1815:A:OP1	1.96	0.48
26:DA:900:A:H2'	26:DA:901:A:H8	1.79	0.48
26:DA:385:C:O2	36:DP:71:VAL:HG21	2.13	0.48
16:AP:19:ILE:HG22	16:AP:37:GLY:C	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:484:C:H2'	26:BA:485:C:H6	1.78	0.48
26:BA:652(C):G:N2	26:BA:653:A:H1'	2.28	0.48
33:DI:31:LEU:HD21	33:DI:38:LEU:HG	1.95	0.48
8:CH:64:LYS:HD2	8:CH:79:VAL:HG21	1.96	0.48
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.14	0.48
26:DA:957:A:H5'	37:DQ:76:LYS:HG3	1.94	0.48
4:AD:100:ARG:NH1	4:AD:137:SER:OG	2.46	0.48
28:BD:68:LYS:HD3	28:BD:70:TRP:CH2	2.48	0.48
1:AA:1085:U:OP2	61:AA:4141:HOH:O	2.20	0.48
26:BA:2836:U:H2'	26:BA:2837:G:C8	2.49	0.48
26:BA:2651:C:H2'	26:BA:2652:C:C6	2.48	0.48
1:AA:1171:G:C2'	1:AA:1172:C:H5'	2.44	0.48
1:CA:922:G:H1	1:CA:1395:C:H42	1.62	0.48
27:DB:32:C:C2	27:DB:51:G:N1	2.81	0.48
26:DA:2302:G:C2'	26:DA:2303:G:H5'	2.43	0.48
27:DB:117:G:O2'	39:DS:54:LEU:HD21	2.14	0.48
1:AA:1355:G:H2'	1:AA:1356:G:C8	2.49	0.48
26:DA:307:G:N2	26:DA:309:G:H3'	2.29	0.48
30:BF:34:TRP:HA	36:BP:6:LEU:HD13	1.95	0.48
26:DA:277:C:HO2'	26:DA:278:A:P	2.34	0.48
24:CX:23:C:H2'	24:CX:24:U:H6	1.79	0.48
26:DA:2564:A:C2	26:DA:2647:U:H4'	2.49	0.48
26:DA:93:G:H2'	26:DA:94:C:H6	1.78	0.48
1:CA:222:U:H2'	1:CA:223:U:C6	2.48	0.48
32:DH:56:SER:OG	32:DH:57:ASP:N	2.45	0.48
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.79	0.48
1:CA:567:G:C2	1:CA:568:G:H1'	2.49	0.48
26:DA:1416:G:H1	26:DA:1582:C:H42	1.62	0.48
4:AD:22:LYS:HB2	4:AD:26:CYS:SG	2.53	0.48
17:AQ:62:SER:HB3	17:AQ:72:ARG:HD2	1.96	0.48
37:DQ:21:THR:HG21	37:DQ:101:ARG:HD3	1.95	0.48
3:CC:155:GLY:HA3	3:CC:196:LEU:HD13	1.95	0.48
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.48	0.48
5:AE:110:LEU:HD13	5:AE:118:ILE:HD13	1.95	0.48
3:CC:71:ALA:HB1	3:CC:109:PRO:HG3	1.96	0.48
26:BA:1999:C:H4'	26:BA:2723:C:O2	2.14	0.48
3:AC:82:GLU:HG2	3:AC:85:ARG:HH22	1.78	0.48
1:CA:1002:G:H2'	1:CA:1003:G:C8	2.49	0.48
27:DB:90:A:N7	27:DB:91:C:H1'	2.29	0.48
33:DI:127:VAL:HA	33:DI:140:LEU:O	2.14	0.48
1:AA:292:G:N7	1:AA:293:G:H1'	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2319:G:H22	39:BS:3:ARG:HA	1.77	0.48
1:CA:659:U:H2'	1:CA:660:G:H5'	1.94	0.48
26:BA:1494:A:H2'	26:BA:1495:A:C8	2.48	0.48
31:BG:16:ARG:O	31:BG:20:ILE:HG13	2.14	0.48
1:CA:892:A:O2'	1:CA:1415:G:H4'	2.13	0.48
26:DA:7:G:H2'	26:DA:8:A:C8	2.49	0.48
1:CA:1404:C:H2'	1:CA:1405:G:C8	2.49	0.48
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.13	0.48
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.96	0.48
1:CA:434:U:H2'	1:CA:435:C:C6	2.49	0.48
26:BA:2712:U:H2'	26:BA:2714:G:H5''	1.95	0.48
12:AL:26:ALA:HB1	12:AL:60:LEU:HD23	1.95	0.48
13:AM:19:LEU:HD21	13:AM:56:LEU:HD21	1.96	0.48
26:DA:476:G:H4'	26:DA:502:A:N1	2.28	0.48
1:AA:1516:G:H2'	1:AA:1518:A:OP2	2.13	0.48
26:BA:1341:U:OP2	26:BA:1394:U:O2'	2.23	0.48
26:DA:1221:C:H2'	26:DA:1221(A):C:C6	2.48	0.48
26:DA:1697:G:OP2	26:DA:1698:A:O2'	2.22	0.48
26:BA:1992:G:H4'	26:BA:1993:U:C5	2.49	0.48
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.36	0.48
26:DA:784:A:H5'	26:DA:785:G:OP1	2.13	0.48
2:AB:178:ARG:NH2	8:AH:74:PRO:HB3	2.27	0.48
7:CG:108:ALA:HA	7:CG:111:ARG:HD2	1.96	0.48
4:CD:173:TRP:HB2	4:CD:187:ARG:O	2.14	0.48
26:DA:1695:G:H8	28:DD:8:PRO:O	1.97	0.48
28:BD:134:ARG:HG2	28:BD:187:GLY:O	2.14	0.48
1:AA:339:C:OP2	35:BO:97:ARG:HD3	2.14	0.48
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.48	0.48
26:DA:58:G:O2'	26:DA:73:A:N1	2.43	0.48
9:AI:23:ASN:ND2	9:AI:23:ASN:H	2.12	0.48
26:DA:2773:C:P	29:DE:166:THR:HG1	2.37	0.48
26:DA:753:C:H2'	26:DA:754:C:C6	2.49	0.48
26:DA:2327:A:H2'	26:DA:2328:A:C8	2.49	0.48
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.96	0.48
33:DI:93:THR:HA	33:DI:116:LEU:HD13	1.96	0.48
26:DA:2785:C:HO2'	29:DE:66:HIS:CE1	2.30	0.48
1:CA:441:A:H3'	1:CA:442:C:C6	2.49	0.48
4:CD:90:GLY:HA3	4:CD:200:GLU:HG3	1.94	0.48
12:AL:8:ASN:O	12:AL:12:ARG:HG3	2.14	0.48
26:DA:577:G:H8	26:DA:577:G:O5'	1.97	0.48
4:AD:196:LEU:C	4:AD:198:VAL:H	2.17	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:84:LYS:HD3	15:AO:84:LYS:O	2.13	0.48
1:CA:1137:C:H5''	1:CA:1138:G:OP1	2.14	0.48
26:DA:2336:A:H61	47:D0:43:THR:CG2	2.27	0.48
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.95	0.48
26:BA:1709:U:H2'	26:BA:1710:C:C6	2.49	0.48
31:BG:5:VAL:HG22	31:BG:8:LYS:H	1.79	0.48
26:BA:2171:A:HO2'	26:BA:2172:U:H6	1.59	0.47
54:B7:24:THR:O	54:B7:28:ARG:HG3	2.13	0.47
26:BA:2892:A:C5	26:BA:2893:G:C6	3.02	0.47
26:BA:2629:A:H1'	26:BA:2630:G:H5''	1.96	0.47
26:DA:2821:A:H2'	26:DA:2822:G:C8	2.49	0.47
51:B4:63:TYR:N	51:B4:64:GLY:HA2	2.29	0.47
7:CG:99:LEU:HA	7:CG:102:ARG:NH1	2.29	0.47
33:DI:72:LEU:HD13	33:DI:140:LEU:HB2	1.94	0.47
1:CA:296:U:O2'	1:CA:556:C:O2	2.30	0.47
26:BA:952:G:P	37:BQ:16:ARG:HH21	2.37	0.47
24:AX:61:C:H2'	24:AX:62:C:H6	1.78	0.47
1:CA:1089:G:C6	1:CA:1090:U:C2	3.02	0.47
1:AA:1024:G:N3	1:AA:1024:G:H2'	2.28	0.47
48:B1:3:LYS:HB2	48:B1:61:ARG:NH1	2.29	0.47
4:AD:85:LYS:HG3	4:AD:86:LYS:N	2.28	0.47
29:DE:37:ARG:HB2	29:DE:46:ALA:N	2.29	0.47
1:AA:1258:G:H2'	1:AA:1259:C:H6	1.78	0.47
29:DE:119:ARG:HD2	29:DE:120:TRP:CE2	2.49	0.47
45:BY:6:HIS:H	45:BY:6:HIS:CD2	2.32	0.47
31:DG:173:LEU:HB3	31:DG:178:PHE:CG	2.48	0.47
32:DH:13:LYS:HA	32:DH:14:GLY:HA2	1.58	0.47
35:BO:69:ILE:HG12	35:BO:77:ILE:HG22	1.96	0.47
26:BA:2492:U:H2'	26:BA:2493:U:C6	2.49	0.47
26:BA:1292:U:H2'	26:BA:1293:C:C6	2.49	0.47
20:CT:37:SER:O	20:CT:41:ILE:HD13	2.14	0.47
3:CC:35:GLU:OE2	3:CC:59:ARG:NH2	2.47	0.47
2:CB:8:LYS:HA	2:CB:217:ARG:HE	1.79	0.47
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.96	0.47
7:CG:155:ARG:CZ	7:CG:155:ARG:HB3	2.43	0.47
26:DA:1206:G:H2'	26:DA:1207:C:C6	2.48	0.47
26:DA:1951:U:O2'	26:DA:1953:A:N7	2.43	0.47
26:DA:80:G:H2'	26:DA:81:G:O4'	2.14	0.47
1:CA:1027:C:N4	1:CA:1034:G:N1	2.61	0.47
1:CA:1002:G:N2	1:CA:1039:C:C4	2.82	0.47
1:CA:78:G:N2	1:CA:92:C:O2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2150:U:H2'	26:DA:2151:G:C8	2.49	0.47
1:AA:973:G:OP1	10:AJ:57:LYS:NZ	2.43	0.47
1:AA:406:G:N2	4:AD:119:GLN:HE22	2.13	0.47
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.33	0.47
48:D1:3:LYS:HB2	48:D1:61:ARG:HH12	1.79	0.47
26:DA:1899:G:O2'	26:DA:1900:A:OP2	2.31	0.47
26:BA:84:A:H5'	45:BY:8:LYS:HG2	1.95	0.47
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.96	0.47
26:DA:236:C:H2'	26:DA:237:C:H6	1.79	0.47
1:CA:66:G:OP1	1:CA:66:G:H8	1.97	0.47
10:CJ:16:LEU:HD23	10:CJ:94:VAL:HG22	1.95	0.47
1:CA:974:A:OP1	1:CA:974:A:H8	1.97	0.47
32:DH:154:PRO:HB3	32:DH:163:TYR:CE2	2.49	0.47
2:AB:174:VAL:HG13	2:AB:184:VAL:HG11	1.95	0.47
26:BA:2164:C:H5	26:BA:2165:G:C4	2.32	0.47
1:CA:59:A:H5''	1:CA:387:U:H5''	1.95	0.47
40:BT:23:ARG:HG3	40:BT:120:ARG:NH1	2.29	0.47
1:CA:1206:G:N7	61:CA:4001:HOH:O	2.36	0.47
4:CD:31:CYS:O	4:CD:35:ARG:HG3	2.13	0.47
26:DA:1359:A:C6	26:DA:1360:A:C4	3.02	0.47
1:AA:221:C:H2'	1:AA:222:U:C6	2.43	0.47
26:BA:548:A:N6	42:BV:19:LYS:H	2.11	0.47
1:CA:1221:G:O3'	19:CS:77:THR:HG21	2.13	0.47
1:CA:1060:C:OP1	10:CJ:51:ARG:NH1	2.46	0.47
9:AI:79:LEU:HD22	9:AI:104:ARG:HB2	1.94	0.47
1:CA:45:U:H2'	1:CA:46:G:C8	2.49	0.47
1:CA:953:G:N7	13:CM:104:ARG:NH2	2.62	0.47
26:BA:1301:A:C8	26:BA:1303:G:C8	3.02	0.47
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.96	0.47
26:DA:2732:G:H3'	26:DA:2733:A:O4'	2.14	0.47
1:CA:605:U:C2'	1:CA:606:G:H5'	2.44	0.47
26:DA:236:C:H2'	26:DA:237:C:C6	2.48	0.47
26:DA:83:G:O2'	26:DA:102:G:N2	2.47	0.47
1:AA:381:C:H2'	1:AA:382:A:O4'	2.14	0.47
26:BA:2698:U:H2'	26:BA:2699:C:C6	2.49	0.47
1:AA:950:U:OP2	13:AM:102:ARG:HD3	2.13	0.47
53:B6:14:THR:HB	53:B6:48:VAL:O	2.13	0.47
2:CB:184:VAL:N	2:CB:198:ASP:OD2	2.38	0.47
26:DA:2583:G:OP2	61:DA:3952:HOH:O	2.20	0.47
1:CA:1360:A:C4	14:CN:18:VAL:HG12	2.49	0.47
26:DA:2400:G:H2'	26:DA:2401:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2875:C:O2'	40:DT:2:ASN:OD1	2.21	0.47
1:CA:872:A:O2'	1:CA:873:A:H3'	2.15	0.47
38:DR:87:TYR:OH	38:DR:116:LEU:HB3	2.14	0.47
26:BA:1255:U:O5'	26:BA:1256:G:H5''	2.14	0.47
26:DA:1170:G:H1	26:DA:1179:C:H42	1.62	0.47
26:DA:784:A:C8	26:DA:792:G:C5	3.02	0.47
46:BZ:33:LEU:HD11	46:BZ:90:VAL:HG21	1.97	0.47
1:CA:165:C:H2'	1:CA:166:G:H8	1.79	0.47
40:BT:108:ARG:HA	40:BT:111:ARG:NH1	2.30	0.47
26:BA:309:G:H4'	45:BY:18:GLY:HA2	1.96	0.47
1:AA:58:C:O2'	1:AA:388:G:N7	2.37	0.47
26:DA:191:A:N1	61:DA:4117:HOH:O	2.35	0.47
54:D7:10:ARG:O	54:D7:14:LYS:HB2	2.14	0.47
26:DA:2547:U:O2	35:DO:23:ARG:NH2	2.47	0.47
4:AD:187:ARG:NH1	4:AD:193:ASP:OD2	2.48	0.47
4:AD:164:ALA:O	4:AD:168:ARG:NH1	2.45	0.47
1:CA:1495:U:O2'	26:DA:1919:A:N1	2.40	0.47
26:DA:1783:A:H5'	26:DA:2608:G:H4'	1.96	0.47
26:BA:1406:U:H2'	26:BA:1407:C:C6	2.50	0.47
2:CB:20:GLU:HB2	2:CB:190:THR:OG1	2.14	0.47
26:BA:2493:U:H2'	26:BA:2494:G:O4'	2.14	0.47
26:BA:1274:A:N3	26:BA:1297:C:H1'	2.29	0.47
2:AB:28:PHE:CD1	2:AB:190:THR:HA	2.50	0.47
26:BA:1643:G:H2'	26:BA:1644:C:O4'	2.14	0.47
26:BA:45:C:H2'	26:BA:47:C:C6	2.49	0.47
1:AA:687:A:N1	1:AA:700:G:O2'	2.41	0.47
51:B4:26:SER:OG	51:B4:27:THR:N	2.47	0.47
4:AD:11:LEU:HD23	4:AD:66:ARG:HB3	1.97	0.47
26:DA:2708:G:H1'	38:DR:71:GLN:HE22	1.79	0.47
26:DA:1509(A):A:N3	26:DA:1509(A):A:H5''	2.29	0.47
16:AP:54:GLU:HG3	16:AP:55:ARG:N	2.29	0.47
26:BA:2735:G:H2'	26:BA:2736:G:H8	1.78	0.47
26:BA:2552:U:C2	26:BA:2554:U:H5''	2.48	0.47
26:DA:2140:C:O2	26:DA:2140:C:H2'	2.13	0.47
1:CA:1392:G:H21	1:CA:1502:A:H8	1.61	0.47
26:DA:1171:G:N2	26:DA:1179:C:N3	2.61	0.47
26:BA:2120:G:C2'	26:BA:2121:G:H5'	2.45	0.47
26:BA:1803:A:O2'	28:BD:259:THR:HG21	2.14	0.47
1:CA:1052:U:H5''	1:CA:1053:G:OP2	2.13	0.47
1:AA:1321:C:H5''	1:AA:1322:C:H2'	1.97	0.47
28:BD:108:PRO:HG2	28:BD:111:LEU:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.14	0.47
20:AT:43:LEU:HD13	20:AT:51:GLU:HB3	1.96	0.47
32:BH:56:SER:HB3	32:BH:61:HIS:ND1	2.30	0.47
30:DF:157:VAL:HB	30:DF:194:MET:HG2	1.97	0.47
9:AI:100:GLY:O	9:AI:103:THR:HG23	2.14	0.47
26:BA:1354:A:H2'	26:BA:1355:G:O4'	2.15	0.47
2:AB:71:VAL:HB	2:AB:164:VAL:HG22	1.97	0.47
13:CM:79:LYS:NZ	13:CM:83:ASP:OD2	2.35	0.47
26:DA:603:A:N1	26:DA:625:G:O2'	2.37	0.47
26:DA:608:A:H2'	26:DA:609:A:C8	2.49	0.47
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.97	0.47
26:BA:2674:G:H2'	26:BA:2675:A:C8	2.50	0.47
8:AH:6:ILE:HB	8:AH:85:ARG:NH1	2.28	0.47
8:CH:45:ILE:HD13	8:CH:61:VAL:HG13	1.96	0.47
50:B3:26:LEU:O	50:B3:35:ARG:NE	2.44	0.47
1:CA:6:G:H4'	1:CA:298:A:H4'	1.96	0.47
11:CK:41:THR:OG1	11:CK:42:TRP:N	2.48	0.47
40:BT:106:SER:O	40:BT:110:ILE:HG13	2.14	0.47
1:AA:356:A:N3	1:AA:368:U:O2'	2.42	0.47
46:DZ:144:LEU:HD11	46:DZ:172:ALA:HB1	1.95	0.47
26:BA:1335:U:OP1	44:BX:65:ARG:HD2	2.14	0.47
24:CX:49:G:C2	24:CX:65:C:N3	2.82	0.47
31:DG:43:LEU:HB3	31:DG:44:GLY:H	1.62	0.47
26:BA:1803:A:H4'	28:BD:259:THR:HG23	1.96	0.47
1:AA:1015:A:H2'	1:AA:1016:A:C8	2.50	0.47
38:DR:31:HIS:C	38:DR:33:ARG:H	2.17	0.47
1:CA:499:A:H4'	1:CA:500:G:H5'	1.97	0.47
1:AA:1127:G:H5'	1:AA:1280:A:O2'	2.13	0.47
26:DA:659:C:H2'	26:DA:660:G:C8	2.48	0.47
36:DP:28:GLY:O	36:DP:30:THR:N	2.48	0.47
26:DA:1424:G:H2'	26:DA:1425:G:O4'	2.15	0.47
26:BA:271(K):U:C2	33:BI:50:ARG:HD3	2.49	0.47
26:BA:1641:A:H2'	26:BA:1642:G:O4'	2.15	0.47
26:DA:2308:G:H5''	26:DA:2310:A:OP2	2.14	0.47
26:BA:2625:G:H2'	26:BA:2626:C:C6	2.49	0.47
26:BA:2431:U:O2'	26:BA:2433:A:N7	2.36	0.47
26:DA:1592:C:H2'	26:DA:1593:G:C8	2.50	0.47
37:BQ:85:LYS:HG2	47:B0:7:LEU:HB3	1.96	0.47
1:AA:411:A:OP2	4:AD:25:ARG:NH2	2.48	0.47
1:CA:865:A:H5'	1:CA:1078:U:O4	2.14	0.47
1:CA:7:G:H5'	1:CA:298:A:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:3:ARG:HB3	6:CF:93:SER:HB2	1.97	0.47
38:DR:97:VAL:HG22	38:DR:114:VAL:HG22	1.97	0.47
40:DT:22:PHE:HA	40:DT:91:ARG:HH12	1.78	0.47
1:CA:624:C:H2'	1:CA:625:G:H8	1.79	0.47
1:CA:721:G:H4'	1:CA:722:A:O4'	2.15	0.47
26:BA:94(A):G:H2'	26:BA:95:G:O4'	2.15	0.47
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.29	0.47
40:DT:36:GLU:OE1	40:DT:41:ARG:NE	2.41	0.47
36:DP:143:GLY:O	36:DP:145:PRO:HD3	2.14	0.47
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.42	0.47
1:CA:1004:A:H3'	1:CA:1005:A:C5'	2.45	0.47
1:CA:1400:C:O5'	22:CV:18:G:C2	2.68	0.47
1:CA:986:A:C2	19:CS:52:TYR:HE2	2.32	0.47
26:BA:2137:C:H2'	26:BA:2138:C:C6	2.49	0.47
1:AA:1399:C:C2	1:AA:1502:A:N6	2.82	0.47
26:BA:2103:C:N3	26:BA:2186:G:N2	2.49	0.47
26:BA:303:U:H2'	26:BA:304:G:C8	2.49	0.47
1:CA:1099:G:C5	1:CA:1100:C:N3	2.82	0.47
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.47	0.47
26:BA:990:A:C6	26:BA:1186:G:H1'	2.49	0.47
1:CA:584:G:H5'	17:CQ:91:ARG:NH2	2.30	0.47
26:DA:1579:A:H2'	26:DA:1580:A:C8	2.50	0.47
1:AA:1034:G:H3'	1:AA:1035:A:C8	2.49	0.47
27:DB:55:U:H1'	31:DG:29:TRP:CD1	2.49	0.47
1:CA:545:C:O2'	1:CA:549:C:OP1	2.27	0.47
5:CE:93:PRO:HG2	8:CH:105:ARG:NE	2.29	0.47
41:BU:36:ARG:HD2	41:BU:40:PHE:CZ	2.49	0.47
26:BA:1668:A:O2'	26:BA:1674:G:N7	2.42	0.47
4:AD:61:LYS:HA	4:AD:203:VAL:HG22	1.96	0.47
26:BA:467:G:O6	61:BA:3834:HOH:O	2.19	0.47
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.48	0.47
1:CA:1457:G:H5''	20:CT:35:THR:HG21	1.96	0.47
1:AA:979:C:OP1	1:AA:1223:C:N4	2.48	0.47
1:CA:797:C:C2'	1:CA:798:G:H5'	2.44	0.47
26:DA:990:A:C6	26:DA:1186:G:H1'	2.50	0.47
26:BA:2870:C:H2'	26:BA:2871:C:O4'	2.15	0.47
1:CA:1097:C:H2'	1:CA:1098:C:O4'	2.15	0.47
1:AA:838:G:H1	1:AA:848:C:N4	2.13	0.47
26:DA:2639:A:H2'	26:DA:2640:G:O4'	2.14	0.47
26:BA:242:G:O2'	26:BA:254:G:O6	2.30	0.47
1:AA:659:U:H2'	1:AA:660:G:H5'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1055:A:O2'	3:AC:161:GLU:O	2.23	0.47
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.78	0.47
1:CA:811:C:H4'	1:CA:901:A:H61	1.79	0.47
26:BA:1178:C:H2'	26:BA:1179:C:H6	1.80	0.47
26:BA:1778:U:H2'	26:BA:1784:A:N6	2.30	0.47
26:BA:2848:G:O2'	26:BA:2867:G:N2	2.43	0.47
46:DZ:30:ASN:ND2	46:DZ:90:VAL:HB	2.29	0.47
3:CC:32:LEU:HA	3:CC:35:GLU:HG2	1.96	0.47
26:BA:1297:C:OP1	26:BA:2710:C:H4'	2.14	0.47
26:BA:2735:G:H2'	26:BA:2736:G:C8	2.50	0.47
46:DZ:150:LEU:H	46:DZ:172:ALA:HB3	1.80	0.47
34:DN:4:TYR:CD2	41:DU:100:VAL:HG11	2.49	0.47
1:AA:936:C:O2	1:AA:1382:C:N4	2.31	0.47
1:AA:1112:C:C2	3:AC:178:LEU:HB2	2.49	0.47
10:CJ:9:ARG:HG2	10:CJ:69:ASN:OD1	2.14	0.47
7:CG:73:MET:HG3	7:CG:90:GLU:HA	1.96	0.47
26:BA:141:A:C8	26:BA:1408:C:O2'	2.65	0.47
26:DA:2220:G:H2'	26:DA:2221:G:H8	1.80	0.47
19:AS:39:THR:HG22	19:AS:40:ILE:O	2.15	0.47
26:DA:411:G:C5	36:DP:72:PRO:HB3	2.50	0.47
35:DO:16:ALA:HB2	35:DO:52:VAL:HG21	1.95	0.47
32:DH:106:THR:HG22	32:DH:112:PRO:HB3	1.96	0.47
1:AA:1133:G:H2'	1:AA:1134:G:C8	2.49	0.47
1:AA:783:C:OP1	1:AA:1515:C:O2'	2.32	0.47
46:BZ:146:ILE:HA	46:BZ:147:GLY:HA2	1.63	0.47
56:D9:2:LYS:NZ	56:D9:31:LYS:O	2.28	0.47
30:DF:150:GLY:HA2	30:DF:172:TRP:CD2	2.50	0.47
1:CA:76:C:N4	1:CA:96:U:N3	2.62	0.47
1:CA:1362:C:C2'	1:CA:1363:C:H5''	2.43	0.47
19:CS:36:ARG:HD2	19:CS:52:TYR:O	2.15	0.47
31:DG:48:GLU:O	31:DG:51:ARG:HG3	2.15	0.47
26:BA:2160:G:H2'	26:BA:2161:C:C6	2.50	0.47
1:CA:1281:U:P	1:CA:1282:C:H41	2.38	0.47
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.48	0.47
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.14	0.47
26:DA:2500:U:H2'	26:DA:2504:U:C5	2.50	0.47
26:BA:797:C:H2'	26:BA:798:G:O4'	2.15	0.47
26:BA:2564:A:C2	26:BA:2647:U:H4'	2.49	0.47
1:AA:460:G:O5'	1:AA:460:G:H8	1.97	0.47
12:CL:113:ARG:HB3	12:CL:122:THR:HG21	1.97	0.47
26:BA:2577:A:O4'	52:B5:3:LYS:HB2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2398:U:H2'	26:DA:2399:G:C8	2.50	0.47
16:AP:66:PRO:HB2	16:AP:71:ARG:HB3	1.96	0.47
17:AQ:51:TYR:CZ	17:AQ:73:VAL:HG11	2.50	0.47
4:AD:31:CYS:O	4:AD:35:ARG:HG3	2.13	0.47
3:CC:134:ILE:HD11	3:CC:153:VAL:HG21	1.96	0.47
26:DA:2485:G:C2	26:DA:2486:G:C8	3.03	0.47
26:DA:1910:G:C6	26:DA:1911:U:C4	3.02	0.47
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.50	0.47
26:DA:853:G:H2'	26:DA:854:G:H8	1.79	0.47
1:AA:1425:U:H2'	1:AA:1426:C:C6	2.50	0.47
27:DB:78:A:C2	27:DB:100:A:C4	3.03	0.47
45:DY:12:THR:O	45:DY:75:ILE:N	2.41	0.47
1:CA:1398:A:OP1	1:CA:1401:G:OP1	2.33	0.47
24:CX:41:C:H2'	24:CX:42:G:C8	2.49	0.47
27:DB:8:U:O2'	39:DS:40:ILE:HD13	2.14	0.47
1:AA:1286:A:H2'	1:AA:1287:A:H4'	1.95	0.47
1:AA:765:G:H5''	1:AA:766:A:OP1	2.15	0.47
1:CA:163:C:H2'	1:CA:164:U:O4'	2.14	0.47
26:DA:2199:A:H3'	26:DA:2200:C:H6	1.80	0.47
1:CA:857:C:H2'	1:CA:858:G:O4'	2.15	0.47
48:B1:23:LYS:HB3	48:B1:29:GLY:HA3	1.97	0.47
1:AA:406:G:OP1	4:AD:5:ILE:HD11	2.14	0.47
30:DF:39:TRP:CD1	30:DF:101:LEU:HB2	2.49	0.47
1:CA:1271:G:H5'	1:CA:1314:C:H5''	1.95	0.47
26:BA:2543:G:H2'	26:BA:2544:G:C8	2.50	0.47
3:CC:54:ARG:HB2	3:CC:69:HIS:HB2	1.95	0.47
26:BA:37:C:H2'	26:BA:38:A:C8	2.49	0.47
1:CA:1266:G:N1	1:CA:1269:A:OP2	2.47	0.47
26:DA:1500:G:O2'	28:DD:100:GLY:O	2.29	0.47
26:BA:328:U:H4'	45:BY:68:HIS:CG	2.50	0.47
53:B6:13:CYS:SG	53:B6:47:THR:HG21	2.54	0.47
26:BA:2507:C:H2'	26:BA:2508:G:O4'	2.14	0.47
26:BA:1029:A:OP1	37:BQ:128:LYS:NZ	2.45	0.47
1:CA:493:G:H2'	1:CA:494:U:C5	2.50	0.47
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.97	0.47
26:DA:593:G:C6	26:DA:594:U:C4	3.03	0.47
1:AA:811:C:O2'	1:AA:901:A:N1	2.43	0.47
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.50	0.47
1:CA:1358:U:H5''	14:CN:33:VAL:O	2.15	0.47
31:DG:41:GLN:NE2	31:DG:153:ARG:HB3	2.17	0.47
27:DB:87:G:N2	27:DB:90:A:OP2	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.38	0.47
26:DA:2722:G:H5''	26:DA:2820:A:N7	2.30	0.47
33:DI:127:VAL:HG22	33:DI:139:GLN:OE1	2.15	0.47
1:AA:190:U:H2'	1:AA:191:G:C8	2.50	0.47
26:BA:2238:G:H2'	26:BA:2238:G:N3	2.30	0.47
1:AA:985:C:H2'	1:AA:986:A:C8	2.50	0.47
40:DT:77:PRO:HB2	40:DT:80:SER:HB2	1.97	0.47
1:CA:786:G:C2	1:CA:797:C:C2	3.03	0.47
26:DA:1187:G:H5'	42:DV:81:TYR:CE1	2.50	0.47
26:BA:222:A:H5''	26:BA:421:U:OP1	2.14	0.47
1:AA:1276:G:H2'	1:AA:1277:C:C6	2.50	0.47
26:BA:281:G:H1'	26:BA:360:G:N2	2.29	0.47
1:CA:736:C:H2'	1:CA:737:A:C8	2.50	0.47
29:BE:1:MET:HE3	29:BE:199:ARG:HD2	1.97	0.47
7:AG:136:LYS:O	7:AG:140:ASP:HB2	2.15	0.47
26:DA:2477:C:N4	56:D9:10:ILE:HG23	2.30	0.47
26:BA:869:G:H2'	26:BA:870:A:O4'	2.15	0.47
8:AH:11:THR:HG23	8:AH:14:ARG:HH12	1.79	0.47
38:BR:97:VAL:HG22	38:BR:114:VAL:HG22	1.97	0.47
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.44	0.47
26:DA:2335:A:C8	26:DA:2337:G:C5	3.03	0.47
1:AA:243:A:H4'	1:AA:244:U:H5''	1.97	0.47
11:CK:62:GLN:HB2	11:CK:93:GLN:HG3	1.95	0.47
26:DA:2134:A:O2'	26:DA:2159:G:N3	2.41	0.46
26:DA:2126:A:H2	26:DA:2127:G:N3	2.12	0.46
26:DA:2172:U:O2'	26:DA:2173:A:OP1	2.30	0.46
26:BA:1358:G:O2'	26:BA:1359:A:H5''	2.15	0.46
26:BA:2120:G:H2'	26:BA:2121:G:H5'	1.97	0.46
1:CA:750:G:N2	15:CO:23:GLY:O	2.42	0.46
26:BA:330:A:H2	26:BA:1210:A:O2'	1.96	0.46
28:BD:232:PRO:HB3	28:BD:244:ARG:CZ	2.45	0.46
2:CB:170:GLU:O	2:CB:174:VAL:HG23	2.15	0.46
1:CA:1010:G:H2'	1:CA:1011:G:C8	2.49	0.46
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.50	0.46
15:AO:24:SER:OG	15:AO:25:THR:N	2.49	0.46
1:AA:934:C:H5	1:AA:1344:C:H2'	1.79	0.46
18:CR:45:SER:OG	18:CR:47:THR:HG22	2.16	0.46
26:BA:2564:A:OP1	26:BA:2648:C:H4'	2.16	0.46
27:DB:42:C:O2	31:DG:93:THR:N	2.38	0.46
1:AA:841:U:H5	1:AA:848:C:H1'	1.77	0.46
1:AA:1036:G:N2	1:AA:1037:C:H1'	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:119:A:H4'	26:BA:120:U:OP1	2.16	0.46
24:AX:19:G:H4'	24:AX:20:U:OP2	2.15	0.46
1:AA:1095:U:OP2	1:AA:1108:G:N1	2.43	0.46
45:BY:6:HIS:HE1	45:BY:72:VAL:O	1.98	0.46
26:DA:1935:G:H1'	26:DA:1964:G:N2	2.31	0.46
26:DA:601:C:O2'	26:DA:605:C:OP1	2.32	0.46
28:BD:275:LYS:HB3	28:BD:276:LYS:H	1.47	0.46
4:CD:23:GLY:O	4:CD:26:CYS:HB2	2.14	0.46
1:AA:134:A:H61	16:AP:25:ARG:NH1	2.13	0.46
1:AA:1014:A:H4'	19:AS:14:HIS:CE1	2.49	0.46
1:AA:520:A:N1	1:AA:536:C:H1'	2.30	0.46
26:BA:998:C:OP1	61:BA:4488:HOH:O	2.21	0.46
40:DT:23:ARG:HG3	40:DT:120:ARG:NH1	2.30	0.46
1:CA:1356:G:H8	1:CA:1356:G:O5'	1.98	0.46
1:CA:1153:C:N4	1:CA:1154:G:H21	2.10	0.46
26:BA:2392:A:O3'	55:B8:27:THR:HB	2.15	0.46
33:DI:52:ARG:HH11	33:DI:52:ARG:HG3	1.79	0.46
19:AS:66:MET:HA	51:B4:58:ARG:NH1	2.30	0.46
26:DA:1021:A:C8	26:DA:1021:A:H3'	2.50	0.46
26:BA:832:G:N3	36:BP:53:GLY:HA3	2.30	0.46
27:DB:37:C:C5	27:DB:38:C:C4	3.04	0.46
1:AA:358:U:H2'	1:AA:359:U:H6	1.80	0.46
24:CX:53:G:C5	24:CX:54:5MU:H72	2.50	0.46
14:CN:48:ALA:HB2	14:CN:53:LEU:HD12	1.97	0.46
26:BA:280:C:H2'	26:BA:281:G:O4'	2.15	0.46
26:BA:27:G:N2	26:BA:512:G:H1'	2.30	0.46
2:CB:97:TRP:CZ2	2:CB:102:LEU:HD13	2.50	0.46
4:AD:20:TYR:HA	4:AD:26:CYS:SG	2.56	0.46
26:DA:96:G:H4'	49:D2:48:HIS:CD2	2.50	0.46
38:BR:38:VAL:HG22	38:BR:112:ALA:HB2	1.97	0.46
26:BA:2845:G:H2'	26:BA:2846:G:C8	2.50	0.46
30:DF:154:VAL:HG22	30:DF:191:ARG:HB2	1.98	0.46
26:BA:2398:U:H2'	26:BA:2399:G:C8	2.51	0.46
26:BA:744:G:H5''	26:BA:1658:C:H5''	1.97	0.46
11:AK:78:GLN:O	11:AK:103:LEU:HD22	2.15	0.46
26:DA:2845:G:H5''	40:DT:54:ARG:O	2.15	0.46
26:DA:2753:A:N3	56:D9:15:LYS:NZ	2.55	0.46
1:AA:967:C:H3'	1:AA:968:A:H2'	1.97	0.46
1:CA:1166:G:H8	1:CA:1166:G:O5'	1.98	0.46
26:DA:2886:G:H2'	26:DA:2887:U:H6	1.79	0.46
1:CA:313:A:H2'	1:CA:314:C:C6	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CN:26:ARG:HD3	14:CN:43:CYS:SG	2.54	0.46
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.16	0.46
1:AA:1165:C:N3	1:AA:1171:G:O6	2.49	0.46
1:CA:77:G:C5	1:CA:93:G:C2	3.04	0.46
2:CB:16:HIS:O	2:CB:18:GLY:N	2.48	0.46
26:BA:1171:G:H3'	26:BA:1173:G:H5'	1.98	0.46
26:DA:1394:U:C4	26:DA:1395:A:C5	3.03	0.46
36:DP:21:ARG:HA	36:DP:21:ARG:HD3	1.70	0.46
1:AA:606:G:H1'	1:AA:632:A:H61	1.80	0.46
26:BA:1459:G:H5''	26:BA:1460:A:OP2	2.16	0.46
27:BB:48:A:H2'	27:BB:49:C:C6	2.50	0.46
1:AA:107:G:H2'	1:AA:108:G:O4'	2.15	0.46
26:BA:271(R):G:C2'	26:BA:271(S):G:H5''	2.42	0.46
4:CD:108:LEU:HD12	4:CD:108:LEU:HA	1.68	0.46
17:CQ:64:PRO:HB3	17:CQ:70:ARG:NH1	2.30	0.46
1:AA:826:C:H2'	1:AA:827:U:C6	2.50	0.46
9:AI:47:LEU:O	9:AI:50:LEU:HG	2.15	0.46
24:AX:61:C:H2'	24:AX:62:C:C6	2.50	0.46
1:CA:765:G:N1	1:CA:812:C:O2'	2.40	0.46
26:DA:725:G:C6	26:DA:726:G:N1	2.83	0.46
26:DA:320:A:H4'	26:DA:322:A:N7	2.30	0.46
26:BA:2207:G:H2'	26:BA:2208:A:C2	2.49	0.46
26:BA:2801(A):A:N3	26:BA:2895:U:H1'	2.30	0.46
26:BA:2335:A:C8	26:BA:2337:G:C5	3.03	0.46
28:BD:97:TYR:HE1	28:BD:103:ARG:HG3	1.80	0.46
26:DA:1820:U:C4	28:DD:202:LYS:HD3	2.50	0.46
35:BO:98:VAL:HG22	35:BO:118:ALA:HA	1.97	0.46
26:DA:666:G:H4'	36:DP:49:ARG:NH2	2.30	0.46
26:BA:754:C:H2'	26:BA:755:C:C6	2.49	0.46
26:DA:1547:C:O2'	26:DA:1548:C:H5'	2.15	0.46
26:DA:471:A:H2'	26:DA:472:A:O4'	2.15	0.46
26:DA:1486:A:H2'	26:DA:1487:G:H8	1.81	0.46
1:AA:1404:C:H2'	1:AA:1405:G:C8	2.49	0.46
26:BA:1412:A:H2'	26:BA:1413:G:C8	2.50	0.46
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.97	0.46
26:DA:2591:C:H2'	26:DA:2592:G:C8	2.51	0.46
26:DA:2406:U:H2'	26:DA:2406:U:OP2	2.15	0.46
1:AA:1092:A:H5'	1:AA:1092:A:H8	1.80	0.46
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.36	0.46
2:CB:223:ILE:HA	2:CB:226:ARG:HG2	1.97	0.46
1:CA:335:C:H2'	1:CA:336:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2148:G:H2'	26:DA:2149:G:H8	1.80	0.46
1:CA:1402:C:H2'	1:CA:1403:C:O4'	2.15	0.46
26:BA:2127:G:O2'	26:BA:2128:C:O4'	2.34	0.46
26:BA:2162:G:C5'	26:BA:2172:U:H2'	2.46	0.46
27:DB:32:C:N3	27:DB:33:G:C5	2.84	0.46
1:AA:598:U:H2'	1:AA:599:C:C6	2.50	0.46
1:CA:1055:A:H5'	1:CA:1055:A:H8	1.80	0.46
24:CX:19:G:H1	24:CX:56:C:N4	2.09	0.46
1:CA:1295:G:O2'	13:CM:14:ARG:NH1	2.48	0.46
26:BA:826:U:C4'	36:BP:55:ARG:HB2	2.45	0.46
25:AY:75:C:H5''	25:AY:76:A:OP1	2.14	0.46
29:DE:72:VAL:HG22	29:DE:73:GLU:HB3	1.96	0.46
26:BA:196:A:O2'	26:BA:805:G:O6	2.26	0.46
36:DP:47:ASP:OD2	36:DP:50:ARG:NH2	2.49	0.46
1:CA:229:U:H2'	1:CA:230:G:C8	2.51	0.46
26:BA:2695:C:H2'	26:BA:2696:U:C6	2.51	0.46
26:BA:666:G:C2'	26:BA:667:U:H5'	2.45	0.46
26:DA:2017:U:O2	52:D5:10:LYS:HB2	2.15	0.46
1:CA:18:C:H5'	1:CA:1079:G:H1'	1.95	0.46
46:DZ:119:GLU:HG2	46:DZ:119:GLU:H	1.49	0.46
26:BA:1341:U:O2	44:BX:80:ILE:HD12	2.15	0.46
26:BA:2345:G:N3	26:BA:2381:C:H2'	2.30	0.46
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.61	0.46
4:AD:33:MET:HB2	58:AD:302:SF4:S2	2.55	0.46
26:BA:64:A:C5	44:BX:66:LEU:HD12	2.50	0.46
20:CT:40:ALA:HB2	20:CT:55:ILE:HG22	1.97	0.46
26:DA:1399:C:OP1	44:DX:25:LYS:NZ	2.48	0.46
26:DA:1649:G:O2'	38:DR:107:ASP:OD2	2.21	0.46
26:DA:2823:A:OP1	29:DE:113:PHE:HB2	2.15	0.46
28:DD:276:LYS:H	28:DD:276:LYS:HD3	1.81	0.46
26:BA:569:U:O2'	26:BA:983:A:N1	2.41	0.46
3:CC:124:ILE:HD11	3:CC:189:ALA:HB1	1.98	0.46
1:CA:1038:C:H2'	1:CA:1039:C:C6	2.51	0.46
24:CX:49:G:N1	24:CX:65:C:C4	2.71	0.46
27:DB:31:C:C5	27:DB:32:C:H5	2.33	0.46
1:AA:975:A:N6	1:AA:1367:C:O4'	2.48	0.46
26:DA:1359:A:N6	26:DA:1372:U:C4	2.83	0.46
26:DA:2712:U:O2'	26:DA:2713:A:H5'	2.16	0.46
26:DA:1578:U:C2'	26:DA:1579:A:H5'	2.46	0.46
26:DA:2199:A:H3'	26:DA:2200:C:C6	2.51	0.46
4:CD:155:LEU:HD23	4:CD:156:GLU:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DO:1:MET:HG3	35:DO:67:LYS:HG2	1.97	0.46
26:BA:768:G:O2'	26:BA:1379:A:N1	2.41	0.46
27:DB:43:C:H2'	27:DB:44:G:H5''	1.98	0.46
51:B4:54:GLY:HA2	51:B4:55:ARG:HA	1.48	0.46
1:CA:130:A:N3	1:CA:263:A:O2'	2.37	0.46
26:BA:34:C:H41	26:BA:447:A:N6	2.14	0.46
1:CA:448:A:P	1:CA:485:G:H22	2.38	0.46
1:AA:49:U:O2'	1:AA:50:A:H2'	2.14	0.46
1:CA:342:C:C2'	1:CA:343:U:H5'	2.46	0.46
26:BA:385:C:O2	36:BP:71:VAL:HG21	2.15	0.46
6:AF:21:LEU:O	6:AF:25:ILE:HG12	2.15	0.46
42:BV:23:GLU:OE1	42:BV:89:GLN:NE2	2.47	0.46
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.98	0.46
26:BA:2512:C:H2'	26:BA:2513:G:O4'	2.15	0.46
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.15	0.46
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.16	0.46
26:BA:969:U:H2'	26:BA:970:C:C6	2.51	0.46
26:BA:1783:A:H5'	26:BA:2608:G:H4'	1.97	0.46
26:BA:2461:C:H2'	26:BA:2462:U:C6	2.51	0.46
26:BA:1430:C:H2'	26:BA:1431:U:C6	2.49	0.46
26:BA:2094:G:OP1	33:BI:22:LYS:HD2	2.14	0.46
26:BA:674:G:H1'	30:BF:74:ARG:HD3	1.97	0.46
26:DA:898:C:H2'	26:DA:899:A:O4'	2.16	0.46
26:BA:1814:G:H4'	28:BD:51:VAL:HG21	1.98	0.46
1:CA:512:U:O4'	4:CD:43:HIS:HE1	1.98	0.46
26:DA:2808:U:H2'	26:DA:2891:G:N1	2.30	0.46
1:AA:1493:A:H2'	26:BA:1913:A:N1	2.30	0.46
32:DH:7:LEU:O	32:DH:69:ARG:NH1	2.47	0.46
1:CA:1442:G:HO2'	1:CA:1442(A):G:P	2.35	0.46
4:AD:103:ASN:O	4:AD:107:ARG:HG2	2.15	0.46
28:DD:3:VAL:HG13	28:DD:17:THR:HB	1.96	0.46
1:AA:1025:U:O2	1:AA:1036:G:O6	2.34	0.46
10:CJ:44:VAL:HG13	10:CJ:66:ARG:HG2	1.97	0.46
1:AA:674:G:H2'	1:AA:675:A:C8	2.50	0.46
26:DA:2370:G:C6	26:DA:2371:G:C6	3.03	0.46
1:CA:1456:G:O6	20:CT:54:LYS:HE3	2.15	0.46
29:DE:116:VAL:HG11	29:DE:138:PRO:HB3	1.98	0.46
26:BA:1794:U:H2'	26:BA:1795:C:H6	1.80	0.46
3:AC:85:ARG:O	3:AC:89:GLU:N	2.47	0.46
35:DO:52:VAL:HG12	35:DO:94:ARG:NH2	2.31	0.46
26:DA:1654:A:C1'	26:DA:2823:A:H5'	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:344:A:H4'	1:CA:345:C:OP2	2.16	0.46
7:CG:29:LYS:HG3	7:CG:101:LEU:HB3	1.97	0.46
31:DG:68:PRO:HG2	31:DG:90:LEU:HD22	1.97	0.46
6:CF:75:LEU:O	6:CF:79:LEU:HG	2.15	0.46
26:DA:1353:A:H2'	26:DA:1354:A:C8	2.51	0.46
30:DF:129:PHE:CE2	30:DF:163:VAL:HG11	2.51	0.46
33:BI:85:GLU:O	33:BI:123:LEU:HD12	2.15	0.46
2:AB:21:ARG:H	2:AB:21:ARG:HD2	1.80	0.46
4:AD:81:GLU:OE1	4:AD:139:ARG:NH1	2.36	0.46
41:DU:58:ARG:HA	41:DU:61:TRP:CE3	2.51	0.46
9:CI:73:GLN:HA	9:CI:76:ALA:HB3	1.98	0.46
1:CA:1025:U:N3	1:CA:1036:G:N1	2.64	0.46
1:CA:90:U:O2'	1:CA:91:C:H5'	2.15	0.46
2:CB:204:ASN:O	2:CB:210:SER:OG	2.24	0.46
1:CA:994:A:C5	1:CA:1216:G:H4'	2.50	0.46
1:CA:1127:G:H5'	1:CA:1281:U:O2	2.16	0.46
26:DA:994:C:H1'	42:DV:10:LYS:HE3	1.97	0.46
28:DD:183:ARG:HG3	28:DD:270:ILE:HG12	1.97	0.46
1:AA:976:G:C8	1:AA:1362:C:N4	2.83	0.46
1:AA:56:U:H2'	1:AA:57:G:H8	1.76	0.46
26:DA:2815:C:H2'	26:DA:2816:C:C6	2.51	0.46
1:CA:967:C:H2'	1:CA:968:A:C8	2.51	0.46
1:CA:419:C:H5''	1:CA:513:C:H1'	1.98	0.46
9:AI:77:ILE:O	9:AI:81:ILE:HG22	2.15	0.46
26:DA:1230:C:H2'	26:DA:1231:G:C8	2.48	0.46
26:BA:2646:C:OP2	26:BA:2732:G:O2'	2.34	0.46
50:D3:8:LEU:O	50:D3:32:GLN:N	2.36	0.46
1:AA:951:G:C2'	1:AA:952:U:H5'	2.46	0.46
40:BT:53:ARG:CZ	40:BT:53:ARG:HB3	2.46	0.46
2:CB:19:HIS:CD2	2:CB:20:GLU:H	2.34	0.46
1:AA:189(C):C:H2'	1:AA:189(D):C:O4'	2.16	0.46
27:BB:87:G:N2	27:BB:90:A:OP2	2.44	0.46
1:CA:1316:G:N2	1:CA:1318:A:H3'	2.31	0.46
1:CA:269:C:H2'	1:CA:270:A:C8	2.51	0.46
41:DU:28:ARG:NH1	41:DU:38:THR:OG1	2.43	0.46
26:BA:2693:A:H2'	26:BA:2694:G:H8	1.80	0.46
46:DZ:5:LEU:HG	46:DZ:47:VAL:HG21	1.98	0.46
13:AM:59:TYR:O	13:AM:63:THR:OG1	2.25	0.46
2:AB:223:ILE:HA	2:AB:226:ARG:HG2	1.97	0.46
30:BF:8:GLN:HE22	30:BF:21:ALA:HB2	1.81	0.46
26:BA:2610:C:O2	61:BA:4295:HOH:O	2.20	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:82:ARG:HG2	2:CB:83:MET:N	2.31	0.46
46:BZ:150:LEU:O	46:BZ:171:ILE:HG13	2.15	0.46
26:BA:2162:G:N1	26:BA:2163:C:C4	2.84	0.46
26:BA:1359:A:C6	26:BA:1372:U:N3	2.82	0.46
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.98	0.46
26:BA:631:A:H2'	26:BA:632:A:O4'	2.14	0.46
1:CA:838:G:C6	1:CA:848:C:N4	2.82	0.46
26:DA:1851:U:C4	26:DA:1852:C:C4	3.04	0.46
26:DA:1853:A:N3	26:DA:2233:U:O2'	2.38	0.46
26:DA:2741:A:OP1	56:D9:22:ARG:NH2	2.45	0.46
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.81	0.46
5:AE:103:GLY:O	5:AE:106:PRO:HD2	2.16	0.46
1:AA:1492:A:H2'	1:AA:1493:A:C8	2.51	0.46
1:AA:1273:G:H3'	1:AA:1274:G:C8	2.51	0.46
26:BA:252:G:OP1	36:BP:50:ARG:NH1	2.43	0.46
26:DA:910:A:N1	26:DA:2277:G:H1'	2.31	0.46
26:DA:1429:G:H2'	26:DA:1430:C:C6	2.51	0.46
32:DH:70:THR:HG22	32:DH:74:ASN:ND2	2.31	0.46
26:DA:195:A:H61	26:DA:198:C:H3'	1.81	0.46
26:DA:30:G:H2'	26:DA:31:C:H6	1.79	0.46
1:AA:309:G:H2'	1:AA:310:G:H8	1.81	0.46
26:DA:754:C:H2'	26:DA:755:C:C6	2.51	0.46
1:AA:539:A:H2'	1:AA:540:G:C8	2.50	0.46
37:DQ:26:TYR:CD1	37:DQ:28:ALA:HB2	2.51	0.46
2:CB:97:TRP:CH2	2:CB:101:MET:HB2	2.51	0.46
26:BA:2723:C:H4'	38:BR:1:MET:HG3	1.98	0.46
9:CI:86:VAL:HA	9:CI:89:ASN:O	2.16	0.46
43:DW:46:PHE:O	43:DW:50:VAL:HG23	2.16	0.46
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.30	0.46
26:BA:911:A:H2'	37:BQ:9:TYR:OH	2.16	0.46
11:AK:29:ILE:HG23	11:AK:44:SER:HB3	1.98	0.46
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.41	0.46
1:AA:1414:U:H3	1:AA:1486:G:H1	1.63	0.46
41:BU:28:ARG:NH1	41:BU:38:THR:OG1	2.43	0.46
61:BA:4873:HOH:O	29:BE:162:ALA:HB3	2.16	0.46
26:DA:652:C:C2'	26:DA:652(A):A:H5'	2.46	0.46
26:DA:1474:C:H2'	26:DA:1475:G:C8	2.51	0.46
26:BA:2179:C:H2'	26:BA:2180:U:C6	2.50	0.46
26:DA:2881:C:H2'	26:DA:2882:A:O4'	2.16	0.46
8:AH:33:GLU:HG2	8:AH:48:TYR:CE2	2.50	0.46
28:BD:79:VAL:HG12	28:BD:113:VAL:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2242:G:H2'	26:DA:2243:U:O4'	2.16	0.46
1:AA:814:A:H2'	1:AA:816:A:H5''	1.98	0.46
26:BA:2478:A:OP2	56:B9:2:LYS:NZ	2.41	0.46
1:AA:1165:C:N4	1:AA:1166:G:C6	2.84	0.46
26:DA:2153:G:H3'	26:DA:2154:G:C8	2.50	0.46
24:CX:29:G:C6	24:CX:30:G:C5	3.04	0.46
1:AA:43:C:H2'	1:AA:44:G:O4'	2.15	0.46
26:DA:2200:C:O2	26:DA:2226:C:N4	2.49	0.46
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.98	0.46
51:B4:61:ARG:HG3	51:B4:62:ARG:H	1.81	0.46
1:AA:600:C:H5'	8:AH:129:VAL:HA	1.98	0.46
4:AD:172:PRO:HB2	4:AD:187:ARG:NH2	2.31	0.46
26:DA:1913:A:H4'	26:DA:1914:C:C5'	2.46	0.46
1:AA:762:C:H2'	1:AA:763:G:H8	1.80	0.46
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.51	0.46
26:DA:320:A:H4'	26:DA:322:A:C8	2.51	0.46
32:BH:4:ILE:O	32:BH:69:ARG:HG2	2.16	0.46
26:DA:566:U:H2'	26:DA:567:A:O4'	2.16	0.46
1:CA:262:A:C6	1:CA:263:A:C6	3.04	0.46
26:DA:1243:G:H2'	26:DA:1244:G:O4'	2.15	0.46
26:DA:1375:C:H2'	26:DA:1376:C:C6	2.51	0.46
26:DA:773:U:H2'	26:DA:774:A:H5'	1.98	0.46
1:CA:973:G:H3'	1:CA:974:A:H5''	1.97	0.46
1:AA:1065:U:H4'	1:AA:1066:C:O5'	2.15	0.46
40:BT:60:THR:HG22	40:BT:77:PRO:HA	1.97	0.46
1:AA:927:G:H1	1:AA:1390:U:H3	1.63	0.46
28:DD:73:VAL:HG13	28:DD:120:GLY:HA3	1.98	0.46
42:DV:21:ARG:HG2	42:DV:91:TYR:CD2	2.51	0.46
26:BA:2328:A:H2'	26:BA:2329:G:C8	2.50	0.46
24:AX:31:G:C8	24:AX:32:5MC:HM52	2.51	0.46
7:CG:75:VAL:HG13	7:CG:145:ALA:HA	1.98	0.46
3:CC:191:THR:HG21	3:CC:193:TYR:CZ	2.51	0.46
26:DA:1184:G:OP1	50:D3:30:ARG:HD2	2.16	0.46
26:BA:2282:G:OP1	26:BA:2283:C:H1'	2.16	0.46
30:DF:24:LEU:HD21	30:DF:114:VAL:HG12	1.97	0.46
1:CA:98:G:C6	1:CA:99:U:C4	3.03	0.46
22:AV:13:A:H4'	22:AV:14:A:OP2	2.16	0.46
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.51	0.46
27:DB:63:G:H2'	27:DB:64:C:C6	2.50	0.46
26:DA:717:G:H2'	26:DA:718:A:O4'	2.17	0.46
26:DA:784:A:C6	28:DD:229:VAL:HG21	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.15	0.46
26:DA:2493:U:H2'	26:DA:2494:G:O4'	2.16	0.46
51:B4:68:ARG:HD2	51:B4:69:LYS:N	2.29	0.46
1:CA:685:G:C2	1:CA:686:U:C4	3.04	0.46
26:DA:1021:A:H3'	26:DA:1021:A:H8	1.80	0.46
1:AA:600:C:O2'	1:AA:601:C:H5'	2.16	0.46
33:DI:88:ILE:HG21	33:DI:144:VAL:CG1	2.46	0.46
24:CX:22:G:H2'	24:CX:23:C:C6	2.51	0.46
34:BN:12:ARG:NH1	34:BN:38:HIS:HE2	2.14	0.46
26:BA:2032:G:H1'	29:BE:145:LYS:HD3	1.98	0.46
26:BA:1045:A:OP1	26:BA:1047:G:H5''	2.16	0.46
1:CA:634:C:H2'	1:CA:635:G:H8	1.81	0.46
1:CA:262:A:H2'	1:CA:263:A:C8	2.51	0.46
1:CA:1352:C:OP1	21:CU:3:LYS:NZ	2.33	0.46
1:AA:189(C):C:N4	1:AA:189(H):G:H1	2.14	0.46
26:DA:576:U:H2'	26:DA:577:G:C8	2.51	0.46
27:DB:80:U:H2'	27:DB:81:G:C8	2.50	0.46
8:CH:34:GLU:OE1	8:CH:37:ARG:NH1	2.49	0.46
41:BU:108:GLU:O	41:BU:112:ARG:HG2	2.15	0.46
34:DN:115:ARG:HA	34:DN:118:LYS:HE3	1.98	0.46
1:CA:748:C:H4'	1:CA:749:C:O5'	2.16	0.46
26:BA:931:G:O2'	50:B3:24:LYS:HD3	2.16	0.46
26:DA:2419:U:H2'	26:DA:2420:C:C6	2.51	0.46
35:BO:4:PRO:O	35:BO:5:GLN:HB2	2.16	0.46
26:DA:2133:G:O2'	26:DA:2157:G:N2	2.31	0.45
26:DA:2137:C:N4	26:DA:2154:G:N1	2.29	0.45
26:BA:2139:C:C2	26:BA:2153:G:C2	3.05	0.45
1:CA:407:G:N1	1:CA:436:C:C2	2.83	0.45
1:AA:348:G:C2'	1:AA:349:A:H5'	2.46	0.45
26:DA:2820:A:OP2	38:DR:2:ARG:NH2	2.49	0.45
24:CX:19:G:H4'	24:CX:20:U:OP2	2.15	0.45
24:CX:60:U:H3'	24:CX:61:C:H6	1.81	0.45
27:DB:1:U:H2'	27:DB:2:C:C6	2.51	0.45
27:DB:16:G:H2'	27:DB:17:C:C6	2.51	0.45
4:CD:112:VAL:HG22	4:CD:116:GLN:OE1	2.16	0.45
1:AA:1216:G:H5''	14:AN:5:ALA:CB	2.46	0.45
31:BG:43:LEU:C	31:BG:45:GLU:H	2.19	0.45
26:BA:1654:A:C1'	26:BA:2823:A:H5'	2.46	0.45
61:DA:4083:HOH:O	36:DP:16:ARG:HG3	2.15	0.45
26:DA:448:U:C4	26:DA:583:G:H1'	2.51	0.45
15:CO:5:LYS:O	15:CO:9:GLN:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1932:A:H2'	26:DA:1933:G:O4'	2.16	0.45
24:AX:50:U:O5'	24:AX:50:U:H6	1.99	0.45
1:AA:779:C:H2'	1:AA:780:A:O4'	2.16	0.45
26:BA:722:A:H2'	26:BA:723:G:C8	2.51	0.45
30:BF:178:PRO:HB2	30:BF:201:VAL:CG2	2.47	0.45
42:BV:55:ALA:HB2	42:BV:101:GLY:HA2	1.98	0.45
26:DA:2082:A:H3'	26:DA:2083:G:H8	1.81	0.45
2:AB:35:GLU:OE1	2:AB:38:GLY:HA2	2.17	0.45
38:BR:44:LEU:HD22	38:BR:48:VAL:HG23	1.99	0.45
34:DN:104:LYS:HA	34:DN:107:LEU:HD12	1.98	0.45
1:CA:375:U:O3'	16:CP:6:LEU:HB2	2.17	0.45
36:DP:6:LEU:HA	36:DP:6:LEU:HD23	1.79	0.45
1:AA:143:A:H2'	1:AA:143:A:N3	2.31	0.45
1:CA:779:C:H2'	1:CA:780:A:O4'	2.16	0.45
26:BA:144:C:H5'	44:BX:2:LYS:HE2	1.98	0.45
26:DA:1220:A:OP2	41:DU:19:LYS:NZ	2.46	0.45
1:AA:102:G:O2'	1:AA:151:A:N3	2.31	0.45
1:CA:90:U:C2'	1:CA:91:C:H5'	2.46	0.45
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.84	0.45
26:BA:2127:G:C2	26:BA:2128:C:C2	3.04	0.45
26:DA:2124:G:H3'	26:DA:2125:G:H5''	1.96	0.45
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.17	0.45
26:BA:1530:C:H42	26:BA:1539:G:H1	1.65	0.45
1:AA:1252:A:H61	1:AA:1285:A:N6	2.05	0.45
1:CA:978:A:O2'	1:CA:1321:C:N4	2.48	0.45
46:BZ:107:THR:HA	46:BZ:108:PRO:HD3	1.73	0.45
26:DA:2203:U:H2'	26:DA:2205:C:H6	1.78	0.45
1:CA:758:G:H5'	1:CA:880:C:H1'	1.98	0.45
1:CA:728:A:OP1	1:CA:742:G:O2'	2.34	0.45
26:BA:1721:G:H5'	26:BA:1722:A:OP2	2.17	0.45
1:AA:93:G:H2'	1:AA:96:U:O4'	2.16	0.45
11:AK:45:GLY:O	11:AK:50:TYR:HB2	2.17	0.45
1:CA:1202:G:H2'	1:CA:1203:C:O4'	2.16	0.45
1:CA:1371:G:C6	1:CA:1372:U:C4	3.04	0.45
3:CC:33:LEU:HD21	14:CN:53:LEU:HD22	1.97	0.45
26:DA:184:C:H2'	26:DA:185:U:H6	1.80	0.45
34:DN:4:TYR:CE2	41:DU:100:VAL:HG11	2.51	0.45
9:CI:72:GLY:O	9:CI:76:ALA:N	2.43	0.45
55:B8:23:VAL:CG1	55:B8:47:LYS:HD3	2.46	0.45
7:CG:51:GLN:HB3	7:CG:51:GLN:HE21	1.64	0.45
26:BA:1916:A:H2'	26:BA:1917:U:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DW:79:GLY:HA3	43:DW:100:THR:HG22	1.97	0.45
26:BA:2065:C:H2'	26:BA:2066:C:C6	2.51	0.45
1:AA:892:A:O2'	1:AA:1415:G:H4'	2.16	0.45
24:CX:38:A:O5'	24:CX:38:A:H8	1.99	0.45
1:CA:72:C:N3	1:CA:97:G:C2	2.83	0.45
23:CW:76:PPU:N	24:CX:76:31H:N3'	2.61	0.45
26:BA:1171:G:H5'	26:BA:1173:G:OP2	2.16	0.45
1:AA:625:G:H4'	16:AP:16:HIS:HB3	1.97	0.45
26:DA:1250:G:N7	36:DP:18:ARG:NH2	2.64	0.45
33:BI:106:GLY:HA2	33:BI:107:VAL:CG2	2.44	0.45
26:DA:1037:G:H2'	26:DA:1038:C:O4'	2.17	0.45
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.82	0.45
1:AA:1152:A:H5'	10:AJ:13:HIS:CG	2.52	0.45
1:AA:1152:A:OP1	10:AJ:70:ARG:NH2	2.50	0.45
26:BA:2075:U:OP2	26:BA:2238:G:O2'	2.28	0.45
26:DA:330:A:C2	26:DA:1210:A:H2'	2.51	0.45
42:DV:60:GLU:N	42:DV:95:LEU:O	2.38	0.45
1:AA:66:G:H2'	1:AA:67:C:H5'	1.98	0.45
1:CA:1464:G:OP1	40:DT:108:ARG:HD3	2.16	0.45
46:BZ:110:GLY:N	46:BZ:144:LEU:O	2.43	0.45
55:D8:9:GLY:O	55:D8:13:ARG:HG2	2.16	0.45
26:DA:2773:C:O2'	26:DA:2774:C:H5'	2.16	0.45
1:AA:22:G:H4'	1:AA:885:G:C8	2.51	0.45
28:DD:121:PRO:HB3	28:DD:135:PHE:CE2	2.51	0.45
1:CA:131:C:H2'	1:CA:132:C:C6	2.51	0.45
38:DR:36:THR:HG22	38:DR:37:THR:H	1.81	0.45
12:AL:97:ARG:HB2	12:AL:98:TYR:CE2	2.51	0.45
11:CK:34:ASP:OD2	11:CK:38:ASN:HB2	2.17	0.45
24:CX:7:G:H5''	24:CX:8:4SU:H5	1.98	0.45
26:DA:2016:U:H2'	26:DA:2017:U:C6	2.52	0.45
26:DA:608:A:OP1	30:DF:100:THR:OG1	2.25	0.45
30:DF:156:LEU:HD21	30:DF:163:VAL:HG12	1.98	0.45
26:DA:947:G:N2	26:DA:971:C:C2	2.84	0.45
26:BA:904:C:H2'	26:BA:905:U:C6	2.52	0.45
1:CA:162:A:N3	1:CA:348:G:H4'	2.31	0.45
26:BA:1639:U:O2'	26:BA:1640:C:H5'	2.17	0.45
26:BA:297:C:OP1	45:BY:87:LYS:NZ	2.42	0.45
30:DF:116:ASP:OD2	36:DP:1:MET:N	2.46	0.45
49:B2:35:LEU:HB3	49:B2:50:ILE:HG12	1.99	0.45
26:DA:629:G:H5''	26:DA:650:C:O2'	2.16	0.45
39:DS:110:LEU:HD12	39:DS:110:LEU:HA	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DY:6:HIS:H	45:DY:6:HIS:CD2	2.34	0.45
26:DA:1265:A:OP1	26:DA:1265:A:H8	2.00	0.45
26:DA:2704:C:H2'	26:DA:2705:A:O4'	2.16	0.45
26:DA:719:C:H2'	26:DA:720:C:C6	2.51	0.45
51:B4:59:PHE:HB2	51:B4:62:ARG:CZ	2.46	0.45
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.29	0.45
1:CA:1255:G:P	10:CJ:45:ARG:HH22	2.40	0.45
1:AA:1030:C:N3	1:AA:1031:G:N2	2.65	0.45
1:AA:1225:A:H2'	1:AA:1226:C:C5	2.51	0.45
26:BA:795:C:H2'	26:BA:796:C:C6	2.52	0.45
26:DA:250:G:C6	26:DA:251:A:C6	3.04	0.45
12:CL:33:ARG:O	12:CL:85:ILE:HG12	2.16	0.45
26:DA:828:U:C5	26:DA:2247:A:H4'	2.52	0.45
26:BA:874:G:C2'	26:BA:875:G:H5'	2.46	0.45
2:AB:146:GLN:O	2:AB:150:SER:HB3	2.16	0.45
26:BA:1045:A:OP1	26:BA:1046:A:H3'	2.16	0.45
49:D2:28:LYS:HB3	49:D2:57:ILE:HG12	1.97	0.45
26:DA:1011:G:H1'	26:DA:1013:C:O4'	2.16	0.45
35:DO:98:VAL:HG22	35:DO:118:ALA:HA	1.99	0.45
26:DA:2016:U:O2'	52:D5:7:PRO:O	2.33	0.45
33:DI:110:ASP:HA	33:DI:111:PRO:HD3	1.80	0.45
1:CA:1080:A:H5''	1:CA:1081:G:OP2	2.17	0.45
3:CC:35:GLU:HG3	3:CC:36:ASP:N	2.31	0.45
26:DA:507:A:H5''	26:DA:508:G:H3'	1.98	0.45
17:AQ:76:LEU:HD12	17:AQ:77:VAL:H	1.82	0.45
1:CA:1176:A:H2'	1:CA:1177:G:O4'	2.16	0.45
26:DA:1613:G:C2	26:DA:1619:G:C5	3.05	0.45
6:AF:12:PRO:HG3	6:AF:57:GLN:O	2.16	0.45
26:DA:815:C:H2'	26:DA:816:C:C6	2.52	0.45
26:BA:1415:U:O2'	26:BA:1417:C:OP1	2.29	0.45
26:DA:196:A:C4	26:DA:805:G:C6	3.04	0.45
19:CS:40:ILE:HD12	19:CS:69:HIS:O	2.16	0.45
1:CA:5:U:H2'	1:CA:5:U:H6	1.53	0.45
26:BA:2439:A:C8	26:BA:2439:A:H5'	2.52	0.45
13:CM:3:ARG:HB3	13:CM:8:GLU:HA	1.99	0.45
1:CA:509:A:H2'	1:CA:510:A:C8	2.50	0.45
1:CA:1002:G:N3	1:CA:1003:G:C8	2.85	0.45
26:DA:2139:C:H3'	26:DA:2140:C:H6	1.80	0.45
1:CA:976:G:OP1	14:CN:32:SER:N	2.38	0.45
26:BA:2167:U:H5'	26:BA:2168:G:OP2	2.17	0.45
1:CA:709:G:H2'	1:CA:710:G:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.52	0.45
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.50	0.45
26:DA:2833:G:H4'	26:DA:2834:G:OP2	2.17	0.45
31:BG:56:ALA:HA	31:BG:153:ARG:NH2	2.31	0.45
4:AD:178:VAL:C	4:AD:180:GLY:H	2.20	0.45
26:BA:957:A:N1	26:BA:2458:G:H4'	2.32	0.45
26:BA:2691:C:O3'	26:BA:2871:C:H4'	2.17	0.45
26:BA:2820:A:P	38:BR:2:ARG:HH22	2.39	0.45
26:DA:71:A:H5''	26:DA:73:A:N9	2.32	0.45
26:DA:754:C:H2'	26:DA:755:C:H6	1.82	0.45
28:DD:132:PRO:HD3	28:DD:190:TYR:CZ	2.51	0.45
1:CA:189(A):C:C2'	1:CA:189(B):C:H5'	2.46	0.45
26:DA:2854:G:H2'	26:DA:2855:C:C6	2.50	0.45
1:CA:1515:C:H2'	1:CA:1516:G:C8	2.52	0.45
26:BA:588:U:H2'	26:BA:589:C:C6	2.51	0.45
1:AA:429:U:H4'	1:AA:430:A:O5'	2.16	0.45
13:AM:19:LEU:HA	13:AM:19:LEU:HD12	1.79	0.45
1:CA:624:C:O2'	1:CA:625:G:H5'	2.17	0.45
7:AG:140:ASP:OD1	7:AG:143:ARG:NH2	2.42	0.45
26:DA:2886:G:H2'	26:DA:2887:U:C6	2.51	0.45
2:AB:80:ILE:HD12	2:AB:211:ILE:HG22	1.98	0.45
26:BA:2478:A:H2'	26:BA:2479:G:O4'	2.16	0.45
1:CA:509:A:H5'	4:CD:54:TYR:HD1	1.81	0.45
15:AO:82:ILE:O	15:AO:86:GLY:N	2.50	0.45
26:DA:222:A:H3'	26:DA:421:U:H5'	1.97	0.45
4:CD:78:LEU:HD22	4:CD:96:LEU:HB3	1.99	0.45
61:BA:4902:HOH:O	55:B8:42:ARG:HD2	2.15	0.45
10:AJ:64:GLU:HG2	14:AN:59:ALA:HB2	1.99	0.45
26:DA:2567:G:H2'	26:DA:2568:C:C6	2.51	0.45
26:DA:2679:A:H4'	29:DE:165:VAL:HG11	1.98	0.45
1:CA:950:U:H2'	1:CA:951:G:H8	1.81	0.45
44:BX:5:TYR:CZ	49:B2:30:ARG:HB2	2.52	0.45
2:AB:82:ARG:NH1	2:AB:86:GLU:OE2	2.50	0.45
32:DH:28:GLY:HA3	32:DH:79:VAL:HB	1.98	0.45
46:BZ:154:ASP:OD1	46:BZ:155:LEU:HD13	2.17	0.45
29:BE:73:GLU:H	29:BE:73:GLU:HG3	1.60	0.45
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.43	0.45
26:BA:145:G:H2'	26:BA:146:G:C8	2.51	0.45
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.49	0.45
16:AP:6:LEU:HB3	16:AP:17:TYR:CD1	2.51	0.45
1:AA:1173:G:N1	1:AA:1174:G:C5	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2152:G:H5'	26:DA:2153:G:OP2	2.17	0.45
1:CA:1400:C:C5	24:CX:35:A:C4	3.05	0.45
26:BA:2134:A:N1	26:BA:2158:A:C8	2.85	0.45
1:AA:79:G:C6	1:AA:90:U:N3	2.84	0.45
1:AA:160:A:H2'	1:AA:161:A:C8	2.52	0.45
1:AA:280:C:N3	17:AQ:39:SER:N	2.65	0.45
1:AA:599:C:H4'	8:AH:130:GLY:C	2.37	0.45
26:BA:2336:A:H61	47:B0:43:THR:CG2	2.27	0.45
4:CD:173:TRP:CH2	4:CD:194:LEU:HD23	2.52	0.45
31:DG:15:VAL:HG22	31:DG:175:LEU:HB3	1.98	0.45
1:AA:1298:C:H2'	7:AG:114:ARG:NH1	2.31	0.45
1:CA:293:G:H5'	1:CA:610:G:C2	2.52	0.45
1:CA:762:C:H2'	1:CA:763:G:C8	2.51	0.45
1:CA:34:C:H2'	1:CA:35:G:C8	2.51	0.45
26:BA:142(A):C:H2'	26:BA:143:G:O4'	2.16	0.45
26:BA:1453:U:H1'	38:BR:60:LEU:HD21	1.98	0.45
26:DA:2427:C:OP1	61:DA:4236:HOH:O	2.21	0.45
1:AA:375:U:OP1	16:AP:69:THR:HG21	2.16	0.45
6:CF:6:VAL:HG13	6:CF:90:VAL:HG22	1.98	0.45
46:BZ:104:PHE:HB3	46:BZ:141:VAL:HG21	1.99	0.45
28:BD:152:GLY:O	28:BD:154:LYS:HG2	2.17	0.45
41:BU:110:VAL:HG12	41:BU:114:LYS:HE2	1.98	0.45
24:AX:13:C:O2'	26:BA:1924:C:H4'	2.15	0.45
1:AA:688:G:H2'	1:AA:689:C:C6	2.51	0.45
40:DT:29:ARG:HB3	40:DT:87:ASP:HB2	1.99	0.45
26:DA:823:G:H2'	26:DA:824:A:C8	2.52	0.45
26:BA:1864:U:OP1	26:BA:2410:G:O2'	2.25	0.45
21:AU:15:ARG:HH11	21:AU:15:ARG:HB2	1.81	0.45
26:DA:118:A:N3	26:DA:178:G:H1'	2.32	0.45
26:DA:2701:C:H2'	26:DA:2702:U:H2'	1.99	0.45
16:AP:59:TRP:HA	16:AP:62:VAL:HG12	1.99	0.45
1:CA:339:C:H2'	1:CA:340:U:C6	2.52	0.45
26:DA:2129:C:O2'	26:DA:2130:U:H5'	2.16	0.45
1:CA:1292:U:OP2	7:CG:41:ARG:NH2	2.50	0.45
24:CX:65:C:N4	24:CX:66:C:C4	2.85	0.45
2:AB:207:ALA:O	2:AB:210:SER:HB3	2.16	0.45
26:DA:2114:A:H2'	26:DA:2114:A:N3	2.32	0.45
1:AA:1044:A:C5	1:AA:1045:C:H1'	2.52	0.45
36:BP:63:PRO:HB2	55:B8:30:ARG:NH2	2.32	0.45
30:BF:56:GLU:OE2	30:BF:93:LYS:NZ	2.46	0.45
26:DA:1817:G:H2'	26:DA:1818:U:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2312:U:H2'	26:DA:2313:C:C6	2.52	0.45
26:BA:1798:U:H5'	28:BD:259:THR:CG2	2.45	0.45
47:B0:43:THR:O	47:B0:43:THR:HG23	2.16	0.45
35:BO:63:VAL:HB	35:BO:102:VAL:HG12	1.99	0.45
26:DA:2697:G:H2'	26:DA:2698:U:O4'	2.17	0.45
26:BA:2319:G:H22	39:BS:3:ARG:NE	2.15	0.45
26:BA:2319:G:C2	39:BS:3:ARG:HA	2.51	0.45
1:CA:791:G:N2	1:CA:1497:G:O3'	2.49	0.45
26:DA:2572:A:OP1	26:DA:2574:G:O2'	2.35	0.45
26:DA:856:C:HO2'	26:DA:857:C:P	2.38	0.45
26:DA:724:U:H2'	26:DA:725:G:O4'	2.16	0.45
43:BW:18:ARG:HG3	43:BW:76:VAL:HB	1.99	0.45
1:AA:370:C:H2'	1:AA:371:G:C8	2.52	0.45
1:AA:192:U:H2'	1:AA:193:C:C6	2.52	0.45
26:DA:858:U:O2	26:DA:2268:A:H2'	2.17	0.45
26:BA:656:G:H2'	26:BA:657:U:O4'	2.16	0.45
2:AB:92:TYR:OH	2:AB:150:SER:OG	2.34	0.45
1:CA:1327:C:H5''	21:CU:20:LYS:HB3	1.99	0.45
1:AA:1095:U:P	1:AA:1108:G:H1	2.39	0.45
4:CD:70:ILE:HD11	4:CD:74:GLN:HB3	1.99	0.45
5:CE:92:LYS:HB3	5:CE:119:LEU:HB2	1.98	0.45
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.52	0.45
26:DA:17:G:H4'	41:DU:25:TRP:NE1	2.31	0.45
26:BA:2785:C:H2'	26:BA:2786:U:O4'	2.17	0.45
32:DH:43:VAL:HG13	32:DH:52:VAL:HG22	1.99	0.45
28:BD:145:VAL:HG13	28:BD:191:ALA:HB2	1.99	0.45
1:AA:1310:G:H1	1:AA:1327:C:H42	1.63	0.45
37:DQ:62:GLY:HA2	46:DZ:116:VAL:HG21	1.99	0.45
32:BH:150:ALA:HA	32:BH:153:LYS:HG3	1.98	0.45
50:D3:18:ASP:OD1	50:D3:18:ASP:N	2.50	0.45
1:AA:1431:C:H2'	1:AA:1432:G:O4'	2.16	0.45
32:BH:23:ARG:HD2	32:BH:34:GLU:OE1	2.16	0.45
50:D3:46:ASN:O	50:D3:50:VAL:HG22	2.17	0.45
19:CS:14:HIS:O	19:CS:18:LYS:HG3	2.16	0.45
24:CX:41:C:C2	24:CX:42:G:C8	3.04	0.45
1:CA:1118:C:C2	1:CA:1119:C:C5	3.05	0.45
26:DA:2114:A:C8	26:DA:2168:G:H1'	2.51	0.45
26:DA:1394:U:H4'	26:DA:1603:A:H4'	1.99	0.45
36:DP:65:ARG:HG3	55:D8:25:MET:CG	2.47	0.45
36:BP:65:ARG:HG3	55:B8:25:MET:CG	2.47	0.45
26:DA:2302:G:C2	26:DA:2315:G:C2	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BF:18:ARG:HG2	30:BF:19:GLU:H	1.81	0.45
19:AS:65:ASN:ND2	19:AS:66:MET:HG2	2.32	0.45
26:BA:228:A:H3'	26:BA:229:A:C5'	2.47	0.45
26:BA:2277:G:P	47:B0:10:THR:HG21	2.57	0.45
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.17	0.45
36:DP:38:GLN:O	36:DP:39:LYS:HB3	2.16	0.45
1:AA:581:G:OP1	15:AO:61:GLY:HA3	2.17	0.45
20:CT:57:ARG:HH12	20:CT:100:ILE:HD12	1.82	0.45
1:AA:178:C:H2'	1:AA:179:A:C8	2.52	0.45
4:AD:128:VAL:HG12	4:AD:129:ASN:ND2	2.31	0.45
26:BA:573:G:O2'	26:BA:574:C:H3'	2.16	0.45
4:AD:18:LYS:HE3	4:AD:20:TYR:OH	2.17	0.45
3:AC:21:ARG:NH1	3:AC:56:ASP:OD2	2.50	0.45
1:CA:737:A:O2'	1:CA:738:C:H5'	2.16	0.45
1:CA:936:C:H1'	1:CA:1382:C:H42	1.80	0.45
26:DA:455:C:N3	26:DA:472:A:H2'	2.31	0.45
31:BG:108:ASN:HD22	51:B4:22:ILE:HG21	1.82	0.45
31:BG:61:ALA:O	31:BG:65:GLY:N	2.39	0.45
26:BA:639:U:H2'	26:BA:640:C:C6	2.52	0.45
26:DA:79:G:O2'	26:DA:346:A:N3	2.35	0.45
42:BV:14:VAL:HB	42:BV:96:ILE:HG13	1.97	0.45
26:BA:1932:A:H2'	26:BA:1933:G:O4'	2.17	0.45
1:CA:193:C:H2'	1:CA:194:C:H6	1.82	0.45
26:DA:1721:G:H5'	26:DA:1722:A:H5''	1.99	0.45
33:BI:122:GLU:HB2	33:BI:126:TYR:OH	2.17	0.45
26:DA:2416:C:O2'	26:DA:2417:C:H5'	2.17	0.45
26:DA:940:G:O2'	61:DA:3711:HOH:O	2.18	0.45
1:AA:397:A:N3	1:AA:397:A:H3'	2.32	0.45
10:AJ:5:ARG:NH2	10:AJ:71:LEU:HD21	2.32	0.45
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	1.99	0.45
26:BA:1557:C:H5''	26:BA:1558:A:OP2	2.17	0.45
26:DA:2315:G:C6	26:DA:2316:C:N4	2.85	0.45
1:CA:1099:G:C2	1:CA:1100:C:O2	2.70	0.45
1:CA:1053:G:H4'	1:CA:1054:C:H5'	1.99	0.45
26:DA:893:C:H5'	26:DA:894:C:OP2	2.17	0.45
13:CM:82:MET:O	13:CM:93:ARG:NH2	2.48	0.45
26:DA:191:A:H2'	26:DA:192:C:C6	2.52	0.45
24:CX:15:G:C4	24:CX:59:A:N6	2.85	0.45
1:AA:1291:G:H4'	9:AI:39:GLY:HA3	1.99	0.45
43:DW:72:LYS:N	43:DW:106:ILE:O	2.48	0.45
1:AA:922:G:H2'	1:AA:923:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:67:C:H2'	1:AA:68:G:H8	1.79	0.45
29:BE:31:CYS:HB3	29:BE:49:LEU:HG	1.99	0.45
6:CF:2:ARG:CZ	6:CF:69:GLU:HG2	2.46	0.45
26:BA:242:G:C8	55:B8:5:LYS:HG2	2.51	0.45
26:DA:1557:C:H5''	26:DA:1558:A:OP2	2.17	0.45
28:DD:77:ALA:HB2	28:DD:97:TYR:CD2	2.52	0.45
7:CG:42:ILE:HG22	7:CG:120:ILE:HD12	1.98	0.45
5:AE:143:ARG:NH1	8:AH:77:GLU:OE2	2.49	0.45
1:AA:1136:U:H5''	1:AA:1137:C:C2	2.52	0.45
44:BX:65:ARG:HB2	44:BX:70:LEU:HD23	1.99	0.45
1:AA:1133:G:H2'	1:AA:1134:G:H8	1.81	0.45
26:DA:1473:G:H2'	26:DA:1474:C:O4'	2.16	0.45
40:BT:127:ALA:O	40:BT:128:GLU:HB2	2.17	0.45
31:BG:124:SER:HB2	31:BG:131:TYR:CE1	2.52	0.45
26:DA:265:A:C8	26:DA:266:G:H1'	2.52	0.45
54:D7:13:ALA:HB2	54:D7:46:VAL:HG21	1.99	0.45
26:BA:1113:U:H2'	26:BA:1114:G:C8	2.52	0.45
13:AM:51:ALA:HA	13:AM:54:VAL:HG22	1.98	0.45
29:DE:101:ARG:CZ	29:DE:171:GLU:HB2	2.47	0.45
26:BA:340:A:H2'	26:BA:341:G:O4'	2.17	0.45
1:CA:982:U:H4'	1:CA:983:A:O5'	2.16	0.45
26:DA:2153:G:C6	26:DA:2154:G:C6	3.05	0.45
24:CX:30:G:C6	24:CX:31:G:N7	2.85	0.45
10:AJ:5:ARG:HE	10:AJ:5:ARG:HB3	1.48	0.45
26:BA:2161:C:O2'	26:BA:2173:A:H4'	2.17	0.45
1:CA:1124:G:O2'	1:CA:1145:C:C4	2.70	0.45
1:CA:1280:A:H2'	1:CA:1281:U:N3	2.31	0.45
1:CA:1064:G:H1'	1:CA:1065:U:OP2	2.16	0.45
39:DS:38:GLN:HA	39:DS:50:SER:HA	1.99	0.45
10:AJ:57:LYS:HD2	10:AJ:60:ARG:HH21	1.81	0.45
26:DA:1359:A:N1	26:DA:1372:U:O4	2.50	0.45
31:DG:111:LEU:O	31:DG:114:ILE:HB	2.17	0.45
3:AC:16:ARG:HH22	3:AC:183:ASP:CG	2.20	0.45
26:DA:1826:G:H2'	26:DA:1827:C:C6	2.51	0.45
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.98	0.45
26:BA:466:A:O3'	54:B7:33:ARG:NH1	2.48	0.45
8:CH:81:HIS:N	8:CH:138:TRP:O	2.50	0.45
1:CA:1405:G:H2'	1:CA:1406:U:C6	2.51	0.45
28:BD:101:GLU:HG2	28:BD:103:ARG:HD3	1.98	0.45
51:D4:15:ILE:N	51:D4:31:ILE:O	2.32	0.45
1:CA:624:C:O2'	16:CP:10:GLY:HA2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:779:C:O2'	11:CK:120:ARG:HD3	2.17	0.45
6:AF:89:MET:HG2	6:AF:91:VAL:HG23	1.99	0.45
33:DI:14:ASP:N	33:DI:17:GLN:OE1	2.43	0.45
1:CA:266:G:O3'	17:CQ:67:LYS:HB2	2.16	0.45
26:DA:1660:C:H2'	26:DA:1661:G:H8	1.82	0.45
26:BA:1842:G:O2'	28:BD:253:GLN:NE2	2.38	0.45
26:DA:1903:G:OP1	28:DD:241:PRO:HB2	2.16	0.45
31:DG:61:ALA:O	31:DG:65:GLY:N	2.44	0.45
27:BB:96:U:OP1	46:BZ:14:LYS:NZ	2.49	0.45
26:DA:2675:A:H5'	35:DO:29:ASN:O	2.17	0.45
8:CH:9:MET:HG3	8:CH:26:VAL:HG21	1.99	0.45
2:CB:207:ALA:O	2:CB:211:ILE:HG13	2.17	0.44
1:CA:922:G:H2'	1:CA:923:A:C8	2.52	0.44
1:AA:1124:G:H5''	10:AJ:35:SER:OG	2.17	0.44
41:BU:50:ARG:HG2	41:BU:53:ARG:NH2	2.32	0.44
26:DA:2127:G:C6	26:DA:2161:C:N3	2.84	0.44
42:DV:85:LYS:HB2	42:DV:85:LYS:HE3	1.72	0.44
26:DA:182:A:H2	26:DA:433:C:O2	2.00	0.44
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.82	0.44
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.22	0.44
26:BA:1186:G:H2'	26:BA:1187:G:O4'	2.17	0.44
24:CX:19:G:P	24:CX:60:U:H3	2.40	0.44
1:AA:708:C:H2'	1:AA:709:G:H8	1.82	0.44
1:CA:707:C:H5''	11:CK:85:ARG:NH1	2.32	0.44
26:DA:884:C:H2'	26:DA:885:C:O4'	2.17	0.44
26:DA:1183:G:H4'	50:D3:29:ARG:HH22	1.82	0.44
26:DA:466:A:O3'	54:D7:33:ARG:NH1	2.50	0.44
1:AA:1052:U:H5''	1:AA:1053:G:OP2	2.17	0.44
26:DA:539:G:H2'	26:DA:540:C:H6	1.82	0.44
26:BA:288:C:H2'	26:BA:289:A:H8	1.82	0.44
26:BA:271(F):C:H2'	26:BA:271(G):C:C6	2.52	0.44
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.98	0.44
26:BA:141:A:H8	26:BA:1408:C:HO2'	1.56	0.44
26:DA:601:C:O2'	26:DA:605:C:H5''	2.18	0.44
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.57	0.44
26:DA:2416:C:C2'	26:DA:2417:C:H5'	2.47	0.44
26:DA:1287:A:C5	26:DA:1288:U:C4	3.05	0.44
26:BA:1446:C:O2'	26:BA:1545:A:O2'	2.33	0.44
26:DA:2273:A:O2'	26:DA:2274:A:H5'	2.17	0.44
26:BA:2118:U:H4'	26:BA:2119:A:OP1	2.16	0.44
1:CA:1171:G:O2'	1:CA:1172:C:H5'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1447:G:N2	26:BA:1464:C:O2	2.25	0.44
1:AA:937:A:H2'	1:AA:938:A:H5'	1.99	0.44
1:CA:630:G:H2'	1:CA:631:G:C8	2.52	0.44
37:DQ:38:GLU:HB2	37:DQ:127:ILE:HG22	1.99	0.44
26:BA:2467:C:H4'	37:BQ:123:HIS:CG	2.52	0.44
42:DV:89:GLN:HA	42:DV:90:PRO:HD3	1.88	0.44
36:BP:98:GLU:O	36:BP:101:VAL:HB	2.16	0.44
1:CA:688:G:H5'	11:CK:46:GLY:C	2.37	0.44
20:CT:62:LEU:HD23	20:CT:62:LEU:HA	1.82	0.44
1:CA:690:G:H8	1:CA:690:G:O5'	1.99	0.44
30:DF:164:ARG:O	30:DF:168:ARG:HB2	2.16	0.44
32:DH:144:VAL:O	32:DH:148:ILE:HG12	2.17	0.44
26:BA:1963:U:H4'	26:BA:1964:G:OP1	2.17	0.44
1:AA:1187:G:H2'	1:AA:1188:A:C8	2.52	0.44
11:CK:92:GLU:OE2	11:CK:96:ARG:NH1	2.50	0.44
1:CA:73:G:C6	1:CA:76:C:C5	3.05	0.44
24:CX:29:G:N1	24:CX:30:G:C4	2.85	0.44
27:DB:114:C:H2'	27:DB:115:G:O4'	2.17	0.44
26:DA:2683:C:O2	35:DO:70:LYS:NZ	2.31	0.44
1:CA:164:U:H2'	1:CA:165:C:C6	2.52	0.44
26:BA:307:G:H21	26:BA:330:A:H62	1.66	0.44
1:AA:1278:U:H5'	1:AA:1279:A:O4'	2.17	0.44
1:CA:1417:G:H22	1:CA:1482:G:H2'	1.81	0.44
26:DA:2552:U:C2	26:DA:2554:U:H5''	2.51	0.44
45:BY:54:LYS:HA	45:BY:56:PRO:HD3	2.00	0.44
26:DA:444:C:H4'	30:DF:49:ALA:HB2	1.99	0.44
26:DA:210:C:H2'	26:DA:211:A:C8	2.52	0.44
1:CA:937:A:H2'	1:CA:938:A:H5'	1.99	0.44
53:B6:11:LEU:HB3	53:B6:49:HIS:HB3	1.99	0.44
1:AA:573:A:N3	1:AA:883:C:O2'	2.41	0.44
26:DA:2657:A:O3'	32:DH:160:LYS:NZ	2.45	0.44
45:DY:9:LYS:HA	45:DY:10:GLY:HA2	1.56	0.44
17:CQ:45:HIS:HD2	17:CQ:65:ILE:HG12	1.82	0.44
26:DA:1223:G:N2	26:DA:1227:G:C4	2.85	0.44
26:DA:339:U:O5'	26:DA:339:U:H6	2.00	0.44
24:AX:9:G:N3	24:AX:45:G:H2'	2.31	0.44
26:DA:1676:A:H2'	26:DA:1677:A:O4'	2.18	0.44
26:DA:2063:C:C4	26:DA:2064:C:C4	3.05	0.44
51:D4:26:SER:OG	51:D4:27:THR:N	2.48	0.44
14:CN:3:ARG:HD2	14:CN:4:LYS:N	2.32	0.44
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2131:G:C8	26:DA:2133:G:N1	2.86	0.44
26:DA:2101:G:H2'	26:DA:2102:U:O4'	2.17	0.44
26:DA:2187:G:C2	26:DA:2188:C:C2	3.05	0.44
1:CA:1216:G:OP1	14:CN:2:ALA:HA	2.18	0.44
1:CA:1261:A:C6	1:CA:1262:C:C2	3.05	0.44
26:DA:1608:A:H1'	26:DA:1610:A:OP2	2.17	0.44
1:CA:1159:U:O4'	1:CA:1182:G:N2	2.50	0.44
26:BA:2181:G:HO2'	26:BA:2182:G:P	2.41	0.44
1:AA:1262:C:N3	1:AA:1273:G:C6	2.85	0.44
1:CA:19:C:H4'	1:CA:864:A:O4'	2.17	0.44
26:DA:1826:G:H4'	28:DD:242:ARG:NH1	2.32	0.44
26:DA:1826:G:H4'	28:DD:242:ARG:CZ	2.47	0.44
10:AJ:47:PHE:CZ	14:AN:37:PHE:HE1	2.36	0.44
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.53	0.44
26:DA:2667:C:N3	32:DH:110:SER:OG	2.29	0.44
1:CA:1405:G:O4'	1:CA:1519:A:H4'	2.17	0.44
1:AA:1107:C:C4	1:AA:1108:G:C8	3.05	0.44
1:CA:936:C:H2'	1:CA:937:A:O4'	2.18	0.44
26:DA:854:G:H2'	26:DA:855:G:H8	1.82	0.44
53:D6:14:THR:O	53:D6:17:LYS:NZ	2.47	0.44
26:DA:1978:A:H2'	26:DA:1979:C:O4'	2.17	0.44
1:AA:920:U:H2'	1:AA:921:U:C6	2.52	0.44
30:BF:129:PHE:HA	30:BF:142:TRP:NE1	2.31	0.44
6:CF:46:ARG:HB3	6:CF:60:PHE:CE1	2.51	0.44
26:DA:248:G:O5'	26:DA:249:C:H5''	2.17	0.44
26:BA:571:A:N6	26:BA:2499:C:O3'	2.47	0.44
26:BA:292:C:H2'	26:BA:293:U:C6	2.52	0.44
61:DA:3809:HOH:O	30:DF:68:LYS:HE2	2.17	0.44
31:BG:15:VAL:HG21	31:BG:176:LEU:HD23	2.00	0.44
38:DR:72:ASP:OD2	38:DR:75:LEU:HB2	2.18	0.44
6:CF:24:GLU:HG3	6:CF:28:ARG:HD3	1.99	0.44
26:BA:2728:U:H2'	26:BA:2729:G:C8	2.53	0.44
2:CB:224:GLN:HA	2:CB:228:GLY:O	2.18	0.44
1:AA:1173:G:C6	1:AA:1174:G:C5	3.06	0.44
26:DA:2140:C:C2	26:DA:2152:G:C2	3.05	0.44
26:DA:2151:G:H2'	26:DA:2152:G:C8	2.41	0.44
1:CA:1400:C:N4	24:CX:34:C:H2'	2.26	0.44
26:BA:2163:C:C4	26:BA:2164:C:O2	2.71	0.44
1:AA:1008:C:H2'	1:AA:1009:G:O4'	2.16	0.44
26:DA:1359:A:C6	26:DA:1372:U:O4	2.69	0.44
26:DA:2031:A:C6	26:DA:2498:C:H1'	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:286:C:H2'	26:BA:287:C:C6	2.53	0.44
26:DA:1370:C:N4	26:DA:1371:G:C6	2.86	0.44
1:AA:985:C:H2'	1:AA:986:A:H8	1.82	0.44
1:AA:986:A:H2'	1:AA:987:G:C8	2.53	0.44
24:AX:16:C:H5''	24:AX:17:C:C5	2.53	0.44
31:BG:41:GLN:HB3	31:BG:43:LEU:HD13	1.99	0.44
29:DE:36:ARG:NH2	29:DE:86:PRO:O	2.47	0.44
5:CE:41:VAL:O	5:CE:67:VAL:HG13	2.17	0.44
26:BA:1793:C:H2'	26:BA:1794:U:C6	2.53	0.44
1:CA:66:G:H2'	1:CA:67:C:H5'	1.98	0.44
32:DH:26:VAL:HB	32:DH:33:LEU:HD12	1.99	0.44
11:AK:41:THR:OG1	11:AK:42:TRP:N	2.51	0.44
1:AA:499:A:H4'	1:AA:500:G:H5'	1.99	0.44
26:BA:1501:C:H2'	26:BA:1502:C:C6	2.52	0.44
2:CB:103:THR:HA	2:CB:180:LEU:HD11	1.99	0.44
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.99	0.44
42:DV:29:PRO:HA	42:DV:61:VAL:HG22	1.99	0.44
26:BA:811:U:P	36:BP:29:LYS:H	2.40	0.44
26:BA:123:G:H2'	26:BA:124:G:O4'	2.18	0.44
1:CA:1112:C:C2	3:CC:178:LEU:HB2	2.52	0.44
31:BG:7:LEU:HD23	31:BG:7:LEU:HA	1.85	0.44
26:BA:871:U:OP1	37:BQ:5:ARG:HD3	2.17	0.44
37:DQ:1:MET:N	37:DQ:1:MET:SD	2.82	0.44
1:AA:715:A:H2'	1:AA:716:A:C8	2.53	0.44
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.18	0.44
44:DX:12:VAL:HG21	44:DX:27:THR:HG22	1.99	0.44
26:DA:2137:C:C4	26:DA:2138:C:N4	2.85	0.44
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.80	0.44
1:CA:1118:C:OP1	9:CI:9:ARG:HD2	2.17	0.44
26:DA:1224:C:O2'	42:DV:85:LYS:HA	2.18	0.44
26:DA:1422:G:H1'	26:DA:1496:A:N1	2.33	0.44
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.53	0.44
26:DA:1333:C:H2'	26:DA:1334:G:H8	1.83	0.44
1:AA:1366:C:HO2'	10:AJ:60:ARG:HH22	1.64	0.44
1:CA:156:G:N1	1:CA:165:C:N3	2.39	0.44
1:AA:222:U:H2'	1:AA:223:U:C6	2.52	0.44
51:B4:59:PHE:O	51:B4:62:ARG:NE	2.47	0.44
1:AA:1442(A):G:C8	40:BT:118:ARG:HG2	2.53	0.44
26:BA:1182:A:H2'	26:BA:1183:G:C8	2.53	0.44
26:DA:469:G:O6	54:D7:37:LYS:HE2	2.17	0.44
26:DA:1857:G:C6	26:DA:1858:G:N1	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:560:U:O2'	1:CA:561:U:OP2	2.32	0.44
24:AX:16:C:H5''	24:AX:17:C:H5	1.83	0.44
1:CA:765:G:H5''	1:CA:766:A:OP1	2.18	0.44
44:BX:50:LYS:HB3	44:BX:87:GLN:HE22	1.82	0.44
1:CA:775:G:N2	1:CA:804:U:O4	2.51	0.44
32:BH:54:ARG:HD3	32:BH:65:HIS:ND1	2.32	0.44
32:BH:61:HIS:O	32:BH:65:HIS:HB2	2.18	0.44
26:DA:2328:A:H2'	26:DA:2329:G:C8	2.53	0.44
10:CJ:55:LYS:HG3	10:CJ:56:HIS:N	2.31	0.44
28:BD:38:LYS:HD2	28:BD:38:LYS:HA	1.87	0.44
26:DA:1963:U:H4'	26:DA:1964:G:OP1	2.17	0.44
1:AA:110:C:O2'	16:AP:25:ARG:O	2.30	0.44
35:BO:122:LEU:HD13	40:BT:72:VAL:HG11	1.98	0.44
13:AM:14:ARG:HB2	13:AM:16:ASP:OD1	2.16	0.44
26:BA:189:G:O6	26:BA:205:G:O2'	2.29	0.44
3:AC:180:ALA:O	3:AC:182:ILE:N	2.51	0.44
26:BA:1270:C:O2'	26:BA:1648:C:OP2	2.35	0.44
26:BA:554:U:C4	26:BA:555:U:C4	3.06	0.44
26:DA:340:A:H2'	26:DA:341:G:O4'	2.17	0.44
26:DA:2489:G:C6	26:DA:2490:G:C6	3.06	0.44
26:DA:483:A:O4'	45:DY:48:ALA:HB1	2.17	0.44
26:DA:2357:U:OP1	47:D0:20:ARG:HD3	2.18	0.44
26:BA:1155:A:OP1	41:BU:55:ARG:HD3	2.17	0.44
27:BB:6:C:H2'	27:BB:7:G:H5''	2.00	0.44
36:BP:27:HIS:O	36:BP:31:ALA:HA	2.16	0.44
46:DZ:92:SER:O	46:DZ:130:PRO:HG2	2.17	0.44
41:BU:86:ALA:HB2	41:BU:116:ALA:HB2	1.98	0.44
2:CB:210:SER:O	2:CB:214:ILE:HG12	2.18	0.44
24:CX:30:G:C4	24:CX:31:G:C8	3.05	0.44
30:BF:74:ARG:H	30:BF:74:ARG:HG3	1.50	0.44
26:BA:1529:G:C6	26:BA:1530:C:N4	2.86	0.44
39:BS:15:ARG:HE	39:BS:88:ASP:CG	2.19	0.44
11:AK:99:GLN:HE21	11:AK:108:ILE:HD11	1.82	0.44
8:AH:25:ASP:OD1	8:AH:60:ARG:HG3	2.17	0.44
26:BA:247:G:H4'	26:BA:386:G:C5	2.52	0.44
26:DA:1126:A:H4'	26:DA:1127:A:O5'	2.18	0.44
26:BA:2384:G:P	47:B0:55:ARG:HH12	2.40	0.44
1:CA:1010:G:H2'	1:CA:1011:G:H8	1.83	0.44
13:AM:84:ILE:HD12	19:AS:74:PHE:CE2	2.52	0.44
31:BG:16:ARG:HH21	31:BG:31:VAL:HG11	1.81	0.44
26:DA:2248:C:OP2	61:DA:3945:HOH:O	2.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:828:A:N6	1:AA:858:G:O2'	2.51	0.44
1:CA:598:U:H4'	8:CH:94:TYR:CD2	2.52	0.44
1:AA:164:U:H2'	1:AA:165:C:C6	2.52	0.44
26:DA:2442:C:H2'	26:DA:2443:C:H6	1.83	0.44
1:AA:509:A:H5'	4:AD:54:TYR:HD2	1.82	0.44
26:BA:2038:G:H2'	26:BA:2039:C:O4'	2.18	0.44
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	1.98	0.44
3:CC:36:ASP:O	3:CC:39:ILE:HB	2.18	0.44
40:DT:2:ASN:O	40:DT:6:LEU:HD22	2.18	0.44
26:DA:815:C:H2'	26:DA:816:C:H6	1.81	0.44
31:DG:125:PHE:CZ	31:DG:170:ARG:HA	2.53	0.44
1:CA:616:G:C2	1:CA:617:G:C8	3.06	0.44
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.99	0.44
12:CL:97:ARG:HB2	12:CL:98:TYR:CE2	2.52	0.44
26:BA:363(C):G:H2'	26:BA:363(D):G:C8	2.53	0.44
5:CE:68:GLU:OE1	5:CE:70:PRO:HG3	2.17	0.44
40:BT:37:GLY:HA2	40:BT:38:ASN:HA	1.69	0.44
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.81	0.44
44:BX:35:THR:HG22	44:BX:38:GLU:HB2	2.00	0.44
26:DA:2024:G:N7	61:DA:3704:HOH:O	2.36	0.44
12:CL:34:ARG:HB3	12:CL:34:ARG:HE	1.47	0.44
24:CX:13:C:O2'	26:DA:1924:C:H4'	2.18	0.44
26:DA:2230:G:H1'	48:D1:45:ASN:CG	2.38	0.44
5:AE:79:GLU:HG3	5:AE:93:PRO:HD2	2.00	0.44
32:DH:95:ARG:HG2	32:DH:96:ALA:N	2.32	0.44
1:CA:1038:C:O2'	1:CA:1039:C:H5'	2.17	0.44
26:DA:2138:C:N3	26:DA:2153:G:N2	2.59	0.44
1:CA:976:G:O2'	1:CA:1362:C:N4	2.50	0.44
24:CX:30:G:H2'	24:CX:31:G:O4'	2.17	0.44
1:AA:1503:A:N3	22:AV:13:A:C6	2.85	0.44
26:DA:2166:G:H5'	26:DA:2167:U:O5'	2.18	0.44
1:CA:337:C:H2'	1:CA:338:A:H8	1.83	0.44
1:AA:1252:A:N6	1:AA:1285:A:H61	2.06	0.44
1:AA:1250:A:H4'	9:AI:68:GLY:N	2.33	0.44
30:BF:184:TYR:O	30:BF:188:ARG:HG3	2.18	0.44
26:DA:1470:G:H5''	26:DA:1471:A:OP1	2.17	0.44
26:BA:1459:G:C3'	26:BA:1460:A:H5''	2.47	0.44
29:BE:51:PHE:O	29:BE:77:ILE:HD12	2.18	0.44
5:AE:102:ALA:HB2	5:AE:120:THR:HG21	2.00	0.44
19:CS:9:VAL:HB	51:D4:67:TYR:CD2	2.47	0.44
5:AE:31:LEU:HD11	5:AE:129:ILE:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:614:A:C2'	1:AA:615:C:H5'	2.48	0.44
46:BZ:117:LEU:HD23	46:BZ:119:GLU:OE1	2.18	0.44
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	1.99	0.44
1:AA:53:A:H61	1:AA:358:U:H3	1.65	0.44
26:BA:2625:G:H2'	26:BA:2626:C:H6	1.83	0.44
26:DA:375:C:H2'	26:DA:376:C:H6	1.82	0.44
34:BN:4:TYR:CE2	41:BU:100:VAL:HG11	2.52	0.44
46:DZ:69:THR:HG22	46:DZ:90:VAL:HG13	2.00	0.44
26:DA:2389:G:H5''	26:DA:2390:U:O4'	2.18	0.44
4:AD:63:LYS:HG3	4:AD:198:VAL:HG22	2.00	0.44
2:CB:162:ILE:HG13	2:CB:162:ILE:O	2.17	0.44
11:AK:69:ALA:O	11:AK:73:MET:HG3	2.18	0.44
26:DA:265:A:H1'	26:DA:266:G:O4'	2.18	0.44
1:CA:982:U:H5	14:CN:31:ARG:HH22	1.62	0.44
1:AA:938:A:C6	1:AA:939:G:C5	3.06	0.44
26:DA:1321:A:H2'	26:DA:1322:A:O4'	2.17	0.44
26:DA:1232:G:C2	26:DA:1233:C:C2	3.05	0.44
5:CE:72:GLN:O	5:CE:75:THR:HG22	2.18	0.44
54:D7:12:ARG:NH2	54:D7:44:PRO:HB3	2.32	0.44
3:AC:27:LYS:NZ	3:AC:27:LYS:HA	2.32	0.44
1:AA:1330:U:H4'	13:AM:23:TYR:CZ	2.53	0.44
45:BY:5:MET:HE1	45:BY:32:PRO:HA	2.00	0.44
4:AD:118:ARG:HG3	4:AD:136:PRO:HB3	2.00	0.44
8:CH:14:ARG:O	8:CH:18:ARG:HD3	2.18	0.44
1:AA:1165:C:H2'	1:AA:1166:G:O4'	2.17	0.44
31:DG:138:GLN:NE2	31:DG:153:ARG:HB2	2.33	0.44
26:BA:2165:G:H1	26:BA:2172:U:H5	1.62	0.44
1:CA:1121:U:C2'	1:CA:1122:U:H5'	2.47	0.44
1:AA:1010:G:N2	1:AA:1020:U:H1'	2.33	0.44
1:AA:90:U:O2'	1:AA:91:C:H5'	2.18	0.44
1:AA:605:U:C2'	1:AA:606:G:H5'	2.47	0.44
46:BZ:111:VAL:O	46:BZ:112:ARG:HB2	2.17	0.44
1:CA:683:G:H2'	1:CA:684:A:C8	2.52	0.44
26:BA:818:G:H4'	26:BA:838:C:O3'	2.17	0.44
27:DB:13:A:N3	27:DB:16:G:H1'	2.33	0.44
39:DS:15:ARG:HE	39:DS:88:ASP:CG	2.18	0.44
2:CB:76:GLN:HB2	2:CB:208:ILE:HG12	1.99	0.44
19:AS:22:LEU:HB3	19:AS:27:GLU:HG3	2.00	0.44
1:CA:1095:U:H5''	1:CA:1109:C:O2	2.17	0.44
26:DA:2773:C:OP1	29:DE:164:ARG:NE	2.41	0.44
1:CA:1286:A:H2	21:CU:18:TYR:HH	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:92:TYR:HE2	2:AB:94:ASN:HB2	1.83	0.44
26:BA:468:G:N7	54:B7:39:ARG:NH2	2.66	0.44
3:CC:33:LEU:HD21	14:CN:53:LEU:CD2	2.47	0.44
3:AC:118:GLN:HG2	3:AC:118:GLN:H	1.51	0.44
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.18	0.44
26:BA:629:G:N3	26:BA:639:U:O2'	2.49	0.44
36:BP:19:VAL:HG12	36:BP:27:HIS:HB3	2.00	0.44
42:BV:5:VAL:HG21	42:BV:35:LEU:HD23	1.99	0.44
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	2.00	0.44
43:BW:86:LEU:HD12	43:BW:87:PRO:HD2	2.00	0.44
1:CA:1350:A:C5	1:CA:1351:U:C4	3.05	0.44
3:AC:39:ILE:O	3:AC:43:LEU:HG	2.17	0.44
26:DA:1614:A:C2	43:DW:93:ALA:HB2	2.52	0.44
48:B1:52:ARG:HH12	48:B1:57:GLU:HB2	1.83	0.44
3:CC:105:GLU:HG3	3:CC:105:GLU:H	1.54	0.44
2:AB:20:GLU:O	2:AB:40:HIS:HB2	2.18	0.44
26:BA:2133:G:N2	26:BA:2158:A:C2	2.86	0.44
26:BA:2134:A:N3	26:BA:2134:A:C2'	2.80	0.44
26:DA:1420:U:HO2'	26:DA:1421:G:P	2.41	0.44
27:DB:28:C:H5''	39:DS:31:SER:HB3	1.99	0.44
26:DA:2302:G:C2	26:DA:2303:G:C8	3.05	0.44
16:CP:21:VAL:HG11	16:CP:59:TRP:NE1	2.33	0.44
19:AS:37:ARG:H	19:AS:37:ARG:HG3	1.38	0.44
1:CA:958:A:N6	19:CS:77:THR:HG23	2.32	0.44
26:BA:172:C:H2'	26:BA:173:G:O4'	2.18	0.44
1:CA:1046:A:H61	1:CA:1213:A:H61	1.64	0.44
35:DO:63:VAL:HG12	35:DO:106:LEU:HD11	1.99	0.44
9:CI:96:LEU:HD23	9:CI:96:LEU:HA	1.84	0.44
37:BQ:56:ARG:HG2	37:BQ:56:ARG:HH11	1.83	0.44
9:AI:21:PRO:HA	9:AI:59:PHE:HA	2.00	0.44
1:AA:69:G:H2'	1:AA:70:G:H8	1.83	0.44
1:AA:418:C:H1'	1:AA:540:G:O2'	2.16	0.44
3:AC:22:TRP:CE2	14:AN:54:PRO:HG3	2.52	0.44
1:CA:486:U:H2'	1:CA:487:A:H8	1.82	0.44
1:CA:1076:C:OP1	2:CB:175:ARG:NH1	2.51	0.44
26:BA:709:U:H2'	26:BA:710:G:C8	2.53	0.44
47:D0:82:ARG:HA	47:D0:83:PRO:HD3	1.79	0.44
1:AA:679:C:C2'	1:AA:680:C:H5'	2.47	0.44
43:BW:20:VAL:HG11	43:BW:44:ALA:HA	2.00	0.44
5:AE:36:ASP:OD2	5:AE:40:ARG:HB2	2.18	0.44
26:DA:1007:C:C2	26:DA:1008:C:C5	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2686:G:C2	26:DA:2724:C:O2	2.71	0.44
3:AC:13:GLY:HA3	14:AN:57:ARG:NH2	2.33	0.44
26:DA:1742:G:H8	26:DA:1742:G:O5'	2.00	0.44
42:DV:40:LEU:HB2	42:DV:46:VAL:HG13	1.99	0.44
26:BA:1996:C:H4'	26:BA:1997:G:OP1	2.16	0.44
1:AA:547:A:H4'	1:AA:548:G:O5'	2.18	0.44
26:BA:2742:C:H5''	56:B9:1:MET:HE2	2.00	0.44
1:CA:1001(A):G:H3'	1:CA:1002:G:O4'	2.17	0.43
1:AA:1503:A:N3	22:AV:13:A:N6	2.65	0.43
26:BA:2134:A:C2	26:BA:2159:G:H1'	2.52	0.43
1:CA:1125:U:C3'	1:CA:1126:U:H5''	2.48	0.43
26:DA:1421:G:C2	26:DA:1422:G:C8	3.06	0.43
1:AA:993:G:N3	1:AA:993:G:H2'	2.33	0.43
26:BA:2285:C:N4	53:B6:24:GLU:OE1	2.50	0.43
1:CA:1100:C:H5	2:CB:96:ARG:HH22	1.66	0.43
26:DA:1849:G:H2'	26:DA:1850:G:H8	1.82	0.43
1:CA:164:U:H2'	1:CA:165:C:H6	1.83	0.43
27:DB:104:U:O3'	46:DZ:72:ARG:HD2	2.17	0.43
28:BD:134:ARG:HG3	28:BD:135:PHE:CE2	2.53	0.43
46:DZ:53:ILE:HG22	46:DZ:71:VAL:O	2.18	0.43
44:BX:32:PRO:HA	44:BX:77:LYS:HB2	1.99	0.43
1:CA:991:U:H3'	1:CA:1212:U:H3	1.82	0.43
33:DI:87:LYS:CA	33:DI:122:GLU:HA	2.47	0.43
3:CC:126:ARG:HB2	3:CC:128:PHE:CE1	2.53	0.43
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	2.00	0.43
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.33	0.43
26:DA:1165:U:H2'	26:DA:1166:C:C6	2.53	0.43
1:AA:738:C:H2'	1:AA:739:C:C6	2.53	0.43
4:AD:85:LYS:HG3	4:AD:86:LYS:HG2	1.99	0.43
1:CA:321:A:C2	1:CA:333:G:C2	3.06	0.43
1:CA:763:G:H2'	1:CA:764:C:H5'	1.99	0.43
26:DA:839:U:H1'	26:DA:1191:G:H1'	2.00	0.43
1:AA:189(A):C:C2'	1:AA:189(B):C:H5'	2.48	0.43
26:DA:1593:G:H2'	26:DA:1594:G:C8	2.53	0.43
26:DA:1411:C:H2'	26:DA:1412:A:H8	1.82	0.43
1:CA:66:G:C2'	1:CA:67:C:H5'	2.48	0.43
1:AA:1134:G:C2	1:AA:1141:C:C2	3.06	0.43
1:CA:344:A:H5''	1:CA:345:C:H5	1.81	0.43
1:AA:38:G:H22	1:AA:397:A:H5''	1.83	0.43
26:BA:566:U:P	36:BP:29:LYS:HZ2	2.41	0.43
39:DS:95:HIS:CG	39:DS:96:GLY:N	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DH:12:PRO:O	32:DH:15:VAL:HG13	2.18	0.43
1:AA:288:A:H2'	1:AA:289:G:H4'	1.99	0.43
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.80	0.43
48:D1:83:GLU:HA	48:D1:84:GLY:HA2	1.62	0.43
1:CA:881:G:P	12:CL:12:ARG:HH22	2.40	0.43
26:DA:1264:G:O5'	26:DA:1264:G:H8	2.01	0.43
37:DQ:86:GLY:HA3	47:D0:10:THR:CG2	2.48	0.43
36:DP:59:LEU:HD23	55:D8:58:ILE:HD13	2.00	0.43
26:DA:1484:G:O6	26:DA:1505:C:N4	2.47	0.43
39:BS:105:ALA:O	39:BS:110:LEU:HB2	2.18	0.43
56:D9:29:ASN:HB3	56:D9:32:HIS:ND1	2.33	0.43
27:BB:66:A:H61	27:BB:108:U:H2'	1.83	0.43
32:BH:13:LYS:HA	32:BH:14:GLY:HA2	1.58	0.43
45:BY:9:LYS:HA	45:BY:10:GLY:HA2	1.69	0.43
26:DA:200:U:O2	26:DA:386:G:N2	2.51	0.43
1:AA:421:U:H2'	1:AA:421:U:O2	2.16	0.43
20:CT:24:LEU:HD12	20:CT:24:LEU:HA	1.76	0.43
42:DV:37:VAL:O	42:DV:51:VAL:HG23	2.18	0.43
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.54	0.43
1:CA:73:G:N1	1:CA:76:C:C5	2.86	0.43
26:BA:2188:C:H2'	26:BA:2189:U:O4'	2.18	0.43
1:CA:1361:G:H8	1:CA:1361:G:O5'	2.01	0.43
5:AE:52:PRO:HG2	5:AE:53:LEU:HD12	1.99	0.43
1:AA:1168:A:C6	1:AA:1169:A:C6	3.07	0.43
1:CA:731:G:H5'	1:CA:766:A:H4'	2.00	0.43
26:BA:2543:G:H21	26:BA:2646:C:H5''	1.82	0.43
26:DA:1860:G:H1	26:DA:1882:C:N4	2.16	0.43
2:CB:125:PRO:O	2:CB:127:ILE:N	2.51	0.43
27:DB:42:C:N3	31:DG:93:THR:HB	2.33	0.43
11:AK:50:TYR:HE1	11:AK:54:ARG:HE	1.64	0.43
4:CD:11:LEU:O	4:CD:15:GLU:HB2	2.18	0.43
9:AI:3:GLN:HG3	9:AI:20:ARG:HE	1.83	0.43
26:BA:1047:G:HO2'	26:BA:1048:A:P	2.40	0.43
1:CA:110:C:O2'	16:CP:25:ARG:O	2.31	0.43
26:BA:1582:C:O2'	26:BA:1586:A:N3	2.51	0.43
24:CX:54:5MU:O4	24:CX:58:A:N7	2.51	0.43
27:BB:83:G:H4'	50:B3:52:HIS:CG	2.53	0.43
16:CP:43:LYS:HG2	16:CP:48:TRP:CD2	2.53	0.43
26:DA:2785:C:OP1	29:DE:41:LYS:NZ	2.45	0.43
26:DA:854:G:H2'	26:DA:855:G:C8	2.53	0.43
28:BD:145:VAL:HG11	28:BD:175:LEU:HD11	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1263:U:C4	26:DA:1264:G:C6	3.06	0.43
26:BA:700:G:O2'	26:BA:1632:A:N3	2.42	0.43
1:AA:1397:C:H4'	22:AV:23:A:C2	2.53	0.43
45:DY:20:TYR:CE1	45:DY:43:ASN:HA	2.52	0.43
26:DA:2469:A:H5''	26:DA:2470:G:OP2	2.18	0.43
6:CF:95:GLU:HA	6:CF:96:PRO:HD3	1.90	0.43
26:BA:1111:A:N3	26:BA:1112:G:H1'	2.33	0.43
46:BZ:92:SER:O	46:BZ:130:PRO:HG2	2.17	0.43
26:DA:1959:G:C6	26:DA:1960:A:C5	3.06	0.43
1:AA:453:A:C5	1:AA:454:C:C4	3.06	0.43
2:AB:24:TRP:CZ3	2:AB:26:PRO:HA	2.53	0.43
26:DA:863:A:H2'	26:DA:864:G:C8	2.53	0.43
1:CA:829:G:H1	1:CA:857:C:H42	1.65	0.43
26:DA:2893:G:H4'	26:DA:2894:G:O5'	2.18	0.43
2:CB:166:ASP:O	2:CB:170:GLU:N	2.44	0.43
26:DA:1826:G:H2'	26:DA:1827:C:H6	1.82	0.43
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.32	0.43
1:CA:419:C:H5''	1:CA:513:C:C1'	2.49	0.43
26:DA:1028:A:H61	26:DA:1125:G:H2'	1.82	0.43
26:DA:1513:C:H2'	26:DA:1514:U:C6	2.54	0.43
9:CI:23:ASN:HD22	9:CI:25:LYS:H	1.67	0.43
26:DA:923:C:H2'	26:DA:924:C:H6	1.83	0.43
26:DA:619:G:O5'	26:DA:620:G:N2	2.51	0.43
1:CA:635:G:H2'	1:CA:636:U:O4'	2.18	0.43
26:DA:900:A:O2'	26:DA:901:A:OP1	2.34	0.43
33:DI:75:LEU:HD11	33:DI:105:HIS:CD2	2.53	0.43
26:DA:271(Q):G:H2'	26:DA:271(R):G:H8	1.82	0.43
1:CA:619:U:O2	4:CD:133:VAL:HA	2.18	0.43
7:AG:76:ARG:NH2	7:AG:156:TRP:HZ2	2.16	0.43
26:DA:185:U:H2'	26:DA:186:G:C8	2.53	0.43
26:DA:211:A:H2'	26:DA:212:G:O4'	2.18	0.43
1:CA:392:G:H2'	1:CA:393:A:H8	1.82	0.43
1:AA:748:C:H4'	1:AA:749:C:O5'	2.19	0.43
6:AF:17:SER:O	6:AF:21:LEU:HG	2.18	0.43
1:CA:340:U:H2'	1:CA:341:C:C6	2.54	0.43
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.19	0.43
20:AT:36:LEU:HD22	20:AT:55:ILE:HG23	2.00	0.43
2:AB:139:LYS:O	2:AB:143:GLU:HG3	2.18	0.43
39:BS:59:LYS:HE3	39:BS:60:GLY:H	1.82	0.43
46:BZ:124:ILE:HG23	46:BZ:126:VAL:HG23	2.00	0.43
42:BV:21:ARG:HG2	42:BV:91:TYR:CD1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BV:29:PRO:HA	42:BV:61:VAL:HG22	2.00	0.43
43:DW:84:ARG:HG3	43:DW:98:LYS:HD2	2.00	0.43
26:DA:2483:C:N3	37:DQ:124:LYS:NZ	2.59	0.43
26:BA:579:G:H2'	26:BA:580:C:C6	2.53	0.43
26:DA:938:G:OP1	55:D8:52:LYS:HD2	2.18	0.43
8:AH:103:VAL:HG21	8:AH:110:ALA:HB2	2.00	0.43
24:AX:7:G:O2'	24:AX:49:G:H5'	2.18	0.43
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.36	0.43
26:BA:535:C:O3'	41:BU:53:ARG:NH1	2.51	0.43
26:DA:1493:C:H41	26:DA:2206:G:C2'	2.31	0.43
26:BA:2791:C:H5'	26:BA:2893:G:N2	2.32	0.43
1:AA:321:A:N7	1:AA:328:C:O2'	2.37	0.43
26:BA:2287:A:C4	26:BA:2289:G:C8	3.07	0.43
1:AA:1304:G:C5	1:AA:1305:G:C6	3.06	0.43
1:CA:1055:A:H62	1:CA:1200:C:N4	2.16	0.43
24:CX:19:G:C4	24:CX:57:A:C2	3.06	0.43
26:BA:330:A:C2	26:BA:1210:A:H2'	2.52	0.43
46:DZ:157:LEU:HB3	46:DZ:161:VAL:HG13	2.00	0.43
3:AC:16:ARG:HH22	3:AC:183:ASP:HA	1.82	0.43
26:DA:2651:C:C2'	26:DA:2652:C:H5'	2.48	0.43
26:DA:2492:U:H2'	26:DA:2493:U:C6	2.54	0.43
30:DF:184:TYR:O	30:DF:188:ARG:HG3	2.18	0.43
26:DA:330:A:H2	26:DA:1210:A:C2'	2.32	0.43
35:DO:23:ARG:HG3	35:DO:24:VAL:N	2.32	0.43
1:AA:310:G:H5'	16:AP:31:LYS:HB2	1.99	0.43
1:CA:1235:U:H2'	1:CA:1236:A:O4'	2.18	0.43
26:DA:51:G:H1'	26:DA:119:A:N1	2.33	0.43
1:CA:1091:U:O2'	1:CA:1093:A:N7	2.46	0.43
26:DA:7:G:H5'	34:DN:130:HIS:CE1	2.53	0.43
1:AA:271:C:H2'	1:AA:272:C:C6	2.53	0.43
26:BA:1364:G:OP2	48:B1:3:LYS:HG3	2.18	0.43
28:DD:132:PRO:HG2	28:DD:135:PHE:HD2	1.81	0.43
26:DA:523:C:H4'	26:DA:540:C:O2	2.19	0.43
1:CA:1104:G:C2'	1:CA:1105:A:H5'	2.48	0.43
26:DA:1570:A:C6	26:DA:1571:A:C6	3.05	0.43
46:DZ:149:SER:HB2	46:DZ:172:ALA:O	2.18	0.43
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.18	0.43
21:AU:15:ARG:NH1	21:AU:15:ARG:HB2	2.33	0.43
26:DA:2489:G:C6	26:DA:2490:G:N1	2.87	0.43
1:AA:1469:G:H2'	1:AA:1470:G:C8	2.53	0.43
29:BE:96:PHE:O	29:BE:175:VAL:HG11	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AS:53:ASN:OD1	19:AS:56:GLN:N	2.37	0.43
1:AA:105:G:H2'	1:AA:106:C:C6	2.54	0.43
51:D4:64:GLY:C	51:D4:66:SER:H	2.22	0.43
28:DD:223:GLY:HA3	28:DD:231:HIS:CE1	2.54	0.43
26:DA:2846:G:H2'	26:DA:2847:U:O4'	2.18	0.43
1:AA:593:G:C2	1:AA:594:G:C4	3.06	0.43
46:BZ:93:ASP:HB2	46:BZ:131:ARG:NH2	2.33	0.43
26:BA:493:G:H2'	26:BA:494:G:O4'	2.17	0.43
1:AA:1525:G:OP2	11:AK:120:ARG:NH2	2.52	0.43
45:BY:13:VAL:HG12	45:BY:74:PRO:HA	2.01	0.43
26:BA:2256:G:H2'	26:BA:2257:U:O4'	2.19	0.43
28:BD:72:LYS:HB3	28:BD:72:LYS:HE3	1.82	0.43
40:BT:8:LYS:HD3	40:BT:8:LYS:HA	1.79	0.43
1:CA:399:G:H2'	1:CA:400:C:C6	2.54	0.43
31:DG:18:GLU:OE2	31:DG:21:ARG:NH2	2.51	0.43
26:DA:873:G:H1	26:DA:904:C:H42	1.66	0.43
1:CA:77:G:C6	1:CA:93:G:C6	3.06	0.43
1:CA:1400:C:N3	24:CX:34:C:C2	2.87	0.43
23:AW:76:PPU:HD1	26:BA:2506:U:O4'	2.19	0.43
1:CA:1144:G:C6	1:CA:1145:C:N4	2.86	0.43
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.53	0.43
1:CA:1507:A:H2'	1:CA:1508:G:O4'	2.19	0.43
26:DA:1334:G:C6	26:DA:1335:U:C4	3.06	0.43
26:DA:1652:A:H2'	26:DA:1653:G:H5'	2.01	0.43
1:AA:1017:G:H2'	1:AA:1018:C:O4'	2.19	0.43
1:CA:828:A:C2	1:CA:829:G:H1'	2.53	0.43
26:DA:1693:U:O2'	28:DD:14:ARG:NH2	2.51	0.43
26:DA:1827:C:OP2	28:DD:222:ARG:HD2	2.18	0.43
1:AA:600:C:N3	1:AA:639:G:C2	2.87	0.43
26:DA:2831:G:O2'	26:DA:2883:A:H2'	2.18	0.43
26:DA:2748:A:H5'	32:DH:4:ILE:HD12	2.00	0.43
1:AA:1003:G:N1	1:AA:1004:A:N3	2.66	0.43
36:BP:6:LEU:HD23	36:BP:6:LEU:HA	1.75	0.43
1:CA:1432:G:OP1	40:DT:108:ARG:HB2	2.17	0.43
26:DA:753:C:H2'	26:DA:754:C:H6	1.83	0.43
1:AA:22:G:C6	1:AA:23:C:C4	3.06	0.43
1:AA:542:G:OP1	4:AD:10:ARG:NH2	2.50	0.43
36:DP:121:LYS:O	36:DP:123:LEU:N	2.48	0.43
26:DA:2695:C:H2'	26:DA:2696:U:H6	1.81	0.43
32:BH:56:SER:OG	32:BH:57:ASP:N	2.49	0.43
26:BA:2801(A):A:H1'	26:BA:2895:U:H1'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BS:49:VAL:HG22	39:BS:73:LEU:HD12	2.00	0.43
32:DH:38:SER:OG	32:DH:40:GLU:HG3	2.19	0.43
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	2.01	0.43
24:AX:31:G:N7	24:AX:32:5MC:HM52	2.33	0.43
33:DI:8:PRO:HB3	33:DI:14:ASP:OD1	2.19	0.43
26:BA:444:C:H4'	30:BF:49:ALA:HB2	2.00	0.43
3:CC:131:ARG:NH1	5:CE:50:GLU:HG3	2.34	0.43
26:BA:459:U:H5''	54:B7:40:TRP:CD2	2.53	0.43
7:AG:28:ASN:HA	7:AG:31:MET:HE2	2.00	0.43
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.33	0.43
14:AN:15:LYS:HE2	14:AN:16:PHE:CE1	2.53	0.43
26:DA:1159:U:H2'	26:DA:1160:G:H8	1.84	0.43
26:DA:2094:G:P	33:DI:22:LYS:HD2	2.58	0.43
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.50	0.43
35:DO:73:ASP:HB2	40:DT:82:LEU:HD13	2.00	0.43
26:DA:271(F):C:H2'	26:DA:271(G):C:C6	2.53	0.43
1:AA:182:U:H5'	1:AA:182:U:H6	1.83	0.43
43:BW:51:LEU:HD23	43:BW:105:VAL:HG11	1.99	0.43
26:DA:2341:G:H2'	26:DA:2342:C:O4'	2.17	0.43
26:DA:2110:G:OP1	26:DA:2118:U:N3	2.51	0.43
1:CA:971:G:O6	1:CA:1364:U:O2'	2.32	0.43
1:CA:1272:G:C2'	1:CA:1273:G:H5'	2.48	0.43
1:CA:1148:U:O2'	9:CI:66:ARG:NH1	2.51	0.43
1:AA:991:U:O2'	1:AA:992:U:OP2	2.26	0.43
27:BB:105:A:H2'	27:BB:106:G:O4'	2.18	0.43
51:D4:40:HIS:HA	51:D4:41:PRO:HD2	1.76	0.43
26:BA:1142(A):A:C4	26:BA:1144:G:C8	3.07	0.43
1:CA:515:G:C5	1:CA:516:U:C4	3.06	0.43
26:DA:1359:A:N6	26:DA:1372:U:N3	2.67	0.43
26:DA:2378:A:H4'	39:DS:23:ARG:HD2	2.00	0.43
1:CA:265:G:H5'	17:CQ:64:PRO:O	2.17	0.43
31:DG:11:TYR:HA	31:DG:15:VAL:HB	2.00	0.43
1:CA:647:C:H2'	1:CA:648:A:H8	1.84	0.43
36:DP:38:GLN:HG2	36:DP:45:LEU:N	2.33	0.43
26:BA:1858:G:N2	26:BA:1883:G:H2'	2.34	0.43
3:CC:54:ARG:HB3	3:CC:54:ARG:HH11	1.83	0.43
1:AA:99:U:H2'	1:AA:100:C:C6	2.53	0.43
26:BA:1257:C:H4'	30:BF:83:PHE:CE1	2.52	0.43
34:BN:4:TYR:HE2	34:BN:41:ASP:HB2	1.83	0.43
4:CD:61:LYS:NZ	4:CD:72:GLU:OE2	2.42	0.43
28:BD:223:GLY:HA3	28:BD:231:HIS:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CS:11:VAL:HG13	19:CS:38:SER:HB3	2.01	0.43
26:BA:2357:U:OP1	47:B0:20:ARG:NH1	2.51	0.43
37:BQ:21:THR:HG21	37:BQ:101:ARG:HD3	2.00	0.43
30:BF:132:VAL:HA	30:BF:138:GLU:HB3	2.00	0.43
1:AA:575:G:O2'	1:AA:821:G:H5'	2.18	0.43
54:D7:34:ARG:NH1	54:D7:41:ARG:O	2.52	0.43
42:DV:25:LEU:H	42:DV:92:THR:HG1	1.62	0.43
32:BH:154:PRO:HB3	32:BH:163:TYR:CZ	2.53	0.43
18:CR:32:ARG:HA	18:CR:69:THR:HG21	2.01	0.43
3:CC:34:LEU:HD22	14:CN:25:VAL:HG11	2.00	0.43
26:BA:1121:C:H2'	26:BA:1122:G:O4'	2.18	0.43
8:AH:69:ARG:HB2	8:AH:69:ARG:HE	1.52	0.43
30:DF:93:LYS:HA	30:DF:93:LYS:HD3	1.91	0.43
1:AA:262:A:H2'	1:AA:263:A:C8	2.53	0.43
4:CD:103:ASN:O	4:CD:107:ARG:HG2	2.19	0.43
1:AA:1173:G:C6	1:AA:1174:G:N7	2.86	0.43
1:CA:96:U:O2'	1:CA:97:G:C8	2.65	0.43
26:BA:2099:U:H2'	26:BA:2100:G:C8	2.54	0.43
1:CA:1122:U:H2'	1:CA:1123:A:C8	2.54	0.43
33:BI:92:VAL:HG11	33:BI:144:VAL:HG11	2.01	0.43
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.53	0.43
26:DA:2526:G:H5'	26:DA:2742:C:O2'	2.18	0.43
3:CC:6:HIS:HA	3:CC:7:PRO:HD3	1.80	0.43
4:CD:108:LEU:HB3	4:CD:110:PHE:CE1	2.54	0.43
1:CA:1222:G:H5'	19:CS:77:THR:HG21	2.00	0.43
36:BP:50:ARG:HG2	55:B8:61:LEU:HD11	1.99	0.43
26:DA:746:A:O2'	26:DA:2611:U:O2'	2.26	0.43
26:BA:185:U:H4'	26:BA:218:A:H4'	2.01	0.43
26:DA:1709:U:H2'	26:DA:1710:C:C6	2.54	0.43
1:CA:410:G:P	4:CD:30:LYS:HZ3	2.36	0.43
1:CA:766:A:H2'	1:CA:767:A:O4'	2.18	0.43
31:BG:16:ARG:HE	31:BG:31:VAL:HG11	1.84	0.43
1:CA:243:A:H4'	1:CA:244:U:H5''	2.00	0.43
26:DA:1364:G:OP2	48:D1:3:LYS:HG3	2.19	0.43
26:DA:466:A:N3	26:DA:683:C:H1'	2.34	0.43
26:BA:1857:G:C6	26:BA:1858:G:C6	3.07	0.43
26:DA:2848:G:C8	40:DT:97:ALA:HB2	2.53	0.43
2:CB:84:GLU:HB3	2:CB:219:VAL:HG21	2.00	0.43
1:CA:189:G:H2'	1:CA:189(A):C:C6	2.54	0.43
1:AA:401:C:H2'	1:AA:402:G:H8	1.83	0.43
1:AA:792:A:H4'	1:AA:793:U:C5'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1179:A:H4'	9:AI:103:THR:HA	2.00	0.43
4:CD:133:VAL:HG11	4:CD:138:TYR:CD2	2.54	0.43
26:DA:2274:A:C5	26:DA:2276:G:C8	3.06	0.43
14:CN:4:LYS:HA	14:CN:7:ILE:HG12	2.01	0.43
48:D1:72:GLU:HG2	48:D1:76:ARG:HD3	2.00	0.43
6:CF:8:ILE:HG22	6:CF:10:LEU:HD13	2.00	0.43
15:CO:58:MET:O	15:CO:62:GLN:N	2.40	0.43
26:DA:614(B):G:H1'	30:DF:44:ARG:HB2	2.00	0.43
13:AM:13:LYS:HA	13:AM:44:ARG:HH11	1.84	0.43
36:DP:58:THR:O	36:DP:62:LEU:HG	2.18	0.43
34:DN:23:LEU:HD12	34:DN:99:LEU:HD23	2.00	0.43
26:BA:2490:G:H8	26:BA:2490:G:OP2	2.01	0.43
19:CS:56:GLN:HB3	19:CS:56:GLN:HE21	1.59	0.43
12:CL:84:LEU:HB2	12:CL:105:TYR:CE2	2.54	0.43
26:DA:851:U:O2'	50:D3:42:ALA:O	2.29	0.43
1:CA:1005:A:H3'	1:CA:1006:C:O4'	2.19	0.43
1:CA:1007:C:H6	1:CA:1007:C:O5'	2.02	0.43
26:DA:2108:C:H2'	26:DA:2109:U:H6	1.83	0.43
1:CA:1277:C:O2'	1:CA:1279:A:H8	2.01	0.43
1:CA:1320:C:O4'	19:CS:73:GLU:HG3	2.19	0.43
1:CA:626:U:H2'	1:CA:627:G:O4'	2.19	0.43
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.54	0.43
24:CX:19:G:N1	24:CX:56:C:N4	2.56	0.43
26:DA:2224:G:H4'	26:DA:2226:C:C2	2.53	0.43
26:DA:573:G:H1	26:DA:2031:A:P	2.41	0.43
26:DA:2807:G:N1	26:DA:2808:U:N3	2.67	0.43
26:BA:2175:C:C2'	26:BA:2176:A:H5'	2.48	0.43
13:AM:91:ARG:NE	13:AM:97:PRO:O	2.51	0.43
1:CA:1343:G:H2'	1:CA:1344:C:H6	1.80	0.43
31:DG:10:LYS:HG3	31:DG:14:GLU:OE1	2.19	0.43
1:AA:1316:G:H4'	14:AN:18:VAL:HG13	2.01	0.43
1:AA:309:G:H1'	1:AA:608:A:C2	2.54	0.43
26:DA:279:C:H2'	26:DA:280:C:C6	2.54	0.43
26:DA:1688:U:O2	26:DA:1700:A:H8	2.02	0.43
26:BA:2544:G:H2'	26:BA:2545:G:O4'	2.18	0.43
1:CA:1095:U:C4	1:CA:1096:C:C4	3.07	0.43
26:BA:272:G:N7	26:BA:421:U:H2'	2.34	0.43
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.53	0.43
26:DA:557:U:H2'	26:DA:558:G:C8	2.54	0.43
33:BI:72:LEU:O	33:BI:74:ASN:N	2.48	0.43
26:DA:797:C:H2'	26:DA:798:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:189(K):U:H2'	1:CA:189(L):G:C8	2.53	0.43
1:CA:944:G:N1	1:CA:1338:G:OP2	2.41	0.43
26:BA:2657:A:H1'	26:BA:2665:A:N6	2.34	0.43
1:CA:1352:C:N3	1:CA:1371:G:C6	2.87	0.43
1:CA:35:G:C4	1:CA:550:G:N2	2.87	0.43
1:CA:1073:U:H2'	1:CA:1074:G:H8	1.84	0.43
26:BA:262:A:H2'	26:BA:263:C:O4'	2.18	0.43
26:DA:616:G:H5'	30:DF:205:ARG:HD2	2.01	0.43
26:BA:746:A:H2'	26:BA:2612:C:H5''	1.99	0.43
1:CA:860:A:OP2	61:CA:4111:HOH:O	2.21	0.43
7:AG:23:VAL:O	7:AG:27:ILE:HG12	2.18	0.43
26:DA:987:G:O2'	26:DA:1000:A:N3	2.41	0.43
26:DA:602:G:O2'	26:DA:655:A:N6	2.51	0.43
26:DA:1782:C:O2'	26:DA:2609:U:H5''	2.19	0.43
26:DA:1778:U:H2'	26:DA:1784:A:N6	2.34	0.43
26:DA:2153:G:N3	26:DA:2153:G:H2'	2.33	0.43
1:CA:1392:G:O2'	1:CA:1393:U:H5'	2.19	0.43
26:DA:1394:U:OP1	61:DA:3949:HOH:O	2.20	0.43
1:CA:1208:C:H2'	1:CA:1209:C:O4'	2.19	0.43
26:DA:1359:A:N1	26:DA:1372:U:C4	2.86	0.43
26:BA:848:G:N9	26:BA:933:A:H8	2.17	0.43
1:CA:255:G:C6	1:CA:256:U:C4	3.07	0.43
1:AA:173:U:C5	1:AA:198:G:H8	2.37	0.43
26:BA:1127:A:N3	26:BA:2518:A:H5''	2.34	0.43
3:AC:138:VAL:HG23	3:AC:151:VAL:HG23	2.01	0.43
35:DO:78:ARG:HH22	40:DT:75:ILE:HD11	1.84	0.43
43:DW:13:SER:HA	43:DW:14:PRO:HD3	1.89	0.43
26:DA:557:U:H2'	26:DA:558:G:H8	1.84	0.43
26:BA:1364:G:OP1	48:B1:2:SER:HA	2.19	0.43
32:BH:35:VAL:HA	32:BH:36:PRO:HD2	1.92	0.43
26:DA:1153:C:OP1	41:DU:92:ARG:NH1	2.50	0.43
1:CA:664:G:P	18:CR:64:ARG:HH21	2.42	0.43
26:DA:2352:A:N6	26:DA:2365:G:O2'	2.51	0.43
27:BB:78:A:H2'	27:BB:79:C:O4'	2.19	0.43
26:DA:27:G:O2'	26:DA:28:A:OP2	2.32	0.43
26:DA:2336:A:H61	47:D0:43:THR:HG22	1.84	0.43
1:AA:1112:C:C4	3:AC:178:LEU:HD23	2.54	0.43
26:BA:755:C:H2'	26:BA:756:C:H6	1.84	0.43
26:DA:1486:A:H2'	26:DA:1487:G:C8	2.54	0.43
26:DA:1288:U:C2	26:DA:1327:C:C2	3.07	0.43
53:D6:6:ARG:HH11	53:D6:26:ASN:HB2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:422:A:H2'	26:DA:423:A:C8	2.54	0.43
26:BA:2591:C:H2'	26:BA:2592:G:C8	2.54	0.43
26:BA:844:C:C2'	26:BA:845:G:H5'	2.49	0.43
29:BE:167:VAL:HG12	29:BE:189:PRO:HD3	2.01	0.43
26:BA:1489:U:HO2'	26:BA:1490:A:H8	1.67	0.43
26:DA:1641:A:H2'	26:DA:1642:G:O4'	2.18	0.43
4:CD:120:LEU:HA	4:CD:120:LEU:HD23	1.88	0.43
5:CE:36:ASP:C	5:CE:38:GLN:H	2.22	0.43
1:AA:255:G:H1'	17:AQ:16:GLN:NE2	2.34	0.43
32:BH:18:GLU:HB3	32:BH:25:LYS:HB2	2.00	0.43
41:BU:66:ASN:O	41:BU:70:ARG:HG3	2.18	0.43
26:DA:2109:U:N3	26:DA:2110:G:N7	2.66	0.43
1:AA:1089:G:HO2'	1:AA:1170:A:H2	1.64	0.43
26:BA:2125:G:H1	26:BA:2172:U:P	2.40	0.43
1:CA:1064:G:OP1	1:CA:1386:G:H4'	2.19	0.43
26:DA:1449:A:H8	26:DA:1449:A:OP2	2.02	0.43
1:CA:585:G:N3	1:CA:879:C:H4'	2.34	0.43
35:BO:120:GLU:OE1	40:BT:67:SER:OG	2.29	0.43
31:BG:148:MET:HB2	31:BG:148:MET:HE3	1.82	0.43
40:DT:59:THR:HG23	40:DT:78:LEU:CB	2.46	0.43
26:DA:171:G:H2'	26:DA:172:C:H6	1.83	0.43
1:CA:1109:C:H2'	1:CA:1110:A:O4'	2.19	0.43
4:CD:8:VAL:O	4:CD:11:LEU:HB2	2.19	0.43
1:AA:683:G:H2'	1:AA:684:A:H8	1.84	0.43
1:AA:408:A:H2'	1:AA:409:G:O4'	2.18	0.43
29:DE:37:ARG:NH1	29:DE:42:ASP:OD1	2.49	0.43
1:CA:1137:C:H6	1:CA:1137:C:O5'	2.02	0.43
1:CA:417:C:O5'	1:CA:417:C:H6	2.02	0.43
1:CA:950:U:H2'	1:CA:951:G:C8	2.53	0.43
26:BA:445:C:O2'	26:BA:446:G:H5'	2.19	0.43
26:DA:414:C:H2'	26:DA:415:A:C8	2.54	0.43
1:CA:358:U:H2'	1:CA:359:U:C6	2.54	0.43
26:BA:1309:G:H4'	54:B7:7:PRO:HB2	2.01	0.43
8:CH:44:PHE:HE2	8:CH:109:ILE:HG12	1.84	0.43
26:DA:355:G:H2'	26:DA:356:G:C8	2.54	0.43
3:CC:22:TRP:CD1	3:CC:57:ILE:HG22	2.54	0.43
15:AO:3:ILE:HG12	15:AO:3:ILE:O	2.19	0.43
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.19	0.43
26:BA:236:C:H2'	26:BA:237:C:C6	2.53	0.43
26:DA:2706:G:O2'	38:DR:64:ARG:HD3	2.19	0.43
23:CW:76:PPU:H102	26:DA:2584:U:H4'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1013:G:N2	1:CA:1015:A:H3'	2.34	0.42
26:BA:2821:A:H2'	26:BA:2822:G:O4'	2.18	0.42
26:BA:303:U:H2'	26:BA:304:G:H8	1.84	0.42
1:CA:1227:A:OP2	13:CM:111:LYS:HE3	2.18	0.42
51:D4:40:HIS:ND1	51:D4:43:TYR:HD2	2.17	0.42
1:CA:1512:U:H2'	1:CA:1513:A:C8	2.53	0.42
13:AM:4:ILE:HA	13:AM:5:ALA:HA	1.81	0.42
26:BA:250:G:OP2	55:B8:13:ARG:NH2	2.52	0.42
26:BA:962:G:H4'	26:BA:2496:C:O2'	2.19	0.42
5:CE:93:PRO:HG2	8:CH:105:ARG:CZ	2.49	0.42
36:DP:46:LYS:HE3	36:DP:46:LYS:HB3	1.80	0.42
1:AA:201:C:N4	1:AA:216:G:H22	2.17	0.42
1:CA:1090:U:H2'	1:CA:1091:U:C6	2.53	0.42
26:BA:1654:A:H2'	26:BA:1655:A:H8	1.83	0.42
27:DB:43:C:C4	27:DB:45:A:C6	3.07	0.42
26:DA:2052:G:H4'	29:DE:143:ASN:O	2.19	0.42
41:BU:10:ARG:NH2	61:BU:301:HOH:O	2.52	0.42
30:BF:106:ARG:HG2	30:BF:106:ARG:H	1.49	0.42
42:DV:57:VAL:HG12	42:DV:99:ILE:HG12	2.00	0.42
1:AA:300:A:H1'	1:AA:565:U:O2	2.19	0.42
4:CD:12:CYS:SG	4:CD:19:LEU:HB2	2.58	0.42
26:DA:2070:G:C2	26:DA:2442:C:C2	3.07	0.42
26:BA:947:G:OP2	61:BA:4650:HOH:O	2.22	0.42
26:BA:2836:U:C4	26:BA:2883:A:N6	2.87	0.42
26:BA:2712:U:OP1	26:BA:2714:G:H4'	2.19	0.42
26:BA:2554:U:H2'	26:BA:2555:U:C6	2.53	0.42
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.18	0.42
28:DD:38:LYS:HA	28:DD:38:LYS:HD2	1.83	0.42
28:BD:146:GLU:HG2	28:BD:152:GLY:C	2.40	0.42
46:DZ:91:LEU:HD23	46:DZ:130:PRO:HB3	2.01	0.42
26:DA:872:A:H2'	26:DA:873:G:O4'	2.19	0.42
20:AT:29:LYS:HB2	20:AT:71:THR:HG21	2.01	0.42
1:CA:679:C:C2'	1:CA:680:C:H5'	2.49	0.42
26:BA:828:U:H2'	26:BA:829:A:C8	2.54	0.42
35:DO:4:PRO:O	35:DO:5:GLN:HB2	2.19	0.42
52:D5:49:CYS:SG	52:D5:51:TYR:HB2	2.58	0.42
1:CA:1101:A:N6	2:CB:176:GLU:OE2	2.51	0.42
26:BA:1934:C:H4'	26:BA:1974:C:O3'	2.19	0.42
26:BA:2636:U:H1'	26:BA:2783:G:N2	2.35	0.42
1:AA:864:A:H2'	1:AA:865:A:C8	2.53	0.42
1:AA:718:G:C8	11:AK:116:HIS:HB3	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DH:58:GLU:O	32:DH:62:LYS:HG3	2.19	0.42
26:BA:1317:A:H2'	26:BA:1318:C:C6	2.53	0.42
31:DG:143:GLU:H	31:DG:143:GLU:HG2	1.32	0.42
13:CM:50:GLU:HG3	13:CM:54:VAL:HG13	2.00	0.42
27:DB:68:C:H2'	27:DB:69:G:O4'	2.18	0.42
26:BA:2557:G:H2'	26:BA:2558:C:C6	2.53	0.42
1:CA:1007:C:O2	1:CA:1022:G:N1	2.31	0.42
26:DA:2110:G:C2	26:DA:2120:G:H1'	2.53	0.42
26:DA:2139:C:N4	26:DA:2153:G:C2	2.87	0.42
2:CB:16:HIS:HD2	2:CB:204:ASN:N	2.17	0.42
1:CA:1400:C:O4'	22:CV:18:G:H1'	2.19	0.42
24:AX:5:G:N2	24:AX:68:C:N3	2.58	0.42
24:CX:42:G:H2'	24:CX:43:A:C8	2.51	0.42
26:DA:2303:G:H2'	26:DA:2304:G:O4'	2.19	0.42
26:DA:1530:C:O2'	26:DA:1531:C:P	2.77	0.42
1:AA:630:G:H2'	1:AA:631:G:H8	1.84	0.42
55:D8:30:ARG:HD3	55:D8:30:ARG:HA	1.57	0.42
46:BZ:111:VAL:C	46:BZ:113:ALA:H	2.22	0.42
1:AA:1322:C:H4'	1:AA:1323:G:OP1	2.20	0.42
26:BA:812:C:H5''	26:BA:1250:G:O2'	2.19	0.42
26:DA:2494:G:O2'	37:DQ:80:GLU:HA	2.19	0.42
13:AM:88:ARG:HG3	13:AM:98:VAL:HG12	2.01	0.42
1:AA:1355:G:H2'	1:AA:1356:G:H8	1.84	0.42
1:AA:1417:G:C6	1:AA:1482:G:C6	3.08	0.42
1:AA:762:C:H2'	1:AA:763:G:C8	2.55	0.42
43:DW:69:LEU:HD22	43:DW:107:LEU:HB3	2.00	0.42
18:CR:53:ARG:HA	18:CR:56:THR:OG1	2.18	0.42
1:CA:892:A:C6	1:CA:893:C:C4	3.08	0.42
36:DP:44:GLY:HA3	36:DP:45:LEU:HB2	2.01	0.42
1:AA:952:U:H2'	1:AA:953:G:C8	2.54	0.42
1:CA:598:U:H2'	1:CA:599:C:H6	1.83	0.42
1:CA:49:U:H3	1:CA:362:G:H1'	1.84	0.42
26:BA:1790:C:H2'	26:BA:1791:A:C5	2.54	0.42
26:BA:1820:U:C4	28:BD:160:GLY:HA3	2.54	0.42
26:DA:83:G:N2	26:DA:102:G:H1'	2.34	0.42
46:DZ:141:VAL:HG12	46:DZ:144:LEU:HD12	2.00	0.42
2:CB:55:PHE:O	2:CB:59:GLU:N	2.32	0.42
40:DT:92:GLY:O	40:DT:120:ARG:NH2	2.51	0.42
26:BA:2607:G:H2'	26:BA:2608:G:O4'	2.19	0.42
26:DA:506:G:O3'	26:DA:507:A:H8	2.02	0.42
1:CA:630:G:H2'	1:CA:631:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BZ:48:PHE:CE1	46:BZ:71:VAL:HG11	2.55	0.42
26:DA:819:A:H5'	26:DA:973:A:N1	2.34	0.42
1:CA:524:G:H2'	1:CA:525:C:C6	2.54	0.42
26:BA:1828:G:H4'	26:BA:1829:A:OP1	2.18	0.42
35:BO:92:GLU:HG3	35:BO:93:PRO:HD2	2.00	0.42
26:DA:1439:A:H2'	26:DA:1440:G:O4'	2.19	0.42
26:BA:2315:G:H2'	26:BA:2316:C:C6	2.55	0.42
37:BQ:34:LEU:HD11	37:BQ:129:THR:HB	2.00	0.42
46:BZ:98:MET:O	46:BZ:125:LEU:HA	2.20	0.42
26:BA:670:A:H4'	26:BA:671:C:O5'	2.20	0.42
37:DQ:118:LEU:HB2	37:DQ:131:ILE:HD13	2.02	0.42
26:BA:919:G:N2	26:BA:2269:A:OP2	2.52	0.42
21:CU:9:ARG:O	21:CU:13:ILE:HG13	2.19	0.42
55:D8:10:ALA:HB3	55:D8:62:LEU:HD21	2.01	0.42
18:CR:76:LEU:HA	18:CR:76:LEU:HD12	1.76	0.42
33:BI:140:LEU:HA	33:BI:140:LEU:HD23	1.86	0.42
30:DF:149:ASP:OD1	30:DF:149:ASP:N	2.47	0.42
51:B4:41:PRO:HG3	51:B4:49:PHE:CE2	2.54	0.42
4:CD:50:ARG:HA	4:CD:51:PRO:HD3	1.85	0.42
1:AA:266:G:H5''	1:AA:268:C:H41	1.84	0.42
26:DA:2395:C:O2'	48:D1:30:VAL:HG22	2.19	0.42
26:BA:2284:C:OP1	53:B6:3:SER:OG	2.32	0.42
46:DZ:158:PRO:HA	46:DZ:159:PRO:HD3	1.90	0.42
26:DA:226:G:H21	26:DA:228:A:H62	1.68	0.42
1:CA:1400:C:H4'	22:CV:18:G:O2'	2.19	0.42
19:CS:27:GLU:HG2	19:CS:47:HIS:CD2	2.54	0.42
27:DB:30:C:O2	27:DB:31:C:C6	2.72	0.42
26:BA:1992:G:H4'	26:BA:1993:U:H5	1.84	0.42
36:BP:3:LEU:HA	36:BP:3:LEU:HD12	1.84	0.42
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.84	0.42
1:AA:1445:C:C2	1:AA:1458:G:C2	3.07	0.42
1:AA:1202:G:O2'	14:AN:29:ARG:HG3	2.19	0.42
24:CX:61:C:H2'	24:CX:62:C:C6	2.54	0.42
20:AT:10:LEU:HD23	20:AT:11:SER:H	1.83	0.42
13:CM:60:VAL:HG23	13:CM:64:TRP:CZ3	2.53	0.42
26:BA:1131:G:O6	26:BA:2040:C:H1'	2.20	0.42
1:AA:1130:A:H5'	9:AI:18:PHE:CE2	2.54	0.42
1:AA:503:C:H2'	1:AA:504:C:C6	2.54	0.42
12:CL:33:ARG:HG2	12:CL:60:LEU:HD12	2.02	0.42
26:BA:1423:G:H2'	26:BA:1424:G:H8	1.84	0.42
34:BN:112:LEU:O	34:BN:116:LEU:HG	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DE:176:ILE:HG22	29:DE:178:GLU:HG2	2.01	0.42
26:BA:1665:A:H2'	26:BA:1666:G:O4'	2.18	0.42
26:DA:676:A:H1'	26:DA:2443:C:H1'	2.00	0.42
3:CC:115:LEU:HD12	3:CC:115:LEU:HA	1.82	0.42
1:CA:435:C:O5'	1:CA:435:C:H6	2.01	0.42
2:AB:170:GLU:O	2:AB:174:VAL:HG23	2.20	0.42
26:BA:744:G:OP1	29:BE:132:HIS:ND1	2.50	0.42
26:BA:135:G:C6	26:BA:145:G:C6	3.07	0.42
26:DA:1721:G:H2'	26:DA:1740:G:O6	2.19	0.42
26:BA:18:C:O2'	26:BA:554:U:OP1	2.36	0.42
26:BA:1477:A:H2'	26:BA:1478:G:O4'	2.19	0.42
36:BP:138:LEU:HD23	36:BP:145:PRO:HG3	2.01	0.42
30:BF:150:GLY:HA2	30:BF:172:TRP:CD2	2.55	0.42
1:CA:831:U:C2'	1:CA:832:C:H5'	2.50	0.42
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.19	0.42
4:AD:108:LEU:HD12	4:AD:108:LEU:HA	1.83	0.42
26:DA:67:U:H2'	26:DA:68:G:O4'	2.19	0.42
7:AG:55:GLY:O	7:AG:56:GLN:HG3	2.19	0.42
3:CC:114:PRO:HA	3:CC:185:GLY:HA3	2.00	0.42
48:B1:7:ILE:HG23	48:B1:98:LEU:HD11	2.01	0.42
26:DA:876:C:H2'	26:DA:877:U:O4'	2.19	0.42
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.55	0.42
40:BT:22:PHE:HA	40:BT:91:ARG:HH12	1.84	0.42
1:AA:991:U:H6	1:AA:991:U:H2'	1.65	0.42
1:AA:730:G:C5	1:AA:731:G:H1'	2.55	0.42
27:DB:6:C:H2'	27:DB:7:G:H5''	2.00	0.42
26:DA:2316:C:O2'	26:DA:2317:C:H5'	2.19	0.42
8:AH:86:ILE:HG12	8:AH:135:CYS:HA	2.01	0.42
26:DA:1384:A:N3	26:DA:1405:U:H1'	2.33	0.42
26:DA:911:A:H2'	37:DQ:9:TYR:OH	2.19	0.42
29:DE:72:VAL:HG13	29:DE:73:GLU:O	2.19	0.42
30:DF:53:THR:HG23	30:DF:55:GLY:N	2.31	0.42
33:DI:88:ILE:HG23	33:DI:123:LEU:HA	2.00	0.42
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.07	0.42
36:DP:39:LYS:CB	36:DP:45:LEU:HG	2.48	0.42
26:BA:2108:C:H2'	26:BA:2109:U:O4'	2.19	0.42
8:CH:94:TYR:HD1	8:CH:132:GLU:HA	1.84	0.42
26:BA:38:A:H2'	26:BA:39:C:C6	2.55	0.42
26:DA:1191:G:H2'	26:DA:1192:G:H8	1.84	0.42
1:CA:723:U:HO2'	1:CA:724:G:H5'	1.84	0.42
11:CK:38:ASN:HA	11:CK:39:PRO:HD3	1.94	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:208:C:H2'	26:DA:209:C:H6	1.82	0.42
3:CC:115:LEU:O	3:CC:118:GLN:HG2	2.19	0.42
8:CH:97:VAL:HA	8:CH:100:ILE:HG13	2.01	0.42
4:CD:175:SER:HB3	4:CD:186:LEU:HD21	2.01	0.42
11:AK:73:MET:HG2	11:AK:103:LEU:HD21	2.00	0.42
11:CK:120:ARG:HA	11:CK:121:PRO:HD3	1.82	0.42
26:BA:2742:C:OP1	56:B9:35:ARG:HD3	2.19	0.42
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	2.02	0.42
26:BA:536:A:H2'	26:BA:537:C:C6	2.55	0.42
32:DH:10:PRO:O	32:DH:76:VAL:HG21	2.19	0.42
9:AI:5:TYR:HH	9:AI:7:THR:HG1	1.59	0.42
7:CG:46:ALA:HA	7:CG:49:ILE:HD12	2.02	0.42
1:AA:384:G:H2'	1:AA:385:C:C6	2.53	0.42
26:DA:108:U:C2	26:DA:109:G:C8	3.07	0.42
38:DR:38:VAL:HB	38:DR:39:PRO:HD3	2.00	0.42
35:BO:15:GLY:O	35:BO:47:ILE:HG12	2.19	0.42
20:CT:47:GLY:HA2	20:CT:48:LYS:C	2.39	0.42
1:CA:38:G:H1	1:CA:397:A:H5''	1.84	0.42
28:DD:134:ARG:O	28:DD:168:ARG:NH2	2.52	0.42
34:DN:96:GLU:H	34:DN:96:GLU:CD	2.23	0.42
26:BA:774:A:N3	26:BA:774:A:H2'	2.35	0.42
33:DI:125:GLU:HA	33:DI:142:VAL:O	2.20	0.42
8:AH:23:SER:HB3	8:AH:62:TYR:CD2	2.54	0.42
33:DI:83:ALA:C	33:DI:89:TYR:HD2	2.23	0.42
1:CA:972:C:OP2	10:CJ:57:LYS:NZ	2.30	0.42
1:CA:71:C:H42	1:CA:98:G:H1	1.66	0.42
26:DA:2151:G:C4	26:DA:2152:G:C8	3.07	0.42
24:CX:31:G:C5	24:CX:32:5MC:C4	3.07	0.42
1:CA:1120:G:C5	1:CA:1121:U:C5	3.07	0.42
1:CA:838:G:C2	1:CA:849:C:C2	3.07	0.42
1:CA:581:G:O2'	1:CA:582:U:H5'	2.19	0.42
26:DA:272(G):C:N4	26:DA:363(C):G:H1	2.11	0.42
2:CB:96:ARG:NE	2:CB:98:LEU:HD13	2.34	0.42
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.35	0.42
7:CG:113:GLU:CG	7:CG:119:ARG:HG2	2.49	0.42
1:CA:1513:A:C6	1:CA:1514:C:N4	2.88	0.42
7:AG:126:ASP:O	7:AG:131:LYS:N	2.50	0.42
1:CA:153:C:H2'	1:CA:154:C:C6	2.55	0.42
26:BA:286:C:H2'	26:BA:287:C:H6	1.85	0.42
1:AA:1509:C:H2'	1:AA:1510:U:O4'	2.20	0.42
26:BA:2040:C:H2'	26:BA:2041:U:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DQ:29:PHE:HB2	37:DQ:105:GLU:OE2	2.19	0.42
26:DA:362:U:H3'	26:DA:362:U:OP1	2.20	0.42
26:DA:329:G:OP1	26:DA:329:G:H8	2.02	0.42
26:DA:2630:G:H2'	26:DA:2631:G:H8	1.82	0.42
26:DA:1913:A:H4'	26:DA:1914:C:O5'	2.19	0.42
1:CA:1089:G:C2	1:CA:1097:C:C2	3.07	0.42
7:CG:27:ILE:O	7:CG:31:MET:N	2.53	0.42
1:AA:192:U:H4'	20:AT:57:ARG:HD3	2.00	0.42
45:BY:86:ARG:HD2	45:BY:100:ALA:HA	2.01	0.42
1:CA:189:G:H2'	1:CA:189(A):C:O4'	2.20	0.42
1:CA:333:G:H4'	20:CT:16:HIS:CE1	2.54	0.42
33:DI:62:LYS:HE2	33:DI:133:HIS:NE2	2.34	0.42
1:CA:625:G:H4'	16:CP:16:HIS:HB3	2.02	0.42
26:DA:2758:A:C4	32:DH:67:LEU:HD21	2.55	0.42
3:CC:124:ILE:HD11	3:CC:189:ALA:CB	2.49	0.42
26:DA:1674:G:N2	26:DA:1677:A:N1	2.53	0.42
53:B6:8:LYS:HG2	55:B8:34:TRP:CD1	2.55	0.42
40:DT:11:GLU:OE1	40:DT:57:PHE:HB3	2.19	0.42
51:B4:16:CYS:SG	51:B4:17:GLY:N	2.92	0.42
15:CO:31:LEU:HD23	15:CO:31:LEU:HA	1.87	0.42
2:AB:61:LEU:HA	2:AB:61:LEU:HD12	1.85	0.42
26:BA:1015:G:N2	26:BA:1147:C:O2	2.47	0.42
13:CM:57:ARG:NE	51:D4:34:GLU:HB3	2.34	0.42
16:AP:2:VAL:HG22	16:AP:64:ALA:HA	2.01	0.42
26:BA:786:C:H5''	26:BA:1780:A:C8	2.55	0.42
26:DA:2176:A:H2'	26:DA:2177:C:C6	2.55	0.42
1:CA:76:C:N4	1:CA:96:U:C2	2.88	0.42
1:CA:1400:C:C6	22:CV:18:G:C2	3.08	0.42
26:BA:2096:U:O4	26:BA:2193:G:O6	2.36	0.42
1:CA:1272:G:H2'	1:CA:1273:G:H5'	2.01	0.42
27:DB:30:C:OP2	39:DS:32:LEU:HD11	2.20	0.42
31:DG:27:ASN:HB3	31:DG:30:GLU:HB2	2.02	0.42
7:AG:29:LYS:HD3	7:AG:29:LYS:HA	1.94	0.42
35:DO:47:ILE:HB	35:DO:48:PRO:HD2	2.02	0.42
1:CA:582:U:C2	1:CA:760:G:C6	3.07	0.42
1:CA:1055:A:C8	1:CA:1206:G:C2	3.07	0.42
1:AA:1366:C:H2'	1:AA:1367:C:H6	1.85	0.42
27:DB:4:C:H42	27:DB:117:G:H1	1.67	0.42
26:DA:2662:A:H2'	26:DA:2663:G:O4'	2.19	0.42
13:AM:3:ARG:O	13:AM:57:ARG:NH2	2.48	0.42
13:CM:44:ARG:HB2	13:CM:47:ASP:OD1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:910:A:H62	37:BQ:12:GLN:HA	1.85	0.42
26:BA:2544:G:H1'	26:BA:2646:C:H4'	2.01	0.42
1:AA:194:C:O3'	20:AT:68:LYS:HD2	2.19	0.42
1:AA:1053:G:H4'	1:AA:1054:C:H5'	2.01	0.42
51:D4:16:CYS:SG	51:D4:17:GLY:N	2.93	0.42
26:DA:1009:A:O5'	26:DA:1009:A:H8	2.02	0.42
26:DA:1034:G:OP1	26:DA:1034:G:H8	2.02	0.42
4:CD:125:HIS:O	4:CD:149:ALA:N	2.42	0.42
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	2.01	0.42
9:AI:26:VAL:HG22	9:AI:61:ALA:HB3	2.01	0.42
1:CA:1075:C:C2'	1:CA:1076:C:H5'	2.50	0.42
26:DA:2400:G:H2'	26:DA:2401:U:H6	1.83	0.42
8:AH:11:THR:HG23	8:AH:14:ARG:NH1	2.34	0.42
26:DA:2243:U:H2'	26:DA:2244:U:C6	2.54	0.42
1:CA:374:A:C6	1:CA:375:U:C4	3.07	0.42
34:DN:36:GLY:HA3	34:DN:49:GLY:HA2	2.02	0.42
1:CA:1342:C:O2'	9:CI:124:GLN:HG3	2.19	0.42
46:BZ:68:PRO:O	46:BZ:91:LEU:HB2	2.19	0.42
1:AA:399:G:H2'	1:AA:400:C:C6	2.54	0.42
26:BA:478:A:C6	26:BA:480:A:C6	3.07	0.42
6:AF:11:ASN:HB3	6:AF:14:LEU:HG	2.00	0.42
1:CA:918:A:H2'	1:CA:919:A:C8	2.53	0.42
26:BA:2236:C:H2'	26:BA:2237:G:O4'	2.20	0.42
26:BA:1208:C:C4	26:BA:1209:G:N7	2.88	0.42
43:BW:24:ILE:HA	43:BW:27:LYS:HG3	2.01	0.42
1:CA:33:A:N3	12:CL:32:PHE:HE2	2.17	0.42
26:DA:925:C:H2'	26:DA:926:A:H8	1.85	0.42
26:DA:1836:C:H2'	26:DA:1837:C:H6	1.84	0.42
26:BA:1285:G:N2	26:BA:1328:G:H5''	2.35	0.42
32:DH:126:PRO:HG2	32:DH:130:ARG:HD2	2.00	0.42
51:B4:40:HIS:O	51:B4:43:TYR:N	2.53	0.42
26:DA:1026:U:H4'	26:DA:1027:A:OP1	2.19	0.42
29:DE:170:LEU:HB3	29:DE:184:VAL:CG2	2.50	0.42
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	2.01	0.42
26:DA:2106:G:H2'	26:DA:2107:C:O4'	2.20	0.42
26:BA:2139:C:H5'	26:BA:2140:C:OP2	2.19	0.42
1:CA:1132:C:H42	1:CA:1142:G:H1	1.67	0.42
46:BZ:150:LEU:HG	46:BZ:151:HIS:H	1.84	0.42
26:DA:2164:C:H5''	26:DA:2165:G:C8	2.54	0.42
53:B6:6:ARG:HH12	53:B6:26:ASN:HB2	1.83	0.42
1:CA:1227:A:H3'	1:CA:1227:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:486:U:H2'	1:AA:487:A:H8	1.84	0.42
1:CA:514:C:N4	1:CA:515:G:O6	2.52	0.42
1:CA:1087:G:C4	1:CA:1099:G:N2	2.87	0.42
26:DA:2722:G:H2'	26:DA:2723:C:C6	2.54	0.42
3:AC:131:ARG:HH12	5:AE:50:GLU:HG3	1.84	0.42
36:BP:52:GLU:HB3	36:BP:55:ARG:NH1	2.35	0.42
26:DA:2611:U:C4	52:D5:3:LYS:HG2	2.54	0.42
1:CA:1250:A:O3'	9:CI:67:GLY:HA2	2.20	0.42
46:DZ:53:ILE:HG13	46:DZ:53:ILE:H	1.70	0.42
39:BS:3:ARG:HE	39:BS:4:LEU:N	2.18	0.42
26:DA:801:G:OP2	30:DF:55:GLY:HA2	2.20	0.42
18:CR:74:ARG:HB3	18:CR:81:PHE:CZ	2.55	0.42
1:CA:1442(A):G:O2'	40:DT:118:ARG:HG2	2.20	0.42
26:DA:2787:C:H2'	26:DA:2788:C:C6	2.55	0.42
29:BE:49:LEU:HD12	29:BE:49:LEU:HA	1.77	0.42
1:CA:1095:U:H2'	1:CA:1096:C:O4'	2.20	0.42
26:BA:272:G:O2'	26:BA:421:U:OP2	2.27	0.42
26:BA:1424:G:H2'	26:BA:1425:G:O4'	2.19	0.42
26:DA:448:U:O4	26:DA:583:G:H1'	2.20	0.42
26:DA:2848:G:H1'	26:DA:2867:G:N2	2.33	0.42
1:AA:736:C:H2'	1:AA:737:A:C8	2.55	0.42
51:D4:62:ARG:HB2	51:D4:63:TYR:CD1	2.54	0.42
26:DA:253:C:H2'	26:DA:254:G:O4'	2.20	0.42
30:BF:167:ALA:O	30:BF:170:LEU:HB2	2.20	0.42
17:AQ:64:PRO:HB3	17:AQ:70:ARG:NH1	2.34	0.42
26:BA:151:C:H2'	26:BA:152:G:H8	1.85	0.42
26:DA:2220:G:H2'	26:DA:2221:G:C8	2.55	0.42
26:BA:2259:G:C2	26:BA:2282:G:N1	2.88	0.42
26:DA:271(F):C:H2'	26:DA:271(G):C:O4'	2.20	0.42
26:BA:1902:C:H5'	28:BD:246:PRO:HD3	2.01	0.42
31:BG:179:PRO:HG3	51:B4:43:TYR:OH	2.20	0.42
41:DU:69:CYS:HB3	41:DU:74:LEU:HD13	2.01	0.42
53:D6:23:THR:OG1	53:D6:24:GLU:N	2.53	0.42
26:DA:2099:U:H3	26:DA:2190:G:H1	1.66	0.42
1:AA:112:G:OP2	16:AP:27:LYS:HD2	2.18	0.42
26:BA:2537:U:H2'	26:BA:2538:C:C6	2.54	0.42
26:DA:634:C:H2'	26:DA:635:C:C6	2.54	0.42
54:D7:8:ASN:HB3	54:D7:11:LYS:HB3	2.01	0.42
26:BA:954:G:H5''	37:BQ:13:GLN:HB3	2.01	0.42
16:AP:28:ARG:NH1	16:AP:29:ASP:OD2	2.45	0.42
1:AA:899:C:H6	1:AA:899:C:O5'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:866:A:H2'	26:DA:866:A:N3	2.35	0.42
39:DS:80:LEU:HD12	39:DS:80:LEU:HA	1.82	0.42
31:BG:128:ARG:HE	31:BG:128:ARG:HB2	1.38	0.42
26:DA:928:G:O5'	26:DA:928:G:H8	2.02	0.42
33:DI:80:PRO:HA	33:DI:145:VAL:O	2.20	0.42
40:BT:94:ALA:HB1	40:BT:99:LEU:HD21	2.01	0.42
26:BA:1525:G:H2'	26:BA:1526:G:O4'	2.20	0.42
26:BA:2784:C:O2'	29:BE:42:ASP:OD1	2.21	0.42
26:BA:2567:G:H2'	26:BA:2568:C:C6	2.55	0.42
26:DA:2135:A:H61	26:DA:2157:G:N2	2.18	0.42
26:DA:2153:G:H3'	26:DA:2154:G:H8	1.84	0.42
26:BA:2141:G:C6	26:BA:2142:C:C2	3.07	0.42
26:DA:2584:U:O2'	61:DA:3701:HOH:O	2.17	0.42
1:CA:1128:C:C2	1:CA:1147:C:N4	2.87	0.42
26:BA:2124:G:N2	26:BA:2174:C:N3	2.58	0.42
27:DB:33:G:C5	27:DB:34:U:C4	3.07	0.42
9:CI:8:GLY:HA2	9:CI:79:LEU:HB3	2.01	0.42
26:DA:2162:G:O3'	26:DA:2172:U:H6	2.03	0.42
1:CA:656:C:H2'	1:CA:657:G:O4'	2.20	0.42
26:DA:2721:A:H2'	26:DA:2722:G:O4'	2.19	0.42
1:AA:681:C:C2	1:AA:710:G:C2	3.07	0.42
26:DA:1637:A:H4'	26:DA:2711:A:O2'	2.20	0.42
1:CA:1525:G:H2'	1:CA:1526:G:O4'	2.20	0.42
26:DA:2498:C:O2'	26:DA:2499:C:H5'	2.20	0.42
1:AA:758:G:H5'	1:AA:880:C:H1'	2.01	0.42
1:CA:1252:A:H61	1:CA:1285:A:H61	1.65	0.42
26:BA:1022:G:C5	26:BA:1140:C:C4	3.07	0.42
1:AA:1239:A:C4	1:AA:1298:C:N4	2.87	0.42
1:CA:593:G:C6	1:CA:647:C:N3	2.88	0.42
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.40	0.42
31:BG:56:ALA:HA	31:BG:153:ARG:HH21	1.85	0.42
26:DA:1166:C:H2'	26:DA:1167:U:H6	1.84	0.42
27:BB:30:C:H2'	27:BB:31:C:C5'	2.49	0.42
26:DA:2078:C:C4	26:DA:2079:U:C4	3.07	0.42
1:AA:840:C:H4'	1:AA:841:U:OP1	2.20	0.42
1:AA:495:A:H4'	1:AA:496:A:OP1	2.18	0.42
26:DA:1598:C:O3'	44:DX:35:THR:OG1	2.37	0.42
26:BA:1107:G:O2'	26:BA:1108:U:H5'	2.20	0.42
43:BW:13:SER:HA	43:BW:14:PRO:HD3	1.84	0.42
26:DA:2359:C:H2'	26:DA:2360:A:O4'	2.19	0.42
3:AC:22:TRP:CD1	3:AC:59:ARG:HD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:DT:73:GLU:OE1	40:DT:103:ARG:NE	2.53	0.42
1:CA:486:U:H2'	1:CA:487:A:C8	2.55	0.42
1:CA:737:A:H2'	1:CA:738:C:C6	2.54	0.42
4:AD:15:GLU:CG	4:AD:63:LYS:HB3	2.49	0.42
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.55	0.42
42:BV:89:GLN:HA	42:BV:90:PRO:HD3	1.97	0.42
26:BA:2471:C:H2'	26:BA:2472:G:O4'	2.20	0.42
4:CD:88:VAL:O	4:CD:92:VAL:HG23	2.20	0.42
26:DA:1227:G:OP1	41:DU:13:LYS:HG2	2.20	0.42
26:DA:321:G:C5	26:DA:341:G:H4'	2.54	0.42
4:CD:102:ASP:OD1	4:CD:103:ASN:N	2.53	0.42
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.20	0.42
26:BA:1316:U:H2'	26:BA:1317:A:C8	2.55	0.42
29:DE:170:LEU:HB3	29:DE:184:VAL:HG22	2.01	0.42
8:CH:31:PHE:O	8:CH:35:ILE:HG13	2.20	0.42
26:BA:1540:U:H2'	26:BA:1541:G:O4'	2.20	0.42
18:CR:24:ALA:C	18:CR:26:LEU:H	2.23	0.42
26:DA:2467:C:C4	26:DA:2468:G:C6	3.07	0.42
7:CG:22:LEU:HG	7:CG:62:PHE:CZ	2.55	0.42
1:AA:1203:C:C2'	1:AA:1204:A:H5'	2.49	0.42
1:CA:288:A:H2'	1:CA:289:G:H4'	2.01	0.42
26:DA:859:G:N2	26:DA:917:A:OP2	2.53	0.42
44:BX:24:GLY:O	44:BX:83:VAL:HG22	2.20	0.42
32:DH:71:LEU:O	32:DH:75:ALA:N	2.53	0.42
31:DG:33:ARG:HB2	31:DG:33:ARG:NH1	2.34	0.42
26:DA:1156:A:OP1	26:DA:1156:A:H8	2.03	0.42
29:BE:9:VAL:HG22	29:BE:25:VAL:HB	2.01	0.42
1:CA:124:G:P	1:CA:310:G:H21	2.42	0.42
2:AB:12:GLU:HG3	2:AB:13:ALA:N	2.35	0.42
30:BF:64:ILE:HD12	30:BF:65:TRP:CZ3	2.55	0.42
1:CA:1004:A:H62	1:CA:1037:C:H2'	1.85	0.42
26:DA:2120:G:C2	26:DA:2121:G:C8	3.07	0.42
26:DA:2187:G:C5	26:DA:2188:C:C4	3.08	0.42
26:BA:2141:G:N7	26:BA:2151:G:C2	2.88	0.42
26:DA:1313:U:H2'	26:DA:1610:A:C2	2.55	0.42
26:DA:1496:A:H2'	26:DA:1498:C:C5	2.55	0.42
54:B7:24:THR:HA	54:B7:25:PRO:HD3	1.96	0.42
26:DA:846:C:H4'	26:DA:847:U:O4'	2.19	0.42
26:BA:1566:A:OP1	28:BD:211:ARG:NH1	2.53	0.42
26:DA:864:G:OP2	37:DQ:22:LYS:HE2	2.20	0.42
1:AA:1358:U:H2'	1:AA:1359:C:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1636:C:H2'	26:DA:1637:A:H8	1.85	0.42
26:BA:1800:C:H3'	28:BD:147:LEU:HD23	2.02	0.42
46:DZ:10:ARG:HG3	46:DZ:36:LYS:HB3	2.01	0.42
39:DS:11:LYS:O	39:DS:15:ARG:HG3	2.20	0.42
31:BG:138:GLN:HB3	31:BG:153:ARG:O	2.19	0.42
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.35	0.42
1:AA:979:C:O2	14:AN:19:ARG:HG2	2.20	0.42
26:DA:918:A:C5	26:DA:919:G:H1'	2.55	0.42
44:DX:54:VAL:HG22	44:DX:81:VAL:HG12	2.01	0.42
26:DA:2870:C:H2'	26:DA:2871:C:O4'	2.20	0.42
29:BE:144:ARG:HB3	29:BE:145:LYS:H	1.52	0.42
1:CA:362:G:N1	1:CA:365:U:OP2	2.50	0.42
26:BA:1889:A:N1	26:BA:2234:G:H1'	2.34	0.42
26:BA:2492:U:H2'	26:BA:2493:U:H6	1.85	0.42
1:AA:375:U:O2'	16:AP:6:LEU:O	2.36	0.42
3:AC:35:GLU:O	3:AC:39:ILE:HG13	2.20	0.42
37:BQ:21:THR:HG21	37:BQ:101:ARG:HB2	2.02	0.42
1:AA:262:A:C6	1:AA:263:A:C6	3.08	0.42
26:DA:1248:G:C2	41:DU:3:ARG:HD2	2.55	0.42
5:CE:90:VAL:O	5:CE:120:THR:HA	2.20	0.42
28:DD:158:ALA:O	28:DD:161:THR:OG1	2.30	0.42
27:BB:55:U:H2'	27:BB:56:G:O4'	2.20	0.42
26:DA:1351:C:C2	26:DA:1381:G:C2	3.08	0.42
26:BA:1311:G:N7	54:B7:9:ARG:NH2	2.67	0.42
29:DE:174:ASP:OD1	29:DE:175:VAL:N	2.53	0.42
27:DB:71:C:H1'	27:DB:107:G:N2	2.34	0.42
10:CJ:65:LEU:HB2	14:CN:56:VAL:HG22	2.01	0.42
1:CA:1026:G:N3	1:CA:1026:G:H3'	2.35	0.42
26:DA:2129:C:H2'	26:DA:2130:U:C6	2.55	0.42
1:CA:1277:C:HO2'	1:CA:1279:A:C1'	2.30	0.42
26:DA:2105:C:H2'	26:DA:2106:G:C8	2.54	0.42
1:CA:1134:G:N3	1:CA:1134:G:H2'	2.35	0.42
23:CW:76:PPU:C5'	23:CW:76:PPU:H8	2.36	0.42
23:CW:76:PPU:HD2	26:DA:2451:A:C4	2.54	0.42
16:CP:28:ARG:HH11	16:CP:29:ASP:CG	2.20	0.42
33:DI:52:ARG:CG	33:DI:52:ARG:HH11	2.33	0.42
7:CG:111:ARG:HB2	7:CG:119:ARG:HD2	2.01	0.42
26:BA:330:A:O2'	26:BA:331:A:H8	2.02	0.42
13:AM:3:ARG:HH22	13:AM:11:ARG:HE	1.68	0.42
26:DA:2376:A:H2'	26:DA:2377:A:O4'	2.20	0.42
1:AA:692:U:H2'	1:AA:694:A:OP2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:885:G:O2'	1:CA:886:G:H5'	2.20	0.42
26:DA:528:A:O2'	26:DA:529:A:H5'	2.19	0.42
1:CA:1060:C:C5	3:CC:2:GLY:HA2	2.55	0.42
6:CF:14:LEU:HD22	6:CF:18:GLN:HB3	2.02	0.42
27:DB:24:G:H5'	27:DB:25:A:N6	2.32	0.42
26:DA:2001:A:H2'	26:DA:2002:G:H8	1.80	0.42
35:DO:24:VAL:HG12	35:DO:39:ILE:HG22	2.02	0.42
26:DA:1973:G:H2'	26:DA:1974:C:C6	2.55	0.42
1:CA:45:U:OP1	1:CA:307:C:O2'	2.27	0.42
1:CA:608:A:H2'	1:CA:609:A:O4'	2.20	0.42
26:BA:1655:A:H4'	29:BE:115:GLY:N	2.35	0.42
26:DA:1363:C:H2'	26:DA:1364:G:H8	1.85	0.42
27:BB:4:C:H2'	27:BB:5:C:O4'	2.19	0.42
1:AA:841:U:O4'	1:AA:841:U:P	2.78	0.42
14:AN:48:ALA:HB2	14:AN:53:LEU:HD12	2.02	0.42
31:DG:31:VAL:HA	31:DG:32:PRO:HD2	1.68	0.42
28:DD:12:SER:HB3	28:DD:208:LYS:HB3	2.02	0.42
39:BS:83:LYS:HB2	39:BS:83:LYS:HE2	1.92	0.42
1:CA:382:A:H2'	1:CA:383:A:H8	1.82	0.42
26:DA:522:G:C6	26:DA:523:C:C4	3.08	0.42
26:DA:39:C:H2'	26:DA:40:C:H6	1.85	0.42
50:B3:8:LEU:O	50:B3:32:GLN:N	2.40	0.42
26:DA:2784:C:H1'	29:DE:37:ARG:HH12	1.84	0.42
1:AA:430:A:OP2	4:AD:8:VAL:HG12	2.19	0.42
10:CJ:40:LEU:HD12	10:CJ:69:ASN:HB3	2.02	0.42
26:DA:1475:G:C2	26:DA:1517:G:C2	3.08	0.42
30:BF:178:PRO:HB2	30:BF:201:VAL:HG21	2.02	0.42
1:CA:193:C:H2'	1:CA:194:C:C6	2.55	0.42
26:DA:1894:C:H2'	26:DA:1895:C:H6	1.85	0.42
5:CE:57:LYS:HG2	5:CE:61:TYR:HE2	1.85	0.42
4:CD:134:ASP:O	4:CD:136:PRO:HD3	2.20	0.42
7:CG:50:ILE:HD11	7:CG:58:PRO:HB3	2.01	0.42
24:CX:72:A:H5''	24:CX:73:A:OP2	2.20	0.42
26:BA:479:A:N3	26:BA:481:G:H5''	2.34	0.42
26:DA:357:A:H2'	26:DA:358:U:C6	2.55	0.42
28:BD:264:LYS:HA	28:BD:265:PRO:HD3	1.91	0.42
29:DE:11:MET:HG2	29:DE:24:THR:HB	2.01	0.42
27:BB:103:G:O2'	46:BZ:73:GLN:NE2	2.53	0.42
33:BI:83:ALA:HB2	33:BI:88:ILE:HA	2.01	0.42
26:BA:1983:C:H4'	26:BA:2606:C:H4'	2.01	0.42
4:AD:120:LEU:HA	4:AD:120:LEU:HD23	1.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BI:10:GLU:H	33:BI:10:GLU:HG3	1.35	0.42
1:AA:1517:G:H1'	26:BA:1919:A:O3'	2.18	0.42
50:D3:4:LEU:O	50:D3:36:VAL:HA	2.20	0.42
26:DA:407:G:H2'	26:DA:408:G:C8	2.55	0.42
1:CA:1002:G:C4	1:CA:1003:G:C8	3.08	0.41
26:DA:2120:G:N2	26:DA:2179:C:C2	2.88	0.41
26:DA:2153:G:C2	26:DA:2154:G:C4	3.08	0.41
26:BA:2142:C:N3	26:BA:2149:G:C6	2.88	0.41
26:BA:2153:G:C2	26:BA:2154:G:C8	3.07	0.41
1:CA:1134:G:H2'	1:CA:1135:U:H5'	2.02	0.41
1:CA:999:C:C2	1:CA:1042:G:N2	2.81	0.41
26:BA:2506:U:C2	26:BA:2585:U:O4	2.73	0.41
1:CA:1127:G:N2	1:CA:1147:C:H41	2.18	0.41
1:CA:1126:U:C2	1:CA:1281:U:O4	2.73	0.41
26:BA:1445:A:H1'	26:BA:1460:A:C2	2.55	0.41
1:CA:683:G:C6	1:CA:684:A:C6	3.08	0.41
1:AA:283:C:C2'	1:AA:284:G:H5'	2.51	0.41
26:BA:2144:U:O2'	26:BA:2145:C:H2'	2.20	0.41
36:DP:96:THR:HA	36:DP:126:VAL:HB	2.01	0.41
1:CA:427:U:H3'	1:CA:428:G:H2'	2.01	0.41
1:CA:1251:A:O2'	1:CA:1369:C:O2'	2.23	0.41
44:BX:31:HIS:CD2	44:BX:33:LYS:HB2	2.55	0.41
43:DW:66:GLU:HA	43:DW:69:LEU:HD12	2.02	0.41
40:DT:108:ARG:HA	40:DT:111:ARG:NH1	2.35	0.41
26:DA:1364:G:P	48:D1:3:LYS:HG3	2.59	0.41
26:BA:1748:G:H2'	26:BA:1749:A:O4'	2.20	0.41
1:CA:712:A:N6	1:CA:713:G:C6	2.88	0.41
20:AT:53:LEU:HD13	20:AT:100:ILE:O	2.20	0.41
26:BA:1608:A:H1'	26:BA:1610:A:OP2	2.20	0.41
28:DD:276:LYS:H	28:DD:276:LYS:CD	2.32	0.41
8:CH:30:ARG:O	8:CH:34:GLU:HG2	2.19	0.41
26:DA:106:C:H2'	26:DA:107:C:H6	1.84	0.41
26:DA:1721:G:H8	26:DA:1741:A:H62	1.67	0.41
20:AT:55:ILE:HA	20:AT:55:ILE:HD13	1.90	0.41
1:CA:894:G:C6	1:CA:895:G:C5	3.08	0.41
26:BA:1448:G:H5''	26:BA:1542:A:OP2	2.20	0.41
1:AA:1001:A:N1	1:AA:1040:U:O4	2.53	0.41
1:AA:831:U:C2'	1:AA:832:C:H5'	2.50	0.41
26:BA:272(J):C:H2'	26:BA:274:G:C8	2.55	0.41
36:DP:101:VAL:HG23	36:DP:106:LEU:HD13	2.02	0.41
1:CA:926:G:H5''	1:CA:927:G:O5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2356:C:OP1	47:B0:24:LYS:NZ	2.39	0.41
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.84	0.41
26:BA:322:A:H3'	30:BF:169:ASN:ND2	2.35	0.41
26:BA:596:G:H2'	26:BA:597:U:O4'	2.20	0.41
3:AC:77:ILE:HG13	3:AC:78:GLY:N	2.35	0.41
26:BA:662:G:H5''	36:BP:16:ARG:HG2	2.02	0.41
34:BN:48:MET:H	34:BN:48:MET:HG3	1.77	0.41
30:BF:196:LEU:HA	30:BF:196:LEU:HD23	1.81	0.41
26:DA:780:G:O5'	26:DA:780:G:H8	2.02	0.41
44:BX:88:LYS:HE3	44:BX:88:LYS:HB2	1.84	0.41
38:BR:118:GLU:H	38:BR:118:GLU:CD	2.23	0.41
26:DA:64:A:O3'	44:DX:71:GLY:HA3	2.20	0.41
12:CL:103:GLY:N	12:CL:107:ALA:O	2.48	0.41
26:BA:2812:G:H2'	26:BA:2813:A:O4'	2.20	0.41
39:DS:37:ALA:N	39:DS:51:ALA:O	2.52	0.41
16:AP:14:ASN:N	16:AP:15:PRO:HD3	2.35	0.41
41:BU:69:CYS:HB3	41:BU:74:LEU:HD13	2.02	0.41
3:CC:125:GLU:HG3	3:CC:190:ARG:HG2	2.02	0.41
26:DA:870:A:OP1	37:DQ:6:ARG:NE	2.49	0.41
29:BE:182:LEU:HD21	29:BE:198:VAL:HG11	2.02	0.41
1:CA:1245:A:N1	1:CA:1292:U:O2	2.53	0.41
1:CA:1014:A:P	1:CA:1014:A:H8	2.43	0.41
1:CA:1118:C:H2'	1:CA:1119:C:H6	1.85	0.41
1:AA:1007:C:N3	1:AA:1022:G:O6	2.52	0.41
26:DA:1422:G:C4	26:DA:1423:G:C8	3.08	0.41
26:DA:1012:U:C5	34:DN:28:THR:HG21	2.55	0.41
1:AA:1304:G:C6	1:AA:1305:G:N1	2.88	0.41
26:BA:1021:A:C3'	26:BA:1021:A:C8	3.00	0.41
26:DA:1372:U:O4	26:DA:1373:A:C5	2.74	0.41
26:BA:171:G:C2'	26:BA:172:C:H5'	2.50	0.41
1:AA:58:C:O5'	1:AA:58:C:H6	2.02	0.41
1:CA:265:G:N2	1:CA:267:C:H5'	2.35	0.41
1:CA:967:C:H2'	1:CA:968:A:N7	2.34	0.41
1:AA:875:C:H1'	8:AH:15:ASN:OD1	2.20	0.41
1:AA:1071:C:H42	1:AA:1104:G:H1	1.68	0.41
26:BA:795:C:H2'	26:BA:796:C:H6	1.85	0.41
1:AA:626:U:H2'	1:AA:627:G:O4'	2.20	0.41
1:CA:1493:A:H2'	26:DA:1913:A:N6	2.34	0.41
26:DA:1015:G:O2'	26:DA:1016:G:H5'	2.19	0.41
26:DA:729:G:H5'	26:DA:730:C:C5'	2.50	0.41
26:BA:2364:C:O2	47:B0:36:ILE:HD11	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:321:A:N7	1:CA:328:C:O2'	2.31	0.41
26:BA:2014:A:H2'	26:BA:2015:A:C8	2.55	0.41
37:DQ:52:VAL:HA	37:DQ:55:VAL:HG12	2.03	0.41
26:DA:1832:C:N4	26:DA:1833:U:C4	2.88	0.41
26:DA:271(Q):G:C2	26:DA:271(R):G:C5	3.08	0.41
26:BA:288:C:H2'	26:BA:289:A:C8	2.56	0.41
26:BA:817:C:H4'	26:BA:932:G:C5	2.55	0.41
1:AA:411:A:O2'	1:AA:413:G:H5'	2.20	0.41
1:CA:1330:U:H4'	13:CM:23:TYR:CZ	2.55	0.41
2:AB:71:VAL:HG12	2:AB:170:GLU:HG3	2.02	0.41
26:DA:1354:A:H2'	26:DA:1355:G:O4'	2.19	0.41
2:CB:82:ARG:HH11	2:CB:83:MET:HE1	1.84	0.41
3:CC:159:GLY:HA2	3:CC:193:TYR:CE1	2.56	0.41
1:CA:348:G:O2'	1:CA:349:A:H5'	2.19	0.41
1:CA:690:G:C6	1:CA:691:G:C6	3.08	0.41
26:BA:1111:A:H4'	26:BA:1112:G:OP1	2.21	0.41
39:BS:59:LYS:CE	39:BS:60:GLY:H	2.34	0.41
11:AK:120:ARG:HA	11:AK:121:PRO:HD3	1.86	0.41
3:CC:131:ARG:O	3:CC:135:LYS:HB2	2.21	0.41
26:DA:2269:A:OP1	61:DA:4046:HOH:O	2.22	0.41
26:BA:2391:G:O6	26:BA:2425:A:H8	2.03	0.41
26:BA:2390:U:P	55:B8:35:GLN:HE22	2.44	0.41
26:DA:1897:G:C6	26:DA:1898:U:C4	3.08	0.41
13:AM:70:LEU:O	13:AM:74:VAL:HG23	2.20	0.41
37:BQ:57:HIS:CD2	37:BQ:117:ALA:HB2	2.55	0.41
1:CA:909:A:H2'	1:CA:910:C:O4'	2.20	0.41
20:CT:30:LYS:O	20:CT:34:LYS:HG3	2.20	0.41
5:AE:33:VAL:HG21	5:AE:109:ILE:HG12	2.02	0.41
1:CA:746:A:H4'	1:CA:837:G:O2'	2.20	0.41
26:BA:109:G:H2'	26:BA:110:G:O4'	2.20	0.41
1:AA:228:A:H2'	1:AA:229:U:O4'	2.20	0.41
55:D8:63:PRO:HG2	55:D8:64:TYR:CE2	2.55	0.41
45:DY:19:LYS:HB3	45:DY:19:LYS:HE2	1.70	0.41
1:CA:185:A:O5'	1:CA:185:A:H8	2.03	0.41
55:B8:60:LEU:HD23	55:B8:60:LEU:HA	1.91	0.41
34:DN:138:LEU:HA	34:DN:138:LEU:HD23	1.84	0.41
15:AO:62:GLN:HA	15:AO:65:ARG:NH1	2.34	0.41
17:CQ:95:TYR:O	17:CQ:98:LEU:HB2	2.20	0.41
1:CA:8:A:N7	4:CD:209:ARG:HA	2.35	0.41
50:D3:41:PRO:HA	50:D3:44:ARG:HB3	2.01	0.41
1:AA:1172:C:C5	1:AA:1173:G:N7	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1132:C:C4	1:CA:1133:G:N7	2.88	0.41
26:BA:2789:C:O4'	26:BA:2892:A:H2	2.04	0.41
26:DA:1529:G:O2'	26:DA:1530:C:H5'	2.20	0.41
1:CA:44:G:H1	1:CA:398:C:N4	2.10	0.41
1:CA:515:G:C6	1:CA:516:U:C4	3.09	0.41
26:DA:1359:A:N1	26:DA:1360:A:C5	2.88	0.41
26:BA:307:G:N2	26:BA:309:G:H3'	2.35	0.41
1:CA:829:G:O6	61:CA:4089:HOH:O	2.19	0.41
1:CA:503:C:OP2	12:CL:116:SER:HB3	2.20	0.41
13:CM:65:LYS:CB	51:D4:50:VAL:HG11	2.47	0.41
31:DG:97:ASP:O	31:DG:101:ILE:HG13	2.21	0.41
33:DI:87:LYS:CB	33:DI:122:GLU:HA	2.49	0.41
26:DA:1688:U:H3	26:DA:1700:A:C5'	2.33	0.41
27:DB:42:C:O2'	31:DG:66:GLN:HG2	2.19	0.41
26:DA:565:C:H2'	26:DA:566:U:O4'	2.20	0.41
9:CI:23:ASN:HD22	9:CI:25:LYS:HG2	1.86	0.41
1:AA:636:U:H5'	17:AQ:2:PRO:HG3	2.03	0.41
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.20	0.41
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.55	0.41
29:DE:176:ILE:HB	29:DE:181:LEU:HB2	2.02	0.41
29:DE:122:PHE:HZ	29:DE:155:LYS:HB2	1.84	0.41
26:DA:347:A:H2'	26:DA:348:G:H8	1.85	0.41
1:CA:939:G:P	7:CG:95:ARG:HH12	2.43	0.41
26:BA:2786:U:H2'	26:BA:2787:C:C6	2.54	0.41
28:BD:142:VAL:HG13	28:BD:191:ALA:HB1	2.02	0.41
26:BA:1446:C:HO2'	26:BA:1545:A:HO2'	1.65	0.41
15:AO:3:ILE:H	15:AO:3:ILE:HD13	1.84	0.41
26:BA:814:C:H4'	26:BA:1224:C:O2	2.20	0.41
30:BF:31:HIS:NE2	30:BF:35:GLU:OE2	2.53	0.41
8:CH:58:TYR:O	8:CH:59:LEU:HD23	2.19	0.41
1:CA:304:U:H2'	1:CA:305:G:C8	2.56	0.41
26:BA:1930:G:N2	26:BA:1968:G:H2'	2.35	0.41
44:DX:59:VAL:HG21	44:DX:78:LYS:HE3	2.02	0.41
1:AA:1409:C:H2'	1:AA:1410:G:H8	1.85	0.41
26:DA:2506:U:C2	26:DA:2585:U:O4	2.73	0.41
26:DA:2588:G:H2'	26:DA:2589:A:O4'	2.19	0.41
39:BS:87:PHE:HB2	39:BS:112:PHE:CE2	2.55	0.41
46:DZ:76:LEU:HA	46:DZ:76:LEU:HD12	1.85	0.41
1:AA:981:U:H6	1:AA:981:U:O5'	2.03	0.41
26:DA:2145:C:H2'	26:DA:2145:C:H6	1.65	0.41
40:BT:35:LYS:HB2	40:BT:35:LYS:HE3	1.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2232:U:P	48:D1:40:ARG:HH12	2.43	0.41
1:AA:489:C:OP1	4:AD:132:ARG:NH2	2.53	0.41
28:BD:215:LEU:HD13	28:BD:217:ARG:NH2	2.35	0.41
5:AE:84:PHE:CE2	5:AE:133:TYR:HD2	2.38	0.41
1:CA:1367:C:OP1	9:CI:114:TYR:HA	2.20	0.41
26:DA:2101:G:C6	26:DA:2102:U:N3	2.89	0.41
1:AA:1125:U:H4'	10:AJ:5:ARG:NH2	2.31	0.41
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.56	0.41
1:CA:1153:C:N4	1:CA:1154:G:N2	2.68	0.41
46:DZ:156:LYS:HE3	46:DZ:156:LYS:HB3	1.55	0.41
26:DA:2168:G:H5'	26:DA:2169:A:OP2	2.19	0.41
53:B6:6:ARG:NE	53:B6:24:GLU:OE1	2.38	0.41
1:AA:328:C:H4'	1:AA:329:A:H5'	2.02	0.41
1:AA:35:G:H2'	1:AA:36:C:C6	2.55	0.41
26:DA:2302:G:N3	26:DA:2315:G:N2	2.68	0.41
26:BA:1020:A:N1	26:BA:1141:U:O2'	2.40	0.41
29:BE:93:VAL:HG13	61:BE:3106:HOH:O	2.20	0.41
1:CA:1295:G:O3'	13:CM:14:ARG:NH1	2.53	0.41
1:CA:1157:A:H5'	1:CA:1158:C:N1	2.35	0.41
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.20	0.41
26:DA:910:A:C6	26:DA:911:A:C6	3.08	0.41
26:BA:2277:G:OP2	47:B0:12:ASN:HB2	2.20	0.41
15:AO:70:LEU:HD11	15:AO:77:ARG:HB2	2.03	0.41
1:CA:1494:G:H5'	26:DA:1913:A:C5	2.56	0.41
1:CA:789:U:H2'	1:CA:791:G:OP2	2.21	0.41
31:BG:16:ARG:HB2	31:BG:17:PRO:HD3	2.02	0.41
32:DH:3:ARG:HB3	32:DH:3:ARG:HH11	1.85	0.41
26:DA:874:G:C8	26:DA:874:G:H5'	2.53	0.41
18:CR:61:LYS:HA	18:CR:64:ARG:NH1	2.36	0.41
26:BA:1045:A:OP1	26:BA:1045:A:H4'	2.20	0.41
20:CT:54:LYS:N	20:CT:100:ILE:HD11	2.34	0.41
26:BA:324:A:H2'	26:BA:325:G:O4'	2.20	0.41
26:DA:2292:C:H2'	26:DA:2293:C:C6	2.55	0.41
26:DA:1445(A):C:H2'	26:DA:1446:C:C6	2.54	0.41
1:CA:408:A:C2	1:CA:435:C:O2	2.74	0.41
1:AA:1112:C:O5'	1:AA:1112:C:H6	2.03	0.41
26:DA:853:G:H2'	26:DA:854:G:C8	2.55	0.41
1:AA:110:C:H2'	1:AA:111:G:O4'	2.19	0.41
26:DA:1654:A:H1'	26:DA:2823:A:H5'	2.03	0.41
1:CA:951:G:C6	1:CA:952:U:C4	3.09	0.41
1:CA:615:C:H2'	1:CA:616:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1614:A:P	26:DA:1614:A:H8	2.43	0.41
19:AS:3:ARG:HH11	19:AS:10:PHE:HB2	1.86	0.41
53:D6:6:ARG:NH1	53:D6:26:ASN:HB2	2.35	0.41
1:CA:942:G:H21	9:CI:124:GLN:NE2	2.19	0.41
1:AA:830:G:H2'	1:AA:831:U:O4'	2.21	0.41
36:DP:81:GLN:HB3	36:DP:106:LEU:HD23	2.02	0.41
5:CE:59:GLY:O	5:CE:62:ALA:HB3	2.20	0.41
5:AE:77:PRO:HG2	5:AE:142:LEU:HD22	2.03	0.41
9:AI:4:TYR:CE1	9:AI:88:TYR:HD1	2.38	0.41
5:CE:76:ILE:HB	5:CE:77:PRO:HD2	2.03	0.41
8:AH:82:HIS:NE2	8:AH:84:ARG:HG2	2.35	0.41
28:BD:166:GLN:HB2	28:BD:174:ILE:HG22	2.02	0.41
32:DH:45:VAL:HA	32:DH:50:VAL:HG22	2.01	0.41
29:BE:19:ARG:CZ	35:BO:72:PRO:HB3	2.50	0.41
26:DA:1816:G:H3'	28:DD:62:TYR:CE1	2.56	0.41
26:DA:701:G:O2'	26:DA:1631(A):A:N1	2.53	0.41
37:BQ:70:PRO:HA	37:BQ:94:VAL:O	2.20	0.41
26:DA:1377:G:OP2	61:DA:4242:HOH:O	2.21	0.41
13:CM:20:THR:HA	13:CM:25:ILE:HG22	2.01	0.41
26:DA:45:C:H2'	26:DA:47:C:C6	2.56	0.41
1:CA:114:U:H2'	1:CA:115:G:C8	2.55	0.41
28:BD:5:LYS:HB3	28:BD:5:LYS:HE3	1.55	0.41
26:DA:1303:G:C6	26:DA:1304:C:C4	3.07	0.41
26:DA:2245:U:O2'	26:DA:2436:G:OP2	2.19	0.41
26:DA:2155:G:O6	26:DA:2156:G:C2	2.74	0.41
1:CA:1276:G:H2'	1:CA:1277:C:H6	1.85	0.41
1:CA:986:A:C6	1:CA:1220:G:C2	3.09	0.41
1:CA:1120:G:N1	1:CA:1154:G:C2	2.88	0.41
26:BA:2849:U:OP2	40:BT:95:ARG:NH1	2.53	0.41
27:DB:63:G:H2'	27:DB:64:C:H6	1.85	0.41
1:AA:345:C:H4'	1:AA:346:G:N3	2.35	0.41
1:CA:580:U:H2'	1:CA:581:G:O4'	2.20	0.41
26:DA:363(C):G:H8	26:DA:363(C):G:O5'	2.03	0.41
26:DA:1580:A:OP2	26:DA:1580:A:H8	2.04	0.41
1:CA:1255:G:O3'	1:CA:1258:G:H1'	2.20	0.41
26:DA:2492:U:H2'	26:DA:2493:U:H6	1.84	0.41
9:AI:50:LEU:HD23	9:AI:81:ILE:CD1	2.50	0.41
1:AA:922:G:N3	1:AA:1398:A:H2	2.19	0.41
26:DA:606:U:H4'	26:DA:658:C:H4'	2.01	0.41
2:CB:122:PHE:HD1	2:CB:123:ALA:H	1.67	0.41
13:CM:68:GLY:HA3	31:DG:116:ASP:CG	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AN:37:PHE:CE2	14:AN:53:LEU:HD13	2.55	0.41
29:BE:119:ARG:CG	29:BE:160:TYR:HB2	2.51	0.41
6:AF:97:PHE:HB3	18:AR:32:ARG:HD3	2.03	0.41
26:BA:858:U:O2	26:BA:2268:A:H2'	2.21	0.41
1:CA:229:U:H5''	16:CP:33:ILE:HD12	2.01	0.41
36:DP:100:LEU:HD23	36:DP:100:LEU:HA	1.82	0.41
26:DA:1114:G:H2'	26:DA:1115:G:O4'	2.20	0.41
20:CT:56:MET:HG3	20:CT:57:ARG:N	2.36	0.41
26:BA:338:G:C2'	26:BA:339:U:H5'	2.51	0.41
35:DO:104:ARG:NH2	35:DO:121:VAL:O	2.53	0.41
26:DA:271(H):G:O2'	26:DA:271(I):G:OP2	2.38	0.41
26:DA:2515:C:H2'	26:DA:2516:G:C8	2.54	0.41
1:CA:1327:C:H2'	1:CA:1328:C:C6	2.55	0.41
26:DA:2784:C:O2'	29:DE:42:ASP:OD1	2.27	0.41
1:AA:967:C:H4'	9:AI:125:TYR:HE1	1.85	0.41
1:AA:688:G:H2'	1:AA:689:C:H6	1.86	0.41
26:DA:966:G:C6	26:DA:967:C:N4	2.89	0.41
26:DA:16:G:H2'	26:DA:17:G:H8	1.85	0.41
39:BS:110:LEU:HD12	39:BS:110:LEU:HA	1.80	0.41
34:DN:34:LEU:O	34:DN:49:GLY:HA3	2.21	0.41
26:DA:2467:C:OP1	56:D9:8:LYS:NZ	2.41	0.41
26:DA:1248:G:C5	41:DU:3:ARG:HB2	2.55	0.41
27:BB:24:G:O2'	27:BB:56:G:N7	2.48	0.41
48:D1:75:GLU:HA	48:D1:78:LYS:HE3	2.02	0.41
26:BA:2396:G:OP1	48:B1:25:LYS:NZ	2.34	0.41
32:DH:24:VAL:HG13	32:DH:37:VAL:HG21	2.01	0.41
2:AB:41:ILE:HD13	2:AB:41:ILE:HA	1.95	0.41
51:D4:54:GLY:HA2	51:D4:55:ARG:HA	1.53	0.41
1:CA:638:G:H2'	1:CA:639:G:O4'	2.20	0.41
26:BA:2776:A:C6	26:BA:2778:A:C6	3.09	0.41
46:DZ:44:PHE:CZ	46:DZ:86:VAL:HG11	2.56	0.41
26:BA:1682:G:C4	26:BA:1757:U:C2	3.08	0.41
49:B2:32:LEU:HD13	49:B2:36:ARG:NH1	2.35	0.41
26:BA:857:C:OP1	47:B0:77:ARG:NH2	2.52	0.41
26:BA:1614:A:H8	26:BA:1614:A:P	2.43	0.41
31:BG:66:GLN:HE21	31:BG:66:GLN:HB3	1.59	0.41
1:CA:203:U:H2'	1:CA:203:U:OP2	2.20	0.41
26:BA:1017:G:N2	26:BA:1145:C:O2	2.38	0.41
1:AA:1379:G:N7	7:AG:2:ALA:HB3	2.35	0.41
31:DG:165:THR:OG1	31:DG:168:GLU:HG3	2.21	0.41
1:AA:1164:G:C5	1:AA:1173:G:C2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1162:C:C2	1:CA:1175:G:C2	3.09	0.41
10:CJ:59:SER:O	10:CJ:60:ARG:HD3	2.21	0.41
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	2.03	0.41
26:DA:1600:C:O2'	26:DA:1601:G:H5'	2.21	0.41
26:DA:1449:A:HO2'	26:DA:1529:G:N2	2.15	0.41
26:DA:1359:A:N6	26:DA:1360:A:C2	2.89	0.41
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.51	0.41
1:AA:1027:C:H2'	1:AA:1028:C:C5	2.55	0.41
1:CA:1368:G:C2'	1:CA:1369:C:H5'	2.50	0.41
31:BG:17:PRO:HA	31:BG:20:ILE:HD12	2.03	0.41
1:AA:952:U:H2'	1:AA:953:G:H8	1.86	0.41
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.36	0.41
26:DA:1152:C:H2'	26:DA:1153:C:H6	1.85	0.41
1:AA:782:A:H4'	1:AA:1514:C:O2'	2.21	0.41
26:DA:493:G:H2'	26:DA:494:G:O4'	2.20	0.41
40:BT:24:PRO:HD3	40:BT:52:ILE:HD12	2.01	0.41
1:AA:909:A:H2'	1:AA:910:C:O4'	2.20	0.41
33:DI:93:THR:HG22	33:DI:116:LEU:HD22	2.02	0.41
4:AD:28:SER:O	4:AD:31:CYS:HB3	2.21	0.41
26:DA:2416:C:H2'	26:DA:2417:C:H6	1.86	0.41
11:CK:92:GLU:HB3	11:CK:96:ARG:NH1	2.35	0.41
12:CL:34:ARG:HG2	12:CL:35:GLY:N	2.35	0.41
26:BA:1328:G:O2'	26:BA:1329:U:H2'	2.20	0.41
30:BF:32:LEU:HB3	30:BF:112:MET:HE1	2.02	0.41
19:AS:45:VAL:HA	19:AS:62:ILE:HG22	2.02	0.41
26:DA:2542:A:H4'	26:DA:2543:G:C8	2.56	0.41
44:DX:4:ALA:HB1	44:DX:42:ALA:HA	2.03	0.41
37:BQ:115:MET:SD	37:BQ:131:ILE:HG21	2.61	0.41
7:AG:88:PRO:HB3	7:AG:145:ALA:O	2.20	0.41
26:DA:2653:U:H5''	26:DA:2654:A:OP2	2.21	0.41
9:CI:47:LEU:O	9:CI:50:LEU:HG	2.21	0.41
45:DY:65:ALA:HA	45:DY:66:PRO:HD3	1.93	0.41
1:CA:866:C:C4	1:CA:867:G:H1'	2.55	0.41
7:AG:21:VAL:O	7:AG:24:THR:OG1	2.34	0.41
41:BU:61:TRP:CH2	41:BU:93:LYS:HB2	2.56	0.41
7:AG:109:ASN:HA	7:AG:119:ARG:HE	1.85	0.41
26:BA:2443:C:OP1	30:BF:68:LYS:HD3	2.20	0.41
1:CA:1120:G:C6	1:CA:1154:G:C2	3.09	0.41
1:CA:1047:G:H8	1:CA:1047:G:O5'	2.04	0.41
26:DA:993:G:C6	26:DA:994:C:C4	3.08	0.41
27:DB:20:C:N4	27:DB:21:G:C6	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1850:G:H2'	26:DA:1851:U:O4'	2.20	0.41
12:CL:56:ALA:HB3	12:CL:100:ILE:HD11	2.03	0.41
1:CA:583:A:O2'	17:CQ:91:ARG:NE	2.54	0.41
26:DA:2711:A:OP1	26:DA:2712:U:H3'	2.20	0.41
33:DI:40:THR:HG23	33:DI:43:ASN:ND2	2.32	0.41
1:CA:1158:C:O3'	2:CB:133:LYS:NZ	2.54	0.41
4:CD:13:ARG:NH1	4:CD:38:TYR:O	2.52	0.41
26:DA:192:C:O2'	26:DA:802:A:N3	2.50	0.41
44:BX:31:HIS:HA	44:BX:32:PRO:HD3	1.91	0.41
1:CA:1010:G:C4	1:CA:1011:G:C8	3.08	0.41
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	2.03	0.41
1:AA:890:G:N2	1:AA:906:G:H2'	2.36	0.41
26:DA:2787:C:H2'	26:DA:2788:C:H6	1.86	0.41
2:AB:187:LEU:HD23	2:AB:201:ILE:HB	2.02	0.41
1:AA:167:G:H2'	1:AA:168:G:C8	2.54	0.41
26:BA:1796:U:H2'	26:BA:1797:C:H6	1.84	0.41
16:CP:33:ILE:H	16:CP:33:ILE:HG12	1.73	0.41
51:D4:59:PHE:HA	51:D4:60:GLN:C	2.40	0.41
35:DO:77:ILE:HA	40:DT:73:GLU:O	2.21	0.41
48:D1:52:ARG:NH1	48:D1:57:GLU:OE2	2.53	0.41
1:AA:203:U:H2'	1:AA:203:U:OP2	2.20	0.41
26:DA:270:A:C2	26:DA:366:C:H4'	2.56	0.41
51:D4:57:GLU:HA	51:D4:58:ARG:HA	1.67	0.41
29:DE:37:ARG:HB2	29:DE:46:ALA:H	1.85	0.41
26:BA:2011:U:H2'	26:BA:2012:G:O4'	2.20	0.41
26:BA:2774:C:H2'	26:BA:2775:A:O4'	2.21	0.41
36:DP:138:LEU:HD23	36:DP:145:PRO:HG3	2.03	0.41
3:CC:130:VAL:O	3:CC:134:ILE:HD13	2.21	0.41
26:BA:2845:G:H2'	26:BA:2846:G:H8	1.84	0.41
35:BO:98:VAL:HG13	35:BO:117:LEU:HB3	2.03	0.41
26:BA:64:A:O3'	44:BX:71:GLY:HA3	2.20	0.41
30:DF:129:PHE:CD2	30:DF:163:VAL:HG21	2.56	0.41
26:DA:649:G:H2'	26:DA:650:C:O4'	2.20	0.41
1:CA:950:U:OP2	13:CM:102:ARG:HD3	2.20	0.41
26:DA:118:A:H1'	26:DA:178:G:O4'	2.21	0.41
26:BA:1113:U:H2'	26:BA:1114:G:H8	1.85	0.41
26:DA:247:G:H4'	26:DA:386:G:C5	2.56	0.41
26:BA:419:C:H2'	26:BA:420:C:O4'	2.20	0.41
26:BA:1448:G:H1'	26:BA:1528:A:N1	2.35	0.41
26:BA:22:C:H2'	26:BA:23:G:O4'	2.20	0.41
26:BA:1636:C:H2'	26:BA:1637:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1190:G:H5''	36:DP:32:THR:HA	2.02	0.41
6:CF:34:GLY:O	6:CF:67:MET:HA	2.21	0.41
3:CC:154:SER:O	3:CC:197:GLY:N	2.49	0.41
37:BQ:54:MET:HG3	37:BQ:121:ALA:HB2	2.01	0.41
26:BA:1853:A:H2'	26:BA:1854:A:C8	2.56	0.41
26:DA:2250:G:O2'	26:DA:2496:C:OP1	2.32	0.41
11:CK:81:ASP:OD1	11:CK:106:LYS:HE2	2.20	0.41
26:DA:1745(A):C:H5'	26:DA:1746:G:OP2	2.20	0.41
1:CA:1067:A:O5'	1:CA:1067:A:H8	2.04	0.41
26:DA:1647:G:H3'	26:DA:1647:G:P	2.60	0.41
31:BG:122:PRO:HD3	31:BG:181:ARG:HG2	2.02	0.41
26:BA:2634:G:C2	26:BA:2635:C:C2	3.08	0.41
34:BN:62:VAL:CG1	34:BN:66:LYS:HB2	2.51	0.41
34:BN:108:PRO:O	34:BN:113:GLY:HA3	2.20	0.41
26:DA:1408:C:H2'	26:DA:1409:C:C6	2.56	0.41
26:DA:141:A:H8	26:DA:1408:C:HO2'	1.58	0.41
1:AA:1173:G:C2	1:AA:1174:G:C4	3.08	0.41
1:CA:1262:C:C2'	1:CA:1263:C:H5'	2.51	0.41
26:BA:2162:G:H5'	26:BA:2172:U:H2'	2.02	0.41
26:BA:1359:A:C2	26:BA:1372:U:C4	3.08	0.41
26:DA:1495:A:H2'	26:DA:1496:A:C8	2.55	0.41
27:DB:90:A:C5	27:DB:91:C:H1'	2.56	0.41
1:AA:1250:A:C2	1:AA:1370:G:H1'	2.55	0.41
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	2.03	0.41
26:BA:271(S):G:H2'	26:BA:271(T):C:O4'	2.21	0.41
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.56	0.41
36:BP:58:THR:O	36:BP:62:LEU:HG	2.21	0.41
26:DA:1124:C:H1'	56:D9:36:GLN:NE2	2.36	0.41
1:CA:552:U:O2	12:CL:31:PRO:HB3	2.21	0.41
34:DN:62:VAL:CG1	34:DN:66:LYS:HB2	2.50	0.41
1:AA:1298:C:H4'	1:AA:1299:A:C4	2.55	0.41
30:BF:33:LEU:HA	30:BF:33:LEU:HD12	1.92	0.41
1:CA:1068:G:N3	1:CA:1191:A:C2	2.89	0.41
26:DA:974:G:C6	26:DA:1186:G:C6	3.09	0.41
1:CA:861:G:HO2'	1:CA:874:G:HO2'	1.68	0.41
26:BA:1230:C:H2'	26:BA:1231:G:C8	2.55	0.41
1:CA:1056:U:H4'	3:CC:163:ALA:HB2	2.02	0.41
1:CA:1410:G:H2'	1:CA:1411:C:C6	2.56	0.41
32:BH:3:ARG:NE	32:BH:3:ARG:HA	2.34	0.41
38:DR:24:GLN:HE22	38:DR:36:THR:HG21	1.86	0.41
1:CA:1352:C:N4	1:CA:1370:G:H1	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:74:LEU:HG	16:AP:79:VAL:HG21	2.03	0.41
26:BA:324:A:N6	26:BA:338:G:O2'	2.49	0.41
1:AA:189(B):C:H2'	1:AA:189(C):C:C6	2.56	0.41
1:AA:451:A:H61	1:AA:480:U:H2'	1.85	0.41
26:DA:370:G:OP1	26:DA:403:U:N3	2.42	0.41
26:BA:973:A:C8	26:BA:1188:U:C2	3.08	0.41
8:AH:4:ASP:OD2	8:AH:85:ARG:NH1	2.54	0.41
45:BY:87:LYS:HB3	45:BY:95:LYS:HD3	2.03	0.41
26:DA:503:A:C5	26:DA:506:G:C6	3.08	0.41
44:BX:5:TYR:CE1	49:B2:30:ARG:HB2	2.55	0.41
26:BA:123:G:O3'	26:BA:1376:C:H4'	2.20	0.41
41:BU:86:ALA:O	42:BV:49:THR:HG23	2.21	0.41
1:AA:37:U:O2'	1:AA:547:A:N1	2.52	0.41
2:CB:158:LEU:HD12	2:CB:158:LEU:H	1.84	0.41
26:DA:1819:A:H5''	28:DD:161:THR:HG21	2.03	0.41
7:AG:74:GLU:HG2	7:AG:91:VAL:HG22	2.03	0.41
1:CA:527:G:O6	12:CL:49:ASN:ND2	2.53	0.41
26:DA:152:G:H2'	26:DA:153:C:C6	2.56	0.41
34:BN:23:LEU:HD12	34:BN:99:LEU:HD23	2.03	0.41
9:CI:32:ASP:HB3	9:CI:35:GLU:HG3	2.02	0.41
26:BA:471:A:H2'	26:BA:472:A:O4'	2.20	0.41
6:CF:76:ALA:O	6:CF:80:ARG:HG3	2.21	0.41
38:BR:74:LYS:HG2	38:BR:77:ARG:HH21	1.86	0.41
26:DA:1341:U:O2	44:DX:80:ILE:HD12	2.21	0.41
26:DA:1279:G:H2'	26:DA:1280:G:O4'	2.21	0.41
51:B4:28:LYS:HD3	51:B4:31:ILE:HD11	2.02	0.41
1:AA:942:G:C2	1:AA:1342:C:C2	3.09	0.41
26:BA:1805:U:O2	28:BD:50:THR:HB	2.21	0.41
7:CG:18:TYR:CG	7:CG:59:LEU:HD13	2.56	0.41
51:B4:6:HIS:HA	51:B4:7:PRO:HD3	1.95	0.41
26:DA:328:U:H4'	45:DY:68:HIS:CG	2.56	0.41
1:CA:667:G:O2'	15:CO:49:ASP:OD1	2.20	0.41
1:CA:1005:A:H2'	1:CA:1005:A:N3	2.35	0.41
1:CA:1022:G:H2'	1:CA:1023:G:H8	1.86	0.41
1:AA:1164:G:C2'	1:AA:1165:C:H5'	2.51	0.41
26:DA:2142:C:H2'	26:DA:2143:C:H6	1.83	0.41
1:CA:1291:G:C6	1:CA:1292:U:C4	3.08	0.41
26:BA:2168:G:O6	26:BA:2171:A:H8	2.03	0.41
1:CA:1155:G:N7	1:CA:1156:G:C5	2.89	0.41
26:DA:2126:A:C5	26:DA:2163:C:H1'	2.56	0.41
40:BT:95:ARG:HH11	40:BT:95:ARG:CG	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.56	0.41
26:DA:1140:C:O3'	34:DN:25:ARG:NH1	2.53	0.41
4:AD:155:LEU:HD23	4:AD:156:GLU:N	2.36	0.41
26:BA:245:G:O5'	36:BP:73:GLY:HA2	2.20	0.41
1:AA:350:G:O2'	1:AA:351:G:H5'	2.21	0.41
8:AH:21:LYS:HD2	8:AH:21:LYS:HA	1.85	0.41
33:DI:72:LEU:HD12	33:DI:138:ILE:HG22	2.03	0.41
26:DA:573:G:O2'	26:DA:574:C:H3'	2.20	0.41
1:CA:578:C:O2'	1:CA:728:A:N3	2.41	0.41
26:DA:82:G:O6	61:DA:4071:HOH:O	2.21	0.41
1:CA:502:G:H2'	1:CA:503:C:O4'	2.21	0.41
5:CE:93:PRO:HA	5:CE:118:ILE:HD12	2.02	0.41
2:AB:105:PHE:CZ	2:AB:155:LEU:HD12	2.55	0.41
26:DA:460:A:C2	26:DA:470:A:C4	3.09	0.41
1:CA:968:A:H8	1:CA:968:A:O5'	2.03	0.41
1:CA:60:A:N3	1:CA:61:G:H1'	2.36	0.41
1:CA:475:G:H2'	1:CA:476:G:C8	2.56	0.41
4:CD:112:VAL:HG13	4:CD:161:ASN:OD1	2.21	0.41
32:DH:70:THR:HG22	32:DH:74:ASN:HD21	1.86	0.41
30:DF:39:TRP:CG	30:DF:101:LEU:HB2	2.56	0.41
26:BA:1692:U:O2'	26:BA:1693:U:H2'	2.20	0.41
1:AA:1216:G:H5''	14:AN:5:ALA:HB2	2.03	0.41
31:BG:41:GLN:NE2	31:BG:153:ARG:HB3	2.34	0.41
18:CR:51:LEU:HA	18:CR:52:PRO:HD3	1.90	0.41
1:AA:1003:G:N3	1:AA:1004:A:H1'	2.36	0.41
40:DT:56:GLY:O	40:DT:59:THR:HG22	2.21	0.41
31:BG:14:GLU:O	31:BG:17:PRO:HD2	2.21	0.41
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.35	0.41
26:BA:2820:A:C6	38:BR:4:LEU:HD11	2.56	0.41
26:DA:2646:C:O5'	26:DA:2646:C:H6	2.04	0.41
1:CA:1325:C:O2'	1:CA:1326:C:H5'	2.20	0.41
1:AA:738:C:H2'	1:AA:739:C:H6	1.86	0.41
1:CA:764:C:H4'	15:CO:50:HIS:HB3	2.03	0.41
45:BY:54:LYS:HA	45:BY:55:TYR:HA	1.89	0.41
1:AA:407:G:N2	1:AA:436:C:C2	2.89	0.41
54:D7:9:ARG:HE	54:D7:47:ARG:HG3	1.86	0.41
1:AA:265:G:H5'	17:AQ:64:PRO:O	2.21	0.41
1:CA:1079:G:O3'	5:CE:14:ARG:NH2	2.54	0.41
1:AA:748:C:H1'	1:AA:749:C:OP2	2.20	0.41
1:CA:1381:U:H2'	1:CA:1382:C:H5'	2.03	0.41
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BR:38:VAL:HB	38:BR:39:PRO:HD3	2.02	0.41
26:DA:1820:U:C2	28:DD:202:LYS:HB3	2.55	0.41
2:AB:211:ILE:HG13	2:AB:211:ILE:H	1.66	0.41
1:CA:1249:C:O2'	9:CI:73:GLN:NE2	2.54	0.41
1:CA:949:A:C6	1:CA:950:U:C4	3.09	0.41
1:CA:266:G:H8	1:CA:266:G:H2'	1.62	0.41
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.85	0.41
42:BV:65:GLY:HA3	42:BV:91:TYR:CZ	2.56	0.41
13:CM:50:GLU:O	13:CM:54:VAL:HG13	2.21	0.41
51:D4:34:GLU:OE2	51:D4:35:VAL:HG12	2.20	0.41
26:BA:1527:G:H5''	26:BA:1528:A:OP1	2.20	0.41
16:AP:8:ARG:NH2	16:AP:15:PRO:HG3	2.35	0.41
9:AI:4:TYR:CE2	9:AI:88:TYR:HA	2.56	0.41
26:DA:45:C:H2'	26:DA:47:C:H6	1.86	0.41
3:AC:87:LEU:O	3:AC:91:LEU:N	2.30	0.41
39:BS:20:ARG:NH2	47:B0:48:GLY:O	2.54	0.41
10:CJ:11:PHE:HE1	10:CJ:67:THR:HB	1.85	0.41
2:CB:91:PRO:HG3	2:CB:154:LEU:HD12	2.03	0.41
26:BA:2760:C:H2'	26:BA:2761:G:H5''	2.02	0.41
54:D7:22:MET:HA	54:D7:28:ARG:HG2	2.03	0.41
8:AH:104:ARG:HG3	8:AH:138:TRP:CD2	2.56	0.41
1:CA:192:U:O2'	20:CT:60:GLU:OE2	2.22	0.41
9:CI:100:GLY:O	9:CI:103:THR:HG22	2.21	0.41
3:CC:24:ALA:HB1	3:CC:28:GLN:O	2.20	0.41
26:BA:2516:G:C6	26:BA:2517:C:C4	3.09	0.41
17:AQ:10:VAL:HG13	17:AQ:19:VAL:HB	2.02	0.41
26:BA:2080:G:OP1	48:B1:35:THR:HG21	2.20	0.41
26:DA:1906:G:C8	26:DA:1929:G:H2'	2.55	0.41
1:CA:945:G:C2	1:CA:946:A:C8	3.09	0.41
48:B1:95:LEU:HA	48:B1:95:LEU:HD12	1.87	0.41
33:BI:43:ASN:C	33:BI:43:ASN:HD22	2.24	0.41
1:AA:1263:C:H2'	1:AA:1264:C:C6	2.56	0.41
26:BA:2516:G:C5	26:BA:2517:C:C4	3.09	0.41
30:DF:31:HIS:HB2	36:DP:9:ASN:OD1	2.21	0.41
33:DI:114:LEU:HD11	33:DI:128:LEU:HD13	2.02	0.41
1:CA:522:C:H5''	12:CL:120:TYR:OH	2.21	0.41
11:AK:20:TYR:O	11:AK:30:VAL:HA	2.21	0.41
1:AA:472:A:H5''	16:AP:80:PHE:HB3	2.02	0.41
26:DA:2693:A:C2	26:DA:2694:G:C8	3.09	0.41
19:AS:36:ARG:HD2	19:AS:52:TYR:O	2.21	0.41
5:CE:135:THR:O	5:CE:139:LEU:HG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CE:106:PRO:HB3	5:CE:135:THR:OG1	2.20	0.41
2:AB:101:MET:HA	2:AB:108:ILE:HD12	2.02	0.41
26:DA:2563:U:H4'	35:DO:28:SER:HA	2.02	0.41
1:CA:1194:U:H4'	5:CE:22:GLY:O	2.21	0.41
26:BA:1395:A:C6	26:BA:1398:C:C2	3.09	0.41
29:DE:141:ILE:O	29:DE:154:LYS:HE2	2.21	0.41
29:BE:170:LEU:HB3	29:BE:184:VAL:HG22	2.02	0.41
26:BA:2347:C:H2'	26:BA:2348:U:C6	2.55	0.41
33:BI:12:LEU:HD23	33:BI:12:LEU:HA	1.79	0.41
48:B1:97:LEU:HD23	48:B1:97:LEU:HA	1.86	0.41
31:DG:181:ARG:HE	31:DG:181:ARG:HB3	1.78	0.41
51:D4:61:ARG:O	51:D4:61:ARG:NE	2.53	0.41
38:DR:100:LEU:HA	38:DR:100:LEU:HD13	1.86	0.41
26:DA:2884:U:C4	26:DA:2885:C:C2	3.09	0.41
26:DA:735:A:N7	26:DA:761:A:H2	2.18	0.41
30:BF:60:SER:OG	30:BF:61:GLY:N	2.53	0.41
1:AA:691:G:P	11:AK:26:ASN:HD22	2.44	0.41
1:CA:77:G:C6	1:CA:78:G:C6	3.09	0.41
26:BA:2135:A:O5'	26:BA:2135:A:H8	2.04	0.41
26:BA:2162:G:C6	26:BA:2163:C:N4	2.89	0.41
40:BT:91:ARG:HH11	40:BT:120:ARG:NH1	2.19	0.41
26:DA:848:G:C2	26:DA:933:A:H1'	2.56	0.41
13:AM:3:ARG:HG3	13:AM:4:ILE:N	2.36	0.41
26:BA:2144:U:H2'	26:BA:2146:C:C5	2.56	0.41
1:CA:1221:G:H4'	19:CS:77:THR:OG1	2.21	0.41
1:CA:728:A:O4'	15:CO:54:ARG:NH2	2.54	0.41
13:AM:91:ARG:HA	13:AM:91:ARG:HD2	1.86	0.41
26:BA:952:G:OP1	37:BQ:16:ARG:NH2	2.54	0.41
15:AO:74:ASP:HA	15:AO:75:PRO:HD2	1.94	0.41
26:BA:1653:G:H4'	26:BA:1654:A:O5'	2.21	0.41
26:DA:565:C:C5	42:DV:78:LYS:HE3	2.56	0.41
1:AA:1024:G:H2'	1:AA:1025:U:H5'	2.02	0.41
26:DA:535:C:H2'	26:DA:536:A:O4'	2.21	0.41
6:CF:2:ARG:NE	6:CF:69:GLU:HG2	2.36	0.41
26:BA:874:G:H2'	26:BA:875:G:H5'	2.02	0.41
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.46	0.41
26:DA:2514:U:H2'	26:DA:2515:C:C6	2.56	0.41
2:AB:60:ASP:OD1	2:AB:64:ARG:NE	2.48	0.41
4:CD:92:VAL:O	4:CD:96:LEU:HD22	2.21	0.41
26:BA:1935:G:H1'	26:BA:1964:G:N2	2.35	0.41
26:DA:1232:G:H2'	26:DA:1233:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:223:A:N1	26:BA:407:G:O2'	2.37	0.41
34:DN:30:ILE:O	34:DN:34:LEU:HD22	2.21	0.41
1:AA:1409:C:H2'	1:AA:1410:G:C8	2.56	0.41
26:BA:809:G:C5	26:BA:810:U:C4	3.09	0.41
26:BA:2480:C:N4	26:BA:2481:G:C6	2.89	0.41
24:AX:12:G:H4'	26:BA:1908:C:O2	2.21	0.41
46:DZ:54:HIS:CG	46:DZ:101:PRO:HG3	2.56	0.41
1:AA:1019:C:H5'	1:AA:1019:C:H6	1.86	0.41
1:CA:751:U:O4'	15:CO:24:SER:HA	2.20	0.41
1:CA:698:G:C6	1:CA:699:C:C4	3.09	0.41
27:DB:59:A:H2'	27:DB:60:C:O4'	2.22	0.41
26:BA:1649:G:C6	26:BA:2009:G:C6	3.10	0.41
1:CA:1005:A:OP2	1:CA:1024:G:N1	2.54	0.40
1:CA:92:C:N4	1:CA:93:G:N7	2.68	0.40
26:BA:2116:G:N2	26:BA:2162:G:OP1	2.54	0.40
1:AA:1009:G:N2	1:AA:1020:U:O2	2.44	0.40
1:AA:78:G:C6	1:AA:91:C:N4	2.81	0.40
26:DA:2793:G:H2'	26:DA:2794:C:O4'	2.21	0.40
1:CA:1064:G:N2	1:CA:1190:G:H2'	2.36	0.40
26:BA:1530:C:HO2'	26:BA:1531:C:P	2.40	0.40
26:BA:1530:C:O2'	26:BA:1531:C:P	2.79	0.40
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.87	0.40
24:CX:60:U:H3'	24:CX:61:C:C6	2.56	0.40
1:CA:512:U:OP1	4:CD:46:LYS:HE2	2.21	0.40
1:CA:1524:C:H2'	1:CA:1525:G:O4'	2.21	0.40
26:BA:848:G:N3	26:BA:933:A:H1'	2.36	0.40
8:AH:51:VAL:HG12	8:AH:52:ASP:N	2.37	0.40
27:DB:73:A:C4	27:DB:105:A:C2	3.09	0.40
26:DA:2808:U:O2'	26:DA:2809:A:H5'	2.20	0.40
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.40	0.40
1:AA:1226:C:P	13:AM:91:ARG:HH12	2.44	0.40
28:BD:134:ARG:HG3	28:BD:135:PHE:CD2	2.56	0.40
1:CA:1368:G:OP2	9:CI:112:LYS:HG3	2.21	0.40
26:BA:958:U:HO2'	26:BA:959:A:P	2.43	0.40
1:CA:1304:G:C6	1:CA:1305:G:C6	3.09	0.40
26:DA:1914:C:H2'	26:DA:1915:U:H6	1.85	0.40
26:DA:565:C:H4'	26:DA:1253:A:C6	2.55	0.40
26:BA:253:C:OP2	55:B8:5:LYS:NZ	2.31	0.40
2:AB:231:GLU:HB2	2:AB:232:PRO:CD	2.50	0.40
1:AA:300:A:O2'	1:AA:564:C:O2	2.37	0.40
1:CA:221:C:H2'	1:CA:222:U:H6	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:686:G:N2	26:BA:788:A:H61	2.19	0.40
26:BA:2685:G:H5'	35:BO:68:GLU:CD	2.41	0.40
16:CP:20:VAL:HG21	16:CP:32:TYR:CD2	2.56	0.40
5:CE:41:VAL:HG22	5:CE:69:VAL:HG11	2.03	0.40
26:DA:2283:C:C2	26:DA:2389:G:C2	3.08	0.40
8:AH:14:ARG:O	8:AH:18:ARG:HD3	2.21	0.40
26:DA:2882:A:OP1	38:DR:96:ARG:NE	2.48	0.40
26:DA:1007:C:OP2	61:DA:4086:HOH:O	2.21	0.40
51:D4:34:GLU:H	51:D4:34:GLU:CD	2.24	0.40
39:BS:87:PHE:HB2	39:BS:112:PHE:CD2	2.56	0.40
1:AA:26:A:N6	1:AA:558:G:O2'	2.52	0.40
1:CA:355:C:H2'	1:CA:356:A:O4'	2.21	0.40
26:BA:2019:A:H5''	41:BU:27:LEU:HD12	2.02	0.40
35:DO:60:ALA:HB1	35:DO:84:ALA:HB1	2.04	0.40
54:D7:26:GLY:O	54:D7:30:VAL:HG23	2.22	0.40
26:BA:2533:A:H2'	26:BA:2534:A:O4'	2.20	0.40
43:DW:86:LEU:HA	43:DW:87:PRO:HD3	1.94	0.40
1:CA:97:G:N1	1:CA:98:G:C5	2.89	0.40
31:DG:60:LEU:HD13	31:DG:60:LEU:HA	1.89	0.40
26:BA:2129:C:N3	26:BA:2160:G:C2	2.89	0.40
1:CA:1120:G:C6	1:CA:1121:U:C4	3.08	0.40
26:DA:2125:G:N2	26:DA:2173:A:C8	2.86	0.40
9:CI:33:PHE:HZ	9:CI:46:ALA:HB3	1.86	0.40
26:DA:1533:G:C6	26:DA:1537:G:C6	3.09	0.40
1:CA:977:A:O3'	1:CA:980:C:N4	2.48	0.40
55:B8:7:HIS:HB3	55:B8:61:LEU:HB3	2.03	0.40
2:AB:90:MET:HA	2:AB:91:PRO:HD3	1.92	0.40
26:DA:2830:G:O2'	26:DA:2883:A:N1	2.41	0.40
12:AL:42:THR:HA	12:AL:53:ARG:O	2.22	0.40
1:CA:1517:G:H1'	26:DA:1919:A:O3'	2.21	0.40
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	2.03	0.40
12:CL:60:LEU:HD23	12:CL:66:VAL:HG22	2.02	0.40
26:DA:6:A:C2'	26:DA:7:G:H5'	2.50	0.40
6:CF:2:ARG:NH2	15:CO:2:PRO:HD2	2.34	0.40
26:DA:1188:U:C4'	42:DV:79:VAL:HG22	2.51	0.40
15:CO:50:HIS:O	15:CO:53:HIS:HB3	2.21	0.40
1:CA:636:U:H2'	1:CA:637:G:C8	2.55	0.40
1:CA:1107:C:C4	1:CA:1108:G:C8	3.09	0.40
26:DA:271(H):G:O6	26:DA:271(Q):G:C6	2.74	0.40
4:CD:175:SER:OG	4:CD:184:LYS:HB2	2.21	0.40
1:AA:16:A:N3	1:AA:1080:A:O2'	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1354:A:H5''	28:DD:38:LYS:HD3	2.02	0.40
1:AA:937:A:C2'	1:AA:938:A:H5'	2.51	0.40
8:CH:44:PHE:CE2	8:CH:109:ILE:HG12	2.55	0.40
1:CA:1342:C:H4'	9:CI:125:TYR:O	2.21	0.40
2:AB:18:GLY:HA3	2:AB:41:ILE:HD13	2.03	0.40
26:DA:311:A:C6	26:DA:328:U:C4	3.10	0.40
26:DA:979:G:H5''	26:DA:980:A:H5''	2.03	0.40
26:BA:732:C:H2'	26:BA:733:G:O4'	2.20	0.40
38:BR:109:ALA:HA	38:BR:110:PRO:HD2	1.92	0.40
26:BA:69:C:O2	26:BA:73:A:O2'	2.31	0.40
1:CA:1471:G:C2'	1:CA:1472:U:H5'	2.51	0.40
11:CK:48:ILE:O	11:CK:50:TYR:N	2.53	0.40
38:BR:29:LEU:HA	38:BR:29:LEU:HD12	1.82	0.40
1:CA:718:G:H5'	11:CK:117:ASN:ND2	2.36	0.40
26:BA:1512:U:H2'	26:BA:1513:C:C6	2.56	0.40
26:DA:2154:G:C2	26:DA:2155:G:N7	2.89	0.40
26:BA:2141:G:N1	26:BA:2142:C:O2	2.54	0.40
24:CX:6:G:C2	24:CX:68:C:C2	3.10	0.40
1:AA:347:G:C6	1:AA:348:G:C5	3.09	0.40
26:DA:1448:G:H5''	26:DA:1449:A:OP1	2.21	0.40
19:AS:69:HIS:N	51:B4:58:ARG:NH2	2.70	0.40
26:DA:1182:A:H2'	26:DA:1183:G:C8	2.56	0.40
26:BA:250:G:P	55:B8:13:ARG:NH2	2.95	0.40
2:AB:155:LEU:HD11	2:AB:159:PRO:HD3	2.03	0.40
26:BA:1815:A:H8	26:BA:1815:A:OP1	2.05	0.40
2:AB:126:GLU:HB3	2:AB:127:ILE:H	1.67	0.40
26:BA:467:G:O2'	26:BA:796:C:O2'	2.32	0.40
31:DG:97:ASP:HA	31:DG:100:TRP:HD1	1.87	0.40
26:BA:1569:A:H2'	26:BA:1570:A:O4'	2.21	0.40
26:DA:360:G:H2'	26:DA:361:G:H8	1.85	0.40
31:BG:10:LYS:HG3	31:BG:14:GLU:OE1	2.22	0.40
26:DA:975(A):G:H1'	26:DA:990:A:C2	2.57	0.40
26:DA:2263:C:H41	47:D0:15:ASP:HA	1.87	0.40
26:BA:1231:G:H2'	26:BA:1232:G:C8	2.56	0.40
15:AO:17:ARG:HD3	15:AO:26:GLU:CD	2.41	0.40
26:DA:1152:C:H2'	26:DA:1153:C:C6	2.57	0.40
8:CH:20:TYR:HA	8:CH:65:TYR:OH	2.21	0.40
26:BA:1791:A:C8	26:BA:1792:G:C8	3.09	0.40
26:BA:1791:A:OP2	26:BA:1791:A:H8	2.05	0.40
1:CA:636:U:O2'	1:CA:637:G:H5'	2.22	0.40
26:DA:2849:U:H4'	26:DA:2868:A:C2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DG:73:ALA:O	31:DG:84:LYS:HG3	2.21	0.40
1:CA:17:U:H2'	1:CA:18:C:H6	1.86	0.40
29:DE:120:TRP:CD1	29:DE:155:LYS:HB3	2.57	0.40
29:BE:181:LEU:HD12	29:BE:181:LEU:HA	1.83	0.40
1:CA:444:C:H2'	1:CA:445:G:C8	2.57	0.40
26:BA:2699:C:H2'	26:BA:2700:C:O4'	2.21	0.40
26:BA:868:U:C4	26:BA:869:G:N7	2.90	0.40
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	2.03	0.40
26:BA:755:C:H2'	26:BA:756:C:C6	2.56	0.40
1:CA:949:A:C5	1:CA:950:U:C4	3.10	0.40
26:DA:422:A:C6	26:DA:423:A:C6	3.10	0.40
1:CA:830:G:H2'	1:CA:831:U:O4'	2.21	0.40
26:DA:2099:U:H2'	26:DA:2100:G:H8	1.86	0.40
10:CJ:43:ARG:HB2	10:CJ:67:THR:HG23	2.04	0.40
53:B6:10:LEU:HG	53:B6:54:ILE:HG13	2.01	0.40
30:DF:37:VAL:O	30:DF:41:LEU:HG	2.21	0.40
26:BA:1194:A:H2'	26:BA:1195:G:O4'	2.22	0.40
1:AA:582:U:H2'	1:AA:583:A:C8	2.57	0.40
32:DH:42:ARG:HD3	32:DH:44:VAL:HG23	2.04	0.40
1:CA:120:A:C6	1:CA:122:G:C2	3.09	0.40
26:DA:638:G:H2'	26:DA:639:U:O4'	2.21	0.40
26:DA:453:C:H5''	61:DA:4438:HOH:O	2.20	0.40
48:B1:17:SER:HB2	48:B1:40:ARG:HG2	2.02	0.40
47:B0:50:ASN:HB3	47:B0:63:VAL:HG22	2.03	0.40
39:DS:43:GLU:OE1	47:D0:49:LYS:NZ	2.31	0.40
45:BY:34:LYS:HG2	45:BY:34:LYS:O	2.21	0.40
24:AX:43:A:H2'	24:AX:44:A:C8	2.57	0.40
17:AQ:32:TYR:O	17:AQ:34:LYS:N	2.54	0.40
3:CC:112:SER:O	3:CC:116:VAL:HG23	2.21	0.40
26:BA:435:C:H2'	26:BA:436:C:H5'	2.03	0.40
1:AA:1368:G:C2'	1:AA:1369:C:H5'	2.51	0.40
4:AD:88:VAL:HG22	5:AE:97:GLY:HA2	2.04	0.40
1:AA:1174:G:H5''	1:AA:1174:G:H8	1.87	0.40
26:DA:2141:G:H2'	26:DA:2142:C:O4'	2.21	0.40
26:DA:2151:G:N3	26:DA:2152:G:C8	2.89	0.40
26:DA:2104:G:O2'	26:DA:2105:C:O4'	2.36	0.40
26:BA:2127:G:H1'	26:BA:2173:A:C2	2.56	0.40
26:DA:1203:G:H2'	26:DA:1241:A:N6	2.37	0.40
51:B4:57:GLU:OE2	51:B4:58:ARG:HG3	2.21	0.40
26:DA:2723:C:P	29:DE:109:LYS:HZ3	2.44	0.40
26:BA:2317:C:H2'	26:BA:2318:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1210:A:H4'	26:BA:1211:U:O5'	2.21	0.40
26:BA:2393:A:O2'	36:BP:60:MET:O	2.32	0.40
13:CM:33:ALA:HA	13:CM:59:TYR:CE2	2.56	0.40
1:AA:875:C:C4	1:AA:876:G:N7	2.90	0.40
27:DB:16:G:O6	27:DB:66:A:H2	2.04	0.40
26:BA:196:A:H2'	26:BA:196:A:N3	2.36	0.40
39:DS:11:LYS:HD2	39:DS:15:ARG:NH1	2.37	0.40
26:BA:528:A:C2	26:BA:2043:C:H5'	2.56	0.40
26:DA:660:G:C6	26:DA:661:C:C4	3.10	0.40
24:CX:22:G:H2'	24:CX:23:C:H6	1.86	0.40
26:DA:466:A:H1'	26:DA:683:C:O4'	2.20	0.40
26:BA:531:C:H4'	26:BA:532:A:H5''	2.03	0.40
1:CA:1409:C:H2'	1:CA:1410:G:H8	1.85	0.40
26:BA:469:G:O6	54:B7:37:LYS:HE2	2.21	0.40
1:CA:1106:G:C6	1:CA:1107:C:C4	3.09	0.40
30:DF:34:TRP:CZ2	36:DP:8:PRO:HG3	2.57	0.40
1:AA:265:G:N2	1:AA:267:C:H5'	2.37	0.40
26:DA:183:C:C2'	26:DA:184:C:H5'	2.51	0.40
26:DA:1790:C:H2'	26:DA:1791:A:C5	2.56	0.40
29:DE:119:ARG:HH11	29:DE:119:ARG:HD3	1.77	0.40
1:AA:428:G:H4'	1:AA:429:U:O5'	2.21	0.40
31:DG:107:LEU:HD21	31:DG:178:PHE:CE1	2.56	0.40
7:AG:26:PHE:CE2	7:AG:30:ILE:HD11	2.57	0.40
27:BB:96:U:H2'	27:BB:97:G:C8	2.56	0.40
38:DR:70:LEU:HD13	38:DR:75:LEU:HD13	2.03	0.40
26:DA:873:G:H1	26:DA:904:C:N4	2.19	0.40
32:BH:11:VAL:HG21	32:BH:50:VAL:HG23	2.03	0.40
26:DA:2093:G:C6	26:DA:2225:A:C8	3.10	0.40
26:BA:2051:A:H4'	29:BE:141:ILE:HG12	2.03	0.40
26:BA:255:A:H1'	26:BA:384:U:C6	2.57	0.40
31:BG:126:ASP:HB2	31:BG:130:ASN:HB2	2.04	0.40
26:DA:260:G:C6	26:DA:261:G:C8	3.09	0.40
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.21	0.40
50:D3:19:GLN:O	50:D3:23:LEU:HD22	2.22	0.40
49:B2:29:LYS:HG2	49:B2:57:ILE:HD13	2.02	0.40
10:AJ:81:THR:HA	10:AJ:84:GLN:HB3	2.03	0.40
39:DS:35:ILE:HG22	39:DS:53:SER:HB3	2.04	0.40
26:BA:128:C:H2'	26:BA:129:C:O4'	2.22	0.40
26:BA:1052:C:H6	26:BA:1052:C:O5'	2.04	0.40
51:B4:48:ARG:HA	51:B4:48:ARG:CZ	2.52	0.40
14:CN:6:LEU:HA	14:CN:6:LEU:HD12	1.95	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CO:48:LYS:HD3	15:CO:48:LYS:HA	1.83	0.40
7:CG:52:GLU:H	7:CG:52:GLU:HG2	1.69	0.40
26:DA:2286:A:N3	26:DA:2286:A:H2'	2.36	0.40
4:CD:168:ARG:H	4:CD:168:ARG:HG2	1.65	0.40
43:BW:33:ARG:NE	43:BW:52:GLU:OE1	2.50	0.40
37:DQ:17:LEU:HD21	37:DQ:96:VAL:HG13	2.03	0.40
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.87	0.40
26:DA:786:C:H5''	26:DA:1780:A:N7	2.36	0.40
1:CA:1025:U:C4	1:CA:1036:G:O6	2.75	0.40
1:CA:1392:G:N2	1:CA:1502:A:H8	2.18	0.40
1:CA:1125:U:O2'	1:CA:1126:U:C2'	2.68	0.40
1:AA:146:G:C2	1:AA:147:G:C4	3.10	0.40
4:CD:46:LYS:O	4:CD:47:ARG:HB3	2.22	0.40
35:BO:101:PRO:HG3	40:BT:67:SER:OG	2.22	0.40
50:B3:10:LYS:HB3	50:B3:53:LEU:HA	2.04	0.40
26:DA:452:G:C4	26:DA:458:G:C6	3.09	0.40
26:BA:1674:G:H1'	26:BA:1676:A:N6	2.35	0.40
1:CA:538:G:H5''	12:CL:114:LYS:HB2	2.03	0.40
35:DO:63:VAL:HB	35:DO:102:VAL:HG12	2.03	0.40
27:DB:108:U:H5'	27:DB:109:C:OP2	2.22	0.40
26:DA:2298:A:H2	26:DA:2321:G:C5	2.39	0.40
37:BQ:12:GLN:HG2	37:BQ:73:PRO:HD2	2.03	0.40
1:AA:1531:A:H2'	1:AA:1532:U:C4	2.56	0.40
26:BA:780:G:H1'	26:BA:785:G:C2	2.56	0.40
26:DA:729:G:H2'	26:DA:1775:U:O2	2.20	0.40
26:BA:117:G:OP2	26:BA:119:A:O2'	2.33	0.40
4:AD:86:LYS:HG2	4:AD:86:LYS:H	1.61	0.40
26:DA:1598:C:H2'	26:DA:1599:C:C6	2.57	0.40
32:BH:117:PRO:HG3	32:BH:123:PHE:CD2	2.56	0.40
26:DA:300:A:OP1	45:DY:86:ARG:NH2	2.52	0.40
1:CA:485:G:O2'	1:CA:486:U:OP2	2.39	0.40
26:BA:26:G:H1'	26:BA:515:A:H61	1.86	0.40
37:DQ:76:LYS:HB3	37:DQ:91:GLU:HG3	2.03	0.40
26:BA:2651:C:H2'	26:BA:2652:C:H6	1.85	0.40
55:B8:39:LYS:HA	55:B8:42:ARG:NH1	2.37	0.40
1:AA:715:A:H1'	1:AA:777:A:N1	2.35	0.40
44:DX:12:VAL:HG22	44:DX:29:TRP:CE2	2.57	0.40
20:AT:36:LEU:HA	20:AT:36:LEU:HD23	1.84	0.40
26:DA:996:A:N6	26:DA:1160:G:C6	2.89	0.40
43:DW:86:LEU:HD22	43:DW:96:ILE:HD11	2.04	0.40
26:BA:438:G:H2'	26:BA:440:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:D4:18:CYS:HB3	51:D4:39:CYS:HB3	2.04	0.40
26:DA:2623:G:H4'	26:DA:2825:C:O2	2.22	0.40
30:BF:183:VAL:O	30:BF:187:VAL:HG23	2.21	0.40
37:BQ:104:PHE:HE2	37:BQ:125:LEU:HD11	1.87	0.40
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.21	0.40
39:BS:41:ASP:HB2	39:BS:48:LEU:HD21	2.03	0.40
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.52	0.40
34:DN:75:TYR:CE2	34:DN:77:GLY:HA2	2.56	0.40
9:AI:97:LYS:HB3	9:AI:98:PRO:HD3	2.04	0.40
38:BR:87:TYR:OH	38:BR:116:LEU:HB3	2.21	0.40
1:AA:1060:C:P	14:AN:45:ARG:HH22	2.44	0.40
49:B2:48:HIS:CE1	49:B2:49:LYS:HG3	2.57	0.40
29:BE:35:GLN:OE1	29:BE:66:HIS:HE1	2.05	0.40
26:DA:1002:G:H2'	26:DA:1003:G:O4'	2.21	0.40
16:AP:60:LEU:HA	16:AP:60:LEU:HD13	1.83	0.40
33:DI:44:LEU:HA	33:DI:44:LEU:HD13	1.92	0.40
3:AC:115:LEU:HA	3:AC:115:LEU:HD12	1.88	0.40
47:D0:27:GLU:HG3	47:D0:68:GLU:HA	2.04	0.40
26:DA:959:A:N3	26:DA:2457:U:O2'	2.47	0.40
37:BQ:37:LEU:HD21	37:BQ:130:LYS:HE2	2.04	0.40
26:BA:1168:G:O2'	26:BA:1169:G:H5'	2.22	0.40
32:DH:150:ALA:HA	32:DH:153:LYS:HG3	2.02	0.40
26:BA:2001:A:H2'	26:BA:2002:G:C8	2.56	0.40

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

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

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	229/256 (90%)	204 (89%)	21 (9%)	4 (2%)	11	36
2	CB	229/256 (90%)	204 (89%)	14 (6%)	11 (5%)	3	9
3	AC	204/239 (85%)	189 (93%)	13 (6%)	2 (1%)	19	52
3	CC	204/239 (85%)	188 (92%)	15 (7%)	1 (0%)	34	69
4	AD	206/209 (99%)	198 (96%)	7 (3%)	1 (0%)	34	69
4	CD	206/209 (99%)	196 (95%)	7 (3%)	3 (2%)	13	40
5	AE	146/162 (90%)	136 (93%)	9 (6%)	1 (1%)	26	62
5	CE	146/162 (90%)	135 (92%)	10 (7%)	1 (1%)	26	62
6	AF	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
6	CF	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
7	AG	153/156 (98%)	143 (94%)	7 (5%)	3 (2%)	9	30
7	CG	153/156 (98%)	143 (94%)	9 (6%)	1 (1%)	26	62
8	AH	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
8	CH	135/138 (98%)	130 (96%)	4 (3%)	1 (1%)	26	62
9	AI	125/128 (98%)	118 (94%)	7 (6%)	0	100	100
9	CI	125/128 (98%)	118 (94%)	6 (5%)	1 (1%)	24	58
10	AJ	95/105 (90%)	83 (87%)	5 (5%)	7 (7%)	1	3
10	CJ	94/105 (90%)	83 (88%)	6 (6%)	5 (5%)	2	7
11	AK	112/129 (87%)	106 (95%)	5 (4%)	1 (1%)	21	55
11	CK	112/129 (87%)	105 (94%)	6 (5%)	1 (1%)	21	55
12	AL	120/132 (91%)	116 (97%)	4 (3%)	0	100	100
12	CL	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
13	AM	121/126 (96%)	113 (93%)	6 (5%)	2 (2%)	11	36
13	CM	120/126 (95%)	110 (92%)	9 (8%)	1 (1%)	24	58
14	AN	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
14	CN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
15	AO	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
15	CO	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	AP	80/88 (91%)	75 (94%)	5 (6%)	0	100	100
16	CP	80/88 (91%)	76 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	AQ	97/105 (92%)	90 (93%)	7 (7%)	0	100	100
17	CQ	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
18	AR	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
18	CR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
19	AS	81/93 (87%)	70 (86%)	11 (14%)	0	100	100
19	CS	81/93 (87%)	71 (88%)	8 (10%)	2 (2%)	7	24
20	AT	94/106 (89%)	85 (90%)	3 (3%)	6 (6%)	2	4
20	CT	94/106 (89%)	84 (89%)	6 (6%)	4 (4%)	3	10
21	AU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
21	CU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
28	BD	273/276 (99%)	263 (96%)	9 (3%)	1 (0%)	39	74
28	DD	273/276 (99%)	261 (96%)	10 (4%)	2 (1%)	26	62
29	BE	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	34	69
29	DE	202/206 (98%)	193 (96%)	7 (4%)	2 (1%)	19	52
30	BF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	34	69
30	DF	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	19	52
31	BG	179/182 (98%)	166 (93%)	9 (5%)	4 (2%)	8	28
31	DG	179/182 (98%)	166 (93%)	9 (5%)	4 (2%)	8	28
32	BH	172/180 (96%)	161 (94%)	9 (5%)	2 (1%)	16	47
32	DH	172/180 (96%)	163 (95%)	7 (4%)	2 (1%)	16	47
33	BI	144/148 (97%)	132 (92%)	9 (6%)	3 (2%)	9	29
33	DI	144/148 (97%)	130 (90%)	12 (8%)	2 (1%)	14	42
34	BN	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
34	DN	138/140 (99%)	132 (96%)	5 (4%)	1 (1%)	26	62
35	BO	120/122 (98%)	114 (95%)	5 (4%)	1 (1%)	24	58
35	DO	120/122 (98%)	115 (96%)	4 (3%)	1 (1%)	24	58
36	BP	147/150 (98%)	138 (94%)	8 (5%)	1 (1%)	26	62
36	DP	147/150 (98%)	133 (90%)	13 (9%)	1 (1%)	26	62
37	BQ	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
37	DQ	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
38	BR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	DR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
39	BS	108/112 (96%)	104 (96%)	4 (4%)	0	100	100
39	DS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	21	55
40	BT	129/146 (88%)	121 (94%)	8 (6%)	0	100	100
40	DT	129/146 (88%)	125 (97%)	3 (2%)	1 (1%)	24	58
41	BU	114/118 (97%)	114 (100%)	0	0	100	100
41	DU	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
42	BV	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	19	52
42	DV	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	19	52
43	BW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
43	DW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
44	BX	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
44	DX	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
45	BY	105/110 (96%)	95 (90%)	10 (10%)	0	100	100
45	DY	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
46	BZ	169/206 (82%)	148 (88%)	19 (11%)	2 (1%)	16	47
46	DZ	172/206 (84%)	156 (91%)	14 (8%)	2 (1%)	16	47
47	B0	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
47	D0	81/85 (95%)	77 (95%)	4 (5%)	0	100	100
48	B1	95/98 (97%)	94 (99%)	0	1 (1%)	17	50
48	D1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	17	50
49	B2	68/72 (94%)	68 (100%)	0	0	100	100
49	D2	68/72 (94%)	68 (100%)	0	0	100	100
50	B3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
50	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
51	B4	67/71 (94%)	54 (81%)	8 (12%)	5 (8%)	1	3
51	D4	67/71 (94%)	53 (79%)	10 (15%)	4 (6%)	2	5
52	B5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
52	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
53	B6	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
53	D6	51/54 (94%)	50 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	B7	46/49 (94%)	46 (100%)	0	0	100	100
54	D7	46/49 (94%)	45 (98%)	0	1 (2%)	8	28
55	B8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
55	D8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
56	B9	35/37 (95%)	35 (100%)	0	0	100	100
56	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11409/12128 (94%)	10783 (94%)	516 (4%)	110 (1%)	19	52

All (110) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	231	GLU
4	AD	166	LYS
7	AG	80	VAL
10	AJ	55	LYS
20	AT	10	LEU
28	BD	275	LYS
30	BF	130	ALA
31	BG	49	ASP
31	BG	51	ARG
32	BH	92	ILE
46	BZ	152	ALA
51	B4	62	ARG
2	CB	8	LYS
2	CB	16	HIS
2	CB	20	GLU
2	CB	126	GLU
9	CI	54	ASP
13	CM	85	GLY
20	CT	99	LEU
30	DF	21	ALA
30	DF	130	ALA
31	DG	81	LYS
33	DI	10	GLU
36	DP	29	LYS
48	D1	3	LYS
51	D4	39	CYS
51	D4	62	ARG
54	D7	46	VAL
10	AJ	31	GLY

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Mol	Chain	Res	Type
10	AJ	56	HIS
10	AJ	77	PRO
11	AK	49	GLY
20	AT	47	GLY
20	AT	68	LYS
20	AT	96	GLY
48	B1	3	LYS
51	B4	45	GLY
51	B4	65	ASP
2	CB	17	PHE
2	CB	121	LEU
2	CB	128	GLU
4	CD	47	ARG
4	CD	167	GLY
7	CG	7	ALA
10	CJ	79	ARG
20	CT	47	GLY
31	DG	43	LEU
32	DH	47	GLU
33	DI	81	VAL
40	DT	100	TYR
51	D4	45	GLY
10	AJ	79	ARG
10	AJ	91	PRO
29	BE	52	LEU
31	BG	43	LEU
46	BZ	114	GLY
2	CB	122	PHE
10	CJ	77	PRO
10	CJ	78	ASN
19	CS	12	ASP
19	CS	65	ASN
20	CT	102	GLY
28	DD	239	ARG
29	DE	52	LEU
29	DE	73	GLU
31	DG	32	PRO
46	DZ	101	PRO
5	AE	85	GLY
7	AG	6	ARG
7	AG	81	GLY
13	AM	67	GLU

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Mol	Chain	Res	Type
20	AT	102	GLY
31	BG	32	PRO
35	BO	5	GLN
36	BP	29	LYS
51	B4	58	ARG
2	CB	10	LEU
2	CB	78	GLN
20	CT	95	ALA
28	DD	3	VAL
31	DG	51	ARG
32	DH	126	PRO
34	DN	2	LYS
35	DO	5	GLN
39	DS	84	GLN
51	D4	38	LYS
3	AC	181	ASN
20	AT	100	ILE
32	BH	47	GLU
33	BI	107	VAL
51	B4	57	GLU
2	CB	231	GLU
4	CD	46	LYS
5	CE	69	VAL
2	AB	78	GLN
13	AM	4	ILE
33	BI	73	GLU
8	CH	73	ASP
3	AC	66	VAL
10	AJ	75	ILE
42	BV	79	VAL
10	CJ	75	ILE
42	DV	79	VAL
33	BI	119	PRO
3	CC	108	ASN
10	CJ	91	PRO
2	AB	124	SER
2	AB	125	PRO
11	CK	49	GLY
46	DZ	114	GLY

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	192/220 (87%)	161 (84%)	31 (16%)	3	9
2	CB	187/220 (85%)	161 (86%)	26 (14%)	4	13
3	AC	143/188 (76%)	131 (92%)	12 (8%)	14	37
3	CC	140/188 (74%)	127 (91%)	13 (9%)	11	32
4	AD	170/181 (94%)	153 (90%)	17 (10%)	9	27
4	CD	173/181 (96%)	157 (91%)	16 (9%)	11	32
5	AE	113/123 (92%)	106 (94%)	7 (6%)	23	54
5	CE	114/123 (93%)	105 (92%)	9 (8%)	15	40
6	AF	83/90 (92%)	78 (94%)	5 (6%)	24	56
6	CF	85/90 (94%)	79 (93%)	6 (7%)	18	46
7	AG	119/127 (94%)	107 (90%)	12 (10%)	9	27
7	CG	120/127 (94%)	108 (90%)	12 (10%)	9	27
8	AH	114/119 (96%)	109 (96%)	5 (4%)	35	69
8	CH	114/119 (96%)	106 (93%)	8 (7%)	19	47
9	AI	90/99 (91%)	76 (84%)	14 (16%)	3	9
9	CI	89/99 (90%)	78 (88%)	11 (12%)	6	17
10	AJ	66/92 (72%)	60 (91%)	6 (9%)	12	33
10	CJ	69/92 (75%)	63 (91%)	6 (9%)	13	35
11	AK	82/99 (83%)	76 (93%)	6 (7%)	17	44
11	CK	83/99 (84%)	79 (95%)	4 (5%)	31	66
12	AL	97/109 (89%)	91 (94%)	6 (6%)	23	54
12	CL	97/109 (89%)	94 (97%)	3 (3%)	47	81
13	AM	93/101 (92%)	82 (88%)	11 (12%)	6	19
13	CM	92/101 (91%)	81 (88%)	11 (12%)	6	19
14	AN	49/50 (98%)	43 (88%)	6 (12%)	6	18
14	CN	49/50 (98%)	43 (88%)	6 (12%)	6	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	AO	78/80 (98%)	66 (85%)	12 (15%)	3	10
15	CO	78/80 (98%)	70 (90%)	8 (10%)	9	26
16	AP	69/74 (93%)	60 (87%)	9 (13%)	5	15
16	CP	68/74 (92%)	62 (91%)	6 (9%)	12	35
17	AQ	94/97 (97%)	91 (97%)	3 (3%)	46	80
17	CQ	94/97 (97%)	87 (93%)	7 (7%)	17	43
18	AR	59/77 (77%)	54 (92%)	5 (8%)	13	36
18	CR	59/77 (77%)	54 (92%)	5 (8%)	13	36
19	AS	69/80 (86%)	61 (88%)	8 (12%)	7	20
19	CS	67/80 (84%)	62 (92%)	5 (8%)	17	43
20	AT	70/82 (85%)	60 (86%)	10 (14%)	4	12
20	CT	70/82 (85%)	63 (90%)	7 (10%)	9	27
21	AU	18/22 (82%)	16 (89%)	2 (11%)	8	23
21	CU	18/22 (82%)	17 (94%)	1 (6%)	26	59
28	BD	215/218 (99%)	201 (94%)	14 (6%)	21	52
28	DD	215/218 (99%)	200 (93%)	15 (7%)	19	47
29	BE	164/166 (99%)	144 (88%)	20 (12%)	6	18
29	DE	164/166 (99%)	147 (90%)	17 (10%)	9	25
30	BF	160/166 (96%)	145 (91%)	15 (9%)	11	31
30	DF	159/166 (96%)	146 (92%)	13 (8%)	14	38
31	BG	143/156 (92%)	128 (90%)	15 (10%)	8	24
31	DG	142/156 (91%)	122 (86%)	20 (14%)	4	12
32	BH	144/148 (97%)	138 (96%)	6 (4%)	36	71
32	DH	144/148 (97%)	132 (92%)	12 (8%)	14	38
33	BI	110/124 (89%)	90 (82%)	20 (18%)	2	6
33	DI	104/124 (84%)	87 (84%)	17 (16%)	3	8
34	BN	118/119 (99%)	103 (87%)	15 (13%)	5	16
34	DN	118/119 (99%)	108 (92%)	10 (8%)	13	36
35	BO	100/100 (100%)	94 (94%)	6 (6%)	24	56
35	DO	100/100 (100%)	96 (96%)	4 (4%)	38	73
36	BP	115/116 (99%)	105 (91%)	10 (9%)	13	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	DP	115/116 (99%)	103 (90%)	12 (10%)	9	25
37	BQ	111/111 (100%)	100 (90%)	11 (10%)	10	28
37	DQ	111/111 (100%)	100 (90%)	11 (10%)	10	28
38	BR	101/101 (100%)	82 (81%)	19 (19%)	2	6
38	DR	101/101 (100%)	84 (83%)	17 (17%)	2	8
39	BS	87/88 (99%)	79 (91%)	8 (9%)	11	32
39	DS	85/88 (97%)	75 (88%)	10 (12%)	6	19
40	BT	115/127 (91%)	106 (92%)	9 (8%)	16	41
40	DT	113/127 (89%)	103 (91%)	10 (9%)	12	35
41	BU	93/94 (99%)	86 (92%)	7 (8%)	17	43
41	DU	93/94 (99%)	88 (95%)	5 (5%)	27	60
42	BV	80/82 (98%)	68 (85%)	12 (15%)	3	11
42	DV	80/82 (98%)	72 (90%)	8 (10%)	9	27
43	BW	90/92 (98%)	84 (93%)	6 (7%)	20	50
43	DW	90/92 (98%)	82 (91%)	8 (9%)	12	34
44	BX	77/78 (99%)	74 (96%)	3 (4%)	39	74
44	DX	77/78 (99%)	72 (94%)	5 (6%)	21	52
45	BY	85/91 (93%)	77 (91%)	8 (9%)	11	31
45	DY	85/91 (93%)	78 (92%)	7 (8%)	14	38
46	BZ	145/179 (81%)	131 (90%)	14 (10%)	10	29
46	DZ	145/179 (81%)	127 (88%)	18 (12%)	6	17
47	B0	65/67 (97%)	62 (95%)	3 (5%)	33	67
47	D0	65/67 (97%)	62 (95%)	3 (5%)	33	67
48	B1	80/83 (96%)	72 (90%)	8 (10%)	9	27
48	D1	80/83 (96%)	73 (91%)	7 (9%)	12	35
49	B2	65/67 (97%)	56 (86%)	9 (14%)	4	13
49	D2	65/67 (97%)	59 (91%)	6 (9%)	11	32
50	B3	51/52 (98%)	45 (88%)	6 (12%)	6	19
50	D3	50/52 (96%)	47 (94%)	3 (6%)	24	56
51	B4	59/63 (94%)	47 (80%)	12 (20%)	1	4
51	D4	53/63 (84%)	46 (87%)	7 (13%)	5	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	B5	50/52 (96%)	48 (96%)	2 (4%)	38	73
52	D5	50/52 (96%)	48 (96%)	2 (4%)	38	73
53	B6	51/52 (98%)	44 (86%)	7 (14%)	4	13
53	D6	50/52 (96%)	48 (96%)	2 (4%)	38	73
54	B7	41/42 (98%)	38 (93%)	3 (7%)	17	44
54	D7	41/42 (98%)	38 (93%)	3 (7%)	17	44
55	B8	53/55 (96%)	49 (92%)	4 (8%)	17	43
55	D8	54/55 (98%)	53 (98%)	1 (2%)	65	91
56	B9	34/34 (100%)	31 (91%)	3 (9%)	12	35
56	D9	34/34 (100%)	33 (97%)	1 (3%)	50	83
All	All	9319/10066 (93%)	8433 (90%)	886 (10%)	11	30

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

Mol	Chain	Res	Type
2	AB	8	LYS
2	AB	11	LEU
2	AB	17	PHE
2	AB	20	GLU
2	AB	21	ARG
2	AB	24	TRP
2	AB	80	ILE
2	AB	81	VAL
2	AB	96	ARG
2	AB	108	ILE
2	AB	114	ARG
2	AB	124	SER
2	AB	127	ILE
2	AB	142	LEU
2	AB	145	LEU
2	AB	155	LEU
2	AB	156	LYS
2	AB	157	ARG
2	AB	169	LYS
2	AB	170	GLU
2	AB	185	ILE
2	AB	187	LEU
2	AB	189	ASP

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Mol	Chain	Res	Type
2	AB	200	ILE
2	AB	205	ASP
2	AB	209	ARG
2	AB	217	ARG
2	AB	221	LEU
2	AB	223	ILE
2	AB	224	GLN
2	AB	233	SER
3	AC	3	ASN
3	AC	17	ASP
3	AC	37	GLN
3	AC	54	ARG
3	AC	104	GLN
3	AC	115	LEU
3	AC	118	GLN
3	AC	119	ARG
3	AC	131	ARG
3	AC	181	ASN
3	AC	196	LEU
3	AC	204	LEU
4	AD	5	ILE
4	AD	13	ARG
4	AD	31	CYS
4	AD	49	ARG
4	AD	58	LEU
4	AD	85	LYS
4	AD	86	LYS
4	AD	91	SER
4	AD	108	LEU
4	AD	118	ARG
4	AD	127	THR
4	AD	135	LEU
4	AD	138	TYR
4	AD	157	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	187	ARG
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	60	TYR
5	AE	67	VAL

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Mol	Chain	Res	Type
5	AE	71	LEU
5	AE	126	ARG
6	AF	17	SER
6	AF	69	GLU
6	AF	70	ASP
6	AF	81	ILE
6	AF	82	ARG
7	AG	8	GLU
7	AG	10	ARG
7	AG	12	LEU
7	AG	13	GLN
7	AG	52	GLU
7	AG	53	LYS
7	AG	76	ARG
7	AG	79	ARG
7	AG	104	LEU
7	AG	113	GLU
7	AG	114	ARG
7	AG	138	LYS
8	AH	91	ARG
8	AH	112	LEU
8	AH	115	SER
8	AH	127	LEU
8	AH	133	LEU
9	AI	17	VAL
9	AI	23	ASN
9	AI	42	ARG
9	AI	50	LEU
9	AI	53	VAL
9	AI	64	THR
9	AI	81	ILE
9	AI	89	ASN
9	AI	92	TYR
9	AI	103	THR
9	AI	105	ASP
9	AI	108	VAL
9	AI	127	LYS
9	AI	128	ARG
10	AJ	5	ARG
10	AJ	7	LYS
10	AJ	38	ILE
10	AJ	43	ARG

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Mol	Chain	Res	Type
10	AJ	67	THR
10	AJ	81	THR
11	AK	14	VAL
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	96	ARG
11	AK	104	GLN
12	AL	33	ARG
12	AL	52	LEU
12	AL	57	LYS
12	AL	60	LEU
12	AL	83	VAL
12	AL	116	SER
13	AM	3	ARG
13	AM	4	ILE
13	AM	19	LEU
13	AM	43	THR
13	AM	49	THR
13	AM	73	GLU
13	AM	78	ILE
13	AM	84	ILE
13	AM	102	ARG
13	AM	110	ARG
13	AM	121	LYS
14	AN	3	ARG
14	AN	7	ILE
14	AN	18	VAL
14	AN	22	THR
14	AN	23	ARG
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	24	SER
15	AO	26	GLU
15	AO	38	ARG
15	AO	39	LEU
15	AO	41	GLU
15	AO	47	LYS
15	AO	64	ARG
15	AO	66	LEU
15	AO	71	GLN

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Mol	Chain	Res	Type
15	AO	83	GLU
16	AP	11	SER
16	AP	19	ILE
16	AP	27	LYS
16	AP	32	TYR
16	AP	33	ILE
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	67	THR
17	AQ	6	LEU
17	AQ	24	GLU
17	AQ	74	LEU
18	AR	28	GLU
18	AR	31	LEU
18	AR	35	ARG
18	AR	38	GLU
18	AR	76	LEU
19	AS	9	VAL
19	AS	12	ASP
19	AS	17	GLU
19	AS	28	LYS
19	AS	37	ARG
19	AS	41	VAL
19	AS	65	ASN
19	AS	66	MET
20	AT	8	ARG
20	AT	9	ASN
20	AT	10	LEU
20	AT	24	LEU
20	AT	45	GLN
20	AT	54	LYS
20	AT	62	LEU
20	AT	71	THR
20	AT	74	LYS
20	AT	90	GLN
21	AU	9	ARG
21	AU	10	ARG
28	BD	37	LEU
28	BD	61	LEU
28	BD	94	LEU
28	BD	99	ASP

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Mol	Chain	Res	Type
28	BD	103	ARG
28	BD	126	GLN
28	BD	142	VAL
28	BD	211	ARG
28	BD	221	VAL
28	BD	229	VAL
28	BD	242	ARG
28	BD	257	LEU
28	BD	260	ARG
28	BD	275	LYS
29	BE	9	VAL
29	BE	12	THR
29	BE	21	VAL
29	BE	24	THR
29	BE	33	VAL
29	BE	34	VAL
29	BE	45	THR
29	BE	47	VAL
29	BE	49	LEU
29	BE	73	GLU
29	BE	77	ILE
29	BE	78	LEU
29	BE	111	ARG
29	BE	116	VAL
29	BE	119	ARG
29	BE	144	ARG
29	BE	154	LYS
29	BE	163	GLU
29	BE	178	GLU
29	BE	181	LEU
30	BF	19	GLU
30	BF	20	LEU
30	BF	24	LEU
30	BF	33	LEU
30	BF	53	THR
30	BF	57	VAL
30	BF	74	ARG
30	BF	106	ARG
30	BF	110	LEU
30	BF	125	LEU
30	BF	132	VAL
30	BF	140	LEU

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Mol	Chain	Res	Type
30	BF	170	LEU
30	BF	192	LEU
30	BF	197	ASP
31	BG	3	LEU
31	BG	7	LEU
31	BG	21	ARG
31	BG	43	LEU
31	BG	45	GLU
31	BG	60	LEU
31	BG	81	LYS
31	BG	82	LEU
31	BG	128	ARG
31	BG	133	LEU
31	BG	136	ARG
31	BG	140	ILE
31	BG	143	GLU
31	BG	148	MET
31	BG	170	ARG
32	BH	2	SER
32	BH	6	ARG
32	BH	41	MET
32	BH	69	ARG
32	BH	84	SER
32	BH	95	ARG
33	BI	5	LEU
33	BI	9	LEU
33	BI	10	GLU
33	BI	12	LEU
33	BI	20	ASP
33	BI	38	LEU
33	BI	40	THR
33	BI	43	ASN
33	BI	47	LEU
33	BI	48	GLU
33	BI	50	ARG
33	BI	57	ARG
33	BI	61	ARG
33	BI	66	GLU
33	BI	91	SER
33	BI	92	VAL
33	BI	96	ASP
33	BI	101	LEU

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Mol	Chain	Res	Type
33	BI	140	LEU
33	BI	142	VAL
34	BN	1	MET
34	BN	10	GLU
34	BN	28	THR
34	BN	33	LEU
34	BN	34	LEU
34	BN	38	HIS
34	BN	46	VAL
34	BN	48	MET
34	BN	61	ARG
34	BN	68	GLU
34	BN	83	LYS
34	BN	87	LEU
34	BN	99	LEU
34	BN	120	LEU
34	BN	133	GLN
35	BO	8	LEU
35	BO	10	VAL
35	BO	24	VAL
35	BO	92	GLU
35	BO	94	ARG
35	BO	97	ARG
36	BP	42	SER
36	BP	55	ARG
36	BP	65	ARG
36	BP	70	GLN
36	BP	76	LYS
36	BP	95	VAL
36	BP	106	LEU
36	BP	112	LEU
36	BP	148	LEU
36	BP	149	GLU
37	BQ	5	ARG
37	BQ	21	THR
37	BQ	35	VAL
37	BQ	45	GLN
37	BQ	55	VAL
37	BQ	56	ARG
37	BQ	59	ARG
37	BQ	60	ARG
37	BQ	75	THR

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Mol	Chain	Res	Type
37	BQ	109	VAL
37	BQ	110	THR
38	BR	1	MET
38	BR	6	SER
38	BR	15	SER
38	BR	18	LEU
38	BR	24	GLN
38	BR	28	LEU
38	BR	29	LEU
38	BR	33	ARG
38	BR	36	THR
38	BR	44	LEU
38	BR	54	LEU
38	BR	60	LEU
38	BR	63	ARG
38	BR	65	LEU
38	BR	67	LEU
38	BR	75	LEU
38	BR	79	LEU
38	BR	100	LEU
38	BR	111	LEU
39	BS	20	ARG
39	BS	48	LEU
39	BS	49	VAL
39	BS	57	LYS
39	BS	59	LYS
39	BS	61	ASN
39	BS	78	LEU
39	BS	83	LYS
40	BT	6	LEU
40	BT	16	ARG
40	BT	23	ARG
40	BT	49	VAL
40	BT	64	ARG
40	BT	96	ARG
40	BT	108	ARG
40	BT	113	LYS
40	BT	118	ARG
41	BU	5	LYS
41	BU	8	VAL
41	BU	36	ARG
41	BU	74	LEU

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Mol	Chain	Res	Type
41	BU	83	LEU
41	BU	92	ARG
41	BU	104	GLN
42	BV	6	LYS
42	BV	18	LEU
42	BV	28	GLU
42	BV	43	GLU
42	BV	46	VAL
42	BV	51	VAL
42	BV	52	VAL
42	BV	61	VAL
42	BV	73	SER
42	BV	79	VAL
42	BV	95	LEU
42	BV	100	ARG
43	BW	4	LYS
43	BW	11	ARG
43	BW	17	VAL
43	BW	23	LEU
43	BW	51	LEU
43	BW	100	THR
44	BX	57	LEU
44	BX	65	ARG
44	BX	88	LYS
45	BY	1	MET
45	BY	7	VAL
45	BY	11	ASP
45	BY	23	ARG
45	BY	31	LEU
45	BY	43	ASN
45	BY	90	LEU
45	BY	91	GLU
46	BZ	5	LEU
46	BZ	6	LYS
46	BZ	19	ARG
46	BZ	58	VAL
46	BZ	61	LEU
46	BZ	72	ARG
46	BZ	76	LEU
46	BZ	107	THR
46	BZ	129	SER
46	BZ	136	PHE

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Mol	Chain	Res	Type
46	BZ	142	SER
46	BZ	144	LEU
46	BZ	154	ASP
46	BZ	155	LEU
47	B0	7	LEU
47	B0	20	ARG
47	B0	55	ARG
48	B1	21	ARG
48	B1	35	THR
48	B1	40	ARG
48	B1	52	ARG
48	B1	75	GLU
48	B1	78	LYS
48	B1	89	GLU
48	B1	95	LEU
49	B2	3	LEU
49	B2	28	LYS
49	B2	30	ARG
49	B2	32	LEU
49	B2	52	ASP
49	B2	53	LEU
49	B2	55	ARG
49	B2	64	LEU
49	B2	70	GLN
50	B3	8	LEU
50	B3	23	LEU
50	B3	31	LEU
50	B3	40	THR
50	B3	54	VAL
50	B3	60	GLU
51	B4	3	GLU
51	B4	28	LYS
51	B4	34	GLU
51	B4	46	GLN
51	B4	49	PHE
51	B4	56	VAL
51	B4	59	PHE
51	B4	60	GLN
51	B4	61	ARG
51	B4	67	TYR
51	B4	68	ARG
51	B4	69	LYS

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Mol	Chain	Res	Type
52	B5	29	THR
52	B5	40	LYS
53	B6	4	GLU
53	B6	6	ARG
53	B6	14	THR
53	B6	18	ARG
53	B6	28	ARG
53	B6	48	VAL
53	B6	52	VAL
54	B7	1	MET
54	B7	24	THR
54	B7	34	ARG
55	B8	14	VAL
55	B8	23	VAL
55	B8	31	HIS
55	B8	32	LEU
56	B9	4	ARG
56	B9	22	ARG
56	B9	27	CYS
2	CB	10	LEU
2	CB	17	PHE
2	CB	24	TRP
2	CB	35	GLU
2	CB	80	ILE
2	CB	82	ARG
2	CB	96	ARG
2	CB	97	TRP
2	CB	98	LEU
2	CB	117	GLU
2	CB	119	GLU
2	CB	126	GLU
2	CB	128	GLU
2	CB	142	LEU
2	CB	150	SER
2	CB	154	LEU
2	CB	155	LEU
2	CB	163	PHE
2	CB	185	ILE
2	CB	187	LEU
2	CB	189	ASP
2	CB	200	ILE
2	CB	217	ARG

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Mol	Chain	Res	Type
2	CB	221	LEU
2	CB	230	VAL
2	CB	233	SER
3	CC	3	ASN
3	CC	15	THR
3	CC	20	SER
3	CC	21	ARG
3	CC	28	GLN
3	CC	32	LEU
3	CC	105	GLU
3	CC	115	LEU
3	CC	118	GLN
3	CC	125	GLU
3	CC	126	ARG
3	CC	131	ARG
3	CC	152	ILE
4	CD	5	ILE
4	CD	13	ARG
4	CD	31	CYS
4	CD	34	GLU
4	CD	47	ARG
4	CD	58	LEU
4	CD	85	LYS
4	CD	96	LEU
4	CD	108	LEU
4	CD	135	LEU
4	CD	138	TYR
4	CD	155	LEU
4	CD	168	ARG
4	CD	170	VAL
4	CD	191	ARG
4	CD	194	LEU
5	CE	10	MET
5	CE	12	LEU
5	CE	24	ARG
5	CE	38	GLN
5	CE	41	VAL
5	CE	47	LYS
5	CE	60	TYR
5	CE	78	HIS
5	CE	120	THR
6	CF	10	LEU

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Mol	Chain	Res	Type
6	CF	28	ARG
6	CF	41	GLU
6	CF	75	LEU
6	CF	81	ILE
6	CF	94	GLN
7	CG	9	VAL
7	CG	10	ARG
7	CG	32	ARG
7	CG	51	GLN
7	CG	72	ARG
7	CG	73	MET
7	CG	75	VAL
7	CG	76	ARG
7	CG	104	LEU
7	CG	113	GLU
7	CG	144	MET
7	CG	155	ARG
8	CH	21	LYS
8	CH	26	VAL
8	CH	78	GLN
8	CH	84	ARG
8	CH	112	LEU
8	CH	115	SER
8	CH	133	LEU
8	CH	135	CYS
9	CI	7	THR
9	CI	14	VAL
9	CI	17	VAL
9	CI	23	ASN
9	CI	53	VAL
9	CI	56	LEU
9	CI	64	THR
9	CI	81	ILE
9	CI	102	LEU
9	CI	108	VAL
9	CI	128	ARG
10	CJ	6	ILE
10	CJ	29	ARG
10	CJ	59	SER
10	CJ	67	THR
10	CJ	81	THR
10	CJ	100	THR

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Mol	Chain	Res	Type
11	CK	14	VAL
11	CK	54	ARG
11	CK	96	ARG
11	CK	104	GLN
12	CL	33	ARG
12	CL	83	VAL
12	CL	124	LYS
13	CM	4	ILE
13	CM	15	VAL
13	CM	19	LEU
13	CM	27	LYS
13	CM	49	THR
13	CM	56	LEU
13	CM	70	LEU
13	CM	78	ILE
13	CM	102	ARG
13	CM	110	ARG
13	CM	121	LYS
14	CN	3	ARG
14	CN	12	ARG
14	CN	18	VAL
14	CN	22	THR
14	CN	23	ARG
14	CN	33	VAL
15	CO	3	ILE
15	CO	5	LYS
15	CO	10	LYS
15	CO	24	SER
15	CO	38	ARG
15	CO	39	LEU
15	CO	41	GLU
15	CO	83	GLU
16	CP	28	ARG
16	CP	32	TYR
16	CP	33	ILE
16	CP	60	LEU
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	36	ILE
17	CQ	49	GLU
17	CQ	60	ILE

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Mol	Chain	Res	Type
17	CQ	74	LEU
17	CQ	96	GLU
17	CQ	99	SER
18	CR	25	THR
18	CR	26	LEU
18	CR	35	ARG
18	CR	41	LYS
18	CR	76	LEU
19	CS	28	LYS
19	CS	56	GLN
19	CS	65	ASN
19	CS	66	MET
19	CS	77	THR
20	CT	24	LEU
20	CT	41	ILE
20	CT	45	GLN
20	CT	56	MET
20	CT	71	THR
20	CT	80	ARG
20	CT	90	GLN
21	CU	10	ARG
28	DD	13	ARG
28	DD	54	ARG
28	DD	94	LEU
28	DD	99	ASP
28	DD	106	ILE
28	DD	126	GLN
28	DD	134	ARG
28	DD	138	VAL
28	DD	169	GLU
28	DD	211	ARG
28	DD	221	VAL
28	DD	242	ARG
28	DD	257	LEU
28	DD	260	ARG
28	DD	276	LYS
29	DE	9	VAL
29	DE	21	VAL
29	DE	24	THR
29	DE	33	VAL
29	DE	52	LEU
29	DE	72	VAL

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Mol	Chain	Res	Type
29	DE	73	GLU
29	DE	78	LEU
29	DE	89	ASP
29	DE	111	ARG
29	DE	116	VAL
29	DE	119	ARG
29	DE	144	ARG
29	DE	154	LYS
29	DE	163	GLU
29	DE	175	VAL
29	DE	181	LEU
30	DF	19	GLU
30	DF	20	LEU
30	DF	24	LEU
30	DF	33	LEU
30	DF	57	VAL
30	DF	74	ARG
30	DF	88	VAL
30	DF	106	ARG
30	DF	107	LYS
30	DF	110	LEU
30	DF	135	LYS
30	DF	170	LEU
30	DF	192	LEU
31	DG	3	LEU
31	DG	7	LEU
31	DG	9	ARG
31	DG	16	ARG
31	DG	21	ARG
31	DG	35	GLU
31	DG	36	LYS
31	DG	43	LEU
31	DG	45	GLU
31	DG	47	LYS
31	DG	60	LEU
31	DG	98	ARG
31	DG	115	ARG
31	DG	128	ARG
31	DG	133	LEU
31	DG	136	ARG
31	DG	140	ILE
31	DG	143	GLU

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Mol	Chain	Res	Type
31	DG	148	MET
31	DG	170	ARG
32	DH	2	SER
32	DH	3	ARG
32	DH	33	LEU
32	DH	34	GLU
32	DH	43	VAL
32	DH	49	VAL
32	DH	69	ARG
32	DH	76	VAL
32	DH	81	GLU
32	DH	95	ARG
32	DH	116	GLU
32	DH	171	LEU
33	DI	5	LEU
33	DI	9	LEU
33	DI	12	LEU
33	DI	20	ASP
33	DI	40	THR
33	DI	43	ASN
33	DI	44	LEU
33	DI	50	ARG
33	DI	52	ARG
33	DI	57	ARG
33	DI	68	LEU
33	DI	75	LEU
33	DI	77	LEU
33	DI	87	LYS
33	DI	92	VAL
33	DI	93	THR
33	DI	101	LEU
34	DN	1	MET
34	DN	28	THR
34	DN	33	LEU
34	DN	34	LEU
34	DN	46	VAL
34	DN	48	MET
34	DN	85	ILE
34	DN	87	LEU
34	DN	99	LEU
34	DN	120	LEU
35	DO	8	LEU

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Mol	Chain	Res	Type
35	DO	10	VAL
35	DO	69	ILE
35	DO	94	ARG
36	DP	1	MET
36	DP	45	LEU
36	DP	55	ARG
36	DP	59	LEU
36	DP	65	ARG
36	DP	70	GLN
36	DP	83	VAL
36	DP	95	VAL
36	DP	99	LEU
36	DP	106	LEU
36	DP	112	LEU
36	DP	148	LEU
37	DQ	1	MET
37	DQ	16	ARG
37	DQ	21	THR
37	DQ	45	GLN
37	DQ	54	MET
37	DQ	55	VAL
37	DQ	56	ARG
37	DQ	60	ARG
37	DQ	75	THR
37	DQ	109	VAL
37	DQ	131	ILE
38	DR	1	MET
38	DR	6	SER
38	DR	15	SER
38	DR	24	GLN
38	DR	28	LEU
38	DR	29	LEU
38	DR	33	ARG
38	DR	36	THR
38	DR	44	LEU
38	DR	54	LEU
38	DR	63	ARG
38	DR	65	LEU
38	DR	67	LEU
38	DR	75	LEU
38	DR	79	LEU
38	DR	100	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
38	DR	111	LEU
39	DS	20	ARG
39	DS	35	ILE
39	DS	36	TYR
39	DS	44	LYS
39	DS	57	LYS
39	DS	67	ARG
39	DS	68	GLN
39	DS	71	ARG
39	DS	75	GLU
39	DS	80	LEU
40	DT	6	LEU
40	DT	16	ARG
40	DT	17	THR
40	DT	23	ARG
40	DT	64	ARG
40	DT	82	LEU
40	DT	96	ARG
40	DT	108	ARG
40	DT	113	LYS
40	DT	118	ARG
41	DU	36	ARG
41	DU	74	LEU
41	DU	89	GLU
41	DU	92	ARG
41	DU	104	GLN
42	DV	15	GLU
42	DV	46	VAL
42	DV	52	VAL
42	DV	57	VAL
42	DV	61	VAL
42	DV	62	LEU
42	DV	73	SER
42	DV	79	VAL
43	DW	4	LYS
43	DW	11	ARG
43	DW	17	VAL
43	DW	19	LEU
43	DW	23	LEU
43	DW	51	LEU
43	DW	63	ASP
43	DW	100	THR

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Mol	Chain	Res	Type
44	DX	1	MET
44	DX	57	LEU
44	DX	88	LYS
44	DX	90	GLU
44	DX	92	LEU
45	DY	6	HIS
45	DY	7	VAL
45	DY	19	LYS
45	DY	23	ARG
45	DY	43	ASN
45	DY	72	VAL
45	DY	90	LEU
46	DZ	5	LEU
46	DZ	11	GLU
46	DZ	18	LEU
46	DZ	19	ARG
46	DZ	50	GLN
46	DZ	61	LEU
46	DZ	72	ARG
46	DZ	74	VAL
46	DZ	76	LEU
46	DZ	86	VAL
46	DZ	107	THR
46	DZ	119	GLU
46	DZ	120	ILE
46	DZ	136	PHE
46	DZ	144	LEU
46	DZ	154	ASP
46	DZ	155	LEU
46	DZ	170	THR
47	D0	19	LYS
47	D0	20	ARG
47	D0	24	LYS
48	D1	4	VAL
48	D1	21	ARG
48	D1	35	THR
48	D1	40	ARG
48	D1	59	THR
48	D1	78	LYS
48	D1	95	LEU
49	D2	30	ARG
49	D2	32	LEU

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Mol	Chain	Res	Type
49	D2	45	SER
49	D2	53	LEU
49	D2	55	ARG
49	D2	70	GLN
50	D3	8	LEU
50	D3	23	LEU
50	D3	40	THR
51	D4	3	GLU
51	D4	34	GLU
51	D4	52	THR
51	D4	56	VAL
51	D4	58	ARG
51	D4	68	ARG
51	D4	69	LYS
52	D5	29	THR
52	D5	40	LYS
53	D6	6	ARG
53	D6	48	VAL
54	D7	1	MET
54	D7	14	LYS
54	D7	34	ARG
55	D8	31	HIS
56	D9	4	ARG

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

Mol	Chain	Res	Type
2	AB	94	ASN
3	AC	6	HIS
3	AC	37	GLN
3	AC	102	ASN
3	AC	104	GLN
3	AC	123	GLN
3	AC	136	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	77	ASN
4	AD	123	HIS
4	AD	129	ASN
4	AD	161	ASN
5	AE	20	GLN
5	AE	38	GLN

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Mol	Chain	Res	Type
6	AF	100	ASN
7	AG	13	GLN
7	AG	28	ASN
7	AG	56	GLN
7	AG	148	ASN
9	AI	23	ASN
9	AI	31	GLN
9	AI	73	GLN
9	AI	89	ASN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	93	GLN
11	AK	104	GLN
12	AL	78	GLN
15	AO	28	GLN
15	AO	62	GLN
19	AS	56	GLN
19	AS	57	HIS
19	AS	65	ASN
19	AS	83	HIS
20	AT	9	ASN
20	AT	45	GLN
20	AT	90	GLN
28	BD	87	ASN
28	BD	164	GLN
28	BD	166	GLN
28	BD	253	GLN
30	BF	8	GLN
30	BF	69	HIS
30	BF	169	ASN
30	BF	203	GLN
31	BG	40	ASN
31	BG	108	ASN
33	BI	43	ASN
33	BI	54	GLN
33	BI	105	HIS
36	BP	38	GLN
36	BP	70	GLN
37	BQ	45	GLN
37	BQ	57	HIS
39	BS	95	HIS
40	BT	43	GLN

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Mol	Chain	Res	Type
40	BT	123	GLN
41	BU	117	GLN
44	BX	31	HIS
45	BY	6	HIS
45	BY	43	ASN
46	BZ	73	GLN
46	BZ	118	GLN
46	BZ	132	ASN
49	B2	48	HIS
49	B2	70	GLN
51	B4	46	GLN
52	B5	23	HIS
56	B9	36	GLN
2	CB	16	HIS
2	CB	19	HIS
2	CB	40	HIS
2	CB	146	GLN
2	CB	224	GLN
3	CC	6	HIS
3	CC	28	GLN
3	CC	102	ASN
3	CC	118	GLN
3	CC	123	GLN
3	CC	136	GLN
4	CD	45	GLN
4	CD	77	ASN
4	CD	123	HIS
4	CD	129	ASN
6	CF	100	ASN
7	CG	28	ASN
7	CG	51	GLN
7	CG	109	ASN
9	CI	23	ASN
9	CI	58	HIS
9	CI	73	GLN
9	CI	124	GLN
10	CJ	13	HIS
10	CJ	62	HIS
12	CL	78	GLN
15	CO	28	GLN
15	CO	62	GLN
17	CQ	16	GLN

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Mol	Chain	Res	Type
19	CS	23	ASN
19	CS	56	GLN
20	CT	45	GLN
28	DD	164	GLN
28	DD	166	GLN
28	DD	253	GLN
29	DE	143	ASN
30	DF	69	HIS
30	DF	203	GLN
31	DG	40	ASN
31	DG	41	GLN
33	DI	43	ASN
33	DI	54	GLN
33	DI	104	GLN
33	DI	133	HIS
36	DP	38	GLN
36	DP	70	GLN
37	DQ	45	GLN
37	DQ	123	HIS
38	DR	13	HIS
38	DR	71	GLN
39	DS	68	GLN
40	DT	58	ASN
40	DT	79	HIS
43	DW	60	ASN
44	DX	31	HIS
44	DX	82	GLN
45	DY	43	ASN
46	DZ	55	HIS
56	D9	36	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1521 (98%)	407 (27%)	26 (1%)
1	CA	1501/1521 (98%)	413 (27%)	28 (1%)
22	AV	12/24 (50%)	7 (58%)	0
22	CV	5/24 (20%)	4 (80%)	0
23	AW	1/3 (33%)	0	0
23	CW	1/3 (33%)	0	0
24	AX	74/77 (96%)	26 (35%)	2 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	CX	74/77 (96%)	31 (41%)	4 (5%)
25	AY	4/76 (5%)	1 (25%)	0
25	CY	4/76 (5%)	1 (25%)	0
26	BA	2811/2915 (96%)	529 (18%)	30 (1%)
26	DA	2791/2915 (95%)	595 (21%)	30 (1%)
27	BB	120/121 (99%)	16 (13%)	2 (1%)
27	DB	119/121 (98%)	31 (26%)	0
All	All	9012/9474 (95%)	2061 (22%)	122 (1%)

All (2061) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	7	G
1	AA	9	G
1	AA	15	G
1	AA	22	G
1	AA	29	G
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	50	A
1	AA	51	A
1	AA	55	A
1	AA	61	G
1	AA	68	G
1	AA	69	G
1	AA	73	G
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	96	U
1	AA	100	C
1	AA	101	A
1	AA	111	G
1	AA	112	G
1	AA	115	G
1	AA	116	A
1	AA	121	C
1	AA	129(A)	G
1	AA	131	C

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Mol	Chain	Res	Type
1	AA	144	G
1	AA	146	G
1	AA	155	C
1	AA	163	C
1	AA	170	U
1	AA	171	A
1	AA	173	U
1	AA	174	C
1	AA	178	C
1	AA	180	U
1	AA	182	U
1	AA	189(A)	C
1	AA	189(B)	C
1	AA	189(D)	C
1	AA	189(H)	G
1	AA	189(J)	G
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	221	C
1	AA	230	G
1	AA	247	G
1	AA	248	C
1	AA	251	G
1	AA	258	G
1	AA	259	G
1	AA	266	G
1	AA	267	C
1	AA	274	A
1	AA	280	C
1	AA	283	C
1	AA	289	G
1	AA	301	G
1	AA	318	G
1	AA	320	C
1	AA	321	A
1	AA	328	C

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Mol	Chain	Res	Type
1	AA	329	A
1	AA	332	G
1	AA	343	U
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	374	A
1	AA	383	A
1	AA	384	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	409	G
1	AA	412	A
1	AA	413	G
1	AA	414	A
1	AA	421	U
1	AA	422	C
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	432	A
1	AA	439	A
1	AA	442	C
1	AA	445	G
1	AA	452	A
1	AA	457	C
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	484	G
1	AA	485	G
1	AA	495	A
1	AA	496	A
1	AA	498	U

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Mol	Chain	Res	Type
1	AA	504	C
1	AA	505	G
1	AA	508	C
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	519	C
1	AA	521	G
1	AA	524	G
1	AA	527	G
1	AA	528	C
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	544	G
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	562	C
1	AA	571	U
1	AA	572	A
1	AA	573	A
1	AA	575	G
1	AA	576	G
1	AA	577	G
1	AA	581	G
1	AA	592	G
1	AA	593	G
1	AA	596	C
1	AA	604	G
1	AA	606	G
1	AA	611	A
1	AA	615	C
1	AA	622	A
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	645	C
1	AA	646	U

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Mol	Chain	Res	Type
1	AA	647	C
1	AA	648	A
1	AA	649	G
1	AA	653	A
1	AA	660	G
1	AA	665	A
1	AA	671	G
1	AA	673	G
1	AA	677	U
1	AA	680	C
1	AA	684	A
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	701	C
1	AA	710	G
1	AA	711	G
1	AA	717	C
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	733	A
1	AA	748	C
1	AA	749	C
1	AA	752	G
1	AA	755	G
1	AA	759	A
1	AA	764	C
1	AA	766	A
1	AA	777	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	798	G
1	AA	802	A
1	AA	806	C
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	821	G
1	AA	828	A

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Mol	Chain	Res	Type
1	AA	832	C
1	AA	833	U
1	AA	835	U
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	849	C
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	860	A
1	AA	868	C
1	AA	869	G
1	AA	874	G
1	AA	885	G
1	AA	886	G
1	AA	902	G
1	AA	913	A
1	AA	914	A
1	AA	922	G
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	936	C
1	AA	938	A
1	AA	942	G
1	AA	945	G
1	AA	952	U
1	AA	954	G
1	AA	960	U
1	AA	961	U
1	AA	965	A
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	973	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	979	C
1	AA	981	U

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Mol	Chain	Res	Type
1	AA	982	U
1	AA	983	A
1	AA	992	U
1	AA	993	G
1	AA	999	C
1	AA	1000	U
1	AA	1001(A)	G
1	AA	1002	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1011	G
1	AA	1017	G
1	AA	1019	C
1	AA	1020	U
1	AA	1021	G
1	AA	1022	G
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1036	G
1	AA	1037	C
1	AA	1039	C
1	AA	1043	C
1	AA	1045	C
1	AA	1052	U
1	AA	1054	C
1	AA	1055	A
1	AA	1056	U
1	AA	1057	G
1	AA	1063	C
1	AA	1064	G
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1076	C

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Mol	Chain	Res	Type
1	AA	1081	G
1	AA	1092	A
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1122	U
1	AA	1124	G
1	AA	1125	U
1	AA	1126	U
1	AA	1128	C
1	AA	1130	A
1	AA	1132	C
1	AA	1134	G
1	AA	1135	U
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1145	C
1	AA	1146	A
1	AA	1152	A
1	AA	1157	A
1	AA	1158	C
1	AA	1159	U
1	AA	1160	G
1	AA	1164	G
1	AA	1165	C
1	AA	1169	A
1	AA	1174	G
1	AA	1176	A
1	AA	1181	G
1	AA	1183	A
1	AA	1184	G
1	AA	1185	G
1	AA	1196	U
1	AA	1197	G
1	AA	1199	U
1	AA	1200	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	AA	1202	G
1	AA	1204	A
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1218	C
1	AA	1227	A
1	AA	1228	C
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1244	C
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1262	C
1	AA	1264	C
1	AA	1265	G
1	AA	1270	C
1	AA	1273	G
1	AA	1274	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1286	A
1	AA	1287	A
1	AA	1296	C
1	AA	1297	C
1	AA	1298	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1317	C
1	AA	1320	C
1	AA	1321	C
1	AA	1322	C
1	AA	1326	C
1	AA	1338	G
1	AA	1340	A
1	AA	1342	C
1	AA	1347	G

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Mol	Chain	Res	Type
1	AA	1360	A
1	AA	1363	C
1	AA	1365	G
1	AA	1370	G
1	AA	1371	G
1	AA	1376	U
1	AA	1377	A
1	AA	1379	G
1	AA	1383	C
1	AA	1396	A
1	AA	1397	C
1	AA	1398	A
1	AA	1402	C
1	AA	1419	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1457	G
1	AA	1458	G
1	AA	1472	U
1	AA	1475	G
1	AA	1487	G
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1507	A
1	AA	1517	G
1	AA	1520	G
1	AA	1525	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	13	A

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Mol	Chain	Res	Type
22	AV	15	A
22	AV	18	G
22	AV	19	U
22	AV	20	U
22	AV	23	A
22	AV	24	A
24	AX	9	G
24	AX	13	C
24	AX	16	C
24	AX	17	C
24	AX	17(A)	U
24	AX	18	G
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	25	C
24	AX	27	U
24	AX	31	G
24	AX	41	C
24	AX	45	G
24	AX	47	U
24	AX	48	C
24	AX	52	G
24	AX	56	C
24	AX	59	A
24	AX	61	C
24	AX	62	C
24	AX	66	C
24	AX	67	C
24	AX	68	C
24	AX	70	G
24	AX	72	A
25	AY	75	C
26	BA	7	G
26	BA	10	G
26	BA	12	U
26	BA	13	A
26	BA	27	G
26	BA	34	C
26	BA	45	C
26	BA	61	G
26	BA	71	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	BA	72	U
26	BA	74	A
26	BA	75	G
26	BA	84	A
26	BA	95	G
26	BA	102	G
26	BA	118	A
26	BA	119	A
26	BA	120	U
26	BA	122	G
26	BA	125	G
26	BA	140	G
26	BA	172	C
26	BA	177	G
26	BA	182	A
26	BA	188	G
26	BA	196	A
26	BA	199	A
26	BA	205	G
26	BA	215	G
26	BA	216	A
26	BA	221	A
26	BA	222	A
26	BA	225	A
26	BA	229	A
26	BA	233	A
26	BA	243	U
26	BA	244	A
26	BA	248	G
26	BA	267	C
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(S)	G
26	BA	272(A)	U
26	BA	272(B)	G
26	BA	272(G)	C
26	BA	272(H)	C
26	BA	279	C
26	BA	282	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	BA	311	A
26	BA	329	G
26	BA	330	A
26	BA	339	U
26	BA	345	A
26	BA	352	G
26	BA	356	G
26	BA	357	A
26	BA	359	A
26	BA	363	G
26	BA	380	U
26	BA	386	G
26	BA	396	G
26	BA	405	U
26	BA	407	G
26	BA	411	G
26	BA	412	A
26	BA	421	U
26	BA	428	A
26	BA	436	C
26	BA	442	G
26	BA	443	A
26	BA	444	C
26	BA	448	U
26	BA	451	C
26	BA	454	A
26	BA	456	C
26	BA	457	A
26	BA	481	G
26	BA	494	G
26	BA	504	U
26	BA	505	A
26	BA	508	G
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

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Mol	Chain	Res	Type
26	BA	563	G
26	BA	568	U
26	BA	573	G
26	BA	574	C
26	BA	575	A
26	BA	593	G
26	BA	603	A
26	BA	604	G
26	BA	607	U
26	BA	610	G
26	BA	614(B)	G
26	BA	615	G
26	BA	619	G
26	BA	627	A
26	BA	637	A
26	BA	645	C
26	BA	646	A
26	BA	647	G
26	BA	652(D)	C
26	BA	652(E)	G
26	BA	652(F)	G
26	BA	652(T)	C
26	BA	652(U)	G
26	BA	667	U
26	BA	669	G
26	BA	676	A
26	BA	677	A
26	BA	686	G
26	BA	714	U
26	BA	717	G
26	BA	726	G
26	BA	730	C
26	BA	764	A
26	BA	771	G
26	BA	775	G
26	BA	776	G
26	BA	782	A
26	BA	784	A
26	BA	785	G
26	BA	789	A
26	BA	792	G
26	BA	793	A

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Mol	Chain	Res	Type
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	875	G
26	BA	879	G
26	BA	880	G
26	BA	881	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	895	U
26	BA	896	A
26	BA	897	C
26	BA	907	U
26	BA	910	A
26	BA	914	C
26	BA	931	G
26	BA	932	G
26	BA	941	A
26	BA	945	A
26	BA	946	G
26	BA	953	A
26	BA	958	U
26	BA	959	A
26	BA	961	C
26	BA	974	G
26	BA	975	C
26	BA	975(A)	G
26	BA	983	A
26	BA	996	A
26	BA	1012	U
26	BA	1013	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	BA	1022	G
26	BA	1026	U
26	BA	1033	U
26	BA	1038	C
26	BA	1039	G
26	BA	1040	C
26	BA	1042	G
26	BA	1045	A
26	BA	1046	A
26	BA	1107	G
26	BA	1108	U
26	BA	1109	C
26	BA	1110	G
26	BA	1111	A
26	BA	1112	G
26	BA	1128	A
26	BA	1129	A
26	BA	1130	U
26	BA	1135	C
26	BA	1136	G
26	BA	1139	G
26	BA	1141	U
26	BA	1149	G
26	BA	1155	A
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	1178	C
26	BA	1210	A
26	BA	1211	U
26	BA	1218	C
26	BA	1220	A
26	BA	1244	G
26	BA	1250	G
26	BA	1253	A
26	BA	1256	G
26	BA	1271	G
26	BA	1272	A
26	BA	1273	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	BA	1300	U
26	BA	1301	A
26	BA	1303	G
26	BA	1308	A
26	BA	1314	C
26	BA	1319	G
26	BA	1320	C
26	BA	1321	A
26	BA	1335	U
26	BA	1352	U
26	BA	1359	A
26	BA	1365	A
26	BA	1369	G
26	BA	1370	C
26	BA	1380	G
26	BA	1384	A
26	BA	1385	G
26	BA	1386	C
26	BA	1395	A
26	BA	1416	G
26	BA	1417	C
26	BA	1420	U
26	BA	1421	G
26	BA	1428	C
26	BA	1437	C
26	BA	1445	A
26	BA	1449	A
26	BA	1450	G
26	BA	1455	G
26	BA	1458	C
26	BA	1459	G
26	BA	1460	A
26	BA	1467	C
26	BA	1471	A
26	BA	1478	G
26	BA	1482	G
26	BA	1490	A
26	BA	1491	G
26	BA	1492	G
26	BA	1493	C
26	BA	1496	A
26	BA	1505	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	BA	1507	A
26	BA	1508	A
26	BA	1509	C
26	BA	1509(A)	A
26	BA	1513	C
26	BA	1525	G
26	BA	1531	C
26	BA	1532	C
26	BA	1541	G
26	BA	1543	C
26	BA	1547	C
26	BA	1554	A
26	BA	1555	G
26	BA	1558	A
26	BA	1566	A
26	BA	1569	A
26	BA	1578	U
26	BA	1581	G
26	BA	1584	C
26	BA	1586	A
26	BA	1608	A
26	BA	1610	A
26	BA	1644	C
26	BA	1647	G
26	BA	1648	C
26	BA	1654	A
26	BA	1664	A
26	BA	1667	G
26	BA	1674	G
26	BA	1691	C
26	BA	1696	G
26	BA	1700	A
26	BA	1701	A
26	BA	1703	G
26	BA	1721	G
26	BA	1722	A
26	BA	1746	G
26	BA	1747(A)	G
26	BA	1748	G
26	BA	1756	G
26	BA	1762	A
26	BA	1763	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	BA	1764	G
26	BA	1773	A
26	BA	1777	U
26	BA	1779	U
26	BA	1780	A
26	BA	1782	C
26	BA	1786	A
26	BA	1791	A
26	BA	1800	C
26	BA	1801	G
26	BA	1816	G
26	BA	1827	C
26	BA	1829	A
26	BA	1847	A
26	BA	1877	A
26	BA	1878	G
26	BA	1889	A
26	BA	1900	A
26	BA	1906	G
26	BA	1912	A
26	BA	1913	A
26	BA	1915	U
26	BA	1919	A
26	BA	1924	C
26	BA	1927	A
26	BA	1929	G
26	BA	1930	G
26	BA	1936	A
26	BA	1937	A
26	BA	1938	A
26	BA	1940	U
26	BA	1941	C
26	BA	1955	U
26	BA	1963	U
26	BA	1964	G
26	BA	1967	C
26	BA	1969	A
26	BA	1970	A
26	BA	1971	A
26	BA	1972	A
26	BA	1984	G
26	BA	1991	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	BA	1992	G
26	BA	1993	U
26	BA	1996	C
26	BA	1997	G
26	BA	2023	G
26	BA	2027	G
26	BA	2031	A
26	BA	2032	G
26	BA	2033	A
26	BA	2035	G
26	BA	2043	C
26	BA	2051	A
26	BA	2055	C
26	BA	2056	G
26	BA	2060	A
26	BA	2061	G
26	BA	2062	A
26	BA	2069	G
26	BA	2093	G
26	BA	2096	U
26	BA	2097	C
26	BA	2100	G
26	BA	2101	G
26	BA	2102	U
26	BA	2106	G
26	BA	2117	A
26	BA	2118	U
26	BA	2119	A
26	BA	2121	G
26	BA	2123	G
26	BA	2125	G
26	BA	2127	G
26	BA	2128	C
26	BA	2129	C
26	BA	2130	U
26	BA	2131	G
26	BA	2132	U
26	BA	2134	A
26	BA	2135	A
26	BA	2136	C
26	BA	2140	C
26	BA	2141	G

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Mol	Chain	Res	Type
26	BA	2142	C
26	BA	2145	C
26	BA	2147	G
26	BA	2148	G
26	BA	2157	G
26	BA	2158	A
26	BA	2159	G
26	BA	2160	G
26	BA	2164	C
26	BA	2166	G
26	BA	2167	U
26	BA	2168	G
26	BA	2169	A
26	BA	2170	A
26	BA	2171	A
26	BA	2172	U
26	BA	2173	A
26	BA	2175	C
26	BA	2176	A
26	BA	2178	C
26	BA	2181	G
26	BA	2182	G
26	BA	2184	G
26	BA	2188	C
26	BA	2189	U
26	BA	2190	G
26	BA	2192	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	2219	G
26	BA	2225	A
26	BA	2238	G
26	BA	2239	G
26	BA	2268	A
26	BA	2269	A
26	BA	2279	G
26	BA	2283	C
26	BA	2287	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	BA	2305	A
26	BA	2308	G
26	BA	2316	C
26	BA	2320	A
26	BA	2325	G
26	BA	2326	C
26	BA	2334	G
26	BA	2335	A
26	BA	2336	A
26	BA	2343	C
26	BA	2347	C
26	BA	2350	C
26	BA	2361	A
26	BA	2372	G
26	BA	2383	G
26	BA	2385	C
26	BA	2389	G
26	BA	2396	G
26	BA	2406	U
26	BA	2410	G
26	BA	2424	C
26	BA	2425	A
26	BA	2429	G
26	BA	2430	A
26	BA	2432	A
26	BA	2434	A
26	BA	2435	A
26	BA	2439	A
26	BA	2440	C
26	BA	2441	C
26	BA	2445	G
26	BA	2448	A
26	BA	2469	A
26	BA	2474	C
26	BA	2476	A
26	BA	2484	G
26	BA	2487	G
26	BA	2490	G
26	BA	2491	U
26	BA	2494	G
26	BA	2502	G
26	BA	2505	G

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Mol	Chain	Res	Type
26	BA	2518	A
26	BA	2525	G
26	BA	2529	G
26	BA	2531	A
26	BA	2536	G
26	BA	2538	C
26	BA	2554	U
26	BA	2566	A
26	BA	2567	G
26	BA	2573	C
26	BA	2579	C
26	BA	2582	G
26	BA	2585	U
26	BA	2602	A
26	BA	2609	U
26	BA	2610	C
26	BA	2611	U
26	BA	2612	C
26	BA	2629	A
26	BA	2630	G
26	BA	2646	C
26	BA	2654	A
26	BA	2669	G
26	BA	2689	U
26	BA	2690	C
26	BA	2702	U
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	2755	C
26	BA	2757	A
26	BA	2758	A
26	BA	2761	G
26	BA	2764	A
26	BA	2765	A
26	BA	2766	G
26	BA	2778	A
26	BA	2790	A
26	BA	2791	C

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Mol	Chain	Res	Type
26	BA	2792	G
26	BA	2793	G
26	BA	2802	G
26	BA	2807	G
26	BA	2818	G
26	BA	2820	A
26	BA	2821	A
26	BA	2835	A
26	BA	2872	G
26	BA	2873	A
26	BA	2876	G
26	BA	2880	C
26	BA	2884	U
26	BA	2892	A
26	BA	2893	G
26	BA	2894	G
27	BB	2	C
27	BB	7	G
27	BB	13	A
27	BB	24	G
27	BB	32	C
27	BB	51	G
27	BB	52	A
27	BB	53	A
27	BB	56	G
27	BB	63	G
27	BB	73	A
27	BB	75	G
27	BB	85	G
27	BB	93	G
27	BB	106	G
27	BB	110	G
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	15	G
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	47	C

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Mol	Chain	Res	Type
1	CA	48	C
1	CA	50	A
1	CA	51	A
1	CA	55	A
1	CA	58	C
1	CA	61	G
1	CA	66	G
1	CA	68	G
1	CA	69	G
1	CA	72	C
1	CA	73	G
1	CA	79	G
1	CA	88	A
1	CA	91	C
1	CA	96	U
1	CA	97	G
1	CA	100	C
1	CA	101	A
1	CA	105	G
1	CA	111	G
1	CA	112	G
1	CA	115	G
1	CA	116	A
1	CA	121	C
1	CA	129(A)	G
1	CA	131	C
1	CA	139	G
1	CA	144	G
1	CA	146	G
1	CA	155	C
1	CA	156	G
1	CA	163	C
1	CA	170	U
1	CA	171	A
1	CA	173	U
1	CA	174	C
1	CA	178	C
1	CA	180	U
1	CA	182	U
1	CA	189(A)	C
1	CA	189(B)	C
1	CA	189(D)	C

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Mol	Chain	Res	Type
1	CA	189(H)	G
1	CA	190	U
1	CA	195	A
1	CA	197	A
1	CA	200	G
1	CA	201	C
1	CA	202	U
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	221	C
1	CA	226	G
1	CA	230	G
1	CA	247	G
1	CA	248	C
1	CA	251	G
1	CA	258	G
1	CA	259	G
1	CA	266	G
1	CA	267	C
1	CA	274	A
1	CA	280	C
1	CA	283	C
1	CA	289	G
1	CA	301	G
1	CA	318	G
1	CA	320	C
1	CA	321	A
1	CA	328	C
1	CA	329	A
1	CA	332	G
1	CA	343	U
1	CA	344	A
1	CA	346	G
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	374	A

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Mol	Chain	Res	Type
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	409	G
1	CA	412	A
1	CA	413	G
1	CA	414	A
1	CA	421	U
1	CA	422	C
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	432	A
1	CA	434	U
1	CA	439	A
1	CA	442	C
1	CA	452	A
1	CA	456	C
1	CA	461	A
1	CA	470	C
1	CA	471	G
1	CA	484	G
1	CA	485	G
1	CA	495	A
1	CA	496	A
1	CA	498	U
1	CA	504	C
1	CA	505	G
1	CA	508	C
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	519	C
1	CA	521	G
1	CA	527	G
1	CA	528	C
1	CA	531	U
1	CA	532	A
1	CA	533	A

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Mol	Chain	Res	Type
1	CA	544	G
1	CA	547	A
1	CA	559	A
1	CA	560	U
1	CA	561	U
1	CA	562	C
1	CA	571	U
1	CA	572	A
1	CA	573	A
1	CA	575	G
1	CA	576	G
1	CA	577	G
1	CA	581	G
1	CA	592	G
1	CA	593	G
1	CA	596	C
1	CA	604	G
1	CA	606	G
1	CA	611	A
1	CA	612	C
1	CA	615	C
1	CA	622	A
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	645	C
1	CA	646	U
1	CA	647	C
1	CA	649	G
1	CA	653	A
1	CA	660	G
1	CA	665	A
1	CA	671	G
1	CA	673	G
1	CA	677	U
1	CA	680	C
1	CA	684	A
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	701	C
1	CA	710	G

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Mol	Chain	Res	Type
1	CA	711	G
1	CA	717	C
1	CA	721	G
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	733	A
1	CA	748	C
1	CA	749	C
1	CA	752	G
1	CA	755	G
1	CA	759	A
1	CA	764	C
1	CA	766	A
1	CA	777	A
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	798	G
1	CA	802	A
1	CA	806	C
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	821	G
1	CA	826	C
1	CA	828	A
1	CA	832	C
1	CA	833	U
1	CA	835	U
1	CA	838	G
1	CA	840	C
1	CA	841	U
1	CA	848	C
1	CA	849	C
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	860	A
1	CA	868	C
1	CA	869	G
1	CA	874	G

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Mol	Chain	Res	Type
1	CA	885	G
1	CA	886	G
1	CA	887	G
1	CA	902	G
1	CA	913	A
1	CA	914	A
1	CA	922	G
1	CA	926	G
1	CA	927	G
1	CA	934	C
1	CA	936	C
1	CA	938	A
1	CA	942	G
1	CA	945	G
1	CA	952	U
1	CA	954	G
1	CA	960	U
1	CA	961	U
1	CA	965	A
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	973	G
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	979	C
1	CA	981	U
1	CA	982	U
1	CA	983	A
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	1002	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1011	G
1	CA	1017	G
1	CA	1018	C
1	CA	1020	U

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Mol	Chain	Res	Type
1	CA	1022	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1030(D)	A
1	CA	1036	G
1	CA	1037	C
1	CA	1038	C
1	CA	1039	C
1	CA	1041	A
1	CA	1043	C
1	CA	1045	C
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1056	U
1	CA	1057	G
1	CA	1063	C
1	CA	1064	G
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1086	U
1	CA	1092	A
1	CA	1093	A
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1117	G
1	CA	1122	U
1	CA	1124	G
1	CA	1125	U
1	CA	1126	U

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Mol	Chain	Res	Type
1	CA	1128	C
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1145	C
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1157	A
1	CA	1158	C
1	CA	1159	U
1	CA	1160	G
1	CA	1165	C
1	CA	1170	A
1	CA	1174	G
1	CA	1176	A
1	CA	1181	G
1	CA	1183	A
1	CA	1184	G
1	CA	1185	G
1	CA	1196	U
1	CA	1197	G
1	CA	1199	U
1	CA	1200	C
1	CA	1202	G
1	CA	1204	A
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1214	C
1	CA	1218	C
1	CA	1227	A
1	CA	1228	C
1	CA	1236	A
1	CA	1240	U
1	CA	1244	C

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Mol	Chain	Res	Type
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1264	C
1	CA	1265	G
1	CA	1270	C
1	CA	1274	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1284	C
1	CA	1287	A
1	CA	1296	C
1	CA	1297	C
1	CA	1298	C
1	CA	1300	G
1	CA	1316	G
1	CA	1317	C
1	CA	1321	C
1	CA	1322	C
1	CA	1326	C
1	CA	1338	G
1	CA	1340	A
1	CA	1342	C
1	CA	1347	G
1	CA	1360	A
1	CA	1363	C
1	CA	1365	G
1	CA	1370	G
1	CA	1376	U
1	CA	1377	A
1	CA	1379	G
1	CA	1383	C
1	CA	1396	A
1	CA	1397	C
1	CA	1398	A
1	CA	1400	C
1	CA	1402	C
1	CA	1419	G
1	CA	1442	G
1	CA	1442(A)	G

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Mol	Chain	Res	Type
1	CA	1442(B)	A
1	CA	1446	U
1	CA	1447	A
1	CA	1452	C
1	CA	1457	G
1	CA	1458	G
1	CA	1472	U
1	CA	1475	G
1	CA	1487	G
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G
1	CA	1497	G
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1507	A
1	CA	1517	G
1	CA	1520	G
1	CA	1525	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	15	A
22	CV	16	A
22	CV	18	G
22	CV	19	U
24	CX	4	G
24	CX	8	4SU
24	CX	9	G
24	CX	13	C
24	CX	16	C
24	CX	17	C
24	CX	17(A)	U
24	CX	18	G
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	25	C
24	CX	27	U

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Mol	Chain	Res	Type
24	CX	31	G
24	CX	41	C
24	CX	42	G
24	CX	45	G
24	CX	47	U
24	CX	48	C
24	CX	52	G
24	CX	56	C
24	CX	59	A
24	CX	60	U
24	CX	61	C
24	CX	62	C
24	CX	65	C
24	CX	66	C
24	CX	67	C
24	CX	68	C
24	CX	70	G
24	CX	72	A
25	CY	76	A
26	DA	7	G
26	DA	9	U
26	DA	10	G
26	DA	11	G
26	DA	12	U
26	DA	13	A
26	DA	15	G
26	DA	34	C
26	DA	35	G
26	DA	45	C
26	DA	50	U
26	DA	61	G
26	DA	63	U
26	DA	68	G
26	DA	71	A
26	DA	74	A
26	DA	75	G
26	DA	78	A
26	DA	84	A
26	DA	95	G
26	DA	102	G
26	DA	118	A
26	DA	119	A

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Mol	Chain	Res	Type
26	DA	120	U
26	DA	122	G
26	DA	131	G
26	DA	139	G
26	DA	141	A
26	DA	154(A)	C
26	DA	157	U
26	DA	181	A
26	DA	182	A
26	DA	184	C
26	DA	196	A
26	DA	199	A
26	DA	205	G
26	DA	213	A
26	DA	214	G
26	DA	216	A
26	DA	221	A
26	DA	222	A
26	DA	224	G
26	DA	225	A
26	DA	229	A
26	DA	233	A
26	DA	245	G
26	DA	248	G
26	DA	250	G
26	DA	260	G
26	DA	261	G
26	DA	264	C
26	DA	265	A
26	DA	266	G
26	DA	271(D)	G
26	DA	271(I)	G
26	DA	271(K)	U
26	DA	271(L)	U
26	DA	271(M)	G
26	DA	271(N)	U
26	DA	271(O)	C
26	DA	272(A)	U
26	DA	272(B)	G
26	DA	274	G
26	DA	277	C
26	DA	278	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	DA	285	C
26	DA	292	C
26	DA	302	C
26	DA	311	A
26	DA	317	G
26	DA	324	A
26	DA	327	G
26	DA	329	G
26	DA	330	A
26	DA	345	A
26	DA	352	G
26	DA	363	G
26	DA	363(B)	G
26	DA	363(E)	U
26	DA	363(F)	A
26	DA	372	G
26	DA	386	G
26	DA	391	G
26	DA	396	G
26	DA	405	U
26	DA	411	G
26	DA	412	A
26	DA	415	A
26	DA	416	C
26	DA	421	U
26	DA	422	A
26	DA	428	A
26	DA	442	G
26	DA	443	A
26	DA	444	C
26	DA	446	G
26	DA	455	C
26	DA	456	C
26	DA	457	A
26	DA	470	A
26	DA	474	G
26	DA	481	G
26	DA	482	A
26	DA	487	C
26	DA	496	G
26	DA	504	U
26	DA	505	A

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Mol	Chain	Res	Type
26	DA	508	G
26	DA	509	C
26	DA	519	U
26	DA	530	G
26	DA	531	C
26	DA	532	A
26	DA	533	G
26	DA	536	A
26	DA	545	G
26	DA	556	G
26	DA	563	G
26	DA	573	G
26	DA	575	A
26	DA	586	A
26	DA	595	C
26	DA	603	A
26	DA	604	G
26	DA	607	U
26	DA	614(B)	G
26	DA	615	G
26	DA	627	A
26	DA	637	A
26	DA	640	C
26	DA	645	C
26	DA	646	A
26	DA	647	G
26	DA	651	G
26	DA	652(A)	A
26	DA	652(B)	A
26	DA	652(C)	G
26	DA	652(U)	G
26	DA	653	A
26	DA	669	G
26	DA	670	A
26	DA	677	A
26	DA	686	G
26	DA	708	C
26	DA	709	U
26	DA	717	G
26	DA	729	G
26	DA	730	C
26	DA	740	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	DA	753	C
26	DA	759	G
26	DA	765	G
26	DA	771	G
26	DA	775	G
26	DA	776	G
26	DA	782	A
26	DA	783	A
26	DA	784	A
26	DA	785	G
26	DA	790	C
26	DA	792	G
26	DA	805	G
26	DA	812	C
26	DA	819	A
26	DA	821	A
26	DA	827	U
26	DA	828	U
26	DA	847	U
26	DA	857	C
26	DA	859	G
26	DA	866	A
26	DA	869	G
26	DA	874	G
26	DA	875	G
26	DA	879	G
26	DA	880	G
26	DA	882	G
26	DA	884	C
26	DA	886	C
26	DA	887	A
26	DA	888	C
26	DA	889	C
26	DA	890	A
26	DA	894	C
26	DA	896	A
26	DA	900	A
26	DA	901	A
26	DA	910	A
26	DA	912	C
26	DA	915	C
26	DA	917	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	DA	921	G
26	DA	932	G
26	DA	933	A
26	DA	941	A
26	DA	945	A
26	DA	946	G
26	DA	953	A
26	DA	961	C
26	DA	974	G
26	DA	975	C
26	DA	979	G
26	DA	980	A
26	DA	983	A
26	DA	996	A
26	DA	1012	U
26	DA	1013	C
26	DA	1017	G
26	DA	1020	A
26	DA	1022	G
26	DA	1025	G
26	DA	1026	U
26	DA	1027	A
26	DA	1033	U
26	DA	1038	C
26	DA	1039	G
26	DA	1042	G
26	DA	1043	C
26	DA	1114	G
26	DA	1116	C
26	DA	1127	A
26	DA	1128	A
26	DA	1129	A
26	DA	1130	U
26	DA	1135	C
26	DA	1136	G
26	DA	1139	G
26	DA	1142(A)	A
26	DA	1166	C
26	DA	1170	G
26	DA	1171	G
26	DA	1206	G
26	DA	1210	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	DA	1211	U
26	DA	1212	G
26	DA	1220	A
26	DA	1229	G
26	DA	1244	G
26	DA	1249	U
26	DA	1253	A
26	DA	1256	G
26	DA	1271	G
26	DA	1272	A
26	DA	1273	U
26	DA	1296	G
26	DA	1300	U
26	DA	1301	A
26	DA	1303	G
26	DA	1308	A
26	DA	1314	C
26	DA	1320	C
26	DA	1341	U
26	DA	1342	A
26	DA	1352	U
26	DA	1357	U
26	DA	1358	G
26	DA	1359	A
26	DA	1365	A
26	DA	1370	C
26	DA	1379	A
26	DA	1380	G
26	DA	1384	A
26	DA	1385	G
26	DA	1386	C
26	DA	1392	A
26	DA	1395	A
26	DA	1412	A
26	DA	1416	G
26	DA	1417	C
26	DA	1419	A
26	DA	1420	U
26	DA	1421	G
26	DA	1428	C
26	DA	1437	C
26	DA	1445	A

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Mol	Chain	Res	Type
26	DA	1449	A
26	DA	1450	G
26	DA	1451	C
26	DA	1455	G
26	DA	1459	G
26	DA	1467	C
26	DA	1471	A
26	DA	1482	G
26	DA	1488	G
26	DA	1493	C
26	DA	1494	A
26	DA	1497	U
26	DA	1504	C
26	DA	1508	A
26	DA	1509	C
26	DA	1509(A)	A
26	DA	1509(B)	A
26	DA	1512	U
26	DA	1520	G
26	DA	1523	U
26	DA	1525	G
26	DA	1530	C
26	DA	1531	C
26	DA	1532	C
26	DA	1542	A
26	DA	1545	A
26	DA	1547	C
26	DA	1548	C
26	DA	1558	A
26	DA	1559	G
26	DA	1569	A
26	DA	1578	U
26	DA	1579	A
26	DA	1583	A
26	DA	1586	A
26	DA	1592	C
26	DA	1597	A
26	DA	1598	C
26	DA	1608	A
26	DA	1610	A
26	DA	1631	C
26	DA	1636	C

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Mol	Chain	Res	Type
26	DA	1640	C
26	DA	1645	G
26	DA	1647	G
26	DA	1648	C
26	DA	1653	G
26	DA	1654	A
26	DA	1674	G
26	DA	1684	C
26	DA	1696	G
26	DA	1700	A
26	DA	1701	A
26	DA	1703	G
26	DA	1721	G
26	DA	1722	A
26	DA	1740	G
26	DA	1742	G
26	DA	1743	C
26	DA	1744	C
26	DA	1745(A)	C
26	DA	1746	G
26	DA	1750	G
26	DA	1756	G
26	DA	1762	A
26	DA	1763	G
26	DA	1764	G
26	DA	1773	A
26	DA	1780	A
26	DA	1791	A
26	DA	1800	C
26	DA	1801	G
26	DA	1812	A
26	DA	1816	G
26	DA	1829	A
26	DA	1831	G
26	DA	1835	G
26	DA	1839	G
26	DA	1840	G
26	DA	1847	A
26	DA	1848	A
26	DA	1859	A
26	DA	1862	G
26	DA	1866	C

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Mol	Chain	Res	Type
26	DA	1877	A
26	DA	1878	G
26	DA	1882	C
26	DA	1889	A
26	DA	1896	G
26	DA	1900	A
26	DA	1906	G
26	DA	1913	A
26	DA	1914	C
26	DA	1915	U
26	DA	1929	G
26	DA	1930	G
26	DA	1936	A
26	DA	1937	A
26	DA	1938	A
26	DA	1940	U
26	DA	1955	U
26	DA	1960	A
26	DA	1963	U
26	DA	1967	C
26	DA	1970	A
26	DA	1971	A
26	DA	1972	A
26	DA	1984	G
26	DA	1993	U
26	DA	1997	G
26	DA	2020	A
26	DA	2023	G
26	DA	2024	G
26	DA	2031	A
26	DA	2033	A
26	DA	2043	C
26	DA	2055	C
26	DA	2056	G
26	DA	2060	A
26	DA	2061	G
26	DA	2062	A
26	DA	2069	G
26	DA	2093	G
26	DA	2097	C
26	DA	2104	G
26	DA	2105	C

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Mol	Chain	Res	Type
26	DA	2106	G
26	DA	2111	C
26	DA	2113	U
26	DA	2114	A
26	DA	2115	G
26	DA	2119	A
26	DA	2120	G
26	DA	2122	U
26	DA	2123	G
26	DA	2125	G
26	DA	2126	A
26	DA	2127	G
26	DA	2128	C
26	DA	2129	C
26	DA	2130	U
26	DA	2131	G
26	DA	2132	U
26	DA	2133	G
26	DA	2134	A
26	DA	2135	A
26	DA	2136	C
26	DA	2137	C
26	DA	2138	C
26	DA	2139	C
26	DA	2140	C
26	DA	2141	G
26	DA	2143	C
26	DA	2144	U
26	DA	2146	C
26	DA	2150	U
26	DA	2151	G
26	DA	2153	G
26	DA	2154	G
26	DA	2157	G
26	DA	2158	A
26	DA	2159	G
26	DA	2164	C
26	DA	2165	G
26	DA	2166	G
26	DA	2167	U
26	DA	2168	G
26	DA	2169	A

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Mol	Chain	Res	Type
26	DA	2170	A
26	DA	2172	U
26	DA	2173	A
26	DA	2174	C
26	DA	2175	C
26	DA	2178	C
26	DA	2181	G
26	DA	2184	G
26	DA	2185	C
26	DA	2189	U
26	DA	2192	G
26	DA	2193	G
26	DA	2198	A
26	DA	2200	C
26	DA	2206	G
26	DA	2207	G
26	DA	2208	A
26	DA	2218	U
26	DA	2219	G
26	DA	2225	A
26	DA	2238	G
26	DA	2239	G
26	DA	2274	A
26	DA	2275	C
26	DA	2279	G
26	DA	2283	C
26	DA	2287	A
26	DA	2288	A
26	DA	2291	U
26	DA	2303	G
26	DA	2305	A
26	DA	2308	G
26	DA	2318	G
26	DA	2319	G
26	DA	2320	A
26	DA	2325	G
26	DA	2333	A
26	DA	2334	G
26	DA	2336	A
26	DA	2337	G
26	DA	2342	C
26	DA	2343	C

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Mol	Chain	Res	Type
26	DA	2347	C
26	DA	2349	G
26	DA	2354	G
26	DA	2377	A
26	DA	2379	G
26	DA	2383	G
26	DA	2385	C
26	DA	2388	A
26	DA	2402	C
26	DA	2406	U
26	DA	2410	G
26	DA	2417	C
26	DA	2418	A
26	DA	2422	A
26	DA	2425	A
26	DA	2427	C
26	DA	2429	G
26	DA	2430	A
26	DA	2435	A
26	DA	2439	A
26	DA	2440	C
26	DA	2441	C
26	DA	2448	A
26	DA	2453	A
26	DA	2459	A
26	DA	2460	U
26	DA	2465	C
26	DA	2469	A
26	DA	2476	A
26	DA	2477	C
26	DA	2480	C
26	DA	2484	G
26	DA	2487	G
26	DA	2490	G
26	DA	2502	G
26	DA	2505	G
26	DA	2518	A
26	DA	2529	G
26	DA	2532	G
26	DA	2535	G
26	DA	2536	G
26	DA	2542	A

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Mol	Chain	Res	Type
26	DA	2549	G
26	DA	2554	U
26	DA	2562	U
26	DA	2566	A
26	DA	2567	G
26	DA	2569	G
26	DA	2602	A
26	DA	2603	G
26	DA	2609	U
26	DA	2610	C
26	DA	2611	U
26	DA	2612	C
26	DA	2615	U
26	DA	2627	G
26	DA	2629	A
26	DA	2630	G
26	DA	2632	A
26	DA	2634	G
26	DA	2641	G
26	DA	2652	C
26	DA	2654	A
26	DA	2660	A
26	DA	2661	G
26	DA	2663	G
26	DA	2669	G
26	DA	2689	U
26	DA	2690	C
26	DA	2702	U
26	DA	2703	C
26	DA	2706	G
26	DA	2707	G
26	DA	2712(A)	A
26	DA	2713	A
26	DA	2714	G
26	DA	2721	A
26	DA	2726	U
26	DA	2733	A
26	DA	2746	U
26	DA	2751	G
26	DA	2757	A
26	DA	2758	A
26	DA	2759	G

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Mol	Chain	Res	Type
26	DA	2764	A
26	DA	2765	A
26	DA	2766	G
26	DA	2774	C
26	DA	2775	A
26	DA	2778	A
26	DA	2780	G
26	DA	2789	C
26	DA	2794	C
26	DA	2802	G
26	DA	2803	C
26	DA	2809	A
26	DA	2810	A
26	DA	2818	G
26	DA	2820	A
26	DA	2821	A
26	DA	2834	G
26	DA	2835	A
26	DA	2861	G
26	DA	2872	G
26	DA	2879	C
26	DA	2880	C
26	DA	2892	A
26	DA	2894	G
26	DA	2895	U
26	DA	2897	U
27	DB	2	C
27	DB	3	C
27	DB	7	G
27	DB	8	U
27	DB	9	G
27	DB	11	C
27	DB	12	C
27	DB	13	A
27	DB	15	A
27	DB	25	A
27	DB	30	C
27	DB	31	C
27	DB	33	G
27	DB	39	A
27	DB	41	U
27	DB	42	C

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Mol	Chain	Res	Type
27	DB	44	G
27	DB	54	G
27	DB	56	G
27	DB	59	A
27	DB	67	G
27	DB	73	A
27	DB	75	G
27	DB	85	G
27	DB	91	C
27	DB	93	G
27	DB	101	G
27	DB	108	U
27	DB	110	G
27	DB	111	G
27	DB	115	G

All (122) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	250	A
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1027	C
1	AA	1054	C
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1201	A
1	AA	1212	U
1	AA	1256	A
1	AA	1285	A
1	AA	1299	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	AA	1442	G
1	AA	1447	A
1	AA	1492	A
24	AX	16	C
24	AX	47	U
26	BA	71	A
26	BA	271(J)	C
26	BA	271(K)	U
26	BA	271(M)	G
26	BA	278	A
26	BA	827	U
26	BA	958	U
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	1379	A
26	BA	1530	C
26	BA	1653	G
26	BA	1828	G
26	BA	1992	G
26	BA	2126	A
26	BA	2127	G
26	BA	2158	A
26	BA	2170	A
26	BA	2181	G
26	BA	2183	C
26	BA	2187	G
26	BA	2406	U
26	BA	2439	A
26	BA	2689	U
26	BA	2756	U
26	BA	2893	G
27	BB	1	U
27	BB	52	A
1	CA	60	A
1	CA	65	U
1	CA	88	A
1	CA	96	U
1	CA	115	G

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Mol	Chain	Res	Type
1	CA	250	A
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	687	A
1	CA	748	C
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1054	C
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1183	A
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1442	G
1	CA	1447	A
1	CA	1492	A
24	CX	16	C
24	CX	18	G
24	CX	41	C
24	CX	46	G
26	DA	271(K)	U
26	DA	271(M)	G
26	DA	277	C
26	DA	362	U
26	DA	669	G
26	DA	752	A
26	DA	774	A
26	DA	856	C
26	DA	900	A
26	DA	1026	U
26	DA	1210	A
26	DA	1395	A
26	DA	1420	U
26	DA	1427	A
26	DA	1493	C

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Mol	Chain	Res	Type
26	DA	1530	C
26	DA	1558	A
26	DA	1653	G
26	DA	1913	A
26	DA	1992	G
26	DA	2104	G
26	DA	2110	G
26	DA	2282	G
26	DA	2406	U
26	DA	2422	A
26	DA	2428	G
26	DA	2439	A
26	DA	2602	A
26	DA	2689	U
26	DA	2756	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
23	PPU	AW	76	26,23	30,40,41	0.97	1 (3%)	37,57,60	1.90	10 (27%)
24	5MC	AX	32	24	13,22,23	1.32	1 (7%)	15,32,35	1.03	1 (6%)
24	5MU	AX	54	24	12,22,23	0.30	0	14,32,35	2.18	2 (14%)
24	PSU	AX	55	24	13,21,22	1.22	1 (7%)	18,30,33	3.26	6 (33%)
24	31H	AX	76	24,57	23,32,35	1.07	2 (8%)	24,45,50	3.07	5 (20%)
24	4SU	AX	8	24	11,21,22	1.20	1 (9%)	13,30,33	1.72	1 (7%)
23	PPU	CW	76	26,23	30,40,41	0.92	1 (3%)	37,57,60	2.01	11 (29%)
24	5MC	CX	32	24	13,22,23	1.35	1 (7%)	15,32,35	1.03	1 (6%)
24	5MU	CX	54	24	12,22,23	0.34	0	14,32,35	2.20	2 (14%)
24	PSU	CX	55	24	13,21,22	1.35	1 (7%)	18,30,33	3.45	6 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
24	31H	CX	76	24,60,57	25,34,35	1.19	3 (12%)	26,47,50	3.07	7 (26%)
24	4SU	CX	8	24	11,21,22	1.22	1 (9%)	13,30,33	1.29	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	PPU	AW	76	26,23	-	0/21/43/44	0/4/4/4
24	5MC	AX	32	24	-	0/3/25/26	0/2/2/2
24	5MU	AX	54	24	-	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	-	0/15/37/41	0/3/3/3
24	4SU	AX	8	24	-	0/3/25/26	0/2/2/2
23	PPU	CW	76	26,23	-	0/21/43/44	0/4/4/4
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	24,60,57	-	1/18/40/41	0/3/3/3
24	4SU	CX	8	24	-	0/3/25/26	0/2/2/2

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CX	55	PSU	C5-C1'	-4.39	1.48	1.52
24	AX	55	PSU	C5-C1'	-3.84	1.48	1.52
24	CX	8	4SU	C4-S4	-3.84	1.60	1.67
24	AX	8	4SU	C4-S4	-3.79	1.60	1.67
24	CX	76	31H	C5-C4	-3.19	1.33	1.40
24	AX	76	31H	C5-C4	-2.95	1.33	1.40
24	CX	76	31H	C5-N7	-2.26	1.31	1.39
24	AX	76	31H	C3'-N3'	2.08	1.49	1.45
24	CX	76	31H	C3'-N3'	2.46	1.49	1.45
23	CW	76	PPU	C5-C4	3.27	1.47	1.40
23	AW	76	PPU	C5-C4	3.49	1.48	1.40
24	AX	32	5MC	C5-C4	4.54	1.48	1.41
24	CX	32	5MC	C5-C4	4.70	1.48	1.41

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	76	31H	N3-C2-N1	-12.05	119.67	128.89
24	CX	76	31H	N3-C2-N1	-11.87	119.81	128.89
24	CX	55	PSU	N1-C2-N3	-10.74	121.48	128.33
24	AX	55	PSU	N1-C2-N3	-10.14	121.86	128.33
24	AX	8	4SU	C5-C4-N3	-5.67	118.07	123.63
23	CW	76	PPU	N3-C2-N1	-5.66	124.56	128.89
24	AX	76	31H	C4'-O4'-C1'	-5.62	103.54	109.72
24	AX	54	5MU	C5-C4-N3	-5.46	119.06	125.14
24	CX	54	5MU	C5-C4-N3	-5.34	119.19	125.14
23	AW	76	PPU	N3-C2-N1	-5.00	125.06	128.89
24	CX	8	4SU	C5-C4-N3	-4.33	119.39	123.63
24	CX	55	PSU	C5-C6-N1	-3.94	118.83	124.39
23	AW	76	PPU	C4-C5-N7	-3.63	106.14	109.48
24	AX	76	31H	C4-C5-N7	-3.51	106.25	109.48
24	AX	55	PSU	C5-C6-N1	-3.46	119.52	124.39
23	CW	76	PPU	C10-N6-C9	-3.31	105.02	115.96
24	CX	76	31H	OCN-CN-N	-3.23	120.11	124.76
23	CW	76	PPU	C9-N6-C6	-3.03	109.94	119.48
23	AW	76	PPU	C10-N6-C6	-3.02	109.95	119.48
24	AX	76	31H	C4'-C3'-N3'	-2.98	107.40	113.61
24	AX	55	PSU	C5-C1'-C2'	-2.97	110.25	115.52
23	CW	76	PPU	C4-C5-N7	-2.95	106.76	109.48
23	AW	76	PPU	C3'-N3'-C	-2.71	118.91	123.18
24	CX	55	PSU	C5-C1'-C2'	-2.60	110.90	115.52
24	CX	76	31H	CA-N-CN	-2.45	119.06	122.82
23	AW	76	PPU	C10-N6-C9	-2.26	108.50	115.96
23	AW	76	PPU	C4'-C3'-N3'	-2.26	108.90	113.61
23	CW	76	PPU	C10-N6-C6	-2.18	112.62	119.48
23	CW	76	PPU	C2'-C1'-N9	-2.10	111.08	114.29
23	CW	76	PPU	C3'-N3'-C	-2.04	119.97	123.18
24	CX	76	31H	C2'-C1'-N9	-2.03	111.19	114.29
23	CW	76	PPU	C4'-O4'-C1'	2.03	111.95	109.72
23	AW	76	PPU	C2'-C3'-N3'	2.04	118.43	113.18
24	CX	76	31H	O2'-C2'-C3'	2.08	115.53	110.62
23	CW	76	PPU	O4'-C4'-C3'	2.11	106.94	103.93
24	CX	32	5MC	N4-C4-N3	2.55	120.64	116.95
24	AX	55	PSU	O4'-C1'-C2'	2.75	107.53	104.73
24	AX	32	5MC	N4-C4-N3	2.76	120.95	116.95
23	AW	76	PPU	O4'-C4'-C3'	2.82	107.96	103.93
24	CX	55	PSU	O4'-C1'-C2'	3.09	107.88	104.73
23	AW	76	PPU	N1-C6-N6	3.48	120.83	117.05
24	CX	76	31H	O4'-C4'-C3'	3.48	108.91	103.93
24	AX	55	PSU	C6-N1-C2	3.98	121.87	115.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	76	31H	O4'-C1'-N9	4.31	117.12	108.10
24	CX	55	PSU	C6-N1-C2	4.38	122.51	115.47
23	CW	76	PPU	C2-N1-C6	4.52	121.05	111.43
23	AW	76	PPU	C2-N1-C6	4.84	121.73	111.43
23	CW	76	PPU	N1-C6-N6	5.11	122.61	117.05
24	AX	54	5MU	C4-N3-C2	5.77	120.23	115.25
24	CX	54	5MU	C4-N3-C2	5.93	120.37	115.25
24	AX	55	PSU	C4-N3-C2	6.33	120.72	115.25
24	CX	55	PSU	C4-N3-C2	6.47	120.84	115.25
24	CX	76	31H	O4'-C1'-N9	7.33	123.44	108.10

There are no chirality outliers.

All (1) torsion outliers are listed below:

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

There are no ring outliers.

11 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	AW	76	PPU	5	0
24	AX	32	5MC	2	0
24	AX	54	5MU	1	0
24	AX	55	PSU	1	0
24	AX	8	4SU	2	0
23	CW	76	PPU	11	0
24	CX	32	5MC	3	0
24	CX	54	5MU	2	0
24	CX	55	PSU	1	0
24	CX	76	31H	4	0
24	CX	8	4SU	2	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 1916 ligands modelled in this entry, 1914 are monoatomic - leaving 2 for Mogul analysis.



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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
58	SF4	AD	302	4	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	302	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	302	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	AA	1498/1521 (98%)	0.23	20 (1%) 79 71	39, 73, 93, 105	0
1	CA	1503/1521 (98%)	0.17	25 (1%) 73 63	41, 75, 94, 106	0
2	AB	231/256 (90%)	0.53	15 (6%) 22 13	69, 82, 91, 101	0
2	CB	231/256 (90%)	2.20	109 (47%) 0 0	71, 84, 93, 101	0
3	AC	206/239 (86%)	0.47	6 (2%) 55 43	67, 79, 89, 95	0
3	CC	206/239 (86%)	1.91	87 (42%) 0 0	70, 81, 91, 95	0
4	AD	208/209 (99%)	0.59	13 (6%) 23 14	57, 74, 85, 91	0
4	CD	208/209 (99%)	0.81	20 (9%) 10 5	57, 75, 85, 92	0
5	AE	148/162 (91%)	0.52	6 (4%) 41 29	59, 71, 82, 90	0
5	CE	148/162 (91%)	1.04	30 (20%) 1 1	59, 73, 84, 91	0
6	AF	100/101 (99%)	0.45	4 (4%) 42 30	54, 69, 78, 83	0
6	CF	100/101 (99%)	0.27	5 (5%) 32 21	56, 71, 80, 83	0
7	AG	155/156 (99%)	0.58	15 (9%) 10 5	64, 76, 86, 92	0
7	CG	155/156 (99%)	1.10	28 (18%) 2 1	67, 78, 88, 92	0
8	AH	137/138 (99%)	0.43	6 (4%) 38 26	60, 72, 80, 85	0
8	CH	137/138 (99%)	1.38	35 (25%) 1 0	62, 74, 82, 85	0
9	AI	127/128 (99%)	0.85	18 (14%) 4 2	64, 83, 91, 96	0
9	CI	127/128 (99%)	1.64	47 (37%) 0 0	69, 84, 91, 98	0
10	AJ	97/105 (92%)	0.74	10 (10%) 9 4	66, 83, 92, 94	0
10	CJ	96/105 (91%)	2.09	54 (56%) 0 0	69, 85, 93, 94	0
11	AK	114/129 (88%)	0.70	10 (8%) 12 6	46, 70, 81, 85	0
11	CK	114/129 (88%)	0.64	14 (12%) 5 3	50, 71, 82, 85	0
12	AL	122/132 (92%)	0.54	3 (2%) 61 48	50, 64, 73, 81	0
12	CL	122/132 (92%)	0.72	13 (10%) 8 4	52, 65, 75, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
13	AM	123/126 (97%)	0.66	13 (10%) 8 4	58, 72, 83, 90	0
13	CM	122/126 (96%)	1.51	33 (27%) 1 0	72, 85, 93, 100	0
14	AN	60/61 (98%)	0.65	6 (10%) 9 4	65, 75, 81, 82	0
14	CN	60/61 (98%)	2.24	31 (51%) 0 0	69, 78, 83, 86	0
15	AO	88/89 (98%)	0.77	3 (3%) 49 36	54, 69, 81, 85	0
15	CO	88/89 (98%)	0.61	9 (10%) 9 4	53, 71, 82, 87	0
16	AP	82/88 (93%)	0.82	11 (13%) 4 2	59, 72, 82, 85	0
16	CP	82/88 (93%)	0.53	5 (6%) 25 15	57, 71, 81, 85	0
17	AQ	99/105 (94%)	0.64	3 (3%) 54 41	58, 71, 80, 83	0
17	CQ	99/105 (94%)	1.15	19 (19%) 2 1	56, 72, 81, 83	0
18	AR	68/88 (77%)	0.84	8 (11%) 6 3	59, 70, 80, 84	0
18	CR	68/88 (77%)	0.57	6 (8%) 12 6	60, 71, 82, 85	0
19	AS	83/93 (89%)	0.86	12 (14%) 3 2	72, 82, 89, 93	0
19	CS	83/93 (89%)	2.26	48 (57%) 0 0	73, 84, 91, 95	0
20	AT	96/106 (90%)	1.08	18 (18%) 2 1	60, 71, 83, 85	0
20	CT	96/106 (90%)	1.10	20 (20%) 1 1	56, 71, 83, 85	0
21	AU	23/27 (85%)	0.89	1 (4%) 39 27	69, 74, 79, 85	0
21	CU	23/27 (85%)	0.58	3 (13%) 5 2	71, 76, 84, 86	0
22	AV	13/24 (54%)	1.52	2 (15%) 3 1	56, 88, 93, 97	0
22	CV	6/24 (25%)	1.03	1 (16%) 2 1	59, 76, 95, 96	0
23	AW	2/3 (66%)	0.39	0 100 100	30, 30, 30, 37	0
23	CW	2/3 (66%)	0.73	0 100 100	50, 50, 50, 57	0
24	AX	71/77 (92%)	0.22	0 100 100	27, 70, 84, 92	0
24	CX	71/77 (92%)	0.28	0 100 100	30, 75, 86, 93	0
25	AY	5/76 (6%)	0.10	0 100 100	51, 76, 87, 94	0
25	CY	5/76 (6%)	1.37	1 (20%) 1 1	60, 79, 90, 91	0
26	BA	2819/2915 (96%)	0.24	27 (0%) 84 77	20, 42, 89, 107	0
26	DA	2800/2915 (96%)	-0.00	49 (1%) 71 61	22, 46, 90, 107	0
27	BB	120/121 (99%)	0.10	0 100 100	37, 63, 77, 88	0
27	DB	120/121 (99%)	0.14	5 (4%) 40 28	42, 68, 80, 91	0
28	BD	275/276 (99%)	0.21	2 (0%) 89 84	21, 41, 58, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
28	DD	275/276 (99%)	0.01	1 (0%) 93 90	23, 43, 61, 80	0
29	BE	204/206 (99%)	0.21	1 (0%) 91 88	21, 46, 65, 82	0
29	DE	204/206 (99%)	-0.05	1 (0%) 91 88	23, 48, 67, 84	0
30	BF	203/210 (96%)	0.23	2 (0%) 84 77	22, 51, 73, 87	0
30	DF	203/210 (96%)	0.07	1 (0%) 91 88	24, 54, 74, 86	0
31	BG	181/182 (99%)	0.37	7 (3%) 43 31	55, 70, 82, 93	0
31	DG	181/182 (99%)	1.36	52 (28%) 1 0	59, 74, 85, 93	0
32	BH	174/180 (96%)	0.14	1 (0%) 90 86	49, 65, 77, 81	0
32	DH	174/180 (96%)	1.25	40 (22%) 1 1	52, 70, 80, 84	0
33	BI	146/148 (98%)	0.73	13 (8%) 12 6	47, 81, 90, 95	0
33	DI	146/148 (98%)	3.04	80 (54%) 0 0	46, 84, 94, 99	0
34	BN	140/140 (100%)	0.27	1 (0%) 89 84	29, 49, 72, 82	0
34	DN	140/140 (100%)	0.09	2 (1%) 78 69	33, 53, 74, 83	0
35	BO	122/122 (100%)	-0.02	1 (0%) 87 81	26, 42, 61, 65	0
35	DO	122/122 (100%)	-0.03	0 100 100	36, 57, 70, 79	0
36	BP	149/150 (99%)	0.33	2 (1%) 79 71	25, 52, 76, 85	0
36	DP	149/150 (99%)	0.54	7 (4%) 35 24	28, 54, 78, 86	0
37	BQ	141/141 (100%)	0.25	0 100 100	29, 51, 65, 78	0
37	DQ	141/141 (100%)	0.71	17 (12%) 6 3	31, 55, 69, 79	0
38	BR	118/118 (100%)	-0.10	0 100 100	23, 37, 56, 63	0
38	DR	118/118 (100%)	0.18	0 100 100	31, 50, 64, 71	0
39	BS	110/112 (98%)	0.19	1 (0%) 85 79	33, 51, 63, 76	0
39	DS	110/112 (98%)	0.80	11 (10%) 9 4	55, 76, 86, 89	0
40	BT	131/146 (89%)	-0.18	0 100 100	27, 44, 73, 86	0
40	DT	131/146 (89%)	0.06	1 (0%) 87 81	42, 59, 78, 86	0
41	BU	116/118 (98%)	-0.06	1 (0%) 85 79	18, 32, 52, 73	0
41	DU	116/118 (98%)	0.28	2 (1%) 73 63	37, 58, 75, 80	0
42	BV	101/101 (100%)	-0.02	0 100 100	20, 43, 61, 76	0
42	DV	101/101 (100%)	0.87	12 (11%) 6 3	36, 67, 81, 87	0
43	BW	112/113 (99%)	0.06	1 (0%) 85 79	20, 33, 51, 84	0
43	DW	112/113 (99%)	0.30	1 (0%) 85 79	32, 47, 65, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
44	BX	95/96 (98%)	0.12	0 100 100	22, 37, 57, 82	0
44	DX	95/96 (98%)	0.71	8 (8%) 14 6	39, 59, 73, 82	0
45	BY	107/110 (97%)	0.01	0 100 100	32, 48, 70, 81	0
45	DY	107/110 (97%)	0.99	15 (14%) 4 2	48, 68, 78, 89	0
46	BZ	171/206 (83%)	0.48	5 (2%) 55 43	40, 63, 83, 88	0
46	DZ	174/206 (84%)	1.70	60 (34%) 0 0	64, 82, 94, 97	0
47	B0	83/85 (97%)	-0.06	0 100 100	23, 38, 52, 66	0
47	D0	83/85 (97%)	0.77	8 (9%) 10 5	36, 61, 72, 81	0
48	B1	97/98 (98%)	0.03	2 (2%) 67 56	21, 42, 65, 74	0
48	D1	97/98 (98%)	0.43	3 (3%) 52 40	30, 54, 76, 82	0
49	B2	70/72 (97%)	0.12	0 100 100	32, 48, 63, 87	0
49	D2	70/72 (97%)	0.50	4 (5%) 27 17	50, 67, 78, 83	0
50	B3	59/60 (98%)	-0.11	0 100 100	21, 37, 62, 81	0
50	D3	59/60 (98%)	1.01	6 (10%) 9 4	44, 60, 77, 87	0
51	B4	69/71 (97%)	0.64	11 (15%) 3 1	54, 76, 91, 98	0
51	D4	69/71 (97%)	1.58	24 (34%) 0 0	80, 90, 95, 99	0
52	B5	59/60 (98%)	-0.08	1 (1%) 73 63	19, 33, 53, 65	0
52	D5	59/60 (98%)	-0.03	0 100 100	28, 48, 69, 72	0
53	B6	53/54 (98%)	-0.05	0 100 100	28, 40, 60, 64	0
53	D6	53/54 (98%)	0.47	3 (5%) 27 17	43, 59, 72, 82	0
54	B7	48/49 (97%)	-0.05	0 100 100	18, 25, 54, 63	0
54	D7	48/49 (97%)	0.01	1 (2%) 67 56	29, 39, 63, 81	0
55	B8	64/65 (98%)	-0.03	0 100 100	23, 32, 46, 61	0
55	D8	64/65 (98%)	0.44	0 100 100	37, 55, 66, 70	0
56	B9	37/37 (100%)	0.50	1 (2%) 58 45	27, 49, 67, 71	0
56	D9	37/37 (100%)	0.92	5 (13%) 4 2	46, 54, 67, 74	0
All	All	20640/21602 (95%)	0.43	1345 (6%) 22 13	18, 63, 89, 107	0

All (1345) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
33	DI	119	PRO	11.8
33	DI	65	ALA	11.6

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Mol	Chain	Res	Type	RSRZ
33	DI	128	LEU	10.9
13	CM	124	PRO	10.8
33	DI	85	GLU	10.6
33	DI	146	ALA	10.6
33	DI	58	LEU	10.3
33	DI	111	PRO	9.9
33	DI	137	PRO	9.3
33	DI	87	LYS	9.2
33	DI	89	TYR	8.9
51	D4	45	GLY	8.9
33	DI	100	ALA	8.8
50	D3	2	PRO	8.4
33	DI	145	VAL	8.2
33	DI	114	LEU	8.1
33	DI	83	ALA	7.9
13	CM	123	ALA	7.9
33	DI	129	THR	7.8
3	CC	87	LEU	7.8
33	DI	86	THR	7.7
33	DI	122	GLU	7.6
33	DI	99	GLU	7.5
33	DI	96	ASP	7.5
13	AM	124	PRO	7.3
33	DI	84	GLY	7.2
1	CA	1030(B)	C	6.9
46	DZ	124	ILE	6.9
44	DX	92	LEU	6.8
14	CN	53	LEU	6.7
10	CJ	6	ILE	6.7
2	CB	232	PRO	6.6
33	DI	112	LYS	6.6
33	DI	118	LYS	6.6
2	CB	70	PHE	6.5
3	CC	71	ALA	6.5
33	DI	54	GLN	6.4
33	DI	68	LEU	6.4
13	CM	119	GLY	6.3
45	DY	1	MET	6.3
3	CC	80	GLY	6.3
9	CI	19	LEU	6.3
3	CC	81	GLY	6.2
51	D4	52	THR	6.1

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Mol	Chain	Res	Type	RSRZ
22	AV	24	A	6.1
3	CC	167	TRP	6.0
2	CB	230	VAL	6.0
33	DI	72	LEU	6.0
14	CN	37	PHE	5.9
32	DH	115	VAL	5.9
14	CN	25	VAL	5.9
14	CN	44	LEU	5.9
33	DI	108	THR	5.8
37	DQ	136	ALA	5.8
7	CG	80	VAL	5.8
2	CB	214	ILE	5.8
33	DI	130	TYR	5.8
4	AD	167	GLY	5.8
46	DZ	125	LEU	5.7
8	CH	80	ILE	5.7
2	CB	21	ARG	5.7
2	CB	200	ILE	5.6
31	DG	109	VAL	5.6
56	D9	12	ASP	5.6
46	DZ	171	ILE	5.5
50	D3	60	GLU	5.4
14	CN	22	THR	5.4
36	DP	108	LYS	5.4
2	CB	81	VAL	5.4
32	DH	107	VAL	5.4
13	CM	75	ALA	5.4
7	CG	81	GLY	5.4
31	DG	28	VAL	5.3
42	DV	1	MET	5.3
7	AG	79	ARG	5.3
26	DA	2155	G	5.3
33	DI	88	ILE	5.2
2	CB	112	VAL	5.2
2	CB	93	VAL	5.2
2	CB	207	ALA	5.2
2	CB	77	ALA	5.2
2	CB	163	PHE	5.1
10	CJ	48	THR	5.1
33	DI	109	ILE	5.1
5	CE	94	ALA	5.1
3	CC	199	LYS	5.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
7	CG	18	TYR	5.0
14	CN	42	ILE	5.0
2	CB	83	MET	5.0
13	CM	66	LEU	5.0
46	DZ	155	LEU	5.0
3	CC	170	GLN	5.0
10	CJ	62	HIS	5.0
19	CS	16	LEU	5.0
13	CM	120	LYS	5.0
2	CB	29	ALA	4.9
3	CC	143	GLU	4.9
2	CB	231	GLU	4.9
3	CC	146	ALA	4.9
13	CM	121	LYS	4.9
19	CS	20	LEU	4.9
46	DZ	142	SER	4.8
1	AA	1030(B)	C	4.8
19	CS	71	LEU	4.8
33	DI	69	LYS	4.8
33	DI	61	ARG	4.8
10	CJ	85	LEU	4.8
43	BW	111	HIS	4.8
39	DS	56	LEU	4.8
2	CB	116	GLU	4.8
2	CB	188	ALA	4.8
31	DG	41	GLN	4.8
2	CB	97	TRP	4.8
19	CS	45	VAL	4.7
2	CB	222	ILE	4.7
46	DZ	96	VAL	4.7
10	CJ	47	PHE	4.7
19	CS	50	ALA	4.7
19	CS	28	LYS	4.7
33	BI	84	GLY	4.7
2	AB	188	ALA	4.7
26	DA	2131	G	4.7
32	DH	2	SER	4.6
2	CB	177	ALA	4.6
14	CN	8	GLU	4.6
2	CB	187	LEU	4.6
47	D0	69	PHE	4.6
42	DV	20	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
33	DI	93	THR	4.6
7	CG	78	ARG	4.6
39	DS	58	LEU	4.6
19	CS	32	LYS	4.5
9	CI	7	THR	4.5
26	DA	2156	G	4.5
9	CI	41	VAL	4.5
33	DI	144	VAL	4.5
19	CS	79	THR	4.5
31	DG	140	ILE	4.5
3	CC	37	GLN	4.5
3	CC	201	TYR	4.5
2	CB	101	MET	4.5
51	D4	40	HIS	4.5
45	DY	55	TYR	4.5
2	CB	181	PHE	4.5
7	CG	83	ALA	4.5
37	DQ	104	PHE	4.4
33	DI	134	PRO	4.4
2	CB	100	GLY	4.4
3	AC	80	GLY	4.4
43	DW	112	GLY	4.4
46	DZ	50	GLN	4.4
46	DZ	162	GLU	4.4
9	CI	52	ALA	4.4
33	DI	124	GLY	4.4
2	CB	229	VAL	4.4
2	CB	45	GLN	4.4
7	CG	82	GLY	4.4
31	DG	2	PRO	4.4
51	D4	44	THR	4.4
8	CH	83	ILE	4.3
7	AG	82	GLY	4.3
31	DG	29	TRP	4.3
3	CC	152	ILE	4.3
3	CC	53	ALA	4.3
3	CC	117	ALA	4.3
7	AG	83	ALA	4.3
3	CC	187	ALA	4.3
46	DZ	121	HIS	4.3
3	CC	165	THR	4.3
3	CC	204	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
2	CB	103	THR	4.2
51	B4	46	GLN	4.2
19	CS	52	TYR	4.2
31	DG	136	ARG	4.2
51	B4	49	PHE	4.2
51	B4	50	VAL	4.2
2	CB	102	LEU	4.2
18	AR	42	ARG	4.2
31	DG	178	PHE	4.2
20	AT	72	LEU	4.2
1	CA	1030(A)	G	4.2
42	DV	43	GLU	4.2
46	DZ	93	ASP	4.2
46	DZ	114	GLY	4.2
8	CH	82	HIS	4.1
9	CI	57	GLY	4.1
9	CI	61	ALA	4.1
2	AB	126	GLU	4.1
2	CB	201	ILE	4.1
3	CC	206	GLU	4.1
3	CC	189	ALA	4.1
3	CC	12	LEU	4.1
8	CH	81	HIS	4.1
2	CB	227	GLY	4.1
2	CB	92	TYR	4.1
3	AC	87	LEU	4.1
7	CG	84	ASN	4.1
9	CI	64	THR	4.1
14	CN	36	PHE	4.1
11	AK	13	GLN	4.0
46	DZ	5	LEU	4.0
2	CB	90	MET	4.0
2	AB	133	LYS	4.0
26	DA	2133	G	4.0
3	CC	91	LEU	4.0
10	CJ	65	LEU	4.0
36	DP	78	PRO	4.0
31	BG	49	ASP	4.0
3	CC	139	GLN	4.0
48	B1	98	LEU	4.0
46	DZ	4	ARG	4.0
9	CI	115	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
26	DA	2157	G	4.0
2	CB	184	VAL	4.0
33	DI	17	GLN	3.9
7	CG	23	VAL	3.9
13	CM	102	ARG	3.9
2	CB	185	ILE	3.9
9	CI	26	VAL	3.9
17	CQ	39	SER	3.9
29	BE	89	ASP	3.9
32	DH	123	PHE	3.9
51	B4	48	ARG	3.9
3	CC	142	MET	3.9
7	CG	85	TYR	3.9
3	CC	149	ALA	3.9
8	CH	122	ARG	3.9
2	CB	40	HIS	3.9
31	DG	137	GLU	3.9
46	DZ	172	ALA	3.9
2	CB	69	LEU	3.9
10	CJ	74	ILE	3.9
2	CB	76	GLN	3.9
19	CS	13	ASP	3.8
2	CB	197	VAL	3.8
3	CC	78	GLY	3.8
2	CB	165	VAL	3.8
32	DH	35	VAL	3.8
2	CB	215	LEU	3.8
7	AG	156	TRP	3.8
26	DA	2112	G	3.8
42	DV	101	GLY	3.8
3	CC	108	ASN	3.8
46	DZ	146	ILE	3.8
26	DA	2125	G	3.8
2	CB	11	LEU	3.8
3	CC	134	ILE	3.8
32	DH	105	LEU	3.8
3	CC	10	PHE	3.8
20	CT	80	ARG	3.8
2	AB	37	ASN	3.8
33	DI	12	LEU	3.8
33	DI	103	ARG	3.8
19	CS	49	ILE	3.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
12	CL	64	TYR	3.7
51	D4	49	PHE	3.7
19	CS	35	SER	3.7
3	CC	22	TRP	3.7
10	CJ	93	GLY	3.7
46	DZ	143	GLY	3.7
2	CB	113	HIS	3.7
13	CM	92	HIS	3.7
26	DA	1509	C	3.7
26	DA	2138	C	3.7
46	BZ	105	VAL	3.7
20	AT	74	LYS	3.7
8	CH	130	GLY	3.7
13	CM	69	GLU	3.7
51	D4	64	GLY	3.7
28	DD	2	ALA	3.7
46	DZ	130	PRO	3.7
48	D1	2	SER	3.7
2	CB	178	ARG	3.7
1	AA	1024	G	3.7
14	CN	34	TYR	3.7
19	CS	66	MET	3.7
2	CB	205	ASP	3.7
19	AS	67	VAL	3.7
46	DZ	140	ASP	3.7
3	CC	8	ILE	3.7
10	CJ	98	ILE	3.7
33	DI	62	LYS	3.7
26	DA	883	G	3.7
18	CR	46	GLU	3.7
33	DI	91	SER	3.7
32	DH	76	VAL	3.7
1	CA	1001(A)	G	3.6
46	DZ	55	HIS	3.6
26	BA	2804	C	3.6
4	CD	152	SER	3.6
7	CG	79	ARG	3.6
14	CN	11	LYS	3.6
32	DH	95	ARG	3.6
13	CM	96	LEU	3.6
8	CH	74	PRO	3.6
8	CH	95	VAL	3.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
26	DA	2116	G	3.6
26	DA	2173	A	3.6
2	CB	89	GLY	3.6
3	CC	148	GLY	3.6
33	DI	121	LYS	3.6
39	DS	33	LYS	3.6
46	DZ	111	VAL	3.6
3	CC	57	ILE	3.6
9	CI	63	ILE	3.6
51	D4	35	VAL	3.6
51	D4	50	VAL	3.6
3	CC	180	ALA	3.6
19	CS	46	GLY	3.6
19	CS	69	HIS	3.6
1	AA	1447	A	3.5
7	AG	85	TYR	3.5
14	CN	46	GLU	3.5
3	CC	20	SER	3.5
20	AT	13	LEU	3.5
4	CD	150	GLU	3.5
46	DZ	133	ILE	3.5
47	D0	75	LEU	3.5
13	CM	4	ILE	3.5
14	CN	58	LYS	3.5
46	DZ	53	ILE	3.5
56	D9	13	LYS	3.5
8	CH	135	CYS	3.5
5	CE	10	MET	3.5
14	CN	50	LYS	3.5
1	AA	1030(C)	G	3.5
2	CB	48	MET	3.5
2	CB	158	LEU	3.5
2	CB	164	VAL	3.5
51	D4	56	VAL	3.5
33	DI	4	ILE	3.5
8	CH	71	GLY	3.5
9	CI	54	ASP	3.5
3	CC	190	ARG	3.5
26	DA	2127	G	3.5
46	DZ	150	LEU	3.5
2	CB	43	ASP	3.5
33	BI	112	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
4	AD	157	LEU	3.4
8	CH	2	LEU	3.4
3	CC	138	VAL	3.4
5	CE	148	VAL	3.4
26	DA	2132	U	3.4
2	CB	132	LYS	3.4
2	CB	49	GLU	3.4
13	CM	78	ILE	3.4
26	BA	2145	C	3.4
26	DA	2139	C	3.4
51	D4	51	ASP	3.4
11	AK	92	GLU	3.4
2	CB	115	LEU	3.4
19	CS	30	LEU	3.4
33	BI	86	THR	3.4
46	DZ	105	VAL	3.4
3	CC	54	ARG	3.4
3	CC	48	TYR	3.4
7	AG	154	TYR	3.4
7	CG	37	ASN	3.4
26	DA	2154	G	3.4
37	DQ	63	LYS	3.4
39	DS	57	LYS	3.4
31	BG	120	LEU	3.4
2	CB	57	PHE	3.4
13	AM	123	ALA	3.4
9	CI	36	TYR	3.4
13	CM	90	LEU	3.4
51	D4	53	GLU	3.4
10	CJ	96	ILE	3.4
2	CB	196	LEU	3.4
13	CM	122	LYS	3.4
31	DG	85	GLY	3.3
2	CB	68	ILE	3.3
31	DG	39	ILE	3.3
46	DZ	151	HIS	3.3
26	DA	229	A	3.3
1	AA	1027	C	3.3
2	CB	162	ILE	3.3
3	CC	186	PHE	3.3
17	CQ	44	ALA	3.3
41	BU	117	GLN	3.3

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Mol	Chain	Res	Type	RSRZ
50	D3	26	LEU	3.3
18	CR	84	LYS	3.3
26	DA	896	A	3.3
54	D7	48	LYS	3.3
2	CB	44	LEU	3.3
31	DG	135	LEU	3.3
33	DI	16	GLY	3.3
33	DI	73	GLU	3.3
33	DI	97	ILE	3.3
10	CJ	63	PHE	3.3
33	BI	85	GLU	3.3
12	CL	69	TYR	3.3
9	CI	56	LEU	3.3
2	CB	37	ASN	3.3
8	CH	134	ILE	3.3
2	CB	202	PRO	3.3
14	CN	29	ARG	3.3
11	CK	25	TYR	3.3
19	AS	18	LYS	3.3
32	DH	114	VAL	3.3
51	D4	57	GLU	3.3
42	DV	54	GLY	3.3
32	DH	88	LEU	3.3
46	DZ	8	TYR	3.3
26	BA	2120	G	3.2
5	CE	81	GLU	3.2
51	B4	56	VAL	3.2
2	CB	127	ILE	3.2
10	CJ	10	GLY	3.2
33	DI	59	ALA	3.2
19	CS	53	ASN	3.2
3	CC	76	VAL	3.2
3	CC	207	VAL	3.2
5	CE	90	VAL	3.2
7	CG	26	PHE	3.2
9	CI	45	ALA	3.2
16	AP	80	PHE	3.2
9	AI	7	THR	3.2
13	CM	94	ARG	3.2
16	AP	39	TYR	3.2
2	CB	99	GLY	3.2
19	CS	82	GLY	3.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
51	D4	69	LYS	3.2
39	DS	39	ILE	3.2
33	DI	125	GLU	3.2
2	AB	215	LEU	3.2
14	CN	61	TRP	3.2
13	CM	80	ARG	3.2
19	CS	65	ASN	3.2
2	CB	91	PRO	3.2
32	DH	94	TYR	3.2
2	CB	53	ARG	3.2
26	BA	1509	C	3.2
14	CN	39	LEU	3.2
16	CP	48	TRP	3.2
1	CA	80	G	3.2
8	AH	2	LEU	3.2
19	CS	27	GLU	3.2
20	AT	95	ALA	3.2
33	DI	55	ALA	3.2
33	DI	79	ILE	3.2
46	DZ	156	LYS	3.2
11	AK	17	GLY	3.1
33	BI	103	ARG	3.1
31	DG	48	GLU	3.1
32	DH	44	VAL	3.1
2	CB	41	ILE	3.1
10	AJ	71	LEU	3.1
19	CS	12	ASP	3.1
13	CM	60	VAL	3.1
31	DG	52	ILE	3.1
2	CB	67	THR	3.1
33	DI	82	ARG	3.1
39	DS	32	LEU	3.1
10	CJ	17	ASP	3.1
10	CJ	69	ASN	3.1
31	DG	157	ILE	3.1
8	AH	119	LEU	3.1
31	DG	97	ASP	3.1
22	AV	23	A	3.1
3	CC	23	TYR	3.1
19	AS	15	LEU	3.1
4	CD	134	ASP	3.1
2	CB	15	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
5	CE	6	PHE	3.1
9	AI	59	PHE	3.1
14	AN	15	LYS	3.1
1	AA	1033	G	3.1
17	CQ	65	ILE	3.1
5	CE	79	GLU	3.1
9	CI	79	LEU	3.1
10	CJ	59	SER	3.1
45	DY	51	VAL	3.1
46	DZ	161	VAL	3.1
19	AS	71	LEU	3.1
30	BF	17	ARG	3.1
33	DI	35	LEU	3.1
46	BZ	112	ARG	3.1
32	DH	13	LYS	3.1
10	CJ	92	THR	3.1
10	CJ	50	ILE	3.1
33	DI	71	ILE	3.1
26	DA	2142	C	3.1
4	AD	23	GLY	3.1
33	DI	140	LEU	3.1
11	AK	82	VAL	3.1
16	AP	7	ALA	3.1
3	CC	82	GLU	3.1
9	AI	81	ILE	3.1
31	DG	138	GLN	3.1
3	CC	13	GLY	3.1
8	CH	107	LEU	3.1
17	CQ	89	LEU	3.1
46	DZ	160	GLY	3.1
51	D4	39	CYS	3.1
16	AP	1	MET	3.0
31	BG	146	TYR	3.0
1	CA	1002	G	3.0
13	CM	109	THR	3.0
26	BA	2157	G	3.0
27	DB	118	G	3.0
42	DV	42	GLY	3.0
19	AS	59	PRO	3.0
2	CB	63	MET	3.0
10	CJ	100	THR	3.0
32	DH	101	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
4	AD	110	PHE	3.0
3	CC	184	TYR	3.0
19	CS	57	HIS	3.0
45	DY	44	ILE	3.0
2	CB	98	LEU	3.0
19	CS	24	ALA	3.0
19	CS	47	HIS	3.0
33	BI	89	TYR	3.0
5	CE	13	ILE	3.0
7	AG	78	ARG	3.0
33	BI	109	ILE	3.0
51	B4	53	GLU	3.0
9	CI	37	PHE	3.0
32	DH	128	PRO	3.0
32	DH	111	HIS	3.0
16	AP	19	ILE	3.0
6	AF	17	SER	3.0
13	AM	2	ALA	3.0
10	CJ	75	ILE	3.0
46	BZ	52	SER	3.0
18	AR	25	THR	3.0
3	CC	145	GLY	3.0
10	CJ	61	GLU	3.0
13	AM	22	ILE	3.0
37	DQ	137	TYR	3.0
10	CJ	67	THR	3.0
2	CB	160	ASP	3.0
10	CJ	72	VAL	3.0
9	AI	23	ASN	3.0
20	CT	42	GLN	3.0
46	DZ	138	GLU	3.0
20	CT	24	LEU	3.0
31	DG	102	PHE	3.0
17	CQ	21	VAL	2.9
31	DG	120	LEU	2.9
32	DH	25	LYS	2.9
2	CB	31	TYR	2.9
19	CS	80	TYR	2.9
4	CD	208	SER	2.9
10	CJ	64	GLU	2.9
2	CB	183	PRO	2.9
31	DG	115	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
46	DZ	120	ILE	2.9
17	CQ	22	LEU	2.9
4	CD	23	GLY	2.9
11	CK	49	GLY	2.9
26	DA	2149	G	2.9
46	BZ	106	GLY	2.9
9	AI	98	PRO	2.9
19	CS	81	ARG	2.9
2	AB	66	GLY	2.9
11	CK	13	GLN	2.9
8	AH	3	THR	2.9
13	CM	105	THR	2.9
19	AS	49	ILE	2.9
2	AB	63	MET	2.9
13	CM	98	VAL	2.9
3	CC	83	ARG	2.9
44	DX	89	ILE	2.9
53	D6	54	ILE	2.9
9	CI	102	LEU	2.9
17	CQ	84	LEU	2.9
20	CT	34	LYS	2.9
26	DA	2160	G	2.9
1	CA	1532	U	2.9
10	AJ	34	VAL	2.9
3	CC	172	ARG	2.9
8	CH	123	GLU	2.9
2	CB	71	VAL	2.9
5	CE	67	VAL	2.9
26	BA	2174	C	2.9
9	AI	19	LEU	2.9
14	AN	37	PHE	2.9
13	AM	62	ASN	2.9
32	DH	108	GLY	2.9
11	AK	89	ALA	2.9
2	AB	33	TYR	2.9
8	CH	116	LYS	2.9
2	CB	198	ASP	2.9
4	AD	176	LEU	2.9
10	CJ	71	LEU	2.9
13	AM	121	LYS	2.9
5	CE	100	VAL	2.8
31	DG	92	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
31	DG	149	VAL	2.8
46	DZ	128	VAL	2.8
9	CI	9	ARG	2.8
32	DH	151	ILE	2.8
51	B4	41	PRO	2.8
13	AM	122	LYS	2.8
19	CS	68	GLY	2.8
10	CJ	27	ALA	2.8
46	DZ	132	ASN	2.8
3	CC	132	ARG	2.8
3	CC	178	LEU	2.8
46	DZ	137	ILE	2.8
30	DF	21	ALA	2.8
31	DG	161	THR	2.8
6	AF	55	ASP	2.8
18	CR	76	LEU	2.8
33	DI	77	LEU	2.8
47	D0	84	LEU	2.8
51	B4	54	GLY	2.8
19	CS	2	PRO	2.8
31	DG	112	PRO	2.8
2	AB	135	GLN	2.8
14	CN	12	ARG	2.8
33	DI	18	VAL	2.8
27	DB	120	A	2.8
3	CC	101	LEU	2.8
36	BP	105	LEU	2.8
13	AM	6	GLY	2.8
14	CN	35	ARG	2.8
1	AA	1030(A)	G	2.8
1	CA	1202	G	2.8
33	BI	121	LYS	2.8
6	AF	48	LEU	2.8
33	DI	14	ASP	2.8
33	DI	38	LEU	2.8
36	DP	123	LEU	2.8
2	CB	75	LYS	2.8
2	CB	131	PRO	2.8
26	DA	886	C	2.8
33	DI	46	ALA	2.8
33	DI	104	GLN	2.8
3	CC	177	THR	2.8

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Mol	Chain	Res	Type	RSRZ
12	CL	60	LEU	2.8
15	AO	89	GLY	2.8
31	DG	51	ARG	2.8
44	DX	69	TYR	2.8
46	DZ	57	ILE	2.8
36	DP	1	MET	2.8
56	D9	11	CYS	2.8
3	CC	86	VAL	2.8
7	CG	77	SER	2.8
14	CN	45	ARG	2.8
51	D4	68	ARG	2.8
8	CH	86	ILE	2.8
9	CI	47	LEU	2.8
9	CI	81	ILE	2.8
20	AT	21	LYS	2.8
26	DA	2123	G	2.8
31	DG	164	GLU	2.8
33	DI	138	ILE	2.8
46	DZ	154	ASP	2.8
42	DV	92	THR	2.8
10	CJ	43	ARG	2.8
1	CA	1115	C	2.8
4	CD	2	GLY	2.8
4	CD	167	GLY	2.8
3	CC	14	ILE	2.8
7	CG	16	LEU	2.8
1	CA	1156	G	2.8
10	CJ	77	PRO	2.8
31	DG	37	VAL	2.8
3	CC	17	ASP	2.7
32	DH	98	LEU	2.7
2	CB	30	ARG	2.7
15	CO	68	ARG	2.7
5	CE	145	LYS	2.7
9	CI	70	LYS	2.7
14	AN	2	ALA	2.7
26	DA	2135	A	2.7
51	B4	43	TYR	2.7
34	DN	9	VAL	2.7
7	CG	12	LEU	2.7
10	CJ	88	LEU	2.7
8	CH	76	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
32	DH	19	VAL	2.7
26	DA	2147	G	2.7
46	DZ	24	LEU	2.7
20	CT	77	ALA	2.7
8	AH	94	TYR	2.7
31	DG	35	GLU	2.7
51	D4	67	TYR	2.7
3	AC	66	VAL	2.7
9	CI	14	VAL	2.7
32	DH	106	THR	2.7
5	CE	96	PRO	2.7
46	DZ	163	LEU	2.7
8	CH	54	ASP	2.7
26	DA	2128	C	2.7
2	AB	123	ALA	2.7
10	AJ	20	ALA	2.7
13	CM	73	GLU	2.7
2	CB	66	GLY	2.7
3	CC	171	GLY	2.7
15	CO	60	VAL	2.7
17	AQ	10	VAL	2.7
20	CT	29	LYS	2.7
33	DI	92	VAL	2.7
31	DG	117	PHE	2.7
31	DG	152	LEU	2.7
39	DS	54	LEU	2.7
19	CS	14	HIS	2.7
2	CB	218	ALA	2.7
45	DY	35	TYR	2.7
33	BI	80	PRO	2.7
51	D4	41	PRO	2.7
11	CK	21	ILE	2.7
11	CK	95	ILE	2.7
2	AB	129	GLU	2.7
2	CB	109	SER	2.7
2	CB	62	ALA	2.7
20	AT	87	LYS	2.7
26	DA	645	C	2.7
4	CD	130	GLY	2.7
13	CM	103	THR	2.7
10	CJ	55	LYS	2.7
17	CQ	58	GLU	2.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	CB	161	ALA	2.7
37	DQ	33	GLY	2.7
10	CJ	34	VAL	2.7
9	AI	5	TYR	2.7
19	CS	61	TYR	2.7
5	CE	88	LYS	2.7
20	AT	14	LYS	2.7
7	CG	156	TRP	2.7
51	D4	47	GLN	2.7
33	DI	15	VAL	2.7
1	CA	1531	A	2.6
20	AT	20	LEU	2.6
26	BA	2131	G	2.6
32	DH	87	LEU	2.6
45	DY	61	ILE	2.6
2	CB	16	HIS	2.6
17	CQ	87	LYS	2.6
37	DQ	106	VAL	2.6
26	DA	2146	C	2.6
2	AB	200	ILE	2.6
1	AA	1026	G	2.6
3	CC	51	GLY	2.6
44	DX	33	LYS	2.6
4	CD	170	VAL	2.6
8	CH	138	TRP	2.6
15	CO	7	GLU	2.6
2	CB	51	LEU	2.6
16	CP	19	ILE	2.6
2	CB	123	ALA	2.6
15	CO	16	ALA	2.6
1	CA	1034	G	2.6
20	AT	71	THR	2.6
8	CH	39	LEU	2.6
12	AL	64	TYR	2.6
45	DY	57	GLN	2.6
1	CA	1026	G	2.6
5	CE	24	ARG	2.6
45	DY	60	PHE	2.6
4	CD	20	TYR	2.6
9	CI	62	TYR	2.6
9	CI	106	ALA	2.6
9	CI	119	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
10	CJ	41	PRO	2.6
13	CM	112	GLY	2.6
51	D4	46	GLN	2.6
10	AJ	72	VAL	2.6
33	BI	107	VAL	2.6
42	DV	47	VAL	2.6
26	BA	2805	G	2.6
27	DB	56	G	2.6
46	DZ	117	LEU	2.6
17	CQ	80	GLY	2.6
20	CT	41	ILE	2.6
4	CD	169	LYS	2.6
5	AE	92	LYS	2.6
5	CE	120	THR	2.6
2	CB	233	SER	2.6
20	CT	36	LEU	2.6
32	DH	110	SER	2.6
37	DQ	30	GLY	2.6
37	DQ	62	GLY	2.6
2	CB	85	ALA	2.6
2	CB	133	LYS	2.6
10	CJ	44	VAL	2.6
14	CN	56	VAL	2.6
19	CS	51	VAL	2.6
3	CC	47	LEU	2.6
2	CB	72	GLY	2.6
2	CB	8	LYS	2.6
10	AJ	6	ILE	2.6
20	CT	51	GLU	2.6
46	DZ	145	GLU	2.6
32	DH	96	ALA	2.6
1	CA	1447	A	2.6
26	DA	2170	A	2.6
46	DZ	72	ARG	2.5
3	CC	188	LEU	2.5
3	CC	205	GLY	2.5
17	CQ	100	LYS	2.5
18	AR	46	GLU	2.5
4	CD	158	ILE	2.5
33	BI	88	ILE	2.5
5	CE	113	ALA	2.5
9	AI	43	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
12	CL	68	ALA	2.5
8	CH	72	PRO	2.5
20	AT	98	PRO	2.5
2	CB	130	ARG	2.5
17	CQ	24	GLU	2.5
31	BG	103	LEU	2.5
10	CJ	23	ILE	2.5
51	B4	52	THR	2.5
42	DV	12	TYR	2.5
51	D4	43	TYR	2.5
5	CE	8	GLU	2.5
26	BA	2162	G	2.5
53	D6	11	LEU	2.5
3	CC	79	ARG	2.5
7	CG	150	ALA	2.5
9	AI	52	ALA	2.5
8	CH	9	MET	2.5
2	CB	94	ASN	2.5
2	CB	52	GLU	2.5
46	DZ	134	PRO	2.5
13	AM	56	LEU	2.5
20	CT	91	LEU	2.5
26	DA	890	A	2.5
27	DB	58	A	2.5
33	DI	57	ARG	2.5
2	CB	58	ILE	2.5
1	AA	1257	U	2.5
2	CB	88	ALA	2.5
9	CI	122	ALA	2.5
14	CN	10	ALA	2.5
31	DG	169	ALA	2.5
37	DQ	121	ALA	2.5
9	CI	53	VAL	2.5
33	DI	3	VAL	2.5
52	B5	60	VAL	2.5
9	AI	85	LEU	2.5
10	CJ	8	LEU	2.5
18	AR	40	LEU	2.5
18	AR	66	LEU	2.5
37	DQ	5	ARG	2.5
26	DA	2804	C	2.5
46	DZ	59	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
19	CS	7	LYS	2.5
19	CS	40	ILE	2.5
12	CL	67	THR	2.5
42	DV	26	ASP	2.5
7	AG	91	VAL	2.5
10	CJ	46	ARG	2.5
12	CL	101	VAL	2.5
14	AN	16	PHE	2.5
19	AS	60	VAL	2.5
10	CJ	31	GLY	2.5
10	CJ	37	PRO	2.5
11	AK	25	TYR	2.5
31	DG	107	LEU	2.5
21	AU	14	TRP	2.5
37	DQ	135	ASP	2.5
6	CF	40	VAL	2.5
14	CN	60	SER	2.5
19	AS	39	THR	2.5
5	CE	119	LEU	2.5
7	AG	112	PRO	2.5
3	CC	169	ALA	2.5
44	DX	1	MET	2.5
41	DU	90	VAL	2.5
2	CB	33	TYR	2.5
9	CI	4	TYR	2.5
10	CJ	26	ALA	2.5
19	AS	27	GLU	2.5
37	DQ	139	GLU	2.5
26	DA	884	C	2.5
32	DH	113	VAL	2.5
9	CI	126	SER	2.4
26	DA	2166	G	2.4
32	DH	116	GLU	2.4
7	CG	152	ALA	2.4
2	CB	105	PHE	2.4
17	CQ	71	PHE	2.4
5	CE	12	LEU	2.4
3	CC	191	THR	2.4
2	CB	199	TYR	2.4
5	AE	102	ALA	2.4
5	AE	23	GLY	2.4
31	BG	178	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
32	DH	93	GLY	2.4
51	B4	51	ASP	2.4
3	CC	68	VAL	2.4
19	CS	34	TRP	2.4
4	AD	179	GLU	2.4
33	DI	117	GLU	2.4
39	BS	24	LEU	2.4
13	AM	4	ILE	2.4
3	CC	30	ARG	2.4
46	DZ	131	ARG	2.4
4	CD	180	GLY	2.4
14	AN	36	PHE	2.4
2	AB	165	VAL	2.4
3	CC	147	LYS	2.4
8	CH	79	VAL	2.4
9	CI	116	LYS	2.4
34	BN	140	VAL	2.4
46	DZ	97	GLU	2.4
2	CB	10	LEU	2.4
10	CJ	40	LEU	2.4
16	AP	6	LEU	2.4
4	CD	29	PRO	2.4
39	DS	79	ALA	2.4
46	DZ	164	ALA	2.4
37	DQ	130	LYS	2.4
2	CB	59	GLU	2.4
32	DH	43	VAL	2.4
32	DH	159	GLU	2.4
20	CT	55	ILE	2.4
36	DP	109	GLY	2.4
4	CD	24	GLU	2.4
7	CG	129	GLU	2.4
48	D1	60	PHE	2.4
5	CE	33	VAL	2.4
7	CG	91	VAL	2.4
8	CH	93	VAL	2.4
9	AI	17	VAL	2.4
31	DG	155	MET	2.4
37	DQ	56	ARG	2.4
1	CA	1036	G	2.4
26	BA	2116	G	2.4
49	D2	9	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
2	CB	228	GLY	2.4
8	CH	115	SER	2.4
10	CJ	36	GLY	2.4
15	CO	89	GLY	2.4
47	D0	76	GLY	2.4
6	CF	55	ASP	2.4
17	CQ	23	VAL	2.4
21	CU	6	ARG	2.4
45	DY	24	VAL	2.4
3	AC	196	LEU	2.4
3	CC	52	LEU	2.4
19	CS	44	MET	2.4
14	CN	48	ALA	2.4
26	BA	2803	C	2.4
26	DA	2168	G	2.4
2	CB	152	PHE	2.4
3	CC	144	SER	2.4
5	CE	152	ARG	2.4
3	CC	43	LEU	2.4
8	AH	32	LYS	2.4
37	DQ	28	ALA	2.4
26	BA	2140	C	2.4
5	CE	150	ARG	2.4
44	DX	86	GLY	2.4
9	CI	127	LYS	2.4
12	CL	28	LYS	2.4
19	AS	19	VAL	2.4
5	CE	31	LEU	2.3
26	DA	887	A	2.3
7	CG	40	ALA	2.3
9	CI	42	ARG	2.3
2	CB	139	LYS	2.3
9	CI	123	PRO	2.3
31	DG	49	ASP	2.3
32	DH	17	VAL	2.3
33	DI	19	VAL	2.3
1	CA	1024	G	2.3
4	AD	135	LEU	2.3
5	CE	123	LEU	2.3
14	CN	47	LEU	2.3
22	CV	18	G	2.3
26	BA	2793	G	2.3

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Mol	Chain	Res	Type	RSRZ
3	CC	105	GLU	2.3
20	AT	23	ARG	2.3
27	DB	25	A	2.3
4	AD	16	GLY	2.3
1	AA	1029	C	2.3
33	DI	8	PRO	2.3
4	CD	198	VAL	2.3
9	AI	26	VAL	2.3
10	CJ	35	SER	2.3
13	CM	3	ARG	2.3
20	AT	24	LEU	2.3
1	CA	1021	G	2.3
11	CK	31	THR	2.3
26	DA	652(U)	G	2.3
7	CG	132	GLY	2.3
49	D2	1	MET	2.3
51	D4	54	GLY	2.3
9	CI	18	PHE	2.3
1	AA	1030	C	2.3
13	CM	97	PRO	2.3
26	BA	2161	C	2.3
11	CK	84	VAL	2.3
16	AP	17	TYR	2.3
36	DP	110	TYR	2.3
13	CM	30	ALA	2.3
14	CN	38	GLY	2.3
26	BA	1913	A	2.3
28	BD	2	ALA	2.3
1	AA	1023	G	2.3
26	DA	2159	G	2.3
10	CJ	29	ARG	2.3
20	CT	30	LYS	2.3
26	DA	34	C	2.3
18	AR	85	LEU	2.3
56	B9	12	ASP	2.3
32	BH	2	SER	2.3
2	CB	237	ALA	2.3
10	AJ	68	HIS	2.3
50	D3	40	THR	2.3
51	D4	42	PHE	2.3
2	AB	202	PRO	2.3
10	CJ	91	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
16	AP	15	PRO	2.3
31	DG	159	VAL	2.3
1	CA	1028	C	2.3
16	AP	68	ASP	2.3
26	DA	2137	C	2.3
26	DA	2174	C	2.3
31	DG	108	ASN	2.3
3	CC	124	ILE	2.3
4	CD	146	ILE	2.3
17	AQ	65	ILE	2.3
17	CQ	15	MET	2.3
5	CE	45	PHE	2.3
12	AL	65	GLU	2.3
1	CA	1030(C)	G	2.3
45	DY	74	PRO	2.3
20	CT	45	GLN	2.3
31	DG	62	LEU	2.3
13	CM	72	ALA	2.3
19	AS	44	MET	2.3
19	CS	31	ILE	2.3
19	CS	62	ILE	2.3
5	AE	135	THR	2.3
18	CR	47	THR	2.3
33	DI	78	THR	2.3
4	AD	170	VAL	2.3
32	DH	97	ARG	2.3
42	DV	5	VAL	2.3
6	CF	79	LEU	2.3
11	CK	98	LEU	2.3
1	AA	1001(A)	G	2.3
20	AT	66	ALA	2.3
3	AC	206	GLU	2.3
7	AG	50	ILE	2.3
3	CC	55	VAL	2.3
3	CC	130	VAL	2.3
11	CK	30	VAL	2.3
17	CQ	77	VAL	2.3
31	BG	160	VAL	2.3
33	BI	81	VAL	2.3
3	CC	72	LYS	2.3
20	CT	90	GLN	2.3
46	DZ	159	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
16	CP	7	ALA	2.2
46	DZ	51	ALA	2.2
7	AG	62	PHE	2.2
33	DI	120	ILE	2.2
1	CA	1035	A	2.2
9	AI	6	GLY	2.2
11	CK	118	GLY	2.2
20	CT	62	LEU	2.2
14	CN	2	ALA	2.2
33	DI	80	PRO	2.2
41	DU	21	ALA	2.2
46	DZ	109	ALA	2.2
2	CB	19	HIS	2.2
3	AC	201	TYR	2.2
11	AK	32	ILE	2.2
20	CT	9	ASN	2.2
26	DA	2161	C	2.2
4	CD	137	SER	2.2
26	BA	2792	G	2.2
3	CC	116	VAL	2.2
10	CJ	94	VAL	2.2
10	CJ	90	LEU	2.2
31	DG	177	GLY	2.2
8	CH	132	GLU	2.2
9	CI	49	PRO	2.2
10	CJ	89	ASP	2.2
20	CT	46	GLU	2.2
10	CJ	54	PHE	2.2
7	AG	153	HIS	2.2
8	CH	113	SER	2.2
19	CS	38	SER	2.2
46	DZ	99	TYR	2.2
1	AA	1036	G	2.2
9	CI	44	VAL	2.2
12	CL	63	GLY	2.2
19	CS	41	VAL	2.2
3	CC	21	ARG	2.2
4	CD	11	LEU	2.2
33	DI	47	LEU	2.2
47	D0	68	GLU	2.2
48	D1	75	GLU	2.2
51	D4	34	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
46	DZ	25	PRO	2.2
15	CO	87	ILE	2.2
46	DZ	54	HIS	2.2
26	BA	2108	C	2.2
46	DZ	98	MET	2.2
7	CG	4	ARG	2.2
8	CH	41	ARG	2.2
12	CL	96	VAL	2.2
13	CM	88	ARG	2.2
14	AN	56	VAL	2.2
32	DH	67	LEU	2.2
14	CN	9	LYS	2.2
19	AS	13	ASP	2.2
34	DN	43	THR	2.2
3	CC	5	ILE	2.2
8	CH	109	ILE	2.2
9	AI	30	GLY	2.2
9	CI	23	ASN	2.2
45	DY	72	VAL	2.2
9	CI	99	LEU	2.2
46	DZ	18	LEU	2.2
11	AK	81	ASP	2.2
18	AR	20	ALA	2.2
31	DG	116	ASP	2.2
1	AA	1031	G	2.2
9	CI	21	PRO	2.2
5	CE	143	ARG	2.2
18	AR	56	THR	2.2
50	D3	57	GLU	2.2
8	CH	19	VAL	2.2
19	CS	60	VAL	2.2
8	CH	63	LEU	2.2
1	AA	1532	U	2.2
11	AK	57	THR	2.2
18	CR	56	THR	2.2
20	AT	69	GLY	2.2
9	CI	92	TYR	2.2
15	CO	71	GLN	2.2
29	DE	52	LEU	2.2
31	DG	106	LEU	2.2
42	DV	35	LEU	2.2
12	CL	26	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	CA	1492	A	2.2
3	CC	150	LYS	2.2
46	DZ	48	PHE	2.2
10	CJ	38	ILE	2.2
18	CR	25	THR	2.2
7	CG	5	ARG	2.2
16	CP	6	LEU	2.2
26	BA	2125	G	2.2
26	DA	2805	G	2.2
33	DI	37	VAL	2.2
56	D9	16	VAL	2.2
13	CM	76	ALA	2.2
13	CM	118	ALA	2.2
32	DH	84	SER	2.1
44	DX	34	ALA	2.2
2	CB	55	PHE	2.1
2	CB	220	ASP	2.1
56	D9	15	LYS	2.1
46	DZ	88	PHE	2.1
8	AH	13	ILE	2.1
31	DG	24	GLY	2.1
31	DG	179	PRO	2.1
39	DS	71	ARG	2.1
6	AF	88	VAL	2.1
9	CI	17	VAL	2.1
19	CS	5	LEU	2.1
1	CA	1190	G	2.1
11	CK	94	ALA	2.1
28	BD	276	LYS	2.1
45	DY	20	TYR	2.1
17	AQ	12	SER	2.1
45	DY	29	GLU	2.1
3	CC	158	GLY	2.1
5	CE	77	PRO	2.1
7	AG	155	ARG	2.1
8	CH	66	GLY	2.1
13	AM	102	ARG	2.1
14	CN	57	ARG	2.1
39	DS	45	GLY	2.1
5	CE	105	VAL	2.1
13	AM	105	THR	2.1
21	CU	14	TRP	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	CA	79	G	2.1
2	AB	42	ILE	2.1
12	CL	29	GLY	2.1
19	CS	26	GLY	2.1
26	DA	652(B)	A	2.1
5	CE	106	PRO	2.1
15	AO	19	PRO	2.1
20	CT	74	LYS	2.1
46	DZ	62	PRO	2.1
9	AI	41	VAL	2.1
9	AI	87	GLN	2.1
6	CF	21	LEU	2.1
9	CI	85	LEU	2.1
31	DG	34	LEU	2.1
33	DI	127	VAL	2.1
10	CJ	42	THR	2.1
37	DQ	115	MET	2.1
20	AT	59	ALA	2.1
20	CT	28	ALA	2.1
1	CA	1257	U	2.1
9	CI	20	ARG	2.1
9	CI	88	TYR	2.1
31	DG	25	TYR	2.1
33	DI	20	ASP	2.1
30	BF	172	TRP	2.1
17	CQ	14	LYS	2.1
33	DI	13	GLY	2.1
26	BA	2121	G	2.1
26	DA	888	C	2.1
33	DI	51	ILE	2.1
3	CC	7	PRO	2.1
4	AD	37	PRO	2.1
33	BI	137	PRO	2.1
9	CI	10	ARG	2.1
12	AL	93	LEU	2.1
31	DG	3	LEU	2.1
31	DG	173	LEU	2.1
33	DI	5	LEU	2.1
2	CB	148	TYR	2.1
7	AG	26	PHE	2.1
16	AP	38	TYR	2.1
47	D0	52	GLY	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	CC	77	ILE	2.1
10	AJ	98	ILE	2.1
26	BA	2128	C	2.1
8	CH	27	PRO	2.1
19	CS	59	PRO	2.1
1	AA	216	G	2.1
1	AA	1002	G	2.1
8	CH	22	GLU	2.1
13	CM	67	GLU	2.1
26	BA	2110	G	2.1
32	DH	49	VAL	2.1
31	DG	86	MET	2.1
17	CQ	32	TYR	2.1
11	CK	108	ILE	2.1
3	CC	85	ARG	2.1
10	CJ	5	ARG	2.1
10	CJ	45	ARG	2.1
20	AT	25	ARG	2.1
25	CY	74	C	2.1
26	BA	2142	C	2.1
19	CS	6	LYS	2.1
20	AT	68	LYS	2.1
20	CT	66	ALA	2.1
14	CN	49	HIS	2.1
3	CC	102	ASN	2.1
8	CH	38	ILE	2.1
10	AJ	96	ILE	2.1
31	DG	88	ILE	2.1
37	DQ	47	ILE	2.1
10	CJ	7	LYS	2.1
39	DS	68	GLN	2.1
45	DY	46	LYS	2.1
1	CA	1493	A	2.1
7	AG	80	VAL	2.1
26	BA	2146	C	2.1
26	DA	652(T)	C	2.1
31	DG	139	LEU	2.1
46	DZ	91	LEU	2.1
4	AD	111	ALA	2.1
11	CK	15	ALA	2.1
14	CN	59	ALA	2.1
1	CA	1011	G	2.1

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Mol	Chain	Res	Type	RSRZ
14	CN	23	ARG	2.1
2	CB	190	THR	2.1
10	AJ	64	GLU	2.1
10	AJ	75	ILE	2.1
31	DG	93	THR	2.1
19	CS	23	ASN	2.1
19	CS	64	GLU	2.1
11	AK	107	SER	2.1
9	CI	98	PRO	2.1
49	D2	64	LEU	2.1
1	AA	163	C	2.1
1	AA	1007	C	2.1
20	AT	52	ALA	2.1
36	BP	12	ALA	2.1
10	CJ	86	MET	2.0
5	CE	75	THR	2.0
13	CM	43	THR	2.0
15	AO	87	ILE	2.0
17	CQ	36	ILE	2.0
32	DH	124	GLU	2.0
33	DI	135	GLU	2.0
33	DI	76	THR	2.0
11	CK	117	ASN	2.0
3	CC	59	ARG	2.0
3	CC	173	VAL	2.0
13	AM	60	VAL	2.0
15	CO	67	LEU	2.0
33	DI	142	VAL	2.0
46	DZ	144	LEU	2.0
32	DH	150	ALA	2.0
4	CD	87	GLY	2.0
26	BA	652(S)	C	2.0
26	BA	885	C	2.0
26	DA	2140	C	2.0
26	DA	2794	C	2.0
36	DP	149	GLU	2.0
44	DX	80	ILE	2.0
9	CI	124	GLN	2.0
7	CG	61	VAL	2.0
19	CS	22	LEU	2.0
26	BA	2155	G	2.0
9	AI	106	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
48	B1	2	SER	2.0
31	BG	48	GLU	2.0
35	BO	112	MET	2.0
21	CU	5	ASP	2.0
46	BZ	45	ASP	2.0
4	AD	168	ARG	2.0
47	D0	3	HIS	2.0
49	D2	57	ILE	2.0
51	D4	55	ARG	2.0
7	CG	17	VAL	2.0
31	DG	165	THR	2.0
2	CB	186	ALA	2.0
4	AD	180	GLY	2.0
16	CP	9	PHE	2.0
26	DA	2110	G	2.0
26	DA	2153	G	2.0
32	DH	82	GLY	2.0
3	CC	44	GLU	2.0
6	CF	51	PRO	2.0
12	CL	48	PRO	2.0
19	CS	17	GLU	2.0
15	CO	77	ARG	2.0
26	BA	2111	C	2.0
40	DT	1	MET	2.0
53	D6	28	ARG	2.0
16	AP	59	TRP	2.0
5	AE	88	LYS	2.0
31	DG	182	LYS	2.0
32	DH	138	LYS	2.0
7	CG	38	LEU	2.0
7	CG	44	TYR	2.0
3	CC	9	GLY	2.0
5	AE	98	THR	2.0
12	CL	55	VAL	2.0
32	DH	157	TYR	2.0
46	DZ	41	LEU	2.0
50	D3	59	VAL	2.0
9	AI	24	GLY	2.0
45	DY	43	ASN	2.0
47	D0	54	GLY	2.0
10	CJ	83	GLU	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
23	PPU	AW	76	37/38	0.97	0.20	-	12,29,37,42	0
24	5MC	CX	32	21/22	0.85	0.22	-	68,80,88,99	0
24	PSU	AX	55	20/21	0.93	0.16	-	58,70,77,82	0
24	PSU	CX	55	20/21	0.91	0.16	-	61,72,81,89	0
24	5MU	CX	54	21/22	0.92	0.13	-	71,79,92,107	0
24	5MC	AX	32	21/22	0.95	0.18	-	46,55,75,77	0
24	5MU	AX	54	21/22	0.95	0.16	-	57,67,82,96	0
24	4SU	AX	8	20/21	0.95	0.17	-	47,59,67,84	0
24	31H	AX	76	30/33	0.96	0.26	-	14,31,55,77	8
24	31H	CX	76	32/33	0.95	0.23	-	23,42,61,84	10
24	4SU	CX	8	20/21	0.90	0.17	-	61,80,93,118	0
23	PPU	CW	76	37/38	0.97	0.23	-	27,41,53,63	0

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
57	MG	BA	3027	1/1	0.89	1.04	67.56	36,36,36,36	0
57	MG	BA	3036	1/1	0.95	0.64	63.42	42,42,42,42	0
57	MG	DA	3238	1/1	0.98	0.43	33.85	31,31,31,31	0
57	MG	DA	3141	1/1	0.87	0.23	28.27	37,37,37,37	0
57	MG	BA	3244	1/1	0.96	0.39	27.78	29,29,29,29	0
57	MG	DA	3039	1/1	0.94	0.39	27.40	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	CA	3126	1/1	0.83	0.37	25.78	73,73,73,73	0
57	MG	BA	3226	1/1	0.96	0.43	25.58	36,36,36,36	0
57	MG	DA	3001	1/1	0.89	0.37	25.38	45,45,45,45	0
57	MG	DA	3277	1/1	0.95	0.44	23.93	50,50,50,50	0
57	MG	BA	3185	1/1	0.98	0.50	23.04	34,34,34,34	0
57	MG	BA	3401	1/1	0.93	0.28	22.75	31,31,31,31	0
57	MG	DA	3042	1/1	0.95	0.32	22.56	37,37,37,37	0
57	MG	DA	3533	1/1	0.81	0.48	21.51	47,47,47,47	0
57	MG	DA	3173	1/1	0.97	0.34	20.81	42,42,42,42	0
57	MG	BA	3125	1/1	0.98	0.39	20.78	30,30,30,30	0
57	MG	BQ	3003	1/1	0.83	0.73	20.07	68,68,68,68	0
57	MG	DA	3177	1/1	0.94	0.34	19.16	29,29,29,29	0
57	MG	BA	3277	1/1	0.95	0.30	17.04	34,34,34,34	0
57	MG	DA	3210	1/1	0.94	0.44	16.68	57,57,57,57	0
57	MG	DA	3350	1/1	0.93	0.36	16.45	44,44,44,44	0
57	MG	DA	3456	1/1	0.96	0.35	15.88	59,59,59,59	0
57	MG	DA	3351	1/1	0.96	0.34	15.62	45,45,45,45	0
57	MG	DE	302	1/1	0.94	0.60	15.38	51,51,51,51	0
57	MG	DA	3267	1/1	0.89	0.29	14.97	45,45,45,45	0
57	MG	DA	3579	1/1	0.99	0.30	14.29	58,58,58,58	0
57	MG	BA	3533	1/1	0.89	0.28	14.20	45,45,45,45	0
57	MG	BA	3267	1/1	0.95	0.36	13.68	33,33,33,33	0
57	MG	DA	3609	1/1	0.66	0.26	13.56	55,55,55,55	0
57	MG	BA	3602	1/1	0.96	0.34	13.41	65,65,65,65	0
57	MG	BA	3271	1/1	0.95	0.34	13.25	45,45,45,45	0
57	MG	DA	3170	1/1	0.94	0.37	12.80	47,47,47,47	0
57	MG	BA	3131	1/1	0.97	0.38	12.70	31,31,31,31	0
57	MG	BA	3514	1/1	0.87	0.37	12.47	36,36,36,36	0
57	MG	DA	3257	1/1	0.91	0.33	12.38	46,46,46,46	0
57	MG	DA	3619	1/1	0.86	0.43	12.34	63,63,63,63	0
57	MG	BU	204	1/1	0.96	0.33	12.12	38,38,38,38	0
57	MG	BU	208	1/1	0.92	0.44	12.10	39,39,39,39	0
57	MG	BN	3006	1/1	0.95	0.62	11.96	47,47,47,47	0
57	MG	CA	3116	1/1	0.64	0.33	11.89	74,74,74,74	0
57	MG	BW	202	1/1	0.95	0.60	11.83	41,41,41,41	0
57	MG	BA	3384	1/1	0.97	0.29	11.81	19,19,19,19	0
57	MG	BA	3461	1/1	0.97	0.25	11.68	32,32,32,32	0
57	MG	BA	3412	1/1	0.87	0.40	11.36	44,44,44,44	0
57	MG	AA	3055	1/1	0.91	0.31	11.27	53,53,53,53	0
57	MG	BA	3245	1/1	0.98	0.31	11.21	37,37,37,37	0
57	MG	DA	3373	1/1	0.98	0.23	11.10	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BN	3004	1/1	0.95	0.56	10.97	49,49,49,49	0
57	MG	BA	3105	1/1	0.92	0.25	10.92	45,45,45,45	0
57	MG	DA	3614	1/1	0.97	0.49	10.79	56,56,56,56	0
57	MG	DA	3602	1/1	0.86	0.25	10.61	50,50,50,50	0
57	MG	BA	3698	1/1	0.92	0.30	10.21	51,51,51,51	0
57	MG	BE	3001	1/1	0.98	0.34	10.08	48,48,48,48	0
57	MG	BP	3001	1/1	0.94	0.43	10.06	49,49,49,49	0
57	MG	CA	3054	1/1	0.85	0.36	9.90	53,53,53,53	0
57	MG	BE	3002	1/1	0.88	0.44	9.85	50,50,50,50	0
57	MG	CA	3017	1/1	0.85	0.29	9.46	69,69,69,69	0
57	MG	BA	3534	1/1	0.88	0.28	9.43	23,23,23,23	0
57	MG	BA	3101	1/1	0.98	0.29	9.31	29,29,29,29	0
57	MG	DD	306	1/1	0.94	0.38	9.27	44,44,44,44	0
57	MG	BA	3651	1/1	0.81	0.26	9.24	62,62,62,62	0
57	MG	DA	3255	1/1	0.90	0.28	9.20	34,34,34,34	0
57	MG	BD	301	1/1	0.96	0.37	9.11	37,37,37,37	0
57	MG	DA	3559	1/1	0.94	0.21	8.96	31,31,31,31	0
57	MG	DA	3440	1/1	0.95	0.26	8.77	44,44,44,44	0
57	MG	DA	3234	1/1	0.93	0.30	8.73	34,34,34,34	0
57	MG	DA	3258	1/1	0.97	0.26	8.65	32,32,32,32	0
57	MG	DA	3441	1/1	0.95	0.27	8.60	43,43,43,43	0
57	MG	DB	3005	1/1	0.94	0.20	8.57	54,54,54,54	0
57	MG	BD	310	1/1	0.91	0.40	8.46	34,34,34,34	0
57	MG	BA	3663	1/1	0.95	0.24	8.44	36,36,36,36	0
57	MG	DA	3274	1/1	0.95	0.22	8.37	45,45,45,45	0
57	MG	BA	3257	1/1	0.90	0.31	8.22	40,40,40,40	0
57	MG	BA	3111	1/1	0.90	0.29	8.15	51,51,51,51	0
57	MG	BA	3054	1/1	0.93	0.25	8.05	44,44,44,44	0
57	MG	DA	3628	1/1	0.85	0.57	7.85	59,59,59,59	0
57	MG	DA	3426	1/1	0.90	0.34	7.84	38,38,38,38	0
57	MG	AA	3113	1/1	0.87	0.29	7.77	54,54,54,54	0
57	MG	BA	3490	1/1	0.96	0.28	7.65	17,17,17,17	0
57	MG	BA	3707	1/1	0.95	0.36	7.49	34,34,34,34	0
57	MG	DA	3216	1/1	0.92	0.30	7.47	43,43,43,43	0
57	MG	BQ	3001	1/1	0.95	0.32	7.45	51,51,51,51	0
57	MG	DA	3251	1/1	0.93	0.28	7.42	34,34,34,34	0
57	MG	BA	3259	1/1	0.97	0.29	7.40	40,40,40,40	0
57	MG	BA	3498	1/1	0.97	0.23	7.20	45,45,45,45	0
57	MG	AX	3007	1/1	0.95	0.27	7.01	54,54,54,54	0
57	MG	AA	3024	1/1	0.97	0.24	6.90	49,49,49,49	0
57	MG	BU	206	1/1	0.91	0.35	6.87	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3376	1/1	0.93	0.24	6.82	40,40,40,40	0
57	MG	BA	3405	1/1	0.96	0.24	6.71	31,31,31,31	0
57	MG	BA	3283	1/1	0.97	0.23	6.60	22,22,22,22	0
57	MG	DA	3116	1/1	0.90	0.23	6.53	36,36,36,36	0
57	MG	BA	3709	1/1	0.88	0.33	6.52	45,45,45,45	0
57	MG	DU	3001	1/1	0.97	0.62	6.52	56,56,56,56	0
57	MG	BA	3530	1/1	0.94	0.26	6.46	20,20,20,20	0
57	MG	DD	305	1/1	0.88	0.36	6.38	48,48,48,48	0
57	MG	BA	3160	1/1	0.97	0.25	6.33	23,23,23,23	0
57	MG	BA	3067	1/1	0.95	0.25	6.28	26,26,26,26	0
57	MG	DA	3004	1/1	0.96	0.28	6.26	32,32,32,32	0
57	MG	DA	3242	1/1	0.96	0.20	6.21	48,48,48,48	0
57	MG	DA	3127	1/1	0.97	0.35	6.21	40,40,40,40	0
57	MG	BA	3118	1/1	0.94	0.24	6.17	28,28,28,28	0
57	MG	BA	3677	1/1	0.95	0.24	6.10	30,30,30,30	0
57	MG	BA	3396	1/1	0.82	0.24	6.08	20,20,20,20	0
57	MG	DA	3501	1/1	0.93	0.24	6.03	47,47,47,47	0
57	MG	DA	3061	1/1	0.89	0.27	5.85	36,36,36,36	0
57	MG	BA	3212	1/1	0.98	0.29	5.83	24,24,24,24	0
57	MG	BN	3001	1/1	0.96	0.47	5.83	46,46,46,46	0
57	MG	DA	3444	1/1	0.86	0.25	5.78	37,37,37,37	0
57	MG	DA	3410	1/1	0.82	0.23	5.78	37,37,37,37	0
57	MG	AA	3144	1/1	0.94	0.28	5.75	44,44,44,44	0
57	MG	BA	3281	1/1	0.87	0.26	5.70	46,46,46,46	0
57	MG	DA	3448	1/1	0.90	0.25	5.59	36,36,36,36	0
57	MG	AA	3172	1/1	0.85	0.28	5.52	54,54,54,54	0
57	MG	DA	3621	1/1	0.96	0.46	5.49	61,61,61,61	0
57	MG	BA	3114	1/1	0.96	0.24	5.39	41,41,41,41	0
57	MG	BD	311	1/1	0.92	0.36	5.38	60,60,60,60	0
57	MG	DA	3369	1/1	0.85	0.26	5.37	36,36,36,36	0
57	MG	AA	3074	1/1	0.95	0.27	5.36	38,38,38,38	0
57	MG	DA	3162	1/1	0.81	0.44	5.34	58,58,58,58	0
57	MG	DA	3030	1/1	0.97	0.39	5.31	32,32,32,32	0
57	MG	BA	3133	1/1	0.96	0.24	5.28	29,29,29,29	0
57	MG	AA	3030	1/1	0.94	0.27	5.22	41,41,41,41	0
57	MG	DA	3015	1/1	0.98	0.25	5.18	41,41,41,41	0
57	MG	DA	3192	1/1	0.97	0.23	5.15	31,31,31,31	0
57	MG	DA	3185	1/1	0.94	0.20	5.13	57,57,57,57	0
57	MG	BA	3041	1/1	0.96	0.25	5.10	39,39,39,39	0
57	MG	DA	3538	1/1	0.93	0.23	5.08	77,77,77,77	0
57	MG	AA	3083	1/1	0.98	0.29	5.07	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3705	1/1	0.96	0.32	5.04	32,32,32,32	0
57	MG	BA	3423	1/1	0.96	0.25	5.04	26,26,26,26	0
57	MG	DA	3161	1/1	0.89	0.23	5.00	35,35,35,35	0
57	MG	DA	3106	1/1	0.74	0.21	4.91	52,52,52,52	0
57	MG	DA	3174	1/1	0.95	0.19	4.88	38,38,38,38	0
57	MG	DA	3474	1/1	0.97	0.22	4.88	52,52,52,52	0
57	MG	BA	3403	1/1	0.96	0.23	4.78	22,22,22,22	0
57	MG	BR	203	1/1	0.94	0.28	4.76	31,31,31,31	0
57	MG	BQ	3002	1/1	0.97	0.30	4.71	39,39,39,39	0
57	MG	BD	303	1/1	0.97	0.32	4.67	42,42,42,42	0
57	MG	DA	3100	1/1	0.98	0.20	4.62	38,38,38,38	0
57	MG	DA	3552	1/1	0.94	0.23	4.57	43,43,43,43	0
57	MG	DA	3307	1/1	0.80	0.21	4.50	51,51,51,51	0
57	MG	BA	3391	1/1	0.95	0.24	4.50	30,30,30,30	0
57	MG	B7	102	1/1	0.90	0.32	4.47	53,53,53,53	0
57	MG	CA	3097	1/1	0.91	0.22	4.43	43,43,43,43	0
57	MG	CA	3058	1/1	0.83	0.35	4.39	70,70,70,70	0
57	MG	AA	3116	1/1	0.96	0.26	4.38	41,41,41,41	0
57	MG	BA	3152	1/1	0.91	0.25	4.38	45,45,45,45	0
57	MG	BA	3509	1/1	0.91	0.32	4.34	34,34,34,34	0
57	MG	DA	3462	1/1	0.97	0.27	4.33	35,35,35,35	0
57	MG	BA	3310	1/1	0.93	0.21	4.31	43,43,43,43	0
57	MG	DA	3312	1/1	0.87	0.20	4.25	30,30,30,30	0
57	MG	BD	306	1/1	0.91	0.31	4.15	30,30,30,30	0
57	MG	DA	3363	1/1	0.99	0.21	4.15	35,35,35,35	0
57	MG	BF	304	1/1	0.90	0.26	4.10	35,35,35,35	0
57	MG	BA	3436	1/1	0.95	0.22	4.09	21,21,21,21	0
57	MG	DA	3166	1/1	0.95	0.20	4.04	47,47,47,47	0
57	MG	BA	3303	1/1	0.78	0.23	4.04	39,39,39,39	0
57	MG	BA	3706	1/1	0.98	0.25	4.02	27,27,27,27	0
57	MG	DA	3152	1/1	0.96	0.20	4.02	38,38,38,38	0
57	MG	DA	3319	1/1	0.91	0.33	3.95	45,45,45,45	0
57	MG	AA	3090	1/1	0.89	0.20	3.86	70,70,70,70	0
57	MG	DA	3103	1/1	0.90	0.32	3.84	55,55,55,55	0
57	MG	DA	3473	1/1	0.92	0.20	3.83	32,32,32,32	0
57	MG	CA	3070	1/1	0.92	0.24	3.80	42,42,42,42	0
57	MG	BA	3200	1/1	0.94	0.24	3.80	39,39,39,39	0
57	MG	AA	3204	1/1	0.96	0.23	3.73	64,64,64,64	0
57	MG	BA	3529	1/1	0.97	0.28	3.71	29,29,29,29	0
57	MG	DA	3119	1/1	0.82	0.20	3.65	52,52,52,52	0
57	MG	BA	3532	1/1	0.90	0.24	3.64	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	CA	3095	1/1	0.90	0.25	3.64	52,52,52,52	0
57	MG	DA	3017	1/1	0.94	0.17	3.62	58,58,58,58	0
57	MG	DA	3230	1/1	0.95	0.22	3.59	46,46,46,46	0
57	MG	DA	3594	1/1	0.97	0.17	3.58	51,51,51,51	0
57	MG	DA	3023	1/1	0.88	0.21	3.57	35,35,35,35	0
57	MG	DA	3466	1/1	0.98	0.24	3.57	41,41,41,41	0
57	MG	BA	3150	1/1	0.97	0.21	3.52	40,40,40,40	0
57	MG	BA	3183	1/1	0.89	0.25	3.44	50,50,50,50	0
57	MG	DA	3348	1/1	0.96	0.20	3.41	33,33,33,33	0
57	MG	DA	3483	1/1	0.96	0.28	3.39	41,41,41,41	0
57	MG	BA	3314	1/1	0.95	0.25	3.35	42,42,42,42	0
57	MG	DF	3004	1/1	0.93	0.27	3.27	56,56,56,56	0
57	MG	DA	3371	1/1	0.92	0.23	3.24	47,47,47,47	0
57	MG	DA	3171	1/1	0.94	0.21	3.17	38,38,38,38	0
57	MG	DA	3387	1/1	0.96	0.18	3.16	29,29,29,29	0
57	MG	DA	3417	1/1	0.91	0.20	3.16	46,46,46,46	0
57	MG	AA	3091	1/1	0.97	0.24	3.13	35,35,35,35	0
57	MG	BA	3253	1/1	0.95	0.22	3.11	28,28,28,28	0
57	MG	BA	3437	1/1	0.92	0.23	3.07	52,52,52,52	0
57	MG	BA	3385	1/1	0.86	0.27	3.06	34,34,34,34	0
57	MG	DA	3183	1/1	0.98	0.21	3.05	31,31,31,31	0
57	MG	BA	3190	1/1	0.98	0.23	3.05	24,24,24,24	0
57	MG	BA	3443	1/1	0.94	0.24	3.03	38,38,38,38	0
57	MG	BA	3366	1/1	0.83	0.22	3.02	38,38,38,38	0
57	MG	DP	202	1/1	0.93	0.28	3.00	48,48,48,48	0
57	MG	BA	3246	1/1	0.96	0.23	2.96	46,46,46,46	0
57	MG	BA	3546	1/1	0.97	0.24	2.96	27,27,27,27	0
57	MG	DA	3020	1/1	0.96	0.19	2.94	32,32,32,32	0
57	MG	DA	3207	1/1	0.97	0.24	2.86	39,39,39,39	0
57	MG	DA	3430	1/1	0.85	0.20	2.86	26,26,26,26	0
57	MG	BA	3026	1/1	0.99	0.25	2.84	36,36,36,36	0
57	MG	DA	3096	1/1	0.97	0.21	2.83	52,52,52,52	0
57	MG	DA	3243	1/1	0.97	0.30	2.79	41,41,41,41	0
57	MG	BA	3193	1/1	0.98	0.20	2.77	30,30,30,30	0
57	MG	BA	3432	1/1	0.97	0.26	2.72	35,35,35,35	0
57	MG	DA	3624	1/1	0.83	0.27	2.66	66,66,66,66	0
57	MG	AA	3155	1/1	0.90	0.24	2.65	65,65,65,65	0
57	MG	DA	3145	1/1	0.96	0.21	2.65	38,38,38,38	0
57	MG	DA	3453	1/1	0.91	0.22	2.61	44,44,44,44	0
57	MG	BA	3686	1/1	0.96	0.22	2.59	36,36,36,36	0
57	MG	BA	3431	1/1	0.93	0.21	2.56	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	CA	3074	1/1	0.96	0.23	2.55	51,51,51,51	0
57	MG	DD	303	1/1	0.98	0.24	2.52	42,42,42,42	0
57	MG	BA	3294	1/1	0.94	0.21	2.51	37,37,37,37	0
57	MG	AA	3089	1/1	0.90	0.20	2.46	61,61,61,61	0
57	MG	BA	3508	1/1	0.94	0.19	2.40	52,52,52,52	0
57	MG	DA	3058	1/1	0.94	0.21	2.40	47,47,47,47	0
57	MG	DA	3471	1/1	0.96	0.23	2.38	23,23,23,23	0
57	MG	BD	308	1/1	0.85	0.32	2.36	41,41,41,41	0
57	MG	DA	3475	1/1	0.95	0.19	2.35	35,35,35,35	0
57	MG	BF	307	1/1	0.97	0.24	2.31	25,25,25,25	0
57	MG	DA	3291	1/1	0.87	0.21	2.25	56,56,56,56	0
57	MG	DA	3228	1/1	0.94	0.24	2.19	49,49,49,49	0
57	MG	DA	3059	1/1	0.86	0.16	2.12	60,60,60,60	0
57	MG	DA	3382	1/1	0.98	0.22	2.12	20,20,20,20	0
57	MG	DV	201	1/1	0.96	0.30	2.09	49,49,49,49	0
57	MG	DA	3044	1/1	0.99	0.18	2.08	38,38,38,38	0
57	MG	BA	3148	1/1	0.94	0.20	2.05	44,44,44,44	0
57	MG	CA	3047	1/1	0.98	0.20	2.05	50,50,50,50	0
57	MG	DA	3537	1/1	0.94	0.20	2.02	45,45,45,45	0
57	MG	BA	3545	1/1	0.96	0.24	2.01	34,34,34,34	0
57	MG	BA	3053	1/1	0.97	0.20	2.00	33,33,33,33	0
57	MG	DA	3494	1/1	0.96	0.19	2.00	56,56,56,56	0
57	MG	DA	3014	1/1	0.96	0.19	2.00	45,45,45,45	0
57	MG	BA	3418	1/1	0.97	0.23	1.96	26,26,26,26	0
57	MG	BV	201	1/1	0.98	0.22	1.86	33,33,33,33	0
57	MG	BA	3045	1/1	0.95	0.21	1.85	33,33,33,33	0
57	MG	DA	3427	1/1	0.91	0.20	1.84	26,26,26,26	0
57	MG	DA	3315	1/1	0.97	0.16	1.84	57,57,57,57	0
57	MG	BX	101	1/1	0.94	0.28	1.83	36,36,36,36	0
57	MG	BA	3364	1/1	0.94	0.21	1.82	37,37,37,37	0
57	MG	BA	3347	1/1	0.84	0.22	1.80	32,32,32,32	0
57	MG	DA	3296	1/1	0.97	0.20	1.78	46,46,46,46	0
57	MG	DA	3565	1/1	0.79	0.20	1.72	49,49,49,49	0
57	MG	BA	3510	1/1	0.92	0.24	1.72	20,20,20,20	0
57	MG	CA	3107	1/1	0.77	0.21	1.70	89,89,89,89	0
57	MG	BD	309	1/1	0.97	0.25	1.63	33,33,33,33	0
57	MG	B5	101	1/1	0.87	0.21	1.54	30,30,30,30	0
57	MG	AW	101	1/1	0.96	0.24	1.50	24,24,24,24	0
57	MG	AA	3137	1/1	0.98	0.28	1.48	66,66,66,66	0
57	MG	DA	3625	1/1	0.86	0.26	1.45	57,57,57,57	0
57	MG	DA	3098	1/1	0.96	0.19	1.43	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3520	1/1	0.96	0.21	1.43	46,46,46,46	0
57	MG	DA	3041	1/1	0.95	0.18	1.34	36,36,36,36	0
57	MG	DA	3514	1/1	0.92	0.20	1.34	34,34,34,34	0
57	MG	DA	3517	1/1	0.91	0.18	1.33	36,36,36,36	0
57	MG	DA	3005	1/1	0.98	0.20	1.32	29,29,29,29	0
57	MG	BA	3609	1/1	0.96	0.18	1.32	47,47,47,47	0
57	MG	BB	3002	1/1	0.97	0.19	1.29	44,44,44,44	0
57	MG	DA	3229	1/1	0.95	0.17	1.25	39,39,39,39	0
57	MG	BA	3189	1/1	0.95	0.19	1.25	33,33,33,33	0
57	MG	BA	3056	1/1	0.95	0.20	1.19	21,21,21,21	0
57	MG	BA	3558	1/1	0.94	0.17	1.13	63,63,63,63	0
57	MG	DA	3549	1/1	0.96	0.20	1.11	47,47,47,47	0
57	MG	BA	3400	1/1	0.95	0.20	1.05	33,33,33,33	0
57	MG	AA	3076	1/1	0.87	0.19	1.01	62,62,62,62	0
57	MG	DA	3032	1/1	0.91	0.18	0.97	34,34,34,34	0
57	MG	BA	3186	1/1	0.97	0.23	0.95	42,42,42,42	0
57	MG	BA	3411	1/1	0.92	0.23	0.93	24,24,24,24	0
57	MG	BA	3162	1/1	0.89	0.20	0.91	39,39,39,39	0
57	MG	DU	3004	1/1	0.92	0.18	0.90	69,69,69,69	0
57	MG	DA	3357	1/1	0.96	0.19	0.89	29,29,29,29	0
57	MG	BD	302	1/1	0.94	0.24	0.88	38,38,38,38	0
57	MG	BA	3043	1/1	0.97	0.17	0.88	44,44,44,44	0
57	MG	CA	3133	1/1	0.82	0.19	0.85	69,69,69,69	0
57	MG	DA	3543	1/1	0.92	0.14	0.85	61,61,61,61	0
57	MG	DA	3489	1/1	0.97	0.15	0.81	38,38,38,38	0
57	MG	DA	3213	1/1	0.93	0.30	0.79	51,51,51,51	0
57	MG	BA	3445	1/1	0.85	0.21	0.78	35,35,35,35	0
57	MG	DA	3511	1/1	0.91	0.17	0.76	40,40,40,40	0
57	MG	BA	3047	1/1	0.89	0.23	0.71	44,44,44,44	0
57	MG	AA	3108	1/1	0.97	0.21	0.67	54,54,54,54	0
57	MG	DA	3347	1/1	0.92	0.19	0.65	32,32,32,32	0
57	MG	CA	3025	1/1	0.66	0.17	0.63	66,66,66,66	0
57	MG	BA	3285	1/1	0.98	0.18	0.61	21,21,21,21	0
57	MG	BA	3407	1/1	0.98	0.19	0.58	29,29,29,29	0
57	MG	BA	3628	1/1	0.93	0.17	0.54	60,60,60,60	0
57	MG	DA	3112	1/1	0.93	0.15	0.54	63,63,63,63	0
57	MG	CA	3076	1/1	0.96	0.20	0.54	59,59,59,59	0
57	MG	AA	3194	1/1	0.98	0.21	0.51	41,41,41,41	0
57	MG	BA	3408	1/1	0.96	0.21	0.50	42,42,42,42	0
57	MG	DA	3570	1/1	0.98	0.18	0.49	28,28,28,28	0
57	MG	BA	3716	1/1	0.98	0.17	0.49	53,53,53,53	0
57	MG	AA	3021	1/1	0.93	0.16	0.48	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3340	1/1	0.98	0.17	0.47	38,38,38,38	0
57	MG	AX	3002	1/1	0.94	0.18	0.43	67,67,67,67	0
57	MG	BR	201	1/1	0.96	0.23	0.42	30,30,30,30	0
57	MG	BA	3154	1/1	0.97	0.20	0.40	36,36,36,36	0
57	MG	DA	3345	1/1	0.88	0.18	0.40	28,28,28,28	0
57	MG	BA	3316	1/1	0.88	0.18	0.39	49,49,49,49	0
57	MG	BA	3571	1/1	0.88	0.20	0.36	24,24,24,24	0
57	MG	CA	3158	1/1	0.76	0.18	0.29	66,66,66,66	0
57	MG	BN	3003	1/1	0.93	0.26	0.29	61,61,61,61	0
57	MG	DA	3582	1/1	0.93	0.16	0.25	24,24,24,24	0
57	MG	DE	304	1/1	0.96	0.15	0.24	47,47,47,47	0
57	MG	BA	3549	1/1	0.85	0.18	0.23	55,55,55,55	0
57	MG	BA	3695	1/1	0.95	0.20	0.20	19,19,19,19	0
57	MG	DA	3499	1/1	0.86	0.14	0.17	47,47,47,47	0
57	MG	BA	3720	1/1	0.95	0.22	0.17	48,48,48,48	0
57	MG	BA	3587	1/1	0.79	0.18	0.16	51,51,51,51	0
57	MG	BA	3051	1/1	0.96	0.18	0.16	36,36,36,36	0
57	MG	DA	3443	1/1	0.94	0.18	0.15	27,27,27,27	0
57	MG	CW	101	1/1	0.86	0.19	0.12	43,43,43,43	0
59	ZN	D5	102	1/1	0.99	0.17	0.10	58,58,58,58	0
57	MG	BA	3247	1/1	0.89	0.18	0.10	37,37,37,37	0
57	MG	BA	3109	1/1	0.82	0.14	0.09	53,53,53,53	0
57	MG	CA	3037	1/1	0.95	0.17	0.09	60,60,60,60	0
57	MG	AA	3094	1/1	0.94	0.19	0.08	54,54,54,54	0
57	MG	DB	3006	1/1	0.97	0.13	0.08	44,44,44,44	0
57	MG	BF	303	1/1	0.98	0.19	0.06	35,35,35,35	0
57	MG	AX	3012	1/1	0.94	0.21	0.03	15,15,15,15	0
57	MG	CK	3001	1/1	0.94	0.18	-0.02	57,57,57,57	0
57	MG	DA	3378	1/1	0.97	0.15	-0.03	33,33,33,33	0
57	MG	DA	3479	1/1	0.95	0.17	-0.06	45,45,45,45	0
57	MG	BA	3274	1/1	0.99	0.17	-0.07	44,44,44,44	0
57	MG	AA	3017	1/1	0.90	0.15	-0.07	63,63,63,63	0
57	MG	AA	3047	1/1	0.85	0.21	-0.07	59,59,59,59	0
57	MG	AA	3011	1/1	0.86	0.16	-0.08	67,67,67,67	0
57	MG	BP	3002	1/1	0.95	0.20	-0.08	32,32,32,32	0
57	MG	DA	3393	1/1	0.97	0.16	-0.08	41,41,41,41	0
57	MG	DA	3364	1/1	0.90	0.17	-0.08	49,49,49,49	0
57	MG	DE	303	1/1	0.79	0.17	-0.10	49,49,49,49	0
57	MG	BA	3334	1/1	0.85	0.18	-0.14	37,37,37,37	0
57	MG	BA	3350	1/1	0.88	0.16	-0.14	43,43,43,43	0
57	MG	BG	3001	1/1	0.94	0.18	-0.14	44,44,44,44	0
57	MG	BA	3701	1/1	0.96	0.20	-0.14	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3572	1/1	0.96	0.20	-0.15	27,27,27,27	0
57	MG	DA	3361	1/1	0.97	0.18	-0.16	32,32,32,32	0
57	MG	DA	3045	1/1	0.94	0.13	-0.16	39,39,39,39	0
57	MG	BA	3097	1/1	0.87	0.20	-0.19	44,44,44,44	0
57	MG	DA	3620	1/1	0.98	0.17	-0.21	47,47,47,47	0
57	MG	CA	3075	1/1	0.91	0.16	-0.22	48,48,48,48	0
59	ZN	B5	102	1/1	0.99	0.16	-0.22	41,41,41,41	0
57	MG	BU	207	1/1	0.99	0.16	-0.23	23,23,23,23	0
57	MG	CA	3104	1/1	0.96	0.16	-0.24	37,37,37,37	0
57	MG	BV	202	1/1	0.98	0.20	-0.26	29,29,29,29	0
57	MG	CA	3105	1/1	0.93	0.17	-0.26	76,76,76,76	0
57	MG	BA	3464	1/1	0.95	0.20	-0.27	26,26,26,26	0
57	MG	BA	3025	1/1	0.97	0.20	-0.27	12,12,12,12	0
57	MG	AA	3183	1/1	0.97	0.19	-0.28	43,43,43,43	0
57	MG	BA	3204	1/1	0.89	0.13	-0.29	61,61,61,61	0
57	MG	BA	3511	1/1	0.92	0.20	-0.29	41,41,41,41	0
57	MG	BA	3421	1/1	0.93	0.18	-0.30	29,29,29,29	0
57	MG	CA	3059	1/1	0.84	0.18	-0.31	60,60,60,60	0
57	MG	BA	3144	1/1	0.86	0.19	-0.33	42,42,42,42	0
57	MG	DA	3617	1/1	0.91	0.18	-0.34	40,40,40,40	0
57	MG	BD	307	1/1	0.97	0.18	-0.35	40,40,40,40	0
57	MG	BA	3469	1/1	0.94	0.18	-0.35	42,42,42,42	0
57	MG	DA	3167	1/1	0.93	0.17	-0.36	26,26,26,26	0
57	MG	AA	3025	1/1	0.93	0.17	-0.36	46,46,46,46	0
57	MG	DA	3029	1/1	0.98	0.16	-0.37	44,44,44,44	0
57	MG	BA	3021	1/1	0.86	0.19	-0.38	35,35,35,35	0
57	MG	BU	203	1/1	0.98	0.18	-0.38	35,35,35,35	0
57	MG	DA	3339	1/1	0.98	0.17	-0.43	23,23,23,23	0
57	MG	DA	3270	1/1	0.94	0.15	-0.44	57,57,57,57	0
57	MG	BF	308	1/1	0.94	0.19	-0.45	46,46,46,46	0
57	MG	AA	3028	1/1	0.88	0.18	-0.46	58,58,58,58	0
57	MG	DA	3268	1/1	0.92	0.12	-0.48	35,35,35,35	0
57	MG	DA	3435	1/1	0.94	0.14	-0.48	59,59,59,59	0
57	MG	AA	3006	1/1	0.93	0.16	-0.49	62,62,62,62	0
57	MG	DA	3154	1/1	0.86	0.16	-0.50	40,40,40,40	0
57	MG	D3	3001	1/1	0.97	0.17	-0.50	54,54,54,54	0
57	MG	B7	101	1/1	0.98	0.18	-0.53	48,48,48,48	0
57	MG	BA	3615	1/1	0.88	0.13	-0.53	60,60,60,60	0
59	ZN	D4	501	1/1	0.76	0.19	-0.56	154,154,154,154	0
57	MG	DU	3003	1/1	0.97	0.20	-0.57	60,60,60,60	0
57	MG	CA	3146	1/1	0.96	0.15	-0.60	74,74,74,74	0
59	ZN	D6	501	1/1	0.98	0.16	-0.63	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3718	1/1	0.98	0.17	-0.63	36,36,36,36	0
57	MG	CA	3038	1/1	0.81	0.14	-0.64	68,68,68,68	0
57	MG	DA	3359	1/1	0.97	0.16	-0.67	42,42,42,42	0
57	MG	DA	3300	1/1	0.95	0.14	-0.68	38,38,38,38	0
57	MG	BA	3380	1/1	0.86	0.16	-0.70	55,55,55,55	0
57	MG	DA	3623	1/1	0.96	0.16	-0.70	31,31,31,31	0
57	MG	CA	3007	1/1	0.84	0.14	-0.70	55,55,55,55	0
57	MG	BA	3497	1/1	0.92	0.19	-0.72	41,41,41,41	0
57	MG	DA	3495	1/1	0.84	0.10	-0.72	48,48,48,48	0
57	MG	BA	3541	1/1	0.96	0.17	-0.72	43,43,43,43	0
57	MG	DF	3003	1/1	0.93	0.17	-0.75	36,36,36,36	0
57	MG	BA	3305	1/1	0.97	0.18	-0.75	45,45,45,45	0
57	MG	DA	3379	1/1	0.92	0.16	-0.75	37,37,37,37	0
57	MG	CA	3115	1/1	0.97	0.14	-0.76	59,59,59,59	0
57	MG	BW	203	1/1	0.92	0.17	-0.79	39,39,39,39	0
57	MG	AA	3007	1/1	0.68	0.20	-0.80	47,47,47,47	0
57	MG	BW	204	1/1	0.98	0.17	-0.83	27,27,27,27	0
57	MG	CA	3044	1/1	0.75	0.14	-0.86	59,59,59,59	0
57	MG	BA	3135	1/1	0.92	0.19	-0.87	48,48,48,48	0
57	MG	AA	3050	1/1	0.93	0.17	-0.88	49,49,49,49	0
57	MG	BA	3492	1/1	0.87	0.18	-0.90	30,30,30,30	0
57	MG	BA	3181	1/1	0.94	0.18	-0.91	49,49,49,49	0
57	MG	AA	3174	1/1	0.95	0.14	-0.93	64,64,64,64	0
57	MG	DA	3031	1/1	0.99	0.14	-0.94	36,36,36,36	0
57	MG	BA	3093	1/1	0.93	0.16	-0.94	23,23,23,23	0
57	MG	BA	3327	1/1	0.93	0.18	-0.94	32,32,32,32	0
57	MG	BF	301	1/1	0.98	0.18	-0.95	30,30,30,30	0
59	ZN	B6	501	1/1	0.99	0.14	-0.96	43,43,43,43	0
57	MG	DA	3349	1/1	0.98	0.16	-0.99	35,35,35,35	0
57	MG	DA	3203	1/1	0.97	0.17	-1.00	46,46,46,46	0
57	MG	BA	3374	1/1	0.91	0.15	-1.01	48,48,48,48	0
57	MG	DA	3583	1/1	0.96	0.14	-1.02	44,44,44,44	0
57	MG	CA	3063	1/1	0.94	0.11	-1.03	59,59,59,59	0
57	MG	BY	201	1/1	0.98	0.16	-1.04	51,51,51,51	0
57	MG	CA	3029	1/1	0.87	0.16	-1.05	48,48,48,48	0
57	MG	AA	3130	1/1	0.94	0.16	-1.05	52,52,52,52	0
57	MG	BA	3410	1/1	0.93	0.19	-1.06	40,40,40,40	0
57	MG	D8	101	1/1	0.92	0.15	-1.08	60,60,60,60	0
57	MG	DA	3126	1/1	0.96	0.13	-1.09	39,39,39,39	0
57	MG	BA	3559	1/1	0.92	0.17	-1.10	36,36,36,36	0
57	MG	AA	3103	1/1	0.95	0.15	-1.11	42,42,42,42	0
57	MG	CA	3021	1/1	0.94	0.15	-1.14	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3394	1/1	0.96	0.17	-1.14	22,22,22,22	0
57	MG	AE	3002	1/1	0.96	0.15	-1.15	61,61,61,61	0
57	MG	AA	3052	1/1	0.97	0.16	-1.16	53,53,53,53	0
57	MG	CA	3055	1/1	0.83	0.13	-1.16	66,66,66,66	0
57	MG	AA	3004	1/1	0.84	0.17	-1.17	61,61,61,61	0
57	MG	CA	3125	1/1	0.91	0.14	-1.19	64,64,64,64	0
57	MG	DA	3205	1/1	0.87	0.13	-1.19	52,52,52,52	0
57	MG	DA	3467	1/1	0.94	0.15	-1.20	28,28,28,28	0
57	MG	DA	3314	1/1	0.89	0.14	-1.24	56,56,56,56	0
57	MG	BA	3588	1/1	0.99	0.18	-1.25	19,19,19,19	0
57	MG	DA	3414	1/1	0.95	0.15	-1.28	37,37,37,37	0
57	MG	DR	3002	1/1	0.96	0.14	-1.28	51,51,51,51	0
57	MG	CA	3141	1/1	0.96	0.15	-1.29	69,69,69,69	0
57	MG	BA	3426	1/1	0.90	0.18	-1.29	30,30,30,30	0
57	MG	BA	3343	1/1	0.97	0.18	-1.31	18,18,18,18	0
57	MG	CA	3079	1/1	0.97	0.14	-1.34	42,42,42,42	0
57	MG	CA	3043	1/1	0.84	0.13	-1.35	68,68,68,68	0
57	MG	DA	3342	1/1	0.76	0.15	-1.35	49,49,49,49	0
57	MG	AA	3095	1/1	0.98	0.15	-1.38	44,44,44,44	0
57	MG	DA	3021	1/1	0.91	0.13	-1.38	50,50,50,50	0
59	ZN	CN	501	1/1	0.82	0.07	-1.38	101,101,101,101	0
59	ZN	AN	501	1/1	0.95	0.12	-1.38	71,71,71,71	0
57	MG	DA	3510	1/1	0.94	0.13	-1.40	52,52,52,52	0
57	MG	AN	503	1/1	0.95	0.13	-1.42	61,61,61,61	0
57	MG	AA	3170	1/1	0.83	0.15	-1.43	70,70,70,70	0
57	MG	BA	3145	1/1	0.98	0.16	-1.44	41,41,41,41	0
57	MG	DF	3002	1/1	0.94	0.12	-1.44	51,51,51,51	0
57	MG	AN	502	1/1	0.75	0.17	-1.45	61,61,61,61	0
57	MG	BA	3491	1/1	0.96	0.16	-1.45	33,33,33,33	0
57	MG	BA	3352	1/1	0.96	0.14	-1.46	29,29,29,29	0
57	MG	CA	3061	1/1	0.95	0.10	-1.48	87,87,87,87	0
57	MG	CA	3077	1/1	0.97	0.13	-1.48	63,63,63,63	0
57	MG	DD	304	1/1	0.97	0.15	-1.52	40,40,40,40	0
57	MG	BQ	3005	1/1	0.95	0.17	-1.52	39,39,39,39	0
57	MG	AA	3015	1/1	0.94	0.17	-1.55	28,28,28,28	0
57	MG	AA	3003	1/1	0.92	0.10	-1.55	53,53,53,53	0
58	SF4	AD	302	8/8	0.98	0.14	-1.55	59,71,78,78	0
57	MG	BU	205	1/1	0.93	0.15	-1.56	32,32,32,32	0
57	MG	DA	3344	1/1	0.92	0.13	-1.61	42,42,42,42	0
57	MG	BA	3128	1/1	0.98	0.16	-1.62	33,33,33,33	0
57	MG	BA	3694	1/1	0.97	0.19	-1.63	11,11,11,11	0
57	MG	AA	3189	1/1	0.95	0.12	-1.63	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
59	ZN	DY	501	1/1	0.98	0.10	-1.64	88,88,88,88	0
59	ZN	B9	501	1/1	0.96	0.13	-1.64	59,59,59,59	0
57	MG	DA	3033	1/1	0.97	0.13	-1.64	46,46,46,46	0
57	MG	DF	3001	1/1	0.83	0.12	-1.65	36,36,36,36	0
59	ZN	B4	501	1/1	0.95	0.06	-1.67	94,94,94,94	0
57	MG	BA	3134	1/1	0.93	0.16	-1.70	43,43,43,43	0
57	MG	CA	3045	1/1	0.92	0.15	-1.70	53,53,53,53	0
57	MG	BA	3715	1/1	0.93	0.14	-1.71	33,33,33,33	0
57	MG	BA	3057	1/1	0.98	0.18	-1.71	21,21,21,21	0
57	MG	BA	3566	1/1	0.87	0.17	-1.74	31,31,31,31	0
58	SF4	CD	501	8/8	0.97	0.12	-1.76	59,71,83,91	0
57	MG	CA	3159	1/1	0.94	0.14	-1.76	46,46,46,46	0
57	MG	AA	3018	1/1	0.92	0.14	-1.77	62,62,62,62	0
57	MG	CF	3001	1/1	0.92	0.17	-1.78	51,51,51,51	0
57	MG	BA	3064	1/1	0.93	0.16	-1.79	38,38,38,38	0
57	MG	BA	3024	1/1	0.91	0.15	-1.81	42,42,42,42	0
57	MG	BA	3528	1/1	0.99	0.17	-1.81	37,37,37,37	0
57	MG	BA	3046	1/1	0.95	0.18	-1.81	30,30,30,30	0
57	MG	DA	3513	1/1	0.87	0.11	-1.85	49,49,49,49	0
59	ZN	D9	501	1/1	0.89	0.07	-1.86	75,75,75,75	0
57	MG	DA	3524	1/1	0.91	0.10	-1.86	40,40,40,40	0
57	MG	BA	3276	1/1	0.97	0.16	-1.88	19,19,19,19	0
57	MG	DG	3001	1/1	0.78	0.09	-1.91	49,49,49,49	0
57	MG	DA	3434	1/1	0.94	0.10	-1.94	48,48,48,48	0
57	MG	DA	3432	1/1	0.93	0.12	-1.94	33,33,33,33	0
57	MG	AM	201	1/1	0.92	0.05	-1.96	43,43,43,43	0
57	MG	BA	3286	1/1	0.93	0.15	-1.96	33,33,33,33	0
57	MG	BD	304	1/1	0.98	0.19	-1.97	36,36,36,36	0
57	MG	BA	3452	1/1	0.95	0.18	-1.98	15,15,15,15	0
57	MG	DQ	3001	1/1	0.95	0.08	-1.99	58,58,58,58	0
57	MG	BA	3048	1/1	0.94	0.14	-2.01	44,44,44,44	0
57	MG	DA	3297	1/1	0.83	0.14	-2.04	48,48,48,48	0
57	MG	CA	3094	1/1	0.89	0.09	-2.07	80,80,80,80	0
57	MG	BA	3710	1/1	0.93	0.11	-2.07	21,21,21,21	0
57	MG	BA	3713	1/1	0.94	0.14	-2.08	63,63,63,63	0
57	MG	AA	3119	1/1	0.96	0.13	-2.11	50,50,50,50	0
57	MG	DA	3011	1/1	0.87	0.12	-2.12	36,36,36,36	0
57	MG	AK	3001	1/1	0.96	0.12	-2.13	55,55,55,55	0
57	MG	DA	3052	1/1	0.96	0.11	-2.14	33,33,33,33	0
57	MG	DA	3221	1/1	0.92	0.13	-2.15	49,49,49,49	0
57	MG	BA	3137	1/1	0.94	0.17	-2.16	57,57,57,57	0
57	MG	BA	3213	1/1	0.93	0.15	-2.16	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	AA	3001	1/1	0.80	0.13	-2.18	72,72,72,72	0
57	MG	DA	3470	1/1	0.97	0.14	-2.20	34,34,34,34	0
57	MG	DA	3060	1/1	0.94	0.11	-2.23	50,50,50,50	0
57	MG	AA	3157	1/1	0.96	0.13	-2.27	38,38,38,38	0
57	MG	DA	3299	1/1	0.95	0.13	-2.27	32,32,32,32	0
57	MG	BA	3039	1/1	0.96	0.15	-2.35	27,27,27,27	0
57	MG	AA	3008	1/1	0.82	0.11	-2.37	65,65,65,65	0
57	MG	BA	3383	1/1	0.97	0.13	-2.37	37,37,37,37	0
57	MG	CT	3001	1/1	0.92	0.07	-2.40	59,59,59,59	0
57	MG	CA	3052	1/1	0.83	0.09	-2.42	61,61,61,61	0
57	MG	BA	3089	1/1	0.94	0.13	-2.43	30,30,30,30	0
57	MG	DA	3265	1/1	0.91	0.14	-2.43	33,33,33,33	0
57	MG	AA	3140	1/1	0.96	0.12	-2.44	56,56,56,56	0
57	MG	B9	502	1/1	0.91	0.12	-2.48	31,31,31,31	0
57	MG	AA	3104	1/1	0.88	0.15	-2.48	47,47,47,47	0
57	MG	BA	3619	1/1	0.96	0.13	-2.48	54,54,54,54	0
57	MG	AA	3187	1/1	0.96	0.14	-2.49	47,47,47,47	0
57	MG	BA	3023	1/1	0.94	0.16	-2.51	25,25,25,25	0
57	MG	BA	3028	1/1	0.95	0.13	-2.55	31,31,31,31	0
57	MG	DA	3449	1/1	0.91	0.09	-2.56	52,52,52,52	0
57	MG	CA	3039	1/1	0.94	0.10	-2.59	52,52,52,52	0
57	MG	DA	3063	1/1	0.89	0.10	-2.60	40,40,40,40	0
57	MG	BA	3395	1/1	0.95	0.18	-2.63	19,19,19,19	0
57	MG	DA	3223	1/1	0.86	0.11	-2.66	56,56,56,56	0
57	MG	BA	3393	1/1	0.94	0.15	-2.67	30,30,30,30	0
57	MG	DA	3212	1/1	0.92	0.08	-2.67	47,47,47,47	0
57	MG	BA	3077	1/1	0.95	0.12	-2.68	33,33,33,33	0
57	MG	DA	3218	1/1	0.94	0.09	-2.70	36,36,36,36	0
57	MG	AA	3032	1/1	0.92	0.11	-2.70	80,80,80,80	0
57	MG	BA	3302	1/1	0.97	0.17	-2.71	50,50,50,50	0
57	MG	BA	3187	1/1	0.97	0.15	-2.71	35,35,35,35	0
57	MG	DA	3389	1/1	0.91	0.15	-2.73	31,31,31,31	0
57	MG	DB	3003	1/1	0.92	0.06	-2.73	76,76,76,76	0
57	MG	CX	3003	1/1	0.94	0.13	-2.76	53,53,53,53	0
57	MG	DA	3146	1/1	0.89	0.11	-2.77	44,44,44,44	0
57	MG	BA	3037	1/1	0.97	0.17	-2.79	38,38,38,38	0
57	MG	BA	3381	1/1	0.90	0.17	-2.81	30,30,30,30	0
57	MG	AA	3206	1/1	0.96	0.06	-2.82	62,62,62,62	0
57	MG	BA	3081	1/1	0.96	0.14	-2.83	26,26,26,26	0
59	ZN	BY	202	1/1	0.98	0.12	-2.89	70,70,70,70	0
57	MG	AA	3037	1/1	0.93	0.11	-2.89	48,48,48,48	0
57	MG	BA	3237	1/1	0.92	0.15	-2.91	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3498	1/1	0.92	0.08	-2.92	66,66,66,66	0
57	MG	DA	3541	1/1	0.97	0.15	-2.92	40,40,40,40	0
57	MG	B0	103	1/1	0.90	0.12	-2.95	38,38,38,38	0
57	MG	DA	3131	1/1	0.98	0.11	-2.97	34,34,34,34	0
57	MG	DA	3512	1/1	0.97	0.13	-2.97	24,24,24,24	0
57	MG	DA	3007	1/1	0.90	0.08	-2.98	48,48,48,48	0
57	MG	AA	3121	1/1	0.85	0.10	-2.98	66,66,66,66	0
57	MG	BA	3439	1/1	0.95	0.16	-3.00	12,12,12,12	0
57	MG	AA	3026	1/1	0.91	0.08	-3.00	61,61,61,61	0
57	MG	DA	3531	1/1	0.96	0.07	-3.01	40,40,40,40	0
57	MG	BD	305	1/1	0.96	0.16	-3.05	41,41,41,41	0
57	MG	CA	3049	1/1	0.97	0.11	-3.07	42,42,42,42	0
57	MG	CA	3151	1/1	0.93	0.12	-3.08	58,58,58,58	0
57	MG	DA	3332	1/1	0.95	0.11	-3.08	52,52,52,52	0
57	MG	CA	3065	1/1	0.95	0.08	-3.14	60,60,60,60	0
57	MG	BF	306	1/1	0.94	0.08	-3.24	43,43,43,43	0
57	MG	BA	3523	1/1	0.89	0.14	-3.24	31,31,31,31	0
57	MG	DA	3508	1/1	0.90	0.10	-3.25	58,58,58,58	0
57	MG	AA	3061	1/1	0.95	0.10	-3.32	65,65,65,65	0
57	MG	DA	3075	1/1	0.92	0.11	-3.46	40,40,40,40	0
57	MG	DA	3272	1/1	0.97	0.08	-3.47	29,29,29,29	0
57	MG	AA	3164	1/1	0.96	0.12	-3.48	54,54,54,54	0
57	MG	BA	3522	1/1	0.93	0.11	-3.48	34,34,34,34	0
57	MG	BU	201	1/1	0.87	0.11	-3.51	36,36,36,36	0
57	MG	DA	3320	1/1	0.97	0.12	-3.52	19,19,19,19	0
57	MG	DA	3009	1/1	0.98	0.14	-3.55	39,39,39,39	0
57	MG	BA	3084	1/1	0.94	0.14	-3.55	37,37,37,37	0
57	MG	CA	3057	1/1	0.90	0.12	-3.57	48,48,48,48	0
57	MG	AA	3112	1/1	0.95	0.14	-3.57	44,44,44,44	0
57	MG	CA	3024	1/1	0.92	0.07	-3.64	58,58,58,58	0
57	MG	AJ	201	1/1	0.90	0.08	-3.69	67,67,67,67	0
57	MG	DA	3343	1/1	0.92	0.10	-3.75	37,37,37,37	0
57	MG	BA	3206	1/1	0.96	0.13	-3.76	37,37,37,37	0
57	MG	AA	3034	1/1	0.93	0.08	-3.76	47,47,47,47	0
57	MG	B3	3001	1/1	0.96	0.12	-3.78	43,43,43,43	0
57	MG	BB	3004	1/1	0.89	0.11	-3.79	43,43,43,43	0
57	MG	BA	3693	1/1	0.95	0.14	-3.83	48,48,48,48	0
57	MG	CA	3145	1/1	0.95	0.10	-3.87	49,49,49,49	0
57	MG	BA	3315	1/1	0.96	0.10	-3.87	42,42,42,42	0
57	MG	BA	3288	1/1	0.96	0.10	-3.89	37,37,37,37	0
57	MG	BA	3399	1/1	0.93	0.15	-3.89	26,26,26,26	0
57	MG	AA	3149	1/1	0.91	0.14	-3.89	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	CA	3031	1/1	0.84	0.10	-3.91	55,55,55,55	0
57	MG	DA	3480	1/1	0.97	0.11	-3.96	28,28,28,28	0
57	MG	BB	3015	1/1	0.98	0.11	-3.96	42,42,42,42	0
57	MG	DA	3038	1/1	0.91	0.11	-4.00	39,39,39,39	0
57	MG	BA	3337	1/1	0.89	0.15	-4.05	51,51,51,51	0
57	MG	DA	3502	1/1	0.94	0.14	-4.06	51,51,51,51	0
57	MG	DA	3401	1/1	0.96	0.12	-4.12	36,36,36,36	0
57	MG	BA	3040	1/1	0.96	0.14	-4.14	28,28,28,28	0
57	MG	DA	3588	1/1	0.97	0.13	-4.14	21,21,21,21	0
57	MG	CA	3005	1/1	0.82	0.12	-4.17	81,81,81,81	0
57	MG	AX	3004	1/1	0.97	0.12	-4.27	45,45,45,45	0
57	MG	AA	3162	1/1	0.89	0.10	-4.31	40,40,40,40	0
57	MG	BE	3007	1/1	0.99	0.10	-4.37	31,31,31,31	0
57	MG	AA	3096	1/1	0.91	0.06	-4.43	57,57,57,57	0
57	MG	AA	3057	1/1	0.95	0.12	-4.47	38,38,38,38	0
57	MG	BA	3042	1/1	0.97	0.14	-4.49	34,34,34,34	0
57	MG	BV	204	1/1	0.97	0.09	-4.50	36,36,36,36	0
57	MG	DA	3184	1/1	0.95	0.09	-4.51	44,44,44,44	0
57	MG	BB	3007	1/1	0.94	0.10	-4.57	51,51,51,51	0
57	MG	BA	3458	1/1	0.94	0.14	-4.67	40,40,40,40	0
57	MG	BA	3009	1/1	0.97	0.09	-4.68	34,34,34,34	0
57	MG	DA	3164	1/1	0.97	0.08	-4.75	44,44,44,44	0
57	MG	DA	3589	1/1	0.95	0.14	-4.85	52,52,52,52	0
57	MG	AA	3023	1/1	0.96	0.07	-4.90	60,60,60,60	0
57	MG	BE	3004	1/1	0.97	0.12	-4.93	49,49,49,49	0
57	MG	BA	3340	1/1	0.94	0.10	-5.06	59,59,59,59	0
57	MG	BA	3390	1/1	0.96	0.09	-5.07	31,31,31,31	0
57	MG	AA	3066	1/1	0.87	0.09	-5.11	66,66,66,66	0
57	MG	DA	3114	1/1	0.85	0.13	-5.16	51,51,51,51	0
57	MG	BA	3621	1/1	0.93	0.13	-5.17	18,18,18,18	0
57	MG	BA	3284	1/1	0.92	0.12	-5.20	41,41,41,41	0
57	MG	AA	3065	1/1	0.88	0.12	-5.21	48,48,48,48	0
57	MG	BA	3345	1/1	0.95	0.12	-5.26	36,36,36,36	0
57	MG	BA	3172	1/1	0.94	0.17	-5.29	27,27,27,27	0
57	MG	BA	3697	1/1	0.97	0.16	-5.29	23,23,23,23	0
57	MG	BA	3624	1/1	0.97	0.11	-5.35	26,26,26,26	0
57	MG	DA	3121	1/1	0.95	0.12	-5.39	39,39,39,39	0
57	MG	BA	3593	1/1	0.98	0.11	-5.48	36,36,36,36	0
57	MG	AA	3122	1/1	0.73	0.10	-5.48	52,52,52,52	0
57	MG	DA	3022	1/1	0.99	0.08	-5.62	27,27,27,27	0
57	MG	AA	3022	1/1	0.96	0.07	-5.69	57,57,57,57	0
57	MG	BA	3008	1/1	0.95	0.11	-5.70	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3689	1/1	0.87	0.14	-5.73	46,46,46,46	0
57	MG	BA	3589	1/1	0.95	0.13	-5.80	35,35,35,35	0
57	MG	BA	3625	1/1	0.86	0.12	-5.98	46,46,46,46	0
57	MG	BA	3289	1/1	0.95	0.12	-6.09	41,41,41,41	0
57	MG	AA	3153	1/1	0.96	0.09	-6.09	46,46,46,46	0
57	MG	BA	3517	1/1	0.96	0.13	-6.09	20,20,20,20	0
57	MG	BA	3313	1/1	0.93	0.15	-6.26	30,30,30,30	0
57	MG	AA	3152	1/1	0.95	0.09	-6.29	64,64,64,64	0
57	MG	BB	3017	1/1	0.98	0.09	-6.35	28,28,28,28	0
57	MG	BA	3646	1/1	0.96	0.09	-6.36	43,43,43,43	0
57	MG	AA	3036	1/1	0.93	0.11	-6.54	51,51,51,51	0
57	MG	BA	3124	1/1	0.97	0.12	-6.55	31,31,31,31	0
57	MG	BA	3278	1/1	0.94	0.07	-6.63	38,38,38,38	0
57	MG	BA	3565	1/1	0.89	0.10	-6.78	50,50,50,50	0
57	MG	AA	3167	1/1	0.96	0.06	-6.83	65,65,65,65	0
57	MG	BA	3618	1/1	0.85	0.10	-7.53	64,64,64,64	0
57	MG	DA	3012	1/1	0.97	0.08	-7.66	42,42,42,42	0
57	MG	DA	3525	1/1	0.94	0.08	-8.08	40,40,40,40	0
57	MG	DA	3264	1/1	0.92	0.10	-8.18	33,33,33,33	0
57	MG	BA	3554	1/1	0.97	0.08	-8.41	44,44,44,44	0
57	MG	BA	3586	1/1	0.99	0.11	-8.59	33,33,33,33	0
57	MG	B0	102	1/1	0.92	0.13	-8.71	53,53,53,53	0
57	MG	BA	3379	1/1	0.91	0.10	-8.75	69,69,69,69	0
57	MG	DA	3092	1/1	0.96	0.09	-8.91	29,29,29,29	0
57	MG	BA	3420	1/1	0.97	0.11	-9.38	23,23,23,23	0
57	MG	BA	3348	1/1	0.97	0.12	-9.59	17,17,17,17	0
57	MG	BA	3506	1/1	0.96	0.12	-10.04	39,39,39,39	0
57	MG	BA	3501	1/1	0.90	0.07	-11.21	67,67,67,67	0
57	MG	BA	3354	1/1	0.96	0.11	-11.21	31,31,31,31	0
57	MG	BA	3479	1/1	0.99	0.13	-11.32	22,22,22,22	0
57	MG	BA	3038	1/1	0.96	0.06	-11.71	38,38,38,38	0
57	MG	BA	3672	1/1	0.93	0.10	-12.65	28,28,28,28	0
57	MG	BA	3335	1/1	0.94	0.09	-13.85	26,26,26,26	0
57	MG	BA	3341	1/1	0.96	0.06	-19.83	52,52,52,52	0
57	MG	BB	3012	1/1	0.92	0.16	-	33,33,33,33	0
57	MG	CA	3109	1/1	0.90	0.19	-	61,61,61,61	0
57	MG	BF	310	1/1	0.96	0.12	-	51,51,51,51	0
57	MG	BA	3699	1/1	0.91	0.09	-	33,33,33,33	0
57	MG	DA	3461	1/1	0.88	0.13	-	55,55,55,55	0
57	MG	DA	3219	1/1	0.88	0.22	-	54,54,54,54	0
57	MG	DA	3283	1/1	0.83	0.14	-	40,40,40,40	0
57	MG	BA	3113	1/1	0.71	0.23	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3142	1/1	0.97	0.20	-	35,35,35,35	0
57	MG	DA	3476	1/1	0.96	0.14	-	49,49,49,49	0
57	MG	AA	3038	1/1	0.96	0.22	-	58,58,58,58	0
57	MG	BA	3032	1/1	0.91	0.23	-	30,30,30,30	0
57	MG	CA	3066	1/1	0.81	0.18	-	69,69,69,69	0
57	MG	DA	3550	1/1	0.72	0.28	-	63,63,63,63	0
57	MG	AA	3068	1/1	0.92	0.12	-	64,64,64,64	0
57	MG	DA	3503	1/1	0.88	0.18	-	51,51,51,51	0
57	MG	AA	3002	1/1	0.95	0.13	-	58,58,58,58	0
57	MG	BA	3499	1/1	0.93	0.22	-	51,51,51,51	0
57	MG	DB	3001	1/1	0.98	0.07	-	50,50,50,50	0
57	MG	CA	3124	1/1	0.87	0.17	-	57,57,57,57	0
57	MG	BA	3696	1/1	0.96	0.11	-	41,41,41,41	0
57	MG	BA	3451	1/1	0.96	0.17	-	59,59,59,59	0
57	MG	CA	3001	1/1	0.86	0.09	-	53,53,53,53	0
57	MG	BA	3688	1/1	0.92	0.33	-	46,46,46,46	0
57	MG	DA	3094	1/1	0.92	0.19	-	38,38,38,38	0
57	MG	DA	3572	1/1	0.91	0.14	-	46,46,46,46	0
57	MG	BN	3002	1/1	0.90	0.25	-	46,46,46,46	0
57	MG	DA	3616	1/1	0.93	0.13	-	28,28,28,28	0
57	MG	BA	3503	1/1	0.98	0.11	-	50,50,50,50	0
57	MG	DA	3156	1/1	0.95	0.16	-	46,46,46,46	0
57	MG	BA	3224	1/1	0.93	0.44	-	48,48,48,48	0
57	MG	BA	3678	1/1	0.94	0.19	-	49,49,49,49	0
57	MG	DA	3601	1/1	0.88	0.11	-	43,43,43,43	0
57	MG	BA	3293	1/1	0.77	0.16	-	43,43,43,43	0
57	MG	DA	3530	1/1	0.92	0.09	-	43,43,43,43	0
57	MG	DA	3198	1/1	0.92	0.08	-	41,41,41,41	0
57	MG	DA	3573	1/1	0.97	0.08	-	49,49,49,49	0
57	MG	BA	3473	1/1	0.97	0.18	-	31,31,31,31	0
57	MG	AA	3100	1/1	0.69	0.17	-	69,69,69,69	0
57	MG	DA	3558	1/1	0.88	0.09	-	45,45,45,45	0
57	MG	CA	3090	1/1	0.93	0.44	-	64,64,64,64	0
57	MG	DA	3108	1/1	0.94	0.15	-	50,50,50,50	0
57	MG	DA	3532	1/1	0.95	0.10	-	43,43,43,43	0
57	MG	BA	3090	1/1	0.94	0.20	-	50,50,50,50	0
57	MG	DA	3250	1/1	0.92	0.16	-	41,41,41,41	0
57	MG	DA	3172	1/1	0.97	0.09	-	32,32,32,32	0
57	MG	AA	3005	1/1	0.90	0.16	-	66,66,66,66	0
57	MG	BA	3079	1/1	0.82	0.23	-	55,55,55,55	0
57	MG	AX	3006	1/1	0.91	0.27	-	59,59,59,59	0
57	MG	AA	3125	1/1	0.80	0.11	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3031	1/1	0.90	0.13	-	51,51,51,51	0
57	MG	AA	3045	1/1	0.95	0.12	-	44,44,44,44	0
57	MG	BA	3692	1/1	0.91	0.17	-	64,64,64,64	0
57	MG	AA	3086	1/1	0.91	0.13	-	45,45,45,45	0
57	MG	BA	3474	1/1	0.84	0.17	-	64,64,64,64	0
57	MG	BA	3668	1/1	0.95	0.20	-	39,39,39,39	0
57	MG	BA	3052	1/1	0.85	0.24	-	44,44,44,44	0
57	MG	BA	3599	1/1	0.96	0.19	-	43,43,43,43	0
57	MG	BA	3442	1/1	0.96	0.14	-	51,51,51,51	0
57	MG	DA	3085	1/1	0.95	0.13	-	27,27,27,27	0
57	MG	BA	3304	1/1	0.85	0.26	-	49,49,49,49	0
57	MG	DA	3540	1/1	0.95	0.09	-	43,43,43,43	0
57	MG	CJ	5001	1/1	0.90	0.12	-	51,51,51,51	0
57	MG	BA	3066	1/1	0.86	0.20	-	53,53,53,53	0
57	MG	DY	502	1/1	0.96	0.12	-	56,56,56,56	0
57	MG	DA	3423	1/1	0.98	0.24	-	33,33,33,33	0
57	MG	DA	3008	1/1	0.90	0.22	-	26,26,26,26	0
57	MG	DA	3321	1/1	0.97	0.17	-	40,40,40,40	0
57	MG	CA	3102	1/1	0.89	0.12	-	56,56,56,56	0
57	MG	BA	3085	1/1	0.97	0.15	-	18,18,18,18	0
57	MG	BA	3016	1/1	0.96	0.15	-	35,35,35,35	0
57	MG	BA	3235	1/1	0.87	0.19	-	52,52,52,52	0
57	MG	BA	3132	1/1	0.94	0.18	-	52,52,52,52	0
57	MG	DA	3055	1/1	0.95	0.08	-	35,35,35,35	0
57	MG	BA	3552	1/1	0.93	0.11	-	59,59,59,59	0
57	MG	BA	3355	1/1	0.86	0.12	-	30,30,30,30	0
57	MG	CA	3062	1/1	0.86	0.09	-	73,73,73,73	0
57	MG	DA	3420	1/1	0.96	0.10	-	41,41,41,41	0
57	MG	AA	3084	1/1	0.92	0.14	-	43,43,43,43	0
57	MG	DW	202	1/1	0.90	0.18	-	43,43,43,43	0
57	MG	AA	3175	1/1	0.94	0.32	-	61,61,61,61	0
57	MG	CA	3009	1/1	0.94	0.12	-	44,44,44,44	0
57	MG	DA	3293	1/1	0.88	0.19	-	41,41,41,41	0
57	MG	BA	3369	1/1	0.94	0.16	-	57,57,57,57	0
57	MG	AA	3160	1/1	0.91	0.23	-	58,58,58,58	0
57	MG	CA	3022	1/1	0.88	0.28	-	55,55,55,55	0
57	MG	D5	101	1/1	0.94	0.20	-	42,42,42,42	0
57	MG	DA	3522	1/1	0.91	0.17	-	41,41,41,41	0
57	MG	DA	3627	1/1	0.90	0.23	-	56,56,56,56	0
57	MG	AA	3195	1/1	0.92	0.10	-	58,58,58,58	0
57	MG	DA	3515	1/1	0.90	0.17	-	53,53,53,53	0
57	MG	AA	3101	1/1	0.96	0.19	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3358	1/1	0.94	0.53	-	45,45,45,45	0
57	MG	BA	3071	1/1	0.94	0.20	-	48,48,48,48	0
57	MG	DA	3497	1/1	0.91	0.17	-	61,61,61,61	0
57	MG	AA	3088	1/1	0.96	0.22	-	40,40,40,40	0
57	MG	AA	3062	1/1	0.87	0.23	-	57,57,57,57	0
57	MG	DA	3439	1/1	0.83	0.17	-	44,44,44,44	0
57	MG	BA	3562	1/1	0.96	0.16	-	47,47,47,47	0
57	MG	BA	3657	1/1	0.96	0.12	-	55,55,55,55	0
57	MG	DA	3093	1/1	0.91	0.13	-	45,45,45,45	0
57	MG	DA	3240	1/1	0.98	0.24	-	36,36,36,36	0
57	MG	DA	3053	1/1	0.95	0.22	-	50,50,50,50	0
60	K	AX	3001	1/1	0.94	0.10	-	39,39,39,39	0
57	MG	DA	3091	1/1	0.91	0.22	-	37,37,37,37	0
57	MG	BA	3372	1/1	0.89	0.08	-	58,58,58,58	0
57	MG	BA	3579	1/1	0.81	0.32	-	44,44,44,44	0
57	MG	BA	3120	1/1	0.92	0.36	-	52,52,52,52	0
57	MG	DA	3079	1/1	0.95	0.14	-	41,41,41,41	0
57	MG	BA	3112	1/1	0.85	0.28	-	58,58,58,58	0
57	MG	BA	3389	1/1	0.94	0.11	-	57,57,57,57	0
57	MG	AF	3001	1/1	0.73	0.20	-	58,58,58,58	0
57	MG	AA	3178	1/1	0.96	0.18	-	67,67,67,67	0
57	MG	DA	3395	1/1	0.99	0.11	-	31,31,31,31	0
57	MG	BA	3171	1/1	0.95	0.36	-	44,44,44,44	0
57	MG	DA	3220	1/1	0.93	0.20	-	54,54,54,54	0
57	MG	CA	3157	1/1	0.94	0.09	-	61,61,61,61	0
57	MG	BA	3168	1/1	0.93	0.19	-	32,32,32,32	0
57	MG	BA	3658	1/1	0.92	0.22	-	16,16,16,16	0
57	MG	AA	3161	1/1	0.96	0.20	-	28,28,28,28	0
57	MG	BA	3671	1/1	0.93	0.15	-	55,55,55,55	0
57	MG	CA	3018	1/1	0.92	0.13	-	47,47,47,47	0
57	MG	DA	3237	1/1	0.97	0.31	-	41,41,41,41	0
57	MG	BU	202	1/1	0.95	0.10	-	45,45,45,45	0
57	MG	BA	3115	1/1	0.92	0.48	-	49,49,49,49	0
57	MG	CA	3056	1/1	0.75	0.12	-	56,56,56,56	0
57	MG	CA	3106	1/1	0.88	0.14	-	65,65,65,65	0
57	MG	BA	3332	1/1	0.97	0.22	-	29,29,29,29	0
57	MG	AA	3141	1/1	0.85	0.11	-	54,54,54,54	0
57	MG	BA	3357	1/1	0.93	0.20	-	31,31,31,31	0
57	MG	BA	3301	1/1	0.93	0.23	-	43,43,43,43	0
57	MG	DA	3122	1/1	0.88	0.13	-	58,58,58,58	0
57	MG	BA	3556	1/1	0.91	0.16	-	52,52,52,52	0
57	MG	BA	3367	1/1	0.94	0.06	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3091	1/1	0.85	0.19	-	56,56,56,56	0
57	MG	DA	3308	1/1	0.89	0.14	-	52,52,52,52	0
57	MG	AX	3003	1/1	0.86	0.33	-	66,66,66,66	0
57	MG	BA	3365	1/1	0.96	0.14	-	40,40,40,40	0
57	MG	DA	3089	1/1	0.93	0.19	-	36,36,36,36	0
57	MG	DA	3551	1/1	0.95	0.11	-	57,57,57,57	0
57	MG	DA	3134	1/1	0.81	0.16	-	59,59,59,59	0
57	MG	DA	3067	1/1	0.90	0.13	-	54,54,54,54	0
57	MG	CA	3117	1/1	0.91	0.14	-	100,100,100,100	0
57	MG	BE	3003	1/1	0.95	0.16	-	25,25,25,25	0
57	MG	BA	3402	1/1	0.97	0.22	-	39,39,39,39	0
57	MG	DA	3478	1/1	0.95	0.17	-	57,57,57,57	0
57	MG	DA	3280	1/1	0.90	0.19	-	49,49,49,49	0
57	MG	AA	3190	1/1	0.78	0.12	-	75,75,75,75	0
57	MG	BA	3531	1/1	0.96	0.28	-	20,20,20,20	0
57	MG	DA	3071	1/1	0.98	0.15	-	42,42,42,42	0
57	MG	BB	3003	1/1	0.98	0.17	-	40,40,40,40	0
57	MG	AA	3196	1/1	0.95	0.12	-	60,60,60,60	0
57	MG	DA	3187	1/1	0.87	0.23	-	39,39,39,39	0
57	MG	DA	3190	1/1	0.95	0.26	-	52,52,52,52	0
57	MG	BO	5001	1/1	0.94	0.14	-	49,49,49,49	0
57	MG	DA	3101	1/1	0.97	0.28	-	45,45,45,45	0
57	MG	DA	3608	1/1	0.82	0.15	-	61,61,61,61	0
57	MG	BA	3096	1/1	0.95	0.18	-	39,39,39,39	0
57	MG	AA	3138	1/1	0.97	0.20	-	40,40,40,40	0
57	MG	DA	3302	1/1	0.97	0.18	-	30,30,30,30	0
57	MG	AA	3013	1/1	0.97	0.12	-	53,53,53,53	0
57	MG	BA	3070	1/1	0.88	0.20	-	44,44,44,44	0
57	MG	DA	3303	1/1	0.79	0.18	-	57,57,57,57	0
57	MG	DA	3090	1/1	0.84	0.16	-	52,52,52,52	0
57	MG	DA	3472	1/1	0.95	0.20	-	24,24,24,24	0
57	MG	DA	3051	1/1	0.94	0.09	-	54,54,54,54	0
57	MG	DA	3115	1/1	0.93	0.13	-	58,58,58,58	0
57	MG	DA	3590	1/1	0.93	0.10	-	58,58,58,58	0
57	MG	BA	3666	1/1	0.93	0.17	-	79,79,79,79	0
57	MG	DA	3459	1/1	0.94	0.43	-	40,40,40,40	0
57	MG	DA	3507	1/1	0.97	0.24	-	33,33,33,33	0
57	MG	AA	3093	1/1	0.95	0.20	-	56,56,56,56	0
57	MG	DD	301	1/1	0.97	0.22	-	31,31,31,31	0
57	MG	BA	3262	1/1	0.92	0.27	-	38,38,38,38	0
57	MG	BA	3147	1/1	0.99	0.23	-	34,34,34,34	0
57	MG	DA	3460	1/1	0.94	0.07	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3551	1/1	0.96	0.24	-	17,17,17,17	0
57	MG	BA	3502	1/1	0.50	0.23	-	57,57,57,57	0
57	MG	BA	3163	1/1	0.97	0.26	-	43,43,43,43	0
57	MG	DA	3386	1/1	0.99	0.21	-	39,39,39,39	0
57	MG	DA	3377	1/1	0.94	0.17	-	31,31,31,31	0
57	MG	CA	3100	1/1	0.96	0.20	-	48,48,48,48	0
57	MG	BA	3447	1/1	0.89	0.12	-	44,44,44,44	0
57	MG	BA	3197	1/1	0.97	0.19	-	32,32,32,32	0
57	MG	DV	202	1/1	0.63	0.76	-	75,75,75,75	0
57	MG	CA	3072	1/1	0.95	0.28	-	38,38,38,38	0
57	MG	BA	3690	1/1	0.98	0.17	-	49,49,49,49	0
57	MG	DA	3226	1/1	0.88	0.18	-	54,54,54,54	0
57	MG	BA	3075	1/1	0.92	0.35	-	45,45,45,45	0
57	MG	DA	3043	1/1	0.86	0.15	-	44,44,44,44	0
57	MG	BA	3222	1/1	0.93	0.20	-	52,52,52,52	0
57	MG	BA	3614	1/1	0.94	0.12	-	64,64,64,64	0
57	MG	BA	3017	1/1	0.92	0.23	-	48,48,48,48	0
57	MG	BA	3409	1/1	0.93	0.27	-	27,27,27,27	0
57	MG	DA	3026	1/1	0.96	0.14	-	41,41,41,41	0
57	MG	DA	3372	1/1	0.96	0.10	-	49,49,49,49	0
57	MG	DA	3247	1/1	0.97	0.11	-	43,43,43,43	0
57	MG	BA	3441	1/1	0.98	0.13	-	56,56,56,56	0
57	MG	DA	3241	1/1	0.96	0.18	-	40,40,40,40	0
57	MG	AA	3072	1/1	0.91	0.08	-	65,65,65,65	0
57	MG	BA	3636	1/1	0.88	0.29	-	45,45,45,45	0
57	MG	AA	3173	1/1	0.90	0.21	-	53,53,53,53	0
57	MG	DA	3442	1/1	0.94	0.23	-	34,34,34,34	0
57	MG	DA	3301	1/1	0.97	0.11	-	54,54,54,54	0
57	MG	DA	3346	1/1	0.92	0.12	-	39,39,39,39	0
57	MG	DA	3398	1/1	0.97	0.13	-	37,37,37,37	0
57	MG	BA	3515	1/1	0.87	0.17	-	44,44,44,44	0
57	MG	DA	3561	1/1	0.94	0.13	-	51,51,51,51	0
57	MG	CA	3003	1/1	0.85	0.13	-	74,74,74,74	0
57	MG	AA	3201	1/1	0.96	0.10	-	68,68,68,68	0
57	MG	DA	3422	1/1	0.92	0.26	-	40,40,40,40	0
57	MG	BA	3058	1/1	0.94	0.20	-	24,24,24,24	0
57	MG	DA	3102	1/1	0.74	0.14	-	64,64,64,64	0
57	MG	CA	3118	1/1	0.94	0.17	-	69,69,69,69	0
57	MG	BA	3687	1/1	0.98	0.12	-	30,30,30,30	0
57	MG	BA	3223	1/1	0.89	0.15	-	38,38,38,38	0
57	MG	DA	3385	1/1	0.97	0.09	-	47,47,47,47	0
57	MG	AX	3008	1/1	0.81	0.11	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	AA	3180	1/1	0.87	0.21	-	61,61,61,61	0
57	MG	BA	3368	1/1	0.96	0.32	-	26,26,26,26	0
57	MG	BA	3430	1/1	0.94	0.13	-	54,54,54,54	0
57	MG	DA	3504	1/1	0.95	0.17	-	46,46,46,46	0
57	MG	BA	3564	1/1	0.93	0.19	-	44,44,44,44	0
57	MG	AA	3056	1/1	0.84	0.31	-	66,66,66,66	0
57	MG	BA	3485	1/1	0.97	0.11	-	40,40,40,40	0
57	MG	BA	3230	1/1	0.92	0.35	-	45,45,45,45	0
57	MG	DA	3235	1/1	0.97	0.36	-	48,48,48,48	0
57	MG	BA	3104	1/1	0.87	0.20	-	54,54,54,54	0
57	MG	BF	309	1/1	0.71	0.41	-	61,61,61,61	0
57	MG	DN	5001	1/1	0.98	0.06	-	53,53,53,53	0
57	MG	BA	3270	1/1	0.97	0.41	-	47,47,47,47	0
57	MG	DA	3137	1/1	0.87	0.28	-	48,48,48,48	0
57	MG	DB	3009	1/1	0.91	0.21	-	55,55,55,55	0
57	MG	BA	3563	1/1	0.94	0.10	-	38,38,38,38	0
57	MG	DA	3298	1/1	0.99	0.11	-	35,35,35,35	0
57	MG	BA	3141	1/1	0.97	0.21	-	38,38,38,38	0
57	MG	DA	3189	1/1	0.86	0.19	-	57,57,57,57	0
57	MG	BA	3567	1/1	0.94	0.21	-	55,55,55,55	0
57	MG	DA	3019	1/1	0.91	0.18	-	54,54,54,54	0
57	MG	CA	3127	1/1	0.86	0.33	-	76,76,76,76	0
57	MG	DA	3433	1/1	0.98	0.23	-	27,27,27,27	0
57	MG	DA	3585	1/1	0.97	0.27	-	45,45,45,45	0
57	MG	DA	3110	1/1	0.85	0.10	-	60,60,60,60	0
57	MG	DA	3509	1/1	0.87	0.24	-	42,42,42,42	0
57	MG	DA	3481	1/1	0.95	0.12	-	69,69,69,69	0
57	MG	DA	3353	1/1	0.88	0.11	-	42,42,42,42	0
57	MG	DA	3282	1/1	0.94	0.19	-	36,36,36,36	0
57	MG	BA	3033	1/1	0.89	0.16	-	39,39,39,39	0
57	MG	BA	3548	1/1	0.87	0.18	-	54,54,54,54	0
57	MG	DR	3001	1/1	0.94	1.11	-	66,66,66,66	0
57	MG	DA	3217	1/1	0.83	0.35	-	50,50,50,50	0
57	MG	CA	3015	1/1	0.81	0.11	-	61,61,61,61	0
57	MG	BA	3194	1/1	0.97	0.21	-	42,42,42,42	0
57	MG	BA	3015	1/1	0.92	0.15	-	50,50,50,50	0
57	MG	BA	3598	1/1	0.91	0.22	-	54,54,54,54	0
57	MG	BA	3494	1/1	0.85	0.22	-	30,30,30,30	0
57	MG	DA	3487	1/1	0.97	0.09	-	44,44,44,44	0
57	MG	BA	3700	1/1	0.83	0.20	-	69,69,69,69	0
57	MG	DA	3607	1/1	0.92	0.18	-	73,73,73,73	0
57	MG	BA	3414	1/1	0.97	0.24	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	CA	3048	1/1	0.89	0.18	-	48,48,48,48	0
57	MG	DA	3253	1/1	0.96	0.23	-	34,34,34,34	0
57	MG	CA	3023	1/1	0.83	0.10	-	88,88,88,88	0
57	MG	AA	3019	1/1	0.93	0.12	-	52,52,52,52	0
57	MG	BP	3003	1/1	0.96	0.14	-	42,42,42,42	0
57	MG	BA	3099	1/1	0.92	0.32	-	36,36,36,36	0
57	MG	BA	3568	1/1	0.96	0.25	-	43,43,43,43	0
57	MG	DA	3148	1/1	0.84	0.20	-	45,45,45,45	0
57	MG	DA	3491	1/1	0.85	0.17	-	43,43,43,43	0
57	MG	BA	3638	1/1	0.95	0.09	-	41,41,41,41	0
57	MG	CA	3138	1/1	0.95	0.15	-	66,66,66,66	0
57	MG	DA	3606	1/1	0.97	0.19	-	54,54,54,54	0
57	MG	AA	3051	1/1	0.84	0.27	-	51,51,51,51	0
57	MG	DA	3028	1/1	0.90	0.15	-	52,52,52,52	0
57	MG	DA	3081	1/1	0.91	0.30	-	45,45,45,45	0
57	MG	BA	3641	1/1	0.93	0.18	-	33,33,33,33	0
57	MG	DA	3328	1/1	0.78	0.15	-	66,66,66,66	0
57	MG	BA	3184	1/1	0.96	0.26	-	42,42,42,42	0
57	MG	CA	3010	1/1	0.92	0.20	-	56,56,56,56	0
57	MG	BA	3110	1/1	0.98	0.18	-	40,40,40,40	0
57	MG	AA	3053	1/1	0.89	0.16	-	54,54,54,54	0
57	MG	AA	3193	1/1	0.89	0.31	-	77,77,77,77	0
57	MG	DA	3199	1/1	0.94	0.07	-	41,41,41,41	0
57	MG	AA	3115	1/1	0.93	0.33	-	38,38,38,38	0
57	MG	DA	3404	1/1	0.95	0.08	-	48,48,48,48	0
57	MG	BA	3526	1/1	0.90	0.16	-	48,48,48,48	0
57	MG	DA	3176	1/1	0.97	0.15	-	42,42,42,42	0
57	MG	CA	3050	1/1	0.87	0.12	-	56,56,56,56	0
57	MG	BA	3082	1/1	0.95	0.16	-	57,57,57,57	0
57	MG	BA	3539	1/1	0.95	0.22	-	18,18,18,18	0
57	MG	DA	3322	1/1	0.90	0.18	-	51,51,51,51	0
57	MG	BZ	3001	1/1	0.81	0.27	-	56,56,56,56	0
57	MG	DA	3451	1/1	0.99	0.21	-	39,39,39,39	0
57	MG	DA	3138	1/1	0.89	0.21	-	39,39,39,39	0
57	MG	DA	3383	1/1	0.92	0.13	-	45,45,45,45	0
57	MG	DA	3362	1/1	0.89	0.27	-	48,48,48,48	0
57	MG	BA	3504	1/1	0.97	0.24	-	33,33,33,33	0
57	MG	BA	3339	1/1	0.96	0.40	-	52,52,52,52	0
57	MG	BA	3382	1/1	0.96	0.19	-	31,31,31,31	0
57	MG	BA	3220	1/1	0.96	0.23	-	54,54,54,54	0
57	MG	DA	3276	1/1	0.80	0.17	-	56,56,56,56	0
57	MG	AA	3171	1/1	0.92	0.16	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3121	1/1	0.97	0.24	-	48,48,48,48	0
57	MG	BA	3216	1/1	0.79	0.17	-	35,35,35,35	0
57	MG	DA	3168	1/1	0.98	0.32	-	50,50,50,50	0
57	MG	BA	3123	1/1	0.92	0.12	-	56,56,56,56	0
57	MG	DA	3109	1/1	0.92	0.17	-	45,45,45,45	0
57	MG	DA	3144	1/1	0.94	0.08	-	48,48,48,48	0
57	MG	BE	3005	1/1	0.96	0.16	-	15,15,15,15	0
57	MG	BA	3478	1/1	0.96	0.15	-	22,22,22,22	0
57	MG	BA	3378	1/1	0.93	0.18	-	45,45,45,45	0
57	MG	BA	3088	1/1	0.89	0.41	-	59,59,59,59	0
57	MG	DA	3445	1/1	0.97	0.09	-	59,59,59,59	0
57	MG	CA	3012	1/1	0.85	0.34	-	45,45,45,45	0
57	MG	DA	3034	1/1	0.90	0.26	-	46,46,46,46	0
57	MG	DA	3169	1/1	0.98	0.20	-	45,45,45,45	0
57	MG	AA	3124	1/1	0.90	0.21	-	58,58,58,58	0
60	K	CX	3001	1/1	0.96	0.08	-	54,54,54,54	0
57	MG	DA	3317	1/1	0.92	0.24	-	42,42,42,42	0
57	MG	AA	3148	1/1	0.97	0.16	-	61,61,61,61	0
57	MG	DA	3356	1/1	0.88	0.22	-	53,53,53,53	0
57	MG	BA	3535	1/1	0.91	0.25	-	29,29,29,29	0
57	MG	CA	3004	1/1	0.67	0.23	-	70,70,70,70	0
57	MG	DA	3367	1/1	0.85	0.15	-	24,24,24,24	0
57	MG	AA	3067	1/1	0.94	0.13	-	47,47,47,47	0
57	MG	BA	3584	1/1	0.91	0.10	-	59,59,59,59	0
57	MG	BA	3061	1/1	0.90	0.10	-	58,58,58,58	0
57	MG	DA	3013	1/1	0.85	0.15	-	43,43,43,43	0
57	MG	BA	3375	1/1	0.95	0.26	-	46,46,46,46	0
57	MG	AA	3073	1/1	0.89	0.12	-	59,59,59,59	0
57	MG	BA	3149	1/1	0.91	0.19	-	40,40,40,40	0
57	MG	DA	3539	1/1	0.90	0.26	-	52,52,52,52	0
57	MG	DA	3571	1/1	0.93	0.18	-	54,54,54,54	0
57	MG	BA	3373	1/1	0.95	0.24	-	46,46,46,46	0
57	MG	DA	3437	1/1	0.94	0.17	-	48,48,48,48	0
57	MG	B2	3001	1/1	0.95	0.11	-	43,43,43,43	0
57	MG	BA	3419	1/1	0.90	0.24	-	58,58,58,58	0
57	MG	BA	3550	1/1	0.96	0.15	-	60,60,60,60	0
57	MG	BA	3662	1/1	0.98	0.25	-	62,62,62,62	0
57	MG	DA	3438	1/1	0.96	0.13	-	42,42,42,42	0
57	MG	BA	3165	1/1	0.95	0.22	-	34,34,34,34	0
57	MG	DA	3496	1/1	0.87	0.19	-	63,63,63,63	0
57	MG	BA	3440	1/1	0.97	0.23	-	40,40,40,40	0
57	MG	BA	3146	1/1	0.89	0.20	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3252	1/1	0.98	0.22	-	30,30,30,30	0
57	MG	CA	3020	1/1	0.92	0.06	-	51,51,51,51	0
57	MG	DA	3463	1/1	0.96	0.08	-	54,54,54,54	0
57	MG	BA	3637	1/1	0.99	0.15	-	40,40,40,40	0
57	MG	DA	3254	1/1	0.94	0.27	-	42,42,42,42	0
57	MG	BA	3719	1/1	0.88	0.09	-	53,53,53,53	0
57	MG	BA	3682	1/1	0.94	0.19	-	30,30,30,30	0
57	MG	BA	3065	1/1	0.93	0.27	-	43,43,43,43	0
57	MG	BA	3322	1/1	0.90	0.18	-	40,40,40,40	0
57	MG	BA	3453	1/1	0.90	0.11	-	47,47,47,47	0
57	MG	DA	3516	1/1	0.96	0.07	-	43,43,43,43	0
57	MG	AA	3082	1/1	0.96	0.15	-	55,55,55,55	0
57	MG	DW	201	1/1	0.62	0.20	-	70,70,70,70	0
57	MG	BA	3585	1/1	0.93	0.15	-	45,45,45,45	0
57	MG	BA	3459	1/1	0.94	0.28	-	44,44,44,44	0
57	MG	AA	3176	1/1	0.92	0.09	-	43,43,43,43	0
57	MG	BA	3468	1/1	0.96	0.14	-	42,42,42,42	0
57	MG	BA	3512	1/1	0.97	0.10	-	32,32,32,32	0
57	MG	DA	3027	1/1	0.76	0.18	-	42,42,42,42	0
57	MG	BA	3078	1/1	0.87	0.20	-	55,55,55,55	0
57	MG	BA	3003	1/1	0.72	0.16	-	44,44,44,44	0
57	MG	BA	3577	1/1	0.89	0.24	-	35,35,35,35	0
57	MG	DA	3529	1/1	0.95	0.12	-	43,43,43,43	0
57	MG	DA	3178	1/1	0.91	0.21	-	39,39,39,39	0
57	MG	DA	3535	1/1	0.94	0.22	-	21,21,21,21	0
57	MG	CA	3148	1/1	0.64	0.17	-	81,81,81,81	0
57	MG	CA	3082	1/1	0.78	0.14	-	71,71,71,71	0
57	MG	DA	3132	1/1	0.82	0.14	-	53,53,53,53	0
57	MG	DA	3450	1/1	0.92	0.17	-	34,34,34,34	0
57	MG	DA	3113	1/1	0.92	0.24	-	42,42,42,42	0
57	MG	CA	3064	1/1	0.90	0.16	-	64,64,64,64	0
57	MG	BA	3083	1/1	0.94	0.18	-	33,33,33,33	0
57	MG	DA	3153	1/1	0.92	0.15	-	34,34,34,34	0
57	MG	DA	3227	1/1	0.94	0.13	-	57,57,57,57	0
57	MG	BA	3256	1/1	0.99	0.10	-	36,36,36,36	0
57	MG	DA	3155	1/1	0.92	0.21	-	34,34,34,34	0
57	MG	DA	3049	1/1	0.94	0.15	-	46,46,46,46	0
57	MG	AA	3127	1/1	0.82	0.27	-	73,73,73,73	0
57	MG	DA	3506	1/1	0.94	0.21	-	38,38,38,38	0
57	MG	CA	3144	1/1	0.97	0.23	-	58,58,58,58	0
57	MG	BQ	3004	1/1	0.95	0.26	-	35,35,35,35	0
57	MG	BA	3455	1/1	0.92	0.17	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3629	1/1	0.94	0.19	-	37,37,37,37	0
57	MG	DA	3306	1/1	0.94	0.12	-	31,31,31,31	0
57	MG	AA	3079	1/1	0.94	0.06	-	62,62,62,62	0
57	MG	DA	3587	1/1	0.87	0.20	-	35,35,35,35	0
57	MG	BA	3318	1/1	0.94	0.18	-	39,39,39,39	0
57	MG	BA	3537	1/1	0.94	0.18	-	35,35,35,35	0
57	MG	CA	3040	1/1	0.79	0.26	-	67,67,67,67	0
57	MG	DA	3003	1/1	0.81	0.19	-	56,56,56,56	0
57	MG	BA	3312	1/1	0.95	0.16	-	44,44,44,44	0
57	MG	DA	3311	1/1	0.86	0.18	-	42,42,42,42	0
57	MG	DA	3618	1/1	0.97	0.16	-	46,46,46,46	0
57	MG	AA	3151	1/1	0.86	0.16	-	72,72,72,72	0
57	MG	DA	3505	1/1	0.97	0.07	-	41,41,41,41	0
57	MG	DA	3324	1/1	0.96	0.26	-	42,42,42,42	0
57	MG	DA	3469	1/1	0.98	0.31	-	41,41,41,41	0
57	MG	BA	3282	1/1	0.94	0.10	-	44,44,44,44	0
57	MG	DA	3072	1/1	0.85	0.37	-	46,46,46,46	0
57	MG	BA	3174	1/1	0.91	0.16	-	44,44,44,44	0
57	MG	BA	3062	1/1	0.75	0.26	-	52,52,52,52	0
57	MG	CA	3002	1/1	0.96	0.20	-	66,66,66,66	0
57	MG	DA	3070	1/1	0.85	0.22	-	35,35,35,35	0
57	MG	BA	3416	1/1	0.86	0.14	-	73,73,73,73	0
57	MG	BA	3320	1/1	0.93	0.12	-	56,56,56,56	0
57	MG	DA	3547	1/1	0.84	0.25	-	68,68,68,68	0
57	MG	DA	3163	1/1	0.95	0.27	-	43,43,43,43	0
57	MG	BA	3547	1/1	0.93	0.18	-	33,33,33,33	0
57	MG	BA	3035	1/1	0.94	0.21	-	28,28,28,28	0
57	MG	AA	3179	1/1	0.97	0.12	-	56,56,56,56	0
57	MG	AA	3035	1/1	0.96	0.39	-	52,52,52,52	0
57	MG	AA	3064	1/1	0.68	0.14	-	65,65,65,65	0
57	MG	DA	3130	1/1	0.74	0.23	-	55,55,55,55	0
57	MG	DA	3209	1/1	0.94	0.17	-	53,53,53,53	0
57	MG	DA	3215	1/1	0.97	0.18	-	35,35,35,35	0
57	MG	DA	3200	1/1	0.93	0.18	-	38,38,38,38	0
57	MG	AA	3197	1/1	0.93	0.14	-	50,50,50,50	0
57	MG	DA	3289	1/1	0.98	0.25	-	50,50,50,50	0
57	MG	BA	3607	1/1	0.96	0.19	-	41,41,41,41	0
57	MG	DA	3622	1/1	0.91	1.07	-	58,58,58,58	0
57	MG	DA	3281	1/1	0.89	0.13	-	37,37,37,37	0
57	MG	BA	3505	1/1	0.93	0.20	-	16,16,16,16	0
57	MG	DA	3574	1/1	0.88	0.14	-	59,59,59,59	0
57	MG	BA	3360	1/1	0.87	0.16	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3703	1/1	0.94	0.09	-	47,47,47,47	0
57	MG	BA	3192	1/1	0.97	0.10	-	35,35,35,35	0
57	MG	BA	3346	1/1	0.98	0.23	-	29,29,29,29	0
57	MG	DA	3603	1/1	0.93	0.14	-	40,40,40,40	0
57	MG	BA	3242	1/1	0.88	0.22	-	45,45,45,45	0
57	MG	AA	3041	1/1	0.67	0.19	-	62,62,62,62	0
57	MG	AA	3128	1/1	0.93	0.23	-	53,53,53,53	0
57	MG	BA	3191	1/1	0.97	0.09	-	22,22,22,22	0
57	MG	BA	3643	1/1	0.98	0.15	-	47,47,47,47	0
57	MG	DA	3088	1/1	0.87	0.20	-	41,41,41,41	0
57	MG	BA	3632	1/1	0.90	0.10	-	43,43,43,43	0
57	MG	BA	3049	1/1	0.93	0.25	-	53,53,53,53	0
57	MG	BA	3645	1/1	0.98	0.14	-	43,43,43,43	0
57	MG	DA	3553	1/1	0.36	0.40	-	75,75,75,75	0
57	MG	AA	3177	1/1	0.97	0.15	-	66,66,66,66	0
57	MG	AA	3111	1/1	0.79	0.13	-	70,70,70,70	0
57	MG	BA	3456	1/1	0.97	0.13	-	44,44,44,44	0
57	MG	AA	3120	1/1	0.95	0.13	-	53,53,53,53	0
57	MG	BA	3006	1/1	0.93	0.14	-	38,38,38,38	0
57	MG	BA	3685	1/1	0.98	0.18	-	40,40,40,40	0
57	MG	BA	3542	1/1	0.88	0.12	-	40,40,40,40	0
57	MG	BA	3074	1/1	0.94	0.12	-	43,43,43,43	0
57	MG	AA	3078	1/1	0.97	0.17	-	66,66,66,66	0
57	MG	CA	3013	1/1	0.91	0.17	-	45,45,45,45	0
57	MG	BA	3007	1/1	0.96	0.13	-	39,39,39,39	0
57	MG	BB	3020	1/1	0.81	0.16	-	55,55,55,55	0
57	MG	AA	3063	1/1	0.16	0.12	-	89,89,89,89	0
57	MG	DA	3400	1/1	0.96	0.13	-	33,33,33,33	0
57	MG	DA	3316	1/1	0.97	0.17	-	39,39,39,39	0
57	MG	DA	3010	1/1	0.95	0.12	-	51,51,51,51	0
57	MG	BA	3180	1/1	0.83	0.27	-	32,32,32,32	0
57	MG	BA	3392	1/1	0.94	0.18	-	27,27,27,27	0
57	MG	BA	3069	1/1	0.95	0.21	-	48,48,48,48	0
57	MG	DA	3087	1/1	0.82	0.14	-	65,65,65,65	0
57	MG	DE	301	1/1	0.90	0.10	-	52,52,52,52	0
57	MG	AA	3166	1/1	0.61	0.20	-	70,70,70,70	0
57	MG	DA	3464	1/1	0.98	0.15	-	51,51,51,51	0
57	MG	BA	3298	1/1	0.87	0.25	-	50,50,50,50	0
57	MG	BA	3376	1/1	0.99	0.21	-	21,21,21,21	0
57	MG	DA	3160	1/1	0.57	0.11	-	65,65,65,65	0
57	MG	BA	3358	1/1	0.97	0.09	-	35,35,35,35	0
57	MG	DA	3352	1/1	0.95	0.24	-	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3191	1/1	0.84	0.08	-	54,54,54,54	0
57	MG	BA	3044	1/1	0.94	0.07	-	40,40,40,40	0
57	MG	CA	3147	1/1	0.90	0.12	-	56,56,56,56	0
57	MG	BA	3477	1/1	0.98	0.14	-	19,19,19,19	0
57	MG	BA	3207	1/1	0.92	0.16	-	55,55,55,55	0
57	MG	DA	3368	1/1	0.84	0.09	-	58,58,58,58	0
57	MG	DA	3006	1/1	0.95	0.14	-	40,40,40,40	0
57	MG	BA	3633	1/1	0.95	0.14	-	54,54,54,54	0
57	MG	AX	3011	1/1	0.92	0.37	-	73,73,73,73	0
57	MG	BA	3211	1/1	0.95	0.16	-	50,50,50,50	0
57	MG	BA	3261	1/1	0.80	0.19	-	52,52,52,52	0
57	MG	CA	3143	1/1	0.96	0.12	-	59,59,59,59	0
57	MG	BA	3338	1/1	0.95	0.08	-	50,50,50,50	0
57	MG	BA	3691	1/1	0.87	0.32	-	54,54,54,54	0
57	MG	BA	3151	1/1	0.95	0.13	-	42,42,42,42	0
57	MG	CA	3129	1/1	0.90	0.22	-	83,83,83,83	0
57	MG	BB	3009	1/1	0.91	0.18	-	63,63,63,63	0
57	MG	DA	3409	1/1	0.94	0.08	-	70,70,70,70	0
57	MG	DA	3083	1/1	0.85	0.24	-	30,30,30,30	0
57	MG	BA	3225	1/1	0.95	0.12	-	45,45,45,45	0
57	MG	BA	3258	1/1	0.83	0.22	-	35,35,35,35	0
57	MG	DA	3278	1/1	0.93	0.07	-	38,38,38,38	0
57	MG	BA	3654	1/1	0.97	0.19	-	42,42,42,42	0
57	MG	AA	3039	1/1	0.90	0.28	-	62,62,62,62	0
57	MG	DA	3076	1/1	0.93	0.34	-	53,53,53,53	0
57	MG	BA	3424	1/1	0.93	0.21	-	29,29,29,29	0
57	MG	AA	3169	1/1	0.99	0.13	-	48,48,48,48	0
57	MG	DA	3025	1/1	0.96	0.18	-	35,35,35,35	0
57	MG	CA	3120	1/1	0.85	0.27	-	72,72,72,72	0
57	MG	BA	3518	1/1	0.96	0.22	-	48,48,48,48	0
57	MG	BA	3030	1/1	0.98	0.12	-	44,44,44,44	0
57	MG	BA	3604	1/1	0.79	0.10	-	62,62,62,62	0
57	MG	BA	3544	1/1	0.94	0.17	-	52,52,52,52	0
57	MG	CA	3060	1/1	0.87	0.16	-	78,78,78,78	0
57	MG	BA	3415	1/1	0.92	0.23	-	61,61,61,61	0
57	MG	DA	3521	1/1	0.92	0.09	-	57,57,57,57	0
57	MG	B1	101	1/1	0.94	0.42	-	37,37,37,37	0
57	MG	DA	3231	1/1	0.97	0.28	-	33,33,33,33	0
57	MG	AA	3070	1/1	0.91	0.24	-	43,43,43,43	0
57	MG	BA	3202	1/1	0.95	0.17	-	42,42,42,42	0
57	MG	CA	3152	1/1	0.88	0.15	-	66,66,66,66	0
57	MG	BA	3156	1/1	0.93	0.12	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BB	3011	1/1	0.95	0.12	-	40,40,40,40	0
57	MG	DA	3194	1/1	0.92	0.28	-	43,43,43,43	0
57	MG	BA	3072	1/1	0.94	0.12	-	32,32,32,32	0
57	MG	BA	3635	1/1	0.92	0.11	-	59,59,59,59	0
57	MG	BA	3170	1/1	0.96	0.18	-	41,41,41,41	0
57	MG	BA	3103	1/1	0.86	0.50	-	62,62,62,62	0
57	MG	BA	3576	1/1	0.95	0.26	-	29,29,29,29	0
57	MG	BA	3428	1/1	0.97	0.17	-	54,54,54,54	0
57	MG	BA	3218	1/1	0.91	0.59	-	52,52,52,52	0
57	MG	DA	3545	1/1	0.80	0.18	-	70,70,70,70	0
57	MG	DA	3180	1/1	0.95	0.30	-	41,41,41,41	0
57	MG	DA	3150	1/1	0.98	0.36	-	41,41,41,41	0
57	MG	DA	3325	1/1	0.95	0.12	-	43,43,43,43	0
57	MG	AA	3012	1/1	0.95	0.23	-	61,61,61,61	0
57	MG	BA	3076	1/1	0.97	0.24	-	34,34,34,34	0
57	MG	DA	3310	1/1	0.98	0.16	-	43,43,43,43	0
57	MG	DA	3458	1/1	0.87	0.08	-	44,44,44,44	0
57	MG	DU	3002	1/1	0.94	0.42	-	67,67,67,67	0
57	MG	BA	3601	1/1	0.89	0.18	-	69,69,69,69	0
57	MG	BA	3178	1/1	0.84	0.24	-	52,52,52,52	0
57	MG	BA	3470	1/1	0.78	0.13	-	69,69,69,69	0
57	MG	BA	3143	1/1	0.88	0.18	-	41,41,41,41	0
57	MG	DO	5001	1/1	0.89	0.16	-	53,53,53,53	0
57	MG	DA	3391	1/1	0.94	0.21	-	39,39,39,39	0
57	MG	DA	3129	1/1	0.91	0.13	-	41,41,41,41	0
57	MG	BA	3513	1/1	0.93	0.12	-	55,55,55,55	0
57	MG	BA	3251	1/1	0.94	0.27	-	48,48,48,48	0
57	MG	BA	3597	1/1	0.92	0.29	-	56,56,56,56	0
57	MG	BA	3106	1/1	0.97	0.25	-	24,24,24,24	0
57	MG	BA	3493	1/1	0.97	0.13	-	39,39,39,39	0
57	MG	B0	101	1/1	0.94	0.11	-	33,33,33,33	0
57	MG	BA	3417	1/1	0.94	0.17	-	49,49,49,49	0
57	MG	BA	3311	1/1	0.97	0.07	-	42,42,42,42	0
57	MG	DA	3596	1/1	0.88	0.25	-	71,71,71,71	0
57	MG	CA	3046	1/1	0.95	0.18	-	53,53,53,53	0
57	MG	BA	3140	1/1	0.99	0.20	-	26,26,26,26	0
57	MG	AA	3146	1/1	0.79	0.12	-	81,81,81,81	0
57	MG	CA	3149	1/1	0.86	0.10	-	49,49,49,49	0
57	MG	CA	3081	1/1	0.86	0.13	-	67,67,67,67	0
57	MG	CA	3085	1/1	0.78	0.32	-	71,71,71,71	0
57	MG	DA	3149	1/1	0.94	0.19	-	42,42,42,42	0
57	MG	CA	3111	1/1	0.93	0.07	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3486	1/1	0.94	0.16	-	37,37,37,37	0
57	MG	BA	3610	1/1	0.85	0.19	-	60,60,60,60	0
57	MG	BA	3300	1/1	0.92	0.12	-	55,55,55,55	0
57	MG	DA	3097	1/1	0.93	0.16	-	50,50,50,50	0
57	MG	AA	3202	1/1	0.93	0.06	-	60,60,60,60	0
57	MG	DA	3262	1/1	0.93	0.08	-	39,39,39,39	0
57	MG	CA	3068	1/1	0.93	0.12	-	53,53,53,53	0
57	MG	CA	3067	1/1	0.84	0.14	-	45,45,45,45	0
57	MG	BA	3467	1/1	0.80	0.24	-	51,51,51,51	0
57	MG	B8	101	1/1	0.95	0.15	-	34,34,34,34	0
57	MG	DA	3104	1/1	0.92	0.19	-	47,47,47,47	0
57	MG	DA	3604	1/1	0.96	0.28	-	61,61,61,61	0
57	MG	DQ	3002	1/1	0.96	0.15	-	45,45,45,45	0
57	MG	DA	3195	1/1	0.97	0.26	-	42,42,42,42	0
57	MG	AA	3199	1/1	0.92	0.17	-	58,58,58,58	0
57	MG	CA	3155	1/1	0.87	0.16	-	66,66,66,66	0
57	MG	BA	3291	1/1	0.87	0.18	-	44,44,44,44	0
57	MG	BA	3177	1/1	0.84	0.20	-	39,39,39,39	0
57	MG	BA	3356	1/1	0.97	0.11	-	36,36,36,36	0
57	MG	BA	3331	1/1	0.82	0.26	-	39,39,39,39	0
57	MG	AA	3077	1/1	0.96	0.27	-	52,52,52,52	0
57	MG	BA	3126	1/1	0.94	0.28	-	34,34,34,34	0
57	MG	CA	3028	1/1	0.96	0.31	-	57,57,57,57	0
57	MG	BA	3102	1/1	0.97	0.26	-	43,43,43,43	0
57	MG	DA	3064	1/1	0.89	0.31	-	52,52,52,52	0
57	MG	DD	302	1/1	0.93	0.14	-	50,50,50,50	0
57	MG	BA	3581	1/1	0.90	0.08	-	55,55,55,55	0
57	MG	BA	3005	1/1	0.86	0.19	-	44,44,44,44	0
57	MG	CA	3096	1/1	0.83	0.18	-	51,51,51,51	0
57	MG	DA	3107	1/1	0.92	0.17	-	39,39,39,39	0
57	MG	DA	3335	1/1	0.98	0.13	-	48,48,48,48	0
57	MG	DA	3054	1/1	0.81	0.17	-	40,40,40,40	0
57	MG	DA	3567	1/1	0.97	0.09	-	49,49,49,49	0
57	MG	CA	3026	1/1	0.87	0.13	-	59,59,59,59	0
57	MG	AA	3139	1/1	0.97	0.13	-	51,51,51,51	0
57	MG	DA	3419	1/1	0.93	0.20	-	37,37,37,37	0
57	MG	BA	3444	1/1	0.96	0.23	-	32,32,32,32	0
57	MG	BA	3215	1/1	0.93	0.10	-	53,53,53,53	0
57	MG	BA	3595	1/1	0.89	0.21	-	52,52,52,52	0
57	MG	AA	3054	1/1	0.71	0.16	-	62,62,62,62	0
57	MG	DA	3397	1/1	0.96	0.08	-	46,46,46,46	0
57	MG	BA	3060	1/1	0.87	0.22	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	B0	104	1/1	0.98	0.10	-	49,49,49,49	0
57	MG	BA	3457	1/1	0.98	0.11	-	41,41,41,41	0
57	MG	AA	3133	1/1	0.94	0.16	-	59,59,59,59	0
57	MG	DA	3518	1/1	0.98	0.08	-	42,42,42,42	0
57	MG	BA	3351	1/1	0.82	0.11	-	62,62,62,62	0
57	MG	DA	3286	1/1	0.94	0.25	-	45,45,45,45	0
57	MG	AA	3131	1/1	0.93	0.20	-	56,56,56,56	0
57	MG	DA	3252	1/1	0.83	0.12	-	63,63,63,63	0
57	MG	BA	3287	1/1	0.85	0.27	-	42,42,42,42	0
57	MG	DA	3105	1/1	0.83	0.21	-	37,37,37,37	0
57	MG	BA	3466	1/1	0.89	0.25	-	57,57,57,57	0
57	MG	AA	3059	1/1	0.92	0.30	-	61,61,61,61	0
57	MG	DA	3527	1/1	0.91	0.26	-	52,52,52,52	0
57	MG	BA	3608	1/1	0.81	0.09	-	50,50,50,50	0
57	MG	CA	3101	1/1	0.97	0.14	-	41,41,41,41	0
57	MG	DA	3338	1/1	0.93	0.11	-	36,36,36,36	0
57	MG	DA	3018	1/1	0.91	0.33	-	51,51,51,51	0
57	MG	DA	3165	1/1	0.95	0.14	-	54,54,54,54	0
57	MG	CA	3080	1/1	0.97	0.16	-	61,61,61,61	0
57	MG	BA	3650	1/1	0.90	0.10	-	49,49,49,49	0
57	MG	BA	3631	1/1	0.95	0.12	-	53,53,53,53	0
57	MG	D8	102	1/1	0.89	0.25	-	63,63,63,63	0
57	MG	CA	3006	1/1	0.96	0.12	-	43,43,43,43	0
57	MG	CA	3086	1/1	0.94	0.14	-	56,56,56,56	0
57	MG	BA	3616	1/1	0.91	0.17	-	32,32,32,32	0
57	MG	AA	3110	1/1	0.95	0.19	-	52,52,52,52	0
57	MG	BA	3155	1/1	0.92	0.20	-	44,44,44,44	0
57	MG	BA	3233	1/1	0.68	0.31	-	55,55,55,55	0
57	MG	BA	3538	1/1	0.95	0.17	-	25,25,25,25	0
57	MG	BA	3507	1/1	0.84	0.18	-	48,48,48,48	0
57	MG	BA	3173	1/1	0.91	0.27	-	28,28,28,28	0
57	MG	BA	3199	1/1	0.81	0.26	-	60,60,60,60	0
57	MG	CA	3154	1/1	0.86	0.14	-	68,68,68,68	0
57	MG	DA	3519	1/1	0.67	0.17	-	60,60,60,60	0
57	MG	DA	3259	1/1	0.87	0.14	-	39,39,39,39	0
57	MG	AA	3106	1/1	0.93	0.07	-	53,53,53,53	0
57	MG	CA	3122	1/1	0.91	0.09	-	50,50,50,50	0
57	MG	DB	3010	1/1	0.92	0.19	-	55,55,55,55	0
57	MG	AA	3060	1/1	0.94	0.38	-	49,49,49,49	0
57	MG	BA	3108	1/1	0.93	0.15	-	36,36,36,36	0
57	MG	DA	3374	1/1	0.76	0.15	-	42,42,42,42	0
57	MG	DA	3493	1/1	0.95	0.10	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	AA	3075	1/1	0.96	0.14	-	57,57,57,57	0
57	MG	DA	3069	1/1	0.63	0.49	-	59,59,59,59	0
57	MG	DA	3457	1/1	0.78	0.22	-	45,45,45,45	0
57	MG	DA	3605	1/1	0.88	0.08	-	64,64,64,64	0
57	MG	BA	3669	1/1	0.90	0.19	-	34,34,34,34	0
57	MG	BF	302	1/1	0.92	0.18	-	59,59,59,59	0
57	MG	DA	3412	1/1	0.86	0.09	-	60,60,60,60	0
57	MG	CA	3131	1/1	0.94	0.14	-	57,57,57,57	0
57	MG	BA	3319	1/1	0.96	0.15	-	37,37,37,37	0
57	MG	BB	3010	1/1	0.98	0.10	-	28,28,28,28	0
57	MG	DA	3179	1/1	0.98	0.24	-	50,50,50,50	0
57	MG	BA	3446	1/1	0.94	0.09	-	49,49,49,49	0
57	MG	BA	3377	1/1	0.93	0.25	-	58,58,58,58	0
57	MG	DA	3520	1/1	0.80	0.20	-	51,51,51,51	0
57	MG	BA	3068	1/1	0.92	0.15	-	46,46,46,46	0
57	MG	CA	3035	1/1	0.84	0.28	-	63,63,63,63	0
57	MG	BA	3521	1/1	0.93	0.28	-	32,32,32,32	0
57	MG	BA	3209	1/1	0.97	0.23	-	32,32,32,32	0
57	MG	DA	3542	1/1	0.96	0.10	-	44,44,44,44	0
57	MG	BA	3482	1/1	0.87	0.13	-	56,56,56,56	0
57	MG	AA	3203	1/1	0.94	0.10	-	42,42,42,42	0
57	MG	CA	3112	1/1	0.95	0.10	-	31,31,31,31	0
57	MG	BA	3119	1/1	0.94	0.24	-	41,41,41,41	0
57	MG	BA	3268	1/1	0.93	0.16	-	45,45,45,45	0
57	MG	BA	3594	1/1	0.95	0.11	-	34,34,34,34	0
57	MG	BA	3317	1/1	0.92	0.14	-	49,49,49,49	0
57	MG	BA	3136	1/1	0.84	0.21	-	56,56,56,56	0
57	MG	DA	3528	1/1	0.93	0.12	-	60,60,60,60	0
57	MG	AA	3043	1/1	0.81	0.27	-	59,59,59,59	0
57	MG	AA	3154	1/1	0.90	0.19	-	46,46,46,46	0
57	MG	BA	3613	1/1	0.91	0.09	-	74,74,74,74	0
57	MG	BA	3434	1/1	0.93	0.21	-	27,27,27,27	0
57	MG	BA	3296	1/1	0.96	0.24	-	31,31,31,31	0
57	MG	BA	3059	1/1	0.94	0.29	-	50,50,50,50	0
57	MG	BB	3005	1/1	0.90	0.17	-	42,42,42,42	0
57	MG	BA	3203	1/1	0.89	0.23	-	56,56,56,56	0
57	MG	DA	3429	1/1	0.96	0.15	-	38,38,38,38	0
57	MG	BA	3606	1/1	0.96	0.18	-	39,39,39,39	0
57	MG	BA	3116	1/1	0.94	0.28	-	54,54,54,54	0
57	MG	DA	3197	1/1	0.85	0.15	-	35,35,35,35	0
57	MG	CA	3137	1/1	0.81	0.17	-	81,81,81,81	0
57	MG	DA	3073	1/1	0.98	0.31	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	AA	3107	1/1	0.94	0.14	-	50,50,50,50	0
57	MG	AA	3042	1/1	0.78	0.17	-	52,52,52,52	0
57	MG	BA	3325	1/1	0.95	0.12	-	38,38,38,38	0
57	MG	DA	3577	1/1	0.85	0.18	-	25,25,25,25	0
57	MG	BA	3387	1/1	0.94	0.16	-	29,29,29,29	0
57	MG	BA	3622	1/1	0.95	0.13	-	24,24,24,24	0
57	MG	BA	3681	1/1	0.96	0.22	-	42,42,42,42	0
57	MG	DA	3157	1/1	0.95	0.18	-	44,44,44,44	0
57	MG	DA	3181	1/1	0.97	0.21	-	36,36,36,36	0
57	MG	BA	3159	1/1	0.95	0.26	-	43,43,43,43	0
57	MG	DA	3233	1/1	0.97	0.28	-	41,41,41,41	0
57	MG	DA	3275	1/1	0.95	0.18	-	36,36,36,36	0
57	MG	DA	3261	1/1	0.96	0.23	-	38,38,38,38	0
57	MG	BA	3195	1/1	0.96	0.28	-	46,46,46,46	0
57	MG	DA	3288	1/1	0.91	0.24	-	32,32,32,32	0
57	MG	BV	203	1/1	0.97	0.10	-	31,31,31,31	0
57	MG	BA	3425	1/1	0.87	0.20	-	28,28,28,28	0
57	MG	DA	3355	1/1	0.95	0.20	-	48,48,48,48	0
57	MG	CA	3032	1/1	0.87	0.42	-	58,58,58,58	0
57	MG	BA	3580	1/1	0.98	0.27	-	13,13,13,13	0
57	MG	CA	3030	1/1	0.82	0.09	-	75,75,75,75	0
57	MG	DA	3597	1/1	0.88	0.09	-	42,42,42,42	0
57	MG	BA	3574	1/1	0.90	0.12	-	41,41,41,41	0
57	MG	DA	3490	1/1	0.93	0.10	-	62,62,62,62	0
57	MG	DQ	3003	1/1	0.90	0.28	-	59,59,59,59	0
57	MG	DA	3208	1/1	0.95	0.13	-	50,50,50,50	0
57	MG	DA	3188	1/1	0.94	0.21	-	48,48,48,48	0
57	MG	DA	3331	1/1	0.93	0.26	-	54,54,54,54	0
57	MG	BA	3164	1/1	0.87	0.27	-	44,44,44,44	0
57	MG	BA	3232	1/1	0.90	0.18	-	31,31,31,31	0
57	MG	BA	3540	1/1	0.94	0.20	-	24,24,24,24	0
57	MG	AA	3010	1/1	0.95	0.05	-	54,54,54,54	0
57	MG	DA	3599	1/1	0.99	0.23	-	36,36,36,36	0
57	MG	BA	3433	1/1	0.93	0.12	-	32,32,32,32	0
57	MG	DA	3566	1/1	0.86	0.08	-	40,40,40,40	0
57	MG	DD	307	1/1	0.81	0.12	-	50,50,50,50	0
57	MG	BA	3264	1/1	0.96	0.09	-	47,47,47,47	0
57	MG	DA	3292	1/1	0.89	0.12	-	29,29,29,29	0
57	MG	DA	3354	1/1	0.99	0.26	-	25,25,25,25	0
57	MG	BA	3361	1/1	0.90	0.08	-	38,38,38,38	0
57	MG	BA	3342	1/1	0.92	0.20	-	38,38,38,38	0
57	MG	AA	3147	1/1	0.94	0.06	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3613	1/1	0.91	0.37	-	45,45,45,45	0
57	MG	DA	3256	1/1	0.89	0.12	-	52,52,52,52	0
57	MG	BW	201	1/1	0.92	0.18	-	48,48,48,48	0
57	MG	DA	3211	1/1	0.95	0.15	-	43,43,43,43	0
57	MG	BA	3702	1/1	0.92	0.12	-	41,41,41,41	0
57	MG	DA	3610	1/1	0.89	0.16	-	42,42,42,42	0
57	MG	DA	3556	1/1	0.97	0.14	-	49,49,49,49	0
57	MG	DA	3612	1/1	0.95	0.11	-	64,64,64,64	0
57	MG	DA	3384	1/1	0.93	0.09	-	41,41,41,41	0
57	MG	BA	3406	1/1	0.85	0.22	-	24,24,24,24	0
57	MG	AA	3186	1/1	0.97	0.10	-	43,43,43,43	0
57	MG	AA	3081	1/1	0.98	0.09	-	44,44,44,44	0
57	MG	BA	3386	1/1	0.98	0.25	-	30,30,30,30	0
57	MG	BA	3087	1/1	0.94	0.21	-	44,44,44,44	0
57	MG	BA	3336	1/1	0.93	0.10	-	47,47,47,47	0
57	MG	BA	3704	1/1	0.92	0.13	-	31,31,31,31	0
57	MG	BA	3263	1/1	0.86	0.30	-	50,50,50,50	0
57	MG	BA	3205	1/1	0.93	0.12	-	52,52,52,52	0
57	MG	DA	3580	1/1	0.73	0.11	-	47,47,47,47	0
57	MG	BA	3363	1/1	0.96	0.21	-	31,31,31,31	0
57	MG	DA	3084	1/1	0.95	0.17	-	42,42,42,42	0
57	MG	CA	3114	1/1	0.85	0.24	-	96,96,96,96	0
57	MG	DA	3402	1/1	0.88	0.15	-	47,47,47,47	0
57	MG	BA	3228	1/1	0.93	0.28	-	33,33,33,33	0
57	MG	BA	3094	1/1	0.85	0.15	-	46,46,46,46	0
57	MG	DA	3484	1/1	0.91	0.10	-	41,41,41,41	0
57	MG	BA	3011	1/1	0.89	0.18	-	32,32,32,32	0
57	MG	BA	3272	1/1	0.98	0.21	-	38,38,38,38	0
57	MG	BA	3018	1/1	0.91	0.21	-	58,58,58,58	0
57	MG	BA	3012	1/1	0.95	0.16	-	38,38,38,38	0
57	MG	DA	3232	1/1	0.96	0.07	-	48,48,48,48	0
57	MG	DA	3586	1/1	0.95	0.13	-	21,21,21,21	0
57	MG	AA	3033	1/1	0.90	0.19	-	43,43,43,43	0
57	MG	CA	3139	1/1	0.87	0.09	-	82,82,82,82	0
57	MG	BA	3660	1/1	0.93	0.11	-	62,62,62,62	0
57	MG	DA	3062	1/1	0.92	0.24	-	49,49,49,49	0
57	MG	DA	3388	1/1	0.93	0.22	-	33,33,33,33	0
57	MG	BA	3655	1/1	0.99	0.09	-	68,68,68,68	0
57	MG	DA	3294	1/1	0.96	0.17	-	18,18,18,18	0
57	MG	CA	3132	1/1	0.95	0.13	-	51,51,51,51	0
57	MG	BA	3349	1/1	0.89	0.19	-	55,55,55,55	0
57	MG	BA	3620	1/1	0.98	0.13	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3182	1/1	0.86	0.18	-	36,36,36,36	0
57	MG	BA	3266	1/1	0.92	0.21	-	53,53,53,53	0
57	MG	BA	3483	1/1	0.94	0.14	-	36,36,36,36	0
57	MG	DA	3196	1/1	0.91	0.23	-	46,46,46,46	0
57	MG	AA	3163	1/1	0.87	0.17	-	70,70,70,70	0
57	MG	AA	3136	1/1	0.97	0.15	-	43,43,43,43	0
57	MG	BA	3575	1/1	0.94	0.17	-	30,30,30,30	0
57	MG	BA	3524	1/1	0.93	0.12	-	39,39,39,39	0
57	MG	AA	3048	1/1	0.93	0.19	-	42,42,42,42	0
57	MG	CA	3033	1/1	0.83	0.15	-	67,67,67,67	0
57	MG	BA	3275	1/1	0.99	0.10	-	38,38,38,38	0
57	MG	DA	3086	1/1	0.96	0.08	-	41,41,41,41	0
57	MG	CA	3121	1/1	0.97	0.20	-	51,51,51,51	0
57	MG	BA	3117	1/1	0.98	0.17	-	24,24,24,24	0
57	MG	AA	3198	1/1	0.74	0.12	-	66,66,66,66	0
57	MG	DA	3263	1/1	0.91	0.13	-	47,47,47,47	0
57	MG	BA	3157	1/1	0.94	0.12	-	42,42,42,42	0
57	MG	DA	3066	1/1	0.89	0.10	-	55,55,55,55	0
57	MG	BA	3472	1/1	0.94	0.10	-	39,39,39,39	0
57	MG	CA	3083	1/1	0.91	0.27	-	71,71,71,71	0
57	MG	AA	3184	1/1	0.97	0.11	-	56,56,56,56	0
57	MG	DA	3202	1/1	0.95	0.48	-	41,41,41,41	0
57	MG	BA	3309	1/1	0.99	0.10	-	31,31,31,31	0
57	MG	BA	3388	1/1	0.89	0.15	-	31,31,31,31	0
57	MG	DA	3136	1/1	0.96	0.18	-	62,62,62,62	0
57	MG	DA	3562	1/1	0.89	0.09	-	58,58,58,58	0
57	MG	DA	3313	1/1	0.95	0.04	-	51,51,51,51	0
57	MG	CA	3016	1/1	0.93	0.05	-	52,52,52,52	0
57	MG	DA	3047	1/1	0.88	0.19	-	44,44,44,44	0
57	MG	CA	3110	1/1	0.90	0.19	-	56,56,56,56	0
57	MG	BA	3098	1/1	0.93	0.58	-	50,50,50,50	0
57	MG	BA	3674	1/1	0.56	0.19	-	59,59,59,59	0
57	MG	BB	3019	1/1	0.91	0.15	-	62,62,62,62	0
57	MG	BA	3527	1/1	0.87	0.17	-	37,37,37,37	0
57	MG	BA	3656	1/1	0.91	0.15	-	57,57,57,57	0
57	MG	DA	3323	1/1	0.95	0.11	-	39,39,39,39	0
57	MG	BA	3661	1/1	0.94	0.19	-	56,56,56,56	0
57	MG	BA	3591	1/1	0.93	0.10	-	42,42,42,42	0
57	MG	BA	3248	1/1	0.96	0.24	-	32,32,32,32	0
57	MG	AX	3005	1/1	0.93	0.32	-	57,57,57,57	0
57	MG	BA	3371	1/1	0.90	0.16	-	53,53,53,53	0
57	MG	DA	3554	1/1	0.84	0.18	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3626	1/1	0.94	0.22	-	48,48,48,48	0
57	MG	DA	3095	1/1	0.90	0.25	-	45,45,45,45	0
57	MG	AA	3029	1/1	0.97	0.07	-	42,42,42,42	0
57	MG	BA	3489	1/1	0.96	0.22	-	36,36,36,36	0
57	MG	DB	3008	1/1	0.75	0.10	-	59,59,59,59	0
57	MG	BA	3647	1/1	0.96	0.12	-	41,41,41,41	0
57	MG	BA	3002	1/1	0.82	0.14	-	45,45,45,45	0
57	MG	BA	3238	1/1	0.90	0.26	-	26,26,26,26	0
57	MG	AA	3097	1/1	0.83	0.16	-	45,45,45,45	0
57	MG	BA	3561	1/1	0.94	0.18	-	37,37,37,37	0
57	MG	BA	3100	1/1	0.94	0.20	-	40,40,40,40	0
57	MG	BA	3449	1/1	0.95	0.15	-	31,31,31,31	0
57	MG	DA	3546	1/1	0.83	0.14	-	41,41,41,41	0
57	MG	BA	3073	1/1	0.94	0.29	-	39,39,39,39	0
57	MG	AV	3001	1/1	0.92	0.20	-	59,59,59,59	0
57	MG	BA	3169	1/1	0.96	0.15	-	40,40,40,40	0
57	MG	DA	3002	1/1	0.94	0.31	-	44,44,44,44	0
57	MG	DA	3186	1/1	0.95	0.08	-	33,33,33,33	0
57	MG	DA	3285	1/1	0.92	0.12	-	50,50,50,50	0
57	MG	DA	3488	1/1	0.92	0.14	-	47,47,47,47	0
57	MG	BA	3013	1/1	0.95	0.28	-	36,36,36,36	0
57	MG	BA	3398	1/1	0.94	0.25	-	36,36,36,36	0
57	MG	BA	3328	1/1	0.80	0.09	-	55,55,55,55	0
57	MG	BA	3095	1/1	0.97	0.23	-	29,29,29,29	0
57	MG	BA	3022	1/1	0.92	0.23	-	47,47,47,47	0
57	MG	BA	3673	1/1	0.93	0.11	-	55,55,55,55	0
57	MG	AA	3182	1/1	0.98	0.15	-	40,40,40,40	0
57	MG	DA	3050	1/1	0.98	0.14	-	48,48,48,48	0
57	MG	BA	3210	1/1	0.91	0.15	-	42,42,42,42	0
57	MG	DA	3128	1/1	0.95	0.20	-	45,45,45,45	0
57	MG	DA	3477	1/1	0.96	0.10	-	37,37,37,37	0
57	MG	AA	3165	1/1	0.97	0.24	-	47,47,47,47	0
57	MG	BA	3055	1/1	0.93	0.20	-	43,43,43,43	0
57	MG	BA	3630	1/1	0.95	0.13	-	72,72,72,72	0
57	MG	DA	3436	1/1	0.81	0.12	-	61,61,61,61	0
57	MG	DA	3304	1/1	0.81	0.14	-	44,44,44,44	0
57	MG	DA	3143	1/1	0.90	0.22	-	47,47,47,47	0
57	MG	AA	3205	1/1	0.86	0.26	-	48,48,48,48	0
57	MG	DA	3077	1/1	0.88	0.19	-	58,58,58,58	0
57	MG	DA	3204	1/1	0.88	0.19	-	39,39,39,39	0
57	MG	BA	3138	1/1	0.93	0.26	-	57,57,57,57	0
57	MG	BA	3496	1/1	0.98	0.29	-	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	AA	3049	1/1	0.95	0.19	-	43,43,43,43	0
57	MG	CA	3019	1/1	0.83	0.13	-	57,57,57,57	0
57	MG	DA	3249	1/1	0.96	0.19	-	48,48,48,48	0
57	MG	BA	3486	1/1	0.95	0.16	-	32,32,32,32	0
57	MG	BA	3569	1/1	0.97	0.24	-	46,46,46,46	0
57	MG	BA	3344	1/1	0.92	0.19	-	48,48,48,48	0
57	MG	BA	3249	1/1	0.93	0.22	-	44,44,44,44	0
57	MG	AA	3156	1/1	0.87	0.15	-	86,86,86,86	0
57	MG	DA	3037	1/1	0.87	0.16	-	41,41,41,41	0
57	MG	AA	3027	1/1	0.91	0.18	-	55,55,55,55	0
57	MG	DA	3600	1/1	0.87	0.10	-	45,45,45,45	0
57	MG	AA	3181	1/1	0.80	0.07	-	82,82,82,82	0
57	MG	DA	3182	1/1	0.92	0.39	-	52,52,52,52	0
57	MG	DA	3593	1/1	0.93	0.20	-	49,49,49,49	0
57	MG	BA	3665	1/1	0.89	0.14	-	50,50,50,50	0
57	MG	DB	3004	1/1	0.97	0.11	-	38,38,38,38	0
57	MG	BA	3676	1/1	0.97	0.18	-	44,44,44,44	0
57	MG	BA	3623	1/1	0.86	0.14	-	42,42,42,42	0
57	MG	BA	3308	1/1	0.93	0.15	-	14,14,14,14	0
57	MG	BA	3321	1/1	0.97	0.16	-	31,31,31,31	0
57	MG	BA	3605	1/1	0.93	0.25	-	44,44,44,44	0
57	MG	BA	3269	1/1	0.98	0.24	-	30,30,30,30	0
57	MG	BA	3603	1/1	0.72	0.18	-	42,42,42,42	0
57	MG	BA	3644	1/1	0.94	0.19	-	48,48,48,48	0
57	MG	BA	3050	1/1	0.95	0.10	-	44,44,44,44	0
57	MG	BA	3711	1/1	0.94	0.19	-	46,46,46,46	0
57	MG	AA	3009	1/1	0.97	0.09	-	40,40,40,40	0
57	MG	AA	3109	1/1	0.75	0.26	-	75,75,75,75	0
57	MG	BA	3717	1/1	0.93	0.44	-	40,40,40,40	0
57	MG	DA	3318	1/1	0.93	0.19	-	39,39,39,39	0
57	MG	DA	3327	1/1	0.91	0.12	-	49,49,49,49	0
57	MG	BP	3004	1/1	0.96	0.11	-	41,41,41,41	0
57	MG	DA	3111	1/1	0.77	0.25	-	54,54,54,54	0
57	MG	CA	3011	1/1	0.96	0.28	-	39,39,39,39	0
57	MG	BF	305	1/1	0.88	0.15	-	33,33,33,33	0
57	MG	BA	3254	1/1	0.96	0.20	-	30,30,30,30	0
57	MG	DA	3222	1/1	0.96	0.22	-	38,38,38,38	0
57	MG	BA	3234	1/1	0.89	0.43	-	39,39,39,39	0
57	MG	BA	3297	1/1	0.93	0.22	-	36,36,36,36	0
57	MG	CA	3123	1/1	0.98	0.09	-	53,53,53,53	0
57	MG	DA	3536	1/1	0.96	0.15	-	48,48,48,48	0
57	MG	DA	3560	1/1	0.98	0.20	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3240	1/1	0.94	0.33	-	52,52,52,52	0
57	MG	CA	3108	1/1	0.97	0.15	-	51,51,51,51	0
57	MG	DA	3548	1/1	0.66	0.15	-	58,58,58,58	0
57	MG	BA	3592	1/1	0.99	0.18	-	14,14,14,14	0
57	MG	DA	3416	1/1	0.97	0.09	-	46,46,46,46	0
57	MG	BA	3560	1/1	0.95	0.16	-	54,54,54,54	0
57	MG	DA	3446	1/1	0.82	0.23	-	37,37,37,37	0
57	MG	BA	3034	1/1	0.96	0.11	-	21,21,21,21	0
57	MG	DA	3239	1/1	0.98	0.31	-	51,51,51,51	0
57	MG	BA	3292	1/1	0.96	0.17	-	26,26,26,26	0
57	MG	CA	3014	1/1	0.94	0.12	-	58,58,58,58	0
57	MG	DA	3260	1/1	0.74	0.20	-	43,43,43,43	0
57	MG	AA	3016	1/1	0.91	0.14	-	52,52,52,52	0
57	MG	CA	3073	1/1	0.98	0.09	-	57,57,57,57	0
57	MG	DA	3117	1/1	0.88	0.12	-	40,40,40,40	0
57	MG	DA	3309	1/1	0.96	0.12	-	34,34,34,34	0
57	MG	BA	3219	1/1	0.97	0.42	-	42,42,42,42	0
57	MG	DA	3396	1/1	0.95	0.11	-	43,43,43,43	0
57	MG	DA	3024	1/1	0.98	0.09	-	29,29,29,29	0
57	MG	DA	3557	1/1	0.90	0.07	-	54,54,54,54	0
57	MG	DA	3159	1/1	0.93	0.14	-	32,32,32,32	0
57	MG	AX	3010	1/1	0.88	0.15	-	61,61,61,61	0
57	MG	BA	3495	1/1	0.95	0.22	-	47,47,47,47	0
57	MG	BA	3127	1/1	0.96	0.24	-	41,41,41,41	0
57	MG	BA	3010	1/1	0.97	0.20	-	45,45,45,45	0
57	MG	BA	3329	1/1	0.94	0.12	-	21,21,21,21	0
57	MG	BA	3684	1/1	0.92	0.10	-	47,47,47,47	0
57	MG	BA	3231	1/1	0.89	0.21	-	42,42,42,42	0
57	MG	AA	3159	1/1	0.95	0.14	-	31,31,31,31	0
57	MG	BA	3480	1/1	0.95	0.27	-	50,50,50,50	0
57	MG	CA	3087	1/1	0.98	0.14	-	50,50,50,50	0
57	MG	BA	3167	1/1	0.99	0.23	-	51,51,51,51	0
57	MG	AA	3105	1/1	0.82	0.26	-	59,59,59,59	0
57	MG	BA	3450	1/1	0.93	0.07	-	45,45,45,45	0
57	MG	CA	3134	1/1	0.94	0.18	-	72,72,72,72	0
57	MG	AA	3080	1/1	0.78	0.16	-	82,82,82,82	0
57	MG	DA	3425	1/1	0.85	0.12	-	40,40,40,40	0
57	MG	BA	3198	1/1	0.95	0.19	-	45,45,45,45	0
57	MG	BA	3708	1/1	0.94	0.16	-	38,38,38,38	0
57	MG	BA	3427	1/1	0.98	0.16	-	23,23,23,23	0
57	MG	DA	3078	1/1	0.97	0.04	-	49,49,49,49	0
57	MG	CA	3042	1/1	0.80	0.16	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3370	1/1	0.87	0.11	-	72,72,72,72	0
57	MG	AA	3040	1/1	0.75	0.21	-	67,67,67,67	0
57	MG	DA	3615	1/1	0.88	0.15	-	36,36,36,36	0
57	MG	BA	3362	1/1	0.97	0.13	-	43,43,43,43	0
57	MG	BA	3583	1/1	0.88	0.10	-	54,54,54,54	0
57	MG	BA	3413	1/1	0.85	0.09	-	50,50,50,50	0
57	MG	BA	3648	1/1	0.95	0.13	-	50,50,50,50	0
57	MG	CA	3103	1/1	0.95	0.16	-	71,71,71,71	0
57	MG	BA	3475	1/1	0.97	0.10	-	31,31,31,31	0
57	MG	DA	3564	1/1	0.88	0.17	-	48,48,48,48	0
57	MG	BB	3014	1/1	0.95	0.08	-	41,41,41,41	0
57	MG	BA	3019	1/1	0.94	0.15	-	30,30,30,30	0
57	MG	BA	3307	1/1	0.96	0.26	-	31,31,31,31	0
57	MG	BB	3013	1/1	0.98	0.18	-	43,43,43,43	0
57	MG	BA	3129	1/1	0.88	0.13	-	30,30,30,30	0
57	MG	CA	3071	1/1	0.95	0.40	-	49,49,49,49	0
57	MG	DA	3290	1/1	0.95	0.14	-	43,43,43,43	0
57	MG	CA	3113	1/1	0.80	0.17	-	75,75,75,75	0
57	MG	DA	3578	1/1	0.76	0.23	-	63,63,63,63	0
57	MG	DA	3016	1/1	0.97	0.13	-	34,34,34,34	0
57	MG	BA	3578	1/1	0.95	0.14	-	43,43,43,43	0
57	MG	AA	3143	1/1	0.88	0.15	-	32,32,32,32	0
57	MG	DA	3629	1/1	0.97	0.22	-	40,40,40,40	0
57	MG	AX	3009	1/1	0.96	0.13	-	50,50,50,50	0
57	MG	DA	3365	1/1	0.96	0.08	-	54,54,54,54	0
57	MG	AA	3114	1/1	0.74	0.31	-	57,57,57,57	0
57	MG	AA	3192	1/1	0.92	0.12	-	72,72,72,72	0
57	MG	DA	3403	1/1	0.96	0.13	-	31,31,31,31	0
57	MG	BN	3005	1/1	0.97	0.22	-	31,31,31,31	0
57	MG	CA	3034	1/1	0.93	0.27	-	49,49,49,49	0
57	MG	DA	3399	1/1	0.99	0.13	-	26,26,26,26	0
57	MG	AA	3188	1/1	0.89	0.10	-	62,62,62,62	0
57	MG	DA	3523	1/1	0.97	0.15	-	45,45,45,45	0
57	MG	DA	3452	1/1	0.88	0.19	-	40,40,40,40	0
57	MG	BB	3001	1/1	0.90	0.16	-	44,44,44,44	0
57	MG	BA	3516	1/1	0.93	0.14	-	32,32,32,32	0
57	MG	BG	3002	1/1	0.86	0.12	-	65,65,65,65	0
57	MG	CA	3119	1/1	0.90	0.09	-	74,74,74,74	0
57	MG	DA	3366	1/1	0.86	0.16	-	40,40,40,40	0
57	MG	BA	3236	1/1	0.96	0.15	-	39,39,39,39	0
57	MG	DA	3584	1/1	0.98	0.14	-	63,63,63,63	0
57	MG	CA	3142	1/1	0.87	0.20	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3201	1/1	0.90	0.27	-	42,42,42,42	0
57	MG	BA	3712	1/1	0.90	0.11	-	30,30,30,30	0
57	MG	BA	3404	1/1	0.91	0.22	-	30,30,30,30	0
57	MG	DA	3375	1/1	0.90	0.23	-	30,30,30,30	0
57	MG	DA	3465	1/1	0.96	0.14	-	45,45,45,45	0
57	MG	BA	3208	1/1	0.95	0.10	-	33,33,33,33	0
57	MG	BA	3175	1/1	0.82	0.18	-	55,55,55,55	0
57	MG	BA	3330	1/1	0.99	0.17	-	14,14,14,14	0
57	MG	BA	3536	1/1	0.97	0.11	-	42,42,42,42	0
57	MG	BA	3465	1/1	0.90	0.17	-	44,44,44,44	0
57	MG	BA	3500	1/1	0.91	0.10	-	54,54,54,54	0
57	MG	DA	3333	1/1	0.97	0.12	-	41,41,41,41	0
57	MG	DA	3394	1/1	0.91	0.11	-	48,48,48,48	0
57	MG	BA	3166	1/1	0.83	0.26	-	45,45,45,45	0
57	MG	DA	3224	1/1	0.83	0.29	-	60,60,60,60	0
57	MG	BA	3063	1/1	0.88	0.14	-	39,39,39,39	0
57	MG	DA	3279	1/1	0.96	0.32	-	50,50,50,50	0
57	MG	CA	3084	1/1	0.86	0.15	-	58,58,58,58	0
57	MG	DA	3334	1/1	0.96	0.13	-	31,31,31,31	0
57	MG	DA	3056	1/1	0.89	0.08	-	35,35,35,35	0
57	MG	BA	3611	1/1	0.83	0.12	-	61,61,61,61	0
57	MG	BA	3229	1/1	0.89	0.51	-	52,52,52,52	0
57	MG	BA	3642	1/1	0.93	0.18	-	50,50,50,50	0
57	MG	BA	3476	1/1	0.92	0.14	-	37,37,37,37	0
57	MG	BA	3487	1/1	0.80	0.11	-	70,70,70,70	0
57	MG	BA	3460	1/1	0.93	0.14	-	43,43,43,43	0
57	MG	AA	3118	1/1	0.95	0.17	-	50,50,50,50	0
57	MG	AD	301	1/1	0.95	0.10	-	47,47,47,47	0
57	MG	BA	3454	1/1	0.92	0.15	-	45,45,45,45	0
57	MG	DA	3147	1/1	0.91	0.18	-	42,42,42,42	0
57	MG	AA	3102	1/1	0.96	0.29	-	52,52,52,52	0
57	MG	BA	3359	1/1	0.96	0.14	-	56,56,56,56	0
57	MG	BA	3573	1/1	0.96	0.15	-	29,29,29,29	0
57	MG	CA	3008	1/1	0.72	0.13	-	67,67,67,67	0
57	MG	DA	3336	1/1	0.98	0.21	-	38,38,38,38	0
57	MG	BA	3683	1/1	0.88	0.27	-	44,44,44,44	0
57	MG	DA	3626	1/1	0.89	0.22	-	38,38,38,38	0
57	MG	BA	3652	1/1	0.96	0.19	-	65,65,65,65	0
57	MG	DA	3418	1/1	0.94	0.21	-	41,41,41,41	0
57	MG	CA	3069	1/1	0.91	0.33	-	56,56,56,56	0
57	MG	DA	3035	1/1	0.92	0.19	-	45,45,45,45	0
57	MG	BA	3188	1/1	0.96	0.19	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3048	1/1	0.93	0.16	-	53,53,53,53	0
57	MG	BA	3370	1/1	0.98	0.21	-	32,32,32,32	0
57	MG	AA	3126	1/1	0.76	0.17	-	52,52,52,52	0
57	MG	DA	3415	1/1	0.92	0.36	-	55,55,55,55	0
57	MG	BA	3679	1/1	0.94	0.15	-	38,38,38,38	0
57	MG	DA	3140	1/1	0.98	0.25	-	38,38,38,38	0
57	MG	CA	3053	1/1	0.91	0.17	-	59,59,59,59	0
57	MG	BA	3265	1/1	0.98	0.14	-	30,30,30,30	0
57	MG	DA	3534	1/1	0.97	0.12	-	30,30,30,30	0
57	MG	BA	3092	1/1	0.91	0.14	-	32,32,32,32	0
57	MG	DA	3455	1/1	0.88	0.35	-	34,34,34,34	0
57	MG	BA	3217	1/1	0.90	0.36	-	57,57,57,57	0
57	MG	DA	3065	1/1	0.96	0.14	-	38,38,38,38	0
57	MG	BA	3617	1/1	0.97	0.13	-	59,59,59,59	0
57	MG	DA	3592	1/1	0.89	0.14	-	62,62,62,62	0
57	MG	AA	3020	1/1	0.93	0.18	-	62,62,62,62	0
57	MG	DA	3485	1/1	0.94	0.20	-	41,41,41,41	0
57	MG	AA	3099	1/1	0.94	0.11	-	59,59,59,59	0
57	MG	DA	3563	1/1	0.91	0.15	-	55,55,55,55	0
57	MG	CA	3036	1/1	0.91	0.10	-	47,47,47,47	0
57	MG	DA	3206	1/1	0.98	0.22	-	37,37,37,37	0
57	MG	BA	3525	1/1	0.89	0.18	-	49,49,49,49	0
57	MG	CA	3027	1/1	0.88	0.08	-	62,62,62,62	0
57	MG	BA	3429	1/1	0.89	0.13	-	37,37,37,37	0
57	MG	DA	3575	1/1	0.89	0.21	-	19,19,19,19	0
57	MG	AA	3145	1/1	0.78	0.23	-	71,71,71,71	0
57	MG	BB	3016	1/1	0.98	0.06	-	39,39,39,39	0
57	MG	BA	3659	1/1	0.97	0.22	-	47,47,47,47	0
57	MG	AS	101	1/1	0.88	0.09	-	55,55,55,55	0
57	MG	BA	3570	1/1	0.81	0.12	-	48,48,48,48	0
57	MG	BA	3273	1/1	0.93	0.17	-	30,30,30,30	0
57	MG	DA	3555	1/1	0.82	0.15	-	70,70,70,70	0
57	MG	CA	3089	1/1	0.96	0.12	-	65,65,65,65	0
57	MG	DA	3569	1/1	0.91	0.15	-	42,42,42,42	0
57	MG	BA	3639	1/1	0.73	0.15	-	46,46,46,46	0
57	MG	AA	3129	1/1	0.98	0.15	-	37,37,37,37	0
57	MG	CA	3160	1/1	0.94	0.38	-	49,49,49,49	0
57	MG	BA	3290	1/1	0.98	0.14	-	43,43,43,43	0
57	MG	BA	3020	1/1	0.83	0.30	-	55,55,55,55	0
57	MG	CX	3002	1/1	0.73	0.35	-	75,75,75,75	0
57	MG	AA	3071	1/1	0.97	0.39	-	41,41,41,41	0
57	MG	BA	3107	1/1	0.93	0.28	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	DA	3057	1/1	0.96	0.25	-	22,22,22,22	0
57	MG	AA	3031	1/1	0.92	0.10	-	41,41,41,41	0
57	MG	AA	3168	1/1	0.89	0.09	-	56,56,56,56	0
57	MG	DA	3193	1/1	0.83	0.21	-	43,43,43,43	0
57	MG	BA	3243	1/1	0.87	0.24	-	46,46,46,46	0
57	MG	AA	3158	1/1	0.92	0.09	-	72,72,72,72	0
57	MG	DA	3214	1/1	0.93	0.13	-	43,43,43,43	0
57	MG	B3	3002	1/1	0.97	0.17	-	58,58,58,58	0
57	MG	BA	3306	1/1	0.72	0.20	-	32,32,32,32	0
57	MG	DA	3266	1/1	0.85	0.14	-	45,45,45,45	0
57	MG	DB	3002	1/1	0.86	0.07	-	75,75,75,75	0
57	MG	DA	3544	1/1	0.94	0.08	-	59,59,59,59	0
57	MG	AA	3085	1/1	0.73	0.15	-	69,69,69,69	0
57	MG	DA	3337	1/1	0.84	0.22	-	46,46,46,46	0
57	MG	BA	3295	1/1	0.86	0.14	-	56,56,56,56	0
57	MG	DA	3142	1/1	0.93	0.23	-	50,50,50,50	0
57	MG	B7	103	1/1	0.85	0.21	-	51,51,51,51	0
57	MG	DA	3125	1/1	0.92	0.11	-	48,48,48,48	0
57	MG	AA	3092	1/1	0.94	0.15	-	36,36,36,36	0
57	MG	AA	3014	1/1	0.90	0.14	-	73,73,73,73	0
57	MG	CA	3091	1/1	0.93	0.20	-	75,75,75,75	0
57	MG	BA	3555	1/1	0.93	0.08	-	62,62,62,62	0
57	MG	BA	3130	1/1	0.83	0.39	-	39,39,39,39	0
57	MG	DA	3380	1/1	0.90	0.13	-	65,65,65,65	0
57	MG	DA	3246	1/1	0.92	0.30	-	57,57,57,57	0
57	MG	BA	3438	1/1	0.96	0.16	-	19,19,19,19	0
57	MG	AA	3134	1/1	0.86	0.15	-	59,59,59,59	0
57	MG	BA	3627	1/1	0.97	0.09	-	28,28,28,28	0
57	MG	BA	3670	1/1	0.98	0.11	-	25,25,25,25	0
57	MG	DA	3120	1/1	0.87	0.26	-	55,55,55,55	0
57	MG	DA	3151	1/1	0.96	0.20	-	48,48,48,48	0
57	MG	DA	3390	1/1	0.70	0.17	-	54,54,54,54	0
57	MG	DA	3360	1/1	0.93	0.11	-	54,54,54,54	0
57	MG	DA	3244	1/1	0.86	0.22	-	43,43,43,43	0
57	MG	BA	3640	1/1	0.96	0.15	-	53,53,53,53	0
57	MG	DA	3411	1/1	0.93	0.10	-	51,51,51,51	0
57	MG	DB	3007	1/1	0.98	0.09	-	55,55,55,55	0
57	MG	CA	3092	1/1	0.83	0.16	-	76,76,76,76	0
57	MG	DA	3595	1/1	0.89	0.14	-	65,65,65,65	0
57	MG	DA	3526	1/1	0.96	0.10	-	41,41,41,41	0
57	MG	BA	3299	1/1	0.85	0.20	-	27,27,27,27	0
57	MG	BA	3422	1/1	0.80	0.15	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3600	1/1	0.96	0.25	-	59,59,59,59	0
57	MG	BA	3435	1/1	0.96	0.24	-	31,31,31,31	0
57	MG	BA	3582	1/1	0.95	0.16	-	23,23,23,23	0
57	MG	DA	3124	1/1	0.97	0.26	-	30,30,30,30	0
57	MG	BA	3260	1/1	0.94	0.26	-	45,45,45,45	0
57	MG	DA	3074	1/1	0.94	0.18	-	38,38,38,38	0
57	MG	DA	3305	1/1	0.88	0.07	-	48,48,48,48	0
57	MG	AA	3150	1/1	0.89	0.09	-	65,65,65,65	0
57	MG	BB	3018	1/1	0.92	0.09	-	43,43,43,43	0
57	MG	BA	3553	1/1	0.98	0.19	-	41,41,41,41	0
57	MG	CA	3041	1/1	0.84	0.10	-	62,62,62,62	0
57	MG	BA	3179	1/1	0.93	0.20	-	49,49,49,49	0
57	MG	BA	3239	1/1	0.99	0.17	-	42,42,42,42	0
57	MG	BA	3014	1/1	0.98	0.13	-	46,46,46,46	0
57	MG	DA	3135	1/1	0.65	0.18	-	61,61,61,61	0
57	MG	DA	3581	1/1	0.93	0.17	-	53,53,53,53	0
57	MG	BA	3675	1/1	0.92	0.19	-	41,41,41,41	0
57	MG	DA	3118	1/1	0.94	0.09	-	46,46,46,46	0
57	MG	CE	3001	1/1	0.81	0.19	-	80,80,80,80	0
57	MG	BA	3519	1/1	0.89	0.16	-	26,26,26,26	0
57	MG	DA	3408	1/1	0.94	0.10	-	44,44,44,44	0
57	MG	DA	3123	1/1	0.97	0.16	-	45,45,45,45	0
57	MG	CA	3098	1/1	0.88	0.07	-	76,76,76,76	0
57	MG	AA	3132	1/1	0.96	0.20	-	67,67,67,67	0
57	MG	DA	3611	1/1	0.91	0.17	-	58,58,58,58	0
57	MG	DA	3468	1/1	0.96	0.26	-	64,64,64,64	0
57	MG	DA	3133	1/1	0.91	0.14	-	52,52,52,52	0
57	MG	DA	3225	1/1	0.93	0.14	-	42,42,42,42	0
57	MG	DA	3454	1/1	0.97	0.27	-	28,28,28,28	0
57	MG	DA	3082	1/1	0.93	0.17	-	47,47,47,47	0
57	MG	BA	3001	1/1	0.91	0.20	-	48,48,48,48	0
57	MG	BE	3006	1/1	0.90	0.34	-	72,72,72,72	0
57	MG	DA	3576	1/1	0.91	0.27	-	46,46,46,46	0
57	MG	CA	3128	1/1	0.93	0.12	-	43,43,43,43	0
57	MG	BA	3255	1/1	0.98	0.06	-	37,37,37,37	0
57	MG	DA	3036	1/1	0.87	0.14	-	48,48,48,48	0
57	MG	AA	3117	1/1	0.96	0.12	-	55,55,55,55	0
57	MG	DA	3139	1/1	0.86	0.20	-	49,49,49,49	0
57	MG	DA	3598	1/1	0.90	0.11	-	48,48,48,48	0
57	MG	BA	3612	1/1	0.95	0.23	-	58,58,58,58	0
57	MG	BW	205	1/1	0.98	0.14	-	30,30,30,30	0
57	MG	BA	3488	1/1	0.97	0.05	-	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BB	3008	1/1	0.92	0.11	-	60,60,60,60	0
57	MG	DA	3492	1/1	0.91	0.10	-	45,45,45,45	0
57	MG	BA	3653	1/1	0.98	0.21	-	51,51,51,51	0
57	MG	BA	3176	1/1	0.92	0.23	-	35,35,35,35	0
57	MG	BA	3326	1/1	0.85	0.15	-	40,40,40,40	0
57	MG	DA	3080	1/1	0.96	0.10	-	64,64,64,64	0
57	MG	DA	3568	1/1	0.85	0.14	-	45,45,45,45	0
57	MG	DA	3287	1/1	0.89	0.29	-	58,58,58,58	0
57	MG	DA	3482	1/1	0.99	0.25	-	31,31,31,31	0
57	MG	CA	3153	1/1	0.96	0.15	-	57,57,57,57	0
57	MG	BA	3214	1/1	0.90	0.22	-	48,48,48,48	0
57	MG	BA	3139	1/1	0.90	0.32	-	45,45,45,45	0
57	MG	BA	3250	1/1	0.93	0.15	-	47,47,47,47	0
57	MG	BA	3280	1/1	0.98	0.17	-	46,46,46,46	0
57	MG	B5	103	1/1	0.96	0.08	-	50,50,50,50	0
57	MG	BA	3634	1/1	0.95	0.23	-	58,58,58,58	0
57	MG	BA	3397	1/1	0.92	0.11	-	33,33,33,33	0
57	MG	DA	3248	1/1	0.89	0.20	-	59,59,59,59	0
57	MG	CA	3130	1/1	0.85	0.16	-	88,88,88,88	0
57	MG	CA	3150	1/1	0.95	0.11	-	66,66,66,66	0
57	MG	BA	3029	1/1	0.86	0.19	-	53,53,53,53	0
57	MG	BA	3201	1/1	0.94	0.17	-	44,44,44,44	0
57	MG	BA	3080	1/1	0.94	0.20	-	51,51,51,51	0
57	MG	AA	3185	1/1	0.91	0.15	-	50,50,50,50	0
57	MG	CA	3099	1/1	0.88	0.22	-	50,50,50,50	0
57	MG	BA	3353	1/1	0.94	0.08	-	46,46,46,46	0
57	MG	DA	3591	1/1	0.88	0.10	-	69,69,69,69	0
57	MG	BA	3596	1/1	0.98	0.14	-	56,56,56,56	0
57	MG	DP	201	1/1	0.95	0.25	-	61,61,61,61	0
57	MG	AA	3142	1/1	0.95	0.29	-	53,53,53,53	0
57	MG	BA	3481	1/1	0.97	0.23	-	35,35,35,35	0
57	MG	BA	3333	1/1	0.89	0.10	-	58,58,58,58	0
57	MG	AA	3098	1/1	0.90	0.14	-	42,42,42,42	0
57	MG	BR	202	1/1	0.90	0.18	-	49,49,49,49	0
57	MG	BA	3714	1/1	0.95	0.10	-	42,42,42,42	0
57	MG	AA	3191	1/1	0.95	0.21	-	56,56,56,56	0
57	MG	CA	3093	1/1	0.93	0.16	-	69,69,69,69	0
57	MG	CA	3135	1/1	0.84	0.10	-	85,85,85,85	0
57	MG	DA	3424	1/1	0.95	0.08	-	56,56,56,56	0
57	MG	DA	3500	1/1	0.96	0.15	-	32,32,32,32	0
57	MG	BB	3006	1/1	0.95	0.19	-	42,42,42,42	0
57	MG	BA	3471	1/1	0.94	0.10	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	BA	3664	1/1	0.93	0.14	-	66,66,66,66	0
57	MG	AA	3058	1/1	0.86	0.21	-	48,48,48,48	0
57	MG	DA	3392	1/1	0.98	0.23	-	40,40,40,40	0
57	MG	BA	3324	1/1	0.92	0.20	-	61,61,61,61	0
57	MG	AA	3123	1/1	0.86	0.10	-	59,59,59,59	0
57	MG	CA	3051	1/1	0.93	0.30	-	57,57,57,57	0
57	MG	BA	3196	1/1	0.97	0.27	-	51,51,51,51	0
57	MG	AA	3087	1/1	0.86	0.13	-	57,57,57,57	0
57	MG	DA	3413	1/1	0.93	0.29	-	30,30,30,30	0
57	MG	AA	3135	1/1	0.94	0.07	-	52,52,52,52	0
57	MG	BA	3649	1/1	0.95	0.14	-	65,65,65,65	0
57	MG	DA	3175	1/1	0.96	0.24	-	42,42,42,42	0
57	MG	AA	3207	1/1	0.95	0.10	-	57,57,57,57	0
57	MG	DA	3326	1/1	0.91	0.09	-	40,40,40,40	0
57	MG	BA	3221	1/1	0.83	0.25	-	59,59,59,59	0
57	MG	DA	3269	1/1	0.98	0.16	-	40,40,40,40	0
57	MG	BA	3279	1/1	0.92	0.21	-	48,48,48,48	0
57	MG	DA	3158	1/1	0.78	0.13	-	52,52,52,52	0
57	MG	BA	3153	1/1	0.87	0.12	-	53,53,53,53	0
57	MG	DA	3273	1/1	0.96	0.21	-	41,41,41,41	0
57	MG	BA	3122	1/1	0.92	0.22	-	39,39,39,39	0
57	MG	BA	3590	1/1	0.91	0.24	-	62,62,62,62	0
57	MG	DA	3431	1/1	0.92	0.15	-	56,56,56,56	0
57	MG	DA	3447	1/1	0.95	0.14	-	48,48,48,48	0
57	MG	DA	3245	1/1	0.96	0.12	-	46,46,46,46	0
57	MG	BA	3227	1/1	0.97	0.19	-	39,39,39,39	0
57	MG	BA	3557	1/1	0.93	0.17	-	35,35,35,35	0
57	MG	BA	3004	1/1	0.98	0.18	-	26,26,26,26	0
57	MG	AA	3200	1/1	0.94	0.10	-	58,58,58,58	0
57	MG	BA	3086	1/1	0.98	0.22	-	15,15,15,15	0
57	MG	AE	3001	1/1	0.93	0.37	-	85,85,85,85	0
57	MG	BA	3462	1/1	0.95	0.23	-	51,51,51,51	0
57	MG	DA	3099	1/1	0.92	0.15	-	40,40,40,40	0
57	MG	AD	303	1/1	0.89	0.20	-	60,60,60,60	0
57	MG	BA	3543	1/1	0.84	0.11	-	69,69,69,69	0
57	MG	AA	3044	1/1	0.94	0.14	-	46,46,46,46	0
57	MG	CA	3136	1/1	0.92	0.11	-	68,68,68,68	0
57	MG	BA	3241	1/1	0.91	0.33	-	53,53,53,53	0
57	MG	DA	3330	1/1	0.95	0.18	-	49,49,49,49	0
57	MG	CA	3078	1/1	0.90	0.18	-	63,63,63,63	0
57	MG	BA	3667	1/1	0.94	0.18	-	31,31,31,31	0
57	MG	DA	3046	1/1	0.87	0.33	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	CA	3140	1/1	0.90	0.07	-	48,48,48,48	0
57	MG	BA	3484	1/1	0.96	0.08	-	50,50,50,50	0
57	MG	DA	3236	1/1	0.94	0.10	-	45,45,45,45	0
57	MG	BA	3161	1/1	0.96	0.21	-	54,54,54,54	0
57	MG	DA	3406	1/1	0.82	0.15	-	62,62,62,62	0
57	MG	BA	3323	1/1	0.94	0.10	-	59,59,59,59	0
57	MG	DA	3284	1/1	0.86	0.20	-	51,51,51,51	0
57	MG	DA	3405	1/1	0.96	0.08	-	45,45,45,45	0
57	MG	DA	3295	1/1	0.96	0.08	-	58,58,58,58	0
57	MG	DA	3381	1/1	0.93	0.22	-	55,55,55,55	0
57	MG	BA	3158	1/1	0.79	0.28	-	48,48,48,48	0
57	MG	DA	3341	1/1	0.94	0.14	-	32,32,32,32	0
57	MG	DA	3407	1/1	0.76	0.16	-	67,67,67,67	0
57	MG	DA	3421	1/1	0.87	0.07	-	31,31,31,31	0
57	MG	CA	3088	1/1	0.88	0.11	-	61,61,61,61	0
57	MG	AA	3069	1/1	0.82	0.11	-	75,75,75,75	0
57	MG	AA	3046	1/1	0.91	0.18	-	72,72,72,72	0
57	MG	BA	3463	1/1	0.94	0.12	-	43,43,43,43	0
57	MG	DA	3271	1/1	0.92	0.22	-	47,47,47,47	0
57	MG	DA	3068	1/1	0.90	0.17	-	48,48,48,48	0
57	MG	BA	3448	1/1	0.94	0.08	-	42,42,42,42	0
57	MG	BA	3680	1/1	0.86	0.13	-	46,46,46,46	0
57	MG	DA	3428	1/1	0.90	0.19	-	46,46,46,46	0
57	MG	DA	3329	1/1	0.99	0.25	-	54,54,54,54	0
57	MG	CA	3156	1/1	0.98	0.05	-	57,57,57,57	0
57	MG	DA	3040	1/1	0.92	0.43	-	48,48,48,48	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.