



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 06:21 am BST

PDB ID : 4W2H
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in complex with pactamycin (co-crystallized), mRNA and deacylated tRNA in the P site
Authors : Polikanov, Y.S.; Osterman, I.A.; Szal, T.; Tashlitsky, V.N.; Serebryakova, M.V.; Kusochev, P.; Bulkley, D.; Malanicheva, I.A.; Efimenko, T.A.; Efremenkova, O.V.; Konevega, A.L.; Shaw, K.J.; Bogdanov, A.A.; Rodnina, M.V.; Dontsova, O.A.; Mankin, A.S.; Steitz, T.A.; Sergiev, P.V.
Deposited on : 2014-09-12
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

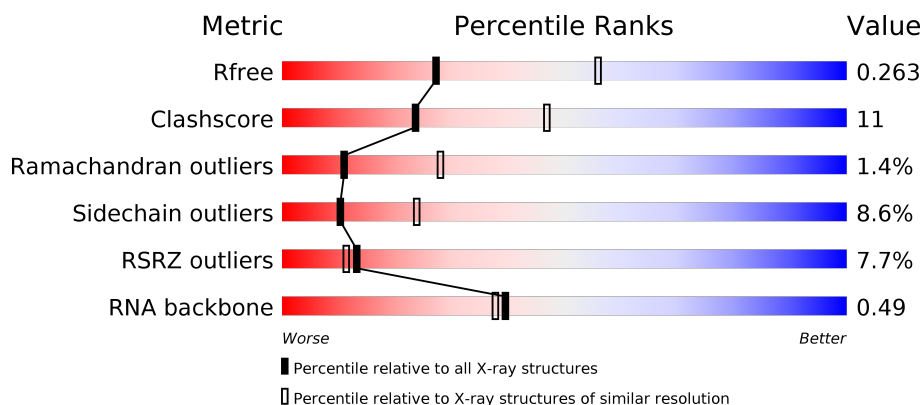
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)
RNA backbone	3102	1159 (3.00-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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>0%</div> <div> <div></div> <div>45%</div> <div>40%</div> <div>12%</div> <div>..</div> </div> </div>
1	CA	1521	<div> <div>2%</div> <div> <div></div> <div>44%</div> <div>40%</div> <div>14%</div> <div>..</div> </div> </div>
2	AB	256	<div> <div>4%</div> <div> <div></div> <div>43%</div> <div>36%</div> <div>12%</div> <div>10%</div> </div> </div>
2	CB	256	<div> <div>23%</div> <div> <div></div> <div>43%</div> <div>39%</div> <div>8%</div> <div>10%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	AC	239	
3	CC	239	
4	AD	209	
4	CD	209	
5	AE	162	
5	CE	162	
6	AF	101	
6	CF	101	
7	AG	156	
7	CG	156	
8	AH	138	
8	CH	138	
9	AI	128	
9	CI	128	
10	AJ	105	
10	CJ	105	
11	AK	129	
11	CK	129	
12	AL	132	
12	CL	132	
13	AM	126	
13	CM	126	
14	AN	61	
14	CN	61	
15	AO	89	



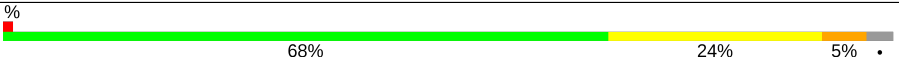
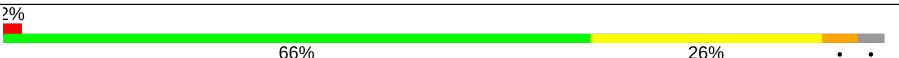
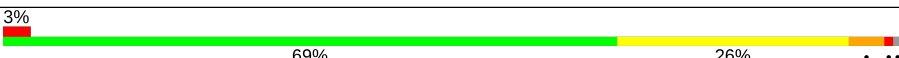

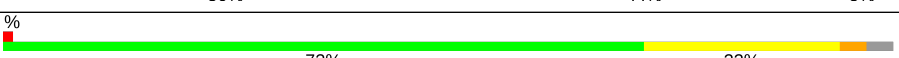
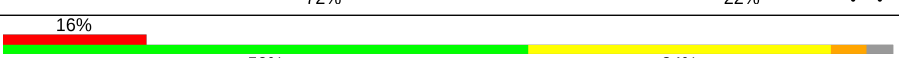
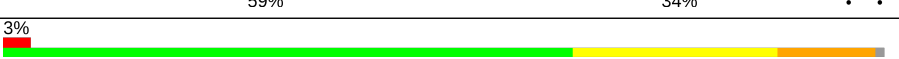

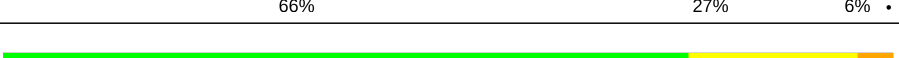







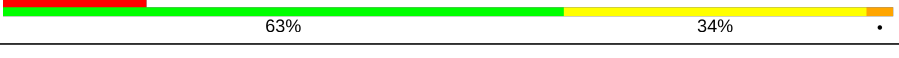
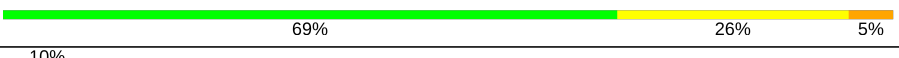

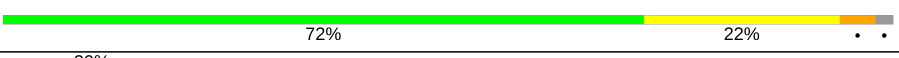



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Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AX	77	
23	CX	77	
24	AY	76	
24	CY	76	
25	BA	2915	
25	DA	2915	
26	BB	121	
26	DB	121	
27	BD	276	
27	DD	276	

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

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Mol	Chain	Length	Quality of chain
40	DU	118	
41	BV	101	
41	DV	101	
42	BW	113	
42	DW	113	
43	BX	96	
43	DX	96	
44	BY	110	
44	DY	110	
45	BZ	206	
45	DZ	206	
46	B0	85	
46	D0	85	
47	B1	98	
47	D1	98	
48	B2	72	
48	D2	72	
49	B3	60	
49	D3	60	
50	B4	71	
50	D4	71	
51	B5	60	
51	D5	60	
52	B6	54	
52	D6	54	

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Mol	Chain	Length	Quality of chain
53	B7	49	
53	D7	49	
54	B8	65	
54	D8	65	
55	B9	37	
55	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
56	MG	AA	3166	-	-	-	X
56	MG	BA	3048	-	-	-	X
56	MG	BE	306	-	-	-	X
56	MG	CA	3174	-	-	-	X
56	MG	DA	3640	-	-	-	X
56	MG	DA	3647	-	-	-	X
56	MG	DA	3655	-	-	-	X
57	PCY	CA	3176	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 290807 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1497	Total	C	N	O	P	0	0	0
			32183	14323	5965	10398	1497			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1552	976	302	273	1			
3	CC	206	Total	C	N	O	S	0	0	0
			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	120	Total	C	N	O	S		
			937	578	194	163	2	0	0
13	CM	118	Total	C	N	O	S		
			920	566	191	161	2	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	8	Total	C	N	O	P	0	0	0
			169	76	29	56	8			
22	CV	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AX	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
23	CX	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 24 is a RNA chain called E-site tRNA Acceptor Stem.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	AY	18	Total	C	N	O	P	0	0	0
			385	171	71	125	18			
24	CY	5	Total	C	N	O	P	0	0	0
			104	47	19	33	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2822	Total	C	N	O	P	0	0	0
			60792	27054	11380	19537	2821			
25	DA	2800	Total	C	N	O	P	0	0	0
			60311	26840	11284	19388	2799			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B4	69	Total	C	N	O	S	0	0	0
			558	352	102	99	5			
50	D4	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	B4	1	Total	Mg	0	0
			1	1		
56	BA	814	Total	Mg	0	0
			814	814		
56	CA	175	Total	Mg	0	0
			175	175		
56	DQ	3	Total	Mg	0	0
			3	3		
56	D3	1	Total	Mg	0	0
			1	1		
56	DF	5	Total	Mg	0	0
			5	5		
56	B8	2	Total	Mg	0	0
			2	2		
56	BE	7	Total	Mg	0	0
			7	7		
56	DU	4	Total	Mg	0	0
			4	4		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AN	1	Total 1	Mg 1	0	0
56	BP	4	Total 4	Mg 4	0	0
56	AX	9	Total 9	Mg 9	0	0
56	DN	1	Total 1	Mg 1	0	0
56	DD	8	Total 8	Mg 8	0	0
56	B5	4	Total 4	Mg 4	0	0
56	BB	22	Total 22	Mg 22	0	0
56	D8	1	Total 1	Mg 1	0	0
56	AE	3	Total 3	Mg 3	0	0
56	DG	1	Total 1	Mg 1	0	0
56	B9	1	Total 1	Mg 1	0	0
56	BF	9	Total 9	Mg 9	0	0
56	BX	2	Total 2	Mg 2	0	0
56	B2	1	Total 1	Mg 1	0	0
56	AA	190	Total 190	Mg 190	0	0
56	BQ	4	Total 4	Mg 4	0	0
56	CX	2	Total 2	Mg 2	0	0
56	DV	3	Total 3	Mg 3	0	0
56	B6	2	Total 2	Mg 2	0	0
56	AM	1	Total 1	Mg 1	0	0
56	BU	9	Total 9	Mg 9	0	0

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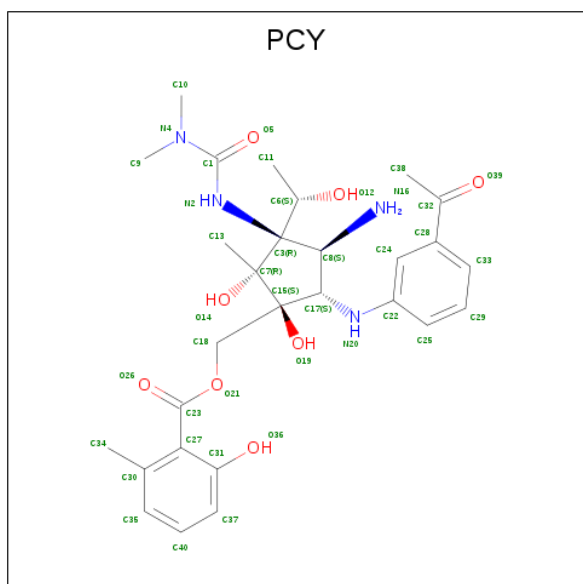
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	DR	1	Total 1	Mg 1	0	0
56	AD	1	Total 1	Mg 1	0	0
56	BN	7	Total 7	Mg 7	0	0
56	CT	1	Total 1	Mg 1	0	0
56	D0	2	Total 2	Mg 2	0	0
56	BG	2	Total 2	Mg 2	0	0
56	BY	3	Total 3	Mg 3	0	0
56	DE	5	Total 5	Mg 5	0	0
56	B3	1	Total 1	Mg 1	0	0
56	CJ	1	Total 1	Mg 1	0	0
56	BR	3	Total 3	Mg 3	0	0
56	DA	674	Total 674	Mg 674	0	0
56	DP	2	Total 2	Mg 2	0	0
56	DW	2	Total 2	Mg 2	0	0
56	B7	5	Total 5	Mg 5	0	0
56	CF	1	Total 1	Mg 1	0	0
56	BV	4	Total 4	Mg 4	0	0
56	DO	1	Total 1	Mg 1	0	0
56	BO	1	Total 1	Mg 1	0	0
56	AQ	1	Total 1	Mg 1	0	0
56	D1	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	BZ	2	Total	Mg	0	0
			2	2		
56	DY	1	Total	Mg	0	0
			1	1		
56	BD	9	Total	Mg	0	0
			9	9		
56	B0	5	Total	Mg	0	0
			5	5		
56	CE	2	Total	Mg	0	0
			2	2		
56	BW	4	Total	Mg	0	0
			4	4		
56	AF	1	Total	Mg	0	0
			1	1		
56	DB	10	Total	Mg	0	0
			10	10		

- Molecule 57 is Pactamycin (three-letter code: PCY) (formula: $C_{28}H_{38}N_4O_8$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
57	AA	1	Total	C	N	O	0	0
			40	28	4	8		
57	CA	1	Total	C	N	O	0	0
			40	28	4	8		

- Molecule 58 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



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	175	Total 175	O 175	0	0
61	AJ	2	Total 2	O 2	0	0
61	AL	1	Total 1	O 1	0	0
61	AM	1	Total 1	O 1	0	0
61	AO	1	Total 1	O 1	0	0
61	AV	1	Total 1	O 1	0	0
61	AX	8	Total 8	O 8	0	0
61	BA	1294	Total 1294	O 1294	0	0
61	BB	34	Total 34	O 34	0	0
61	BD	16	Total 16	O 16	0	0
61	BE	12	Total 12	O 12	0	0
61	BF	7	Total 7	O 7	0	0
61	BG	3	Total 3	O 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BI	1	Total 1	O 1	0	0
61	BN	1	Total 1	O 1	0	0
61	BO	4	Total 4	O 4	0	0
61	BP	15	Total 15	O 15	0	0
61	BQ	5	Total 5	O 5	0	0
61	BR	1	Total 1	O 1	0	0
61	BU	2	Total 2	O 2	0	0
61	BV	2	Total 2	O 2	0	0
61	BW	3	Total 3	O 3	0	0
61	BX	5	Total 5	O 5	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	4	Total 4	O 4	0	0
61	B6	1	Total 1	O 1	0	0
61	B7	1	Total 1	O 1	0	0
61	B8	10	Total 10	O 10	0	0
61	CA	137	Total 137	O 137	0	0
61	CD	1	Total 1	O 1	0	0
61	CJ	2	Total 2	O 2	0	0
61	CL	1	Total 1	O 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	CN	1	Total 1	O 1	0	0
61	CT	1	Total 1	O 1	0	0
61	CX	2	Total 2	O 2	0	0
61	DA	924	Total 924	O 924	0	0
61	DB	8	Total 8	O 8	0	0
61	DD	18	Total 18	O 18	0	0
61	DE	9	Total 9	O 9	0	0
61	DF	5	Total 5	O 5	0	0
61	DN	1	Total 1	O 1	0	0
61	DO	1	Total 1	O 1	0	0
61	DP	14	Total 14	O 14	0	0
61	DR	1	Total 1	O 1	0	0
61	DT	1	Total 1	O 1	0	0
61	DU	3	Total 3	O 3	0	0
61	DV	1	Total 1	O 1	0	0
61	DW	1	Total 1	O 1	0	0
61	DX	1	Total 1	O 1	0	0
61	DY	1	Total 1	O 1	0	0
61	D0	7	Total 7	O 7	0	0
61	D1	1	Total 1	O 1	0	0
61	D3	1	Total 1	O 1	0	0

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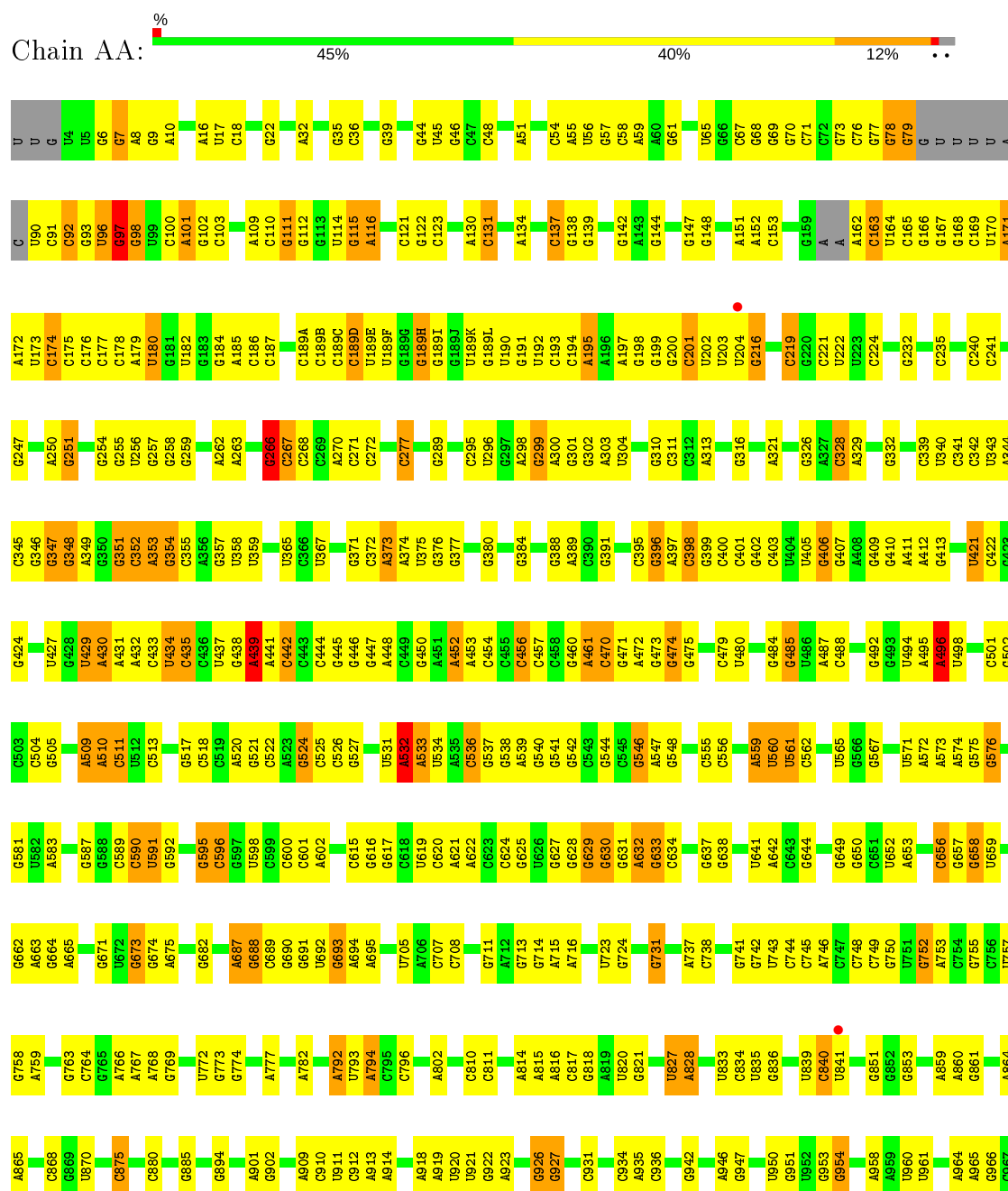
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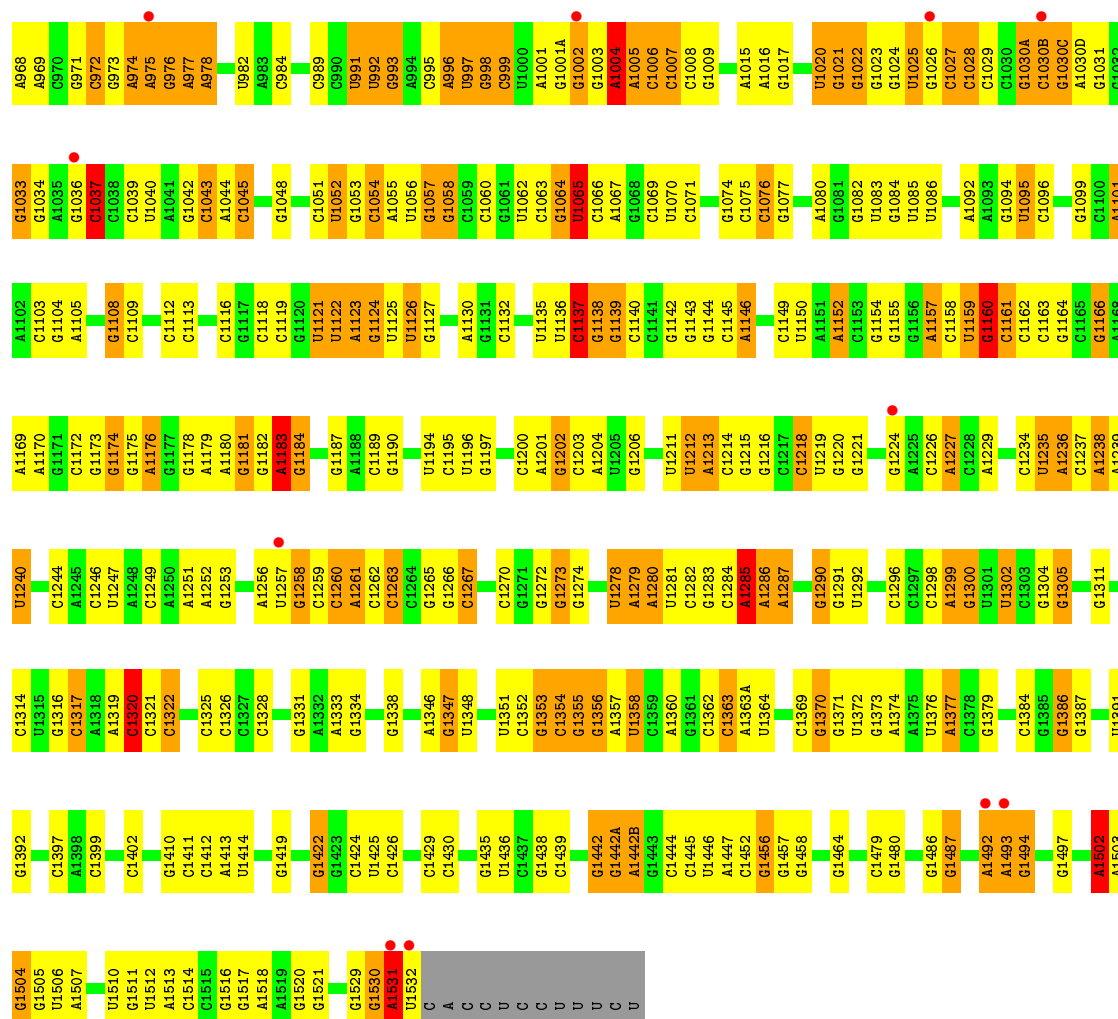
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	D8	4	Total	O	0	0
			4	4		

3 Residue-property plots

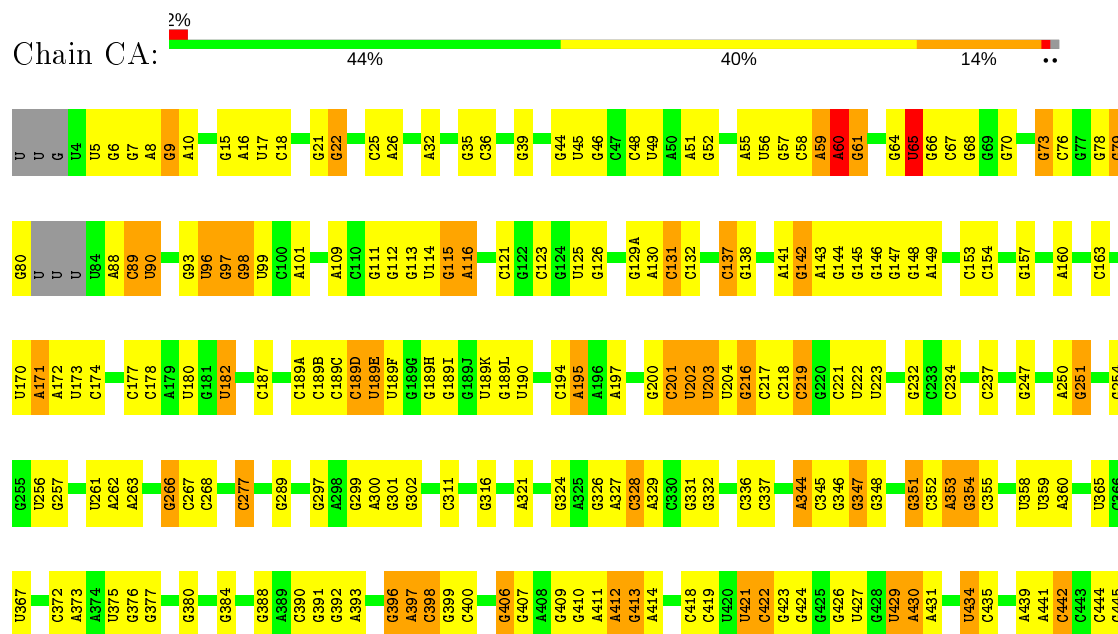
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

• Molecule 1: 16S Ribosomal RNA

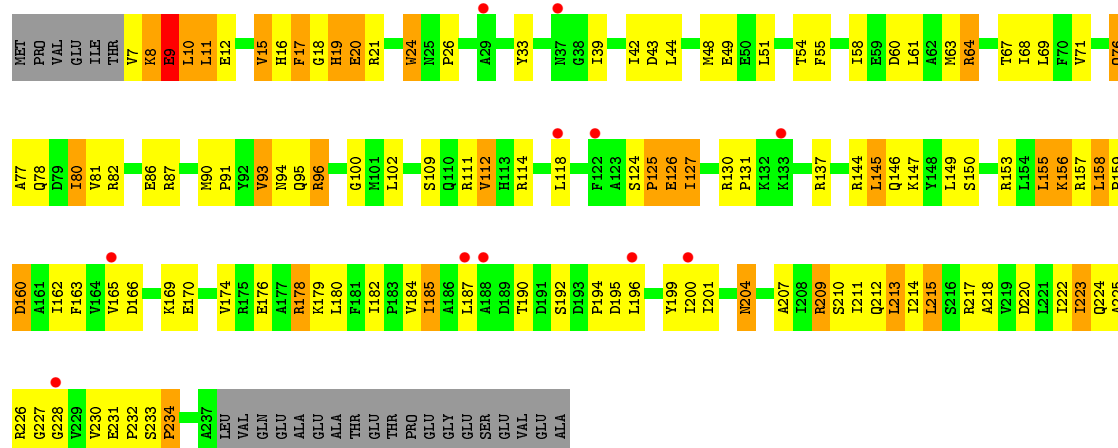
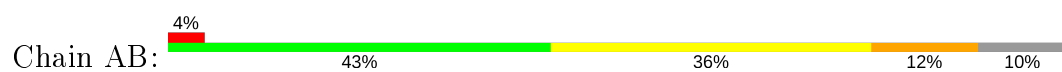




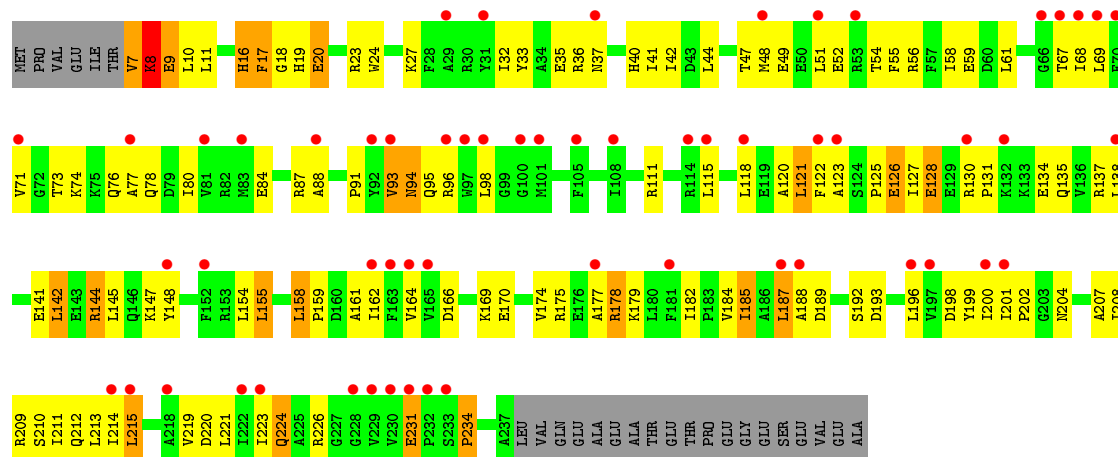
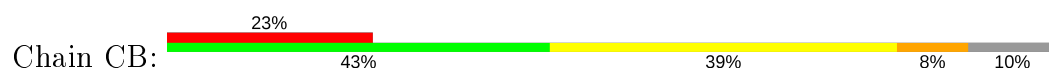
- Molecule 1: 16S Ribosomal RNA



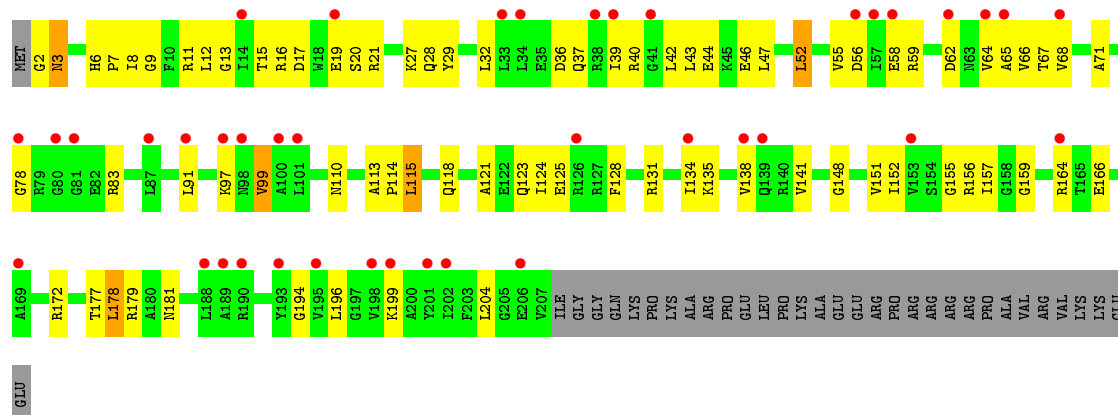




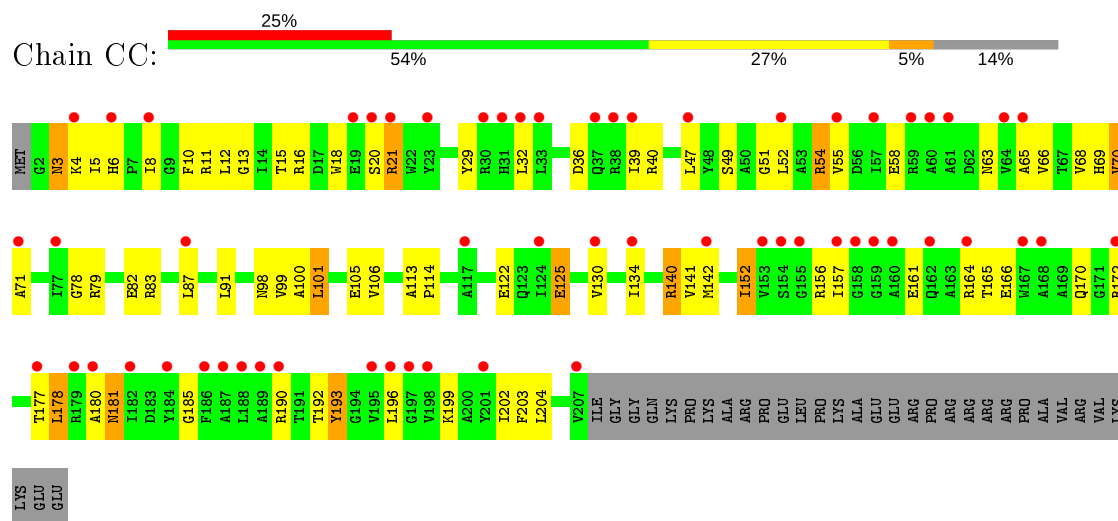
• Molecule 2: 30S Ribosomal Protein S2



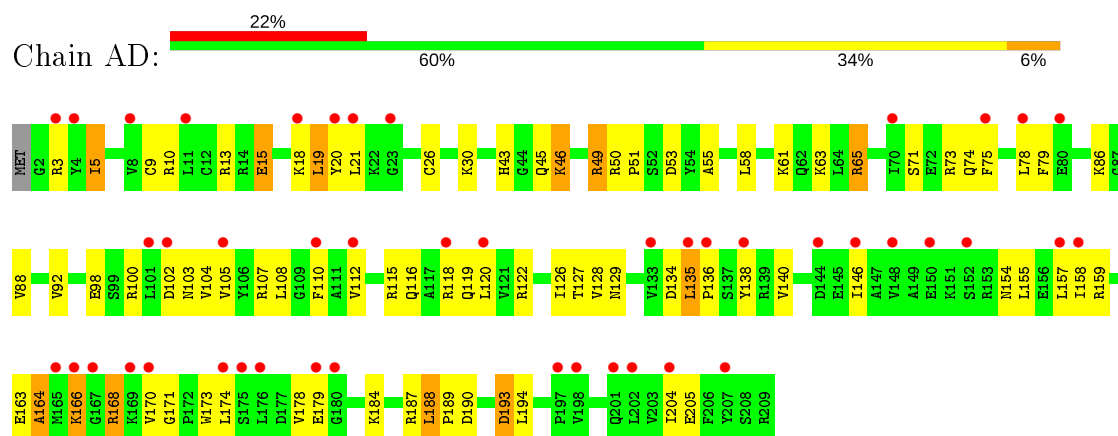
• Molecule 3: 30S Ribosomal Protein S3



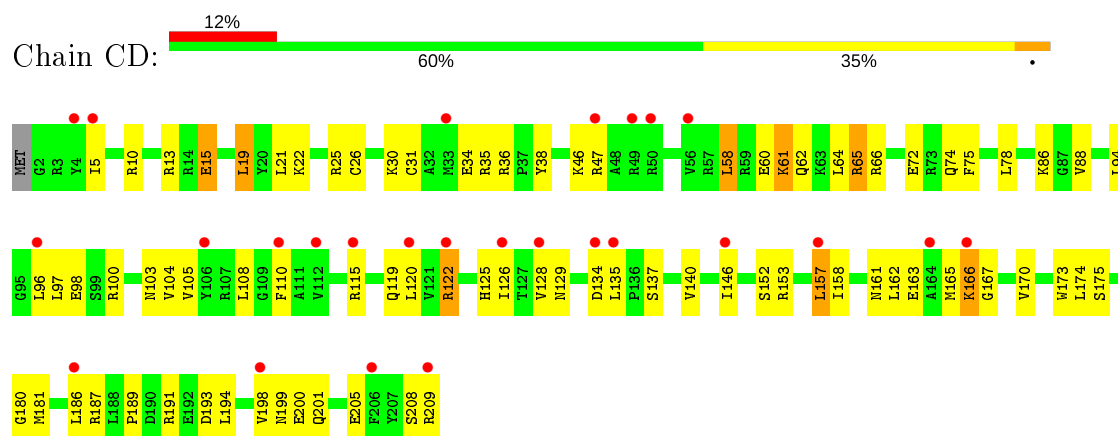
- Molecule 3: 30S Ribosomal Protein S3



- Molecule 4: 30S Ribosomal Protein S4

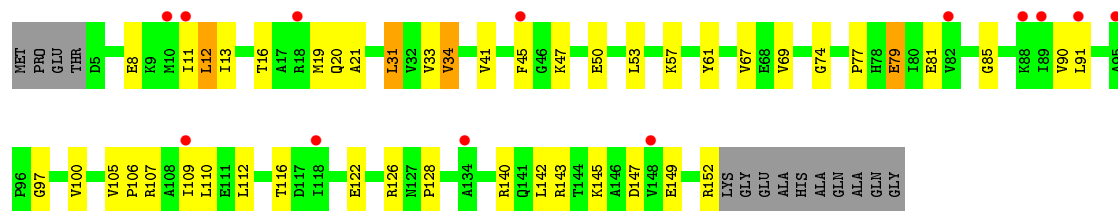


- Molecule 4: 30S Ribosomal Protein S4

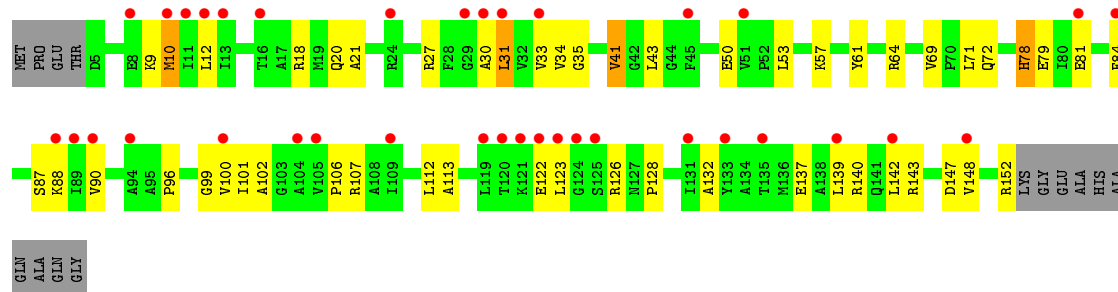


- Molecule 5: 30S Ribosomal Protein S5

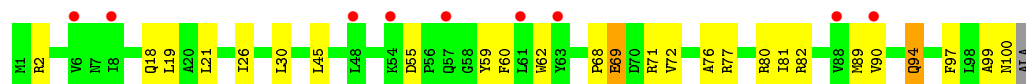
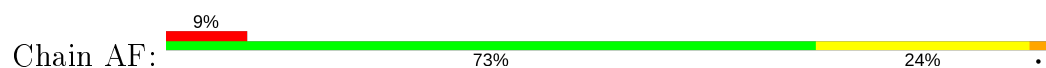




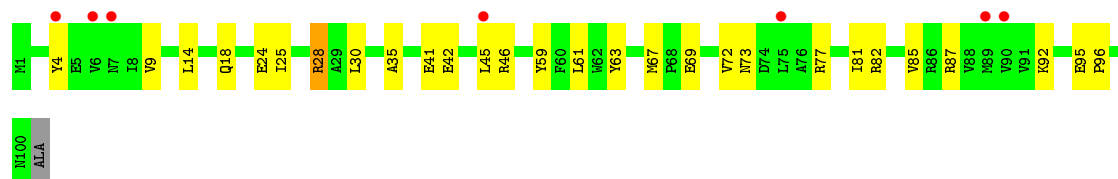
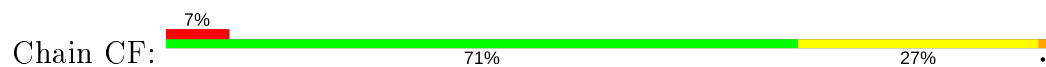
• Molecule 5: 30S Ribosomal Protein S5



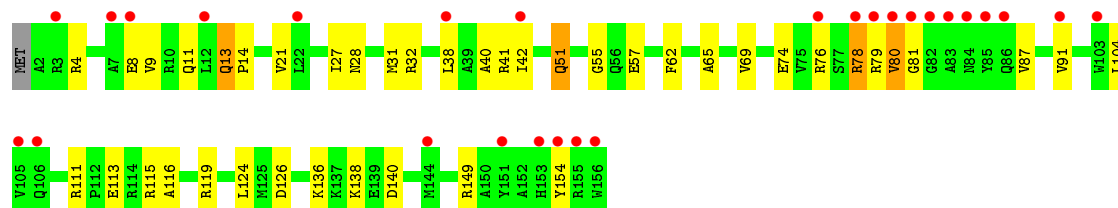
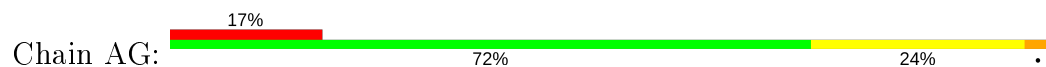
• Molecule 6: 30S Ribosomal Protein S6



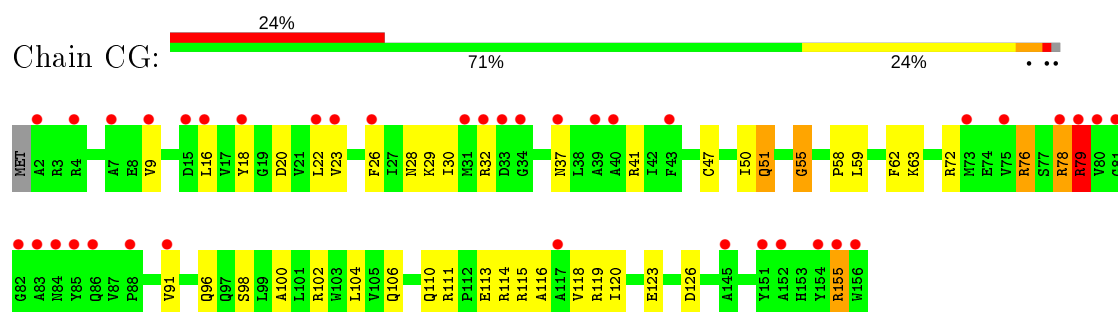
• Molecule 6: 30S Ribosomal Protein S6



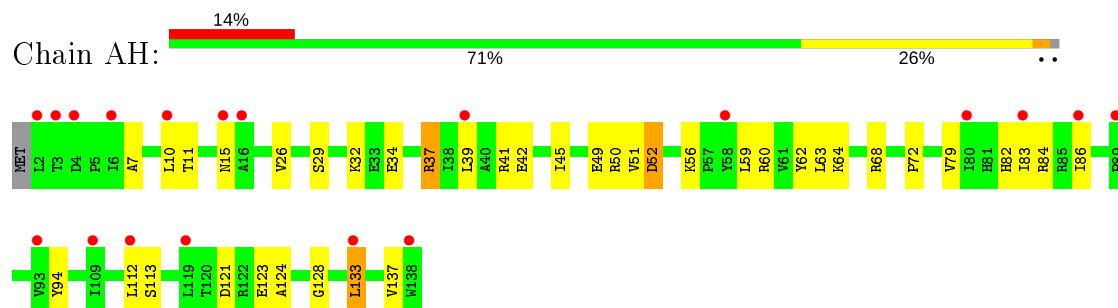
• Molecule 7: 30S Ribosomal Protein S7



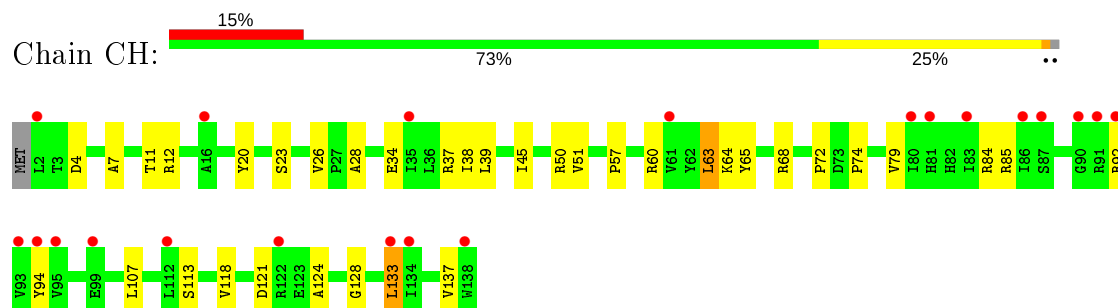
• Molecule 7: 30S Ribosomal Protein S7



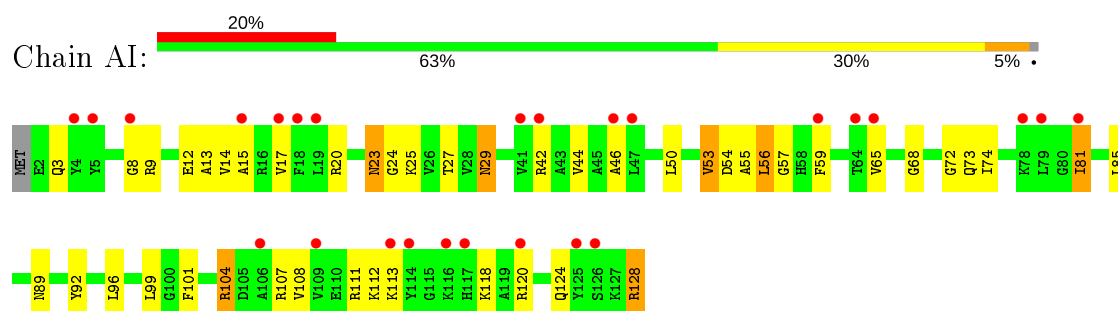
- Molecule 8: 30S Ribosomal Protein S8



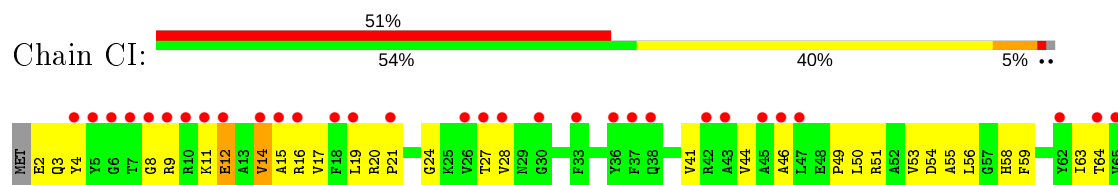
- Molecule 8: 30S Ribosomal Protein S8



- Molecule 9: 30S Ribosomal Protein S9

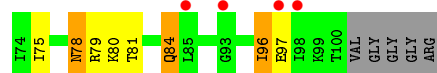
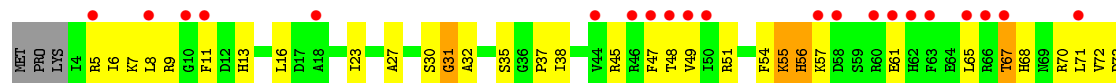


- Molecule 9: 30S Ribosomal Protein S9

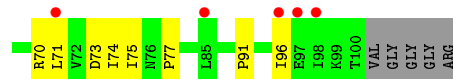
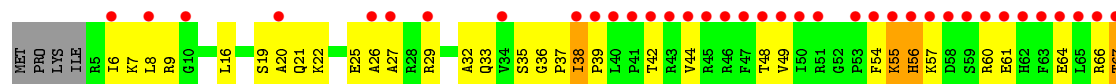
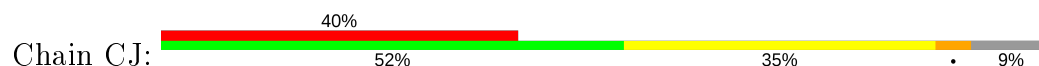




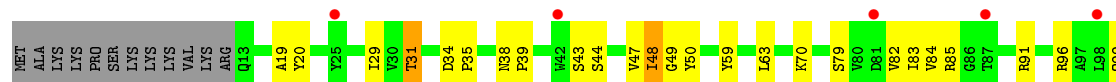
• Molecule 10: 30S Ribosomal Protein S10



• Molecule 10: 30S Ribosomal Protein S10



• Molecule 11: 30S Ribosomal Protein S11

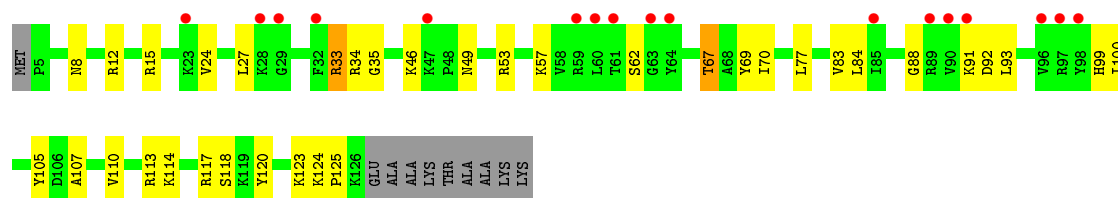


• Molecule 11: 30S Ribosomal Protein S11

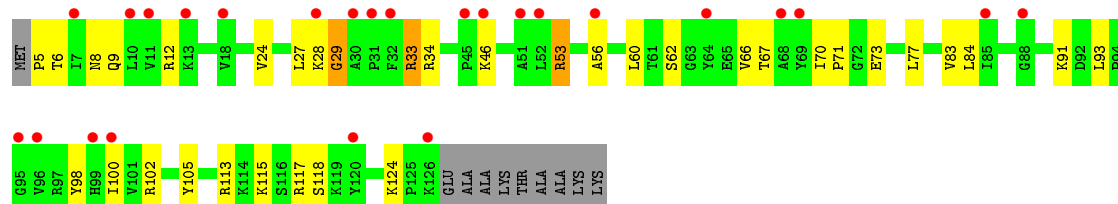


• Molecule 12: 30S Ribosomal Protein S12

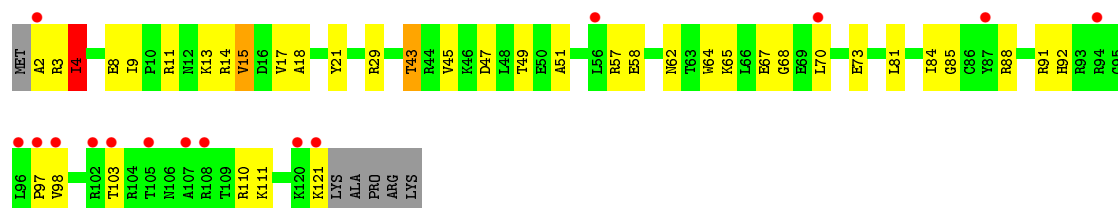




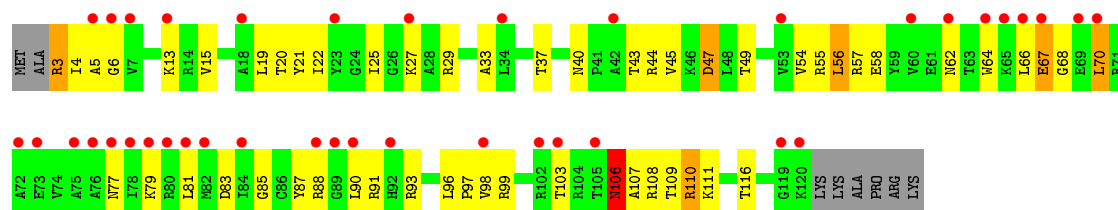
• Molecule 12: 30S Ribosomal Protein S12



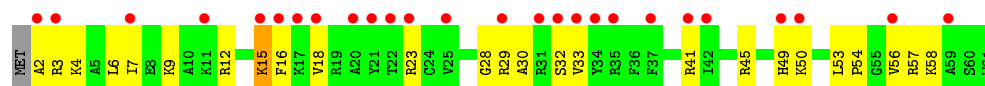
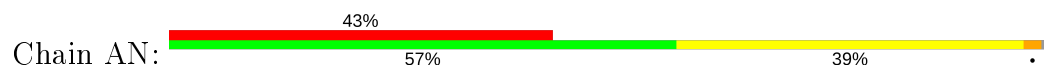
• Molecule 13: 30S Ribosomal Protein S13



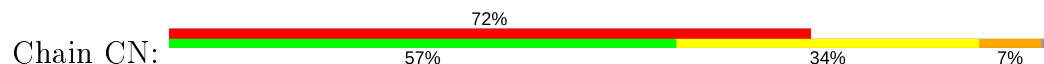
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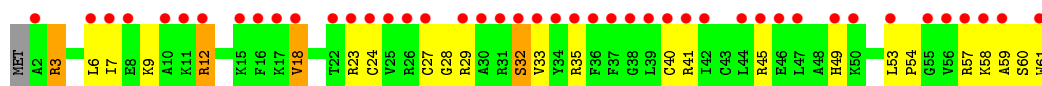


• Molecule 14: 30S Ribosomal Protein S14

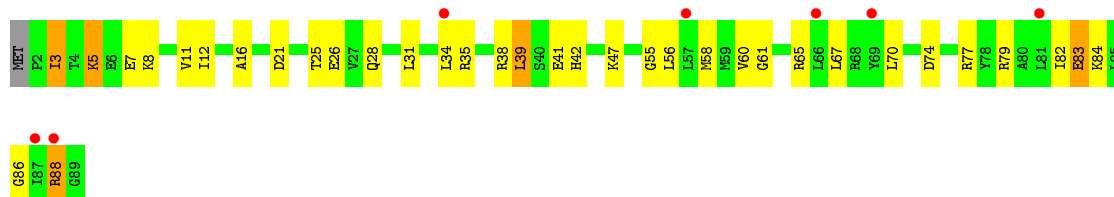


• Molecule 14: 30S Ribosomal Protein S14

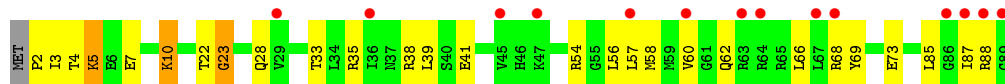




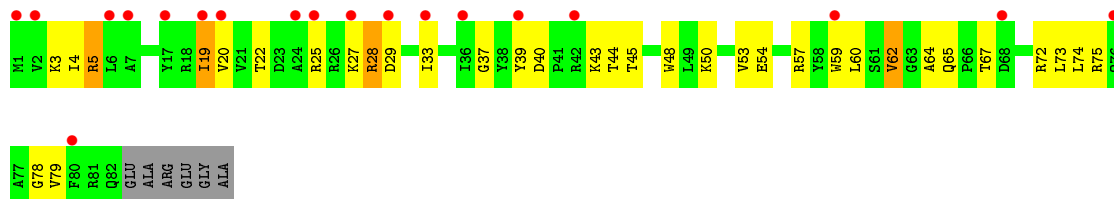
• Molecule 15: 30S Ribosomal Protein S15



• Molecule 15: 30S Ribosomal Protein S15



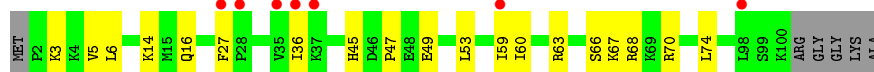
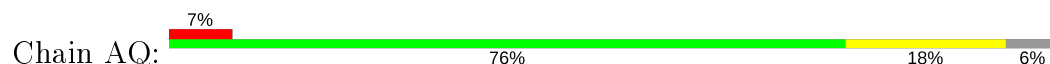
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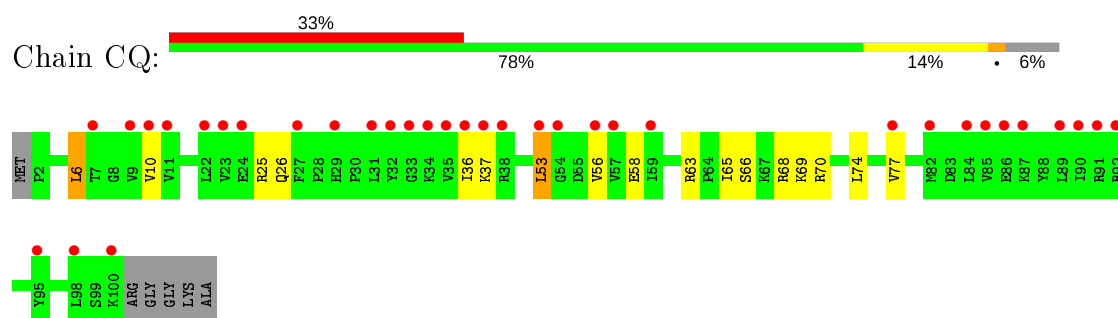
• Molecule 16: 30S Ribosomal Protein S16



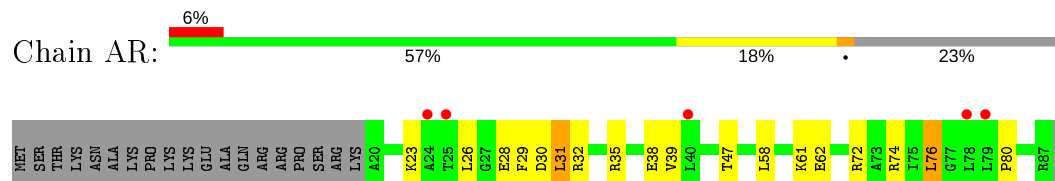
• Molecule 17: 30S Ribosomal Protein S17



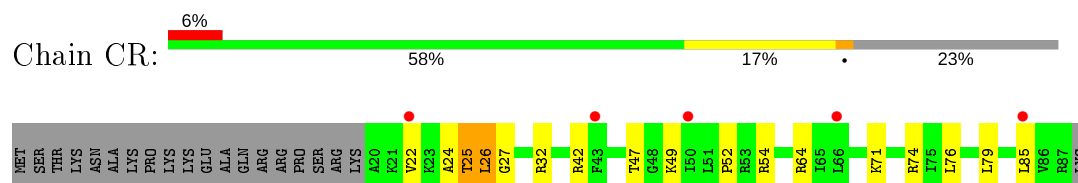
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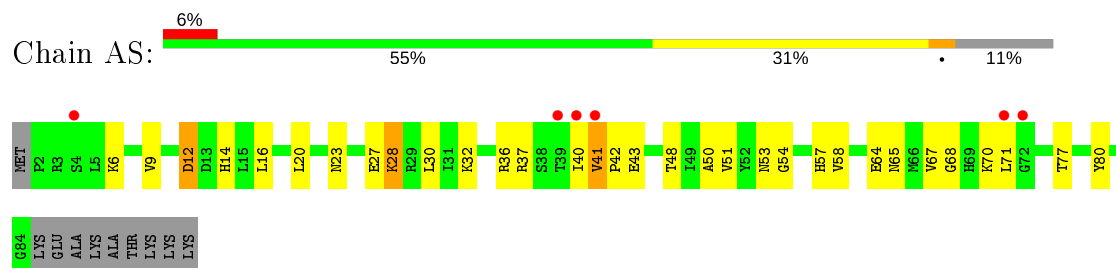
- Molecule 18: 30S Ribosomal Protein S18



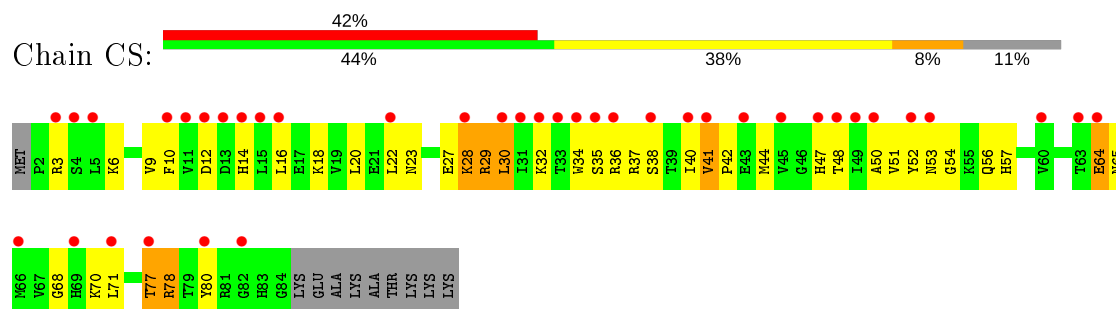
- Molecule 18: 30S Ribosomal Protein S18



- Molecule 19: 30S Ribosomal Protein S19

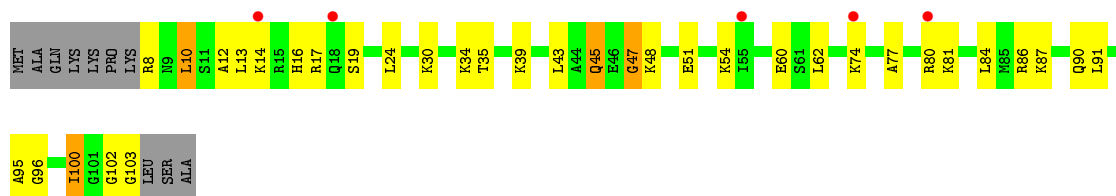


- Molecule 19: 30S Ribosomal Protein S19

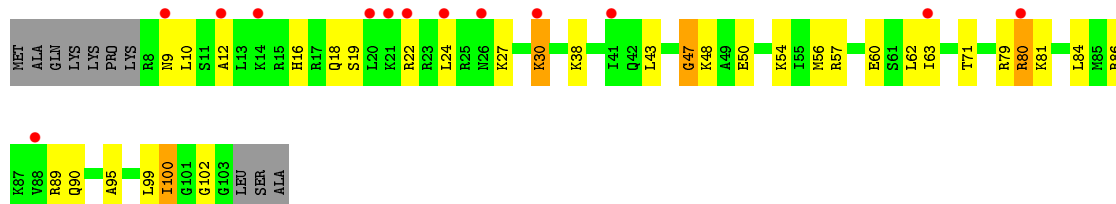


- Molecule 20: 30S Ribosomal Protein S20

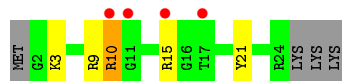




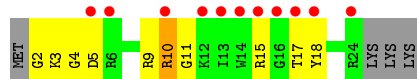
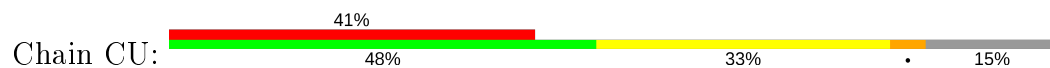
- Molecule 20: 30S Ribosomal Protein S20



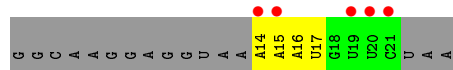
- Molecule 21: 30S Ribosomal Protein THX



- Molecule 21: 30S Ribosomal Protein THX



- Molecule 22: mRNA

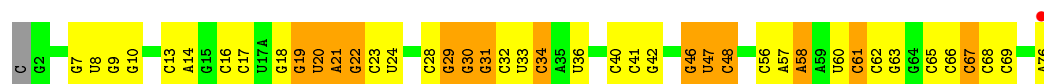


- Molecule 22: mRNA



- Molecule 23: P-site tRNA





• Molecule 23: P-site tRNA



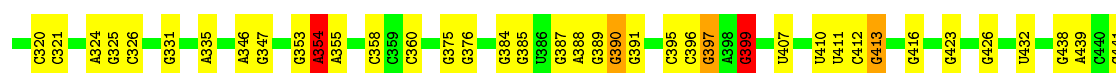
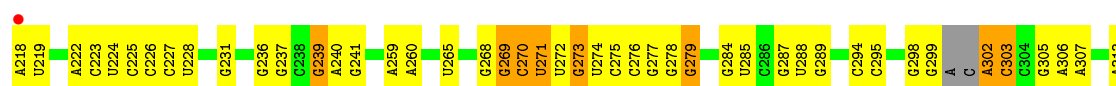
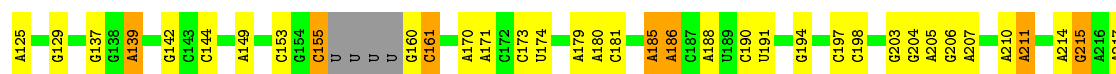
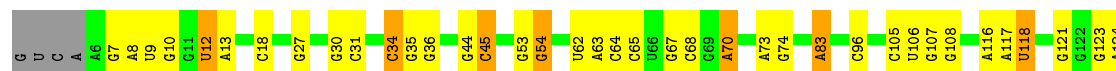
• Molecule 24: E-site tRNA Acceptor Stem



• Molecule 24: E-site tRNA Acceptor Stem



• Molecule 25: 23S Ribosomal RNA

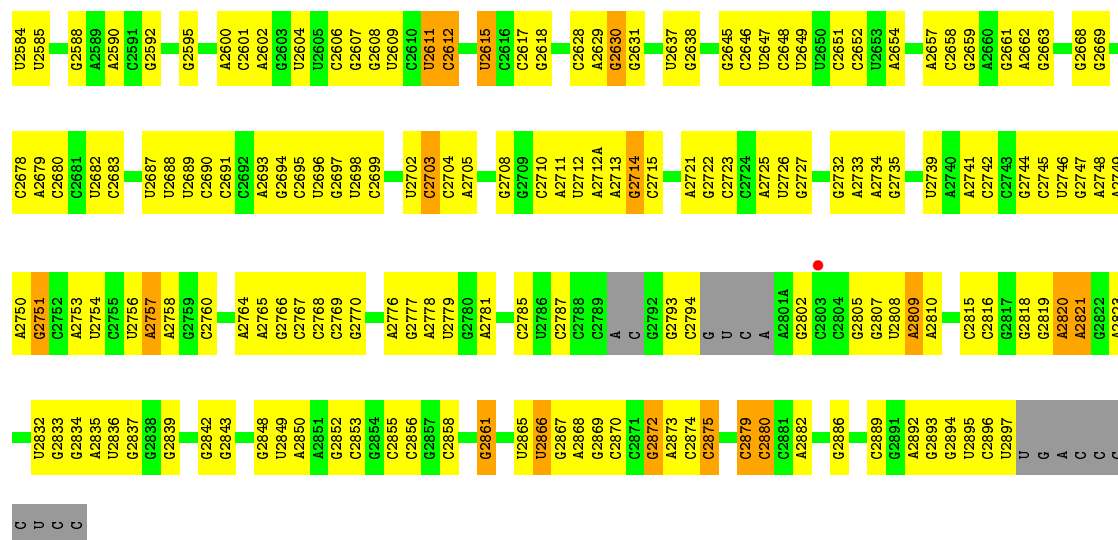


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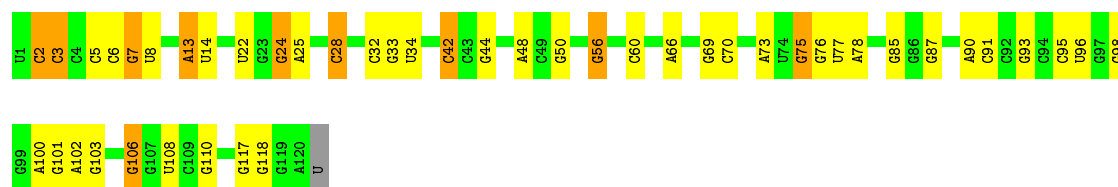
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G2255	G2256	G2257	G2258	G2261	U2262	A2267	A2268	A2269	G2273	A2274	G2275	G2276	G2277	A2278	G2279	G2280	G2283	G2284	G2285	A2286	G2287	A2288	U2291	G2292	G2293	G2294	G2295	G2296	G2297	A2298	G2302	G2303	G2304	A2305	G2308	G2309	A2310	U2311	U2312	G2313	G2314	G2315	G2318	G2319	A2320	G2321	G2322	G2323	G2324	G2325	G2326							
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G2100	G2101	U2102	G2103	G2104	G2105	G2106	G2107	G2108	U2109	G2110	G2111	G2112	U2113	A2114	G2115	G2116	A2117	G2118	A2119	G2120	G2121	U2122	G2125	A2126	G2127	G2128	G2129	U2130	G2131	U2132	G2133	A2134	A2135	G2136	G2137	G2138	G2139	G2140	G2141	G2142	U2143	U2144	G2145	G2146	G2147	G2148	U2149	U2150	G2151	G2152	G2153	G2154	G2155	G2156	G2157	A2158	G2159	G2160
A2020	G2021	U2022	G2023	G2024	G2025	G2026	G2029	A2030	A2031	G2032	A2033	U2034	G2035	G2036	G2037	G2038	G2039	G2040	U2041	A2042	G2043	G2044	G2045	G2046	A2051	A2054	G2055	G2056	A2057	A2058	A2059	G2060	G2061	A2062	G2063	G2064	G2065	G2066	G2069	U2074	U2075	U2076	U2077	G2078	U2079	G2080	G2081	U2086	G2087	G2094	U2099							
A1927	G1928	G1929	G1930	U1931	A1932	G1933	A1936	A1937	U1938	U1939	U1946	C1947	G1948	U1949	U1955	U1956	U1957	C1958	G1959	U1963	G1964	G1967	A1970	A1971	A1972	A1978	C1979	G1980	A1981	A1989	A1990	C1994	C1995	G1996	G1997	G1998	C1999	G2000	G2001	G2002	C2006	G2010	U2011	U2012	A2013	A2014	A2019											
A1815	G1816	G1822	G1823	G1826	G1827	G1828	G1835	G1836	C1837	G1842	G1846	A1847	A1848	A1849	G1850	C1852	A1859	G1865	A1877	C1878	G1879	G1883	A1889	A1890	C1894	C1895	G1896	G1897	U1898	G1899	A1900	G1906	G1907	C1908	A1912	A1913	C1914	U1915	A1916	U1917	U1918	A1919	G1922	U1923														
G1705	A1710	C1711	G1716	A1721	A1722	U1723	G1740	A1741	G1742	G1743	G1746	C1751	G1756	A1759	A1762	G1763	G1764	G1772	A1773	U1778	U1779	A1780	A1783	A1784	A1785	A1786	A1789	C1790	A1791	G1792	U1796	C1797	U1798	G1799	G1800	G1801	A1802	A1803	C1804	U1805	A1809	A1810	G1811	A1812	G1813	G1814												
A1610	A1614	G1615	A1616	U1617	A1618	G1626	G1627	G1628	U1629	G1633	G1636	A1637	C1638	U1639	C1640	G1647	G1648	G1651	A1652	G1653	A1654	A1656	U1659	C1660	A1664	G1666	G1667	A1668	A1669	C1670	G1674	G1686	G1687	U1688	A1689	U1692	U1693	G1696	G1697	C1698	A1699	G1699	G1700	A1701	G1702	G1703	G1704											
C1530	C1531	G1532	G1533	U1534	G1536	G1537	G1538	U1539	U1540	G1541	A1542	C1543	C1546	C1547	C1548	U1549	A1554	C1557	A1558	G1559	A1566	U1569	U1578	A1579	A1580	G1581	C1582	G1583	C1584	A1586	G1587	C1588	C1589	U1590	G1591	G1592	G1593	G1594	G1595	A1596	A1597	G1598	G1599	C1600	A1601	U1602	C1607	A1608	C1609									
G1447	G1448	A1449	G1450	A1452	U1453	G1455	G1459	U1460	G1461	G1462	G1465	G1466	C1467	A1471	A1472	A1477	G1478	G1482	A1486	G1487	G1492	C1493	A1494	A1495	U1496	U1497	G1498	C1499	G1500	C1505	U1506	A1507	A1508	C1509	A1509A	U1509B	G1510	U1514	G1515	G1519	G1524	G1525	G1526	G1527	A1528	C1445A	G1529											
G1368	G1369	G1370	U1371	U1372	A1373	C1376	G1377	U1378	A1379	A1384	G1385	G1389	U1390	U1391	A1392	A1393	U1396	U1397	C1398	C1399	G1400	U1405	U1406	G1410	A1494	A1411	A1412	U1415	G1416	C1417	G1418	A1419	U1420	G1421	G1422	G1423	G1424	A1427	C1428	G1429	C1430	U1431	A1434	G1435	G1436	C1437	A1445	C1446A	C1446									



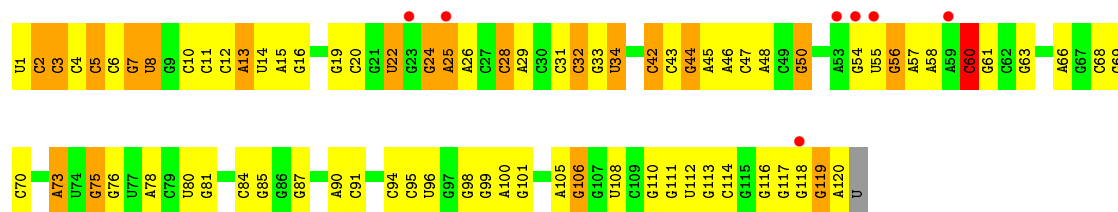
• Molecule 26: 5S Ribosomal RNA

Chain BB: 61% 30% 8% .



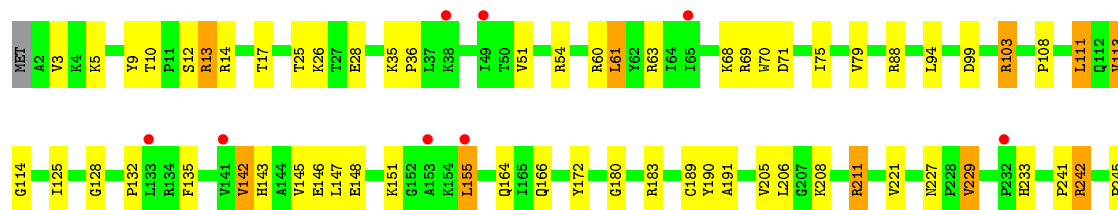
• Molecule 26: 5S Ribosomal RNA

Chain DB: 6% 35% 47% 17% ..



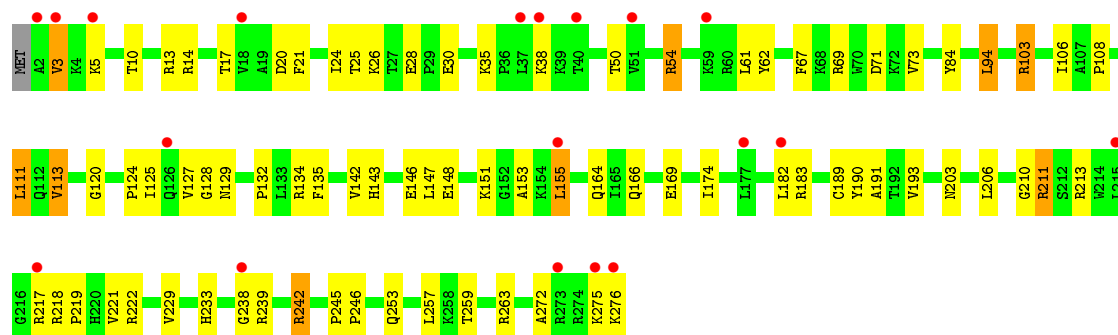
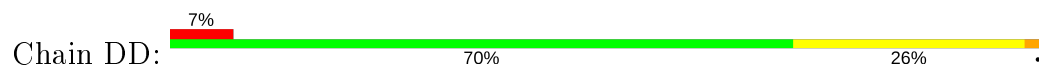
• Molecule 27: 50S Ribosomal Protein L2

Chain BD: 4% 73% 23% .

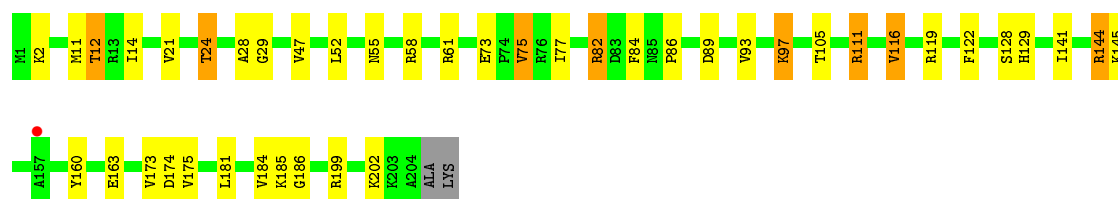
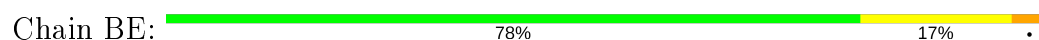




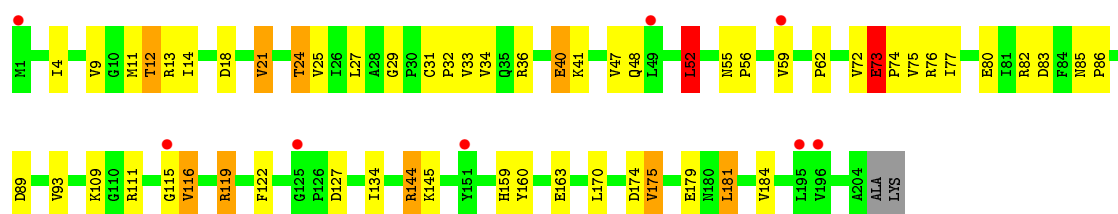
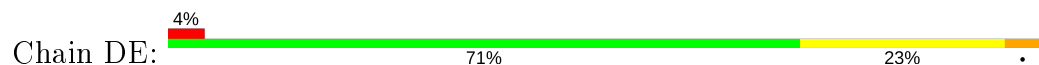
• Molecule 27: 50S Ribosomal Protein L2



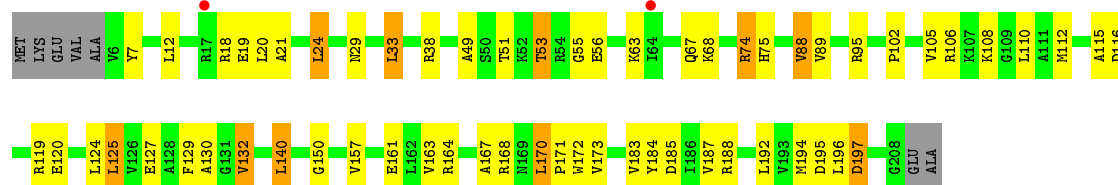
• Molecule 28: 50S Ribosomal Protein L3



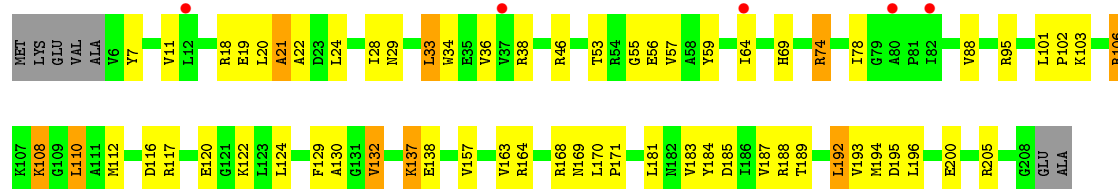
• Molecule 28: 50S Ribosomal Protein L3



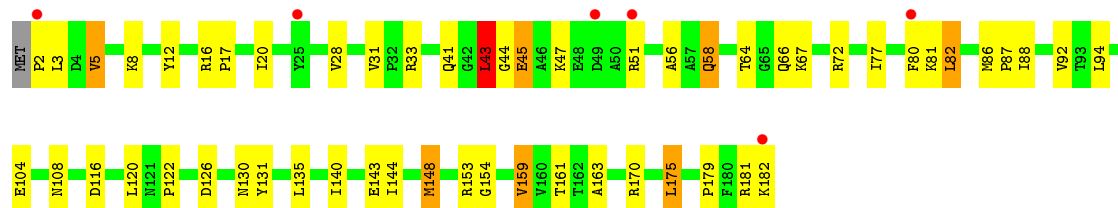
• Molecule 29: 50S Ribosomal Protein L4



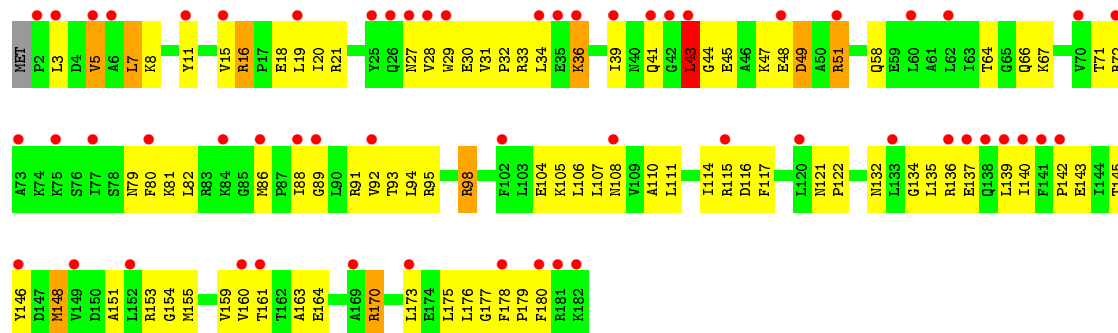
• Molecule 29: 50S Ribosomal Protein L4



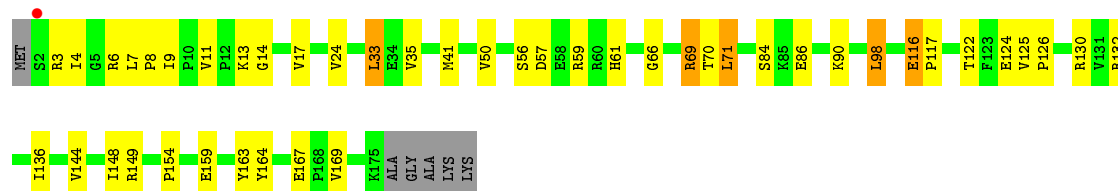
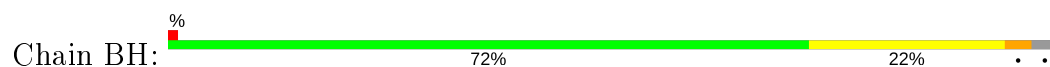
• Molecule 30: 50S Ribosomal Protein L5



• Molecule 30: 50S Ribosomal Protein L5

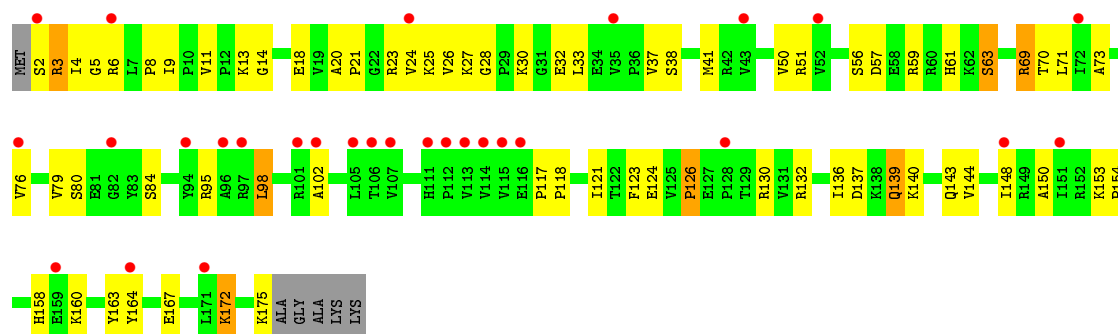


• Molecule 31: 50S Ribosomal Protein L6

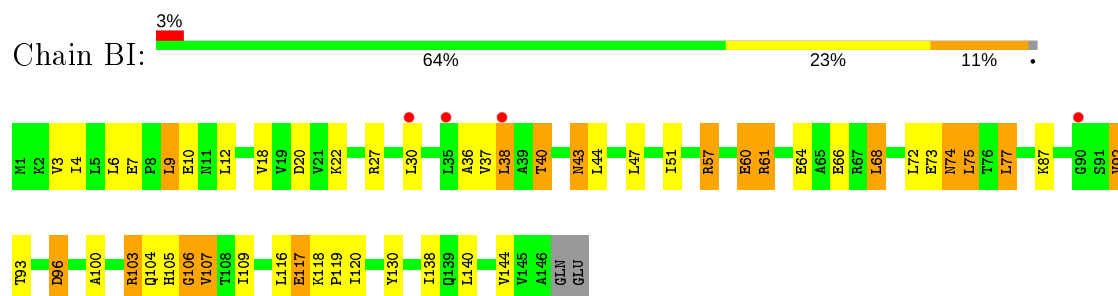


• Molecule 31: 50S Ribosomal Protein L6

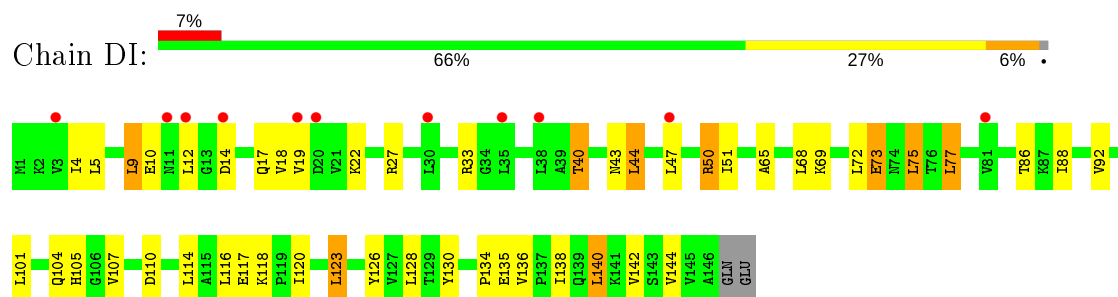




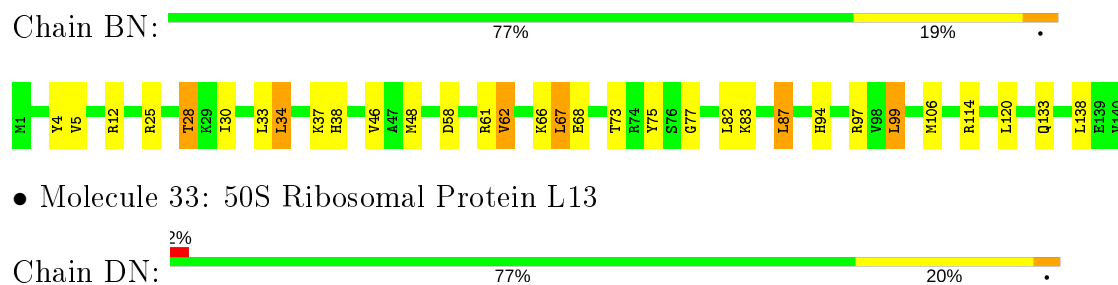
• Molecule 32: 50S Ribosomal Protein L9



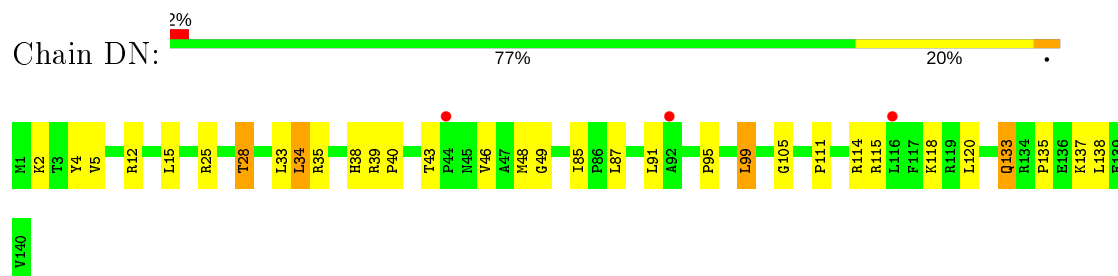
• Molecule 32: 50S Ribosomal Protein L9



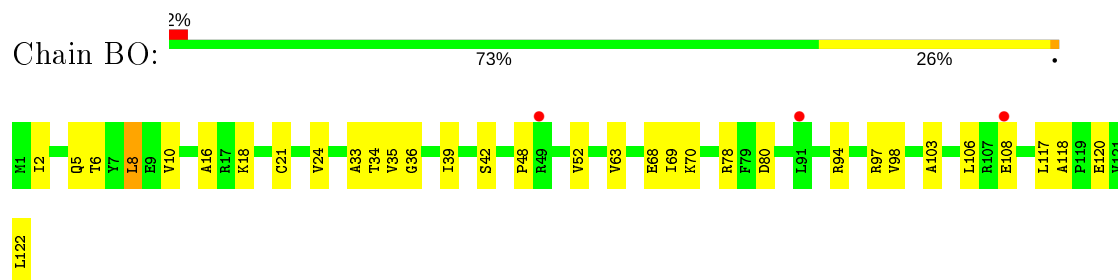
• Molecule 33: 50S Ribosomal Protein L13



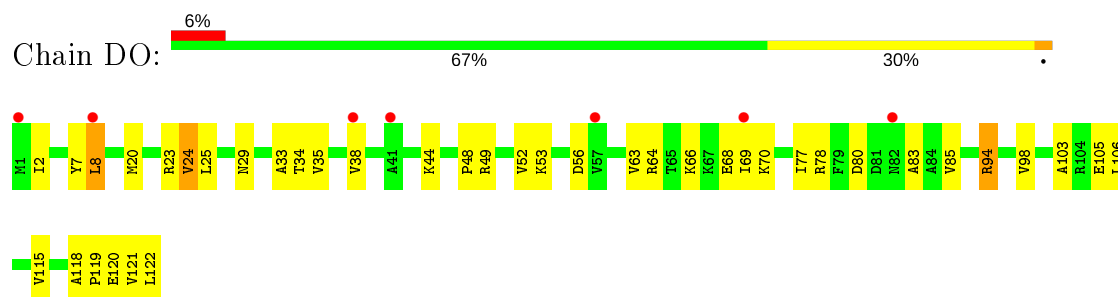
• Molecule 33: 50S Ribosomal Protein L13



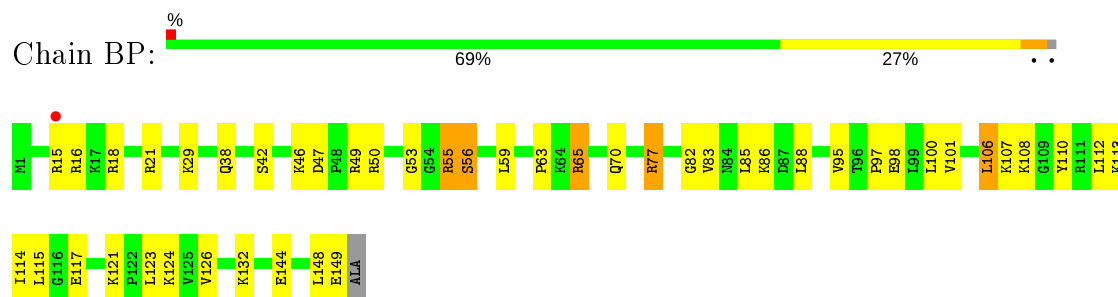
• Molecule 34: 50S Ribosomal Protein L14



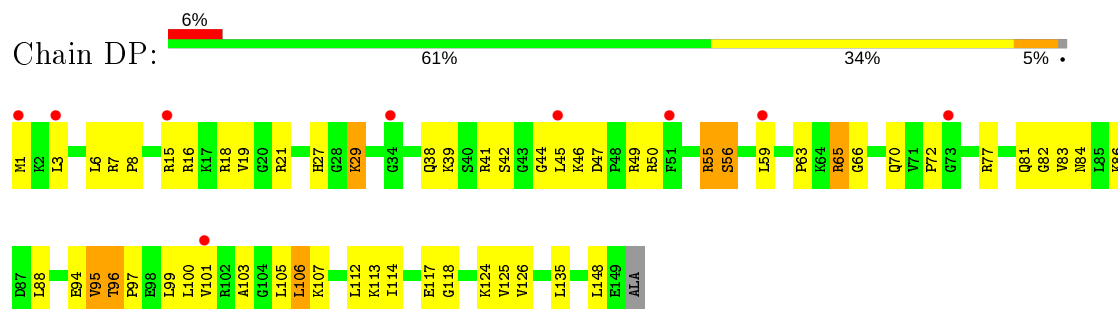
• Molecule 34: 50S Ribosomal Protein L14



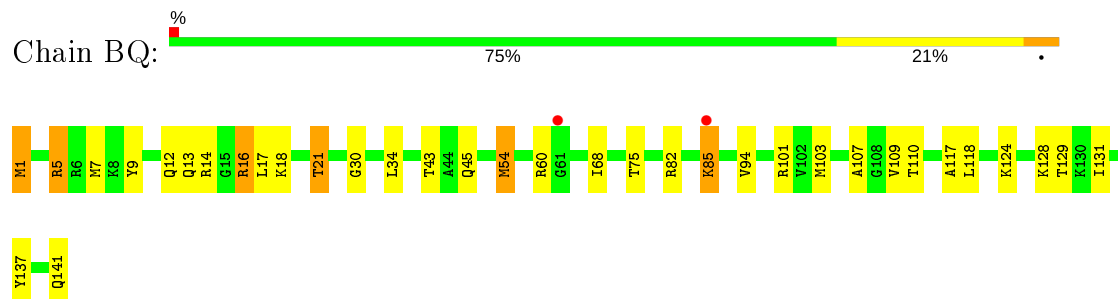
• Molecule 35: 50S Ribosomal Protein L15



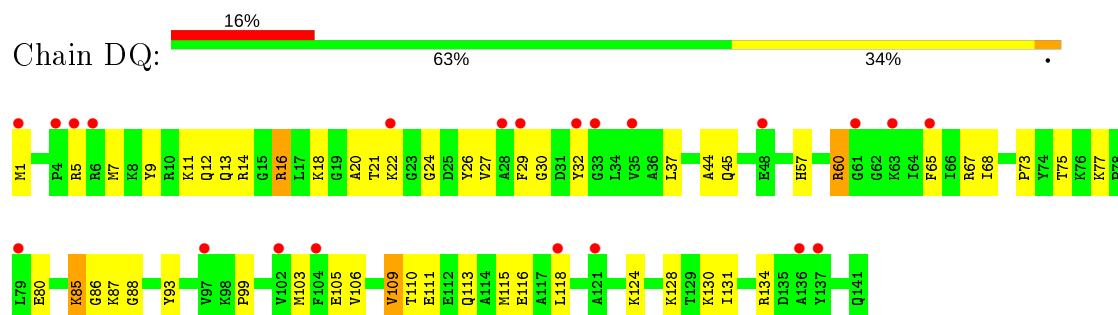
• Molecule 35: 50S Ribosomal Protein L15



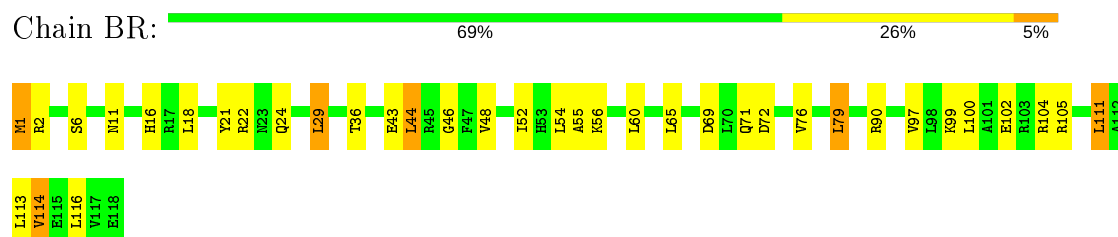
• Molecule 36: 50S Ribosomal Protein L16



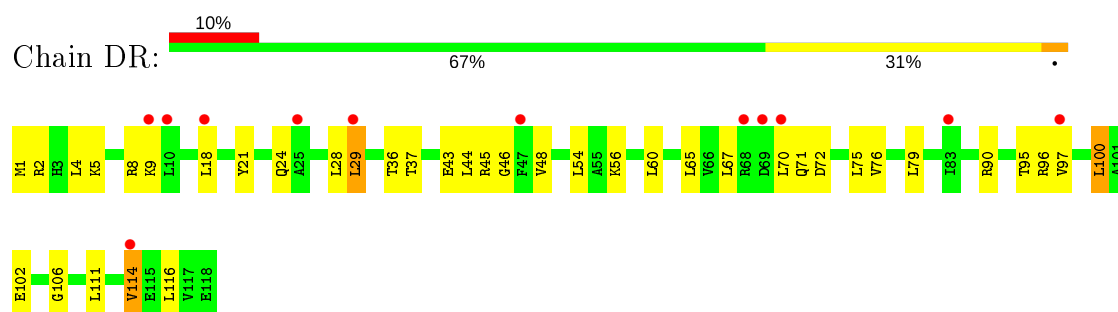
- Molecule 36: 50S Ribosomal Protein L16



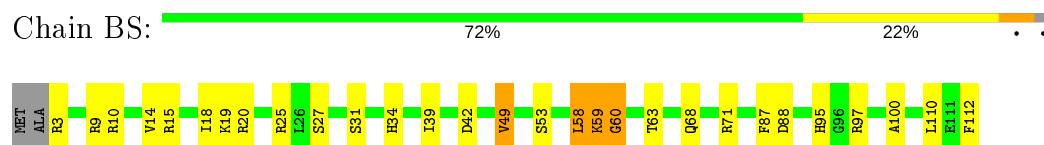
- Molecule 37: 50S Ribosomal Protein L17



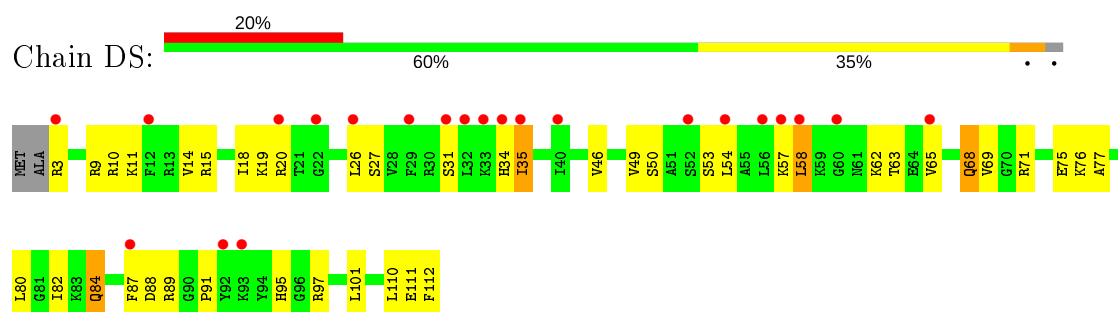
- Molecule 37: 50S Ribosomal Protein L17



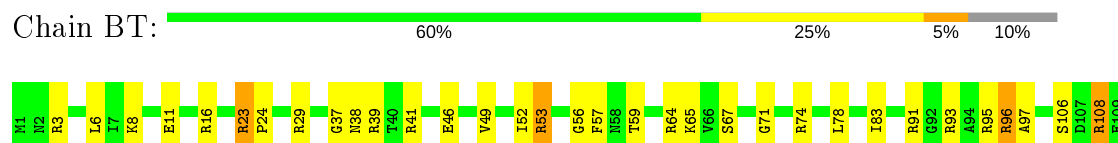
- Molecule 38: 50S Ribosomal Protein L18



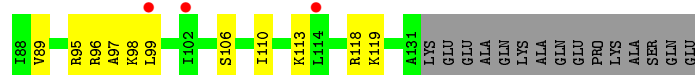
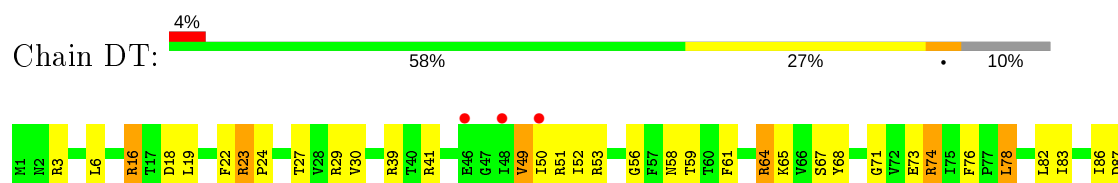
- Molecule 38: 50S Ribosomal Protein L18



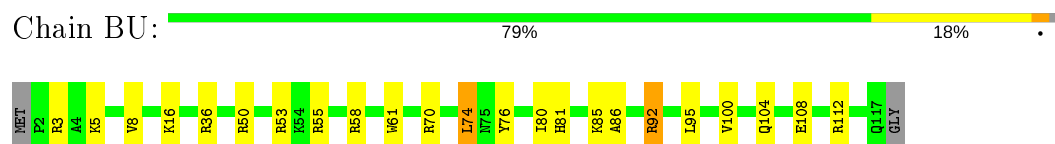
- Molecule 39: 50S Ribosomal Protein L19



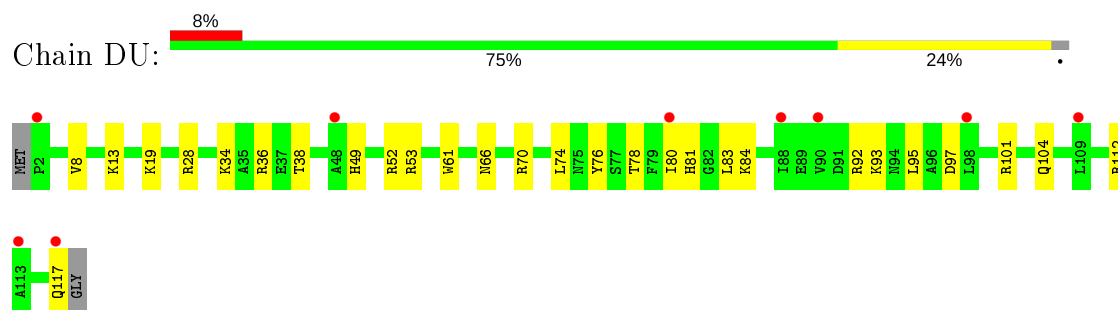
- Molecule 39: 50S Ribosomal Protein L19



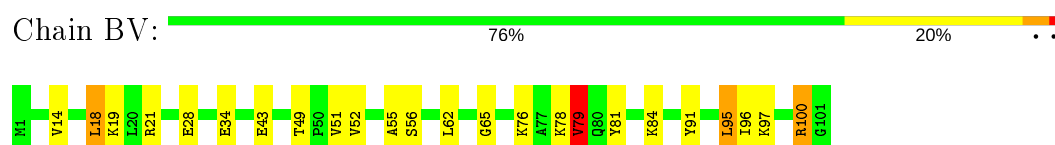
- Molecule 40: 50S Ribosomal Protein L20



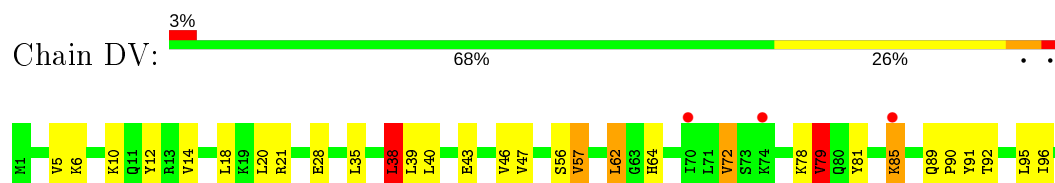
- Molecule 40: 50S Ribosomal Protein L20



- Molecule 41: 50S Ribosomal Protein L21

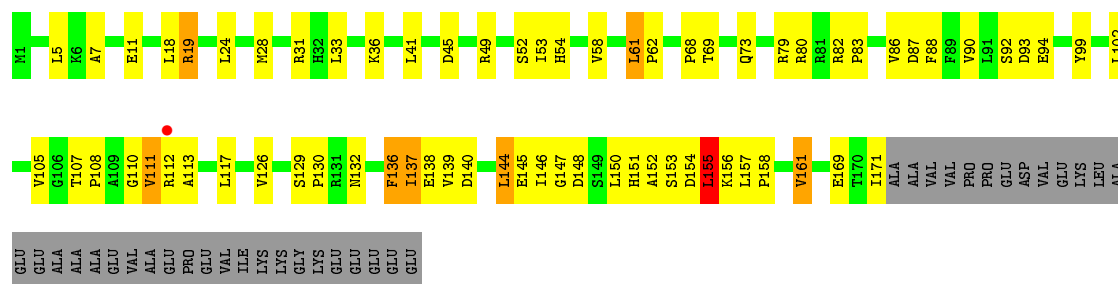


- Molecule 41: 50S Ribosomal Protein L21



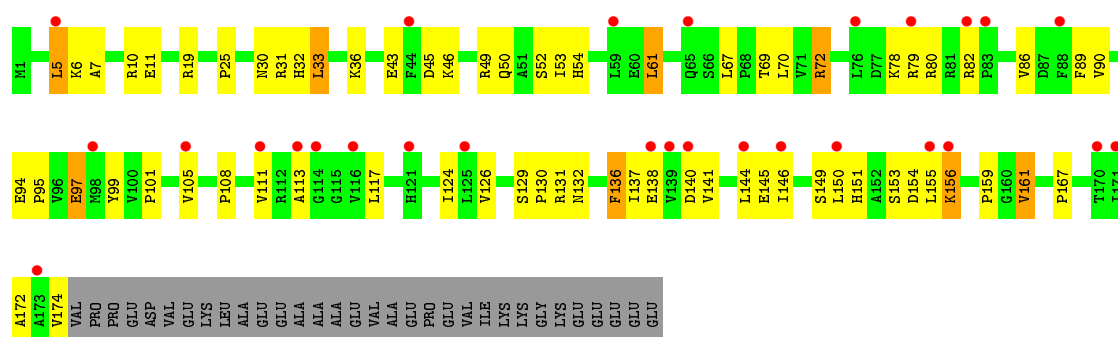
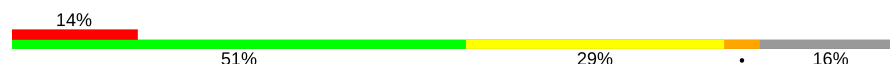
- Molecule 45: 50S Ribosomal Protein L25

Chain BZ:



- Molecule 45: 50S Ribosomal Protein L25

Chain DZ:



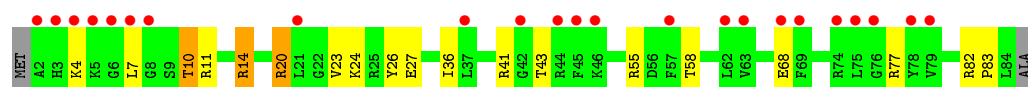
- Molecule 46: 50S Ribosomal Protein L27

Chain B0:



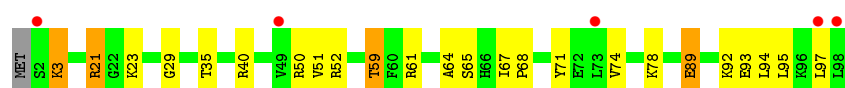
- Molecule 46: 50S Ribosomal Protein L27

Chain D0:



- Molecule 47: 50S Ribosomal Protein L28

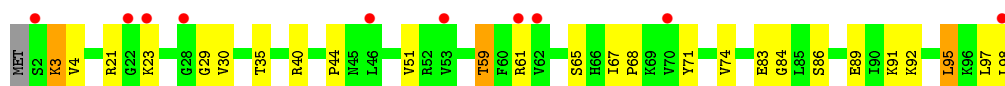
Chain B1:



- Molecule 47: 50S Ribosomal Protein L28

Chain D1:

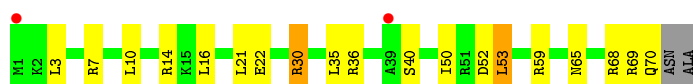




• Molecule 48: 50S Ribosomal Protein L29



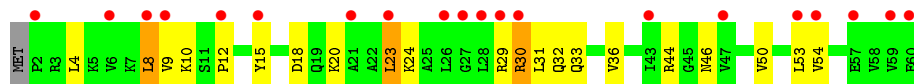
• Molecule 48: 50S Ribosomal Protein L29



• Molecule 49: 50S Ribosomal Protein L30



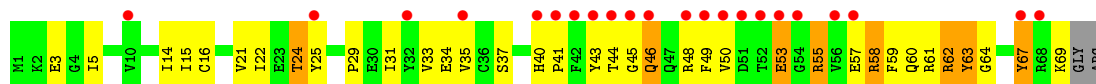
• Molecule 49: 50S Ribosomal Protein L30



• Molecule 50: 50S Ribosomal Protein L31



• Molecule 50: 50S Ribosomal Protein L31

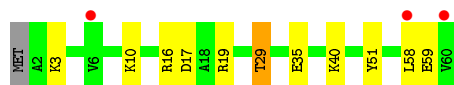
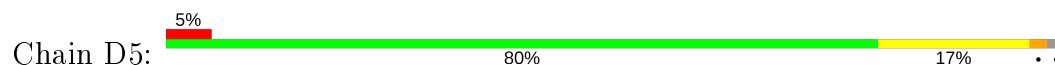


• Molecule 51: 50S Ribosomal Protein L32





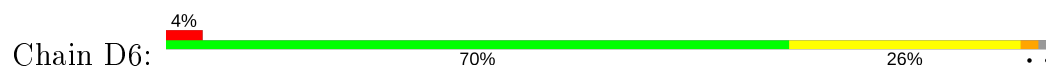
- Molecule 51: 50S Ribosomal Protein L32



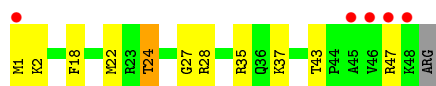
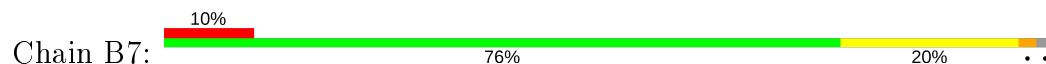
- Molecule 52: 50S Ribosomal Protein L33



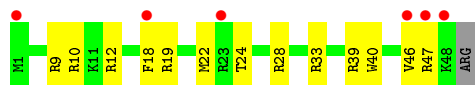
- Molecule 52: 50S Ribosomal Protein L33



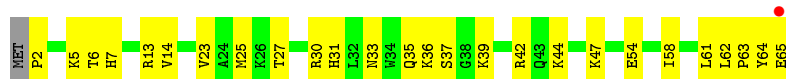
- Molecule 53: 50S Ribosomal Protein L34



- Molecule 53: 50S Ribosomal Protein L34

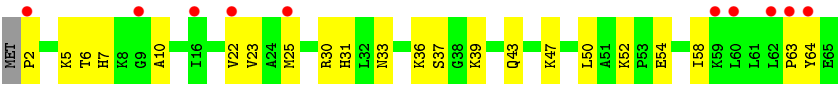


- Molecule 54: 50S Ribosomal Protein L35

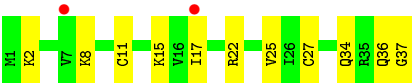


- Molecule 54: 50S Ribosomal Protein L35

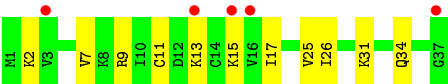




● Molecule 55: 50S Ribosomal Protein L36



● Molecule 55: 50S Ribosomal Protein L36



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	208.93Å 446.95Å 619.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	144.86 – 2.70 254.67 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (144.86-2.70) 99.6 (254.67-2.70)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.215 , 0.262 0.215 , 0.263	Depositor DCC
R_{free} test set	78302 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	53.5	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 59.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	290807	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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, PCY, K, ZN, 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	1.31	15/36024 (0.0%)	1.16	60/56222 (0.1%)
1	CA	0.43	0/36170	0.97	61/56452 (0.1%)
2	AB	0.34	0/1881	0.62	1/2542 (0.0%)
2	CB	0.35	0/1860	0.62	1/2518 (0.0%)
3	AC	0.30	0/1576	0.51	0/2130
3	CC	0.33	0/1566	0.59	1/2119 (0.0%)
4	AD	0.31	0/1689	0.55	0/2267
4	CD	0.31	0/1704	0.55	0/2284
5	AE	0.31	0/1145	0.53	0/1543
5	CE	0.33	0/1149	0.57	0/1548
6	AF	0.30	0/819	0.52	0/1111
6	CF	0.32	0/829	0.54	0/1123
7	AG	0.29	0/1250	0.50	0/1679
7	CG	0.31	0/1254	0.53	0/1683
8	AH	0.30	0/1108	0.52	0/1494
8	CH	0.29	0/1108	0.52	0/1494
9	AI	0.29	0/1002	0.55	0/1346
9	CI	0.33	0/997	0.58	1/1343 (0.1%)
10	AJ	0.29	0/722	0.54	0/982
10	CJ	0.34	0/727	0.59	0/988
11	AK	0.32	0/844	0.51	0/1145
11	CK	0.30	0/848	0.53	0/1149
12	AL	0.33	0/946	0.51	0/1274
12	CL	0.33	0/946	0.60	1/1274 (0.1%)
13	AM	0.29	0/947	0.58	0/1272
13	CM	0.31	0/930	0.55	0/1250
14	AN	0.31	0/501	0.54	0/664
14	CN	0.34	0/501	0.52	0/664
15	AO	0.31	0/739	0.53	0/985
15	CO	0.32	0/739	0.53	0/985
16	AP	0.31	0/697	0.53	0/939
16	CP	0.32	0/693	0.51	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.32	0/836	0.52	0/1117
17	CQ	0.31	0/836	0.48	0/1117
18	AR	0.32	0/560	0.53	0/746
18	CR	0.30	0/560	0.51	0/746
19	AS	0.31	0/667	0.53	0/900
19	CS	0.33	0/661	0.65	1/893 (0.1%)
20	AT	0.31	0/730	0.56	0/965
20	CT	0.29	0/729	0.53	0/965
21	AU	0.29	0/203	0.51	0/266
21	CU	0.35	0/203	0.55	0/266
22	AV	0.56	0/188	1.13	0/290
22	CV	0.62	0/122	1.18	0/188
23	AX	0.56	2/1725 (0.1%)	1.16	18/2689 (0.7%)
23	CX	0.55	1/1725 (0.1%)	1.20	18/2689 (0.7%)
24	AY	0.72	1/428 (0.2%)	0.91	0/661
24	CY	0.48	0/115	1.02	0/176
25	BA	0.67	6/68083 (0.0%)	1.04	144/106274 (0.1%)
25	DA	0.51	3/67542 (0.0%)	1.00	78/105428 (0.1%)
26	BB	0.51	0/2878	0.91	0/4490
26	DB	0.57	0/2878	1.01	2/4490 (0.0%)
27	BD	0.44	0/2186	0.60	0/2944
27	DD	0.39	0/2186	0.59	0/2944
28	BE	0.45	0/1592	0.60	0/2149
28	DE	0.38	0/1592	0.62	0/2149
29	BF	0.43	0/1619	0.58	0/2193
29	DF	0.36	0/1615	0.59	0/2188
30	BG	0.33	0/1450	0.55	1/1959 (0.1%)
30	DG	0.36	0/1449	0.57	0/1958
31	BH	0.36	0/1356	0.54	0/1834
31	DH	0.34	0/1356	0.54	0/1834
32	BI	0.32	0/1100	0.58	0/1501
32	DI	0.32	0/1076	0.57	0/1471
33	BN	0.39	0/1144	0.54	0/1543
33	DN	0.36	0/1144	0.57	0/1543
34	BO	0.45	0/943	0.59	1/1269 (0.1%)
34	DO	0.37	0/943	0.60	1/1269 (0.1%)
35	BP	0.42	0/1152	0.60	0/1533
35	DP	0.38	0/1152	0.64	1/1533 (0.1%)
36	BQ	0.44	0/1143	0.58	0/1527
36	DQ	0.36	0/1143	0.57	0/1527
37	BR	0.44	0/982	0.66	0/1312
37	DR	0.33	0/982	0.57	0/1312
38	BS	0.39	0/887	0.62	0/1180

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DS	0.33	0/880	0.55	0/1172
39	BT	0.38	0/1105	0.60	0/1477
39	DT	0.35	0/1097	0.57	1/1468 (0.1%)
40	BU	0.48	0/977	0.61	0/1301
40	DU	0.33	0/977	0.53	0/1301
41	BV	0.44	0/782	0.64	0/1049
41	DV	0.34	0/782	0.55	1/1049 (0.1%)
42	BW	0.50	0/897	0.62	0/1205
42	DW	0.34	0/897	0.53	0/1205
43	BX	0.45	0/764	0.58	0/1025
43	DX	0.34	0/764	0.54	1/1025 (0.1%)
44	BY	0.40	0/819	0.62	0/1095
44	DY	0.33	0/819	0.57	0/1095
45	BZ	0.35	0/1379	0.62	0/1873
45	DZ	0.31	0/1390	0.54	0/1890
46	B0	0.45	0/662	0.65	0/881
46	D0	0.33	0/662	0.55	0/881
47	B1	0.40	0/762	0.55	0/1014
47	D1	0.36	0/762	0.56	0/1014
48	B2	0.39	0/590	0.59	0/781
48	D2	0.29	0/590	0.50	0/781
49	B3	0.41	0/474	0.59	0/635
49	D3	0.30	0/469	0.53	0/630
50	B4	0.36	0/571	0.68	0/768
50	D4	0.34	0/545	0.62	0/737
51	B5	0.50	1/469 (0.2%)	0.77	0/635
51	D5	0.35	0/469	0.59	1/635 (0.2%)
52	B6	0.60	1/460 (0.2%)	0.67	1/613 (0.2%)
52	D6	0.36	0/456	0.52	0/608
53	B7	0.48	0/426	0.62	0/561
53	D7	0.37	0/426	0.57	0/561
54	B8	0.44	0/519	0.61	0/684
54	D8	0.36	0/525	0.54	0/691
55	B9	0.50	0/310	0.65	1/407 (0.2%)
55	D9	0.38	0/310	0.62	0/407
All	All	0.65	30/310558 (0.0%)	0.94	397/464586 (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
1	AA	0	1
7	CG	0	2
38	BS	0	1
50	B4	0	1
50	D4	0	1
All	All	0	6

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	439	A	C5-C4	145.31	2.40	1.38
1	AA	496	A	C6-N1	114.63	2.15	1.35
1	AA	439	A	N3-C4	59.27	1.70	1.34
1	AA	496	A	C2-N3	54.84	1.82	1.33
1	AA	439	A	C6-N1	53.24	1.72	1.35
1	AA	439	A	N9-C4	44.55	1.64	1.37
1	AA	439	A	C5-C6	42.20	1.79	1.41
1	AA	439	A	N7-C5	41.35	1.64	1.39
1	AA	439	A	N1-C2	40.66	1.71	1.34
1	AA	439	A	C2-N3	38.98	1.68	1.33
1	AA	439	A	C8-N7	32.92	1.54	1.31
1	AA	439	A	N9-C8	32.75	1.64	1.37
1	AA	496	A	N3-C4	19.92	1.46	1.34
1	AA	496	A	C5-C4	-14.32	1.28	1.38
1	AA	496	A	N1-C2	11.06	1.44	1.34
24	AY	1	G	OP3-P	-10.29	1.48	1.61
25	BA	1188	A	N9-C4	-9.37	1.32	1.37
25	BA	354	A	N9-C4	-6.52	1.33	1.37
25	BA	553	A	N9-C4	-6.46	1.33	1.37
25	BA	1067	A	N9-C4	-6.36	1.34	1.37
23	CX	22	G	N7-C5	6.34	1.43	1.39
23	AX	22	G	N7-C5	6.23	1.43	1.39
25	BA	2299	A	N9-C4	-6.16	1.34	1.37
52	B6	43	CYS	CB-SG	6.08	1.92	1.82
25	DA	528	A	N9-C4	-5.97	1.34	1.37
25	DA	2287	A	N9-C4	-5.93	1.34	1.37
51	B5	36	CYS	CB-SG	5.47	1.91	1.82
23	AX	14	A	N7-C5	-5.44	1.35	1.39
25	BA	990	A	N9-C4	-5.24	1.34	1.37
25	DA	1142(A)	A	N9-C4	-5.09	1.34	1.37

All (397) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	496	A	C2-N3-C4	97.04	159.12	110.60
1	AA	496	A	N1-C2-N3	-89.99	84.31	129.30
1	AA	496	A	C5-C6-N6	-36.75	94.30	123.70
1	AA	496	A	C5-C6-N1	31.98	133.69	117.70
1	AA	496	A	C4-C5-C6	-28.65	102.68	117.00
1	AA	439	A	N3-C4-N9	27.30	149.24	127.40
1	AA	439	A	C4-C5-N7	-26.92	97.24	110.70
1	AA	439	A	C6-C5-N7	26.20	150.64	132.30
1	AA	439	A	N9-C4-C5	-25.41	95.64	105.80
1	AA	439	A	C2-N3-C4	25.16	123.18	110.60
1	AA	496	A	N1-C6-N6	22.35	132.01	118.60
1	AA	439	A	C5-N7-C8	18.86	113.33	103.90
1	AA	439	A	C6-N1-C2	18.43	129.66	118.60
1	AA	439	A	N3-C4-C5	-18.40	113.92	126.80
1	AA	439	A	C8-N9-C4	17.01	112.60	105.80
1	AA	439	A	N7-C8-N9	14.77	121.19	113.80
1	CA	1119	C	C2-N3-C4	14.01	126.91	119.90
1	CA	1154	G	C5-C6-O6	13.13	136.48	128.60
1	AA	496	A	C6-C5-N7	12.69	141.18	132.30
1	AA	439	A	C4-C5-C6	-11.90	111.05	117.00
1	AA	439	A	N1-C2-N3	-11.72	123.44	129.30
25	BA	1686	U	O5'-P-OP2	-11.30	95.53	105.70
25	BA	2083	G	O5'-P-OP2	-11.14	95.67	105.70
1	AA	496	A	C4-C5-N7	10.89	116.14	110.70
25	DA	2061	G	O5'-P-OP2	-10.55	96.20	105.70
25	BA	840	A	O5'-P-OP2	-10.40	96.34	105.70
1	CA	1119	C	N1-C2-O2	10.32	125.09	118.90
25	BA	139	A	N7-C8-N9	10.30	118.95	113.80
25	BA	553	A	C2-N3-C4	-10.10	105.55	110.60
1	AA	496	A	N3-C4-N9	9.95	135.36	127.40
25	BA	354	A	C2-N3-C4	-9.87	105.66	110.60
25	BA	990	A	N1-C6-N6	9.81	124.48	118.60
25	BA	1067	A	C2-N3-C4	-9.77	105.71	110.60
23	CX	46	G	C6-N1-C2	-9.77	119.24	125.10
23	AX	14	A	C4-C5-C6	9.68	121.84	117.00
25	BA	31	C	O5'-P-OP1	-9.51	97.14	105.70
25	DA	2155	G	N3-C4-N9	9.44	131.67	126.00
1	CA	1119	C	N3-C4-C5	-9.39	118.14	121.90
1	CA	1154	G	N1-C6-O6	-9.38	114.27	119.90
1	AA	496	A	N3-C4-C5	-9.27	120.31	126.80
25	BA	139	A	C5-N7-C8	-9.25	99.27	103.90
25	BA	2162	C	N1-C2-O2	9.14	124.39	118.90
1	AA	1161	C	N1-C2-O2	9.11	124.36	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AX	14	A	C5-N7-C8	9.10	108.45	103.90
25	BA	1807	G	O5'-P-OP2	-9.09	97.52	105.70
25	DA	528	A	C2-N3-C4	-8.98	106.11	110.60
25	BA	1188	A	C2-N3-C4	-8.97	106.12	110.60
25	BA	855	G	O5'-P-OP2	-8.89	97.69	105.70
1	AA	1030(B)	C	N1-C2-O2	8.82	124.19	118.90
25	BA	990	A	C2-N3-C4	-8.75	106.23	110.60
1	AA	1030(B)	C	C2-N1-C1'	8.73	128.41	118.80
23	CX	20	U	N1-C2-O2	8.63	128.84	122.80
1	CA	1119	C	C5-C4-N4	8.54	126.18	120.20
1	AA	1161	C	N3-C2-O2	-8.51	115.94	121.90
25	BA	537	G	O4'-C1'-N9	8.49	114.99	108.20
25	BA	139	A	C8-N9-C4	-8.33	102.47	105.80
23	AX	46	G	C6-N1-C2	-8.30	120.12	125.10
25	BA	1188	A	N3-C4-N9	-8.15	120.88	127.40
25	DA	2577	A	O5'-P-OP1	-8.11	98.40	105.70
25	BA	553	A	N3-C4-N9	-8.10	120.92	127.40
23	CX	14	A	C4-C5-C6	8.04	121.02	117.00
23	CX	20	U	N3-C2-O2	-8.02	116.59	122.20
25	BA	2162	C	C2-N1-C1'	7.94	127.53	118.80
25	DA	645	C	C2-N1-C1'	7.92	127.51	118.80
25	BA	1188	A	N3-C4-C5	7.84	132.29	126.80
23	AX	22	G	C4-C5-C6	-7.82	114.11	118.80
1	CA	1023	G	N3-C4-N9	7.80	130.68	126.00
23	AX	22	G	N1-C6-O6	-7.79	115.23	119.90
1	AA	1160	G	N7-C8-N9	7.71	116.95	113.10
25	BA	354	A	N1-C2-N3	7.70	133.15	129.30
25	BA	553	A	N3-C4-C5	7.64	132.15	126.80
1	AA	496	A	C5-N7-C8	-7.64	100.08	103.90
25	BA	2299	A	C2-N3-C4	-7.64	106.78	110.60
23	CX	46	G	C5-C6-O6	-7.62	124.03	128.60
25	DA	1204	A	O4'-C1'-N9	7.55	114.24	108.20
25	BA	215	G	O4'-C1'-N9	7.48	114.19	108.20
25	BA	990	A	C5-N7-C8	-7.43	100.18	103.90
25	BA	990	A	C4-C5-N7	7.41	114.40	110.70
25	BA	2162	C	N3-C2-O2	-7.39	116.73	121.90
1	CA	1037	C	C6-N1-C2	-7.35	117.36	120.30
23	AX	22	G	N3-C4-N9	-7.31	121.61	126.00
1	AA	254	G	O5'-P-OP1	-7.26	99.16	105.70
25	BA	1581	U	N3-C2-O2	-7.21	117.15	122.20
1	CA	1003	G	N7-C8-N9	7.19	116.70	113.10
25	DA	2276	G	O5'-P-OP1	-7.16	99.25	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1030(B)	C	N3-C2-O2	-7.15	116.90	121.90
23	CX	22	G	C4-C5-C6	-7.13	114.52	118.80
25	DA	2155	G	N3-C4-C5	-7.11	125.05	128.60
25	DA	1774	C	O5'-P-OP1	-7.07	99.33	105.70
25	BA	2122	G	C5-C6-O6	-7.07	124.36	128.60
25	BA	848	G	O5'-P-OP2	-7.06	99.34	105.70
1	CA	1003	G	C8-N9-C4	-6.97	103.61	106.40
1	CA	1263	C	C2-N3-C4	6.94	123.37	119.90
25	DA	2155	G	C6-C5-N7	-6.94	126.24	130.40
25	DA	645	C	N1-C2-O2	6.93	123.06	118.90
25	DA	512	G	O4'-C1'-N9	6.92	113.73	108.20
23	CX	14	A	C5-N7-C8	6.92	107.36	103.90
25	BA	1361	C	O5'-P-OP2	-6.89	99.50	105.70
23	AX	14	A	C5-C6-N1	-6.89	114.26	117.70
25	DA	2167	U	N1-C2-O2	6.88	127.62	122.80
1	CA	1158	C	N1-C2-O2	6.86	123.01	118.90
25	BA	1067	A	N1-C2-N3	6.85	132.73	129.30
25	BA	2091	G	O5'-P-OP2	-6.84	99.55	105.70
25	DA	2167	U	N3-C2-O2	-6.82	117.42	122.20
1	AA	1285	A	P-O3'-C3'	6.81	127.87	119.70
25	BA	2858	G	O4'-C1'-N9	6.81	113.65	108.20
25	BA	1068	G	N3-C4-N9	-6.80	121.92	126.00
23	AX	22	G	C6-C5-N7	6.79	134.47	130.40
25	DA	2155	G	N3-C2-N2	6.78	124.64	119.90
1	CA	1003	G	C4-N9-C1'	6.71	135.22	126.50
25	BA	990	A	C6-C5-N7	-6.71	127.61	132.30
23	CX	22	G	C5-N7-C8	-6.70	100.95	104.30
23	AX	22	G	C8-N9-C1'	6.70	135.71	127.00
25	BA	993	G	O5'-P-OP1	-6.69	99.68	105.70
25	BA	986	A	O5'-P-OP1	-6.67	99.69	105.70
25	BA	1068	G	N3-C2-N2	-6.67	115.23	119.90
1	CA	1023	G	C4-N9-C1'	6.62	135.11	126.50
23	CX	22	G	N1-C6-O6	-6.62	115.93	119.90
25	DA	2139	C	C2-N1-C1'	6.60	126.06	118.80
1	CA	1002	G	N3-C2-N2	-6.60	115.28	119.90
25	BA	1311	A	O5'-P-OP2	-6.59	99.77	105.70
1	CA	1158	C	C2-N1-C1'	6.58	126.04	118.80
1	AA	1030(B)	C	C6-N1-C2	-6.57	117.67	120.30
23	CX	20	U	C2-N1-C1'	6.54	125.54	117.70
25	BA	1810	U	O5'-P-OP1	-6.53	99.82	105.70
1	CA	754	C	C2-N1-C1'	6.51	125.96	118.80
25	DA	2155	G	N1-C2-N2	-6.50	110.35	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	DX	57	LEU	CA-CB-CG	6.44	130.11	115.30
25	BA	12	U	C2-N1-C1'	6.43	125.42	117.70
25	DA	2287	A	C2-N3-C4	-6.42	107.39	110.60
1	CA	1119	C	C6-N1-C2	-6.42	117.73	120.30
1	CA	1003	G	N3-C4-C5	-6.42	125.39	128.60
23	CX	22	G	C5-C6-N1	6.41	114.70	111.50
23	CX	46	G	C5-C6-N1	6.41	114.70	111.50
25	DA	1828	G	O5'-P-OP1	-6.39	99.94	105.70
25	BA	874	U	O5'-P-OP2	-6.37	99.97	105.70
25	DA	2155	G	C4-N9-C1'	6.36	134.77	126.50
25	BA	2566	U	O5'-P-OP1	-6.34	100.00	105.70
25	BA	2348	A	N9-C4-C5	-6.33	103.27	105.80
1	AA	1160	G	C8-N9-C4	-6.32	103.87	106.40
25	BA	1232	G	N1-C6-O6	-6.31	116.11	119.90
1	CA	1225	A	C5-C6-N6	6.31	128.75	123.70
12	CL	29	GLY	N-CA-C	-6.25	97.47	113.10
25	BA	733	G	N9-C4-C5	-6.23	102.91	105.40
1	AA	1161	C	C4-C5-C6	6.22	120.51	117.40
25	BA	978	A	C5-N7-C8	-6.22	100.79	103.90
25	BA	2260	C	O5'-P-OP2	-6.21	100.11	105.70
25	BA	2627	U	O5'-P-OP1	-6.19	100.13	105.70
25	DA	2473	U	N1-C2-O2	6.17	127.12	122.80
25	BA	139	A	C6-C5-N7	-6.17	127.98	132.30
1	CA	1220	G	N3-C2-N2	-6.17	115.58	119.90
1	CA	1119	C	C5-C6-N1	6.16	124.08	121.00
34	BO	8	LEU	CA-CB-CG	6.15	129.44	115.30
25	DA	277	C	N1-C2-O2	6.14	122.59	118.90
1	CA	1023	G	C6-C5-N7	-6.13	126.72	130.40
25	BA	856	G	N1-C6-O6	-6.12	116.23	119.90
25	BA	978	A	N7-C8-N9	6.09	116.85	113.80
25	BA	2122	G	N1-C6-O6	6.09	123.55	119.90
23	AX	22	G	C5-N7-C8	-6.08	101.26	104.30
25	DA	1021	A	C2-N3-C4	-6.08	107.56	110.60
25	DA	949	C	N1-C2-O2	-6.07	115.26	118.90
25	BA	593	G	C5-C6-N1	6.07	114.54	111.50
25	DA	2473	U	N3-C2-O2	-6.07	117.95	122.20
23	AX	22	G	C4-N9-C1'	-6.06	118.62	126.50
1	CA	1158	C	N3-C2-O2	-6.05	117.66	121.90
1	CA	960	U	C2-N1-C1'	6.05	124.96	117.70
1	AA	1285	A	OP2-P-O3'	6.03	118.47	105.20
25	BA	1067	A	C8-N9-C4	-6.03	103.39	105.80
34	DO	8	LEU	CA-CB-CG	6.01	129.13	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1154	G	C6-N1-C2	6.00	128.70	125.10
1	CA	1220	G	N3-C4-N9	-5.98	122.41	126.00
25	DA	2889	C	N1-C2-O2	5.98	122.49	118.90
25	BA	1745	A	C2-N3-C4	-5.97	107.61	110.60
25	DA	2136	C	N1-C2-O2	5.96	122.48	118.90
25	BA	139	A	O4'-C1'-N9	5.96	112.97	108.20
25	BA	2162	C	C6-N1-C2	-5.96	117.92	120.30
25	BA	555	G	N3-C4-C5	5.96	131.58	128.60
25	BA	179	A	O5'-P-OP2	-5.95	100.34	105.70
25	BA	1249	A	O4'-C1'-N9	5.92	112.93	108.20
25	DA	2473	U	C2-N1-C1'	5.91	124.79	117.70
25	DA	2138	C	N1-C2-O2	5.90	122.44	118.90
25	DA	645	C	C6-N1-C1'	-5.89	113.73	120.80
25	DA	1142(A)	A	C2-N3-C4	-5.87	107.67	110.60
1	AA	1030(B)	C	C6-N1-C1'	-5.86	113.77	120.80
25	BA	1067	A	C5-N7-C8	-5.86	100.97	103.90
25	DA	945	A	O4'-C1'-N9	5.86	112.88	108.20
1	CA	1225	A	N1-C6-N6	-5.85	115.09	118.60
1	CA	1023	G	C8-N9-C1'	-5.85	119.39	127.00
1	CA	1263	C	C5-C6-N1	5.83	123.92	121.00
25	BA	990	A	C5-C6-N6	-5.83	119.04	123.70
1	AA	1502	A	N1-C2-N3	5.83	132.21	129.30
25	BA	1067	A	N3-C4-N9	-5.82	122.75	127.40
1	AA	1025	U	N1-C2-O2	5.80	126.86	122.80
25	DA	141	A	N7-C8-N9	5.79	116.70	113.80
1	AA	1160	G	C4-N9-C1'	5.79	134.03	126.50
25	BA	934	A	O4'-C1'-N9	5.79	112.83	108.20
1	CA	1119	C	N3-C2-O2	-5.79	117.84	121.90
25	BA	1745	A	O4'-C1'-N9	5.79	112.83	108.20
25	BA	1067	A	N7-C8-N9	5.79	116.69	113.80
25	BA	831	A	O4'-C1'-N9	5.78	112.83	108.20
25	BA	2014	G	P-O3'-C3'	5.78	126.64	119.70
25	DA	1314	C	C2-N1-C1'	5.77	125.14	118.80
25	DA	2153	G	C5-C6-O6	-5.74	125.15	128.60
25	BA	1858	C	N3-C2-O2	-5.73	117.89	121.90
25	DA	2155	G	C8-N9-C1'	-5.73	119.56	127.00
25	BA	2348	A	N1-C6-N6	5.72	122.03	118.60
25	BA	2605	U	N3-C4-O4	-5.72	115.39	119.40
1	CA	79	G	C5-C6-O6	5.71	132.03	128.60
25	DA	277	C	N3-C2-O2	-5.71	117.91	121.90
25	DA	2108	C	C2-N3-C4	5.71	122.75	119.90
23	AX	22	G	N3-C4-C5	5.70	131.45	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2054	G	C4-C5-N7	-5.70	108.52	110.80
1	CA	1190	G	N9-C1'-C2'	-5.70	105.73	112.00
25	BA	1985	U	C2-N1-C1'	5.70	124.54	117.70
9	CI	102	LEU	CA-CB-CG	5.69	128.39	115.30
25	DA	1313	U	C2-N1-C1'	5.68	124.52	117.70
1	CA	1003	G	N3-C4-N9	5.68	129.41	126.00
25	BA	139	A	C4-C5-N7	5.67	113.53	110.70
25	BA	2210	C	C6-N1-C2	-5.66	118.03	120.30
25	DA	856	C	C6-N1-C2	-5.66	118.03	120.30
25	BA	354	A	N3-C4-N9	-5.66	122.88	127.40
25	DA	528	A	N1-C2-N3	5.65	132.13	129.30
30	BG	82	LEU	CA-CB-CG	5.64	128.28	115.30
25	DA	748	G	C4-N9-C1'	-5.63	119.17	126.50
25	DA	1653	G	P-O3'-C3'	5.62	126.45	119.70
25	BA	2441	G	OP1-P-OP2	-5.62	111.18	119.60
25	BA	2299	A	N3-C4-C5	5.61	130.73	126.80
3	CC	101	LEU	CA-CB-CG	5.61	128.19	115.30
25	BA	637	U	N3-C2-O2	-5.59	118.29	122.20
25	BA	892	G	O4'-C1'-N9	5.59	112.67	108.20
25	BA	1418	U	N3-C4-O4	5.59	123.31	119.40
41	DV	38	LEU	CA-CB-CG	5.58	128.13	115.30
25	DA	2160	G	N3-C4-N9	5.58	129.35	126.00
23	AX	14	A	C8-N9-C1'	-5.56	117.69	127.70
25	BA	1343	C	OP1-P-O3'	5.56	117.44	105.20
25	DA	1022	G	C4-C5-N7	-5.55	108.58	110.80
25	BA	470	C	O5'-P-OP1	5.54	117.35	110.70
25	BA	2211	U	N1-C2-O2	5.54	126.68	122.80
26	DB	1	U	C2-N1-C1'	5.54	124.35	117.70
1	AA	997	U	C5-C4-O4	5.53	129.22	125.90
23	AX	10	G	N3-C2-N2	-5.53	116.03	119.90
25	BA	139	A	N1-C6-N6	5.53	121.92	118.60
1	AA	1160	G	N3-C4-C5	-5.53	125.84	128.60
25	DA	614	U	N3-C2-O2	-5.52	118.33	122.20
1	AA	1183	A	P-O3'-C3'	5.52	126.32	119.70
25	DA	2287	A	N3-C4-C5	5.52	130.66	126.80
1	AA	1137	C	C6-N1-C2	-5.51	118.09	120.30
25	DA	1022	G	N3-C4-N9	-5.51	122.69	126.00
1	CA	1004	A	N7-C8-N9	-5.51	111.05	113.80
23	CX	17	C	C2-N1-C1'	5.51	124.86	118.80
19	CS	16	LEU	CA-CB-CG	5.50	127.96	115.30
1	CA	1220	G	N9-C4-C5	5.49	107.60	105.40
1	CA	1030(B)	C	C6-N1-C2	-5.49	118.10	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1256	A	N1-C6-N6	5.47	121.88	118.60
25	BA	1660	A	O5'-P-OP1	-5.47	100.78	105.70
23	CX	14	A	C4-N9-C1'	5.47	136.15	126.30
51	D5	58	LEU	CA-CB-CG	5.47	127.88	115.30
25	DA	195	A	P-O3'-C3'	5.46	126.26	119.70
26	DB	60	C	C5-C6-N1	5.46	123.73	121.00
1	AA	365	U	C2-N1-C1'	-5.45	111.17	117.70
25	DA	2153	G	N1-C6-O6	5.45	123.17	119.90
1	AA	1042	G	O4'-C1'-N9	5.43	112.54	108.20
25	BA	1153	G	N3-C4-C5	-5.42	125.89	128.60
25	BA	1091	A	C2-N3-C4	5.42	113.31	110.60
23	CX	22	G	C6-C5-N7	5.42	133.65	130.40
25	BA	2045	G	O5'-P-OP1	-5.41	100.83	105.70
25	DA	2167	U	C2-N1-C1'	5.41	124.19	117.70
52	B6	13	CYS	CA-CB-SG	5.39	123.71	114.00
25	DA	2725	A	N1-C6-N6	5.39	121.84	118.60
23	CX	14	A	C8-N9-C1'	-5.39	118.00	127.70
25	BA	2250	G	OP1-P-OP2	5.39	127.68	119.60
25	BA	555	G	C4-C5-N7	5.38	112.95	110.80
23	AX	14	A	C4-N9-C1'	5.38	135.98	126.30
1	CA	992	U	P-O3'-C3'	5.38	126.15	119.70
25	BA	1431	G	O4'-C1'-N9	5.38	112.50	108.20
1	CA	955	U	C2-N3-C4	5.37	130.22	127.00
25	BA	2713	C	C6-N1-C2	-5.36	118.16	120.30
25	BA	1343	C	OP2-P-O3'	-5.36	93.40	105.20
25	BA	1745	A	N1-C2-N3	5.36	131.98	129.30
25	BA	1249	A	C5-N7-C8	-5.36	101.22	103.90
1	CA	1006	C	N1-C2-O2	5.36	122.11	118.90
25	DA	2252	G	N3-C4-N9	-5.35	122.79	126.00
1	AA	532	A	OP1-P-O3'	5.35	116.97	105.20
25	BA	1359	U	C2-N1-C1'	5.35	124.12	117.70
25	BA	827	G	O5'-P-OP2	-5.34	100.89	105.70
25	BA	36	G	O5'-P-OP2	-5.33	100.90	105.70
1	CA	1183	A	P-O3'-C3'	5.33	126.10	119.70
1	CA	1023	G	N3-C4-C5	-5.33	125.94	128.60
25	DA	528	A	N3-C4-N9	-5.32	123.14	127.40
25	BA	1768	U	C2-N1-C1'	5.32	124.08	117.70
25	BA	869	U	N3-C2-O2	-5.29	118.49	122.20
25	DA	801	G	O5'-P-OP2	-5.29	100.93	105.70
25	BA	894	U	C5-C6-N1	-5.29	120.06	122.70
25	BA	978	A	O4'-C1'-N9	5.29	112.43	108.20
25	BA	2054	G	N9-C4-C5	5.29	107.51	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2072	C	N1-C2-O2	-5.28	115.73	118.90
25	BA	1200	G	OP2-P-O3'	5.28	116.81	105.20
25	DA	2155	G	N9-C4-C5	-5.28	103.29	105.40
25	BA	2162	C	C6-N1-C1'	-5.28	114.47	120.80
25	BA	1188	A	C5-C6-N1	-5.27	115.06	117.70
1	CA	65	U	P-O3'-C3'	5.27	126.03	119.70
25	BA	715	G	OP2-P-O3'	5.27	116.80	105.20
25	BA	2077	C	OP1-P-O3'	5.27	116.79	105.20
25	DA	1558	A	P-O3'-C3'	5.26	126.02	119.70
25	DA	2139	C	C6-N1-C1'	-5.26	114.48	120.80
25	BA	1220	U	P-O3'-C3'	5.26	126.01	119.70
25	DA	2207	G	N1-C6-O6	5.26	123.06	119.90
25	BA	2701	U	C5-C6-N1	5.26	125.33	122.70
25	BA	1235	G	C5-N7-C8	5.24	106.92	104.30
23	CX	67	C	C5-C6-N1	5.24	123.62	121.00
25	BA	2024	G	N3-C2-N2	-5.24	116.23	119.90
25	DA	528	A	N3-C4-C5	5.24	130.47	126.80
1	AA	97	G	N3-C4-N9	5.24	129.14	126.00
1	AA	421	U	N1-C2-O2	5.24	126.47	122.80
1	CA	532	A	OP1-P-O3'	5.23	116.71	105.20
25	DA	2139	C	N1-C2-O2	5.23	122.04	118.90
25	BA	1581	U	N1-C2-O2	5.23	126.46	122.80
25	DA	141	A	N1-C2-N3	5.22	131.91	129.30
1	AA	266	G	P-O3'-C3'	5.22	125.96	119.70
25	BA	847	A	OP1-P-OP2	5.22	127.43	119.60
1	AA	299	G	C5-C6-O6	-5.21	125.47	128.60
35	DP	44	GLY	C-N-CA	5.21	134.73	121.70
1	CA	1064	G	P-O3'-C3'	5.21	125.95	119.70
23	AX	46	G	N1-C2-N3	5.20	127.02	123.90
25	BA	354	A	N3-C4-C5	5.20	130.44	126.80
25	BA	2627	U	OP1-P-OP2	5.20	127.41	119.60
25	BA	2211	U	C2-N1-C1'	5.19	123.93	117.70
25	DA	1210	A	P-O3'-C3'	5.19	125.93	119.70
1	AA	1030(B)	C	C5-C6-N1	5.19	123.60	121.00
25	BA	399	G	O4'-C1'-N9	5.19	112.35	108.20
25	DA	2267	A	OP1-P-OP2	5.18	127.37	119.60
25	BA	410	U	C2-N1-C1'	-5.18	111.49	117.70
25	BA	2601	A	C8-N9-C4	5.17	107.87	105.80
25	BA	2209	G	P-O3'-C3'	5.17	125.90	119.70
25	BA	733	G	C4-C5-N7	5.17	112.87	110.80
25	BA	1249	A	C2-N3-C4	-5.17	108.02	110.60
25	DA	1530	C	P-O3'-C3'	5.16	125.89	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1768	U	N1-C2-O2	5.16	126.41	122.80
2	AB	9	GLU	N-CA-C	5.15	124.92	111.00
25	BA	2883	A	O4'-C1'-N9	5.15	112.32	108.20
1	CA	1002	G	N1-C2-N2	5.15	120.84	116.20
1	CA	1054	C	C2-N1-C1'	5.15	124.46	118.80
1	CA	913	A	P-O3'-C3'	5.14	125.87	119.70
2	CB	231	GLU	C-N-CD	5.14	139.19	128.40
1	CA	1154	G	N3-C2-N2	5.14	123.50	119.90
1	AA	1004	A	C8-N9-C4	-5.13	103.75	105.80
25	DA	2166	G	P-O3'-C3'	5.13	125.86	119.70
25	BA	2250	G	N3-C4-N9	5.12	129.07	126.00
1	AA	1183	A	O4'-C1'-N9	-5.12	104.10	108.20
1	CA	60	A	P-O3'-C3'	5.12	125.85	119.70
1	CA	1263	C	C6-N1-C2	-5.12	118.25	120.30
25	BA	1700	G	P-O3'-C3'	5.12	125.84	119.70
23	AX	22	G	C5-C6-N1	5.12	114.06	111.50
1	CA	1023	G	C4-C5-N7	5.12	112.85	110.80
55	B9	11	CYS	CA-CB-SG	-5.12	104.79	114.00
25	BA	2189	U	C2-N1-C1'	5.11	123.83	117.70
25	DA	2149	G	N3-C4-N9	5.11	129.06	126.00
25	BA	2168	C	C2-N1-C1'	5.11	124.42	118.80
25	DA	2108	C	N1-C2-O2	5.11	121.96	118.90
39	DT	78	LEU	CA-CB-CG	5.11	127.04	115.30
23	CX	46	G	N1-C2-N3	5.10	126.96	123.90
25	DA	141	A	C5-N7-C8	-5.10	101.35	103.90
25	BA	842	C	N1-C2-O2	5.10	121.96	118.90
25	BA	2515	A	N1-C2-N3	-5.09	126.76	129.30
25	DA	1783	A	C8-N9-C4	5.08	107.83	105.80
25	BA	1218	G	O4'-C1'-N9	5.08	112.26	108.20
1	CA	1128	C	P-O3'-C3'	5.08	125.80	119.70
25	BA	555	G	C5-N7-C8	-5.08	101.76	104.30
1	AA	1160	G	N3-C4-N9	5.08	129.05	126.00
1	AA	1037	C	N1-C2-O2	5.07	121.94	118.90
25	BA	2027	A	OP1-P-O3'	5.07	116.35	105.20
1	AA	1531	A	O4'-C1'-N9	-5.06	104.15	108.20
25	BA	1874	C	C6-N1-C2	5.06	122.33	120.30
25	DA	751	A	O5'-P-OP1	-5.06	101.14	105.70
25	DA	2139	C	C5-C6-N1	5.06	123.53	121.00
1	CA	1023	G	N9-C4-C5	-5.06	103.38	105.40
1	CA	1272	G	C6-N1-C2	5.05	128.13	125.10
25	DA	2554	U	O5'-P-OP1	-5.05	101.15	105.70
1	CA	993	G	N3-C4-C5	-5.05	126.08	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1263	C	N3-C4-C5	-5.05	119.88	121.90
25	DA	141	A	O4'-C1'-N9	5.05	112.24	108.20
1	AA	615	C	C6-N1-C2	-5.04	118.28	120.30
25	BA	598	A	O5'-P-OP1	-5.03	101.17	105.70
25	BA	1068	G	N3-C4-C5	5.03	131.12	128.60
25	DA	2152	G	C5-C6-O6	-5.03	125.58	128.60
25	DA	2318	G	N3-C4-C5	-5.03	126.08	128.60
25	BA	2449	U	C5-C6-N1	-5.03	120.19	122.70
1	CA	1004	A	C4-N9-C1'	-5.02	117.26	126.30
23	AX	14	A	C4-C5-N7	-5.02	108.19	110.70
1	CA	1256	A	N9-C4-C5	-5.01	103.79	105.80
25	DA	1022	G	N9-C4-C5	5.01	107.41	105.40
1	AA	1320	C	C5-C6-N1	5.01	123.50	121.00
25	DA	798	G	N3-C4-N9	-5.01	123.00	126.00
1	AA	1065	U	P-O3'-C3'	5.00	125.71	119.70
1	AA	782	A	O5'-P-OP1	-5.00	101.20	105.70
25	BA	2078	G	O4'-C1'-N9	-5.00	104.20	108.20
1	CA	1183	A	OP1-P-O3'	5.00	116.21	105.20

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	439	A	Sidechain
50	B4	59	PHE	Peptide
38	BS	58	LEU	Peptide
7	CG	78	ARG	Peptide
7	CG	79	ARG	Peptide
50	D4	67	TYR	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	32183	0	16244	640	0
1	CA	32312	0	16308	675	0
2	AB	1846	0	1867	88	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	CB	1825	0	1828	91	0
3	AC	1552	0	1546	53	0
3	CC	1542	0	1517	52	0
4	AD	1659	0	1676	71	0
4	CD	1674	0	1714	52	0
5	AE	1129	0	1185	32	0
5	CE	1133	0	1191	37	0
6	AF	806	0	793	19	0
6	CF	816	0	808	16	0
7	AG	1231	0	1238	22	0
7	CG	1235	0	1249	37	0
8	AH	1088	0	1126	28	0
8	CH	1088	0	1126	26	0
9	AI	983	0	986	30	0
9	CI	978	0	966	47	0
10	AJ	709	0	650	34	0
10	CJ	714	0	672	34	0
11	AK	829	0	825	20	0
11	CK	833	0	836	16	0
12	AL	930	0	980	25	0
12	CL	930	0	980	28	0
13	AM	937	0	977	27	0
13	CM	920	0	950	37	0
14	AN	492	0	529	21	0
14	CN	492	0	529	25	0
15	AO	728	0	760	22	0
15	CO	728	0	760	24	0
16	AP	681	0	697	23	0
16	CP	677	0	686	17	0
17	AQ	823	0	891	11	0
17	CQ	823	0	891	10	0
18	AR	555	0	618	13	0
18	CR	555	0	618	12	0
19	AS	652	0	662	25	0
19	CS	646	0	644	39	0
20	AT	728	0	798	21	0
20	CT	727	0	796	16	0
21	AU	199	0	208	4	0
21	CU	199	0	208	9	0
22	AV	169	0	86	4	0
22	CV	109	0	55	5	0
23	AX	1625	0	828	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	CX	1625	0	829	27	0
24	AY	385	0	199	11	0
24	CY	104	0	56	6	0
25	BA	60792	0	30653	698	0
25	DA	60311	0	30414	981	0
26	BB	2573	0	1306	23	0
26	DB	2573	0	1306	73	0
27	BD	2136	0	2218	60	0
27	DD	2136	0	2218	66	0
28	BE	1559	0	1618	27	0
28	DE	1559	0	1618	41	0
29	BF	1584	0	1625	45	0
29	DF	1580	0	1619	51	0
30	BG	1425	0	1443	43	0
30	DG	1424	0	1434	67	0
31	BH	1330	0	1407	24	0
31	DH	1330	0	1407	49	0
32	BI	1085	0	1114	35	0
32	DI	1061	0	1080	30	0
33	BN	1117	0	1183	19	0
33	DN	1117	0	1184	17	0
34	BO	933	0	996	23	0
34	DO	933	0	996	29	0
35	BP	1135	0	1212	34	0
35	DP	1135	0	1212	53	0
36	BQ	1122	0	1179	26	0
36	DQ	1122	0	1179	37	0
37	BR	968	0	1033	20	0
37	DR	968	0	1033	25	0
38	BS	877	0	938	26	0
38	DS	870	0	923	29	0
39	BT	1091	0	1151	38	0
39	DT	1083	0	1136	36	0
40	BU	959	0	1019	18	0
40	DU	959	0	1019	18	0
41	BV	771	0	830	13	0
41	DV	771	0	830	20	0
42	BW	886	0	940	18	0
42	DW	886	0	940	16	0
43	BX	750	0	814	22	0
43	DX	750	0	814	18	0
44	BY	806	0	881	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	DY	806	0	881	21	0
45	BZ	1349	0	1355	45	0
45	DZ	1360	0	1363	44	0
46	B0	653	0	674	15	0
46	D0	653	0	674	22	0
47	B1	755	0	826	21	0
47	D1	755	0	826	19	0
48	B2	588	0	643	10	0
48	D2	588	0	643	12	0
49	B3	469	0	518	10	0
49	D3	464	0	514	12	0
50	B4	558	0	544	36	0
50	D4	532	0	503	27	0
51	B5	455	0	465	9	0
51	D5	455	0	465	9	0
52	B6	453	0	473	10	0
52	D6	449	0	469	10	0
53	B7	418	0	467	7	0
53	D7	418	0	467	9	0
54	B8	511	0	571	22	0
54	D8	517	0	582	16	0
55	B9	307	0	335	8	0
55	D9	307	0	335	7	0
56	AA	190	0	0	0	0
56	AD	1	0	0	0	0
56	AE	3	0	0	0	0
56	AF	1	0	0	0	0
56	AM	1	0	0	0	0
56	AN	1	0	0	0	0
56	AQ	1	0	0	0	0
56	AX	9	0	0	0	0
56	B0	5	0	0	0	0
56	B2	1	0	0	0	0
56	B3	1	0	0	0	0
56	B4	1	0	0	0	0
56	B5	4	0	0	0	0
56	B6	2	0	0	0	0
56	B7	5	0	0	0	0
56	B8	2	0	0	0	0
56	B9	1	0	0	0	0
56	BA	814	0	0	0	0
56	BB	22	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	BD	9	0	0	0	0
56	BE	7	0	0	0	0
56	BF	9	0	0	0	0
56	BG	2	0	0	0	0
56	BN	7	0	0	0	0
56	BO	1	0	0	0	0
56	BP	4	0	0	0	0
56	BQ	4	0	0	0	0
56	BR	3	0	0	0	0
56	BU	9	0	0	0	0
56	BV	4	0	0	0	0
56	BW	4	0	0	0	0
56	BX	2	0	0	0	0
56	BY	3	0	0	0	0
56	BZ	2	0	0	0	0
56	CA	175	0	0	0	0
56	CE	2	0	0	0	0
56	CF	1	0	0	0	0
56	CJ	1	0	0	0	0
56	CT	1	0	0	0	0
56	CX	2	0	0	0	0
56	D0	2	0	0	0	0
56	D1	1	0	0	0	0
56	D3	1	0	0	0	0
56	D8	1	0	0	0	0
56	DA	674	0	0	0	0
56	DB	10	0	0	0	0
56	DD	8	0	0	0	0
56	DE	5	0	0	0	0
56	DF	5	0	0	0	0
56	DG	1	0	0	0	0
56	DN	1	0	0	0	0
56	DO	1	0	0	0	0
56	DP	2	0	0	0	0
56	DQ	3	0	0	0	0
56	DR	1	0	0	0	0
56	DU	4	0	0	0	0
56	DV	3	0	0	0	0
56	DW	2	0	0	0	0
56	DY	1	0	0	0	0
57	AA	40	0	38	6	0
57	CA	40	0	38	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	AD	8	0	0	1	0
58	CD	8	0	0	0	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	175	0	0	13	0
61	AJ	2	0	0	0	0
61	AL	1	0	0	0	0
61	AM	1	0	0	0	0
61	AO	1	0	0	0	0
61	AV	1	0	0	0	0
61	AX	8	0	0	0	0
61	B0	4	0	0	0	0
61	B1	1	0	0	0	0
61	B3	1	0	0	0	0
61	B5	4	0	0	1	0
61	B6	1	0	0	0	0
61	B7	1	0	0	0	0
61	B8	10	0	0	1	0
61	BA	1294	0	0	49	0
61	BB	34	0	0	1	0
61	BD	16	0	0	1	0
61	BE	12	0	0	1	0
61	BF	7	0	0	1	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BN	1	0	0	0	0
61	BO	4	0	0	0	0
61	BP	15	0	0	1	0
61	BQ	5	0	0	0	0
61	BR	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	BU	2	0	0	0	0
61	BV	2	0	0	0	0
61	BW	3	0	0	0	0
61	BX	5	0	0	0	0
61	CA	137	0	0	12	0
61	CD	1	0	0	0	0
61	CJ	2	0	0	0	0
61	CL	1	0	0	1	0
61	CN	1	0	0	0	0
61	CT	1	0	0	0	0
61	CX	2	0	0	0	0
61	D0	7	0	0	0	0
61	D1	1	0	0	0	0
61	D3	1	0	0	0	0
61	D8	4	0	0	0	0
61	DA	924	0	0	75	0
61	DB	8	0	0	0	0
61	DD	18	0	0	3	0
61	DE	9	0	0	1	0
61	DF	5	0	0	0	0
61	DN	1	0	0	0	0
61	DO	1	0	0	0	0
61	DP	14	0	0	1	0
61	DR	1	0	0	0	0
61	DT	1	0	0	0	0
61	DU	3	0	0	0	0
61	DV	1	0	0	0	0
61	DW	1	0	0	0	0
61	DX	1	0	0	0	0
61	DY	1	0	0	0	0
All	All	290807	0	193177	5129	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (5129) 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:AA:439:A:N3	1:AA:439:A:C2	1.68	1.62
1:AA:439:A:C5	1:AA:439:A:C6	1.79	1.62
1:AA:439:A:N3	1:AA:439:A:C4	1.70	1.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:439:A:N1	1:AA:439:A:C6	1.72	1.55
1:AA:439:A:N1	1:AA:439:A:C2	1.70	1.54
1:AA:439:A:C4	1:AA:496:A:C6	1.95	1.53
1:AA:439:A:C5	1:AA:496:A:C6	1.97	1.50
1:AA:496:A:C2	1:AA:496:A:N3	1.82	1.47
1:AA:439:A:C2	1:AA:496:A:N3	1.92	1.35
1:AA:439:A:C5	1:AA:496:A:N3	1.94	1.35
1:AA:439:A:C4	1:AA:496:A:N3	1.93	1.35
1:AA:439:A:C6	1:AA:496:A:N3	1.95	1.34
1:AA:439:A:N1	1:AA:496:A:N3	1.82	1.25
1:AA:439:A:C8	1:AA:496:A:C6	2.30	1.19
1:AA:439:A:C6	1:AA:496:A:C2	2.31	1.18
1:AA:496:A:C6	1:AA:496:A:N1	2.15	1.14
1:AA:439:A:N3	1:AA:496:A:N3	1.98	1.11
1:CA:1162:C:N4	1:CA:1174:G:H1	1.49	1.08
1:AA:439:A:N9	1:AA:496:A:C6	2.21	1.07
1:AA:439:A:N7	1:AA:496:A:C6	2.25	1.03
1:AA:439:A:N3	1:AA:496:A:C2	2.28	1.00
1:AA:439:A:C2	1:AA:496:A:C2	2.49	1.00
25:DA:2138:C:N4	25:DA:2153:G:H1	1.61	0.99
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.44	0.97
25:DA:2104:G:H1	25:DA:2185:C:H42	1.12	0.97
25:BA:1065:U:HO2'	25:BA:1067:A:H2	1.01	0.96
1:CA:998:G:H1	1:CA:1043:C:H42	0.98	0.95
1:CA:1029:C:N4	1:CA:1032:G:H1	1.62	0.95
22:CV:16:A:H61	23:CX:36:U:H3	1.05	0.95
1:AA:1161:C:N4	1:AA:1175:G:H1	1.64	0.94
1:CA:1262:C:H42	1:CA:1273:G:H1	1.14	0.94
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.50	0.94
25:DA:1359:A:N1	25:DA:1372:U:N3	2.16	0.93
1:AA:997:U:H3	1:AA:1044:A:H61	1.04	0.93
1:AA:1161:C:H42	1:AA:1175:G:H1	1.04	0.92
1:AA:1162:C:H42	1:AA:1174:G:H1	1.07	0.91
1:AA:439:A:C8	1:AA:496:A:N6	2.39	0.91
1:CA:1025:U:H3	1:CA:1036:G:H1	1.11	0.91
1:AA:78:G:H1	1:AA:91:C:H42	1.17	0.91
1:CA:1162:C:N3	1:CA:1174:G:N2	2.19	0.90
1:AA:984:C:H42	1:AA:1221:G:H1	1.18	0.90
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.51	0.90
25:BA:927:G:N2	25:BA:944:C:N3	2.21	0.89
22:CV:16:A:N6	23:CX:36:U:H3	1.69	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:620:G:H4'	25:DA:621:A:H5'	1.53	0.89
25:DA:2138:C:H42	25:DA:2153:G:H1	0.92	0.89
1:CA:1029:C:N3	1:CA:1032:G:N2	2.21	0.89
1:AA:496:A:N3	1:AA:496:A:N1	2.21	0.88
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.54	0.88
35:BP:126:VAL:HG12	35:BP:148:LEU:HD22	1.55	0.88
35:DP:126:VAL:HG12	35:DP:148:LEU:HD22	1.56	0.88
1:CA:975:A:H4'	1:CA:976:G:H5''	1.56	0.88
1:CA:998:G:H1	1:CA:1043:C:N4	1.71	0.88
1:CA:1162:C:H42	1:CA:1174:G:H1	0.91	0.87
25:DA:2046:G:H5'	51:D5:19:ARG:HA	1.54	0.87
25:DA:2166:G:H3'	25:DA:2167:U:H5''	1.54	0.87
1:AA:1502:A:H2	1:AA:1505:G:H1	1.21	0.87
1:AA:439:A:C5	1:AA:496:A:C4	2.61	0.87
1:AA:1162:C:N4	1:AA:1174:G:H1	1.73	0.87
2:CB:16:HIS:HB3	2:CB:210:SER:HB2	1.57	0.86
25:BA:2118:U:H3	25:BA:2215:G:H1	1.20	0.86
4:AD:107:ARG:HH22	4:AD:194:LEU:HD22	1.36	0.86
1:AA:439:A:N1	1:AA:496:A:C2	2.44	0.86
1:AA:439:A:C4	1:AA:496:A:C4	2.63	0.85
1:CA:1000:U:H3	1:CA:1041:A:H61	1.19	0.85
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.09	0.85
25:DA:880:G:N1	25:DA:898:C:O2	2.09	0.85
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	1.57	0.85
2:AB:16:HIS:CD2	2:AB:17:PHE:H	1.94	0.84
25:BA:656:A:OP1	35:BP:65:ARG:NH1	2.10	0.84
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.43	0.84
25:DA:2401:U:H5'	52:D6:18:ARG:HH12	1.41	0.84
46:B0:11:ARG:O	46:B0:14:ARG:NH2	2.10	0.84
25:BA:1360:C:OP1	61:BA:4706:HOH:O	1.95	0.83
25:BA:839:G:O6	61:BA:4691:HOH:O	1.95	0.83
10:CJ:8:LEU:HB2	10:CJ:70:ARG:HB2	1.60	0.83
1:AA:201:C:H42	1:AA:216:G:H1	1.27	0.82
25:BA:2163:G:O6	25:BA:2172:U:O2	1.95	0.82
1:CA:1154:G:H2'	1:CA:1155:G:H8	1.44	0.82
25:DA:1798:U:H5'	27:DD:259:THR:HG22	1.59	0.82
1:AA:1027:C:C2	1:AA:1034:G:N1	2.46	0.82
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.58	0.82
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.42	0.82
25:DA:740:U:OP2	61:DA:4497:HOH:O	1.96	0.82
33:DN:15:LEU:HB2	33:DN:135:PRO:HB2	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.62	0.81
1:AA:997:U:H3	1:AA:1044:A:N6	1.77	0.81
25:DA:2807:G:N1	25:DA:2893:G:O6	2.10	0.81
43:DX:53:LYS:HB3	43:DX:82:GLN:HB3	1.61	0.81
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.14	0.81
25:DA:1271:G:OP2	61:DA:4489:HOH:O	1.98	0.81
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.61	0.81
1:CA:1007:C:N3	1:CA:1022:G:O6	2.14	0.81
26:DB:2:C:O2	26:DB:119:G:N2	2.13	0.81
25:DA:1153:C:OP2	61:DA:4453:HOH:O	2.00	0.80
25:DA:1721:G:H8	25:DA:1741:A:H62	1.26	0.80
32:BI:92:VAL:HG13	32:BI:120:ILE:HB	1.63	0.80
25:DA:1602:U:O4	61:DA:4187:HOH:O	2.00	0.80
31:DH:24:VAL:HG13	31:DH:37:VAL:HG21	1.63	0.80
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.46	0.80
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.14	0.80
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.00	0.80
1:AA:1158:C:C4	1:AA:1160:G:H8	1.99	0.80
25:BA:388:A:H2'	25:BA:389:G:H8	1.47	0.80
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.15	0.80
25:DA:1204:A:H2	25:DA:1241:A:H62	1.27	0.79
4:CD:122:ARG:NH1	4:CD:134:ASP:O	2.16	0.79
25:DA:1332:G:OP1	61:DA:4448:HOH:O	1.99	0.79
2:AB:127:ILE:HD12	2:AB:130:ARG:HD3	1.63	0.79
29:DF:53:THR:HG23	29:DF:55:GLY:H	1.47	0.79
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.48	0.79
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.64	0.79
53:B7:24:THR:HG22	53:B7:27:GLY:H	1.48	0.79
25:DA:1022:G:H22	25:DA:1142(A):A:H2	1.27	0.79
37:DR:97:VAL:HG22	37:DR:114:VAL:HG13	1.65	0.79
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.00	0.79
25:DA:2502:G:N7	61:DA:4677:HOH:O	2.14	0.79
25:BA:932:C:H3'	25:BA:933:C:H5''	1.65	0.79
1:CA:1422:G:H5'	34:DO:48:PRO:HB3	1.65	0.79
1:AA:642:A:N3	8:AH:113:SER:OG	2.15	0.78
1:CA:1119:C:H42	1:CA:1154:G:H1	1.31	0.78
1:CA:953:G:H5'	1:CA:965:A:H61	1.48	0.78
25:DA:631:A:OP1	35:DP:65:ARG:NH1	2.16	0.78
1:AA:894:G:N7	61:AA:4102:HOH:O	2.15	0.78
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.65	0.78
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:191:A:N1	61:DA:4501:HOH:O	2.15	0.78
1:AA:1422:G:H5'	34:BO:48:PRO:HB3	1.65	0.78
1:CA:1028:C:N3	1:CA:1033:G:C6	2.51	0.78
25:DA:2104:G:H1	25:DA:2185:C:N4	1.81	0.78
25:DA:994:C:OP1	40:DU:53:ARG:NH2	2.17	0.78
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.63	0.78
1:AA:76:C:H42	1:AA:93:G:H1	1.30	0.78
1:AA:975:A:H4'	1:AA:976:G:H5''	1.65	0.78
1:CA:596:C:O2	1:CA:644:G:N2	2.13	0.78
25:BA:2831:A:OP2	61:BA:5266:HOH:O	2.02	0.78
22:AV:16:A:H61	23:AX:36:U:H3	1.31	0.78
1:AA:78:G:N2	1:AA:91:C:N3	2.33	0.77
2:AB:231:GLU:HB3	2:AB:232:PRO:HD2	1.64	0.77
1:AA:78:G:H1	1:AA:91:C:N4	1.81	0.77
25:DA:602:G:O2'	25:DA:655:A:N6	2.16	0.77
27:DD:238:GLY:O	61:DD:407:HOH:O	2.02	0.77
25:BA:2163:G:H1	25:BA:2171:G:H22	1.29	0.77
25:BA:1829:U:H5'	27:BD:259:THR:HG22	1.66	0.77
1:AA:266:G:H5''	1:AA:268:C:H41	1.48	0.77
1:AA:1007:C:N3	1:AA:1022:G:O6	2.17	0.77
1:CA:664:G:H22	1:CA:741:G:H1	1.31	0.77
1:AA:953:G:H5'	1:AA:965:A:H61	1.48	0.77
25:BA:2251:G:OP2	61:BA:4424:HOH:O	2.02	0.77
27:BD:71:ASP:HB3	27:BD:103:ARG:HH22	1.49	0.77
25:DA:1689:A:H62	25:DA:1698:A:H2	1.31	0.77
1:CA:1026:G:H5'	1:CA:1027:C:O5'	1.83	0.77
29:BF:185:ASP:HA	29:BF:188:ARG:HD3	1.67	0.76
25:BA:1577:C:O2'	25:BA:1578:C:O5'	2.03	0.76
25:BA:2832:G:OP2	61:BA:5266:HOH:O	2.03	0.76
1:CA:771:G:N7	61:CA:4031:HOH:O	2.18	0.76
25:DA:1250:G:N7	35:DP:18:ARG:NH2	2.34	0.76
25:DA:1030:G:OP2	36:DQ:128:LYS:NZ	2.18	0.76
25:DA:2114:A:N6	25:DA:2119:A:N7	2.34	0.76
25:BA:894:U:OP2	61:BA:4495:HOH:O	2.02	0.76
50:D4:24:THR:OG1	50:D4:25:TYR:N	2.16	0.76
4:AD:108:LEU:HD13	4:AD:174:LEU:HD13	1.67	0.76
25:BA:2299:A:H62	25:BA:2356:U:H3	1.33	0.76
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.18	0.76
1:CA:504:C:OP1	61:CA:4008:HOH:O	2.04	0.76
1:AA:627:G:H2'	1:AA:628:G:H8	1.51	0.75
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:563:G:OP2	61:DA:4452:HOH:O	2.05	0.75
25:BA:1981:G:N7	61:BA:4103:HOH:O	2.20	0.75
25:BA:478:G:OP2	61:BA:5249:HOH:O	2.04	0.75
1:CA:1165:C:H42	1:CA:1171:G:H1	1.35	0.75
1:CA:1221:G:OP1	1:CA:1320:C:N4	2.19	0.75
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.69	0.75
13:CM:22:ILE:HG23	13:CM:67:GLU:HG2	1.69	0.75
25:DA:2126:A:N6	25:DA:2162:G:O2'	2.19	0.75
25:BA:591:U:O4	61:BA:4249:HOH:O	2.05	0.75
45:BZ:129:SER:HB2	45:BZ:132:ASN:HB2	1.69	0.75
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.20	0.75
25:DA:1140:C:O3'	33:DN:25:ARG:NH1	2.20	0.75
25:DA:2268:A:OP1	61:DA:4414:HOH:O	2.05	0.75
25:DA:2312:U:H5'	30:DG:88:ILE:HD11	1.69	0.75
25:DA:2430:A:OP2	61:DA:4569:HOH:O	2.05	0.74
10:AJ:7:LYS:HE2	10:AJ:9:ARG:HH12	1.52	0.74
25:BA:1378:G:OP1	61:BA:4706:HOH:O	2.06	0.74
1:CA:1183:A:O2'	1:CA:1184:G:OP1	2.04	0.74
25:BA:1480:A:H61	25:BA:1605:A:H62	1.33	0.74
15:CO:22:THR:OG1	15:CO:23:GLY:N	2.20	0.74
25:DA:587:C:OP2	35:DP:21:ARG:NH2	2.20	0.74
1:AA:439:A:C6	1:AA:496:A:C4	2.76	0.74
44:BY:92:ASN:HB3	44:BY:94:LYS:H	1.52	0.74
25:DA:1783:A:OP1	61:DA:4497:HOH:O	2.04	0.74
25:BA:2015:U:OP2	61:BA:5270:HOH:O	2.05	0.74
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.35	0.74
9:CI:53:VAL:O	9:CI:55:ALA:N	2.20	0.74
25:DA:64:A:N6	25:DA:90:U:O4	2.19	0.74
25:DA:971:C:OP2	61:DA:4841:HOH:O	2.06	0.74
25:BA:1462:G:N2	25:BA:1629:C:O2	2.17	0.74
25:DA:2308:G:O6	25:DA:2311:A:N6	2.16	0.74
1:AA:652:U:O4	1:AA:752:G:O2'	2.05	0.74
2:CB:123:ALA:H	2:CB:127:ILE:HD12	1.53	0.74
1:CA:1114:C:O2'	14:CN:60:SER:O	2.05	0.74
1:AA:574:A:OP2	61:AA:4007:HOH:O	2.04	0.74
4:AD:104:VAL:HG11	4:AD:146:ILE:HD13	1.68	0.74
25:DA:568:U:O4	61:DA:4154:HOH:O	2.06	0.74
1:AA:1158:C:H5	1:AA:1181:G:H1	1.36	0.73
25:BA:2877:G:OP2	39:BT:119:LYS:NZ	2.21	0.73
1:AA:1166:G:N2	1:AA:1170:A:OP2	2.18	0.73
11:CK:48:ILE:O	11:CK:50:TYR:N	2.17	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1019:U:H3	25:DA:1142(A):A:H62	1.36	0.73
25:DA:2638:G:P	28:DE:82:ARG:HH22	2.11	0.73
1:AA:972:C:OP1	61:AA:4128:HOH:O	2.07	0.73
1:CA:1507:A:N6	1:CA:1528:U:O4	2.16	0.73
35:BP:42:SER:O	61:BP:305:HOH:O	2.06	0.73
1:CA:76:C:H42	1:CA:93:G:H1	1.36	0.73
30:DG:80:PHE:O	30:DG:82:LEU:N	2.21	0.73
1:AA:316:G:OP2	1:AA:351:G:O2'	2.05	0.73
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.22	0.73
25:DA:2867:G:OP2	39:DT:119:LYS:NZ	2.20	0.73
25:DA:573:G:OP2	41:DV:78:LYS:NZ	2.21	0.73
3:AC:8:ILE:HG23	3:AC:16:ARG:HG2	1.70	0.73
9:AI:17:VAL:HG21	9:AI:81:ILE:HG22	1.70	0.73
51:D5:16:ARG:NH1	51:D5:17:ASP:OD1	2.21	0.73
26:DB:22:U:H3	26:DB:61:G:H1	1.34	0.73
1:AA:400:C:H5''	4:AD:73:ARG:HH22	1.53	0.73
39:BT:16:ARG:NH2	39:BT:83:ILE:O	2.21	0.73
1:AA:78:G:N1	1:AA:91:C:N4	2.36	0.73
1:CA:419:C:OP1	1:CA:513:C:O2'	2.05	0.73
19:AS:20:LEU:HD23	19:AS:23:ASN:HD22	1.52	0.73
25:BA:2324:U:H5'	30:BG:88:ILE:HD11	1.71	0.73
2:CB:87:ARG:HD3	2:CB:234:PRO:HD2	1.70	0.73
30:DG:7:LEU:HD13	30:DG:104:GLU:HA	1.70	0.73
25:DA:1327:C:OP2	61:DA:4194:HOH:O	2.06	0.72
25:DA:792:G:O6	61:DA:4438:HOH:O	2.06	0.72
1:AA:439:A:C5	1:AA:496:A:C5	2.75	0.72
25:DA:2285:C:OP2	52:D6:6:ARG:NH1	2.22	0.72
1:CA:1004:A:N6	1:CA:1037:C:N3	2.37	0.72
27:DD:148:GLU:HB2	27:DD:151:LYS:HD2	1.72	0.72
29:DF:21:ALA:HB3	29:DF:22:ALA:HA	1.70	0.72
35:DP:42:SER:O	61:DP:303:HOH:O	2.06	0.72
39:DT:16:ARG:NH1	39:DT:18:ASP:OD1	2.21	0.72
40:DU:78:THR:O	40:DU:117:GLN:NE2	2.22	0.72
25:BA:1094:A:OP2	25:BA:1155:C:N4	2.15	0.72
1:CA:1048:G:OP1	14:CN:3:ARG:NH2	2.22	0.72
25:DA:2183:C:H2'	25:DA:2184:G:H8	1.54	0.72
1:AA:567:G:N3	61:AA:4097:HOH:O	2.22	0.72
19:AS:68:GLY:H	50:B4:58:ARG:HD3	1.54	0.72
28:BE:105:THR:OG1	28:BE:199:ARG:NH2	2.22	0.72
1:CA:1183:A:O2'	1:CA:1185:G:OP2	2.08	0.72
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1315:C:OP2	61:DA:4448:HOH:O	2.06	0.72
25:DA:1530:C:O2'	25:DA:1531:C:O5'	2.07	0.72
27:BD:108:PRO:HB3	27:BD:143:HIS:CE1	2.25	0.72
51:D5:16:ARG:HG2	51:D5:16:ARG:HH11	1.54	0.72
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.22	0.72
25:DA:2595:G:N7	61:DA:4581:HOH:O	2.22	0.72
2:AB:201:ILE:HG21	2:AB:214:ILE:HG21	1.72	0.72
52:B6:35:GLU:OE2	52:B6:50:ARG:NH1	2.23	0.71
27:BD:17:THR:O	27:BD:211:ARG:NH2	2.23	0.71
1:CA:1123:A:H4'	10:CJ:36:GLY:HA3	1.72	0.71
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.23	0.71
16:AP:22:THR:HA	16:AP:33:ILE:HG12	1.73	0.71
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.08	0.71
1:AA:664:G:H22	1:AA:741:G:H1	1.35	0.71
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	1.72	0.71
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.72	0.71
25:BA:2162:C:C2	25:BA:2173:G:N1	2.57	0.71
25:DA:131:G:OP1	61:DA:4106:HOH:O	2.07	0.71
49:B3:8:LEU:HD13	49:B3:31:LEU:HD23	1.71	0.71
25:BA:973:G:N7	61:BA:4494:HOH:O	2.24	0.71
45:BZ:111:VAL:HG12	45:BZ:112:ARG:H	1.55	0.71
1:AA:339:C:OP2	34:BO:97:ARG:NH1	2.23	0.71
25:BA:2125:C:H42	25:BA:2208:G:H1	1.39	0.71
26:BB:48:A:H4'	38:BS:95:HIS:HD2	1.55	0.71
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.72	0.71
1:CA:1187:G:H5'	9:CI:113:LYS:HE2	1.71	0.71
25:DA:1010:A:OP2	61:DA:4463:HOH:O	2.09	0.71
1:AA:1027:C:O2'	1:AA:1034:G:N2	2.24	0.71
57:AA:3191:PCY:O21	57:AA:3191:PCY:O14	2.08	0.71
25:BA:2343:G:O2'	25:BA:2348:A:N1	2.19	0.71
38:BS:25:ARG:NH1	38:BS:42:ASP:OD1	2.23	0.71
1:CA:798:G:N7	61:CA:4027:HOH:O	2.24	0.71
7:CG:16:LEU:HD23	9:CI:41:VAL:HG12	1.73	0.71
3:AC:3:ASN:N	3:AC:3:ASN:OD1	2.23	0.71
25:BA:1370:G:O6	61:BA:4308:HOH:O	2.09	0.71
44:BY:54:LYS:HA	44:BY:56:PRO:HD3	1.72	0.71
25:BA:2340:A:H2'	25:BA:2341:G:C8	2.26	0.71
20:CT:50:GLU:HG3	20:CT:100:ILE:HD13	1.71	0.71
25:DA:2584:U:H2'	25:DA:2585:U:H2'	1.71	0.71
1:CA:1029:C:H42	1:CA:1032:G:H1	0.80	0.70
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:95:LYS:HA	9:CI:99:LEU:HD13	1.72	0.70
25:DA:1114:G:H2'	25:DA:1115:G:H8	1.56	0.70
25:DA:11:G:H2'	25:DA:12:U:H5''	1.73	0.70
25:DA:2849:U:O4	39:DT:23:ARG:NH2	2.24	0.70
1:AA:1086:U:H3	1:AA:1099:G:H22	1.38	0.70
25:BA:426:G:OP2	61:BA:5008:HOH:O	2.09	0.70
27:BD:69:ARG:NH2	27:BD:128:GLY:O	2.24	0.70
47:D1:59:THR:O	47:D1:91:LYS:NZ	2.23	0.70
32:DI:27:ARG:HD2	47:D1:71:TYR:CE1	2.26	0.70
1:AA:1183:A:H8	1:AA:1183:A:H5''	1.55	0.70
25:DA:89:G:H3'	25:DA:90:U:H5''	1.73	0.70
25:BA:2138:G:N2	25:BA:2184:G:OP1	2.24	0.70
25:BA:1740:U:O2'	27:BD:14:ARG:NH2	2.25	0.70
25:BA:1296:G:N7	35:BP:18:ARG:NH2	2.39	0.70
39:BT:95:ARG:HH11	39:BT:95:ARG:HG2	1.54	0.70
3:CC:164:ARG:NH1	3:CC:166:GLU:OE1	2.24	0.70
46:D0:11:ARG:O	46:D0:14:ARG:NH2	2.23	0.70
29:DF:185:ASP:HA	29:DF:188:ARG:HD3	1.72	0.70
43:DX:11:PRO:HB3	43:DX:92:LEU:HD11	1.73	0.70
55:D9:25:VAL:HB	55:D9:34:GLN:HB2	1.73	0.70
25:DA:2042:A:OP1	61:DA:4176:HOH:O	2.10	0.70
25:DA:71:A:H5''	25:DA:73:A:C8	2.26	0.70
26:DB:20:C:H42	26:DB:63:G:H1	1.39	0.70
25:DA:2748:A:H5'	31:DH:4:ILE:HD12	1.74	0.70
34:BO:35:VAL:HG11	34:BO:103:ALA:HB3	1.72	0.70
1:CA:201:C:H42	1:CA:216:G:H1	1.38	0.70
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.72	0.70
14:CN:9:LYS:HG3	14:CN:12:ARG:HH11	1.55	0.70
25:BA:2339:A:H2'	25:BA:2340:A:C8	2.26	0.70
35:BP:50:ARG:HD3	54:B8:7:HIS:CD2	2.26	0.70
1:CA:1000:U:H3	1:CA:1041:A:N6	1.90	0.70
25:BA:2802:C:O2	25:BA:2903:G:N2	2.21	0.70
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.25	0.70
25:DA:2682:U:OP2	61:DA:4144:HOH:O	2.10	0.70
25:DA:954:G:H5''	36:DQ:13:GLN:HB3	1.74	0.70
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.09	0.70
1:CA:1237:C:HO2'	1:CA:1300:G:H1	1.37	0.70
1:CA:346:G:OP1	39:DT:41:ARG:NH2	2.22	0.70
10:CJ:61:GLU:OE1	14:CN:58:LYS:NZ	2.24	0.70
25:BA:932:C:N3	25:BA:937:A:N6	2.40	0.70
43:BX:53:LYS:HB3	43:BX:82:GLN:HB3	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BZ:139:VAL:HG22	45:BZ:155:LEU:HD11	1.74	0.70
1:CA:1262:C:N4	1:CA:1273:G:H1	1.87	0.70
1:AA:46:G:O6	61:AA:4149:HOH:O	2.07	0.69
1:AA:596:C:OP2	61:AA:4065:HOH:O	2.10	0.69
25:BA:832:G:OP2	61:BA:4267:HOH:O	2.10	0.69
1:CA:673:G:H2'	1:CA:674:G:C8	2.28	0.69
12:AL:33:ARG:HD3	12:AL:62:SER:HB3	1.73	0.69
25:DA:123:G:N7	61:DA:4069:HOH:O	2.24	0.69
25:BA:1249:A:H2	25:BA:1287:A:H62	1.40	0.69
31:BH:98:LEU:HD13	31:BH:125:VAL:HG23	1.74	0.69
34:BO:63:VAL:HG12	34:BO:106:LEU:HD11	1.73	0.69
1:CA:1086:U:H3	1:CA:1099:G:H22	1.40	0.69
25:DA:2183:C:H2'	25:DA:2184:G:C8	2.27	0.69
25:DA:2198:A:OP1	32:DI:33:ARG:NH2	2.24	0.69
25:BA:2145:G:H1	25:BA:2197:C:H42	1.40	0.69
3:CC:58:GLU:HB2	3:CC:65:ALA:HB3	1.75	0.69
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.24	0.69
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.75	0.69
25:BA:1199:C:OP1	40:BU:92:ARG:NH1	2.24	0.69
25:BA:2695:C:O2	34:BO:70:LYS:NZ	2.20	0.69
43:BX:57:LEU:HD11	43:BX:78:LYS:HE2	1.74	0.69
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.75	0.69
25:DA:2504:U:OP2	61:DA:4445:HOH:O	2.09	0.69
1:AA:439:A:C4	1:AA:496:A:C5	2.76	0.69
25:BA:1170:C:OP1	61:BA:4957:HOH:O	2.09	0.69
25:BA:709:G:OP1	61:BA:4721:HOH:O	2.10	0.69
1:CA:1154:G:H2'	1:CA:1155:G:C8	2.27	0.69
1:AA:984:C:N4	1:AA:1221:G:H1	1.88	0.69
25:BA:1018:A:OP2	61:BA:4249:HOH:O	2.11	0.69
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.26	0.69
25:DA:731:C:OP1	61:DA:4606:HOH:O	2.10	0.69
34:DO:35:VAL:HG11	34:DO:103:ALA:HB3	1.74	0.69
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.73	0.69
25:BA:153:C:OP2	47:B1:92:LYS:NZ	2.26	0.69
35:BP:100:LEU:HD12	35:BP:112:LEU:HD11	1.73	0.69
1:CA:1132:C:H42	1:CA:1142:G:H1	1.38	0.69
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.73	0.69
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.26	0.68
25:DA:2206:G:H3'	25:DA:2207:G:N7	2.07	0.68
1:AA:532:A:O2'	1:AA:533:A:OP1	2.11	0.68
25:BA:96:C:OP1	48:B2:2:LYS:NZ	2.25	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1317:C:N3	19:CS:37:ARG:NH2	2.41	0.68
25:DA:2820:A:OP2	37:DR:2:ARG:NH2	2.26	0.68
9:AI:53:VAL:O	9:AI:55:ALA:N	2.25	0.68
25:BA:1067:A:H62	25:BA:1186:U:H3	1.41	0.68
25:BA:542:C:OP1	51:B5:16:ARG:NH2	2.26	0.68
2:CB:120:ALA:O	2:CB:122:PHE:N	2.26	0.68
9:CI:17:VAL:HG21	9:CI:81:ILE:HG22	1.74	0.68
1:AA:839:U:O2'	1:AA:840:C:OP1	2.09	0.68
8:AH:64:LYS:HG2	8:AH:79:VAL:HG21	1.75	0.68
54:D8:33:ASN:HA	54:D8:36:LYS:HD2	1.76	0.68
25:BA:2162:C:O2	25:BA:2173:G:N1	2.26	0.68
20:CT:60:GLU:HG3	20:CT:81:LYS:HD2	1.75	0.68
1:CA:1493:A:H2'	25:DA:1913:A:H61	1.59	0.68
25:DA:2121:G:H1	25:DA:2177:C:H42	1.41	0.68
25:BA:1218:G:O2'	25:BA:1219:A:O4'	2.10	0.68
1:CA:728:A:H2'	1:CA:729:A:C8	2.29	0.68
24:AY:76:A:N6	25:BA:2434:A:O4'	2.26	0.68
25:BA:2465:A:OP1	61:BA:4680:HOH:O	2.10	0.68
25:BA:303:C:H42	25:BA:385:G:H1	1.41	0.68
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.94	0.68
25:DA:2805:G:H2'	25:DA:2807:G:C8	2.28	0.68
25:BA:129:G:OP1	61:BA:4179:HOH:O	2.12	0.68
31:BH:86:GLU:OE2	31:BH:132:ARG:NH2	2.27	0.68
35:BP:86:LYS:HE3	35:BP:117:GLU:HB3	1.74	0.68
25:DA:2574:G:OP1	61:DA:4879:HOH:O	2.11	0.68
28:DE:36:ARG:HD3	28:DE:85:ASN:HD21	1.59	0.68
29:DF:184:TYR:CE2	29:DF:188:ARG:HD2	2.29	0.68
25:BA:1827:U:H2'	25:BA:1828:C:C6	2.28	0.68
1:CA:768:A:OP2	61:CA:4016:HOH:O	2.10	0.68
16:CP:9:PHE:CE1	16:CP:18:ARG:HD2	2.28	0.68
25:DA:2693:A:H2'	25:DA:2694:G:H8	1.57	0.68
28:DE:72:VAL:HA	28:DE:73:GLU:HB3	1.76	0.68
1:AA:1069:C:OP2	61:AA:4170:HOH:O	2.10	0.68
1:AA:517:G:N2	1:AA:533:A:OP2	2.25	0.68
1:CA:1007:C:O2	1:CA:1022:G:N1	2.22	0.68
20:CT:10:LEU:HD23	20:CT:12:ALA:HB2	1.75	0.68
31:DH:3:ARG:HH12	31:DH:5:GLY:N	1.91	0.68
2:AB:87:ARG:NH2	2:AB:220:ASP:OD1	2.24	0.67
1:CA:1502:A:H2	1:CA:1505:G:H1	1.42	0.67
25:DA:2138:C:N3	25:DA:2153:G:N2	2.38	0.67
1:AA:1030(A):G:O2'	1:AA:1030(C):G:N7	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:67:C:H2'	1:AA:68:G:C8	2.29	0.67
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.27	0.67
25:DA:1658:C:OP1	61:DA:4482:HOH:O	2.11	0.67
25:BA:388:A:H2'	25:BA:389:G:C8	2.28	0.67
40:BU:76:TYR:OH	40:BU:92:ARG:NH1	2.27	0.67
3:AC:11:ARG:HB3	3:AC:15:THR:HB	1.74	0.67
1:CA:521:G:H4'	12:CL:73:GLU:HG2	1.77	0.67
25:DA:2010:G:N7	61:DA:4368:HOH:O	2.26	0.67
1:AA:79:G:C2	1:AA:90:U:O2	2.48	0.67
35:BP:65:ARG:HG3	54:B8:25:MET:HG3	1.77	0.67
2:AB:212:GLN:NE2	2:AB:234:PRO:O	2.27	0.67
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.27	0.67
12:AL:70:ILE:HD13	12:AL:77:LEU:HD12	1.75	0.67
25:BA:2367:C:H1'	46:B0:39:ARG:HH21	1.59	0.67
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.27	0.67
1:AA:1172:C:H2'	1:AA:1173:G:H8	1.60	0.67
25:BA:1491:A:N7	61:BA:4087:HOH:O	2.26	0.67
5:CE:148:VAL:HG21	8:CH:107:LEU:HD13	1.75	0.67
25:DA:987:G:O2'	25:DA:1000:A:N3	2.25	0.67
25:DA:1114:G:H2'	25:DA:1115:G:C8	2.29	0.67
39:DT:59:THR:HG23	39:DT:78:LEU:HB3	1.77	0.67
25:BA:206:G:OP2	61:BA:5041:HOH:O	2.13	0.67
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.59	0.67
25:DA:2206:G:H3'	25:DA:2207:G:C8	2.29	0.67
25:DA:880:G:H22	25:DA:898:C:H1'	1.59	0.67
30:DG:11:TYR:HB2	30:DG:176:LEU:HD21	1.76	0.67
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.22	0.67
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.77	0.67
25:DA:320:A:OP2	29:DF:137:LYS:NZ	2.25	0.67
4:AD:122:ARG:NH2	4:AD:134:ASP:OD1	2.28	0.67
9:AI:9:ARG:HG2	9:AI:14:VAL:HG13	1.77	0.67
26:BB:106:G:H5'	45:BZ:31:ARG:HG2	1.77	0.67
25:DA:956:G:H5''	36:DQ:77:LYS:HD2	1.77	0.67
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.74	0.66
6:AF:69:GLU:O	6:AF:72:VAL:HG12	1.95	0.66
1:CA:1005:A:O2'	1:CA:1037:C:O2'	2.12	0.66
25:DA:2062:A:OP1	61:DA:4140:HOH:O	2.11	0.66
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.10	0.66
25:BA:1431:G:O2'	25:BA:1442:U:O2	2.09	0.66
35:BP:88:LEU:HD11	35:BP:114:ILE:HD12	1.76	0.66
1:CA:532:A:O2'	1:CA:533:A:OP1	2.12	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:974:A:OP2	14:CN:29:ARG:NH2	2.28	0.66
9:CI:17:VAL:HG23	9:CI:63:ILE:HG12	1.77	0.66
25:DA:2176:A:H2'	25:DA:2177:C:C6	2.31	0.66
25:DA:2323:G:O6	25:DA:2332:U:N3	2.18	0.66
26:DB:106:G:H5'	45:DZ:31:ARG:HG2	1.76	0.66
1:AA:991:U:O2'	1:AA:992:U:OP2	2.13	0.66
11:AK:48:ILE:HG21	11:AK:63:LEU:HB3	1.78	0.66
29:BF:53:THR:HG22	29:BF:55:GLY:H	1.60	0.66
1:CA:35:G:O2'	12:CL:118:SER:O	2.07	0.66
25:DA:2126:A:H62	25:DA:2172:U:H5'	1.61	0.66
25:DA:574:C:OP1	61:DA:4132:HOH:O	2.12	0.66
25:DA:2748:A:O2'	31:DH:63:SER:O	2.10	0.66
36:DQ:85:LYS:HG2	46:D0:7:LEU:HB3	1.76	0.66
7:AG:9:VAL:O	7:AG:11:GLN:NE2	2.28	0.66
1:CA:782:A:OP1	61:CA:4023:HOH:O	2.12	0.66
1:CA:794:A:OP2	61:CA:4023:HOH:O	2.14	0.66
25:DA:1189:A:OP2	61:DA:4459:HOH:O	2.14	0.66
25:DA:2162:G:H4'	25:DA:2172:U:H2'	1.75	0.66
25:DA:1693:U:O2'	27:DD:14:ARG:NH2	2.28	0.66
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.29	0.66
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.29	0.66
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.28	0.66
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.28	0.66
46:B0:27:GLU:HG3	46:B0:68:GLU:HA	1.77	0.66
25:DA:1648:C:OP1	61:DA:4489:HOH:O	2.14	0.66
26:DB:84:C:OP1	49:D3:15:TYR:OH	2.12	0.66
1:AA:1027:C:C4	1:AA:1034:G:O6	2.49	0.66
28:BE:47:VAL:HG21	28:BE:86:PRO:HD2	1.78	0.66
38:BS:39:ILE:HB	38:BS:49:VAL:HG13	1.78	0.66
1:CA:316:G:OP2	1:CA:351:G:O2'	2.13	0.66
25:DA:2113:U:H3	25:DA:2170:A:H61	1.43	0.66
38:DS:49:VAL:HG23	38:DS:80:LEU:HD22	1.77	0.66
25:DA:1371:G:H2'	25:DA:1372:U:H5	1.60	0.66
28:DE:73:GLU:HG3	28:DE:73:GLU:O	1.95	0.66
34:DO:115:VAL:HG13	34:DO:121:VAL:HG21	1.76	0.66
30:BG:56:ALA:HA	30:BG:153:ARG:HH21	1.61	0.66
1:CA:1347:G:H5''	9:CI:107:ARG:HB3	1.78	0.66
48:D2:22:GLU:OE2	48:D2:68:ARG:NH2	2.29	0.66
43:DX:8:ILE:O	48:D2:36:ARG:NH2	2.28	0.66
45:DZ:72:ARG:NH2	45:DZ:97:GLU:O	2.25	0.66
2:CB:221:LEU:HD23	2:CB:224:GLN:HE22	1.59	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:162:LEU:HD13	4:CD:181:MET:HG2	1.79	0.65
25:DA:2296:U:OP2	38:DS:9:ARG:NH2	2.28	0.65
39:DT:65:LYS:HE2	39:DT:67:SER:HB2	1.77	0.65
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.09	0.65
1:CA:815:A:N7	1:CA:1509:C:O2'	2.27	0.65
1:AA:1003:G:N2	1:AA:1004:A:N3	2.44	0.65
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.29	0.65
25:DA:1418:G:OP2	61:DA:4396:HOH:O	2.13	0.65
3:AC:39:ILE:HG23	3:AC:91:LEU:HD11	1.78	0.65
25:BA:118:U:OP2	61:BA:4118:HOH:O	2.14	0.65
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.96	0.65
2:CB:201:ILE:HG21	2:CB:214:ILE:HG21	1.79	0.65
25:DA:2127:G:O6	25:DA:2161:C:N3	2.28	0.65
2:AB:87:ARG:CZ	2:AB:233:SER:HB3	2.27	0.65
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.77	0.65
25:BA:2122:G:H1	25:BA:2211:U:H3	0.73	0.65
25:DA:2638:G:OP2	28:DE:82:ARG:NH2	2.26	0.65
1:AA:1530:G:H2'	1:AA:1531:A:O4'	1.97	0.65
29:BF:51:THR:HB	29:BF:88:VAL:HG11	1.77	0.65
1:CA:1320:C:H5"	19:CS:70:LYS:HG3	1.78	0.65
2:AB:126:GLU:HG2	2:AB:127:ILE:HG12	1.78	0.65
16:AP:74:LEU:HG	16:AP:79:VAL:HG21	1.78	0.65
38:BS:15:ARG:O	38:BS:19:LYS:HG2	1.97	0.65
43:BX:35:THR:HG22	43:BX:38:GLU:H	1.61	0.65
41:DV:35:LEU:HB2	41:DV:57:VAL:HG23	1.79	0.65
25:BA:2495:C:N3	36:BQ:124:LYS:NZ	2.44	0.65
32:BI:3:VAL:HG12	32:BI:38:LEU:HA	1.79	0.65
25:BA:872:C:O2	35:BP:55:ARG:NH2	2.25	0.65
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.11	0.65
1:CA:142:G:H2'	1:CA:143:A:C8	2.31	0.65
29:DF:103:LYS:HA	29:DF:106:ARG:HG3	1.78	0.65
25:BA:1299:A:OP1	61:BA:4949:HOH:O	2.14	0.65
6:CF:81:ILE:HD11	27:DD:125:ILE:HB	1.77	0.65
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.77	0.65
25:DA:1237:A:OP1	61:DA:4740:HOH:O	2.14	0.65
35:DP:95:VAL:HA	35:DP:99:LEU:HD21	1.77	0.65
25:DA:770:G:OP2	61:DA:4536:HOH:O	2.13	0.65
31:DH:9:ILE:HB	31:DH:50:VAL:HB	1.78	0.65
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.27	0.64
57:AA:3191:PCY:H162	57:AA:3191:PCY:H25	1.62	0.64
25:BA:1815:A:OP2	61:BA:4761:HOH:O	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2122:G:O6	25:BA:2211:U:O4	2.15	0.64
50:B4:15:ILE:HG23	50:B4:21:VAL:HG22	1.79	0.64
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.79	0.64
39:DT:95:ARG:HG2	39:DT:95:ARG:HH11	1.60	0.64
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.32	0.64
2:CB:212:GLN:NE2	2:CB:234:PRO:O	2.30	0.64
5:CE:10:MET:N	5:CE:10:MET:SD	2.71	0.64
25:DA:2163:C:OP1	25:DA:2165:G:N2	2.30	0.64
45:DZ:153:SER:HB3	45:DZ:167:PRO:HB3	1.80	0.64
1:AA:1352:C:OP1	21:AU:3:LYS:NZ	2.24	0.64
4:AD:166:LYS:HA	4:AD:178:VAL:HG21	1.79	0.64
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HD23	1.80	0.64
37:BR:104:ARG:HG3	37:BR:111:LEU:HD21	1.78	0.64
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.79	0.64
25:DA:994:C:O2'	25:DA:996:A:OP1	2.10	0.64
1:AA:79:G:C2	1:AA:90:U:C2	2.85	0.64
25:BA:2239:A:N7	61:BA:4799:HOH:O	2.29	0.64
25:BA:2658:C:OP2	25:BA:2745:G:O2'	2.12	0.64
41:BV:95:LEU:HD13	41:BV:97:LYS:HD3	1.79	0.64
29:DF:29:ASN:H	29:DF:112:MET:HE1	1.63	0.64
25:BA:139:A:H8	25:BA:1454:C:HO2'	1.45	0.64
25:BA:30:G:OP2	40:BU:5:LYS:NZ	2.30	0.64
1:CA:1023:G:H3'	1:CA:1024:G:H8	1.63	0.64
26:DB:76:G:N2	26:DB:101:G:O6	2.28	0.64
39:DT:16:ARG:NH2	39:DT:83:ILE:O	2.30	0.64
41:DV:40:LEU:HB2	41:DV:46:VAL:HG13	1.80	0.64
1:AA:1158:C:C4	1:AA:1160:G:C8	2.85	0.64
1:AA:310:G:OP2	16:AP:27:LYS:NZ	2.24	0.64
4:AD:187:ARG:NH1	4:AD:190:ASP:OD1	2.31	0.64
25:BA:610:C:OP2	35:BP:21:ARG:NH2	2.30	0.64
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.28	0.64
25:DA:2125:G:H22	25:DA:2172:U:H5'	1.62	0.64
25:DA:1278:A:OP1	37:DR:36:THR:HG23	1.97	0.64
39:DT:50:ILE:HA	39:DT:99:LEU:HD12	1.79	0.64
4:AD:98:GLU:HG2	4:AD:189:PRO:HG2	1.78	0.64
25:BA:2442:A:N3	25:BA:2442:A:H2'	2.12	0.64
30:BG:41:GLN:HE22	30:BG:153:ARG:HB3	1.63	0.64
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.33	0.64
25:DA:997:G:OP1	40:DU:92:ARG:HG2	1.98	0.64
25:DA:1814:G:O3'	27:DD:54:ARG:NH2	2.31	0.64
28:DE:59:VAL:HG21	28:DE:74:PRO:HB3	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:52:SER:OG	45:DZ:53:ILE:N	2.31	0.64
25:BA:1201:A:OP1	40:BU:55:ARG:HD3	1.98	0.64
26:DB:10:C:O2	26:DB:111:G:N2	2.19	0.64
27:DD:3:VAL:HG21	27:DD:203:ASN:HB2	1.80	0.64
1:CA:578:C:OP1	61:CA:4043:HOH:O	2.14	0.64
25:DA:2122:U:O4	25:DA:2176:A:N1	2.31	0.64
31:DH:59:ARG:O	31:DH:63:SER:OG	2.16	0.64
25:BA:1221:G:H1'	25:BA:1222:A:H5'	1.79	0.63
2:CB:19:HIS:HB2	2:CB:204:ASN:HB2	1.79	0.63
24:CY:76:A:O5'	61:DA:4895:HOH:O	2.14	0.63
25:BA:2113:U:O4	61:BA:4797:HOH:O	2.14	0.63
25:BA:2130:C:H42	25:BA:2203:G:H1	1.44	0.63
1:CA:532:A:H61	3:CC:193:TYR:HB3	1.62	0.63
2:CB:80:ILE:HD13	2:CB:211:ILE:HB	1.80	0.63
25:DA:2364:C:OP1	46:D0:55:ARG:NH1	2.31	0.63
14:CN:3:ARG:HB3	14:CN:3:ARG:HH21	1.63	0.63
25:DA:143:G:H4'	43:DX:35:THR:HG21	1.80	0.63
1:AA:1004:A:N6	1:AA:1036:G:N7	2.46	0.63
13:CM:96:LEU:O	13:CM:110:ARG:NH1	2.31	0.63
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.28	0.63
13:AM:65:LYS:NZ	50:B4:53:GLU:OE1	2.25	0.63
25:DA:2287:A:H62	25:DA:2344:U:H3	1.46	0.63
25:BA:611:U:H2'	25:BA:612:C:C6	2.34	0.63
20:CT:43:LEU:O	20:CT:47:GLY:N	2.25	0.63
25:BA:902:G:O2'	46:B0:27:GLU:OE2	2.13	0.63
25:BA:1890:A:N6	25:BA:1905:G:O2'	2.32	0.63
25:DA:1889:A:H2'	25:DA:1890:A:C8	2.34	0.63
2:AB:95:GLN:HG3	2:AB:147:LYS:HD3	1.81	0.63
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.34	0.63
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.26	0.63
1:CA:444:C:H2'	1:CA:445:G:H8	1.62	0.63
1:CA:839:U:O2'	1:CA:840:C:OP1	2.16	0.63
28:DE:47:VAL:HG11	28:DE:86:PRO:HD2	1.80	0.63
32:DI:12:LEU:HD22	32:DI:19:VAL:HG21	1.81	0.63
37:DR:36:THR:HG22	37:DR:37:THR:H	1.63	0.63
2:AB:17:PHE:HD2	2:AB:44:LEU:HD21	1.64	0.63
22:AV:16:A:N6	23:AX:36:U:H3	1.96	0.63
25:BA:630:U:OP1	29:BF:102:PRO:HA	1.98	0.63
32:BI:92:VAL:HG11	32:BI:144:VAL:HG11	1.81	0.63
42:BW:4:LYS:HD3	42:BW:6:ILE:HD11	1.80	0.63
42:BW:14:PRO:HG2	42:BW:78:GLU:HG2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BZ:11:GLU:O	45:BZ:36:LYS:NZ	2.20	0.63
1:CA:142:G:H2'	1:CA:143:A:H8	1.63	0.63
38:BS:27:SER:HA	38:BS:88:ASP:HB3	1.80	0.62
1:CA:1279:A:O2'	1:CA:1282:C:N4	2.32	0.62
4:CD:61:LYS:NZ	4:CD:72:GLU:OE2	2.22	0.62
26:DB:45:A:O4'	30:DG:95:ARG:NH1	2.32	0.62
36:DQ:109:VAL:HG13	36:DQ:113:GLN:HB3	1.80	0.62
25:BA:2162:C:N3	25:BA:2173:G:O6	2.32	0.62
25:BA:591:U:O2'	61:BA:5137:HOH:O	2.15	0.62
36:BQ:54:MET:HG3	36:BQ:117:ALA:HB1	1.79	0.62
45:BZ:136:PHE:O	45:BZ:137:ILE:HG13	1.99	0.62
25:DA:1266:G:O5'	42:DW:15:ARG:NH2	2.32	0.62
40:BU:81:HIS:CE1	40:BU:85:LYS:HD2	2.33	0.62
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.32	0.62
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.63	0.62
28:DE:72:VAL:HG13	28:DE:73:GLU:O	1.98	0.62
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.80	0.62
25:BA:2297:C:OP2	52:B6:6:ARG:NH1	2.33	0.62
45:BZ:117:LEU:HD11	45:BZ:144:LEU:HD23	1.81	0.62
45:BZ:52:SER:OG	45:BZ:53:ILE:N	2.32	0.62
1:CA:1023:G:H3'	1:CA:1024:G:C8	2.35	0.62
1:CA:1029:C:N4	1:CA:1032:G:N1	2.33	0.62
1:CA:1127:G:H5'	1:CA:1280:A:O2'	2.00	0.62
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.32	0.62
12:CL:70:ILE:HG12	12:CL:100:ILE:HD12	1.79	0.62
25:DA:2070:G:OP2	61:DA:4726:HOH:O	2.16	0.62
25:DA:322:A:OP2	29:DF:169:ASN:HB2	1.98	0.62
35:DP:86:LYS:HB3	35:DP:118:GLY:HA3	1.81	0.62
1:AA:1145:C:H4'	1:AA:1146:A:H5'	1.80	0.62
1:AA:1521:G:N3	61:AA:4051:HOH:O	2.31	0.62
25:BA:1185:C:O3'	33:BN:25:ARG:NH1	2.32	0.62
32:BI:93:THR:HG22	32:BI:119:PRO:HB3	1.82	0.62
39:BT:53:ARG:NH1	39:BT:53:ARG:HB3	2.14	0.62
1:CA:998:G:N2	1:CA:1043:C:N3	2.43	0.62
1:CA:1157:A:H4'	1:CA:1158:C:O5'	1.99	0.62
1:CA:1321:C:H5''	1:CA:1322:C:H2'	1.80	0.62
2:CB:128:GLU:OE1	2:CB:135:GLN:NE2	2.33	0.62
1:CA:1179:A:H4'	9:CI:103:THR:HA	1.81	0.62
30:DG:41:GLN:HE22	30:DG:153:ARG:HB3	1.64	0.62
41:DV:5:VAL:HG11	41:DV:57:VAL:HG21	1.81	0.62
1:AA:221:C:H2'	1:AA:222:U:H6	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:5:LYS:HE2	15:AO:5:LYS:H	1.63	0.62
25:BA:2579:G:H2'	25:BA:2580:C:C6	2.34	0.62
25:BA:602:G:H2'	25:BA:603:C:C6	2.34	0.62
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.18	0.62
26:DB:14:U:OP2	26:DB:70:C:O2'	2.15	0.62
1:AA:277:C:H5''	17:AQ:68:ARG:NH2	2.14	0.62
25:BA:1093:G:H2'	25:BA:1156:G:H1	1.65	0.62
30:BG:41:GLN:NE2	30:BG:154:GLY:O	2.33	0.62
1:CA:1392:G:H21	1:CA:1502:A:H8	1.48	0.62
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.82	0.62
30:DG:108:ASN:HD22	50:D4:22:ILE:HG12	1.64	0.62
25:DA:1557:C:OP2	25:DA:1558:A:O2'	2.17	0.62
25:DA:1653:G:H3'	37:DR:2:ARG:HD3	1.81	0.62
25:DA:2483:C:N3	36:DQ:124:LYS:NZ	2.47	0.62
29:DF:157:VAL:HB	29:DF:194:MET:HG2	1.81	0.62
40:DU:76:TYR:OH	40:DU:92:ARG:NH1	2.32	0.62
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.32	0.62
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.16	0.62
52:B6:6:ARG:NH1	52:B6:26:ASN:HB2	2.15	0.62
25:BA:2369:U:OP1	46:B0:20:ARG:NH1	2.32	0.62
34:BO:2:ILE:HD12	34:BO:6:THR:HG21	1.79	0.62
1:AA:79:G:C6	1:AA:90:U:N3	2.68	0.62
25:BA:2374:G:OP1	54:B8:44:LYS:NZ	2.28	0.62
25:BA:271:U:O2'	25:BA:273:G:N2	2.32	0.62
25:DA:1300:U:H4'	25:DA:1301:A:H5''	1.82	0.62
25:DA:2273:A:H2'	25:DA:2274:A:C8	2.35	0.62
1:AA:1314:C:OP1	19:AS:6:LYS:NZ	2.24	0.62
25:BA:1714:G:O2'	25:BA:2013:U:O4	2.14	0.62
1:CA:1003:G:H2'	1:CA:1004:A:O4'	2.00	0.62
1:CA:977:A:O2'	1:CA:981:U:N3	2.32	0.62
8:CH:4:ASP:OD2	8:CH:85:ARG:NH1	2.32	0.62
49:D3:8:LEU:HD13	49:D3:31:LEU:HD23	1.82	0.62
25:DA:2356:C:OP1	46:D0:24:LYS:NZ	2.28	0.62
32:DI:114:LEU:HD11	32:DI:128:LEU:HD13	1.82	0.62
1:AA:1158:C:N4	1:AA:1160:G:H8	1.97	0.61
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.33	0.61
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.33	0.61
49:B3:3:ARG:NH1	49:B3:60:GLU:OE2	2.33	0.61
25:BA:2145:G:H2'	25:BA:2146:G:H8	1.65	0.61
25:BA:354:A:H2	25:BA:1255:A:HO2'	1.47	0.61
31:BH:149:ARG:NH1	31:BH:167:GLU:OE2	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.31	0.61
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.15	0.61
25:DA:848:G:H2'	25:DA:849:A:C8	2.35	0.61
1:AA:79:G:N1	1:AA:90:U:C2	2.69	0.61
9:AI:3:GLN:HG2	9:AI:20:ARG:HE	1.65	0.61
2:CB:48:MET:HA	2:CB:51:LEU:HD12	1.82	0.61
9:CI:16:ARG:HB2	9:CI:64:THR:HB	1.82	0.61
25:DA:1033:U:OP1	55:D9:9:ARG:NH2	2.33	0.61
44:DY:23:ARG:HG2	44:DY:42:VAL:HG22	1.81	0.61
1:AA:1174:G:H2'	1:AA:1175:G:H8	1.63	0.61
25:BA:1211:U:H2'	25:BA:1212:C:C6	2.35	0.61
25:BA:671:A:H2'	25:BA:672:G:O4'	2.01	0.61
25:BA:83:A:H5''	44:BY:8:LYS:HE3	1.82	0.61
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.36	0.61
25:DA:2166:G:N7	25:DA:2168:G:N2	2.45	0.61
25:DA:2314:C:H2'	25:DA:2315:G:C8	2.36	0.61
1:AA:1226:C:O2'	13:AM:111:LYS:NZ	2.32	0.61
11:AK:48:ILE:H	11:AK:48:ILE:HD13	1.65	0.61
25:BA:2754:A:OP1	55:B9:22:ARG:NH2	2.21	0.61
3:CC:13:GLY:HA3	14:CN:57:ARG:HH21	1.63	0.61
25:DA:2167:U:O2'	25:DA:2168:G:N3	2.34	0.61
37:DR:21:TYR:CZ	37:DR:43:GLU:HG2	2.35	0.61
1:AA:1203:C:H2'	1:AA:1204:A:H8	1.65	0.61
1:AA:439:A:C2	1:AA:496:A:C4	2.86	0.61
50:B4:48:ARG:NH1	50:B4:48:ARG:HA	2.16	0.61
1:CA:1166:G:N2	1:CA:1170:A:OP2	2.33	0.61
2:CB:125:PRO:O	2:CB:127:ILE:N	2.33	0.61
13:CM:54:VAL:HA	13:CM:57:ARG:HB3	1.82	0.61
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.81	0.61
25:DA:1762:A:N1	61:DA:4564:HOH:O	2.30	0.61
25:DA:2074:U:H2'	25:DA:2075:U:C6	2.35	0.61
25:DA:2114:A:N1	25:DA:2117:A:N6	2.49	0.61
1:AA:946:A:H2'	1:AA:947:G:C8	2.35	0.61
3:AC:62:ASP:HA	3:AC:97:LYS:HD3	1.81	0.61
25:BA:1040:C:OP1	40:BU:53:ARG:NH2	2.34	0.61
25:BA:2348:A:H61	46:B0:43:THR:CG2	2.13	0.61
25:DA:2147:G:C2	25:DA:2148:G:H1'	2.36	0.61
25:DA:2753:A:N3	55:D9:15:LYS:NZ	2.46	0.61
13:CM:13:LYS:NZ	13:CM:21:TYR:OH	2.34	0.61
25:DA:2646:C:OP2	25:DA:2732:G:O2'	2.18	0.61
25:BA:929:G:H22	25:BA:940:C:H42	1.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1051:C:H2'	1:CA:1052:U:C6	2.36	0.61
1:CA:56:U:H2'	1:CA:57:G:C8	2.36	0.61
25:DA:1231:G:H2'	25:DA:1232:G:H8	1.65	0.61
25:DA:1778:U:H2'	25:DA:1784:A:N6	2.15	0.61
27:DD:108:PRO:HB3	27:DD:143:HIS:CE1	2.35	0.61
42:DW:71:VAL:HA	42:DW:107:LEU:HD12	1.83	0.61
8:AH:112:LEU:HB3	8:AH:133:LEU:HA	1.81	0.61
25:BA:1076:G:OP2	36:BQ:128:LYS:NZ	2.33	0.61
25:BA:2255:U:H2'	25:BA:2256:U:C6	2.36	0.61
25:BA:965:G:N2	25:BA:2281:A:OP2	2.34	0.61
25:BA:934:A:O2'	25:BA:935:C:OP2	2.18	0.61
27:BD:132:PRO:HD3	27:BD:190:TYR:CZ	2.35	0.61
29:BF:20:LEU:HD22	29:BF:21:ALA:H	1.66	0.61
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.20	0.61
13:CM:33:ALA:O	13:CM:37:THR:OG1	2.15	0.61
31:DH:144:VAL:O	31:DH:148:ILE:HG12	2.00	0.61
25:BA:646:A:OP2	35:BP:108:LYS:NZ	2.33	0.61
13:CM:47:ASP:N	13:CM:47:ASP:OD2	2.34	0.61
25:DA:2661:G:H2'	25:DA:2662:A:C8	2.36	0.61
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.33	0.60
47:B1:50:ARG:HG2	47:B1:59:THR:HB	1.83	0.60
25:BA:1312:G:O5'	42:BW:15:ARG:NH2	2.34	0.60
25:BA:397:G:H5"	25:BA:450:A:N6	2.16	0.60
25:BA:70:A:N7	43:BX:31:HIS:HE1	1.99	0.60
1:CA:1235:U:O2'	1:CA:1305:G:OP1	2.16	0.60
11:CK:82:VAL:HB	11:CK:108:ILE:HG12	1.83	0.60
25:DA:1371:G:H2'	25:DA:1372:U:C5	2.36	0.60
27:DD:108:PRO:HG2	27:DD:111:LEU:HG	1.83	0.60
45:DZ:45:ASP:OD1	45:DZ:49:ARG:NH1	2.34	0.60
1:AA:1161:C:N3	1:AA:1175:G:N2	2.36	0.60
2:AB:163:PHE:HA	2:AB:185:ILE:HG13	1.83	0.60
45:BZ:145:GLU:O	45:BZ:148:ASP:N	2.26	0.60
3:CC:52:LEU:HD21	3:CC:55:VAL:HG23	1.82	0.60
29:DF:101:LEU:O	29:DF:106:ARG:NH1	2.30	0.60
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.34	0.60
25:BA:1338:U:H2'	25:BA:1339:C:C6	2.37	0.60
1:CA:1381:U:H1'	7:CG:79:ARG:HD3	1.83	0.60
25:DA:1292:U:H2'	25:DA:1293:C:C6	2.36	0.60
25:DA:479:A:N3	25:DA:481:G:H5"	2.15	0.60
25:DA:588:U:H2'	25:DA:589:C:C6	2.35	0.60
25:DA:958:U:OP2	36:DQ:14:ARG:NH1	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:108:PRO:HG2	45:DZ:117:LEU:HD13	1.83	0.60
1:AA:1002:G:H3'	1:AA:1003:G:C8	2.36	0.60
5:CE:20:GLN:NE2	5:CE:21:ALA:O	2.35	0.60
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.31	0.60
7:CG:18:TYR:HB3	7:CG:59:LEU:HD13	1.83	0.60
7:CG:50:ILE:HD11	7:CG:58:PRO:HA	1.82	0.60
8:CH:34:GLU:OE1	8:CH:37:ARG:NH1	2.35	0.60
25:DA:2061:G:H5''	25:DA:2503:A:C2	2.36	0.60
25:DA:2125:G:N1	25:DA:2172:U:O5'	2.35	0.60
1:AA:954:G:H21	1:AA:1227:A:H62	1.49	0.60
25:BA:1405:A:H2'	25:BA:1406:A:H5'	1.83	0.60
25:BA:1846:A:N1	61:BA:4015:HOH:O	2.30	0.60
1:AA:1020:U:H2'	1:AA:1021:G:H8	1.65	0.60
1:AA:1502:A:H2	1:AA:1505:G:N1	1.96	0.60
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.83	0.60
25:BA:997:G:OP1	36:BQ:16:ARG:NH2	2.35	0.60
31:BH:56:SER:OG	31:BH:57:ASP:N	2.35	0.60
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.35	0.60
1:AA:1052:U:H2'	1:AA:1055:A:OP2	2.01	0.60
1:AA:97:G:O2'	1:AA:98:G:H5''	2.01	0.60
23:AX:8:4SU:H6	23:AX:8:4SU:O5'	2.01	0.60
25:BA:1899:A:H5'	25:BA:1900:G:OP2	2.02	0.60
30:BG:77:ILE:HG22	30:BG:80:PHE:H	1.65	0.60
31:BH:159:GLU:HG3	31:BH:169:VAL:HG11	1.84	0.60
32:BI:130:TYR:HB3	32:BI:138:ILE:HB	1.84	0.60
1:CA:977:A:HO2'	1:CA:981:U:H3	1.49	0.60
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	1.83	0.60
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.34	0.60
25:DA:2109:U:H4'	25:DA:2149:G:H21	1.67	0.60
31:DH:38:SER:HB3	31:DH:41:MET:HG2	1.84	0.60
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.37	0.60
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.37	0.60
5:AE:57:LYS:HD3	5:AE:61:TYR:HE2	1.66	0.60
29:BF:157:VAL:HB	29:BF:194:MET:HG2	1.84	0.60
45:BZ:80:ARG:HB3	45:BZ:82:ARG:HG3	1.84	0.60
1:CA:757:U:H2'	1:CA:758:G:O4'	2.02	0.60
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.84	0.60
25:DA:153:C:OP2	47:D1:92:LYS:NZ	2.34	0.60
25:DA:807:U:OP2	35:DP:41:ARG:NH2	2.35	0.60
25:DA:2723:C:OP2	28:DE:109:LYS:NZ	2.35	0.60
25:DA:1041:C:OP1	45:DZ:46:LYS:NZ	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.83	0.60
18:AR:26:LEU:HD21	18:AR:39:VAL:HG13	1.83	0.60
25:BA:1410:G:OP2	47:B1:3:LYS:HG3	2.02	0.60
27:BD:12:SER:HB3	27:BD:208:LYS:HB3	1.84	0.60
26:BB:103:G:O2'	45:BZ:73:GLN:NE2	2.35	0.60
1:CA:677:U:H3	1:CA:713:G:H22	1.50	0.60
3:CC:130:VAL:O	3:CC:134:ILE:HG12	2.02	0.60
25:DA:1028:A:N6	25:DA:1125:G:H2'	2.16	0.60
30:DG:41:GLN:NE2	30:DG:154:GLY:O	2.35	0.60
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.01	0.59
32:BI:103:ARG:HG2	32:BI:104:GLN:N	2.17	0.59
45:BZ:58:VAL:HG12	45:BZ:68:PRO:HA	1.82	0.59
1:CA:123:C:OP1	1:CA:311:C:O2'	2.17	0.59
1:CA:693:G:O6	57:CA:3176:PCY:N16	2.34	0.59
1:CA:396:G:O2'	1:CA:398:C:OP1	2.16	0.59
25:DA:2630:G:H2'	25:DA:2631:G:C8	2.37	0.59
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.85	0.59
1:CA:627:G:H2'	1:CA:628:G:H8	1.66	0.59
25:DA:307:G:N1	25:DA:310:A:OP2	2.35	0.59
25:DA:792:G:OP2	61:DA:4161:HOH:O	2.16	0.59
36:DQ:32:TYR:OH	36:DQ:111:GLU:OE1	2.19	0.59
25:BA:173:C:H2'	25:BA:174:U:C6	2.37	0.59
1:CA:694:A:H62	57:CA:3176:PCY:H93	1.67	0.59
1:CA:692:U:O2'	1:CA:694:A:N7	2.33	0.59
2:CB:61:LEU:HD23	2:CB:68:ILE:HD11	1.83	0.59
25:DA:125:G:H5''	53:D7:19:ARG:HD3	1.83	0.59
25:DA:2134:A:H62	25:DA:2157:G:H4'	1.67	0.59
25:DA:2291:U:H2'	25:DA:2292:C:C6	2.37	0.59
25:DA:2648:C:H2'	25:DA:2649:U:C6	2.38	0.59
28:DE:111:ARG:HG3	28:DE:160:TYR:CD2	2.36	0.59
1:AA:629:G:H2'	1:AA:630:G:O4'	2.03	0.59
7:AG:62:PHE:HA	7:AG:124:LEU:HD22	1.84	0.59
10:AJ:27:ALA:HA	10:AJ:81:THR:HG21	1.85	0.59
19:AS:67:VAL:HB	50:B4:58:ARG:HB3	1.83	0.59
25:BA:1793:A:H2'	61:BA:5153:HOH:O	2.03	0.59
42:BW:69:LEU:HD13	42:BW:107:LEU:HD23	1.84	0.59
1:CA:448:A:P	1:CA:485:G:H22	2.26	0.59
1:CA:67:C:H2'	1:CA:68:G:C8	2.37	0.59
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.83	0.59
10:CJ:55:LYS:O	10:CJ:57:LYS:N	2.34	0.59
25:DA:1991:U:H2'	25:DA:1992:G:H5''	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DD:242:ARG:N	27:DD:242:ARG:HD3	2.17	0.59
42:DW:34:ASN:OD1	42:DW:37:ARG:NH2	2.35	0.59
1:AA:411:A:OP1	4:AD:30:LYS:NZ	2.35	0.59
19:AS:9:VAL:HG21	50:B4:61:ARG:HH12	1.67	0.59
25:BA:1221:G:H1'	25:BA:1222:A:C5'	2.32	0.59
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.66	0.59
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.37	0.59
2:CB:71:VAL:HA	2:CB:93:VAL:HG23	1.85	0.59
23:CX:8:4SU:O5'	23:CX:8:4SU:H6	2.02	0.59
25:DA:2127:G:N1	25:DA:2161:C:O2	2.28	0.59
43:DX:4:ALA:HB1	43:DX:42:ALA:HA	1.85	0.59
45:DZ:80:ARG:HB3	45:DZ:82:ARG:HG3	1.85	0.59
7:AG:113:GLU:HG2	7:AG:119:ARG:HG2	1.84	0.59
1:AA:1347:G:H5''	9:AI:107:ARG:HB3	1.84	0.59
10:AJ:30:SER:OG	10:AJ:84:GLN:NE2	2.36	0.59
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.84	0.59
25:BA:53:G:O2'	53:B7:35:ARG:HD3	2.03	0.59
25:BA:1219:A:H4'	25:BA:1220:U:OP1	2.01	0.59
25:BA:1700:G:H3'	37:BR:2:ARG:HD3	1.83	0.59
6:CF:30:LEU:O	6:CF:35:ALA:HB3	2.03	0.59
25:DA:1803:A:O2'	27:DD:259:THR:HG21	2.02	0.59
26:DB:5:C:H42	26:DB:116:G:H1	1.50	0.59
26:DB:90:A:C5	26:DB:91:C:H1'	2.37	0.59
29:DF:110:LEU:HD21	29:DF:181:LEU:HG	1.84	0.59
1:AA:1414:U:H3	1:AA:1486:G:H1	1.50	0.59
20:AT:60:GLU:HG3	20:AT:81:LYS:HD2	1.83	0.59
25:BA:1613:A:OP1	27:BD:211:ARG:NH1	2.36	0.59
19:CS:53:ASN:HB2	19:CS:77:THR:HA	1.84	0.59
25:DA:2357:U:OP1	46:D0:20:ARG:NH1	2.36	0.59
25:DA:1600:C:OP1	43:DX:58:HIS:NE2	2.26	0.59
25:DA:2532:G:O2'	25:DA:2657:A:N1	2.35	0.59
25:DA:796:C:H2'	25:DA:797:C:C6	2.38	0.59
45:DZ:69:THR:HG22	45:DZ:90:VAL:HA	1.84	0.59
1:AA:1320:C:H5''	19:AS:70:LYS:HG3	1.84	0.59
25:BA:2163:G:C6	25:BA:2172:U:O2	2.56	0.59
25:BA:667:G:H21	25:BA:671:A:H2	1.50	0.59
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.30	0.59
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.38	0.59
25:DA:1021:A:H62	25:DA:1141:U:H3	1.50	0.59
25:DA:322:A:OP1	29:DF:168:ARG:HD2	2.02	0.59
34:DO:77:ILE:HB	39:DT:74:ARG:HD3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1001:A:N1	1:AA:1040:U:O4	2.36	0.59
1:AA:1005:A:H5''	1:AA:1006:C:OP2	2.03	0.59
3:AC:20:SER:HB2	3:AC:40:ARG:HH12	1.67	0.59
1:AA:671:G:H5'	6:AF:77:ARG:HH22	1.68	0.59
25:BA:1074:A:N6	25:BA:1171:G:H2'	2.18	0.59
40:BU:3:ARG:HH12	40:BU:5:LYS:HD3	1.67	0.59
25:DA:1405:U:H2'	25:DA:1406:U:C6	2.37	0.59
25:DA:1971:A:OP2	27:DD:242:ARG:NH2	2.33	0.59
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.28	0.59
1:AA:144:G:H1	1:AA:178:C:H42	1.50	0.59
2:AB:137:ARG:CZ	2:AB:137:ARG:HB3	2.32	0.59
4:AD:178:VAL:HG12	4:AD:179:GLU:H	1.68	0.59
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.29	0.59
48:B2:65:ASN:OD1	48:B2:69:ARG:NH1	2.35	0.59
25:DA:299:A:N1	25:DA:322:A:O2'	2.32	0.59
25:DA:529:A:H62	25:DA:2041:U:H3	1.49	0.59
25:DA:607:U:OP1	29:DF:102:PRO:HA	2.03	0.59
29:DF:64:ILE:HG21	29:DF:78:ILE:HG23	1.85	0.59
25:BA:1785:C:OP1	39:BT:96:ARG:NH1	2.35	0.58
25:BA:2416:C:O3'	35:BP:77:ARG:NH2	2.36	0.58
25:BA:918:U:OP1	36:BQ:5:ARG:HD3	2.02	0.58
1:CA:26:A:N6	1:CA:558:G:O2'	2.35	0.58
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.20	0.58
4:CD:104:VAL:HG11	4:CD:146:ILE:HD13	1.84	0.58
25:DA:2693:A:H2'	25:DA:2694:G:C8	2.37	0.58
37:DR:67:LEU:HD22	37:DR:76:VAL:HG21	1.85	0.58
10:AJ:78:ASN:O	10:AJ:80:LYS:N	2.36	0.58
25:BA:121:G:OP2	61:BA:4119:HOH:O	2.16	0.58
25:BA:2490:A:OP2	55:B9:2:LYS:NZ	2.35	0.58
26:BB:77:U:OP1	45:BZ:19:ARG:NH2	2.36	0.58
35:DP:63:PRO:HG2	54:D8:25:MET:HB2	1.85	0.58
25:DA:1316:U:H2'	25:DA:1317:A:C8	2.38	0.58
31:DH:8:PRO:O	31:DH:69:ARG:NH1	2.36	0.58
1:AA:376:G:H4'	16:AP:5:ARG:HE	1.67	0.58
2:AB:15:VAL:O	2:AB:16:HIS:ND1	2.37	0.58
31:BH:11:VAL:HG21	31:BH:50:VAL:HG23	1.85	0.58
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.83	0.58
25:DA:1038:C:H42	25:DA:1117:G:H1	1.50	0.58
25:DA:577:G:O2'	25:DA:1254:A:OP1	2.19	0.58
28:DE:174:ASP:OD1	28:DE:175:VAL:N	2.36	0.58
1:CA:974:A:P	14:CN:29:ARG:HH21	2.27	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:49:PRO:HD2	9:CI:81:ILE:HD11	1.85	0.58
9:CI:85:LEU:HB3	9:CI:92:TYR:CD2	2.39	0.58
13:CM:85:GLY:HA2	13:CM:93:ARG:HH22	1.67	0.58
25:DA:1446:C:H42	25:DA:1465:G:H1	1.51	0.58
25:DA:2126:A:N6	25:DA:2162:G:HO2'	2.02	0.58
25:DA:2104:G:N2	25:DA:2185:C:N3	2.42	0.58
32:DI:40:THR:O	32:DI:44:LEU:HB2	2.02	0.58
34:DO:63:VAL:HG12	34:DO:106:LEU:HD11	1.85	0.58
45:DZ:129:SER:HB3	45:DZ:132:ASN:HB2	1.86	0.58
1:AA:139:G:N2	1:AA:224:C:O2	2.30	0.58
1:AA:501:C:OP1	12:AL:117:ARG:NH2	2.24	0.58
47:B1:3:LYS:HB2	47:B1:61:ARG:HH12	1.68	0.58
25:BA:1153:G:N2	25:BA:1154:U:O4	2.37	0.58
25:BA:989:G:O3'	61:BA:4867:HOH:O	2.17	0.58
32:BI:27:ARG:HD2	47:B1:71:TYR:CE1	2.38	0.58
41:BV:14:VAL:HB	41:BV:96:ILE:HG13	1.84	0.58
1:CA:1172:C:H2'	1:CA:1173:G:C8	2.38	0.58
1:CA:148:G:H2'	1:CA:149:A:H8	1.68	0.58
25:DA:1800:C:OP2	27:DD:183:ARG:NH2	2.33	0.58
27:DD:206:LEU:HD22	27:DD:211:ARG:HG2	1.85	0.58
32:DI:117:GLU:HG3	32:DI:118:LYS:H	1.69	0.58
42:DW:14:PRO:HG2	42:DW:78:GLU:HG2	1.84	0.58
1:AA:693:G:C6	57:AA:3191:PCY:H25	2.39	0.58
18:AR:31:LEU:H	18:AR:31:LEU:HD23	1.69	0.58
25:BA:1249:A:H61	25:BA:1286:U:H2'	1.69	0.58
25:DA:247:G:H4'	25:DA:386:G:C5	2.38	0.58
25:DA:539:G:H2'	25:DA:540:C:C6	2.39	0.58
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.36	0.58
1:AA:262:A:H2'	1:AA:263:A:C8	2.37	0.58
10:AJ:65:LEU:HD13	14:AN:56:VAL:HG22	1.84	0.58
25:BA:1346:U:H4'	25:BA:1347:A:H5''	1.84	0.58
25:BA:313:A:N6	25:BA:375:G:O2'	2.37	0.58
30:BG:16:ARG:NE	30:BG:31:VAL:HG11	2.18	0.58
1:CA:45:U:H2'	1:CA:46:G:C8	2.39	0.58
3:CC:71:ALA:HA	3:CC:106:VAL:HB	1.86	0.58
25:DA:2327:A:H2'	25:DA:2328:A:C8	2.39	0.58
34:DO:120:GLU:HG2	34:DO:122:LEU:HG	1.84	0.58
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.19	0.58
2:AB:18:GLY:HA2	2:AB:42:ILE:HG13	1.85	0.58
12:AL:57:LYS:HD3	12:AL:67:THR:HG23	1.85	0.58
25:BA:139:A:H8	25:BA:1454:C:O2'	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:904:C:OP1	46:B0:77:ARG:NH2	2.36	0.58
2:CB:95:GLN:HG3	2:CB:147:LYS:HD3	1.85	0.58
2:CB:155:LEU:HD21	2:CB:159:PRO:HG3	1.84	0.58
1:CA:598:U:H4'	8:CH:94:TYR:CD2	2.39	0.58
16:CP:23:ASP:OD2	16:CP:25:ARG:NH1	2.36	0.58
30:DG:151:ALA:HB3	30:DG:153:ARG:HH11	1.68	0.58
1:AA:1160:G:C5	1:AA:1161:C:H5	2.21	0.58
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.35	0.58
25:BA:2745:G:H3'	25:BA:2746:A:O4'	2.04	0.58
32:BI:106:GLY:HA2	32:BI:107:VAL:O	2.03	0.58
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.38	0.58
1:CA:457:C:H42	1:CA:474:G:H1	1.51	0.58
1:CA:975:A:H5''	1:CA:1363(A):A:N6	2.19	0.58
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.84	0.58
25:DA:854:G:H2'	25:DA:855:G:C8	2.39	0.58
30:DG:3:LEU:HD13	50:D4:25:TYR:CZ	2.39	0.58
1:AA:589:C:C2'	1:AA:590:C:H5'	2.34	0.58
9:AI:85:LEU:HB3	9:AI:92:TYR:HD2	1.69	0.58
25:BA:1154:U:O2'	25:BA:1155:C:O4'	2.22	0.58
25:BA:325:G:OP2	44:BY:84:ARG:NH2	2.37	0.58
1:CA:997:U:H3	1:CA:1044:A:H61	1.52	0.58
3:CC:20:SER:HB2	3:CC:40:ARG:HH12	1.67	0.58
25:DA:1325:G:OP1	25:DA:1647:G:O2'	2.11	0.58
25:DA:492:A:H2'	25:DA:493:G:O4'	2.04	0.58
25:DA:2303:G:O2'	30:DG:132:ASN:HB2	2.04	0.58
2:AB:187:LEU:HA	2:AB:201:ILE:HB	1.85	0.57
2:AB:8:LYS:HG2	2:AB:9:GLU:H	1.68	0.57
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.86	0.57
25:BA:1053:C:OP1	33:BN:37:LYS:NZ	2.37	0.57
25:BA:469:A:H1'	25:BA:1246:C:O4'	2.04	0.57
27:BD:148:GLU:HB2	27:BD:151:LYS:HD2	1.86	0.57
25:BA:346:A:OP1	29:BF:168:ARG:HD2	2.04	0.57
32:BI:68:LEU:HD11	32:BI:109:ILE:HD11	1.86	0.57
1:CA:36:C:O2'	12:CL:117:ARG:NH2	2.37	0.57
4:AD:49:ARG:HE	4:AD:49:ARG:H	1.50	0.57
5:AE:81:GLU:HG2	5:AE:90:VAL:HG13	1.86	0.57
28:BE:14:ILE:HD11	28:BE:173:VAL:HG11	1.86	0.57
25:DA:1342:A:O2'	25:DA:1344:G:OP2	2.15	0.57
25:DA:2570:G:O6	61:DA:4792:HOH:O	2.17	0.57
28:DE:127:ASP:OD2	61:DE:409:HOH:O	2.17	0.57
25:DA:637:A:H8	35:DP:117:GLU:HG3	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DQ:22:LYS:O	45:DZ:78:LYS:NZ	2.29	0.57
25:DA:2880:C:O3'	37:DR:90:ARG:NH1	2.37	0.57
1:AA:123:C:OP1	1:AA:311:C:O2'	2.19	0.57
1:AA:964:A:OP1	61:AA:4146:HOH:O	2.17	0.57
4:CD:88:VAL:HG22	5:CE:96:PRO:HB2	1.85	0.57
19:CS:52:TYR:HB2	19:CS:57:HIS:CE1	2.39	0.57
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.39	0.57
1:AA:1173:G:C2'	1:AA:1174:G:H5'	2.34	0.57
1:AA:1262:C:H2'	1:AA:1263:C:C6	2.40	0.57
1:AA:1239:A:H62	1:AA:1299:A:N6	2.02	0.57
1:AA:649:G:H2'	1:AA:650:G:H8	1.68	0.57
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	1.86	0.57
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.19	0.57
25:BA:1736:A:H62	25:BA:1745:A:H2	1.51	0.57
25:BA:2701:U:H4'	25:BA:2702:C:H5'	1.85	0.57
26:BB:33:G:H5'	30:BG:2:PRO:HD3	1.86	0.57
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.86	0.57
23:CX:23:C:H2'	23:CX:24:U:C6	2.39	0.57
25:DA:566:U:H5''	35:DP:29:LYS:HE3	1.86	0.57
27:DD:142:VAL:HG22	27:DD:193:VAL:HA	1.85	0.57
38:DS:84:GLN:H	38:DS:111:GLU:HB2	1.68	0.57
1:AA:76:C:N4	1:AA:93:G:H1	1.98	0.57
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.85	0.57
25:BA:2594:G:OP2	61:BA:4493:HOH:O	2.17	0.57
25:BA:572:A:O2'	25:BA:573:G:OP1	2.23	0.57
26:BB:102:A:N7	61:BB:315:HOH:O	2.32	0.57
2:CB:178:ARG:NH1	2:CB:196:LEU:O	2.38	0.57
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.86	0.57
25:DA:2879:C:OP2	61:DA:4411:HOH:O	2.17	0.57
25:DA:41:C:H2'	25:DA:42:G:H8	1.69	0.57
25:DA:852:G:H2'	25:DA:853:G:C8	2.39	0.57
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.39	0.57
1:AA:1239:A:H62	1:AA:1299:A:H62	1.52	0.57
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.85	0.57
1:CA:1150:U:O4	1:CA:1151:A:N6	2.37	0.57
4:CD:30:LYS:HA	4:CD:35:ARG:HD2	1.85	0.57
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.69	0.57
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.87	0.57
25:DA:1588:C:H2'	25:DA:1589:C:C6	2.39	0.57
25:DA:643:A:N1	25:DA:2369:A:O2'	2.37	0.57
25:DA:1012:U:H5	33:DN:28:THR:HG21	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:682:G:H1	1:AA:708:C:H42	1.53	0.57
2:AB:18:GLY:O	2:AB:19:HIS:HB3	2.04	0.57
9:AI:13:ALA:HB2	9:AI:68:GLY:HA3	1.86	0.57
47:B1:23:LYS:HB3	47:B1:29:GLY:HA3	1.86	0.57
3:CC:180:ALA:HB1	3:CC:203:PHE:HE1	1.69	0.57
25:DA:2113:U:H3	25:DA:2170:A:N6	2.02	0.57
24:CY:76:A:N3	25:DA:2394:C:N4	2.52	0.57
25:DA:2557:G:H2'	25:DA:2558:C:C6	2.39	0.57
25:DA:323:G:O2'	25:DA:1205:U:N3	2.35	0.57
25:DA:842:G:N7	61:DA:4699:HOH:O	2.32	0.57
26:DB:44:G:OP1	30:DG:98:ARG:NH2	2.36	0.57
28:DE:36:ARG:HG2	28:DE:47:VAL:HG12	1.86	0.57
13:CM:68:GLY:HA3	30:DG:116:ASP:OD1	2.04	0.57
2:AB:10:LEU:O	2:AB:12:GLU:N	2.36	0.57
23:AX:23:C:H2'	23:AX:24:U:C6	2.39	0.57
32:BI:93:THR:OG1	32:BI:96:ASP:OD1	2.17	0.57
1:CA:737:A:H1'	6:CF:73:ASN:HD21	1.69	0.57
22:CV:16:A:N1	23:CX:36:U:O2	2.38	0.57
25:DA:2537:U:H2'	25:DA:2538:C:C6	2.40	0.57
15:AO:11:VAL:HG21	15:AO:34:LEU:HD22	1.85	0.57
44:BY:5:MET:HE1	44:BY:32:PRO:HA	1.86	0.57
1:CA:1239:A:H4'	1:CA:1240:U:H5''	1.86	0.57
1:CA:76:C:N4	1:CA:93:G:H1	2.03	0.57
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.69	0.57
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.86	0.57
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.87	0.57
19:CS:28:LYS:HB3	19:CS:28:LYS:HZ2	1.69	0.57
25:DA:2079:U:O3'	47:D1:35:THR:OG1	2.23	0.57
52:D6:10:LEU:HD23	52:D6:22:ALA:HB2	1.87	0.57
25:DA:2721:A:OP1	61:DA:4144:HOH:O	2.16	0.57
25:DA:889:C:H2'	25:DA:890:A:O4'	2.04	0.57
27:DD:10:THR:OG1	27:DD:13:ARG:HG2	2.05	0.57
1:AA:1162:C:N3	1:AA:1174:G:N2	2.43	0.57
1:AA:992:U:O2	1:AA:1043:C:N4	2.38	0.57
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.87	0.57
25:BA:2825:C:H5'	51:B5:29:THR:HG21	1.87	0.57
28:BE:174:ASP:OD1	28:BE:175:VAL:N	2.38	0.57
33:BN:94:HIS:HB3	33:BN:97:ARG:HD3	1.87	0.57
1:CA:1051:C:H2'	1:CA:1052:U:H6	1.70	0.57
1:CA:583:A:N6	1:CA:758:G:O2'	2.38	0.57
2:CB:161:ALA:HB1	2:CB:185:ILE:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:24:GLU:HG3	6:CF:28:ARG:NH1	2.19	0.57
50:D4:62:ARG:O	50:D4:64:GLY:N	2.38	0.57
25:DA:2139:C:H42	25:DA:2152:G:H1	1.51	0.57
25:DA:2543:G:H2'	25:DA:2544:G:C8	2.40	0.57
43:DX:32:PRO:HA	43:DX:77:LYS:HD2	1.87	0.57
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.19	0.56
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.37	0.56
45:BZ:111:VAL:C	45:BZ:113:ALA:H	2.07	0.56
45:BZ:41:LEU:HD21	45:BZ:83:PRO:HG2	1.85	0.56
1:CA:145:G:H1	1:CA:177:C:H42	1.52	0.56
1:CA:524:G:O5'	1:CA:524:G:H8	1.87	0.56
1:CA:826:C:H2'	1:CA:827:U:C6	2.40	0.56
29:DF:11:VAL:HB	29:DF:18:ARG:HB3	1.85	0.56
13:AM:92:HIS:CE1	13:AM:98:VAL:HG11	2.40	0.56
51:B5:16:ARG:HG2	51:B5:16:ARG:HH11	1.69	0.56
25:BA:1071:G:C4	25:BA:1180:C:H1'	2.40	0.56
25:BA:1091:A:OP1	25:BA:1091:A:H4'	2.06	0.56
25:BA:1503:G:OP2	61:BA:4135:HOH:O	2.16	0.56
25:BA:2163:G:H1	25:BA:2171:G:N2	2.02	0.56
25:BA:2545:A:H2'	25:BA:2546:A:O4'	2.06	0.56
25:BA:9:U:H3	25:BA:2641:A:H2	1.52	0.56
1:CA:572:A:OP1	61:CA:4039:HOH:O	2.17	0.56
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.37	0.56
49:D3:46:ASN:O	49:D3:50:VAL:HG22	2.05	0.56
25:DA:1588:C:H2'	25:DA:1589:C:H6	1.70	0.56
25:DA:2331:G:O2'	25:DA:2336:A:N1	2.28	0.56
31:DH:3:ARG:HB3	31:DH:3:ARG:HH11	1.71	0.56
37:DR:21:TYR:OH	37:DR:43:GLU:HG2	2.05	0.56
1:AA:1238:A:OP2	61:AA:4121:HOH:O	2.18	0.56
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.37	0.56
51:B5:16:ARG:HD2	51:B5:20:ARG:NH1	2.20	0.56
25:BA:1033:G:O2'	25:BA:1046:A:N3	2.36	0.56
25:BA:2023:A:H2'	25:BA:2024:G:C8	2.40	0.56
30:BG:3:LEU:HD12	30:BG:5:VAL:HG12	1.87	0.56
1:CA:1179:A:H2'	1:CA:1180:A:O4'	2.06	0.56
25:DA:647:G:H8	25:DA:647:G:O5'	1.88	0.56
1:AA:1033:G:H2'	1:AA:1034:G:C8	2.35	0.56
1:AA:1053:G:N2	61:AA:4025:HOH:O	2.39	0.56
1:AA:1183:A:H5''	1:AA:1183:A:C8	2.39	0.56
1:AA:167:G:H2'	1:AA:168:G:H8	1.69	0.56
6:AF:60:PHE:HE2	18:AR:76:LEU:HD12	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:707:C:OP1	11:AK:85:ARG:NH1	2.39	0.56
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.38	0.56
31:BH:56:SER:HB3	31:BH:61:HIS:ND1	2.20	0.56
1:CA:664:G:N2	1:CA:741:G:H1	2.02	0.56
28:DE:116:VAL:HG13	28:DE:122:PHE:HB2	1.86	0.56
30:DG:16:ARG:O	30:DG:20:ILE:HG13	2.04	0.56
25:DA:2744:G:N2	31:DH:143:GLN:OE1	2.39	0.56
32:DI:130:TYR:HB3	32:DI:138:ILE:HB	1.87	0.56
35:DP:82:GLY:HA2	35:DP:113:LYS:O	2.05	0.56
1:CA:345:C:OP2	39:DT:39:ARG:NH2	2.36	0.56
29:BF:53:THR:CG2	29:BF:55:GLY:H	2.18	0.56
36:BQ:16:ARG:HG3	36:BQ:17:LEU:H	1.71	0.56
37:BR:21:TYR:OH	37:BR:43:GLU:HG2	2.05	0.56
45:BZ:111:VAL:O	45:BZ:113:ALA:N	2.35	0.56
2:CB:8:LYS:HD2	2:CB:9:GLU:H	1.71	0.56
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.38	0.56
7:CG:111:ARG:HD2	7:CG:123:GLU:HB2	1.88	0.56
25:DA:1946:U:H2'	25:DA:1947:C:C6	2.40	0.56
25:DA:572:A:H5''	25:DA:573:G:OP2	2.05	0.56
35:DP:50:ARG:HD3	54:D8:7:HIS:CD2	2.39	0.56
39:DT:27:THR:HB	39:DT:89:VAL:HG22	1.88	0.56
43:DX:31:HIS:CD2	43:DX:33:LYS:HB2	2.40	0.56
1:AA:445:G:H2'	1:AA:446:G:C8	2.40	0.56
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.88	0.56
4:AD:188:LEU:H	4:AD:188:LEU:HD23	1.70	0.56
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.39	0.56
27:BD:132:PRO:HG2	27:BD:135:PHE:CD2	2.41	0.56
1:CA:839:U:H3'	1:CA:840:C:C5	2.41	0.56
13:CM:91:ARG:HB2	13:CM:98:VAL:HG13	1.86	0.56
25:DA:500:G:N1	25:DA:503:A:OP2	2.37	0.56
26:DB:13:A:N1	26:DB:69:G:O2'	2.31	0.56
32:DI:72:LEU:HD21	32:DI:107:VAL:HG11	1.86	0.56
1:AA:814:A:H2'	1:AA:816:A:H5''	1.87	0.56
25:BA:139:A:C8	25:BA:1454:C:O2'	2.59	0.56
25:BA:287:G:H4'	25:BA:288:U:H5''	1.87	0.56
29:BF:116:ASP:OD1	29:BF:119:ARG:NH2	2.39	0.56
45:BZ:45:ASP:OD2	45:BZ:49:ARG:NH1	2.38	0.56
1:CA:1028:C:C2	1:CA:1033:G:N1	2.74	0.56
1:CA:589:C:C2'	1:CA:590:C:H5'	2.36	0.56
9:CI:97:LYS:HA	9:CI:102:LEU:HG	1.87	0.56
25:DA:1639:U:H2'	25:DA:1640:C:H5''	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2429:G:OP2	61:DA:4569:HOH:O	2.18	0.56
25:DA:2708:G:H1'	37:DR:71:GLN:HE22	1.70	0.56
26:DB:48:A:H4'	38:DS:95:HIS:HD2	1.71	0.56
35:DP:100:LEU:HD12	35:DP:112:LEU:HD11	1.87	0.56
40:DU:97:ASP:OD1	40:DU:101:ARG:HD2	2.05	0.56
1:AA:56:U:H2'	1:AA:57:G:C8	2.41	0.56
25:BA:1827:U:H2'	25:BA:1828:C:H6	1.70	0.56
25:BA:1834:A:O2'	27:BD:259:THR:HG21	2.05	0.56
25:BA:354:A:H2	25:BA:1255:A:O2'	1.89	0.56
25:BA:934:A:H4'	25:BA:935:C:H5	1.71	0.56
1:CA:1318:A:OP1	19:CS:3:ARG:NH1	2.39	0.56
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.12	0.56
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.29	0.56
1:AA:193:C:H2'	1:AA:194:C:H6	1.71	0.56
50:B4:44:THR:O	50:B4:46:GLN:N	2.39	0.56
25:BA:1466:U:O2'	25:BA:1467:G:OP1	2.24	0.56
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.86	0.56
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.21	0.56
25:DA:1316:U:H2'	25:DA:1317:A:H8	1.69	0.56
25:DA:299:A:H5''	44:DY:86:ARG:HH21	1.69	0.56
26:DB:29:A:O2'	26:DB:58:A:N1	2.32	0.56
25:DA:301:G:OP2	44:DY:84:ARG:NH2	2.39	0.56
43:BX:57:LEU:CD1	43:BX:78:LYS:HG2	2.36	0.56
23:CX:40:C:H2'	23:CX:41:C:H6	1.69	0.56
47:D1:23:LYS:HB3	47:D1:29:GLY:HA3	1.87	0.56
25:DA:635:C:O2'	25:DA:639:U:OP1	2.22	0.56
29:DF:192:LEU:HD22	29:DF:194:MET:HG3	1.87	0.56
1:AA:1027:C:N3	1:AA:1034:G:O6	2.38	0.56
25:BA:1500:A:OP2	61:BA:4134:HOH:O	2.18	0.56
25:BA:2331:G:H22	38:BS:3:ARG:NE	2.04	0.56
40:BU:76:TYR:CZ	40:BU:80:ILE:HG13	2.40	0.56
1:CA:160:A:H61	1:CA:347:G:H1'	1.70	0.56
1:CA:489:C:H2'	1:CA:490:G:H8	1.71	0.56
11:CK:110:ASP:HB3	18:CR:85:LEU:HB3	1.88	0.56
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.05	0.56
20:CT:16:HIS:O	20:CT:19:SER:OG	2.20	0.56
23:CX:23:C:H2'	23:CX:24:U:H6	1.71	0.56
25:DA:2165:G:N2	25:DA:2172:U:O4	2.38	0.56
25:DA:816:C:O2'	25:DA:932:G:O6	2.19	0.56
25:DA:952:G:OP1	36:DQ:16:ARG:NH2	2.39	0.56
44:DY:43:ASN:CG	44:DY:65:ALA:HB3	2.26	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.34	0.55
25:BA:1541:A:H2'	25:BA:1542:A:C8	2.42	0.55
25:BA:191:U:OP1	61:BA:4909:HOH:O	2.18	0.55
25:BA:2188:G:N7	25:BA:2190:G:N2	2.54	0.55
30:BG:131:TYR:HB3	30:BG:159:VAL:HG13	1.88	0.55
32:BI:104:GLN:O	32:BI:106:GLY:N	2.34	0.55
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.38	0.55
3:CC:157:ILE:HD12	3:CC:164:ARG:HB3	1.87	0.55
25:DA:1913:A:H4'	25:DA:1914:C:C5'	2.36	0.55
1:AA:757:U:H2'	1:AA:758:G:O4'	2.06	0.55
2:AB:178:ARG:HG2	8:AH:72:PRO:HA	1.88	0.55
4:AD:65:ARG:HG2	4:AD:75:PHE:CD2	2.40	0.55
25:BA:1451:U:H2'	25:BA:1452:U:C6	2.42	0.55
25:BA:2858:G:C8	39:BT:97:ALA:HB2	2.40	0.55
27:BD:147:LEU:HD13	27:BD:155:LEU:HD21	1.87	0.55
1:CA:1063:C:H3'	1:CA:1064:G:H2'	1.87	0.55
1:CA:646:U:H2'	1:CA:647:C:C6	2.42	0.55
12:CL:33:ARG:HG2	12:CL:60:LEU:HD12	1.89	0.55
18:CR:26:LEU:HD12	18:CR:27:GLY:H	1.71	0.55
29:DF:53:THR:HG22	29:DF:56:GLU:HG3	1.88	0.55
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.54	0.55
1:AA:439:A:C2	1:AA:496:A:H1'	2.41	0.55
2:AB:213:LEU:HD22	2:AB:214:ILE:HD13	1.88	0.55
25:BA:553:A:C2	25:BA:2065:C:H4'	2.42	0.55
1:CA:1173:G:H2'	1:CA:1174:G:C8	2.41	0.55
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.88	0.55
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.38	0.55
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.06	0.55
46:D0:27:GLU:HG3	46:D0:68:GLU:HA	1.89	0.55
25:DA:1796:U:H2'	25:DA:1797:C:C6	2.41	0.55
34:DO:68:GLU:OE2	34:DO:78:ARG:NH1	2.39	0.55
1:AA:1442:G:HO2'	1:AA:1442(A):G:P	2.29	0.55
25:BA:1735:U:O2	25:BA:1747:A:H5'	2.07	0.55
35:BP:63:PRO:HD3	54:B8:27:THR:HG22	1.88	0.55
25:BA:956:A:H62	36:BQ:12:GLN:HA	1.72	0.55
43:BX:11:PRO:HB3	43:BX:92:LEU:HD11	1.88	0.55
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.41	0.55
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	1.87	0.55
25:DA:194:G:H2'	25:DA:195:A:O4'	2.06	0.55
25:DA:764:A:H5'	27:DD:210:GLY:HA2	1.87	0.55
1:AA:114:U:H1'	1:AA:353:A:H1'	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.53	0.55
28:BE:11:MET:HG2	28:BE:24:THR:HB	1.89	0.55
25:BA:878:G:N2	35:BP:53:GLY:O	2.39	0.55
35:BP:59:LEU:HD23	54:B8:58:ILE:HD13	1.88	0.55
44:BY:7:VAL:HG21	44:BY:72:VAL:HG12	1.89	0.55
1:CA:1093:A:H2'	1:CA:1095:U:H5'	1.87	0.55
1:CA:596:C:N3	1:CA:644:G:N1	2.43	0.55
1:CA:833:U:H2'	1:CA:834:C:C6	2.41	0.55
1:CA:1074:G:OP1	5:CE:64:ARG:NH2	2.40	0.55
15:CO:54:ARG:O	15:CO:58:MET:HG3	2.07	0.55
25:DA:2369:A:H2'	25:DA:2370:G:H8	1.71	0.55
25:DA:41:C:H2'	25:DA:42:G:C8	2.41	0.55
30:DG:170:ARG:HH21	30:DG:180:PHE:HB2	1.71	0.55
31:DH:3:ARG:HH12	31:DH:5:GLY:H	1.51	0.55
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.06	0.55
13:AM:49:THR:HG22	13:AM:51:ALA:H	1.70	0.55
28:BE:29:GLY:HA3	61:BE:405:HOH:O	2.06	0.55
25:BA:709:G:H5''	35:BP:16:ARG:HG2	1.89	0.55
51:D5:16:ARG:HG2	51:D5:16:ARG:NH1	2.22	0.55
27:DD:108:PRO:HB3	27:DD:143:HIS:HE1	1.70	0.55
31:DH:56:SER:OG	31:DH:57:ASP:N	2.38	0.55
1:AA:1399:C:C2	1:AA:1502:A:N6	2.74	0.55
1:AA:627:G:H2'	1:AA:628:G:C8	2.36	0.55
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.88	0.55
4:AD:18:LYS:HG2	58:AD:501:SF4:S1	2.47	0.55
25:BA:1219:A:H1'	25:BA:1220:U:H5''	1.88	0.55
25:BA:2212:G:H2'	25:BA:2213:G:O4'	2.07	0.55
25:BA:2804:C:H2'	25:BA:2805:G:H8	1.70	0.55
39:BT:127:ALA:O	39:BT:129:ARG:N	2.40	0.55
1:CA:1134:G:H1	1:CA:1140:C:H42	1.55	0.55
1:CA:959:A:HO2'	1:CA:984:C:HO2'	1.49	0.55
52:D6:13:CYS:SG	52:D6:47:THR:HG21	2.47	0.55
25:DA:1614:A:H8	25:DA:1614:A:P	2.30	0.55
25:DA:2126:A:H2	25:DA:2127:G:N3	2.05	0.55
25:DA:2184:G:H2'	25:DA:2185:C:H5'	1.88	0.55
25:DA:39:C:O2	29:DF:46:ARG:NH2	2.39	0.55
31:DH:154:PRO:HB3	31:DH:163:TYR:CZ	2.42	0.55
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.54	0.55
1:AA:1258:G:H2'	1:AA:1259:C:C6	2.42	0.55
1:AA:201:C:N4	1:AA:216:G:H1	1.99	0.55
1:AA:621:A:H2'	1:AA:622:A:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AQ:27:PHE:CZ	17:AQ:36:ILE:HD11	2.42	0.55
25:BA:1269:G:N2	25:BA:1272:A:OP2	2.37	0.55
25:BA:1634:C:H2'	25:BA:1635:C:C6	2.41	0.55
41:BV:21:ARG:HG2	41:BV:91:TYR:CD1	2.41	0.55
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.42	0.55
1:CA:489:C:H2'	1:CA:490:G:C8	2.42	0.55
1:CA:798:G:O6	61:CA:4029:HOH:O	2.17	0.55
29:DF:120:GLU:HB2	29:DF:122:LYS:HG2	1.89	0.55
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.20	0.55
1:AA:673:G:H2'	1:AA:674:G:C8	2.41	0.55
45:BZ:108:PRO:HB2	45:BZ:111:VAL:HG23	1.89	0.55
1:CA:1190:G:OP1	3:CC:5:ILE:N	2.39	0.55
1:CA:972:C:OP1	61:CA:4116:HOH:O	2.18	0.55
25:DA:1357:U:H2'	25:DA:1358:G:O4'	2.07	0.55
25:DA:220:G:O2'	25:DA:233:A:N3	2.38	0.55
25:DA:289:A:H2'	25:DA:290:G:O4'	2.05	0.55
31:DH:69:ARG:HG3	31:DH:70:THR:N	2.22	0.55
1:AA:1039:C:H2'	1:AA:1040:U:C6	2.41	0.55
1:AA:448:A:O5'	1:AA:485:G:N2	2.24	0.55
1:AA:78:G:C2	1:AA:91:C:N3	2.75	0.55
1:AA:1372:U:OP1	9:AI:72:GLY:N	2.40	0.55
13:AM:88:ARG:HG3	13:AM:98:VAL:HG12	1.89	0.55
15:AO:79:ARG:O	15:AO:83:GLU:HB2	2.07	0.55
1:AA:376:G:H5''	16:AP:5:ARG:HB2	1.88	0.55
25:BA:1588:G:H3'	25:BA:1589:A:H2'	1.89	0.55
25:BA:1961:U:OP1	25:BA:2616:U:O2'	2.23	0.55
25:BA:2303:U:H2'	25:BA:2304:C:C6	2.42	0.55
25:BA:1874:C:H5'	27:BD:253:GLN:NE2	2.22	0.55
31:BH:164:TYR:HB2	31:BH:167:GLU:HB2	1.89	0.55
34:BO:2:ILE:HB	34:BO:33:ALA:HB3	1.89	0.55
1:CA:472:A:H2'	1:CA:473:G:O4'	2.06	0.55
25:DA:48:G:O6	61:DA:4033:HOH:O	2.15	0.55
1:AA:1051:C:H2'	1:AA:1052:U:C6	2.42	0.54
1:AA:537:G:H2'	1:AA:538:G:H8	1.71	0.54
4:AD:19:LEU:HB3	4:AD:21:LEU:HD21	1.88	0.54
25:BA:878:G:O2'	35:BP:38:GLN:NE2	2.39	0.54
1:CA:1131:G:H2'	1:CA:1132:C:C6	2.42	0.54
3:CC:40:ARG:NH2	3:CC:55:VAL:O	2.39	0.54
4:CD:19:LEU:HB3	4:CD:21:LEU:HD21	1.89	0.54
1:CA:986:A:H1'	19:CS:54:GLY:O	2.07	0.54
25:DA:1376:C:OP2	61:DA:4086:HOH:O	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DO:2:ILE:HB	34:DO:33:ALA:HB3	1.90	0.54
1:AA:1007:C:O2	1:AA:1022:G:N1	2.25	0.54
1:AA:1095:U:P	1:AA:1108:G:H1	2.30	0.54
1:AA:976:G:N2	1:AA:1363:C:OP2	2.35	0.54
25:BA:1627:A:OP2	25:BA:1627:A:H8	1.90	0.54
25:BA:1829:U:OP2	27:BD:274:ARG:NH2	2.39	0.54
33:BN:67:LEU:HD12	33:BN:87:LEU:HD13	1.89	0.54
1:CA:56:U:H2'	1:CA:57:G:H8	1.71	0.54
25:DA:1012:U:C5	33:DN:28:THR:HG21	2.41	0.54
43:DX:31:HIS:CD2	43:DX:33:LYS:H	2.25	0.54
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.54	0.54
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.88	0.54
23:AX:23:C:H2'	23:AX:24:U:H6	1.73	0.54
25:BA:939:C:H2'	25:BA:940:C:C6	2.42	0.54
32:BI:61:ARG:HA	32:BI:61:ARG:HH11	1.72	0.54
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.40	0.54
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.41	0.54
2:CB:76:GLN:HB2	2:CB:208:ILE:HG12	1.89	0.54
25:DA:571:A:H5'	25:DA:2030:A:N7	2.21	0.54
26:DB:114:C:H4'	38:DS:46:VAL:HG22	1.89	0.54
1:AA:166:G:H2'	1:AA:167:G:H8	1.72	0.54
1:AA:598:U:O4	61:AA:4065:HOH:O	2.17	0.54
50:B4:47:GLN:HG2	50:B4:49:PHE:H	1.72	0.54
26:BB:6:C:H2'	26:BB:7:G:H5"	1.89	0.54
19:CS:44:MET:O	19:CS:47:HIS:HB2	2.08	0.54
25:DA:1010:A:H1'	25:DA:1153:C:H1'	1.90	0.54
25:DA:2180:U:H2'	25:DA:2181:G:O4'	2.08	0.54
25:DA:2747:G:H1	25:DA:2754:U:H2'	1.72	0.54
31:DH:18:GLU:HB3	31:DH:25:LYS:HB2	1.90	0.54
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.27	0.54
1:AA:1278:U:H5'	1:AA:1279:A:O4'	2.08	0.54
2:AB:55:PHE:HA	2:AB:58:ILE:HB	1.90	0.54
13:AM:58:GLU:O	13:AM:62:ASN:ND2	2.28	0.54
24:AY:71:G:H4'	25:BA:1882:U:H4'	1.88	0.54
27:BD:145:VAL:HG12	27:BD:146:GLU:O	2.08	0.54
1:CA:1028:C:N3	1:CA:1033:G:O6	2.39	0.54
1:CA:1220:G:H5'	19:CS:34:TRP:O	2.06	0.54
7:CG:106:GLN:O	7:CG:110:GLN:HG3	2.08	0.54
1:CA:975:A:N1	10:CJ:48:THR:HB	2.21	0.54
25:DA:1011:G:OP2	40:DU:66:ASN:ND2	2.39	0.54
25:DA:1410:G:H2'	25:DA:1411:C:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2820:A:C5	37:DR:4:LEU:HD11	2.43	0.54
25:DA:459:U:H5''	53:D7:40:TRP:CD2	2.43	0.54
25:DA:622:G:H2'	25:DA:623:G:H8	1.72	0.54
25:DA:740:U:H2'	25:DA:741:G:C8	2.43	0.54
26:DB:95:C:H2'	26:DB:96:U:C6	2.42	0.54
34:DO:77:ILE:HG13	39:DT:74:ARG:HG2	1.88	0.54
45:DZ:19:ARG:HG3	45:DZ:25:PRO:HD3	1.88	0.54
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.07	0.54
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.42	0.54
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.08	0.54
11:AK:29:ILE:HG23	11:AK:44:SER:HB3	1.90	0.54
1:AA:958:A:N6	19:AS:77:THR:O	2.41	0.54
25:BA:2135:U:N3	25:BA:2136:A:N7	2.56	0.54
25:BA:34:C:H5''	25:BA:35:G:OP2	2.07	0.54
40:BU:3:ARG:NH1	40:BU:5:LYS:HD3	2.22	0.54
25:DA:1005:C:H2'	25:DA:1006:C:C6	2.42	0.54
25:DA:603:A:H4'	25:DA:604:G:H5'	1.89	0.54
25:DA:1188:U:H4'	41:DV:79:VAL:HG22	1.89	0.54
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.43	0.54
1:AA:1272:G:H2'	1:AA:1273:G:O4'	2.07	0.54
25:BA:1014:U:H2'	25:BA:1015:C:C6	2.42	0.54
25:BA:2044:U:O2'	25:BA:2629:C:H5'	2.08	0.54
38:BS:34:HIS:ND1	38:BS:53:SER:OG	2.38	0.54
1:CA:1155:G:N2	1:CA:1156:G:H1'	2.23	0.54
1:CA:89:C:H2'	1:CA:90:U:O4'	2.07	0.54
50:D4:53:GLU:HG2	50:D4:55:ARG:H	1.72	0.54
25:DA:14:A:N1	25:DA:2044:C:O2'	2.34	0.54
25:DA:857:C:H1'	46:D0:26:TYR:HE1	1.71	0.54
26:DB:6:C:H2'	26:DB:7:G:H5''	1.89	0.54
39:DT:30:VAL:HG22	39:DT:86:ILE:HG12	1.88	0.54
1:AA:1320:C:H5'	1:AA:1320:C:H6	1.73	0.54
1:AA:688:G:H2'	1:AA:689:C:H6	1.72	0.54
25:BA:1249:A:N6	25:BA:1286:U:H2'	2.23	0.54
25:BA:1003:U:H5''	36:BQ:14:ARG:HD3	1.90	0.54
36:BQ:43:THR:HG22	36:BQ:94:VAL:HG12	1.90	0.54
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.89	0.54
3:CC:180:ALA:HB1	3:CC:203:PHE:CE1	2.42	0.54
9:CI:3:GLN:HG2	9:CI:20:ARG:HE	1.72	0.54
19:CS:32:LYS:HE3	19:CS:57:HIS:CD2	2.43	0.54
25:DA:1341:U:OP1	25:DA:1397:U:N3	2.38	0.54
25:DA:2126:A:N6	25:DA:2172:U:H5'	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2552:U:H2'	25:DA:2554:U:H5''	1.90	0.54
25:DA:1842:G:O2'	27:DD:253:GLN:NE2	2.41	0.54
45:DZ:99:TYR:HA	45:DZ:124:ILE:O	2.08	0.54
45:DZ:70:LEU:O	45:DZ:89:PHE:N	2.37	0.54
1:AA:931:C:H42	1:AA:1386:G:H1	1.54	0.54
25:BA:2340:A:H2'	25:BA:2341:G:H8	1.72	0.54
25:BA:2879:G:H2'	25:BA:2880:C:O4'	2.07	0.54
25:BA:331:G:H21	25:BA:354:A:H62	1.55	0.54
1:CA:452:A:O2'	1:CA:453:A:OP2	2.23	0.54
1:CA:1495:U:O2'	25:DA:1919:A:N1	2.32	0.54
25:DA:863:A:H2'	25:DA:864:G:C8	2.43	0.54
35:DP:94:GLU:HG3	35:DP:124:LYS:HD3	1.90	0.54
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.42	0.54
1:AA:479:C:N4	1:AA:480:U:O4	2.41	0.54
2:AB:231:GLU:HB3	2:AB:232:PRO:CD	2.33	0.54
9:AI:8:GLY:O	9:AI:15:ALA:N	2.41	0.54
1:AA:1456:G:N2	20:AT:43:LEU:HD11	2.22	0.54
48:B2:22:GLU:OE2	48:B2:68:ARG:NH2	2.41	0.54
32:BI:75:LEU:HD22	32:BI:105:HIS:CG	2.43	0.54
39:BT:59:THR:HG23	39:BT:78:LEU:HB3	1.90	0.54
1:CA:1269:A:H2	1:CA:1312:G:N3	2.06	0.54
25:DA:1827:C:OP2	27:DD:222:ARG:NH1	2.38	0.54
25:DA:2022:U:O2'	25:DA:2617:C:H5'	2.07	0.54
26:DB:50:G:OP1	38:DS:63:THR:N	2.40	0.54
1:AA:976:G:H5'	1:AA:1358:U:O2'	2.07	0.53
10:AJ:54:PHE:O	10:AJ:56:HIS:N	2.36	0.53
25:BA:1425:A:H4'	25:BA:1426:G:OP2	2.08	0.53
1:CA:1173:G:H2'	1:CA:1174:G:H8	1.72	0.53
1:CA:922:G:N3	1:CA:1398:A:H2	2.05	0.53
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.26	0.53
25:DA:2305:A:H5''	30:DG:134:GLY:HA3	1.91	0.53
38:DS:35:ILE:HD12	38:DS:101:LEU:HD12	1.89	0.53
44:DY:1:MET:HG2	44:DY:2:ARG:H	1.73	0.53
1:AA:1493:A:H5''	1:AA:1494:G:OP2	2.08	0.53
1:AA:56:U:H2'	1:AA:57:G:H8	1.72	0.53
3:AC:71:ALA:HB2	3:AC:115:LEU:HD21	1.90	0.53
10:AJ:5:ARG:HD3	10:AJ:71:LEU:HD11	1.90	0.53
1:AA:1456:G:H22	20:AT:43:LEU:HD11	1.73	0.53
24:AY:67:C:H2'	24:AY:68:C:C6	2.42	0.53
27:BD:9:TYR:CZ	27:BD:13:ARG:HG2	2.44	0.53
29:BF:197:ASP:OD1	29:BF:197:ASP:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:BY:6:HIS:H	44:BY:6:HIS:CD2	2.26	0.53
45:BZ:7:ALA:HB3	45:BZ:61:LEU:HD12	1.90	0.53
1:CA:1324:A:O4'	1:CA:1362:C:H4'	2.09	0.53
1:CA:153:C:H2'	1:CA:154:C:C6	2.43	0.53
1:CA:937:A:H1'	1:CA:1379:G:N2	2.23	0.53
2:CB:223:ILE:HA	2:CB:226:ARG:HG2	1.89	0.53
2:CB:73:THR:HB	2:CB:95:GLN:O	2.08	0.53
1:CA:1338:G:H21	23:CX:41:C:H1'	1.73	0.53
25:DA:18:C:H2'	25:DA:19:C:C6	2.44	0.53
25:DA:692:C:O2'	27:DD:38:LYS:NZ	2.41	0.53
25:DA:903:C:H2'	25:DA:904:C:C6	2.43	0.53
31:DH:56:SER:HB3	31:DH:61:HIS:ND1	2.23	0.53
1:AA:1006:C:H42	1:AA:1023:G:H1	1.57	0.53
25:BA:270:C:H4'	25:BA:271:U:OP1	2.08	0.53
45:BZ:92:SER:O	45:BZ:130:PRO:HG2	2.08	0.53
1:CA:1292:U:OP2	7:CG:41:ARG:NH2	2.42	0.53
1:CA:920:U:H2'	1:CA:921:U:C6	2.44	0.53
7:CG:113:GLU:HG3	7:CG:118:VAL:HG12	1.89	0.53
25:DA:203:C:OP1	61:DA:4577:HOH:O	2.19	0.53
28:DE:82:ARG:HG2	28:DE:83:ASP:N	2.23	0.53
30:DG:114:ILE:HB	30:DG:117:PHE:HB2	1.90	0.53
31:DH:3:ARG:HB3	31:DH:6:ARG:HG2	1.90	0.53
32:DI:104:GLN:O	32:DI:105:HIS:ND1	2.42	0.53
1:AA:1095:U:H5''	1:AA:1109:C:O2	2.08	0.53
1:AA:96:U:O2'	1:AA:97:G:H5'	2.09	0.53
2:AB:77:ALA:HB2	2:AB:165:VAL:HG11	1.90	0.53
25:BA:2130:C:N4	25:BA:2203:G:H1	2.06	0.53
25:BA:2187:G:H1	25:BA:2194:U:H5	1.56	0.53
2:CB:189:ASP:HB3	2:CB:204:ASN:HA	1.90	0.53
23:CX:21:A:H3'	23:CX:46:G:O6	2.08	0.53
25:DA:2184:G:C2'	25:DA:2185:C:H5'	2.39	0.53
25:DA:2364:C:H2'	25:DA:2365:G:O4'	2.07	0.53
38:DS:34:HIS:O	38:DS:97:ARG:NH2	2.41	0.53
1:AA:1137:C:H4'	1:AA:1138:G:C2	2.42	0.53
1:AA:950:U:H2'	1:AA:951:G:H8	1.73	0.53
25:BA:1361:C:OP2	61:BA:4706:HOH:O	2.19	0.53
25:BA:2776:G:OP2	61:BA:4759:HOH:O	2.17	0.53
44:BY:102:CYS:SG	44:BY:103:GLY:N	2.81	0.53
52:D6:9:LEU:HA	52:D6:54:ILE:HB	1.91	0.53
25:DA:154(A):C:H2'	25:DA:157:U:H5'	1.91	0.53
25:DA:493:G:H2'	25:DA:494:G:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.43	0.53
1:AA:17:U:H2'	1:AA:18:C:C6	2.43	0.53
2:AB:145:LEU:HD12	2:AB:149:LEU:HD12	1.91	0.53
2:AB:71:VAL:HA	2:AB:93:VAL:HG23	1.90	0.53
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.41	0.53
19:AS:40:ILE:HD11	19:AS:71:LEU:HD23	1.90	0.53
25:BA:1834:A:H4'	27:BD:259:THR:HG23	1.89	0.53
25:BA:2101:U:O3'	47:B1:35:THR:OG1	2.27	0.53
1:CA:1095:U:P	1:CA:1108:G:H1	2.32	0.53
1:CA:221:C:H2'	1:CA:222:U:H6	1.73	0.53
1:CA:324:G:N7	61:CA:4062:HOH:O	2.33	0.53
1:CA:97:G:O2'	1:CA:98:G:H5''	2.08	0.53
13:CM:88:ARG:HG3	13:CM:98:VAL:HG12	1.90	0.53
19:CS:20:LEU:HD23	19:CS:23:ASN:HD22	1.73	0.53
25:DA:1688:U:O2	25:DA:1700:A:H5'	2.08	0.53
25:DA:1721:G:H2'	25:DA:1740:G:O6	2.09	0.53
25:DA:1816:G:O6	27:DD:35:LYS:NZ	2.22	0.53
25:DA:191:A:H2'	25:DA:192:C:C6	2.42	0.53
25:DA:644:A:H4'	25:DA:645:C:C5	2.44	0.53
25:DA:646:A:H2'	25:DA:647:G:O4'	2.08	0.53
25:DA:2751:G:H5'	31:DH:2:SER:HA	1.90	0.53
45:DZ:108:PRO:HG3	45:DZ:141:VAL:HB	1.90	0.53
1:AA:1203:C:H2'	1:AA:1204:A:C8	2.43	0.53
19:AS:41:VAL:HG13	19:AS:43:GLU:H	1.74	0.53
27:BD:146:GLU:HB2	27:BD:189:CYS:HB3	1.90	0.53
34:BO:16:ALA:HB2	34:BO:52:VAL:HG21	1.89	0.53
1:CA:1272:G:H2'	1:CA:1273:G:O4'	2.08	0.53
1:CA:1376:U:H2'	1:CA:1377:A:H8	1.71	0.53
1:CA:328:C:H4'	1:CA:329:A:H5'	1.91	0.53
1:CA:532:A:N6	3:CC:193:TYR:HB3	2.24	0.53
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.90	0.53
25:DA:667:U:O2	54:D8:2:PRO:HD2	2.08	0.53
25:DA:1996:C:H4'	25:DA:1997:G:OP1	2.09	0.53
25:DA:2283:C:H2'	25:DA:2284:C:O4'	2.09	0.53
25:DA:400:G:N7	61:DA:4657:HOH:O	2.33	0.53
25:DA:902:C:H2'	25:DA:903:C:H6	1.74	0.53
35:DP:59:LEU:HD23	54:D8:58:ILE:HD13	1.90	0.53
1:AA:347:G:H2'	1:AA:348:G:O4'	2.09	0.53
3:AC:44:GLU:HA	3:AC:52:LEU:HD12	1.91	0.53
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.09	0.53
1:AA:617:G:H4'	16:AP:44:THR:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:16:HIS:O	20:AT:19:SER:OG	2.24	0.53
35:BP:63:PRO:HG2	54:B8:25:MET:HB2	1.91	0.53
54:B8:42:ARG:HD2	61:B8:206:HOH:O	2.07	0.53
25:BA:1067:A:H3'	25:BA:1067:A:C8	2.44	0.53
25:BA:1513:G:O2'	25:BA:1593:C:O2'	2.26	0.53
39:BT:65:LYS:HE2	39:BT:67:SER:HB2	1.91	0.53
1:CA:991:U:C4	1:CA:1212:U:H1'	2.44	0.53
2:CB:71:VAL:HB	2:CB:164:VAL:HG13	1.89	0.53
50:D4:60:GLN:HA	50:D4:62:ARG:HG2	1.90	0.53
25:DA:27:G:O2'	25:DA:28:A:OP2	2.25	0.53
25:DA:465:G:OP1	53:D7:12:ARG:NH2	2.35	0.53
25:DA:910:A:H62	36:DQ:12:GLN:HA	1.74	0.53
26:DB:20:C:N4	26:DB:63:G:H1	2.05	0.53
28:DE:14:ILE:HG13	28:DE:21:VAL:HG13	1.90	0.53
33:DN:43:THR:N	33:DN:48:MET:SD	2.80	0.53
5:AE:33:VAL:HG21	5:AE:109:ILE:HA	1.91	0.53
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.74	0.53
47:B1:51:VAL:HG11	47:B1:74:VAL:HG21	1.91	0.53
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.44	0.53
1:CA:452:A:OP1	16:CP:43:LYS:NZ	2.37	0.53
2:CB:84:GLU:HB3	2:CB:219:VAL:HG21	1.91	0.53
50:D4:15:ILE:HG23	50:D4:21:VAL:HG22	1.90	0.53
25:DA:1423:G:H2'	25:DA:1424:G:H8	1.74	0.53
25:DA:1802:A:N1	25:DA:1822:G:H1'	2.24	0.53
27:DD:132:PRO:HD3	27:DD:190:TYR:CZ	2.43	0.53
1:AA:1298:C:H4'	1:AA:1299:A:O4'	2.08	0.53
1:AA:997:U:H2'	1:AA:998:G:H8	1.74	0.53
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.43	0.53
9:AI:50:LEU:HD13	9:AI:56:LEU:HA	1.90	0.53
25:BA:714:U:O2	54:B8:2:PRO:HD2	2.09	0.53
25:BA:211:A:H5''	25:BA:448:U:OP1	2.09	0.53
25:BA:922:G:H2'	25:BA:923:C:O4'	2.09	0.53
25:BA:1742:G:N7	27:BD:14:ARG:NH2	2.56	0.53
38:BS:14:VAL:O	38:BS:18:ILE:HG12	2.09	0.53
44:BY:92:ASN:N	44:BY:93:GLY:HA2	2.24	0.53
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.23	0.53
1:CA:1288:A:N3	1:CA:1352:C:O2'	2.40	0.53
2:CB:142:LEU:HA	2:CB:145:LEU:HD12	1.91	0.53
4:CD:165:MET:O	4:CD:167:GLY:N	2.42	0.53
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.09	0.53
25:DA:2227:A:OP2	61:DA:4521:HOH:O	2.19	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2556:C:H2'	25:DA:2557:G:O4'	2.09	0.53
25:DA:342:G:O6	61:DA:4680:HOH:O	2.15	0.53
25:DA:999:U:OP2	61:DA:4453:HOH:O	2.19	0.53
28:DE:9:VAL:HG13	28:DE:25:VAL:O	2.08	0.53
31:DH:98:LEU:HD12	31:DH:102:ALA:O	2.09	0.53
29:DF:34:TRP:CE2	35:DP:8:PRO:HG3	2.44	0.53
35:DP:97:PRO:HD3	35:DP:126:VAL:O	2.09	0.53
1:AA:1392:G:N2	1:AA:1502:A:H8	2.06	0.52
1:AA:193:C:H2'	1:AA:194:C:C6	2.43	0.52
1:AA:232:G:H1'	1:AA:262:A:N1	2.25	0.52
25:BA:1781:G:O2'	25:BA:2870:A:N1	2.34	0.52
1:CA:1028:C:C4	1:CA:1033:G:O6	2.62	0.52
1:CA:1054:C:H4'	1:CA:1055:A:OP1	2.08	0.52
8:CH:7:ALA:O	8:CH:11:THR:OG1	2.22	0.52
48:D2:65:ASN:OD1	48:D2:69:ARG:NH1	2.41	0.52
25:DA:2704:C:H2'	25:DA:2705:A:O4'	2.09	0.52
25:DA:527:C:H3'	61:DA:4467:HOH:O	2.08	0.52
25:DA:852:G:H2'	25:DA:853:G:H8	1.72	0.52
28:DE:48:GLN:HA	28:DE:80:GLU:HA	1.91	0.52
30:DG:19:LEU:HD22	30:DG:32:PRO:HG2	1.91	0.52
32:DI:120:ILE:HG21	32:DI:126:TYR:CE2	2.44	0.52
32:DI:128:LEU:O	32:DI:140:LEU:N	2.36	0.52
43:DX:12:VAL:HG22	43:DX:29:TRP:CE2	2.45	0.52
1:AA:405:U:O2'	1:AA:496:A:O2'	2.25	0.52
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.74	0.52
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.91	0.52
23:AX:7:G:H1	23:AX:66:C:H42	1.57	0.52
25:BA:2145:G:H1	25:BA:2197:C:N4	2.06	0.52
25:BA:2784:C:H2'	25:BA:2785:C:C6	2.44	0.52
25:BA:801:C:H2'	25:BA:802:C:H6	1.74	0.52
25:BA:1993:A:OP2	27:BD:242:ARG:NH2	2.42	0.52
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.40	0.52
7:CG:20:ASP:HB3	7:CG:23:VAL:HB	1.91	0.52
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.44	0.52
25:DA:2815:C:C5'	51:D5:29:THR:HG21	2.39	0.52
25:DA:1467:C:C5	25:DA:1546:C:H2'	2.45	0.52
25:DA:1593:G:H2'	25:DA:1594:G:C8	2.44	0.52
25:DA:1664:A:OP1	61:DA:4762:HOH:O	2.19	0.52
25:DA:2131:G:N7	25:DA:2133:G:N2	2.58	0.52
25:DA:403:U:H4'	25:DA:404:C:H5'	1.91	0.52
41:DV:43:GLU:OE2	41:DV:43:GLU:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:396:G:O2'	1:AA:398:C:OP1	2.16	0.52
25:BA:2740:G:O2'	34:BO:70:LYS:NZ	2.40	0.52
25:BA:236:G:H4'	25:BA:413:G:C5	2.44	0.52
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.45	0.52
1:CA:1174:G:H2'	1:CA:1175:G:H8	1.74	0.52
1:CA:1284:C:H5	1:CA:1285:A:HO2'	1.56	0.52
1:CA:17:U:H2'	1:CA:18:C:C6	2.45	0.52
1:CA:460:G:N2	1:CA:471:G:OP2	2.28	0.52
2:CB:138:LEU:HA	2:CB:141:GLU:HB3	1.92	0.52
9:CI:8:GLY:O	9:CI:15:ALA:N	2.39	0.52
25:DA:2206:G:H5'	25:DA:2207:G:N7	2.23	0.52
25:DA:223:A:O2'	25:DA:420:C:O2	2.27	0.52
28:DE:170:LEU:HB3	28:DE:184:VAL:HG22	1.92	0.52
30:DG:5:VAL:HG22	30:DG:8:LYS:H	1.74	0.52
1:AA:192:U:H2'	1:AA:193:C:C6	2.44	0.52
16:AP:3:LYS:HG2	16:AP:65:GLN:HB2	1.92	0.52
25:BA:1848:G:OP1	27:BD:88:ARG:NH2	2.40	0.52
37:BR:100:LEU:HD11	37:BR:113:LEU:HD23	1.92	0.52
5:CE:78:HIS:CE1	5:CE:143:ARG:H	2.27	0.52
25:DA:2309:A:H61	30:DG:79:ASN:ND2	2.08	0.52
31:DH:137:ASP:HB3	31:DH:140:LYS:HB3	1.92	0.52
1:AA:270:A:H2'	1:AA:271:C:C6	2.44	0.52
1:AA:576:G:O6	1:AA:880:C:O2'	2.25	0.52
1:AA:57:G:H2'	1:AA:58:C:C6	2.45	0.52
4:AD:105:VAL:HG13	4:AD:110:PHE:HB2	1.90	0.52
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.24	0.52
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.44	0.52
25:BA:1001:G:OP2	36:BQ:14:ARG:NH2	2.36	0.52
25:BA:2584:A:N7	28:BE:144:ARG:HD2	2.24	0.52
1:CA:1399:C:C2	1:CA:1502:A:N6	2.77	0.52
1:CA:954:G:H21	1:CA:1227:A:H62	1.56	0.52
1:CA:959:A:O2'	1:CA:984:C:O2'	2.21	0.52
48:D2:10:LEU:HD13	48:D2:14:ARG:HH12	1.74	0.52
50:D4:16:CYS:HA	50:D4:33:VAL:HB	1.91	0.52
25:DA:2473:U:O2	25:DA:2473:U:H2'	2.09	0.52
28:DE:72:VAL:HA	28:DE:73:GLU:CB	2.38	0.52
45:DZ:108:PRO:HB2	45:DZ:111:VAL:HG23	1.90	0.52
4:AD:168:ARG:H	4:AD:168:ARG:CD	2.23	0.52
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.92	0.52
8:AH:49:GLU:HG2	8:AH:62:TYR:HE1	1.74	0.52
25:BA:2053:A:C6	25:BA:2510:C:H1'	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BG:5:VAL:HG23	30:BG:104:GLU:OE2	2.09	0.52
39:BT:96:ARG:CZ	39:BT:96:ARG:HB3	2.38	0.52
1:CA:1002:G:H2'	1:CA:1003:G:H8	1.73	0.52
25:DA:2134:A:H2'	25:DA:2135:A:O4'	2.10	0.52
25:DA:212:G:H2'	25:DA:213:A:O4'	2.10	0.52
25:DA:236:C:H2'	25:DA:237:C:C6	2.45	0.52
30:DG:33:ARG:O	30:DG:34:LEU:HD23	2.10	0.52
28:DE:18:ASP:HB3	39:DT:82:LEU:HD21	1.91	0.52
1:AA:1051:C:H2'	1:AA:1052:U:H6	1.74	0.52
25:BA:1594:C:H2'	25:BA:1595:C:C6	2.44	0.52
25:BA:2108:U:H2'	25:BA:2109:G:C8	2.45	0.52
25:BA:2235:G:OP1	27:BD:172:TYR:OH	2.22	0.52
25:BA:934:A:H4'	25:BA:935:C:C5	2.44	0.52
32:BI:72:LEU:C	32:BI:74:ASN:H	2.13	0.52
25:BA:1233:U:H4'	41:BV:79:VAL:HG22	1.92	0.52
45:BZ:24:LEU:HB2	45:BZ:41:LEU:HD23	1.92	0.52
1:CA:1238:A:OP2	61:CA:4060:HOH:O	2.19	0.52
1:CA:975:A:C4'	1:CA:976:G:H5''	2.35	0.52
13:CM:3:ARG:HA	50:D4:34:GLU:HG2	1.92	0.52
25:DA:1636:C:H2'	25:DA:1637:A:C8	2.45	0.52
25:DA:2371:G:O6	61:DA:4325:HOH:O	2.17	0.52
13:CM:6:GLY:O	30:DG:115:ARG:NH2	2.42	0.52
1:AA:1124:G:N7	1:AA:1145:C:O2'	2.35	0.52
1:AA:1256:A:N6	1:AA:1278:U:O4'	2.40	0.52
1:AA:520:A:N1	1:AA:536:C:H1'	2.25	0.52
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.74	0.52
25:BA:1814:A:H5'	25:BA:2620:G:H4'	1.92	0.52
1:CA:629:G:H2'	1:CA:630:G:O4'	2.10	0.52
8:CH:28:ALA:HB3	8:CH:57:PRO:HB2	1.91	0.52
46:D0:68:GLU:HB2	46:D0:82:ARG:HH11	1.75	0.52
25:DA:128:C:H2'	25:DA:129:C:H6	1.74	0.52
25:DA:857:C:OP2	46:D0:77:ARG:NH2	2.43	0.52
25:DA:902:C:H2'	25:DA:903:C:C6	2.44	0.52
1:AA:1003:G:H2'	1:AA:1004:A:H4'	1.92	0.52
1:AA:501:C:H2'	1:AA:502:G:C8	2.45	0.52
25:BA:2123:G:H2'	25:BA:2124:U:C6	2.45	0.52
32:BI:4:ILE:HG12	32:BI:18:VAL:HG22	1.91	0.52
39:BT:112:ARG:HG3	39:BT:115:ARG:HH21	1.74	0.52
1:CA:1376:U:OP1	7:CG:98:SER:OG	2.19	0.52
1:CA:422:C:H4'	1:CA:423:G:C4	2.43	0.52
1:CA:688:G:H2'	1:CA:689:C:H6	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.25	0.52
1:CA:735:C:H2'	1:CA:736:C:H6	1.75	0.52
1:CA:827:U:H5''	1:CA:828:A:OP2	2.10	0.52
1:CA:922:G:H2'	1:CA:923:A:C8	2.45	0.52
1:CA:96:U:O2'	1:CA:97:G:H5'	2.09	0.52
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.45	0.52
19:CS:14:HIS:O	19:CS:18:LYS:HG3	2.10	0.52
47:D1:3:LYS:HB2	47:D1:61:ARG:HH12	1.74	0.52
25:DA:1530:C:HO2'	25:DA:1531:C:P	2.33	0.52
25:DA:27:G:N2	25:DA:512:G:H1'	2.24	0.52
25:DA:637:A:H5''	35:DP:117:GLU:HG2	1.92	0.52
25:DA:652(T):C:H2'	25:DA:652(U):G:C8	2.45	0.52
31:DH:20:ALA:HB1	31:DH:21:PRO:HD2	1.90	0.52
1:AA:439:A:C8	1:AA:439:A:H3'	2.45	0.52
1:AA:600:C:H2'	1:AA:601:C:C6	2.45	0.52
9:AI:23:ASN:HD22	9:AI:25:LYS:HG2	1.75	0.52
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.33	0.52
30:BG:66:GLN:NE2	30:BG:94:LEU:HD23	2.25	0.52
43:BX:57:LEU:HD11	43:BX:78:LYS:HG2	1.92	0.52
2:CB:158:LEU:HD23	2:CB:182:ILE:HD11	1.92	0.52
1:CA:261:U:OP2	20:CT:79:ARG:NH2	2.43	0.52
25:DA:1430:C:H2'	25:DA:1431:U:C6	2.44	0.52
25:DA:1264:G:H2'	25:DA:2014:A:N6	2.25	0.52
25:DA:526:A:N3	25:DA:2044:C:H1'	2.25	0.52
25:DA:2110:G:C2	25:DA:2120:G:H1'	2.44	0.52
39:DT:16:ARG:HH12	39:DT:19:LEU:HG	1.75	0.52
1:AA:1030(D):A:N6	1:AA:1031:G:H21	2.08	0.51
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.93	0.51
11:AK:99:GLN:HG3	11:AK:105:VAL:HG11	1.91	0.51
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.92	0.51
45:BZ:110:GLY:N	45:BZ:144:LEU:O	2.42	0.51
45:BZ:45:ASP:O	45:BZ:49:ARG:HG3	2.09	0.51
1:CA:1165:C:N4	1:CA:1171:G:H1	2.04	0.51
1:CA:336:C:H2'	1:CA:337:C:C6	2.45	0.51
1:CA:421:U:O2'	1:CA:423:G:N7	2.43	0.51
4:CD:157:LEU:O	4:CD:161:ASN:ND2	2.44	0.51
8:CH:34:GLU:HB3	8:CH:118:VAL:HG21	1.92	0.51
30:DG:64:THR:HB	30:DG:94:LEU:HD21	1.91	0.51
25:DA:2839:G:H5'	37:DR:46:GLY:HA2	1.90	0.51
1:AA:1063:C:H3'	1:AA:1064:G:H2'	1.93	0.51
27:BD:26:LYS:HE2	27:BD:28:GLU:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BE:21:VAL:HG23	28:BE:185:LYS:HD2	1.93	0.51
42:BW:18:ARG:NH1	42:BW:76:VAL:O	2.43	0.51
1:CA:992:U:H4'	1:CA:993:G:O5'	2.10	0.51
2:CB:221:LEU:HD23	2:CB:224:GLN:NE2	2.24	0.51
3:CC:32:LEU:O	3:CC:36:ASP:HB2	2.10	0.51
5:CE:81:GLU:HG2	5:CE:90:VAL:HG13	1.92	0.51
8:CH:64:LYS:HG2	8:CH:79:VAL:HG21	1.92	0.51
25:DA:857:C:H4'	46:D0:23:VAL:HG21	1.92	0.51
25:DA:1449:A:O2'	25:DA:1529:G:N2	2.21	0.51
25:DA:2075:U:OP2	25:DA:2238:G:O2'	2.26	0.51
25:DA:686:G:N2	25:DA:788:A:H61	2.08	0.51
26:DB:3:C:H2'	26:DB:4:C:H6	1.75	0.51
30:DG:137:GLU:HB3	30:DG:139:LEU:HG	1.91	0.51
31:DH:20:ALA:HB3	31:DH:23:ARG:HG3	1.92	0.51
25:DA:2849:U:P	39:DT:95:ARG:HH12	2.34	0.51
1:AA:1003:G:C2	1:AA:1004:A:N3	2.79	0.51
1:AA:1260:C:O5'	1:AA:1284:C:H4'	2.11	0.51
1:AA:1328:C:OP1	21:AU:21:TYR:OH	2.13	0.51
1:AA:192:U:H2'	1:AA:193:C:H6	1.76	0.51
14:AN:23:ARG:HD2	14:AN:28:GLY:O	2.10	0.51
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.10	0.51
25:BA:1639:G:H2'	25:BA:1640:G:C8	2.46	0.51
25:BA:174:U:H4'	25:BA:207:A:H4'	1.93	0.51
25:BA:395:C:OP2	61:BA:4985:HOH:O	2.19	0.51
25:BA:27:G:N2	25:BA:537:G:H1'	2.26	0.51
32:BI:27:ARG:HD2	47:B1:71:TYR:CZ	2.44	0.51
34:BO:98:VAL:HG13	34:BO:117:LEU:HB3	1.92	0.51
36:BQ:85:LYS:HD3	46:B0:7:LEU:HG	1.92	0.51
1:CA:834:C:H2'	1:CA:835:U:C6	2.45	0.51
8:CH:4:ASP:OD1	8:CH:7:ALA:N	2.27	0.51
19:CS:40:ILE:HD12	19:CS:71:LEU:HD12	1.91	0.51
25:DA:1231:G:H2'	25:DA:1232:G:C8	2.46	0.51
25:DA:1751:C:HO2'	25:DA:2861:G:HO2'	1.56	0.51
25:DA:2552:U:C2	25:DA:2554:U:H5'	2.46	0.51
25:DA:309:G:N3	25:DA:329:G:O2'	2.41	0.51
25:DA:839:U:H1'	25:DA:1191:G:H1'	1.92	0.51
25:DA:859:G:O2'	25:DA:916:G:O6	2.23	0.51
25:DA:323:G:C8	29:DF:171:PRO:HG3	2.45	0.51
1:AA:353:A:H5'	1:AA:353:A:H8	1.75	0.51
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.43	0.51
10:AJ:16:LEU:HD22	10:AJ:68:HIS:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:48:ILE:O	11:AK:50:TYR:N	2.36	0.51
47:B1:3:LYS:HB2	47:B1:61:ARG:NH1	2.25	0.51
25:BA:957:A:H2'	36:BQ:9:TYR:OH	2.09	0.51
36:BQ:30:GLY:HA2	36:BQ:107:ALA:HB2	1.92	0.51
1:CA:148:G:H2'	1:CA:149:A:C8	2.45	0.51
1:CA:992:U:H6	1:CA:992:U:H5'	1.76	0.51
2:CB:184:VAL:N	2:CB:198:ASP:OD2	2.28	0.51
2:CB:19:HIS:CG	2:CB:20:GLU:H	2.28	0.51
1:CA:671:G:H5'	6:CF:77:ARG:HH22	1.76	0.51
12:CL:56:ALA:HB2	12:CL:70:ILE:HD11	1.92	0.51
25:DA:1187:G:H5'	41:DV:81:TYR:CE1	2.45	0.51
25:DA:2286:A:H4'	25:DA:2287:A:O4'	2.11	0.51
25:DA:571:A:N6	25:DA:2499:C:O3'	2.43	0.51
25:DA:2657:A:O3'	31:DH:160:LYS:NZ	2.42	0.51
38:DS:77:ALA:HB1	38:DS:82:ILE:HB	1.93	0.51
33:DN:4:TYR:HB2	40:DU:101:ARG:NH1	2.26	0.51
41:DV:72:VAL:HG22	41:DV:85:LYS:HB3	1.93	0.51
1:AA:1052:U:H5''	1:AA:1053:G:OP2	2.11	0.51
25:BA:1410:G:P	47:B1:3:LYS:HG3	2.50	0.51
25:BA:185:A:H2'	25:BA:185:A:N3	2.26	0.51
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.46	0.51
5:CE:137:GLU:HA	5:CE:140:ARG:HB3	1.93	0.51
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.92	0.51
47:D1:95:LEU:HD12	47:D1:98:LEU:HD12	1.93	0.51
25:DA:1499:C:H2'	25:DA:1500:G:H8	1.76	0.51
25:DA:2646:C:H2'	25:DA:2647:U:O4'	2.11	0.51
25:DA:2823:A:OP1	28:DE:159:HIS:NE2	2.40	0.51
42:DW:12:ILE:O	42:DW:101:SER:OG	2.25	0.51
1:AA:1125:U:H1'	1:AA:1126:U:H6	1.74	0.51
1:AA:1161:C:O2'	1:AA:1162:C:H5'	2.11	0.51
1:AA:395:C:N4	61:AA:4042:HOH:O	2.43	0.51
1:AA:456:C:H2'	1:AA:457:C:C6	2.46	0.51
1:AA:984:C:N3	1:AA:1221:G:N2	2.50	0.51
1:AA:997:U:H2'	1:AA:998:G:C8	2.45	0.51
17:AQ:67:LYS:HA	17:AQ:70:ARG:HH12	1.76	0.51
44:BY:1:MET:HE3	44:BY:2:ARG:H	1.76	0.51
1:CA:991:U:H2'	1:CA:1212:U:C4	2.45	0.51
1:CA:997:U:C2'	1:CA:998:G:H5'	2.40	0.51
9:CI:24:GLY:HA2	9:CI:59:PHE:O	2.11	0.51
10:CJ:54:PHE:O	10:CJ:56:HIS:N	2.37	0.51
18:CR:26:LEU:HD22	18:CR:42:ARG:HE	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:839:U:H2'	25:DA:840:C:C6	2.45	0.51
32:DI:92:VAL:HG23	32:DI:120:ILE:HB	1.91	0.51
26:DB:75:G:O2'	45:DZ:10:ARG:NH2	2.44	0.51
1:AA:1004:A:N6	1:AA:1036:G:C5	2.77	0.51
1:AA:403:C:O2'	4:AD:122:ARG:NH1	2.43	0.51
1:AA:447:G:O6	1:AA:485:G:O2'	2.23	0.51
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	1.93	0.51
3:AC:64:VAL:HG13	3:AC:99:VAL:HA	1.92	0.51
50:B4:63:TYR:N	50:B4:64:GLY:HA2	2.25	0.51
55:B9:15:LYS:HE2	55:B9:17:ILE:HD13	1.92	0.51
25:BA:1091:A:H1'	25:BA:1093:G:N3	2.26	0.51
25:BA:260:A:N3	25:BA:395:C:O2'	2.38	0.51
28:BE:47:VAL:HG23	28:BE:84:PHE:O	2.10	0.51
30:BG:16:ARG:HB2	30:BG:17:PRO:HD3	1.92	0.51
32:BI:4:ILE:HD11	32:BI:44:LEU:HD12	1.93	0.51
1:CA:1128:C:H1'	1:CA:1147:C:N4	2.19	0.51
1:CA:954:G:H21	1:CA:1227:A:N6	2.09	0.51
1:CA:1402:C:H2'	1:CA:1403:C:O4'	2.11	0.51
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.76	0.51
25:DA:1288:U:C2	25:DA:1327:C:O2	2.64	0.51
25:DA:30:G:H2'	25:DA:31:C:C6	2.46	0.51
35:DP:59:LEU:HD21	54:D8:10:ALA:HA	1.91	0.51
38:DS:14:VAL:O	38:DS:18:ILE:HG12	2.11	0.51
44:DY:102:CYS:SG	44:DY:103:GLY:N	2.83	0.51
1:AA:946:A:O2'	1:AA:1333:A:N3	2.36	0.51
4:AD:3:ARG:HE	4:AD:118:ARG:HD3	1.76	0.51
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	1.92	0.51
50:B4:43:TYR:O	50:B4:45:GLY:N	2.44	0.51
25:BA:2402:U:P	54:B8:35:GLN:HE22	2.34	0.51
25:BA:2157:A:N6	25:BA:2178:G:O2'	2.36	0.51
25:BA:2021:C:H5''	25:BA:2736:C:O2'	2.11	0.51
1:CA:447:G:O6	1:CA:485:G:O2'	2.19	0.51
5:CE:57:LYS:HD3	5:CE:61:TYR:HE2	1.75	0.51
25:DA:2135:A:N7	25:DA:2136:C:N4	2.58	0.51
25:DA:2142:C:H2'	25:DA:2143:C:O4'	2.11	0.51
25:DA:221:A:C4	25:DA:266:G:N7	2.79	0.51
30:DG:170:ARG:HH21	30:DG:180:PHE:CB	2.23	0.51
42:DW:88:ARG:NH1	42:DW:94:ASP:OD2	2.43	0.51
1:AA:1530:G:H4'	1:AA:1530:G:OP1	2.10	0.51
1:AA:77:G:H2'	1:AA:78:G:H5'	1.93	0.51
1:AA:864:A:H2'	1:AA:865:A:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:918:A:H2'	1:AA:919:A:C8	2.46	0.51
12:AL:77:LEU:HD21	12:AL:107:ALA:HB2	1.92	0.51
13:AM:2:ALA:N	13:AM:8:GLU:OE1	2.44	0.51
25:BA:1831:C:OP1	27:BD:264:LYS:NZ	2.38	0.51
25:BA:1921:G:H2'	25:BA:1921:G:N3	2.25	0.51
25:BA:2203:G:O2'	25:BA:2204:G:OP1	2.28	0.51
25:BA:2125:C:N4	25:BA:2208:G:H1	2.06	0.51
25:BA:2576:A:C2	25:BA:2659:U:H4'	2.45	0.51
25:BA:441:C:H2'	25:BA:442:A:C8	2.46	0.51
25:BA:596:G:OP2	41:BV:78:LYS:NZ	2.39	0.51
25:BA:624:C:OP1	29:BF:108:LYS:HE3	2.11	0.51
30:BG:33:ARG:O	30:BG:161:THR:HG23	2.11	0.51
45:BZ:69:THR:HG22	45:BZ:90:VAL:HA	1.92	0.51
1:CA:1003:G:N2	1:CA:1025:U:O4	2.43	0.51
1:CA:1262:C:N3	1:CA:1273:G:N2	2.54	0.51
1:CA:972:C:O2'	10:CJ:55:LYS:O	2.29	0.51
25:DA:2849:U:OP2	39:DT:95:ARG:NH1	2.44	0.51
32:DI:5:LEU:HD12	32:DI:9:LEU:HD23	1.93	0.51
1:AA:267:C:OP1	17:AQ:67:LYS:HD2	2.11	0.51
1:CA:663:A:O3'	18:CR:64:ARG:NH2	2.38	0.51
10:CJ:25:GLU:O	10:CJ:29:ARG:HG2	2.11	0.51
1:CA:664:G:P	18:CR:64:ARG:HH21	2.34	0.51
52:D6:10:LEU:HG	52:D6:54:ILE:HG13	1.93	0.51
25:DA:2141:G:O6	25:DA:2150:U:O2	2.29	0.51
25:DA:2808:U:C2'	25:DA:2809:A:H5'	2.41	0.51
25:DA:392:C:H5''	25:DA:409:C:H5''	1.93	0.51
25:DA:484:C:H2'	25:DA:485:C:C6	2.47	0.51
25:DA:623:G:H2'	25:DA:624:C:C6	2.46	0.51
1:AA:184:G:H2'	1:AA:185:A:H8	1.76	0.50
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.44	0.50
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.91	0.50
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.76	0.50
51:B5:16:ARG:NH1	51:B5:17:ASP:OD1	2.44	0.50
25:BA:505:A:N3	25:BA:507:G:H5''	2.25	0.50
43:BX:1:MET:HE1	48:B2:26:ARG:HH21	1.76	0.50
44:BY:35:TYR:CE2	44:BY:69:ALA:HB3	2.46	0.50
1:CA:58:C:O2'	1:CA:388:G:N7	2.35	0.50
1:CA:735:C:H2'	1:CA:736:C:C6	2.45	0.50
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.93	0.50
24:CY:72:C:H4'	25:DA:1852:C:H5''	1.93	0.50
25:DA:1899:G:N3	25:DA:1899:G:H2'	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2348:A:H61	46:B0:43:THR:HG21	1.74	0.50
25:BA:1073:A:C2	25:BA:2500:A:H5'	2.47	0.50
25:BA:1320:A:N3	25:BA:1343:C:H1'	2.26	0.50
25:BA:1634:C:H2'	25:BA:1635:C:H6	1.77	0.50
25:BA:1817:A:H1'	25:BA:1960:A:N6	2.27	0.50
25:BA:2724:U:O2'	25:BA:2726:A:H5'	2.10	0.50
25:BA:956:A:N3	25:BA:2276:C:O2'	2.39	0.50
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.26	0.50
3:CC:66:VAL:HB	3:CC:101:LEU:HA	1.94	0.50
13:CM:19:LEU:HD21	13:CM:56:LEU:HD11	1.93	0.50
25:DA:1477:A:H2'	25:DA:1478:G:O4'	2.11	0.50
25:DA:195:A:H61	25:DA:198:C:H3'	1.74	0.50
25:DA:539:G:H2'	25:DA:540:C:H6	1.76	0.50
36:DQ:65:PHE:HB2	36:DQ:105:GLU:HB2	1.92	0.50
36:DQ:20:ALA:HA	36:DQ:99:PRO:HD2	1.92	0.50
1:AA:1226:C:P	13:AM:91:ARG:HH12	2.34	0.50
2:AB:19:HIS:NE2	2:AB:20:GLU:OE2	2.45	0.50
5:AE:152:ARG:HD3	8:AH:42:GLU:O	2.12	0.50
16:AP:57:ARG:NH2	16:AP:79:VAL:O	2.43	0.50
25:BA:2073:A:H4'	28:BE:141:ILE:HG12	1.94	0.50
25:BA:298:G:H2'	25:BA:299:G:H8	1.77	0.50
25:BA:876:A:N7	25:BA:2259:A:O2'	2.42	0.50
27:BD:145:VAL:HB	27:BD:155:LEU:HB2	1.92	0.50
27:BD:180:GLY:HA3	27:BD:275:LYS:HG3	1.92	0.50
30:BG:161:THR:HG22	30:BG:163:ALA:H	1.75	0.50
35:BP:97:PRO:HD3	35:BP:126:VAL:O	2.11	0.50
25:DA:2750:A:H8	25:DA:2750:A:OP1	1.94	0.50
33:DN:34:LEU:O	33:DN:49:GLY:HA3	2.10	0.50
1:AA:1060:C:OP1	14:AN:45:ARG:NH2	2.40	0.50
1:AA:1174:G:H2'	1:AA:1175:G:C8	2.46	0.50
2:AB:218:ALA:O	2:AB:222:ILE:HG13	2.10	0.50
52:B6:11:LEU:HB3	52:B6:49:HIS:HB3	1.93	0.50
25:BA:1952:G:O2'	25:BA:1990:G:O6	2.20	0.50
25:BA:2132:G:C2	25:BA:2142:G:H1'	2.46	0.50
25:BA:2230:U:O4'	47:B1:52:ARG:NH2	2.45	0.50
25:BA:2807:C:N4	25:BA:2813:G:H1	2.09	0.50
27:BD:242:ARG:HD3	27:BD:242:ARG:N	2.26	0.50
1:CA:1119:C:OP1	9:CI:83:ARG:NH1	2.44	0.50
1:CA:1244:C:H42	1:CA:1293:G:H1	1.59	0.50
1:CA:1338:G:H2'	1:CA:1339:A:C8	2.47	0.50
1:CA:222:U:H2'	1:CA:223:U:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:427:U:OP2	4:CD:36:ARG:NH2	2.45	0.50
4:CD:173:TRP:CZ3	4:CD:193:ASP:HB3	2.46	0.50
25:DA:2336:A:H61	46:D0:43:THR:HG22	1.77	0.50
32:DI:110:ASP:N	32:DI:130:TYR:OH	2.24	0.50
39:DT:106:SER:O	39:DT:110:ILE:HG13	2.12	0.50
40:DU:81:HIS:HD2	40:DU:84:LYS:HD3	1.77	0.50
25:DA:2012:G:OP1	42:DW:11:ARG:NH2	2.43	0.50
42:DW:60:ASN:HD22	42:DW:60:ASN:N	2.10	0.50
1:AA:1144:G:N2	1:AA:1146:A:H62	2.09	0.50
1:AA:540:G:H2'	1:AA:541:G:O4'	2.12	0.50
1:AA:664:G:N2	1:AA:741:G:H1	2.06	0.50
3:AC:124:ILE:HD12	3:AC:196:LEU:HD12	1.94	0.50
39:BT:29:ARG:HG3	39:BT:46:GLU:HB2	1.93	0.50
1:CA:1002:G:N1	1:CA:1038:C:O2	2.41	0.50
2:CB:174:VAL:O	2:CB:178:ARG:HB3	2.10	0.50
9:CI:96:LEU:HD22	9:CI:101:PHE:HB2	1.94	0.50
25:DA:2001:A:H2'	25:DA:2002:G:C8	2.46	0.50
25:DA:601:C:O2	25:DA:605:C:H4'	2.12	0.50
26:DB:8:U:H3	26:DB:113:G:H1	1.60	0.50
26:DB:31:C:H4'	30:DG:29:TRP:CZ2	2.47	0.50
32:DI:4:ILE:HG12	32:DI:18:VAL:HG22	1.93	0.50
1:AA:950:U:H2'	1:AA:951:G:C8	2.46	0.50
9:AI:29:ASN:OD1	9:AI:65:VAL:N	2.32	0.50
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.34	0.50
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.92	0.50
25:BA:1698:G:N7	37:BR:11:ASN:ND2	2.60	0.50
25:BA:2166:U:H2'	25:BA:2168:C:H5	1.77	0.50
25:BA:2177:G:H2'	25:BA:2178:G:O4'	2.12	0.50
25:BA:241:G:OP1	35:BP:50:ARG:NH1	2.45	0.50
25:BA:1002:A:N1	25:BA:2470:G:H4'	2.27	0.50
1:CA:1362:C:C2'	1:CA:1363:C:H5''	2.42	0.50
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.93	0.50
1:CA:716:A:N3	11:CK:118:GLY:HA2	2.25	0.50
3:CC:113:ALA:HB2	3:CC:202:ILE:HG13	1.94	0.50
15:CO:54:ARG:HG2	15:CO:58:MET:HE2	1.93	0.50
21:CU:15:ARG:HB2	21:CU:15:ARG:HH11	1.77	0.50
25:DA:2169:A:H2'	25:DA:2170:A:C8	2.47	0.50
25:DA:422:A:H2'	25:DA:423:A:C8	2.46	0.50
25:DA:455:C:N3	25:DA:472:A:H2'	2.26	0.50
25:DA:821:A:H2'	25:DA:946:G:H5''	1.92	0.50
26:DB:15:A:OP2	26:DB:69:G:N2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:DU:49:HIS:HA	40:DU:52:ARG:HB3	1.94	0.50
50:B4:59:PHE:N	50:B4:59:PHE:CD1	2.80	0.50
25:BA:2162:C:O2	25:BA:2162:C:H2'	2.10	0.50
25:BA:795:G:O6	42:BW:90:ARG:NH1	2.45	0.50
1:CA:1132:C:N4	1:CA:1142:G:H1	2.07	0.50
10:CJ:8:LEU:HD23	10:CJ:96:ILE:HG23	1.93	0.50
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.94	0.50
25:DA:1354:A:H2'	25:DA:1355:G:O4'	2.11	0.50
25:DA:2869:G:H2'	25:DA:2870:C:O4'	2.12	0.50
25:DA:921:G:C6	25:DA:922:U:C4	3.00	0.50
1:AA:473:G:C2'	1:AA:474:G:H5'	2.40	0.50
1:AA:504:C:H2'	1:AA:511:C:H5	1.77	0.50
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.94	0.50
24:AY:75:C:H5''	24:AY:76:A:H5'	1.94	0.50
50:B4:63:TYR:CD1	50:B4:63:TYR:N	2.80	0.50
51:B5:11:THR:HG23	51:B5:15:ARG:HB3	1.93	0.50
25:BA:2018:C:H4'	25:BA:2019:G:OP1	2.12	0.50
25:BA:2398:C:H2'	25:BA:2399:U:C6	2.47	0.50
29:BF:18:ARG:HG2	29:BF:19:GLU:H	1.75	0.50
1:CA:1353:G:OP1	21:CU:10:ARG:NH1	2.44	0.50
1:CA:707:C:H2'	1:CA:708:C:C6	2.47	0.50
25:DA:2059:A:O2'	29:DF:69:HIS:HD2	1.95	0.50
25:DA:253:C:OP2	54:D8:5:LYS:NZ	2.30	0.50
25:DA:586:A:N1	25:DA:809:G:O2'	2.34	0.50
30:DG:28:VAL:O	30:DG:31:VAL:HG12	2.12	0.50
1:AA:461:A:O2'	1:AA:470:C:H5'	2.12	0.50
2:AB:61:LEU:HD23	2:AB:68:ILE:HD11	1.94	0.50
6:AF:89:MET:HE1	18:AR:72:ARG:HB3	1.94	0.50
55:B9:25:VAL:HB	55:B9:34:GLN:HB2	1.92	0.50
25:BA:1809:U:H2'	25:BA:1815:A:N6	2.27	0.50
25:BA:2169:G:H2'	25:BA:2170:G:O4'	2.12	0.50
25:BA:559:U:H2'	25:BA:560:C:C6	2.47	0.50
39:BT:108:ARG:HH22	39:BT:112:ARG:NH1	2.09	0.50
1:CA:1119:C:N4	1:CA:1154:G:H1	2.05	0.50
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.45	0.50
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.94	0.50
11:CK:62:GLN:HG3	11:CK:97:ALA:HB2	1.92	0.50
23:CX:48:C:C2	23:CX:59:A:H1'	2.47	0.50
25:DA:61:G:H5'	48:D2:50:ILE:HG21	1.94	0.50
25:DA:1184:G:OP1	49:D3:30:ARG:HD2	2.11	0.50
25:DA:1528(A):A:H2'	25:DA:1529:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1590:U:H2'	25:DA:1591:G:H8	1.77	0.50
25:DA:817:C:H2'	25:DA:818:G:O4'	2.12	0.50
26:DB:3:C:H2'	26:DB:4:C:C6	2.47	0.50
29:DF:129:PHE:CD2	29:DF:163:VAL:HG21	2.47	0.50
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.47	0.49
1:CA:1037:C:H6	1:CA:1037:C:O5'	1.95	0.49
1:CA:429:U:H1'	1:CA:430:A:H5''	1.93	0.49
1:CA:620:C:H2'	1:CA:621:A:O4'	2.12	0.49
1:CA:953:G:H5'	1:CA:965:A:N6	2.23	0.49
7:CG:91:VAL:HB	7:CG:96:GLN:HG2	1.93	0.49
23:CX:61:C:H2'	23:CX:62:C:H6	1.76	0.49
47:D1:3:LYS:HB2	47:D1:61:ARG:NH1	2.26	0.49
25:DA:100:G:O2'	48:D2:7:ARG:NH2	2.43	0.49
25:DA:528:A:C2	25:DA:2042:A:H2'	2.47	0.49
30:DG:173:LEU:HB3	30:DG:178:PHE:CD1	2.47	0.49
31:DH:30:LYS:HG3	31:DH:80:SER:O	2.12	0.49
39:DT:22:PHE:CE2	39:DT:52:ILE:HD11	2.47	0.49
1:AA:1213:A:O2'	1:AA:1215:G:N7	2.34	0.49
4:AD:102:ASP:OD2	4:AD:118:ARG:NH1	2.44	0.49
4:AD:107:ARG:NH2	4:AD:194:LEU:HD22	2.17	0.49
25:BA:2549:U:H2'	25:BA:2550:C:C6	2.48	0.49
1:CA:297:G:N2	1:CA:300:A:OP2	2.43	0.49
1:CA:64:G:H4'	1:CA:65:U:H3'	1.94	0.49
1:CA:839:U:H3'	1:CA:840:C:C6	2.46	0.49
6:CF:4:TYR:HD1	6:CF:92:LYS:HA	1.77	0.49
25:DA:1772:G:OP1	61:DA:4511:HOH:O	2.19	0.49
25:DA:1667:G:O2'	25:DA:1991:U:O4	2.24	0.49
25:DA:2166:G:H5'	25:DA:2167:U:OP2	2.12	0.49
25:DA:2355:C:O3'	46:D0:24:LYS:HD2	2.11	0.49
45:DZ:54:HIS:CG	45:DZ:101:PRO:HG3	2.46	0.49
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.94	0.49
1:AA:662:G:H2'	1:AA:663:A:C8	2.47	0.49
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.93	0.49
1:AA:191:G:N2	20:AT:103:GLY:HA2	2.27	0.49
25:BA:768:C:H2'	25:BA:769:A:C8	2.47	0.49
1:CA:1118:C:H2'	1:CA:1119:C:C6	2.48	0.49
1:CA:1258:G:H21	1:CA:1279:A:H62	1.60	0.49
25:DA:1197:G:H2'	25:DA:1198:U:H6	1.77	0.49
25:DA:1581:G:H2'	25:DA:1582:C:O4'	2.12	0.49
25:DA:1363:C:O2'	25:DA:1809:A:N3	2.43	0.49
25:DA:2637:U:H5''	28:DE:82:ARG:NH2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DI:130:TYR:HD2	32:DI:138:ILE:HD12	1.77	0.49
36:DQ:75:THR:HG21	36:DQ:87:LYS:NZ	2.27	0.49
1:AA:1075:C:H2'	1:AA:1076:C:H5'	1.93	0.49
1:AA:16:A:O2'	5:AE:16:THR:HB	2.13	0.49
24:AY:71:G:H2'	24:AY:72:C:C6	2.48	0.49
25:BA:2152:U:H2'	25:BA:2153:G:N2	2.27	0.49
25:BA:18:C:O2'	25:BA:577:U:OP1	2.26	0.49
31:BH:144:VAL:O	31:BH:148:ILE:HG13	2.13	0.49
1:CA:1029:C:N3	1:CA:1032:G:C2	2.81	0.49
1:CA:1052:U:H5'	1:CA:1053:G:OP2	2.13	0.49
1:CA:937:A:H1'	1:CA:1379:G:H22	1.78	0.49
1:CA:532:A:H61	3:CC:193:TYR:CB	2.24	0.49
1:CA:863:U:O2'	1:CA:865:A:N7	2.39	0.49
2:CB:95:GLN:HB2	2:CB:148:TYR:HD1	1.77	0.49
2:CB:55:PHE:O	2:CB:59:GLU:N	2.35	0.49
13:CM:106:ASN:N	13:CM:106:ASN:OD1	2.44	0.49
25:DA:2394:C:OP2	54:D8:30:ARG:NH1	2.45	0.49
25:DA:39:C:H2'	25:DA:40:C:C6	2.47	0.49
27:DD:28:GLU:OE1	61:DD:413:HOH:O	2.19	0.49
36:DQ:37:LEU:HD11	36:DQ:130:LYS:HB2	1.94	0.49
1:AA:1027:C:O2	1:AA:1034:G:N1	2.45	0.49
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.34	0.49
1:AA:713:G:H2'	1:AA:714:G:C8	2.47	0.49
19:AS:41:VAL:HG22	19:AS:42:PRO:HD2	1.95	0.49
25:BA:904:C:N4	25:BA:905:U:O4	2.46	0.49
1:CA:1028:C:O2	1:CA:1033:G:N1	2.45	0.49
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.47	0.49
13:CM:79:LYS:NZ	13:CM:83:ASP:OD2	2.39	0.49
25:DA:82:G:N1	25:DA:103:A:OP2	2.42	0.49
25:DA:2035:G:OP1	61:DA:4476:HOH:O	2.19	0.49
25:DA:606:U:H4'	25:DA:658:C:H4'	1.95	0.49
25:DA:709:U:H2'	25:DA:710:G:C8	2.47	0.49
26:DB:33:G:C6	26:DB:34:U:C4	3.01	0.49
29:DF:184:TYR:CE1	35:DP:3:LEU:HD21	2.48	0.49
36:DQ:57:HIS:NE2	36:DQ:116:GLU:HB3	2.28	0.49
37:DR:72:ASP:OD2	37:DR:75:LEU:HB2	2.11	0.49
1:AA:741:G:H2'	1:AA:742:G:O4'	2.13	0.49
1:AA:743:U:H2'	1:AA:744:C:C6	2.48	0.49
2:AB:20:GLU:HB3	2:AB:190:THR:OG1	2.12	0.49
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.13	0.49
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1153:G:H2'	25:BA:1153:G:N3	2.28	0.49
25:BA:2157:A:H61	25:BA:2178:G:C2'	2.26	0.49
25:BA:2285:A:H2'	25:BA:2286:A:C8	2.47	0.49
25:BA:2045:G:H5'	25:BA:2629:C:H4'	1.95	0.49
25:BA:305:G:H1'	25:BA:384:G:N2	2.27	0.49
44:BY:1:MET:HE2	44:BY:1:MET:H3	1.78	0.49
1:CA:950:U:H2'	1:CA:951:G:H8	1.78	0.49
10:CJ:38:ILE:HG12	10:CJ:71:LEU:O	2.13	0.49
23:CX:76:A:H3'	25:DA:2585:U:C5	2.47	0.49
25:DA:2787:C:H1'	28:DE:62:PRO:HG3	1.93	0.49
25:DA:745:G:O6	61:DA:4342:HOH:O	2.19	0.49
35:DP:88:LEU:HD11	35:DP:114:ILE:HD12	1.93	0.49
1:AA:45:U:H2'	1:AA:46:G:C8	2.47	0.49
1:AA:589:C:H2'	1:AA:590:C:H5'	1.95	0.49
1:AA:839:U:H3'	1:AA:840:C:C5	2.47	0.49
1:AA:839:U:HO2'	1:AA:840:C:P	2.32	0.49
3:AC:42:LEU:O	3:AC:46:GLU:HG2	2.13	0.49
49:B3:29:ARG:N	49:B3:33:GLN:OE1	2.43	0.49
50:B4:46:GLN:N	50:B4:46:GLN:HE21	2.10	0.49
25:BA:2008:A:OP1	61:BA:4484:HOH:O	2.20	0.49
25:BA:2202:U:H2'	25:BA:2203:G:O4'	2.12	0.49
25:BA:225:C:H2'	25:BA:226:C:C6	2.48	0.49
25:BA:2624:C:OP2	51:B5:2:ALA:N	2.46	0.49
29:BF:29:ASN:H	29:BF:112:MET:CE	2.24	0.49
44:BY:15:VAL:HG21	44:BY:42:VAL:HG11	1.93	0.49
1:CA:189(K):U:H2'	1:CA:189(L):G:C8	2.47	0.49
1:CA:820:U:H4'	1:CA:821:G:OP2	2.13	0.49
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.95	0.49
3:CC:125:GLU:HG3	3:CC:190:ARG:O	2.12	0.49
1:CA:1106:G:H5''	3:CC:172:ARG:HG2	1.94	0.49
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.12	0.49
25:DA:2329:G:N2	46:D0:41:ARG:HB3	2.28	0.49
25:DA:112:U:H2'	25:DA:113:G:O4'	2.13	0.49
25:DA:1759:A:H4'	25:DA:2715:C:O4'	2.13	0.49
25:DA:297:C:H2'	25:DA:298:G:O4'	2.12	0.49
25:DA:800:A:OP1	25:DA:800:A:H8	1.95	0.49
31:DH:118:PRO:HG2	31:DH:121:ILE:HG13	1.95	0.49
33:DN:111:PRO:HA	33:DN:114:ARG:NH1	2.27	0.49
1:AA:1262:C:H2'	1:AA:1263:C:H6	1.78	0.49
1:AA:258:G:H2'	1:AA:259:G:H8	1.78	0.49
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:454:C:OP1	16:AP:75:ARG:NH2	2.45	0.49
49:B3:18:ASP:N	49:B3:18:ASP:OD1	2.46	0.49
25:BA:1219:A:H1'	25:BA:1220:U:C5'	2.43	0.49
25:BA:1232:G:H5''	41:BV:81:TYR:CE1	2.48	0.49
25:BA:1553:A:O2'	25:BA:1554:A:O4'	2.31	0.49
25:BA:2860:A:OP2	25:BA:2876:U:H5	1.96	0.49
30:BG:44:GLY:N	30:BG:88:ILE:O	2.45	0.49
36:BQ:118:LEU:HB2	36:BQ:131:ILE:HD13	1.95	0.49
1:CA:1122:U:H2'	1:CA:1123:A:C8	2.48	0.49
1:CA:1119:C:N3	1:CA:1154:G:N2	2.61	0.49
1:CA:1410:G:H2'	1:CA:1411:C:C6	2.48	0.49
1:CA:441:A:H3'	1:CA:442:C:C6	2.48	0.49
1:CA:627:G:H2'	1:CA:628:G:C8	2.46	0.49
3:CC:98:ASN:O	3:CC:100:ALA:N	2.46	0.49
10:CJ:20:ALA:HB1	10:CJ:37:PRO:HB3	1.94	0.49
53:D7:24:THR:O	53:D7:28:ARG:HG3	2.12	0.49
25:DA:1359:A:N1	25:DA:1372:U:C4	2.80	0.49
25:DA:2351:G:HO2'	25:DA:2352:A:H8	1.59	0.49
25:DA:2417:C:OP1	35:DP:65:ARG:NH2	2.44	0.49
32:DI:14:ASP:N	32:DI:17:GLN:OE1	2.43	0.49
41:DV:21:ARG:HG2	41:DV:91:TYR:CD2	2.47	0.49
1:AA:792:A:O2'	1:AA:794:A:N7	2.42	0.49
2:AB:24:TRP:CZ3	2:AB:26:PRO:HA	2.48	0.49
6:AF:81:ILE:HD11	27:BD:125:ILE:HB	1.94	0.49
23:AX:47:U:H5'	23:AX:48:C:H5'	1.95	0.49
25:BA:1039:G:OP1	40:BU:50:ARG:NH2	2.45	0.49
25:BA:1874:C:H5'	27:BD:253:GLN:HE22	1.76	0.49
1:CA:1427:U:H2'	1:CA:1428:A:C8	2.48	0.49
1:CA:218:C:C2'	1:CA:219:C:H5'	2.43	0.49
1:CA:35:G:H2'	1:CA:36:C:C6	2.47	0.49
1:CA:537:G:H2'	1:CA:538:G:C8	2.47	0.49
2:CB:94:ASN:HB3	2:CB:95:GLN:NE2	2.27	0.49
3:CC:54:ARG:HG3	3:CC:69:HIS:HB2	1.95	0.49
4:CD:98:GLU:HG2	4:CD:189:PRO:HG2	1.94	0.49
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.43	0.49
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	1.95	0.49
9:CI:128:ARG:NH2	23:CX:33:U:OP2	2.46	0.49
47:D1:91:LYS:HG2	47:D1:95:LEU:HD22	1.95	0.49
25:DA:143:G:H2'	25:DA:143(A):C:C6	2.48	0.49
25:DA:1508:A:H5'	25:DA:1509(A):A:N7	2.28	0.49
25:DA:1608:A:H1'	25:DA:1610:A:OP2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1889:A:N1	25:DA:2234:G:H1'	2.28	0.49
25:DA:468:G:N7	53:D7:39:ARG:NH2	2.56	0.49
1:AA:1095:U:OP1	1:AA:1108:G:N2	2.45	0.49
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.95	0.49
1:AA:1048:G:OP1	14:AN:3:ARG:HB3	2.13	0.49
20:AT:14:LYS:HG3	20:AT:17:ARG:NH2	2.27	0.49
45:BZ:151:HIS:C	45:BZ:153:SER:H	2.17	0.49
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.48	0.49
1:CA:194:C:H2'	1:CA:195:A:H5''	1.94	0.49
1:CA:520:A:N1	1:CA:536:C:H1'	2.28	0.49
1:CA:742:G:OP1	15:CO:35:ARG:NH2	2.46	0.49
1:CA:838:G:H1	1:CA:848:C:H42	1.60	0.49
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.78	0.49
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.13	0.49
25:DA:1865:G:N2	25:DA:1877:A:OP2	2.43	0.49
25:DA:2103:C:H2'	25:DA:2104:G:O4'	2.12	0.49
28:DE:179:GLU:HB3	28:DE:181:LEU:HD22	1.94	0.49
31:DH:73:ALA:O	31:DH:76:VAL:HG12	2.13	0.49
32:DI:88:ILE:HG12	32:DI:123:LEU:HD13	1.94	0.49
25:DA:2094:G:OP1	32:DI:22:LYS:HD2	2.13	0.49
1:AA:1172:C:H2'	1:AA:1173:G:C8	2.44	0.48
1:AA:1260:C:OP1	1:AA:1284:C:O2'	2.31	0.48
1:AA:1369:C:H2'	1:AA:1370:G:C8	2.48	0.48
1:AA:501:C:H2'	1:AA:502:G:H8	1.78	0.48
1:AA:539:A:H2'	1:AA:540:G:C8	2.47	0.48
1:AA:715:A:H2'	1:AA:716:A:C8	2.47	0.48
2:AB:78:GLN:O	2:AB:94:ASN:ND2	2.46	0.48
14:AN:4:LYS:C	14:AN:6:LEU:H	2.15	0.48
24:AY:4:C:H5'	25:BA:1907:A:H5''	1.95	0.48
25:BA:2377:G:O6	54:B8:39:LYS:HE3	2.13	0.48
25:BA:1444:C:OP1	43:BX:53:LYS:NZ	2.40	0.48
25:BA:2772:G:N7	61:BA:4232:HOH:O	2.35	0.48
25:BA:553:A:N1	25:BA:2064:A:H2'	2.28	0.48
28:BE:144:ARG:HB3	28:BE:145:LYS:H	1.43	0.48
32:BI:100:ALA:HA	32:BI:103:ARG:HD2	1.95	0.48
25:BA:1272:A:OP1	41:BV:84:LYS:HE2	2.13	0.48
1:CA:427:U:O2'	1:CA:541:G:OP1	2.27	0.48
2:CB:91:PRO:HG2	2:CB:155:LEU:HD23	1.95	0.48
25:DA:2121:G:H1	25:DA:2177:C:N4	2.08	0.48
25:DA:880:G:H2'	25:DA:881:G:H5'	1.95	0.48
3:AC:43:LEU:HD21	3:AC:91:LEU:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.78	0.48
12:AL:84:LEU:HB2	12:AL:105:TYR:CE2	2.48	0.48
50:B4:57:GLU:HB3	50:B4:58:ARG:HA	1.95	0.48
51:B5:5:PRO:O	61:B5:4001:HOH:O	2.20	0.48
25:BA:1223:C:H2'	25:BA:1224:C:H6	1.78	0.48
25:BA:1879:A:H2'	25:BA:1880:G:H8	1.78	0.48
25:BA:909:G:H2'	25:BA:910:A:O4'	2.13	0.48
27:BD:108:PRO:HG2	27:BD:111:LEU:HG	1.94	0.48
1:CA:444:C:H2'	1:CA:445:G:C8	2.47	0.48
25:DA:1591:G:H2'	25:DA:1592:C:C6	2.47	0.48
25:DA:1798:U:H5'	27:DD:259:THR:CG2	2.38	0.48
25:DA:2695:C:H2'	25:DA:2696:U:C6	2.48	0.48
26:DB:73:A:C4	26:DB:105:A:C2	3.00	0.48
29:DF:20:LEU:HA	29:DF:20:LEU:HD23	1.67	0.48
32:DI:77:LEU:HD12	32:DI:140:LEU:HD11	1.94	0.48
38:DS:10:ARG:HH21	38:DS:91:PRO:HB2	1.78	0.48
1:AA:1039:C:H2'	1:AA:1040:U:H6	1.78	0.48
1:AA:1304:G:C6	1:AA:1305:G:N1	2.81	0.48
16:AP:19:ILE:HG23	16:AP:37:GLY:C	2.33	0.48
25:BA:1475:G:H2'	25:BA:1476:C:C6	2.47	0.48
25:BA:2509:A:H5''	61:BA:4109:HOH:O	2.12	0.48
25:BA:886:U:H2'	25:BA:887:C:C6	2.49	0.48
31:BH:24:VAL:HG22	31:BH:35:VAL:HB	1.94	0.48
1:CA:359:U:H2'	1:CA:360:A:C8	2.48	0.48
1:CA:628:G:C2'	1:CA:629:G:H5'	2.42	0.48
3:CC:39:ILE:HG23	3:CC:91:LEU:HD11	1.94	0.48
25:DA:1495:A:H2'	25:DA:1496:A:C8	2.48	0.48
25:DA:1462:C:H4'	25:DA:2703:C:H5'	1.95	0.48
35:DP:38:GLN:O	35:DP:39:LYS:HB3	2.14	0.48
1:AA:1121:U:C2'	1:AA:1122:U:H5'	2.44	0.48
1:AA:166:G:H2'	1:AA:167:G:C8	2.48	0.48
1:AA:977:A:H1'	1:AA:982:U:O4	2.14	0.48
4:AD:154:ASN:HA	4:AD:159:ARG:HH21	1.78	0.48
13:AM:29:ARG:HD3	13:AM:64:TRP:CD2	2.49	0.48
25:BA:1091:A:OP1	25:BA:1092:A:H3'	2.14	0.48
25:BA:186:A:N6	25:BA:2442:A:O2'	2.46	0.48
25:BA:2658:C:H2'	25:BA:2659:U:O4'	2.14	0.48
25:BA:721:G:O2'	29:BF:74:ARG:HD3	2.14	0.48
25:BA:895:G:O6	25:BA:974:G:H2'	2.14	0.48
25:BA:895:G:N3	25:BA:978:A:H1'	2.28	0.48
29:BF:29:ASN:H	29:BF:112:MET:HE1	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BZ:105:VAL:O	45:BZ:140:ASP:HA	2.14	0.48
1:CA:1262:C:O2'	1:CA:1263:C:H5'	2.13	0.48
1:CA:73:G:C6	1:CA:97:G:C6	3.02	0.48
3:CC:47:LEU:HD12	3:CC:68:VAL:HG11	1.95	0.48
4:CD:78:LEU:HD22	4:CD:96:LEU:HB3	1.96	0.48
25:DA:1364:G:OP2	47:D1:3:LYS:HG3	2.13	0.48
54:D8:22:VAL:HG12	54:D8:50:LEU:HD12	1.94	0.48
25:DA:2006:C:O5'	25:DA:2006:C:H6	1.95	0.48
25:DA:2276:G:H5'	36:DQ:86:GLY:HA2	1.96	0.48
25:DA:625:G:N7	35:DP:107:LYS:NZ	2.51	0.48
25:DA:994:C:H1'	41:DV:10:LYS:HE3	1.94	0.48
25:DA:863:A:OP1	36:DQ:22:LYS:HG3	2.13	0.48
37:DR:2:ARG:NH1	37:DR:5:LYS:O	2.44	0.48
44:DY:9:LYS:HA	44:DY:10:GLY:HA2	1.51	0.48
1:AA:909:A:H2'	1:AA:910:C:O4'	2.14	0.48
3:AC:164:ARG:HD2	3:AC:166:GLU:HG2	1.95	0.48
15:AO:82:ILE:HD11	15:AO:88:ARG:HH11	1.77	0.48
50:B4:61:ARG:HG3	50:B4:62:ARG:N	2.27	0.48
25:BA:1411:A:OP2	47:B1:3:LYS:HG2	2.13	0.48
25:BA:1800:G:O2'	25:BA:1980:C:OP1	2.26	0.48
25:BA:2087:C:H2'	25:BA:2088:C:C6	2.48	0.48
25:BA:2376:C:H2'	25:BA:2377:G:O4'	2.13	0.48
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.14	0.48
1:CA:1362:C:H2'	1:CA:1363:C:H5''	1.95	0.48
2:CB:27:LYS:HD3	2:CB:193:ASP:OD1	2.14	0.48
25:DA:2161:C:H2'	25:DA:2162:G:C8	2.47	0.48
25:DA:2369:A:H2'	25:DA:2370:G:C8	2.48	0.48
25:DA:2557:G:H2'	25:DA:2558:C:H6	1.79	0.48
25:DA:271(P):C:H2'	25:DA:271(Q):G:O4'	2.13	0.48
25:DA:570:G:H5''	61:DA:4155:HOH:O	2.13	0.48
25:DA:705:A:H2'	25:DA:706:A:O4'	2.14	0.48
29:DF:117:ARG:NH2	29:DF:189:THR:O	2.46	0.48
30:DG:106:LEU:HA	30:DG:110:ALA:HB3	1.96	0.48
30:DG:105:LYS:NZ	30:DG:143:GLU:OE2	2.47	0.48
34:DO:63:VAL:HG11	34:DO:85:VAL:HG23	1.96	0.48
36:DQ:26:TYR:O	36:DQ:67:ARG:NH1	2.46	0.48
36:DQ:68:ILE:HG23	36:DQ:103:MET:HA	1.95	0.48
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.79	0.48
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.79	0.48
1:AA:429:U:H1'	1:AA:430:A:H5''	1.96	0.48
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:11:ILE:HB	5:AE:31:LEU:HB3	1.96	0.48
25:BA:287:G:N7	25:BA:448:U:H2'	2.29	0.48
25:BA:354:A:HO2'	25:BA:355:A:H8	1.59	0.48
25:BA:390:G:H2'	25:BA:391:G:C8	2.49	0.48
27:BD:10:THR:OG1	27:BD:13:ARG:HB2	2.14	0.48
25:BA:2650:G:OP1	28:BE:82:ARG:NH2	2.46	0.48
31:BH:124:GLU:HB2	31:BH:132:ARG:HB3	1.95	0.48
25:BA:2858:G:H8	39:BT:97:ALA:HB2	1.78	0.48
1:CA:299:G:H2'	1:CA:300:A:C8	2.49	0.48
1:CA:434:U:H2'	1:CA:435:C:C6	2.49	0.48
7:CG:47:CYS:HA	7:CG:50:ILE:HG12	1.95	0.48
19:CS:20:LEU:HA	19:CS:23:ASN:HB2	1.95	0.48
53:D7:9:ARG:HE	53:D7:47:ARG:HG3	1.78	0.48
25:DA:1378:A:OP1	53:D7:10:ARG:NH2	2.47	0.48
25:DA:1429:G:H2'	25:DA:1430:C:C6	2.48	0.48
25:DA:1939:U:OP1	25:DA:2604:U:O2'	2.32	0.48
25:DA:857:C:H1'	46:D0:26:TYR:CE1	2.49	0.48
25:DA:8:A:H2'	25:DA:9:U:H6	1.78	0.48
27:DD:17:THR:O	27:DD:211:ARG:NH2	2.47	0.48
31:DH:27:LYS:NZ	31:DH:32:GLU:OE2	2.41	0.48
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.02	0.48
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.49	0.48
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.13	0.48
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.77	0.48
1:AA:175:C:H2'	1:AA:176:C:H6	1.79	0.48
1:AA:389:A:N3	1:AA:389:A:H2'	2.29	0.48
1:AA:688:G:H2'	1:AA:689:C:C6	2.49	0.48
1:AA:97:G:O2'	1:AA:98:G:H8	1.96	0.48
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.13	0.48
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.28	0.48
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.34	0.48
23:AX:21:A:H5'	23:AX:22:G:OP1	2.13	0.48
50:B4:56:VAL:HG23	50:B4:57:GLU:HG3	1.95	0.48
25:BA:1495:G:H4'	25:BA:1589:A:OP1	2.13	0.48
25:BA:2186:C:H5	25:BA:2187:G:N3	2.12	0.48
25:BA:223:C:H2'	25:BA:224:U:H6	1.79	0.48
25:BA:2760:G:O6	25:BA:2768:C:H5''	2.12	0.48
25:BA:927:G:H2'	25:BA:928:G:H8	1.79	0.48
29:BF:164:ARG:O	29:BF:168:ARG:HB2	2.13	0.48
32:BI:43:ASN:HD22	32:BI:43:ASN:C	2.17	0.48
45:BZ:150:LEU:O	45:BZ:171:ILE:HG13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.48	0.48
57:CA:3176:PCY:H8	57:CA:3176:PCY:H181	1.55	0.48
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.96	0.48
3:CC:125:GLU:OE2	3:CC:125:GLU:N	2.46	0.48
25:DA:938:G:OP1	54:D8:52:LYS:HD2	2.14	0.48
25:DA:1637:A:H4'	25:DA:2711:A:O2'	2.14	0.48
1:CA:1494:G:N2	25:DA:1912:A:N3	2.61	0.48
1:CA:1493:A:H8	25:DA:1913:A:N1	2.12	0.48
25:DA:2776:A:H4'	25:DA:2777:G:H5''	1.95	0.48
25:DA:2809:A:H2'	25:DA:2810:A:C8	2.49	0.48
27:DD:3:VAL:HG13	27:DD:17:THR:HB	1.94	0.48
27:DD:182:LEU:HB2	27:DD:272:ALA:HB3	1.95	0.48
31:DH:9:ILE:HG12	31:DH:69:ARG:HD2	1.96	0.48
25:DA:1288:U:O4	37:DR:106:GLY:HA3	2.14	0.48
1:AA:153:C:H42	1:AA:169:C:N4	2.12	0.48
1:AA:495:A:N3	1:AA:496:A:C8	2.82	0.48
2:AB:81:VAL:HG12	2:AB:215:LEU:HD11	1.95	0.48
7:AG:149:ARG:HD2	11:AK:59:TYR:CE1	2.49	0.48
25:BA:155:C:H6	25:BA:155:C:OP2	1.97	0.48
25:BA:715:G:H5'	25:BA:716:G:OP2	2.13	0.48
25:BA:999:G:H5''	36:BQ:13:GLN:HB3	1.95	0.48
30:BG:144:ILE:HA	30:BG:148:MET:HE1	1.95	0.48
37:BR:55:ALA:HB2	37:BR:79:LEU:HD13	1.96	0.48
26:BB:28:C:H5''	38:BS:31:SER:HB3	1.95	0.48
42:BW:51:LEU:HD23	42:BW:105:VAL:HG11	1.95	0.48
1:CA:1036:G:H3'	1:CA:1037:C:C6	2.49	0.48
1:CA:302:G:N3	1:CA:556:C:H4'	2.29	0.48
1:CA:918:A:H2'	1:CA:919:A:C8	2.49	0.48
2:CB:166:ASP:HB3	2:CB:169:LYS:HB3	1.94	0.48
4:CD:74:GLN:NE2	4:CD:137:SER:OG	2.47	0.48
25:DA:2815:C:H2'	25:DA:2816:C:C6	2.49	0.48
25:DA:530:G:N1	61:DA:4457:HOH:O	2.17	0.48
27:DD:73:VAL:HG13	27:DD:120:GLY:HA3	1.96	0.48
28:DE:11:MET:HG2	28:DE:24:THR:HB	1.95	0.48
1:AA:921:U:O2	5:AE:19:MET:HB2	2.12	0.48
13:AM:9:ILE:HB	13:AM:18:ALA:HB1	1.96	0.48
30:BG:66:GLN:HG3	50:B4:1:MET:CE	2.44	0.48
54:B8:6:THR:HG22	54:B8:63:PRO:HD2	1.95	0.48
25:BA:1954:A:H2'	25:BA:1955:G:O4'	2.13	0.48
25:BA:275:C:H2'	25:BA:276:C:C6	2.48	0.48
25:BA:2818:U:H5''	25:BA:2900:G:O6	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BP:107:LYS:O	35:BP:110:TYR:HB2	2.13	0.48
36:BQ:1:MET:SD	36:BQ:1:MET:N	2.82	0.48
37:BR:22:ARG:NE	37:BR:69:ASP:OD1	2.41	0.48
1:CA:1057:G:C2'	1:CA:1058:G:H5'	2.44	0.48
1:CA:1095:U:H5''	1:CA:1109:C:O2	2.14	0.48
1:CA:1122:U:C4	1:CA:1123:A:N7	2.81	0.48
1:CA:539:A:H2'	1:CA:540:G:C8	2.48	0.48
3:CC:181:ASN:HD21	3:CC:204:LEU:HD12	1.77	0.48
25:DA:1796:U:H2'	25:DA:1797:C:H6	1.78	0.48
25:DA:2745:C:C4	25:DA:2746:U:C4	3.02	0.48
25:DA:642:G:H21	25:DA:646:A:H2	1.60	0.48
1:AA:1273:G:H3'	1:AA:1274:G:H8	1.79	0.48
2:AB:10:LEU:C	2:AB:12:GLU:H	2.17	0.48
3:AC:157:ILE:HD12	3:AC:164:ARG:HB3	1.96	0.48
5:AE:77:PRO:HD2	5:AE:142:LEU:HD22	1.95	0.48
25:BA:2101:U:OP1	47:B1:21:ARG:NH2	2.47	0.48
48:B2:32:LEU:HD13	48:B2:36:ARG:NH1	2.29	0.48
25:BA:197:C:H2'	25:BA:198:C:C6	2.49	0.48
25:BA:482:C:H4'	61:BA:4029:HOH:O	2.14	0.48
25:BA:661:G:OP1	35:BP:132:LYS:HE2	2.13	0.48
1:CA:600:C:H2'	1:CA:601:C:C6	2.49	0.48
1:CA:911:U:H2'	1:CA:912:C:C6	2.49	0.48
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.40	0.48
19:CS:3:ARG:HH22	19:CS:10:PHE:HD2	1.61	0.48
25:DA:1290:C:H2'	25:DA:1291:C:H6	1.79	0.48
25:DA:1899:G:O2'	25:DA:1900:A:OP2	2.29	0.48
25:DA:2647:U:H2'	25:DA:2648:C:C6	2.49	0.48
25:DA:2680:C:OP2	28:DE:111:ARG:NH2	2.47	0.48
25:DA:911:A:H2'	36:DQ:9:TYR:OH	2.13	0.48
28:DE:12:THR:HG22	39:DT:58:ASN:OD1	2.14	0.48
30:DG:3:LEU:HD12	30:DG:5:VAL:HG12	1.95	0.48
45:DZ:7:ALA:HB3	45:DZ:61:LEU:HD12	1.96	0.48
1:AA:911:U:H2'	1:AA:912:C:C6	2.49	0.47
12:AL:88:GLY:O	12:AL:99:HIS:HD2	1.96	0.47
19:AS:9:VAL:HG11	50:B4:61:ARG:NH2	2.29	0.47
30:BG:108:ASN:HD22	50:B4:22:ILE:HG21	1.79	0.47
54:B8:23:VAL:HG11	54:B8:47:LYS:HD3	1.94	0.47
25:BA:1629:C:O2'	25:BA:1632:A:N3	2.39	0.47
25:BA:207:A:C2	25:BA:224:U:H4'	2.49	0.47
25:BA:2162:C:N3	25:BA:2173:G:C6	2.82	0.47
43:BX:61:GLY:HA3	43:BX:73:ARG:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:83:A:H5'	44:BY:8:LYS:HG2	1.95	0.47
1:CA:1028:C:C2	1:CA:1033:G:C6	3.02	0.47
1:CA:1097:C:H1'	1:CA:1170:A:H1'	1.95	0.47
1:CA:880:C:OP1	12:CL:8:ASN:ND2	2.45	0.47
1:CA:984:C:H2'	1:CA:985:C:H6	1.78	0.47
1:CA:407:G:O4'	4:CD:119:GLN:NE2	2.47	0.47
1:CA:10:A:OP2	5:CE:126:ARG:HD2	2.14	0.47
25:DA:467:G:OP1	53:D7:33:ARG:HD2	2.13	0.47
25:DA:2114:A:N6	25:DA:2115:G:H21	2.12	0.47
25:DA:2131:G:C8	25:DA:2133:G:C2	3.02	0.47
25:DA:2734:A:H2'	25:DA:2735:G:O4'	2.13	0.47
25:DA:818:G:O2'	25:DA:838:C:O2'	2.23	0.47
26:DB:31:C:C2'	26:DB:32:C:H5'	2.44	0.47
30:DG:7:LEU:HD11	30:DG:107:LEU:HD12	1.95	0.47
32:DI:47:LEU:O	32:DI:51:ILE:HG13	2.14	0.47
42:DW:51:LEU:HD23	42:DW:105:VAL:HG11	1.96	0.47
1:AA:1392:G:H21	1:AA:1502:A:H8	1.59	0.47
25:BA:215:G:H21	25:BA:217:A:H62	1.61	0.47
25:BA:2798:C:H2'	25:BA:2799:U:O4'	2.14	0.47
25:BA:2804:C:H2'	25:BA:2805:G:C8	2.48	0.47
25:BA:842:C:H2'	25:BA:843:C:C6	2.49	0.47
25:BA:923:C:H2'	25:BA:924:U:O4'	2.14	0.47
44:BY:9:LYS:HA	44:BY:10:GLY:HA2	1.67	0.47
1:CA:814:A:N7	1:CA:816:A:C4	2.82	0.47
1:CA:938:A:C6	1:CA:939:G:C5	3.02	0.47
1:CA:739:C:OP1	15:CO:2:PRO:HD3	2.14	0.47
16:CP:3:LYS:HG2	16:CP:65:GLN:HB2	1.95	0.47
26:DB:2:C:H2'	26:DB:3:C:C6	2.49	0.47
45:DZ:5:LEU:HD13	45:DZ:6:LYS:O	2.14	0.47
1:AA:1149:C:H2'	1:AA:1150:U:C6	2.49	0.47
1:AA:1237:C:O2'	1:AA:1300:G:N2	2.33	0.47
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.49	0.47
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.96	0.47
1:AA:833:U:H2'	1:AA:834:C:C6	2.49	0.47
1:AA:96:U:H2'	1:AA:97:G:C8	2.50	0.47
1:AA:991:U:HO2'	1:AA:992:U:P	2.34	0.47
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.15	0.47
25:BA:1218:G:O2'	25:BA:1219:A:O5'	2.32	0.47
25:BA:2183:C:O2'	25:BA:2195:A:H4'	2.14	0.47
25:BA:2331:G:N2	38:BS:3:ARG:HA	2.30	0.47
25:BA:2596:U:H2'	25:BA:2597:U:H2'	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2885:C:OP1	39:BT:3:ARG:NH1	2.43	0.47
1:CA:1151:A:O2'	1:CA:1152:A:H8	1.98	0.47
1:CA:1238:A:C2	1:CA:1303:C:H4'	2.50	0.47
1:CA:1309:G:O2'	13:CM:77:ASN:ND2	2.47	0.47
1:CA:59:A:H3'	1:CA:331:G:H22	1.79	0.47
1:CA:750:G:H1'	15:CO:22:THR:HG1	1.78	0.47
50:D4:59:PHE:HA	50:D4:60:GLN:C	2.34	0.47
25:DA:1186:G:C2	25:DA:1187:G:H1'	2.49	0.47
25:DA:898:C:H2'	25:DA:899:A:O4'	2.14	0.47
26:DB:32:C:H2'	26:DB:33:G:O4'	2.15	0.47
30:DG:43:LEU:C	30:DG:45:GLU:H	2.17	0.47
34:DO:119:PRO:HB2	39:DT:68:TYR:CE2	2.48	0.47
25:DA:2683:C:P	39:DT:53:ARG:HH22	2.36	0.47
45:DZ:31:ARG:HD2	45:DZ:94:GLU:OE2	2.13	0.47
1:AA:1005:A:N3	1:AA:1036:G:N2	2.56	0.47
1:AA:1057:G:C2'	1:AA:1058:G:H5'	2.44	0.47
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.49	0.47
1:AA:144:G:H1	1:AA:178:C:N4	2.11	0.47
1:AA:649:G:H2'	1:AA:650:G:C8	2.47	0.47
3:AC:9:GLY:N	14:AN:49:HIS:O	2.46	0.47
25:BA:2623:U:H6	25:BA:2623:U:H5'	1.79	0.47
25:BA:302:A:H4'	25:BA:303:C:OP1	2.14	0.47
25:BA:662:A:H8	35:BP:117:GLU:HG3	1.79	0.47
1:AA:1464:G:OP2	39:BT:111:ARG:NH2	2.48	0.47
41:BV:34:GLU:HB3	41:BV:56:SER:HB2	1.97	0.47
1:CA:1057:G:H2'	1:CA:1058:G:H5'	1.95	0.47
1:CA:1165:C:N3	1:CA:1171:G:N2	2.63	0.47
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.49	0.47
1:CA:1465:C:H2'	1:CA:1466:C:O4'	2.15	0.47
1:CA:1493:A:H5''	1:CA:1494:G:OP2	2.14	0.47
2:CB:123:ALA:N	2:CB:127:ILE:HD12	2.27	0.47
25:DA:1131:G:C8	25:DA:2025:C:H4'	2.49	0.47
25:DA:2144:U:H1'	25:DA:2148:G:N2	2.29	0.47
25:DA:875:G:O2'	45:DZ:151:HIS:HE1	1.97	0.47
29:DF:137:LYS:HB3	29:DF:137:LYS:NZ	2.29	0.47
31:DH:118:PRO:HD2	31:DH:121:ILE:HG21	1.96	0.47
35:DP:39:LYS:HD2	35:DP:45:LEU:HD11	1.95	0.47
38:DS:50:SER:O	38:DS:76:LYS:NZ	2.45	0.47
41:DV:6:LYS:HB2	41:DV:38:LEU:HD21	1.95	0.47
45:DZ:50:GLN:OE1	45:DZ:50:GLN:N	2.47	0.47
1:AA:1239:A:H4'	1:AA:1240:U:H5''	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:542:G:OP1	4:AD:10:ARG:NH2	2.37	0.47
1:AA:630:G:O2'	1:AA:631:G:H5'	2.14	0.47
1:AA:818:G:HO2'	1:AA:820:U:H6	1.62	0.47
10:AJ:13:HIS:HA	10:AJ:16:LEU:HB3	1.97	0.47
1:AA:391:G:P	16:AP:28:ARG:HH12	2.37	0.47
26:BB:24:G:N7	26:BB:56:G:H2'	2.29	0.47
38:BS:59:LYS:HB2	38:BS:60:GLY:H	1.51	0.47
40:BU:86:ALA:O	41:BV:49:THR:HG23	2.15	0.47
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.29	0.47
1:CA:1342:C:H1'	9:CI:124:GLN:NE2	2.30	0.47
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.50	0.47
1:CA:728:A:H2'	1:CA:729:A:H8	1.76	0.47
1:CA:976:G:P	14:CN:32:SER:H	2.38	0.47
13:CM:81:LEU:HD22	13:CM:88:ARG:HB3	1.96	0.47
14:CN:24:CYS:O	14:CN:28:GLY:N	2.43	0.47
47:D1:83:GLU:HA	47:D1:84:GLY:HA2	1.66	0.47
19:CS:64:GLU:HB2	50:D4:59:PHE:CE1	2.49	0.47
25:DA:1149:G:H2'	25:DA:1150:C:C6	2.49	0.47
25:DA:1209:G:O2'	25:DA:1237:A:N1	2.38	0.47
25:DA:1486:A:O2'	25:DA:1487:G:H5'	2.14	0.47
25:DA:1505:C:H2'	25:DA:1506:C:C6	2.50	0.47
25:DA:1448:G:H4'	25:DA:1542:A:OP1	2.14	0.47
25:DA:2106:G:H2'	25:DA:2107:C:O4'	2.15	0.47
25:DA:2137:C:H2'	25:DA:2138:C:C5	2.49	0.47
25:DA:2483:C:H2'	25:DA:2484:G:O4'	2.15	0.47
25:DA:2615:U:OP1	61:DA:4295:HOH:O	2.20	0.47
25:DA:307:G:N2	25:DA:310:A:O5'	2.39	0.47
25:DA:484:C:H2'	25:DA:485:C:H6	1.80	0.47
43:DX:43:VAL:HG21	43:DX:81:VAL:HG11	1.95	0.47
44:DY:28:LYS:HD2	44:DY:40:GLU:HG3	1.95	0.47
1:AA:407:G:OP1	4:AD:115:ARG:HD3	2.15	0.47
1:AA:620:C:H2'	1:AA:621:A:O4'	2.13	0.47
4:AD:166:LYS:HD3	4:AD:178:VAL:HG11	1.96	0.47
4:AD:61:LYS:O	4:AD:65:ARG:HB2	2.15	0.47
8:AH:26:VAL:HG22	8:AH:59:LEU:HB2	1.97	0.47
24:AY:69:G:C2	24:AY:70:G:H1'	2.50	0.47
49:B3:26:LEU:O	49:B3:35:ARG:NE	2.46	0.47
25:BA:1189:A:OP1	33:BN:25:ARG:NH2	2.48	0.47
25:BA:777:C:H3'	61:BA:4849:HOH:O	2.15	0.47
25:BA:895:G:N9	25:BA:978:A:H8	2.12	0.47
45:BZ:138:GLU:N	45:BZ:156:LYS:HD3	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:359:U:H2'	1:CA:360:A:H8	1.78	0.47
1:CA:642:A:N3	8:CH:113:SER:OG	2.45	0.47
10:CJ:42:THR:HG21	10:CJ:66:ARG:HB3	1.96	0.47
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.54	0.47
25:DA:1131:G:H8	25:DA:2025:C:H4'	1.78	0.47
25:DA:2320:A:N3	25:DA:2320:A:H2'	2.30	0.47
25:DA:2579:C:H4'	28:DE:134:ILE:HG12	1.97	0.47
25:DA:797:C:H2'	25:DA:798:G:O4'	2.15	0.47
29:DF:29:ASN:H	29:DF:112:MET:CE	2.26	0.47
29:DF:164:ARG:O	29:DF:168:ARG:HB2	2.13	0.47
25:DA:2562:U:H1'	34:DO:23:ARG:HH11	1.80	0.47
38:DS:62:LYS:HA	38:DS:65:VAL:HB	1.96	0.47
1:AA:1442(B):A:C4	39:BT:118:ARG:NH2	2.83	0.47
1:AA:373:A:H2'	1:AA:374:A:H8	1.79	0.47
1:AA:439:A:N3	1:AA:496:A:C4	2.82	0.47
1:AA:472:A:H2'	1:AA:473:G:O4'	2.15	0.47
1:AA:745:C:H2'	1:AA:746:A:C8	2.49	0.47
2:AB:170:GLU:O	2:AB:174:VAL:HG23	2.15	0.47
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.47	0.47
20:AT:48:LYS:HD3	20:AT:48:LYS:HA	1.70	0.47
25:BA:1604:C:OP2	25:BA:1605:A:O2'	2.21	0.47
25:BA:2204:G:H2'	25:BA:2205:C:C6	2.49	0.47
25:BA:2639:G:O2'	25:BA:2794:A:N1	2.37	0.47
25:BA:831:A:C6	27:BD:229:VAL:HG11	2.50	0.47
30:BG:16:ARG:CZ	30:BG:31:VAL:HG11	2.44	0.47
1:CA:662:G:H2'	1:CA:663:A:C8	2.49	0.47
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.29	0.47
3:CC:164:ARG:HG2	3:CC:165:THR:H	1.79	0.47
5:CE:137:GLU:HG2	5:CE:140:ARG:HH11	1.78	0.47
7:CG:111:ARG:NH2	7:CG:126:ASP:OD2	2.46	0.47
1:CA:1118:C:OP1	9:CI:9:ARG:HD2	2.15	0.47
1:CA:750:G:H1'	15:CO:22:THR:OG1	2.14	0.47
47:D1:51:VAL:HG11	47:D1:74:VAL:HG21	1.95	0.47
25:DA:10:G:H2'	25:DA:11:G:C8	2.50	0.47
25:DA:1342:A:H2	25:DA:1396:U:HO2'	1.62	0.47
25:DA:1509(B):A:H2'	25:DA:1510:G:H8	1.79	0.47
1:CA:1493:A:H3'	25:DA:1913:A:N1	2.29	0.47
25:DA:2617:C:H2'	25:DA:2618:G:O4'	2.15	0.47
25:DA:948:G:H21	25:DA:985:C:P	2.37	0.47
26:DB:31:C:H2'	26:DB:32:C:H5'	1.95	0.47
30:DG:106:LEU:O	30:DG:111:LEU:HG	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DO:68:GLU:HB3	34:DO:78:ARG:HB2	1.96	0.47
36:DQ:75:THR:HG21	36:DQ:87:LYS:HZ2	1.79	0.47
36:DQ:11:LYS:NZ	36:DQ:88:GLY:O	2.33	0.47
38:DS:11:LYS:HD3	38:DS:91:PRO:HD3	1.95	0.47
1:AA:221:C:H2'	1:AA:222:U:C6	2.48	0.47
1:AA:811:C:O2'	1:AA:901:A:N1	2.43	0.47
25:BA:1974:A:C6	25:BA:1975:A:N1	2.83	0.47
25:BA:2156:A:HO2'	25:BA:2157:A:P	2.38	0.47
25:BA:484:G:C8	53:B7:37:LYS:HG2	2.49	0.47
25:BA:762:G:H2'	25:BA:763:A:O4'	2.15	0.47
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.80	0.47
1:CA:300:A:H1'	1:CA:565:U:O2	2.15	0.47
57:CA:3176:PCY:N20	57:CA:3176:PCY:O21	2.48	0.47
1:CA:390:C:H2'	1:CA:391:G:C8	2.50	0.47
1:CA:509:A:O2'	1:CA:510:A:OP1	2.26	0.47
1:CA:1375:A:O2'	7:CG:29:LYS:NZ	2.44	0.47
13:CM:91:ARG:NE	13:CM:97:PRO:O	2.48	0.47
15:CO:62:GLN:HE21	15:CO:66:LEU:HD13	1.79	0.47
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.96	0.47
23:CX:4:G:H1	23:CX:69:C:H42	1.62	0.47
47:D1:67:ILE:N	47:D1:68:PRO:HD2	2.30	0.47
49:D3:29:ARG:N	49:D3:33:GLN:OE1	2.36	0.47
25:DA:1639:U:C2'	25:DA:1640:C:H5''	2.44	0.47
25:DA:1697:G:OP2	25:DA:1698:A:O2'	2.21	0.47
25:DA:2019:A:H4'	40:DU:34:LYS:HD2	1.97	0.47
25:DA:2261:C:O2'	25:DA:2262:U:H5'	2.15	0.47
25:DA:325:G:H2'	25:DA:326:G:O4'	2.15	0.47
25:DA:864:G:N2	25:DA:913:U:C2	2.83	0.47
1:AA:1112:C:H1'	3:AC:179:ARG:HG2	1.95	0.47
1:AA:240:C:H2'	1:AA:241:C:C6	2.50	0.47
1:AA:250:A:H4'	1:AA:251:G:O5'	2.15	0.47
4:AD:170:VAL:HG12	4:AD:171:GLY:H	1.80	0.47
6:AF:62:TRP:CD1	18:AR:35:ARG:HD2	2.50	0.47
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.14	0.47
10:AJ:5:ARG:HB3	10:AJ:73:ASP:OD1	2.14	0.47
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.96	0.47
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	1.95	0.47
25:BA:1552:C:H2'	25:BA:1553:A:H8	1.79	0.47
25:BA:756:U:H2'	25:BA:757:G:C8	2.50	0.47
25:BA:801:C:H2'	25:BA:802:C:C6	2.50	0.47
26:BB:87:G:N2	26:BB:90:A:OP2	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BF:51:THR:HB	29:BF:88:VAL:CG1	2.45	0.47
1:CA:232:G:H1'	1:CA:262:A:N1	2.29	0.47
1:CA:690:G:C6	1:CA:691:G:C6	3.03	0.47
2:CB:207:ALA:O	2:CB:210:SER:HB3	2.15	0.47
4:CD:128:VAL:HG12	4:CD:129:ASN:ND2	2.29	0.47
4:CD:65:ARG:HG2	4:CD:75:PHE:CD1	2.50	0.47
25:DA:1686:C:H2'	25:DA:1687:G:O4'	2.14	0.47
25:DA:172:C:H2'	25:DA:173:G:C8	2.50	0.47
25:DA:1786:A:H1'	25:DA:1938:A:N6	2.29	0.47
25:DA:528:A:C2'	25:DA:529:A:H5''	2.44	0.47
25:DA:579:G:H2'	25:DA:580:C:C6	2.50	0.47
25:DA:761:A:OP2	61:DA:4073:HOH:O	2.20	0.47
26:DB:119:G:H2'	26:DB:120:A:C8	2.50	0.47
27:DD:124:PRO:HG2	27:DD:129:ASN:HD21	1.79	0.47
25:DA:2590:A:OP2	27:DD:238:GLY:HA2	2.14	0.47
32:DI:86:THR:O	32:DI:123:LEU:HD22	2.14	0.47
34:DO:34:THR:OG1	34:DO:35:VAL:N	2.47	0.47
38:DS:34:HIS:ND1	38:DS:53:SER:OG	2.41	0.47
44:DY:44:ILE:HA	44:DY:63:LYS:O	2.13	0.47
45:DZ:145:GLU:HG3	45:DZ:146:ILE:H	1.79	0.47
1:AA:1169:A:H2'	1:AA:1170:A:C8	2.50	0.47
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.97	0.47
8:AH:11:THR:HG22	8:AH:15:ASN:ND2	2.30	0.47
48:B2:23:LYS:O	48:B2:27:GLU:HG3	2.14	0.47
25:BA:895:G:C4	25:BA:978:A:H8	2.33	0.47
25:BA:1857:G:H4'	27:BD:242:ARG:CZ	2.45	0.47
31:BH:17:VAL:HG21	31:BH:50:VAL:HG21	1.97	0.47
37:BR:29:LEU:HD12	37:BR:116:LEU:HD11	1.97	0.47
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.14	0.47
4:CD:100:ARG:NH1	4:CD:137:SER:OG	2.48	0.47
20:CT:47:GLY:HA2	20:CT:48:LYS:C	2.36	0.47
1:CA:1326:C:H5''	21:CU:18:TYR:O	2.15	0.47
25:DA:579:G:O2'	25:DA:2019:A:OP1	2.28	0.47
25:DA:67:U:H2'	25:DA:68:G:H8	1.80	0.47
26:DB:11:C:OP2	26:DB:12:C:N4	2.36	0.47
29:DF:29:ASN:N	29:DF:112:MET:HE1	2.30	0.47
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.50	0.47
1:AA:1160:G:C6	1:AA:1161:C:C5	3.03	0.47
1:AA:189(K):U:H2'	1:AA:189(L):G:C8	2.50	0.47
2:AB:223:ILE:HA	2:AB:226:ARG:HG2	1.97	0.47
3:AC:131:ARG:NH1	3:AC:135:LYS:HE3	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:105:VAL:HG21	5:AE:128:PRO:HB3	1.97	0.47
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.50	0.47
13:AM:4:ILE:HG13	13:AM:57:ARG:HA	1.97	0.47
50:B4:68:ARG:HD2	50:B4:68:ARG:HA	1.62	0.47
25:BA:1074:A:H61	25:BA:1171:G:H2'	1.80	0.47
25:BA:555:G:C5	25:BA:2044:U:H5''	2.50	0.47
26:BB:48:A:H4'	38:BS:95:HIS:CD2	2.43	0.47
1:CA:1064:G:H4'	1:CA:1065:U:O5'	2.15	0.47
1:CA:1075:C:H2'	1:CA:1076:C:H5'	1.96	0.47
1:CA:114:U:H2'	1:CA:115:G:C8	2.50	0.47
1:CA:1159:U:O4'	1:CA:1182:G:N2	2.47	0.47
1:CA:266:G:H5''	1:CA:268:C:H41	1.79	0.47
1:CA:609:A:C5	1:CA:610:G:C8	3.03	0.47
1:CA:838:G:H1	1:CA:848:C:N4	2.13	0.47
1:CA:1279:A:OP2	10:CJ:9:ARG:NH1	2.48	0.47
25:DA:1266:G:O4'	42:DW:15:ARG:NH2	2.46	0.47
25:DA:1593:G:H2'	25:DA:1594:G:H8	1.79	0.47
25:DA:2065:C:H2'	25:DA:2066:C:C6	2.50	0.47
25:DA:2408:U:H2'	25:DA:2409:G:C8	2.49	0.47
25:DA:2687:U:H2'	25:DA:2688:U:O4'	2.14	0.47
25:DA:784:A:C8	25:DA:792:G:C5	3.02	0.47
29:DF:18:ARG:HG2	29:DF:19:GLU:H	1.80	0.47
30:DG:72:ARG:HA	30:DG:86:MET:O	2.15	0.47
32:DI:14:ASP:O	32:DI:17:GLN:HB3	2.15	0.47
38:DS:84:GLN:HA	38:DS:111:GLU:O	2.14	0.47
45:DZ:31:ARG:HB2	45:DZ:32:HIS:CD2	2.49	0.47
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.50	0.46
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.97	0.46
25:BA:1217:G:H3'	25:BA:1218:G:H5'	1.98	0.46
25:BA:600:G:O2'	25:BA:1300:A:OP1	2.30	0.46
25:BA:2298:A:H4'	25:BA:2299:A:O5'	2.15	0.46
25:BA:2348:A:H61	46:B0:43:THR:HG22	1.77	0.46
25:BA:2707:C:H2'	25:BA:2708:U:C6	2.50	0.46
25:BA:561:A:H2'	25:BA:562:C:C6	2.50	0.46
43:BX:47:PHE:O	43:BX:49:VAL:HG13	2.15	0.46
1:CA:25:C:H5'	1:CA:524:G:H1'	1.97	0.46
1:CA:838:G:H3'	1:CA:840:C:H41	1.78	0.46
1:CA:948:C:H2'	1:CA:949:A:H8	1.80	0.46
25:DA:128:C:H2'	25:DA:129:C:C6	2.50	0.46
25:DA:2171:A:H1'	25:DA:2172:U:C6	2.50	0.46
25:DA:71:A:H5''	25:DA:73:A:N9	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:774:A:H2'	25:DA:774:A:N3	2.30	0.46
37:DR:56:LYS:NZ	37:DR:90:ARG:O	2.47	0.46
45:DZ:61:LEU:HD22	45:DZ:67:LEU:HG	1.97	0.46
45:DZ:95:PRO:HA	45:DZ:130:PRO:HD3	1.97	0.46
1:AA:1003:G:N2	1:AA:1004:A:H1'	2.31	0.46
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.16	0.46
1:AA:165:C:H2'	1:AA:166:G:C8	2.50	0.46
1:AA:67:C:O2'	1:AA:171:A:N3	2.34	0.46
1:AA:429:U:H3'	4:AD:9:CYS:SG	2.55	0.46
1:AA:452:A:O2'	1:AA:453:A:OP2	2.26	0.46
1:AA:546:G:O2'	1:AA:548:G:O2'	2.27	0.46
2:AB:146:GLN:O	2:AB:150:SER:HB3	2.15	0.46
3:AC:78:GLY:HA3	3:AC:83:ARG:H	1.81	0.46
1:AA:407:G:OP1	4:AD:115:ARG:NH2	2.48	0.46
1:AA:8:A:N6	4:AD:205:GLU:O	2.48	0.46
6:AF:100:ASN:HB2	18:AR:28:GLU:HA	1.96	0.46
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.80	0.46
25:BA:1171:G:H5'	55:B9:37:GLY:HA2	1.97	0.46
25:BA:142:G:H1'	43:BX:37:THR:HG21	1.97	0.46
25:BA:1577:C:HO2'	25:BA:1578:C:P	2.37	0.46
25:BA:2158:C:H42	25:BA:2177:G:H1	1.63	0.46
25:BA:231:G:C8	54:B8:5:LYS:HG2	2.50	0.46
29:BF:129:PHE:CD2	29:BF:163:VAL:HG21	2.50	0.46
1:CA:1173:G:C2'	1:CA:1174:G:H5'	2.44	0.46
1:CA:234:C:H5''	17:CQ:70:ARG:HH21	1.81	0.46
2:CB:52:GLU:HG2	2:CB:56:ARG:NH2	2.31	0.46
23:CX:20:U:O2	23:CX:20:U:H2'	2.16	0.46
25:DA:1499:C:H2'	25:DA:1500:G:C8	2.50	0.46
25:DA:2147:G:H2'	25:DA:2148:G:H4'	1.96	0.46
25:DA:2322:A:H2'	25:DA:2323:G:O4'	2.16	0.46
25:DA:262:A:H2'	25:DA:263:C:O4'	2.14	0.46
25:DA:2848:G:C8	39:DT:97:ALA:HB2	2.51	0.46
25:DA:873:G:N2	25:DA:905:U:C2	2.82	0.46
25:DA:90:U:H1'	25:DA:92:A:C8	2.51	0.46
27:DD:71:ASP:HB3	27:DD:103:ARG:NH2	2.30	0.46
42:DW:45:TYR:CZ	42:DW:49:LYS:HE3	2.50	0.46
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.34	0.46
1:AA:1362:C:H2'	1:AA:1363:C:H5''	1.97	0.46
1:AA:328:C:H4'	1:AA:329:A:H5'	1.97	0.46
1:AA:300:A:H1'	1:AA:565:U:O2	2.15	0.46
7:AG:136:LYS:O	7:AG:140:ASP:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:97:PRO:HG2	13:AM:103:THR:HG22	1.97	0.46
25:BA:105:C:H2'	25:BA:106:U:H6	1.79	0.46
25:BA:2482:G:O6	25:BA:2488:A:O2'	2.25	0.46
25:BA:843:C:H2'	25:BA:844:C:C6	2.51	0.46
25:BA:932:C:H3'	25:BA:933:C:C5'	2.42	0.46
26:BB:76:G:N2	26:BB:101:G:O6	2.45	0.46
28:BE:116:VAL:HG13	28:BE:122:PHE:HB2	1.97	0.46
34:BO:35:VAL:HG11	34:BO:103:ALA:CB	2.41	0.46
25:BA:956:A:C5	36:BQ:13:GLN:HG3	2.51	0.46
1:CA:853:G:H2'	1:CA:854:G:H8	1.80	0.46
4:CD:105:VAL:HG13	4:CD:110:PHE:HB2	1.98	0.46
9:CI:20:ARG:HA	9:CI:21:PRO:HD3	1.82	0.46
25:DA:1710:C:H2'	25:DA:1711:C:C6	2.50	0.46
25:DA:2110:G:OP1	25:DA:2118:U:N3	2.40	0.46
28:DE:13:ARG:HG2	39:DT:58:ASN:HD21	1.81	0.46
31:DH:164:TYR:HB2	31:DH:167:GLU:HB2	1.97	0.46
1:AA:342:C:C2	1:AA:348:G:N2	2.83	0.46
1:AA:926:G:C6	1:AA:1505:G:C6	3.03	0.46
4:AD:164:ALA:O	4:AD:168:ARG:HD3	2.15	0.46
1:AA:975:A:N1	10:AJ:48:THR:HB	2.30	0.46
1:AA:1302:U:H5	13:AM:17:VAL:HG21	1.81	0.46
1:AA:103:C:P	20:AT:17:ARG:HH21	2.37	0.46
25:BA:1452:U:H2'	25:BA:1453:C:C6	2.51	0.46
25:BA:1715:A:H4'	25:BA:1716:A:O5'	2.16	0.46
25:BA:1841:A:H2'	25:BA:1842:G:O4'	2.15	0.46
25:BA:2308:U:OP2	38:BS:9:ARG:NH2	2.45	0.46
27:BD:61:LEU:O	27:BD:63:ARG:NH1	2.48	0.46
29:BF:33:LEU:HD13	29:BF:112:MET:HE2	1.96	0.46
38:BS:10:ARG:O	38:BS:14:VAL:HG13	2.16	0.46
1:CA:1005:A:OP2	1:CA:1006:C:N4	2.49	0.46
1:CA:1286:A:H2	21:CU:18:TYR:OH	1.99	0.46
11:CK:99:GLN:O	11:CK:101:SER:N	2.37	0.46
15:CO:5:LYS:NZ	15:CO:5:LYS:H	2.14	0.46
25:DA:1916:A:H2'	25:DA:1917:U:O4'	2.15	0.46
25:DA:18:C:H2'	25:DA:19:C:H6	1.79	0.46
25:DA:861:A:C2	25:DA:917:A:C4	3.03	0.46
30:DG:148:MET:HG3	30:DG:148:MET:H	1.47	0.46
30:DG:15:VAL:HG13	30:DG:175:LEU:HD23	1.97	0.46
1:AA:1429:C:H2'	1:AA:1430:C:C6	2.50	0.46
1:AA:79:G:N1	1:AA:90:U:N3	2.63	0.46
2:AB:207:ALA:O	2:AB:210:SER:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:217:A:H2'	25:BA:219:U:O4'	2.16	0.46
25:BA:2372:A:H2'	25:BA:2373:A:O4'	2.15	0.46
25:BA:2859:U:H4'	25:BA:2878:A:C2	2.50	0.46
25:BA:287:G:O2'	25:BA:448:U:OP2	2.23	0.46
25:BA:664:U:H2'	25:BA:665:C:C6	2.51	0.46
25:BA:904:C:H4'	46:B0:23:VAL:HG21	1.97	0.46
28:BE:12:THR:HG21	39:BT:11:GLU:HG2	1.98	0.46
30:BG:126:ASP:OD2	30:BG:130:ASN:ND2	2.48	0.46
32:BI:75:LEU:HD22	32:BI:105:HIS:ND1	2.30	0.46
1:CA:1203:C:H2'	1:CA:1204:A:O4'	2.15	0.46
1:CA:984:C:O5'	1:CA:984:C:H6	1.98	0.46
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.14	0.46
19:CS:30:LEU:HD11	19:CS:32:LYS:HG3	1.98	0.46
25:DA:570:G:H2'	25:DA:2030:A:C5	2.50	0.46
25:DA:2727:G:O2'	34:DO:70:LYS:NZ	2.48	0.46
25:DA:784:A:OP1	25:DA:2588:G:H5''	2.15	0.46
25:DA:912:C:N4	25:DA:913:U:O4	2.48	0.46
30:DG:173:LEU:HB3	30:DG:178:PHE:CG	2.51	0.46
35:DP:135:LEU:HD23	35:DP:135:LEU:HA	1.73	0.46
1:AA:189(C):C:H2'	1:AA:189(D):C:O4'	2.15	0.46
1:AA:401:C:H2'	1:AA:402:G:C8	2.50	0.46
1:AA:433:C:C2'	1:AA:434:U:H5'	2.46	0.46
2:AB:156:LYS:HB3	2:AB:156:LYS:HE2	1.72	0.46
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.50	0.46
10:AJ:5:ARG:HE	10:AJ:5:ARG:HB3	1.53	0.46
20:AT:45:GLN:HB3	20:AT:45:GLN:HE21	1.59	0.46
25:BA:1055:A:OP2	33:BN:37:LYS:NZ	2.44	0.46
25:BA:1067:A:H3'	25:BA:1067:A:H8	1.81	0.46
25:BA:1081:U:H2'	25:BA:1082:G:C8	2.50	0.46
25:BA:2332:A:H2'	25:BA:2332:A:N3	2.31	0.46
1:CA:1227:A:H3'	1:CA:1227:A:C8	2.51	0.46
1:CA:1401:G:C2	1:CA:1402:C:H1'	2.51	0.46
1:CA:397:A:H3'	1:CA:397:A:N3	2.29	0.46
1:CA:615:C:H2'	1:CA:616:G:O4'	2.16	0.46
1:CA:784:C:H4'	25:DA:1837:C:OP1	2.16	0.46
1:CA:814:A:H2'	1:CA:816:A:H5''	1.97	0.46
5:CE:88:LYS:HB3	5:CE:123:LEU:HB2	1.97	0.46
6:CF:45:LEU:HD12	6:CF:59:TYR:HD2	1.81	0.46
7:CG:111:ARG:HB3	7:CG:113:GLU:OE2	2.16	0.46
7:CG:116:ALA:O	7:CG:120:ILE:HG13	2.15	0.46
25:DA:1131:G:O6	25:DA:2040:C:H1'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1638:C:H4'	25:DA:2710:C:O2	2.16	0.46
25:DA:2308:G:H5''	25:DA:2310:A:OP2	2.15	0.46
25:DA:2395:C:O2'	47:D1:30:VAL:HG13	2.15	0.46
25:DA:2577:A:OP2	51:D5:3:LYS:NZ	2.43	0.46
25:DA:271(K):U:O2	32:DI:50:ARG:NE	2.49	0.46
38:DS:27:SER:HA	38:DS:88:ASP:HB3	1.98	0.46
1:AA:109:A:H2'	1:AA:326:G:N2	2.31	0.46
17:AQ:5:VAL:HA	17:AQ:59:ILE:O	2.15	0.46
49:B3:19:GLN:OE1	49:B3:52:HIS:NE2	2.40	0.46
50:B4:46:GLN:O	50:B4:46:GLN:HG2	2.16	0.46
52:B6:50:ARG:HB2	52:B6:50:ARG:HE	1.53	0.46
25:BA:239:G:OP2	54:B8:13:ARG:NH2	2.48	0.46
25:BA:1093:G:H2'	25:BA:1156:G:H22	1.81	0.46
25:BA:1790:A:H1'	25:BA:2723:A:C2	2.51	0.46
25:BA:2786:C:H2'	25:BA:2787:C:H6	1.80	0.46
25:BA:2856:G:H2'	25:BA:2857:U:O4'	2.16	0.46
32:BI:6:LEU:HD11	32:BI:37:VAL:HG23	1.98	0.46
33:BN:12:ARG:HH12	33:BN:38:HIS:HE2	1.64	0.46
33:BN:138:LEU:HA	33:BN:138:LEU:HD23	1.72	0.46
1:CA:1256:A:N6	1:CA:1278:U:O2'	2.48	0.46
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.46	0.46
1:CA:1298:C:H2'	7:CG:114:ARG:HH12	1.81	0.46
1:CA:421:U:H6	1:CA:421:U:H5'	1.81	0.46
1:CA:688:G:H2'	1:CA:689:C:C6	2.49	0.46
1:CA:951:G:N3	1:CA:970:C:O2'	2.39	0.46
2:CB:16:HIS:CB	2:CB:210:SER:HB2	2.37	0.46
8:CH:38:ILE:HD12	8:CH:118:VAL:HG12	1.98	0.46
25:DA:1651:G:H2'	25:DA:1652:A:O4'	2.15	0.46
25:DA:658:C:H2'	25:DA:659:C:C6	2.50	0.46
25:DA:662:G:H5''	35:DP:16:ARG:HG2	1.96	0.46
26:DB:19:G:H2'	26:DB:20:C:O4'	2.16	0.46
1:AA:1479:C:H2'	1:AA:1480:G:H8	1.80	0.46
1:AA:820:U:H4'	1:AA:821:G:OP2	2.16	0.46
2:AB:162:ILE:HD11	2:AB:184:VAL:HG22	1.97	0.46
9:AI:24:GLY:HA3	9:AI:57:GLY:HA2	1.97	0.46
25:BA:1159:U:H2'	25:BA:1160:G:C8	2.50	0.46
25:BA:1417:G:H2'	25:BA:1418:U:H5	1.79	0.46
25:BA:794:U:O2	25:BA:2036:A:H1'	2.15	0.46
25:BA:223:C:H2'	25:BA:224:U:C6	2.51	0.46
25:BA:555:G:O4'	25:BA:555:G:N3	2.46	0.46
25:BA:831:A:O4'	27:BD:227:ASN:ND2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BO:120:GLU:HG2	34:BO:122:LEU:HG	1.98	0.46
36:BQ:68:ILE:HG23	36:BQ:103:MET:HA	1.98	0.46
1:CA:1151:A:N3	10:CJ:39:PRO:HG3	2.31	0.46
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.16	0.46
1:CA:978:A:O2'	1:CA:1321:C:N4	2.49	0.46
1:CA:1374:A:O2'	7:CG:28:ASN:HB3	2.16	0.46
1:CA:171:A:H2'	1:CA:172:A:C8	2.51	0.46
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.98	0.46
53:D7:18:PHE:CE1	53:D7:22:MET:HG3	2.51	0.46
25:DA:656:G:H2'	25:DA:657:U:O4'	2.14	0.46
31:DH:118:PRO:O	31:DH:121:ILE:HB	2.16	0.46
33:DN:99:LEU:HD23	33:DN:99:LEU:HA	1.82	0.46
37:DR:95:THR:HG22	37:DR:116:LEU:HD23	1.98	0.46
26:DB:28:C:H5''	38:DS:31:SER:HB3	1.97	0.46
39:DT:51:ARG:HG3	39:DT:98:LYS:HD2	1.98	0.46
1:AA:1125:U:H1'	1:AA:1126:U:C6	2.50	0.46
1:AA:130:A:O2'	1:AA:131:C:O5'	2.31	0.46
1:AA:148:G:H1	1:AA:174:C:N4	2.14	0.46
1:AA:189(D):C:O2	1:AA:189(H):G:C6	2.69	0.46
1:AA:833:U:H2'	1:AA:834:C:H6	1.80	0.46
1:AA:542:G:P	4:AD:10:ARG:HH22	2.39	0.46
48:B2:32:LEU:HD13	48:B2:36:ARG:HH11	1.81	0.46
50:B4:33:VAL:HG12	50:B4:35:VAL:H	1.81	0.46
25:BA:1223:C:H2'	25:BA:1224:C:C6	2.51	0.46
25:BA:1633:A:H2'	25:BA:1634:C:C6	2.51	0.46
25:BA:1904:C:H2'	25:BA:1905:G:O4'	2.16	0.46
25:BA:2165:C:H2'	25:BA:2166:U:O4'	2.16	0.46
25:BA:2177:G:C2	25:BA:2178:G:H1'	2.51	0.46
25:BA:2236:G:H4'	25:BA:2238:C:C2	2.51	0.46
25:BA:553:A:OP2	33:BN:114:ARG:NH1	2.49	0.46
25:BA:624:C:O2'	25:BA:628:C:OP1	2.29	0.46
25:BA:936:C:H2'	25:BA:936:C:OP2	2.15	0.46
25:BA:1823:G:H5'	27:BD:205:VAL:HG13	1.98	0.46
34:BO:68:GLU:HB3	34:BO:78:ARG:HB2	1.97	0.46
35:BP:55:ARG:HG2	35:BP:56:SER:N	2.30	0.46
1:CA:1289:A:OP1	21:CU:9:ARG:NH2	2.48	0.46
1:CA:1236:A:O2'	1:CA:1304:G:H4'	2.15	0.46
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.15	0.46
1:CA:947:G:H2'	1:CA:948:C:O4'	2.16	0.46
5:CE:35:GLY:HA3	5:CE:112:LEU:HB3	1.98	0.46
7:CG:100:ALA:O	7:CG:104:LEU:HD13	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:51:ARG:HG2	9:CI:56:LEU:HD21	1.98	0.46
49:D3:24:LYS:HE3	49:D3:24:LYS:HB2	1.63	0.46
25:DA:195:A:H2'	25:DA:198:C:N4	2.30	0.46
25:DA:2156:G:H3'	25:DA:2157:G:C5	2.51	0.46
26:DB:16:G:N2	26:DB:68:C:O2	2.49	0.46
26:DB:46:A:C5	26:DB:47:C:C4	3.04	0.46
34:DO:23:ARG:HG3	34:DO:24:VAL:N	2.31	0.46
35:DP:96:THR:HG23	35:DP:99:LEU:HD23	1.98	0.46
1:AA:262:A:C6	1:AA:263:A:C6	3.03	0.46
6:AF:68:PRO:HB2	6:AF:71:ARG:HG3	1.97	0.46
9:AI:92:TYR:O	9:AI:96:LEU:HB2	2.16	0.46
25:BA:211:A:H3'	25:BA:448:U:H5'	1.98	0.46
25:BA:2186:C:H5	25:BA:2187:G:C4	2.34	0.46
31:BH:90:LYS:HD3	31:BH:159:GLU:HG2	1.97	0.46
33:BN:73:THR:OG1	33:BN:82:LEU:HD11	2.16	0.46
39:BT:8:LYS:HD3	39:BT:8:LYS:HA	1.77	0.46
1:CA:1220:G:O3'	19:CS:36:ARG:HD3	2.15	0.46
1:CA:202:U:H3'	1:CA:203:U:C6	2.51	0.46
7:CG:22:LEU:HD23	7:CG:63:LYS:HG2	1.98	0.46
1:CA:502:G:OP1	12:CL:118:SER:HB3	2.16	0.46
20:CT:54:LYS:HA	20:CT:57:ARG:NH2	2.31	0.46
23:CX:10:G:N2	23:CX:26:G:H1'	2.31	0.46
30:DG:108:ASN:HA	50:D4:37:SER:HB2	1.96	0.46
25:DA:1547:C:H2'	25:DA:1548:C:H6	1.81	0.46
25:DA:2712:U:OP1	25:DA:2714:G:H4'	2.16	0.46
30:DG:151:ALA:O	30:DG:153:ARG:HD3	2.16	0.46
30:DG:71:THR:N	30:DG:89:GLY:O	2.42	0.46
25:DA:832:G:H5'	35:DP:45:LEU:HD21	1.97	0.46
1:AA:1236:A:H4'	1:AA:1304:G:H4'	1.98	0.45
1:AA:1320:C:H2'	1:AA:1321:C:O4'	2.16	0.45
1:AA:1492:A:H2'	1:AA:1493:A:C8	2.50	0.45
1:AA:153:C:H42	1:AA:169:C:H42	1.63	0.45
1:AA:7:G:H5''	1:AA:298:A:O4'	2.16	0.45
57:AA:3191:PCY:C1	57:AA:3191:PCY:H112	2.46	0.45
1:AA:524:G:H2'	1:AA:525:C:C6	2.52	0.45
2:AB:192:SER:O	2:AB:194:PRO:HD3	2.16	0.45
2:AB:82:ARG:NH1	2:AB:86:GLU:OE2	2.49	0.45
50:B4:26:SER:OG	50:B4:27:THR:N	2.49	0.45
25:BA:1501:U:O2'	25:BA:1502:G:N7	2.41	0.45
25:BA:1759:C:H2'	25:BA:1760:U:O4'	2.16	0.45
25:BA:2301:G:OP1	61:BA:4230:HOH:O	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2418:U:H2'	25:BA:2418:U:OP2	2.16	0.45
25:BA:2541:G:H5''	25:BA:2542:A:H5''	1.98	0.45
25:BA:670:C:H5''	25:BA:671:A:OP2	2.16	0.45
33:BN:4:TYR:CD2	40:BU:100:VAL:HG11	2.51	0.45
25:BA:2331:G:H22	38:BS:3:ARG:CZ	2.27	0.45
1:CA:324:G:N1	1:CA:327:A:OP2	2.48	0.45
1:CA:461:A:O2'	1:CA:470:C:H5'	2.15	0.45
1:CA:909:A:H2'	1:CA:910:C:O4'	2.17	0.45
1:CA:9:G:H2'	1:CA:10:A:H8	1.81	0.45
25:DA:1789:A:H2'	25:DA:1790:C:C6	2.51	0.45
25:DA:1913:A:H4'	25:DA:1914:C:O5'	2.15	0.45
25:DA:2238:G:N3	25:DA:2238:G:H2'	2.31	0.45
25:DA:2432:A:H5''	25:DA:2433:A:OP2	2.15	0.45
25:DA:2850:A:N7	25:DA:2868:A:O2'	2.31	0.45
25:DA:2865:U:C4	25:DA:2866:U:C4	3.04	0.45
30:DG:105:LYS:HB3	30:DG:142:PRO:HG3	1.99	0.45
30:DG:44:GLY:N	30:DG:88:ILE:O	2.48	0.45
25:DA:637:A:H2'	35:DP:117:GLU:OE2	2.16	0.45
1:AA:175:C:H2'	1:AA:176:C:C6	2.51	0.45
1:AA:437:U:OP1	4:AD:155:LEU:HD21	2.16	0.45
18:AR:26:LEU:HD23	18:AR:29:PHE:CD2	2.50	0.45
25:BA:1580:G:H3'	25:BA:1581:U:O2	2.15	0.45
25:BA:2556:G:H1'	25:BA:2658:C:H4'	1.98	0.45
25:BA:636:G:O2'	25:BA:640:A:N1	2.45	0.45
33:BN:62:VAL:CG1	33:BN:66:LYS:HB2	2.46	0.45
39:BT:37:GLY:HA2	39:BT:38:ASN:HA	1.64	0.45
40:BU:112:ARG:H	40:BU:112:ARG:HG2	1.57	0.45
45:BZ:158:PRO:HG2	45:BZ:161:VAL:HG11	1.98	0.45
1:CA:1030(C):G:H2'	1:CA:1030(D):A:C8	2.51	0.45
1:CA:1353:G:H2'	1:CA:1354:C:C6	2.51	0.45
1:CA:137:C:H2'	1:CA:138:G:H8	1.82	0.45
1:CA:392:G:H2'	1:CA:393:A:C8	2.51	0.45
1:CA:637:G:H2'	1:CA:638:G:C8	2.51	0.45
3:CC:10:PHE:O	3:CC:178:LEU:HD11	2.16	0.45
3:CC:8:ILE:HG23	3:CC:16:ARG:HG2	1.97	0.45
4:CD:60:GLU:OE1	4:CD:199:ASN:N	2.34	0.45
50:D4:62:ARG:HD3	50:D4:62:ARG:H	1.81	0.45
25:DA:108:U:H2'	25:DA:109:G:C8	2.51	0.45
25:DA:1547:C:H2'	25:DA:1548:C:C6	2.52	0.45
25:DA:1970:A:OP1	61:DA:4253:HOH:O	2.21	0.45
25:DA:854:G:H2'	25:DA:855:G:H8	1.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DI:72:LEU:HA	32:DI:75:LEU:HD22	1.96	0.45
1:AA:1054:C:H4'	1:AA:1055:A:OP1	2.16	0.45
1:AA:1516:G:H2'	1:AA:1518:A:OP2	2.16	0.45
5:AE:79:GLU:H	5:AE:79:GLU:HG3	1.47	0.45
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.98	0.45
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.96	0.45
50:B4:68:ARG:HB3	50:B4:69:LYS:H	1.51	0.45
25:BA:1985:U:H4'	25:BA:1986:G:OP1	2.16	0.45
25:BA:2820:A:N6	25:BA:2900:G:O2'	2.44	0.45
25:BA:552:C:C5	25:BA:2792:U:H2'	2.51	0.45
30:BG:58:GLN:HE21	30:BG:58:GLN:HA	1.81	0.45
1:CA:1353:G:H2'	1:CA:1354:C:H6	1.80	0.45
1:CA:580:U:H2'	1:CA:581:G:O4'	2.16	0.45
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.56	0.45
5:CE:43:LEU:HD21	5:CE:132:ALA:HB1	1.98	0.45
7:CG:113:GLU:CG	7:CG:119:ARG:HG2	2.39	0.45
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.44	0.45
16:CP:19:ILE:HG22	16:CP:36:ILE:HG13	1.98	0.45
18:CR:22:VAL:HA	18:CR:25:THR:HG22	1.98	0.45
25:DA:973:A:C8	25:DA:1188:U:C2	3.04	0.45
25:DA:1214:A:N6	25:DA:1235:G:H1'	2.32	0.45
25:DA:1268:A:OP1	61:DA:4293:HOH:O	2.21	0.45
25:DA:1592:C:H2'	25:DA:1593:G:H8	1.82	0.45
25:DA:234:C:H2'	25:DA:235:U:C6	2.51	0.45
25:DA:2722:G:H2'	25:DA:2723:C:C6	2.51	0.45
25:DA:2645:G:N2	25:DA:2767:C:OP2	2.48	0.45
25:DA:286:C:H2'	25:DA:287:C:H6	1.81	0.45
25:DA:315:G:H2'	25:DA:316:C:C6	2.52	0.45
25:DA:362:U:O2'	25:DA:363:G:H5'	2.16	0.45
25:DA:729:G:OP2	27:DD:13:ARG:HD3	2.17	0.45
25:DA:819:A:C4	25:DA:1189:A:C2	3.05	0.45
25:DA:923:C:O5'	25:DA:923:C:H6	1.99	0.45
25:DA:1816:G:H3'	27:DD:62:TYR:CE1	2.51	0.45
1:AA:1285:A:O2'	1:AA:1286:A:OP2	2.34	0.45
1:AA:441:A:H3'	1:AA:442:C:C6	2.51	0.45
1:AA:509:A:H5''	4:AD:55:ALA:HB2	1.99	0.45
1:AA:691:G:H2'	1:AA:692:U:C6	2.52	0.45
1:AA:834:C:H2'	1:AA:835:U:C6	2.52	0.45
5:AE:105:VAL:O	5:AE:109:ILE:HD12	2.17	0.45
7:AG:78:ARG:NE	7:AG:154:TYR:O	2.48	0.45
46:B0:36:ILE:HD13	46:B0:58:THR:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B6:12:GLU:OE2	52:B6:52:VAL:HG21	2.15	0.45
25:BA:734:C:H5''	53:B7:2:LYS:HE2	1.98	0.45
25:BA:1087:C:H42	25:BA:1160:G:H1	1.63	0.45
25:BA:397:G:H8	25:BA:397:G:OP2	1.98	0.45
26:BB:13:A:N1	26:BB:69:G:O2'	2.42	0.45
27:BD:111:LEU:HA	27:BD:111:LEU:HD23	1.86	0.45
27:BD:275:LYS:HB3	27:BD:276:LYS:H	1.41	0.45
30:BG:64:THR:HB	30:BG:94:LEU:HD21	1.99	0.45
32:BI:40:THR:O	32:BI:44:LEU:HB2	2.17	0.45
32:BI:57:ARG:HA	32:BI:60:GLU:HB3	1.97	0.45
1:CA:1222:G:H5'	19:CS:77:THR:HG21	1.99	0.45
2:CB:121:LEU:H	2:CB:125:PRO:HG2	1.80	0.45
3:CC:122:GLU:HA	3:CC:125:GLU:OE1	2.15	0.45
4:CD:108:LEU:HD13	4:CD:174:LEU:HD13	1.98	0.45
1:CA:8:A:N6	4:CD:205:GLU:O	2.47	0.45
5:CE:84:PHE:N	5:CE:87:SER:O	2.48	0.45
25:DA:1509(A):A:H3'	25:DA:1509(B):A:H8	1.82	0.45
25:DA:271(D):G:H2'	25:DA:271(E):U:C6	2.51	0.45
25:DA:2785:C:OP1	28:DE:41:LYS:NZ	2.47	0.45
25:DA:300:A:OP1	44:DY:86:ARG:NH2	2.40	0.45
25:DA:307:G:H2'	25:DA:309:G:OP2	2.17	0.45
25:DA:687:C:N3	25:DA:788:A:H5'	2.31	0.45
25:DA:900:A:O2'	25:DA:901:A:OP1	2.30	0.45
26:DB:16:G:H1	26:DB:68:C:H42	1.63	0.45
26:DB:87:G:N2	26:DB:90:A:OP2	2.45	0.45
1:AA:1371:G:C6	1:AA:1372:U:C4	3.05	0.45
1:AA:162:A:H3'	1:AA:163:C:O4'	2.17	0.45
1:AA:171:A:H2'	1:AA:172:A:C8	2.51	0.45
1:AA:345:C:OP2	39:BT:39:ARG:NH2	2.46	0.45
1:AA:473:G:O2'	1:AA:474:G:H5'	2.17	0.45
1:AA:693:G:H2'	1:AA:694:A:C8	2.51	0.45
2:AB:55:PHE:HD1	2:AB:58:ILE:HD12	1.80	0.45
4:AD:116:GLN:NE2	4:AD:157:LEU:HD11	2.32	0.45
4:AD:88:VAL:O	4:AD:92:VAL:HG23	2.16	0.45
9:AI:55:ALA:HB1	9:AI:59:PHE:CD2	2.52	0.45
11:AK:38:ASN:HA	11:AK:39:PRO:HD3	1.84	0.45
11:AK:70:LYS:HB2	11:AK:70:LYS:HE2	1.71	0.45
48:B2:10:LEU:HD23	48:B2:10:LEU:HA	1.86	0.45
25:BA:1057:G:OP2	40:BU:70:ARG:NH2	2.49	0.45
25:BA:354:A:H2	25:BA:1255:A:C2'	2.29	0.45
25:BA:1387:U:OP2	25:BA:1440:U:O2'	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1688:A:H2'	25:BA:1689:G:O4'	2.17	0.45
25:BA:1845:G:H4'	27:BD:51:VAL:HG21	1.97	0.45
25:BA:2357:G:N3	25:BA:2393:C:H2'	2.32	0.45
25:BA:2564:U:C2	25:BA:2566:U:H5'	2.51	0.45
38:BS:87:PHE:HB2	38:BS:112:PHE:CE2	2.52	0.45
1:CA:1005:A:H3'	1:CA:1006:C:H5''	1.98	0.45
1:CA:21:G:H2'	1:CA:22:G:C8	2.51	0.45
1:CA:587:G:N2	1:CA:754:C:OP2	2.48	0.45
3:CC:79:ARG:H	3:CC:82:GLU:HB3	1.81	0.45
5:CE:12:LEU:O	5:CE:30:ALA:HA	2.17	0.45
25:DA:1999:C:H4'	25:DA:2723:C:O2	2.17	0.45
25:DA:2436:G:C6	25:DA:2437:U:C4	3.05	0.45
25:DA:2497:A:H5''	61:DA:4062:HOH:O	2.16	0.45
25:DA:2836:U:H2'	25:DA:2837:G:C8	2.51	0.45
26:DB:42:C:O2	30:DG:93:THR:N	2.27	0.45
36:DQ:118:LEU:HB2	36:DQ:131:ILE:HD13	1.99	0.45
1:AA:1149:C:H2'	1:AA:1150:U:H6	1.81	0.45
1:AA:1218:C:OP2	14:AN:9:LYS:NZ	2.33	0.45
1:AA:1486:G:H2'	1:AA:1487:G:O4'	2.16	0.45
1:AA:444:C:H2'	1:AA:445:G:C8	2.52	0.45
1:AA:537:G:H2'	1:AA:538:G:C8	2.49	0.45
12:AL:124:LYS:HA	12:AL:125:PRO:HD3	1.79	0.45
1:AA:581:G:OP1	15:AO:65:ARG:NH2	2.49	0.45
25:BA:2507:G:H5''	36:BQ:82:ARG:HG2	1.98	0.45
25:BA:776:G:OP2	27:BD:13:ARG:NH1	2.49	0.45
28:BE:24:THR:HG23	28:BE:184:VAL:HG12	1.98	0.45
37:BR:56:LYS:NZ	37:BR:90:ARG:O	2.50	0.45
1:CA:1005:A:HO2'	1:CA:1006:C:P	2.40	0.45
1:CA:1142:G:H3'	1:CA:1143:G:H8	1.81	0.45
1:CA:187:C:O2'	20:CT:89:ARG:NH2	2.49	0.45
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.50	0.45
1:CA:693:G:H2'	1:CA:694:A:C8	2.52	0.45
1:CA:70:G:H1	1:CA:99:U:H3	1.65	0.45
2:CB:169:LYS:HD3	2:CB:169:LYS:O	2.17	0.45
2:CB:161:ALA:HB1	2:CB:185:ILE:CD1	2.47	0.45
1:CA:537:G:H5''	12:CL:113:ARG:NH1	2.32	0.45
21:CU:2:GLY:O	21:CU:4:GLY:N	2.49	0.45
50:D4:40:HIS:O	50:D4:44:THR:N	2.43	0.45
25:DA:1197:G:H2'	25:DA:1198:U:C6	2.52	0.45
25:DA:443:A:H1'	25:DA:1201:C:O4'	2.17	0.45
25:DA:1266:G:O2'	25:DA:2012:G:O6	2.23	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1638:C:H5''	25:DA:2710:C:O2'	2.15	0.45
25:DA:414:C:H2'	25:DA:415:A:C8	2.52	0.45
31:DH:126:PRO:HD2	31:DH:130:ARG:O	2.17	0.45
31:DH:175:LYS:HB2	31:DH:175:LYS:HE3	1.76	0.45
25:BA:2132:G:O2'	25:BA:2142:G:OP2	2.35	0.45
25:BA:2240:G:OP1	27:BD:261:LYS:NZ	2.34	0.45
25:BA:240:A:C5	25:BA:241:G:H1'	2.51	0.45
25:BA:2902:G:H4'	25:BA:2903:G:O5'	2.17	0.45
1:CA:1125:U:C2	10:CJ:38:ILE:HD12	2.52	0.45
1:CA:1174:G:H2'	1:CA:1175:G:C8	2.51	0.45
2:CB:33:TYR:N	2:CB:41:ILE:O	2.41	0.45
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.98	0.45
19:CS:23:ASN:HA	19:CS:27:GLU:CD	2.37	0.45
25:DA:1262:A:H2	51:D5:10:LYS:HD2	1.80	0.45
25:DA:1002:G:H22	25:DA:1154:G:H1'	1.82	0.45
25:DA:1452:A:O2'	25:DA:1453:U:H2'	2.17	0.45
25:DA:1688:U:H2'	25:DA:1698:A:N6	2.32	0.45
25:DA:1779:U:H2'	61:DA:4760:HOH:O	2.15	0.45
25:DA:2114:A:C2	25:DA:2115:G:H1'	2.52	0.45
25:DA:2224:G:H4'	25:DA:2226:C:C2	2.51	0.45
25:DA:2741:A:H2'	25:DA:2742:C:O4'	2.16	0.45
25:DA:906:G:O2'	36:DQ:67:ARG:NH2	2.39	0.45
26:DB:42:C:O2'	30:DG:66:GLN:HG2	2.16	0.45
30:DG:15:VAL:HG12	30:DG:19:LEU:HD12	1.98	0.45
32:DI:65:ALA:O	32:DI:69:LYS:N	2.49	0.45
34:DO:29:ASN:OD1	34:DO:29:ASN:N	2.49	0.45
37:DR:28:LEU:HD12	37:DR:48:VAL:HG11	1.99	0.45
1:AA:1221:G:H4'	19:AS:53:ASN:O	2.16	0.45
1:AA:303:A:H2'	1:AA:304:U:O4'	2.17	0.45
1:AA:116:A:H61	1:AA:313:A:H1'	1.81	0.45
1:AA:624:C:H2'	1:AA:625:G:H8	1.82	0.45
2:AB:109:SER:HA	2:AB:112:VAL:HG13	1.97	0.45
5:AE:12:LEU:HD22	5:AE:13:ILE:N	2.32	0.45
13:AM:3:ARG:HD2	13:AM:9:ILE:CG1	2.46	0.45
25:BA:1388:A:O2'	25:BA:1390:G:OP2	2.26	0.45
25:BA:1405:A:N1	25:BA:1418:U:C4	2.85	0.45
25:BA:144:C:H5'	43:BX:2:LYS:HE2	1.99	0.45
25:BA:2660:C:H2'	25:BA:2661:U:C6	2.52	0.45
25:BA:537:G:OP1	25:BA:1280:U:O2'	2.30	0.45
34:BO:34:THR:OG1	34:BO:35:VAL:N	2.50	0.45
25:BA:950:C:H4'	45:BZ:169:GLU:OE2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1142:G:C2	1:CA:1143:G:H1'	2.52	0.45
1:CA:1228:C:P	13:CM:108:ARG:HH12	2.39	0.45
1:CA:1268:A:N3	1:CA:1326:C:O2'	2.47	0.45
1:CA:1353:G:O2'	1:CA:1354:C:H5'	2.15	0.45
1:CA:113:G:O4'	1:CA:354:G:H4'	2.16	0.45
1:CA:501:C:H2'	1:CA:502:G:C8	2.51	0.45
1:CA:637:G:H2'	1:CA:638:G:H8	1.82	0.45
1:CA:792:A:H4'	1:CA:793:U:H5''	1.99	0.45
1:CA:993:G:H1	1:CA:1045:C:H42	1.64	0.45
3:CC:3:ASN:N	3:CC:3:ASN:OD1	2.49	0.45
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.98	0.45
10:CJ:22:LYS:O	10:CJ:26:ALA:N	2.50	0.45
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.82	0.45
13:CM:97:PRO:HG2	13:CM:103:THR:HG22	1.99	0.45
25:DA:1399:C:C2'	25:DA:1400:G:H5'	2.47	0.45
25:DA:1913:A:H4'	25:DA:1914:C:H5''	1.99	0.45
25:DA:345:A:OP2	25:DA:345:A:H8	1.99	0.45
25:DA:528:A:H2'	25:DA:529:A:H5''	1.98	0.45
25:DA:631:A:H1'	35:DP:66:GLY:HA2	1.99	0.45
26:DB:60:C:H6	26:DB:60:C:O5'	2.00	0.45
26:DB:98:G:H2'	26:DB:99:G:O4'	2.17	0.45
35:DP:38:GLN:HG2	35:DP:45:LEU:H	1.81	0.45
41:DV:89:GLN:HA	41:DV:90:PRO:HD3	1.85	0.45
1:AA:1178:G:N2	1:AA:1181:G:OP2	2.47	0.45
1:AA:942:G:H21	9:AI:124:GLN:NE2	2.15	0.45
2:AB:220:ASP:O	2:AB:223:ILE:HG12	2.17	0.45
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.99	0.45
5:AE:45:PHE:CE2	5:AE:47:LYS:HE3	2.52	0.45
18:AR:74:ARG:HG2	18:AR:80:PRO:O	2.16	0.45
22:AV:16:A:H2'	22:AV:17:U:O4'	2.17	0.45
25:BA:933:C:N3	25:BA:934:A:H8	2.15	0.45
26:BB:66:A:H61	26:BB:108:U:H2'	1.82	0.45
31:BH:3:ARG:HH22	31:BH:66:GLY:HA3	1.82	0.45
39:BT:112:ARG:HG3	39:BT:115:ARG:NH2	2.31	0.45
1:CA:1492:A:H4'	1:CA:1493:A:OP1	2.17	0.45
1:CA:848:C:O5'	1:CA:848:C:H6	2.00	0.45
1:CA:953:G:C2	1:CA:954:G:H1'	2.52	0.45
2:CB:44:LEU:H	2:CB:44:LEU:HD22	1.81	0.45
3:CC:140:ARG:HH22	3:CC:141:VAL:HG23	1.82	0.45
5:CE:78:HIS:CD2	5:CE:142:LEU:HD23	2.52	0.45
11:CK:20:TYR:CZ	11:CK:83:ILE:HD12	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:D4:48:ARG:O	50:D4:50:VAL:N	2.50	0.45
25:DA:1846:G:H1	25:DA:1894:C:H42	1.65	0.45
25:DA:2135:A:H61	25:DA:2157:G:H21	1.65	0.45
25:DA:2155:G:C5	25:DA:2156:G:H1'	2.52	0.45
25:DA:2207:G:H3'	25:DA:2208:A:H5''	1.98	0.45
25:DA:510:C:H2'	25:DA:511:U:O4'	2.17	0.45
25:DA:565:C:H2'	25:DA:566:U:O4'	2.17	0.45
25:DA:515:A:H1'	25:DA:581:C:H1'	1.99	0.45
26:DB:112:U:H2'	26:DB:113:G:H8	1.81	0.45
26:DB:24:G:H5''	26:DB:25:A:N7	2.32	0.45
35:DP:101:VAL:HA	35:DP:106:LEU:O	2.17	0.45
39:DT:16:ARG:HH11	39:DT:16:ARG:HB3	1.81	0.45
1:AA:1084:G:C5	1:AA:1085:U:C4	3.05	0.45
1:AA:110:C:H2'	1:AA:111:G:O4'	2.16	0.45
1:AA:1267:C:H6	1:AA:1267:C:O5'	1.99	0.45
1:AA:70:G:H2'	1:AA:71:C:C6	2.52	0.45
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.17	0.45
16:AP:28:ARG:HG2	16:AP:29:ASP:OD1	2.16	0.45
25:BA:1077:G:H21	55:B9:36:GLN:HE22	1.65	0.45
27:BD:233:HIS:HA	61:BD:3406:HOH:O	2.17	0.45
25:BA:1846:A:P	27:BD:54:ARG:HH22	2.39	0.45
29:BF:125:LEU:HD12	29:BF:194:MET:HB2	1.99	0.45
29:BF:7:TYR:CD2	29:BF:24:LEU:HB2	2.52	0.45
32:BI:9:LEU:HB3	32:BI:12:LEU:HB2	1.99	0.45
1:CA:1002:G:O6	1:CA:1038:C:N3	2.50	0.45
1:CA:130:A:O2'	1:CA:131:C:O5'	2.26	0.45
1:CA:250:A:H4'	1:CA:251:G:O5'	2.16	0.45
1:CA:302:G:O2'	1:CA:556:C:H5''	2.17	0.45
1:CA:375:U:C4	1:CA:376:G:N7	2.85	0.45
1:CA:411:A:H2'	1:CA:412:A:H4'	1.99	0.45
6:CF:82:ARG:HB2	6:CF:85:VAL:HG23	1.99	0.45
12:CL:113:ARG:NH2	61:CL:201:HOH:O	2.50	0.45
19:CS:41:VAL:HG22	19:CS:42:PRO:HD2	1.99	0.45
23:CX:40:C:H2'	23:CX:41:C:C6	2.51	0.45
54:D8:54:GLU:O	54:D8:58:ILE:HG13	2.17	0.45
25:DA:1539:G:H2'	25:DA:1540:U:O4'	2.17	0.45
25:DA:1922:G:H2'	25:DA:1923:U:O4'	2.17	0.45
25:DA:2332:U:O2'	25:DA:2335:A:N3	2.40	0.45
25:DA:2529:G:OP1	31:DH:172:LYS:HE2	2.17	0.45
25:DA:25:U:C4	25:DA:26:G:C6	3.05	0.45
25:DA:940:G:H2'	25:DA:941:A:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DE:144:ARG:HB3	28:DE:145:LYS:H	1.41	0.45
29:DF:7:TYR:O	29:DF:22:ALA:N	2.50	0.45
37:DR:29:LEU:HD23	37:DR:70:LEU:HD11	1.98	0.45
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.43	0.44
1:AA:137:C:H2'	1:AA:138:G:C8	2.52	0.44
1:AA:54:C:H2'	1:AA:352:C:H41	1.81	0.44
1:AA:538:G:H2'	1:AA:539:A:H8	1.82	0.44
2:AB:102:LEU:HD23	2:AB:182:ILE:HD12	1.99	0.44
2:AB:224:GLN:HA	2:AB:228:GLY:O	2.17	0.44
16:AP:5:ARG:HH11	16:AP:22:THR:HG23	1.82	0.44
25:BA:1577:C:O2'	25:BA:1578:C:P	2.75	0.44
25:BA:1480:A:N6	25:BA:1605:A:H62	2.09	0.44
25:BA:2163:G:O6	25:BA:2172:U:C2	2.67	0.44
29:BF:161:GLU:HG2	29:BF:164:ARG:NH2	2.32	0.44
35:BP:82:GLY:HA2	35:BP:113:LYS:O	2.18	0.44
34:BO:80:ASP:OD2	39:BT:71:GLY:HA3	2.17	0.44
1:CA:1050:G:H1'	1:CA:1214:C:O2	2.17	0.44
1:CA:1347:G:O2'	1:CA:1348:U:OP2	2.33	0.44
1:CA:495:A:H4'	1:CA:496:A:OP1	2.16	0.44
1:CA:964:A:N3	1:CA:969:A:O2'	2.44	0.44
3:CC:63:ASN:HB3	3:CC:98:ASN:HD22	1.82	0.44
8:CH:51:VAL:HG21	8:CH:60:ARG:HH11	1.81	0.44
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.98	0.44
25:DA:2001:A:OP1	37:DR:9:LYS:NZ	2.45	0.44
25:DA:2064:C:H2'	25:DA:2065:C:C6	2.51	0.44
25:DA:2569:G:C2	25:DA:2570:G:C8	3.05	0.44
25:DA:530:G:O4'	25:DA:530:G:N3	2.48	0.44
34:DO:53:LYS:HG2	34:DO:56:ASP:OD1	2.16	0.44
25:DA:2318:G:H22	38:DS:3:ARG:NH1	2.15	0.44
38:DS:84:GLN:HG3	38:DS:111:GLU:OE2	2.17	0.44
1:AA:358:U:H2'	1:AA:359:U:C6	2.52	0.44
1:AA:111:G:HO2'	1:AA:389:A:HO2'	1.63	0.44
1:AA:445:G:H2'	1:AA:446:G:H8	1.82	0.44
1:AA:600:C:O2'	1:AA:601:C:H5'	2.17	0.44
3:AC:123:GLN:HG2	3:AC:128:PHE:CD2	2.53	0.44
5:AE:8:GLU:HG3	5:AE:34:VAL:HG23	1.99	0.44
12:AL:53:ARG:HB3	12:AL:93:LEU:HD11	1.98	0.44
54:B8:61:LEU:O	54:B8:63:PRO:HD3	2.17	0.44
25:BA:1555:C:H4'	25:BA:1556:A:OP2	2.17	0.44
25:BA:227:C:H2'	25:BA:228:U:O4'	2.18	0.44
25:BA:44:G:H5''	25:BA:45:C:OP1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BD:142:VAL:HG13	27:BD:191:ALA:HB1	1.98	0.44
1:CA:1066:C:H2'	1:CA:1067:A:C8	2.52	0.44
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.17	0.44
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.17	0.44
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.16	0.44
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.33	0.44
1:CA:595:G:H1'	1:CA:596:C:H5	1.82	0.44
1:CA:691:G:H2'	1:CA:692:U:C6	2.52	0.44
1:CA:1206:G:H4'	3:CC:192:THR:O	2.18	0.44
7:CG:18:TYR:CD1	7:CG:59:LEU:HB2	2.52	0.44
12:CL:60:LEU:HD21	12:CL:66:VAL:HG22	1.99	0.44
14:CN:29:ARG:HD3	14:CN:40:CYS:HB2	1.99	0.44
23:CX:21:A:H5'	23:CX:22:G:OP1	2.17	0.44
25:DA:1038:C:N4	25:DA:1117:G:H1	2.14	0.44
25:DA:1411:C:H2'	25:DA:1412:A:C8	2.52	0.44
25:DA:1592:C:H2'	25:DA:1593:G:C8	2.53	0.44
25:DA:1983:C:H4'	25:DA:2606:C:H4'	1.99	0.44
25:DA:2126:A:N3	25:DA:2127:G:H1'	2.32	0.44
25:DA:2134:A:H3'	25:DA:2135:A:C8	2.52	0.44
25:DA:2144:U:H1'	25:DA:2148:G:H22	1.81	0.44
25:DA:641:C:O2'	25:DA:2350:C:OP1	2.22	0.44
25:DA:26:G:C6	25:DA:27:G:N1	2.86	0.44
25:DA:821:A:N1	61:DA:4375:HOH:O	2.36	0.44
25:DA:866:A:H2'	25:DA:866:A:N3	2.32	0.44
1:AA:1479:C:H2'	1:AA:1480:G:C8	2.52	0.44
57:AA:3191:PCY:N16	57:AA:3191:PCY:O5	2.48	0.44
1:AA:442:C:H42	1:AA:492:G:H1	1.64	0.44
4:AD:168:ARG:H	4:AD:168:ARG:HD2	1.80	0.44
10:AJ:78:ASN:C	10:AJ:80:LYS:H	2.20	0.44
11:AK:19:ALA:HB3	11:AK:82:VAL:HA	1.99	0.44
25:BA:1398:U:OP1	61:BA:4203:HOH:O	2.21	0.44
25:BA:1517:G:N2	25:BA:1568:G:OP2	2.30	0.44
1:AA:1494:G:H4'	25:BA:1935:A:C8	2.52	0.44
25:BA:609:A:N1	25:BA:856:G:O2'	2.44	0.44
27:BD:75:ILE:HD13	27:BD:99:ASP:OD2	2.17	0.44
30:BG:45:GLU:HG2	30:BG:45:GLU:H	1.52	0.44
40:BU:74:LEU:H	40:BU:74:LEU:HD12	1.81	0.44
1:CA:1157:A:C6	1:CA:1180:A:C5	3.05	0.44
1:CA:1058:G:H1	1:CA:1199:U:H3	1.65	0.44
1:CA:520:A:C2	1:CA:536:C:H1'	2.52	0.44
1:CA:743:U:H2'	1:CA:744:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:20:SER:HB2	3:CC:40:ARG:NH1	2.32	0.44
3:CC:83:ARG:O	3:CC:87:LEU:HG	2.18	0.44
1:CA:1309:G:N7	13:CM:99:ARG:NH2	2.65	0.44
14:CN:32:SER:OG	14:CN:32:SER:O	2.33	0.44
23:CX:61:C:H2'	23:CX:62:C:C6	2.52	0.44
25:DA:1165:U:H2'	25:DA:1166:C:C6	2.53	0.44
25:DA:1221(A):C:C2	25:DA:1229:G:C2	3.05	0.44
25:DA:1288:U:O2'	25:DA:1647:G:N2	2.50	0.44
25:DA:2332:U:H5'	25:DA:2336:A:N6	2.32	0.44
25:DA:2526:G:H5'	25:DA:2742:C:O2'	2.16	0.44
25:DA:271(E):U:H2'	25:DA:271(F):C:C6	2.53	0.44
25:DA:2832:U:OP2	61:DA:4417:HOH:O	2.20	0.44
25:DA:526:A:OP1	61:DA:4468:HOH:O	2.21	0.44
29:DF:116:ASP:O	29:DF:120:GLU:HG3	2.17	0.44
34:DO:80:ASP:OD2	39:DT:71:GLY:HA3	2.18	0.44
41:DV:85:LYS:HB2	41:DV:85:LYS:HE3	1.72	0.44
44:DY:1:MET:HG2	44:DY:2:ARG:N	2.32	0.44
45:DZ:150:LEU:HD12	45:DZ:150:LEU:HA	1.79	0.44
1:AA:997:U:O2	1:AA:1044:A:N1	2.51	0.44
1:AA:993:G:H1	1:AA:1045:C:H42	1.65	0.44
1:AA:1063:C:OP2	1:AA:1064:G:O2'	2.28	0.44
1:AA:1159:U:O2	1:AA:1160:G:N1	2.50	0.44
1:AA:1325:C:O2'	1:AA:1326:C:H5'	2.17	0.44
1:AA:346:G:OP1	39:BT:41:ARG:NH1	2.49	0.44
1:AA:495:A:N3	1:AA:496:A:H8	2.16	0.44
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.99	0.44
8:AH:51:VAL:HG12	8:AH:52:ASP:N	2.33	0.44
13:AM:84:ILE:HG13	13:AM:85:GLY:CA	2.48	0.44
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.51	0.44
1:AA:1220:G:N2	19:AS:54:GLY:O	2.41	0.44
25:BA:1314:A:H2'	25:BA:1315:A:O4'	2.17	0.44
25:BA:1911:A:N1	25:BA:2246:G:H1'	2.33	0.44
25:BA:510:C:H2'	25:BA:511:C:C6	2.53	0.44
25:BA:659:C:H2'	25:BA:660:C:C6	2.53	0.44
29:BF:89:VAL:O	61:BF:403:HOH:O	2.21	0.44
1:CA:1157:A:H5'	1:CA:1158:C:N1	2.31	0.44
1:CA:1227:A:H8	1:CA:1227:A:H3'	1.83	0.44
1:CA:501:C:H2'	1:CA:502:G:H8	1.81	0.44
1:CA:600:C:O2'	1:CA:601:C:H5'	2.17	0.44
1:CA:926:G:H5''	1:CA:927:G:O5'	2.17	0.44
2:CB:32:ILE:HD13	2:CB:40:HIS:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CO:33:THR:HG21	15:CO:85:LEU:HD22	1.98	0.44
54:D8:6:THR:HG22	54:D8:63:PRO:HD2	1.99	0.44
25:DA:1270:C:O2'	25:DA:1325:G:H2'	2.17	0.44
25:DA:1815:A:H8	25:DA:1815:A:OP1	2.01	0.44
23:CX:12:G:H4'	25:DA:1908:C:O2	2.17	0.44
25:DA:2126:A:N1	25:DA:2162:G:H1'	2.33	0.44
25:DA:2154:G:N3	25:DA:2154:G:H2'	2.33	0.44
25:DA:2274:A:C5	25:DA:2276:G:C8	3.05	0.44
25:DA:2023:G:H5'	25:DA:2617:C:H4'	1.98	0.44
25:DA:792:G:H5''	25:DA:793:A:H5'	2.00	0.44
39:DT:24:PRO:HA	39:DT:49:VAL:HG22	1.98	0.44
40:DU:28:ARG:NH1	40:DU:38:THR:OG1	2.49	0.44
1:AA:194:C:H2'	1:AA:195:A:H5''	2.00	0.44
1:AA:58:C:O2'	1:AA:388:G:N7	2.39	0.44
5:AE:152:ARG:HA	8:AH:64:LYS:HE2	1.99	0.44
19:AS:28:LYS:HE3	19:AS:28:LYS:HB3	1.82	0.44
47:B1:94:LEU:O	47:B1:97:LEU:HB2	2.18	0.44
50:B4:54:GLY:O	50:B4:56:VAL:HA	2.18	0.44
25:BA:2707:C:H2'	25:BA:2708:U:H6	1.83	0.44
25:BA:331:G:N7	61:BA:4427:HOH:O	2.36	0.44
25:BA:347:G:C8	29:BF:171:PRO:HG3	2.53	0.44
25:BA:471:C:O2'	25:BA:472:G:H5'	2.17	0.44
25:BA:611:U:H2'	25:BA:612:C:H6	1.82	0.44
25:BA:185:A:O2'	25:BA:852:G:O6	2.29	0.44
26:BB:14:U:OP2	26:BB:70:C:O2'	2.32	0.44
27:BD:206:LEU:HD22	27:BD:211:ARG:HG2	1.98	0.44
34:BO:36:GLY:HA2	34:BO:106:LEU:HD23	2.00	0.44
35:BP:47:ASP:OD2	35:BP:49:ARG:NH2	2.50	0.44
41:BV:76:LYS:HB2	41:BV:81:TYR:HB3	1.98	0.44
1:CA:1027:C:O2'	1:CA:1034:G:N2	2.51	0.44
2:CB:118:LEU:O	2:CB:122:PHE:HB3	2.17	0.44
4:CD:13:ARG:NH1	4:CD:38:TYR:O	2.50	0.44
5:CE:139:LEU:HA	5:CE:142:LEU:HD12	1.99	0.44
6:CF:25:ILE:HD13	6:CF:82:ARG:HE	1.83	0.44
6:CF:95:GLU:HA	6:CF:96:PRO:HD3	1.89	0.44
24:CY:76:A:H3'	61:DA:4895:HOH:O	2.17	0.44
50:D4:33:VAL:HG12	50:D4:35:VAL:H	1.83	0.44
25:DA:1029:A:N1	25:DA:2465:C:O2'	2.47	0.44
25:DA:2313:C:H2'	25:DA:2314:C:C6	2.52	0.44
26:DB:55:U:O3'	30:DG:27:ASN:ND2	2.51	0.44
39:DT:29:ARG:HB3	39:DT:87:ASP:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:138:GLU:H	45:DZ:156:LYS:HZ1	1.64	0.44
1:AA:352:C:H4'	1:AA:354:G:OP1	2.18	0.44
1:AA:431:A:H2'	1:AA:432:A:O4'	2.18	0.44
2:AB:114:ARG:O	2:AB:118:LEU:HG	2.18	0.44
3:AC:134:ILE:O	3:AC:138:VAL:HG23	2.17	0.44
14:AN:9:LYS:HG3	14:AN:12:ARG:HH12	1.83	0.44
15:AO:55:GLY:HA2	15:AO:58:MET:CE	2.48	0.44
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.18	0.44
25:BA:1893:G:H2'	25:BA:1894:G:H8	1.81	0.44
25:BA:2129:C:H2'	25:BA:2130:C:C6	2.53	0.44
25:BA:2162:C:C4	25:BA:2173:G:O6	2.71	0.44
25:BA:416:G:N1	35:BP:70:GLN:HG3	2.33	0.44
25:BA:27:G:C2	25:BA:537:G:N3	2.86	0.44
25:BA:821:A:N3	25:BA:821:A:H2'	2.33	0.44
25:BA:776:G:C6	27:BD:208:LYS:HB2	2.52	0.44
36:BQ:85:LYS:HG2	46:B0:7:LEU:HB3	1.97	0.44
39:BT:106:SER:O	39:BT:110:ILE:HG13	2.17	0.44
43:BX:31:HIS:HA	43:BX:32:PRO:HD3	1.87	0.44
44:BY:1:MET:CE	44:BY:1:MET:H3	2.30	0.44
1:CA:1137:C:O2'	1:CA:1138:G:N2	2.51	0.44
1:CA:1304:G:N2	1:CA:1332:A:OP2	2.41	0.44
1:CA:946:A:H2'	1:CA:947:G:C8	2.53	0.44
4:CD:140:VAL:HG11	4:CD:146:ILE:HD11	1.99	0.44
61:DA:4920:HOH:O	46:D0:4:LYS:NZ	2.50	0.44
49:D3:18:ASP:N	49:D3:18:ASP:OD1	2.51	0.44
25:DA:1927:A:H2'	25:DA:1928:A:C8	2.52	0.44
25:DA:2058:A:N7	61:DA:4182:HOH:O	2.36	0.44
25:DA:2697:G:H2'	25:DA:2698:U:O4'	2.18	0.44
25:DA:602:G:H4'	25:DA:604:G:H4'	2.00	0.44
25:DA:941:A:H2'	25:DA:942:G:O4'	2.18	0.44
26:DB:7:G:H3'	26:DB:8:U:H5''	2.00	0.44
27:DD:169:GLU:OE2	27:DD:174:ILE:HD11	2.18	0.44
30:DG:177:GLY:O	30:DG:179:PRO:HD3	2.18	0.44
31:DH:71:LEU:HA	31:DH:71:LEU:HD12	1.85	0.44
45:DZ:136:PHE:O	45:DZ:137:ILE:HG13	2.17	0.44
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.17	0.44
1:AA:1082:G:H2'	1:AA:1083:U:O4'	2.18	0.44
1:AA:1160:G:C5	1:AA:1161:C:C5	3.05	0.44
1:AA:1166:G:N2	1:AA:1169:A:H3'	2.33	0.44
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.53	0.44
1:AA:1410:G:H2'	1:AA:1411:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:44:G:H2'	1:AA:45:U:O4'	2.18	0.44
1:AA:714:G:H2'	1:AA:715:A:C8	2.53	0.44
1:AA:745:C:H2'	1:AA:746:A:H8	1.83	0.44
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.49	0.44
1:AA:406:G:H21	4:AD:119:GLN:HE22	1.64	0.44
4:AD:50:ARG:HA	4:AD:51:PRO:HD3	1.86	0.44
1:AA:1187:G:H5'	9:AI:113:LYS:HE2	1.98	0.44
13:AM:3:ARG:NH2	13:AM:11:ARG:HH21	2.16	0.44
52:B6:14:THR:HG21	52:B6:48:VAL:HG22	1.99	0.44
25:BA:1052:C:O2'	33:BN:106:MET:HB3	2.18	0.44
25:BA:2145:G:H2'	25:BA:2146:G:C8	2.49	0.44
25:BA:2228:G:H2'	25:BA:2229:A:C2	2.53	0.44
25:BA:950:C:H2'	25:BA:951:U:C6	2.53	0.44
25:BA:1925:G:OP1	27:BD:241:PRO:HB2	2.17	0.44
28:BE:55:ASN:HB3	28:BE:58:ARG:HG3	2.00	0.44
29:BF:184:TYR:CE2	29:BF:188:ARG:HD2	2.53	0.44
38:BS:15:ARG:NE	38:BS:88:ASP:OD2	2.50	0.44
1:CA:1034:G:H5''	1:CA:1035:A:OP2	2.18	0.44
1:CA:1381:U:C2'	1:CA:1382:C:H5'	2.48	0.44
2:CB:121:LEU:N	2:CB:125:PRO:HG2	2.33	0.44
15:CO:54:ARG:HH11	15:CO:58:MET:HE1	1.82	0.44
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.31	0.44
25:DA:1314:C:OP1	61:DA:4448:HOH:O	2.20	0.44
25:DA:2207:G:H8	25:DA:2207:G:P	2.41	0.44
25:DA:2356:C:H2'	25:DA:2357:U:O4'	2.18	0.44
25:DA:2607:G:H2'	25:DA:2608:G:O4'	2.18	0.44
25:DA:67:U:H2'	25:DA:68:G:C8	2.53	0.44
25:DA:815:C:C2	25:DA:1193:G:C2	3.05	0.44
29:DF:183:VAL:O	29:DF:187:VAL:HG23	2.17	0.44
29:DF:36:VAL:HG11	29:DF:183:VAL:HG11	1.99	0.44
35:DP:19:VAL:HG12	35:DP:27:HIS:HB3	1.99	0.44
41:DV:56:SER:OG	41:DV:100:ARG:HD2	2.17	0.44
44:DY:94:LYS:HD3	44:DY:94:LYS:HA	1.81	0.44
45:DZ:131:ARG:HD2	45:DZ:131:ARG:H	1.83	0.44
1:AA:346:G:H3'	1:AA:346:G:N3	2.33	0.44
1:AA:926:G:H5''	1:AA:927:G:O5'	2.18	0.44
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.99	0.44
3:AC:155:GLY:HA3	3:AC:196:LEU:HD22	1.99	0.44
3:AC:58:GLU:HB2	3:AC:65:ALA:HB3	1.99	0.44
53:B7:24:THR:O	53:B7:28:ARG:HG3	2.18	0.44
25:BA:1594:C:H2'	25:BA:1595:C:H6	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2156:A:O2'	25:BA:2157:A:OP1	2.29	0.44
25:BA:2316:G:H22	25:BA:2324:U:H3	1.65	0.44
25:BA:502:G:H4'	25:BA:527:A:N1	2.33	0.44
25:BA:596:G:O2'	25:BA:597:C:H3'	2.18	0.44
27:BD:79:VAL:O	27:BD:114:GLY:N	2.45	0.44
28:BE:24:THR:HG22	28:BE:186:GLY:O	2.18	0.44
13:AM:68:GLY:HA3	30:BG:116:ASP:OD1	2.17	0.44
30:BG:67:LYS:HD3	50:B4:5:ILE:HB	1.99	0.44
36:BQ:16:ARG:HG2	36:BQ:18:LYS:HG3	2.00	0.44
38:BS:3:ARG:HA	38:BS:3:ARG:HE	1.82	0.44
45:BZ:73:GLN:HB3	45:BZ:87:ASP:HB2	2.00	0.44
1:CA:1134:G:H1	1:CA:1140:C:N4	2.15	0.44
1:CA:1392:G:N2	1:CA:1502:A:H8	2.13	0.44
1:CA:542:G:P	4:CD:10:ARG:HH22	2.40	0.44
25:DA:1344:G:O2'	25:DA:1385:G:H2'	2.17	0.44
25:DA:1531:C:H42	25:DA:1538:G:H1	1.66	0.44
25:DA:807:U:O2'	25:DA:2060:A:N1	2.42	0.44
25:DA:2280:G:N7	61:DA:4535:HOH:O	2.36	0.44
25:DA:2525:G:C2	25:DA:2539:C:C2	3.06	0.44
26:DB:2:C:OP2	26:DB:2:C:H3'	2.18	0.44
26:DB:45:A:C6	26:DB:46:A:C5	3.05	0.44
26:DB:57:A:O4'	30:DG:30:GLU:HG3	2.18	0.44
34:DO:64:ARG:HB2	34:DO:83:ALA:HB3	1.99	0.44
1:AA:1127:G:H5'	1:AA:1280:A:O2'	2.17	0.44
1:AA:1511:G:H2'	1:AA:1512:U:O4'	2.18	0.44
4:AD:15:GLU:HG3	4:AD:63:LYS:HE2	1.99	0.44
4:AD:71:SER:OG	4:AD:74:GLN:HB2	2.18	0.44
11:AK:84:VAL:HG11	11:AK:91:ARG:HH11	1.83	0.44
13:AM:14:ARG:H	13:AM:14:ARG:HG3	1.62	0.44
14:AN:53:LEU:HA	14:AN:54:PRO:HD2	1.88	0.44
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.18	0.44
15:AO:74:ASP:HB3	15:AO:77:ARG:HB2	2.00	0.44
19:AS:51:VAL:HG22	19:AS:71:LEU:HD22	1.99	0.44
19:AS:71:LEU:HA	19:AS:71:LEU:HD23	1.89	0.44
25:BA:1405:A:C2	25:BA:1418:U:O4	2.71	0.44
25:BA:2163:G:C6	25:BA:2164:C:C2	3.05	0.44
25:BA:2710:U:H2'	25:BA:2711:C:C6	2.53	0.44
25:BA:2784:C:H2'	25:BA:2785:C:H6	1.82	0.44
25:BA:2880:C:H2'	25:BA:2881:C:O4'	2.18	0.44
31:BH:7:LEU:HA	31:BH:8:PRO:HD3	1.83	0.44
25:BA:2859:U:OP2	39:BT:95:ARG:NH1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1023:G:C4	1:CA:1024:G:C8	3.05	0.44
1:CA:1254:C:O4'	1:CA:1356:G:H5''	2.18	0.44
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.52	0.44
1:CA:344:A:H4'	1:CA:345:C:OP2	2.18	0.44
1:CA:589:C:H2'	1:CA:590:C:H5'	1.99	0.44
1:CA:714:G:H2'	1:CA:715:A:C8	2.52	0.44
4:CD:201:GLN:HE22	5:CE:99:GLY:HA2	1.83	0.44
9:CI:81:ILE:O	9:CI:85:LEU:HG	2.18	0.44
10:CJ:67:THR:O	10:CJ:67:THR:OG1	2.33	0.44
19:CS:22:LEU:HB3	19:CS:27:GLU:HG3	1.99	0.44
25:DA:2029:G:H2'	25:DA:2031:A:OP1	2.18	0.44
25:DA:570:G:H2'	25:DA:2030:A:N7	2.33	0.44
25:DA:2080:G:O2'	25:DA:2081:C:H5'	2.17	0.44
25:DA:2117:A:O2'	25:DA:2118:U:H5''	2.18	0.44
25:DA:2236:C:H2'	25:DA:2237:G:O4'	2.18	0.44
25:DA:918:A:H5''	26:DB:98:G:O2'	2.17	0.44
35:DP:7:ARG:HA	35:DP:8:PRO:HD3	1.90	0.44
36:DQ:29:PHE:HB2	36:DQ:105:GLU:OE2	2.18	0.44
25:DA:2376:A:N1	38:DS:87:PHE:HB3	2.33	0.44
1:AA:67:C:H2'	1:AA:68:G:H8	1.78	0.43
1:AA:767:A:H2'	1:AA:768:A:O4'	2.18	0.43
2:AB:51:LEU:HD21	2:AB:201:ILE:HG23	1.99	0.43
3:AC:156:ARG:NH2	3:AC:159:GLY:O	2.51	0.43
11:AK:44:SER:O	11:AK:48:ILE:HD13	2.18	0.43
13:AM:15:VAL:HG22	13:AM:43:THR:O	2.18	0.43
30:BG:66:GLN:HG3	50:B4:1:MET:HE1	2.00	0.43
25:BA:1056:A:N3	25:BA:1199:C:H1'	2.32	0.43
25:BA:1067:A:H8	25:BA:1068:G:H5''	1.82	0.43
25:BA:1338:U:H2'	25:BA:1339:C:H6	1.83	0.43
25:BA:320:C:H2'	25:BA:321:C:H6	1.81	0.43
25:BA:515:G:H2'	25:BA:516:G:O4'	2.18	0.43
25:BA:898:U:O2'	49:B3:42:ALA:O	2.36	0.43
26:BB:2:C:H2'	26:BB:3:C:C6	2.53	0.43
29:BF:18:ARG:NH2	29:BF:127:GLU:OE1	2.50	0.43
31:BH:154:PRO:HB3	31:BH:163:TYR:CZ	2.53	0.43
25:BA:63:A:O3'	43:BX:71:GLY:HA3	2.18	0.43
1:CA:1177:G:H3'	1:CA:1178:G:H8	1.83	0.43
1:CA:1234:C:H1'	1:CA:1364:U:O2	2.18	0.43
1:CA:254:G:OP1	17:CQ:66:SER:OG	2.21	0.43
1:CA:353:A:H8	1:CA:353:A:H5'	1.82	0.43
1:CA:741:G:H2'	1:CA:742:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CH:39:LEU:HB3	8:CH:45:ILE:HG12	1.99	0.43
12:CL:71:PRO:O	12:CL:102:ARG:HD2	2.18	0.43
18:CR:74:ARG:HG3	18:CR:79:LEU:HB2	2.00	0.43
49:D3:4:LEU:O	49:D3:36:VAL:HA	2.17	0.43
25:DA:2815:C:H5'	51:D5:29:THR:HG21	2.00	0.43
25:DA:1021:A:H3'	25:DA:1021:A:H8	1.83	0.43
25:DA:1550:C:H2'	25:DA:1551:C:C6	2.53	0.43
25:DA:18:C:O2'	25:DA:554:U:OP1	2.36	0.43
25:DA:2469:A:H2'	25:DA:2470:G:O4'	2.18	0.43
25:DA:2678:C:H2'	25:DA:2679:A:O4'	2.18	0.43
25:DA:411:G:C5	35:DP:72:PRO:HB3	2.53	0.43
25:DA:471:A:H2'	25:DA:472:A:O4'	2.17	0.43
26:DB:105:A:OP1	45:DZ:72:ARG:NH1	2.51	0.43
26:DB:54:G:H21	30:DG:29:TRP:HE1	1.66	0.43
25:DA:2760:C:H1'	31:DH:139:GLN:HE22	1.83	0.43
31:DH:5:GLY:HA2	31:DH:69:ARG:HB3	2.00	0.43
44:DY:6:HIS:CD2	44:DY:6:HIS:H	2.36	0.43
45:DZ:33:LEU:HD21	45:DZ:90:VAL:HG21	1.99	0.43
1:AA:537:G:OP1	12:AL:113:ARG:NH2	2.37	0.43
1:AA:657:G:C2	1:AA:750:G:C5	3.06	0.43
1:AA:860:A:H2'	1:AA:861:G:O4'	2.18	0.43
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.46	0.43
1:AA:1152:A:H5'	10:AJ:13:HIS:CG	2.54	0.43
50:B4:49:PHE:HA	50:B4:49:PHE:HD1	1.69	0.43
25:BA:1810:U:H2'	61:BA:5050:HOH:O	2.18	0.43
28:BE:173:VAL:CG2	28:BE:185:LYS:HB2	2.47	0.43
28:BE:28:ALA:HB3	28:BE:93:VAL:HG12	1.99	0.43
30:BG:17:PRO:HA	30:BG:20:ILE:HD12	2.01	0.43
37:BR:16:HIS:O	37:BR:16:HIS:HD2	2.00	0.43
1:CA:1256:A:H61	1:CA:1278:U:C1'	2.31	0.43
1:CA:1304:G:C6	1:CA:1305:G:N1	2.85	0.43
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.52	0.43
1:CA:685:G:C2	1:CA:686:U:C4	3.06	0.43
1:CA:940:C:H2'	1:CA:941:G:C8	2.53	0.43
1:CA:977:A:H1'	1:CA:982:U:O4	2.18	0.43
1:CA:8:A:H5'	5:CE:101:ILE:HG22	2.01	0.43
13:CM:64:TRP:HB2	13:CM:66:LEU:HD21	1.99	0.43
23:CX:31:G:C5	23:CX:32:5MC:HM52	2.53	0.43
50:D4:40:HIS:HB3	50:D4:43:TYR:HB2	2.00	0.43
25:DA:1021:A:C8	25:DA:1021:A:H3'	2.53	0.43
25:DA:1190:G:O2'	25:DA:1191:G:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1214:A:H61	25:DA:1235:G:H1'	1.83	0.43
25:DA:2128:C:H2'	25:DA:2129:C:O4'	2.17	0.43
25:DA:332:A:O2'	25:DA:334:C:OP2	2.28	0.43
25:DA:601:C:O2'	25:DA:605:C:H5''	2.18	0.43
30:DG:98:ARG:H	30:DG:98:ARG:HG2	1.40	0.43
31:DH:11:VAL:HG21	31:DH:50:VAL:HG23	2.00	0.43
33:DN:115:ARG:HA	33:DN:118:LYS:HE3	1.99	0.43
25:DA:2882:A:OP1	37:DR:96:ARG:NE	2.51	0.43
45:DZ:10:ARG:NH1	45:DZ:36:LYS:HD2	2.33	0.43
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.16	0.43
1:AA:1247:U:H3	1:AA:1290:G:H1	1.65	0.43
1:AA:1355:G:H2'	1:AA:1356:G:C8	2.53	0.43
1:AA:628:G:C2'	1:AA:629:G:H5'	2.48	0.43
2:AB:174:VAL:O	2:AB:178:ARG:HB2	2.18	0.43
3:AC:15:THR:HG23	3:AC:181:ASN:HD22	1.84	0.43
4:AD:18:LYS:NZ	4:AD:26:CYS:O	2.32	0.43
4:AD:43:HIS:HA	4:AD:46:LYS:HD3	1.99	0.43
7:AG:51:GLN:O	7:AG:55:GLY:HA2	2.18	0.43
16:AP:75:ARG:O	16:AP:78:GLY:N	2.46	0.43
1:AA:1229:A:O2'	23:AX:30:G:OP1	2.36	0.43
48:B2:28:LYS:HG3	48:B2:53:LEU:HD21	1.99	0.43
52:B6:15:GLU:HG3	52:B6:47:THR:HG23	1.99	0.43
25:BA:1199:C:H2'	25:BA:1200:G:O4'	2.19	0.43
25:BA:1451:U:H2'	25:BA:1452:U:H6	1.83	0.43
25:BA:1576:G:C2'	25:BA:1577:C:H5'	2.48	0.43
25:BA:1576:G:O2'	25:BA:1577:C:H5'	2.17	0.43
25:BA:1756:U:H2'	25:BA:1757:C:C6	2.53	0.43
25:BA:2005:C:H4'	25:BA:2618:C:H4'	1.99	0.43
28:BE:111:ARG:HG3	28:BE:160:TYR:CD2	2.54	0.43
28:BE:75:VAL:HG13	28:BE:77:ILE:H	1.83	0.43
30:BG:122:PRO:HG3	30:BG:182:LYS:H	1.83	0.43
31:BH:154:PRO:HB3	31:BH:163:TYR:CE2	2.53	0.43
33:BN:30:ILE:HG22	33:BN:34:LEU:HD22	1.99	0.43
1:AA:1422:G:C5'	34:BO:48:PRO:HB3	2.43	0.43
35:BP:85:LEU:HG	35:BP:115:LEU:O	2.18	0.43
26:BB:8:U:O3'	38:BS:25:ARG:NH2	2.52	0.43
25:BA:2331:G:C2	38:BS:3:ARG:HA	2.53	0.43
45:BZ:137:ILE:HA	45:BZ:156:LYS:NZ	2.34	0.43
1:CA:1138:G:C5	1:CA:1140:C:H1'	2.53	0.43
1:CA:1178:G:N2	1:CA:1181:G:OP2	2.47	0.43
1:CA:1485:U:H2'	1:CA:1486:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:560:U:H4'	1:CA:561:U:O5'	2.18	0.43
1:CA:833:U:H2'	1:CA:834:C:H6	1.82	0.43
6:CF:42:GLU:OE1	6:CF:59:TYR:OH	2.33	0.43
23:CX:65:C:H2'	23:CX:66:C:C6	2.54	0.43
24:CY:76:A:H5'	47:D1:30:VAL:HG21	1.99	0.43
49:D3:10:LYS:HB3	49:D3:53:LEU:HA	2.00	0.43
25:DA:1027:A:C6	25:DA:1126:A:C4	3.06	0.43
25:DA:1260:G:C6	25:DA:1261:C:C4	3.07	0.43
25:DA:1530:C:H1'	25:DA:1531:C:OP1	2.18	0.43
25:DA:1654:A:H1'	25:DA:2823:A:H5'	2.00	0.43
25:DA:2136:C:N3	25:DA:2155:G:O6	2.52	0.43
25:DA:27:G:HO2'	25:DA:28:A:P	2.40	0.43
25:DA:632:A:H2'	25:DA:633:A:C8	2.53	0.43
25:DA:674:G:O2'	29:DF:74:ARG:HD3	2.19	0.43
25:DA:746:A:H2'	25:DA:2612:C:H5''	2.00	0.43
27:DD:164:GLN:NE2	27:DD:166:GLN:OE1	2.47	0.43
29:DF:116:ASP:OD2	35:DP:1:MET:N	2.44	0.43
35:DP:95:VAL:HG13	35:DP:125:VAL:HA	2.00	0.43
39:DT:64:ARG:HB2	39:DT:73:GLU:HG2	2.01	0.43
1:AA:1057:G:H2'	1:AA:1058:G:H5'	1.99	0.43
4:AD:187:ARG:NH2	4:AD:193:ASP:OD1	2.46	0.43
7:AG:78:ARG:NH1	7:AG:79:ARG:HD2	2.33	0.43
20:AT:77:ALA:O	20:AT:81:LYS:HG3	2.19	0.43
22:AV:14:A:H2'	22:AV:15:A:H8	1.82	0.43
47:B1:64:ALA:HA	47:B1:67:ILE:HG13	2.00	0.43
49:B3:7:LYS:HE3	49:B3:32:GLN:HE21	1.83	0.43
50:B4:58:ARG:O	50:B4:61:ARG:HB3	2.18	0.43
54:B8:62:LEU:HB3	54:B8:65:GLU:CG	2.48	0.43
25:BA:1314:A:C2	25:BA:2035:A:C4	3.07	0.43
30:BG:16:ARG:O	30:BG:20:ILE:HG13	2.18	0.43
39:BT:23:ARG:HG3	39:BT:120:ARG:NH1	2.33	0.43
44:BY:99:CYS:HB2	44:BY:106:LEU:HD21	2.00	0.43
45:BZ:7:ALA:O	45:BZ:62:PRO:HD3	2.19	0.43
1:CA:1145:C:H4'	1:CA:1146:A:H5'	2.01	0.43
1:CA:1314:C:OP1	19:CS:6:LYS:NZ	2.30	0.43
1:CA:141:A:H1'	1:CA:182:U:O2	2.19	0.43
1:CA:189(C):C:H2'	1:CA:189(D):C:O4'	2.19	0.43
1:CA:950:U:H2'	1:CA:951:G:C8	2.54	0.43
2:CB:144:ARG:NH2	2:CB:148:TYR:OH	2.49	0.43
3:CC:11:ARG:HB3	3:CC:15:THR:HB	2.00	0.43
10:CJ:64:GLU:OE2	10:CJ:66:ARG:NH1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:46:LYS:NZ	12:CL:91:LYS:O	2.42	0.43
25:DA:1220:A:OP2	40:DU:19:LYS:NZ	2.35	0.43
25:DA:1257:C:H2'	25:DA:1258:C:C6	2.53	0.43
25:DA:2349:G:OP1	61:DA:4097:HOH:O	2.21	0.43
25:DA:2695:C:H2'	25:DA:2696:U:H6	1.83	0.43
25:DA:320:A:H4'	25:DA:322:A:C8	2.52	0.43
25:DA:720:C:H2'	25:DA:721:C:C6	2.54	0.43
30:DG:121:ASN:HA	30:DG:122:PRO:HD3	1.80	0.43
36:DQ:111:GLU:O	36:DQ:115:MET:HG2	2.18	0.43
38:DS:58:LEU:HD11	38:DS:65:VAL:HG13	2.00	0.43
40:DU:61:TRP:CH2	40:DU:93:LYS:HB2	2.54	0.43
25:DA:1614:A:C2	42:DW:93:ALA:HB2	2.53	0.43
45:DZ:5:LEU:HD21	45:DZ:43:GLU:HB3	1.99	0.43
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.17	0.43
1:AA:522:C:H41	12:AL:53:ARG:NH2	2.16	0.43
1:AA:737:A:H2'	1:AA:738:C:C6	2.53	0.43
5:AE:145:LYS:O	5:AE:149:GLU:HG2	2.18	0.43
1:AA:526:C:OP2	12:AL:91:LYS:HE3	2.19	0.43
13:AM:11:ARG:HA	13:AM:45:VAL:HB	2.01	0.43
25:BA:1373:C:O2'	37:BR:105:ARG:NH1	2.43	0.43
25:BA:1553:A:O2'	25:BA:1554:A:O5'	2.25	0.43
25:BA:1686:U:O2'	25:BA:1687:C:H5'	2.19	0.43
25:BA:599:U:H2'	25:BA:600:G:C8	2.54	0.43
25:BA:847:A:H8	25:BA:847:A:OP1	2.00	0.43
25:BA:964:A:H5''	26:BB:98:G:O2'	2.18	0.43
25:BA:2761:A:H5'	31:BH:4:ILE:HD12	2.01	0.43
45:BZ:54:HIS:HD2	45:BZ:99:TYR:O	2.01	0.43
1:CA:1492:A:H2'	1:CA:1493:A:C4	2.53	0.43
1:CA:598:U:H2'	1:CA:599:C:C6	2.52	0.43
5:CE:50:GLU:HB2	5:CE:53:LEU:HD13	2.00	0.43
13:CM:13:LYS:O	13:CM:45:VAL:HG23	2.19	0.43
14:CN:59:ALA:HB1	14:CN:61:TRP:HZ3	1.82	0.43
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	2.01	0.43
49:D3:9:VAL:HG12	49:D3:32:GLN:HE22	1.83	0.43
25:DA:1041:C:H42	25:DA:1114:G:H1	1.66	0.43
25:DA:1153:C:H2'	25:DA:1154:G:O4'	2.19	0.43
25:DA:1292:U:H2'	25:DA:1293:C:H6	1.83	0.43
25:DA:149:A:H2'	25:DA:150:C:O4'	2.19	0.43
25:DA:1932:A:H2'	25:DA:1933:G:O4'	2.18	0.43
25:DA:234:C:H2'	25:DA:235:U:H6	1.84	0.43
25:DA:417:C:H1'	25:DA:2407:G:N2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2516:G:C6	25:DA:2517:C:C4	3.07	0.43
25:DA:2051:A:H5'	25:DA:2578:G:O4'	2.19	0.43
25:DA:298:G:H5''	25:DA:299:A:OP1	2.18	0.43
25:DA:1803:A:H4'	27:DD:259:THR:HG23	1.99	0.43
25:DA:2572:A:N7	28:DE:145:LYS:HB2	2.34	0.43
35:DP:38:GLN:HG2	35:DP:45:LEU:N	2.33	0.43
42:DW:18:ARG:HG2	42:DW:76:VAL:HB	2.01	0.43
43:DX:20:GLY:HA2	43:DX:23:GLU:OE2	2.19	0.43
1:AA:1015:A:O3'	14:AN:15:LYS:NZ	2.52	0.43
1:AA:100:C:H2'	1:AA:101:A:C8	2.54	0.43
1:AA:1317:C:N3	19:AS:37:ARG:NH2	2.56	0.43
1:AA:162:A:H5''	1:AA:163:C:OP2	2.18	0.43
1:AA:796:C:H1'	57:AA:3191:PCY:H92	2.00	0.43
1:AA:430:A:OP1	4:AD:9:CYS:N	2.41	0.43
1:AA:534:U:H6	1:AA:534:U:O5'	2.02	0.43
1:AA:560:U:H4'	1:AA:561:U:O5'	2.18	0.43
24:AY:5:G:N2	24:AY:6:G:H1'	2.33	0.43
25:BA:1302:G:O2'	29:BF:75:HIS:HE1	2.02	0.43
25:BA:160:G:O2'	25:BA:161:C:H5'	2.18	0.43
25:BA:197:C:H2'	25:BA:198:C:H6	1.84	0.43
25:BA:1685:C:H5''	25:BA:2722:C:O2'	2.19	0.43
25:BA:2827:G:OP1	37:BR:99:LYS:HE2	2.19	0.43
25:BA:504:A:N1	25:BA:525:G:H4'	2.33	0.43
26:BB:75:G:H8	26:BB:75:G:H5''	1.82	0.43
27:BD:71:ASP:HB3	27:BD:103:ARG:NH2	2.27	0.43
30:BG:72:ARG:NH1	30:BG:87:PRO:HG3	2.33	0.43
38:BS:59:LYS:HE3	38:BS:59:LYS:HB2	1.83	0.43
45:BZ:93:ASP:OD1	45:BZ:94:GLU:N	2.51	0.43
1:CA:1002:G:H3'	1:CA:1003:G:C8	2.53	0.43
1:CA:1371:G:C6	1:CA:1372:U:C4	3.06	0.43
1:CA:1446:U:H4'	1:CA:1447:A:C5	2.52	0.43
1:CA:1496:C:H2'	1:CA:1497:G:O4'	2.19	0.43
1:CA:473:G:C2'	1:CA:474:G:H5'	2.48	0.43
2:CB:87:ARG:NH2	2:CB:220:ASP:OD1	2.48	0.43
1:CA:1055:A:N3	3:CC:156:ARG:HD2	2.34	0.43
11:CK:43:SER:HB3	11:CK:68:ALA:HB2	2.01	0.43
14:CN:24:CYS:HB3	14:CN:29:ARG:H	1.83	0.43
19:CS:20:LEU:HA	19:CS:23:ASN:HD22	1.83	0.43
47:D1:86:SER:OG	47:D1:89:GLU:OE2	2.27	0.43
25:DA:1415:U:O2'	25:DA:1417:C:OP1	2.37	0.43
25:DA:2086:U:H2'	25:DA:2087:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2135:A:H61	25:DA:2157:G:N2	2.17	0.43
25:DA:2545:G:N3	25:DA:2565:A:H2	2.16	0.43
25:DA:2819:G:H2'	25:DA:2821:A:N7	2.34	0.43
25:DA:649:G:H2'	25:DA:650:C:O4'	2.18	0.43
25:DA:893:C:H5'	25:DA:894:C:OP2	2.19	0.43
25:DA:93:G:H2'	25:DA:94:C:C6	2.54	0.43
26:DB:26:A:O5'	26:DB:26:A:H8	2.02	0.43
26:DB:33:G:C2	26:DB:50:G:C2	3.07	0.43
34:DO:98:VAL:HG22	34:DO:118:ALA:HA	2.00	0.43
35:DP:99:LEU:O	35:DP:103:ALA:N	2.50	0.43
36:DQ:24:GLY:HA2	36:DQ:67:ARG:NH2	2.34	0.43
1:AA:1028:C:H2'	1:AA:1029:C:H4'	2.00	0.43
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.19	0.43
1:AA:164:U:H2'	1:AA:165:C:C6	2.54	0.43
1:AA:479:C:C4	1:AA:480:U:C4	3.06	0.43
1:AA:68:G:C2	1:AA:69:G:H1'	2.54	0.43
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.34	0.43
2:AB:71:VAL:HG12	2:AB:170:GLU:HG3	2.01	0.43
2:AB:76:GLN:H	2:AB:76:GLN:CD	2.22	0.43
4:AD:128:VAL:HG12	4:AD:129:ASN:ND2	2.33	0.43
4:AD:166:LYS:HB2	4:AD:168:ARG:NH1	2.33	0.43
6:AF:2:ARG:NE	6:AF:69:GLU:HG2	2.34	0.43
19:AS:23:ASN:HA	19:AS:27:GLU:CD	2.39	0.43
30:BG:179:PRO:HG3	50:B4:43:TYR:OH	2.18	0.43
25:BA:1093:G:O2'	25:BA:1094:A:H8	2.01	0.43
25:BA:553:A:C2	25:BA:2064:A:H2'	2.53	0.43
26:BB:78:A:C2	26:BB:100:A:C4	3.06	0.43
29:BF:132:VAL:HG22	29:BF:163:VAL:HG22	2.01	0.43
36:BQ:21:THR:HG21	36:BQ:101:ARG:HD3	2.00	0.43
42:BW:88:ARG:HG3	42:BW:92:ARG:HH21	1.83	0.43
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.52	0.43
1:CA:1228:C:H4'	13:CM:116:THR:HA	2.01	0.43
1:CA:399:G:H2'	1:CA:400:C:C6	2.53	0.43
2:CB:178:ARG:NH2	8:CH:68:ARG:HH12	2.16	0.43
6:CF:61:LEU:HD23	6:CF:63:TYR:HE1	1.84	0.43
9:CI:67:GLY:O	9:CI:73:GLN:NE2	2.43	0.43
9:CI:99:LEU:HB3	9:CI:101:PHE:HE2	1.83	0.43
11:CK:38:ASN:HA	11:CK:39:PRO:HD3	1.87	0.43
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.83	0.43
24:CY:73:A:H2'	24:CY:74:C:O4'	2.18	0.43
50:D4:57:GLU:HA	50:D4:58:ARG:HA	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:D8:63:PRO:HG2	54:D8:64:TYR:CD2	2.54	0.43
25:DA:1579:A:H2'	25:DA:1580:A:C8	2.54	0.43
25:DA:2025:C:H2'	25:DA:2026:C:C6	2.54	0.43
25:DA:2031:A:N3	25:DA:2455:G:O2'	2.35	0.43
25:DA:2037:G:O2'	25:DA:2038:G:H5'	2.18	0.43
25:DA:2628:C:H1'	25:DA:2781:A:H2'	2.00	0.43
26:DB:13:A:O2'	26:DB:14:U:H3'	2.19	0.43
27:DD:218:ARG:HB3	27:DD:219:PRO:HD2	2.01	0.43
29:DF:34:TRP:CZ2	35:DP:8:PRO:HG3	2.53	0.43
39:DT:56:GLY:O	39:DT:59:THR:HG22	2.18	0.43
1:AA:1092:A:O5'	1:AA:1092:A:H8	2.01	0.43
1:AA:922:G:H2'	1:AA:923:A:C8	2.54	0.43
1:AA:993:G:H2'	1:AA:995:C:H41	1.82	0.43
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.65	0.43
2:AB:196:LEU:HD12	2:AB:196:LEU:HA	1.90	0.43
2:AB:211:ILE:O	2:AB:215:LEU:HB2	2.19	0.43
3:AC:113:ALA:HB3	3:AC:114:PRO:HD3	2.01	0.43
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.48	0.43
5:AE:90:VAL:O	5:AE:91:LEU:HD13	2.19	0.43
1:AA:1351:U:O4	9:AI:118:LYS:NZ	2.51	0.43
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.34	0.43
14:AN:3:ARG:HA	14:AN:3:ARG:HD2	1.58	0.43
16:AP:4:ILE:N	16:AP:65:GLN:O	2.30	0.43
20:AT:43:LEU:O	20:AT:47:GLY:N	2.44	0.43
25:BA:1440:U:H2'	25:BA:1441:A:O4'	2.19	0.43
25:BA:1587:U:H2'	25:BA:1588:G:O4'	2.18	0.43
25:BA:1797:U:H2'	25:BA:1798:C:H6	1.84	0.43
25:BA:2166:U:H2'	25:BA:2168:C:C5	2.53	0.43
25:BA:2897:U:H2'	25:BA:2898:C:C6	2.52	0.43
29:BF:183:VAL:O	29:BF:187:VAL:HG23	2.19	0.43
32:BI:6:LEU:HG	32:BI:36:ALA:HA	2.01	0.43
42:BW:14:PRO:HG2	42:BW:78:GLU:CG	2.48	0.43
1:CA:1039:C:H2'	1:CA:1040:U:C6	2.54	0.43
1:CA:790:A:N6	1:CA:1498:U:OP1	2.52	0.43
1:CA:406:G:H4'	4:CD:5:ILE:HD11	2.00	0.43
1:CA:582:U:OP1	15:CO:68:ARG:NH1	2.51	0.43
1:CA:617:G:H4'	16:CP:44:THR:O	2.17	0.43
2:CB:187:LEU:HD23	2:CB:201:ILE:HB	2.00	0.43
3:CC:51:GLY:O	3:CC:70:VAL:HA	2.19	0.43
9:CI:99:LEU:HB3	9:CI:101:PHE:CE2	2.54	0.43
11:CK:48:ILE:HD11	11:CK:64:ALA:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.18	0.43
17:CQ:56:VAL:O	17:CQ:77:VAL:HB	2.19	0.43
20:CT:86:ARG:O	20:CT:90:GLN:NE2	2.49	0.43
25:DA:1508:A:H4'	25:DA:1509(A):A:C4	2.54	0.43
25:DA:151:C:H42	25:DA:175:G:H1	1.67	0.43
25:DA:1301:A:H2	25:DA:1626:G:N3	2.17	0.43
25:DA:237:C:H2'	25:DA:238:C:C6	2.53	0.43
25:DA:2872:G:O2'	25:DA:2873:A:H5'	2.19	0.43
25:DA:28:A:O2'	25:DA:583:G:H5'	2.18	0.43
25:DA:764:A:H5'	27:DD:210:GLY:CA	2.49	0.43
25:DA:864:G:C6	25:DA:865:C:N4	2.86	0.43
28:DE:52:LEU:O	28:DE:76:ARG:N	2.34	0.43
36:DQ:20:ALA:HB2	45:DZ:79:ARG:HG2	1.99	0.43
38:DS:68:GLN:HE21	38:DS:68:GLN:HA	1.83	0.43
45:DZ:144:LEU:HD23	45:DZ:144:LEU:HA	1.76	0.43
1:AA:1290:G:C4	1:AA:1291:G:C8	3.06	0.43
1:AA:931:C:N4	1:AA:1386:G:H1	2.16	0.43
1:AA:590:C:H2'	1:AA:591:U:C6	2.54	0.43
1:AA:575:G:O2'	1:AA:821:G:OP2	2.28	0.43
10:AJ:8:LEU:HD23	10:AJ:96:ILE:HA	2.01	0.43
19:AS:30:LEU:HD21	19:AS:32:LYS:HG3	2.01	0.43
54:B8:33:ASN:HA	54:B8:36:LYS:HD2	2.01	0.43
25:BA:354:A:H2	25:BA:1255:A:H2'	1.83	0.43
27:BD:5:LYS:HE3	27:BD:5:LYS:HB3	1.57	0.43
30:BG:5:VAL:HG22	30:BG:8:LYS:H	1.84	0.43
40:BU:58:ARG:HA	40:BU:61:TRP:CE3	2.54	0.43
45:BZ:137:ILE:HA	45:BZ:156:LYS:HZ1	1.84	0.43
1:CA:1009:G:C2	1:CA:1010:G:C4	3.07	0.43
1:CA:153:C:H2'	1:CA:154:C:H6	1.83	0.43
1:CA:418:C:H2'	1:CA:419:C:C6	2.53	0.43
1:CA:9:G:H2'	1:CA:10:A:C8	2.54	0.43
12:CL:8:ASN:O	12:CL:12:ARG:HG3	2.19	0.43
13:CM:90:LEU:HD23	13:CM:93:ARG:HE	1.84	0.43
25:DA:1505:C:H2'	25:DA:1506:C:H6	1.84	0.43
1:CA:1493:A:C8	25:DA:1913:A:N1	2.86	0.43
25:DA:2257:U:O2'	25:DA:2258:C:H5'	2.18	0.43
25:DA:2815:C:H2'	25:DA:2816:C:H6	1.82	0.43
25:DA:1188:U:C4'	41:DV:79:VAL:HG22	2.49	0.43
43:DX:35:THR:HB	43:DX:38:GLU:HB2	2.01	0.43
1:AA:271:C:H2'	1:AA:272:C:C6	2.54	0.43
1:AA:299:G:C6	1:AA:300:A:C6	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:444:C:H2'	1:AA:445:G:H8	1.84	0.43
1:AA:920:U:H2'	1:AA:921:U:C6	2.54	0.43
3:AC:138:VAL:HG22	3:AC:151:VAL:HG23	2.00	0.43
4:AD:184:LYS:HB3	4:AD:184:LYS:HE2	1.80	0.43
8:AH:29:SER:HB2	8:AH:32:LYS:HG3	2.01	0.43
20:AT:51:GLU:HG3	20:AT:54:LYS:NZ	2.34	0.43
23:AX:61:C:H2'	23:AX:62:C:H6	1.84	0.43
46:B0:43:THR:HG23	46:B0:43:THR:O	2.19	0.43
51:B5:35:GLU:HG3	51:B5:51:TYR:CD2	2.53	0.43
25:BA:2021:C:H4'	25:BA:2736:C:O2	2.18	0.43
25:BA:2172:U:N3	25:BA:2173:G:N7	2.66	0.43
25:BA:2193:A:H1'	25:BA:2194:U:C6	2.54	0.43
25:BA:411:U:H2'	25:BA:412:C:H6	1.83	0.43
25:BA:543:G:H2'	25:BA:544:U:C6	2.54	0.43
30:BG:41:GLN:C	30:BG:43:LEU:H	2.22	0.43
32:BI:12:LEU:HD23	32:BI:12:LEU:HA	1.71	0.43
25:BA:2116:G:OP1	32:BI:22:LYS:HD2	2.19	0.43
32:BI:72:LEU:O	32:BI:74:ASN:N	2.52	0.43
37:BR:44:LEU:HD22	37:BR:48:VAL:HG23	2.00	0.43
39:BT:24:PRO:HD3	39:BT:52:ILE:HD12	2.00	0.43
1:CA:1008:C:H42	1:CA:1021:G:H1	1.67	0.43
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.99	0.43
8:CH:51:VAL:HG11	8:CH:60:ARG:HH12	1.84	0.43
10:CJ:6:ILE:O	10:CJ:71:LEU:HD12	2.18	0.43
20:CT:57:ARG:HH22	20:CT:100:ILE:HD12	1.84	0.43
25:DA:1022:G:C6	25:DA:1140:C:C4	3.06	0.43
25:DA:1185:C:H5''	25:DA:1186:G:OP1	2.18	0.43
25:DA:749:C:O2	25:DA:1618:A:H2'	2.19	0.43
25:DA:1791:A:H3'	25:DA:1792:G:H8	1.84	0.43
25:DA:1790:C:H5''	25:DA:1791:A:OP1	2.19	0.43
25:DA:829:A:N7	25:DA:2248:C:H5'	2.33	0.43
25:DA:2377:A:H2'	25:DA:2378:A:C8	2.54	0.43
32:DI:77:LEU:HD11	32:DI:101:LEU:HB2	2.00	0.43
45:DZ:146:ILE:H	45:DZ:146:ILE:HG13	1.62	0.43
45:DZ:53:ILE:HG13	45:DZ:53:ILE:H	1.73	0.43
1:AA:240:C:H2'	1:AA:241:C:H6	1.84	0.42
1:AA:371:G:O2'	1:AA:373:A:N7	2.46	0.42
1:AA:302:G:O2'	1:AA:556:C:H5''	2.19	0.42
1:AA:996:A:H2'	1:AA:997:U:O4'	2.19	0.42
11:AK:20:TYR:CZ	11:AK:83:ILE:HD12	2.54	0.42
49:B3:46:ASN:O	49:B3:50:VAL:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:B8:54:GLU:O	54:B8:58:ILE:HG13	2.19	0.42
25:BA:1653:C:H4'	25:BA:1654:A:O5'	2.19	0.42
25:BA:2258:G:H2'	25:BA:2259:A:C8	2.54	0.42
25:BA:284:G:C2	25:BA:285:U:O4	2.72	0.42
25:BA:399:G:H8	47:B1:65:SER:O	2.02	0.42
30:BG:43:LEU:HD11	30:BG:153:ARG:HG2	2.01	0.42
39:BT:11:GLU:OE1	39:BT:57:PHE:HB3	2.19	0.42
1:CA:1118:C:H1'	1:CA:1179:A:C6	2.54	0.42
1:CA:630:G:O2'	1:CA:631:G:H5'	2.19	0.42
2:CB:170:GLU:O	2:CB:174:VAL:HG23	2.19	0.42
4:CD:153:ARG:NH2	4:CD:180:GLY:O	2.51	0.42
1:CA:1240:U:O2	7:CG:32:ARG:HB2	2.19	0.42
1:CA:742:G:P	15:CO:35:ARG:HH21	2.42	0.42
50:D4:14:ILE:HG23	50:D4:31:ILE:HB	2.01	0.42
52:D6:11:LEU:HB2	52:D6:21:TYR:HB2	2.00	0.42
25:DA:977:G:N3	25:DA:1001:A:H2	2.16	0.42
25:DA:980:A:C4	25:DA:1136:G:O4'	2.72	0.42
25:DA:1227:G:OP1	40:DU:13:LYS:HG2	2.19	0.42
25:DA:1721:G:N3	25:DA:1721:G:H5''	2.34	0.42
25:DA:1878:G:H2'	25:DA:1879:C:C6	2.54	0.42
25:DA:2128:C:H5'	25:DA:2173:A:C2	2.54	0.42
25:DA:2330:G:H2'	25:DA:2331:G:O4'	2.18	0.42
25:DA:2261:C:H1'	25:DA:2388:A:N3	2.34	0.42
25:DA:272(E):G:C2	25:DA:364:C:C2	3.07	0.42
25:DA:699:A:C2	25:DA:1633:G:N3	2.87	0.42
25:DA:818:G:H4'	25:DA:838:C:O3'	2.19	0.42
25:DA:956:G:OP2	36:DQ:14:ARG:NH2	2.50	0.42
26:DB:16:G:C6	26:DB:69:G:C2	3.07	0.42
27:DD:276:LYS:H	27:DD:276:LYS:HG2	1.63	0.42
29:DF:132:VAL:HA	29:DF:138:GLU:HB3	2.00	0.42
32:DI:69:LYS:O	32:DI:73:GLU:HB2	2.19	0.42
34:DO:52:VAL:HG12	34:DO:94:ARG:HH22	1.84	0.42
41:DV:64:HIS:CE1	41:DV:92:THR:HG1	2.36	0.42
1:AA:1027:C:H2'	1:AA:1028:C:C5	2.55	0.42
1:AA:1252:A:H2'	1:AA:1253:G:O4'	2.19	0.42
1:AA:198:G:O6	1:AA:219:C:N4	2.52	0.42
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.34	0.42
1:AA:690:G:C6	1:AA:691:G:C6	3.07	0.42
2:AB:209:ARG:HH11	2:AB:209:ARG:HB2	1.84	0.42
7:AG:13:GLN:HA	7:AG:14:PRO:HD3	1.90	0.42
10:AJ:27:ALA:HA	10:AJ:81:THR:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AL:110:VAL:HG23	12:AL:120:TYR:HB3	2.01	0.42
1:AA:35:G:O2'	12:AL:118:SER:O	2.32	0.42
50:B4:62:ARG:HB2	50:B4:63:TYR:CD1	2.54	0.42
25:BA:1903:C:H2'	25:BA:1904:C:H6	1.83	0.42
25:BA:2320:G:O2'	25:BA:2322:A:N7	2.51	0.42
25:BA:2339:A:H2'	25:BA:2340:A:H8	1.82	0.42
29:BF:53:THR:HB	29:BF:56:GLU:OE2	2.19	0.42
30:BG:120:LEU:HD23	30:BG:120:LEU:HA	1.88	0.42
34:BO:98:VAL:HG22	34:BO:118:ALA:HA	2.01	0.42
35:BP:121:LYS:O	35:BP:123:LEU:N	2.52	0.42
37:BR:72:ASP:O	37:BR:76:VAL:HG23	2.19	0.42
41:BV:18:LEU:HD22	41:BV:19:LYS:N	2.34	0.42
1:CA:1142:G:H2'	1:CA:1143:G:O4'	2.19	0.42
1:CA:1183:A:H3'	1:CA:1184:G:H5''	2.01	0.42
1:CA:1355:G:C2'	1:CA:1356:G:H5'	2.48	0.42
1:CA:411:A:C6	1:CA:429:U:C4	3.07	0.42
1:CA:857:C:H2'	1:CA:858:G:O4'	2.18	0.42
1:CA:982:U:N3	1:CA:1223:C:N3	2.67	0.42
2:CB:16:HIS:HB2	2:CB:204:ASN:CB	2.33	0.42
7:CG:16:LEU:H	7:CG:16:LEU:HD22	1.84	0.42
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	2.01	0.42
10:CJ:44:VAL:HG13	10:CJ:66:ARG:HG2	2.01	0.42
15:CO:10:LYS:HE2	15:CO:10:LYS:HB2	1.72	0.42
48:D2:10:LEU:HB3	48:D2:14:ARG:NH1	2.34	0.42
55:D9:17:ILE:HD12	55:D9:17:ILE:HA	1.82	0.42
25:DA:1007:C:OP1	33:DN:35:ARG:NH1	2.49	0.42
25:DA:1337:G:H2'	25:DA:1338:G:O4'	2.19	0.42
25:DA:2335:A:O2'	25:DA:2336:A:H5''	2.20	0.42
25:DA:2647:U:O2'	25:DA:2648:C:H5'	2.19	0.42
25:DA:271(U):G:H2'	25:DA:271(V):G:H8	1.82	0.42
25:DA:2768:C:C4	25:DA:2769:C:C5	3.07	0.42
26:DB:80:U:H2'	26:DB:81:G:C8	2.54	0.42
28:DE:4:ILE:HD11	28:DE:29:GLY:HA2	2.02	0.42
31:DH:28:GLY:HA3	31:DH:79:VAL:HB	2.00	0.42
33:DN:91:LEU:HA	33:DN:95:PRO:HA	2.00	0.42
34:DO:7:TYR:HE1	34:DO:20:MET:HE3	1.83	0.42
35:DP:84:ASN:HB3	35:DP:117:GLU:O	2.19	0.42
42:DW:80:PRO:O	42:DW:100:THR:HB	2.19	0.42
1:AA:657:G:C2	1:AA:658:G:C8	3.07	0.42
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.54	0.42
50:B4:54:GLY:O	50:B4:55:ARG:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:805:C:O2'	25:BA:2003:A:N3	2.38	0.42
25:BA:2034:G:OP1	42:BW:11:ARG:NH2	2.44	0.42
25:BA:2023:A:H5''	25:BA:2701:U:H2'	2.00	0.42
25:BA:298:G:H2'	25:BA:299:G:C8	2.54	0.42
25:BA:518:G:H2'	25:BA:519:G:O4'	2.19	0.42
25:BA:895:G:H2'	25:BA:896:A:C8	2.54	0.42
25:BA:1615:G:H5'	27:BD:60:ARG:HA	2.01	0.42
29:BF:116:ASP:O	29:BF:120:GLU:HG3	2.18	0.42
31:BH:9:ILE:HG12	31:BH:69:ARG:HH11	1.82	0.42
28:BE:111:ARG:HA	37:BR:1:MET:SD	2.59	0.42
37:BR:97:VAL:HG22	37:BR:114:VAL:HG13	2.00	0.42
44:BY:55:TYR:CE1	44:BY:61:ILE:HG21	2.55	0.42
45:BZ:79:ARG:HB3	45:BZ:80:ARG:NH1	2.34	0.42
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.49	0.42
1:CA:392:G:H2'	1:CA:393:A:H8	1.83	0.42
1:CA:487:A:H2'	1:CA:488:C:O4'	2.19	0.42
2:CB:147:LYS:HD2	2:CB:148:TYR:CE1	2.54	0.42
2:CB:213:LEU:HD22	2:CB:214:ILE:HD13	2.02	0.42
3:CC:11:ARG:NH2	3:CC:177:THR:O	2.52	0.42
6:CF:14:LEU:HD22	6:CF:18:GLN:HB3	2.02	0.42
9:CI:46:ALA:HA	9:CI:78:LYS:HB2	2.01	0.42
11:CK:65:ALA:HB1	11:CK:98:LEU:HD23	2.02	0.42
12:CL:6:THR:HG23	12:CL:9:GLN:OE1	2.20	0.42
1:CA:1204:A:P	14:CN:3:ARG:HH11	2.42	0.42
14:CN:6:LEU:HA	14:CN:6:LEU:HD12	1.90	0.42
25:DA:1272:A:H3'	25:DA:1273:U:H5''	2.00	0.42
25:DA:1896:G:H2'	25:DA:1897:G:H8	1.84	0.42
25:DA:185:U:H4'	25:DA:218:A:H4'	2.00	0.42
25:DA:2651:C:H2'	25:DA:2652:C:C6	2.54	0.42
27:DD:24:ILE:HD13	27:DD:84:TYR:HB2	2.01	0.42
31:DH:13:LYS:HA	31:DH:14:GLY:HA2	1.76	0.42
35:DP:46:LYS:HE3	35:DP:46:LYS:HB3	1.76	0.42
35:DP:55:ARG:HG2	35:DP:56:SER:O	2.19	0.42
43:DX:35:THR:HG22	43:DX:37:THR:N	2.34	0.42
44:DY:54:LYS:O	44:DY:56:PRO:HD3	2.19	0.42
1:AA:110:C:C2'	1:AA:111:G:H5'	2.48	0.42
1:AA:978:A:O2'	1:AA:1322:C:N3	2.41	0.42
1:AA:102:G:O2'	1:AA:151:A:N3	2.42	0.42
1:AA:348:G:C2'	1:AA:349:A:H5'	2.49	0.42
1:AA:460:G:H21	1:AA:472:A:H62	1.68	0.42
1:AA:595:G:H1'	1:AA:596:C:H5	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:166:ASP:OD2	2:AB:169:LYS:HB2	2.19	0.42
3:AC:110:ASN:O	3:AC:141:VAL:HG22	2.19	0.42
3:AC:118:GLN:HG2	3:AC:118:GLN:H	1.62	0.42
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.34	0.42
4:AD:138:TYR:CE1	4:AD:140:VAL:HA	2.54	0.42
4:AD:188:LEU:H	4:AD:188:LEU:CD2	2.31	0.42
13:AM:3:ARG:HG2	13:AM:8:GLU:HA	2.00	0.42
25:BA:2032:G:H5''	42:BW:42:ARG:HB2	2.00	0.42
25:BA:2589:A:H5''	25:BA:2590:G:H5'	2.01	0.42
25:BA:515:G:N7	42:BW:49:LYS:NZ	2.64	0.42
25:BA:704:U:H2'	25:BA:705:C:C6	2.54	0.42
25:BA:990:A:C4	25:BA:2460:A:C2	3.07	0.42
25:BA:992:G:H2'	25:BA:993:G:C8	2.54	0.42
33:BN:75:TYR:CE2	33:BN:77:GLY:HA2	2.55	0.42
1:CA:1005:A:O2'	1:CA:1006:C:OP1	2.35	0.42
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.54	0.42
1:CA:1261:A:C5	1:CA:1262:C:C4	3.06	0.42
1:CA:143:A:O3'	1:CA:144:G:H8	2.02	0.42
1:CA:1442:G:HO2'	1:CA:1442(A):G:P	2.38	0.42
1:CA:15:G:C4	1:CA:16:A:C8	3.07	0.42
1:CA:532:A:H5'	3:CC:161:GLU:OE2	2.20	0.42
1:CA:767:A:H2'	1:CA:768:A:O4'	2.19	0.42
8:CH:23:SER:HA	8:CH:63:LEU:HD22	2.00	0.42
14:CN:53:LEU:HA	14:CN:54:PRO:HD2	1.92	0.42
16:CP:14:ASN:OD1	16:CP:42:ARG:NH2	2.53	0.42
25:DA:372:G:H8	47:D1:65:SER:O	2.02	0.42
25:DA:1524:G:N2	25:DA:1525:G:H1'	2.34	0.42
25:DA:2376:A:H3'	25:DA:2377:A:H8	1.84	0.42
25:DA:251:A:C5	25:DA:252:G:H1'	2.54	0.42
25:DA:348:G:H2'	25:DA:349:G:C8	2.54	0.42
25:DA:652(D):C:H42	25:DA:652(U):G:H1	1.66	0.42
25:DA:921:G:H4'	25:DA:2269:A:C5	2.54	0.42
25:DA:954:G:C5	25:DA:955:C:C5	3.07	0.42
25:DA:984:A:H5''	25:DA:985:C:H5	1.85	0.42
27:DD:147:LEU:HD13	27:DD:155:LEU:HD21	2.01	0.42
28:DE:115:GLY:O	28:DE:119:ARG:HB2	2.20	0.42
29:DF:196:LEU:HA	29:DF:196:LEU:HD23	1.79	0.42
36:DQ:18:LYS:HE3	36:DQ:18:LYS:HB2	1.75	0.42
45:DZ:117:LEU:HD12	45:DZ:174:VAL:HG22	2.00	0.42
1:AA:1353:G:O2'	1:AA:1354:C:H5'	2.20	0.42
1:AA:1362:C:C2'	1:AA:1363:C:H5''	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:439:A:N1	1:AA:496:A:C4	2.78	0.42
1:AA:406:G:N2	4:AD:119:GLN:HE22	2.18	0.42
8:AH:11:THR:HG22	8:AH:15:ASN:HD21	1.83	0.42
47:B1:89:GLU:HG2	47:B1:89:GLU:H	1.47	0.42
54:B8:61:LEU:C	54:B8:63:PRO:HD3	2.40	0.42
25:BA:1077:G:H5''	55:B9:8:LYS:HE3	2.01	0.42
25:BA:1576:G:C6	25:BA:1577:C:N4	2.88	0.42
25:BA:2247:G:H2'	25:BA:2248:C:C6	2.54	0.42
25:BA:2556:G:H2'	25:BA:2557:G:O4'	2.19	0.42
25:BA:2849:G:H5'	37:BR:46:GLY:HA2	2.01	0.42
25:BA:324:A:H2'	25:BA:358:C:H1'	2.02	0.42
25:BA:496:A:H2'	25:BA:497:A:O4'	2.20	0.42
25:BA:672:G:H8	25:BA:672:G:O5'	2.03	0.42
31:BH:69:ARG:HG3	31:BH:70:THR:N	2.33	0.42
39:BT:108:ARG:HH22	39:BT:112:ARG:HH11	1.67	0.42
39:BT:53:ARG:O	39:BT:59:THR:HA	2.20	0.42
43:BX:31:HIS:CD2	43:BX:33:LYS:H	2.37	0.42
1:CA:1095:U:C4	1:CA:1096:C:C4	3.07	0.42
1:CA:407:G:OP1	4:CD:115:ARG:HD3	2.19	0.42
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.85	0.42
8:CH:124:ALA:O	8:CH:128:GLY:N	2.51	0.42
1:CA:1124:G:H5''	10:CJ:35:SER:OG	2.20	0.42
10:CJ:70:ARG:HA	10:CJ:70:ARG:HD3	1.91	0.42
13:CM:57:ARG:NH1	50:D4:34:GLU:HA	2.34	0.42
46:D0:82:ARG:HA	46:D0:83:PRO:HD3	1.79	0.42
25:DA:271(R):G:H5''	47:D1:97:LEU:HD21	2.00	0.42
43:DX:5:TYR:CE1	48:D2:30:ARG:HB2	2.55	0.42
19:CS:68:GLY:H	50:D4:58:ARG:NH1	2.18	0.42
30:DG:67:LYS:HE2	50:D4:5:ILE:HD12	2.01	0.42
25:DA:2365:G:O6	54:D8:39:LYS:HE3	2.19	0.42
55:D9:7:VAL:HG12	55:D9:34:GLN:HB3	2.02	0.42
25:DA:1212:G:C2	25:DA:1236:G:C4	3.07	0.42
25:DA:1262:A:C5	25:DA:1263:U:C5	3.07	0.42
25:DA:1514:U:H2'	25:DA:1515:G:C8	2.55	0.42
25:DA:2365:G:O6	54:D8:43:GLN:NE2	2.52	0.42
25:DA:236:C:H2'	25:DA:237:C:H6	1.85	0.42
25:DA:2531:A:N3	25:DA:2658:C:O2'	2.43	0.42
25:DA:463:G:N2	25:DA:466:A:OP2	2.38	0.42
28:DE:181:LEU:HD12	28:DE:181:LEU:HA	1.86	0.42
36:DQ:110:THR:HG23	36:DQ:113:GLN:OE1	2.20	0.42
42:DW:13:SER:HA	42:DW:14:PRO:HD3	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:176:C:H2'	1:AA:177:C:C6	2.54	0.42
1:AA:186:C:H2'	1:AA:187:C:C6	2.54	0.42
1:AA:555:C:H2'	1:AA:556:C:C6	2.55	0.42
1:AA:687:A:N3	1:AA:688:G:H1'	2.34	0.42
2:AB:77:ALA:CB	2:AB:165:VAL:HG11	2.50	0.42
4:AD:134:ASP:O	4:AD:136:PRO:HD3	2.19	0.42
8:AH:82:HIS:CE1	8:AH:84:ARG:HD2	2.55	0.42
54:B8:6:THR:HG23	54:B8:64:TYR:HD2	1.84	0.42
25:BA:1220:U:O3'	25:BA:1221:G:H4'	2.19	0.42
25:BA:180:A:H2'	25:BA:181:C:C6	2.55	0.42
25:BA:1940:A:O2'	25:BA:1942:C:N4	2.53	0.42
25:BA:2170:G:OP2	25:BA:2170:G:H8	2.02	0.42
25:BA:876:A:N7	25:BA:2260:C:H5'	2.35	0.42
25:BA:2787:C:H2'	25:BA:2788:A:O4'	2.20	0.42
25:BA:278:G:H2'	25:BA:279:G:H5''	2.02	0.42
29:BF:140:LEU:HD21	29:BF:170:LEU:HD11	2.01	0.42
31:BH:116:GLU:HA	31:BH:117:PRO:HD3	1.95	0.42
39:BT:124:ASP:O	39:BT:128:GLU:HG3	2.19	0.42
42:BW:2:GLU:OE2	42:BW:72:LYS:NZ	2.36	0.42
1:CA:1032:G:H2'	1:CA:1033:G:C8	2.55	0.42
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.37	0.42
1:CA:988:G:C2	1:CA:989:C:H1'	2.55	0.42
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.55	0.42
1:CA:26:A:O2'	4:CD:209:ARG:NH2	2.52	0.42
9:CI:50:LEU:HD21	9:CI:81:ILE:HD12	2.01	0.42
54:D8:23:VAL:HG11	54:D8:47:LYS:HD3	2.00	0.42
25:DA:1005:C:H2'	25:DA:1006:C:H6	1.84	0.42
25:DA:1810:A:H2'	25:DA:1811:G:O4'	2.19	0.42
25:DA:2114:A:O2'	25:DA:2167:U:H1'	2.20	0.42
25:DA:858:U:H1'	25:DA:2268:A:H2'	2.01	0.42
27:DD:142:VAL:CG1	27:DD:191:ALA:HB1	2.49	0.42
31:DH:8:PRO:HB3	31:DH:51:ARG:HG2	2.02	0.42
25:DA:2820:A:C6	37:DR:4:LEU:HD11	2.55	0.42
25:DA:2294:C:P	38:DS:89:ARG:HH22	2.43	0.42
44:DY:90:LEU:HB2	44:DY:92:ASN:HB3	2.01	0.42
1:AA:10:A:OP2	5:AE:126:ARG:HD2	2.20	0.42
1:AA:1125:U:H5''	10:AJ:5:ARG:HH22	1.85	0.42
1:AA:590:C:H2'	1:AA:591:U:H6	1.85	0.42
2:AB:55:PHE:CD1	2:AB:58:ILE:HD12	2.55	0.42
7:AG:28:ASN:HA	7:AG:31:MET:HE2	2.01	0.42
14:AN:2:ALA:HB1	14:AN:6:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:82:ILE:O	15:AO:86:GLY:N	2.51	0.42
16:AP:39:TYR:CG	16:AP:73:LEU:HD13	2.54	0.42
47:B1:89:GLU:O	47:B1:93:GLU:HG2	2.20	0.42
48:B2:2:LYS:O	48:B2:6:VAL:HG23	2.18	0.42
25:BA:1583:C:H2'	25:BA:1584:G:O4'	2.19	0.42
25:BA:1597:C:OP1	25:BA:1765:U:O2'	2.23	0.42
25:BA:2050:U:H2'	25:BA:2051:G:O4'	2.19	0.42
25:BA:2127:C:H2'	25:BA:2128:G:C8	2.54	0.42
25:BA:2430:A:H2'	25:BA:2431:U:C6	2.54	0.42
25:BA:2736:C:H4'	37:BR:1:MET:HG3	2.02	0.42
25:BA:2648:U:H1'	25:BA:2796:G:N2	2.34	0.42
25:BA:484:G:O2'	25:BA:495:G:O6	2.28	0.42
25:BA:764:G:H2'	25:BA:765:A:O4'	2.20	0.42
29:BF:150:GLY:HA2	29:BF:172:TRP:CD2	2.55	0.42
38:BS:63:THR:HG23	38:BS:100:ALA:HB2	2.01	0.42
44:BY:7:VAL:HG21	44:BY:72:VAL:CG1	2.50	0.42
1:CA:1502:A:H2	1:CA:1505:G:N1	2.13	0.42
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.19	0.42
2:CB:179:LYS:HG3	8:CH:72:PRO:HG3	2.02	0.42
22:CV:16:A:N1	23:CX:36:U:C2	2.88	0.42
23:CX:65:C:H2'	23:CX:66:C:H6	1.84	0.42
51:D5:35:GLU:HG3	51:D5:51:TYR:CD2	2.54	0.42
52:D6:40:CYS:HA	52:D6:41:PRO:HD3	1.82	0.42
25:DA:1124:C:H2'	25:DA:1125:G:O4'	2.19	0.42
25:DA:1628:G:H2'	25:DA:1629:U:C6	2.55	0.42
25:DA:2137:C:C2	25:DA:2138:C:H5	2.38	0.42
25:DA:2567:G:H2'	25:DA:2568:C:C6	2.54	0.42
25:DA:805:G:H5''	35:DP:38:GLN:HG3	2.02	0.42
26:DB:94:C:H2'	26:DB:95:C:C6	2.55	0.42
27:DD:146:GLU:HB2	27:DD:189:CYS:HB3	2.02	0.42
27:DD:25:THR:HG21	27:DD:113:VAL:HG11	2.01	0.42
36:DQ:73:PRO:HA	36:DQ:93:TYR:CD1	2.54	0.42
41:DV:39:LEU:HD12	41:DV:47:VAL:HA	2.02	0.42
1:AA:1438:G:H2'	1:AA:1439:C:C6	2.55	0.42
1:AA:179:A:H2'	1:AA:180:U:C6	2.54	0.42
1:AA:91:C:H2'	1:AA:92:C:C6	2.54	0.42
24:AY:5:G:C2	24:AY:69:G:C4	3.07	0.42
49:B3:24:LYS:HE2	49:B3:24:LYS:HB2	1.83	0.42
53:B7:18:PHE:CE2	53:B7:22:MET:HG3	2.55	0.42
25:BA:1432:C:H2'	25:BA:1433:C:C6	2.54	0.42
25:BA:1566:U:H2'	25:BA:1567:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2284:U:H5''	25:BA:2285:A:OP1	2.20	0.42
25:BA:2699:U:H2'	25:BA:2700:U:O4'	2.19	0.42
29:BF:24:LEU:HB3	29:BF:115:ALA:HB2	2.00	0.42
34:BO:21:CYS:HB2	34:BO:39:ILE:HD12	2.02	0.42
25:BA:1387:U:O4'	43:BX:57:LEU:HD23	2.19	0.42
43:BX:43:VAL:HG21	43:BX:81:VAL:HG11	2.02	0.42
1:CA:868:C:H2'	1:CA:869:G:O4'	2.20	0.42
1:CA:890:G:O2'	1:CA:906:G:O6	2.28	0.42
4:CD:125:HIS:HD2	4:CD:152:SER:OG	2.03	0.42
13:CM:20:THR:HA	13:CM:25:ILE:HG22	2.01	0.42
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.19	0.42
19:CS:51:VAL:O	19:CS:57:HIS:HA	2.20	0.42
22:CV:14:A:H3'	22:CV:15:A:H8	1.85	0.42
50:D4:40:HIS:HA	50:D4:41:PRO:HD2	1.82	0.42
25:DA:1138:G:O2'	33:DN:105:GLY:HA3	2.19	0.42
25:DA:1978:A:H2'	25:DA:1979:C:O4'	2.20	0.42
25:DA:2298:A:N6	25:DA:2318:G:C8	2.88	0.42
25:DA:2852:G:H2'	25:DA:2853:C:O4'	2.20	0.42
25:DA:300:A:N3	25:DA:319:C:H1'	2.34	0.42
25:DA:266:G:N2	25:DA:427:U:H1'	2.34	0.42
25:DA:7:G:H2'	25:DA:8:A:H8	1.85	0.42
25:DA:927:G:H2'	25:DA:928:G:O4'	2.20	0.42
26:DB:78:A:C2	26:DB:100:A:C4	3.08	0.42
29:DF:124:LEU:HB3	29:DF:193:VAL:HG22	2.02	0.42
36:DQ:1:MET:HG3	36:DQ:44:ALA:HB1	2.02	0.42
41:DV:62:LEU:HD21	41:DV:95:LEU:HB2	2.01	0.42
43:DX:31:HIS:HA	43:DX:32:PRO:HD3	1.85	0.42
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.55	0.42
1:AA:122:G:H2'	1:AA:123:C:O4'	2.20	0.42
1:AA:1234:C:C2'	1:AA:1235:U:H5'	2.50	0.42
1:AA:763:G:H2'	1:AA:764:C:C6	2.55	0.42
1:AA:92:C:H2'	1:AA:93:G:C8	2.55	0.42
1:AA:997:U:C2'	1:AA:998:G:H5'	2.49	0.42
2:AB:124:SER:HA	2:AB:125:PRO:HA	1.77	0.42
3:AC:32:LEU:HD13	3:AC:59:ARG:HD3	2.01	0.42
6:AF:19:LEU:HD11	6:AF:59:TYR:CE2	2.54	0.42
6:AF:72:VAL:HG23	6:AF:90:VAL:HG11	2.02	0.42
25:BA:2161:C:O5'	25:BA:2161:C:H6	2.02	0.42
25:BA:2800:C:H2'	25:BA:2801:C:C6	2.55	0.42
27:BD:79:VAL:HG12	27:BD:113:VAL:HA	2.01	0.42
31:BH:33:LEU:HD23	31:BH:136:ILE:HG13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BB:91:C:OP1	36:BQ:16:ARG:HG3	2.20	0.42
43:BX:12:VAL:HG21	43:BX:27:THR:HG22	2.02	0.42
43:BX:60:ARG:NH1	53:B7:47:ARG:HH22	2.17	0.42
1:CA:1080:A:H5''	1:CA:1081:G:OP2	2.20	0.42
1:CA:115:G:H1'	1:CA:116:A:N7	2.34	0.42
1:CA:131:C:H2'	1:CA:132:C:C6	2.54	0.42
1:CA:1328:C:H2'	1:CA:1329:A:O4'	2.19	0.42
1:CA:411:A:C4	1:CA:413:G:O4'	2.72	0.42
1:CA:765:G:N1	1:CA:812:C:O2'	2.40	0.42
1:CA:933:G:C6	1:CA:1385:G:C6	3.08	0.42
1:CA:93:G:O2'	1:CA:96:U:H5'	2.20	0.42
2:CB:177:ALA:HB1	2:CB:182:ILE:HB	2.01	0.42
6:CF:35:ALA:HB2	6:CF:67:MET:HB3	2.01	0.42
8:CH:12:ARG:HD2	8:CH:26:VAL:HG12	2.01	0.42
12:CL:117:ARG:NH2	12:CL:124:LYS:HB2	2.35	0.42
13:CM:25:ILE:HD12	13:CM:66:LEU:HD22	2.02	0.42
18:CR:24:ALA:C	18:CR:26:LEU:H	2.23	0.42
48:D2:16:LEU:HB2	48:D2:21:LEU:HD22	2.02	0.42
25:DA:1359:A:C2	25:DA:1372:U:O4	2.72	0.42
25:DA:1434:A:H61	25:DA:1558:A:H62	1.66	0.42
25:DA:1607:C:H4'	25:DA:1608:A:O5'	2.19	0.42
25:DA:172:C:H2'	25:DA:173:G:H8	1.84	0.42
25:DA:1849:G:H2'	25:DA:1850:G:H8	1.85	0.42
25:DA:2386:C:H2'	25:DA:2387:U:C6	2.54	0.42
25:DA:2410:G:C2	25:DA:2411:A:H1'	2.54	0.42
25:DA:271(H):G:N3	25:DA:271(I):G:C8	2.88	0.42
25:DA:2849:U:H4'	25:DA:2868:A:C2	2.54	0.42
25:DA:601:C:OP1	29:DF:108:LYS:NZ	2.38	0.42
25:DA:900:A:H2'	25:DA:901:A:C8	2.54	0.42
25:DA:1823:G:OP1	27:DD:54:ARG:NH1	2.53	0.42
27:DD:5:LYS:HE3	27:DD:5:LYS:HB3	1.55	0.42
30:DG:164:GLU:N	30:DG:164:GLU:OE2	2.53	0.42
36:DQ:30:GLY:O	36:DQ:134:ARG:HD3	2.19	0.42
1:AA:1160:G:C6	1:AA:1161:C:H5	2.37	0.42
1:AA:1261:A:H5''	1:AA:1262:C:OP2	2.20	0.42
1:AA:1458:G:OP1	20:AT:35:THR:OG1	2.26	0.42
1:AA:16:A:N1	1:AA:919:A:H2	2.16	0.42
6:AF:94:GLN:HE21	6:AF:94:GLN:HB2	1.62	0.42
7:AG:78:ARG:HB3	7:AG:87:VAL:HG21	2.02	0.42
25:BA:1249:A:H2	25:BA:1287:A:N6	2.12	0.42
25:BA:2149:G:H2'	25:BA:2150:C:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2605:U:H2'	25:BA:2606:C:C6	2.55	0.42
25:BA:276:C:H2'	25:BA:277:G:O4'	2.20	0.42
25:BA:629:U:H4'	25:BA:705:C:H4'	2.01	0.42
29:BF:167:ALA:HB1	29:BF:173:VAL:HG11	2.02	0.42
29:BF:63:LYS:HE2	29:BF:67:GLN:HB2	2.02	0.42
32:BI:6:LEU:C	32:BI:7:GLU:HG2	2.40	0.42
1:CA:1074:G:C6	1:CA:1075:C:C4	3.08	0.42
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.32	0.42
1:CA:262:A:H2'	1:CA:263:A:C8	2.55	0.42
1:CA:977:A:O2'	1:CA:979:C:OP2	2.38	0.42
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	2.02	0.42
4:CD:163:GLU:O	4:CD:166:LYS:HG2	2.20	0.42
5:CE:9:LYS:HB2	5:CE:112:LEU:HD11	2.02	0.42
11:CK:43:SER:HA	11:CK:47:VAL:HG21	2.02	0.42
17:CQ:10:VAL:O	17:CQ:53:LEU:HD12	2.19	0.42
48:D2:35:LEU:HD12	48:D2:53:LEU:HD12	2.01	0.42
25:DA:1410:G:H2'	25:DA:1411:C:H6	1.84	0.42
25:DA:1514:U:H2'	25:DA:1515:G:H8	1.85	0.42
25:DA:2133:G:N2	25:DA:2157:G:H1'	2.35	0.42
25:DA:2337:G:C2	25:DA:2338:G:C8	3.08	0.42
25:DA:2355:C:H1'	46:D0:36:ILE:HD12	2.02	0.42
25:DA:2683:C:OP1	39:DT:53:ARG:NH2	2.34	0.42
25:DA:622:G:H2'	25:DA:623:G:C8	2.52	0.42
25:DA:700:G:H2'	25:DA:701:G:O4'	2.20	0.42
25:DA:736:C:O5'	25:DA:736:C:H6	2.03	0.42
25:DA:2227:A:OP1	27:DD:263:ARG:HD2	2.20	0.42
27:DD:275:LYS:HD3	27:DD:275:LYS:HA	1.65	0.42
29:DF:29:ASN:O	29:DF:33:LEU:HD22	2.20	0.42
1:AA:1137:C:H4'	1:AA:1138:G:N3	2.35	0.41
1:AA:1187:G:H4'	9:AI:111:ARG:HH11	1.85	0.41
1:AA:374:A:C6	1:AA:375:U:C4	3.08	0.41
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.87	0.41
6:AF:60:PHE:CE2	18:AR:76:LEU:HD12	2.52	0.41
19:AS:64:GLU:O	19:AS:67:VAL:HG23	2.19	0.41
23:AX:13:C:O2'	25:BA:1946:C:H4'	2.20	0.41
25:BA:1549:U:H2'	25:BA:1550:C:C6	2.55	0.41
25:BA:1821:C:H5''	25:BA:1822:A:OP1	2.20	0.41
25:BA:2255:U:H2'	25:BA:2256:U:H6	1.83	0.41
25:BA:390:G:H2'	25:BA:391:G:H8	1.84	0.41
25:BA:1075:A:H5''	36:BQ:128:LYS:HZ3	1.85	0.41
39:BT:91:ARG:HD2	39:BT:120:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1007:C:N3	1:CA:1022:G:C6	2.85	0.41
1:CA:1023:G:C3'	1:CA:1024:G:H8	2.31	0.41
1:CA:1224:G:O2'	1:CA:1322:C:OP1	2.30	0.41
1:CA:510:A:H5''	1:CA:511:C:P	2.59	0.41
1:CA:690:G:H8	1:CA:690:G:O5'	2.03	0.41
1:CA:707:C:H2'	1:CA:708:C:H6	1.83	0.41
1:CA:736:C:H2'	1:CA:737:A:C8	2.55	0.41
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.34	0.41
18:CR:26:LEU:HD13	18:CR:42:ARG:HH11	1.84	0.41
20:CT:63:ILE:HD13	20:CT:80:ARG:HB3	2.02	0.41
25:DA:1297:C:H5''	61:DA:4283:HOH:O	2.19	0.41
25:DA:2114:A:H2'	25:DA:2114:A:N3	2.35	0.41
25:DA:2494:G:C4	25:DA:2495:G:C8	3.08	0.41
25:DA:2611:U:OP2	25:DA:2611:U:H3'	2.20	0.41
25:DA:774:A:N6	61:DA:4022:HOH:O	2.52	0.41
30:DG:145:THR:OG1	30:DG:146:TYR:N	2.52	0.41
30:DG:41:GLN:C	30:DG:43:LEU:H	2.22	0.41
31:DH:124:GLU:HB2	31:DH:132:ARG:HB3	2.02	0.41
25:DA:2659:G:P	31:DH:158:HIS:HE2	2.43	0.41
31:DH:26:VAL:HG12	31:DH:79:VAL:HG11	2.00	0.41
41:DV:14:VAL:HB	41:DV:96:ILE:HG13	2.02	0.41
43:DX:84:ALA:HB3	43:DX:87:GLN:NE2	2.35	0.41
45:DZ:105:VAL:O	45:DZ:140:ASP:HA	2.20	0.41
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.50	0.41
1:AA:1424:C:H2'	1:AA:1425:U:O4'	2.20	0.41
1:AA:1492:A:H4'	1:AA:1493:A:OP1	2.20	0.41
1:AA:255:G:H1'	17:AQ:16:GLN:NE2	2.35	0.41
1:AA:399:G:H2'	1:AA:400:C:C6	2.55	0.41
3:AC:121:ALA:O	3:AC:125:GLU:HG3	2.20	0.41
7:AG:51:GLN:HB3	7:AG:51:GLN:HE21	1.69	0.41
1:AA:875:C:H1'	8:AH:15:ASN:OD1	2.19	0.41
11:AK:34:ASP:HB2	11:AK:35:PRO:HD2	2.02	0.41
13:AM:81:LEU:HD22	13:AM:88:ARG:HB3	2.02	0.41
1:AA:1226:C:H4'	19:AS:80:TYR:OH	2.21	0.41
23:AX:28:C:C2'	23:AX:29:G:H5'	2.50	0.41
23:AX:47:U:H5'	23:AX:48:C:C5'	2.50	0.41
50:B4:59:PHE:HD1	50:B4:59:PHE:H	1.64	0.41
52:B6:25:LYS:NZ	52:B6:51:GLU:OE2	2.42	0.41
25:BA:1343:C:O2'	25:BA:1348:A:N1	2.48	0.41
25:BA:1563:G:H2'	25:BA:1564:C:C6	2.55	0.41
25:BA:2149:G:N2	25:BA:2195:A:H1'	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2245:U:H2'	25:BA:2246:G:C8	2.55	0.41
25:BA:2342:G:H2'	25:BA:2343:G:O4'	2.20	0.41
25:BA:738:C:H2'	25:BA:739:C:C6	2.55	0.41
28:BE:2:LYS:HG2	28:BE:2:LYS:H	1.61	0.41
29:BF:170:LEU:HA	29:BF:171:PRO:HD3	1.91	0.41
30:BG:66:GLN:HE21	30:BG:92:VAL:CG2	2.33	0.41
35:BP:124:LYS:HA	35:BP:144:GLU:HB3	2.01	0.41
39:BT:56:GLY:O	39:BT:59:THR:HG22	2.20	0.41
1:CA:644:G:H4'	8:CH:92:ARG:NH2	2.35	0.41
1:CA:952:U:H2'	1:CA:953:G:H8	1.84	0.41
2:CB:162:ILE:O	2:CB:185:ILE:HG12	2.20	0.41
3:CC:114:PRO:HA	3:CC:185:GLY:HA3	2.01	0.41
1:CA:8:A:C6	4:CD:209:ARG:HG3	2.55	0.41
10:CJ:35:SER:CB	10:CJ:73:ASP:HB2	2.45	0.41
15:CO:56:LEU:O	15:CO:60:VAL:HG23	2.20	0.41
19:CS:9:VAL:HG11	50:D4:61:ARG:HH21	1.84	0.41
52:D6:23:THR:OG1	52:D6:24:GLU:N	2.52	0.41
25:DA:1278:A:H2'	25:DA:1279:G:C8	2.55	0.41
25:DA:1319:G:C6	25:DA:1320:C:N4	2.88	0.41
25:DA:1389:G:C2	25:DA:1390:U:C2	3.08	0.41
25:DA:1704:G:H2'	25:DA:1705:G:O4'	2.21	0.41
25:DA:1791:A:H5'	25:DA:1792:G:OP2	2.20	0.41
25:DA:2065:C:H2'	25:DA:2066:C:H6	1.84	0.41
25:DA:2139:C:N4	25:DA:2152:G:H1	2.16	0.41
25:DA:2370:G:H2'	25:DA:2371:G:C8	2.55	0.41
25:DA:255:A:C6	25:DA:256:A:C5	3.08	0.41
25:DA:598:G:H2'	25:DA:599:G:O4'	2.20	0.41
25:DA:855:G:C6	25:DA:856:C:N4	2.89	0.41
25:DA:7:G:H2'	25:DA:8:A:C8	2.56	0.41
25:DA:616:G:H5'	29:DF:205:ARG:HD2	2.01	0.41
34:DO:103:ALA:HB1	34:DO:105:GLU:OE1	2.19	0.41
25:DA:2019:A:C4'	40:DU:34:LYS:HD2	2.51	0.41
1:AA:1139:G:N2	1:AA:1143:G:C6	2.89	0.41
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.35	0.41
1:AA:152:A:N6	1:AA:170:U:C2	2.88	0.41
1:AA:266:G:H5'	1:AA:266:G:C8	2.56	0.41
1:AA:616:G:O2'	1:AA:617:G:H5'	2.19	0.41
1:AA:658:G:H2'	1:AA:659:U:H6	1.85	0.41
1:AA:954:G:H21	1:AA:1227:A:N6	2.17	0.41
1:AA:993:G:C2'	1:AA:995:C:H41	2.33	0.41
3:AC:178:LEU:HA	3:AC:178:LEU:HD12	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:96:LEU:HA	9:AI:96:LEU:HD23	1.94	0.41
15:AO:39:LEU:O	15:AO:42:HIS:N	2.54	0.41
25:BA:1044:C:H2'	25:BA:1045:U:O4'	2.20	0.41
25:BA:2697:G:H5'	34:BO:68:GLU:OE1	2.21	0.41
25:BA:2800:C:H2'	25:BA:2801:C:H6	1.85	0.41
25:BA:67:G:H2'	25:BA:68:C:O4'	2.19	0.41
31:BH:13:LYS:HA	31:BH:14:GLY:HA2	1.80	0.41
32:BI:30:LEU:HD23	32:BI:30:LEU:HA	1.80	0.41
45:BZ:150:LEU:HA	45:BZ:150:LEU:HD12	1.88	0.41
45:BZ:28:MET:HA	45:BZ:88:PHE:O	2.20	0.41
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.21	0.41
1:CA:1428:A:H2'	1:CA:1429:C:O4'	2.20	0.41
1:CA:1446:U:O2'	1:CA:1447:A:O5'	2.22	0.41
1:CA:1517:G:H1'	25:DA:1919:A:O3'	2.20	0.41
1:CA:582:U:OP1	15:CO:68:ARG:NH2	2.51	0.41
1:CA:922:G:C6	1:CA:923:A:C6	3.09	0.41
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.87	0.41
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.20	0.41
7:CG:115:ARG:O	7:CG:119:ARG:HG3	2.20	0.41
7:CG:155:ARG:CZ	7:CG:155:ARG:HB3	2.48	0.41
9:CI:104:ARG:HG2	9:CI:105:ASP:N	2.35	0.41
15:CO:57:LEU:HA	15:CO:57:LEU:HD23	1.86	0.41
50:D4:46:GLN:HG3	50:D4:48:ARG:CZ	2.50	0.41
25:DA:1142(A):A:C4	25:DA:1144:G:C8	3.07	0.41
25:DA:1420:U:O2'	25:DA:1421:G:OP1	2.34	0.41
25:DA:2054:A:OP1	25:DA:2055:C:O2'	2.24	0.41
25:DA:242:G:N2	25:DA:254:G:H2'	2.35	0.41
25:DA:276:A:H5''	25:DA:277:C:H5'	2.02	0.41
25:DA:396:G:O3'	47:D1:44:PRO:HA	2.20	0.41
25:DA:776:G:N7	25:DA:793:A:O2'	2.49	0.41
26:DB:5:C:N4	26:DB:116:G:H1	2.16	0.41
26:DB:11:C:H3'	26:DB:12:C:C6	2.56	0.41
26:DB:47:C:C4	26:DB:48:A:N7	2.88	0.41
30:DG:18:GLU:OE2	30:DG:21:ARG:NH1	2.53	0.41
25:DA:2547:U:O2	34:DO:23:ARG:NH2	2.53	0.41
39:DT:19:LEU:HD22	39:DT:86:ILE:HG13	2.03	0.41
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.21	0.41
1:AA:1425:U:H2'	1:AA:1426:C:C6	2.55	0.41
1:AA:376:G:O2'	1:AA:377:G:H5'	2.19	0.41
1:AA:624:C:H2'	1:AA:625:G:C8	2.56	0.41
4:AD:45:GLN:HB3	4:AD:45:GLN:HE21	1.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.85	0.41
8:AH:34:GLU:OE1	8:AH:37:ARG:NH2	2.53	0.41
23:AX:66:C:H2'	23:AX:67:C:O4'	2.21	0.41
54:B8:62:LEU:HB3	54:B8:65:GLU:HG3	2.01	0.41
25:BA:54:G:O2'	25:BA:125:A:N1	2.41	0.41
25:BA:2405:A:O2'	54:B8:13:ARG:NH1	2.51	0.41
25:BA:738:C:H2'	25:BA:739:C:H6	1.86	0.41
25:BA:782:A:N7	25:BA:808:A:H2	2.19	0.41
26:BB:42:C:O2'	30:BG:66:GLN:HG2	2.21	0.41
32:BI:96:ASP:OD1	32:BI:96:ASP:N	2.53	0.41
39:BT:118:ARG:HD2	39:BT:118:ARG:HA	1.57	0.41
39:BT:6:LEU:HD13	39:BT:6:LEU:HA	1.86	0.41
44:BY:90:LEU:HD21	44:BY:96:ILE:HG12	2.02	0.41
1:CA:1077:G:N1	1:CA:1081:G:C6	2.88	0.41
1:CA:1277:C:O2'	1:CA:1279:A:C8	2.69	0.41
1:CA:1314:C:H2'	1:CA:1315:U:C6	2.55	0.41
1:CA:1342:C:O2'	9:CI:124:GLN:HG3	2.21	0.41
1:CA:202:U:H3'	1:CA:203:U:C5	2.56	0.41
1:CA:580:U:H5''	15:CO:58:MET:HG2	2.02	0.41
1:CA:836:G:C6	1:CA:851:G:C6	3.09	0.41
3:CC:181:ASN:ND2	3:CC:204:LEU:HD12	2.34	0.41
5:CE:12:LEU:HD12	5:CE:128:PRO:HB2	2.02	0.41
9:CI:96:LEU:HD23	9:CI:96:LEU:HA	1.98	0.41
10:CJ:57:LYS:HE2	10:CJ:60:ARG:NH2	2.35	0.41
13:CM:29:ARG:HD3	13:CM:64:TRP:CE2	2.56	0.41
1:CA:1316:G:H4'	14:CN:18:VAL:HG13	2.02	0.41
25:DA:76:C:O3'	48:D2:59:ARG:HG3	2.20	0.41
25:DA:118:A:H1'	25:DA:178:G:O4'	2.20	0.41
25:DA:1282:U:H2'	25:DA:1283:G:O4'	2.21	0.41
25:DA:1652:A:OP1	37:DR:8:ARG:NH1	2.49	0.41
25:DA:2153:G:H3'	25:DA:2154:G:H8	1.85	0.41
25:DA:2134:A:H4'	25:DA:2159:G:H21	1.84	0.41
25:DA:2350:C:H2'	25:DA:2351:G:O4'	2.20	0.41
25:DA:2721:A:O2'	25:DA:2874:C:H5'	2.20	0.41
25:DA:335:C:H2'	25:DA:336:C:H6	1.84	0.41
27:DD:67:PHE:CD1	27:DD:153:ALA:HB3	2.55	0.41
28:DE:40:GLU:H	28:DE:40:GLU:HG2	1.46	0.41
28:DE:33:VAL:HG13	28:DE:89:ASP:HA	2.02	0.41
33:DN:138:LEU:HA	33:DN:138:LEU:HD23	1.74	0.41
39:DT:61:PHE:CE1	39:DT:76:PHE:HB2	2.55	0.41
40:DU:76:TYR:CZ	40:DU:80:ILE:HG13	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.55	0.41
1:AA:1279:A:O2'	1:AA:1282:C:N4	2.53	0.41
1:AA:1353:G:H2'	1:AA:1354:C:H6	1.84	0.41
1:AA:633:G:H2'	1:AA:634:C:C6	2.56	0.41
1:AA:637:G:H2'	1:AA:638:G:H8	1.85	0.41
1:AA:923:A:OP1	5:AE:21:ALA:HB2	2.20	0.41
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	2.01	0.41
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.85	0.41
4:AD:120:LEU:HB3	4:AD:126:ILE:HD11	2.03	0.41
7:AG:74:GLU:HG2	7:AG:91:VAL:HG22	2.02	0.41
8:AH:56:LYS:HD3	8:AH:56:LYS:HA	1.89	0.41
11:AK:43:SER:HA	11:AK:47:VAL:HG21	2.02	0.41
1:AA:537:G:H5''	12:AL:113:ARG:NH1	2.35	0.41
16:AP:40:ASP:O	16:AP:48:TRP:HB2	2.20	0.41
19:AS:36:ARG:NH1	19:AS:53:ASN:HA	2.35	0.41
20:AT:100:ILE:HG12	20:AT:100:ILE:H	1.69	0.41
25:BA:1765:U:H2'	25:BA:1766:G:O4'	2.21	0.41
26:BB:95:C:H2'	26:BB:96:U:C6	2.54	0.41
29:BF:7:TYR:O	29:BF:21:ALA:HA	2.20	0.41
30:BG:12:TYR:HA	30:BG:16:ARG:HG2	2.02	0.41
31:BH:71:LEU:HA	31:BH:71:LEU:HD12	1.82	0.41
32:BI:77:LEU:HA	32:BI:77:LEU:HD23	1.68	0.41
33:BN:34:LEU:HD12	33:BN:34:LEU:HA	1.94	0.41
37:BR:52:ILE:HD11	37:BR:116:LEU:HD22	2.00	0.41
39:BT:95:ARG:HH11	39:BT:95:ARG:CG	2.28	0.41
42:BW:9:TYR:HA	42:BW:100:THR:CG2	2.51	0.41
45:BZ:157:LEU:HA	45:BZ:158:PRO:HD2	1.85	0.41
1:CA:44:G:H2'	1:CA:45:U:O4'	2.20	0.41
4:CD:58:LEU:HD22	4:CD:62:GLN:HG2	2.02	0.41
4:CD:94:LEU:HD23	4:CD:97:LEU:HD12	2.01	0.41
5:CE:78:HIS:ND1	8:CH:107:LEU:HD12	2.35	0.41
9:CI:16:ARG:HD3	9:CI:64:THR:HG21	2.00	0.41
10:CJ:27:ALA:HB1	10:CJ:74:ILE:HD13	2.02	0.41
25:DA:1230:C:H2'	25:DA:1231:G:C8	2.54	0.41
25:DA:2118:U:C2	25:DA:2149:G:H1'	2.55	0.41
25:DA:1710:C:H4'	25:DA:2858:C:O2	2.20	0.41
25:DA:328:U:H4'	44:DY:68:HIS:CG	2.55	0.41
25:DA:460:A:C2	25:DA:470:A:C4	3.09	0.41
25:DA:804:A:H5''	25:DA:805:G:OP1	2.20	0.41
27:DD:124:PRO:HG2	27:DD:129:ASN:ND2	2.35	0.41
37:DR:100:LEU:HA	37:DR:100:LEU:HD12	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DS:15:ARG:O	38:DS:19:LYS:HG2	2.21	0.41
1:AA:339:C:H2'	1:AA:340:U:C6	2.56	0.41
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.42	0.41
17:AQ:45:HIS:NE2	17:AQ:47:PRO:HG3	2.36	0.41
25:BA:1188:A:C4	25:BA:1190:G:C8	3.09	0.41
25:BA:2191:A:H2'	25:BA:2191:A:N3	2.36	0.41
25:BA:2568:C:H2'	25:BA:2569:G:O4'	2.21	0.41
25:BA:2592:U:C5	25:BA:2593:G:C6	3.09	0.41
25:BA:2544:G:O2'	25:BA:2669:A:N1	2.49	0.41
27:BD:35:LYS:HB2	27:BD:36:PRO:HD2	2.02	0.41
28:BE:97:LYS:NZ	28:BE:97:LYS:HB3	2.36	0.41
30:BG:3:LEU:HD13	50:B4:25:TYR:CZ	2.55	0.41
40:BU:108:GLU:O	40:BU:112:ARG:HG2	2.21	0.41
40:BU:16:LYS:HE2	40:BU:16:LYS:HB3	1.89	0.41
1:CA:1424:C:H2'	1:CA:1425:U:O4'	2.20	0.41
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.48	0.41
1:CA:93:G:H2'	1:CA:96:U:O4'	2.20	0.41
1:CA:991:U:O2'	1:CA:992:U:P	2.79	0.41
2:CB:16:HIS:O	2:CB:18:GLY:N	2.53	0.41
4:CD:191:ARG:NE	4:CD:200:GLU:OE2	2.52	0.41
13:CM:40:ASN:HB3	13:CM:43:THR:HG23	2.02	0.41
19:CS:38:SER:HB2	19:CS:71:LEU:HD13	2.03	0.41
49:D3:12:PRO:HB2	49:D3:20:LYS:HG2	2.03	0.41
30:DG:105:LYS:NZ	50:D4:25:TYR:O	2.46	0.41
25:DA:2360:A:H8	25:DA:2360:A:O5'	2.04	0.41
25:DA:2519:U:C6	25:DA:2542:A:N6	2.89	0.41
25:DA:2698:U:H2'	25:DA:2699:C:C6	2.56	0.41
25:DA:984:A:H5''	25:DA:985:C:C5	2.56	0.41
26:DB:45:A:C4	26:DB:46:A:C8	3.09	0.41
26:DB:66:A:H61	26:DB:108:U:H3'	1.86	0.41
27:DD:127:VAL:HA	27:DD:193:VAL:HG22	2.03	0.41
32:DI:134:PRO:C	32:DI:136:VAL:H	2.24	0.41
35:DP:47:ASP:OD2	35:DP:49:ARG:NH2	2.53	0.41
25:DA:389:G:N1	35:DP:70:GLN:HG3	2.36	0.41
1:AA:115:G:H4'	1:AA:116:A:O5'	2.21	0.41
1:AA:266:G:O3'	17:AQ:67:LYS:HB2	2.20	0.41
1:AA:583:A:N6	1:AA:758:G:O2'	2.53	0.41
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.77	0.41
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.35	0.41
8:AH:7:ALA:O	8:AH:11:THR:OG1	2.28	0.41
23:AX:19:G:H4'	23:AX:20:U:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1293:A:OP1	29:BF:95:ARG:NH2	2.50	0.41
25:BA:1467:G:C2	25:BA:1468:G:C8	3.09	0.41
25:BA:645:G:H5'	25:BA:645:G:N3	2.35	0.41
25:BA:7:G:H2'	25:BA:8:A:O4'	2.21	0.41
27:BD:245:PRO:HA	27:BD:246:PRO:HD3	1.90	0.41
29:BF:102:PRO:HB2	29:BF:105:VAL:HG23	2.02	0.41
30:BG:41:GLN:NE2	30:BG:153:ARG:HB3	2.32	0.41
42:BW:25:ARG:NH2	42:BW:74:ALA:O	2.47	0.41
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.85	0.41
1:CA:1186:G:H21	14:CN:61:TRP:C	2.23	0.41
1:CA:1486:G:H2'	1:CA:1487:G:O4'	2.20	0.41
1:CA:170:U:O2'	1:CA:171:A:H5'	2.21	0.41
1:CA:144:G:H1	1:CA:178:C:H42	1.68	0.41
1:CA:952:U:H2'	1:CA:953:G:C8	2.56	0.41
7:CG:114:ARG:O	7:CG:119:ARG:NH1	2.54	0.41
15:CO:4:THR:HG1	15:CO:7:GLU:HG3	1.86	0.41
25:DA:1297:C:H2'	25:DA:1298:C:C6	2.55	0.41
25:DA:173:G:C2	25:DA:174:C:C2	3.09	0.41
25:DA:1859:A:N6	25:DA:1883:G:O2'	2.54	0.41
25:DA:2167:U:H2'	25:DA:2168:G:H21	1.85	0.41
25:DA:2371:G:C2	25:DA:2372:G:C8	3.09	0.41
25:DA:2769:C:H2'	25:DA:2770:G:O4'	2.21	0.41
25:DA:724:U:H2'	25:DA:725:G:O4'	2.21	0.41
29:DF:59:TYR:CD2	29:DF:78:ILE:HG13	2.56	0.41
30:DG:39:ILE:HB	30:DG:92:VAL:HG13	2.03	0.41
36:DQ:32:TYR:HB2	36:DQ:106:VAL:HG23	2.02	0.41
42:DW:18:ARG:NH1	42:DW:76:VAL:O	2.52	0.41
43:DX:47:PHE:O	43:DX:49:VAL:HG13	2.21	0.41
1:AA:1064:G:N2	1:AA:1190:G:O2'	2.54	0.41
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.20	0.41
1:AA:357:G:O2'	1:AA:358:U:H5'	2.21	0.41
1:AA:400:C:H5''	4:AD:73:ARG:NH2	2.30	0.41
1:AA:632:A:C3'	1:AA:633:G:H5'	2.51	0.41
1:AA:731:G:OP1	1:AA:766:A:H1'	2.20	0.41
1:AA:1206:G:O4'	3:AC:194:GLY:HA2	2.21	0.41
3:AC:181:ASN:OD1	3:AC:204:LEU:HB2	2.21	0.41
5:AE:106:PRO:O	5:AE:110:LEU:HG	2.20	0.41
7:AG:38:LEU:O	7:AG:42:ILE:HG13	2.20	0.41
7:AG:65:ALA:O	7:AG:69:VAL:HG23	2.20	0.41
8:AH:124:ALA:O	8:AH:128:GLY:N	2.51	0.41
12:AL:8:ASN:O	12:AL:12:ARG:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:29:ARG:HD3	13:AM:64:TRP:CE2	2.56	0.41
14:AN:15:LYS:HD2	14:AN:16:PHE:CZ	2.56	0.41
15:AO:7:GLU:H	15:AO:7:GLU:HG3	1.70	0.41
24:AY:4:C:N3	24:AY:70:G:N2	2.69	0.41
55:B9:17:ILE:HD12	55:B9:17:ILE:HA	1.91	0.41
25:BA:1219:A:N3	25:BA:1220:U:H5''	2.35	0.41
25:BA:2184:G:H4'	25:BA:2194:U:H3'	2.02	0.41
25:BA:2227:G:H5'	25:BA:2228:G:N7	2.36	0.41
25:BA:2326:C:H2'	25:BA:2327:G:C8	2.56	0.41
25:BA:2724:U:H1'	25:BA:2725:A:C8	2.56	0.41
25:BA:354:A:O2'	25:BA:355:A:H8	2.03	0.41
25:BA:181:C:O2'	25:BA:849:A:N3	2.46	0.41
25:BA:865:G:H4'	25:BA:885:C:O3'	2.20	0.41
32:BI:117:GLU:HG3	32:BI:117:GLU:H	1.55	0.41
33:BN:99:LEU:HA	33:BN:99:LEU:HD23	1.84	0.41
1:CA:1002:G:N2	1:CA:1039:C:C2	2.89	0.41
1:CA:567:G:O6	12:CL:5:PRO:HD3	2.21	0.41
1:CA:633:G:H2'	1:CA:634:C:C6	2.55	0.41
1:CA:690:G:H2'	1:CA:691:G:O4'	2.20	0.41
1:CA:737:A:H2'	1:CA:738:C:C6	2.56	0.41
2:CB:134:GLU:O	2:CB:137:ARG:HB2	2.21	0.41
2:CB:47:THR:HA	2:CB:202:PRO:HG2	2.02	0.41
4:CD:120:LEU:HB3	4:CD:126:ILE:HD11	2.02	0.41
7:CG:102:ARG:O	7:CG:106:GLN:HG3	2.20	0.41
7:CG:76:ARG:HH11	7:CG:76:ARG:HB2	1.86	0.41
12:CL:53:ARG:HB3	12:CL:93:LEU:HD11	2.03	0.41
13:CM:70:LEU:HD23	13:CM:70:LEU:HA	1.83	0.41
15:CO:39:LEU:HD23	15:CO:39:LEU:HA	1.83	0.41
25:DA:2280:G:O6	46:D0:14:ARG:HD2	2.21	0.41
55:D9:11:CYS:SG	55:D9:13:LYS:HB2	2.60	0.41
25:DA:1472:A:N6	25:DA:1519:G:H1'	2.36	0.41
25:DA:1526:G:H2'	25:DA:1527:G:O4'	2.21	0.41
25:DA:1659:U:C4	25:DA:1660:C:C5	3.09	0.41
25:DA:1805:U:O2	27:DD:50:THR:HB	2.20	0.41
25:DA:1957:C:H2'	25:DA:1958:C:C6	2.56	0.41
25:DA:2055:C:OP1	25:DA:2056:G:H4'	2.20	0.41
25:DA:2277:G:OP2	46:D0:10:THR:HG21	2.21	0.41
25:DA:2855:C:H2'	25:DA:2856:C:C6	2.56	0.41
25:DA:359:A:H2'	25:DA:360:G:O4'	2.20	0.41
25:DA:590:A:OP1	29:DF:95:ARG:NH1	2.53	0.41
25:DA:718:A:H3'	25:DA:719:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DD:26:LYS:NZ	27:DD:30:GLU:OE1	2.53	0.41
29:DF:184:TYR:HE1	35:DP:3:LEU:HD21	1.84	0.41
25:DA:2751:G:H8	31:DH:2:SER:N	2.19	0.41
34:DO:20:MET:HE3	34:DO:44:LYS:HE3	2.03	0.41
34:DO:25:LEU:HD12	34:DO:38:VAL:HG12	2.02	0.41
35:DP:3:LEU:HD12	35:DP:3:LEU:HA	1.88	0.41
44:DY:13:VAL:HB	44:DY:72:VAL:HG13	2.03	0.41
44:DY:7:VAL:HG21	44:DY:72:VAL:HG12	2.03	0.41
45:DZ:30:ASN:HA	45:DZ:89:PHE:HE1	1.85	0.41
1:AA:1161:C:N4	1:AA:1176:A:C6	2.88	0.41
1:AA:1429:C:H2'	1:AA:1430:C:H6	1.85	0.41
1:AA:341:C:H2'	1:AA:342:C:C6	2.56	0.41
1:AA:991:U:C4	1:AA:1212:U:H1'	2.55	0.41
1:AA:991:U:O2'	1:AA:992:U:P	2.78	0.41
3:AC:181:ASN:OD1	3:AC:204:LEU:HD12	2.21	0.41
4:AD:20:TYR:HA	4:AD:26:CYS:SG	2.60	0.41
23:AX:57:A:H2'	23:AX:58:A:H5'	2.02	0.41
25:BA:1387:U:O4	43:BX:16:LYS:HE2	2.19	0.41
25:BA:789:G:H4'	25:BA:1723:A:H5'	2.03	0.41
25:BA:2086:C:H2'	25:BA:2087:C:C6	2.56	0.41
25:BA:2172:U:C2	25:BA:2173:G:N7	2.89	0.41
25:BA:905:U:O2	25:BA:2280:A:H2'	2.20	0.41
27:BD:25:THR:HG21	27:BD:113:VAL:HG11	2.02	0.41
33:BN:58:ASP:OD1	33:BN:58:ASP:N	2.42	0.41
35:BP:148:LEU:H	35:BP:148:LEU:HD23	1.85	0.41
38:BS:34:HIS:O	38:BS:97:ARG:NH2	2.54	0.41
42:BW:9:TYR:HA	42:BW:100:THR:HG23	2.03	0.41
45:BZ:144:LEU:HG	45:BZ:148:ASP:HB2	2.03	0.41
1:CA:1028:C:O2	1:CA:1033:G:C2	2.73	0.41
1:CA:1057:G:C4	1:CA:1204:A:C2	3.08	0.41
1:CA:1067:A:H3'	1:CA:1094:G:OP1	2.21	0.41
1:CA:1423:G:OP1	34:DO:49:ARG:NH2	2.50	0.41
1:CA:1469:G:H2'	1:CA:1470:G:C8	2.56	0.41
1:CA:1511:G:H2'	1:CA:1512:U:O4'	2.21	0.41
1:CA:358:U:H2'	1:CA:359:U:C6	2.56	0.41
1:CA:604:G:H2'	1:CA:605:U:O4'	2.21	0.41
5:CE:57:LYS:HD3	5:CE:61:TYR:CE2	2.55	0.41
1:CA:1123:A:C2	10:CJ:39:PRO:HD2	2.55	0.41
11:CK:27:ASN:ND2	11:CK:55:LYS:HD2	2.35	0.41
23:CX:53:G:C5	23:CX:54:5MU:H72	2.56	0.41
25:DA:1668:A:N3	25:DA:1670:C:C4	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2165:G:H2'	25:DA:2166:G:C8	2.56	0.41
25:DA:2540:C:H2'	25:DA:2541:A:O4'	2.21	0.41
25:DA:2658:C:H2'	25:DA:2659:G:O4'	2.20	0.41
25:DA:2747:G:H1'	25:DA:2757:A:H61	1.84	0.41
25:DA:2875:C:OP1	39:DT:3:ARG:NH1	2.52	0.41
25:DA:336:C:O2'	44:DY:35:TYR:OH	2.36	0.41
25:DA:624:C:O2'	25:DA:657:U:H5''	2.20	0.41
25:DA:900:A:H2'	25:DA:901:A:H8	1.85	0.41
25:DA:975(A):G:C2	25:DA:990:A:C8	3.08	0.41
26:DB:33:G:C6	26:DB:34:U:N3	2.89	0.41
27:DD:69:ARG:NH2	27:DD:128:GLY:O	2.53	0.41
29:DF:21:ALA:CB	29:DF:22:ALA:HA	2.44	0.41
30:DG:179:PRO:HG3	50:D4:43:TYR:OH	2.20	0.41
30:DG:48:GLU:O	30:DG:51:ARG:HG3	2.21	0.41
35:DP:6:LEU:HA	35:DP:6:LEU:HD23	1.83	0.41
38:DS:57:LYS:HB2	38:DS:57:LYS:HE2	1.89	0.41
1:AA:1002:G:C6	1:AA:1003:G:C2	3.09	0.41
1:AA:1112:C:O2	3:AC:179:ARG:N	2.51	0.41
1:AA:674:G:O2'	1:AA:675:A:H5'	2.21	0.41
1:AA:827:U:H5''	1:AA:828:A:OP2	2.20	0.41
1:AA:972:C:O2'	10:AJ:57:LYS:HB2	2.20	0.41
5:AE:50:GLU:HB2	5:AE:53:LEU:CD1	2.51	0.41
1:AA:836:G:P	18:AR:61:LYS:HZ2	2.44	0.41
23:AX:31:G:N7	23:AX:32:5MC:HM52	2.36	0.41
47:B1:67:ILE:N	47:B1:68:PRO:HD2	2.35	0.41
25:BA:1086:C:H2'	25:BA:1087:C:O4'	2.21	0.41
25:BA:1616:A:H2'	25:BA:1617:A:O4'	2.21	0.41
25:BA:1797:U:H2'	25:BA:1798:C:C6	2.56	0.41
25:BA:1820:A:H2'	25:BA:1821:C:O4'	2.21	0.41
25:BA:2134:G:N2	25:BA:2135:U:H1'	2.36	0.41
25:BA:2148:A:H4'	25:BA:2149:G:OP1	2.21	0.41
25:BA:2162:C:H2'	25:BA:2173:G:H22	1.85	0.41
25:BA:259:A:N1	25:BA:396:C:H4'	2.36	0.41
25:BA:64:C:H2'	25:BA:65:C:H6	1.86	0.41
39:BT:127:ALA:C	39:BT:129:ARG:N	2.74	0.41
45:BZ:111:VAL:C	45:BZ:113:ALA:N	2.72	0.41
1:CA:1076:C:H6	1:CA:1076:C:H5'	1.85	0.41
1:CA:1014:A:N3	1:CA:1219:U:H1'	2.36	0.41
1:CA:1221:G:O3'	19:CS:77:THR:HG21	2.20	0.41
1:CA:1372:U:H2'	1:CA:1373:G:O4'	2.21	0.41
1:CA:1414:U:H3	1:CA:1486:G:H1	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1508:G:H2'	1:CA:1509:C:O4'	2.20	0.41
1:CA:237:C:H5''	17:CQ:25:ARG:NE	2.36	0.41
1:CA:892:A:H2'	1:CA:893:C:C6	2.56	0.41
3:CC:140:ARG:H	3:CC:140:ARG:HG3	1.47	0.41
3:CC:5:ILE:HG12	3:CC:6:HIS:N	2.36	0.41
5:CE:78:HIS:HE2	5:CE:142:LEU:HA	1.85	0.41
1:CA:1291:G:OP1	7:CG:37:ASN:ND2	2.53	0.41
11:CK:22:HIS:O	11:CK:29:ILE:N	2.33	0.41
16:CP:74:LEU:HG	16:CP:79:VAL:HG21	2.02	0.41
55:D9:2:LYS:HE2	55:D9:31:LYS:O	2.20	0.41
25:DA:1002:G:N2	25:DA:1154:G:H1'	2.36	0.41
25:DA:1596:A:H2'	25:DA:1597:A:O4'	2.21	0.41
25:DA:1894:C:H2'	25:DA:1895:C:H6	1.85	0.41
25:DA:1991:U:C2'	25:DA:1992:G:H5''	2.50	0.41
25:DA:2490:G:H8	25:DA:2490:G:OP2	2.03	0.41
25:DA:2808:U:O2'	25:DA:2809:A:H5'	2.21	0.41
25:DA:36:G:N3	25:DA:450:G:O2'	2.53	0.41
25:DA:45:C:H2'	25:DA:47:C:C6	2.56	0.41
25:DA:708:C:H42	25:DA:723:G:H1	1.69	0.41
26:DB:68:C:H2'	26:DB:69:G:H8	1.86	0.41
30:DG:161:THR:HG22	30:DG:163:ALA:H	1.86	0.41
35:DP:84:ASN:OD1	35:DP:117:GLU:HB2	2.21	0.41
37:DR:36:THR:HG22	37:DR:37:THR:N	2.31	0.41
38:DS:26:LEU:HD22	38:DS:87:PHE:CE1	2.56	0.41
40:DU:112:ARG:H	40:DU:112:ARG:HG2	1.65	0.41
41:DV:12:TYR:CG	41:DV:20:LEU:HD21	2.56	0.41
44:DY:52:SER:HB2	44:DY:53:PRO:HD2	2.02	0.41
45:DZ:159:PRO:HA	45:DZ:161:VAL:N	2.36	0.41
1:AA:35:G:H2'	1:AA:36:C:C6	2.56	0.41
1:AA:434:U:H2'	1:AA:435:C:C6	2.56	0.41
1:AA:438:G:O2'	1:AA:494:U:O4	2.29	0.41
1:AA:509:A:O2'	1:AA:510:A:OP1	2.23	0.41
1:AA:658:G:H5''	15:AO:31:LEU:HD11	2.03	0.41
1:AA:93:G:O2'	1:AA:96:U:H5'	2.21	0.41
10:AJ:23:ILE:HA	10:AJ:23:ILE:HD12	1.78	0.41
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.41	0.41
20:AT:30:LYS:O	20:AT:34:LYS:HG3	2.21	0.41
25:BA:1067:A:C3'	25:BA:1067:A:C8	3.04	0.41
25:BA:1214:G:H1	25:BA:1226:C:H42	1.69	0.41
25:BA:1468:G:H1'	25:BA:1542:A:N1	2.35	0.41
25:BA:2387:G:O6	61:BA:4806:HOH:O	2.22	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:732:A:C8	25:BA:821:A:C6	3.09	0.41
28:BE:128:SER:OG	28:BE:129:HIS:N	2.54	0.41
29:BF:12:LEU:HB2	29:BF:124:LEU:HD11	2.03	0.41
30:BG:175:LEU:HD12	30:BG:175:LEU:HA	1.96	0.41
34:BO:35:VAL:HG21	34:BO:69:ILE:HD13	2.02	0.41
41:BV:52:VAL:HG22	41:BV:55:ALA:HB3	2.03	0.41
1:CA:1249:C:O4'	9:CI:70:LYS:HE2	2.20	0.41
1:CA:125:U:H2'	1:CA:126:G:C8	2.56	0.41
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.56	0.41
1:CA:49:U:O4	1:CA:365:U:H5	2.04	0.41
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.36	0.41
15:CO:87:ILE:HG22	15:CO:88:ARG:N	2.36	0.41
1:CA:1222:G:H5''	19:CS:78:ARG:NH2	2.36	0.41
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.21	0.41
25:DA:1196:C:C4	25:DA:1197:G:N7	2.89	0.41
25:DA:140:G:N3	25:DA:142:A:N6	2.63	0.41
25:DA:1826:G:H4'	27:DD:242:ARG:NH1	2.36	0.41
25:DA:184:C:H2'	25:DA:185:U:C6	2.56	0.41
25:DA:2078:C:C4	25:DA:2079:U:C4	3.08	0.41
25:DA:2134:A:C8	25:DA:2158:A:N3	2.89	0.41
25:DA:2365:G:P	46:D0:55:ARG:HG2	2.61	0.41
25:DA:342:G:H2'	25:DA:343:C:H6	1.86	0.41
25:DA:603:A:N1	25:DA:625:G:O2'	2.44	0.41
25:DA:760:G:H2'	25:DA:761:A:O4'	2.20	0.41
25:DA:869:G:C4	25:DA:870:A:C8	3.10	0.41
25:DA:918:A:C5	25:DA:919:G:HI'	2.56	0.41
27:DD:132:PRO:HG2	27:DD:135:PHE:CD2	2.56	0.41
29:DF:195:ASP:OD1	29:DF:196:LEU:N	2.54	0.41
30:DG:36:LYS:HG2	30:DG:160:VAL:HB	2.02	0.41
31:DH:117:PRO:HG3	31:DH:123:PHE:CD2	2.56	0.41
31:DH:150:ALA:HA	31:DH:153:LYS:HG3	2.03	0.41
32:DI:101:LEU:O	32:DI:105:HIS:HB2	2.21	0.41
38:DS:54:LEU:O	38:DS:57:LYS:HD3	2.20	0.41
1:AA:1015:A:C6	1:AA:1016:A:C6	3.09	0.40
1:AA:251:G:C6	1:AA:266:G:C6	3.09	0.40
1:AA:353:A:C8	1:AA:353:A:H5'	2.53	0.40
1:AA:526:C:P	12:AL:91:LYS:HE3	2.61	0.40
2:AB:160:ASP:N	2:AB:160:ASP:OD2	2.52	0.40
2:AB:169:LYS:O	2:AB:169:LYS:HD3	2.21	0.40
7:AG:79:ARG:HB3	7:AG:80:VAL:H	1.59	0.40
15:AO:3:ILE:H	15:AO:3:ILE:HD13	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AS:12:ASP:HB3	19:AS:14:HIS:CD2	2.56	0.40
23:AX:20:U:H5''	23:AX:21:A:OP2	2.21	0.40
24:AY:70:G:C2'	24:AY:71:G:H5'	2.51	0.40
25:BA:160:G:C2'	25:BA:161:C:H5'	2.50	0.40
25:BA:1974:A:OP1	34:BO:42:SER:OG	2.34	0.40
25:BA:2713:C:H2'	25:BA:2714:U:H2'	2.03	0.40
25:BA:2801:C:OP1	28:BE:61:ARG:NH2	2.37	0.40
25:BA:2803:A:N3	25:BA:2803:A:H2'	2.36	0.40
25:BA:556:C:H4'	25:BA:557:A:H5''	2.01	0.40
29:BF:196:LEU:HA	29:BF:196:LEU:HD23	1.90	0.40
36:BQ:34:LEU:HD11	36:BQ:129:THR:HB	2.02	0.40
36:BQ:137:TYR:O	36:BQ:141:GLN:HG2	2.20	0.40
25:BA:795:G:C8	42:BW:89:ALA:HB1	2.56	0.40
44:BY:34:LYS:HG2	44:BY:34:LYS:O	2.21	0.40
45:BZ:129:SER:O	45:BZ:132:ASN:N	2.51	0.40
1:CA:1237:C:O2'	1:CA:1300:G:N1	2.34	0.40
1:CA:397:A:H5'	1:CA:398:C:OP1	2.21	0.40
1:CA:448:A:O5'	1:CA:485:G:N2	2.50	0.40
1:CA:60:A:H4'	1:CA:61:G:O5'	2.20	0.40
1:CA:991:U:O2'	1:CA:992:U:OP2	2.36	0.40
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.21	0.40
2:CB:54:THR:HG21	2:CB:201:ILE:HD11	2.04	0.40
4:CD:158:ILE:HG22	4:CD:162:LEU:HD12	2.02	0.40
5:CE:41:VAL:HG22	5:CE:113:ALA:HA	2.02	0.40
2:CB:178:ARG:NE	8:CH:74:PRO:HG3	2.36	0.40
16:CP:15:PRO:O	16:CP:16:HIS:ND1	2.54	0.40
16:CP:4:ILE:HA	16:CP:20:VAL:O	2.21	0.40
1:CA:1222:G:H5''	19:CS:78:ARG:HH21	1.85	0.40
20:CT:27:LYS:HA	20:CT:30:LYS:HE2	2.03	0.40
23:CX:3:C:H5'	25:DA:2255:G:O2'	2.21	0.40
46:D0:36:ILE:HD13	46:D0:58:THR:HG21	2.02	0.40
52:D6:16:CYS:SG	52:D6:18:ARG:HD2	2.61	0.40
25:DA:1164:G:H2'	25:DA:1165:U:C6	2.56	0.40
25:DA:940:G:N3	25:DA:1191:G:H4'	2.35	0.40
25:DA:2038:G:H2'	25:DA:2039:C:O4'	2.20	0.40
25:DA:2135:A:C5	25:DA:2136:C:N4	2.88	0.40
25:DA:2302:G:C2	25:DA:2303:G:C8	3.09	0.40
25:DA:2507:C:H5''	25:DA:2573:C:N4	2.36	0.40
25:DA:1654:A:C1'	25:DA:2823:A:H5'	2.50	0.40
25:DA:182:A:H2	25:DA:433:C:O2	2.05	0.40
25:DA:830:G:H4'	25:DA:831:G:OP2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DD:206:LEU:HD23	27:DD:206:LEU:HA	1.83	0.40
27:DD:26:LYS:HE2	27:DD:28:GLU:O	2.21	0.40
28:DE:31:CYS:HA	28:DE:32:PRO:HD2	1.80	0.40
30:DG:49:ASP:N	30:DG:49:ASP:OD1	2.54	0.40
31:DH:98:LEU:HA	31:DH:98:LEU:HD12	1.93	0.40
33:DN:133:GLN:H	33:DN:133:GLN:HG2	1.64	0.40
25:DA:1666:G:OP1	34:DO:66:LYS:HD3	2.20	0.40
40:DU:66:ASN:HD21	40:DU:70:ARG:HH21	1.68	0.40
1:AA:1104:G:H2'	1:AA:1105:A:O4'	2.21	0.40
1:AA:1194:U:H2'	1:AA:1195:C:C6	2.56	0.40
1:AA:432:A:H3'	1:AA:433:C:H6	1.86	0.40
2:AB:166:ASP:HB3	2:AB:169:LYS:HB3	2.03	0.40
2:AB:16:HIS:CE1	2:AB:214:ILE:HD11	2.56	0.40
2:AB:90:MET:HA	2:AB:91:PRO:HD3	1.96	0.40
3:AC:118:GLN:HA	3:AC:121:ALA:HB3	2.04	0.40
3:AC:37:GLN:HE21	3:AC:40:ARG:HD2	1.85	0.40
4:AD:100:ARG:HH22	4:AD:118:ARG:HH22	1.69	0.40
4:AD:159:ARG:O	4:AD:163:GLU:HG3	2.21	0.40
5:AE:33:VAL:HG13	5:AE:112:LEU:HD12	2.03	0.40
12:AL:53:ARG:HG2	12:AL:69:TYR:HE1	1.87	0.40
15:AO:67:LEU:HA	15:AO:67:LEU:HD23	1.88	0.40
16:AP:59:TRP:HA	16:AP:62:VAL:HG12	2.02	0.40
19:AS:50:ALA:HA	19:AS:58:VAL:O	2.22	0.40
21:AU:15:ARG:HH11	21:AU:15:ARG:HB2	1.86	0.40
25:BA:1676:G:H2'	25:BA:1677:C:C6	2.57	0.40
25:BA:1699:A:C2'	25:BA:1700:G:H5'	2.51	0.40
25:BA:2199:C:H2'	25:BA:2200:C:O4'	2.21	0.40
25:BA:2455:C:OP1	29:BF:68:LYS:HD3	2.21	0.40
25:BA:2672:A:H2'	25:BA:2673:G:O4'	2.20	0.40
29:BF:33:LEU:HD12	29:BF:33:LEU:HA	1.89	0.40
41:BV:65:GLY:HA3	41:BV:91:TYR:CZ	2.56	0.40
1:CA:1125:U:HO2'	1:CA:1126:U:H2'	1.82	0.40
1:CA:1125:U:H5''	1:CA:1127:G:O6	2.21	0.40
1:CA:1172:C:H2'	1:CA:1173:G:H8	1.86	0.40
1:CA:1499:A:H1'	1:CA:1520:G:H5'	2.03	0.40
1:CA:414:A:C5	1:CA:431:A:C2	3.09	0.40
1:CA:583:A:H2'	1:CA:584:G:O4'	2.21	0.40
1:CA:791:G:C6	1:CA:792:A:N7	2.88	0.40
7:CG:115:ARG:HG2	7:CG:118:VAL:HG23	2.03	0.40
1:CA:393:A:OP1	16:CP:13:HIS:HE1	2.04	0.40
1:CA:277:C:H5''	17:CQ:68:ARG:NH2	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CQ:65:ILE:HB	17:CQ:69:LYS:HB3	2.02	0.40
19:CS:22:LEU:HB3	19:CS:27:GLU:CG	2.51	0.40
25:DA:1270:C:H5''	25:DA:1271:G:O5'	2.22	0.40
25:DA:1692:U:O2'	25:DA:1693:U:H2'	2.21	0.40
25:DA:2328:A:H2'	25:DA:2329:G:C8	2.55	0.40
25:DA:2397:G:N2	25:DA:2420:C:H1'	2.36	0.40
25:DA:244:A:C2	25:DA:255:A:C4	3.09	0.40
25:DA:2600:A:C6	25:DA:2601:C:N4	2.89	0.40
25:DA:527:C:C4	25:DA:2779:U:H2'	2.56	0.40
25:DA:645:C:O2	25:DA:645:C:H2'	2.21	0.40
25:DA:901:A:H2'	25:DA:902:C:O4'	2.21	0.40
26:DB:94:C:H2'	26:DB:95:C:H6	1.85	0.40
33:DN:38:HIS:CE1	33:DN:39:ARG:HG3	2.56	0.40
38:DS:87:PHE:HB2	38:DS:112:PHE:CE2	2.56	0.40
1:AA:1004:A:C5	1:AA:1037:C:N3	2.89	0.40
1:AA:148:G:H1	1:AA:174:C:H42	1.68	0.40
1:AA:194:C:C2'	1:AA:195:A:H5''	2.52	0.40
1:AA:487:A:H2'	1:AA:488:C:O4'	2.22	0.40
1:AA:998:G:H2'	1:AA:999:C:O4'	2.22	0.40
2:AB:48:MET:HA	2:AB:51:LEU:HD12	2.03	0.40
4:AD:108:LEU:HD12	4:AD:108:LEU:HA	1.64	0.40
10:AJ:49:VAL:HG21	14:AN:41:ARG:O	2.22	0.40
17:AQ:3:LYS:HD2	17:AQ:60:ILE:HD11	2.03	0.40
20:AT:10:LEU:HD13	20:AT:12:ALA:HB2	2.03	0.40
1:AA:966:G:C2	23:AX:34:C:H5'	2.56	0.40
30:BG:179:PRO:HB2	50:B4:42:PHE:HE2	1.86	0.40
25:BA:1540:A:H2'	25:BA:1541:A:C8	2.56	0.40
25:BA:1787:G:H4'	25:BA:1789:G:O4'	2.21	0.40
25:BA:2598:C:OP2	25:BA:2620:G:N1	2.49	0.40
25:BA:2720:G:H1'	37:BR:71:GLN:HE22	1.87	0.40
25:BA:325:G:H1'	25:BA:326:C:C6	2.56	0.40
25:BA:908:A:C2	25:BA:963:A:C4	3.10	0.40
27:BD:183:ARG:HG3	27:BD:270:ILE:HG12	2.03	0.40
35:BP:46:LYS:HE3	35:BP:46:LYS:HB3	1.76	0.40
1:CA:1004:A:N7	1:CA:1037:C:O2	2.54	0.40
1:CA:1148:U:H1'	9:CI:66:ARG:HH12	1.86	0.40
1:CA:1250:A:H2	1:CA:1370:G:H1'	1.87	0.40
1:CA:794:A:H4'	1:CA:1521:G:O2'	2.21	0.40
1:CA:109:A:C6	1:CA:326:G:C6	3.10	0.40
1:CA:376:G:O2'	1:CA:377:G:H5'	2.21	0.40
1:CA:577:G:C8	1:CA:816:A:C6	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:16:A:N1	1:CA:919:A:H2	2.20	0.40
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.91	0.40
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	2.03	0.40
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.57	0.40
9:CI:2:GLU:O	9:CI:20:ARG:HG2	2.21	0.40
9:CI:71:SER:HA	9:CI:74:ILE:HD12	2.04	0.40
12:CL:34:ARG:HB3	12:CL:34:ARG:HE	1.64	0.40
14:CN:45:ARG:O	14:CN:49:HIS:HD2	2.04	0.40
49:D3:23:LEU:HD13	49:D3:50:VAL:HG11	2.02	0.40
25:DA:1222:C:N3	25:DA:1228:G:C2	2.90	0.40
25:DA:2228:G:C5	25:DA:2229:C:C4	3.09	0.40
25:DA:2445:G:OP1	29:DF:74:ARG:NH2	2.47	0.40
25:DA:2842:G:H2'	25:DA:2843:G:O4'	2.22	0.40
25:DA:589:C:H2'	25:DA:590:A:C8	2.56	0.40
25:DA:670:A:H4'	25:DA:671:C:O5'	2.20	0.40
25:DA:839:U:H2'	25:DA:840:C:H6	1.87	0.40
25:DA:956:G:H2'	25:DA:957:A:H2'	2.03	0.40
26:DB:33:G:N3	26:DB:50:G:N2	2.69	0.40
27:DD:20:ASP:OD1	27:DD:21:PHE:N	2.55	0.40
28:DE:55:ASN:HA	28:DE:56:PRO:HD3	1.88	0.40
44:DY:86:ARG:HB2	44:DY:98:VAL:CG2	2.51	0.40
45:DZ:149:SER:HB2	45:DZ:172:ALA:O	2.22	0.40
1:AA:1286:A:C8	1:AA:1287:A:H4'	2.56	0.40
1:AA:1302:U:OP2	13:AM:21:TYR:OH	2.29	0.40
3:AC:47:LEU:HD12	3:AC:68:VAL:HG11	2.02	0.40
4:AD:78:LEU:HA	4:AD:78:LEU:HD23	1.86	0.40
15:AO:16:ALA:HB1	15:AO:21:ASP:HB3	2.02	0.40
9:AI:128:ARG:NH2	23:AX:33:U:OP2	2.54	0.40
25:BA:2289:G:P	46:B0:10:THR:HG21	2.62	0.40
52:B6:10:LEU:HG	52:B6:54:ILE:HG13	2.02	0.40
25:BA:1258:A:N3	25:BA:1284:G:O2'	2.46	0.40
25:BA:2304:C:H2'	25:BA:2305:C:C6	2.56	0.40
25:BA:268:G:HO2'	25:BA:269:G:H8	1.65	0.40
25:BA:922:G:O3'	45:BZ:151:HIS:HE1	2.05	0.40
27:BD:164:GLN:NE2	27:BD:166:GLN:OE1	2.53	0.40
27:BD:68:LYS:HD3	27:BD:70:TRP:CZ2	2.57	0.40
30:BG:122:PRO:HD3	30:BG:181:ARG:HG2	2.02	0.40
32:BI:118:LYS:HA	32:BI:119:PRO:HD3	1.93	0.40
32:BI:47:LEU:O	32:BI:51:ILE:HG13	2.22	0.40
34:BO:10:VAL:HG21	34:BO:16:ALA:HB3	2.03	0.40
38:BS:58:LEU:HD23	38:BS:58:LEU:HA	1.81	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BX:57:LEU:HD12	43:BX:78:LYS:HG2	2.03	0.40
45:BZ:146:ILE:HA	45:BZ:147:GLY:HA2	1.61	0.40
1:CA:1105:A:H2'	1:CA:1106:G:H8	1.87	0.40
1:CA:1320:C:H5'	1:CA:1320:C:H6	1.85	0.40
1:CA:1325:C:C2'	1:CA:1326:C:H5'	2.51	0.40
1:CA:1288:A:N1	1:CA:1371:G:H1'	2.36	0.40
1:CA:790:A:C6	1:CA:791:G:C6	3.10	0.40
2:CB:36:ARG:O	2:CB:37:ASN:HB2	2.21	0.40
4:CD:25:ARG:NH1	4:CD:30:LYS:HB3	2.36	0.40
4:CD:64:LEU:HB2	4:CD:198:VAL:HG11	2.04	0.40
1:CA:1251:A:H5''	9:CI:12:GLU:OE1	2.22	0.40
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HG2	2.01	0.40
13:CM:87:TYR:HA	13:CM:90:LEU:HD12	2.04	0.40
19:CS:35:SER:O	19:CS:71:LEU:HD22	2.21	0.40
23:CX:43:A:H2'	23:CX:44:A:C8	2.56	0.40
25:DA:1005:C:C2	25:DA:1143:A:C5	3.10	0.40
25:DA:1291:C:O2'	25:DA:1292:U:H5'	2.21	0.40
25:DA:196:A:N3	25:DA:196:A:H2'	2.37	0.40
25:DA:2080:G:N2	25:DA:2241:A:C4	2.89	0.40
25:DA:2182:G:H2'	25:DA:2183:C:C6	2.56	0.40
25:DA:2748:A:C4	25:DA:2749:A:C8	3.10	0.40
25:DA:384:U:H2'	25:DA:385:C:H6	1.85	0.40
25:DA:528:A:C2	25:DA:2043:C:H4'	2.57	0.40
25:DA:639:U:H2'	25:DA:640:C:C6	2.57	0.40
26:DB:43:C:C4	26:DB:45:A:C6	3.10	0.40
25:DA:764:A:O4'	27:DD:213:ARG:HG3	2.22	0.40
27:DD:245:PRO:HA	27:DD:246:PRO:HD3	1.94	0.40
27:DD:38:LYS:HA	27:DD:38:LYS:HD2	1.99	0.40
27:DD:94:LEU:HD23	27:DD:94:LEU:HA	1.95	0.40
25:DA:2494:G:O2'	36:DQ:80:GLU:HA	2.22	0.40
1:AA:1286:A:H2'	1:AA:1287:A:H4'	2.02	0.40
1:AA:295:C:H2'	1:AA:296:U:O4'	2.21	0.40
3:AC:15:THR:CG2	3:AC:181:ASN:HA	2.51	0.40
4:AD:18:LYS:HE2	4:AD:20:TYR:CZ	2.56	0.40
4:AD:88:VAL:HA	5:AE:97:GLY:HA2	2.03	0.40
6:AF:26:ILE:O	6:AF:30:LEU:HG	2.22	0.40
11:AK:19:ALA:HB3	11:AK:82:VAL:HG22	2.04	0.40
16:AP:59:TRP:HB3	16:AP:64:ALA:HB2	2.03	0.40
23:AX:40:C:H2'	23:AX:41:C:H6	1.87	0.40
50:B4:55:ARG:HB3	50:B4:56:VAL:O	2.22	0.40
25:BA:1058:U:C5	33:BN:28:THR:HG21	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:107:G:H2'	25:BA:108:G:O4'	2.22	0.40
25:BA:1052:C:C2	25:BA:1183:G:N2	2.89	0.40
25:BA:1535:U:HO2'	25:BA:1536:A:H8	1.66	0.40
25:BA:1717:C:O2	28:BE:129:HIS:NE2	2.52	0.40
25:BA:2102:G:OP1	47:B1:35:THR:HG21	2.20	0.40
25:BA:470:C:H4'	29:BF:49:ALA:HB2	2.03	0.40
35:BP:101:VAL:HG22	35:BP:106:LEU:O	2.21	0.40
38:BS:3:ARG:HE	38:BS:3:ARG:CA	2.34	0.40
38:BS:68:GLN:HG2	38:BS:71:ARG:HH12	1.86	0.40
42:BW:13:SER:HA	42:BW:14:PRO:HD3	1.94	0.40
1:CA:1262:C:O2'	1:CA:1263:C:C5'	2.69	0.40
1:CA:1325:C:H4'	21:CU:17:THR:HG21	2.02	0.40
1:CA:1502:A:H5''	1:CA:1504:G:N7	2.37	0.40
1:CA:973:G:H3'	1:CA:974:A:H5''	2.03	0.40
2:CB:74:LYS:HG2	2:CB:74:LYS:H	1.52	0.40
2:CB:7:VAL:HB	2:CB:8:LYS:H	1.66	0.40
2:CB:96:ARG:CZ	2:CB:98:LEU:HD13	2.52	0.40
10:CJ:16:LEU:HD23	10:CJ:16:LEU:HA	1.93	0.40
12:CL:84:LEU:HB2	12:CL:105:TYR:CD2	2.56	0.40
48:D2:3:LEU:HD23	48:D2:3:LEU:HA	1.88	0.40
25:DA:1024:G:H21	25:DA:1144:G:C4'	2.35	0.40
25:DA:118:A:OP2	25:DA:119:A:H2'	2.21	0.40
25:DA:1252:G:C2	25:DA:1253:A:C2	3.09	0.40
25:DA:1297:C:H2'	25:DA:1298:C:H6	1.87	0.40
25:DA:1423:G:H2'	25:DA:1424:G:C8	2.56	0.40
25:DA:1448:G:H21	25:DA:1528(A):A:H2	1.69	0.40
25:DA:1999:C:O2	25:DA:2687:U:O2'	2.32	0.40
25:DA:2023:G:H4'	25:DA:2617:C:O3'	2.22	0.40
25:DA:2240:C:O2'	25:DA:2241:A:H5'	2.21	0.40
25:DA:2648:C:H2'	25:DA:2649:U:H6	1.85	0.40
25:DA:71:A:OP2	25:DA:71:A:H3'	2.21	0.40
25:DA:812:C:H5''	25:DA:1250:G:O2'	2.22	0.40
25:DA:867:C:H2'	25:DA:868:U:H6	1.86	0.40
26:DB:56:G:OP1	30:DG:27:ASN:ND2	2.54	0.40
26:DB:57:A:N3	30:DG:29:TRP:HB3	2.36	0.40
27:DD:71:ASP:HB3	27:DD:103:ARG:HH22	1.87	0.40
27:DD:233:HIS:HA	61:DD:406:HOH:O	2.20	0.40
29:DF:36:VAL:HG11	29:DF:183:VAL:CG1	2.51	0.40
30:DG:135:LEU:HB2	30:DG:155:MET:HG2	2.03	0.40
33:DN:39:ARG:HA	33:DN:40:PRO:HD3	1.90	0.40
35:DP:81:GLN:NE2	35:DP:105:LEU:O	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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%)	194 (85%)	24 (10%)	11 (5%)	2	4
2	CB	229/256 (90%)	195 (85%)	24 (10%)	10 (4%)	2	5
3	AC	204/239 (85%)	179 (88%)	23 (11%)	2 (1%)	15	37
3	CC	204/239 (85%)	178 (87%)	23 (11%)	3 (2%)	10	26
4	AD	206/209 (99%)	189 (92%)	15 (7%)	2 (1%)	15	37
4	CD	206/209 (99%)	190 (92%)	14 (7%)	2 (1%)	15	37
5	AE	146/162 (90%)	139 (95%)	5 (3%)	2 (1%)	11	28
5	CE	146/162 (90%)	136 (93%)	8 (6%)	2 (1%)	11	28
6	AF	98/101 (97%)	88 (90%)	10 (10%)	0	100	100
6	CF	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
7	AG	153/156 (98%)	139 (91%)	11 (7%)	3 (2%)	7	19
7	CG	153/156 (98%)	137 (90%)	15 (10%)	1 (1%)	22	46
8	AH	135/138 (98%)	130 (96%)	5 (4%)	0	100	100
8	CH	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	22	46
9	AI	125/128 (98%)	107 (86%)	14 (11%)	4 (3%)	4	9
9	CI	125/128 (98%)	109 (87%)	12 (10%)	4 (3%)	4	9
10	AJ	95/105 (90%)	80 (84%)	9 (10%)	6 (6%)	1	2
10	CJ	94/105 (90%)	83 (88%)	6 (6%)	5 (5%)	2	3
11	AK	112/129 (87%)	103 (92%)	7 (6%)	2 (2%)	8	21
11	CK	112/129 (87%)	101 (90%)	8 (7%)	3 (3%)	5	12
12	AL	120/132 (91%)	111 (92%)	9 (8%)	0	100	100
12	CL	120/132 (91%)	113 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	AM	118/126 (94%)	103 (87%)	13 (11%)	2 (2%)	9	23
13	CM	116/126 (92%)	101 (87%)	11 (10%)	4 (3%)	3	8
14	AN	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
14	CN	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
15	AO	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
15	CO	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	13	32
16	AP	80/88 (91%)	73 (91%)	7 (9%)	0	100	100
16	CP	80/88 (91%)	74 (92%)	5 (6%)	1 (1%)	12	30
17	AQ	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
17	CQ	97/105 (92%)	90 (93%)	7 (7%)	0	100	100
18	AR	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
18	CR	66/88 (75%)	64 (97%)	1 (2%)	1 (2%)	10	26
19	AS	81/93 (87%)	70 (86%)	11 (14%)	0	100	100
19	CS	81/93 (87%)	68 (84%)	11 (14%)	2 (2%)	5	14
20	AT	94/106 (89%)	82 (87%)	6 (6%)	6 (6%)	1	2
20	CT	94/106 (89%)	84 (89%)	5 (5%)	5 (5%)	2	3
21	AU	21/27 (78%)	17 (81%)	4 (19%)	0	100	100
21	CU	21/27 (78%)	16 (76%)	4 (19%)	1 (5%)	2	4
27	BD	273/276 (99%)	258 (94%)	14 (5%)	1 (0%)	34	60
27	DD	273/276 (99%)	257 (94%)	14 (5%)	2 (1%)	22	46
28	BE	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	29	54
28	DE	202/206 (98%)	193 (96%)	7 (4%)	2 (1%)	15	37
29	BF	201/210 (96%)	196 (98%)	4 (2%)	1 (0%)	29	54
29	DF	201/210 (96%)	195 (97%)	4 (2%)	2 (1%)	15	37
30	BG	179/182 (98%)	165 (92%)	11 (6%)	3 (2%)	9	23
30	DG	179/182 (98%)	161 (90%)	14 (8%)	4 (2%)	6	17
31	BH	172/180 (96%)	161 (94%)	10 (6%)	1 (1%)	25	50
31	DH	172/180 (96%)	160 (93%)	11 (6%)	1 (1%)	25	50
32	BI	144/148 (97%)	129 (90%)	12 (8%)	3 (2%)	7	18
32	DI	144/148 (97%)	130 (90%)	12 (8%)	2 (1%)	11	28
33	BN	138/140 (99%)	135 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	DN	138/140 (99%)	133 (96%)	4 (3%)	1 (1%)	22	46
34	BO	120/122 (98%)	114 (95%)	5 (4%)	1 (1%)	19	43
34	DO	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
35	BP	147/150 (98%)	140 (95%)	6 (4%)	1 (1%)	22	46
35	DP	147/150 (98%)	137 (93%)	9 (6%)	1 (1%)	22	46
36	BQ	139/141 (99%)	132 (95%)	6 (4%)	1 (1%)	22	46
36	DQ	139/141 (99%)	132 (95%)	5 (4%)	2 (1%)	11	28
37	BR	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
37	DR	116/118 (98%)	110 (95%)	5 (4%)	1 (1%)	17	40
38	BS	108/112 (96%)	98 (91%)	9 (8%)	1 (1%)	17	40
38	DS	108/112 (96%)	98 (91%)	9 (8%)	1 (1%)	17	40
39	BT	129/146 (88%)	122 (95%)	5 (4%)	2 (2%)	9	24
39	DT	129/146 (88%)	125 (97%)	4 (3%)	0	100	100
40	BU	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
40	DU	114/118 (97%)	112 (98%)	2 (2%)	0	100	100
41	BV	99/101 (98%)	92 (93%)	5 (5%)	2 (2%)	7	19
41	DV	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	15	37
42	BW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
42	DW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
43	BX	93/96 (97%)	88 (95%)	4 (4%)	1 (1%)	14	34
43	DX	93/96 (97%)	88 (95%)	3 (3%)	2 (2%)	6	17
44	BY	105/110 (96%)	97 (92%)	6 (6%)	2 (2%)	8	20
44	DY	105/110 (96%)	99 (94%)	5 (5%)	1 (1%)	15	37
45	BZ	169/206 (82%)	147 (87%)	18 (11%)	4 (2%)	6	15
45	DZ	172/206 (84%)	154 (90%)	17 (10%)	1 (1%)	25	50
46	B0	81/85 (95%)	76 (94%)	4 (5%)	1 (1%)	13	32
46	D0	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
47	B1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	14	34
47	D1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	14	34
48	B2	68/72 (94%)	68 (100%)	0	0	100	100
48	D2	68/72 (94%)	68 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	B3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
49	D3	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
50	B4	67/71 (94%)	50 (75%)	10 (15%)	7 (10%)	0	0
50	D4	67/71 (94%)	53 (79%)	7 (10%)	7 (10%)	0	0
51	B5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
51	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
52	B6	51/54 (94%)	49 (96%)	1 (2%)	1 (2%)	7	19
52	D6	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
53	B7	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
53	D7	46/49 (94%)	45 (98%)	0	1 (2%)	6	17
54	B8	62/65 (95%)	62 (100%)	0	0	100	100
54	D8	62/65 (95%)	62 (100%)	0	0	100	100
55	B9	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
55	D9	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
All	All	11402/12128 (94%)	10561 (93%)	687 (6%)	154 (1%)	11	28

All (154) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	9	GLU
2	AB	10	LEU
2	AB	125	PRO
4	AD	166	LYS
7	AG	80	VAL
9	AI	44	VAL
9	AI	54	ASP
10	AJ	56	HIS
10	AJ	79	ARG
27	BD	275	LYS
29	BF	130	ALA
30	BG	43	LEU
31	BH	126	PRO
32	BI	107	VAL
39	BT	127	ALA
39	BT	128	GLU
47	B1	3	LYS
50	B4	44	THR

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Mol	Chain	Res	Type
50	B4	45	GLY
50	B4	68	ARG
2	CB	16	HIS
2	CB	17	PHE
2	CB	126	GLU
2	CB	231	GLU
3	CC	99	VAL
4	CD	46	LYS
4	CD	166	LYS
9	CI	44	VAL
9	CI	54	ASP
10	CJ	55	LYS
10	CJ	56	HIS
13	CM	67	GLU
13	CM	106	ASN
20	CT	95	ALA
20	CT	99	LEU
29	DF	130	ALA
30	DG	43	LEU
30	DG	47	LYS
30	DG	81	LYS
31	DH	126	PRO
32	DI	10	GLU
36	DQ	60	ARG
41	DV	79	VAL
50	D4	45	GLY
50	D4	49	PHE
50	D4	62	ARG
50	D4	63	TYR
53	D7	46	VAL
2	AB	11	LEU
2	AB	19	HIS
5	AE	85	GLY
7	AG	81	GLY
10	AJ	31	GLY
10	AJ	55	LYS
11	AK	49	GLY
13	AM	67	GLU
20	AT	47	GLY
30	BG	47	LYS
30	BG	51	ARG
32	BI	106	GLY

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Mol	Chain	Res	Type
36	BQ	60	ARG
41	BV	79	VAL
41	BV	100	ARG
43	BX	94	GLY
45	BZ	137	ILE
46	B0	13	GLY
50	B4	49	PHE
52	B6	13	CYS
2	CB	8	LYS
2	CB	10	LEU
2	CB	20	GLU
2	CB	121	LEU
3	CC	4	LYS
3	CC	181	ASN
7	CG	55	GLY
8	CH	133	LEU
10	CJ	75	ILE
10	CJ	77	PRO
11	CK	49	GLY
11	CK	100	ALA
19	CS	30	LEU
20	CT	47	GLY
21	CU	3	LYS
27	DD	239	ARG
29	DF	21	ALA
36	DQ	27	VAL
43	DX	94	GLY
2	AB	126	GLU
10	AJ	75	ILE
10	AJ	78	ASN
20	AT	96	GLY
20	AT	100	ILE
20	AT	102	GLY
28	BE	52	LEU
45	BZ	155	LEU
50	B4	55	ARG
50	B4	62	ARG
2	CB	9	GLU
2	CB	234	PRO
10	CJ	91	PRO
13	CM	5	ALA
18	CR	25	THR

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Mol	Chain	Res	Type
28	DE	52	LEU
38	DS	84	GLN
50	D4	46	GLN
2	AB	131	PRO
4	AD	164	ALA
9	AI	12	GLU
20	AT	10	LEU
20	AT	95	ALA
32	BI	73	GLU
34	BO	5	GLN
44	BY	54	LYS
45	BZ	152	ALA
50	B4	56	VAL
9	CI	11	LYS
13	CM	4	ILE
19	CS	29	ARG
30	DG	51	ARG
32	DI	135	GLU
35	DP	29	LYS
44	DY	54	LYS
47	D1	3	LYS
2	AB	20	GLU
2	AB	213	LEU
2	AB	227	GLY
2	AB	234	PRO
9	AI	29	ASN
13	AM	4	ILE
35	BP	29	LYS
5	CE	27	ARG
9	CI	12	GLU
20	CT	102	GLY
27	DD	3	VAL
33	DN	2	LYS
37	DR	45	ARG
43	DX	2	LYS
45	DZ	113	ALA
50	D4	55	ARG
3	AC	99	VAL
7	AG	4	ARG
16	CP	81	ARG
20	CT	100	ILE
38	BS	60	GLY

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Mol	Chain	Res	Type
15	CO	23	GLY
28	DE	73	GLU
3	AC	66	VAL
44	BY	53	PRO
45	BZ	111	VAL
5	AE	69	VAL
11	AK	105	VAL
50	D4	29	PRO
5	CE	69	VAL
11	CK	105	VAL

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%)	158 (82%)	34 (18%)	2	4
2	CB	187/220 (85%)	161 (86%)	26 (14%)	3	8
3	AC	143/188 (76%)	134 (94%)	9 (6%)	18	40
3	CC	140/188 (74%)	127 (91%)	13 (9%)	9	21
4	AD	170/181 (94%)	154 (91%)	16 (9%)	8	20
4	CD	173/181 (96%)	158 (91%)	15 (9%)	10	23
5	AE	113/123 (92%)	106 (94%)	7 (6%)	18	40
5	CE	114/123 (93%)	103 (90%)	11 (10%)	8	19
6	AF	83/90 (92%)	79 (95%)	4 (5%)	25	53
6	CF	85/90 (94%)	82 (96%)	3 (4%)	36	65
7	AG	119/127 (94%)	108 (91%)	11 (9%)	9	21
7	CG	120/127 (94%)	113 (94%)	7 (6%)	20	43
8	AH	114/119 (96%)	108 (95%)	6 (5%)	22	48
8	CH	114/119 (96%)	109 (96%)	5 (4%)	28	56
9	AI	90/99 (91%)	79 (88%)	11 (12%)	5	11
9	CI	89/99 (90%)	81 (91%)	8 (9%)	9	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	AJ	66/92 (72%)	63 (96%)	3 (4%)	27	55
10	CJ	69/92 (75%)	64 (93%)	5 (7%)	14	34
11	AK	82/99 (83%)	78 (95%)	4 (5%)	25	52
11	CK	83/99 (84%)	79 (95%)	4 (5%)	25	53
12	AL	97/109 (89%)	92 (95%)	5 (5%)	23	49
12	CL	97/109 (89%)	93 (96%)	4 (4%)	30	59
13	AM	91/101 (90%)	83 (91%)	8 (9%)	10	23
13	CM	89/101 (88%)	80 (90%)	9 (10%)	7	17
14	AN	49/50 (98%)	43 (88%)	6 (12%)	5	11
14	CN	49/50 (98%)	42 (86%)	7 (14%)	3	8
15	AO	78/80 (98%)	68 (87%)	10 (13%)	4	10
15	CO	78/80 (98%)	73 (94%)	5 (6%)	17	39
16	AP	69/74 (93%)	59 (86%)	10 (14%)	3	8
16	CP	68/74 (92%)	60 (88%)	8 (12%)	5	12
17	AQ	94/97 (97%)	88 (94%)	6 (6%)	17	39
17	CQ	94/97 (97%)	89 (95%)	5 (5%)	22	48
18	AR	59/77 (77%)	54 (92%)	5 (8%)	10	24
18	CR	59/77 (77%)	55 (93%)	4 (7%)	16	36
19	AS	69/80 (86%)	63 (91%)	6 (9%)	10	23
19	CS	67/80 (84%)	58 (87%)	9 (13%)	4	9
20	AT	70/82 (85%)	62 (89%)	8 (11%)	5	13
20	CT	70/82 (85%)	62 (89%)	8 (11%)	5	13
21	AU	18/22 (82%)	16 (89%)	2 (11%)	6	14
21	CU	18/22 (82%)	17 (94%)	1 (6%)	21	45
27	BD	215/218 (99%)	200 (93%)	15 (7%)	15	35
27	DD	215/218 (99%)	200 (93%)	15 (7%)	15	35
28	BE	164/166 (99%)	150 (92%)	14 (8%)	10	24
28	DE	164/166 (99%)	147 (90%)	17 (10%)	7	16
29	BF	160/166 (96%)	145 (91%)	15 (9%)	8	20
29	DF	159/166 (96%)	144 (91%)	15 (9%)	8	20
30	BG	143/156 (92%)	128 (90%)	15 (10%)	7	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	DG	142/156 (91%)	128 (90%)	14 (10%)	8	18
31	BH	144/148 (97%)	133 (92%)	11 (8%)	13	30
31	DH	144/148 (97%)	134 (93%)	10 (7%)	15	35
32	BI	110/124 (89%)	88 (80%)	22 (20%)	1	3
32	DI	104/124 (84%)	90 (86%)	14 (14%)	4	9
33	BN	118/119 (99%)	103 (87%)	15 (13%)	4	10
33	DN	118/119 (99%)	106 (90%)	12 (10%)	7	17
34	BO	100/100 (100%)	95 (95%)	5 (5%)	24	51
34	DO	100/100 (100%)	96 (96%)	4 (4%)	31	60
35	BP	115/116 (99%)	105 (91%)	10 (9%)	10	23
35	DP	115/116 (99%)	106 (92%)	9 (8%)	12	29
36	BQ	111/111 (100%)	100 (90%)	11 (10%)	8	18
36	DQ	111/111 (100%)	103 (93%)	8 (7%)	14	34
37	BR	101/101 (100%)	87 (86%)	14 (14%)	3	8
37	DR	101/101 (100%)	88 (87%)	13 (13%)	4	10
38	BS	87/88 (99%)	83 (95%)	4 (5%)	27	54
38	DS	85/88 (97%)	77 (91%)	8 (9%)	8	20
39	BT	115/127 (91%)	106 (92%)	9 (8%)	12	29
39	DT	113/127 (89%)	104 (92%)	9 (8%)	12	27
40	BU	93/94 (99%)	87 (94%)	6 (6%)	17	38
40	DU	93/94 (99%)	87 (94%)	6 (6%)	17	38
41	BV	80/82 (98%)	72 (90%)	8 (10%)	7	18
41	DV	80/82 (98%)	72 (90%)	8 (10%)	7	18
42	BW	90/92 (98%)	85 (94%)	5 (6%)	21	45
42	DW	90/92 (98%)	84 (93%)	6 (7%)	16	37
43	BX	77/78 (99%)	73 (95%)	4 (5%)	23	49
43	DX	77/78 (99%)	73 (95%)	4 (5%)	23	49
44	BY	85/91 (93%)	81 (95%)	4 (5%)	26	54
44	DY	85/91 (93%)	78 (92%)	7 (8%)	11	26
45	BZ	145/179 (81%)	131 (90%)	14 (10%)	8	19
45	DZ	145/179 (81%)	132 (91%)	13 (9%)	9	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	B0	65/67 (97%)	62 (95%)	3 (5%)	27	54
46	D0	65/67 (97%)	62 (95%)	3 (5%)	27	54
47	B1	80/83 (96%)	74 (92%)	6 (8%)	13	31
47	D1	80/83 (96%)	75 (94%)	5 (6%)	18	40
48	B2	65/67 (97%)	61 (94%)	4 (6%)	18	40
48	D2	65/67 (97%)	60 (92%)	5 (8%)	13	30
49	B3	51/52 (98%)	46 (90%)	5 (10%)	8	18
49	D3	50/52 (96%)	45 (90%)	5 (10%)	7	18
50	B4	60/63 (95%)	51 (85%)	9 (15%)	3	7
50	D4	53/63 (84%)	46 (87%)	7 (13%)	4	9
51	B5	50/52 (96%)	42 (84%)	8 (16%)	2	6
51	D5	50/52 (96%)	47 (94%)	3 (6%)	19	42
52	B6	51/52 (98%)	45 (88%)	6 (12%)	5	12
52	D6	50/52 (96%)	49 (98%)	1 (2%)	55	81
53	B7	41/42 (98%)	38 (93%)	3 (7%)	14	33
53	D7	41/42 (98%)	41 (100%)	0	100	100
54	B8	53/55 (96%)	49 (92%)	4 (8%)	13	31
54	D8	54/55 (98%)	52 (96%)	2 (4%)	34	63
55	B9	34/34 (100%)	33 (97%)	1 (3%)	42	71
55	D9	34/34 (100%)	33 (97%)	1 (3%)	42	71
All	All	9315/10066 (92%)	8513 (91%)	802 (9%)	10	24

All (802) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	7	VAL
2	AB	8	LYS
2	AB	11	LEU
2	AB	15	VAL
2	AB	17	PHE
2	AB	21	ARG
2	AB	24	TRP
2	AB	39	ILE
2	AB	49	GLU
2	AB	64	ARG

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Mol	Chain	Res	Type
2	AB	67	THR
2	AB	76	GLN
2	AB	80	ILE
2	AB	93	VAL
2	AB	96	ARG
2	AB	112	VAL
2	AB	127	ILE
2	AB	144	ARG
2	AB	145	LEU
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	157	ARG
2	AB	158	LEU
2	AB	160	ASP
2	AB	178	ARG
2	AB	185	ILE
2	AB	200	ILE
2	AB	204	ASN
2	AB	209	ARG
2	AB	215	LEU
2	AB	217	ARG
2	AB	223	ILE
2	AB	230	VAL
3	AC	3	ASN
3	AC	17	ASP
3	AC	21	ARG
3	AC	27	LYS
3	AC	28	GLN
3	AC	29	TYR
3	AC	52	LEU
3	AC	115	LEU
3	AC	178	LEU
4	AD	5	ILE
4	AD	15	GLU
4	AD	19	LEU
4	AD	46	LYS
4	AD	49	ARG
4	AD	53	ASP
4	AD	58	LEU
4	AD	65	ARG
4	AD	86	LYS

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Mol	Chain	Res	Type
4	AD	112	VAL
4	AD	127	THR
4	AD	135	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	188	LEU
4	AD	193	ASP
5	AE	12	LEU
5	AE	31	LEU
5	AE	34	VAL
5	AE	41	VAL
5	AE	67	VAL
5	AE	79	GLU
5	AE	147	ASP
6	AF	55	ASP
6	AF	69	GLU
6	AF	82	ARG
6	AF	94	GLN
7	AG	8	GLU
7	AG	13	GLN
7	AG	21	VAL
7	AG	32	ARG
7	AG	51	GLN
7	AG	57	GLU
7	AG	76	ARG
7	AG	78	ARG
7	AG	104	LEU
7	AG	115	ARG
7	AG	138	LYS
8	AH	37	ARG
8	AH	50	ARG
8	AH	52	ASP
8	AH	63	LEU
8	AH	133	LEU
8	AH	137	VAL
9	AI	23	ASN
9	AI	27	THR
9	AI	42	ARG
9	AI	53	VAL
9	AI	56	LEU
9	AI	81	ILE
9	AI	89	ASN

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Mol	Chain	Res	Type
9	AI	104	ARG
9	AI	108	VAL
9	AI	112	LYS
9	AI	128	ARG
10	AJ	67	THR
10	AJ	84	GLN
10	AJ	96	ILE
11	AK	31	THR
11	AK	48	ILE
11	AK	96	ARG
11	AK	109	VAL
12	AL	33	ARG
12	AL	46	LYS
12	AL	67	THR
12	AL	83	VAL
12	AL	123	LYS
13	AM	4	ILE
13	AM	15	VAL
13	AM	43	THR
13	AM	47	ASP
13	AM	70	LEU
13	AM	73	GLU
13	AM	110	ARG
13	AM	121	LYS
14	AN	7	ILE
14	AN	15	LYS
14	AN	18	VAL
14	AN	32	SER
14	AN	33	VAL
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	26	GLU
15	AO	38	ARG
15	AO	39	LEU
15	AO	41	GLU
15	AO	47	LYS
15	AO	83	GLU
15	AO	84	LYS
15	AO	88	ARG
16	AP	5	ARG
16	AP	19	ILE

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Mol	Chain	Res	Type
16	AP	20	VAL
16	AP	28	ARG
16	AP	45	THR
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	62	VAL
16	AP	67	THR
17	AQ	6	LEU
17	AQ	14	LYS
17	AQ	49	GLU
17	AQ	53	LEU
17	AQ	63	ARG
17	AQ	74	LEU
18	AR	31	LEU
18	AR	32	ARG
18	AR	38	GLU
18	AR	47	THR
18	AR	76	LEU
19	AS	12	ASP
19	AS	16	LEU
19	AS	28	LYS
19	AS	41	VAL
19	AS	48	THR
19	AS	65	ASN
20	AT	8	ARG
20	AT	13	LEU
20	AT	24	LEU
20	AT	45	GLN
20	AT	62	LEU
20	AT	74	LYS
20	AT	80	ARG
20	AT	84	LEU
21	AU	9	ARG
21	AU	10	ARG
27	BD	3	VAL
27	BD	13	ARG
27	BD	61	LEU
27	BD	94	LEU
27	BD	103	ARG
27	BD	111	LEU
27	BD	113	VAL

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Mol	Chain	Res	Type
27	BD	142	VAL
27	BD	155	LEU
27	BD	211	ARG
27	BD	221	VAL
27	BD	229	VAL
27	BD	242	ARG
27	BD	257	LEU
27	BD	260	ARG
28	BE	12	THR
28	BE	24	THR
28	BE	73	GLU
28	BE	75	VAL
28	BE	82	ARG
28	BE	89	ASP
28	BE	97	LYS
28	BE	111	ARG
28	BE	116	VAL
28	BE	119	ARG
28	BE	144	ARG
28	BE	163	GLU
28	BE	181	LEU
28	BE	202	LYS
29	BF	24	LEU
29	BF	33	LEU
29	BF	38	ARG
29	BF	53	THR
29	BF	74	ARG
29	BF	88	VAL
29	BF	106	ARG
29	BF	110	LEU
29	BF	125	LEU
29	BF	132	VAL
29	BF	140	LEU
29	BF	170	LEU
29	BF	192	LEU
29	BF	195	ASP
29	BF	197	ASP
30	BG	5	VAL
30	BG	28	VAL
30	BG	43	LEU
30	BG	45	GLU
30	BG	58	GLN

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Mol	Chain	Res	Type
30	BG	81	LYS
30	BG	82	LEU
30	BG	86	MET
30	BG	135	LEU
30	BG	140	ILE
30	BG	143	GLU
30	BG	148	MET
30	BG	159	VAL
30	BG	170	ARG
30	BG	175	LEU
31	BH	6	ARG
31	BH	33	LEU
31	BH	41	MET
31	BH	59	ARG
31	BH	69	ARG
31	BH	71	LEU
31	BH	84	SER
31	BH	98	LEU
31	BH	116	GLU
31	BH	122	THR
31	BH	130	ARG
32	BI	9	LEU
32	BI	10	GLU
32	BI	20	ASP
32	BI	38	LEU
32	BI	40	THR
32	BI	43	ASN
32	BI	57	ARG
32	BI	60	GLU
32	BI	61	ARG
32	BI	64	GLU
32	BI	66	GLU
32	BI	68	LEU
32	BI	74	ASN
32	BI	75	LEU
32	BI	77	LEU
32	BI	87	LYS
32	BI	92	VAL
32	BI	96	ASP
32	BI	103	ARG
32	BI	116	LEU
32	BI	117	GLU

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Mol	Chain	Res	Type
32	BI	140	LEU
33	BN	5	VAL
33	BN	28	THR
33	BN	33	LEU
33	BN	34	LEU
33	BN	46	VAL
33	BN	48	MET
33	BN	61	ARG
33	BN	62	VAL
33	BN	67	LEU
33	BN	68	GLU
33	BN	83	LYS
33	BN	87	LEU
33	BN	99	LEU
33	BN	120	LEU
33	BN	133	GLN
34	BO	8	LEU
34	BO	18	LYS
34	BO	24	VAL
34	BO	94	ARG
34	BO	108	GLU
35	BP	15	ARG
35	BP	55	ARG
35	BP	56	SER
35	BP	65	ARG
35	BP	77	ARG
35	BP	83	VAL
35	BP	95	VAL
35	BP	98	GLU
35	BP	106	LEU
35	BP	149	GLU
36	BQ	1	MET
36	BQ	5	ARG
36	BQ	7	MET
36	BQ	16	ARG
36	BQ	21	THR
36	BQ	45	GLN
36	BQ	54	MET
36	BQ	75	THR
36	BQ	85	LYS
36	BQ	109	VAL
36	BQ	110	THR

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Mol	Chain	Res	Type
37	BR	1	MET
37	BR	6	SER
37	BR	18	LEU
37	BR	24	GLN
37	BR	29	LEU
37	BR	36	THR
37	BR	44	LEU
37	BR	54	LEU
37	BR	60	LEU
37	BR	65	LEU
37	BR	79	LEU
37	BR	102	GLU
37	BR	111	LEU
37	BR	114	VAL
38	BS	20	ARG
38	BS	49	VAL
38	BS	59	LYS
38	BS	110	LEU
39	BT	23	ARG
39	BT	49	VAL
39	BT	53	ARG
39	BT	64	ARG
39	BT	74	ARG
39	BT	93	ARG
39	BT	96	ARG
39	BT	108	ARG
39	BT	118	ARG
40	BU	8	VAL
40	BU	36	ARG
40	BU	74	LEU
40	BU	92	ARG
40	BU	95	LEU
40	BU	104	GLN
41	BV	18	LEU
41	BV	28	GLU
41	BV	43	GLU
41	BV	51	VAL
41	BV	62	LEU
41	BV	79	VAL
41	BV	95	LEU
41	BV	100	ARG
42	BW	11	ARG

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Mol	Chain	Res	Type
42	BW	17	VAL
42	BW	19	LEU
42	BW	51	LEU
42	BW	107	LEU
43	BX	35	THR
43	BX	66	LEU
43	BX	88	LYS
43	BX	92	LEU
44	BY	1	MET
44	BY	23	ARG
44	BY	43	ASN
44	BY	72	VAL
45	BZ	5	LEU
45	BZ	18	LEU
45	BZ	19	ARG
45	BZ	33	LEU
45	BZ	61	LEU
45	BZ	86	VAL
45	BZ	102	LEU
45	BZ	107	THR
45	BZ	126	VAL
45	BZ	136	PHE
45	BZ	144	LEU
45	BZ	154	ASP
45	BZ	155	LEU
45	BZ	161	VAL
46	B0	14	ARG
46	B0	20	ARG
46	B0	55	ARG
47	B1	21	ARG
47	B1	40	ARG
47	B1	59	THR
47	B1	78	LYS
47	B1	89	GLU
47	B1	95	LEU
48	B2	32	LEU
48	B2	52	ASP
48	B2	64	LEU
48	B2	70	GLN
49	B3	8	LEU
49	B3	23	LEU
49	B3	29	ARG

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Mol	Chain	Res	Type
49	B3	44	ARG
49	B3	54	VAL
50	B4	3	GLU
50	B4	34	GLU
50	B4	46	GLN
50	B4	48	ARG
50	B4	49	PHE
50	B4	58	ARG
50	B4	59	PHE
50	B4	63	TYR
50	B4	68	ARG
51	B5	6	VAL
51	B5	26	THR
51	B5	29	THR
51	B5	33	CYS
51	B5	36	CYS
51	B5	40	LYS
51	B5	49	CYS
51	B5	60	VAL
52	B6	4	GLU
52	B6	6	ARG
52	B6	18	ARG
52	B6	28	ARG
52	B6	40	CYS
52	B6	48	VAL
53	B7	1	MET
53	B7	24	THR
53	B7	43	THR
54	B8	14	VAL
54	B8	30	ARG
54	B8	31	HIS
54	B8	37	SER
55	B9	27	CYS
2	CB	7	VAL
2	CB	8	LYS
2	CB	11	LEU
2	CB	23	ARG
2	CB	24	TRP
2	CB	35	GLU
2	CB	49	GLU
2	CB	67	THR
2	CB	93	VAL

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Mol	Chain	Res	Type
2	CB	94	ASN
2	CB	115	LEU
2	CB	126	GLU
2	CB	128	GLU
2	CB	142	LEU
2	CB	144	ARG
2	CB	154	LEU
2	CB	155	LEU
2	CB	158	LEU
2	CB	175	ARG
2	CB	178	ARG
2	CB	185	ILE
2	CB	187	LEU
2	CB	200	ILE
2	CB	209	ARG
2	CB	215	LEU
2	CB	224	GLN
3	CC	3	ASN
3	CC	21	ARG
3	CC	29	TYR
3	CC	49	SER
3	CC	54	ARG
3	CC	70	VAL
3	CC	105	GLU
3	CC	125	GLU
3	CC	140	ARG
3	CC	152	ILE
3	CC	178	LEU
3	CC	193	TYR
3	CC	196	LEU
4	CD	15	GLU
4	CD	19	LEU
4	CD	31	CYS
4	CD	34	GLU
4	CD	47	ARG
4	CD	58	LEU
4	CD	61	LYS
4	CD	65	ARG
4	CD	86	LYS
4	CD	122	ARG
4	CD	135	LEU
4	CD	157	LEU

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Mol	Chain	Res	Type
4	CD	170	VAL
4	CD	194	LEU
4	CD	208	SER
5	CE	10	MET
5	CE	18	ARG
5	CE	31	LEU
5	CE	34	VAL
5	CE	41	VAL
5	CE	71	LEU
5	CE	72	GLN
5	CE	78	HIS
5	CE	79	GLU
5	CE	147	ASP
5	CE	152	ARG
6	CF	28	ARG
6	CF	41	GLU
6	CF	46	ARG
7	CG	9	VAL
7	CG	51	GLN
7	CG	72	ARG
7	CG	76	ARG
7	CG	78	ARG
7	CG	79	ARG
7	CG	155	ARG
8	CH	50	ARG
8	CH	63	LEU
8	CH	84	ARG
8	CH	133	LEU
8	CH	137	VAL
9	CI	14	VAL
9	CI	27	THR
9	CI	81	ILE
9	CI	92	TYR
9	CI	102	LEU
9	CI	104	ARG
9	CI	108	VAL
9	CI	128	ARG
10	CJ	7	LYS
10	CJ	19	SER
10	CJ	21	GLN
10	CJ	38	ILE
10	CJ	67	THR

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Mol	Chain	Res	Type
11	CK	54	ARG
11	CK	96	ARG
11	CK	109	VAL
11	CK	126	ARG
12	CL	33	ARG
12	CL	53	ARG
12	CL	67	THR
12	CL	83	VAL
13	CM	3	ARG
13	CM	15	VAL
13	CM	27	LYS
13	CM	47	ASP
13	CM	49	THR
13	CM	56	LEU
13	CM	70	LEU
13	CM	106	ASN
13	CM	110	ARG
14	CN	3	ARG
14	CN	7	ILE
14	CN	12	ARG
14	CN	18	VAL
14	CN	23	ARG
14	CN	32	SER
14	CN	33	VAL
15	CO	3	ILE
15	CO	5	LYS
15	CO	10	LYS
15	CO	38	ARG
15	CO	41	GLU
16	CP	5	ARG
16	CP	27	LYS
16	CP	28	ARG
16	CP	45	THR
16	CP	60	LEU
16	CP	62	VAL
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	36	ILE
17	CQ	53	LEU
17	CQ	63	ARG
17	CQ	74	LEU

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Mol	Chain	Res	Type
18	CR	26	LEU
18	CR	32	ARG
18	CR	47	THR
18	CR	76	LEU
19	CS	12	ASP
19	CS	28	LYS
19	CS	41	VAL
19	CS	48	THR
19	CS	56	GLN
19	CS	64	GLU
19	CS	65	ASN
19	CS	77	THR
19	CS	78	ARG
20	CT	24	LEU
20	CT	30	LYS
20	CT	38	LYS
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	84	LEU
21	CU	10	ARG
27	DD	54	ARG
27	DD	61	LEU
27	DD	94	LEU
27	DD	103	ARG
27	DD	106	ILE
27	DD	111	LEU
27	DD	113	VAL
27	DD	134	ARG
27	DD	155	LEU
27	DD	211	ARG
27	DD	217	ARG
27	DD	221	VAL
27	DD	229	VAL
27	DD	242	ARG
27	DD	257	LEU
28	DE	12	THR
28	DE	21	VAL
28	DE	24	THR
28	DE	27	LEU
28	DE	34	VAL

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Mol	Chain	Res	Type
28	DE	40	GLU
28	DE	52	LEU
28	DE	73	GLU
28	DE	75	VAL
28	DE	77	ILE
28	DE	93	VAL
28	DE	116	VAL
28	DE	119	ARG
28	DE	144	ARG
28	DE	163	GLU
28	DE	175	VAL
28	DE	181	LEU
29	DF	24	LEU
29	DF	28	ILE
29	DF	33	LEU
29	DF	38	ARG
29	DF	57	VAL
29	DF	74	ARG
29	DF	88	VAL
29	DF	106	ARG
29	DF	108	LYS
29	DF	110	LEU
29	DF	132	VAL
29	DF	137	LYS
29	DF	170	LEU
29	DF	192	LEU
29	DF	200	GLU
30	DG	5	VAL
30	DG	7	LEU
30	DG	16	ARG
30	DG	36	LYS
30	DG	43	LEU
30	DG	49	ASP
30	DG	58	GLN
30	DG	91	ARG
30	DG	98	ARG
30	DG	136	ARG
30	DG	140	ILE
30	DG	148	MET
30	DG	159	VAL
30	DG	170	ARG
31	DH	3	ARG

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Mol	Chain	Res	Type
31	DH	33	LEU
31	DH	63	SER
31	DH	69	ARG
31	DH	84	SER
31	DH	95	ARG
31	DH	98	LEU
31	DH	136	ILE
31	DH	139	GLN
31	DH	172	LYS
32	DI	9	LEU
32	DI	40	THR
32	DI	43	ASN
32	DI	44	LEU
32	DI	50	ARG
32	DI	68	LEU
32	DI	73	GLU
32	DI	75	LEU
32	DI	77	LEU
32	DI	116	LEU
32	DI	123	LEU
32	DI	140	LEU
32	DI	142	VAL
32	DI	144	VAL
33	DN	5	VAL
33	DN	12	ARG
33	DN	28	THR
33	DN	33	LEU
33	DN	34	LEU
33	DN	46	VAL
33	DN	85	ILE
33	DN	87	LEU
33	DN	99	LEU
33	DN	120	LEU
33	DN	133	GLN
33	DN	137	LYS
34	DO	8	LEU
34	DO	24	VAL
34	DO	69	ILE
34	DO	94	ARG
35	DP	15	ARG
35	DP	55	ARG
35	DP	56	SER

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Mol	Chain	Res	Type
35	DP	65	ARG
35	DP	77	ARG
35	DP	83	VAL
35	DP	95	VAL
35	DP	96	THR
35	DP	106	LEU
36	DQ	5	ARG
36	DQ	7	MET
36	DQ	16	ARG
36	DQ	21	THR
36	DQ	45	GLN
36	DQ	60	ARG
36	DQ	85	LYS
36	DQ	109	VAL
37	DR	1	MET
37	DR	18	LEU
37	DR	24	GLN
37	DR	29	LEU
37	DR	44	LEU
37	DR	54	LEU
37	DR	60	LEU
37	DR	65	LEU
37	DR	79	LEU
37	DR	100	LEU
37	DR	102	GLU
37	DR	111	LEU
37	DR	114	VAL
38	DS	20	ARG
38	DS	35	ILE
38	DS	58	LEU
38	DS	68	GLN
38	DS	69	VAL
38	DS	71	ARG
38	DS	75	GLU
38	DS	110	LEU
39	DT	6	LEU
39	DT	16	ARG
39	DT	23	ARG
39	DT	49	VAL
39	DT	64	ARG
39	DT	74	ARG
39	DT	96	ARG

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Mol	Chain	Res	Type
39	DT	113	LYS
39	DT	118	ARG
40	DU	8	VAL
40	DU	36	ARG
40	DU	74	LEU
40	DU	83	LEU
40	DU	95	LEU
40	DU	104	GLN
41	DV	18	LEU
41	DV	28	GLU
41	DV	38	LEU
41	DV	57	VAL
41	DV	62	LEU
41	DV	72	VAL
41	DV	79	VAL
41	DV	85	LYS
42	DW	11	ARG
42	DW	15	ARG
42	DW	17	VAL
42	DW	51	LEU
42	DW	60	ASN
42	DW	107	LEU
43	DX	57	LEU
43	DX	88	LYS
43	DX	90	GLU
43	DX	92	LEU
44	DY	1	MET
44	DY	23	ARG
44	DY	43	ASN
44	DY	49	VAL
44	DY	72	VAL
44	DY	91	GLU
44	DY	102	CYS
45	DZ	5	LEU
45	DZ	11	GLU
45	DZ	33	LEU
45	DZ	61	LEU
45	DZ	72	ARG
45	DZ	86	VAL
45	DZ	97	GLU
45	DZ	126	VAL
45	DZ	136	PHE

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Mol	Chain	Res	Type
45	DZ	154	ASP
45	DZ	155	LEU
45	DZ	156	LYS
45	DZ	161	VAL
46	D0	10	THR
46	D0	14	ARG
46	D0	20	ARG
47	D1	4	VAL
47	D1	21	ARG
47	D1	40	ARG
47	D1	59	THR
47	D1	95	LEU
48	D2	30	ARG
48	D2	40	SER
48	D2	52	ASP
48	D2	53	LEU
48	D2	70	GLN
49	D3	8	LEU
49	D3	23	LEU
49	D3	30	ARG
49	D3	44	ARG
49	D3	54	VAL
50	D4	3	GLU
50	D4	24	THR
50	D4	53	GLU
50	D4	58	ARG
50	D4	63	TYR
50	D4	67	TYR
50	D4	69	LYS
51	D5	29	THR
51	D5	40	LYS
51	D5	59	GLU
52	D6	6	ARG
54	D8	31	HIS
54	D8	37	SER
55	D9	26	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (147) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	16	HIS
2	AB	94	ASN

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Mol	Chain	Res	Type
3	AC	6	HIS
3	AC	28	GLN
3	AC	37	GLN
3	AC	102	ASN
3	AC	104	GLN
3	AC	136	GLN
4	AD	42	GLN
4	AD	45	GLN
4	AD	77	ASN
4	AD	123	HIS
4	AD	125	HIS
5	AE	20	GLN
5	AE	38	GLN
5	AE	56	GLN
5	AE	73	ASN
5	AE	141	GLN
6	AF	94	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	51	GLN
7	AG	97	GLN
7	AG	148	ASN
9	AI	23	ASN
9	AI	31	GLN
9	AI	58	HIS
9	AI	73	GLN
9	AI	89	ASN
9	AI	124	GLN
10	AJ	56	HIS
10	AJ	84	GLN
11	AK	93	GLN
11	AK	104	GLN
12	AL	78	GLN
12	AL	99	HIS
14	AN	52	GLN
15	AO	28	GLN
15	AO	46	HIS
16	AP	13	HIS
17	AQ	16	GLN
19	AS	23	ASN
19	AS	47	HIS
19	AS	65	ASN

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Mol	Chain	Res	Type
19	AS	83	HIS
20	AT	45	GLN
27	BD	87	ASN
27	BD	253	GLN
29	BF	69	HIS
29	BF	169	ASN
29	BF	203	GLN
30	BG	40	ASN
30	BG	41	GLN
30	BG	58	GLN
30	BG	108	ASN
32	BI	43	ASN
32	BI	54	GLN
35	BP	38	GLN
39	BT	123	GLN
40	BU	81	HIS
40	BU	104	GLN
43	BX	31	HIS
45	BZ	55	HIS
45	BZ	73	GLN
45	BZ	151	HIS
48	B2	70	GLN
49	B3	32	GLN
50	B4	46	GLN
52	B6	20	ASN
55	B9	36	GLN
2	CB	40	HIS
2	CB	76	GLN
2	CB	146	GLN
2	CB	224	GLN
3	CC	28	GLN
3	CC	98	ASN
3	CC	102	ASN
3	CC	104	GLN
3	CC	118	GLN
3	CC	136	GLN
4	CD	74	GLN
4	CD	77	ASN
4	CD	123	HIS
4	CD	125	HIS
4	CD	129	ASN
4	CD	161	ASN

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Mol	Chain	Res	Type
4	CD	201	GLN
5	CE	20	GLN
5	CE	38	GLN
5	CE	56	GLN
5	CE	78	HIS
5	CE	141	GLN
7	CG	28	ASN
7	CG	51	GLN
7	CG	86	GLN
7	CG	97	GLN
7	CG	109	ASN
7	CG	148	ASN
8	CH	82	HIS
9	CI	58	HIS
9	CI	89	ASN
9	CI	117	HIS
9	CI	124	GLN
10	CJ	13	HIS
11	CK	22	HIS
11	CK	93	GLN
12	CL	78	GLN
12	CL	99	HIS
13	CM	77	ASN
15	CO	9	GLN
15	CO	28	GLN
15	CO	62	GLN
16	CP	13	HIS
17	CQ	16	GLN
19	CS	23	ASN
19	CS	47	HIS
19	CS	57	HIS
19	CS	83	HIS
27	DD	87	ASN
27	DD	164	GLN
27	DD	166	GLN
27	DD	253	GLN
28	DE	85	ASN
29	DF	69	HIS
29	DF	169	ASN
29	DF	203	GLN
30	DG	40	ASN
30	DG	41	GLN

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Mol	Chain	Res	Type
30	DG	79	ASN
30	DG	108	ASN
31	DH	139	GLN
35	DP	38	GLN
37	DR	71	GLN
38	DS	68	GLN
40	DU	117	GLN
41	DV	80	GLN
42	DW	60	ASN
43	DX	31	HIS
43	DX	82	GLN
44	DY	43	ASN
45	DZ	32	HIS
45	DZ	34	ASN
45	DZ	55	HIS
45	DZ	151	HIS
48	D2	56	GLN
49	D3	32	GLN
55	D9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1494/1521 (98%)	363 (24%)	26 (1%)
1	CA	1501/1521 (98%)	372 (24%)	32 (2%)
22	AV	7/24 (29%)	0	0
22	CV	4/24 (16%)	1 (25%)	0
23	AX	75/77 (97%)	25 (33%)	0
23	CX	75/77 (97%)	23 (30%)	0
24	AY	16/76 (21%)	7 (43%)	0
24	CY	4/76 (5%)	0	0
25	BA	2814/2915 (96%)	473 (16%)	31 (1%)
25	DA	2791/2915 (95%)	523 (18%)	27 (0%)
26	BB	119/121 (98%)	24 (20%)	0
26	DB	119/121 (98%)	25 (21%)	0
All	All	9019/9468 (95%)	1836 (20%)	116 (1%)

All (1836) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G

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Mol	Chain	Res	Type
1	AA	7	G
1	AA	9	G
1	AA	22	G
1	AA	32	A
1	AA	39	G
1	AA	48	C
1	AA	51	A
1	AA	55	A
1	AA	59	A
1	AA	61	G
1	AA	65	U
1	AA	73	G
1	AA	78	G
1	AA	79	G
1	AA	92	C
1	AA	96	U
1	AA	97	G
1	AA	98	G
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	131	C
1	AA	137	C
1	AA	142	G
1	AA	147	G
1	AA	163	C
1	AA	171	A
1	AA	173	U
1	AA	174	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(E)	U
1	AA	189(F)	U
1	AA	189(H)	G
1	AA	189(I)	G
1	AA	190	U

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Mol	Chain	Res	Type
1	AA	195	A
1	AA	197	A
1	AA	199	G
1	AA	200	G
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	219	C
1	AA	247	G
1	AA	251	G
1	AA	256	U
1	AA	257	G
1	AA	266	G
1	AA	267	C
1	AA	277	C
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	343	U
1	AA	344	A
1	AA	347	G
1	AA	348	G
1	AA	351	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	380	G
1	AA	384	G
1	AA	396	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	409	G
1	AA	412	A

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Mol	Chain	Res	Type
1	AA	413	G
1	AA	421	U
1	AA	422	C
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	434	U
1	AA	435	C
1	AA	439	A
1	AA	442	C
1	AA	452	A
1	AA	456	C
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	474	G
1	AA	475	G
1	AA	484	G
1	AA	485	G
1	AA	496	A
1	AA	498	U
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	521	G
1	AA	524	G
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	536	C
1	AA	544	G
1	AA	546	G
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	571	U
1	AA	572	A

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Mol	Chain	Res	Type
1	AA	573	A
1	AA	576	G
1	AA	587	G
1	AA	590	C
1	AA	591	U
1	AA	592	G
1	AA	595	G
1	AA	596	C
1	AA	602	A
1	AA	629	G
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	641	U
1	AA	644	G
1	AA	653	A
1	AA	656	C
1	AA	658	G
1	AA	665	A
1	AA	673	G
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	695	A
1	AA	705	U
1	AA	711	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	752	G
1	AA	753	A
1	AA	755	G
1	AA	759	A
1	AA	772	U
1	AA	773	G
1	AA	774	G
1	AA	777	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	802	A

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Mol	Chain	Res	Type
1	AA	810	C
1	AA	815	A
1	AA	817	C
1	AA	827	U
1	AA	828	A
1	AA	840	C
1	AA	841	U
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	868	C
1	AA	870	U
1	AA	875	C
1	AA	885	G
1	AA	902	G
1	AA	914	A
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	935	A
1	AA	936	C
1	AA	954	G
1	AA	960	U
1	AA	961	U
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	972	C
1	AA	973	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	978	A
1	AA	989	C
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	998	G
1	AA	999	C
1	AA	1002	G
1	AA	1004	A

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Mol	Chain	Res	Type
1	AA	1005	A
1	AA	1006	C
1	AA	1007	C
1	AA	1008	C
1	AA	1009	G
1	AA	1020	U
1	AA	1021	G
1	AA	1022	G
1	AA	1024	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1033	G
1	AA	1037	C
1	AA	1043	C
1	AA	1045	C
1	AA	1052	U
1	AA	1054	C
1	AA	1056	U
1	AA	1057	G
1	AA	1058	G
1	AA	1065	U
1	AA	1066	C
1	AA	1067	A
1	AA	1076	C
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1101	A
1	AA	1108	G
1	AA	1113	C
1	AA	1116	C
1	AA	1121	U
1	AA	1122	U
1	AA	1123	A
1	AA	1124	G
1	AA	1126	U
1	AA	1130	A
1	AA	1132	C

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Mol	Chain	Res	Type
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	1142	G
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1155	G
1	AA	1157	A
1	AA	1159	U
1	AA	1160	G
1	AA	1163	C
1	AA	1164	G
1	AA	1166	G
1	AA	1174	G
1	AA	1176	A
1	AA	1181	G
1	AA	1182	G
1	AA	1183	A
1	AA	1184	G
1	AA	1196	U
1	AA	1197	G
1	AA	1200	C
1	AA	1202	G
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1216	G
1	AA	1218	C
1	AA	1224	G
1	AA	1227	A
1	AA	1235	U
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1244	C
1	AA	1246	C
1	AA	1257	U
1	AA	1258	G

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Mol	Chain	Res	Type
1	AA	1260	C
1	AA	1261	A
1	AA	1263	C
1	AA	1265	G
1	AA	1266	G
1	AA	1267	C
1	AA	1270	C
1	AA	1273	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1283	G
1	AA	1286	A
1	AA	1287	A
1	AA	1290	G
1	AA	1296	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1305	G
1	AA	1311	G
1	AA	1317	C
1	AA	1320	C
1	AA	1322	C
1	AA	1338	G
1	AA	1347	G
1	AA	1353	G
1	AA	1354	C
1	AA	1355	G
1	AA	1356	G
1	AA	1358	U
1	AA	1360	A
1	AA	1363	C
1	AA	1363(A)	A
1	AA	1364	U
1	AA	1370	G
1	AA	1377	A
1	AA	1379	G
1	AA	1384	C
1	AA	1386	G
1	AA	1387	G
1	AA	1397	C

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Mol	Chain	Res	Type
1	AA	1402	C
1	AA	1419	G
1	AA	1422	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1444	C
1	AA	1445	C
1	AA	1447	A
1	AA	1452	C
1	AA	1456	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	1517	G
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
23	AX	9	G
23	AX	16	C
23	AX	17	C
23	AX	18	G
23	AX	19	G
23	AX	20	U
23	AX	21	A
23	AX	29	G
23	AX	30	G
23	AX	31	G
23	AX	34	C
23	AX	42	G
23	AX	46	G
23	AX	47	U
23	AX	48	C
23	AX	56	C

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Mol	Chain	Res	Type
23	AX	58	A
23	AX	60	U
23	AX	61	C
23	AX	63	G
23	AX	65	C
23	AX	67	C
23	AX	68	C
23	AX	69	C
23	AX	76	A
24	AY	5	G
24	AY	67	C
24	AY	68	C
24	AY	69	G
24	AY	70	G
24	AY	71	G
24	AY	74	C
25	BA	10	G
25	BA	12	U
25	BA	13	A
25	BA	34	C
25	BA	45	C
25	BA	54	G
25	BA	62	U
25	BA	70	A
25	BA	73	A
25	BA	74	G
25	BA	83	A
25	BA	116	A
25	BA	117	A
25	BA	118	U
25	BA	123	G
25	BA	124	A
25	BA	137	G
25	BA	149	A
25	BA	155	C
25	BA	161	C
25	BA	170	A
25	BA	171	A
25	BA	185	A
25	BA	186	A
25	BA	188	A
25	BA	190	C

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Mol	Chain	Res	Type
25	BA	194	G
25	BA	203	G
25	BA	204	G
25	BA	205	A
25	BA	210	A
25	BA	211	A
25	BA	214	A
25	BA	218	A
25	BA	222	A
25	BA	237	G
25	BA	239	G
25	BA	265	U
25	BA	269	G
25	BA	271	U
25	BA	272	U
25	BA	273	G
25	BA	274	U
25	BA	279	G
25	BA	289	G
25	BA	294	C
25	BA	295	C
25	BA	303	C
25	BA	306	A
25	BA	307	A
25	BA	335	A
25	BA	353	G
25	BA	354	A
25	BA	360	C
25	BA	376	G
25	BA	387	G
25	BA	390	G
25	BA	397	G
25	BA	399	G
25	BA	407	U
25	BA	413	G
25	BA	423	G
25	BA	432	U
25	BA	438	G
25	BA	439	A
25	BA	448	U
25	BA	455	A
25	BA	469	A

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Mol	Chain	Res	Type
25	BA	470	C
25	BA	474	U
25	BA	477	C
25	BA	480	A
25	BA	496	A
25	BA	507	G
25	BA	529	U
25	BA	530	A
25	BA	533	G
25	BA	534	C
25	BA	555	G
25	BA	556	C
25	BA	557	A
25	BA	558	G
25	BA	573	G
25	BA	586	G
25	BA	596	G
25	BA	598	A
25	BA	625	G
25	BA	626	A
25	BA	627	G
25	BA	630	U
25	BA	639	G
25	BA	641	G
25	BA	642	G
25	BA	652	A
25	BA	662	A
25	BA	670	C
25	BA	692	C
25	BA	693	G
25	BA	694	G
25	BA	697	C
25	BA	698	G
25	BA	715	G
25	BA	716	G
25	BA	724	A
25	BA	733	G
25	BA	777	C
25	BA	787	U
25	BA	811	A
25	BA	812	G
25	BA	822	G

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Mol	Chain	Res	Type
25	BA	823	G
25	BA	829	A
25	BA	831	A
25	BA	832	G
25	BA	837	C
25	BA	839	G
25	BA	852	G
25	BA	858	U
25	BA	859	C
25	BA	866	A
25	BA	874	U
25	BA	875	U
25	BA	906	G
25	BA	908	A
25	BA	913	A
25	BA	924	U
25	BA	927	G
25	BA	929	G
25	BA	930	G
25	BA	931	C
25	BA	932	C
25	BA	933	C
25	BA	934	A
25	BA	935	C
25	BA	936	C
25	BA	937	A
25	BA	938	G
25	BA	940	C
25	BA	942	A
25	BA	943	C
25	BA	946	A
25	BA	953	U
25	BA	956	A
25	BA	957	A
25	BA	961	C
25	BA	977	G
25	BA	986	A
25	BA	990	A
25	BA	991	G
25	BA	1003	U
25	BA	1004	A
25	BA	1006	C

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Mol	Chain	Res	Type
25	BA	1019	G
25	BA	1020	C
25	BA	1029	A
25	BA	1035	G
25	BA	1042	A
25	BA	1045	U
25	BA	1051	C
25	BA	1054	C
25	BA	1058	U
25	BA	1059	C
25	BA	1068	G
25	BA	1072	U
25	BA	1073	A
25	BA	1079	U
25	BA	1084	C
25	BA	1087	C
25	BA	1090	G
25	BA	1091	A
25	BA	1092	A
25	BA	1093	G
25	BA	1094	A
25	BA	1097	G
25	BA	1153	G
25	BA	1156	G
25	BA	1158	G
25	BA	1175	A
25	BA	1176	U
25	BA	1180	C
25	BA	1181	G
25	BA	1184	G
25	BA	1186	U
25	BA	1195	G
25	BA	1216	G
25	BA	1217	G
25	BA	1218	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1222	A
25	BA	1255	A
25	BA	1256	U
25	BA	1263	C

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Mol	Chain	Res	Type
25	BA	1265	A
25	BA	1287	A
25	BA	1290	G
25	BA	1296	G
25	BA	1299	A
25	BA	1302	G
25	BA	1317	G
25	BA	1318	A
25	BA	1319	U
25	BA	1346	U
25	BA	1347	A
25	BA	1349	G
25	BA	1360	C
25	BA	1366	C
25	BA	1391	C
25	BA	1398	U
25	BA	1405	A
25	BA	1406	A
25	BA	1411	A
25	BA	1416	C
25	BA	1426	G
25	BA	1430	A
25	BA	1431	G
25	BA	1462	G
25	BA	1463	C
25	BA	1466	U
25	BA	1467	G
25	BA	1474	C
25	BA	1491	A
25	BA	1497	G
25	BA	1501	U
25	BA	1502	G
25	BA	1507	A
25	BA	1514	C
25	BA	1518	A
25	BA	1525	G
25	BA	1529	G
25	BA	1539	C
25	BA	1554	A
25	BA	1555	C
25	BA	1556	A
25	BA	1577	C

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Mol	Chain	Res	Type
25	BA	1578	C
25	BA	1580	G
25	BA	1581	U
25	BA	1586	G
25	BA	1589	A
25	BA	1601	A
25	BA	1605	A
25	BA	1613	A
25	BA	1616	A
25	BA	1625	U
25	BA	1627	A
25	BA	1628	G
25	BA	1631	C
25	BA	1632	A
25	BA	1654	A
25	BA	1655	A
25	BA	1656	A
25	BA	1694	G
25	BA	1695	C
25	BA	1701	A
25	BA	1711	A
25	BA	1721	G
25	BA	1742	G
25	BA	1743	G
25	BA	1747	A
25	BA	1748	A
25	BA	1750	G
25	BA	1767	A
25	BA	1768	U
25	BA	1776	G
25	BA	1787	G
25	BA	1794	G
25	BA	1795	G
25	BA	1804	A
25	BA	1811	A
25	BA	1813	C
25	BA	1822	A
25	BA	1831	C
25	BA	1832	G
25	BA	1847	G
25	BA	1848	G
25	BA	1859	G

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Mol	Chain	Res	Type
25	BA	1878	A
25	BA	1879	A
25	BA	1892	G
25	BA	1899	A
25	BA	1900	G
25	BA	1911	A
25	BA	1918	G
25	BA	1922	A
25	BA	1928	G
25	BA	1935	A
25	BA	1936	C
25	BA	1937	U
25	BA	1941	A
25	BA	1951	G
25	BA	1952	G
25	BA	1959	A
25	BA	1960	A
25	BA	1962	U
25	BA	1977	U
25	BA	1985	U
25	BA	1989	C
25	BA	1992	A
25	BA	1993	A
25	BA	1994	A
25	BA	2005	C
25	BA	2014	G
25	BA	2015	U
25	BA	2019	G
25	BA	2023	A
25	BA	2042	A
25	BA	2045	G
25	BA	2053	A
25	BA	2054	G
25	BA	2055	A
25	BA	2061	C
25	BA	2065	C
25	BA	2071	G
25	BA	2074	G
25	BA	2077	C
25	BA	2078	G
25	BA	2082	A
25	BA	2083	G

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Mol	Chain	Res	Type
25	BA	2084	A
25	BA	2091	G
25	BA	2099	A
25	BA	2115	G
25	BA	2120	U
25	BA	2132	G
25	BA	2133	C
25	BA	2135	U
25	BA	2136	A
25	BA	2137	G
25	BA	2138	G
25	BA	2139	A
25	BA	2141	A
25	BA	2143	G
25	BA	2149	G
25	BA	2152	U
25	BA	2153	G
25	BA	2154	U
25	BA	2155	G
25	BA	2156	A
25	BA	2157	A
25	BA	2158	C
25	BA	2161	C
25	BA	2162	C
25	BA	2163	G
25	BA	2164	C
25	BA	2165	C
25	BA	2167	C
25	BA	2168	C
25	BA	2169	G
25	BA	2174	G
25	BA	2178	G
25	BA	2179	G
25	BA	2180	A
25	BA	2185	C
25	BA	2188	G
25	BA	2189	U
25	BA	2190	G
25	BA	2191	A
25	BA	2194	U
25	BA	2196	C
25	BA	2197	C

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Mol	Chain	Res	Type
25	BA	2203	G
25	BA	2204	G
25	BA	2206	G
25	BA	2207	C
25	BA	2209	G
25	BA	2210	C
25	BA	2211	U
25	BA	2212	G
25	BA	2213	G
25	BA	2214	G
25	BA	2220	A
25	BA	2227	G
25	BA	2228	G
25	BA	2229	A
25	BA	2230	U
25	BA	2237	A
25	BA	2250	G
25	BA	2251	G
25	BA	2280	A
25	BA	2281	A
25	BA	2285	A
25	BA	2290	A
25	BA	2295	C
25	BA	2299	A
25	BA	2301	G
25	BA	2310	A
25	BA	2317	A
25	BA	2332	A
25	BA	2333	G
25	BA	2337	G
25	BA	2346	G
25	BA	2347	A
25	BA	2348	A
25	BA	2355	C
25	BA	2359	C
25	BA	2362	C
25	BA	2373	A
25	BA	2384	G
25	BA	2391	G
25	BA	2395	G
25	BA	2397	C
25	BA	2418	U

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Mol	Chain	Res	Type
25	BA	2422	G
25	BA	2426	G
25	BA	2437	A
25	BA	2441	G
25	BA	2442	A
25	BA	2447	A
25	BA	2451	A
25	BA	2453	C
25	BA	2460	A
25	BA	2480	G
25	BA	2481	A
25	BA	2488	A
25	BA	2490	A
25	BA	2499	G
25	BA	2502	G
25	BA	2514	G
25	BA	2517	G
25	BA	2518	U
25	BA	2530	A
25	BA	2541	G
25	BA	2561	G
25	BA	2566	U
25	BA	2576	A
25	BA	2578	A
25	BA	2579	G
25	BA	2585	C
25	BA	2594	G
25	BA	2614	A
25	BA	2621	U
25	BA	2623	U
25	BA	2624	C
25	BA	2641	A
25	BA	2642	G
25	BA	2644	A
25	BA	2653	G
25	BA	2666	A
25	BA	2701	U
25	BA	2702	C
25	BA	2703	C
25	BA	2714	U
25	BA	2715	C
25	BA	2725	A

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Mol	Chain	Res	Type
25	BA	2726	A
25	BA	2727	G
25	BA	2739	U
25	BA	2746	A
25	BA	2770	A
25	BA	2771	A
25	BA	2774	G
25	BA	2777	A
25	BA	2778	A
25	BA	2779	G
25	BA	2791	A
25	BA	2803	A
25	BA	2804	C
25	BA	2807	C
25	BA	2813	G
25	BA	2818	U
25	BA	2828	G
25	BA	2830	A
25	BA	2831	A
25	BA	2844	G
25	BA	2845	A
25	BA	2846	U
25	BA	2882	G
25	BA	2890	C
25	BA	2901	A
25	BA	2902	G
25	BA	2903	G
26	BB	2	C
26	BB	3	C
26	BB	5	C
26	BB	7	G
26	BB	13	A
26	BB	22	U
26	BB	24	G
26	BB	25	A
26	BB	28	C
26	BB	32	C
26	BB	34	U
26	BB	42	C
26	BB	44	G
26	BB	50	G
26	BB	56	G

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Mol	Chain	Res	Type
26	BB	60	C
26	BB	73	A
26	BB	75	G
26	BB	85	G
26	BB	93	G
26	BB	106	G
26	BB	110	G
26	BB	117	G
26	BB	118	G
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	22	G
1	CA	32	A
1	CA	39	G
1	CA	48	C
1	CA	51	A
1	CA	52	G
1	CA	55	A
1	CA	59	A
1	CA	61	G
1	CA	65	U
1	CA	66	G
1	CA	73	G
1	CA	78	G
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	90	U
1	CA	96	U
1	CA	97	G
1	CA	98	G
1	CA	101	A
1	CA	111	G
1	CA	112	G
1	CA	115	G
1	CA	116	A
1	CA	121	C
1	CA	131	C
1	CA	137	C

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Mol	Chain	Res	Type
1	CA	142	G
1	CA	146	G
1	CA	147	G
1	CA	157	G
1	CA	163	C
1	CA	171	A
1	CA	173	U
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(A)	C
1	CA	189(B)	C
1	CA	189(D)	C
1	CA	189(E)	U
1	CA	189(F)	U
1	CA	189(H)	G
1	CA	189(I)	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	217	C
1	CA	219	C
1	CA	247	G
1	CA	251	G
1	CA	256	U
1	CA	257	G
1	CA	266	G
1	CA	267	C
1	CA	277	C
1	CA	289	G
1	CA	301	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	344	A
1	CA	347	G

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Mol	Chain	Res	Type
1	CA	348	G
1	CA	351	G
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	380	G
1	CA	384	G
1	CA	396	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	421	U
1	CA	422	C
1	CA	424	G
1	CA	429	U
1	CA	430	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	474	G
1	CA	484	G
1	CA	485	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C

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Mol	Chain	Res	Type
1	CA	521	G
1	CA	524	G
1	CA	527	G
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	536	C
1	CA	544	G
1	CA	546	G
1	CA	547	A
1	CA	559	A
1	CA	560	U
1	CA	561	U
1	CA	571	U
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	587	G
1	CA	590	C
1	CA	591	U
1	CA	592	G
1	CA	595	G
1	CA	596	C
1	CA	602	A
1	CA	629	G
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	641	U
1	CA	644	G
1	CA	653	A
1	CA	656	C
1	CA	658	G
1	CA	665	A
1	CA	673	G
1	CA	688	G
1	CA	693	G
1	CA	695	A
1	CA	705	U
1	CA	711	G
1	CA	723	U
1	CA	724	G

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Mol	Chain	Res	Type
1	CA	731	G
1	CA	749	C
1	CA	752	G
1	CA	755	G
1	CA	759	A
1	CA	772	U
1	CA	773	G
1	CA	774	G
1	CA	777	A
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	802	A
1	CA	810	C
1	CA	815	A
1	CA	817	C
1	CA	827	U
1	CA	828	A
1	CA	829	G
1	CA	840	C
1	CA	841	U
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	868	C
1	CA	870	U
1	CA	875	C
1	CA	885	G
1	CA	902	G
1	CA	914	A
1	CA	926	G
1	CA	927	G
1	CA	934	C
1	CA	935	A
1	CA	936	C
1	CA	954	G
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	972	C

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Mol	Chain	Res	Type
1	CA	973	G
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	978	A
1	CA	989	C
1	CA	991	U
1	CA	992	U
1	CA	993	G
1	CA	996	A
1	CA	998	G
1	CA	999	C
1	CA	1001(A)	G
1	CA	1002	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1007	C
1	CA	1009	G
1	CA	1020	U
1	CA	1021	G
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	1032	G
1	CA	1033	G
1	CA	1036	G
1	CA	1037	C
1	CA	1041	A
1	CA	1045	C
1	CA	1050	G
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1056	U
1	CA	1057	G

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Mol	Chain	Res	Type
1	CA	1058	G
1	CA	1065	U
1	CA	1066	C
1	CA	1067	A
1	CA	1076	C
1	CA	1081	G
1	CA	1084	G
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1101	A
1	CA	1108	G
1	CA	1113	C
1	CA	1116	C
1	CA	1117	G
1	CA	1122	U
1	CA	1125	U
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	1142	G
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1157	A
1	CA	1159	U
1	CA	1160	G
1	CA	1163	C
1	CA	1164	G
1	CA	1174	G
1	CA	1176	A
1	CA	1180	A
1	CA	1181	G
1	CA	1182	G
1	CA	1183	A
1	CA	1184	G

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Mol	Chain	Res	Type
1	CA	1196	U
1	CA	1197	G
1	CA	1200	C
1	CA	1202	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1214	C
1	CA	1216	G
1	CA	1218	C
1	CA	1224	G
1	CA	1227	A
1	CA	1235	U
1	CA	1236	A
1	CA	1238	A
1	CA	1240	U
1	CA	1244	C
1	CA	1246	C
1	CA	1252	A
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1261	A
1	CA	1263	C
1	CA	1265	G
1	CA	1266	G
1	CA	1267	C
1	CA	1270	C
1	CA	1273	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1283	G
1	CA	1287	A
1	CA	1296	C
1	CA	1300	G
1	CA	1305	G
1	CA	1311	G
1	CA	1317	C

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Mol	Chain	Res	Type
1	CA	1320	C
1	CA	1322	C
1	CA	1338	G
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1354	C
1	CA	1355	G
1	CA	1356	G
1	CA	1358	U
1	CA	1360	A
1	CA	1363	C
1	CA	1363(A)	A
1	CA	1364	U
1	CA	1370	G
1	CA	1377	A
1	CA	1379	G
1	CA	1384	C
1	CA	1397	C
1	CA	1402	C
1	CA	1419	G
1	CA	1422	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1444	C
1	CA	1445	C
1	CA	1447	A
1	CA	1452	C
1	CA	1456	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	1517	G
1	CA	1520	G
1	CA	1529	G

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Mol	Chain	Res	Type
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	16	A
23	CX	9	G
23	CX	16	C
23	CX	17	C
23	CX	18	G
23	CX	19	G
23	CX	20	U
23	CX	21	A
23	CX	29	G
23	CX	30	G
23	CX	31	G
23	CX	34	C
23	CX	42	G
23	CX	46	G
23	CX	47	U
23	CX	48	C
23	CX	56	C
23	CX	58	A
23	CX	60	U
23	CX	61	C
23	CX	65	C
23	CX	67	C
23	CX	68	C
23	CX	76	A
25	DA	10	G
25	DA	12	U
25	DA	15	G
25	DA	34	C
25	DA	35	G
25	DA	36	G
25	DA	45	C
25	DA	51	G
25	DA	55	G
25	DA	61	G
25	DA	71	A
25	DA	74	A
25	DA	75	G
25	DA	79	G
25	DA	83	G

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Mol	Chain	Res	Type
25	DA	84	A
25	DA	90	U
25	DA	94	C
25	DA	95	G
25	DA	100	G
25	DA	102	G
25	DA	118	A
25	DA	119	A
25	DA	120	U
25	DA	125	G
25	DA	139	G
25	DA	141	A
25	DA	149	A
25	DA	154(A)	C
25	DA	157	U
25	DA	173	G
25	DA	181	A
25	DA	182	A
25	DA	196	A
25	DA	199	A
25	DA	205	G
25	DA	214	G
25	DA	215	G
25	DA	216	A
25	DA	221	A
25	DA	222	A
25	DA	228	A
25	DA	229	A
25	DA	233	A
25	DA	248	G
25	DA	250	G
25	DA	271(E)	U
25	DA	271(I)	G
25	DA	271(K)	U
25	DA	271(L)	U
25	DA	271(M)	G
25	DA	271(N)	U
25	DA	271(O)	C
25	DA	272	G
25	DA	272(A)	U
25	DA	272(B)	G
25	DA	277	C

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Mol	Chain	Res	Type
25	DA	278	A
25	DA	292	C
25	DA	294	A
25	DA	311	A
25	DA	324	A
25	DA	327	G
25	DA	329	G
25	DA	330	A
25	DA	332	A
25	DA	333	G
25	DA	338	G
25	DA	345	A
25	DA	346	A
25	DA	352	G
25	DA	362	U
25	DA	363	G
25	DA	370	G
25	DA	372	G
25	DA	386	G
25	DA	396	G
25	DA	399	G
25	DA	405	U
25	DA	407	G
25	DA	411	G
25	DA	412	A
25	DA	415	A
25	DA	422	A
25	DA	428	A
25	DA	444	C
25	DA	455	C
25	DA	456	C
25	DA	457	A
25	DA	470	A
25	DA	481	G
25	DA	501	A
25	DA	504	U
25	DA	505	A
25	DA	509	C
25	DA	530	G
25	DA	531	C
25	DA	532	A
25	DA	533	G

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Mol	Chain	Res	Type
25	DA	545	G
25	DA	563	G
25	DA	573	G
25	DA	575	A
25	DA	587	C
25	DA	588	U
25	DA	603	A
25	DA	604	G
25	DA	607	U
25	DA	614(B)	G
25	DA	615	G
25	DA	621	A
25	DA	622	G
25	DA	627	A
25	DA	637	A
25	DA	645	C
25	DA	646	A
25	DA	647	G
25	DA	652(B)	A
25	DA	652(C)	G
25	DA	669	G
25	DA	686	G
25	DA	701	G
25	DA	715	G
25	DA	717	G
25	DA	726	G
25	DA	730	C
25	DA	744	G
25	DA	752	A
25	DA	753	C
25	DA	764	A
25	DA	765	G
25	DA	771	G
25	DA	775	G
25	DA	776	G
25	DA	779	U
25	DA	782	A
25	DA	784	A
25	DA	785	G
25	DA	790	C
25	DA	792	G
25	DA	805	G

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Mol	Chain	Res	Type
25	DA	812	C
25	DA	819	A
25	DA	827	U
25	DA	828	U
25	DA	832	G
25	DA	848	G
25	DA	857	C
25	DA	859	G
25	DA	866	A
25	DA	867	C
25	DA	874	G
25	DA	879	G
25	DA	880	G
25	DA	881	G
25	DA	882	G
25	DA	883	G
25	DA	884	C
25	DA	886	C
25	DA	887	A
25	DA	888	C
25	DA	889	C
25	DA	890	A
25	DA	893	C
25	DA	895	U
25	DA	896	A
25	DA	897	C
25	DA	898	C
25	DA	899	A
25	DA	900	A
25	DA	901	A
25	DA	910	A
25	DA	917	A
25	DA	923	C
25	DA	932	G
25	DA	933	A
25	DA	938	G
25	DA	941	A
25	DA	944	G
25	DA	945	A
25	DA	946	G
25	DA	953	A
25	DA	959	A

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Mol	Chain	Res	Type
25	DA	961	C
25	DA	963	U
25	DA	974	G
25	DA	975	C
25	DA	983	A
25	DA	996	A
25	DA	1005	C
25	DA	1006	C
25	DA	1012	U
25	DA	1013	C
25	DA	1017	G
25	DA	1018	C
25	DA	1020	A
25	DA	1022	G
25	DA	1026	U
25	DA	1027	A
25	DA	1031	G
25	DA	1033	U
25	DA	1038	C
25	DA	1041	C
25	DA	1042	G
25	DA	1043	C
25	DA	1118	C
25	DA	1130	U
25	DA	1135	C
25	DA	1136	G
25	DA	1139	G
25	DA	1166	C
25	DA	1171	G
25	DA	1205	U
25	DA	1210	A
25	DA	1211	U
25	DA	1212	G
25	DA	1219	G
25	DA	1229	G
25	DA	1233	C
25	DA	1253	A
25	DA	1256	G
25	DA	1271	G
25	DA	1272	A
25	DA	1273	U
25	DA	1300	U

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Mol	Chain	Res	Type
25	DA	1301	A
25	DA	1312	U
25	DA	1314	C
25	DA	1321	A
25	DA	1352	U
25	DA	1359	A
25	DA	1360	A
25	DA	1365	A
25	DA	1368	G
25	DA	1370	C
25	DA	1373	A
25	DA	1379	A
25	DA	1384	A
25	DA	1385	G
25	DA	1391	U
25	DA	1393	A
25	DA	1400	G
25	DA	1416	G
25	DA	1417	C
25	DA	1419	A
25	DA	1420	U
25	DA	1421	G
25	DA	1427	A
25	DA	1428	C
25	DA	1435	G
25	DA	1437	C
25	DA	1445	A
25	DA	1449	A
25	DA	1450	G
25	DA	1455	G
25	DA	1459	G
25	DA	1460	A
25	DA	1467	C
25	DA	1471	A
25	DA	1478	G
25	DA	1482	G
25	DA	1492	G
25	DA	1493	C
25	DA	1494	A
25	DA	1496	A
25	DA	1497	U
25	DA	1508	A

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Mol	Chain	Res	Type
25	DA	1509	C
25	DA	1509(A)	A
25	DA	1524	G
25	DA	1528(A)	A
25	DA	1531	C
25	DA	1541	G
25	DA	1542	A
25	DA	1543	C
25	DA	1547	C
25	DA	1554	A
25	DA	1558	A
25	DA	1559	G
25	DA	1566	A
25	DA	1569	A
25	DA	1578	U
25	DA	1583	A
25	DA	1584	C
25	DA	1586	A
25	DA	1598	C
25	DA	1608	A
25	DA	1609	A
25	DA	1610	A
25	DA	1616	A
25	DA	1640	C
25	DA	1648	C
25	DA	1654	A
25	DA	1669	A
25	DA	1674	G
25	DA	1696	G
25	DA	1700	A
25	DA	1701	A
25	DA	1703	G
25	DA	1721	G
25	DA	1722	A
25	DA	1743	C
25	DA	1746	G
25	DA	1756	G
25	DA	1762	A
25	DA	1763	G
25	DA	1764	G
25	DA	1773	A
25	DA	1780	A

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Mol	Chain	Res	Type
25	DA	1791	A
25	DA	1800	C
25	DA	1801	G
25	DA	1812	A
25	DA	1816	G
25	DA	1828	G
25	DA	1835	G
25	DA	1847	A
25	DA	1848	A
25	DA	1852	C
25	DA	1877	A
25	DA	1900	A
25	DA	1906	G
25	DA	1913	A
25	DA	1914	C
25	DA	1929	G
25	DA	1930	G
25	DA	1936	A
25	DA	1938	A
25	DA	1955	U
25	DA	1963	U
25	DA	1964	G
25	DA	1967	C
25	DA	1970	A
25	DA	1971	A
25	DA	1972	A
25	DA	1981	A
25	DA	1984	G
25	DA	1993	U
25	DA	1997	G
25	DA	2020	A
25	DA	2023	G
25	DA	2031	A
25	DA	2033	A
25	DA	2043	C
25	DA	2046	G
25	DA	2055	C
25	DA	2056	G
25	DA	2060	A
25	DA	2061	G
25	DA	2062	A
25	DA	2069	G

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Mol	Chain	Res	Type
25	DA	2099	U
25	DA	2102	U
25	DA	2105	C
25	DA	2108	C
25	DA	2109	U
25	DA	2110	G
25	DA	2111	C
25	DA	2112	G
25	DA	2115	G
25	DA	2116	G
25	DA	2119	A
25	DA	2122	U
25	DA	2125	G
25	DA	2126	A
25	DA	2127	G
25	DA	2129	C
25	DA	2131	G
25	DA	2132	U
25	DA	2133	G
25	DA	2135	A
25	DA	2136	C
25	DA	2137	C
25	DA	2138	C
25	DA	2140	C
25	DA	2142	C
25	DA	2146	C
25	DA	2148	G
25	DA	2150	U
25	DA	2151	G
25	DA	2153	G
25	DA	2154	G
25	DA	2155	G
25	DA	2157	G
25	DA	2158	A
25	DA	2159	G
25	DA	2163	C
25	DA	2164	C
25	DA	2165	G
25	DA	2166	G
25	DA	2167	U
25	DA	2168	G
25	DA	2169	A

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Mol	Chain	Res	Type
25	DA	2170	A
25	DA	2172	U
25	DA	2173	A
25	DA	2176	A
25	DA	2178	C
25	DA	2181	G
25	DA	2182	G
25	DA	2185	C
25	DA	2186	G
25	DA	2188	C
25	DA	2189	U
25	DA	2192	G
25	DA	2198	A
25	DA	2206	G
25	DA	2207	G
25	DA	2208	A
25	DA	2218	U
25	DA	2219	G
25	DA	2225	A
25	DA	2238	G
25	DA	2239	G
25	DA	2268	A
25	DA	2275	C
25	DA	2279	G
25	DA	2283	C
25	DA	2287	A
25	DA	2288	A
25	DA	2305	A
25	DA	2308	G
25	DA	2309	A
25	DA	2312	U
25	DA	2319	G
25	DA	2320	A
25	DA	2325	G
25	DA	2328	A
25	DA	2336	A
25	DA	2343	C
25	DA	2347	C
25	DA	2350	C
25	DA	2376	A
25	DA	2383	G
25	DA	2385	C

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Mol	Chain	Res	Type
25	DA	2388	A
25	DA	2400	G
25	DA	2402	C
25	DA	2406	U
25	DA	2410	G
25	DA	2417	C
25	DA	2419	U
25	DA	2422	A
25	DA	2423	U
25	DA	2425	A
25	DA	2429	G
25	DA	2430	A
25	DA	2432	A
25	DA	2435	A
25	DA	2439	A
25	DA	2441	C
25	DA	2442	C
25	DA	2445	G
25	DA	2448	A
25	DA	2458	G
25	DA	2465	C
25	DA	2474	C
25	DA	2476	A
25	DA	2490	G
25	DA	2492	U
25	DA	2502	G
25	DA	2505	G
25	DA	2518	A
25	DA	2520	C
25	DA	2529	G
25	DA	2554	U
25	DA	2555	U
25	DA	2566	A
25	DA	2567	G
25	DA	2573	C
25	DA	2582	G
25	DA	2592	G
25	DA	2602	A
25	DA	2609	U
25	DA	2611	U
25	DA	2612	C
25	DA	2615	U

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Mol	Chain	Res	Type
25	DA	2629	A
25	DA	2630	G
25	DA	2654	A
25	DA	2663	G
25	DA	2668	G
25	DA	2669	G
25	DA	2689	U
25	DA	2690	C
25	DA	2691	C
25	DA	2702	U
25	DA	2703	C
25	DA	2712(A)	A
25	DA	2713	A
25	DA	2714	G
25	DA	2726	U
25	DA	2733	A
25	DA	2739	U
25	DA	2751	G
25	DA	2757	A
25	DA	2758	A
25	DA	2764	A
25	DA	2765	A
25	DA	2766	G
25	DA	2778	A
25	DA	2793	G
25	DA	2794	C
25	DA	2802	G
25	DA	2809	A
25	DA	2818	G
25	DA	2820	A
25	DA	2821	A
25	DA	2833	G
25	DA	2834	G
25	DA	2835	A
25	DA	2861	G
25	DA	2866	U
25	DA	2872	G
25	DA	2875	C
25	DA	2879	C
25	DA	2880	C
25	DA	2886	G
25	DA	2892	A

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Mol	Chain	Res	Type
25	DA	2894	G
25	DA	2895	U
25	DA	2896	C
25	DA	2897	U
26	DB	2	C
26	DB	3	C
26	DB	5	C
26	DB	7	G
26	DB	8	U
26	DB	13	A
26	DB	22	U
26	DB	24	G
26	DB	25	A
26	DB	28	C
26	DB	32	C
26	DB	34	U
26	DB	42	C
26	DB	44	G
26	DB	50	G
26	DB	56	G
26	DB	60	C
26	DB	73	A
26	DB	75	G
26	DB	85	G
26	DB	106	G
26	DB	110	G
26	DB	117	G
26	DB	118	G
26	DB	119	G

All (116) RNA pucker outliers are listed below:

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

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Mol	Chain	Res	Type
1	AA	793	U
1	AA	840	C
1	AA	913	A
1	AA	991	U
1	AA	1026	G
1	AA	1064	G
1	AA	1065	U
1	AA	1183	A
1	AA	1201	A
1	AA	1211	U
1	AA	1281	U
1	AA	1285	A
1	AA	1299	A
1	AA	1442	G
1	AA	1446	U
1	AA	1492	A
1	AA	1493	A
25	BA	185	A
25	BA	270	C
25	BA	302	A
25	BA	793	A
25	BA	874	U
25	BA	1019	G
25	BA	1093	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1255	A
25	BA	1286	U
25	BA	1425	A
25	BA	1466	U
25	BA	1577	C
25	BA	1654	A
25	BA	1700	G
25	BA	1710	C
25	BA	2014	G
25	BA	2132	G
25	BA	2156	A
25	BA	2164	C
25	BA	2203	G
25	BA	2205	C
25	BA	2209	G

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Mol	Chain	Res	Type
25	BA	2418	U
25	BA	2442	A
25	BA	2623	U
25	BA	2701	U
25	BA	2769	U
25	BA	2902	G
1	CA	60	A
1	CA	65	U
1	CA	115	G
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	687	A
1	CA	748	C
1	CA	793	U
1	CA	840	C
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1005	A
1	CA	1064	G
1	CA	1065	U
1	CA	1128	C
1	CA	1129	C
1	CA	1183	A
1	CA	1201	A
1	CA	1211	U
1	CA	1212	U
1	CA	1256	A
1	CA	1279	A
1	CA	1281	U
1	CA	1442	G
1	CA	1446	U
1	CA	1492	A
1	CA	1493	A
1	CA	1531	A
25	DA	195	A
25	DA	249	C
25	DA	271(K)	U
25	DA	277	C

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Mol	Chain	Res	Type
25	DA	530	G
25	DA	587	C
25	DA	646	A
25	DA	752	A
25	DA	774	A
25	DA	827	U
25	DA	856	C
25	DA	900	A
25	DA	1026	U
25	DA	1210	A
25	DA	1420	U
25	DA	1530	C
25	DA	1558	A
25	DA	1653	G
25	DA	1913	A
25	DA	1992	G
25	DA	2110	G
25	DA	2126	A
25	DA	2134	A
25	DA	2156	G
25	DA	2406	U
25	DA	2689	U
25	DA	2756	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

8 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	5MU	AX	54	23	15,22,23	1.11	2 (13%)	16,32,35	2.39	2 (12%)
23	PSU	CX	55	23	17,21,22	1.53	2 (11%)	20,30,33	3.21	6 (30%)
23	5MC	AX	32	23	15,22,23	1.38	1 (6%)	19,32,35	1.53	4 (21%)
23	4SU	CX	8	23	14,21,22	1.16	2 (14%)	15,30,33	2.77	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	5MU	CX	54	23	15,22,23	1.12	2 (13%)	16,32,35	2.03	2 (12%)
23	PSU	AX	55	23	17,21,22	1.72	3 (17%)	20,30,33	3.25	6 (30%)
23	4SU	AX	8	23	14,21,22	1.49	2 (14%)	15,30,33	2.76	2 (13%)
23	5MC	CX	32	23	15,22,23	1.24	1 (6%)	19,32,35	1.39	3 (15%)

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	5MU	AX	54	23	-	0/5/25/26	0/2/2/2
23	PSU	CX	55	23	-	0/7/25/26	0/2/2/2
23	5MC	AX	32	23	-	0/5/25/26	0/2/2/2
23	4SU	CX	8	23	-	0/5/25/26	0/2/2/2
23	5MU	CX	54	23	-	0/5/25/26	0/2/2/2
23	PSU	AX	55	23	-	0/7/25/26	0/2/2/2
23	4SU	AX	8	23	-	0/5/25/26	0/2/2/2
23	5MC	CX	32	23	-	0/5/25/26	0/2/2/2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AX	55	PSU	C5-C1'	-5.21	1.47	1.52
23	AX	32	5MC	C5-C4	4.91	1.49	1.41
23	CX	32	5MC	C5-C4	4.41	1.48	1.41
23	AX	8	4SU	C4-S4	-4.15	1.59	1.67
23	CX	55	PSU	C5-C1'	-4.13	1.48	1.52
23	CX	54	5MU	C4-C5	3.48	1.48	1.41
23	AX	8	4SU	C2-N3	-3.39	1.31	1.38
23	CX	55	PSU	C4-C5	3.39	1.48	1.41
23	CX	8	4SU	C4-S4	-3.36	1.61	1.67
23	AX	54	5MU	C4-C5	3.33	1.48	1.41
23	AX	55	PSU	C4-C5	3.01	1.47	1.41
23	CX	8	4SU	C2-N3	-2.34	1.33	1.38
23	AX	54	5MU	C2-N3	-2.31	1.33	1.38
23	AX	55	PSU	O4'-C1'	-2.16	1.41	1.44
23	CX	54	5MU	C2-N3	-2.15	1.33	1.38

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AX	8	4SU	C2-N3-C4	9.61	129.08	115.15
23	CX	8	4SU	C2-N3-C4	9.00	128.20	115.15
23	AX	54	5MU	C4-N3-C2	9.00	122.74	115.14
23	CX	55	PSU	N1-C2-N3	-8.55	121.63	128.43
23	AX	55	PSU	N1-C2-N3	-8.49	121.68	128.43
23	CX	54	5MU	C4-N3-C2	7.26	121.27	115.14
23	CX	55	PSU	C4-N3-C2	6.85	120.93	115.14
23	AX	55	PSU	C4-N3-C2	6.81	120.89	115.14
23	AX	55	PSU	C5-C4-N3	-5.72	117.99	125.36
23	CX	55	PSU	C5-C4-N3	-5.38	118.42	125.36
23	CX	8	4SU	C5-C4-N3	-5.13	116.97	123.83
23	CX	55	PSU	C5-C6-N1	-4.49	118.92	124.44
23	AX	55	PSU	C5-C6-N1	-4.31	119.14	124.44
23	AX	8	4SU	C5-C4-N3	-4.20	118.22	123.83
23	CX	55	PSU	C6-N1-C2	4.08	122.09	115.36
23	AX	55	PSU	C6-N1-C2	4.05	122.04	115.36
23	AX	55	PSU	C5-C1'-C2'	-3.89	108.39	115.32
23	CX	32	5MC	C2-N3-C4	3.41	120.14	116.02
23	AX	32	5MC	C5-C6-N1	-3.22	118.72	122.19
23	AX	32	5MC	C2-N3-C4	3.19	119.87	116.02
23	CX	32	5MC	N4-C4-N3	2.96	121.22	117.03
23	CX	55	PSU	C5-C1'-C2'	-2.90	110.15	115.32
23	CX	54	5MU	C5-C6-N1	-2.56	119.43	122.19
23	AX	32	5MC	CM5-C5-C4	-2.45	119.24	121.72
23	CX	32	5MC	C5-C6-N1	-2.38	119.63	122.19
23	AX	54	5MU	C5-C6-N1	-2.33	119.69	122.19
23	AX	32	5MC	N4-C4-N3	2.18	120.11	117.03
23	CX	8	4SU	C6-N1-C2	-2.04	117.96	121.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	AX	32	5MC	1	0
23	CX	8	4SU	1	0
23	CX	54	5MU	1	0
23	AX	8	4SU	1	0
23	CX	32	5MC	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2061 ligands modelled in this entry, 2057 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	SF4	CD	501	4	0,12,12	0.00	-	-		
57	PCY	AA	3191	-	36,42,42	1.85	5 (13%)	41,65,65	1.52	8 (19%)
57	PCY	CA	3176	-	36,42,42	1.68	5 (13%)	41,65,65	0.96	3 (7%)
58	SF4	AD	501	4	0,12,12	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	CD	501	4	-	-	0/6/5/5
57	PCY	AA	3191	-	-	18/33/67/67	0/3/3/3
57	PCY	CA	3176	-	-	7/33/67/67	0/3/3/3
58	SF4	AD	501	4	-	-	0/6/5/5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	AA	3191	PCY	C34-C30	-5.67	1.39	1.51
57	AA	3191	PCY	C28-C32	-5.48	1.39	1.49
57	CA	3176	PCY	C34-C30	-5.38	1.40	1.51
57	CA	3176	PCY	C28-C32	-4.82	1.40	1.49
57	AA	3191	PCY	C17-N20	4.68	1.51	1.45
57	CA	3176	PCY	C27-C23	-4.53	1.39	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	AA	3191	PCY	C27-C23	-4.11	1.40	1.50
57	CA	3176	PCY	C22-N20	-2.80	1.34	1.39
57	CA	3176	PCY	C17-N20	2.75	1.48	1.45
57	AA	3191	PCY	C22-N20	-2.75	1.34	1.39

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	AA	3191	PCY	O21-C18-C15	4.06	115.29	107.79
57	AA	3191	PCY	O21-C23-C27	4.01	121.35	112.33
57	AA	3191	PCY	C18-O21-C23	-2.79	110.93	116.57
57	CA	3176	PCY	C10-N4-C9	2.46	123.39	115.77
57	AA	3191	PCY	C30-C27-C23	2.43	127.43	120.47
57	AA	3191	PCY	C10-N4-C9	2.42	123.27	115.77
57	AA	3191	PCY	C22-N20-C17	2.36	128.18	123.11
57	CA	3176	PCY	C18-O21-C23	-2.31	111.90	116.57
57	AA	3191	PCY	O36-C31-C27	-2.28	116.88	121.14
57	CA	3176	PCY	O36-C31-C27	-2.21	117.01	121.14
57	AA	3191	PCY	C34-C30-C35	-2.01	116.38	120.31

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	AA	3191	PCY	N2-C3-C6-C11
57	AA	3191	PCY	N2-C3-C6-O12
57	AA	3191	PCY	C7-C3-C6-C11
57	AA	3191	PCY	C7-C3-C6-O12
57	AA	3191	PCY	C8-C3-C6-C11
57	AA	3191	PCY	C8-C3-C6-O12
57	AA	3191	PCY	C7-C15-C18-O21
57	AA	3191	PCY	C17-C15-C18-O21
57	AA	3191	PCY	O19-C15-C18-O21
57	AA	3191	PCY	C8-C17-N20-C22
57	CA	3176	PCY	O26-C23-O21-C18
57	CA	3176	PCY	C27-C23-O21-C18
57	AA	3191	PCY	C24-C22-N20-C17
57	CA	3176	PCY	C24-C28-C32-C38
57	CA	3176	PCY	C24-C28-C32-O39
57	AA	3191	PCY	C25-C22-N20-C17
57	CA	3176	PCY	C33-C28-C32-O39
57	AA	3191	PCY	C24-C28-C32-O39

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Mol	Chain	Res	Type	Atoms
57	CA	3176	PCY	C33-C28-C32-C38
57	AA	3191	PCY	C33-C28-C32-O39
57	AA	3191	PCY	C33-C28-C32-C38
57	AA	3191	PCY	C24-C28-C32-C38
57	CA	3176	PCY	C8-C17-N20-C22
57	AA	3191	PCY	O26-C23-C27-C30
57	AA	3191	PCY	O21-C23-C27-C30

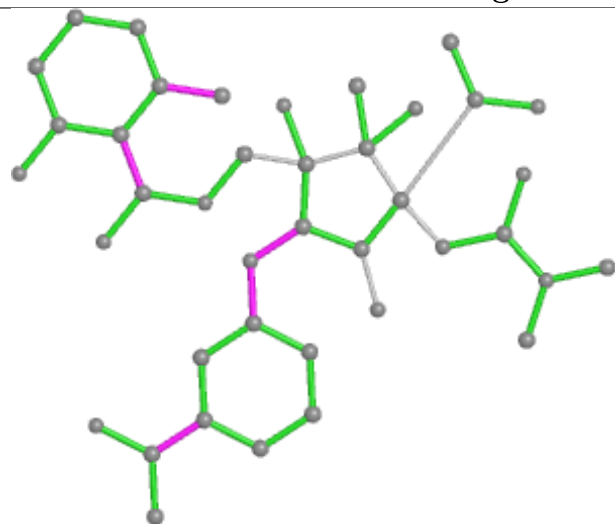
There are no ring outliers.

3 monomers are involved in 11 short contacts:

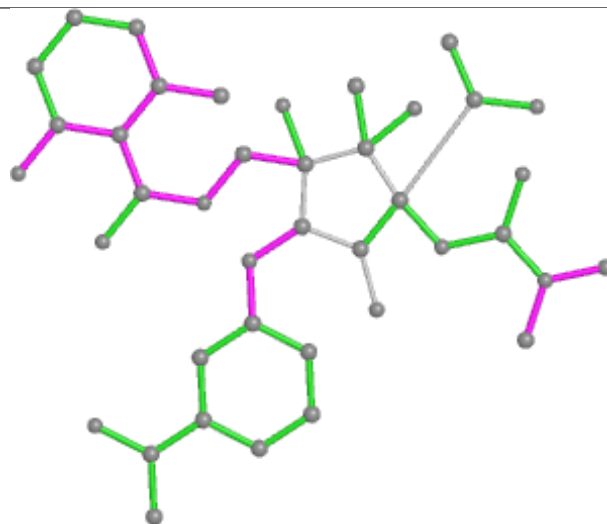
Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	AA	3191	PCY	6	0
57	CA	3176	PCY	4	0
58	AD	501	SF4	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

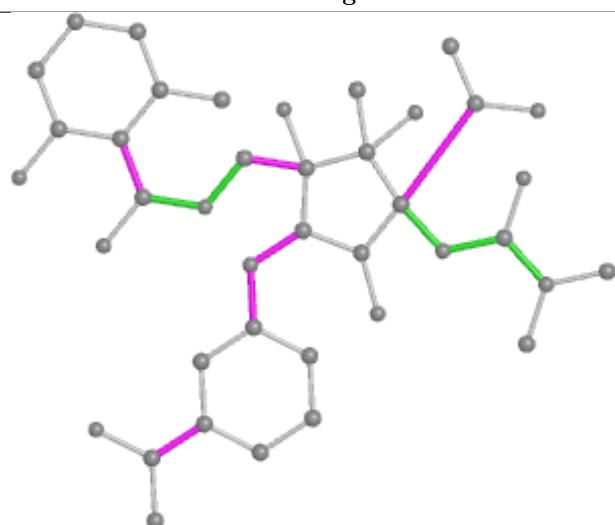
Ligand PCY AA 3191



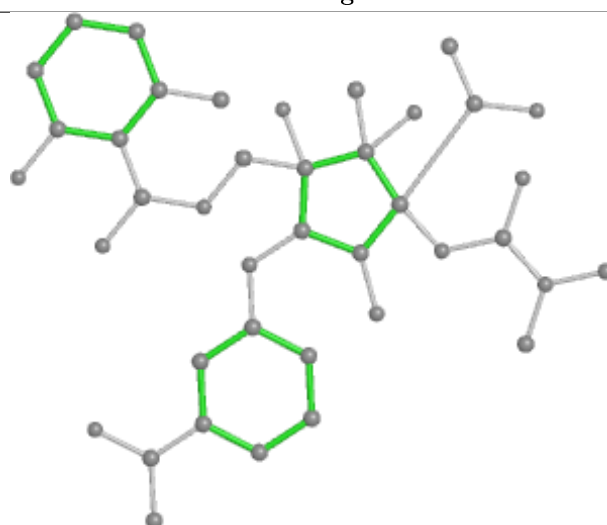
Bond lengths



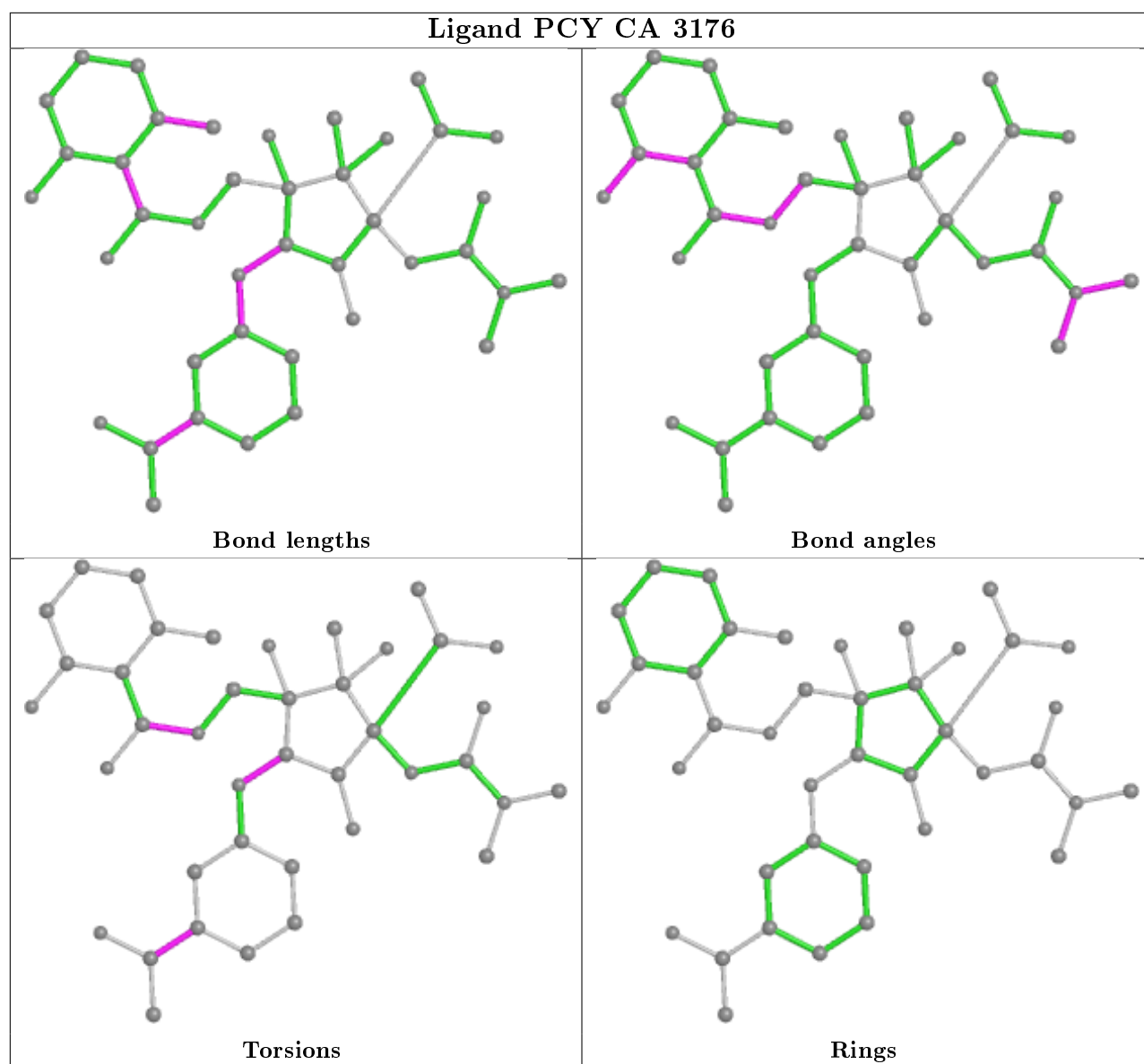
Bond angles



Torsions



Rings



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1497/1521 (98%)	0.03	13 (0%) 84 85	40, 76, 97, 113	0
1	CA	1503/1521 (98%)	0.02	29 (1%) 66 69	42, 77, 97, 113	0
2	AB	231/256 (90%)	0.30	11 (4%) 30 28	71, 85, 93, 98	0
2	CB	231/256 (90%)	1.18	58 (25%) 0 0	71, 86, 94, 98	0
3	AC	206/239 (86%)	1.02	40 (19%) 1 0	69, 83, 91, 95	0
3	CC	206/239 (86%)	1.33	59 (28%) 0 0	69, 84, 92, 96	0
4	AD	208/209 (99%)	1.16	46 (22%) 0 0	60, 76, 86, 91	0
4	CD	208/209 (99%)	0.97	26 (12%) 3 3	60, 76, 84, 89	0
5	AE	148/162 (91%)	0.91	13 (8%) 10 8	56, 72, 81, 88	0
5	CE	148/162 (91%)	1.23	36 (24%) 0 0	58, 74, 83, 89	0
6	AF	100/101 (99%)	0.66	9 (9%) 9 7	61, 74, 82, 85	0
6	CF	100/101 (99%)	0.46	7 (7%) 16 14	62, 75, 83, 86	0
7	AG	155/156 (99%)	1.09	27 (17%) 1 1	69, 79, 89, 98	0
7	CG	155/156 (99%)	1.30	38 (24%) 0 0	70, 80, 90, 99	0
8	AH	137/138 (99%)	0.85	19 (13%) 2 2	61, 74, 81, 85	0
8	CH	137/138 (99%)	0.92	21 (15%) 2 1	63, 75, 83, 88	0
9	AI	127/128 (99%)	1.11	26 (20%) 1 0	63, 85, 91, 94	0
9	CI	127/128 (99%)	2.24	65 (51%) 0 0	70, 86, 92, 96	0
10	AJ	97/105 (92%)	1.18	25 (25%) 0 0	73, 87, 94, 97	0
10	CJ	96/105 (91%)	1.95	42 (43%) 0 0	76, 89, 95, 96	0
11	AK	114/129 (88%)	0.57	5 (4%) 34 33	52, 72, 84, 87	0
11	CK	114/129 (88%)	0.38	5 (4%) 34 33	54, 74, 84, 87	0
12	AL	122/132 (92%)	0.64	17 (13%) 2 2	52, 67, 77, 81	0
12	CL	122/132 (92%)	1.19	25 (20%) 1 0	53, 67, 76, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	120/126 (95%)	0.86	15 (12%) 3 3	53, 75, 85, 93	0
13	CM	118/126 (93%)	1.60	39 (33%) 0 0	71, 88, 94, 98	0
14	AN	60/61 (98%)	1.81	26 (43%) 0 0	74, 80, 88, 90	0
14	CN	60/61 (98%)	3.46	44 (73%) 0 0	75, 83, 88, 92	0
15	AO	88/89 (98%)	0.76	7 (7%) 12 10	55, 69, 81, 85	0
15	CO	88/89 (98%)	1.06	14 (15%) 1 1	58, 71, 82, 86	0
16	AP	82/88 (93%)	1.25	19 (23%) 0 0	64, 75, 84, 91	0
16	CP	82/88 (93%)	1.06	13 (15%) 1 1	63, 73, 83, 89	0
17	AQ	99/105 (94%)	0.76	7 (7%) 16 14	55, 70, 79, 81	0
17	CQ	99/105 (94%)	1.57	35 (35%) 0 0	58, 71, 80, 84	0
18	AR	68/88 (77%)	0.59	5 (7%) 14 12	62, 74, 84, 89	0
18	CR	68/88 (77%)	0.63	5 (7%) 14 12	64, 74, 84, 91	0
19	AS	83/93 (89%)	0.85	6 (7%) 15 13	75, 85, 93, 94	0
19	CS	83/93 (89%)	1.94	39 (46%) 0 0	78, 87, 93, 96	0
20	AT	96/106 (90%)	0.60	5 (5%) 27 25	63, 72, 82, 87	0
20	CT	96/106 (90%)	0.66	13 (13%) 3 2	61, 73, 82, 87	0
21	AU	23/27 (85%)	1.10	4 (17%) 1 1	71, 77, 79, 81	0
21	CU	23/27 (85%)	2.26	11 (47%) 0 0	72, 79, 81, 83	0
22	AV	8/24 (33%)	3.57	5 (62%) 0 0	62, 89, 94, 97	0
22	CV	5/24 (20%)	2.64	3 (60%) 0 0	65, 73, 91, 96	0
23	AX	72/77 (93%)	0.18	1 (1%) 75 77	40, 71, 88, 98	0
23	CX	72/77 (93%)	0.12	3 (4%) 36 35	43, 74, 90, 97	0
24	AY	18/76 (23%)	3.72	13 (72%) 0 0	62, 104, 109, 109	0
24	CY	5/76 (6%)	5.80	5 (100%) 0 0	74, 101, 102, 106	0
25	BA	2822/2915 (96%)	0.54	51 (1%) 68 70	18, 41, 91, 109	0
25	DA	2800/2915 (96%)	-0.04	52 (1%) 66 69	22, 45, 91, 112	0
26	BB	120/121 (99%)	0.36	0 100 100	31, 63, 75, 88	0
26	DB	120/121 (99%)	-0.03	7 (5%) 23 22	38, 69, 81, 91	0
27	BD	275/276 (99%)	0.74	10 (3%) 42 42	20, 39, 58, 77	0
27	DD	275/276 (99%)	0.70	19 (6%) 16 15	22, 42, 60, 78	0
28	BE	204/206 (99%)	0.63	1 (0%) 91 92	19, 44, 64, 86	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DE	204/206 (99%)	0.51	8 (3%) 39 38	22, 48, 66, 86	0
29	BF	203/210 (96%)	0.61	2 (0%) 82 83	21, 50, 74, 91	0
29	DF	203/210 (96%)	0.45	5 (2%) 57 59	24, 55, 77, 90	0
30	BG	181/182 (99%)	0.58	6 (3%) 46 46	55, 71, 83, 96	0
30	DG	181/182 (99%)	1.48	57 (31%) 0 0	60, 75, 84, 95	0
31	BH	174/180 (96%)	0.52	1 (0%) 89 91	45, 64, 75, 84	0
31	DH	174/180 (96%)	0.85	29 (16%) 1 1	53, 68, 79, 86	0
32	BI	146/148 (98%)	0.33	4 (2%) 54 55	48, 75, 84, 88	0
32	DI	146/148 (98%)	0.33	11 (7%) 14 12	51, 75, 84, 88	0
33	BN	140/140 (100%)	0.67	0 100 100	28, 45, 69, 79	0
33	DN	140/140 (100%)	0.50	3 (2%) 63 65	33, 49, 71, 81	0
34	BO	122/122 (100%)	0.64	3 (2%) 57 59	31, 45, 63, 70	0
34	DO	122/122 (100%)	0.56	7 (5%) 23 22	34, 48, 64, 70	0
35	BP	149/150 (99%)	0.62	1 (0%) 87 89	18, 53, 74, 82	0
35	DP	149/150 (99%)	0.60	9 (6%) 21 20	20, 56, 76, 84	0
36	BQ	141/141 (100%)	0.69	2 (1%) 75 77	29, 48, 65, 77	0
36	DQ	141/141 (100%)	1.06	22 (15%) 2 1	32, 52, 69, 78	0
37	BR	118/118 (100%)	0.46	0 100 100	19, 32, 49, 62	0
37	DR	118/118 (100%)	0.94	12 (10%) 6 5	35, 53, 66, 78	0
38	BS	110/112 (98%)	0.32	0 100 100	30, 47, 65, 70	0
38	DS	110/112 (98%)	1.20	22 (20%) 1 0	63, 77, 88, 93	0
39	BT	131/146 (89%)	0.33	0 100 100	30, 43, 71, 85	0
39	DT	131/146 (89%)	0.51	6 (4%) 32 31	43, 59, 78, 88	0
40	BU	116/118 (98%)	0.38	0 100 100	15, 27, 48, 62	0
40	DU	116/118 (98%)	0.82	9 (7%) 13 11	38, 59, 76, 87	0
41	BV	101/101 (100%)	0.22	0 100 100	14, 35, 57, 76	0
41	DV	101/101 (100%)	0.44	3 (2%) 50 51	43, 71, 84, 90	0
42	BW	112/113 (99%)	0.35	0 100 100	17, 28, 50, 75	0
42	DW	112/113 (99%)	0.89	11 (9%) 7 5	34, 50, 68, 92	0
43	BX	95/96 (98%)	0.36	0 100 100	17, 35, 65, 78	0
43	DX	95/96 (98%)	1.61	31 (32%) 0 0	44, 62, 77, 90	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BY	107/110 (97%)	0.38	2 (1%) 66 69	28, 47, 67, 85	0
44	DY	107/110 (97%)	1.24	21 (19%) 1 0	51, 72, 83, 88	0
45	BZ	171/206 (83%)	0.25	1 (0%) 89 91	36, 62, 81, 90	0
45	DZ	174/206 (84%)	1.08	28 (16%) 1 1	66, 83, 93, 96	0
46	B0	83/85 (97%)	0.72	7 (8%) 11 9	12, 33, 66, 84	0
46	D0	83/85 (97%)	1.79	23 (27%) 0 0	34, 64, 78, 91	0
47	B1	97/98 (98%)	0.68	5 (5%) 27 25	19, 43, 69, 72	0
47	D1	97/98 (98%)	0.90	10 (10%) 6 5	37, 57, 78, 82	0
48	B2	70/72 (97%)	0.33	0 100 100	30, 46, 63, 77	0
48	D2	70/72 (97%)	0.53	2 (2%) 51 52	56, 71, 80, 85	0
49	B3	59/60 (98%)	0.28	0 100 100	20, 31, 56, 83	0
49	D3	59/60 (98%)	1.65	20 (33%) 0 0	47, 62, 77, 91	0
50	B4	69/71 (97%)	0.73	6 (8%) 10 8	55, 77, 92, 99	0
50	D4	69/71 (97%)	1.52	22 (31%) 0 0	77, 91, 99, 105	0
51	B5	59/60 (98%)	0.47	2 (3%) 45 45	11, 28, 53, 67	0
51	D5	59/60 (98%)	0.50	3 (5%) 28 26	27, 52, 68, 81	0
52	B6	53/54 (98%)	0.26	0 100 100	27, 39, 56, 67	0
52	D6	53/54 (98%)	0.32	2 (3%) 40 39	45, 62, 73, 79	0
53	B7	48/49 (97%)	0.79	5 (10%) 6 4	16, 23, 52, 68	0
53	D7	48/49 (97%)	1.02	6 (12%) 3 3	29, 40, 64, 77	0
54	B8	64/65 (98%)	0.64	1 (1%) 72 74	24, 31, 43, 61	0
54	D8	64/65 (98%)	1.14	10 (15%) 2 1	44, 53, 63, 72	0
55	B9	37/37 (100%)	0.68	2 (5%) 25 24	28, 45, 67, 72	0
55	D9	37/37 (100%)	1.09	5 (13%) 3 2	44, 55, 68, 75	0
All	All	20640/21596 (95%)	0.56	1586 (7%) 13 11	11, 64, 91, 113	0

All (1586) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	CG	82	GLY	12.8
2	CB	165	VAL	10.4
1	CA	1030(B)	C	9.9
13	AM	2	ALA	9.8
10	CJ	47	PHE	9.7

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Mol	Chain	Res	Type	RSRZ
43	DX	92	LEU	9.4
14	CN	25	VAL	9.3
24	AY	1	G	8.6
46	B0	7	LEU	8.2
7	AG	85	TYR	8.1
22	AV	21	C	7.7
7	AG	82	GLY	7.7
14	CN	2	ALA	7.7
7	CG	79	ARG	7.6
24	CY	73	A	7.4
14	CN	29	ARG	7.2
24	CY	74	C	7.2
30	DG	139	LEU	7.2
7	CG	154	TYR	7.1
14	CN	39	LEU	7.1
46	D0	2	ALA	7.1
7	AG	79	ARG	7.1
14	CN	34	TYR	7.1
14	CN	35	ARG	7.1
13	CM	78	ILE	6.9
10	CJ	63	PHE	6.8
47	D1	2	SER	6.8
10	CJ	65	LEU	6.8
46	B0	4	LYS	6.8
24	CY	75	C	6.8
7	CG	84	ASN	6.7
22	AV	20	U	6.7
24	AY	6	G	6.7
14	CN	30	ALA	6.6
9	AI	19	LEU	6.6
46	B0	3	HIS	6.6
13	CM	120	LYS	6.5
19	CS	49	ILE	6.5
25	DA	2160	G	6.5
25	DA	2144	U	6.5
10	CJ	49	VAL	6.4
46	B0	5	LYS	6.4
14	CN	18	VAL	6.4
46	D0	5	LYS	6.3
10	AJ	8	LEU	6.3
9	CI	6	GLY	6.2
9	CI	15	ALA	6.2

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Mol	Chain	Res	Type	RSRZ
46	D0	7	LEU	6.1
7	AG	78	ARG	6.1
7	CG	16	LEU	6.1
9	CI	9	ARG	6.1
13	CM	7	VAL	6.1
25	DA	2111	C	6.1
19	CS	31	ILE	6.0
3	CC	57	ILE	6.0
25	DA	2147	G	6.0
25	BA	2200	C	6.0
7	AG	156	TRP	5.9
9	CI	36	TYR	5.9
31	DH	115	VAL	5.9
9	CI	115	GLY	5.9
46	D0	4	LYS	5.9
21	CU	14	TRP	5.8
25	BA	2154	U	5.8
7	CG	83	ALA	5.8
9	CI	76	ALA	5.8
7	CG	156	TRP	5.8
9	CI	123	PRO	5.7
14	CN	38	GLY	5.7
46	D0	6	GLY	5.7
46	D0	75	LEU	5.7
20	CT	9	ASN	5.7
24	AY	71	G	5.7
49	D3	60	GLU	5.7
21	CU	6	ARG	5.6
50	D4	45	GLY	5.6
7	CG	78	ARG	5.6
9	AI	47	LEU	5.6
10	CJ	67	THR	5.6
10	CJ	46	ARG	5.5
27	BD	276	LYS	5.5
3	CC	189	ALA	5.5
25	DA	2145	C	5.5
46	B0	6	GLY	5.5
45	DZ	146	ILE	5.5
9	CI	37	PHE	5.5
13	CM	102	ARG	5.5
25	BA	2168	C	5.5
22	CV	14	A	5.5

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Mol	Chain	Res	Type	RSRZ
24	AY	75	C	5.4
9	CI	125	TYR	5.4
30	DG	169	ALA	5.4
9	CI	106	ALA	5.4
19	CS	30	LEU	5.4
10	CJ	50	ILE	5.4
46	D0	3	HIS	5.4
50	D4	49	PHE	5.4
17	CQ	36	ILE	5.4
10	CJ	64	GLU	5.4
9	CI	114	TYR	5.4
13	AM	121	LYS	5.3
1	AA	1257	U	5.3
2	CB	232	PRO	5.3
44	DY	1	MET	5.3
9	CI	66	ARG	5.3
2	CB	70	PHE	5.2
24	AY	2	C	5.2
10	CJ	48	THR	5.2
7	AG	83	ALA	5.2
43	DX	91	ALA	5.2
10	AJ	47	PHE	5.2
14	CN	36	PHE	5.2
50	D4	44	THR	5.2
1	AA	1036	G	5.2
3	CC	159	GLY	5.2
19	AS	71	LEU	5.2
50	D4	40	HIS	5.2
2	CB	200	ILE	5.1
43	DX	69	TYR	5.1
9	CI	7	THR	5.1
45	DZ	144	LEU	5.1
1	CA	1257	U	5.1
7	AG	154	TYR	5.1
13	CM	66	LEU	5.1
13	AM	120	LYS	5.0
1	CA	1492	A	5.0
14	AN	7	ILE	5.0
25	DA	2146	C	5.0
4	AD	3	ARG	5.0
50	D4	56	VAL	5.0
30	DG	2	PRO	5.0

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Mol	Chain	Res	Type	RSRZ
14	CN	31	ARG	5.0
24	AY	5	G	5.0
4	AD	157	LEU	4.9
19	CS	33	THR	4.9
25	BA	2182	G	4.9
25	DA	2159	G	4.9
5	CE	94	ALA	4.9
14	CN	6	LEU	4.9
14	CN	58	LYS	4.9
25	BA	2165	C	4.8
43	DX	68	ARG	4.8
9	CI	33	PHE	4.8
44	DY	35	TYR	4.8
5	CE	12	LEU	4.8
7	CG	85	TYR	4.8
31	DH	112	PRO	4.7
13	CM	80	ARG	4.7
25	BA	2164	C	4.7
9	CI	109	VAL	4.7
7	CG	80	VAL	4.7
22	AV	14	A	4.7
5	CE	13	ILE	4.7
25	BA	2131	U	4.7
2	CB	152	PHE	4.6
25	BA	2167	C	4.6
31	DH	111	HIS	4.6
2	CB	92	TYR	4.6
3	AC	193	TYR	4.6
3	AC	201	TYR	4.6
43	DX	28	PHE	4.6
8	AH	2	LEU	4.6
5	CE	31	LEU	4.6
27	DD	38	LYS	4.6
9	CI	5	TYR	4.6
50	D4	50	VAL	4.6
22	AV	15	A	4.6
2	AB	165	VAL	4.6
9	CI	68	GLY	4.5
2	CB	83	MET	4.5
10	AJ	63	PHE	4.5
9	CI	65	VAL	4.5
2	CB	69	LEU	4.5

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Mol	Chain	Res	Type	RSRZ
30	DG	28	VAL	4.5
53	D7	48	LYS	4.5
10	CJ	66	ARG	4.5
14	CN	23	ARG	4.5
25	BA	2143	G	4.5
30	DG	137	GLU	4.5
14	CN	32	SER	4.5
13	CM	64	TRP	4.5
14	CN	53	LEU	4.5
49	D3	29	ARG	4.5
4	AD	180	GLY	4.5
2	CB	201	ILE	4.5
30	DG	39	ILE	4.5
1	AA	1030(B)	C	4.5
7	AG	80	VAL	4.5
53	D7	46	VAL	4.5
9	CI	110	GLU	4.4
3	CC	21	ARG	4.4
13	CM	92	HIS	4.4
4	CD	47	ARG	4.4
14	CN	41	ARG	4.4
3	CC	186	PHE	4.4
7	CG	2	ALA	4.4
4	AD	23	GLY	4.4
9	CI	67	GLY	4.4
14	CN	50	LYS	4.4
16	AP	68	ASP	4.4
25	BA	935	C	4.4
30	DG	3	LEU	4.4
30	DG	102	PHE	4.4
45	DZ	114	GLY	4.3
4	CD	120	LEU	4.3
55	D9	37	GLY	4.3
43	DX	9	LEU	4.3
30	DG	48	GLU	4.3
14	CN	59	ALA	4.3
25	BA	2151	C	4.3
19	CS	13	ASP	4.3
30	DG	29	TRP	4.3
5	CE	90	VAL	4.3
10	AJ	10	GLY	4.3
36	DQ	104	PHE	4.3

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Mol	Chain	Res	Type	RSRZ
1	CA	1202	G	4.3
9	CI	128	ARG	4.3
14	CN	47	LEU	4.3
1	CA	1036	G	4.3
9	CI	10	ARG	4.3
9	CI	79	LEU	4.3
14	AN	33	VAL	4.3
38	DS	29	PHE	4.3
2	CB	214	ILE	4.3
9	CI	127	LYS	4.2
4	AD	70	ILE	4.2
9	CI	83	ARG	4.2
14	CN	26	ARG	4.2
14	CN	56	VAL	4.2
42	DW	112	GLY	4.2
1	CA	1030(C)	G	4.2
25	BA	1555	C	4.2
47	D1	61	ARG	4.2
1	CA	1493	A	4.2
3	CC	184	TYR	4.2
50	D4	51	ASP	4.2
43	DX	89	ILE	4.2
17	CQ	37	LYS	4.2
50	D4	54	GLY	4.2
43	DX	86	GLY	4.2
30	DG	142	PRO	4.2
24	AY	74	C	4.2
30	DG	19	LEU	4.1
14	CN	37	PHE	4.1
27	DD	2	ALA	4.1
46	D0	45	PHE	4.1
5	CE	29	GLY	4.1
37	DR	68	ARG	4.1
24	AY	3	C	4.1
36	DQ	22	LYS	4.1
2	CB	118	LEU	4.1
30	DG	41	GLN	4.1
2	CB	163	PHE	4.1
50	B4	52	THR	4.1
3	CC	39	ILE	4.1
25	DA	2135	A	4.1
30	DG	27	ASN	4.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1030(A)	G	4.1
47	B1	98	LEU	4.1
12	CL	69	TYR	4.1
7	AG	91	VAL	4.1
50	D4	43	TYR	4.1
4	AD	112	VAL	4.1
38	DS	58	LEU	4.1
13	CM	6	GLY	4.1
7	CG	86	GLN	4.1
10	CJ	54	PHE	4.0
14	CN	44	LEU	4.0
19	CS	35	SER	4.0
24	AY	7	A	4.0
5	AE	89	ILE	4.0
10	AJ	50	ILE	4.0
14	AN	34	TYR	4.0
50	D4	52	THR	4.0
24	CY	72	C	4.0
13	CM	5	ALA	4.0
4	AD	174	LEU	4.0
19	CS	71	LEU	4.0
54	D8	2	PRO	4.0
21	CU	13	ILE	4.0
3	CC	155	GLY	3.9
10	CJ	71	LEU	3.9
50	D4	32	TYR	3.9
53	D7	1	MET	3.9
25	BA	2132	G	3.9
25	BA	2201	C	3.9
12	CL	32	PHE	3.9
11	CK	31	THR	3.9
28	DE	1	MET	3.9
10	AJ	66	ARG	3.9
10	CJ	40	LEU	3.9
48	D2	1	MET	3.9
30	DG	136	ARG	3.9
46	D0	76	GLY	3.9
2	CB	188	ALA	3.9
8	CH	93	VAL	3.9
16	CP	19	ILE	3.9
2	CB	123	ALA	3.9
7	CG	33	ASP	3.9

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Mol	Chain	Res	Type	RSRZ
7	AG	153	HIS	3.9
3	CC	167	TRP	3.9
21	CU	16	GLY	3.9
8	AH	4	ASP	3.9
2	CB	81	VAL	3.9
9	AI	126	SER	3.9
7	AG	76	ARG	3.9
10	CJ	60	ARG	3.9
44	DY	55	TYR	3.9
2	CB	228	GLY	3.9
12	CL	64	TYR	3.9
25	DA	896	A	3.9
36	DQ	5	ARG	3.8
42	DW	81	ALA	3.8
45	DZ	125	LEU	3.8
50	B4	54	GLY	3.8
8	CH	94	TYR	3.8
49	D3	26	LEU	3.8
2	CB	101	MET	3.8
1	CA	1532	U	3.8
30	BG	49	ASP	3.8
9	CI	126	SER	3.8
10	CJ	62	HIS	3.8
14	AN	59	ALA	3.8
38	DS	32	LEU	3.8
14	CN	22	THR	3.8
27	DD	276	LYS	3.8
19	CS	52	TYR	3.8
25	BA	2152	U	3.8
15	CO	87	ILE	3.8
19	AS	39	THR	3.8
9	AI	114	TYR	3.8
42	DW	92	ARG	3.8
14	CN	8	GLU	3.8
13	AM	97	PRO	3.8
7	CG	81	GLY	3.8
32	DI	35	LEU	3.8
7	AG	84	ASN	3.8
37	DR	47	PHE	3.8
9	AI	81	ILE	3.7
3	CC	198	VAL	3.7
46	D0	8	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
17	CQ	32	TYR	3.7
2	CB	177	ALA	3.7
19	AS	40	ILE	3.7
44	DY	45	VAL	3.7
4	AD	118	ARG	3.7
31	DH	105	LEU	3.7
45	DZ	155	LEU	3.7
17	CQ	87	LYS	3.7
25	BA	2155	G	3.7
30	DG	62	LEU	3.7
19	CS	40	ILE	3.7
22	CV	15	A	3.7
49	D3	15	TYR	3.7
31	DH	159	GLU	3.7
13	AM	96	LEU	3.7
12	CL	18	VAL	3.7
10	CJ	41	PRO	3.7
19	CS	38	SER	3.7
9	CI	42	ARG	3.7
1	CA	1026	G	3.7
7	CG	4	ARG	3.7
44	DY	61	ILE	3.7
3	CC	162	GLN	3.7
2	CB	122	PHE	3.6
9	CI	28	VAL	3.6
14	AN	32	SER	3.6
3	AC	126	ARG	3.6
2	CB	187	LEU	3.6
49	D3	53	LEU	3.6
25	BA	2153	G	3.6
7	CG	40	ALA	3.6
9	CI	4	TYR	3.6
9	CI	64	THR	3.6
7	AG	12	LEU	3.6
38	DS	35	ILE	3.6
13	CM	105	THR	3.6
16	AP	17	TYR	3.6
27	BD	275	LYS	3.6
2	AB	118	LEU	3.6
4	AD	120	LEU	3.6
37	DR	70	LEU	3.6
4	AD	179	GLU	3.6

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Mol	Chain	Res	Type	RSRZ
50	D4	35	VAL	3.6
14	CN	17	LYS	3.6
25	BA	2181	G	3.6
25	DA	2104	G	3.6
18	CR	43	PHE	3.6
24	CY	76	A	3.6
14	AN	17	LYS	3.6
25	DA	2140	C	3.6
8	CH	133	LEU	3.6
7	CG	34	GLY	3.6
1	AA	1492	A	3.6
10	CJ	55	LYS	3.6
12	CL	46	LYS	3.6
53	D7	47	ARG	3.6
31	DH	107	VAL	3.6
40	DU	2	PRO	3.6
19	CS	14	HIS	3.6
3	CC	187	ALA	3.6
19	CS	34	TRP	3.6
25	DA	229	A	3.6
12	AL	64	TYR	3.6
16	AP	6	LEU	3.6
16	AP	42	ARG	3.5
17	CQ	98	LEU	3.6
21	CU	15	ARG	3.5
25	DA	2128	C	3.6
46	B0	8	GLY	3.6
30	DG	86	MET	3.5
36	DQ	136	ALA	3.5
24	AY	70	G	3.5
45	DZ	113	ALA	3.5
9	CI	124	GLN	3.5
8	AH	80	ILE	3.5
10	AJ	98	ILE	3.5
8	CH	2	LEU	3.5
38	DS	34	HIS	3.5
4	AD	204	ILE	3.5
19	CS	41	VAL	3.5
5	CE	121	LYS	3.5
20	AT	74	LYS	3.5
13	AM	87	TYR	3.5
17	CQ	95	TYR	3.5

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Mol	Chain	Res	Type	RSRZ
4	CD	49	ARG	3.5
14	AN	15	LYS	3.5
16	CP	12	LYS	3.5
10	CJ	44	VAL	3.5
14	CN	33	VAL	3.5
14	CN	42	ILE	3.5
4	AD	11	LEU	3.5
25	BA	2150	C	3.5
25	DA	2156	G	3.5
53	B7	46	VAL	3.5
44	DY	44	ILE	3.5
14	CN	10	ALA	3.4
3	CC	188	LEU	3.4
5	CE	11	ILE	3.4
13	CM	67	GLU	3.4
13	CM	73	GLU	3.4
44	DY	47	LYS	3.4
17	CQ	9	VAL	3.4
43	DX	43	VAL	3.4
4	AD	176	LEU	3.4
32	DI	12	LEU	3.4
36	DQ	79	LEU	3.4
45	DZ	76	LEU	3.4
12	AL	89	ARG	3.4
43	DX	60	ARG	3.4
46	D0	68	GLU	3.4
9	CI	14	VAL	3.4
13	AM	56	LEU	3.4
17	CQ	84	LEU	3.4
30	DG	120	LEU	3.4
50	B4	50	VAL	3.4
50	B4	55	ARG	3.4
3	CC	195	VAL	3.4
2	AB	200	ILE	3.4
12	AL	91	LYS	3.4
10	AJ	46	ARG	3.4
45	DZ	82	ARG	3.4
21	CU	5	ASP	3.4
25	BA	2163	G	3.4
5	CE	119	LEU	3.4
14	CN	11	LYS	3.4
51	D5	60	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
10	CJ	6	ILE	3.4
16	AP	29	ASP	3.4
25	BA	2157	A	3.4
17	CQ	10	VAL	3.4
27	DD	37	LEU	3.4
5	CE	109	ILE	3.4
25	BA	2166	U	3.4
13	CM	42	ALA	3.4
13	CM	75	ALA	3.4
17	CQ	100	LYS	3.4
52	D6	2	ALA	3.4
15	CO	68	ARG	3.4
49	D3	6	VAL	3.4
19	CS	4	SER	3.3
9	CI	45	ALA	3.3
2	CB	115	LEU	3.3
46	D0	74	ARG	3.3
4	AD	8	VAL	3.3
3	CC	182	ILE	3.3
4	AD	158	ILE	3.3
9	CI	18	PHE	3.3
37	DR	69	ASP	3.3
13	CM	72	ALA	3.3
25	BA	2137	G	3.3
2	AB	196	LEU	3.3
3	AC	33	LEU	3.3
3	AC	188	LEU	3.3
16	CP	51	VAL	3.3
18	CR	22	VAL	3.3
25	DA	2129	C	3.3
3	CC	71	ALA	3.3
30	DG	51	ARG	3.3
16	AP	1	MET	3.3
4	AD	102	ASP	3.3
14	AN	56	VAL	3.3
36	DQ	65	PHE	3.3
7	CG	73	MET	3.3
7	CG	22	LEU	3.3
43	DX	49	VAL	3.3
10	CJ	10	GLY	3.3
30	DG	34	LEU	3.3
32	DI	14	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
45	DZ	139	VAL	3.3
9	CI	117	HIS	3.3
4	CD	146	ILE	3.3
9	CI	102	LEU	3.3
17	CQ	23	VAL	3.3
20	AT	80	ARG	3.3
35	DP	15	ARG	3.3
14	CN	55	GLY	3.3
16	AP	19	ILE	3.3
25	BA	2134	G	3.3
53	B7	1	MET	3.3
7	CG	155	ARG	3.3
13	AM	105	THR	3.2
44	DY	30	VAL	3.2
13	CM	84	ILE	3.2
3	AC	100	ALA	3.2
1	AA	1493	A	3.2
16	CP	59	TRP	3.2
30	DG	152	LEU	3.2
3	CC	19	GLU	3.2
14	AN	16	PHE	3.2
36	DQ	32	TYR	3.2
50	D4	57	GLU	3.2
43	DX	80	ILE	3.2
38	DS	31	SER	3.2
19	CS	43	GLU	3.2
44	DY	58	GLY	3.2
25	DA	2142	C	3.2
3	CC	65	ALA	3.2
44	DY	46	LYS	3.2
53	B7	48	LYS	3.2
4	AD	167	GLY	3.2
12	CL	120	TYR	3.2
32	DI	11	ASN	3.2
5	CE	105	VAL	3.2
19	CS	12	ASP	3.2
4	AD	101	LEU	3.2
9	CI	19	LEU	3.2
7	CG	91	VAL	3.2
17	AQ	35	VAL	3.2
30	DG	5	VAL	3.2
53	B7	45	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
14	CN	57	ARG	3.2
10	CJ	56	HIS	3.2
3	CC	157	ILE	3.2
10	CJ	38	ILE	3.2
9	AI	120	ARG	3.2
25	DA	2138	C	3.1
13	CM	13	LYS	3.1
17	CQ	90	ILE	3.1
31	DH	102	ALA	3.1
4	AD	202	LEU	3.1
35	DP	45	LEU	3.1
36	DQ	61	GLY	3.1
5	CE	125	SER	3.1
19	CS	36	ARG	3.1
19	CS	60	VAL	3.1
25	BA	2135	U	3.1
1	CA	1116	C	3.1
5	AE	95	ALA	3.1
26	DB	118	G	3.1
21	CU	17	THR	3.1
10	AJ	60	ARG	3.1
31	DH	96	ALA	3.1
1	CA	1286	A	3.1
31	BH	2	SER	3.1
25	DA	2179	C	3.1
50	B4	59	PHE	3.1
3	CC	60	ALA	3.1
2	CB	132	LYS	3.1
25	DA	2118	U	3.1
25	BA	1935	A	3.1
5	AE	45	PHE	3.1
29	BF	17	ARG	3.1
30	DG	181	ARG	3.1
40	DU	48	ALA	3.1
25	BA	2142	G	3.1
10	AJ	11	PHE	3.1
45	DZ	170	THR	3.1
2	CB	77	ALA	3.1
18	AR	78	LEU	3.1
7	AG	8	GLU	3.1
17	CQ	86	GLU	3.1
23	CX	70	G	3.1

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Mol	Chain	Res	Type	RSRZ
3	CC	117	ALA	3.1
9	CI	47	LEU	3.1
46	B0	2	ALA	3.1
3	AC	57	ILE	3.1
15	CO	36	ILE	3.1
37	DR	83	ILE	3.1
50	D4	68	ARG	3.1
4	AD	4	TYR	3.0
4	AD	138	TYR	3.0
7	AG	151	TYR	3.0
1	AA	204	U	3.0
5	AE	82	VAL	3.0
9	CI	70	LYS	3.0
2	CB	162	ILE	3.0
52	D6	54	ILE	3.0
25	DA	2134	A	3.0
43	DX	33	LYS	3.0
55	D9	16	VAL	3.0
10	AJ	71	LEU	3.0
19	CS	16	LEU	3.0
21	CU	10	ARG	3.0
12	CL	56	ALA	3.0
30	DG	43	LEU	3.0
40	DU	117	GLN	3.0
20	AT	55	ILE	3.0
25	DA	2133	G	3.0
42	DW	95	ILE	3.0
49	D3	2	PRO	3.0
25	BA	2196	C	3.0
25	DA	1509	C	3.0
2	CB	181	PHE	3.0
9	AI	64	THR	3.0
17	CQ	24	GLU	3.0
2	CB	197	VAL	3.0
19	CS	11	VAL	3.0
30	DG	149	VAL	3.0
47	B1	2	SER	3.0
8	AH	133	LEU	3.0
18	CR	66	LEU	3.0
8	CH	83	ILE	3.0
8	CH	86	ILE	3.0
3	CC	23	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
3	CC	201	TYR	3.0
31	DH	164	TYR	3.0
1	CA	1354	C	3.0
1	CA	1357	A	3.0
5	CE	123	LEU	3.0
18	CR	85	LEU	3.0
12	CL	68	ALA	3.0
3	AC	80	GLY	3.0
8	CH	99	GLU	3.0
14	AN	21	TYR	3.0
43	DX	18	TYR	3.0
1	AA	1026	G	3.0
4	AD	165	MET	3.0
5	CE	16	THR	3.0
43	DX	1	MET	3.0
14	CN	61	TRP	3.0
25	DA	888	C	3.0
7	CG	152	ALA	3.0
27	DD	275	LYS	3.0
7	AG	81	GLY	3.0
15	CO	86	GLY	3.0
10	CJ	43	ARG	3.0
9	AI	59	PHE	3.0
50	D4	42	PHE	3.0
30	DG	84	LYS	3.0
9	AI	109	VAL	3.0
10	CJ	20	ALA	3.0
25	DA	2155	G	3.0
3	CC	134	ILE	3.0
20	CT	41	ILE	3.0
29	DF	82	ILE	3.0
13	CM	79	LYS	3.0
21	CU	18	TYR	3.0
6	AF	61	LEU	3.0
36	DQ	48	GLU	3.0
14	AN	20	ALA	3.0
4	CD	206	PHE	2.9
30	DG	178	PHE	2.9
4	CD	4	TYR	2.9
7	CG	151	TYR	2.9
31	DH	106	THR	2.9
6	CF	45	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
29	DF	12	LEU	2.9
4	CD	209	ARG	2.9
15	CO	88	ARG	2.9
19	CS	45	VAL	2.9
16	AP	7	ALA	2.9
2	CB	31	TYR	2.9
13	CM	23	TYR	2.9
25	DA	2115	G	2.9
17	AQ	98	LEU	2.9
17	CQ	54	GLY	2.9
17	CQ	91	ARG	2.9
36	DQ	1	MET	2.9
38	DS	26	LEU	2.9
53	B7	47	ARG	2.9
13	CM	60	VAL	2.9
25	DA	2158	A	2.9
45	DZ	171	ILE	2.9
2	CB	66	GLY	2.9
25	DA	2139	C	2.9
45	DZ	79	ARG	2.9
15	CO	67	LEU	2.9
8	CH	95	VAL	2.9
13	CM	98	VAL	2.9
25	BA	2203	G	2.9
3	AC	39	ILE	2.9
3	CC	196	LEU	2.9
13	CM	70	LEU	2.9
16	CP	60	LEU	2.9
7	AG	105	VAL	2.9
12	CL	30	ALA	2.9
1	CA	973	G	2.9
31	DH	97	ARG	2.9
21	AU	11	GLY	2.9
46	D0	57	PHE	2.9
45	DZ	5	LEU	2.9
3	AC	64	VAL	2.9
43	DX	7	VAL	2.9
7	CG	37	ASN	2.9
14	AN	35	ARG	2.9
28	DE	125	GLY	2.9
39	DT	48	ILE	2.9
35	DP	51	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
44	DY	60	PHE	2.9
2	CB	196	LEU	2.9
4	AD	166	LYS	2.9
10	AJ	57	LYS	2.9
3	CC	142	MET	2.9
8	AH	93	VAL	2.9
2	CB	37	ASN	2.9
2	CB	97	TRP	2.9
30	DG	108	ASN	2.9
3	CC	154	SER	2.9
24	AY	72	C	2.9
41	DV	74	LYS	2.9
4	CD	157	LEU	2.9
39	DT	99	LEU	2.9
2	CB	96	ARG	2.9
15	AO	69	TYR	2.9
16	AP	24	ALA	2.9
25	DA	2166	G	2.9
22	AV	19	U	2.8
4	AD	80	GLU	2.8
25	DA	2143	C	2.8
46	D0	69	PHE	2.8
17	CQ	56	VAL	2.8
47	B1	49	VAL	2.8
12	CL	95	GLY	2.8
30	DG	89	GLY	2.8
50	D4	53	GLU	2.8
7	AG	42	ILE	2.8
16	CP	33	ILE	2.8
30	DG	88	ILE	2.8
38	DS	40	ILE	2.8
30	DG	141	PHE	2.8
17	CQ	31	LEU	2.8
4	AD	20	TYR	2.8
10	AJ	62	HIS	2.8
10	CJ	59	SER	2.8
16	CP	9	PHE	2.8
17	CQ	38	ARG	2.8
17	CQ	59	ILE	2.8
1	CA	1363(A)	A	2.8
25	DA	2114	A	2.8
19	CS	32	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
30	DG	75	LYS	2.8
44	DY	48	ALA	2.8
4	AD	152	SER	2.8
2	CB	68	ILE	2.8
20	CT	14	LYS	2.8
37	DR	9	LYS	2.8
1	AA	1002	G	2.8
2	CB	71	VAL	2.8
15	CO	89	GLY	2.8
25	DA	883	G	2.8
30	DG	15	VAL	2.8
32	BI	90	GLY	2.8
47	D1	28	GLY	2.8
55	D9	3	VAL	2.8
14	CN	49	HIS	2.8
13	CM	65	LYS	2.8
31	DH	72	ILE	2.8
3	AC	189	ALA	2.8
12	CL	96	VAL	2.8
3	CC	190	ARG	2.8
7	CG	32	ARG	2.8
9	CI	120	ARG	2.8
13	AM	94	ARG	2.8
55	D9	13	LYS	2.8
1	AA	1531	A	2.8
25	BA	2192	A	2.8
6	AF	48	LEU	2.8
13	CM	90	LEU	2.8
2	AB	228	GLY	2.8
3	AC	78	GLY	2.8
38	DS	60	GLY	2.8
9	AI	46	ALA	2.8
2	CB	48	MET	2.8
15	CO	60	VAL	2.8
20	CT	88	VAL	2.8
36	DQ	28	ALA	2.8
3	CC	31	HIS	2.8
8	AH	86	ILE	2.8
12	CL	7	ILE	2.8
13	CM	34	LEU	2.8
25	DA	2110	G	2.8
12	CL	13	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
9	AI	17	VAL	2.7
10	AJ	44	VAL	2.7
30	DG	26	GLN	2.7
31	DH	76	VAL	2.7
7	AG	38	LEU	2.7
15	AO	66	LEU	2.7
5	CE	81	GLU	2.7
14	CN	40	CYS	2.7
10	CJ	34	VAL	2.7
15	CO	45	VAL	2.7
31	DH	52	VAL	2.7
36	DQ	102	VAL	2.7
44	BY	1	MET	2.7
30	DG	173	LEU	2.7
37	DR	29	LEU	2.7
44	DY	50	ARG	2.7
46	D0	44	ARG	2.7
30	DG	35	GLU	2.7
4	AD	170	VAL	2.7
10	CJ	58	ASP	2.7
25	BA	2133	C	2.7
5	CE	24	ARG	2.7
9	CI	121	ARG	2.7
9	CI	62	TYR	2.7
10	CJ	98	ILE	2.7
50	D4	46	GLN	2.7
9	CI	116	LYS	2.7
1	CA	1531	A	2.7
50	B4	4	GLY	2.7
6	CF	4	TYR	2.7
38	DS	12	PHE	2.7
40	DU	88	ILE	2.7
8	CH	87	SER	2.7
38	DS	22	GLY	2.7
47	D1	22	GLY	2.7
49	D3	27	GLY	2.7
2	CB	105	PHE	2.7
3	AC	34	LEU	2.7
12	CL	28	LYS	2.7
14	CN	16	PHE	2.7
19	CS	15	LEU	2.7
15	AO	87	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
9	CI	107	ARG	2.7
49	D3	54	VAL	2.7
16	AP	27	LYS	2.7
19	AS	72	GLY	2.7
13	CM	77	ASN	2.7
15	AO	34	LEU	2.7
16	AP	80	PHE	2.7
20	CT	24	LEU	2.7
16	AP	39	TYR	2.7
10	CJ	45	ARG	2.7
13	AM	108	ARG	2.7
14	AN	3	ARG	2.7
2	AB	29	ALA	2.7
26	DB	25	A	2.7
37	DR	25	ALA	2.7
47	D1	70	VAL	2.7
32	BI	35	LEU	2.7
38	DS	54	LEU	2.7
45	DZ	88	PHE	2.7
3	AC	58	GLU	2.7
5	CE	122	GLU	2.7
14	AN	29	ARG	2.7
10	AJ	48	THR	2.7
36	BQ	85	LYS	2.7
20	AT	18	GLN	2.6
26	DB	55	U	2.6
2	CB	230	VAL	2.6
4	AD	148	VAL	2.6
17	CQ	11	VAL	2.6
47	D1	98	LEU	2.6
25	DA	2148	G	2.6
30	DG	80	PHE	2.6
4	CD	115	ARG	2.6
5	CE	89	ILE	2.6
7	CG	18	TYR	2.6
9	CI	69	GLY	2.6
17	CQ	33	GLY	2.6
17	CQ	77	VAL	2.6
19	CS	47	HIS	2.6
40	DU	90	VAL	2.6
4	AD	135	LEU	2.6
17	CQ	53	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
19	CS	64	GLU	2.6
14	AN	31	ARG	2.6
8	CH	138	TRP	2.6
9	CI	81	ILE	2.6
9	CI	46	ALA	2.6
43	DX	11	PRO	2.6
5	AE	88	LYS	2.6
17	CQ	85	VAL	2.6
38	DS	57	LYS	2.6
46	D0	79	VAL	2.6
13	CM	81	LEU	2.6
13	CM	88	ARG	2.6
14	AN	23	ARG	2.6
15	AO	88	ARG	2.6
25	DA	2113	U	2.6
46	D0	21	LEU	2.6
26	DB	59	A	2.6
19	CS	28	LYS	2.6
50	D4	41	PRO	2.6
3	CC	59	ARG	2.6
3	CC	207	VAL	2.6
16	AP	2	VAL	2.6
25	BA	1221	G	2.6
44	DY	106	LEU	2.6
4	AD	110	PHE	2.6
25	DA	2132	U	2.6
3	AC	97	LYS	2.6
8	CH	90	GLY	2.6
2	CB	223	ILE	2.6
11	CK	25	TYR	2.6
1	CA	1250	A	2.6
4	CD	122	ARG	2.6
19	CS	3	ARG	2.6
25	BA	2191	A	2.6
7	CG	23	VAL	2.6
9	CI	38	GLN	2.6
54	D8	25	MET	2.6
25	DA	2120	G	2.6
30	DG	182	LYS	2.6
10	AJ	97	GLU	2.6
36	DQ	33	GLY	2.6
7	CG	145	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
8	AH	16	ALA	2.6
14	AN	2	ALA	2.6
38	DS	65	VAL	2.6
49	D3	59	VAL	2.6
5	CE	142	LEU	2.6
10	AJ	65	LEU	2.6
32	DI	30	LEU	2.6
3	CC	38	ARG	2.6
30	DG	72	ARG	2.6
3	CC	124	ILE	2.6
6	AF	8	ILE	2.6
30	DG	25	TYR	2.6
4	AD	21	LEU	2.6
10	CJ	85	LEU	2.6
33	DN	116	LEU	2.6
44	BY	91	GLU	2.6
11	CK	49	GLY	2.6
27	DD	238	GLY	2.6
14	CN	24	CYS	2.6
38	DS	87	PHE	2.6
8	CH	122	ARG	2.6
24	AY	73	A	2.6
2	AB	133	LYS	2.5
19	CS	48	THR	2.5
25	DA	2109	U	2.5
30	DG	36	LYS	2.5
30	DG	140	ILE	2.5
7	AG	7	ALA	2.5
9	AI	15	ALA	2.5
19	CS	50	ALA	2.5
3	AC	19	GLU	2.5
54	D8	64	TYR	2.5
4	AD	198	VAL	2.5
9	CI	75	ASP	2.5
12	CL	52	LEU	2.5
17	CQ	35	VAL	2.5
31	DH	114	VAL	2.5
25	BA	2160	C	2.5
3	CC	4	LYS	2.5
4	AD	169	LYS	2.5
9	CI	11	LYS	2.5
30	DG	138	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
9	CI	74	ILE	2.5
7	AG	22	LEU	2.5
9	CI	26	VAL	2.5
10	AJ	49	VAL	2.5
11	AK	98	LEU	2.5
35	DP	59	LEU	2.5
7	AG	155	ARG	2.5
34	BO	49	ARG	2.5
3	CC	6	HIS	2.5
3	CC	160	ALA	2.5
4	AD	146	ILE	2.5
29	BF	64	ILE	2.5
45	DZ	83	PRO	2.5
42	DW	94	ASP	2.5
54	D8	16	ILE	2.5
2	CB	114	ARG	2.5
3	CC	55	VAL	2.5
3	CC	130	VAL	2.5
12	CL	88	GLY	2.5
19	CS	80	TYR	2.5
25	BA	1072	U	2.5
25	BA	2144	U	2.5
25	BA	2518	U	2.5
30	DG	92	VAL	2.5
40	DU	109	LEU	2.5
49	D3	47	VAL	2.5
13	CM	82	MET	2.5
3	CC	168	ALA	2.5
28	BE	157	ALA	2.5
9	CI	8	GLY	2.5
12	AL	63	GLY	2.5
38	DS	20	ARG	2.5
2	CB	51	LEU	2.5
5	AE	148	VAL	2.5
14	AN	25	VAL	2.5
50	D4	67	TYR	2.5
17	AQ	27	PHE	2.5
43	DX	23	GLU	2.5
14	AN	41	ARG	2.5
3	AC	81	GLY	2.5
3	AC	169	ALA	2.5
5	CE	131	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
25	BA	2183	C	2.5
44	DY	65	ALA	2.5
12	CL	10	LEU	2.5
6	AF	88	VAL	2.5
7	CG	9	VAL	2.5
19	CS	66	MET	2.5
44	DY	63	LYS	2.5
25	BA	2156	A	2.5
12	AL	61	THR	2.5
8	AH	83	ILE	2.5
12	CL	100	ILE	2.5
43	DX	31	HIS	2.5
6	AF	57	GLN	2.5
44	DY	29	GLU	2.5
3	AC	195	VAL	2.5
4	AD	105	VAL	2.5
14	CN	27	CYS	2.5
22	CV	18	G	2.5
25	BA	2190	G	2.5
31	DH	2	SER	2.5
7	CG	26	PHE	2.5
7	CG	43	PHE	2.5
5	AE	10	MET	2.5
45	DZ	98	MET	2.5
2	CB	53	ARG	2.5
3	CC	164	ARG	2.5
17	CQ	92	ARG	2.5
44	DY	43	ASN	2.5
45	BZ	112	ARG	2.5
2	CB	29	ALA	2.5
7	AG	86	GLN	2.5
30	DG	161	THR	2.5
1	CA	1251	A	2.5
4	AD	78	LEU	2.5
25	BA	218	A	2.5
5	CE	88	LYS	2.5
32	BI	30	LEU	2.5
32	DI	38	LEU	2.5
38	DS	56	LEU	2.5
2	CB	93	VAL	2.5
32	DI	81	VAL	2.5
45	DZ	105	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
43	DX	26	TYR	2.5
14	CN	46	GLU	2.4
54	D8	9	GLY	2.4
49	D3	12	PRO	2.4
9	AI	117	HIS	2.4
12	CL	126	LYS	2.4
17	AQ	37	LYS	2.4
17	CQ	7	THR	2.4
3	AC	101	LEU	2.4
17	AQ	59	ILE	2.4
18	AR	79	LEU	2.4
49	D3	28	LEU	2.4
15	CO	64	ARG	2.4
23	AX	76	A	2.4
53	D7	18	PHE	2.4
53	D7	23	ARG	2.4
8	AH	15	ASN	2.4
9	AI	4	TYR	2.4
11	AK	25	TYR	2.4
9	CI	105	ASP	2.4
3	AC	139	GLN	2.4
24	AY	4	C	2.4
45	DZ	156	LYS	2.4
12	CL	45	PRO	2.4
4	CD	164	ALA	2.4
13	AM	103	THR	2.4
2	CB	215	LEU	2.4
5	AE	91	LEU	2.4
39	DT	102	ILE	2.4
8	AH	138	TRP	2.4
31	DH	35	VAL	2.4
3	AC	56	ASP	2.4
3	AC	199	LYS	2.4
13	CM	119	GLY	2.4
26	DB	53	A	2.4
35	DP	34	GLY	2.4
1	CA	1149	C	2.4
8	CH	81	HIS	2.4
3	CC	47	LEU	2.4
8	AH	112	LEU	2.4
8	CH	92	ARG	2.4
10	CJ	51	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
25	DA	1026	U	2.4
27	DD	273	ARG	2.4
34	DO	8	LEU	2.4
1	CA	1190	G	2.4
2	CB	231	GLU	2.4
3	CC	153	VAL	2.4
4	CD	198	VAL	2.4
5	CE	148	VAL	2.4
6	CF	6	VAL	2.4
25	DA	2154	G	2.4
19	CS	53	ASN	2.4
46	D0	46	LYS	2.4
9	AI	8	GLY	2.4
25	BA	2180	A	2.4
50	D4	48	ARG	2.4
10	CJ	96	ILE	2.4
14	AN	42	ILE	2.4
2	CB	229	VAL	2.4
7	CG	75	VAL	2.4
14	AN	37	PHE	2.4
25	BA	2169	G	2.4
12	AL	59	ARG	2.4
14	CN	45	ARG	2.4
27	DD	215	LEU	2.4
36	DQ	118	LEU	2.4
43	DX	10	ALA	2.4
11	AK	81	ASP	2.4
45	DZ	140	ASP	2.4
1	CA	979	C	2.4
2	CB	164	VAL	2.4
4	CD	128	VAL	2.4
2	CB	148	TYR	2.4
4	AD	18	LYS	2.4
5	AE	18	ARG	2.4
9	CI	113	LYS	2.4
36	DQ	63	LYS	2.4
45	DZ	121	HIS	2.4
3	AC	87	LEU	2.4
8	CH	112	LEU	2.4
10	CJ	26	ALA	2.4
13	CM	76	ALA	2.4
27	BD	155	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
40	DU	113	ALA	2.4
3	AC	134	ILE	2.4
3	CC	8	ILE	2.4
29	DF	64	ILE	2.4
4	CD	56	VAL	2.4
19	AS	41	VAL	2.4
30	DG	180	PHE	2.4
31	DH	43	VAL	2.4
54	D8	22	VAL	2.4
1	AA	1532	U	2.4
14	AN	50	LYS	2.4
30	BG	182	LYS	2.4
17	CQ	29	HIS	2.4
36	DQ	4	PRO	2.4
2	CB	218	ALA	2.4
8	AH	39	LEU	2.4
43	DX	79	ALA	2.4
44	DY	31	LEU	2.4
54	D8	59	LYS	2.4
3	AC	190	ARG	2.4
13	AM	98	VAL	2.4
14	CN	12	ARG	2.4
42	DW	85	VAL	2.4
4	AD	197	PRO	2.3
25	BA	2141	A	2.3
25	BA	2210	C	2.3
4	CD	135	LEU	2.3
8	CH	16	ALA	2.3
29	DF	80	ALA	2.3
30	DG	6	ALA	2.3
38	DS	52	SER	2.3
45	DZ	59	LEU	2.3
41	DV	85	LYS	2.3
8	AH	109	ILE	2.3
14	CN	7	ILE	2.3
30	DG	115	ARG	2.3
3	AC	68	VAL	2.3
3	AC	198	VAL	2.3
45	DZ	116	VAL	2.3
16	AP	59	TRP	2.3
1	AA	841	U	2.3
4	AD	207	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
10	CJ	57	LYS	2.3
25	DA	2506	U	2.3
46	D0	78	TYR	2.3
7	CG	117	ALA	2.3
10	CJ	8	LEU	2.3
40	DU	98	LEU	2.3
13	CM	103	THR	2.3
19	CS	82	GLY	2.3
28	DE	115	GLY	2.3
3	CC	30	ARG	2.3
34	DO	82	ASN	2.3
2	AB	122	PHE	2.3
9	AI	18	PHE	2.3
29	DF	37	VAL	2.3
3	CC	37	GLN	2.3
7	CG	88	PRO	2.3
1	CA	1224	G	2.3
10	AJ	58	ASP	2.3
2	CB	98	LEU	2.3
9	CI	12	GLU	2.3
10	CJ	61	GLU	2.3
11	CK	50	TYR	2.3
7	AG	3	ARG	2.3
15	AO	57	LEU	2.3
32	DI	47	LEU	2.3
42	DW	9	TYR	2.3
16	CP	7	ALA	2.3
16	CP	26	ARG	2.3
35	DP	73	GLY	2.3
49	D3	23	LEU	2.3
8	AH	3	THR	2.3
19	CS	77	THR	2.3
21	AU	17	THR	2.3
2	CB	108	ILE	2.3
4	CD	126	ILE	2.3
39	DT	50	ILE	2.3
4	AD	75	PHE	2.3
5	CE	45	PHE	2.3
14	AN	18	VAL	2.3
17	CQ	27	PHE	2.3
3	CC	20	SER	2.3
8	AH	10	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
12	AL	29	GLY	2.3
15	CO	63	ARG	2.3
21	AU	10	ARG	2.3
28	DE	151	TYR	2.3
14	AN	11	LYS	2.3
4	CD	5	ILE	2.3
8	CH	35	ILE	2.3
8	CH	80	ILE	2.3
34	DO	69	ILE	2.3
4	CD	112	VAL	2.3
15	CO	29	VAL	2.3
16	CP	21	VAL	2.3
25	DA	2161	C	2.3
5	CE	8	GLU	2.3
23	CX	76	A	2.3
21	AU	15	ARG	2.3
31	DH	6	ARG	2.3
32	DI	20	ASP	2.3
10	AJ	93	GLY	2.3
3	AC	91	LEU	2.3
9	AI	125	TYR	2.3
10	AJ	18	ALA	2.3
12	CL	51	ALA	2.3
30	DG	11	TYR	2.3
30	DG	73	ALA	2.3
17	AQ	36	ILE	2.3
6	AF	90	VAL	2.3
31	DH	24	VAL	2.3
1	CA	1373	G	2.3
25	DA	2178	C	2.3
3	CC	87	LEU	2.3
4	AD	175	SER	2.3
17	CQ	22	LEU	2.3
9	AI	65	VAL	2.3
31	DH	101	ARG	2.3
9	CI	30	GLY	2.3
13	CM	27	LYS	2.3
38	DS	93	LYS	2.3
8	AH	89	PRO	2.3
17	AQ	28	PRO	2.3
42	DW	82	LEU	2.3
45	DZ	65	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
54	D8	62	LEU	2.3
2	AB	188	ALA	2.3
2	CB	88	ALA	2.3
18	AR	24	ALA	2.3
25	DA	2174	C	2.3
3	CC	177	THR	2.3
10	AJ	67	THR	2.3
13	CM	69	GLU	2.3
19	CS	63	THR	2.3
30	DG	146	TYR	2.3
31	DH	94	TYR	2.3
19	CS	10	PHE	2.3
3	AC	153	VAL	2.3
5	CE	124	GLY	2.2
36	BQ	61	GLY	2.2
2	CB	138	LEU	2.2
3	AC	98	ASN	2.2
15	CO	57	LEU	2.2
27	DD	155	LEU	2.2
33	DN	44	PRO	2.2
9	CI	27	THR	2.2
27	DD	40	THR	2.2
3	CC	172	ARG	2.2
8	AH	58	TYR	2.2
25	BA	2199	C	2.2
30	BG	51	ARG	2.2
3	AC	202	ILE	2.2
5	CE	84	PHE	2.2
5	CE	33	VAL	2.2
6	AF	6	VAL	2.2
13	CM	53	VAL	2.2
41	DV	70	ILE	2.2
12	CL	99	HIS	2.2
30	DG	133	LEU	2.2
34	BO	91	LEU	2.2
3	AC	65	ALA	2.2
5	CE	30	ALA	2.2
9	AI	116	LYS	2.2
27	BD	153	ALA	2.2
25	BA	2130	C	2.2
43	DX	47	PHE	2.2
4	AD	201	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
8	CH	61	VAL	2.2
25	BA	2177	G	2.2
25	DA	2121	G	2.2
34	DO	38	VAL	2.2
43	DX	12	VAL	2.2
4	AD	150	GLU	2.2
15	AO	81	LEU	2.2
30	DG	60	LEU	2.2
35	DP	3	LEU	2.2
43	DX	2	LYS	2.2
47	B1	73	LEU	2.2
3	AC	41	GLY	2.2
9	AI	5	TYR	2.2
16	AP	36	ILE	2.2
27	BD	49	ILE	2.2
27	BD	141	VAL	2.2
31	DH	148	ILE	2.2
40	DU	80	ILE	2.2
38	DS	33	LYS	2.2
25	DA	34	C	2.2
9	CI	21	PRO	2.2
18	AR	40	LEU	2.2
26	DB	54	G	2.2
30	BG	2	PRO	2.2
46	D0	62	LEU	2.2
5	AE	134	ALA	2.2
5	CE	10	MET	2.2
7	AG	144	MET	2.2
10	CJ	27	ALA	2.2
5	CE	120	THR	2.2
3	CC	158	GLY	2.2
5	CE	133	TYR	2.2
12	AL	47	LYS	2.2
27	DD	59	LYS	2.2
50	D4	25	TYR	2.2
5	CE	51	VAL	2.2
16	AP	20	VAL	2.2
20	CT	63	ILE	2.2
36	DQ	97	VAL	2.2
37	DR	97	VAL	2.2
9	AI	42	ARG	2.2
3	CC	32	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
4	AD	136	PRO	2.2
17	CQ	34	LYS	2.2
27	DD	126	GLN	2.2
25	BA	2145	G	2.2
25	BA	2178	G	2.2
25	DA	2112	G	2.2
31	DH	116	GLU	2.2
3	AC	164	ARG	2.2
3	CC	64	VAL	2.2
5	AE	109	ILE	2.2
8	CH	134	ILE	2.2
13	CM	62	ASN	2.2
16	CP	79	VAL	2.2
18	CR	50	ILE	2.2
35	DP	101	VAL	2.2
32	BI	38	LEU	2.2
49	D3	8	LEU	2.2
12	AL	23	LYS	2.2
7	CG	31	MET	2.2
34	DO	41	ALA	2.2
49	D3	21	ALA	2.2
2	CB	67	THR	2.2
4	CD	50	ARG	2.2
4	CD	110	PHE	2.2
25	BA	2189	U	2.2
1	CA	1017	G	2.2
25	DA	614(B)	G	2.2
25	DA	2181	G	2.2
27	BD	65	ILE	2.2
51	B5	60	VAL	2.2
3	AC	206	GLU	2.2
14	CN	15	LYS	2.2
15	CO	47	LYS	2.2
7	AG	106	GLN	2.2
19	CS	69	HIS	2.2
28	DE	195	LEU	2.2
31	DH	171	LEU	2.2
39	DT	114	LEU	2.2
45	DZ	138	GLU	2.2
4	CD	134	ASP	2.2
6	CF	89	MET	2.2
7	AG	103	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
34	DO	1	MET	2.2
16	CP	8	ARG	2.2
27	DD	217	ARG	2.2
6	AF	63	TYR	2.1
9	AI	113	LYS	2.1
19	AS	4	SER	2.1
38	DS	92	TYR	2.1
9	AI	41	VAL	2.1
47	D1	53	VAL	2.1
49	D3	43	ILE	2.1
8	AH	119	LEU	2.1
9	AI	79	LEU	2.1
1	CA	1001(A)	G	2.1
12	CL	31	PRO	2.1
28	DE	49	LEU	2.1
25	DA	2100	G	2.1
31	DH	128	PRO	2.1
46	D0	42	GLY	2.1
9	AI	106	ALA	2.1
9	CI	16	ARG	2.1
13	AM	102	ARG	2.1
16	AP	25	ARG	2.1
20	CT	30	LYS	2.1
44	DY	88	LYS	2.1
2	AB	37	ASN	2.1
6	CF	7	ASN	2.1
12	AL	90	VAL	2.1
12	AL	96	VAL	2.1
12	AL	98	TYR	2.1
16	AP	33	ILE	2.1
27	DD	3	VAL	2.1
27	DD	51	VAL	2.1
36	DQ	35	VAL	2.1
43	DX	30	VAL	2.1
45	DZ	111	VAL	2.1
51	D5	6	VAL	2.1
37	DR	10	LEU	2.1
37	DR	18	LEU	2.1
54	D8	60	LEU	2.1
7	CG	7	ALA	2.1
9	CI	122	ALA	2.1
11	AK	42	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
12	AL	28	LYS	2.1
45	DZ	173	ALA	2.1
47	D1	23	LYS	2.1
1	CA	975	A	2.1
12	AL	32	PHE	2.1
30	BG	80	PHE	2.1
45	DZ	44	PHE	2.1
5	CE	100	VAL	2.1
30	DG	70	VAL	2.1
16	CP	49	LEU	2.1
30	DG	77	ILE	2.1
31	DH	151	ILE	2.1
32	DI	3	VAL	2.1
3	CC	33	LEU	2.1
7	CG	15	ASP	2.1
13	CM	89	GLY	2.1
21	CU	24	ARG	2.1
30	DG	42	GLY	2.1
9	AI	78	LYS	2.1
10	AJ	61	GLU	2.1
17	CQ	82	MET	2.1
18	AR	25	THR	2.1
3	AC	138	VAL	2.1
4	AD	133	VAL	2.1
12	AL	60	LEU	2.1
21	CU	12	LYS	2.1
31	DH	113	VAL	2.1
10	CJ	53	PRO	2.1
14	AN	49	HIS	2.1
46	D0	37	LEU	2.1
55	B9	17	ILE	2.1
1	CA	1019	C	2.1
7	CG	39	ALA	2.1
23	CX	65	C	2.1
4	CD	33	MET	2.1
2	CB	233	SER	2.1
36	DQ	29	PHE	2.1
55	D9	15	LYS	2.1
3	AC	62	ASP	2.1
3	CC	52	LEU	2.1
9	CI	72	GLY	2.1
4	CD	106	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
5	AE	11	ILE	2.1
5	CE	139	LEU	2.1
19	CS	22	LEU	2.1
27	DD	18	VAL	2.1
27	DD	177	LEU	2.1
43	DX	70	LEU	2.1
34	BO	108	GLU	2.1
14	AN	22	THR	2.1
20	CT	26	ASN	2.1
27	BD	38	LYS	2.1
2	CB	130	ARG	2.1
38	DS	3	ARG	2.1
3	CC	197	GLY	2.1
27	DD	182	LEU	2.1
37	DR	114	VAL	2.1
55	B9	7	VAL	2.1
10	CJ	39	PRO	2.1
1	AA	975	A	2.1
1	AA	1224	G	2.1
43	DX	42	ALA	2.1
2	CB	100	GLY	2.1
4	AD	144	ASP	2.1
39	DT	46	GLU	2.1
49	D3	57	GLU	2.1
6	CF	75	LEU	2.1
10	AJ	85	LEU	2.1
20	CT	20	LEU	2.1
30	DG	160	VAL	2.1
51	D5	58	LEU	2.1
5	AE	118	ILE	2.1
8	AH	6	ILE	2.1
12	AL	85	ILE	2.1
12	CL	85	ILE	2.1
27	BD	232	PRO	2.1
54	D8	63	PRO	2.1
3	CC	61	ALA	2.1
5	CE	104	ALA	2.1
9	CI	43	ALA	2.1
20	CT	12	ALA	2.1
33	DN	92	ALA	2.1
10	CJ	29	ARG	2.1
20	CT	22	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
5	CE	135	THR	2.1
1	CA	1016	A	2.1
4	CD	96	LEU	2.0
16	AP	76	GLN	2.0
20	AT	14	LYS	2.0
27	DD	5	LYS	2.0
49	D3	9	VAL	2.0
42	DW	96	ILE	2.0
30	BG	25	TYR	2.0
36	DQ	137	TYR	2.0
9	CI	82	ALA	2.0
11	CK	126	ARG	2.0
10	CJ	97	GLU	2.0
13	AM	107	ALA	2.0
36	DQ	6	ARG	2.0
10	CJ	42	THR	2.0
11	AK	87	THR	2.0
35	DP	1	MET	2.0
43	DX	94	GLY	2.0
13	AM	70	LEU	2.0
17	CQ	89	LEU	2.0
19	CS	5	LEU	2.0
27	BD	133	LEU	2.0
42	DW	51	LEU	2.0
45	DZ	150	LEU	2.0
6	CF	90	VAL	2.0
12	CL	11	VAL	2.0
26	DB	23	G	2.0
32	DI	19	VAL	2.0
46	D0	63	VAL	2.0
2	CB	222	ILE	2.0
3	AC	14	ILE	2.0
3	AC	38	ARG	2.0
3	CC	77	ILE	2.0
3	CC	179	ARG	2.0
10	AJ	5	ARG	2.0
12	AL	97	ARG	2.0
25	DA	885	C	2.0
43	DX	65	ARG	2.0
49	D3	30	ARG	2.0
13	CM	18	ALA	2.0
51	B5	2	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
20	CT	21	LYS	2.0
31	DH	82	GLY	2.0
47	B1	97	LEU	2.0
9	CI	108	VAL	2.0
20	CT	80	ARG	2.0
28	DE	59	VAL	2.0
28	DE	196	VAL	2.0
35	BP	15	ARG	2.0
43	DX	39	ILE	2.0
3	CC	180	ALA	2.0
4	CD	166	LYS	2.0
6	AF	54	LYS	2.0
25	DA	2175	C	2.0
25	DA	2803	C	2.0
36	DQ	121	ALA	2.0
48	D2	39	ALA	2.0
2	AB	187	LEU	2.0
4	CD	186	LEU	2.0
8	CH	91	ARG	2.0
44	DY	67	LEU	2.0
47	D1	46	LEU	2.0
54	B8	65	GLU	2.0
17	CQ	57	VAL	2.0
34	DO	57	VAL	2.0
42	DW	105	VAL	2.0
47	D1	62	VAL	2.0
50	D4	10	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
23	4SU	CX	8	20/21	0.90	0.15	73,81,98,100	0
23	PSU	CX	55	20/21	0.91	0.12	56,73,80,86	0
23	5MU	CX	54	21/22	0.93	0.18	69,80,93,106	0
23	5MU	AX	54	21/22	0.94	0.16	60,72,80,91	0
23	PSU	AX	55	20/21	0.95	0.17	56,70,78,80	0
23	5MC	CX	32	21/22	0.95	0.21	66,75,83,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	5MC	AX	32	21/22	0.96	0.24	38,59,69,83	0
23	4SU	AX	8	20/21	0.96	0.18	47,67,77,84	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	3098	1/1	0.38	0.14	71,71,71,71	0
56	MG	DA	3655	1/1	0.40	1.89	74,74,74,74	0
56	MG	BA	3703	1/1	0.52	0.21	57,57,57,57	0
56	MG	BB	205	1/1	0.56	0.18	76,76,76,76	0
56	MG	CA	3043	1/1	0.59	0.14	67,67,67,67	0
56	MG	CX	3002	1/1	0.62	0.16	81,81,81,81	0
56	MG	CA	3081	1/1	0.62	0.16	58,58,58,58	0
56	MG	BA	3237	1/1	0.63	0.32	63,63,63,63	0
56	MG	DA	3242	1/1	0.65	0.16	68,68,68,68	0
56	MG	DA	3484	1/1	0.65	0.16	32,32,32,32	0
56	MG	CA	3084	1/1	0.66	0.14	71,71,71,71	0
56	MG	CA	3158	1/1	0.66	0.14	75,75,75,75	0
56	MG	AA	3038	1/1	0.67	0.20	61,61,61,61	0
56	MG	BA	3044	1/1	0.68	0.29	61,61,61,61	0
56	MG	BB	209	1/1	0.68	0.19	69,69,69,69	0
56	MG	AA	3034	1/1	0.68	0.19	70,70,70,70	0
56	MG	BA	3547	1/1	0.68	0.14	64,64,64,64	0
56	MG	AA	3125	1/1	0.68	0.35	72,72,72,72	0
56	MG	DA	3192	1/1	0.69	0.16	57,57,57,57	0
56	MG	AA	3147	1/1	0.69	0.14	72,72,72,72	0
56	MG	CA	3045	1/1	0.70	0.26	68,68,68,68	0
56	MG	DW	201	1/1	0.71	0.28	67,67,67,67	0
56	MG	CA	3078	1/1	0.71	0.15	64,64,64,64	0
56	MG	DA	3649	1/1	0.71	0.23	53,53,53,53	0
56	MG	AA	3020	1/1	0.72	0.14	71,71,71,71	0
56	MG	CA	3079	1/1	0.72	0.16	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3222	1/1	0.73	0.14	46,46,46,46	0
56	MG	BA	3813	1/1	0.73	0.09	58,58,58,58	0
56	MG	BA	3325	1/1	0.73	0.15	51,51,51,51	0
56	MG	BA	3241	1/1	0.73	0.13	45,45,45,45	0
56	MG	AA	3166	1/1	0.73	0.48	74,74,74,74	0
59	ZN	D4	501	1/1	0.73	0.07	151,151,151,151	0
56	MG	CA	3006	1/1	0.73	0.18	59,59,59,59	0
56	MG	DA	3647	1/1	0.73	0.45	53,53,53,53	0
56	MG	BB	211	1/1	0.74	0.17	81,81,81,81	0
56	MG	BA	3059	1/1	0.74	0.14	49,49,49,49	0
56	MG	DA	3536	1/1	0.74	0.10	44,44,44,44	0
56	MG	DA	3533	1/1	0.74	0.14	52,52,52,52	0
56	MG	DE	303	1/1	0.74	0.40	62,62,62,62	0
56	MG	DA	3640	1/1	0.74	0.43	64,64,64,64	0
56	MG	CA	3082	1/1	0.74	0.23	73,73,73,73	0
56	MG	CA	3001	1/1	0.74	0.09	59,59,59,59	0
56	MG	AA	3184	1/1	0.74	0.12	66,66,66,66	0
56	MG	BE	306	1/1	0.74	0.71	93,93,93,93	0
56	MG	BA	3514	1/1	0.74	0.15	45,45,45,45	0
56	MG	DA	3110	1/1	0.75	0.15	64,64,64,64	0
56	MG	DA	3488	1/1	0.75	0.19	51,51,51,51	0
56	MG	B7	104	1/1	0.75	0.19	64,64,64,64	0
56	MG	BA	3139	1/1	0.75	0.34	53,53,53,53	0
56	MG	DA	3627	1/1	0.75	0.18	64,64,64,64	0
56	MG	BA	3221	1/1	0.75	0.13	39,39,39,39	0
56	MG	DA	3080	1/1	0.76	0.16	49,49,49,49	0
56	MG	CA	3148	1/1	0.76	0.11	88,88,88,88	0
56	MG	CA	3171	1/1	0.77	0.18	65,65,65,65	0
56	MG	CJ	5001	1/1	0.77	0.11	94,94,94,94	0
56	MG	CA	3107	1/1	0.77	0.18	77,77,77,77	0
56	MG	BA	3605	1/1	0.77	0.17	44,44,44,44	0
56	MG	CA	3053	1/1	0.77	0.18	55,55,55,55	0
56	MG	AA	3170	1/1	0.77	0.12	73,73,73,73	0
56	MG	BA	3048	1/1	0.77	0.43	47,47,47,47	0
56	MG	DA	3026	1/1	0.77	0.22	52,52,52,52	0
56	MG	AX	3002	1/1	0.78	0.18	69,69,69,69	0
56	MG	BA	3099	1/1	0.78	0.22	67,67,67,67	0
56	MG	DA	3210	1/1	0.78	0.20	53,53,53,53	0
56	MG	BZ	301	1/1	0.78	0.23	58,58,58,58	0
56	MG	DA	3423	1/1	0.78	0.15	56,56,56,56	0
56	MG	AA	3067	1/1	0.78	0.19	72,72,72,72	0
56	MG	BA	3292	1/1	0.78	0.27	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3083	1/1	0.78	0.17	72,72,72,72	0
56	MG	AA	3169	1/1	0.78	0.26	73,73,73,73	0
56	MG	BA	3092	1/1	0.78	0.22	53,53,53,53	0
56	MG	BA	3657	1/1	0.78	0.15	52,52,52,52	0
56	MG	CA	3124	1/1	0.78	0.20	75,75,75,75	0
56	MG	B2	3001	1/1	0.79	0.20	49,49,49,49	0
56	MG	AA	3124	1/1	0.79	0.10	71,71,71,71	0
56	MG	BA	3447	1/1	0.79	0.15	59,59,59,59	0
56	MG	DA	3074	1/1	0.79	0.11	56,56,56,56	0
56	MG	DA	3255	1/1	0.79	0.12	62,62,62,62	0
56	MG	CE	201	1/1	0.79	0.20	73,73,73,73	0
56	MG	BA	3172	1/1	0.79	0.24	52,52,52,52	0
56	MG	BA	3498	1/1	0.79	0.20	43,43,43,43	0
56	MG	DA	3019	1/1	0.79	0.14	48,48,48,48	0
56	MG	BA	3028	1/1	0.79	0.24	52,52,52,52	0
56	MG	DA	3097	1/1	0.79	0.27	57,57,57,57	0
56	MG	CA	3174	1/1	0.79	0.56	80,80,80,80	0
56	MG	AA	3062	1/1	0.79	0.20	67,67,67,67	0
56	MG	CT	3001	1/1	0.79	0.14	59,59,59,59	0
57	PCY	CA	3176	40/40	0.80	0.43	72,89,98,102	0
56	MG	BA	3512	1/1	0.80	0.32	47,47,47,47	0
56	MG	BA	3375	1/1	0.80	0.13	38,38,38,38	0
56	MG	AA	3059	1/1	0.80	0.15	64,64,64,64	0
56	MG	CA	3016	1/1	0.80	0.15	53,53,53,53	0
56	MG	BU	206	1/1	0.80	1.07	61,61,61,61	0
56	MG	DA	3032	1/1	0.80	0.17	47,47,47,47	0
56	MG	BA	3711	1/1	0.80	0.40	51,51,51,51	0
56	MG	BA	3294	1/1	0.80	0.36	67,67,67,67	0
56	MG	BA	3521	1/1	0.80	0.29	29,29,29,29	0
56	MG	DA	3402	1/1	0.80	0.11	56,56,56,56	0
56	MG	BZ	302	1/1	0.80	0.26	56,56,56,56	0
56	MG	BA	3290	1/1	0.80	0.34	50,50,50,50	0
56	MG	BA	3692	1/1	0.80	0.12	51,51,51,51	0
56	MG	AA	3185	1/1	0.80	0.19	61,61,61,61	0
56	MG	DA	3603	1/1	0.80	0.19	55,55,55,55	0
56	MG	DA	3653	1/1	0.80	0.18	32,32,32,32	0
56	MG	DA	3469	1/1	0.80	0.10	53,53,53,53	0
56	MG	AA	3040	1/1	0.80	0.13	72,72,72,72	0
56	MG	CA	3092	1/1	0.80	0.25	61,61,61,61	0
56	MG	DA	3657	1/1	0.80	0.19	56,56,56,56	0
56	MG	BA	3288	1/1	0.81	0.11	44,44,44,44	0
56	MG	DA	3024	1/1	0.81	0.61	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3030	1/1	0.81	0.15	40,40,40,40	0
56	MG	BA	3199	1/1	0.81	0.44	51,51,51,51	0
56	MG	BA	3607	1/1	0.81	0.17	51,51,51,51	0
56	MG	CA	3009	1/1	0.81	0.27	66,66,66,66	0
56	MG	CA	3011	1/1	0.81	0.13	69,69,69,69	0
56	MG	AF	3001	1/1	0.81	0.16	56,56,56,56	0
56	MG	DA	3644	1/1	0.81	0.12	40,40,40,40	0
56	MG	BA	3296	1/1	0.81	0.21	47,47,47,47	0
56	MG	CA	3097	1/1	0.81	0.22	64,64,64,64	0
56	MG	BA	3050	1/1	0.81	0.16	46,46,46,46	0
56	MG	AA	3094	1/1	0.81	0.12	66,66,66,66	0
56	MG	AA	3049	1/1	0.81	0.28	64,64,64,64	0
56	MG	DA	3083	1/1	0.81	0.20	63,63,63,63	0
56	MG	CA	3129	1/1	0.81	0.11	69,69,69,69	0
56	MG	DA	3455	1/1	0.81	0.20	46,46,46,46	0
56	MG	DA	3389	1/1	0.81	0.10	50,50,50,50	0
56	MG	AA	3084	1/1	0.81	0.11	62,62,62,62	0
56	MG	DB	3001	1/1	0.81	0.17	77,77,77,77	0
56	MG	CA	3131	1/1	0.81	0.14	81,81,81,81	0
56	MG	DA	3286	1/1	0.82	0.15	54,54,54,54	0
56	MG	DV	3003	1/1	0.82	0.10	55,55,55,55	0
56	MG	DA	3043	1/1	0.82	0.11	52,52,52,52	0
56	MG	DA	3586	1/1	0.82	0.12	39,39,39,39	0
56	MG	BA	3256	1/1	0.82	0.24	54,54,54,54	0
56	MG	AA	3048	1/1	0.82	0.22	59,59,59,59	0
56	MG	CA	3067	1/1	0.82	0.18	72,72,72,72	0
56	MG	BA	3111	1/1	0.82	0.09	57,57,57,57	0
56	MG	AA	3171	1/1	0.82	0.17	67,67,67,67	0
56	MG	DA	3612	1/1	0.82	0.16	58,58,58,58	0
56	MG	BA	3040	1/1	0.82	0.20	52,52,52,52	0
56	MG	DA	3069	1/1	0.82	0.13	55,55,55,55	0
56	MG	BA	3475	1/1	0.82	0.12	45,45,45,45	0
56	MG	BA	3109	1/1	0.82	0.21	56,56,56,56	0
56	MG	CA	3022	1/1	0.83	0.18	60,60,60,60	0
56	MG	DA	3643	1/1	0.83	0.18	49,49,49,49	0
56	MG	DA	3087	1/1	0.83	0.32	50,50,50,50	0
56	MG	DF	302	1/1	0.83	0.28	44,44,44,44	0
56	MG	DA	3062	1/1	0.83	0.16	51,51,51,51	0
56	MG	DA	3037	1/1	0.83	0.16	34,34,34,34	0
56	MG	BB	206	1/1	0.83	0.32	58,58,58,58	0
56	MG	DA	3033	1/1	0.83	0.55	54,54,54,54	0
56	MG	AA	3100	1/1	0.83	0.13	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
57	PCY	AA	3191	40/40	0.83	0.43	59,86,97,99	0
56	MG	BA	3525	1/1	0.83	0.23	23,23,23,23	0
56	MG	DA	3164	1/1	0.83	0.20	47,47,47,47	0
56	MG	DA	3673	1/1	0.83	0.52	68,68,68,68	0
56	MG	CA	3032	1/1	0.83	0.10	57,57,57,57	0
56	MG	CA	3089	1/1	0.83	0.09	67,67,67,67	0
56	MG	AA	3076	1/1	0.83	0.16	56,56,56,56	0
56	MG	DA	3075	1/1	0.83	0.30	43,43,43,43	0
56	MG	BA	3168	1/1	0.83	0.23	39,39,39,39	0
56	MG	DA	3115	1/1	0.83	0.12	46,46,46,46	0
56	MG	BA	3437	1/1	0.83	0.24	61,61,61,61	0
56	MG	DA	3180	1/1	0.83	0.77	58,58,58,58	0
56	MG	CA	3087	1/1	0.83	0.12	62,62,62,62	0
56	MG	AX	3003	1/1	0.83	0.23	66,66,66,66	0
56	MG	BA	3604	1/1	0.83	0.25	46,46,46,46	0
56	MG	DA	3181	1/1	0.83	0.18	54,54,54,54	0
56	MG	DA	3607	1/1	0.83	0.17	63,63,63,63	0
56	MG	DD	308	1/1	0.84	0.80	72,72,72,72	0
56	MG	AX	3009	1/1	0.84	0.15	74,74,74,74	0
56	MG	BA	3389	1/1	0.84	0.18	56,56,56,56	0
56	MG	DA	3036	1/1	0.84	0.09	46,46,46,46	0
56	MG	BA	3455	1/1	0.84	0.14	32,32,32,32	0
56	MG	DA	3660	1/1	0.84	0.08	28,28,28,28	0
56	MG	DA	3491	1/1	0.84	0.12	42,42,42,42	0
56	MG	AA	3163	1/1	0.84	0.17	58,58,58,58	0
56	MG	AA	3157	1/1	0.84	0.19	84,84,84,84	0
56	MG	BA	3135	1/1	0.84	0.12	61,61,61,61	0
56	MG	B4	502	1/1	0.84	0.10	77,77,77,77	0
56	MG	AX	3007	1/1	0.84	0.13	69,69,69,69	0
56	MG	BA	3327	1/1	0.84	0.18	37,37,37,37	0
56	MG	BA	3616	1/1	0.84	0.15	51,51,51,51	0
56	MG	DA	3502	1/1	0.84	0.09	48,48,48,48	0
56	MG	BA	3598	1/1	0.84	0.29	53,53,53,53	0
56	MG	DA	3203	1/1	0.84	0.11	50,50,50,50	0
56	MG	BA	3545	1/1	0.84	0.14	36,36,36,36	0
56	MG	BA	3088	1/1	0.84	0.54	49,49,49,49	0
56	MG	DA	3109	1/1	0.84	0.11	68,68,68,68	0
56	MG	DA	3208	1/1	0.84	0.19	44,44,44,44	0
56	MG	DA	3101	1/1	0.84	0.27	55,55,55,55	0
56	MG	BA	3672	1/1	0.84	0.11	62,62,62,62	0
56	MG	AA	3134	1/1	0.84	0.14	65,65,65,65	0
56	MG	BA	3175	1/1	0.84	0.28	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3241	1/1	0.84	0.12	48,48,48,48	0
56	MG	CA	3036	1/1	0.84	0.18	72,72,72,72	0
56	MG	CA	3159	1/1	0.84	0.12	71,71,71,71	0
56	MG	DA	3285	1/1	0.84	0.15	52,52,52,52	0
56	MG	DA	3494	1/1	0.84	0.31	57,57,57,57	0
56	MG	BA	3392	1/1	0.84	0.21	41,41,41,41	0
56	MG	CA	3002	1/1	0.84	0.09	62,62,62,62	0
56	MG	DA	3593	1/1	0.84	0.11	50,50,50,50	0
56	MG	CA	3152	1/1	0.84	0.23	54,54,54,54	0
56	MG	DA	3126	1/1	0.84	0.21	46,46,46,46	0
56	MG	BA	3097	1/1	0.84	0.18	52,52,52,52	0
56	MG	BA	3276	1/1	0.84	0.16	42,42,42,42	0
56	MG	DA	3031	1/1	0.85	0.11	44,44,44,44	0
56	MG	DA	3572	1/1	0.85	0.06	68,68,68,68	0
56	MG	DA	3194	1/1	0.85	0.12	54,54,54,54	0
56	MG	CA	3050	1/1	0.85	0.17	52,52,52,52	0
56	MG	BA	3673	1/1	0.85	0.15	28,28,28,28	0
56	MG	DA	3100	1/1	0.85	0.12	66,66,66,66	0
56	MG	DA	3034	1/1	0.85	0.12	45,45,45,45	0
56	MG	CA	3021	1/1	0.85	0.21	65,65,65,65	0
56	MG	AA	3153	1/1	0.85	0.12	81,81,81,81	0
56	MG	DA	3570	1/1	0.85	0.19	59,59,59,59	0
56	MG	BA	3696	1/1	0.85	0.10	45,45,45,45	0
56	MG	DB	3003	1/1	0.85	0.19	56,56,56,56	0
56	MG	BA	3026	1/1	0.85	0.26	49,49,49,49	0
56	MG	DA	3466	1/1	0.85	0.28	66,66,66,66	0
56	MG	DA	3500	1/1	0.85	0.11	51,51,51,51	0
56	MG	BA	3457	1/1	0.85	0.17	47,47,47,47	0
56	MG	BA	3786	1/1	0.85	0.18	58,58,58,58	0
56	MG	BA	3585	1/1	0.85	0.08	58,58,58,58	0
56	MG	DA	3044	1/1	0.85	0.15	49,49,49,49	0
56	MG	BA	3319	1/1	0.85	0.17	39,39,39,39	0
56	MG	BA	3700	1/1	0.85	0.13	53,53,53,53	0
56	MG	DA	3467	1/1	0.85	0.14	48,48,48,48	0
56	MG	BA	3093	1/1	0.85	0.16	48,48,48,48	0
56	MG	BA	3079	1/1	0.85	0.34	49,49,49,49	0
56	MG	DA	3420	1/1	0.85	0.13	40,40,40,40	0
56	MG	CA	3077	1/1	0.85	0.18	61,61,61,61	0
56	MG	DE	304	1/1	0.85	0.14	40,40,40,40	0
56	MG	DA	3409	1/1	0.85	0.14	55,55,55,55	0
56	MG	DA	3090	1/1	0.85	0.11	48,48,48,48	0
56	MG	BA	3580	1/1	0.85	0.21	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3019	1/1	0.85	0.14	39,39,39,39	0
56	MG	CA	3168	1/1	0.85	0.15	60,60,60,60	0
56	MG	CA	3125	1/1	0.85	0.10	63,63,63,63	0
56	MG	BA	3103	1/1	0.85	0.17	44,44,44,44	0
56	MG	DA	3347	1/1	0.85	0.13	46,46,46,46	0
56	MG	CA	3049	1/1	0.85	0.17	71,71,71,71	0
56	MG	BA	3016	1/1	0.85	0.12	37,37,37,37	0
56	MG	AE	201	1/1	0.85	0.20	64,64,64,64	0
56	MG	BA	3480	1/1	0.85	0.12	50,50,50,50	0
56	MG	BA	3018	1/1	0.85	0.22	63,63,63,63	0
56	MG	BA	3185	1/1	0.85	0.18	52,52,52,52	0
56	MG	DA	3556	1/1	0.85	0.16	55,55,55,55	0
56	MG	DA	3342	1/1	0.85	0.06	46,46,46,46	0
56	MG	BA	3636	1/1	0.85	0.21	52,52,52,52	0
56	MG	CA	3138	1/1	0.85	0.16	65,65,65,65	0
56	MG	AA	3047	1/1	0.85	0.17	63,63,63,63	0
56	MG	BA	3505	1/1	0.86	0.24	33,33,33,33	0
56	MG	DA	3229	1/1	0.86	0.10	64,64,64,64	0
56	MG	DA	3588	1/1	0.86	0.10	65,65,65,65	0
59	ZN	CN	501	1/1	0.86	0.10	103,103,103,103	0
56	MG	BA	3249	1/1	0.86	0.28	40,40,40,40	0
56	MG	BF	308	1/1	0.86	0.37	45,45,45,45	0
56	MG	DA	3244	1/1	0.86	0.26	59,59,59,59	0
56	MG	BA	3468	1/1	0.86	0.15	45,45,45,45	0
56	MG	BA	3460	1/1	0.86	0.15	58,58,58,58	0
56	MG	CA	3029	1/1	0.86	0.09	58,58,58,58	0
56	MG	DA	3125	1/1	0.86	0.19	40,40,40,40	0
56	MG	DA	3042	1/1	0.86	0.11	46,46,46,46	0
56	MG	BA	3120	1/1	0.86	0.20	50,50,50,50	0
56	MG	AA	3079	1/1	0.86	0.21	55,55,55,55	0
56	MG	CA	3105	1/1	0.86	0.12	51,51,51,51	0
56	MG	DA	3264	1/1	0.86	0.18	50,50,50,50	0
56	MG	DA	3294	1/1	0.86	0.08	36,36,36,36	0
56	MG	BA	3609	1/1	0.86	0.14	54,54,54,54	0
56	MG	BA	3381	1/1	0.86	0.13	45,45,45,45	0
56	MG	AE	203	1/1	0.86	0.76	73,73,73,73	0
56	MG	BA	3741	1/1	0.86	0.14	50,50,50,50	0
56	MG	BA	3555	1/1	0.86	0.15	61,61,61,61	0
56	MG	DD	301	1/1	0.86	0.24	43,43,43,43	0
56	MG	AA	3177	1/1	0.86	0.10	80,80,80,80	0
56	MG	DA	3527	1/1	0.86	0.20	61,61,61,61	0
56	MG	BA	3233	1/1	0.86	0.18	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3142	1/1	0.86	0.13	81,81,81,81	0
56	MG	BA	3617	1/1	0.86	0.26	44,44,44,44	0
56	MG	BA	3017	1/1	0.86	0.17	52,52,52,52	0
56	MG	DA	3269	1/1	0.86	0.15	54,54,54,54	0
56	MG	DA	3138	1/1	0.86	0.22	63,63,63,63	0
56	MG	DB	3002	1/1	0.86	0.15	58,58,58,58	0
56	MG	DA	3372	1/1	0.86	0.13	24,24,24,24	0
56	MG	BA	3027	1/1	0.86	0.12	45,45,45,45	0
56	MG	AA	3015	1/1	0.86	0.12	65,65,65,65	0
56	MG	CA	3047	1/1	0.86	0.12	59,59,59,59	0
56	MG	BA	3083	1/1	0.86	0.19	51,51,51,51	0
56	MG	BG	3001	1/1	0.86	0.21	51,51,51,51	0
56	MG	CA	3041	1/1	0.86	0.17	62,62,62,62	0
56	MG	DA	3152	1/1	0.86	0.24	62,62,62,62	0
56	MG	DA	3248	1/1	0.86	0.14	49,49,49,49	0
56	MG	AA	3167	1/1	0.86	0.15	61,61,61,61	0
56	MG	DA	3245	1/1	0.86	0.15	47,47,47,47	0
56	MG	DA	3291	1/1	0.86	0.13	41,41,41,41	0
56	MG	CA	3100	1/1	0.86	0.08	69,69,69,69	0
56	MG	BA	3558	1/1	0.86	0.21	57,57,57,57	0
56	MG	DA	3433	1/1	0.86	0.13	34,34,34,34	0
56	MG	BB	210	1/1	0.86	0.24	55,55,55,55	0
56	MG	DA	3468	1/1	0.86	0.15	37,37,37,37	0
56	MG	BA	3690	1/1	0.86	0.18	52,52,52,52	0
56	MG	BN	3002	1/1	0.86	0.24	57,57,57,57	0
56	MG	BA	3745	1/1	0.86	0.24	58,58,58,58	0
56	MG	DA	3079	1/1	0.86	0.12	32,32,32,32	0
56	MG	DA	3162	1/1	0.87	0.23	37,37,37,37	0
56	MG	BA	3218	1/1	0.87	0.20	34,34,34,34	0
56	MG	DA	3370	1/1	0.87	0.10	50,50,50,50	0
56	MG	BA	3387	1/1	0.87	0.14	45,45,45,45	0
56	MG	DA	3619	1/1	0.87	0.23	54,54,54,54	0
56	MG	BA	3693	1/1	0.87	0.14	74,74,74,74	0
56	MG	BA	3137	1/1	0.87	0.42	40,40,40,40	0
56	MG	BA	3490	1/1	0.87	0.12	60,60,60,60	0
56	MG	AA	3006	1/1	0.87	0.30	71,71,71,71	0
56	MG	DA	3277	1/1	0.87	0.18	54,54,54,54	0
56	MG	BA	3002	1/1	0.87	0.17	57,57,57,57	0
56	MG	BA	3706	1/1	0.87	0.11	63,63,63,63	0
56	MG	BA	3238	1/1	0.87	0.32	41,41,41,41	0
56	MG	DA	3485	1/1	0.87	0.16	43,43,43,43	0
56	MG	CA	3117	1/1	0.87	0.11	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3225	1/1	0.87	0.11	49,49,49,49	0
56	MG	DA	3537	1/1	0.87	0.14	58,58,58,58	0
56	MG	DA	3493	1/1	0.87	0.15	63,63,63,63	0
56	MG	DA	3482	1/1	0.87	0.13	42,42,42,42	0
56	MG	BA	3807	1/1	0.87	0.71	66,66,66,66	0
56	MG	AA	3187	1/1	0.87	0.12	54,54,54,54	0
56	MG	DA	3107	1/1	0.87	0.12	43,43,43,43	0
56	MG	DA	3001	1/1	0.87	0.24	40,40,40,40	0
56	MG	DA	3053	1/1	0.87	0.51	37,37,37,37	0
56	MG	BA	3076	1/1	0.87	0.34	34,34,34,34	0
56	MG	DA	3060	1/1	0.87	0.15	48,48,48,48	0
56	MG	CA	3014	1/1	0.87	0.13	57,57,57,57	0
56	MG	DA	3236	1/1	0.87	0.11	42,42,42,42	0
56	MG	BA	3198	1/1	0.87	0.22	28,28,28,28	0
56	MG	CA	3144	1/1	0.87	0.06	68,68,68,68	0
56	MG	BA	3677	1/1	0.87	0.17	56,56,56,56	0
56	MG	BA	3434	1/1	0.87	0.25	40,40,40,40	0
56	MG	DA	3146	1/1	0.87	0.19	49,49,49,49	0
56	MG	BA	3430	1/1	0.87	0.15	31,31,31,31	0
56	MG	BA	3277	1/1	0.87	0.27	54,54,54,54	0
56	MG	DA	3331	1/1	0.87	0.08	49,49,49,49	0
56	MG	CA	3020	1/1	0.87	0.12	46,46,46,46	0
56	MG	AA	3026	1/1	0.87	0.10	71,71,71,71	0
56	MG	DA	3541	1/1	0.87	0.12	40,40,40,40	0
56	MG	AA	3180	1/1	0.87	0.14	49,49,49,49	0
56	MG	AA	3045	1/1	0.87	0.32	54,54,54,54	0
56	MG	DA	3624	1/1	0.87	0.49	46,46,46,46	0
56	MG	BA	3624	1/1	0.87	0.13	37,37,37,37	0
56	MG	CA	3030	1/1	0.87	0.18	56,56,56,56	0
56	MG	BN	3007	1/1	0.87	0.20	50,50,50,50	0
56	MG	BA	3704	1/1	0.87	0.33	36,36,36,36	0
56	MG	DA	3054	1/1	0.87	0.10	39,39,39,39	0
56	MG	BA	3806	1/1	0.87	0.70	33,33,33,33	0
56	MG	DA	3256	1/1	0.87	0.12	46,46,46,46	0
56	MG	CA	3071	1/1	0.87	0.10	57,57,57,57	0
56	MG	AA	3021	1/1	0.87	0.13	62,62,62,62	0
56	MG	DA	3343	1/1	0.87	0.17	42,42,42,42	0
56	MG	BA	3228	1/1	0.87	0.21	56,56,56,56	0
56	MG	DA	3652	1/1	0.87	0.13	53,53,53,53	0
56	MG	B9	502	1/1	0.87	0.21	47,47,47,47	0
56	MG	DB	3006	1/1	0.87	0.10	60,60,60,60	0
56	MG	BA	3698	1/1	0.87	0.17	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3168	1/1	0.88	0.07	47,47,47,47	0
56	MG	DA	3129	1/1	0.88	0.20	42,42,42,42	0
56	MG	DA	3459	1/1	0.88	0.11	44,44,44,44	0
56	MG	DA	3070	1/1	0.88	0.11	51,51,51,51	0
56	MG	DA	3163	1/1	0.88	0.13	54,54,54,54	0
56	MG	AA	3005	1/1	0.88	0.22	77,77,77,77	0
56	MG	DA	3562	1/1	0.88	0.22	72,72,72,72	0
56	MG	BA	3553	1/1	0.88	0.14	53,53,53,53	0
56	MG	AA	3139	1/1	0.88	0.16	72,72,72,72	0
56	MG	DA	3221	1/1	0.88	0.12	52,52,52,52	0
56	MG	CA	3143	1/1	0.88	0.13	77,77,77,77	0
56	MG	BA	3131	1/1	0.88	0.35	39,39,39,39	0
56	MG	AE	202	1/1	0.88	0.07	74,74,74,74	0
56	MG	DA	3018	1/1	0.88	0.22	51,51,51,51	0
56	MG	BA	3427	1/1	0.88	0.26	52,52,52,52	0
56	MG	BA	3063	1/1	0.88	0.26	54,54,54,54	0
56	MG	BA	3006	1/1	0.88	0.25	52,52,52,52	0
56	MG	BQ	204	1/1	0.88	0.19	43,43,43,43	0
56	MG	BA	3054	1/1	0.88	0.23	43,43,43,43	0
56	MG	BV	204	1/1	0.88	0.22	47,47,47,47	0
56	MG	AA	3001	1/1	0.88	0.17	77,77,77,77	0
56	MG	DA	3281	1/1	0.88	0.15	49,49,49,49	0
56	MG	BA	3112	1/1	0.88	0.20	42,42,42,42	0
56	MG	BA	3499	1/1	0.88	0.21	19,19,19,19	0
56	MG	BA	3259	1/1	0.88	0.22	59,59,59,59	0
56	MG	BA	3720	1/1	0.88	0.11	45,45,45,45	0
56	MG	DA	3338	1/1	0.88	0.19	43,43,43,43	0
56	MG	BA	3351	1/1	0.88	0.19	59,59,59,59	0
56	MG	DG	3001	1/1	0.88	0.07	57,57,57,57	0
56	MG	CA	3005	1/1	0.88	0.10	73,73,73,73	0
56	MG	AA	3156	1/1	0.88	0.12	67,67,67,67	0
56	MG	AA	3043	1/1	0.88	0.12	76,76,76,76	0
56	MG	DA	3630	1/1	0.88	0.10	51,51,51,51	0
56	MG	BA	3062	1/1	0.88	0.17	48,48,48,48	0
56	MG	BA	3114	1/1	0.88	0.15	34,34,34,34	0
56	MG	CA	3019	1/1	0.88	0.06	62,62,62,62	0
56	MG	AA	3107	1/1	0.88	0.13	63,63,63,63	0
56	MG	BA	3404	1/1	0.88	0.23	23,23,23,23	0
56	MG	DA	3103	1/1	0.88	0.08	71,71,71,71	0
56	MG	DA	3238	1/1	0.88	0.13	54,54,54,54	0
56	MG	DA	3114	1/1	0.88	0.11	55,55,55,55	0
56	MG	BA	3232	1/1	0.88	0.18	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	3122	1/1	0.88	0.22	80,80,80,80	0
56	MG	BA	3801	1/1	0.88	0.27	39,39,39,39	0
56	MG	BA	3678	1/1	0.88	0.47	35,35,35,35	0
56	MG	DA	3479	1/1	0.88	0.19	35,35,35,35	0
56	MG	DA	3623	1/1	0.88	0.41	66,66,66,66	0
56	MG	BA	3626	1/1	0.88	0.13	43,43,43,43	0
56	MG	AA	3179	1/1	0.88	0.27	61,61,61,61	0
56	MG	CA	3024	1/1	0.88	0.11	58,58,58,58	0
56	MG	AA	3073	1/1	0.88	0.22	71,71,71,71	0
56	MG	AA	3080	1/1	0.88	0.24	71,71,71,71	0
56	MG	DA	3122	1/1	0.88	0.08	53,53,53,53	0
56	MG	DA	3016	1/1	0.88	0.32	42,42,42,42	0
56	MG	BA	3721	1/1	0.88	0.17	9,9,9,9	0
56	MG	BA	3055	1/1	0.88	0.20	55,55,55,55	0
56	MG	DA	3364	1/1	0.88	0.21	57,57,57,57	0
56	MG	BG	3002	1/1	0.88	0.08	50,50,50,50	0
56	MG	BA	3440	1/1	0.88	0.24	29,29,29,29	0
56	MG	DA	3366	1/1	0.88	0.11	38,38,38,38	0
56	MG	DA	3426	1/1	0.88	0.10	39,39,39,39	0
56	MG	BA	3066	1/1	0.88	0.16	52,52,52,52	0
56	MG	CA	3120	1/1	0.88	0.10	65,65,65,65	0
56	MG	BA	3755	1/1	0.88	0.16	52,52,52,52	0
56	MG	DA	3017	1/1	0.88	0.12	56,56,56,56	0
56	MG	DA	3132	1/1	0.88	0.15	54,54,54,54	0
56	MG	BP	203	1/1	0.88	0.14	49,49,49,49	0
56	MG	CA	3052	1/1	0.88	0.13	69,69,69,69	0
56	MG	DA	3249	1/1	0.88	0.22	65,65,65,65	0
56	MG	DA	3276	1/1	0.88	0.14	54,54,54,54	0
56	MG	DA	3230	1/1	0.88	0.13	52,52,52,52	0
56	MG	BA	3125	1/1	0.88	0.48	49,49,49,49	0
56	MG	DA	3507	1/1	0.88	0.30	57,57,57,57	0
56	MG	BA	3588	1/1	0.89	0.12	29,29,29,29	0
56	MG	DA	3392	1/1	0.89	0.09	50,50,50,50	0
56	MG	BA	3126	1/1	0.89	0.26	47,47,47,47	0
56	MG	BA	3165	1/1	0.89	0.17	50,50,50,50	0
56	MG	DA	3292	1/1	0.89	0.18	40,40,40,40	0
56	MG	BA	3101	1/1	0.89	0.10	39,39,39,39	0
56	MG	AA	3074	1/1	0.89	0.12	51,51,51,51	0
56	MG	AA	3176	1/1	0.89	0.31	57,57,57,57	0
56	MG	CA	3145	1/1	0.89	0.09	68,68,68,68	0
56	MG	DA	3472	1/1	0.89	0.11	60,60,60,60	0
56	MG	BA	3649	1/1	0.89	0.10	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3165	1/1	0.89	0.12	42,42,42,42	0
56	MG	DA	3324	1/1	0.89	0.21	32,32,32,32	0
56	MG	AQ	3001	1/1	0.89	0.19	52,52,52,52	0
56	MG	DA	3282	1/1	0.89	0.16	42,42,42,42	0
56	MG	BA	3506	1/1	0.89	0.14	31,31,31,31	0
56	MG	DA	3592	1/1	0.89	0.11	40,40,40,40	0
56	MG	BA	3471	1/1	0.89	0.19	27,27,27,27	0
56	MG	AA	3168	1/1	0.89	0.11	57,57,57,57	0
56	MG	BA	3539	1/1	0.89	0.27	29,29,29,29	0
56	MG	BA	3295	1/1	0.89	0.23	49,49,49,49	0
56	MG	BA	3567	1/1	0.89	0.17	45,45,45,45	0
56	MG	BF	304	1/1	0.89	0.13	35,35,35,35	0
56	MG	BA	3659	1/1	0.89	0.16	67,67,67,67	0
56	MG	CA	3033	1/1	0.89	0.15	60,60,60,60	0
56	MG	DA	3258	1/1	0.89	0.17	51,51,51,51	0
56	MG	BA	3768	1/1	0.89	0.10	61,61,61,61	0
56	MG	DA	3185	1/1	0.89	0.07	55,55,55,55	0
56	MG	DA	3046	1/1	0.89	0.13	56,56,56,56	0
56	MG	BA	3284	1/1	0.89	0.27	33,33,33,33	0
56	MG	BA	3154	1/1	0.89	0.32	37,37,37,37	0
56	MG	DP	202	1/1	0.89	0.38	55,55,55,55	0
56	MG	DA	3076	1/1	0.89	0.35	39,39,39,39	0
56	MG	AA	3150	1/1	0.89	0.13	66,66,66,66	0
56	MG	DA	3130	1/1	0.89	0.19	54,54,54,54	0
56	MG	CA	3073	1/1	0.89	0.10	55,55,55,55	0
56	MG	BA	3503	1/1	0.89	0.25	64,64,64,64	0
56	MG	AA	3121	1/1	0.89	0.13	33,33,33,33	0
56	MG	BA	3105	1/1	0.89	0.17	39,39,39,39	0
56	MG	DA	3224	1/1	0.89	0.43	47,47,47,47	0
56	MG	BA	3793	1/1	0.89	0.40	52,52,52,52	0
56	MG	BA	3231	1/1	0.89	0.16	51,51,51,51	0
56	MG	DA	3142	1/1	0.89	0.10	50,50,50,50	0
56	MG	BA	3212	1/1	0.89	0.17	26,26,26,26	0
56	MG	BA	3551	1/1	0.89	0.15	49,49,49,49	0
56	MG	DA	3111	1/1	0.89	0.25	53,53,53,53	0
56	MG	DA	3400	1/1	0.89	0.21	56,56,56,56	0
56	MG	BA	3534	1/1	0.89	0.16	44,44,44,44	0
56	MG	DA	3267	1/1	0.89	0.15	41,41,41,41	0
56	MG	DA	3524	1/1	0.89	0.20	59,59,59,59	0
56	MG	BA	3522	1/1	0.89	0.19	16,16,16,16	0
56	MG	DA	3606	1/1	0.89	0.09	48,48,48,48	0
56	MG	BA	3435	1/1	0.89	0.19	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3035	1/1	0.89	0.08	40,40,40,40	0
56	MG	AA	3089	1/1	0.89	0.14	57,57,57,57	0
56	MG	BA	3691	1/1	0.89	0.10	68,68,68,68	0
56	MG	CA	3015	1/1	0.89	0.10	58,58,58,58	0
56	MG	DA	3583	1/1	0.89	0.09	56,56,56,56	0
56	MG	DA	3085	1/1	0.89	0.11	38,38,38,38	0
56	MG	DA	3626	1/1	0.89	0.28	56,56,56,56	0
56	MG	DA	3437	1/1	0.89	0.15	36,36,36,36	0
56	MG	BA	3359	1/1	0.89	0.23	40,40,40,40	0
56	MG	DA	3064	1/1	0.89	0.28	56,56,56,56	0
56	MG	AA	3068	1/1	0.89	0.24	62,62,62,62	0
56	MG	DA	3212	1/1	0.89	0.07	54,54,54,54	0
56	MG	DD	302	1/1	0.89	0.44	73,73,73,73	0
56	MG	BU	201	1/1	0.89	0.23	36,36,36,36	0
56	MG	AA	3025	1/1	0.89	0.24	69,69,69,69	0
56	MG	AA	3066	1/1	0.89	0.13	58,58,58,58	0
56	MG	BE	301	1/1	0.89	0.19	27,27,27,27	0
56	MG	DA	3314	1/1	0.89	0.08	45,45,45,45	0
56	MG	DA	3175	1/1	0.89	0.44	51,51,51,51	0
56	MG	BA	3804	1/1	0.89	0.13	35,35,35,35	0
56	MG	BA	3682	1/1	0.89	0.30	39,39,39,39	0
56	MG	BA	3744	1/1	0.89	0.16	61,61,61,61	0
56	MG	CA	3064	1/1	0.89	0.07	59,59,59,59	0
56	MG	BA	3583	1/1	0.89	0.14	56,56,56,56	0
56	MG	BA	3057	1/1	0.89	0.10	53,53,53,53	0
56	MG	DA	3187	1/1	0.89	0.22	51,51,51,51	0
56	MG	DA	3228	1/1	0.89	0.10	46,46,46,46	0
56	MG	BA	3326	1/1	0.89	0.14	22,22,22,22	0
56	MG	DA	3002	1/1	0.89	0.27	55,55,55,55	0
56	MG	DA	3226	1/1	0.89	0.17	57,57,57,57	0
56	MG	AA	3096	1/1	0.89	0.23	60,60,60,60	0
56	MG	CA	3063	1/1	0.89	0.10	70,70,70,70	0
56	MG	AA	3014	1/1	0.90	0.09	62,62,62,62	0
56	MG	DA	3082	1/1	0.90	0.17	40,40,40,40	0
56	MG	DA	3670	1/1	0.90	0.18	49,49,49,49	0
56	MG	AX	3006	1/1	0.90	0.11	71,71,71,71	0
56	MG	BA	3699	1/1	0.90	0.12	48,48,48,48	0
56	MG	DA	3010	1/1	0.90	0.14	45,45,45,45	0
56	MG	DA	3609	1/1	0.90	0.11	61,61,61,61	0
56	MG	DA	3416	1/1	0.90	0.13	22,22,22,22	0
56	MG	BA	3739	1/1	0.90	0.27	46,46,46,46	0
56	MG	DA	3049	1/1	0.90	0.13	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3666	1/1	0.90	0.13	47,47,47,47	0
56	MG	BA	3571	1/1	0.90	0.13	46,46,46,46	0
56	MG	BA	3554	1/1	0.90	0.15	24,24,24,24	0
56	MG	BA	3461	1/1	0.90	0.09	62,62,62,62	0
56	MG	BA	3767	1/1	0.90	0.23	57,57,57,57	0
56	MG	BA	3161	1/1	0.90	0.48	46,46,46,46	0
56	MG	DA	3567	1/1	0.90	0.06	57,57,57,57	0
56	MG	BA	3394	1/1	0.90	0.20	20,20,20,20	0
56	MG	DA	3405	1/1	0.90	0.12	41,41,41,41	0
56	MG	AA	3138	1/1	0.90	0.09	73,73,73,73	0
56	MG	CA	3151	1/1	0.90	0.20	60,60,60,60	0
56	MG	DA	3057	1/1	0.90	0.32	55,55,55,55	0
56	MG	DA	3332	1/1	0.90	0.22	50,50,50,50	0
56	MG	D1	101	1/1	0.90	0.10	50,50,50,50	0
56	MG	AA	3161	1/1	0.90	0.20	59,59,59,59	0
56	MG	DA	3113	1/1	0.90	0.13	50,50,50,50	0
56	MG	CA	3139	1/1	0.90	0.15	69,69,69,69	0
56	MG	DA	3179	1/1	0.90	0.20	57,57,57,57	0
56	MG	CA	3013	1/1	0.90	0.10	54,54,54,54	0
56	MG	DA	3441	1/1	0.90	0.06	30,30,30,30	0
56	MG	DA	3280	1/1	0.90	0.07	62,62,62,62	0
56	MG	BA	3687	1/1	0.90	0.22	53,53,53,53	0
56	MG	AA	3002	1/1	0.90	0.09	63,63,63,63	0
56	MG	BX	101	1/1	0.90	0.23	36,36,36,36	0
56	MG	BB	218	1/1	0.90	0.16	31,31,31,31	0
56	MG	DA	3213	1/1	0.90	0.42	46,46,46,46	0
56	MG	DA	3135	1/1	0.90	0.14	46,46,46,46	0
56	MG	BA	3266	1/1	0.90	0.21	27,27,27,27	0
56	MG	CA	3068	1/1	0.90	0.23	64,64,64,64	0
56	MG	DA	3363	1/1	0.90	0.15	49,49,49,49	0
56	MG	BA	3283	1/1	0.90	0.16	30,30,30,30	0
56	MG	BA	3594	1/1	0.90	0.17	33,33,33,33	0
56	MG	DA	3521	1/1	0.90	0.45	55,55,55,55	0
56	MG	DA	3358	1/1	0.90	0.14	28,28,28,28	0
56	MG	AN	502	1/1	0.90	0.17	56,56,56,56	0
56	MG	DA	3424	1/1	0.90	0.08	41,41,41,41	0
56	MG	BA	3340	1/1	0.90	0.11	40,40,40,40	0
56	MG	BA	3548	1/1	0.90	0.13	40,40,40,40	0
56	MG	DA	3651	1/1	0.90	0.12	40,40,40,40	0
56	MG	BA	3225	1/1	0.90	0.19	31,31,31,31	0
56	MG	DA	3613	1/1	0.90	0.07	55,55,55,55	0
56	MG	AM	201	1/1	0.90	0.06	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3266	1/1	0.90	0.18	56,56,56,56	0
56	MG	DA	3668	1/1	0.90	1.77	51,51,51,51	0
56	MG	AA	3140	1/1	0.90	0.17	36,36,36,36	0
56	MG	DA	3589	1/1	0.90	0.06	53,53,53,53	0
56	MG	DA	3014	1/1	0.90	0.15	43,43,43,43	0
56	MG	BA	3193	1/1	0.90	0.34	62,62,62,62	0
56	MG	BA	3671	1/1	0.90	0.19	59,59,59,59	0
56	MG	BA	3315	1/1	0.90	0.23	59,59,59,59	0
56	MG	AA	3022	1/1	0.90	0.10	54,54,54,54	0
56	MG	BA	3651	1/1	0.90	0.34	52,52,52,52	0
56	MG	DA	3199	1/1	0.90	0.10	55,55,55,55	0
56	MG	BA	3614	1/1	0.90	0.21	59,59,59,59	0
56	MG	AA	3141	1/1	0.90	0.24	50,50,50,50	0
56	MG	DA	3608	1/1	0.90	0.20	47,47,47,47	0
56	MG	CA	3008	1/1	0.90	0.26	60,60,60,60	0
56	MG	DA	3159	1/1	0.90	0.10	42,42,42,42	0
56	MG	BA	3452	1/1	0.90	0.29	55,55,55,55	0
56	MG	DA	3123	1/1	0.90	0.14	52,52,52,52	0
56	MG	AA	3064	1/1	0.90	0.21	54,54,54,54	0
56	MG	DA	3591	1/1	0.90	0.10	59,59,59,59	0
56	MG	B5	102	1/1	0.90	0.38	45,45,45,45	0
56	MG	B0	103	1/1	0.90	0.20	38,38,38,38	0
56	MG	DA	3218	1/1	0.90	0.27	30,30,30,30	0
56	MG	AA	3007	1/1	0.90	0.12	54,54,54,54	0
56	MG	BA	3264	1/1	0.90	0.34	45,45,45,45	0
56	MG	BA	3082	1/1	0.90	0.26	55,55,55,55	0
56	MG	CA	3044	1/1	0.90	0.10	44,44,44,44	0
56	MG	DA	3124	1/1	0.90	0.09	50,50,50,50	0
56	MG	DA	3360	1/1	0.90	0.13	37,37,37,37	0
56	MG	DA	3605	1/1	0.90	0.16	54,54,54,54	0
56	MG	BA	3194	1/1	0.90	0.17	62,62,62,62	0
56	MG	BA	3200	1/1	0.90	0.18	41,41,41,41	0
56	MG	DA	3663	1/1	0.90	0.13	37,37,37,37	0
56	MG	AA	3004	1/1	0.90	0.19	66,66,66,66	0
56	MG	DA	3395	1/1	0.90	0.10	33,33,33,33	0
56	MG	BA	3663	1/1	0.90	0.23	65,65,65,65	0
56	MG	BA	3219	1/1	0.90	0.14	62,62,62,62	0
56	MG	BA	3401	1/1	0.90	0.20	34,34,34,34	0
56	MG	DA	3377	1/1	0.90	0.15	62,62,62,62	0
56	MG	CA	3115	1/1	0.90	0.09	60,60,60,60	0
56	MG	CA	3149	1/1	0.90	0.24	74,74,74,74	0
56	MG	DA	3510	1/1	0.90	0.18	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3384	1/1	0.90	0.18	63,63,63,63	0
56	MG	AA	3029	1/1	0.90	0.18	43,43,43,43	0
56	MG	DA	3599	1/1	0.90	0.07	47,47,47,47	0
56	MG	BA	3160	1/1	0.90	0.42	40,40,40,40	0
56	MG	BA	3396	1/1	0.90	0.12	41,41,41,41	0
56	MG	AA	3011	1/1	0.90	0.21	56,56,56,56	0
56	MG	DA	3559	1/1	0.90	0.16	61,61,61,61	0
56	MG	BA	3747	1/1	0.90	0.33	33,33,33,33	0
56	MG	BA	3610	1/1	0.90	0.18	39,39,39,39	0
56	MG	BA	3509	1/1	0.90	0.12	39,39,39,39	0
56	MG	BA	3010	1/1	0.91	0.15	41,41,41,41	0
56	MG	AA	3120	1/1	0.91	0.12	49,49,49,49	0
56	MG	BA	3586	1/1	0.91	0.11	60,60,60,60	0
56	MG	BA	3478	1/1	0.91	0.14	59,59,59,59	0
56	MG	BA	3377	1/1	0.91	0.11	48,48,48,48	0
56	MG	BA	3532	1/1	0.91	0.29	30,30,30,30	0
56	MG	BA	3431	1/1	0.91	0.13	63,63,63,63	0
56	MG	BA	3416	1/1	0.91	0.17	36,36,36,36	0
56	MG	DA	3638	1/1	0.91	0.12	42,42,42,42	0
56	MG	BA	3462	1/1	0.91	0.18	49,49,49,49	0
56	MG	B7	103	1/1	0.91	0.20	35,35,35,35	0
56	MG	DA	3313	1/1	0.91	0.05	46,46,46,46	0
56	MG	BA	3746	1/1	0.91	0.16	55,55,55,55	0
56	MG	DA	3333	1/1	0.91	0.09	51,51,51,51	0
56	MG	DA	3063	1/1	0.91	0.08	54,54,54,54	0
56	MG	BA	3064	1/1	0.91	0.17	33,33,33,33	0
56	MG	BA	3731	1/1	0.91	0.14	26,26,26,26	0
56	MG	DU	3004	1/1	0.91	0.19	59,59,59,59	0
56	MG	AA	3044	1/1	0.91	0.24	55,55,55,55	0
56	MG	BA	3068	1/1	0.91	0.24	46,46,46,46	0
56	MG	AA	3149	1/1	0.91	0.12	68,68,68,68	0
56	MG	CA	3136	1/1	0.91	0.08	55,55,55,55	0
56	MG	BA	3128	1/1	0.91	0.14	44,44,44,44	0
56	MG	DA	3597	1/1	0.91	0.09	49,49,49,49	0
56	MG	CA	3069	1/1	0.91	0.06	59,59,59,59	0
56	MG	DA	3274	1/1	0.91	0.07	54,54,54,54	0
56	MG	BA	3759	1/1	0.91	0.07	36,36,36,36	0
56	MG	AA	3039	1/1	0.91	0.16	46,46,46,46	0
56	MG	BU	204	1/1	0.91	0.31	43,43,43,43	0
56	MG	DA	3538	1/1	0.91	0.14	44,44,44,44	0
56	MG	DA	3202	1/1	0.91	0.44	52,52,52,52	0
56	MG	BA	3324	1/1	0.91	0.19	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	3083	1/1	0.91	0.13	53,53,53,53	0
56	MG	BA	3258	1/1	0.91	0.27	61,61,61,61	0
56	MG	DA	3086	1/1	0.91	0.45	36,36,36,36	0
56	MG	B5	103	1/1	0.91	0.16	41,41,41,41	0
56	MG	DA	3440	1/1	0.91	0.12	51,51,51,51	0
56	MG	DA	3415	1/1	0.91	0.14	59,59,59,59	0
56	MG	DA	3247	1/1	0.91	0.19	34,34,34,34	0
56	MG	DA	3499	1/1	0.91	0.06	61,61,61,61	0
56	MG	BA	3674	1/1	0.91	0.17	55,55,55,55	0
56	MG	BA	3419	1/1	0.91	0.17	25,25,25,25	0
56	MG	BA	3592	1/1	0.91	0.10	64,64,64,64	0
56	MG	DA	3182	1/1	0.91	0.08	43,43,43,43	0
56	MG	BA	3479	1/1	0.91	0.13	53,53,53,53	0
56	MG	DU	3003	1/1	0.91	0.46	53,53,53,53	0
56	MG	CA	3104	1/1	0.91	0.09	60,60,60,60	0
56	MG	CA	3085	1/1	0.91	0.21	73,73,73,73	0
56	MG	BA	3025	1/1	0.91	0.11	48,48,48,48	0
56	MG	BA	3751	1/1	0.91	0.36	55,55,55,55	0
56	MG	BA	3679	1/1	0.91	0.22	56,56,56,56	0
56	MG	CA	3025	1/1	0.91	0.20	61,61,61,61	0
56	MG	BA	3529	1/1	0.91	0.20	25,25,25,25	0
56	MG	DA	3200	1/1	0.91	0.11	57,57,57,57	0
56	MG	BA	3157	1/1	0.91	0.83	36,36,36,36	0
56	MG	DR	5001	1/1	0.91	0.12	51,51,51,51	0
56	MG	DA	3454	1/1	0.91	0.09	56,56,56,56	0
56	MG	BA	3576	1/1	0.91	0.17	36,36,36,36	0
56	MG	DA	3150	1/1	0.91	0.18	52,52,52,52	0
56	MG	DA	3316	1/1	0.91	0.09	34,34,34,34	0
56	MG	DA	3438	1/1	0.91	0.14	55,55,55,55	0
56	MG	BA	3034	1/1	0.91	0.17	34,34,34,34	0
56	MG	BA	3725	1/1	0.91	0.20	44,44,44,44	0
56	MG	BA	3464	1/1	0.91	0.16	46,46,46,46	0
56	MG	BA	3495	1/1	0.91	0.14	58,58,58,58	0
56	MG	DA	3118	1/1	0.91	0.14	43,43,43,43	0
56	MG	BA	3169	1/1	0.91	0.41	50,50,50,50	0
56	MG	DB	3005	1/1	0.91	0.14	48,48,48,48	0
56	MG	DA	3391	1/1	0.91	0.10	44,44,44,44	0
56	MG	DA	3270	1/1	0.91	0.25	56,56,56,56	0
56	MG	BF	305	1/1	0.91	0.12	45,45,45,45	0
56	MG	BA	3248	1/1	0.91	0.20	52,52,52,52	0
56	MG	DP	201	1/1	0.91	0.14	58,58,58,58	0
56	MG	CA	3061	1/1	0.91	0.25	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3647	1/1	0.91	0.21	49,49,49,49	0
56	MG	BA	3247	1/1	0.91	0.17	50,50,50,50	0
56	MG	BA	3014	1/1	0.91	0.25	38,38,38,38	0
56	MG	BQ	201	1/1	0.91	0.23	35,35,35,35	0
56	MG	BY	201	1/1	0.91	0.23	52,52,52,52	0
56	MG	B6	102	1/1	0.91	0.19	51,51,51,51	0
56	MG	BA	3144	1/1	0.91	0.32	43,43,43,43	0
56	MG	CA	3155	1/1	0.91	0.08	76,76,76,76	0
56	MG	AA	3037	1/1	0.91	0.19	46,46,46,46	0
56	MG	BA	3760	1/1	0.91	0.17	43,43,43,43	0
56	MG	BA	3305	1/1	0.91	0.13	46,46,46,46	0
56	MG	DA	3260	1/1	0.91	0.11	55,55,55,55	0
56	MG	BA	3562	1/1	0.91	0.27	44,44,44,44	0
56	MG	DA	3149	1/1	0.91	0.62	37,37,37,37	0
56	MG	BA	3204	1/1	0.91	0.15	55,55,55,55	0
56	MG	BB	221	1/1	0.91	0.12	43,43,43,43	0
56	MG	DA	3574	1/1	0.91	0.09	55,55,55,55	0
56	MG	BA	3222	1/1	0.91	0.11	48,48,48,48	0
56	MG	BA	3369	1/1	0.91	0.20	40,40,40,40	0
56	MG	CA	3132	1/1	0.91	0.21	55,55,55,55	0
56	MG	BA	3737	1/1	0.91	0.10	70,70,70,70	0
56	MG	AA	3189	1/1	0.91	0.24	62,62,62,62	0
56	MG	BA	3621	1/1	0.91	0.15	39,39,39,39	0
56	MG	DA	3102	1/1	0.91	0.26	49,49,49,49	0
56	MG	BA	3211	1/1	0.91	0.28	41,41,41,41	0
56	MG	BA	3368	1/1	0.91	0.21	35,35,35,35	0
56	MG	AA	3050	1/1	0.91	0.22	77,77,77,77	0
56	MG	DA	3412	1/1	0.91	0.11	56,56,56,56	0
56	MG	DA	3211	1/1	0.91	0.09	53,53,53,53	0
56	MG	DA	3508	1/1	0.91	0.08	41,41,41,41	0
56	MG	DA	3354	1/1	0.91	0.05	48,48,48,48	0
56	MG	DA	3116	1/1	0.91	0.10	48,48,48,48	0
56	MG	BA	3689	1/1	0.91	0.10	53,53,53,53	0
56	MG	BA	3102	1/1	0.91	0.22	61,61,61,61	0
56	MG	AA	3173	1/1	0.91	0.21	60,60,60,60	0
56	MG	DA	3099	1/1	0.91	0.17	45,45,45,45	0
56	MG	DA	3073	1/1	0.91	0.08	55,55,55,55	0
56	MG	BA	3422	1/1	0.91	0.16	53,53,53,53	0
56	MG	DA	3547	1/1	0.91	0.14	45,45,45,45	0
56	MG	DA	3131	1/1	0.91	0.19	52,52,52,52	0
56	MG	BA	3697	1/1	0.91	0.12	46,46,46,46	0
56	MG	BR	201	1/1	0.91	0.26	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3342	1/1	0.91	0.10	33,33,33,33	0
56	MG	BA	3467	1/1	0.91	0.18	49,49,49,49	0
56	MG	BA	3622	1/1	0.91	0.14	29,29,29,29	0
56	MG	CA	3096	1/1	0.91	0.15	65,65,65,65	0
56	MG	AA	3102	1/1	0.91	0.24	64,64,64,64	0
56	MG	BA	3020	1/1	0.91	0.13	36,36,36,36	0
56	MG	DA	3041	1/1	0.91	0.09	56,56,56,56	0
56	MG	BF	302	1/1	0.91	0.25	56,56,56,56	0
56	MG	BA	3518	1/1	0.91	0.17	65,65,65,65	0
56	MG	DA	3504	1/1	0.91	0.09	41,41,41,41	0
56	MG	DA	3553	1/1	0.91	0.06	46,46,46,46	0
56	MG	DA	3195	1/1	0.91	0.24	58,58,58,58	0
56	MG	BA	3618	1/1	0.91	0.17	56,56,56,56	0
56	MG	BA	3179	1/1	0.91	0.23	41,41,41,41	0
56	MG	BA	3395	1/1	0.91	0.21	36,36,36,36	0
56	MG	BA	3086	1/1	0.91	0.55	49,49,49,49	0
56	MG	DA	3375	1/1	0.91	0.13	37,37,37,37	0
56	MG	BA	3578	1/1	0.91	0.20	20,20,20,20	0
56	MG	CA	3042	1/1	0.91	0.13	70,70,70,70	0
56	MG	BA	3771	1/1	0.91	0.20	52,52,52,52	0
56	MG	BA	3504	1/1	0.92	0.13	40,40,40,40	0
56	MG	BA	3358	1/1	0.92	0.12	40,40,40,40	0
56	MG	CA	3059	1/1	0.92	0.12	75,75,75,75	0
56	MG	BA	3643	1/1	0.92	0.15	58,58,58,58	0
56	MG	B0	101	1/1	0.92	0.09	55,55,55,55	0
56	MG	BA	3110	1/1	0.92	0.17	46,46,46,46	0
56	MG	BA	3186	1/1	0.92	0.14	47,47,47,47	0
56	MG	BA	3577	1/1	0.92	0.24	18,18,18,18	0
56	MG	DA	3341	1/1	0.92	0.23	67,67,67,67	0
56	MG	CA	3103	1/1	0.92	0.11	79,79,79,79	0
56	MG	AA	3164	1/1	0.92	0.24	51,51,51,51	0
56	MG	CA	3017	1/1	0.92	0.14	76,76,76,76	0
56	MG	DA	3318	1/1	0.92	0.07	33,33,33,33	0
56	MG	DA	3345	1/1	0.92	0.23	38,38,38,38	0
56	MG	BA	3162	1/1	0.92	0.34	53,53,53,53	0
56	MG	BA	3192	1/1	0.92	0.21	53,53,53,53	0
56	MG	BA	3728	1/1	0.92	0.30	60,60,60,60	0
56	MG	BA	3785	1/1	0.92	0.13	81,81,81,81	0
56	MG	DA	3197	1/1	0.92	0.83	55,55,55,55	0
56	MG	BA	3774	1/1	0.92	0.09	37,37,37,37	0
56	MG	BA	3787	1/1	0.92	0.16	57,57,57,57	0
56	MG	AA	3151	1/1	0.92	0.12	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3766	1/1	0.92	0.17	59,59,59,59	0
56	MG	BA	3776	1/1	0.92	0.10	48,48,48,48	0
56	MG	BA	3667	1/1	0.92	0.19	39,39,39,39	0
56	MG	B5	101	1/1	0.92	0.42	39,39,39,39	0
56	MG	BA	3213	1/1	0.92	0.20	35,35,35,35	0
56	MG	AA	3097	1/1	0.92	0.18	71,71,71,71	0
56	MG	DA	3610	1/1	0.92	0.17	49,49,49,49	0
56	MG	DA	3544	1/1	0.92	0.22	39,39,39,39	0
56	MG	DA	3283	1/1	0.92	0.14	43,43,43,43	0
56	MG	DA	3495	1/1	0.92	0.15	39,39,39,39	0
56	MG	DD	307	1/1	0.92	0.40	50,50,50,50	0
56	MG	BA	3477	1/1	0.92	0.12	59,59,59,59	0
56	MG	DA	3576	1/1	0.92	0.09	50,50,50,50	0
56	MG	DA	3590	1/1	0.92	0.09	66,66,66,66	0
56	MG	BA	3397	1/1	0.92	0.14	25,25,25,25	0
56	MG	DA	3453	1/1	0.92	0.21	56,56,56,56	0
56	MG	BA	3207	1/1	0.92	0.32	44,44,44,44	0
56	MG	BA	3322	1/1	0.92	0.28	48,48,48,48	0
56	MG	AA	3069	1/1	0.92	0.15	52,52,52,52	0
56	MG	BA	3263	1/1	0.92	0.25	56,56,56,56	0
56	MG	CA	3080	1/1	0.92	0.10	56,56,56,56	0
56	MG	BA	3738	1/1	0.92	0.26	60,60,60,60	0
56	MG	CA	3169	1/1	0.92	0.10	52,52,52,52	0
56	MG	BA	3041	1/1	0.92	0.25	35,35,35,35	0
56	MG	AA	3070	1/1	0.92	0.12	65,65,65,65	0
56	MG	AA	3109	1/1	0.92	0.13	67,67,67,67	0
56	MG	BA	3773	1/1	0.92	0.13	38,38,38,38	0
56	MG	DA	3545	1/1	0.92	0.09	51,51,51,51	0
56	MG	BA	3380	1/1	0.92	0.11	36,36,36,36	0
56	MG	BF	306	1/1	0.92	0.52	30,30,30,30	0
56	MG	BA	3108	1/1	0.92	0.24	64,64,64,64	0
56	MG	DA	3056	1/1	0.92	0.14	60,60,60,60	0
56	MG	DA	3209	1/1	0.92	0.28	46,46,46,46	0
56	MG	CA	3054	1/1	0.92	0.12	70,70,70,70	0
56	MG	BA	3122	1/1	0.92	0.42	46,46,46,46	0
56	MG	BA	3360	1/1	0.92	0.14	21,21,21,21	0
56	MG	BA	3279	1/1	0.92	0.24	45,45,45,45	0
56	MG	BA	3262	1/1	0.92	0.27	54,54,54,54	0
56	MG	BA	3770	1/1	0.92	0.14	47,47,47,47	0
56	MG	DW	202	1/1	0.92	0.43	46,46,46,46	0
56	MG	DA	3628	1/1	0.92	0.08	47,47,47,47	0
56	MG	CF	3001	1/1	0.92	0.10	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	3128	1/1	0.92	0.12	67,67,67,67	0
56	MG	D8	5001	1/1	0.92	0.19	52,52,52,52	0
56	MG	BA	3646	1/1	0.92	0.20	57,57,57,57	0
56	MG	DA	3096	1/1	0.92	0.82	48,48,48,48	0
56	MG	AA	3087	1/1	0.92	0.26	53,53,53,53	0
56	MG	BA	3151	1/1	0.92	0.26	37,37,37,37	0
56	MG	CA	3072	1/1	0.92	0.22	62,62,62,62	0
56	MG	BA	3648	1/1	0.92	0.26	65,65,65,65	0
56	MG	BU	205	1/1	0.92	0.26	43,43,43,43	0
56	MG	BA	3250	1/1	0.92	0.28	42,42,42,42	0
56	MG	DA	3565	1/1	0.92	0.09	45,45,45,45	0
56	MG	DA	3452	1/1	0.92	0.10	37,37,37,37	0
56	MG	BA	3790	1/1	0.92	0.23	29,29,29,29	0
56	MG	B8	102	1/1	0.92	0.15	41,41,41,41	0
56	MG	DA	3388	1/1	0.92	0.14	52,52,52,52	0
56	MG	BA	3531	1/1	0.92	0.28	43,43,43,43	0
56	MG	DA	3376	1/1	0.92	0.15	51,51,51,51	0
56	MG	DA	3497	1/1	0.92	0.13	36,36,36,36	0
56	MG	DA	3431	1/1	0.92	0.09	64,64,64,64	0
56	MG	BA	3439	1/1	0.92	0.14	71,71,71,71	0
56	MG	BA	3217	1/1	0.92	0.20	47,47,47,47	0
56	MG	DA	3147	1/1	0.92	0.12	53,53,53,53	0
56	MG	DA	3369	1/1	0.92	0.10	37,37,37,37	0
56	MG	DA	3322	1/1	0.92	0.12	53,53,53,53	0
56	MG	BB	202	1/1	0.92	0.20	45,45,45,45	0
56	MG	DA	3089	1/1	0.92	0.12	47,47,47,47	0
56	MG	DB	3004	1/1	0.92	0.14	53,53,53,53	0
56	MG	DA	3184	1/1	0.92	0.09	49,49,49,49	0
56	MG	DA	3039	1/1	0.92	0.11	44,44,44,44	0
56	MG	AA	3012	1/1	0.92	0.14	50,50,50,50	0
56	MG	DB	3008	1/1	0.92	0.13	64,64,64,64	0
56	MG	BA	3808	1/1	0.92	0.09	40,40,40,40	0
56	MG	DA	3357	1/1	0.92	0.09	38,38,38,38	0
56	MG	CA	3106	1/1	0.92	0.08	58,58,58,58	0
56	MG	DA	3189	1/1	0.92	0.13	41,41,41,41	0
56	MG	BA	3149	1/1	0.92	0.39	36,36,36,36	0
56	MG	DA	3310	1/1	0.92	0.20	49,49,49,49	0
56	MG	DA	3193	1/1	0.92	0.08	46,46,46,46	0
56	MG	BA	3459	1/1	0.92	0.20	47,47,47,47	0
56	MG	BA	3148	1/1	0.92	0.08	49,49,49,49	0
56	MG	DA	3153	1/1	0.92	0.17	38,38,38,38	0
56	MG	BU	208	1/1	0.92	0.23	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	B0	102	1/1	0.92	0.17	50,50,50,50	0
56	MG	DA	3272	1/1	0.92	0.10	45,45,45,45	0
56	MG	BA	3089	1/1	0.92	0.30	42,42,42,42	0
56	MG	BB	220	1/1	0.92	0.10	51,51,51,51	0
56	MG	BA	3346	1/1	0.92	0.15	29,29,29,29	0
56	MG	BA	3033	1/1	0.92	0.60	42,42,42,42	0
56	MG	DA	3295	1/1	0.92	0.10	30,30,30,30	0
56	MG	AA	3127	1/1	0.92	0.12	79,79,79,79	0
56	MG	DA	3299	1/1	0.92	0.13	40,40,40,40	0
56	MG	AA	3055	1/1	0.92	0.19	69,69,69,69	0
56	MG	BA	3039	1/1	0.92	0.25	58,58,58,58	0
56	MG	BA	3627	1/1	0.92	0.13	57,57,57,57	0
56	MG	BA	3740	1/1	0.92	0.15	35,35,35,35	0
56	MG	BA	3350	1/1	0.92	0.21	28,28,28,28	0
56	MG	DA	3578	1/1	0.92	0.06	40,40,40,40	0
56	MG	BA	3717	1/1	0.92	0.14	54,54,54,54	0
56	MG	DA	3006	1/1	0.92	0.19	58,58,58,58	0
56	MG	DA	3419	1/1	0.92	0.12	45,45,45,45	0
56	MG	DA	3393	1/1	0.92	0.20	48,48,48,48	0
56	MG	BA	3650	1/1	0.92	0.14	48,48,48,48	0
56	MG	BA	3253	1/1	0.92	0.19	47,47,47,47	0
56	MG	BA	3252	1/1	0.92	0.15	44,44,44,44	0
56	MG	BA	3367	1/1	0.92	0.15	34,34,34,34	0
56	MG	BA	3638	1/1	0.92	0.11	56,56,56,56	0
56	MG	DA	3549	1/1	0.92	0.14	32,32,32,32	0
56	MG	DA	3666	1/1	0.92	0.59	47,47,47,47	0
56	MG	DA	3385	1/1	0.92	0.10	32,32,32,32	0
56	MG	DA	3422	1/1	0.92	0.11	51,51,51,51	0
56	MG	BA	3575	1/1	0.92	0.18	27,27,27,27	0
56	MG	CA	3058	1/1	0.92	0.06	59,59,59,59	0
56	MG	DA	3287	1/1	0.92	0.07	39,39,39,39	0
56	MG	DA	3020	1/1	0.92	0.16	32,32,32,32	0
56	MG	DA	3227	1/1	0.92	0.40	49,49,49,49	0
56	MG	CA	3165	1/1	0.92	0.13	60,60,60,60	0
56	MG	BA	3779	1/1	0.92	0.15	45,45,45,45	0
56	MG	DA	3634	1/1	0.92	0.28	61,61,61,61	0
56	MG	CA	3113	1/1	0.92	0.16	49,49,49,49	0
56	MG	DA	3300	1/1	0.92	0.10	41,41,41,41	0
56	MG	AA	3174	1/1	0.93	0.06	54,54,54,54	0
56	MG	BA	3196	1/1	0.93	0.16	40,40,40,40	0
56	MG	DA	3191	1/1	0.93	0.16	46,46,46,46	0
56	MG	BA	3143	1/1	0.93	0.27	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3138	1/1	0.93	0.45	40,40,40,40	0
56	MG	AA	3019	1/1	0.93	0.21	66,66,66,66	0
56	MG	DA	3503	1/1	0.93	0.09	31,31,31,31	0
56	MG	CA	3023	1/1	0.93	0.12	39,39,39,39	0
56	MG	BA	3652	1/1	0.93	0.13	61,61,61,61	0
56	MG	BA	3081	1/1	0.93	0.14	33,33,33,33	0
56	MG	CA	3003	1/1	0.93	0.12	51,51,51,51	0
56	MG	BA	3795	1/1	0.93	0.27	43,43,43,43	0
56	MG	BA	3330	1/1	0.93	0.13	52,52,52,52	0
59	ZN	B4	501	1/1	0.93	0.12	99,99,99,99	0
56	MG	AA	3072	1/1	0.93	0.14	45,45,45,45	0
56	MG	DA	3489	1/1	0.93	0.14	45,45,45,45	0
56	MG	AD	502	1/1	0.93	0.18	56,56,56,56	0
56	MG	DA	3071	1/1	0.93	0.09	48,48,48,48	0
56	MG	BA	3492	1/1	0.93	0.16	47,47,47,47	0
56	MG	BA	3251	1/1	0.93	0.38	52,52,52,52	0
56	MG	DA	3639	1/1	0.93	0.06	52,52,52,52	0
56	MG	DA	3584	1/1	0.93	0.14	31,31,31,31	0
56	MG	BA	3597	1/1	0.93	0.11	40,40,40,40	0
56	MG	BA	3772	1/1	0.93	0.18	56,56,56,56	0
56	MG	BA	3214	1/1	0.93	0.29	44,44,44,44	0
56	MG	DA	3534	1/1	0.93	0.15	67,67,67,67	0
56	MG	DA	3059	1/1	0.93	0.16	40,40,40,40	0
56	MG	DA	3177	1/1	0.93	0.12	46,46,46,46	0
56	MG	BA	3606	1/1	0.93	0.08	67,67,67,67	0
56	MG	DA	3161	1/1	0.93	0.13	37,37,37,37	0
56	MG	BF	303	1/1	0.93	0.31	43,43,43,43	0
56	MG	BA	3633	1/1	0.93	0.25	59,59,59,59	0
56	MG	DV	3002	1/1	0.93	0.64	48,48,48,48	0
56	MG	DA	3528	1/1	0.93	0.08	39,39,39,39	0
56	MG	BA	3783	1/1	0.93	0.15	43,43,43,43	0
56	MG	DA	3143	1/1	0.93	0.61	36,36,36,36	0
56	MG	BA	3265	1/1	0.93	0.09	49,49,49,49	0
56	MG	DA	3563	1/1	0.93	0.14	61,61,61,61	0
56	MG	BA	3426	1/1	0.93	0.18	20,20,20,20	0
56	MG	BA	3224	1/1	0.93	0.44	50,50,50,50	0
56	MG	DA	3012	1/1	0.93	0.10	39,39,39,39	0
56	MG	DA	3134	1/1	0.93	0.07	48,48,48,48	0
56	MG	BA	3408	1/1	0.93	0.14	21,21,21,21	0
56	MG	BA	3045	1/1	0.93	0.17	38,38,38,38	0
56	MG	DA	3571	1/1	0.93	0.12	51,51,51,51	0
56	MG	DA	3665	1/1	0.93	0.42	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3018	1/1	0.93	0.09	52,52,52,52	0
56	MG	BA	3318	1/1	0.93	0.16	25,25,25,25	0
56	MG	DO	5001	1/1	0.93	0.12	55,55,55,55	0
56	MG	DA	3141	1/1	0.93	0.12	46,46,46,46	0
59	ZN	DY	501	1/1	0.93	0.16	97,97,97,97	0
56	MG	CA	3099	1/1	0.93	0.09	58,58,58,58	0
56	MG	DB	3010	1/1	0.93	0.20	53,53,53,53	0
56	MG	AA	3188	1/1	0.93	0.12	49,49,49,49	0
56	MG	CA	3134	1/1	0.93	0.13	65,65,65,65	0
56	MG	DA	3251	1/1	0.93	0.12	46,46,46,46	0
56	MG	DA	3575	1/1	0.93	0.14	51,51,51,51	0
56	MG	BA	3156	1/1	0.93	0.20	32,32,32,32	0
56	MG	DA	3442	1/1	0.93	0.09	37,37,37,37	0
56	MG	BA	3713	1/1	0.93	0.18	26,26,26,26	0
56	MG	DA	3622	1/1	0.93	0.14	35,35,35,35	0
56	MG	BA	3302	1/1	0.93	0.20	24,24,24,24	0
56	MG	DA	3298	1/1	0.93	0.12	55,55,55,55	0
56	MG	BD	3308	1/1	0.93	0.64	60,60,60,60	0
56	MG	DA	3383	1/1	0.93	0.11	31,31,31,31	0
56	MG	BA	3159	1/1	0.93	0.24	40,40,40,40	0
56	MG	BA	3100	1/1	0.93	0.26	53,53,53,53	0
56	MG	BA	3417	1/1	0.93	0.17	32,32,32,32	0
56	MG	BA	3629	1/1	0.93	0.16	57,57,57,57	0
56	MG	BA	3599	1/1	0.93	0.11	45,45,45,45	0
56	MG	BA	3420	1/1	0.93	0.30	46,46,46,46	0
56	MG	BA	3523	1/1	0.93	0.25	47,47,47,47	0
56	MG	DA	3555	1/1	0.93	0.08	56,56,56,56	0
56	MG	DA	3396	1/1	0.93	0.16	47,47,47,47	0
56	MG	BA	3590	1/1	0.93	0.15	60,60,60,60	0
56	MG	CA	3160	1/1	0.93	0.17	61,61,61,61	0
56	MG	DA	3554	1/1	0.93	0.09	47,47,47,47	0
56	MG	DA	3335	1/1	0.93	0.11	43,43,43,43	0
56	MG	DA	3095	1/1	0.93	0.11	43,43,43,43	0
56	MG	DE	305	1/1	0.93	0.14	38,38,38,38	0
56	MG	AA	3172	1/1	0.93	0.22	55,55,55,55	0
56	MG	DA	3058	1/1	0.93	0.37	50,50,50,50	0
56	MG	BA	3091	1/1	0.93	0.20	40,40,40,40	0
56	MG	BW	202	1/1	0.93	0.20	41,41,41,41	0
56	MG	BA	3559	1/1	0.93	0.04	59,59,59,59	0
56	MG	CA	3091	1/1	0.93	0.20	70,70,70,70	0
56	MG	DA	3173	1/1	0.93	0.20	51,51,51,51	0
56	MG	BA	3714	1/1	0.93	0.36	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3272	1/1	0.93	0.14	22,22,22,22	0
56	MG	CA	3127	1/1	0.93	0.17	65,65,65,65	0
56	MG	DA	3465	1/1	0.93	0.16	49,49,49,49	0
56	MG	BB	207	1/1	0.93	0.18	39,39,39,39	0
56	MG	BA	3337	1/1	0.93	0.25	46,46,46,46	0
56	MG	BR	202	1/1	0.93	0.22	42,42,42,42	0
56	MG	BA	3227	1/1	0.93	0.18	34,34,34,34	0
56	MG	DA	3568	1/1	0.93	0.12	66,66,66,66	0
56	MG	BA	3174	1/1	0.93	0.16	50,50,50,50	0
56	MG	DA	3457	1/1	0.93	0.16	43,43,43,43	0
56	MG	BA	3060	1/1	0.93	0.27	26,26,26,26	0
56	MG	BA	3780	1/1	0.93	0.23	54,54,54,54	0
56	MG	BB	216	1/1	0.93	0.11	63,63,63,63	0
56	MG	BA	3281	1/1	0.93	0.15	56,56,56,56	0
56	MG	DA	3253	1/1	0.93	0.11	47,47,47,47	0
56	MG	DA	3268	1/1	0.93	0.13	56,56,56,56	0
56	MG	BA	3425	1/1	0.93	0.14	48,48,48,48	0
56	MG	AA	3133	1/1	0.93	0.23	66,66,66,66	0
56	MG	BA	3582	1/1	0.93	0.20	19,19,19,19	0
56	MG	DA	3104	1/1	0.93	0.16	39,39,39,39	0
56	MG	BA	3065	1/1	0.93	0.20	41,41,41,41	0
56	MG	AA	3142	1/1	0.93	0.09	46,46,46,46	0
56	MG	DA	3305	1/1	0.93	0.12	45,45,45,45	0
56	MG	DA	3413	1/1	0.93	0.08	34,34,34,34	0
56	MG	BA	3613	1/1	0.93	0.18	55,55,55,55	0
56	MG	BA	3061	1/1	0.93	0.30	49,49,49,49	0
56	MG	AA	3160	1/1	0.93	0.14	54,54,54,54	0
56	MG	DA	3279	1/1	0.93	0.11	54,54,54,54	0
56	MG	AA	3031	1/1	0.93	0.12	54,54,54,54	0
56	MG	DA	3140	1/1	0.93	0.35	44,44,44,44	0
56	MG	BA	3299	1/1	0.93	0.16	44,44,44,44	0
56	MG	CA	3173	1/1	0.93	0.10	58,58,58,58	0
56	MG	DA	3564	1/1	0.93	0.10	50,50,50,50	0
56	MG	BA	3723	1/1	0.93	0.15	25,25,25,25	0
56	MG	CA	3026	1/1	0.93	0.12	55,55,55,55	0
56	MG	DA	3648	1/1	0.93	0.18	31,31,31,31	0
56	MG	BA	3595	1/1	0.93	0.62	43,43,43,43	0
56	MG	BA	3724	1/1	0.93	0.17	25,25,25,25	0
56	MG	BA	3612	1/1	0.93	0.16	58,58,58,58	0
56	MG	BA	3013	1/1	0.93	0.17	26,26,26,26	0
56	MG	BA	3163	1/1	0.93	0.33	34,34,34,34	0
56	MG	DA	3460	1/1	0.93	0.10	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3061	1/1	0.93	0.20	41,41,41,41	0
56	MG	AA	3143	1/1	0.93	0.09	57,57,57,57	0
56	MG	BA	3563	1/1	0.93	0.09	44,44,44,44	0
56	MG	AA	3042	1/1	0.93	0.10	55,55,55,55	0
56	MG	AA	3154	1/1	0.93	0.10	50,50,50,50	0
56	MG	DB	3009	1/1	0.93	0.12	58,58,58,58	0
56	MG	BA	3254	1/1	0.93	0.15	55,55,55,55	0
56	MG	DA	3309	1/1	0.93	0.32	46,46,46,46	0
56	MG	BA	3096	1/1	0.93	0.30	61,61,61,61	0
56	MG	BA	3314	1/1	0.93	0.12	44,44,44,44	0
56	MG	DA	3458	1/1	0.93	0.08	57,57,57,57	0
56	MG	DA	3319	1/1	0.93	0.27	52,52,52,52	0
56	MG	DA	3374	1/1	0.93	0.07	31,31,31,31	0
56	MG	BA	3399	1/1	0.93	0.16	61,61,61,61	0
56	MG	BA	3520	1/1	0.93	0.17	50,50,50,50	0
56	MG	DF	303	1/1	0.93	0.08	52,52,52,52	0
56	MG	BA	3566	1/1	0.93	0.19	50,50,50,50	0
56	MG	BA	3722	1/1	0.93	0.19	17,17,17,17	0
56	MG	AA	3145	1/1	0.93	0.12	65,65,65,65	0
56	MG	DA	3522	1/1	0.93	0.28	53,53,53,53	0
56	MG	DA	3418	1/1	0.93	0.11	44,44,44,44	0
56	MG	BA	3443	1/1	0.93	0.17	27,27,27,27	0
56	MG	BA	3347	1/1	0.93	0.16	37,37,37,37	0
56	MG	BA	3694	1/1	0.93	0.14	54,54,54,54	0
56	MG	DA	3617	1/1	0.93	0.10	45,45,45,45	0
56	MG	BA	3178	1/1	0.93	0.65	42,42,42,42	0
56	MG	BA	3133	1/1	0.93	0.16	48,48,48,48	0
56	MG	BA	3538	1/1	0.93	0.18	26,26,26,26	0
56	MG	CA	3121	1/1	0.93	0.16	81,81,81,81	0
56	MG	DA	3490	1/1	0.93	0.12	43,43,43,43	0
56	MG	BA	3121	1/1	0.94	0.43	45,45,45,45	0
56	MG	DA	3183	1/1	0.94	0.13	40,40,40,40	0
56	MG	BA	3049	1/1	0.94	0.13	34,34,34,34	0
56	MG	BA	3308	1/1	0.94	0.12	49,49,49,49	0
56	MG	DA	3631	1/1	0.94	0.10	57,57,57,57	0
56	MG	DA	3051	1/1	0.94	0.08	45,45,45,45	0
56	MG	BA	3637	1/1	0.94	0.10	54,54,54,54	0
56	MG	DA	3220	1/1	0.94	0.07	50,50,50,50	0
56	MG	DA	3259	1/1	0.94	0.15	53,53,53,53	0
56	MG	AA	3036	1/1	0.94	0.19	69,69,69,69	0
56	MG	DA	3445	1/1	0.94	0.16	50,50,50,50	0
56	MG	BB	204	1/1	0.94	0.14	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3429	1/1	0.94	0.13	45,45,45,45	0
56	MG	DA	3535	1/1	0.94	0.07	59,59,59,59	0
56	MG	CA	3126	1/1	0.94	0.09	57,57,57,57	0
56	MG	DA	3361	1/1	0.94	0.11	25,25,25,25	0
56	MG	DA	3463	1/1	0.94	0.06	32,32,32,32	0
56	MG	BA	3494	1/1	0.94	0.13	47,47,47,47	0
56	MG	BA	3072	1/1	0.94	0.15	58,58,58,58	0
56	MG	BA	3732	1/1	0.94	0.17	41,41,41,41	0
56	MG	DA	3252	1/1	0.94	0.10	38,38,38,38	0
56	MG	BA	3702	1/1	0.94	0.23	53,53,53,53	0
56	MG	AA	3158	1/1	0.94	0.09	71,71,71,71	0
56	MG	DA	3025	1/1	0.94	0.14	52,52,52,52	0
56	MG	DA	3604	1/1	0.94	0.14	47,47,47,47	0
56	MG	DA	3091	1/1	0.94	0.11	46,46,46,46	0
56	MG	BA	3402	1/1	0.94	0.14	25,25,25,25	0
56	MG	DA	3067	1/1	0.94	0.12	45,45,45,45	0
56	MG	BA	3798	1/1	0.94	0.09	51,51,51,51	0
56	MG	BA	3719	1/1	0.94	0.16	36,36,36,36	0
56	MG	DA	3008	1/1	0.94	0.14	40,40,40,40	0
56	MG	BA	3240	1/1	0.94	0.10	30,30,30,30	0
56	MG	DA	3625	1/1	0.94	0.18	56,56,56,56	0
56	MG	BA	3449	1/1	0.94	0.19	32,32,32,32	0
56	MG	BA	3600	1/1	0.94	0.17	50,50,50,50	0
56	MG	DA	3410	1/1	0.94	0.10	46,46,46,46	0
56	MG	AA	3052	1/1	0.94	0.15	49,49,49,49	0
56	MG	CA	3004	1/1	0.94	0.09	67,67,67,67	0
56	MG	DA	3284	1/1	0.94	0.18	37,37,37,37	0
56	MG	DA	3516	1/1	0.94	0.28	52,52,52,52	0
56	MG	DA	3398	1/1	0.94	0.14	52,52,52,52	0
56	MG	DA	3611	1/1	0.94	0.20	45,45,45,45	0
56	MG	BA	3639	1/1	0.94	0.15	54,54,54,54	0
56	MG	DA	3072	1/1	0.94	0.13	52,52,52,52	0
56	MG	DA	3297	1/1	0.94	0.12	24,24,24,24	0
56	MG	BA	3260	1/1	0.94	0.10	42,42,42,42	0
56	MG	DA	3178	1/1	0.94	0.28	53,53,53,53	0
56	MG	DA	3551	1/1	0.94	0.07	47,47,47,47	0
56	MG	DA	3365	1/1	0.94	0.08	56,56,56,56	0
56	MG	BA	3466	1/1	0.94	0.19	44,44,44,44	0
56	MG	DA	3659	1/1	0.94	0.48	39,39,39,39	0
56	MG	DA	3015	1/1	0.94	0.54	48,48,48,48	0
56	MG	DA	3386	1/1	0.94	0.08	23,23,23,23	0
56	MG	BA	3335	1/1	0.94	0.20	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3262	1/1	0.94	0.07	46,46,46,46	0
56	MG	AA	3016	1/1	0.94	0.14	55,55,55,55	0
56	MG	BA	3540	1/1	0.94	0.11	57,57,57,57	0
56	MG	DA	3581	1/1	0.94	0.10	35,35,35,35	0
56	MG	BA	3764	1/1	0.94	0.21	44,44,44,44	0
56	MG	DA	3435	1/1	0.94	0.15	55,55,55,55	0
56	MG	CA	3093	1/1	0.94	0.18	65,65,65,65	0
56	MG	BA	3130	1/1	0.94	0.56	41,41,41,41	0
56	MG	CA	3164	1/1	0.94	0.07	73,73,73,73	0
56	MG	BA	3166	1/1	0.94	0.16	46,46,46,46	0
56	MG	AA	3095	1/1	0.94	0.12	50,50,50,50	0
56	MG	AA	3017	1/1	0.94	0.13	69,69,69,69	0
56	MG	DA	3560	1/1	0.94	0.07	47,47,47,47	0
56	MG	BA	3323	1/1	0.94	0.15	43,43,43,43	0
56	MG	BA	3510	1/1	0.94	0.11	42,42,42,42	0
56	MG	BA	3075	1/1	0.94	0.18	21,21,21,21	0
56	MG	DA	3038	1/1	0.94	0.15	28,28,28,28	0
56	MG	BA	3683	1/1	0.94	0.15	43,43,43,43	0
56	MG	DA	3569	1/1	0.94	0.24	59,59,59,59	0
56	MG	BA	3312	1/1	0.94	0.18	35,35,35,35	0
56	MG	BA	3124	1/1	0.94	0.20	35,35,35,35	0
56	MG	BA	3056	1/1	0.94	0.23	50,50,50,50	0
56	MG	BA	3799	1/1	0.94	0.56	50,50,50,50	0
56	MG	DA	3511	1/1	0.94	0.14	54,54,54,54	0
56	MG	DQ	3003	1/1	0.94	0.50	52,52,52,52	0
56	MG	DA	3237	1/1	0.94	0.19	43,43,43,43	0
56	MG	BA	3561	1/1	0.94	0.18	55,55,55,55	0
56	MG	AA	3058	1/1	0.94	0.12	61,61,61,61	0
56	MG	DA	3308	1/1	0.94	0.10	49,49,49,49	0
56	MG	BA	3715	1/1	0.94	0.25	51,51,51,51	0
56	MG	BA	3517	1/1	0.94	0.11	49,49,49,49	0
56	MG	AA	3086	1/1	0.94	0.10	48,48,48,48	0
56	MG	CA	3057	1/1	0.94	0.12	52,52,52,52	0
56	MG	AA	3057	1/1	0.94	0.20	66,66,66,66	0
56	MG	BA	3080	1/1	0.94	0.26	51,51,51,51	0
56	MG	DA	3427	1/1	0.94	0.07	45,45,45,45	0
56	MG	DA	3539	1/1	0.94	0.09	38,38,38,38	0
56	MG	AA	3119	1/1	0.94	0.04	65,65,65,65	0
56	MG	AA	3162	1/1	0.94	0.15	59,59,59,59	0
56	MG	CA	3090	1/1	0.94	0.21	67,67,67,67	0
56	MG	DU	3002	1/1	0.94	0.44	52,52,52,52	0
56	MG	AA	3056	1/1	0.94	0.26	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3778	1/1	0.94	0.11	41,41,41,41	0
56	MG	BA	3150	1/1	0.94	0.19	56,56,56,56	0
56	MG	BA	3433	1/1	0.94	0.17	31,31,31,31	0
56	MG	DA	3275	1/1	0.94	0.09	58,58,58,58	0
56	MG	DA	3430	1/1	0.94	0.11	52,52,52,52	0
56	MG	BA	3484	1/1	0.94	0.16	51,51,51,51	0
56	MG	BA	3366	1/1	0.94	0.11	42,42,42,42	0
56	MG	CA	3112	1/1	0.94	0.10	56,56,56,56	0
56	MG	BA	3501	1/1	0.94	0.13	43,43,43,43	0
56	MG	CX	3003	1/1	0.94	0.16	58,58,58,58	0
56	MG	CA	3154	1/1	0.94	0.19	54,54,54,54	0
56	MG	DF	305	1/1	0.94	0.45	44,44,44,44	0
56	MG	BA	3117	1/1	0.94	0.35	35,35,35,35	0
56	MG	BA	3707	1/1	0.94	0.10	43,43,43,43	0
56	MG	BA	3456	1/1	0.94	0.12	32,32,32,32	0
56	MG	BA	3382	1/1	0.94	0.13	41,41,41,41	0
56	MG	DA	3273	1/1	0.94	0.10	39,39,39,39	0
56	MG	DA	3325	1/1	0.94	0.24	37,37,37,37	0
56	MG	BD	3301	1/1	0.94	0.27	37,37,37,37	0
56	MG	DA	3158	1/1	0.94	0.19	30,30,30,30	0
56	MG	BA	3593	1/1	0.94	0.18	47,47,47,47	0
56	MG	BA	3587	1/1	0.94	0.09	54,54,54,54	0
56	MG	DA	3447	1/1	0.94	0.14	41,41,41,41	0
56	MG	CA	3116	1/1	0.94	0.08	54,54,54,54	0
56	MG	DA	3434	1/1	0.94	0.12	27,27,27,27	0
56	MG	BA	3119	1/1	0.94	0.22	29,29,29,29	0
56	MG	BA	3757	1/1	0.94	0.17	45,45,45,45	0
56	MG	AA	3030	1/1	0.94	0.12	63,63,63,63	0
56	MG	DA	3098	1/1	0.94	0.09	57,57,57,57	0
56	MG	DA	3350	1/1	0.94	0.07	53,53,53,53	0
56	MG	DA	3240	1/1	0.94	0.09	42,42,42,42	0
56	MG	AA	3155	1/1	0.94	0.10	49,49,49,49	0
56	MG	AA	3054	1/1	0.94	0.07	62,62,62,62	0
56	MG	DA	3596	1/1	0.94	0.07	65,65,65,65	0
56	MG	BA	3748	1/1	0.94	0.10	69,69,69,69	0
56	MG	DA	3170	1/1	0.94	0.22	46,46,46,46	0
56	MG	BA	3418	1/1	0.94	0.16	34,34,34,34	0
56	MG	DA	3201	1/1	0.94	0.20	64,64,64,64	0
56	MG	BA	3579	1/1	0.94	0.26	43,43,43,43	0
56	MG	DA	3594	1/1	0.94	0.18	54,54,54,54	0
56	MG	DA	3156	1/1	0.94	0.13	50,50,50,50	0
56	MG	DA	3425	1/1	0.94	0.12	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	3071	1/1	0.94	0.15	51,51,51,51	0
56	MG	DA	3288	1/1	0.94	0.10	48,48,48,48	0
56	MG	BW	201	1/1	0.94	0.25	45,45,45,45	0
56	MG	DA	3337	1/1	0.94	0.13	44,44,44,44	0
56	MG	BA	3239	1/1	0.94	0.17	40,40,40,40	0
56	MG	DA	3615	1/1	0.94	0.09	50,50,50,50	0
56	MG	CA	3027	1/1	0.94	0.18	61,61,61,61	0
56	MG	CA	3088	1/1	0.94	0.15	66,66,66,66	0
56	MG	BA	3182	1/1	0.94	0.19	21,21,21,21	0
56	MG	DA	3579	1/1	0.94	0.15	52,52,52,52	0
56	MG	BA	3268	1/1	0.94	0.32	57,57,57,57	0
56	MG	DA	3023	1/1	0.94	0.19	44,44,44,44	0
56	MG	BA	3777	1/1	0.94	0.15	44,44,44,44	0
56	MG	BA	3310	1/1	0.94	0.17	42,42,42,42	0
56	MG	BA	3695	1/1	0.94	0.28	37,37,37,37	0
56	MG	AA	3008	1/1	0.94	0.14	56,56,56,56	0
56	MG	BA	3073	1/1	0.94	0.20	45,45,45,45	0
56	MG	BA	3242	1/1	0.94	0.10	47,47,47,47	0
56	MG	BA	3021	1/1	0.94	0.17	22,22,22,22	0
56	MG	DA	3030	1/1	0.94	0.09	46,46,46,46	0
56	MG	BA	3524	1/1	0.94	0.16	53,53,53,53	0
56	MG	B5	105	1/1	0.94	0.14	66,66,66,66	0
56	MG	BA	3537	1/1	0.94	0.19	21,21,21,21	0
56	MG	BA	3789	1/1	0.94	0.29	37,37,37,37	0
56	MG	BA	3735	1/1	0.94	0.15	20,20,20,20	0
56	MG	BA	3261	1/1	0.94	0.10	46,46,46,46	0
56	MG	DA	3304	1/1	0.94	0.14	40,40,40,40	0
56	MG	AA	3041	1/1	0.94	0.08	64,64,64,64	0
56	MG	BA	3220	1/1	0.94	0.32	40,40,40,40	0
56	MG	BB	219	1/1	0.94	0.10	74,74,74,74	0
56	MG	BA	3190	1/1	0.94	0.24	50,50,50,50	0
56	MG	BA	3129	1/1	0.94	0.55	38,38,38,38	0
56	MG	DA	3387	1/1	0.94	0.24	39,39,39,39	0
56	MG	BA	3307	1/1	0.94	0.30	50,50,50,50	0
56	MG	DV	3001	1/1	0.94	0.17	61,61,61,61	0
56	MG	BA	3634	1/1	0.94	0.20	47,47,47,47	0
56	MG	DA	3219	1/1	0.94	0.11	36,36,36,36	0
56	MG	BF	309	1/1	0.94	0.10	45,45,45,45	0
56	MG	DE	302	1/1	0.94	0.12	33,33,33,33	0
56	MG	BA	3763	1/1	0.94	0.11	39,39,39,39	0
56	MG	DA	3093	1/1	0.94	0.39	54,54,54,54	0
56	MG	BA	3410	1/1	0.94	0.26	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3071	1/1	0.94	0.16	40,40,40,40	0
56	MG	AA	3105	1/1	0.94	0.14	71,71,71,71	0
56	MG	DA	3443	1/1	0.94	0.11	38,38,38,38	0
56	MG	AA	3182	1/1	0.94	0.14	64,64,64,64	0
56	MG	BA	3317	1/1	0.94	0.21	41,41,41,41	0
56	MG	DA	3379	1/1	0.94	0.09	50,50,50,50	0
59	ZN	AN	501	1/1	0.94	0.15	86,86,86,86	0
56	MG	DA	3582	1/1	0.94	0.14	64,64,64,64	0
56	MG	BA	3411	1/1	0.94	0.26	30,30,30,30	0
56	MG	DA	3436	1/1	0.94	0.11	70,70,70,70	0
56	MG	CA	3040	1/1	0.94	0.14	45,45,45,45	0
56	MG	BN	3003	1/1	0.94	0.19	44,44,44,44	0
56	MG	BA	3153	1/1	0.94	0.14	50,50,50,50	0
56	MG	DA	3486	1/1	0.94	0.34	50,50,50,50	0
56	MG	AA	3009	1/1	0.94	0.11	24,24,24,24	0
56	MG	CA	3123	1/1	0.94	0.16	67,67,67,67	0
56	MG	BA	3210	1/1	0.94	0.24	43,43,43,43	0
56	MG	BA	3067	1/1	0.94	0.20	49,49,49,49	0
56	MG	BA	3012	1/1	0.94	0.34	33,33,33,33	0
56	MG	BA	3158	1/1	0.94	0.30	40,40,40,40	0
56	MG	BA	3116	1/1	0.94	0.11	35,35,35,35	0
56	MG	DA	3206	1/1	0.94	0.09	46,46,46,46	0
56	MG	DA	3176	1/1	0.94	0.34	44,44,44,44	0
56	MG	DA	3151	1/1	0.94	0.09	33,33,33,33	0
56	MG	BA	3229	1/1	0.94	0.32	44,44,44,44	0
56	MG	D0	101	1/1	0.95	0.16	50,50,50,50	0
56	MG	BA	3454	1/1	0.95	0.12	29,29,29,29	0
56	MG	BD	3306	1/1	0.95	0.44	38,38,38,38	0
56	MG	BE	302	1/1	0.95	0.29	40,40,40,40	0
56	MG	BA	3493	1/1	0.95	0.11	49,49,49,49	0
56	MG	DA	3602	1/1	0.95	0.17	51,51,51,51	0
56	MG	DA	3518	1/1	0.95	0.13	58,58,58,58	0
56	MG	DA	3068	1/1	0.95	0.34	47,47,47,47	0
56	MG	DF	301	1/1	0.95	0.16	47,47,47,47	0
56	MG	DA	3171	1/1	0.95	0.14	53,53,53,53	0
56	MG	DA	3642	1/1	0.95	0.09	48,48,48,48	0
56	MG	DA	3633	1/1	0.95	0.06	56,56,56,56	0
56	MG	BA	3047	1/1	0.95	0.12	43,43,43,43	0
56	MG	AA	3104	1/1	0.95	0.25	70,70,70,70	0
56	MG	DD	303	1/1	0.95	0.57	51,51,51,51	0
56	MG	BA	3206	1/1	0.95	0.22	37,37,37,37	0
56	MG	BO	5001	1/1	0.95	0.11	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3473	1/1	0.95	0.09	30,30,30,30	0
56	MG	AA	3024	1/1	0.95	0.20	55,55,55,55	0
56	MG	BA	3809	1/1	0.95	0.12	41,41,41,41	0
56	MG	CA	3150	1/1	0.95	0.12	47,47,47,47	0
56	MG	DA	3411	1/1	0.95	0.25	46,46,46,46	0
56	MG	BA	3574	1/1	0.95	0.17	28,28,28,28	0
56	MG	BA	3344	1/1	0.95	0.21	55,55,55,55	0
56	MG	DA	3439	1/1	0.95	0.20	46,46,46,46	0
56	MG	DA	3662	1/1	0.95	0.14	38,38,38,38	0
56	MG	DA	3198	1/1	0.95	0.30	49,49,49,49	0
56	MG	AA	3091	1/1	0.95	0.16	40,40,40,40	0
56	MG	DN	5001	1/1	0.95	0.10	54,54,54,54	0
56	MG	BA	3015	1/1	0.95	0.14	50,50,50,50	0
56	MG	AA	3010	1/1	0.95	0.12	63,63,63,63	0
56	MG	BA	3497	1/1	0.95	0.13	44,44,44,44	0
56	MG	AA	3175	1/1	0.95	0.10	66,66,66,66	0
56	MG	DA	3172	1/1	0.95	0.11	31,31,31,31	0
56	MG	BP	204	1/1	0.95	0.15	54,54,54,54	0
56	MG	AA	3099	1/1	0.95	0.21	47,47,47,47	0
56	MG	DA	3312	1/1	0.95	0.09	41,41,41,41	0
56	MG	BA	3750	1/1	0.95	0.25	42,42,42,42	0
56	MG	BQ	202	1/1	0.95	0.26	37,37,37,37	0
56	MG	BA	3107	1/1	0.95	0.18	50,50,50,50	0
56	MG	BA	3270	1/1	0.95	0.29	40,40,40,40	0
56	MG	BA	3188	1/1	0.95	0.20	46,46,46,46	0
56	MG	BA	3176	1/1	0.95	0.10	44,44,44,44	0
56	MG	BA	3412	1/1	0.95	0.27	19,19,19,19	0
56	MG	BA	3363	1/1	0.95	0.09	66,66,66,66	0
56	MG	DA	3128	1/1	0.95	0.35	57,57,57,57	0
56	MG	BA	3796	1/1	0.95	0.29	47,47,47,47	0
56	MG	BA	3670	1/1	0.95	0.14	47,47,47,47	0
56	MG	BA	3550	1/1	0.95	0.14	25,25,25,25	0
56	MG	BA	3244	1/1	0.95	0.52	39,39,39,39	0
56	MG	CA	3055	1/1	0.95	0.20	55,55,55,55	0
56	MG	DA	3632	1/1	0.95	0.11	50,50,50,50	0
56	MG	DA	3190	1/1	0.95	0.14	41,41,41,41	0
56	MG	BA	3705	1/1	0.95	0.25	28,28,28,28	0
56	MG	BA	3814	1/1	0.95	0.27	42,42,42,42	0
56	MG	DA	3585	1/1	0.95	0.21	43,43,43,43	0
56	MG	BA	3641	1/1	0.95	0.08	54,54,54,54	0
56	MG	DA	3543	1/1	0.95	0.14	52,52,52,52	0
56	MG	DA	3404	1/1	0.95	0.09	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3743	1/1	0.95	0.15	43,43,43,43	0
56	MG	CA	3156	1/1	0.95	0.16	41,41,41,41	0
56	MG	DA	3446	1/1	0.95	0.17	44,44,44,44	0
56	MG	DA	3661	1/1	0.95	0.22	54,54,54,54	0
56	MG	BA	3177	1/1	0.95	0.30	44,44,44,44	0
56	MG	BA	3029	1/1	0.95	0.18	30,30,30,30	0
56	MG	DA	3401	1/1	0.95	0.08	43,43,43,43	0
56	MG	AX	3004	1/1	0.95	0.12	53,53,53,53	0
56	MG	AA	3046	1/1	0.95	0.15	56,56,56,56	0
56	MG	BA	3267	1/1	0.95	0.14	45,45,45,45	0
56	MG	BA	3429	1/1	0.95	0.16	23,23,23,23	0
56	MG	AX	3010	1/1	0.95	0.09	59,59,59,59	0
56	MG	BA	3348	1/1	0.95	0.19	24,24,24,24	0
56	MG	DA	3326	1/1	0.95	0.17	47,47,47,47	0
56	MG	BA	3357	1/1	0.95	0.19	46,46,46,46	0
56	MG	DA	3340	1/1	0.95	0.10	30,30,30,30	0
56	MG	BA	3257	1/1	0.95	0.20	54,54,54,54	0
56	MG	BA	3189	1/1	0.95	0.23	46,46,46,46	0
56	MG	DA	3257	1/1	0.95	0.22	57,57,57,57	0
56	MG	BA	3205	1/1	0.95	0.38	40,40,40,40	0
56	MG	BA	3716	1/1	0.95	0.37	39,39,39,39	0
56	MG	BA	3556	1/1	0.95	0.11	48,48,48,48	0
56	MG	BA	3123	1/1	0.95	0.23	28,28,28,28	0
56	MG	AA	3103	1/1	0.95	0.17	48,48,48,48	0
56	MG	BA	3269	1/1	0.95	0.21	42,42,42,42	0
56	MG	DA	3307	1/1	0.95	0.13	27,27,27,27	0
56	MG	BA	3361	1/1	0.95	0.16	61,61,61,61	0
56	MG	DA	3290	1/1	0.95	0.10	46,46,46,46	0
56	MG	AA	3130	1/1	0.95	0.06	56,56,56,56	0
56	MG	BA	3236	1/1	0.95	0.36	34,34,34,34	0
56	MG	BA	3007	1/1	0.95	0.10	35,35,35,35	0
56	MG	BD	3307	1/1	0.95	1.03	56,56,56,56	0
56	MG	BA	3090	1/1	0.95	0.22	27,27,27,27	0
56	MG	BA	3752	1/1	0.95	0.08	32,32,32,32	0
56	MG	BV	203	1/1	0.95	0.48	31,31,31,31	0
56	MG	BB	208	1/1	0.95	0.11	36,36,36,36	0
56	MG	AA	3113	1/1	0.95	0.07	67,67,67,67	0
56	MG	BA	3094	1/1	0.95	0.17	44,44,44,44	0
56	MG	BA	3393	1/1	0.95	0.17	22,22,22,22	0
56	MG	DA	3650	1/1	0.95	0.16	46,46,46,46	0
56	MG	AA	3165	1/1	0.95	0.08	49,49,49,49	0
56	MG	DA	3621	1/1	0.95	0.25	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3098	1/1	0.95	0.15	44,44,44,44	0
56	MG	CA	3075	1/1	0.95	0.20	67,67,67,67	0
56	MG	CA	3048	1/1	0.95	0.12	77,77,77,77	0
56	MG	BA	3373	1/1	0.95	0.09	42,42,42,42	0
56	MG	BA	3589	1/1	0.95	0.18	42,42,42,42	0
56	MG	DA	3664	1/1	0.95	0.86	50,50,50,50	0
56	MG	BA	3761	1/1	0.95	0.21	53,53,53,53	0
56	MG	BA	3570	1/1	0.95	0.23	35,35,35,35	0
56	MG	BA	3453	1/1	0.95	0.19	52,52,52,52	0
56	MG	BA	3686	1/1	0.95	0.13	41,41,41,41	0
56	MG	BA	3797	1/1	0.95	0.16	19,19,19,19	0
56	MG	BA	3146	1/1	0.95	0.13	19,19,19,19	0
56	MG	DA	3399	1/1	0.95	0.11	55,55,55,55	0
56	MG	AA	3023	1/1	0.95	0.18	48,48,48,48	0
56	MG	BA	3684	1/1	0.95	0.18	51,51,51,51	0
56	MG	CA	3065	1/1	0.95	0.17	64,64,64,64	0
56	MG	BA	3533	1/1	0.95	0.18	38,38,38,38	0
56	MG	DA	3580	1/1	0.95	0.08	46,46,46,46	0
56	MG	DA	3148	1/1	0.95	0.42	43,43,43,43	0
60	K	CX	3001	1/1	0.95	0.31	77,77,77,77	0
56	MG	BA	3406	1/1	0.95	0.09	32,32,32,32	0
56	MG	BA	3611	1/1	0.95	0.11	45,45,45,45	0
56	MG	BA	3275	1/1	0.95	0.16	34,34,34,34	0
56	MG	DA	3616	1/1	0.95	0.25	43,43,43,43	0
56	MG	DA	3566	1/1	0.95	0.09	62,62,62,62	0
56	MG	BA	3378	1/1	0.95	0.13	47,47,47,47	0
56	MG	AX	3008	1/1	0.95	0.19	37,37,37,37	0
56	MG	BB	215	1/1	0.95	0.20	35,35,35,35	0
56	MG	CA	3166	1/1	0.95	0.16	52,52,52,52	0
56	MG	BA	3414	1/1	0.95	0.22	33,33,33,33	0
56	MG	BA	3701	1/1	0.95	0.20	20,20,20,20	0
56	MG	AA	3112	1/1	0.95	0.14	60,60,60,60	0
56	MG	BA	3765	1/1	0.95	0.09	53,53,53,53	0
56	MG	DA	3428	1/1	0.95	0.05	26,26,26,26	0
56	MG	DA	3557	1/1	0.95	0.17	44,44,44,44	0
56	MG	BA	3565	1/1	0.95	0.09	43,43,43,43	0
56	MG	BA	3541	1/1	0.95	0.17	55,55,55,55	0
56	MG	BN	3005	1/1	0.95	0.21	35,35,35,35	0
56	MG	CA	3128	1/1	0.95	0.14	68,68,68,68	0
56	MG	BA	3669	1/1	0.95	0.11	36,36,36,36	0
56	MG	DA	3003	1/1	0.95	0.12	48,48,48,48	0
56	MG	BA	3132	1/1	0.95	0.22	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3662	1/1	0.95	0.17	52,52,52,52	0
56	MG	BA	3197	1/1	0.95	0.82	51,51,51,51	0
56	MG	AA	3078	1/1	0.95	0.07	72,72,72,72	0
56	MG	BA	3642	1/1	0.95	0.15	36,36,36,36	0
56	MG	B0	105	1/1	0.95	0.07	64,64,64,64	0
56	MG	DA	3658	1/1	0.95	0.33	55,55,55,55	0
56	MG	DA	3278	1/1	0.95	0.14	37,37,37,37	0
56	MG	DA	3050	1/1	0.95	0.10	37,37,37,37	0
56	MG	B6	101	1/1	0.95	0.20	47,47,47,47	0
56	MG	AA	3152	1/1	0.95	0.08	48,48,48,48	0
56	MG	BA	3628	1/1	0.95	0.11	34,34,34,34	0
56	MG	BA	3405	1/1	0.95	0.19	22,22,22,22	0
56	MG	DA	3501	1/1	0.95	0.08	46,46,46,46	0
56	MG	DA	3449	1/1	0.95	0.10	33,33,33,33	0
56	MG	DA	3303	1/1	0.95	0.15	55,55,55,55	0
56	MG	CA	3074	1/1	0.95	0.11	57,57,57,57	0
56	MG	DA	3480	1/1	0.95	0.14	38,38,38,38	0
56	MG	CA	3086	1/1	0.95	0.13	76,76,76,76	0
56	MG	BA	3274	1/1	0.95	0.20	51,51,51,51	0
56	MG	AA	3131	1/1	0.95	0.14	29,29,29,29	0
56	MG	DA	3382	1/1	0.95	0.14	31,31,31,31	0
56	MG	BA	3584	1/1	0.95	0.22	34,34,34,34	0
56	MG	BA	3474	1/1	0.95	0.18	20,20,20,20	0
56	MG	DA	3513	1/1	0.95	0.09	30,30,30,30	0
56	MG	BA	3202	1/1	0.95	0.29	38,38,38,38	0
56	MG	DA	3481	1/1	0.95	0.12	24,24,24,24	0
56	MG	BA	3297	1/1	0.95	0.15	46,46,46,46	0
56	MG	CA	3012	1/1	0.95	0.12	51,51,51,51	0
56	MG	DA	3520	1/1	0.95	0.06	44,44,44,44	0
56	MG	BA	3489	1/1	0.95	0.32	44,44,44,44	0
56	MG	DA	3007	1/1	0.95	0.08	43,43,43,43	0
56	MG	DA	3235	1/1	0.95	0.15	35,35,35,35	0
56	MG	BA	3031	1/1	0.95	0.23	28,28,28,28	0
56	MG	BA	3106	1/1	0.95	0.17	44,44,44,44	0
56	MG	BD	3304	1/1	0.95	0.09	25,25,25,25	0
56	MG	CA	3007	1/1	0.95	0.20	42,42,42,42	0
56	MG	BA	3141	1/1	0.95	0.13	42,42,42,42	0
56	MG	AA	3013	1/1	0.95	0.07	57,57,57,57	0
56	MG	BA	3313	1/1	0.96	0.16	34,34,34,34	0
56	MG	BA	3376	1/1	0.96	0.12	43,43,43,43	0
56	MG	BA	3053	1/1	0.96	0.22	23,23,23,23	0
56	MG	BA	3386	1/1	0.96	0.15	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3160	1/1	0.96	0.20	38,38,38,38	0
56	MG	AA	3123	1/1	0.96	0.18	51,51,51,51	0
56	MG	BA	3171	1/1	0.96	0.19	54,54,54,54	0
56	MG	BA	3681	1/1	0.96	0.16	50,50,50,50	0
56	MG	BA	3271	1/1	0.96	0.14	38,38,38,38	0
56	MG	AA	3090	1/1	0.96	0.23	41,41,41,41	0
56	MG	DA	3352	1/1	0.96	0.11	27,27,27,27	0
56	MG	BA	3469	1/1	0.96	0.13	41,41,41,41	0
56	MG	BA	3432	1/1	0.96	0.12	35,35,35,35	0
56	MG	BA	3058	1/1	0.96	0.13	27,27,27,27	0
60	K	AX	3001	1/1	0.96	0.15	65,65,65,65	0
56	MG	BA	3370	1/1	0.96	0.13	27,27,27,27	0
56	MG	BA	3311	1/1	0.96	0.17	23,23,23,23	0
56	MG	BN	3006	1/1	0.96	0.54	47,47,47,47	0
56	MG	BA	3736	1/1	0.96	0.08	42,42,42,42	0
56	MG	BB	222	1/1	0.96	0.19	50,50,50,50	0
56	MG	BA	3658	1/1	0.96	0.16	51,51,51,51	0
56	MG	AA	3082	1/1	0.96	0.34	51,51,51,51	0
56	MG	AA	3126	1/1	0.96	0.17	57,57,57,57	0
56	MG	DA	3233	1/1	0.96	0.13	40,40,40,40	0
56	MG	DA	3451	1/1	0.96	0.15	20,20,20,20	0
56	MG	BA	3710	1/1	0.96	0.27	28,28,28,28	0
56	MG	BD	3303	1/1	0.96	0.17	33,33,33,33	0
56	MG	DA	3356	1/1	0.96	0.17	37,37,37,37	0
56	MG	BA	3810	1/1	0.96	0.23	43,43,43,43	0
56	MG	BA	3781	1/1	0.96	0.24	47,47,47,47	0
56	MG	DA	3092	1/1	0.96	0.36	48,48,48,48	0
56	MG	AA	3116	1/1	0.96	0.12	32,32,32,32	0
56	MG	BX	102	1/1	0.96	0.15	36,36,36,36	0
56	MG	BA	3569	1/1	0.96	0.16	56,56,56,56	0
56	MG	BA	3316	1/1	0.96	0.23	25,25,25,25	0
56	MG	BA	3450	1/1	0.96	0.15	10,10,10,10	0
56	MG	BA	3287	1/1	0.96	0.27	28,28,28,28	0
56	MG	DA	3301	1/1	0.96	0.11	51,51,51,51	0
56	MG	BA	3754	1/1	0.96	0.10	60,60,60,60	0
56	MG	AA	3065	1/1	0.96	0.08	55,55,55,55	0
56	MG	CA	3062	1/1	0.96	0.18	67,67,67,67	0
56	MG	BA	3660	1/1	0.96	0.17	51,51,51,51	0
56	MG	DA	3620	1/1	0.96	0.17	59,59,59,59	0
56	MG	DA	3397	1/1	0.96	0.09	30,30,30,30	0
56	MG	BA	3536	1/1	0.96	0.23	36,36,36,36	0
56	MG	BA	3022	1/1	0.96	0.14	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3344	1/1	0.96	0.18	46,46,46,46	0
56	MG	BB	217	1/1	0.96	0.16	41,41,41,41	0
56	MG	DA	3667	1/1	0.96	0.14	66,66,66,66	0
56	MG	CA	3102	1/1	0.96	0.12	49,49,49,49	0
56	MG	BA	3549	1/1	0.96	0.15	36,36,36,36	0
56	MG	DA	3421	1/1	0.96	0.07	31,31,31,31	0
56	MG	AA	3106	1/1	0.96	0.10	61,61,61,61	0
56	MG	DA	3381	1/1	0.96	0.19	34,34,34,34	0
56	MG	AA	3081	1/1	0.96	0.23	51,51,51,51	0
56	MG	BA	3246	1/1	0.96	0.12	47,47,47,47	0
56	MG	DA	3311	1/1	0.96	0.12	19,19,19,19	0
56	MG	BA	3483	1/1	0.96	0.20	41,41,41,41	0
56	MG	DA	3674	1/1	0.96	0.80	43,43,43,43	0
56	MG	DA	3496	1/1	0.96	0.42	35,35,35,35	0
56	MG	DA	3106	1/1	0.96	0.06	52,52,52,52	0
56	MG	BA	3775	1/1	0.96	0.07	34,34,34,34	0
56	MG	BA	3591	1/1	0.96	0.13	48,48,48,48	0
56	MG	AA	3144	1/1	0.96	0.10	59,59,59,59	0
56	MG	AA	3148	1/1	0.96	0.09	58,58,58,58	0
56	MG	CA	3039	1/1	0.96	0.15	55,55,55,55	0
56	MG	CA	3111	1/1	0.96	0.10	56,56,56,56	0
56	MG	BA	3304	1/1	0.96	0.12	37,37,37,37	0
56	MG	BA	3216	1/1	0.96	0.10	62,62,62,62	0
56	MG	CA	3122	1/1	0.96	0.10	65,65,65,65	0
56	MG	DA	3243	1/1	0.96	0.15	47,47,47,47	0
56	MG	BA	3136	1/1	0.96	0.29	42,42,42,42	0
56	MG	DA	3265	1/1	0.96	0.18	37,37,37,37	0
56	MG	DA	3011	1/1	0.96	0.53	51,51,51,51	0
56	MG	DA	3444	1/1	0.96	0.12	46,46,46,46	0
56	MG	BA	3635	1/1	0.96	0.08	51,51,51,51	0
56	MG	BA	3803	1/1	0.96	0.17	33,33,33,33	0
56	MG	BA	3791	1/1	0.96	0.18	18,18,18,18	0
56	MG	BA	3615	1/1	0.96	0.08	60,60,60,60	0
56	MG	BA	3564	1/1	0.96	0.18	50,50,50,50	0
56	MG	DD	306	1/1	0.96	0.84	48,48,48,48	0
56	MG	B8	101	1/1	0.96	0.15	36,36,36,36	0
56	MG	DA	3169	1/1	0.96	0.18	44,44,44,44	0
56	MG	BA	3482	1/1	0.96	0.14	42,42,42,42	0
56	MG	BA	3603	1/1	0.96	0.20	42,42,42,42	0
56	MG	DA	3339	1/1	0.96	0.12	60,60,60,60	0
56	MG	BA	3365	1/1	0.96	0.28	37,37,37,37	0
56	MG	BA	3640	1/1	0.96	0.21	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BE	304	1/1	0.96	0.50	43,43,43,43	0
56	MG	CA	3066	1/1	0.96	0.11	47,47,47,47	0
56	MG	BA	3379	1/1	0.96	0.18	39,39,39,39	0
56	MG	BA	3303	1/1	0.96	0.32	37,37,37,37	0
56	MG	BA	3235	1/1	0.96	0.22	26,26,26,26	0
56	MG	BA	3668	1/1	0.96	0.21	48,48,48,48	0
56	MG	DA	3028	1/1	0.96	0.54	45,45,45,45	0
56	MG	DA	3672	1/1	0.96	0.28	59,59,59,59	0
56	MG	BA	3321	1/1	0.96	0.19	21,21,21,21	0
56	MG	DA	3108	1/1	0.96	0.21	46,46,46,46	0
56	MG	BA	3568	1/1	0.96	0.23	26,26,26,26	0
56	MG	BA	3203	1/1	0.96	0.50	38,38,38,38	0
56	MG	BA	3383	1/1	0.96	0.19	20,20,20,20	0
56	MG	DA	3119	1/1	0.96	0.09	40,40,40,40	0
56	MG	BA	3355	1/1	0.96	0.26	28,28,28,28	0
56	MG	DA	3052	1/1	0.96	0.19	26,26,26,26	0
56	MG	BA	3008	1/1	0.96	0.15	26,26,26,26	0
56	MG	BA	3655	1/1	0.96	0.14	54,54,54,54	0
56	MG	DA	3144	1/1	0.96	0.16	39,39,39,39	0
56	MG	CA	3056	1/1	0.96	0.11	60,60,60,60	0
56	MG	DA	3078	1/1	0.96	0.19	35,35,35,35	0
56	MG	BA	3442	1/1	0.96	0.13	36,36,36,36	0
56	MG	DA	3367	1/1	0.96	0.15	55,55,55,55	0
56	MG	DA	3378	1/1	0.96	0.10	34,34,34,34	0
56	MG	DA	3600	1/1	0.96	0.14	43,43,43,43	0
56	MG	BA	3353	1/1	0.96	0.21	49,49,49,49	0
56	MG	BA	3446	1/1	0.96	0.20	31,31,31,31	0
56	MG	CA	3146	1/1	0.96	0.20	65,65,65,65	0
56	MG	DA	3587	1/1	0.96	0.12	52,52,52,52	0
56	MG	B0	104	1/1	0.96	0.18	41,41,41,41	0
56	MG	BA	3243	1/1	0.96	0.31	56,56,56,56	0
56	MG	BA	3502	1/1	0.96	0.11	20,20,20,20	0
56	MG	B7	101	1/1	0.96	0.24	47,47,47,47	0
56	MG	BA	3301	1/1	0.96	0.10	48,48,48,48	0
56	MG	DY	502	1/1	0.96	0.15	58,58,58,58	0
56	MG	BA	3544	1/1	0.96	0.31	45,45,45,45	0
56	MG	DA	3614	1/1	0.96	0.16	61,61,61,61	0
56	MG	DA	3509	1/1	0.96	0.13	55,55,55,55	0
56	MG	B7	105	1/1	0.96	0.27	46,46,46,46	0
56	MG	BA	3664	1/1	0.96	0.19	17,17,17,17	0
56	MG	BA	3762	1/1	0.96	0.16	53,53,53,53	0
56	MG	BA	3515	1/1	0.96	0.17	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BE	305	1/1	0.96	0.21	19,19,19,19	0
56	MG	AA	3114	1/1	0.96	0.17	45,45,45,45	0
56	MG	AA	3146	1/1	0.96	0.13	53,53,53,53	0
56	MG	BA	3733	1/1	0.96	0.09	46,46,46,46	0
56	MG	BA	3444	1/1	0.96	0.22	43,43,43,43	0
56	MG	CA	3147	1/1	0.96	0.13	70,70,70,70	0
56	MG	BA	3756	1/1	0.96	0.06	56,56,56,56	0
56	MG	DA	3293	1/1	0.96	0.14	57,57,57,57	0
56	MG	CA	3051	1/1	0.96	0.15	55,55,55,55	0
56	MG	BA	3596	1/1	0.96	0.08	68,68,68,68	0
56	MG	DA	3406	1/1	0.96	0.12	33,33,33,33	0
56	MG	BA	3230	1/1	0.96	0.51	36,36,36,36	0
56	MG	DQ	3001	1/1	0.96	0.07	45,45,45,45	0
56	MG	BA	3338	1/1	0.96	0.20	43,43,43,43	0
56	MG	DA	3548	1/1	0.96	0.16	55,55,55,55	0
56	MG	DD	304	1/1	0.96	0.08	33,33,33,33	0
56	MG	DA	3105	1/1	0.96	0.10	41,41,41,41	0
56	MG	AA	3018	1/1	0.96	0.15	50,50,50,50	0
56	MG	AA	3137	1/1	0.96	0.11	42,42,42,42	0
56	MG	DA	3525	1/1	0.96	0.12	44,44,44,44	0
56	MG	AA	3088	1/1	0.96	0.10	42,42,42,42	0
56	MG	D3	3001	1/1	0.96	0.42	60,60,60,60	0
56	MG	BA	3104	1/1	0.96	0.25	23,23,23,23	0
56	MG	D0	102	1/1	0.96	0.11	51,51,51,51	0
56	MG	DA	3317	1/1	0.96	0.14	38,38,38,38	0
56	MG	CA	3170	1/1	0.96	0.10	53,53,53,53	0
56	MG	DA	3417	1/1	0.96	0.14	62,62,62,62	0
56	MG	DA	3475	1/1	0.96	0.14	38,38,38,38	0
56	MG	BA	3656	1/1	0.96	0.10	64,64,64,64	0
56	MG	BA	3476	1/1	0.96	0.36	48,48,48,48	0
56	MG	DA	3408	1/1	0.96	0.29	51,51,51,51	0
56	MG	BB	201	1/1	0.96	0.12	65,65,65,65	0
56	MG	BA	3023	1/1	0.96	0.22	35,35,35,35	0
56	MG	DA	3531	1/1	0.96	0.17	62,62,62,62	0
56	MG	BA	3339	1/1	0.96	0.19	23,23,23,23	0
56	MG	DA	3186	1/1	0.96	0.15	54,54,54,54	0
56	MG	BA	3445	1/1	0.96	0.26	48,48,48,48	0
56	MG	DA	3371	1/1	0.96	0.16	22,22,22,22	0
56	MG	AA	3117	1/1	0.96	0.19	34,34,34,34	0
56	MG	DA	3618	1/1	0.96	0.17	64,64,64,64	0
56	MG	DA	3121	1/1	0.96	0.15	40,40,40,40	0
56	MG	CA	3153	1/1	0.96	0.11	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3403	1/1	0.96	0.13	22,22,22,22	0
56	MG	AA	3190	1/1	0.96	0.13	48,48,48,48	0
56	MG	AA	3061	1/1	0.96	0.23	54,54,54,54	0
56	MG	BA	3134	1/1	0.96	0.17	36,36,36,36	0
56	MG	AA	3075	1/1	0.96	0.23	49,49,49,49	0
56	MG	BA	3753	1/1	0.96	0.12	27,27,27,27	0
56	MG	BY	204	1/1	0.96	0.31	52,52,52,52	0
56	MG	AA	3003	1/1	0.96	0.15	63,63,63,63	0
56	MG	BA	3113	1/1	0.96	0.45	39,39,39,39	0
56	MG	BA	3465	1/1	0.96	0.22	47,47,47,47	0
56	MG	BA	3654	1/1	0.96	0.12	49,49,49,49	0
56	MG	BA	3572	1/1	0.96	0.15	52,52,52,52	0
56	MG	BA	3438	1/1	0.96	0.14	21,21,21,21	0
56	MG	BA	3388	1/1	0.96	0.22	27,27,27,27	0
56	MG	DA	3302	1/1	0.96	0.12	32,32,32,32	0
56	MG	AA	3092	1/1	0.96	0.31	54,54,54,54	0
56	MG	CA	3167	1/1	0.96	0.06	47,47,47,47	0
56	MG	BA	3087	1/1	0.96	0.57	40,40,40,40	0
56	MG	AA	3178	1/1	0.96	0.12	59,59,59,59	0
56	MG	BA	3500	1/1	0.96	0.22	32,32,32,32	0
56	MG	DA	3239	1/1	0.96	0.07	51,51,51,51	0
56	MG	DA	3204	1/1	0.96	0.37	50,50,50,50	0
56	MG	DA	3540	1/1	0.96	0.08	56,56,56,56	0
56	MG	DA	3529	1/1	0.96	0.11	57,57,57,57	0
56	MG	BA	3255	1/1	0.96	0.16	41,41,41,41	0
56	MG	DA	3478	1/1	0.96	0.15	67,67,67,67	0
56	MG	BA	3398	1/1	0.96	0.12	51,51,51,51	0
56	MG	BA	3718	1/1	0.96	0.14	53,53,53,53	0
56	MG	DA	3045	1/1	0.96	0.10	60,60,60,60	0
56	MG	DA	3629	1/1	0.96	0.04	61,61,61,61	0
56	MG	DA	3656	1/1	0.96	0.07	57,57,57,57	0
56	MG	DA	3321	1/1	0.96	0.10	30,30,30,30	0
56	MG	BA	3423	1/1	0.96	0.12	31,31,31,31	0
56	MG	AA	3032	1/1	0.96	0.19	59,59,59,59	0
56	MG	DA	3214	1/1	0.96	0.11	51,51,51,51	0
56	MG	BA	3293	1/1	0.96	0.17	40,40,40,40	0
56	MG	DA	3517	1/1	0.96	0.08	57,57,57,57	0
56	MG	BA	3282	1/1	0.96	0.20	41,41,41,41	0
56	MG	DA	3166	1/1	0.96	0.19	35,35,35,35	0
56	MG	BA	3602	1/1	0.96	0.18	32,32,32,32	0
56	MG	BA	3273	1/1	0.96	0.32	41,41,41,41	0
56	MG	CA	3135	1/1	0.96	0.14	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3163	1/1	0.96	0.11	78,78,78,78	0
56	MG	BA	3152	1/1	0.96	0.30	42,42,42,42	0
56	MG	CA	3109	1/1	0.96	0.17	41,41,41,41	0
56	MG	BA	3527	1/1	0.96	0.19	27,27,27,27	0
56	MG	AA	3035	1/1	0.96	0.14	26,26,26,26	0
56	MG	BA	3343	1/1	0.96	0.16	30,30,30,30	0
56	MG	DA	3296	1/1	0.96	0.12	35,35,35,35	0
56	MG	CA	3070	1/1	0.96	0.07	49,49,49,49	0
56	MG	DA	3196	1/1	0.96	0.48	45,45,45,45	0
56	MG	DA	3315	1/1	0.96	0.12	44,44,44,44	0
56	MG	BA	3709	1/1	0.96	0.29	28,28,28,28	0
56	MG	BA	3345	1/1	0.96	0.11	28,28,28,28	0
56	MG	DA	3514	1/1	0.96	0.27	45,45,45,45	0
56	MG	BA	3215	1/1	0.96	0.22	47,47,47,47	0
56	MG	DA	3645	1/1	0.96	0.07	38,38,38,38	0
56	MG	BB	213	1/1	0.96	0.23	30,30,30,30	0
56	MG	BA	3409	1/1	0.97	0.21	21,21,21,21	0
56	MG	BA	3486	1/1	0.97	0.13	22,22,22,22	0
56	MG	BA	3173	1/1	0.97	0.54	41,41,41,41	0
56	MG	DQ	3002	1/1	0.97	0.12	41,41,41,41	0
56	MG	BU	202	1/1	0.97	0.14	29,29,29,29	0
56	MG	BP	201	1/1	0.97	0.38	28,28,28,28	0
56	MG	BA	3436	1/1	0.97	0.20	17,17,17,17	0
56	MG	BA	3127	1/1	0.97	0.28	36,36,36,36	0
56	MG	CA	3010	1/1	0.97	0.13	57,57,57,57	0
56	MG	DA	3355	1/1	0.97	0.12	35,35,35,35	0
56	MG	BA	3286	1/1	0.97	0.33	41,41,41,41	0
56	MG	BA	3003	1/1	0.97	0.13	30,30,30,30	0
56	MG	BA	3528	1/1	0.97	0.29	46,46,46,46	0
56	MG	DA	3327	1/1	0.97	0.11	47,47,47,47	0
56	MG	BD	3309	1/1	0.97	0.14	40,40,40,40	0
56	MG	BA	3458	1/1	0.97	0.14	66,66,66,66	0
56	MG	DA	3306	1/1	0.97	0.28	35,35,35,35	0
56	MG	BA	3354	1/1	0.97	0.17	20,20,20,20	0
56	MG	CA	3133	1/1	0.97	0.11	45,45,45,45	0
56	MG	BA	3542	1/1	0.97	0.17	20,20,20,20	0
56	MG	BA	3676	1/1	0.97	0.17	37,37,37,37	0
56	MG	DA	3234	1/1	0.97	0.18	56,56,56,56	0
56	MG	BA	3749	1/1	0.97	0.11	29,29,29,29	0
56	MG	BA	3726	1/1	0.97	0.09	65,65,65,65	0
56	MG	DA	3021	1/1	0.97	0.45	40,40,40,40	0
56	MG	BA	3608	1/1	0.97	0.15	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3788	1/1	0.97	0.13	10,10,10,10	0
56	MG	BA	3508	1/1	0.97	0.09	34,34,34,34	0
56	MG	BE	307	1/1	0.97	0.12	31,31,31,31	0
56	MG	BF	307	1/1	0.97	0.64	40,40,40,40	0
56	MG	CA	3114	1/1	0.97	0.09	52,52,52,52	0
56	MG	DA	3512	1/1	0.97	0.11	48,48,48,48	0
56	MG	CA	3140	1/1	0.97	0.10	75,75,75,75	0
56	MG	BA	3811	1/1	0.97	0.49	41,41,41,41	0
56	MG	DA	3483	1/1	0.97	0.11	32,32,32,32	0
56	MG	CA	3175	1/1	0.97	0.20	46,46,46,46	0
56	MG	BA	3078	1/1	0.97	0.17	15,15,15,15	0
56	MG	DA	3492	1/1	0.97	0.07	44,44,44,44	0
56	MG	BA	3812	1/1	0.97	0.27	31,31,31,31	0
56	MG	DA	3598	1/1	0.97	0.25	30,30,30,30	0
56	MG	DA	3635	1/1	0.97	0.18	47,47,47,47	0
56	MG	BA	3631	1/1	0.97	0.17	49,49,49,49	0
56	MG	BA	3424	1/1	0.97	0.16	55,55,55,55	0
56	MG	BA	3051	1/1	0.97	0.19	18,18,18,18	0
56	MG	BA	3712	1/1	0.97	0.34	29,29,29,29	0
56	MG	DA	3077	1/1	0.97	0.17	47,47,47,47	0
56	MG	CA	3076	1/1	0.97	0.17	35,35,35,35	0
56	MG	DA	3641	1/1	0.97	0.14	49,49,49,49	0
56	MG	BA	3280	1/1	0.97	0.14	32,32,32,32	0
56	MG	BA	3001	1/1	0.97	0.14	31,31,31,31	0
56	MG	BA	3708	1/1	0.97	0.23	36,36,36,36	0
56	MG	DA	3271	1/1	0.97	0.12	51,51,51,51	0
56	MG	AA	3129	1/1	0.97	0.14	70,70,70,70	0
56	MG	DA	3254	1/1	0.97	0.20	35,35,35,35	0
56	MG	CA	3108	1/1	0.97	0.07	52,52,52,52	0
56	MG	BV	202	1/1	0.97	0.33	33,33,33,33	0
56	MG	AA	3181	1/1	0.97	0.14	63,63,63,63	0
56	MG	BA	3362	1/1	0.97	0.19	40,40,40,40	0
56	MG	DA	3515	1/1	0.97	0.09	39,39,39,39	0
56	MG	BA	3285	1/1	0.97	0.14	54,54,54,54	0
56	MG	DA	3505	1/1	0.97	0.12	45,45,45,45	0
56	MG	BA	3043	1/1	0.97	0.15	35,35,35,35	0
56	MG	BA	3385	1/1	0.97	0.23	41,41,41,41	0
56	MG	BF	301	1/1	0.97	0.49	32,32,32,32	0
56	MG	BA	3009	1/1	0.97	0.16	25,25,25,25	0
56	MG	DA	3223	1/1	0.97	0.20	41,41,41,41	0
56	MG	BA	3320	1/1	0.97	0.17	55,55,55,55	0
56	MG	DA	3013	1/1	0.97	0.06	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3464	1/1	0.97	0.10	24,24,24,24	0
56	MG	BA	3805	1/1	0.97	0.15	30,30,30,30	0
59	ZN	D9	501	1/1	0.97	0.14	65,65,65,65	0
56	MG	DF	304	1/1	0.97	0.88	40,40,40,40	0
56	MG	BA	3632	1/1	0.97	0.24	43,43,43,43	0
56	MG	DA	3055	1/1	0.97	0.07	54,54,54,54	0
56	MG	DA	3348	1/1	0.97	0.11	32,32,32,32	0
56	MG	DA	3188	1/1	0.97	0.07	26,26,26,26	0
56	MG	BA	3487	1/1	0.97	0.21	23,23,23,23	0
56	MG	BA	3390	1/1	0.97	0.21	25,25,25,25	0
56	MG	BA	3769	1/1	0.97	0.10	24,24,24,24	0
56	MG	CA	3157	1/1	0.97	0.09	61,61,61,61	0
56	MG	DD	305	1/1	0.97	0.91	39,39,39,39	0
56	MG	DA	3573	1/1	0.97	0.10	27,27,27,27	0
56	MG	BA	3074	1/1	0.97	0.16	31,31,31,31	0
56	MG	DA	3450	1/1	0.97	0.08	41,41,41,41	0
56	MG	BA	3223	1/1	0.97	0.08	39,39,39,39	0
56	MG	DA	3330	1/1	0.97	0.14	54,54,54,54	0
56	MG	DA	3263	1/1	0.97	0.27	44,44,44,44	0
56	MG	DA	3456	1/1	0.97	0.16	54,54,54,54	0
56	MG	DA	3320	1/1	0.97	0.15	34,34,34,34	0
56	MG	DA	3380	1/1	0.97	0.06	35,35,35,35	0
56	MG	CA	3119	1/1	0.97	0.13	51,51,51,51	0
56	MG	DA	3384	1/1	0.97	0.17	39,39,39,39	0
56	MG	DA	3362	1/1	0.97	0.09	59,59,59,59	0
56	MG	DA	3022	1/1	0.97	0.10	29,29,29,29	0
56	MG	DA	3359	1/1	0.97	0.12	39,39,39,39	0
56	MG	BA	3364	1/1	0.97	0.26	29,29,29,29	0
56	MG	DA	3207	1/1	0.97	0.22	36,36,36,36	0
56	MG	DA	3577	1/1	0.97	0.16	49,49,49,49	0
56	MG	BA	3688	1/1	0.97	0.12	16,16,16,16	0
56	MG	BA	3334	1/1	0.97	0.17	26,26,26,26	0
56	MG	BA	3665	1/1	0.97	0.20	40,40,40,40	0
56	MG	AA	3118	1/1	0.97	0.08	39,39,39,39	0
56	MG	CA	3060	1/1	0.97	0.09	47,47,47,47	0
56	MG	DA	3133	1/1	0.97	0.12	52,52,52,52	0
56	MG	BA	3289	1/1	0.97	0.42	35,35,35,35	0
56	MG	AA	3108	1/1	0.97	0.15	58,58,58,58	0
56	MG	DA	3261	1/1	0.97	0.21	36,36,36,36	0
56	MG	BA	3208	1/1	0.97	0.17	19,19,19,19	0
56	MG	BA	3005	1/1	0.97	0.18	33,33,33,33	0
56	MG	BA	3291	1/1	0.97	0.11	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3415	1/1	0.97	0.18	34,34,34,34	0
56	MG	BA	3758	1/1	0.97	0.15	44,44,44,44	0
56	MG	DA	3215	1/1	0.97	0.06	49,49,49,49	0
56	MG	BA	3140	1/1	0.97	0.25	34,34,34,34	0
56	MG	DA	3047	1/1	0.97	0.09	39,39,39,39	0
56	MG	BA	3428	1/1	0.97	0.26	36,36,36,36	0
56	MG	DA	3394	1/1	0.97	0.15	40,40,40,40	0
56	MG	BA	3032	1/1	0.97	0.42	42,42,42,42	0
56	MG	BA	3623	1/1	0.97	0.10	33,33,33,33	0
56	MG	BA	3448	1/1	0.97	0.22	23,23,23,23	0
56	MG	CA	3118	1/1	0.97	0.09	60,60,60,60	0
56	MG	BA	3183	1/1	0.97	0.17	35,35,35,35	0
56	MG	DA	3414	1/1	0.97	0.07	38,38,38,38	0
56	MG	DB	3007	1/1	0.97	0.17	42,42,42,42	0
56	MG	DA	3669	1/1	0.97	0.38	38,38,38,38	0
56	MG	DA	3231	1/1	0.97	0.27	38,38,38,38	0
56	MG	BA	3332	1/1	0.97	0.21	36,36,36,36	0
56	MG	AA	3093	1/1	0.97	0.14	51,51,51,51	0
56	MG	BY	202	1/1	0.97	0.17	48,48,48,48	0
56	MG	BA	3546	1/1	0.97	0.14	38,38,38,38	0
56	MG	DA	3349	1/1	0.97	0.15	31,31,31,31	0
56	MG	BW	203	1/1	0.97	0.30	37,37,37,37	0
56	MG	BA	3115	1/1	0.97	0.24	33,33,33,33	0
56	MG	BA	3226	1/1	0.97	0.28	25,25,25,25	0
56	MG	AX	3005	1/1	0.97	0.10	64,64,64,64	0
56	MG	DA	3066	1/1	0.97	0.17	47,47,47,47	0
56	MG	BA	3421	1/1	0.97	0.19	48,48,48,48	0
56	MG	DA	3217	1/1	0.97	0.22	34,34,34,34	0
56	MG	CE	202	1/1	0.97	0.07	74,74,74,74	0
56	MG	AA	3027	1/1	0.97	0.11	46,46,46,46	0
56	MG	BA	3653	1/1	0.97	0.15	39,39,39,39	0
56	MG	DA	3390	1/1	0.97	0.11	19,19,19,19	0
56	MG	BA	3661	1/1	0.97	0.11	48,48,48,48	0
56	MG	DA	3145	1/1	0.97	0.09	38,38,38,38	0
56	MG	BA	3372	1/1	0.97	0.15	56,56,56,56	0
56	MG	BA	3519	1/1	0.97	0.25	53,53,53,53	0
56	MG	BV	201	1/1	0.97	0.41	27,27,27,27	0
56	MG	BA	3472	1/1	0.97	0.17	38,38,38,38	0
56	MG	CA	3141	1/1	0.97	0.17	53,53,53,53	0
56	MG	DA	3040	1/1	0.97	0.58	58,58,58,58	0
56	MG	BA	3180	1/1	0.97	0.32	46,46,46,46	0
56	MG	DA	3448	1/1	0.97	0.18	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3523	1/1	0.97	0.28	52,52,52,52	0
56	MG	AA	3101	1/1	0.97	0.17	49,49,49,49	0
56	MG	BA	3511	1/1	0.97	0.22	43,43,43,43	0
56	MG	DA	3088	1/1	0.97	0.10	30,30,30,30	0
56	MG	DA	3065	1/1	0.97	0.08	41,41,41,41	0
56	MG	B3	3001	1/1	0.97	0.20	38,38,38,38	0
56	MG	BA	3331	1/1	0.97	0.16	38,38,38,38	0
56	MG	DA	3558	1/1	0.97	0.04	43,43,43,43	0
56	MG	DA	3094	1/1	0.97	0.15	52,52,52,52	0
56	MG	DA	3671	1/1	0.97	0.24	37,37,37,37	0
56	MG	BA	3118	1/1	0.97	0.55	37,37,37,37	0
56	MG	BA	3181	1/1	0.97	0.20	26,26,26,26	0
56	MG	BA	3187	1/1	0.97	0.22	48,48,48,48	0
56	MG	BA	3685	1/1	0.97	0.14	51,51,51,51	0
56	MG	DA	3368	1/1	0.97	0.14	24,24,24,24	0
56	MG	BA	3300	1/1	0.97	0.30	28,28,28,28	0
56	MG	BA	3352	1/1	0.97	0.17	45,45,45,45	0
56	MG	DA	3029	1/1	0.97	0.26	36,36,36,36	0
56	MG	BA	3038	1/1	0.97	0.39	40,40,40,40	0
56	MG	BA	3201	1/1	0.97	0.39	41,41,41,41	0
56	MG	DA	3155	1/1	0.97	0.21	38,38,38,38	0
56	MG	BA	3485	1/1	0.97	0.14	55,55,55,55	0
56	MG	BA	3298	1/1	0.97	0.20	49,49,49,49	0
56	MG	BA	3800	1/1	0.97	0.09	41,41,41,41	0
56	MG	DA	3328	1/1	0.97	0.16	41,41,41,41	0
56	MG	AA	3033	1/1	0.97	0.23	58,58,58,58	0
56	MG	BA	3496	1/1	0.97	0.06	59,59,59,59	0
56	MG	DA	3487	1/1	0.97	0.16	37,37,37,37	0
56	MG	DA	3216	1/1	0.97	0.11	41,41,41,41	0
56	MG	BA	3024	1/1	0.98	0.41	45,45,45,45	0
56	MG	BA	3035	1/1	0.98	0.48	42,42,42,42	0
56	MG	BA	3328	1/1	0.98	0.15	11,11,11,11	0
56	MG	BA	3095	1/1	0.98	0.14	30,30,30,30	0
56	MG	BA	3543	1/1	0.98	0.23	23,23,23,23	0
56	MG	CA	3038	1/1	0.98	0.09	63,63,63,63	0
56	MG	AA	3111	1/1	0.98	0.14	61,61,61,61	0
56	MG	DA	3353	1/1	0.98	0.14	42,42,42,42	0
56	MG	DA	3373	1/1	0.98	0.09	39,39,39,39	0
56	MG	BA	3507	1/1	0.98	0.22	35,35,35,35	0
56	MG	BA	3451	1/1	0.98	0.15	31,31,31,31	0
56	MG	BA	3530	1/1	0.98	0.20	25,25,25,25	0
56	MG	DU	3001	1/1	0.98	0.56	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3391	1/1	0.98	0.17	26,26,26,26	0
56	MG	BA	3245	1/1	0.98	0.15	61,61,61,61	0
56	MG	DA	3477	1/1	0.98	0.08	30,30,30,30	0
56	MG	BA	3046	1/1	0.98	0.16	34,34,34,34	0
56	MG	DA	3329	1/1	0.98	0.12	47,47,47,47	0
56	MG	DA	3009	1/1	0.98	0.15	29,29,29,29	0
56	MG	BA	3552	1/1	0.98	0.16	46,46,46,46	0
56	MG	DA	3205	1/1	0.98	0.21	34,34,34,34	0
56	MG	DA	3323	1/1	0.98	0.15	29,29,29,29	0
56	MG	DE	301	1/1	0.98	0.26	35,35,35,35	0
56	MG	DA	3506	1/1	0.98	0.11	40,40,40,40	0
56	MG	BE	303	1/1	0.98	0.59	32,32,32,32	0
56	MG	DA	3561	1/1	0.98	0.40	58,58,58,58	0
56	MG	DA	3027	1/1	0.98	0.47	42,42,42,42	0
56	MG	AA	3063	1/1	0.98	0.09	42,42,42,42	0
56	MG	BA	3802	1/1	0.98	0.27	23,23,23,23	0
56	MG	BA	3792	1/1	0.98	0.13	52,52,52,52	0
56	MG	DA	3334	1/1	0.98	0.10	45,45,45,45	0
56	MG	BA	3278	1/1	0.98	0.37	30,30,30,30	0
56	MG	DA	3117	1/1	0.98	0.35	42,42,42,42	0
56	MG	DA	3498	1/1	0.98	0.08	44,44,44,44	0
56	MG	BA	3070	1/1	0.98	0.21	39,39,39,39	0
56	MG	BA	3625	1/1	0.98	0.08	31,31,31,31	0
56	MG	BA	3069	1/1	0.98	0.19	39,39,39,39	0
56	MG	DA	3637	1/1	0.98	0.11	70,70,70,70	0
56	MG	DA	3542	1/1	0.98	0.10	58,58,58,58	0
56	MG	AA	3051	1/1	0.98	0.17	60,60,60,60	0
56	MG	BN	3001	1/1	0.98	0.72	52,52,52,52	0
56	MG	CA	3130	1/1	0.98	0.16	51,51,51,51	0
56	MG	BA	3209	1/1	0.98	0.17	35,35,35,35	0
56	MG	AA	3110	1/1	0.98	0.14	46,46,46,46	0
56	MG	BU	209	1/1	0.98	0.38	27,27,27,27	0
56	MG	BB	212	1/1	0.98	0.19	42,42,42,42	0
56	MG	CA	3037	1/1	0.98	0.19	46,46,46,46	0
56	MG	BA	3333	1/1	0.98	0.11	23,23,23,23	0
56	MG	AA	3028	1/1	0.98	0.17	49,49,49,49	0
56	MG	DA	3004	1/1	0.98	0.12	25,25,25,25	0
56	MG	BA	3782	1/1	0.98	0.42	30,30,30,30	0
59	ZN	B9	501	1/1	0.98	0.18	49,49,49,49	0
59	ZN	B5	104	1/1	0.98	0.20	82,82,82,82	0
56	MG	DA	3250	1/1	0.98	0.21	40,40,40,40	0
56	MG	BA	3734	1/1	0.98	0.16	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3085	1/1	0.98	0.27	23,23,23,23	0
56	MG	BA	3341	1/1	0.98	0.11	43,43,43,43	0
56	MG	BA	3042	1/1	0.98	0.15	41,41,41,41	0
56	MG	DA	3154	1/1	0.98	0.20	52,52,52,52	0
56	MG	DA	3654	1/1	0.98	0.06	50,50,50,50	0
56	MG	BP	202	1/1	0.98	0.13	27,27,27,27	0
56	MG	BA	3191	1/1	0.98	0.12	43,43,43,43	0
56	MG	CA	3031	1/1	0.98	0.10	59,59,59,59	0
56	MG	BQ	203	1/1	0.98	0.32	36,36,36,36	0
56	MG	BA	3329	1/1	0.98	0.19	24,24,24,24	0
56	MG	BA	3473	1/1	0.98	0.14	52,52,52,52	0
56	MG	BA	3371	1/1	0.98	0.10	40,40,40,40	0
56	MG	DA	3636	1/1	0.98	0.11	52,52,52,52	0
56	MG	DA	3232	1/1	0.98	0.08	45,45,45,45	0
56	MG	DA	3346	1/1	0.98	0.12	48,48,48,48	0
56	MG	AA	3159	1/1	0.98	0.07	59,59,59,59	0
56	MG	BA	3234	1/1	0.98	0.31	32,32,32,32	0
56	MG	DA	3461	1/1	0.98	0.23	57,57,57,57	0
56	MG	CA	3034	1/1	0.98	0.13	51,51,51,51	0
56	MG	B7	102	1/1	0.98	0.23	28,28,28,28	0
56	MG	BA	3645	1/1	0.98	0.07	50,50,50,50	0
56	MG	CA	3046	1/1	0.98	0.10	50,50,50,50	0
56	MG	BN	3004	1/1	0.98	0.59	61,61,61,61	0
56	MG	BA	3730	1/1	0.98	0.20	13,13,13,13	0
56	MG	BR	203	1/1	0.98	0.30	34,34,34,34	0
56	MG	CA	3162	1/1	0.98	0.09	42,42,42,42	0
56	MG	BU	207	1/1	0.98	0.43	29,29,29,29	0
56	MG	AA	3132	1/1	0.98	0.14	36,36,36,36	0
56	MG	BA	3742	1/1	0.98	0.28	21,21,21,21	0
58	SF4	CD	501	8/8	0.98	0.16	64,77,89,111	0
56	MG	BA	3077	1/1	0.98	0.37	29,29,29,29	0
56	MG	BA	3170	1/1	0.98	0.18	52,52,52,52	0
56	MG	CA	3101	1/1	0.98	0.11	54,54,54,54	0
56	MG	DA	3137	1/1	0.98	0.23	43,43,43,43	0
56	MG	AA	3085	1/1	0.98	0.17	66,66,66,66	0
56	MG	BA	3184	1/1	0.98	0.23	37,37,37,37	0
56	MG	BA	3784	1/1	0.98	0.17	23,23,23,23	0
56	MG	DA	3081	1/1	0.98	0.17	48,48,48,48	0
56	MG	DA	3351	1/1	0.98	0.12	32,32,32,32	0
56	MG	CA	3137	1/1	0.98	0.15	50,50,50,50	0
56	MG	DA	3289	1/1	0.98	0.07	39,39,39,39	0
56	MG	BA	3195	1/1	0.98	0.33	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3526	1/1	0.98	0.20	35,35,35,35	0
56	MG	BA	3145	1/1	0.98	0.25	41,41,41,41	0
56	MG	DA	3407	1/1	0.98	0.07	28,28,28,28	0
59	ZN	BY	203	1/1	0.98	0.19	54,54,54,54	0
56	MG	CA	3094	1/1	0.98	0.20	68,68,68,68	0
56	MG	BA	3630	1/1	0.98	0.20	43,43,43,43	0
56	MG	BA	3644	1/1	0.98	0.24	50,50,50,50	0
56	MG	DA	3530	1/1	0.98	0.19	47,47,47,47	0
56	MG	BU	203	1/1	0.98	0.21	27,27,27,27	0
56	MG	DA	3127	1/1	0.98	0.17	36,36,36,36	0
56	MG	DA	3403	1/1	0.98	0.15	56,56,56,56	0
56	MG	DA	3470	1/1	0.98	0.15	31,31,31,31	0
56	MG	DA	3139	1/1	0.98	0.12	41,41,41,41	0
56	MG	BA	3004	1/1	0.98	0.15	26,26,26,26	0
56	MG	DA	3048	1/1	0.98	0.17	51,51,51,51	0
56	MG	BA	3167	1/1	0.98	0.33	43,43,43,43	0
56	MG	AA	3115	1/1	0.98	0.24	45,45,45,45	0
56	MG	BA	3309	1/1	0.98	0.06	50,50,50,50	0
56	MG	BA	3147	1/1	0.98	0.12	41,41,41,41	0
56	MG	CA	3028	1/1	0.98	0.11	55,55,55,55	0
56	MG	DA	3552	1/1	0.98	0.12	36,36,36,36	0
56	MG	CA	3110	1/1	0.98	0.13	48,48,48,48	0
56	MG	DA	3174	1/1	0.98	0.07	50,50,50,50	0
56	MG	DA	3546	1/1	0.98	0.07	47,47,47,47	0
56	MG	BA	3620	1/1	0.98	0.19	62,62,62,62	0
56	MG	BA	3581	1/1	0.98	0.09	37,37,37,37	0
56	MG	DA	3532	1/1	0.98	0.12	61,61,61,61	0
56	MG	AA	3135	1/1	0.98	0.08	60,60,60,60	0
56	MG	CA	3172	1/1	0.98	0.07	50,50,50,50	0
56	MG	DA	3474	1/1	0.98	0.06	30,30,30,30	0
56	MG	BA	3164	1/1	0.98	0.44	35,35,35,35	0
58	SF4	AD	501	8/8	0.98	0.18	62,74,91,95	0
56	MG	DA	3167	1/1	0.98	0.14	38,38,38,38	0
56	MG	BA	3400	1/1	0.98	0.12	34,34,34,34	0
56	MG	BA	3306	1/1	0.98	0.21	18,18,18,18	0
56	MG	BA	3463	1/1	0.98	0.13	10,10,10,10	0
56	MG	AA	3053	1/1	0.98	0.11	46,46,46,46	0
56	MG	BA	3491	1/1	0.98	0.19	45,45,45,45	0
56	MG	BA	3573	1/1	0.98	0.17	24,24,24,24	0
56	MG	DA	3646	1/1	0.98	0.11	54,54,54,54	0
56	MG	BW	204	1/1	0.98	0.39	31,31,31,31	0
56	MG	BA	3619	1/1	0.98	0.12	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3349	1/1	0.98	0.21	49,49,49,49	0
56	MG	BA	3142	1/1	0.98	0.32	29,29,29,29	0
56	MG	BA	3011	1/1	0.98	0.10	33,33,33,33	0
56	MG	DA	3462	1/1	0.98	0.09	31,31,31,31	0
56	MG	BA	3413	1/1	0.98	0.16	27,27,27,27	0
56	MG	DA	3595	1/1	0.98	0.07	39,39,39,39	0
56	MG	DA	3432	1/1	0.98	0.10	37,37,37,37	0
56	MG	DA	3476	1/1	0.98	0.24	53,53,53,53	0
56	MG	AA	3183	1/1	0.98	0.08	73,73,73,73	0
56	MG	BB	203	1/1	0.98	0.26	44,44,44,44	0
56	MG	DA	3157	1/1	0.98	0.09	42,42,42,42	0
56	MG	BA	3727	1/1	0.98	0.19	34,34,34,34	0
56	MG	DA	3519	1/1	0.98	0.14	32,32,32,32	0
56	MG	BA	3336	1/1	0.98	0.16	50,50,50,50	0
56	MG	DA	3526	1/1	0.99	0.29	28,28,28,28	0
56	MG	BA	3036	1/1	0.99	0.18	19,19,19,19	0
56	MG	BA	3037	1/1	0.99	0.54	29,29,29,29	0
56	MG	BA	3729	1/1	0.99	0.12	27,27,27,27	0
56	MG	BA	3407	1/1	0.99	0.17	40,40,40,40	0
56	MG	BA	3155	1/1	0.99	0.45	30,30,30,30	0
56	MG	AA	3186	1/1	0.99	0.13	42,42,42,42	0
56	MG	BA	3084	1/1	0.99	0.25	33,33,33,33	0
56	MG	DA	3120	1/1	0.99	0.15	34,34,34,34	0
56	MG	BA	3513	1/1	0.99	0.10	43,43,43,43	0
56	MG	BA	3560	1/1	0.99	0.21	38,38,38,38	0
56	MG	DA	3471	1/1	0.99	0.18	54,54,54,54	0
56	MG	BD	3302	1/1	0.99	0.41	46,46,46,46	0
56	MG	BA	3470	1/1	0.99	0.17	37,37,37,37	0
56	MG	BA	3356	1/1	0.99	0.25	52,52,52,52	0
56	MG	DA	3336	1/1	0.99	0.09	39,39,39,39	0
59	ZN	B6	103	1/1	0.99	0.16	62,62,62,62	0
56	MG	CA	3095	1/1	0.99	0.04	56,56,56,56	0
56	MG	BA	3098	1/1	0.99	0.26	38,38,38,38	0
56	MG	BA	3680	1/1	0.99	0.07	53,53,53,53	0
56	MG	DA	3601	1/1	0.99	0.10	26,26,26,26	0
56	MG	BA	3374	1/1	0.99	0.13	21,21,21,21	0
56	MG	BA	3557	1/1	0.99	0.11	37,37,37,37	0
56	MG	AA	3136	1/1	0.99	0.20	62,62,62,62	0
56	MG	DA	3005	1/1	0.99	0.20	26,26,26,26	0
56	MG	CA	3035	1/1	0.99	0.13	52,52,52,52	0
59	ZN	D6	501	1/1	0.99	0.20	66,66,66,66	0
56	MG	BD	3305	1/1	0.99	0.27	31,31,31,31	0

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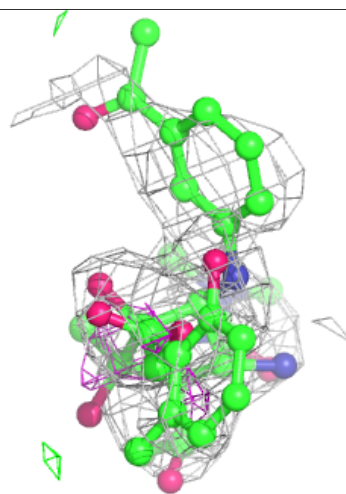
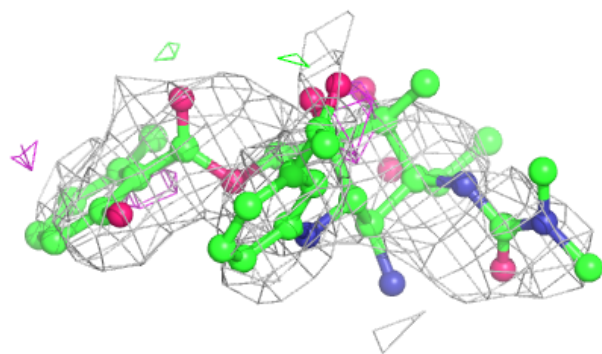
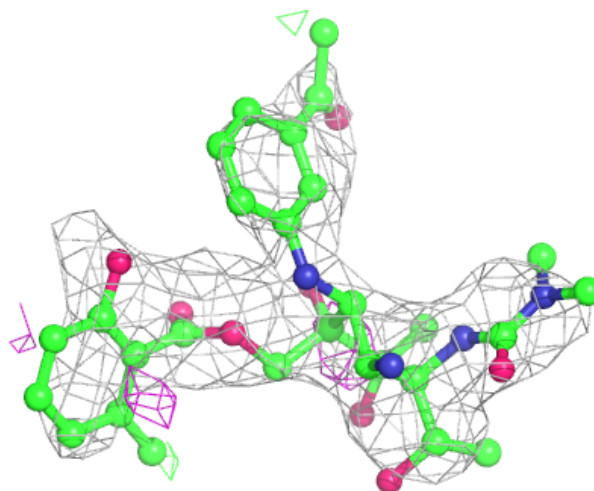
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3675	1/1	0.99	0.23	29,29,29,29	0
56	MG	DA	3112	1/1	0.99	0.15	37,37,37,37	0
56	MG	BA	3601	1/1	0.99	0.14	49,49,49,49	0
56	MG	BB	214	1/1	0.99	0.20	53,53,53,53	0
56	MG	DA	3084	1/1	0.99	0.31	47,47,47,47	0
56	MG	DA	3136	1/1	0.99	0.18	43,43,43,43	0
56	MG	BA	3052	1/1	0.99	0.20	23,23,23,23	0
56	MG	BA	3481	1/1	0.99	0.18	44,44,44,44	0
56	MG	BA	3535	1/1	0.99	0.21	31,31,31,31	0
56	MG	CA	3161	1/1	0.99	0.05	51,51,51,51	0
56	MG	AA	3060	1/1	0.99	0.10	52,52,52,52	0
56	MG	BA	3441	1/1	0.99	0.17	32,32,32,32	0
56	MG	DA	3246	1/1	0.99	0.13	31,31,31,31	0
56	MG	AA	3077	1/1	0.99	0.22	54,54,54,54	0
56	MG	BA	3516	1/1	0.99	0.19	28,28,28,28	0
56	MG	BA	3794	1/1	0.99	0.14	29,29,29,29	0
56	MG	DA	3550	1/1	0.99	0.15	22,22,22,22	0
56	MG	BA	3488	1/1	0.99	0.19	16,16,16,16	0
59	ZN	D5	501	1/1	1.00	0.20	52,52,52,52	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

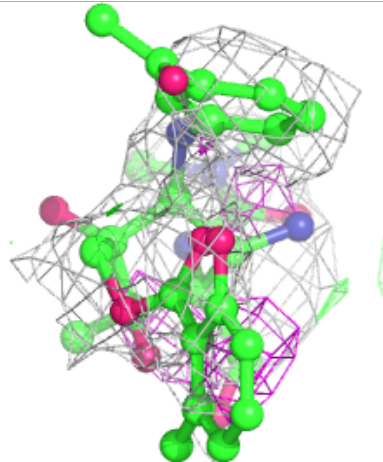
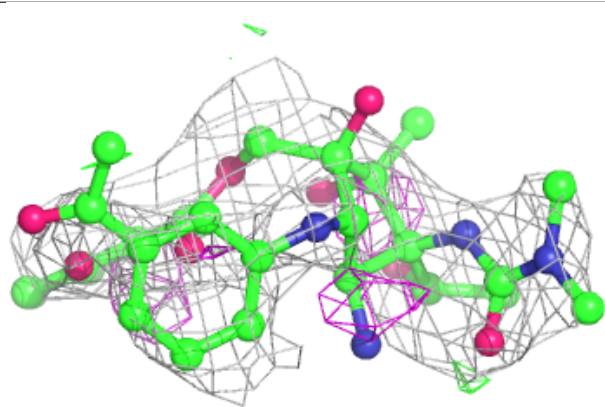
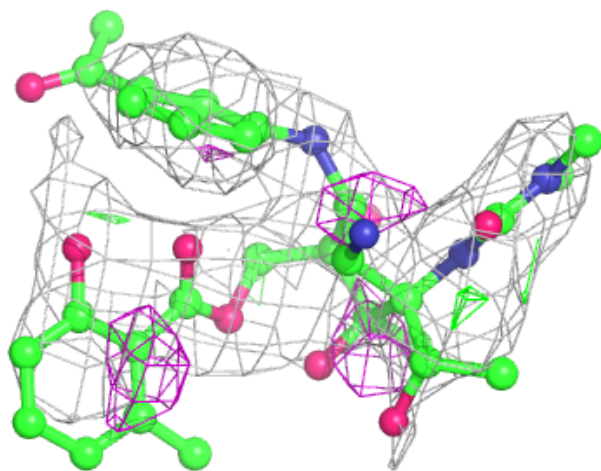
Electron density around PCY CA 3176:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PCY AA 3191:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.