



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 08:58 pm BST

PDB ID : 4W2G
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in complex with pactamycin (soaked), mRNA and three deacylated tRNAs in the A, P and E sites
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 : 2.55 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

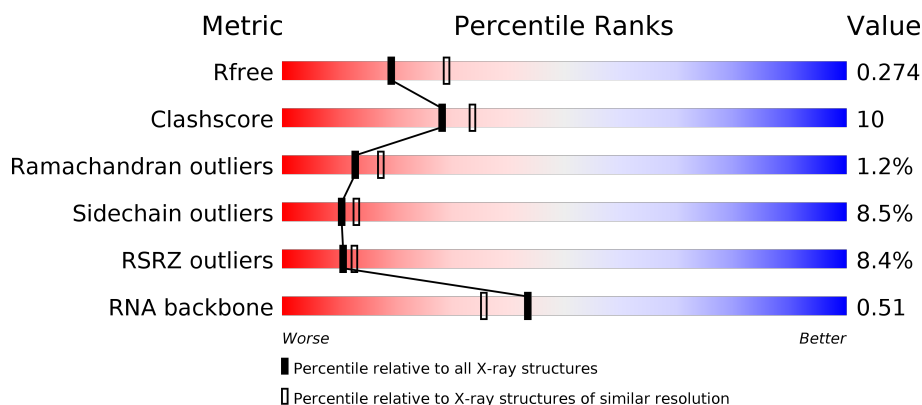
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)
RNA backbone	3102	1026 (2.88-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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>4%</div> <div> <div></div> <div>55%</div> <div>32%</div> <div>10%</div> <div>..</div> </div> </div>
1	CA	1521	<div> <div>3%</div> <div> <div></div> <div>50%</div> <div>37%</div> <div>10%</div> <div>..</div> </div> </div>
2	AB	256	<div> <div>17%</div> <div> <div></div> <div>48%</div> <div>36%</div> <div>5%</div> <div>10%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	CB	256	
3	AC	239	
3	CC	239	
4	AD	209	
4	CD	209	
5	AE	162	
5	CE	162	
6	AF	101	
6	CF	101	
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	














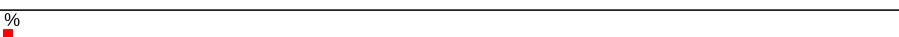











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Mol	Chain	Length	Quality of chain
15	AO	89	
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AW	76	
23	AY	76	
23	CW	76	
23	CY	76	
24	AX	77	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



















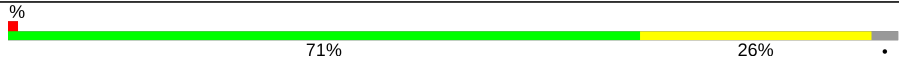
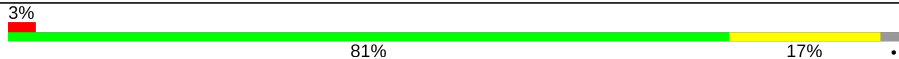
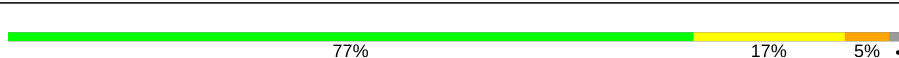


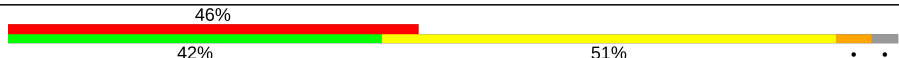
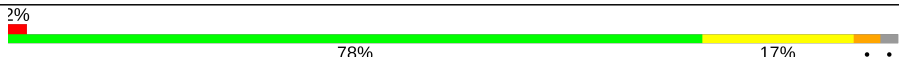
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Mol	Chain	Length	Quality of chain
26	DB	121	
27	BD	276	
27	DD	276	
28	BE	206	
28	DE	206	
29	BF	210	
29	DF	210	
30	BG	182	
30	DG	182	
31	BH	180	
31	DH	180	
32	BI	148	
32	DI	148	
33	BN	140	
33	DN	140	
34	BO	122	
34	DO	122	
35	BP	150	
35	DP	150	
36	BQ	141	
36	DQ	141	
37	BR	118	
37	DR	118	
38	BS	112	
38	DS	112	

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Mol	Chain	Length	Quality of chain
39	BT	146	
39	DT	146	
40	BU	118	
40	DU	118	
41	BV	101	
41	DV	101	
42	BW	113	
42	DW	113	
43	BX	96	
43	DX	96	
44	BY	110	
44	DY	110	
45	BZ	206	
45	DZ	206	
46	B0	85	
46	D0	85	
47	B1	98	
47	D1	98	
48	B2	72	
48	D2	72	
49	B3	60	
49	D3	60	
50	B4	71	
50	D4	71	
51	B5	60	

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Mol	Chain	Length	Quality of chain
51	D5	60	
52	B6	54	
52	D6	54	
53	B7	49	
53	D7	49	
54	B8	65	
54	D8	65	
55	B9	37	
55	D9	37	

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
23	5MU	CY	54	-	-	-	X
56	MG	B1	102	-	-	-	X
56	MG	BR	202	-	-	-	X
56	MG	CA	3027	-	-	-	X
56	MG	CX	3006	-	-	-	X
56	MG	DA	3199	-	-	-	X
56	MG	DA	3596	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 297273 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1498	Total	C	N	O	P	0	0	0
			32205	14333	5970	10404	1498			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 22 is a RNA chain called mRNA.

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

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AW	74	Total	C	N	O	P	S	0	0	0
			1588	713	285	515	73	2			
23	AY	74	Total	C	N	O	P	S	0	0	0
			1581	707	285	515	73	1			
23	CW	72	Total	C	N	O	P	S	0	0	0
			1541	688	278	502	72	1			
23	CY	73	Total	C	N	O	P	S	0	0	0
			1561	698	283	507	72	1			

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

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

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

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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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		0	0	0
			877	553	175	149				
38	DS	110	Total	C	N	O		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			
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			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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	839	Total	Mg	0	0
			839	839		
56	AK	2	Total	Mg	0	0
			2	2		
56	DQ	4	Total	Mg	0	0
			4	4		
56	D3	1	Total	Mg	0	0
			1	1		
56	DF	5	Total	Mg	0	0
			5	5		
56	CV	1	Total	Mg	0	0
			1	1		
56	B8	3	Total	Mg	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	BE	8	Total 8	Mg 8	0	0
56	AW	7	Total 7	Mg 7	0	0
56	DU	2	Total 2	Mg 2	0	0
56	B1	2	Total 2	Mg 2	0	0
56	AN	1	Total 1	Mg 1	0	0
56	BP	3	Total 3	Mg 3	0	0
56	AX	12	Total 12	Mg 12	0	0
56	DN	1	Total 1	Mg 1	0	0
56	CY	1	Total 1	Mg 1	0	0
56	CA	177	Total 177	Mg 177	0	0
56	B5	4	Total 4	Mg 4	0	0
56	BB	23	Total 23	Mg 23	0	0
56	D8	1	Total 1	Mg 1	0	0
56	AE	1	Total 1	Mg 1	0	0
56	DG	1	Total 1	Mg 1	0	0
56	B9	1	Total 1	Mg 1	0	0
56	BF	12	Total 12	Mg 12	0	0
56	AV	1	Total 1	Mg 1	0	0
56	BX	2	Total 2	Mg 2	0	0
56	B2	1	Total 1	Mg 1	0	0
56	AA	230	Total 230	Mg 230	0	0

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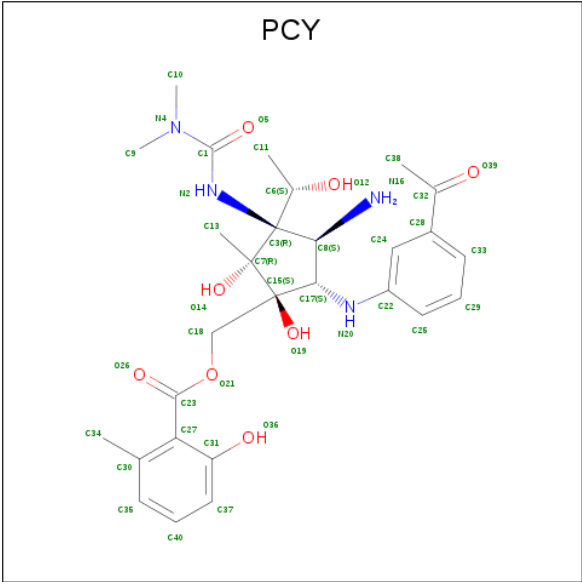
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	BQ	5	Total 5	Mg 5	0	0
56	D7	2	Total 2	Mg 2	0	0
56	CX	5	Total 5	Mg 5	0	0
56	DV	3	Total 3	Mg 3	0	0
56	B6	2	Total 2	Mg 2	0	0
56	AM	1	Total 1	Mg 1	0	0
56	BU	9	Total 9	Mg 9	0	0
56	DR	1	Total 1	Mg 1	0	0
56	AD	1	Total 1	Mg 1	0	0
56	BN	5	Total 5	Mg 5	0	0
56	CT	1	Total 1	Mg 1	0	0
56	D0	2	Total 2	Mg 2	0	0
56	BG	3	Total 3	Mg 3	0	0
56	BY	1	Total 1	Mg 1	0	0
56	DE	4	Total 4	Mg 4	0	0
56	B3	3	Total 3	Mg 3	0	0
56	CJ	1	Total 1	Mg 1	0	0
56	BR	5	Total 5	Mg 5	0	0
56	DA	675	Total 675	Mg 675	0	0
56	DW	3	Total 3	Mg 3	0	0
56	B7	2	Total 2	Mg 2	0	0

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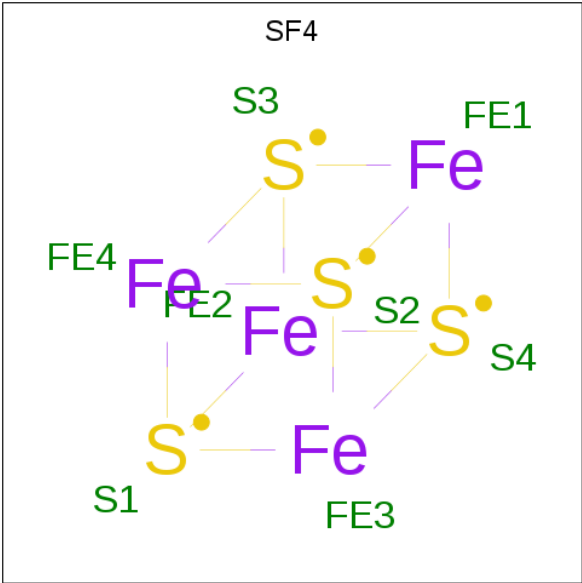
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	CF	1	Total 1	Mg 1	0	0
56	BV	5	Total 5	Mg 5	0	0
56	DO	1	Total 1	Mg 1	0	0
56	BO	1	Total 1	Mg 1	0	0
56	BZ	1	Total 1	Mg 1	0	0
56	DY	1	Total 1	Mg 1	0	0
56	CW	2	Total 2	Mg 2	0	0
56	BD	11	Total 11	Mg 11	0	0
56	B0	3	Total 3	Mg 3	0	0
56	CE	2	Total 2	Mg 2	0	0
56	BW	3	Total 3	Mg 3	0	0
56	AY	3	Total 3	Mg 3	0	0
56	DD	7	Total 7	Mg 7	0	0
56	AF	1	Total 1	Mg 1	0	0
56	DB	11	Total 11	Mg 11	0	0

- 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: Fe₄S₄).



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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	B5	1	Total 1	Zn 1	0	0
59	B4	1	Total 1	Zn 1	0	0
59	CN	1	Total 1	Zn 1	0	0
59	BY	1	Total 1	Zn 1	0	0
59	B9	1	Total 1	Zn 1	0	0
59	DY	1	Total 1	Zn 1	0	0
59	D5	1	Total 1	Zn 1	0	0
59	D4	1	Total 1	Zn 1	0	0
59	AN	1	Total 1	Zn 1	0	0
59	D6	1	Total 1	Zn 1	0	0
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	226	Total 226	O 226	0	0
61	AE	3	Total 3	O 3	0	0
61	AJ	1	Total 1	O 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AL	4	Total 4	O 4	0	0
61	AM	1	Total 1	O 1	0	0
61	AV	4	Total 4	O 4	0	0
61	AW	6	Total 6	O 6	0	0
61	AX	8	Total 8	O 8	0	0
61	AY	3	Total 3	O 3	0	0
61	BA	1411	Total 1411	O 1411	0	0
61	BB	36	Total 36	O 36	0	0
61	BD	16	Total 16	O 16	0	0
61	BE	13	Total 13	O 13	0	0
61	BF	7	Total 7	O 7	0	0
61	BG	3	Total 3	O 3	0	0
61	BI	1	Total 1	O 1	0	0
61	BN	2	Total 2	O 2	0	0
61	BO	3	Total 3	O 3	0	0
61	BP	17	Total 17	O 17	0	0
61	BQ	2	Total 2	O 2	0	0
61	BR	2	Total 2	O 2	0	0
61	BT	1	Total 1	O 1	0	0
61	BU	6	Total 6	O 6	0	0
61	BV	2	Total 2	O 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BW	4	Total 4	O 4	0	0
61	BX	1	Total 1	O 1	0	0
61	B0	4	Total 4	O 4	0	0
61	B1	2	Total 2	O 2	0	0
61	B3	2	Total 2	O 2	0	0
61	B5	5	Total 5	O 5	0	0
61	B6	1	Total 1	O 1	0	0
61	B7	3	Total 3	O 3	0	0
61	B8	11	Total 11	O 11	0	0
61	CA	173	Total 173	O 173	0	0
61	CJ	2	Total 2	O 2	0	0
61	CL	1	Total 1	O 1	0	0
61	CV	2	Total 2	O 2	0	0
61	CW	1	Total 1	O 1	0	0
61	CX	4	Total 4	O 4	0	0
61	DA	1002	Total 1002	O 1002	0	0
61	DB	10	Total 10	O 10	0	0
61	DD	17	Total 17	O 17	0	0
61	DE	11	Total 11	O 11	0	0
61	DF	5	Total 5	O 5	0	0
61	DN	2	Total 2	O 2	0	0

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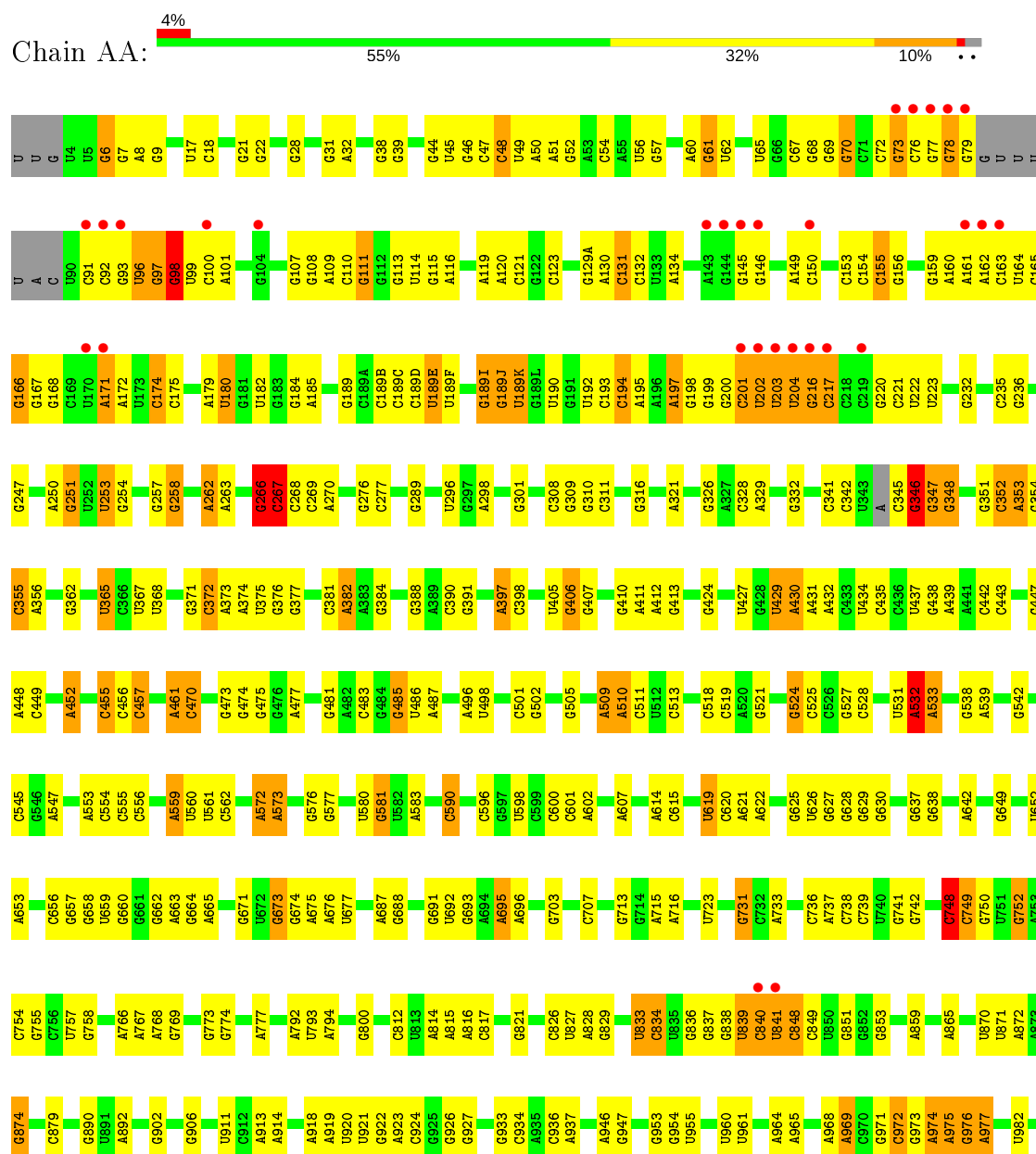
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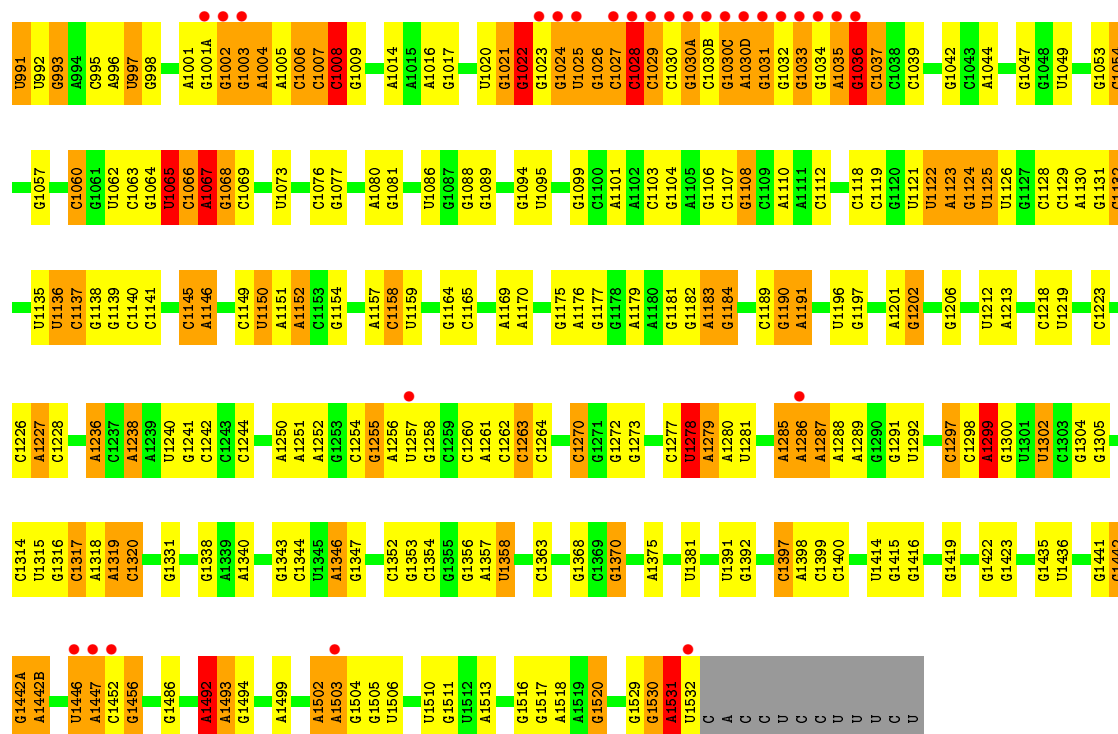
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
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			2	2		
61	DP	8	Total	O	0	0
			8	8		
61	DQ	1	Total	O	0	0
			1	1		
61	DR	1	Total	O	0	0
			1	1		
61	DU	2	Total	O	0	0
			2	2		
61	DW	1	Total	O	0	0
			1	1		
61	DY	1	Total	O	0	0
			1	1		
61	D0	5	Total	O	0	0
			5	5		
61	D3	1	Total	O	0	0
			1	1		
61	D7	3	Total	O	0	0
			3	3		
61	D8	4	Total	O	0	0
			4	4		

3 Residue-property plots [i](#)

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.

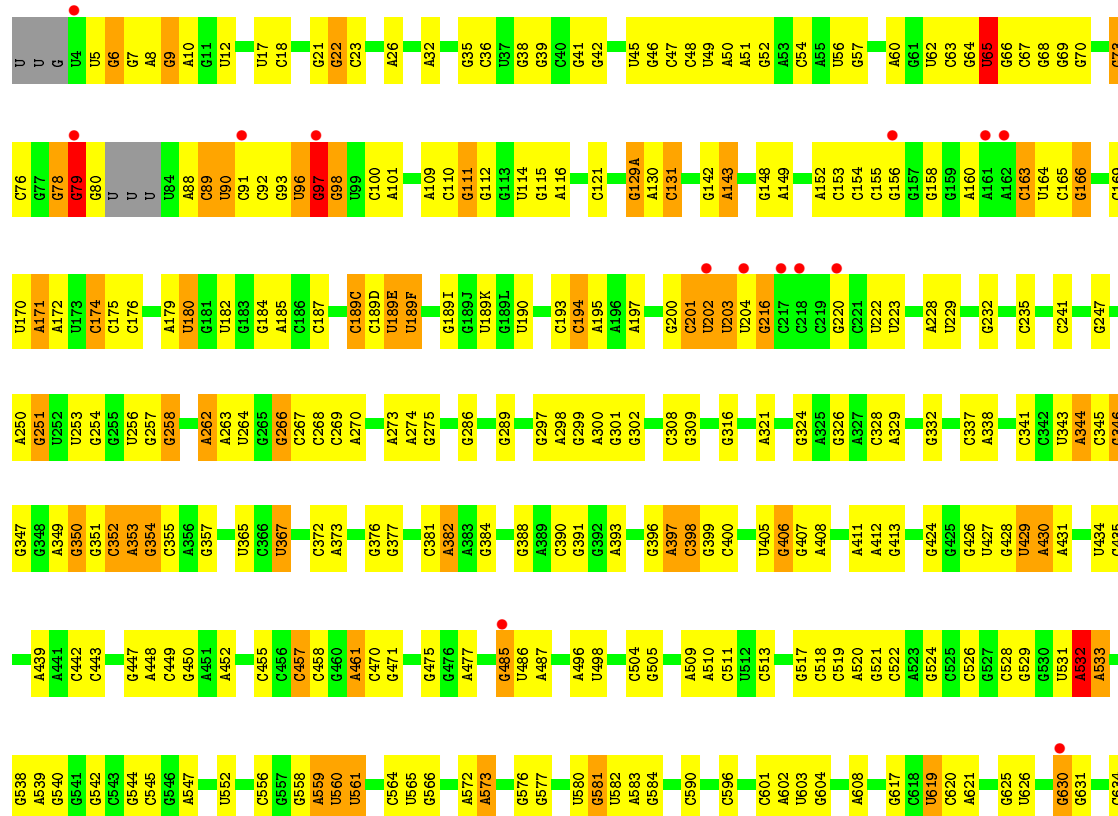
• Molecule 1: 16S Ribosomal RNA



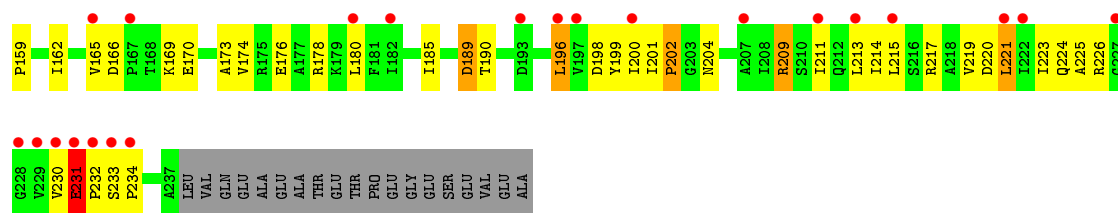


- Molecule 1: 16S Ribosomal RNA

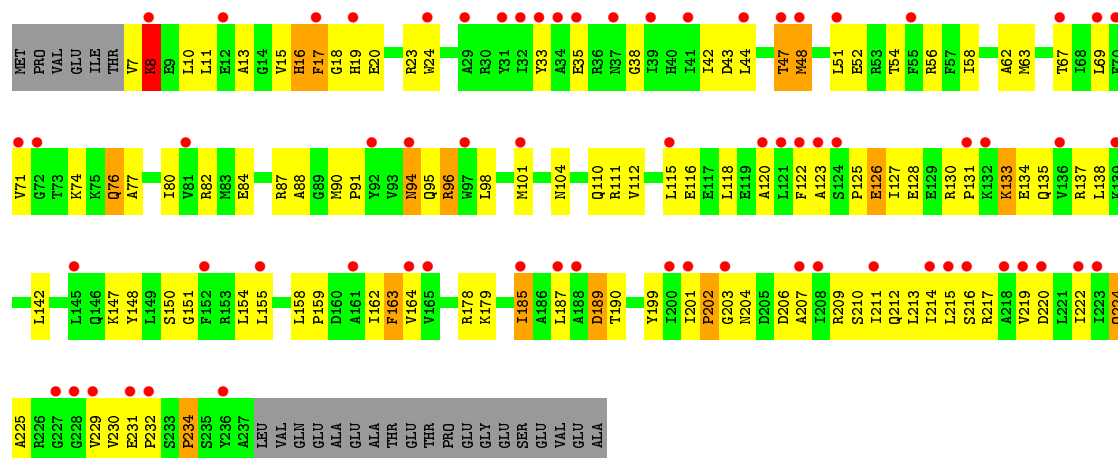
Chain CA: 



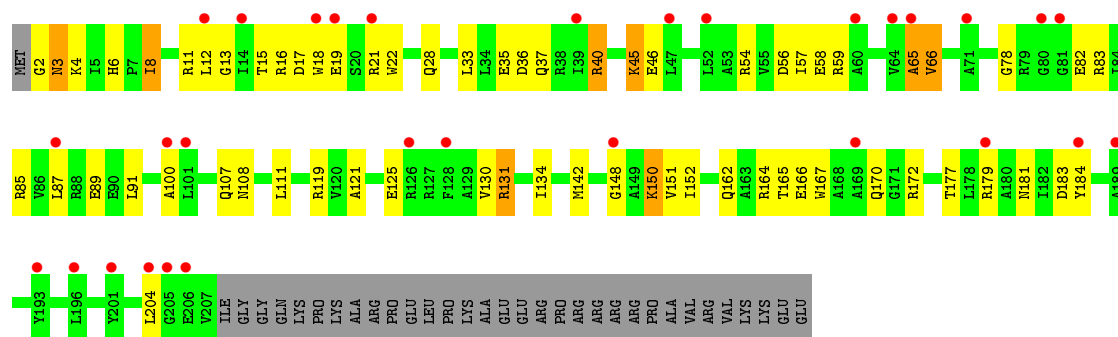




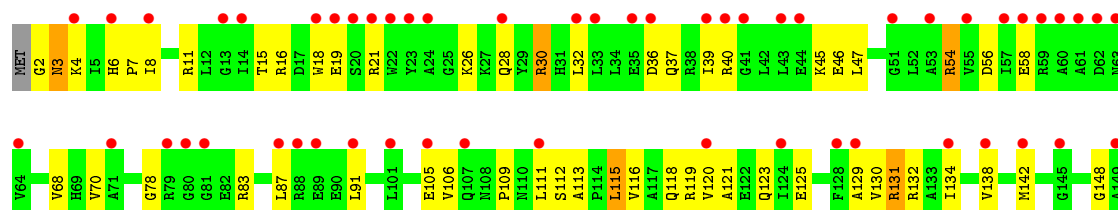
• Molecule 2: 30S Ribosomal Protein S2



• Molecule 3: 30S Ribosomal Protein S3



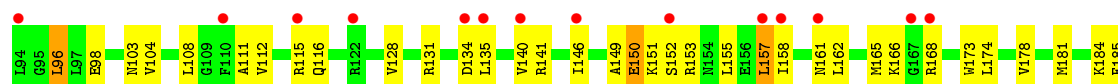
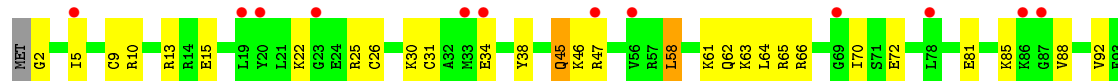
• Molecule 3: 30S Ribosomal Protein S3



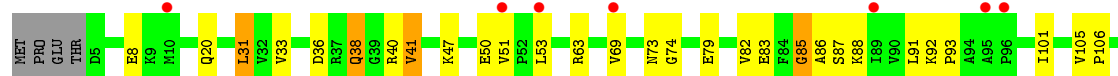
- Molecule 4: 30S Ribosomal Protein S4



- Molecule 4: 30S Ribosomal Protein S4



- Molecule 5: 30S Ribosomal Protein S5

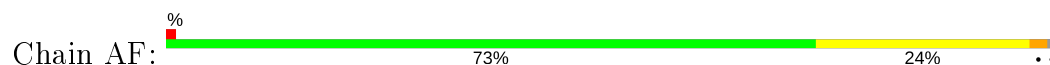


- Molecule 5: 30S Ribosomal Protein S5





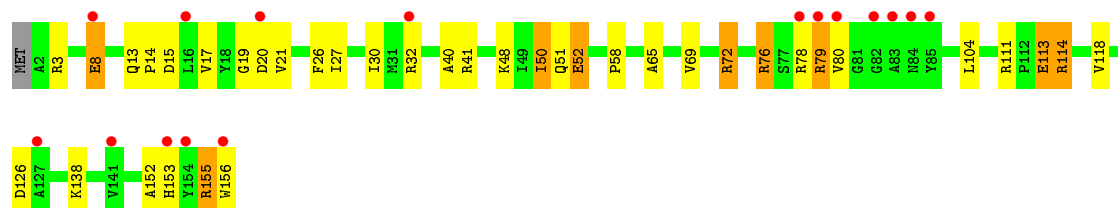
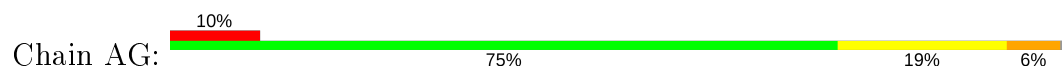
• Molecule 6: 30S Ribosomal Protein S6



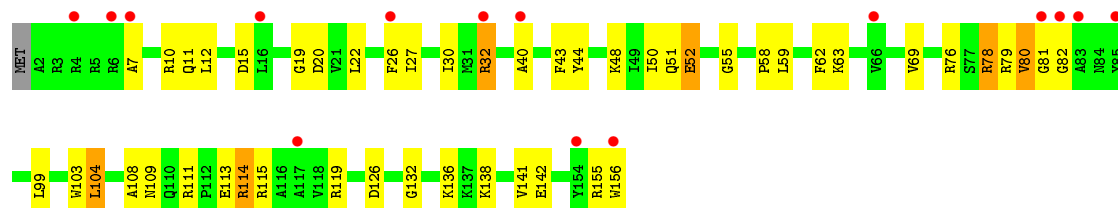
• Molecule 6: 30S Ribosomal Protein S6



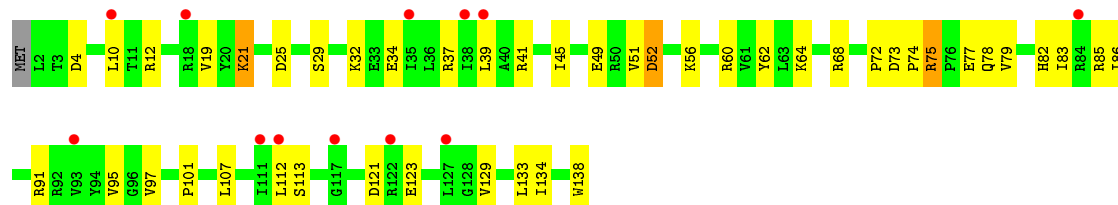
• Molecule 7: 30S Ribosomal Protein S7



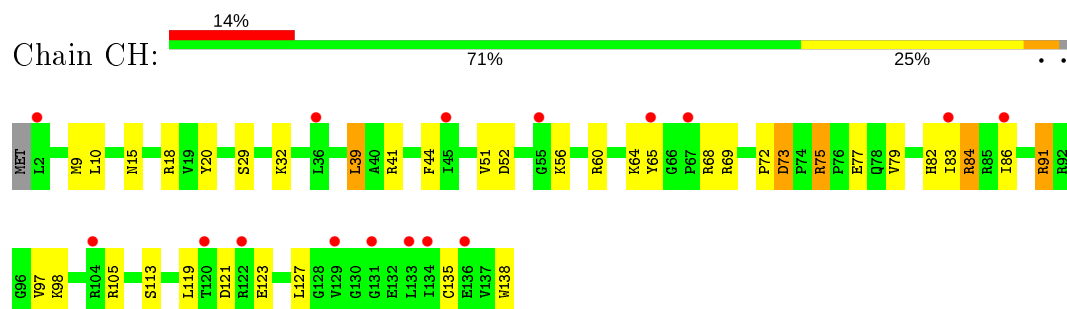
• Molecule 7: 30S Ribosomal Protein S7



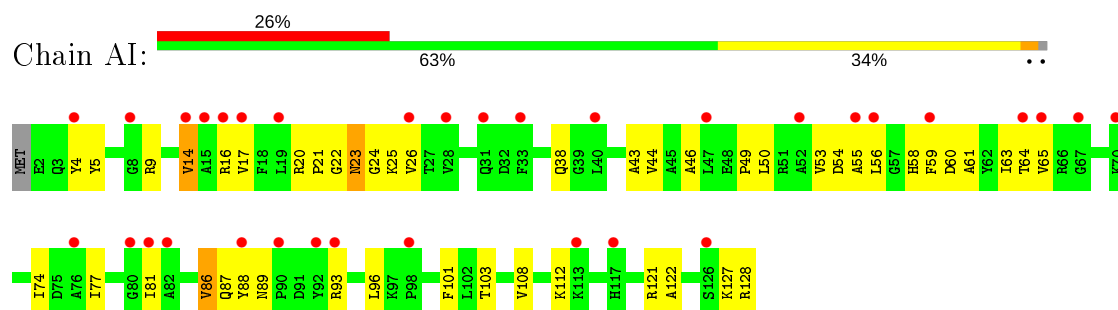
• Molecule 8: 30S Ribosomal Protein S8



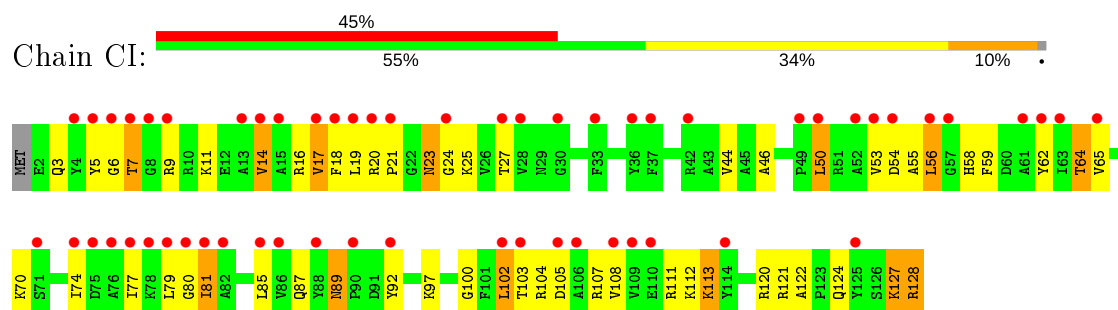
- Molecule 8: 30S Ribosomal Protein S8



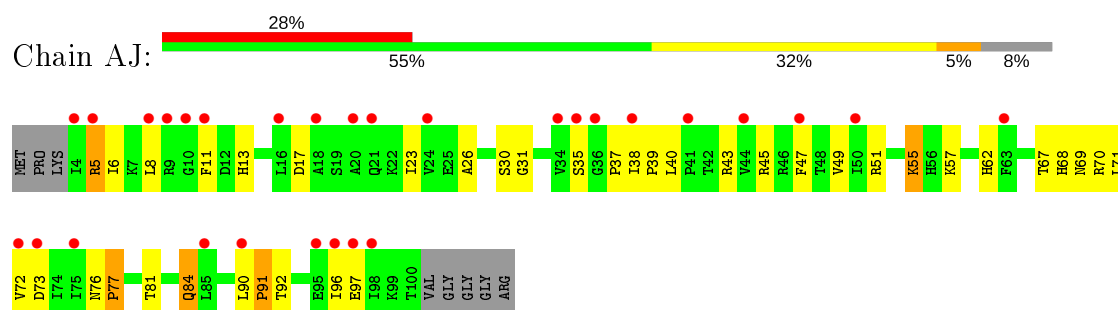
- Molecule 9: 30S Ribosomal Protein S9



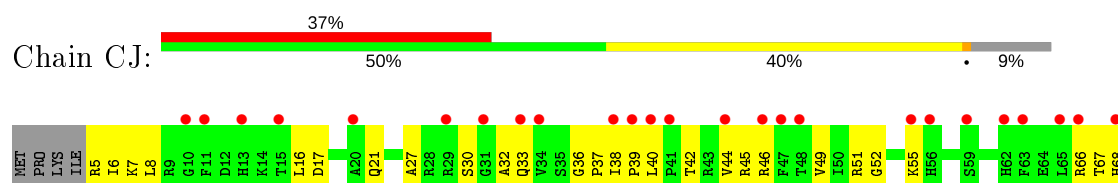
- Molecule 9: 30S Ribosomal Protein S9

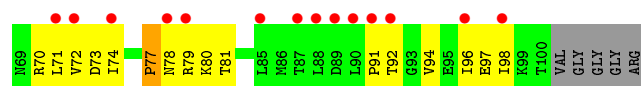


- Molecule 10: 30S Ribosomal Protein S10

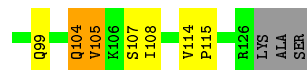
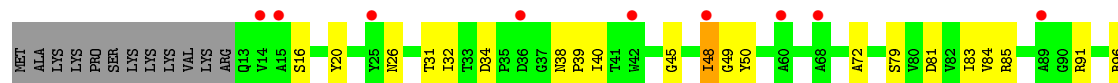


- Molecule 10: 30S Ribosomal Protein S10





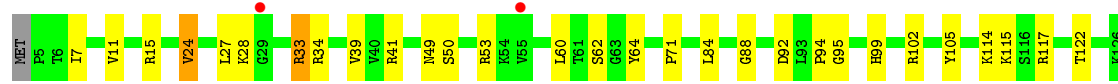
• Molecule 11: 30S Ribosomal Protein S11



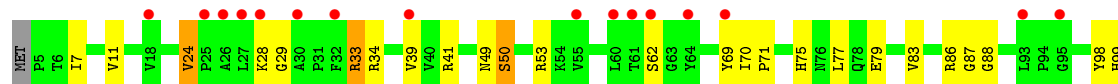
• Molecule 11: 30S Ribosomal Protein S11



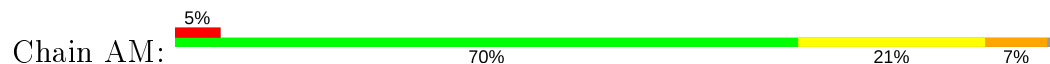
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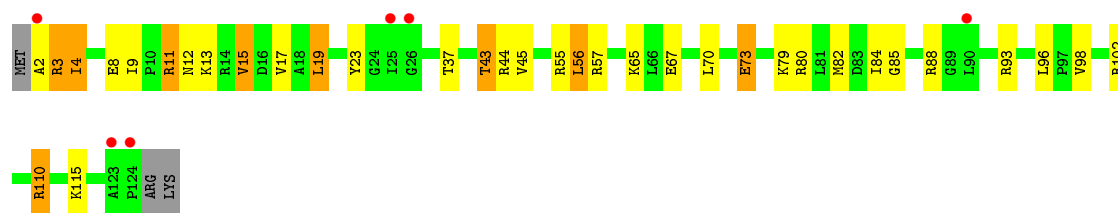


• Molecule 12: 30S Ribosomal Protein S12

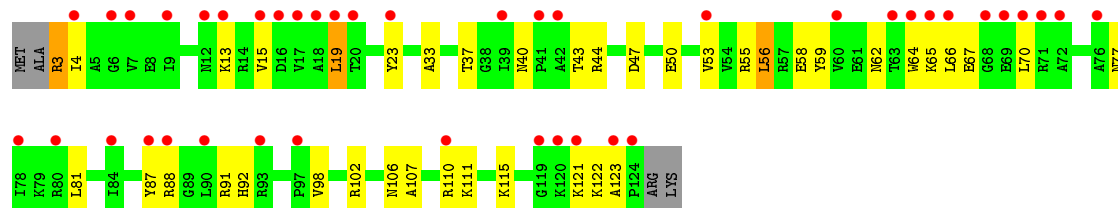


• Molecule 13: 30S Ribosomal Protein S13





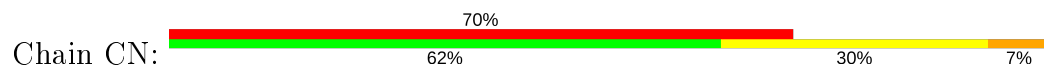
• Molecule 13: 30S Ribosomal Protein S13



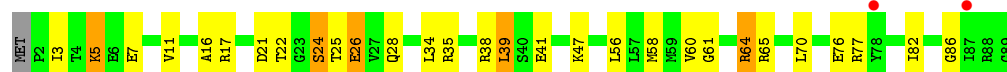
• Molecule 14: 30S Ribosomal Protein S14



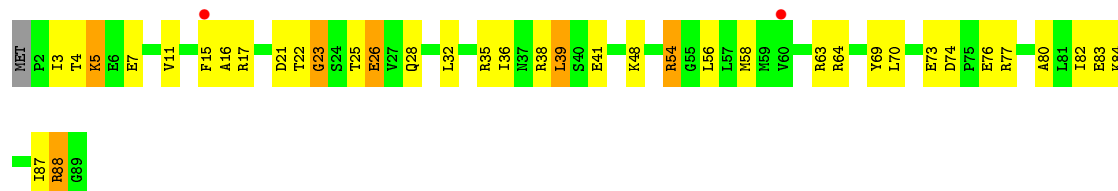
• Molecule 14: 30S Ribosomal Protein S14



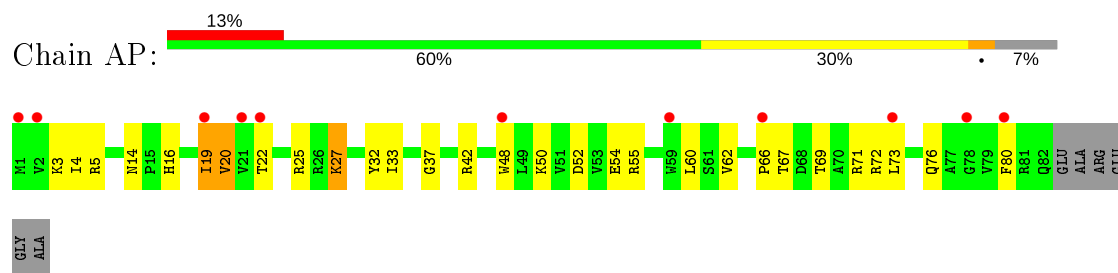
• Molecule 15: 30S Ribosomal Protein S15



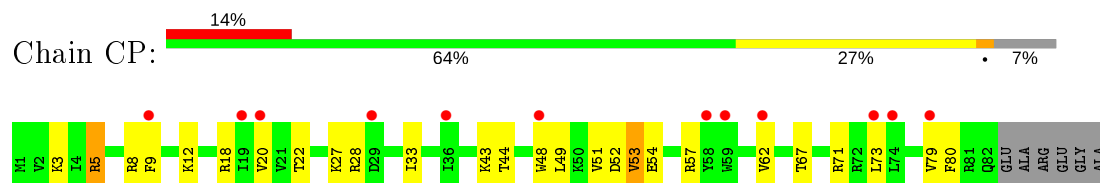
• Molecule 15: 30S Ribosomal Protein S15



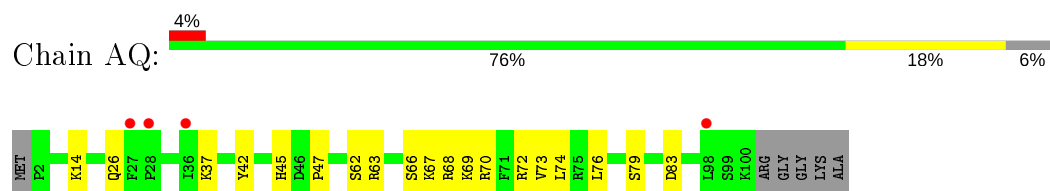
- Molecule 16: 30S Ribosomal Protein S16



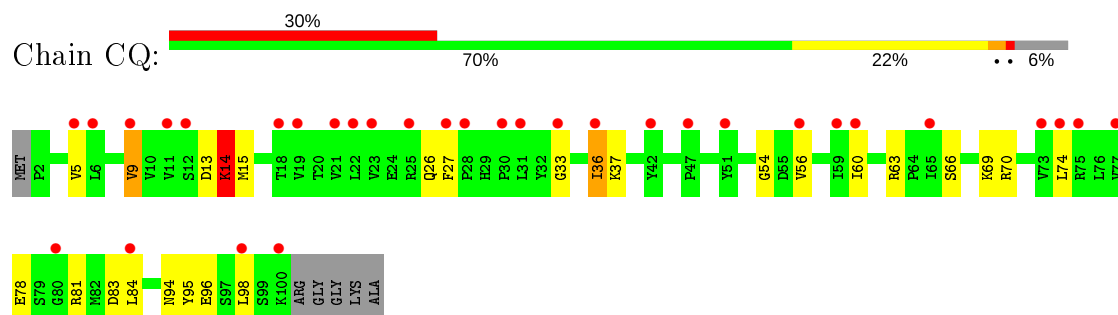
- Molecule 16: 30S Ribosomal Protein S16



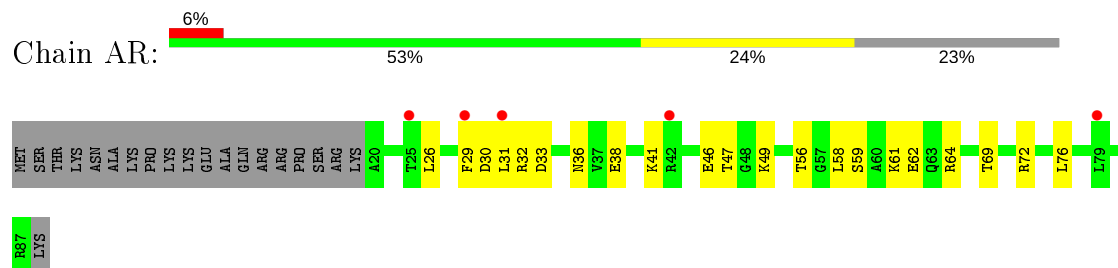
- Molecule 17: 30S Ribosomal Protein S17



- Molecule 17: 30S Ribosomal Protein S17

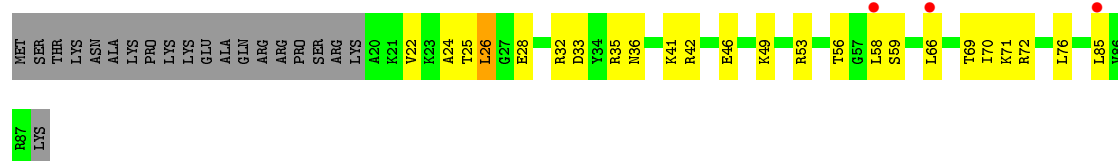


- Molecule 18: 30S Ribosomal Protein S18



- Molecule 18: 30S Ribosomal Protein S18

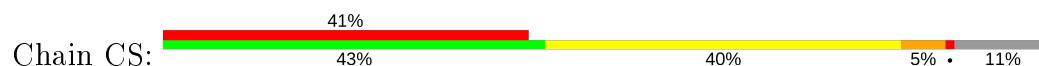




- Molecule 19: 30S Ribosomal Protein S19



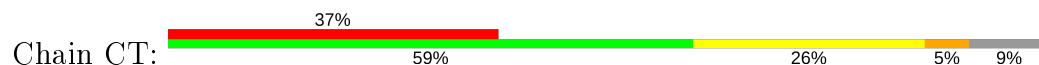
- Molecule 19: 30S Ribosomal Protein S19



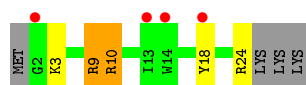
- Molecule 20: 30S Ribosomal Protein S20



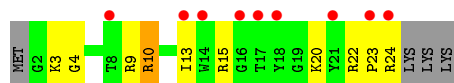
- Molecule 20: 30S Ribosomal Protein S20



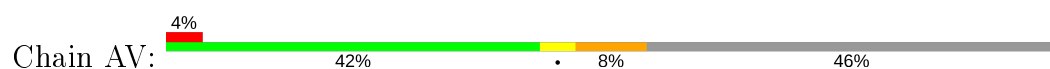
- Molecule 21: 30S Ribosomal Protein THX



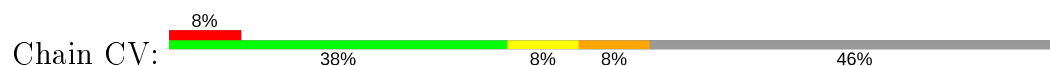
- Molecule 21: 30S Ribosomal Protein THX



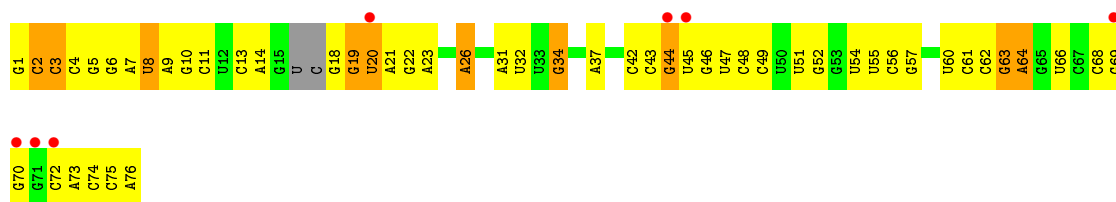
- Molecule 22: mRNA



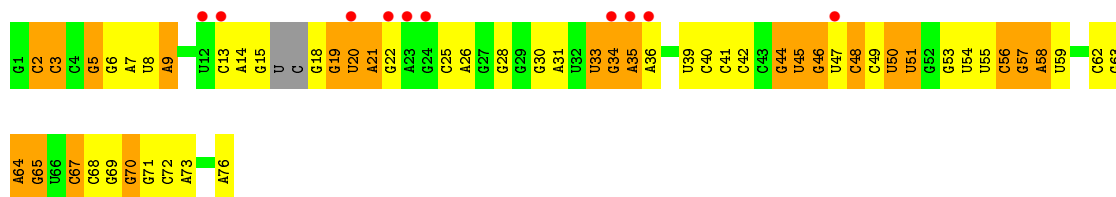
- Molecule 22: mRNA



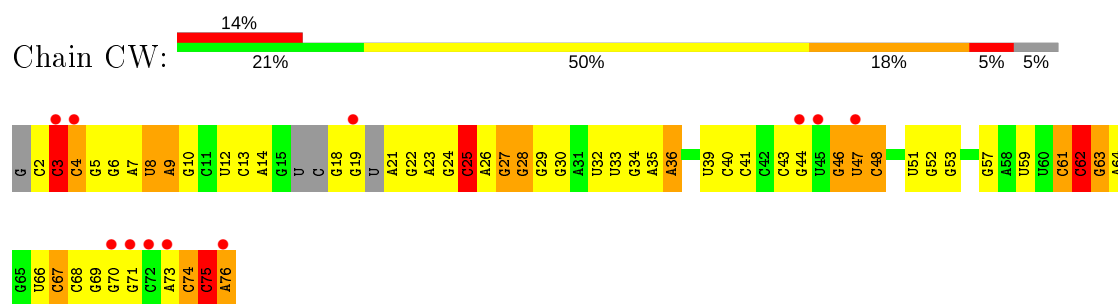
- Molecule 23: A/P-site tRNA



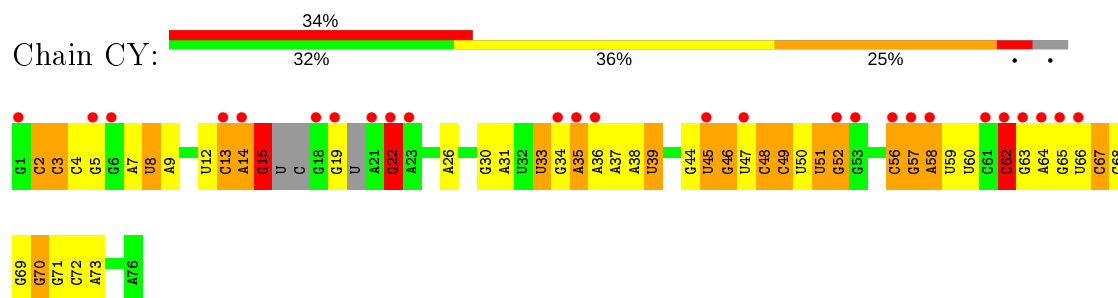
- Molecule 23: A/P-site tRNA



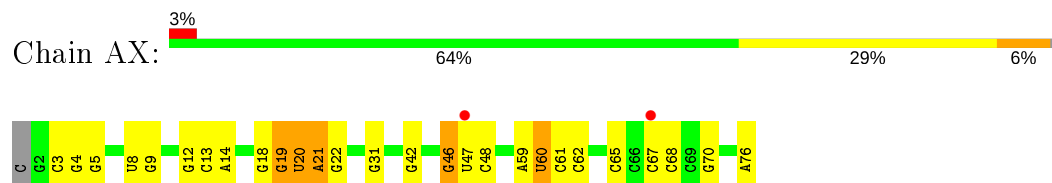
- Molecule 23: A/P-site tRNA



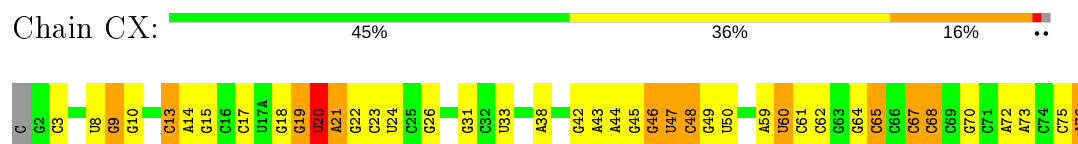
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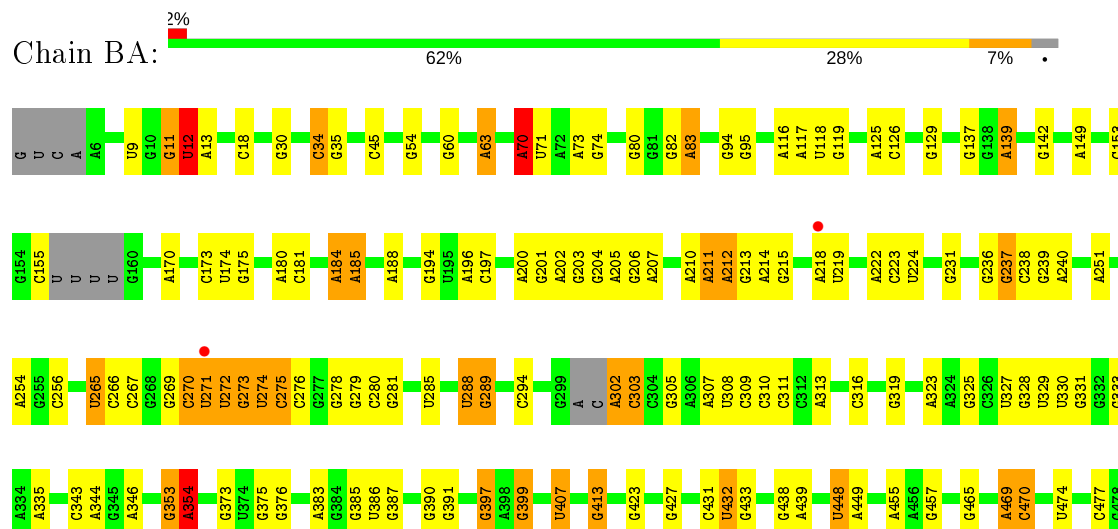
- Molecule 24: E-site tRNA



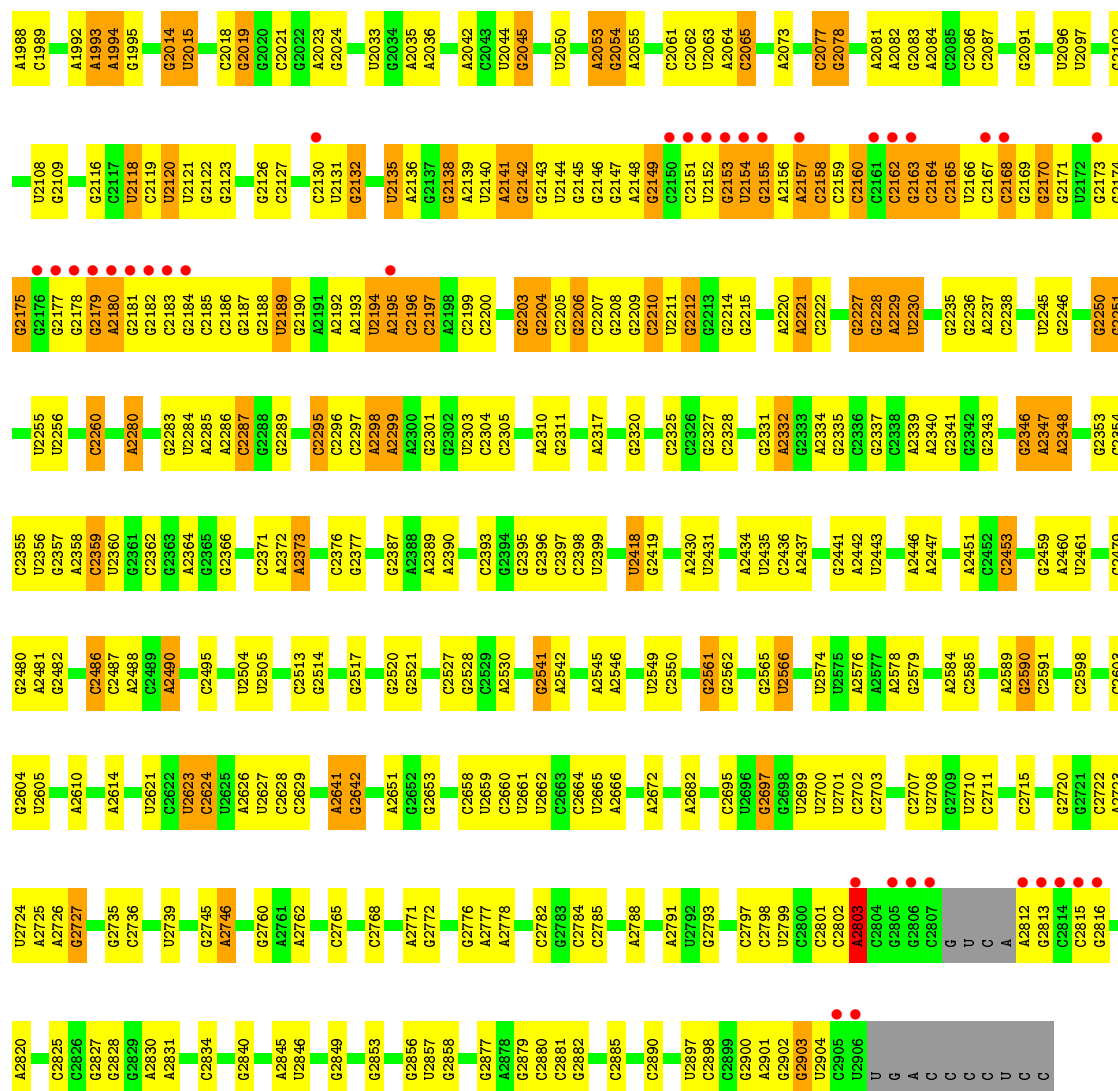
- Molecule 24: E-site tRNA



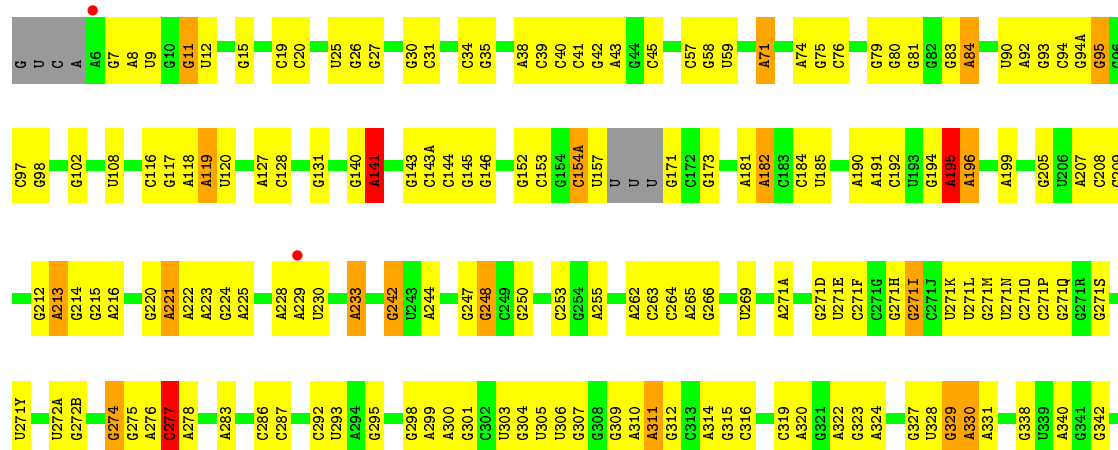
- Molecule 25: 23S Ribosomal RNA



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G3848	G1734	C1595	A1496	C1246	C1083	U982	G877	G776	A690	G887	C481
G1855	U1735	A1604	G1497	C1249	G1085	G983	C885	G777	A691	U591	C482
G1857	A1736	A1605	U1501	U1250	C1086	A986	U886	G778	A692	G593	A483
G3858	U1740	A1613	G1502	A1255	C1087	U989	U894	G779	A693	A594	G484
A1878	G1743	A1616	G1506	U1256	A1091	G989	U895	G786	A694	A595	G489
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G1882	A1745	U1625	G1508	A1258	G1093	G991	C897	U793	A696	C597	G493
C1883	G1746	A1632	U1398	C1263	A1094	G992	U898	U794	A697	A598	G494
A1891	A1747	G1628	A1513	G1264	G1097	G993	C904	G795	A698	G600	A496
G1892	A1748	C1629	C1514	A1265	C1098	G997	U905	G796	A699	A601	A497
U1882	U1756	A1630	A1406	G1269	A	A998	U907	A797	A700	G602	A506
C1883	C1757	A1632	G1407	G1271	A	G1000	A908	A798	A701	C603	A507
G1891	G1766	A1633	A1411	G1272	G	C1001	U907	A801	A702	G604	G507
G1892	A1767	C1634	U1416	A1277	G	A1002	A910	C802	A703	G605	C510
A1899	G1787	G1639	C1416	U1280	G	U1003	A913	A811	A704	G606	C511
G1900	A1790	G1640	U1418	G1284	U	A1004	A913	G812	A705	U611	A526
A1911	U1807	G1644	A1424	G1285	U	A1005	U924	A821	A706	C696	U630
G1921	A1793	C1645	A1425	U1286	G	U1006	A925	G822	A707	C697	U637
A1922	G1795	A1648	A1426	A1287	C	A1018	G926	G823	A708	G698	U638
G1928	A1804	U1648	G1428	G1288	U	A1019	G927	G824	A709	U699	G639
G1929	C1807	C1653	A1429	G1296	A	A1027	G928	A829	A710	G624	A640
C1930	U1808	A1654	A1430	C1297	G	C1028	G931	A831	A711	G625	G637
A1934	U1809	A1655	G1431	G1298	A	A1029	G932	G832	A712	A626	C542
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A1938	A1811	A1660	A1441	G1302	C	C1040	A934	U835	A714	U629	U544
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A1950	A1822	C1687	U1462	A1320	C	C1059	A942	A847	C719	G645	G554
G1951	U1827	G1694	U1467	U1324	A	U1065	A945	G848	A723	G649	G555
G1952	C1828	C1695	C1474	U1334	A	A1067	U953	A851	A724	U652	A557
U1953	U1829	A1699	G1475	U1338	A	G1068	A956	G852	G730	A652	G558
A1958	G1830	G1700	U1477	C1339	G	U1071	A957	G856	A732	A656	C560
A1959	C1831	A1701	C1476	U1343	A	U1072	G962	C859	G733	C659	C562
A1960	U1834	G1708	U1480	C1343	U	A1073	A963	C861	A734	C660	A
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G1986	A1841	G1721	C1483	G1349	U	G1076	C969	A866	C737	U664	U577
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- Molecule 25: 23S Ribosomal RNA

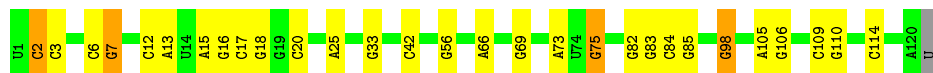


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G1459	G1364	A1274	G1192	G1115	G	G989	G906	G832	G741	G652D	G573	A477	U362
A1460	A1365	A1278	G1193	G1116	G	A990	U907	U833	G741	G652E	G574	A478	G363
G1461	G1201	G1278	G1201	G1117	A	G993	C908	U839	A746	G	A575	A479	G370
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G1466	A1284	A1284	G1203	A1126	U	C995	A911	C995	G748	C	A577	A481	U380
C1467	C1370	G1285	A1204	A1127	U	A996	C912	G845	G748	C	A578	A482	U383
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A1471	C1373	C1207	C1207	U1130	C	C915	C915	G848	C763	C	G582	A493	G386
A1472	A1374	C1208	C1208	G1131	U	G916	G916	A849	A764	G	G583	A494	C392
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C	G2723	G2644	G2533	C2441	G2349	G2277	G2101	G2002	C1888	G1782	A1668
C	G2724	G2645	U2537	C2442	G2350	A2278	C2103	G2003	A1889	A1783	
C	A2725	G2646	C2538	G2443	G2351	G2279					
U	U2726	C2647	C2539	G2444	G2354	C2283					
C	G2727	C2648	G2540	C2355	C2355						

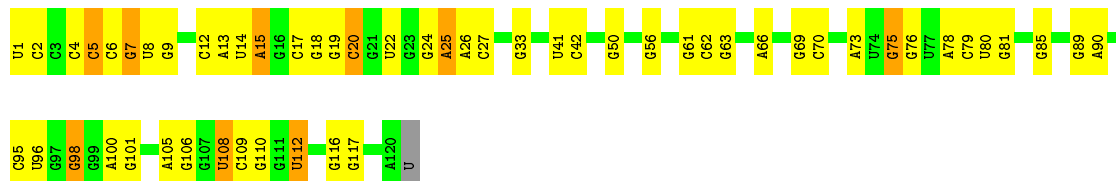
- Molecule 26: 5S Ribosomal RNA

Chain BB:  75% 21%



- Molecule 26: 5S Ribosomal RNA

Chain DB:  54% 38% 7%




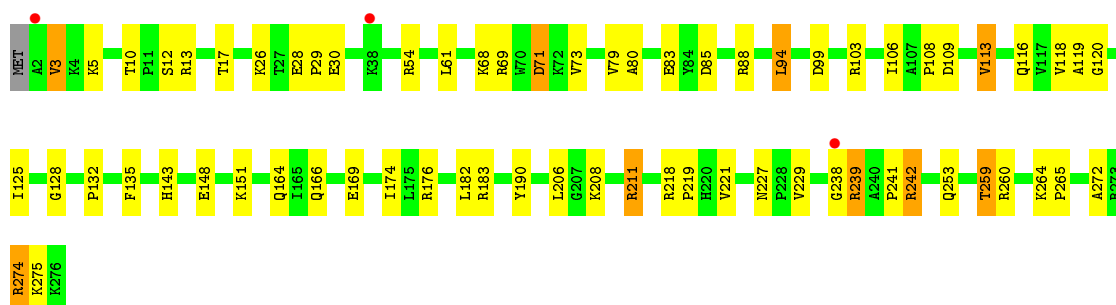
- Molecule 27: 50S Ribosomal Protein L2

Chain BD:  73% 24%



- Molecule 27: 50S Ribosomal Protein L2

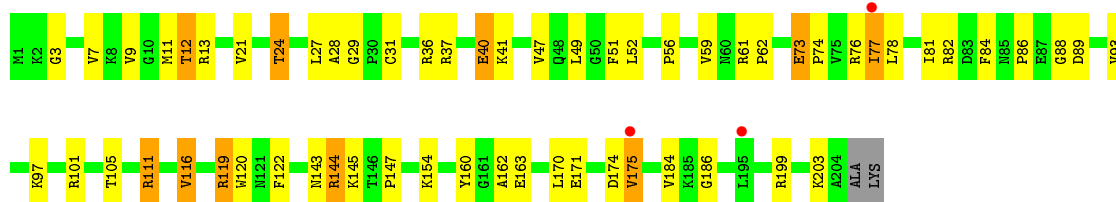
Chain DD:  75% 21%



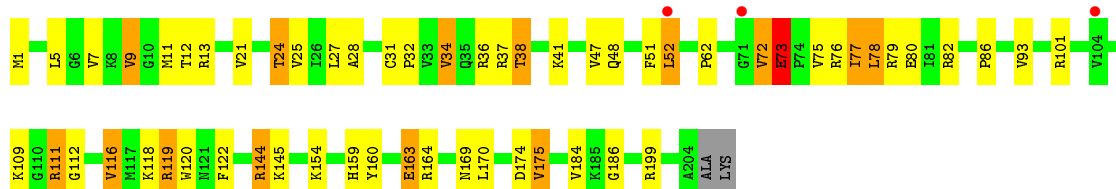
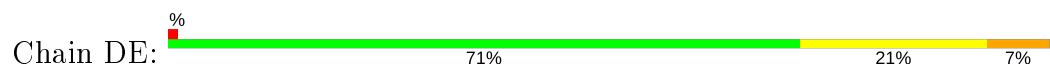
- Molecule 28: 50S Ribosomal Protein L3

Chain BE:  70% 24% 5%

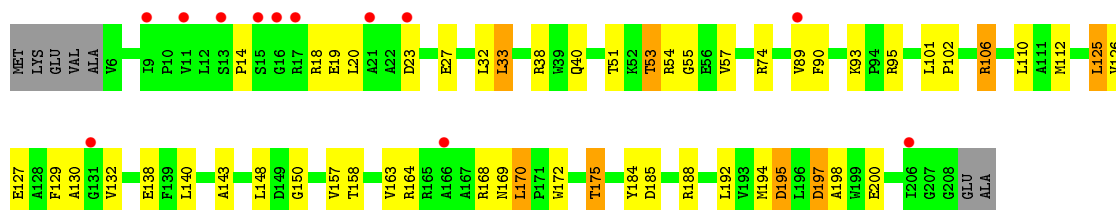
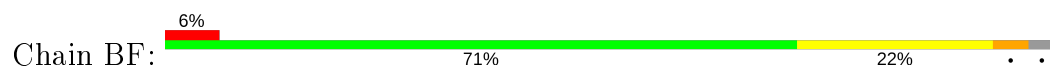




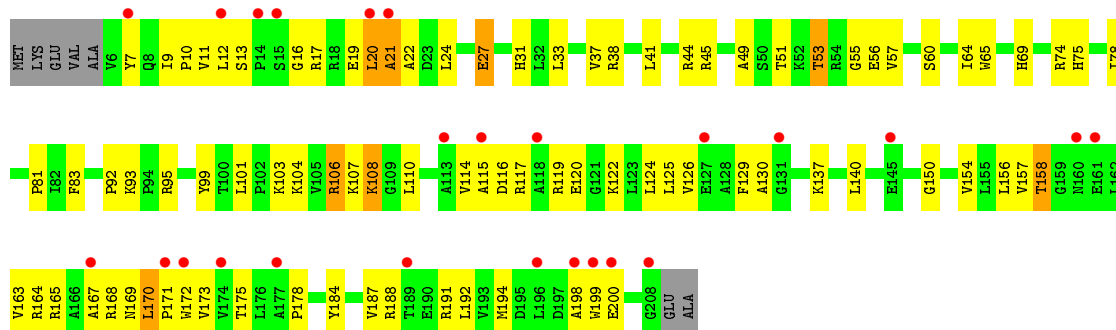
• Molecule 28: 50S Ribosomal Protein L3



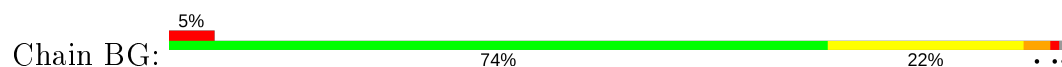
• Molecule 29: 50S Ribosomal Protein L4

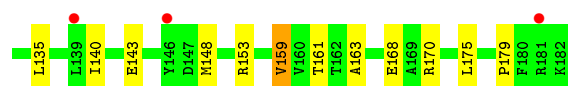


• Molecule 29: 50S Ribosomal Protein L4

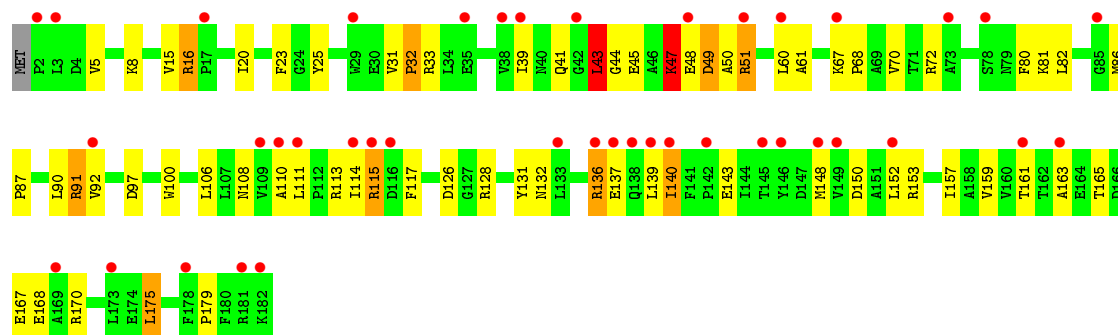


• Molecule 30: 50S Ribosomal Protein L5

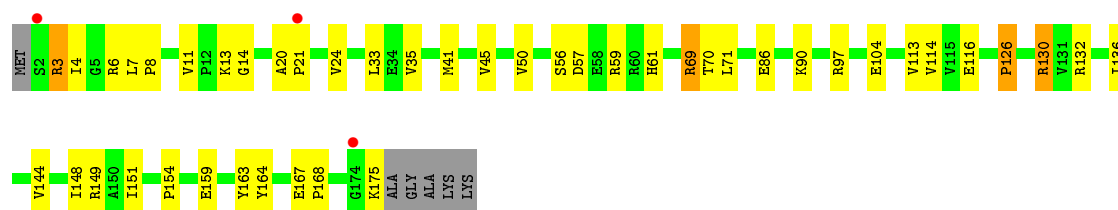
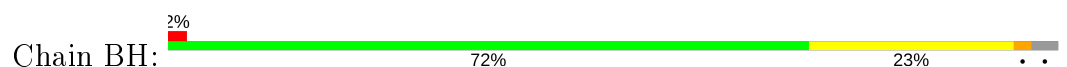




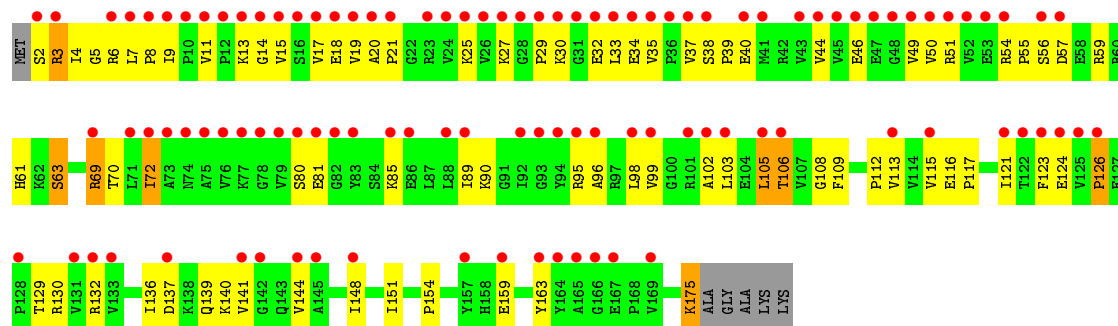
• Molecule 30: 50S Ribosomal Protein L5



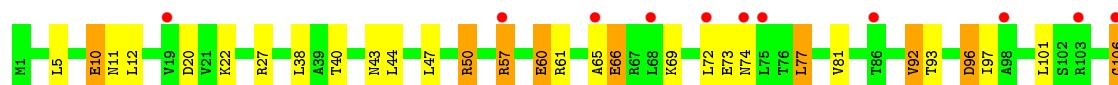
• Molecule 31: 50S Ribosomal Protein L6

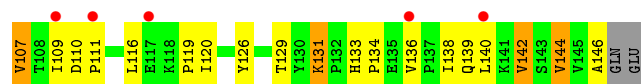


• Molecule 31: 50S Ribosomal Protein L6

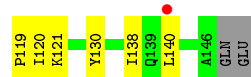
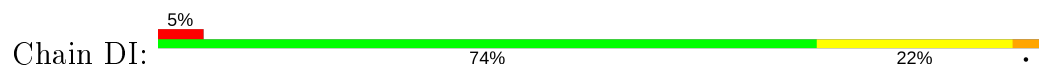


• Molecule 32: 50S Ribosomal Protein L9

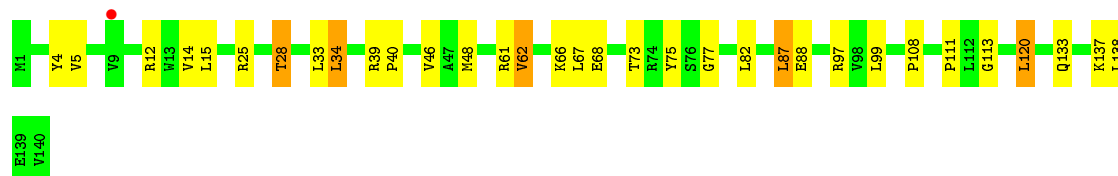
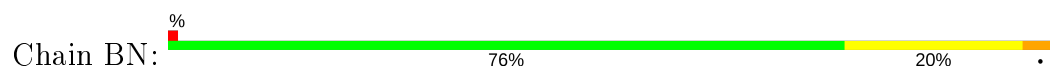




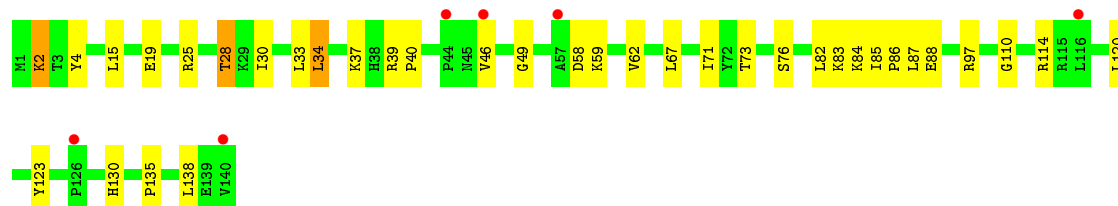
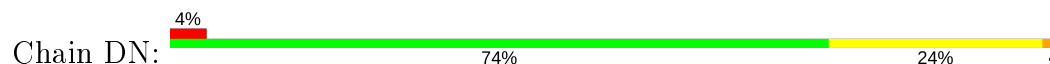
- Molecule 32: 50S Ribosomal Protein L9



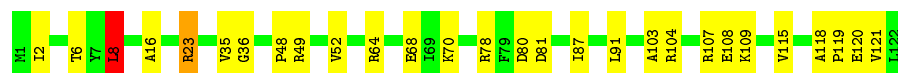
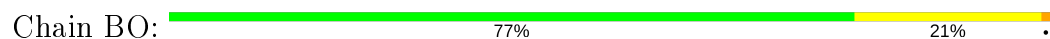
- Molecule 33: 50S Ribosomal Protein L13



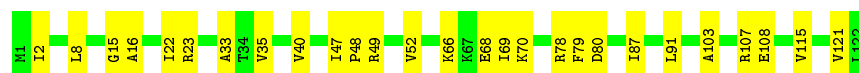
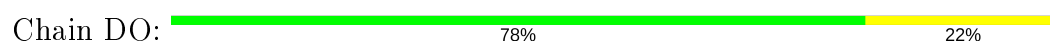
- Molecule 33: 50S Ribosomal Protein L13



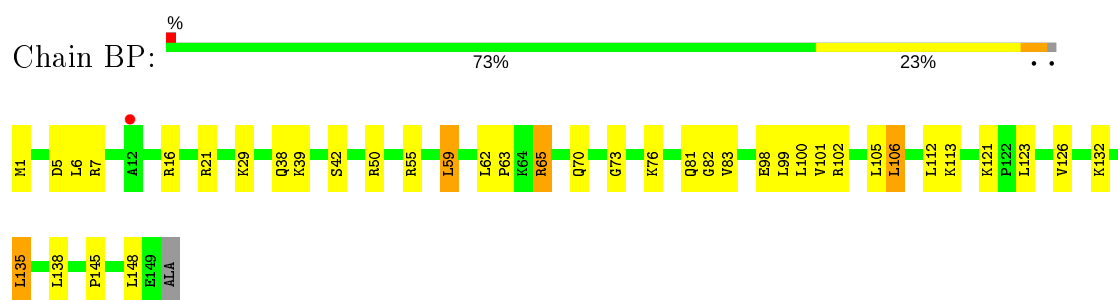
- Molecule 34: 50S Ribosomal Protein L14



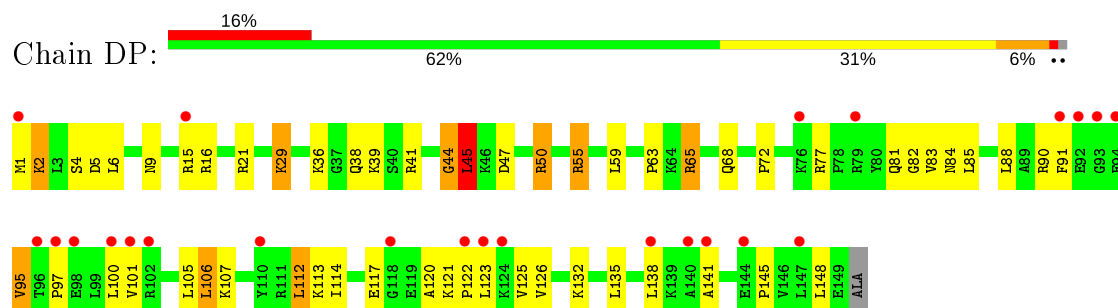
- Molecule 34: 50S Ribosomal Protein L14



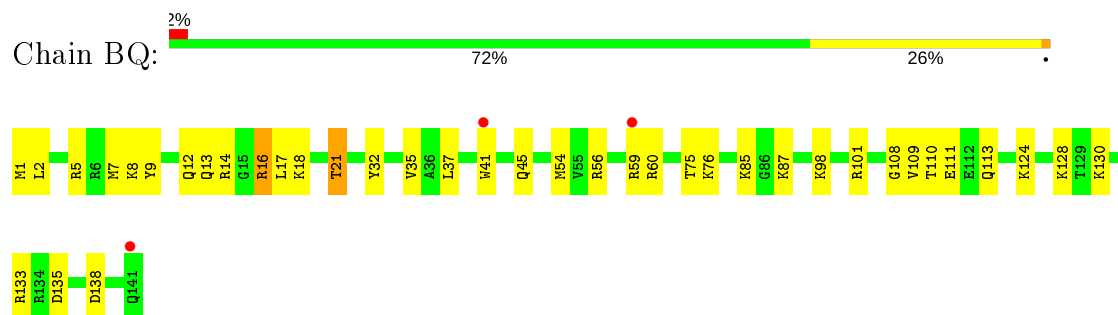
- Molecule 35: 50S Ribosomal Protein L15



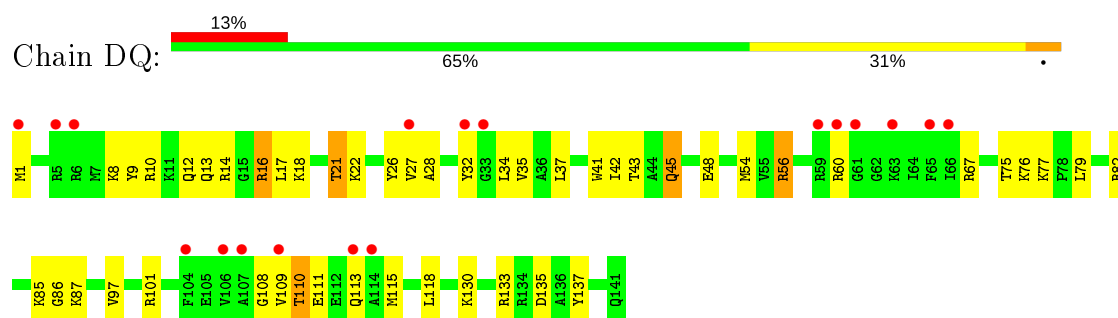
• Molecule 35: 50S Ribosomal Protein L15



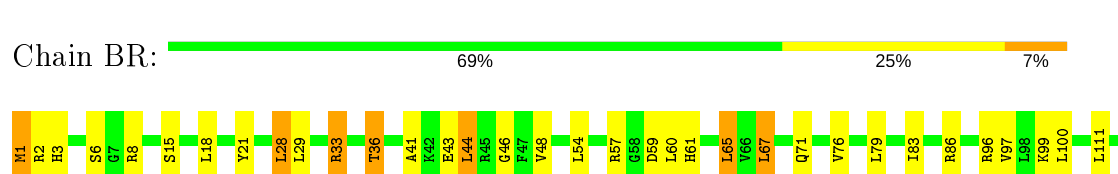
• Molecule 36: 50S Ribosomal Protein L16



• Molecule 36: 50S Ribosomal Protein L16



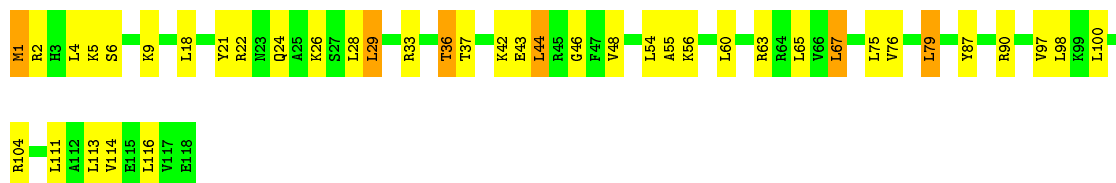
• Molecule 37: 50S Ribosomal Protein L17





• Molecule 37: 50S Ribosomal Protein L17

Chain DR: 65% 30% 5%



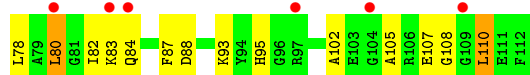
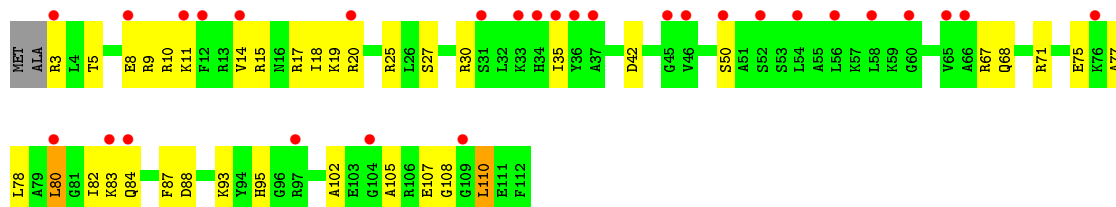
• Molecule 38: 50S Ribosomal Protein L18

Chain BS: 72% 21% 7%



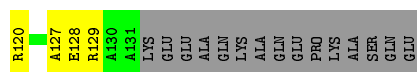
• Molecule 38: 50S Ribosomal Protein L18

Chain DS: 26% 65% 31%



• Molecule 39: 50S Ribosomal Protein L19

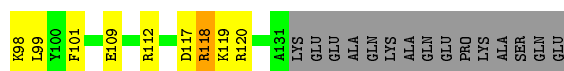
Chain BT: 63% 24% 10%



• Molecule 39: 50S Ribosomal Protein L19

Chain DT: 58% 31% 10%





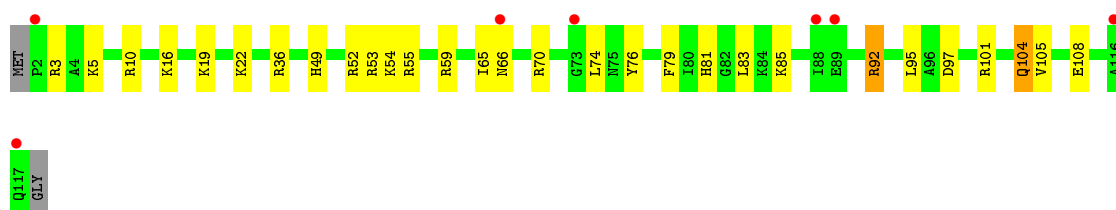
- Molecule 40: 50S Ribosomal Protein L20

Chain BU: 81% 14% ..



- Molecule 40: 50S Ribosomal Protein L20

Chain DU: 6% 74% 23% ..



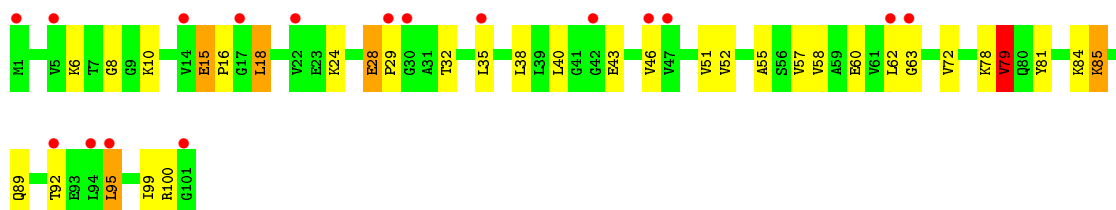
- Molecule 41: 50S Ribosomal Protein L21

Chain BV: 77% 18% 5% ..



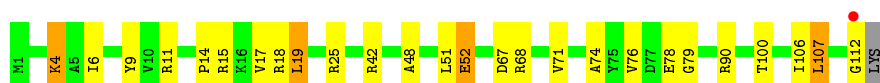
- Molecule 41: 50S Ribosomal Protein L21

Chain DV: 17% 66% 28% 5% ..



- Molecule 42: 50S Ribosomal Protein L22

Chain BW: 76% 19% ..

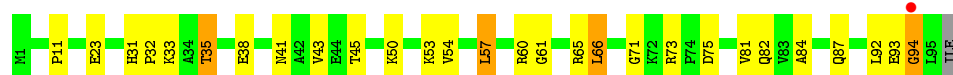


- Molecule 42: 50S Ribosomal Protein L22

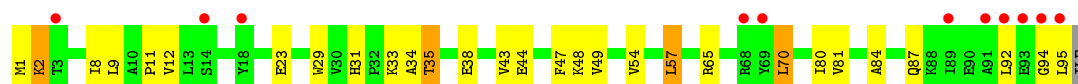
Chain DW: 76% 20% ..



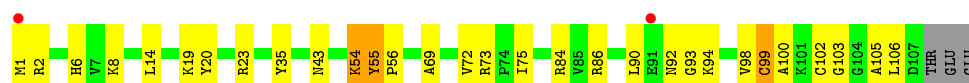
• Molecule 43: 50S Ribosomal Protein L23



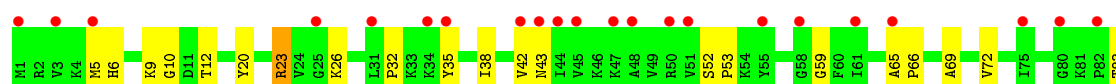
• Molecule 43: 50S Ribosomal Protein L23



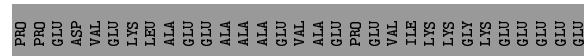
• Molecule 44: 50S Ribosomal Protein L24



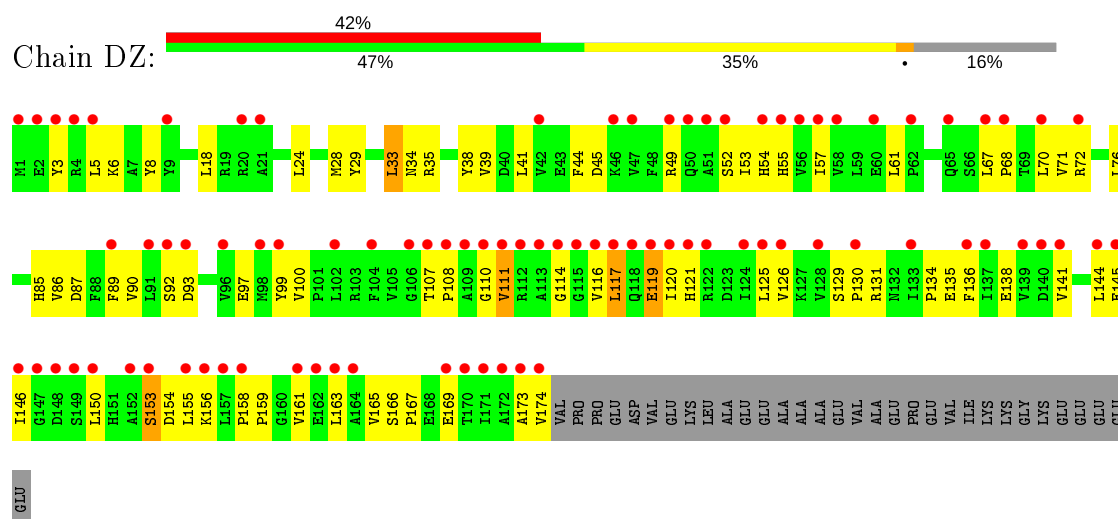
• Molecule 44: 50S Ribosomal Protein L24



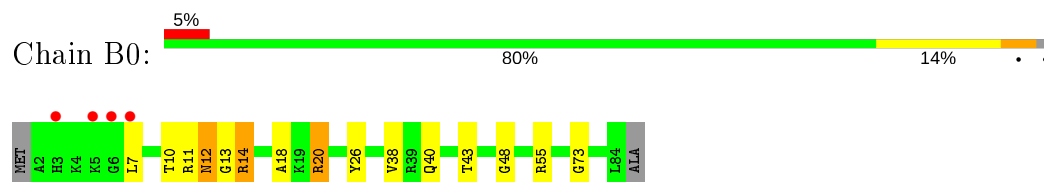
• Molecule 45: 50S Ribosomal Protein L25



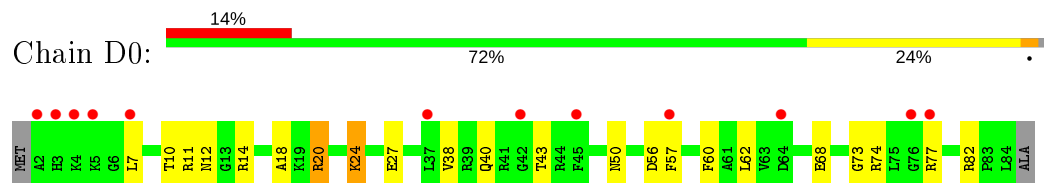
• Molecule 45: 50S Ribosomal Protein L25



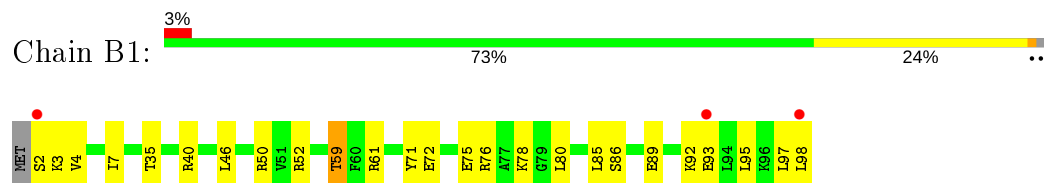
- Molecule 46: 50S Ribosomal Protein L27



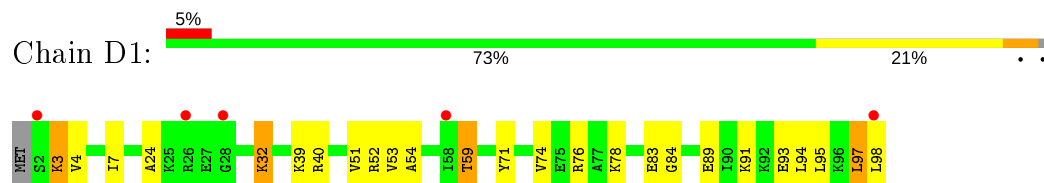
- Molecule 46: 50S Ribosomal Protein L27



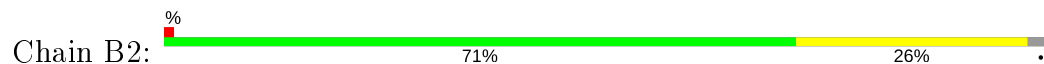
- Molecule 47: 50S Ribosomal Protein L28

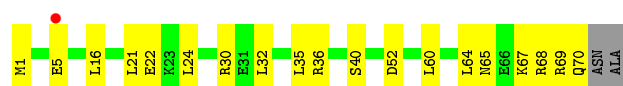


- Molecule 47: 50S Ribosomal Protein L28

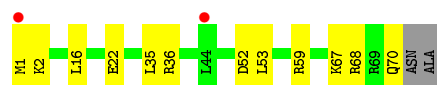
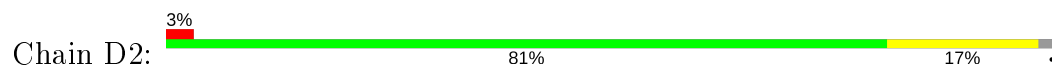


- Molecule 48: 50S Ribosomal Protein L29

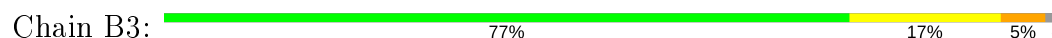




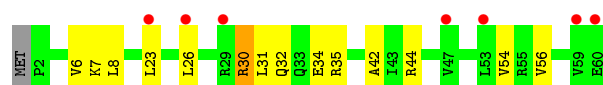
• Molecule 48: 50S Ribosomal Protein L29



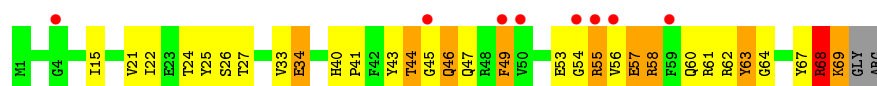
• Molecule 49: 50S Ribosomal Protein L30



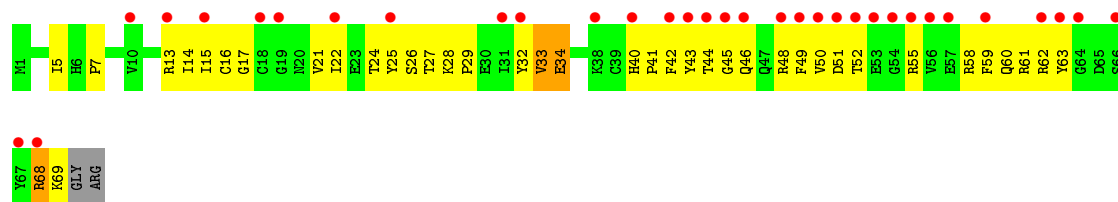
• Molecule 49: 50S Ribosomal Protein L30



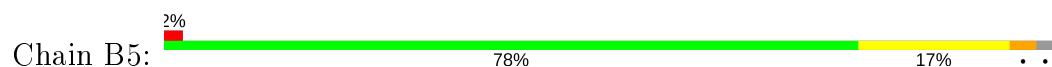
• Molecule 50: 50S Ribosomal Protein L31



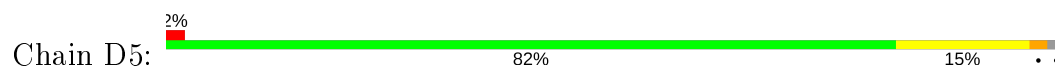
• Molecule 50: 50S Ribosomal Protein L31



• Molecule 51: 50S Ribosomal Protein L32



- Molecule 51: 50S Ribosomal Protein L32



- Molecule 52: 50S Ribosomal Protein L33



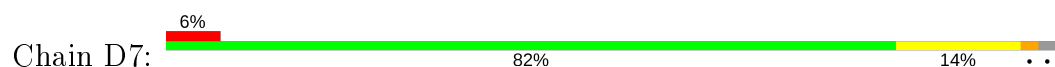
- Molecule 52: 50S Ribosomal Protein L33



- Molecule 53: 50S Ribosomal Protein L34



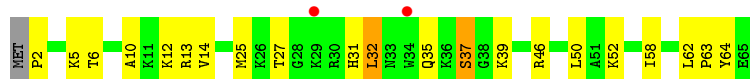
- Molecule 53: 50S Ribosomal Protein L34




- Molecule 54: 50S Ribosomal Protein L35



- Molecule 54: 50S Ribosomal Protein L35




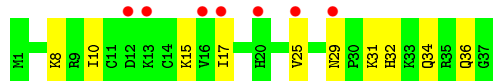
● Molecule 55: 50S Ribosomal Protein L36

Chain B9:  3% 86% 14%



● Molecule 55: 50S Ribosomal Protein L36

Chain D9:  19% 73% 27%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.35Å 449.01Å 621.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	145.52 – 2.55 145.52 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.0 (145.52-2.55) 99.0 (145.52-2.55)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.55Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.225 , 0.273 0.226 , 0.274	Depositor DCC
R_{free} test set	93275 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	48.2	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 58.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	297273	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.48% 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, ZN, PCY, MIA, SF4, MG, 5MC, 4SU, 7MG, K, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AA	0.43	0/36049	0.93	45/56261 (0.1%)
1	CA	0.42	2/36170 (0.0%)	0.95	52/56452 (0.1%)
2	AB	0.31	0/1881	0.62	1/2542 (0.0%)
2	CB	0.32	0/1860	0.59	0/2518
3	AC	0.30	0/1576	0.52	0/2130
3	CC	0.31	0/1566	0.55	0/2119
4	AD	0.32	0/1689	0.53	0/2267
4	CD	0.32	0/1704	0.55	0/2284
5	AE	0.31	0/1145	0.54	0/1543
5	CE	0.33	0/1149	0.59	0/1548
6	AF	0.32	0/819	0.53	0/1111
6	CF	0.30	0/829	0.52	0/1123
7	AG	0.30	0/1250	0.49	0/1679
7	CG	0.30	0/1254	0.50	0/1683
8	AH	0.30	0/1108	0.51	0/1494
8	CH	0.30	0/1108	0.53	0/1494
9	AI	0.32	0/1002	0.56	0/1346
9	CI	0.32	0/997	0.59	0/1343
10	AJ	0.30	0/722	0.56	0/982
10	CJ	0.31	0/727	0.60	0/988
11	AK	0.31	0/844	0.54	0/1145
11	CK	0.30	0/848	0.54	0/1149
12	AL	0.33	0/946	0.53	0/1274
12	CL	0.32	0/946	0.57	0/1274
13	AM	0.30	0/969	0.57	0/1302
13	CM	0.30	0/961	0.53	0/1291
14	AN	0.34	0/501	0.50	0/664
14	CN	0.33	0/501	0.56	0/664
15	AO	0.30	0/739	0.56	0/985
15	CO	0.31	0/739	0.54	0/985
16	AP	0.32	0/697	0.53	0/939
16	CP	0.31	0/693	0.50	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.31	0/836	0.49	0/1117
17	CQ	0.30	0/836	0.52	0/1117
18	AR	0.32	0/560	0.55	0/746
18	CR	0.28	0/560	0.49	0/746
19	AS	0.30	0/667	0.54	0/900
19	CS	0.34	0/661	0.66	0/893
20	AT	0.29	0/730	0.57	0/965
20	CT	0.30	0/729	0.53	0/965
21	AU	0.33	0/203	0.50	0/266
21	CU	0.34	0/203	0.53	0/266
22	AV	0.48	0/310	1.00	0/480
22	CV	0.45	0/310	0.91	2/480 (0.4%)
23	AW	0.48	0/1602	1.06	0/2493
23	AY	0.52	0/1602	1.16	4/2493 (0.2%)
23	CW	0.52	0/1556	1.19	10/2418 (0.4%)
23	CY	0.54	0/1579	1.18	5/2455 (0.2%)
24	AX	0.55	2/1725 (0.1%)	1.16	12/2689 (0.4%)
24	CX	0.56	1/1725 (0.1%)	1.18	18/2689 (0.7%)
25	BA	0.60	6/68013 (0.0%)	1.02	122/106165 (0.1%)
25	DA	0.49	0/67542	0.98	62/105428 (0.1%)
26	BB	0.49	0/2878	0.91	0/4490
26	DB	0.51	0/2878	0.96	1/4490 (0.0%)
27	BD	0.41	0/2186	0.64	1/2944 (0.0%)
27	DD	0.38	0/2186	0.59	1/2944 (0.0%)
28	BE	0.42	0/1592	0.58	0/2149
28	DE	0.36	0/1592	0.58	1/2149 (0.0%)
29	BF	0.40	0/1619	0.58	0/2193
29	DF	0.36	0/1615	0.59	0/2188
30	BG	0.33	0/1450	0.56	1/1959 (0.1%)
30	DG	0.33	0/1449	0.56	0/1958
31	BH	0.34	0/1356	0.52	0/1834
31	DH	0.32	0/1356	0.53	0/1834
32	BI	0.31	0/1100	0.57	0/1501
32	DI	0.29	0/1076	0.56	0/1471
33	BN	0.39	0/1144	0.56	0/1543
33	DN	0.35	0/1144	0.56	0/1543
34	BO	0.42	0/943	0.60	1/1269 (0.1%)
34	DO	0.34	0/943	0.51	0/1269
35	BP	0.38	0/1152	0.59	0/1533
35	DP	0.35	0/1152	0.61	1/1533 (0.1%)
36	BQ	0.41	0/1143	0.55	0/1527
36	DQ	0.36	0/1143	0.55	0/1527
37	BR	0.42	0/982	0.65	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
37	DR	0.31	0/982	0.54	0/1312
38	BS	0.34	0/887	0.59	0/1180
38	DS	0.32	0/880	0.55	0/1172
39	BT	0.39	0/1105	0.60	0/1477
39	DT	0.31	0/1097	0.52	0/1468
40	BU	0.45	0/977	0.62	1/1301 (0.1%)
40	DU	0.32	0/977	0.52	0/1301
41	BV	0.44	0/782	0.61	0/1049
41	DV	0.33	0/782	0.54	0/1049
42	BW	0.44	0/897	0.61	0/1205
42	DW	0.33	0/897	0.53	0/1205
43	BX	0.44	0/764	0.64	1/1025 (0.1%)
43	DX	0.36	0/764	0.57	1/1025 (0.1%)
44	BY	0.42	0/819	0.64	0/1095
44	DY	0.33	0/819	0.52	0/1095
45	BZ	0.35	0/1379	0.60	0/1873
45	DZ	0.33	0/1390	0.56	0/1890
46	B0	0.40	0/662	0.66	1/881 (0.1%)
46	D0	0.33	0/662	0.52	0/881
47	B1	0.40	0/762	0.57	0/1014
47	D1	0.34	0/762	0.56	0/1014
48	B2	0.37	0/590	0.65	0/781
48	D2	0.30	0/590	0.47	0/781
49	B3	0.42	0/474	0.62	0/635
49	D3	0.30	0/469	0.53	0/630
50	B4	0.39	0/571	0.66	0/768
50	D4	0.33	0/545	0.60	0/737
51	B5	0.39	0/469	0.64	0/635
51	D5	0.33	0/469	0.58	0/635
52	B6	0.42	0/460	0.58	0/613
52	D6	0.36	0/456	0.49	0/608
53	B7	0.45	0/426	0.66	0/561
53	D7	0.36	0/426	0.52	0/561
54	B8	0.41	0/519	0.62	0/684
54	D8	0.33	0/525	0.55	0/691
55	B9	0.44	0/310	0.52	0/407
55	D9	0.34	0/310	0.57	0/407
All	All	0.47	11/316672 (0.0%)	0.90	344/474091 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	1
7	AG	0	1
7	CG	0	1
19	CS	0	1
27	DD	0	1
38	BS	0	1
44	BY	0	1
All	All	0	7

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	354	A	N9-C4	-7.89	1.33	1.37
1	CA	1154	G	C6-N1	-7.66	1.34	1.39
25	BA	1188	A	N9-C4	-7.63	1.33	1.37
25	BA	1067	A	N9-C4	-6.49	1.33	1.37
24	AX	14	A	N7-C5	-6.24	1.35	1.39
24	AX	14	A	C8-N7	-6.01	1.27	1.31
25	BA	553	A	N9-C4	-5.68	1.34	1.37
24	CX	22	G	N7-C5	5.39	1.42	1.39
25	BA	593	G	C6-O6	-5.35	1.19	1.24
1	CA	1154	G	N1-C2	-5.31	1.33	1.37
25	BA	990	A	N9-C4	-5.25	1.34	1.37

All (344) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1154	G	C5-C6-O6	17.34	139.00	128.60
1	CA	1119	C	C2-N3-C4	16.52	128.16	119.90
1	CA	1154	G	N3-C2-N2	14.11	129.78	119.90
1	CA	1119	C	N1-C2-O2	14.07	127.34	118.90
1	CA	1154	G	N1-C6-O6	-11.05	113.27	119.90
1	CA	1154	G	N1-C2-N2	-10.96	106.33	116.20
25	BA	354	A	C2-N3-C4	-10.77	105.21	110.60
1	CA	79	G	C5-C6-O6	10.57	134.94	128.60
24	AX	14	A	C4-C5-C6	10.08	122.04	117.00
1	CA	1119	C	N3-C4-C5	-10.03	117.89	121.90
1	CA	1154	G	C6-N1-C2	9.98	131.09	125.10
25	BA	848	G	O5'-P-OP2	-9.83	96.86	105.70
24	AX	46	G	C6-N1-C2	-9.82	119.21	125.10
24	CX	46	G	C6-N1-C2	-9.78	119.23	125.10
1	CA	1119	C	C5-C4-N4	9.74	127.02	120.20
1	CA	1004	A	O4'-C1'-N9	9.72	115.98	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1067	A	C2-N3-C4	-9.68	105.76	110.60
24	AX	14	A	C5-N7-C8	9.60	108.70	103.90
25	DA	2585	U	C5-C4-O4	-9.26	120.35	125.90
25	DA	1776	G	O5'-P-OP2	-9.18	97.44	105.70
25	BA	2162	C	N1-C2-O2	8.97	124.28	118.90
25	BA	1686	U	O5'-P-OP2	-8.95	97.64	105.70
24	CX	14	A	C4-C5-C6	8.89	121.45	117.00
23	AY	64	A	C5-C6-N6	8.55	130.54	123.70
25	BA	593	G	C5-C6-O6	-8.55	123.47	128.60
25	BA	599	U	O5'-P-OP1	-8.44	98.10	105.70
25	BA	2697	G	N1-C6-O6	-8.39	114.86	119.90
1	CA	997	U	C5-C4-O4	8.29	130.87	125.90
25	BA	537	G	O4'-C1'-N9	8.28	114.83	108.20
25	BA	2566	U	O5'-P-OP1	-8.24	98.28	105.70
24	AX	14	A	C5-C6-N1	-8.12	113.64	117.70
25	BA	139	A	N7-C8-N9	8.08	117.84	113.80
24	CX	14	A	C5-N7-C8	8.04	107.92	103.90
25	BA	2160	C	N1-C2-O2	8.02	123.71	118.90
25	BA	2162	C	C2-N1-C1'	8.01	127.61	118.80
25	DA	1352	U	O5'-P-OP1	-7.92	98.57	105.70
23	AY	64	A	N1-C6-N6	-7.87	113.88	118.60
24	AX	22	G	C5-N7-C8	-7.87	100.37	104.30
25	BA	2014	G	P-O3'-C3'	7.82	129.08	119.70
25	BA	1067	A	N1-C2-N3	7.75	133.18	129.30
25	DA	2155	G	N3-C2-N2	7.64	125.25	119.90
1	CA	1119	C	N3-C2-O2	-7.61	116.57	121.90
1	CA	1154	G	C5-C6-N1	-7.61	107.69	111.50
25	BA	990	A	C2-N3-C4	-7.54	106.83	110.60
25	BA	354	A	N3-C4-N9	-7.54	121.37	127.40
25	BA	553	A	C2-N3-C4	-7.54	106.83	110.60
25	BA	2605	U	N3-C4-O4	-7.47	114.17	119.40
24	CX	22	G	C5-N7-C8	-7.45	100.57	104.30
25	BA	1660	A	O5'-P-OP1	-7.41	99.03	105.70
25	BA	139	A	C5-N7-C8	-7.39	100.20	103.90
24	CX	14	A	C5-C6-N1	-7.31	114.04	117.70
1	CA	1119	C	C5-C6-N1	7.31	124.65	121.00
24	CX	22	G	N1-C6-O6	-7.29	115.52	119.90
23	CY	48	C	N1-C2-O2	7.29	123.27	118.90
25	BA	354	A	N1-C2-N3	7.25	132.92	129.30
25	BA	12	U	C2-N1-C1'	7.23	126.38	117.70
25	BA	593	G	C5-C6-N1	7.18	115.09	111.50
1	AA	365	U	C5-C6-N1	-7.12	119.14	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	2585	U	C2-N1-C1'	7.11	126.23	117.70
1	AA	1397	C	O4'-C1'-N1	7.10	113.88	108.20
1	AA	991	U	P-O3'-C3'	7.09	128.21	119.70
25	BA	2162	C	N3-C2-O2	-7.05	116.96	121.90
25	BA	215	G	O4'-C1'-N9	7.05	113.84	108.20
1	AA	254	G	O5'-P-OP1	-7.05	99.36	105.70
23	CW	3	C	N1-C2-O2	7.02	123.11	118.90
1	AA	1030(B)	C	C2-N1-C1'	6.98	126.47	118.80
25	BA	1807	G	O5'-P-OP2	-6.97	99.42	105.70
25	BA	2162	C	C6-N1-C2	-6.95	117.52	120.30
1	CA	1119	C	C6-N1-C2	-6.91	117.54	120.30
25	BA	354	A	N3-C4-C5	6.88	131.62	126.80
25	BA	2260	C	O5'-P-OP2	-6.88	99.50	105.70
1	CA	1004	A	N1-C6-N6	-6.88	114.47	118.60
25	BA	1346	U	P-O3'-C3'	6.87	127.94	119.70
24	AX	46	G	C5-C6-N1	6.87	114.93	111.50
25	BA	1154	U	N3-C2-O2	-6.86	117.40	122.20
27	BD	257	LEU	CA-CB-CG	6.86	131.07	115.30
1	CA	1003	G	N7-C8-N9	6.85	116.53	113.10
25	BA	1188	A	C2-N3-C4	-6.82	107.19	110.60
25	DA	2585	U	C6-N1-C1'	-6.81	111.67	121.20
25	DA	1372	U	N3-C4-O4	6.78	124.15	119.40
25	DA	1698	A	O4'-C1'-N9	6.78	113.62	108.20
1	CA	79	G	N1-C6-O6	-6.77	115.84	119.90
25	DA	2136	C	N1-C2-O2	6.73	122.94	118.90
34	BO	8	LEU	CA-CB-CG	6.73	130.77	115.30
1	CA	1183	A	P-O3'-C3'	6.72	127.76	119.70
25	DA	1372	U	C5-C4-O4	-6.71	121.87	125.90
25	DA	1639	U	O5'-P-OP2	-6.70	99.67	105.70
1	AA	98	G	N3-C4-N9	6.68	130.01	126.00
25	BA	1188	A	N3-C4-C5	6.66	131.46	126.80
1	AA	1278	U	C5-C6-N1	6.64	126.02	122.70
25	BA	139	A	C8-N9-C4	-6.64	103.15	105.80
25	BA	2160	C	N3-C2-O2	-6.63	117.26	121.90
43	BX	57	LEU	CA-CB-CG	6.63	130.56	115.30
1	CA	532	A	P-O3'-C3'	6.62	127.64	119.70
25	DA	2155	G	C6-N1-C2	6.56	129.04	125.10
1	CA	991	U	P-O3'-C3'	6.53	127.53	119.70
1	AA	1002	G	N3-C4-N9	6.53	129.92	126.00
1	AA	98	G	C6-C5-N7	-6.51	126.49	130.40
25	DA	277	C	C6-N1-C2	-6.47	117.71	120.30
1	AA	1030(B)	C	O4'-C1'-N1	6.47	113.37	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	79	G	C6-N1-C2	6.46	128.98	125.10
1	AA	1397	C	C2-N1-C1'	6.42	125.86	118.80
25	BA	989	G	N3-C4-N9	6.42	129.85	126.00
1	CA	754	C	C2-N1-C1'	6.42	125.86	118.80
25	BA	2298	A	N7-C8-N9	6.42	117.01	113.80
25	BA	1188	A	N3-C4-N9	-6.39	122.29	127.40
25	DA	512	G	O4'-C1'-N9	6.38	113.31	108.20
24	CX	20	U	C2-N1-C1'	6.37	125.34	117.70
24	CX	22	G	C4-C5-C6	-6.36	114.98	118.80
1	CA	754	C	N1-C2-O2	6.35	122.71	118.90
25	BA	989	G	N9-C4-C5	-6.33	102.87	105.40
25	BA	2803	A	C2-N3-C4	6.31	113.76	110.60
25	DA	2585	U	N3-C4-O4	6.31	123.82	119.40
25	DA	614	U	N3-C2-O2	-6.30	117.79	122.20
25	BA	1418	U	C5-C4-O4	-6.29	122.12	125.90
25	BA	1154	U	N1-C2-O2	6.29	127.20	122.80
25	BA	986	A	O5'-P-OP1	-6.24	100.08	105.70
25	BA	989	G	C6-C5-N7	-6.23	126.66	130.40
25	BA	2160	C	C6-N1-C2	-6.23	117.81	120.30
25	BA	399	G	O4'-C1'-N9	6.22	113.18	108.20
25	BA	990	A	C5-N7-C8	-6.21	100.79	103.90
22	CV	19	U	C5-C4-O4	6.18	129.61	125.90
1	CA	1492	A	P-O3'-C3'	6.13	127.06	119.70
25	DA	2140	C	N1-C2-O2	6.13	122.58	118.90
1	AA	98	G	N7-C8-N9	6.13	116.17	113.10
1	AA	365	U	C2-N1-C1'	-6.12	110.35	117.70
25	BA	1398	U	O5'-P-OP1	-6.11	100.20	105.70
25	BA	184	A	P-O3'-C3'	6.11	127.03	119.70
25	DA	1191	G	O5'-P-OP2	-6.11	100.20	105.70
1	CA	1003	G	C4-N9-C1'	6.10	134.43	126.50
25	BA	1232	G	N1-C6-O6	-6.09	116.24	119.90
1	CA	1003	G	C8-N9-C4	-6.09	103.96	106.40
25	BA	2050	U	N3-C4-O4	-6.07	115.15	119.40
25	DA	2207	G	C6-C5-N7	-6.04	126.78	130.40
23	CY	4	C	C5-C4-N4	6.03	124.42	120.20
25	BA	2610	A	O5'-P-OP1	-6.02	100.28	105.70
25	BA	553	A	C5-N7-C8	-6.02	100.89	103.90
1	CA	1064	G	P-O3'-C3'	6.02	126.92	119.70
25	BA	2565	G	N3-C4-N9	5.98	129.59	126.00
25	BA	793	A	O4'-C1'-N9	5.98	112.98	108.20
25	BA	1958	A	O4'-C1'-N9	5.96	112.97	108.20
1	AA	1036	G	N1-C6-O6	-5.96	116.32	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CW	36	A	C6-N1-C2	5.96	122.17	118.60
25	BA	139	A	O4'-C1'-N9	5.96	112.96	108.20
25	DA	2685	G	N1-C6-O6	-5.95	116.33	119.90
1	CA	79	G	N3-C4-N9	-5.95	122.43	126.00
25	BA	1539	C	N1-C2-O2	5.94	122.47	118.90
25	BA	2015	U	O5'-P-OP1	-5.94	100.36	105.70
23	CW	67	C	C2-N3-C4	5.93	122.87	119.90
25	BA	637	U	N3-C2-O2	-5.93	118.05	122.20
1	AA	1002	G	N3-C4-C5	-5.92	125.64	128.60
24	CX	46	G	C5-C6-N1	5.92	114.46	111.50
1	CA	90	U	N1-C2-O2	-5.90	118.67	122.80
25	BA	254	A	O4'-C1'-N9	5.87	112.89	108.20
23	CW	25	C	O4'-C1'-N1	5.86	112.89	108.20
25	BA	2014	G	O4'-C1'-N9	-5.85	103.52	108.20
23	AY	64	A	C6-N1-C2	5.84	122.11	118.60
1	CA	1158	C	N1-C2-O2	5.84	122.41	118.90
25	DA	1300	U	P-O3'-C3'	5.84	126.71	119.70
25	BA	1067	A	C5-N7-C8	-5.83	100.98	103.90
25	DA	1128	A	C8-N9-C4	5.82	108.13	105.80
1	AA	98	G	N3-C4-C5	-5.81	125.69	128.60
24	CX	20	U	N1-C2-O2	5.81	126.86	122.80
25	BA	989	G	C8-N9-C1'	-5.80	119.46	127.00
22	CV	19	U	C2-N3-C4	5.77	130.46	127.00
25	DA	2275	C	O4'-C1'-N1	-5.77	103.59	108.20
30	BG	82	LEU	CA-CB-CG	5.76	128.55	115.30
1	AA	267	C	O5'-P-OP1	-5.74	100.54	105.70
25	DA	1368	G	O5'-P-OP2	-5.74	100.54	105.70
1	AA	98	G	C4-N9-C1'	5.73	133.95	126.50
1	AA	1502	A	N7-C8-N9	5.73	116.66	113.80
25	DA	2554	U	O5'-P-OP2	-5.71	100.56	105.70
25	BA	2697	G	C5-C6-O6	5.71	132.02	128.60
26	DB	1	U	C2-N1-C1'	5.70	124.54	117.70
1	CA	1260	C	C6-N1-C2	-5.68	118.03	120.30
25	DA	141	A	N7-C8-N9	5.68	116.64	113.80
23	AY	50	U	C2-N3-C4	5.67	130.40	127.00
25	BA	1745	A	C2-N3-C4	-5.67	107.76	110.60
24	AX	14	A	C8-N9-C1'	-5.66	117.52	127.70
43	DX	57	LEU	CA-CB-CG	5.65	128.29	115.30
25	BA	834	U	O5'-P-OP1	-5.65	100.62	105.70
1	AA	1067	A	P-O3'-C3'	5.64	126.47	119.70
25	DA	2805	G	O4'-C1'-N9	5.64	112.72	108.20
1	AA	266	G	P-O3'-C3'	5.64	126.47	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	137	G	C5-N7-C8	5.64	107.12	104.30
25	DA	1313	U	C2-N1-C1'	5.63	124.46	117.70
25	DA	242	G	N1-C6-O6	-5.62	116.53	119.90
25	DA	2585	U	O4'-C1'-N1	-5.62	103.70	108.20
25	BA	285	U	O4'-C1'-N1	5.62	112.69	108.20
28	DE	72	VAL	C-N-CA	5.62	135.74	121.70
23	CW	67	C	N1-C2-O2	5.60	122.26	118.90
1	AA	1007	C	C2-N3-C4	5.59	122.70	119.90
25	DA	673	C	N1-C2-O2	-5.59	115.55	118.90
25	BA	2189	U	C2-N1-C1'	5.58	124.40	117.70
25	DA	195	A	P-O3'-C3'	5.58	126.39	119.70
1	AA	346	G	C4-N9-C1'	5.57	133.74	126.50
25	BA	1686	U	OP1-P-OP2	5.57	127.95	119.60
24	CX	14	A	C4-N9-C1'	5.56	136.31	126.30
25	BA	978	A	O4'-C1'-N9	5.55	112.64	108.20
25	DA	141	A	O4'-C1'-N9	5.55	112.64	108.20
25	BA	593	G	C4-C5-N7	5.55	113.02	110.80
23	CY	15	G	N3-C2-N2	-5.55	116.01	119.90
25	DA	945	A	C5-N7-C8	-5.55	101.13	103.90
1	AA	1299	A	O5'-P-OP1	5.55	117.36	110.70
23	CW	75	C	P-O3'-C3'	5.54	126.35	119.70
1	AA	1190	G	OP2-P-O3'	5.54	117.39	105.20
23	CW	62	C	C5-C6-N1	5.52	123.76	121.00
25	DA	1992	G	P-O3'-C3'	5.52	126.32	119.70
1	AA	754	C	C2-N1-C1'	5.51	124.86	118.80
24	AX	22	G	N7-C8-N9	5.50	115.85	113.10
25	DA	1996	C	OP1-P-O3'	5.50	117.30	105.20
1	CA	992	U	P-O3'-C3'	5.49	126.29	119.70
1	CA	532	A	OP1-P-O3'	5.48	117.26	105.20
1	AA	1008	C	C2-N3-C4	5.48	122.64	119.90
1	AA	1007	C	N1-C2-O2	5.48	122.19	118.90
25	BA	2298	A	C8-N9-C4	-5.47	103.61	105.80
25	BA	1360	C	O5'-P-OP1	-5.47	100.78	105.70
25	BA	2858	G	O4'-C1'-N9	5.46	112.56	108.20
24	CX	22	G	C5-C6-N1	5.46	114.23	111.50
25	BA	1067	A	N7-C8-N9	5.45	116.52	113.80
1	AA	1022	G	N3-C2-N2	5.45	123.71	119.90
24	CX	46	G	N1-C2-N3	5.44	127.17	123.90
25	BA	1694	G	O4'-C1'-N9	-5.44	103.85	108.20
1	CA	984	C	C2-N3-C4	5.44	122.62	119.90
1	CA	1152	A	O4'-C1'-N9	5.44	112.55	108.20
25	DA	1791	A	O5'-P-OP1	-5.44	100.80	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1183	A	OP1-P-O3'	5.44	117.16	105.20
25	BA	978	A	C5-N7-C8	-5.43	101.19	103.90
25	DA	753	C	O5'-P-OP1	-5.43	100.82	105.70
1	AA	1397	C	C6-N1-C1'	-5.42	114.30	120.80
25	BA	1720	U	C5-C6-N1	-5.42	119.99	122.70
25	BA	993	G	O5'-P-OP1	-5.42	100.83	105.70
23	CY	22	G	N3-C4-N9	5.41	129.25	126.00
25	BA	553	A	N3-C4-N9	-5.41	123.07	127.40
25	DA	2110	G	OP2-P-O3'	5.41	117.10	105.20
2	AB	9	GLU	N-CA-C	5.41	125.60	111.00
25	BA	2162	C	C5-C6-N1	5.41	123.70	121.00
25	DA	277	C	N1-C2-O2	5.41	122.14	118.90
1	CA	65	U	P-O3'-C3'	5.40	126.18	119.70
1	CA	1028	C	C5-C6-N1	5.40	123.70	121.00
24	AX	14	A	C4-N9-C1'	5.40	136.02	126.30
25	BA	2697	G	C6-C5-N7	5.40	133.64	130.40
25	BA	989	G	C4-N9-C1'	5.40	133.51	126.50
1	CA	1190	G	OP2-P-O3'	5.39	117.07	105.20
25	DA	614	U	C5-C4-O4	5.39	129.14	125.90
1	AA	1002	G	C4-N9-C1'	5.38	133.50	126.50
25	DA	2028	U	N3-C4-O4	-5.38	115.64	119.40
1	AA	1285	A	P-O3'-C3'	5.37	126.14	119.70
25	BA	1539	C	C2-N1-C1'	5.37	124.71	118.80
25	BA	70	A	P-O3'-C3'	5.37	126.14	119.70
25	DA	2287	A	C2-N3-C4	-5.36	107.92	110.60
1	CA	97	G	O4'-C1'-N9	5.35	112.48	108.20
25	DA	945	A	N1-C6-N6	5.35	121.81	118.60
25	BA	1539	C	N3-C2-O2	-5.35	118.16	121.90
25	BA	637	U	C5-C4-O4	5.35	129.11	125.90
25	DA	801	G	O5'-P-OP2	-5.35	100.89	105.70
25	DA	1131	G	O4'-C1'-N9	5.34	112.48	108.20
25	DA	277	C	N3-C2-O2	-5.34	118.16	121.90
24	AX	22	G	C4-C5-C6	-5.33	115.60	118.80
1	CA	1158	C	C2-N1-C1'	5.33	124.66	118.80
24	CX	22	G	N7-C8-N9	5.32	115.76	113.10
1	AA	346	G	O4'-C1'-N9	5.32	112.46	108.20
25	DA	1298	C	O5'-P-OP2	-5.32	100.91	105.70
1	AA	1036	G	C4-N9-C1'	5.32	133.42	126.50
25	DA	2155	G	C5-C6-O6	5.31	131.79	128.60
1	CA	1190	G	P-O3'-C3'	5.31	126.07	119.70
24	CX	14	A	C4-C5-N7	-5.30	108.05	110.70
25	DA	574	C	C2-N1-C1'	-5.30	112.97	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1255	A	P-O3'-C3'	5.30	126.06	119.70
24	CX	14	A	C8-N9-C1'	-5.30	118.17	127.70
25	BA	1249	A	O4'-C1'-N9	5.29	112.44	108.20
1	CA	1119	C	C2-N1-C1'	5.29	124.62	118.80
25	BA	1154	U	C2-N1-C1'	5.29	124.05	117.70
25	DA	646	A	O4'-C1'-N9	5.27	112.42	108.20
1	AA	532	A	P-O3'-C3'	5.27	126.03	119.70
25	BA	1233	U	N1-C2-O2	5.27	126.49	122.80
1	CA	1026	G	C4-N9-C1'	5.27	133.35	126.50
25	BA	1235	G	C5-N7-C8	5.26	106.93	104.30
25	DA	271(Y)	U	O4'-C1'-N1	5.26	112.41	108.20
25	BA	1830	G	C4-C5-N7	-5.26	108.69	110.80
25	DA	2136	C	N3-C2-O2	-5.26	118.22	121.90
1	AA	1492	A	P-O3'-C3'	5.26	126.01	119.70
1	AA	1028	C	C6-N1-C2	-5.25	118.20	120.30
25	BA	2287	C	OP1-P-O3'	5.24	116.72	105.20
23	CW	25	C	C6-N1-C1'	5.24	127.08	120.80
27	DD	275	LYS	N-CA-C	-5.23	96.87	111.00
1	AA	98	G	C8-N9-C4	-5.22	104.31	106.40
25	BA	840	A	O5'-P-OP2	-5.22	101.00	105.70
25	BA	2050	U	N1-C2-O2	5.21	126.45	122.80
24	CX	17	C	C2-N1-C1'	5.21	124.53	118.80
25	BA	553	A	N3-C4-C5	5.21	130.44	126.80
25	BA	641	G	N1-C6-O6	-5.21	116.78	119.90
25	BA	598	A	O5'-P-OP1	-5.20	101.02	105.70
25	BA	2347	A	O4'-C1'-N9	5.20	112.36	108.20
25	DA	2447	G	N1-C6-O6	-5.19	116.79	119.90
1	CA	1158	C	C6-N1-C2	-5.18	118.23	120.30
1	AA	1042	G	O4'-C1'-N9	5.18	112.34	108.20
35	DP	44	GLY	C-N-CA	5.18	134.65	121.70
23	CY	62	C	C5-C4-N4	5.18	123.82	120.20
25	BA	1220	U	P-O3'-C3'	5.17	125.91	119.70
24	AX	46	G	C5-C6-O6	-5.17	125.50	128.60
1	AA	1531	A	O4'-C1'-N9	-5.17	104.06	108.20
25	DA	645	C	N1-C2-O2	5.17	122.00	118.90
1	CA	1256	A	O4'-C1'-N9	-5.16	104.07	108.20
25	BA	2163	G	C5-C6-O6	5.16	131.70	128.60
46	B0	12	ASN	N-CA-C	5.15	124.90	111.00
25	BA	593	G	C6-N1-C2	-5.14	122.02	125.10
23	CW	25	C	C2-N1-C1'	-5.14	113.14	118.80
25	BA	649	C	O5'-P-OP1	-5.14	101.08	105.70
1	CA	1154	G	N7-C8-N9	5.13	115.67	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	746	A	O4'-C1'-N9	5.12	112.29	108.20
25	BA	2513	C	C2-N1-C1'	-5.11	113.18	118.80
25	BA	934	A	O4'-C1'-N9	5.11	112.28	108.20
24	CX	46	G	C5-C6-O6	-5.10	125.54	128.60
40	BU	74	LEU	CA-CB-CG	5.10	127.03	115.30
25	BA	1720	U	C2-N1-C1'	-5.10	111.58	117.70
25	BA	1670	G	N1-C6-O6	-5.10	116.84	119.90
25	BA	1985	U	C2-N1-C1'	5.09	123.80	117.70
1	CA	1007	C	C5-C6-N1	5.08	123.54	121.00
25	DA	1558	A	P-O3'-C3'	5.08	125.79	119.70
1	AA	1150	U	C2-N3-C4	5.07	130.04	127.00
24	AX	14	A	N1-C6-N6	5.07	121.64	118.60
1	AA	1502	A	C5-N7-C8	-5.07	101.36	103.90
25	BA	2078	G	O4'-C1'-N9	-5.07	104.15	108.20
25	BA	2298	A	C6-C5-N7	-5.07	128.75	132.30
25	DA	2206	G	C4-N9-C1'	-5.07	119.91	126.50
25	DA	1142	U	C2-N1-C1'	5.06	123.77	117.70
25	DA	748	G	C4-N9-C1'	-5.06	119.93	126.50
1	CA	997	U	N3-C4-O4	-5.05	115.86	119.40
25	BA	847	A	O5'-P-OP1	-5.05	101.16	105.70
25	BA	831	A	OP1-P-O3'	5.05	116.31	105.20
25	BA	2162	C	C6-N1-C1'	-5.05	114.74	120.80
25	DA	2572	A	C8-N9-C4	5.05	107.82	105.80
25	BA	831	A	O4'-C1'-N9	5.04	112.23	108.20
25	BA	2298	A	C5-N7-C8	-5.04	101.38	103.90
1	AA	1065	U	P-O3'-C3'	5.04	125.75	119.70
25	DA	2207	G	C4-N9-C1'	5.03	133.04	126.50
25	BA	1220	U	OP1-P-O3'	5.02	116.25	105.20
23	CW	3	C	C2-N1-C1'	5.02	124.32	118.80
1	AA	1278	U	C6-N1-C2	-5.01	117.99	121.00
25	BA	2077	C	OP1-P-O3'	5.01	116.22	105.20
1	AA	748	C	P-O3'-C3'	5.00	125.71	119.70
25	BA	875	U	C2-N1-C1'	-5.00	111.70	117.70
1	CA	687	A	P-O3'-C3'	5.00	125.70	119.70

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	231	GLU	Peptide
7	AG	78	ARG	Peptide
38	BS	58	LEU	Peptide

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Mol	Chain	Res	Type	Group
44	BY	54	LYS	Peptide
7	CG	78	ARG	Peptide
19	CS	28	LYS	Peptide
27	DD	274	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32205	0	16255	434	0
1	CA	32312	0	16307	550	0
2	AB	1846	0	1867	70	0
2	CB	1825	0	1828	90	0
3	AC	1552	0	1546	45	0
3	CC	1542	0	1517	56	0
4	AD	1659	0	1676	53	0
4	CD	1674	0	1714	54	0
5	AE	1129	0	1185	33	0
5	CE	1133	0	1191	30	0
6	AF	806	0	793	18	0
6	CF	816	0	808	17	0
7	AG	1231	0	1238	22	0
7	CG	1235	0	1249	31	0
8	AH	1088	0	1126	32	0
8	CH	1088	0	1126	31	0
9	AI	983	0	986	28	0
9	CI	978	0	966	46	0
10	AJ	709	0	650	32	0
10	CJ	714	0	672	36	0
11	AK	829	0	825	15	0
11	CK	833	0	836	22	0
12	AL	930	0	980	18	0
12	CL	930	0	980	23	0
13	AM	958	0	1002	26	0
13	CM	950	0	988	24	0
14	AN	492	0	529	20	0
14	CN	492	0	529	17	0
15	AO	728	0	760	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	CO	728	0	760	31	0
16	AP	681	0	697	21	0
16	CP	677	0	686	17	0
17	AQ	823	0	891	16	0
17	CQ	823	0	891	19	0
18	AR	555	0	618	12	0
18	CR	555	0	618	13	0
19	AS	652	0	662	35	0
19	CS	646	0	644	34	0
20	AT	728	0	798	19	0
20	CT	727	0	796	20	0
21	AU	199	0	208	5	0
21	CU	199	0	208	8	0
22	AV	277	0	140	2	0
22	CV	277	0	140	2	0
23	AW	1588	0	820	30	0
23	AY	1581	0	805	57	0
23	CW	1541	0	784	50	0
23	CY	1561	0	796	46	0
24	AX	1625	0	828	11	0
24	CX	1625	0	828	28	0
25	BA	60729	0	30622	619	0
25	DA	60311	0	30414	867	0
26	BB	2573	0	1306	18	0
26	DB	2573	0	1306	38	0
27	BD	2136	0	2218	52	0
27	DD	2136	0	2218	51	0
28	BE	1559	0	1618	38	0
28	DE	1559	0	1618	41	0
29	BF	1584	0	1625	33	0
29	DF	1580	0	1619	64	0
30	BG	1425	0	1443	23	0
30	DG	1424	0	1434	47	0
31	BH	1330	0	1407	26	0
31	DH	1330	0	1407	61	0
32	BI	1085	0	1114	26	0
32	DI	1061	0	1080	19	0
33	BN	1117	0	1184	15	0
33	DN	1117	0	1184	24	0
34	BO	933	0	996	21	0
34	DO	933	0	996	18	0
35	BP	1135	0	1212	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	DP	1135	0	1212	50	0
36	BQ	1122	0	1179	23	0
36	DQ	1122	0	1179	38	0
37	BR	968	0	1033	25	0
37	DR	968	0	1033	26	0
38	BS	877	0	938	26	0
38	DS	870	0	923	23	0
39	BT	1091	0	1151	29	0
39	DT	1083	0	1136	30	0
40	BU	959	0	1019	14	0
40	DU	959	0	1019	28	0
41	BV	771	0	830	17	0
41	DV	771	0	830	21	0
42	BW	886	0	940	15	0
42	DW	886	0	940	13	0
43	BX	750	0	814	23	0
43	DX	750	0	814	22	0
44	BY	806	0	881	21	0
44	DY	806	0	881	20	0
45	BZ	1349	0	1355	41	0
45	DZ	1360	0	1363	63	0
46	B0	653	0	674	16	0
46	D0	653	0	674	24	0
47	B1	755	0	826	17	0
47	D1	755	0	826	15	0
48	B2	588	0	643	9	0
48	D2	588	0	643	8	0
49	B3	469	0	518	8	0
49	D3	464	0	514	9	0
50	B4	558	0	544	34	0
50	D4	532	0	503	25	0
51	B5	455	0	465	11	0
51	D5	455	0	465	8	0
52	B6	453	0	473	7	0
52	D6	449	0	469	8	0
53	B7	418	0	467	11	0
53	D7	418	0	467	6	0
54	B8	511	0	571	18	0
54	D8	517	0	582	21	0
55	B9	307	0	335	4	0
55	D9	307	0	335	8	0
56	AA	230	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	AD	1	0	0	0	0
56	AE	1	0	0	0	0
56	AF	1	0	0	0	0
56	AK	2	0	0	0	0
56	AM	1	0	0	0	0
56	AN	1	0	0	0	0
56	AV	1	0	0	0	0
56	AW	7	0	0	0	0
56	AX	12	0	0	0	0
56	AY	3	0	0	0	0
56	B0	3	0	0	0	0
56	B1	2	0	0	0	0
56	B2	1	0	0	0	0
56	B3	3	0	0	0	0
56	B4	1	0	0	0	0
56	B5	4	0	0	0	0
56	B6	2	0	0	0	0
56	B7	2	0	0	0	0
56	B8	3	0	0	0	0
56	B9	1	0	0	0	0
56	BA	839	0	0	0	0
56	BB	23	0	0	0	0
56	BD	11	0	0	0	0
56	BE	8	0	0	0	0
56	BF	12	0	0	0	0
56	BG	3	0	0	0	0
56	BN	5	0	0	0	0
56	BO	1	0	0	0	0
56	BP	3	0	0	0	0
56	BQ	5	0	0	0	0
56	BR	5	0	0	0	0
56	BU	9	0	0	0	0
56	BV	5	0	0	0	0
56	BW	3	0	0	0	0
56	BX	2	0	0	0	0
56	BY	1	0	0	0	0
56	BZ	1	0	0	0	0
56	CA	177	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	CV	1	0	0	0	0
56	CW	2	0	0	0	0
56	CX	5	0	0	0	0
56	CY	1	0	0	0	0
56	D0	2	0	0	0	0
56	D3	1	0	0	0	0
56	D7	2	0	0	0	0
56	D8	1	0	0	0	0
56	DA	675	0	0	0	0
56	DB	11	0	0	0	0
56	DD	7	0	0	0	0
56	DE	4	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	DQ	4	0	0	0	0
56	DR	1	0	0	0	0
56	DU	2	0	0	0	0
56	DV	3	0	0	0	0
56	DW	3	0	0	0	0
56	DY	1	0	0	0	0
57	AA	40	0	37	7	0
57	CA	40	0	37	9	0
58	AD	8	0	0	0	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	226	0	0	17	0
61	AE	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	AJ	1	0	0	0	0
61	AL	4	0	0	1	0
61	AM	1	0	0	0	0
61	AV	4	0	0	0	0
61	AW	6	0	0	0	0
61	AX	8	0	0	0	0
61	AY	3	0	0	0	0
61	B0	4	0	0	0	0
61	B1	2	0	0	0	0
61	B3	2	0	0	0	0
61	B5	5	0	0	1	0
61	B6	1	0	0	0	0
61	B7	3	0	0	1	0
61	B8	11	0	0	1	0
61	BA	1411	0	0	69	0
61	BB	36	0	0	1	0
61	BD	16	0	0	2	0
61	BE	13	0	0	2	0
61	BF	7	0	0	0	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BN	2	0	0	0	0
61	BO	3	0	0	0	0
61	BP	17	0	0	1	0
61	BQ	2	0	0	0	0
61	BR	2	0	0	0	0
61	BT	1	0	0	0	0
61	BU	6	0	0	0	0
61	BV	2	0	0	0	0
61	BW	4	0	0	0	0
61	BX	1	0	0	0	0
61	CA	173	0	0	15	0
61	CJ	2	0	0	2	0
61	CL	1	0	0	0	0
61	CV	2	0	0	0	0
61	CW	1	0	0	0	0
61	CX	4	0	0	2	0
61	D0	5	0	0	0	0
61	D3	1	0	0	0	0
61	D7	3	0	0	1	0
61	D8	4	0	0	0	0
61	DA	1002	0	0	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	DB	10	0	0	0	0
61	DD	17	0	0	1	0
61	DE	11	0	0	0	0
61	DF	5	0	0	0	0
61	DN	2	0	0	0	0
61	DO	2	0	0	0	0
61	DP	8	0	0	1	0
61	DQ	1	0	0	0	0
61	DR	1	0	0	0	0
61	DU	2	0	0	0	0
61	DW	1	0	0	0	0
61	DY	1	0	0	0	0
All	All	297273	0	196306	4649	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 10.

All (4649) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.25	1.02
1:CA:999:C:N4	1:CA:1042:G:H1	1.59	1.00
1:AA:1025:U:O2	1:AA:1036:G:O6	1.82	0.98
23:CW:27:G:H1	23:CW:43:C:N4	1.62	0.97
1:CA:1029:C:N4	1:CA:1032:G:C6	2.33	0.97
23:CW:27:G:H1	23:CW:43:C:H42	1.01	0.97
23:CY:7:A:H61	23:CY:66:U:H3	1.12	0.97
25:BA:2158:C:H42	25:BA:2177:G:H1	0.98	0.96
25:BA:2145:G:H1	25:BA:2197:C:N4	1.63	0.96
25:DA:83:G:H1	25:DA:102:G:HO2'	1.11	0.95
23:CY:15:G:H22	23:CY:48:C:H42	1.11	0.94
23:AY:2:C:H42	23:AY:71:G:H1	1.15	0.94
23:AY:51:U:H3	23:AY:63:G:H1	0.97	0.93
23:CY:50:U:H3	23:CY:64:A:H61	1.14	0.92
25:DA:1798:U:H5'	27:DD:259:THR:HG22	1.49	0.92
25:DA:826:U:OP1	61:DA:4666:HOH:O	1.88	0.91
25:BA:1736:A:H62	25:BA:1745:A:H2	1.19	0.91
25:BA:591:U:O4	61:BA:4279:HOH:O	1.89	0.90
1:CA:1502:A:H2	1:CA:1505:G:H1	1.20	0.90
23:AY:19:G:N2	23:AY:56:C:N3	2.20	0.90
6:CF:81:ILE:HD11	27:DD:125:ILE:HB	1.53	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:26:A:H61	23:AY:44:G:H1	0.96	0.89
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.54	0.89
23:AY:26:A:N6	23:AY:44:G:H1	1.69	0.89
25:BA:2145:G:H1	25:BA:2197:C:H42	0.90	0.89
7:AG:50:ILE:HD11	7:AG:58:PRO:HA	1.55	0.89
1:AA:266:G:H5''	1:AA:268:C:H41	1.37	0.88
1:AA:376:G:H5''	16:AP:5:ARG:HG2	1.54	0.88
1:CA:532:A:O2'	1:CA:533:A:OP1	1.90	0.88
1:AA:1502:A:H2	1:AA:1505:G:H1	1.19	0.88
53:B7:24:THR:HG22	53:B7:27:GLY:H	1.37	0.88
25:BA:656:A:OP1	35:BP:65:ARG:NH1	2.07	0.88
1:CA:999:C:H42	1:CA:1042:G:H1	0.88	0.88
25:BA:786:G:OP1	61:BA:5273:HOH:O	1.92	0.87
29:DF:53:THR:HG22	29:DF:56:GLU:HG3	1.56	0.87
40:DU:76:TYR:OH	40:DU:92:ARG:NH1	2.06	0.87
25:DA:1315:C:OP2	61:DA:4468:HOH:O	1.91	0.87
39:BT:16:ARG:NH2	39:BT:83:ILE:O	2.08	0.86
46:B0:10:THR:HG22	46:B0:12:ASN:H	1.39	0.86
46:B0:11:ARG:O	46:B0:14:ARG:NH2	2.08	0.86
25:BA:2118:U:H3	25:BA:2215:G:H1	1.24	0.86
25:DA:740:U:OP2	61:DA:4516:HOH:O	1.92	0.86
25:BA:2158:C:N4	25:BA:2177:G:H1	1.72	0.86
30:BG:161:THR:HG22	30:BG:163:ALA:H	1.39	0.86
26:DB:66:A:H61	26:DB:109:C:H5'	1.39	0.86
25:BA:2299:A:H62	25:BA:2356:U:H3	1.22	0.85
1:AA:1025:U:H3	1:AA:1036:G:H1	1.24	0.85
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.57	0.85
1:CA:1189:C:OP1	10:CJ:51:ARG:NH2	2.10	0.85
23:CY:15:G:N2	23:CY:48:C:H42	1.75	0.85
25:BA:1829:U:H5'	27:BD:259:THR:HG22	1.59	0.84
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.59	0.84
25:DA:1689:A:H62	25:DA:1698:A:H2	1.25	0.84
23:CY:56:C:H2'	23:CY:57:G:H8	1.42	0.84
33:DN:123:TYR:HH	33:DN:130:HIS:HE2	1.13	0.84
1:CA:1024:G:H2'	1:CA:1025:U:H5''	1.59	0.84
1:CA:1422:G:H5''	34:DO:48:PRO:HB3	1.60	0.83
25:DA:301:G:OP2	44:DY:84:ARG:NH2	2.11	0.83
19:AS:20:LEU:HD23	19:AS:23:ASN:HD22	1.43	0.83
1:CA:1029:C:N3	1:CA:1032:G:C2	2.46	0.82
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.12	0.82
25:DA:2427:C:OP1	61:DA:4666:HOH:O	1.95	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:153:SER:HB3	45:DZ:167:PRO:HB3	1.62	0.82
35:BP:126:VAL:HG12	35:BP:148:LEU:HD22	1.59	0.82
1:AA:1086:U:H3	1:AA:1099:G:H22	1.23	0.82
30:DG:161:THR:HG22	30:DG:163:ALA:H	1.45	0.82
23:AY:2:C:N4	23:AY:71:G:H1	1.78	0.81
23:CY:15:G:H22	23:CY:48:C:N4	1.78	0.81
29:DF:53:THR:HG23	29:DF:55:GLY:H	1.42	0.81
1:AA:1004:A:N7	1:AA:1036:G:N2	2.28	0.81
1:AA:1158:C:H5	1:AA:1181:G:H1	1.28	0.81
23:CY:50:U:H3	23:CY:64:A:N6	1.78	0.81
25:BA:1094:A:OP2	25:BA:1155:C:N4	2.11	0.81
1:AA:1314:C:OP2	19:AS:4:SER:OG	1.97	0.81
25:DA:882:G:N2	25:DA:894:C:O2	2.14	0.81
1:CA:1029:C:C4	1:CA:1032:G:N1	2.48	0.81
25:DA:1648:C:OP1	61:DA:4508:HOH:O	1.97	0.81
1:CA:972:C:OP1	61:CA:4155:HOH:O	1.97	0.81
2:CB:128:GLU:HG3	2:CB:135:GLN:HE22	1.45	0.81
23:CW:27:G:N2	23:CW:43:C:N3	2.28	0.81
25:BA:2443:U:OP2	61:BA:4398:HOH:O	1.98	0.81
25:DA:2126:A:N6	25:DA:2162:G:O2'	2.13	0.81
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.15	0.80
25:DA:912:C:OP1	36:DQ:8:LYS:NZ	2.14	0.80
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.14	0.80
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.61	0.80
36:BQ:21:THR:HG21	36:BQ:101:ARG:HD3	1.62	0.80
45:DZ:72:ARG:NH2	45:DZ:97:GLU:O	2.13	0.80
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	1.62	0.80
25:BA:2723:A:OP1	61:BA:4496:HOH:O	2.00	0.80
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.29	0.80
38:BS:25:ARG:NH1	38:BS:42:ASP:OD1	2.15	0.80
25:DA:2541:A:N7	61:DA:4301:HOH:O	2.14	0.80
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.61	0.80
1:CA:1352:C:OP1	21:CU:3:LYS:NZ	2.13	0.80
25:DA:994:C:OP1	40:DU:53:ARG:NH2	2.14	0.80
25:DA:2121:G:H1	25:DA:2177:C:H42	1.29	0.80
32:BI:92:VAL:HG13	32:BI:120:ILE:HB	1.65	0.79
47:D1:51:VAL:HG11	47:D1:74:VAL:HG21	1.64	0.79
23:AY:2:C:N3	23:AY:71:G:N2	2.30	0.79
1:CA:953:G:H5'	1:CA:965:A:H61	1.47	0.79
41:DV:40:LEU:HB2	41:DV:46:VAL:HG13	1.65	0.79
1:AA:1008:C:N3	1:AA:1021:G:O6	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2802:C:O2	25:BA:2903:G:N1	2.14	0.79
27:BD:71:ASP:HB3	27:BD:103:ARG:HH22	1.48	0.79
1:CA:838:G:H1	1:CA:848:C:H42	1.30	0.79
25:DA:793:A:O2'	61:DA:4544:HOH:O	1.99	0.79
1:AA:1422:G:H5''	34:BO:48:PRO:HB3	1.65	0.79
3:CC:120:VAL:HA	3:CC:123:GLN:HE21	1.45	0.79
10:CJ:52:GLY:O	14:CN:41:ARG:NH2	2.16	0.79
46:D0:10:THR:HG22	46:D0:12:ASN:H	1.47	0.79
25:DA:2150:U:H2'	25:DA:2151:G:C8	2.18	0.79
1:AA:1503:A:O2'	22:AV:13:A:N1	2.16	0.79
25:BA:615:G:O6	61:BA:5039:HOH:O	1.99	0.79
1:CA:349:A:H2'	1:CA:350:G:H5''	1.64	0.79
29:DF:140:LEU:HD21	29:DF:170:LEU:HD11	1.65	0.79
45:DZ:126:VAL:HG11	45:DZ:161:VAL:HG23	1.64	0.79
25:BA:237:G:OP1	61:BA:5347:HOH:O	2.00	0.78
25:BA:894:U:OP2	61:BA:4544:HOH:O	2.01	0.78
41:BV:72:VAL:HG13	41:BV:85:LYS:HB3	1.66	0.78
1:CA:38:G:H22	1:CA:397:A:H5''	1.48	0.78
15:CO:87:ILE:HG22	15:CO:88:ARG:H	1.48	0.78
25:DA:981:A:OP1	61:DA:4416:HOH:O	2.02	0.78
25:BA:1189:A:OP1	33:BN:25:ARG:NH2	2.16	0.78
1:CA:671:G:H5'	6:CF:77:ARG:HH22	1.48	0.78
23:CY:7:A:N6	23:CY:66:U:H3	1.81	0.78
32:BI:92:VAL:HG11	32:BI:144:VAL:HG11	1.66	0.78
1:AA:160:A:N6	1:AA:345:C:OP2	2.15	0.78
1:CA:504:C:OP1	61:CA:4009:HOH:O	2.02	0.78
51:D5:16:ARG:NH1	51:D5:17:ASP:OD1	2.17	0.78
1:CA:79:G:H1	1:CA:90:U:H3	1.32	0.78
25:DA:956:G:OP2	36:DQ:14:ARG:NH2	2.17	0.78
25:DA:857:C:OP2	46:D0:77:ARG:NH2	2.17	0.77
36:DQ:26:TYR:O	36:DQ:67:ARG:NH1	2.17	0.77
25:BA:1361:C:OP2	61:BA:4775:HOH:O	2.03	0.77
25:DA:1031:G:H5''	55:D9:8:LYS:HE3	1.65	0.77
25:DA:2206:G:H3'	25:DA:2207:G:C8	2.20	0.77
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.65	0.77
23:CW:18:G:O2'	23:CW:57:G:N2	2.15	0.77
25:DA:1970:A:OP1	61:DA:4260:HOH:O	2.02	0.77
9:AI:50:LEU:HD13	9:AI:56:LEU:HA	1.67	0.77
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.15	0.77
25:BA:479:C:OP1	61:BA:4437:HOH:O	2.01	0.77
23:CW:4:C:N3	23:CW:69:G:N2	2.32	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.17	0.77
25:DA:1010:A:OP2	61:DA:4483:HOH:O	2.01	0.77
25:BA:2562:G:OP1	61:BA:5207:HOH:O	2.02	0.77
1:AA:1108:G:O6	61:AA:4156:HOH:O	2.03	0.77
25:DA:2123:G:H1	25:DA:2175:C:H42	1.32	0.77
45:DZ:144:LEU:HD22	45:DZ:174:VAL:HG23	1.66	0.77
8:AH:34:GLU:OE1	8:AH:37:ARG:NH1	2.17	0.77
1:CA:1083:U:OP2	61:CA:4106:HOH:O	2.02	0.77
1:CA:64:G:H4'	1:CA:65:U:H3'	1.67	0.77
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.17	0.76
25:DA:563:G:OP2	61:DA:4472:HOH:O	2.03	0.76
1:AA:975:A:H4'	1:AA:976:G:H5''	1.66	0.76
25:DA:1171:G:H1	25:DA:1178:C:H42	1.31	0.76
25:DA:81:G:N7	61:DA:4462:HOH:O	2.18	0.76
23:AY:50:U:H3	23:AY:64:A:H2	1.31	0.76
24:CX:50:U:H3	24:CX:64:G:H1	1.34	0.76
25:DA:250:G:OP2	54:D8:13:ARG:NH2	2.19	0.76
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.66	0.76
25:BA:1296:G:OP2	35:BP:21:ARG:NH1	2.18	0.76
43:DX:35:THR:HG22	43:DX:38:GLU:H	1.51	0.76
25:BA:1067:A:H62	25:BA:1186:U:H3	1.34	0.76
25:DA:2357:U:OP1	46:D0:20:ARG:NH1	2.19	0.76
25:DA:2285:C:OP2	52:D6:6:ARG:NH1	2.19	0.76
34:DO:35:VAL:HG11	34:DO:103:ALA:HB3	1.67	0.76
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.49	0.76
1:CA:1503:A:O2'	22:CV:13:A:N1	2.19	0.76
25:BA:2459:G:OP2	61:BA:4688:HOH:O	2.03	0.75
25:DA:2151:G:H2'	25:DA:2152:G:H8	1.51	0.75
1:CA:1029:C:C4	1:CA:1032:G:C2	2.75	0.75
25:DA:2139:C:H42	25:DA:2152:G:H1	1.32	0.75
23:CY:26:A:N1	23:CY:44:G:O6	2.20	0.75
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.68	0.75
27:DD:238:GLY:O	61:DD:409:HOH:O	2.03	0.75
25:BA:2720:G:H1'	37:BR:71:GLN:HE22	1.51	0.75
25:DA:2171:A:N3	25:DA:2172:U:N3	2.35	0.75
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HA	1.69	0.75
1:CA:975:A:H4'	1:CA:976:G:H5''	1.69	0.75
25:DA:154(A):C:N4	25:DA:171:G:O6	2.20	0.75
20:CT:60:GLU:HG3	20:CT:81:LYS:HD2	1.69	0.75
25:DA:2317:C:N4	25:DA:2318:G:O6	2.20	0.75
1:AA:201:C:H42	1:AA:216:G:H1	1.35	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.66	0.74
53:B7:34:ARG:NH2	61:B7:201:HOH:O	2.19	0.74
45:DZ:117:LEU:HA	45:DZ:174:VAL:HA	1.67	0.74
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.69	0.74
25:BA:878:G:O2'	35:BP:38:GLN:NE2	2.21	0.74
9:CI:97:LYS:HA	9:CI:102:LEU:HG	1.68	0.74
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.52	0.74
35:DP:126:VAL:HG12	35:DP:148:LEU:HD22	1.69	0.74
25:DA:847:U:OP2	61:DA:4326:HOH:O	2.04	0.74
10:CJ:8:LEU:HB2	10:CJ:70:ARG:HB2	1.67	0.74
26:DB:20:C:N4	26:DB:63:G:O6	2.20	0.74
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.05	0.74
1:CA:152:A:N6	1:CA:169:C:N3	2.35	0.74
23:CW:76:A:OP1	61:DA:4820:HOH:O	2.04	0.74
25:BA:2479:C:OP2	61:BA:5182:HOH:O	2.05	0.74
25:BA:715:G:N7	61:BA:4010:HOH:O	2.20	0.74
42:BW:19:LEU:HB3	51:B5:25:LEU:HD11	1.70	0.74
25:DA:1170:G:H1	25:DA:1179:C:H42	1.36	0.74
1:AA:1069:C:OP2	61:AA:4012:HOH:O	2.05	0.73
23:CY:51:U:O2	23:CY:63:G:N2	2.20	0.73
43:DX:11:PRO:HB3	43:DX:92:LEU:HD11	1.69	0.73
36:DQ:21:THR:HG21	36:DQ:101:ARG:HD3	1.69	0.73
23:AY:26:A:N1	23:AY:44:G:N2	2.35	0.73
43:BX:11:PRO:HB3	43:BX:92:LEU:HD11	1.68	0.73
1:CA:693:G:N7	57:CA:3178:PCY:N16	2.37	0.73
1:CA:353:A:H8	1:CA:353:A:H5'	1.53	0.73
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.22	0.73
25:BA:1648:U:O4	61:BA:4366:HOH:O	2.05	0.73
25:BA:2849:G:H5'	37:BR:46:GLY:HA2	1.70	0.73
1:CA:838:G:H1	1:CA:848:C:N4	1.87	0.73
25:DA:2287:A:H62	25:DA:2344:U:H3	1.34	0.73
1:AA:677:U:H3	1:AA:713:G:H22	1.36	0.73
45:BZ:139:VAL:HG22	45:BZ:155:LEU:HD11	1.71	0.73
11:CK:93:GLN:HA	11:CK:93:GLN:HE21	1.54	0.73
1:CA:999:C:N3	1:CA:1042:G:N2	2.34	0.73
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.70	0.73
1:CA:1255:G:OP1	10:CJ:45:ARG:NH2	2.22	0.73
45:DZ:45:ASP:OD1	45:DZ:49:ARG:NH1	2.22	0.73
30:BG:108:ASN:HB3	50:B4:22:ILE:HD13	1.71	0.72
1:CA:1000:U:H3	1:CA:1041:A:H61	1.36	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)
23:CW:4:C:N4	23:CW:69:G:N1	2.37	0.72
25:DA:2839:G:H5'	37:DR:46:GLY:HA2	1.70	0.72
1:CA:1028:C:N3	1:CA:1033:G:C6	2.56	0.72
3:CC:109:PRO:HB3	3:CC:115:LEU:HD23	1.71	0.72
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.22	0.72
25:DA:2130:U:H4'	25:DA:2133:G:H4'	1.71	0.72
25:DA:2138:C:H42	25:DA:2153:G:H1	1.38	0.72
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.21	0.72
16:CP:52:ASP:O	16:CP:54:GLU:N	2.20	0.72
25:DA:2100:G:H1	25:DA:2189:U:H3	1.34	0.72
25:BA:1018:A:OP2	61:BA:4279:HOH:O	2.08	0.72
9:CI:5:TYR:H	9:CI:87:GLN:HE22	1.38	0.72
25:DA:1602:U:O4	61:DA:4192:HOH:O	2.07	0.72
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.08	0.72
1:AA:664:G:H22	1:AA:741:G:H1	1.38	0.72
53:B7:34:ARG:NH1	53:B7:41:ARG:O	2.23	0.72
25:BA:542:C:OP1	51:B5:16:ARG:NH2	2.23	0.72
25:BA:839:G:O6	61:BA:4760:HOH:O	2.06	0.72
25:DA:1313:U:OP1	61:DA:4343:HOH:O	2.08	0.72
25:DA:2880:C:O3'	37:DR:90:ARG:NH1	2.23	0.72
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	1.71	0.72
23:AY:8:4SU:H4'	23:AY:48:C:H4'	1.72	0.72
54:B8:6:THR:HG22	54:B8:63:PRO:HD2	1.72	0.72
24:CX:75:C:OP1	61:CX:4003:HOH:O	2.06	0.72
25:BA:2776:G:OP2	61:BA:4827:HOH:O	2.06	0.72
57:CA:3178:PCY:N2	57:CA:3178:PCY:O19	2.21	0.72
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.70	0.72
25:BA:2145:G:N2	25:BA:2197:C:N3	2.32	0.72
1:CA:1029:C:N4	1:CA:1032:G:N1	2.37	0.72
25:DA:1352:U:OP2	61:DA:4084:HOH:O	2.08	0.72
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	1.70	0.71
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.23	0.71
50:B4:53:GLU:C	50:B4:55:ARG:H	1.94	0.71
25:BA:1001:G:OP2	36:BQ:14:ARG:NH2	2.22	0.71
1:CA:78:G:H2'	1:CA:79:G:H5''	1.71	0.71
1:AA:1030(C):G:N7	1:AA:1031:G:N2	2.38	0.71
25:BA:2877:G:OP2	39:BT:119:LYS:NZ	2.23	0.71
32:BI:93:THR:HG22	32:BI:119:PRO:HB3	1.72	0.71
25:BA:2396:G:OP2	46:B0:55:ARG:NH1	2.21	0.71
25:BA:2162:C:C2	25:BA:2173:G:N2	2.59	0.71
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.36	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BQ:14:ARG:HG2	36:BQ:41:TRP:HH2	1.55	0.71
9:CI:127:LYS:O	9:CI:128:ARG:HB3	1.91	0.71
24:CX:49:G:H1	24:CX:65:C:H42	1.35	0.71
27:BD:148:GLU:HB2	27:BD:151:LYS:HD2	1.73	0.71
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.24	0.71
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.63	0.71
25:DA:2110:G:O2'	25:DA:2120:G:OP2	2.08	0.71
42:DW:33:ARG:NH2	42:DW:52:GLU:OE1	2.23	0.71
45:DZ:144:LEU:HD21	45:DZ:173:ALA:HA	1.72	0.71
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.71	0.70
1:CA:6:G:H4'	1:CA:298:A:H4'	1.73	0.70
25:DA:320:A:OP2	29:DF:137:LYS:NZ	2.20	0.70
57:AA:3231:PCY:O19	57:AA:3231:PCY:N2	2.24	0.70
25:BA:1378:G:OP1	61:BA:4775:HOH:O	2.08	0.70
25:BA:2157:A:H61	25:BA:2178:G:H1'	1.56	0.70
25:BA:2251:G:OP2	61:BA:4470:HOH:O	2.08	0.70
25:BA:465:G:N7	61:BA:4522:HOH:O	2.24	0.70
36:BQ:109:VAL:HG13	36:BQ:113:GLN:HB3	1.71	0.70
3:AC:78:GLY:HA3	3:AC:83:ARG:H	1.56	0.70
25:BA:2146:G:H1	25:BA:2196:C:H42	1.39	0.70
29:BF:101:LEU:O	29:BF:106:ARG:NH1	2.25	0.70
50:B4:61:ARG:HG3	50:B4:62:ARG:H	1.56	0.70
1:CA:201:C:H42	1:CA:216:G:H1	1.37	0.70
1:CA:346:G:OP1	39:DT:41:ARG:NH2	2.23	0.70
25:DA:1671:U:OP2	61:DA:4069:HOH:O	2.08	0.70
25:BA:1249:A:H2	25:BA:1287:A:H62	1.39	0.70
27:BD:69:ARG:NH2	27:BD:128:GLY:O	2.25	0.70
1:CA:97:G:O2'	1:CA:98:G:O5'	2.09	0.70
23:CY:51:U:N3	23:CY:63:G:N1	2.39	0.70
25:DA:2503:A:O2'	25:DA:2505:G:OP2	2.09	0.70
29:DF:101:LEU:O	29:DF:106:ARG:NH1	2.25	0.70
30:DG:80:PHE:O	30:DG:82:LEU:N	2.24	0.70
25:BA:1700:G:H3'	37:BR:2:ARG:HD3	1.74	0.70
25:BA:30:G:OP2	40:BU:5:LYS:NZ	2.23	0.70
1:CA:1116:C:H2'	1:CA:1117:G:H5''	1.73	0.70
47:D1:76:ARG:HH11	47:D1:97:LEU:HD22	1.56	0.70
5:AE:85:GLY:O	5:AE:87:SER:N	2.24	0.70
1:CA:1118:C:H2'	1:CA:1119:C:H6	1.55	0.70
25:DA:1670:C:OP1	61:DA:4069:HOH:O	2.10	0.70
25:BA:1395:A:OP1	61:BA:5097:HOH:O	2.10	0.70
35:BP:42:SER:O	61:BP:303:HOH:O	2.10	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2447:G:OP2	61:DA:4707:HOH:O	2.10	0.70
27:DD:71:ASP:HB3	27:DD:103:ARG:HH22	1.57	0.70
3:AC:150:LYS:HE2	3:AC:152:ILE:HD11	1.71	0.69
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.24	0.69
25:BA:2143:G:H1	25:BA:2199:C:H42	1.40	0.69
35:DP:36:LYS:O	61:DP:201:HOH:O	2.09	0.69
9:AI:16:ARG:HB2	9:AI:64:THR:HB	1.74	0.69
44:BY:92:ASN:HB3	44:BY:94:LYS:H	1.56	0.69
25:DA:2355:C:H4'	46:D0:24:LYS:HD3	1.74	0.69
25:BA:2130:C:H2'	25:BA:2131:U:H6	1.57	0.69
25:DA:2682:U:OP2	61:DA:4147:HOH:O	2.10	0.69
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.25	0.69
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.73	0.69
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.25	0.69
25:BA:1922:A:OP2	61:BA:4461:HOH:O	2.09	0.69
25:DA:2807:G:N2	25:DA:2893:G:O6	2.25	0.69
25:DA:601:C:O2'	29:DF:104:LYS:NZ	2.24	0.69
1:AA:1129:C:H5''	9:AI:16:ARG:HH12	1.57	0.69
25:BA:1039:G:OP1	40:BU:50:ARG:NH2	2.25	0.69
11:CK:48:ILE:O	11:CK:50:TYR:N	2.22	0.69
1:AA:836:G:OP1	18:AR:61:LYS:NZ	2.23	0.69
25:BA:2081:A:OP2	61:BA:4472:HOH:O	2.11	0.69
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.93	0.69
11:CK:54:ARG:NH2	23:CY:39:PSU:O2'	2.26	0.69
15:CO:22:THR:OG1	15:CO:23:GLY:N	2.21	0.69
1:AA:812:C:N3	61:AA:4050:HOH:O	2.25	0.69
25:DA:2327:A:H2'	25:DA:2328:A:C8	2.28	0.69
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.75	0.69
25:DA:1783:A:OP1	61:DA:4516:HOH:O	2.11	0.69
23:AY:19:G:N1	23:AY:56:C:N4	2.38	0.69
23:AY:67:C:H2'	23:AY:68:C:C6	2.28	0.69
28:BE:47:VAL:HG21	28:BE:86:PRO:HD2	1.73	0.69
23:CW:2:C:N3	23:CW:71:G:O6	2.26	0.69
25:DA:2125:G:H22	25:DA:2172:U:H5'	1.57	0.69
25:DA:2135:A:H61	25:DA:2157:G:H21	1.37	0.69
37:DR:67:LEU:HD13	37:DR:76:VAL:HG21	1.75	0.69
25:BA:139:A:H8	25:BA:1454:C:HO2'	1.40	0.69
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.08	0.69
25:DA:2162:G:H4'	25:DA:2172:U:H2'	1.75	0.69
25:DA:2122:U:O4	25:DA:2176:A:N1	2.24	0.69
25:DA:9:U:H3	25:DA:2629:A:H2	1.39	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1423:G:OP1	34:BO:49:ARG:NH2	2.26	0.68
1:AA:200:G:H1	1:AA:217:C:H42	1.40	0.68
1:AA:539:A:OP2	12:AL:115:LYS:NZ	2.26	0.68
23:AY:44:G:O2'	23:AY:45:U:OP1	2.10	0.68
25:BA:1065:U:HO2'	25:BA:1067:A:H2	1.41	0.68
23:CY:13:C:N3	23:CY:22:G:O6	2.26	0.68
25:DA:2167:U:O2'	25:DA:2168:G:N3	2.25	0.68
25:DA:1012:U:H5	33:DN:28:THR:HG21	1.59	0.68
25:DA:1021:A:H62	25:DA:1141:U:H3	1.39	0.68
25:DA:943:U:OP2	61:DA:4576:HOH:O	2.11	0.68
25:DA:601:C:OP1	29:DF:108:LYS:NZ	2.27	0.68
1:AA:1034:G:H2'	1:AA:1035:A:C8	2.27	0.68
1:AA:44:G:O6	61:AA:4055:HOH:O	2.09	0.68
25:BA:1717:C:OP2	61:BA:5207:HOH:O	2.12	0.68
42:BW:14:PRO:HG2	42:BW:78:GLU:HG2	1.74	0.68
1:CA:1129:C:OP1	9:CI:16:ARG:NH1	2.25	0.68
1:AA:1151:A:HO2'	1:AA:1152:A:H8	1.41	0.68
25:BA:667:G:N2	25:BA:670:C:OP2	2.27	0.68
23:CW:29:G:H1	23:CW:41:C:H42	1.42	0.68
10:AJ:30:SER:O	10:AJ:81:THR:OG1	2.11	0.68
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.22	0.68
25:DA:1817:G:OP1	27:DD:88:ARG:NH2	2.26	0.68
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.10	0.68
23:AY:50:U:O4	23:AY:64:A:N1	2.27	0.68
25:BA:1044:C:OP1	61:BA:4784:HOH:O	2.11	0.68
25:DA:2552:U:H2'	25:DA:2554:U:OP2	1.93	0.68
25:DA:370:G:OP2	61:DA:4103:HOH:O	2.12	0.68
26:DB:13:A:N1	26:DB:69:G:O2'	2.24	0.68
25:BA:2138:G:N7	25:BA:2187:G:N2	2.42	0.68
25:BA:2695:C:O2	34:BO:70:LYS:NZ	2.25	0.68
25:BA:427:G:N7	61:BA:5099:HOH:O	2.26	0.68
25:BA:932:C:H3'	25:BA:933:C:H5''	1.75	0.68
9:CI:17:VAL:HG11	9:CI:81:ILE:HA	1.76	0.68
48:D2:22:GLU:OE2	48:D2:68:ARG:NH2	2.27	0.68
55:D9:25:VAL:HB	55:D9:34:GLN:HB2	1.76	0.68
25:DA:1031:G:H21	55:D9:36:GLN:HE22	1.40	0.68
25:DA:20:C:OP1	40:DU:22:LYS:NZ	2.23	0.68
1:AA:1297:C:O2'	7:AG:114:ARG:NH2	2.27	0.68
23:CY:52:G:O6	23:CY:62:C:N3	2.27	0.68
25:DA:400:G:N7	61:DA:4682:HOH:O	2.27	0.68
25:DA:805:G:OP1	61:DA:4971:HOH:O	2.12	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1271:G:OP2	61:DA:4508:HOH:O	2.11	0.67
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.29	0.67
25:DA:2134:A:O2'	25:DA:2159:G:N3	2.26	0.67
39:DT:65:LYS:HE2	39:DT:67:SER:HB2	1.76	0.67
25:BA:2122:G:H1	25:BA:2211:U:H3	1.41	0.67
32:BI:133:HIS:ND1	32:BI:134:PRO:O	2.26	0.67
1:CA:1075:C:OP1	2:CB:179:LYS:NZ	2.26	0.67
8:CH:10:LEU:HD22	8:CH:83:ILE:HD11	1.76	0.67
10:CJ:44:VAL:HG13	10:CJ:66:ARG:HG2	1.76	0.67
26:DB:75:G:N2	45:DZ:87:ASP:OD1	2.25	0.67
1:CA:766:A:OP2	61:CA:4022:HOH:O	2.11	0.67
3:CC:54:ARG:HH11	3:CC:54:ARG:HB3	1.58	0.67
25:DA:2507:C:H5''	25:DA:2573:C:N4	2.09	0.67
1:CA:1301:U:O2'	1:CA:1302:U:H5'	1.94	0.67
28:DE:47:VAL:HG11	28:DE:86:PRO:HD2	1.76	0.67
1:CA:7:G:O2'	5:CE:120:THR:O	2.13	0.67
36:DQ:110:THR:HG23	36:DQ:113:GLN:HB2	1.76	0.67
1:AA:1352:C:OP1	21:AU:3:LYS:NZ	2.23	0.67
25:BA:70:A:H3'	25:BA:70:A:OP2	1.94	0.67
10:CJ:5:ARG:N	61:CJ:5101:HOH:O	2.28	0.67
29:DF:21:ALA:HB3	29:DF:22:ALA:HA	1.76	0.67
19:AS:41:VAL:HG12	19:AS:43:GLU:H	1.60	0.67
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.42	0.67
5:CE:143:ARG:NH1	8:CH:77:GLU:OE1	2.28	0.67
25:DA:796:C:H2'	25:DA:797:C:C6	2.30	0.67
9:AI:20:ARG:O	9:AI:60:ASP:N	2.23	0.67
1:CA:1312:G:H1	1:CA:1325:C:H42	1.41	0.67
1:CA:986:A:N3	19:CS:52:TYR:OH	2.25	0.67
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	1.76	0.67
3:CC:129:ALA:HB3	3:CC:132:ARG:HB2	1.76	0.67
25:DA:517:C:OP1	51:D5:16:ARG:NH2	2.28	0.67
29:DF:103:LYS:HA	29:DF:106:ARG:HG3	1.76	0.67
29:DF:184:TYR:CE2	29:DF:188:ARG:HD2	2.29	0.67
1:AA:1416:G:N7	61:AA:4106:HOH:O	2.28	0.67
25:BA:2153:G:H5''	25:BA:2154:U:H3'	1.75	0.67
25:BA:2788:A:N7	61:BA:4672:HOH:O	2.27	0.67
25:BA:2793:G:OP1	61:BA:4974:HOH:O	2.13	0.67
25:BA:701:A:N7	61:BA:4847:HOH:O	2.28	0.67
37:BR:67:LEU:HD13	37:BR:76:VAL:HG21	1.77	0.67
18:CR:22:VAL:HB	18:CR:56:THR:HA	1.77	0.67
25:DA:2060:A:N3	61:DA:4409:HOH:O	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:81:G:HO2'	25:DA:295:G:HO2'	1.40	0.67
27:DD:206:LEU:HD22	27:DD:211:ARG:HG2	1.76	0.67
19:AS:68:GLY:H	50:B4:58:ARG:HH12	1.41	0.66
25:BA:2387:G:N7	61:BA:4876:HOH:O	2.29	0.66
25:BA:325:G:OP2	44:BY:84:ARG:NH2	2.28	0.66
4:CD:140:VAL:HG11	4:CD:146:ILE:HD11	1.77	0.66
32:DI:92:VAL:HG22	32:DI:120:ILE:HB	1.77	0.66
1:AA:1392:G:N2	1:AA:1502:A:H8	1.94	0.66
1:AA:572:A:OP1	61:AA:4102:HOH:O	2.12	0.66
27:BD:237:GLU:OE2	61:BD:412:HOH:O	2.14	0.66
1:CA:1002:G:H1	1:CA:1038:C:H42	1.43	0.66
1:CA:1086:U:H3	1:CA:1099:G:H22	1.43	0.66
1:CA:947:G:H1	1:CA:1234:C:H42	1.41	0.66
25:DA:1218:C:H42	25:DA:1231:G:H1	1.43	0.66
25:DA:2006:C:OP2	61:DA:4803:HOH:O	2.13	0.66
25:DA:2046:G:H5'	51:D5:19:ARG:HA	1.76	0.66
1:AA:1238:A:OP2	61:AA:4145:HOH:O	2.12	0.66
1:AA:1152:A:OP1	10:AJ:68:HIS:ND1	2.27	0.66
26:BB:33:G:H5'	30:BG:2:PRO:HD3	1.77	0.66
25:DA:1188:U:H5''	41:DV:79:VAL:HG13	1.76	0.66
25:DA:271(I):G:N2	25:DA:271(O):C:O2	2.27	0.66
1:AA:1255:G:OP1	10:AJ:45:ARG:NH2	2.29	0.66
1:AA:953:G:H5'	1:AA:965:A:H61	1.60	0.66
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.29	0.66
26:DB:12:C:H2'	46:D0:73:GLY:HA3	1.78	0.66
25:DA:1658:C:OP1	61:DA:4502:HOH:O	2.12	0.66
25:DA:1243:G:O2'	35:DP:4:SER:O	2.13	0.66
1:CA:972:C:O2'	10:CJ:55:LYS:O	2.14	0.66
25:DA:1332:G:OP1	61:DA:4468:HOH:O	2.13	0.66
1:CA:1029:C:N3	1:CA:1032:G:N2	2.44	0.66
1:CA:67:C:H2'	1:CA:68:G:C8	2.31	0.66
1:AA:1025:U:O2'	1:AA:1026:G:O4'	2.14	0.66
9:AI:17:VAL:HG23	9:AI:63:ILE:HG12	1.78	0.66
19:AS:68:GLY:HA3	50:B4:58:ARG:HH22	1.61	0.66
31:BH:149:ARG:NH1	31:BH:167:GLU:OE2	2.29	0.66
1:CA:539:A:H2'	1:CA:540:G:C8	2.31	0.66
19:CS:42:PRO:HG3	50:D4:61:ARG:HG3	1.78	0.66
25:DA:304:G:O6	61:DA:4486:HOH:O	2.11	0.66
43:DX:65:ARG:HG3	43:DX:70:LEU:HG	1.77	0.66
23:AW:51:U:H2'	23:AW:52:G:C8	2.30	0.66
27:BD:206:LEU:HD22	27:BD:211:ARG:HG2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:181:ASN:HD21	3:CC:204:LEU:HD12	1.61	0.66
1:AA:310:G:OP2	16:AP:27:LYS:NZ	2.27	0.66
25:BA:2158:C:N3	25:BA:2177:G:N2	2.43	0.66
28:BE:29:GLY:HA3	61:BE:406:HOH:O	1.96	0.66
45:BZ:72:ARG:NH2	45:BZ:97:GLU:O	2.28	0.66
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.77	0.66
25:BA:2362:C:OP2	61:BA:4189:HOH:O	2.13	0.66
23:CW:61:C:O2'	23:CW:62:C:O5'	2.09	0.66
25:DA:307:G:N2	25:DA:310:A:O5'	2.26	0.66
25:DA:526:A:OP1	61:DA:4488:HOH:O	2.14	0.66
1:AA:1392:G:H21	1:AA:1502:A:H8	1.45	0.65
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	1.78	0.65
25:BA:2419:G:OP1	61:BA:4387:HOH:O	2.13	0.65
25:BA:2772:G:N7	61:BA:4262:HOH:O	2.28	0.65
45:BZ:117:LEU:HD11	45:BZ:144:LEU:HB3	1.78	0.65
13:CM:40:ASN:HB3	13:CM:43:THR:HG23	1.78	0.65
1:AA:1530:G:H2'	1:AA:1531:A:O4'	1.96	0.65
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.29	0.65
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.30	0.65
25:BA:2184:G:H5''	25:BA:2194:U:H2'	1.78	0.65
39:BT:65:LYS:HE2	39:BT:67:SER:HB2	1.76	0.65
1:CA:79:G:N2	1:CA:90:U:O2	2.27	0.65
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.14	0.65
25:DA:1996:C:H4'	25:DA:1997:G:OP1	1.96	0.65
24:CX:64:G:H4'	36:DQ:10:ARG:HH12	1.60	0.65
45:DZ:108:PRO:HB2	45:DZ:111:VAL:HG23	1.77	0.65
1:AA:76:C:N3	1:AA:93:G:O6	2.29	0.65
23:AW:19:G:N2	23:AW:56:C:N3	2.44	0.65
43:BX:31:HIS:HD2	43:BX:33:LYS:H	1.44	0.65
1:CA:1002:G:C4	1:CA:1003:G:H8	2.14	0.65
1:CA:1028:C:C4	1:CA:1033:G:O6	2.49	0.65
25:DA:42:G:OP2	61:DA:4954:HOH:O	2.14	0.65
36:DQ:111:GLU:OE1	36:DQ:133:ARG:NH2	2.26	0.65
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.29	0.65
25:DA:30:G:OP2	40:DU:5:LYS:NZ	2.25	0.65
30:DG:114:ILE:HA	30:DG:140:ILE:HD11	1.79	0.65
5:AE:33:VAL:HG21	5:AE:109:ILE:HA	1.77	0.65
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.29	0.65
1:AA:1002:G:H3'	1:AA:1003:G:O4'	1.97	0.65
25:DA:1019:U:H3	25:DA:1142(A):A:H62	1.45	0.65
31:DH:3:ARG:NH2	31:DH:5:GLY:H	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:837:G:H1	1:AA:849:C:H42	1.45	0.65
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.78	0.65
55:B9:25:VAL:HB	55:B9:34:GLN:HB2	1.78	0.65
1:CA:1245:A:H61	1:CA:1292:U:H3	1.45	0.65
1:CA:1417:G:O6	61:CA:4051:HOH:O	2.12	0.65
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.78	0.65
50:D4:44:THR:O	50:D4:46:GLN:N	2.30	0.65
23:CW:51:U:H3	23:CW:63:G:H1	1.45	0.65
34:DO:68:GLU:HB3	34:DO:78:ARG:HB2	1.79	0.65
2:AB:201:ILE:HG21	2:AB:214:ILE:HG21	1.80	0.64
25:BA:11:G:H2'	25:BA:12:U:H5''	1.79	0.64
2:CB:178:ARG:HH22	8:CH:68:ARG:HH12	1.44	0.64
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.30	0.64
25:DA:1204:A:H2	25:DA:1241:A:H62	1.46	0.64
30:DG:15:VAL:HG22	30:DG:175:LEU:HB3	1.79	0.64
33:DN:30:ILE:HG22	33:DN:34:LEU:HD22	1.78	0.64
1:AA:78:G:N2	1:AA:91:C:N3	2.46	0.64
25:BA:2340:A:H2'	25:BA:2341:G:C8	2.32	0.64
19:CS:63:THR:OG1	19:CS:65:ASN:ND2	2.30	0.64
25:DA:631:A:OP1	35:DP:65:ARG:NH1	2.30	0.64
1:AA:1136:U:H5''	1:AA:1137:C:C4	2.31	0.64
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.31	0.64
1:AA:346:G:OP1	39:BT:41:ARG:NH1	2.26	0.64
9:AI:53:VAL:O	9:AI:55:ALA:N	2.31	0.64
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.79	0.64
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.30	0.64
4:CD:157:LEU:O	4:CD:161:ASN:ND2	2.30	0.64
1:AA:1008:C:O2	1:AA:1021:G:N1	2.27	0.64
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.27	0.64
25:BA:2164:C:N3	25:BA:2171:G:O6	2.31	0.64
25:DA:1013:C:H2'	25:DA:1014:U:H6	1.62	0.64
1:AA:97:G:O2'	1:AA:98:G:O4'	2.14	0.64
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.79	0.64
25:BA:1451:U:H2'	25:BA:1452:U:C6	2.32	0.64
33:BN:67:LEU:HB3	33:BN:88:GLU:HG3	1.79	0.64
37:BR:97:VAL:HG22	37:BR:114:VAL:HG13	1.80	0.64
1:CA:1456:G:O6	20:CT:54:LYS:NZ	2.25	0.64
25:DA:1283:G:N2	25:DA:1286:A:OP2	2.31	0.64
25:BA:1222:A:H3'	25:BA:1223:C:C6	2.32	0.64
12:AL:34:ARG:NH2	61:AL:201:HOH:O	2.30	0.64
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:16:ARG:HB2	9:CI:64:THR:HG22	1.79	0.64
23:CY:5:G:H1	23:CY:68:C:H42	1.46	0.64
25:DA:2431:U:OP1	61:DA:4215:HOH:O	2.15	0.64
29:DF:24:LEU:HD23	29:DF:115:ALA:HA	1.79	0.64
1:AA:352:C:OP2	61:AA:4109:HOH:O	2.15	0.64
4:AD:177:ASP:HB3	4:AD:182:LYS:HG2	1.78	0.64
15:CO:22:THR:HG1	15:CO:23:GLY:H	1.46	0.64
23:CY:50:U:O2	23:CY:64:A:N1	2.31	0.64
46:D0:11:ARG:O	46:D0:14:ARG:NH2	2.31	0.64
25:DA:143(A):C:O2'	43:DX:2:LYS:NZ	2.30	0.64
25:DA:2023:G:H5'	25:DA:2617:C:H4'	1.79	0.64
1:CA:1029:C:C2	1:CA:1032:G:N2	2.66	0.64
3:CC:164:ARG:NH1	3:CC:166:GLU:OE1	2.31	0.64
25:DA:1958:C:OP2	61:DA:4696:HOH:O	2.15	0.64
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.80	0.63
23:AW:19:G:H1	23:AW:56:C:H42	1.43	0.63
45:BZ:126:VAL:HG11	45:BZ:161:VAL:HG23	1.81	0.63
45:BZ:138:GLU:H	45:BZ:156:LYS:HD3	1.62	0.63
1:CA:165:C:H2'	1:CA:166:G:H8	1.62	0.63
25:DA:1266:G:O5'	42:DW:15:ARG:NH2	2.31	0.63
25:DA:330:A:H2	25:DA:1210:A:HO2'	1.43	0.63
1:AA:812:C:O2	61:AA:4048:HOH:O	2.14	0.63
16:AP:22:THR:HA	16:AP:33:ILE:HG13	1.80	0.63
25:DA:2123:G:H1	25:DA:2175:C:N4	1.97	0.63
25:DA:2299:G:H2'	25:DA:2300:G:H8	1.64	0.63
25:DA:2360:A:OP2	61:DA:4626:HOH:O	2.15	0.63
25:BA:1219:A:H4'	25:BA:1220:U:OP1	1.97	0.63
25:BA:1431:G:O2'	25:BA:1442:U:O2	2.11	0.63
2:CB:47:THR:HA	2:CB:202:PRO:HG2	1.79	0.63
1:AA:159:G:N2	1:AA:162:A:OP2	2.32	0.63
1:AA:353:A:H5'	1:AA:353:A:H8	1.63	0.63
50:B4:68:ARG:HD2	50:B4:69:LYS:H	1.63	0.63
51:B5:40:LYS:NZ	51:B5:44:THR:O	2.22	0.63
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.14	0.63
24:CX:76:A:H5'	25:DA:2585:U:H5	1.63	0.63
48:D2:1:MET:N	48:D2:52:ASP:OD1	2.23	0.63
1:AA:545:C:OP1	4:AD:61:LYS:NZ	2.31	0.63
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.81	0.63
25:BA:1480:A:H61	25:BA:1605:A:H62	1.45	0.63
28:BE:143:ASN:HD22	28:BE:147:PRO:HD3	1.64	0.63
1:CA:1003:G:N2	1:CA:1025:U:O4	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:307:G:N1	25:DA:310:A:OP2	2.32	0.63
25:DA:468:G:N7	53:D7:39:ARG:NH2	2.44	0.63
26:DB:4:C:H42	26:DB:117:G:H1	1.44	0.63
25:DA:2867:G:OP2	39:DT:119:LYS:NZ	2.32	0.63
2:AB:118:LEU:HB3	2:AB:142:LEU:HD12	1.79	0.63
1:CA:920:U:H2'	1:CA:921:U:C6	2.33	0.63
26:DB:22:U:H3	26:DB:61:G:H1	1.46	0.63
28:DE:36:ARG:HG2	28:DE:47:VAL:HG12	1.80	0.63
1:AA:78:G:N1	1:AA:91:C:N4	2.47	0.63
25:DA:900:A:H2'	25:DA:901:A:H8	1.64	0.63
25:BA:302:A:O2'	25:BA:303:C:OP1	2.17	0.63
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.27	0.63
1:AA:134:A:H61	16:AP:25:ARG:NH1	1.97	0.63
23:AY:19:G:H3'	23:AY:20:U:H6	1.64	0.63
25:BA:2164:C:O2	25:BA:2171:G:N1	2.27	0.63
34:BO:35:VAL:HG11	34:BO:103:ALA:HB3	1.80	0.63
37:BR:44:LEU:HD22	37:BR:48:VAL:HG23	1.81	0.63
45:BZ:92:SER:OG	45:BZ:93:ASP:N	2.31	0.63
25:DA:1283:G:O2'	25:DA:1285:G:N7	2.26	0.63
38:BS:59:LYS:HD2	38:BS:60:GLY:H	1.64	0.62
1:CA:1028:C:C2	1:CA:1033:G:N1	2.67	0.62
1:CA:1132:C:H42	1:CA:1142:G:H1	1.46	0.62
15:CO:5:LYS:HZ2	15:CO:5:LYS:H	1.47	0.62
25:DA:2502:G:N7	61:DA:4706:HOH:O	2.31	0.62
25:DA:7:G:H2'	25:DA:8:A:C8	2.34	0.62
27:DD:12:SER:HB3	27:DD:208:LYS:HB3	1.80	0.62
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.80	0.62
23:AW:7:A:H61	23:AW:66:U:H3	1.45	0.62
25:BA:1312:G:O5'	42:BW:15:ARG:NH2	2.32	0.62
25:DA:1815:A:P	27:DD:54:ARG:HH22	2.22	0.62
28:DE:34:VAL:HG11	28:DE:78:LEU:HD11	1.81	0.62
40:DU:76:TYR:HH	40:DU:92:ARG:NH1	1.96	0.62
1:AA:1002:G:C4	1:AA:1003:G:H1'	2.34	0.62
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.32	0.62
1:CA:1120:G:C6	1:CA:1154:G:N2	2.67	0.62
29:DF:157:VAL:HB	29:DF:194:MET:HG2	1.81	0.62
1:CA:345:C:OP2	39:DT:39:ARG:NH2	2.32	0.62
25:BA:265:U:H2'	25:BA:266:C:C6	2.34	0.62
26:BB:84:C:OP1	49:B3:15:TYR:OH	2.18	0.62
2:CB:178:ARG:NH2	8:CH:68:ARG:HH12	1.97	0.62
50:D4:24:THR:OG1	50:D4:25:TYR:N	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:316:G:OP2	1:AA:351:G:O2'	2.17	0.62
25:BA:2163:G:H1	25:BA:2171:G:H22	1.46	0.62
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.82	0.62
4:CD:191:ARG:NH1	4:CD:191:ARG:O	2.32	0.62
13:CM:33:ALA:HA	13:CM:59:TYR:HE2	1.64	0.62
25:DA:2141:G:O6	25:DA:2150:U:O2	2.17	0.62
25:DA:221:A:N1	25:DA:265:A:O2'	2.32	0.62
1:AA:45:U:H2'	1:AA:46:G:C8	2.35	0.62
1:AA:519:C:OP2	12:AL:50:SER:OG	2.17	0.62
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.82	0.62
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.80	0.62
25:BA:2164:C:H2'	25:BA:2165:C:C6	2.35	0.62
25:BA:278:G:OP1	47:B1:76:ARG:NH1	2.31	0.62
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.82	0.62
3:CC:138:VAL:HG23	3:CC:151:VAL:HG23	1.82	0.62
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.31	0.62
24:CX:21:A:H61	24:CX:46:G:H2'	1.65	0.62
25:DA:2591:C:OP1	27:DD:239:ARG:HD2	2.00	0.62
25:DA:952:G:OP1	36:DQ:16:ARG:NH2	2.33	0.62
2:AB:16:HIS:O	2:AB:18:GLY:N	2.32	0.62
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.82	0.62
20:AT:57:ARG:HH12	20:AT:100:ILE:HD12	1.64	0.62
25:BA:1848:G:OP1	27:BD:88:ARG:NH2	2.33	0.62
25:BA:2163:G:C4	25:BA:2164:C:H1'	2.33	0.62
27:DD:182:LEU:HB2	27:DD:272:ALA:HB3	1.80	0.62
25:DA:1842:G:O2'	27:DD:253:GLN:NE2	2.33	0.62
37:DR:97:VAL:HG22	37:DR:114:VAL:HG13	1.80	0.62
25:BA:2801:C:OP1	28:BE:61:ARG:NH2	2.28	0.62
1:CA:266:G:H5''	1:CA:268:C:H41	1.64	0.62
1:CA:352:C:O2'	1:CA:354:G:OP1	2.14	0.62
54:D8:6:THR:HG22	54:D8:63:PRO:HD2	1.81	0.62
25:DA:2141:G:H2'	25:DA:2142:C:O4'	2.00	0.62
23:CW:74:C:N4	25:DA:2507:C:O2'	2.31	0.62
36:DQ:109:VAL:HG13	36:DQ:113:GLN:HB3	1.81	0.62
37:DR:104:ARG:HG3	37:DR:111:LEU:HD11	1.82	0.62
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.33	0.62
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.32	0.62
46:B0:18:ALA:HB3	46:B0:20:ARG:HH21	1.65	0.62
25:BA:493:G:OP1	53:B7:33:ARG:NH1	2.33	0.62
18:CR:56:THR:HB	18:CR:58:LEU:HD23	1.81	0.62
45:DZ:92:SER:OG	45:DZ:93:ASP:N	2.27	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1223:C:H2'	25:BA:1224:C:H6	1.65	0.62
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.81	0.62
4:CD:104:VAL:HG11	4:CD:146:ILE:HD13	1.82	0.62
25:DA:910:A:H62	36:DQ:12:GLN:HA	1.65	0.62
38:DS:14:VAL:O	38:DS:18:ILE:HG12	2.00	0.62
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.15	0.61
3:CC:47:LEU:HD12	3:CC:68:VAL:HG11	1.81	0.61
1:CA:377:G:OP1	16:CP:3:LYS:HD2	1.99	0.61
20:CT:57:ARG:HH12	20:CT:100:ILE:HD12	1.65	0.61
53:D7:34:ARG:NH1	53:D7:41:ARG:O	2.32	0.61
25:DA:2141:G:C6	25:DA:2150:U:O2	2.52	0.61
25:DA:886:C:O2'	25:DA:889:C:N4	2.32	0.61
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.35	0.61
8:AH:51:VAL:HG21	8:AH:60:ARG:HH11	1.65	0.61
14:AN:23:ARG:HH11	14:AN:30:ALA:HB2	1.64	0.61
49:B3:3:ARG:NH1	49:B3:60:GLU:OE2	2.29	0.61
25:BA:1425:A:H4'	25:BA:1426:G:OP2	2.00	0.61
43:BX:31:HIS:CD2	43:BX:33:LYS:H	2.18	0.61
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.33	0.61
27:DD:148:GLU:HB2	27:DD:151:LYS:HD2	1.82	0.61
1:AA:189(B):C:H42	1:AA:189(I):G:H1	1.48	0.61
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.15	0.61
25:BA:1284:G:OP2	61:BA:5106:HOH:O	2.16	0.61
1:CA:148:G:H2'	1:CA:149:A:H8	1.65	0.61
4:CD:165:MET:SD	4:CD:168:ARG:NH1	2.72	0.61
1:CA:942:G:H21	9:CI:124:GLN:NE2	1.98	0.61
23:CW:9:A:H5'	23:CW:46:7MG:HN22	1.64	0.61
25:DA:2121:G:H1	25:DA:2177:C:N4	1.97	0.61
1:CA:1422:G:O3'	34:DO:49:ARG:NH1	2.31	0.61
1:CA:1441:G:H5''	1:CA:1442:G:H5'	1.81	0.61
16:CP:71:ARG:HG3	16:CP:80:PHE:HE2	1.66	0.61
2:AB:53:ARG:NH2	2:AB:198:ASP:O	2.32	0.61
2:AB:93:VAL:HG21	2:AB:97:TRP:CD1	2.36	0.61
20:AT:60:GLU:HG3	20:AT:81:LYS:HD2	1.80	0.61
48:B2:65:ASN:OD1	48:B2:69:ARG:NH1	2.30	0.61
25:BA:1993:A:OP1	61:BA:4467:HOH:O	2.15	0.61
25:BA:2121:U:H3	25:BA:2212:G:H1	1.47	0.61
25:BA:288:U:O2'	25:BA:289:G:OP1	2.17	0.61
25:DA:2758:A:C2	25:DA:2759:G:H1'	2.36	0.61
25:DA:2843:G:N7	61:DA:4550:HOH:O	2.31	0.61
1:AA:100:C:H2'	1:AA:101:A:C8	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.16	0.61
19:AS:32:LYS:HA	19:AS:50:ALA:HB3	1.83	0.61
25:DA:2611:U:C4	51:D5:3:LYS:HG2	2.35	0.61
19:AS:68:GLY:H	50:B4:58:ARG:NH1	1.99	0.61
25:BA:2303:U:H2'	25:BA:2304:C:C6	2.36	0.61
4:CD:72:GLU:OE1	4:CD:207:TYR:OH	2.18	0.61
7:CG:32:ARG:HH12	7:CG:109:ASN:HD21	1.47	0.61
24:CX:21:A:N6	24:CX:46:G:H2'	2.16	0.61
25:DA:831:G:O2'	35:DP:38:GLN:NE2	2.34	0.61
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.83	0.61
3:AC:13:GLY:HA3	14:AN:57:ARG:NH2	2.16	0.61
1:AA:276:G:O3'	17:AQ:68:ARG:NH1	2.33	0.61
23:AW:18:G:O2'	23:AW:57:G:N2	2.24	0.61
31:BH:3:ARG:HG2	31:BH:6:ARG:HG2	1.82	0.61
36:BQ:108:GLY:HA3	45:BZ:116:VAL:HG13	1.82	0.61
38:BS:27:SER:HA	38:BS:88:ASP:HB3	1.82	0.61
1:CA:1004:A:N6	1:CA:1037:C:C2	2.69	0.61
1:CA:1030(A):G:H2'	1:CA:1030(C):G:OP2	2.00	0.61
1:CA:992:U:H3	1:CA:1044:A:H62	1.49	0.61
13:CM:88:ARG:HG3	13:CM:98:VAL:HG11	1.83	0.61
25:DA:2110:G:H4'	25:DA:2111:C:OP2	2.00	0.61
25:DA:307:G:N7	61:DA:4267:HOH:O	2.31	0.61
2:AB:93:VAL:HG21	2:AB:97:TRP:HD1	1.66	0.61
3:AC:162:GLN:NE2	22:AV:24:A:O2'	2.33	0.61
3:AC:8:ILE:HD13	3:AC:184:TYR:HB3	1.83	0.61
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.34	0.61
25:BA:1343:C:OP1	61:BA:4495:HOH:O	2.16	0.61
31:BH:56:SER:HB3	31:BH:61:HIS:ND1	2.16	0.61
1:CA:36:C:N4	61:CA:4168:HOH:O	2.33	0.61
19:CS:4:SER:HB3	19:CS:7:LYS:HG3	1.82	0.61
23:CY:9:A:H5''	23:CY:46:7MG:H1'	1.81	0.61
47:D1:7:ILE:HG23	47:D1:98:LEU:HD11	1.82	0.61
25:DA:644:A:H4'	25:DA:645:C:C5	2.36	0.61
1:AA:1381:U:H1'	7:AG:79:ARG:HG3	1.83	0.61
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.25	0.61
4:AD:128:VAL:N	4:AD:131:ARG:O	2.30	0.61
23:AW:1:G:O6	23:AW:72:C:N3	2.34	0.61
43:BX:35:THR:HG22	43:BX:38:GLU:H	1.65	0.61
19:CS:32:LYS:HA	19:CS:50:ALA:HB3	1.83	0.61
25:DA:1023:U:OP2	61:DA:4898:HOH:O	2.16	0.61
25:BA:1211:U:H2'	25:BA:1212:C:C6	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:148:G:H2'	1:CA:149:A:C8	2.36	0.60
2:CB:15:VAL:O	2:CB:17:PHE:N	2.34	0.60
29:DF:78:ILE:HA	29:DF:83:PHE:CD1	2.36	0.60
31:DH:99:VAL:N	31:DH:102:ALA:O	2.34	0.60
25:DA:2723:C:H5''	37:DR:1:MET:HE2	1.83	0.60
45:DZ:145:GLU:HG3	45:DZ:146:ILE:H	1.66	0.60
1:AA:1441:G:H5''	1:AA:1442:G:H5'	1.82	0.60
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.19	0.60
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.81	0.60
17:AQ:76:LEU:HD21	17:AQ:79:SER:HB2	1.83	0.60
43:BX:60:ARG:HH22	53:B7:47:ARG:HH22	1.49	0.60
25:BA:1071:G:C4	25:BA:1180:C:H1'	2.36	0.60
25:BA:354:A:H2	25:BA:1255:A:H2'	1.66	0.60
25:DA:2118:U:C4	25:DA:2149:G:H1'	2.37	0.60
29:DF:158:THR:O	29:DF:164:ARG:NH1	2.32	0.60
25:BA:956:A:H62	36:BQ:12:GLN:HA	1.66	0.60
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.84	0.60
50:D4:50:VAL:O	50:D4:52:THR:N	2.33	0.60
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.83	0.60
10:AJ:26:ALA:O	10:AJ:84:GLN:NE2	2.34	0.60
25:BA:1218:G:O2'	25:BA:1219:A:O4'	2.19	0.60
25:BA:1513:G:HO2'	25:BA:1593:C:HO2'	1.46	0.60
25:BA:1846:A:P	27:BD:54:ARG:HH22	2.23	0.60
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.17	0.60
19:CS:38:SER:HB2	19:CS:71:LEU:HD22	1.83	0.60
25:DA:1220:A:OP2	40:DU:19:LYS:NZ	2.31	0.60
25:DA:509:C:OP1	61:DA:4614:HOH:O	2.15	0.60
32:DI:27:ARG:HD2	47:D1:71:TYR:CE1	2.37	0.60
31:BH:86:GLU:OE2	31:BH:132:ARG:NH2	2.34	0.60
1:CA:1028:C:N3	1:CA:1033:G:O6	2.34	0.60
25:DA:1012:U:C5	33:DN:28:THR:HG21	2.37	0.60
1:AA:800:G:O6	61:AA:4021:HOH:O	2.12	0.60
25:BA:1159:U:H2'	25:BA:1160:G:C8	2.36	0.60
1:CA:1007:C:N3	1:CA:1022:G:O6	2.35	0.60
1:CA:1132:C:H2'	1:CA:1133:G:H8	1.65	0.60
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.82	0.60
25:DA:1355:G:O6	61:DA:4421:HOH:O	2.15	0.60
25:DA:993:G:H21	41:DV:89:GLN:HE22	1.50	0.60
25:BA:2166:U:O2'	25:BA:2167:C:H2'	2.01	0.60
25:BA:2173:G:H2'	25:BA:2174:G:C8	2.37	0.60
46:D0:12:ASN:HA	46:D0:14:ARG:HH21	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:299:A:N1	25:DA:322:A:O2'	2.28	0.60
45:DZ:55:HIS:CE1	45:DZ:135:GLU:HG3	2.36	0.60
1:AA:976:G:H5'	1:AA:1358:U:O2'	2.00	0.60
5:AE:151:LEU:HD22	8:AH:79:VAL:HG22	1.84	0.60
47:B1:7:ILE:HG23	47:B1:98:LEU:HD11	1.83	0.60
25:BA:1834:A:O2'	27:BD:259:THR:HG21	2.00	0.60
1:CA:17:U:H2'	1:CA:18:C:C6	2.37	0.60
1:CA:657:G:H21	15:CO:22:THR:HG1	1.49	0.60
47:D1:59:THR:O	47:D1:91:LYS:NZ	2.34	0.60
25:DA:1297:C:OP2	61:DA:4287:HOH:O	2.15	0.60
27:DD:69:ARG:NH2	27:DD:128:GLY:O	2.35	0.60
27:DD:85:ASP:OD2	27:DD:88:ARG:NH1	2.34	0.60
31:DH:3:ARG:HH22	31:DH:5:GLY:H	1.49	0.60
45:DZ:163:LEU:HG	45:DZ:165:VAL:HG22	1.83	0.60
26:BB:6:C:H2'	26:BB:7:G:H5''	1.83	0.60
27:BD:179:SER:O	27:BD:275:LYS:HB2	2.02	0.60
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.37	0.60
2:CB:84:GLU:HB3	2:CB:219:VAL:HG21	1.84	0.60
25:DA:1721:G:H8	25:DA:1741:A:H62	1.48	0.60
25:DA:392:C:OP1	61:DA:4693:HOH:O	2.16	0.60
25:DA:322:A:OP2	29:DF:169:ASN:HB2	2.02	0.60
30:DG:150:ASP:OD2	30:DG:153:ARG:NH1	2.35	0.60
20:AT:43:LEU:O	20:AT:47:GLY:N	2.35	0.60
45:BZ:4:ARG:NE	45:BZ:60:GLU:OE1	2.32	0.60
25:DA:987:G:O2'	25:DA:1000:A:N3	2.32	0.60
31:DH:7:LEU:HD12	31:DH:8:PRO:HD2	1.84	0.60
2:AB:84:GLU:HB3	2:AB:219:VAL:HG21	1.84	0.59
6:AF:42:GLU:OE1	6:AF:59:TYR:OH	2.13	0.59
14:AN:3:ARG:HH21	14:AN:3:ARG:HB3	1.66	0.59
1:AA:625:G:H4'	16:AP:16:HIS:CD2	2.36	0.59
1:CA:1001:A:H2'	1:CA:1001(A):G:H8	1.66	0.59
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.37	0.59
3:CC:30:ARG:HH21	14:CN:38:GLY:HA2	1.67	0.59
29:DF:21:ALA:CB	29:DF:22:ALA:HA	2.32	0.59
25:DA:2495:G:H5''	36:DQ:82:ARG:HG2	1.84	0.59
25:DA:2875:C:O2'	39:DT:2:ASN:OD1	2.19	0.59
4:AD:129:ASN:OD1	4:AD:145:GLU:N	2.33	0.59
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.84	0.59
12:AL:88:GLY:O	12:AL:99:HIS:HD2	1.84	0.59
19:AS:20:LEU:HD13	50:B4:69:LYS:HE2	1.84	0.59
25:BA:83:A:H5'	44:BY:8:LYS:HG2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:646:U:H2'	1:CA:647:C:C6	2.36	0.59
1:CA:811:C:N4	61:CA:4024:HOH:O	2.35	0.59
1:CA:1112:C:H1'	3:CC:179:ARG:HG2	1.83	0.59
9:CI:53:VAL:O	9:CI:55:ALA:N	2.35	0.59
23:CW:29:G:H1	23:CW:41:C:N4	1.99	0.59
25:DA:1639:U:H2'	25:DA:1640:C:H5''	1.84	0.59
51:B5:11:THR:HG23	51:B5:15:ARG:HB3	1.83	0.59
25:BA:1201:A:OP1	40:BU:55:ARG:HD3	2.02	0.59
41:BV:76:LYS:HB2	41:BV:81:TYR:HB3	1.84	0.59
4:CD:98:GLU:HG2	4:CD:189:PRO:HG2	1.83	0.59
35:DP:121:LYS:HB3	35:DP:123:LEU:HG	1.84	0.59
38:DS:25:ARG:NH1	38:DS:42:ASP:OD1	2.35	0.59
25:BA:553:A:N1	25:BA:2064:A:H2'	2.16	0.59
1:CA:934:C:OP1	61:CA:4152:HOH:O	2.17	0.59
2:CB:91:PRO:HD3	2:CB:154:LEU:HD12	1.84	0.59
23:CY:33:U:H2'	23:CY:35:A:OP2	2.01	0.59
25:DA:2169:A:H2'	25:DA:2170:A:C8	2.37	0.59
25:DA:784:A:C6	27:DD:229:VAL:HG11	2.37	0.59
54:B8:42:ARG:HD2	61:B8:207:HOH:O	2.02	0.59
44:BY:102:CYS:SG	44:BY:103:GLY:N	2.75	0.59
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.37	0.59
25:DA:2139:C:N4	25:DA:2152:G:H1	2.00	0.59
25:DA:303:U:H2'	25:DA:304:G:H8	1.67	0.59
25:BA:302:A:H2'	25:BA:303:C:C6	2.38	0.59
45:BZ:152:ALA:HB2	45:BZ:171:ILE:HG21	1.84	0.59
1:CA:450:G:OP1	16:CP:43:LYS:NZ	2.34	0.59
23:CY:62:C:H2'	23:CY:63:G:C8	2.38	0.59
25:DA:1796:U:H2'	25:DA:1797:C:C6	2.38	0.59
25:DA:2137:C:H42	25:DA:2154:G:H1	1.51	0.59
25:DA:2135:A:H61	25:DA:2157:G:N2	2.00	0.59
25:BA:611:U:H2'	25:BA:612:C:C6	2.37	0.59
1:CA:976:G:OP1	14:CN:32:SER:N	2.33	0.59
25:DA:613:G:O2'	25:DA:614(C):A:N1	2.30	0.59
30:DG:136:ARG:HD2	30:DG:137:GLU:HG3	1.85	0.59
44:DY:102:CYS:SG	44:DY:103:GLY:N	2.76	0.59
1:AA:97:G:O2'	1:AA:98:G:H8	1.86	0.59
25:BA:2584:A:N7	28:BE:144:ARG:HD2	2.18	0.59
6:CF:45:LEU:HD12	6:CF:59:TYR:HD2	1.68	0.59
10:CJ:7:LYS:HE3	10:CJ:71:LEU:HD13	1.84	0.59
27:DD:132:PRO:HG2	27:DD:135:PHE:CD2	2.37	0.59
3:AC:57:ILE:HG12	3:AC:66:VAL:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:155:LEU:HD13	4:AD:158:ILE:HD11	1.84	0.59
1:CA:1128:C:O2'	1:CA:1129:C:OP1	2.17	0.59
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.38	0.59
1:CA:316:G:OP2	1:CA:351:G:O2'	2.20	0.59
4:CD:153:ARG:HB2	4:CD:181:MET:SD	2.43	0.59
25:DA:1800:C:OP2	27:DD:183:ARG:NH2	2.35	0.59
25:DA:2140:C:H1'	25:DA:2152:G:N2	2.18	0.59
28:DE:72:VAL:HG13	28:DE:73:GLU:O	2.03	0.59
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.10	0.59
45:BZ:24:LEU:HB2	45:BZ:41:LEU:HD23	1.84	0.59
1:CA:448:A:P	1:CA:485:G:H22	2.26	0.59
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	1.84	0.59
25:DA:2651:C:H42	25:DA:2669:G:H1	1.51	0.59
25:DA:957:A:H5'	36:DQ:76:LYS:HG3	1.84	0.59
30:DG:41:GLN:HE22	30:DG:153:ARG:HB3	1.66	0.59
38:DS:71:ARG:NH1	38:DS:107:GLU:OE1	2.36	0.59
1:AA:1008:C:N3	1:AA:1021:G:C6	2.71	0.58
1:AA:1125:U:H4'	10:AJ:5:ARG:NH2	2.18	0.58
25:BA:2045:G:H5'	25:BA:2629:C:H4'	1.84	0.58
27:BD:17:THR:O	27:BD:211:ARG:NH2	2.36	0.58
31:BH:7:LEU:HD12	31:BH:8:PRO:HD2	1.85	0.58
1:CA:1059:C:OP2	3:CC:199:LYS:NZ	2.33	0.58
9:CI:50:LEU:HB2	9:CI:56:LEU:HD23	1.84	0.58
25:DA:927:G:H2'	25:DA:928:G:O4'	2.02	0.58
28:BE:3:GLY:HA3	28:BE:81:ILE:HD12	1.83	0.58
10:CJ:30:SER:O	10:CJ:81:THR:HG23	2.04	0.58
24:CX:76:A:OP1	61:CX:4003:HOH:O	2.17	0.58
29:DF:116:ASP:OD1	29:DF:119:ARG:NH2	2.35	0.58
5:AE:143:ARG:NH1	8:AH:77:GLU:OE1	2.36	0.58
24:AX:59:A:H2'	24:AX:60:U:H5'	1.83	0.58
25:BA:1232:G:H5''	41:BV:81:TYR:CE1	2.37	0.58
23:CY:36:A:H2'	23:CY:37:MIA:O4'	2.03	0.58
25:DA:2646:C:OP2	25:DA:2732:G:O2'	2.17	0.58
25:BA:1452:U:H2'	25:BA:1453:C:C6	2.38	0.58
28:BE:47:VAL:HG23	28:BE:84:PHE:O	2.03	0.58
1:CA:405:U:O4	4:CD:2:GLY:N	2.36	0.58
7:CG:27:ILE:HD12	7:CG:40:ALA:HA	1.85	0.58
25:DA:1359:A:H61	25:DA:1372:U:H3	1.50	0.58
25:DA:1803:A:O2'	27:DD:259:THR:HG21	2.03	0.58
32:DI:31:LEU:HD21	32:DI:38:LEU:HG	1.84	0.58
8:AH:73:ASP:OD1	8:AH:75:ARG:HD3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1218:G:O2'	25:BA:1219:A:O5'	2.21	0.58
17:AQ:45:HIS:CD2	17:AQ:47:PRO:HG3	2.39	0.58
50:B4:61:ARG:HG3	50:B4:62:ARG:N	2.19	0.58
25:BA:2130:C:H2'	25:BA:2131:U:C6	2.37	0.58
32:BI:27:ARG:HD2	47:B1:71:TYR:CE1	2.39	0.58
28:BE:111:ARG:HG3	28:BE:160:TYR:CD2	2.39	0.58
1:CA:545:C:OP2	4:CD:65:ARG:NH2	2.37	0.58
25:DA:613:G:N2	25:DA:614(C):A:O2'	2.37	0.58
25:DA:871:U:O2	25:DA:906:G:N2	2.30	0.58
33:DN:15:LEU:HB2	33:DN:135:PRO:HB2	1.85	0.58
1:AA:997:U:H3	1:AA:1044:A:H61	1.51	0.58
13:CM:33:ALA:HA	13:CM:59:TYR:CE2	2.39	0.58
25:DA:1204:A:H5'	25:DA:1206:G:H1'	1.86	0.58
25:DA:1250:G:OP2	35:DP:21:ARG:NH1	2.37	0.58
25:DA:1711:C:H2'	25:DA:1712:C:C6	2.38	0.58
34:DO:107:ARG:CZ	39:DT:36:GLU:HG2	2.34	0.58
1:AA:200:G:H1	1:AA:217:C:N4	2.02	0.58
50:B4:57:GLU:HB3	50:B4:58:ARG:HG2	1.86	0.58
25:BA:1827:U:H2'	25:BA:1828:C:C6	2.39	0.58
25:BA:1272:A:OP1	41:BV:84:LYS:HE2	2.04	0.58
25:DA:972:G:OP2	25:DA:973:A:O2'	2.17	0.58
25:BA:303:C:H42	25:BA:385:G:H1	1.51	0.58
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.85	0.58
12:CL:88:GLY:O	12:CL:99:HIS:HD2	1.85	0.58
52:D6:14:THR:OG1	52:D6:48:VAL:O	2.22	0.58
25:DA:2291:U:H2'	25:DA:2292:C:C6	2.39	0.58
25:DA:900:A:H2'	25:DA:901:A:C8	2.38	0.58
26:DB:81:G:H1	26:DB:96:U:H3	1.51	0.58
9:AI:9:ARG:HG2	9:AI:14:VAL:HG12	1.86	0.57
25:BA:2152:U:H2'	25:BA:2153:G:N2	2.19	0.57
25:BA:2820:A:N6	25:BA:2900:G:O2'	2.36	0.57
32:BI:126:TYR:HB2	32:BI:142:VAL:HG23	1.86	0.57
25:BA:83:A:H5''	44:BY:8:LYS:HE3	1.86	0.57
1:CA:517:G:N1	1:CA:533:A:OP2	2.28	0.57
1:CA:775:G:N2	1:CA:804:U:O4	2.36	0.57
2:CB:95:GLN:HG3	2:CB:147:LYS:HD3	1.86	0.57
25:DA:131:G:OP1	61:DA:4107:HOH:O	2.17	0.57
3:CC:18:TRP:H	3:CC:18:TRP:HE3	1.52	0.57
8:CH:64:LYS:HG2	8:CH:79:VAL:HG21	1.86	0.57
20:CT:13:LEU:H	20:CT:13:LEU:HD12	1.68	0.57
24:CX:49:G:H1	24:CX:65:C:N4	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2379:G:O2'	38:DS:17:ARG:NH2	2.22	0.57
25:DA:324:A:N6	25:DA:338:G:O2'	2.37	0.57
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.40	0.57
50:B4:53:GLU:O	50:B4:55:ARG:N	2.35	0.57
25:BA:129:G:OP1	61:BA:4198:HOH:O	2.17	0.57
11:CK:31:THR:HG23	11:CK:42:TRP:HB3	1.85	0.57
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.04	0.57
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.40	0.57
14:AN:27:CYS:SG	14:AN:29:ARG:HB2	2.44	0.57
25:BA:2162:C:C4	25:BA:2173:G:N1	2.71	0.57
25:BA:2299:A:N6	25:BA:2356:U:H3	1.98	0.57
39:BT:24:PRO:HA	39:BT:49:VAL:HG22	1.86	0.57
1:CA:1001:A:H2'	1:CA:1001(A):G:C8	2.38	0.57
25:DA:570:G:H2'	25:DA:2030:A:C5	2.39	0.57
25:DA:833:U:O2	35:DP:55:ARG:NH2	2.36	0.57
24:AX:21:A:N6	24:AX:46:G:H2'	2.19	0.57
25:BA:2227:G:H5'	25:BA:2228:G:N7	2.19	0.57
1:CA:1029:C:N4	1:CA:1032:G:C5	2.72	0.57
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.70	0.57
27:DD:26:LYS:NZ	27:DD:30:GLU:OE1	2.31	0.57
38:DS:27:SER:HA	38:DS:88:ASP:HB3	1.87	0.57
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.27	0.57
23:AY:63:G:H2'	23:AY:64:A:O4'	2.05	0.57
35:BP:63:PRO:HG2	54:B8:25:MET:HB2	1.85	0.57
25:DA:1400:G:H2'	25:DA:1401:G:C8	2.38	0.57
25:DA:1539:G:H2'	25:DA:1540:U:O4'	2.04	0.57
35:DP:97:PRO:HD3	35:DP:126:VAL:O	2.04	0.57
1:AA:1191:A:H5''	3:AC:4:LYS:NZ	2.20	0.57
15:AO:11:VAL:HG21	15:AO:34:LEU:HD22	1.86	0.57
25:BA:2126:G:H2'	25:BA:2127:C:C6	2.40	0.57
25:BA:667:G:H21	25:BA:671:A:H2	1.52	0.57
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.03	0.57
11:CK:110:ASP:HB3	18:CR:85:LEU:HB3	1.86	0.57
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.70	0.57
50:D4:61:ARG:O	50:D4:63:TYR:N	2.38	0.57
25:DA:1400:G:H2'	25:DA:1401:G:H8	1.70	0.57
25:DA:2142:C:H2'	25:DA:2143:C:C6	2.40	0.57
30:DG:39:ILE:HG12	30:DG:157:ILE:HG12	1.87	0.57
1:AA:222:U:H2'	1:AA:223:U:C6	2.39	0.57
2:AB:178:ARG:HG2	8:AH:72:PRO:HA	1.85	0.57
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HD23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:20:U:H4'	23:AY:21:A:OP1	2.04	0.57
38:BS:20:ARG:NH2	46:B0:48:GLY:O	2.37	0.57
37:BR:28:LEU:HD12	37:BR:48:VAL:HG21	1.87	0.57
7:CG:15:ASP:OD2	7:CG:44:TYR:OH	2.18	0.57
7:CG:69:VAL:HG21	7:CG:104:LEU:HD11	1.87	0.57
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.38	0.57
48:D2:35:LEU:HD12	48:D2:53:LEU:HD12	1.87	0.57
25:DA:784:A:C5	27:DD:229:VAL:HG11	2.40	0.57
38:DS:87:PHE:CE1	38:DS:102:ALA:HB2	2.40	0.57
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.40	0.57
1:AA:78:G:C6	1:AA:91:C:N4	2.73	0.57
1:AA:7:G:O2'	5:AE:120:THR:O	2.23	0.57
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.37	0.57
25:BA:572:A:H61	41:BV:19:LYS:H	1.53	0.57
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.37	0.57
1:CA:1317:C:OP1	14:CN:17:LYS:HG2	2.05	0.57
1:CA:673:G:H2'	1:CA:674:G:C8	2.40	0.57
13:CM:81:LEU:HD13	13:CM:88:ARG:HG2	1.87	0.57
25:DA:250:G:P	54:D8:13:ARG:HH22	2.28	0.57
25:DA:1359:A:N6	25:DA:1372:U:H3	2.03	0.57
25:DA:1530:C:N4	25:DA:1539:G:H1	2.03	0.57
25:DA:639:U:H2'	25:DA:640:C:C6	2.40	0.57
29:DF:11:VAL:HG22	29:DF:125:LEU:HB2	1.86	0.57
34:DO:2:ILE:HB	34:DO:33:ALA:HB3	1.87	0.57
1:AA:972:C:OP1	61:AA:4158:HOH:O	2.18	0.57
25:BA:1027:A:OP1	61:BA:4709:HOH:O	2.18	0.57
25:BA:2736:C:OP1	37:BR:3:HIS:ND1	2.22	0.57
25:BA:613:A:OP1	29:BF:95:ARG:NH1	2.38	0.57
27:BD:108:PRO:HB3	27:BD:143:HIS:CE1	2.40	0.57
29:BF:53:THR:HG22	29:BF:55:GLY:H	1.70	0.57
35:BP:81:GLN:NE2	35:BP:105:LEU:O	2.36	0.57
1:CA:1392:G:H21	1:CA:1502:A:H8	1.50	0.57
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.86	0.57
7:CG:78:ARG:NH1	7:CG:79:ARG:HH12	2.03	0.57
10:CJ:78:ASN:O	10:CJ:80:LYS:N	2.38	0.57
26:DB:15:A:OP2	26:DB:69:G:N2	2.37	0.57
25:BA:1346:U:H4'	25:BA:1347:A:C5'	2.35	0.56
25:BA:1475:G:H2'	25:BA:1476:C:C6	2.39	0.56
25:DA:528:A:C2	25:DA:2042:A:H2'	2.40	0.56
34:DO:87:ILE:HD12	34:DO:91:LEU:HA	1.87	0.56
36:DQ:32:TYR:OH	36:DQ:111:GLU:OE1	2.13	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:110:GLY:O	45:DZ:146:ILE:HG13	2.04	0.56
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.06	0.56
1:AA:405:U:OP2	4:AD:3:ARG:NH2	2.38	0.56
1:AA:838:G:H2'	1:AA:839:U:H2'	1.86	0.56
1:AA:977:A:H1'	1:AA:982:U:O4	2.06	0.56
50:B4:33:VAL:HG12	50:B4:34:GLU:H	1.71	0.56
25:BA:1065:U:O2'	25:BA:1067:A:H2	1.88	0.56
25:BA:2840:G:OP1	28:BE:76:ARG:NH2	2.38	0.56
25:BA:346:A:OP1	29:BF:168:ARG:HD2	2.05	0.56
31:BH:113:VAL:HG11	31:BH:151:ILE:HD13	1.87	0.56
25:BA:2331:G:H22	38:BS:3:ARG:NE	2.03	0.56
2:CB:118:LEU:HB3	2:CB:142:LEU:HD12	1.87	0.56
25:DA:1204:A:N6	25:DA:1240:U:H2'	2.20	0.56
25:DA:1430:C:H2'	25:DA:1431:U:C6	2.39	0.56
25:DA:2138:C:N4	25:DA:2153:G:H1	2.03	0.56
24:CX:76:A:H5'	25:DA:2585:U:C5	2.41	0.56
34:DO:115:VAL:HG13	34:DO:121:VAL:HG21	1.87	0.56
25:BA:1613:A:OP1	27:BD:211:ARG:NH1	2.39	0.56
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.20	0.56
20:CT:92:LEU:HA	20:CT:95:ALA:HB3	1.87	0.56
23:CY:62:C:H2'	23:CY:63:G:H8	1.69	0.56
25:DA:1300:U:H4'	25:DA:1301:A:H5'	1.88	0.56
31:DH:96:ALA:HB1	31:DH:103:LEU:HD11	1.87	0.56
3:AC:33:LEU:HD21	14:AN:53:LEU:HD22	1.85	0.56
5:AE:79:GLU:HG3	5:AE:93:PRO:HD2	1.87	0.56
23:AY:33:U:H2'	23:AY:35:A:OP2	2.04	0.56
25:BA:1513:G:H2'	25:BA:1594:C:N4	2.20	0.56
25:BA:1817:A:H1'	25:BA:1960:A:N6	2.20	0.56
25:BA:2310:A:H2'	25:BA:2311:G:O4'	2.05	0.56
1:CA:1151:A:O2'	1:CA:1152:A:H8	1.88	0.56
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.87	0.56
8:CH:41:ARG:NH2	8:CH:123:GLU:OE2	2.38	0.56
19:CS:30:LEU:HA	19:CS:48:THR:O	2.06	0.56
52:D6:6:ARG:NH1	52:D6:26:ASN:HB2	2.20	0.56
25:DA:2506:U:OP1	28:DE:144:ARG:NH2	2.38	0.56
25:DA:994:C:OP2	40:DU:54:LYS:NZ	2.33	0.56
38:DS:68:GLN:HE21	38:DS:71:ARG:HD3	1.69	0.56
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.27	0.56
25:BA:273:G:H4'	25:BA:274:U:OP1	2.04	0.56
29:BF:140:LEU:HD21	29:BF:170:LEU:HD11	1.86	0.56
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.16	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CO:25:THR:HG21	15:CO:70:LEU:HB2	1.86	0.56
25:DA:1434:A:H61	25:DA:1558:A:H62	1.53	0.56
25:DA:1594:G:H2'	25:DA:1595:G:O4'	2.05	0.56
25:DA:2193:G:H2'	25:DA:2194:G:H8	1.71	0.56
1:AA:1007:C:N3	1:AA:1022:G:O6	2.37	0.56
2:AB:15:VAL:HG21	2:AB:209:ARG:HG2	1.87	0.56
3:AC:54:ARG:NH1	3:AC:56:ASP:OD2	2.38	0.56
25:BA:173:C:H2'	25:BA:174:U:C6	2.40	0.56
25:DA:1231:G:H2'	25:DA:1232:G:C8	2.41	0.56
25:DA:1518:U:H2'	25:DA:1519:G:O4'	2.05	0.56
41:DV:43:GLU:OE2	41:DV:43:GLU:N	2.37	0.56
1:AA:17:U:H2'	1:AA:18:C:C6	2.40	0.56
57:AA:3231:PCY:O26	57:AA:3231:PCY:O36	2.22	0.56
4:AD:108:LEU:HD22	4:AD:174:LEU:HD13	1.88	0.56
15:AO:64:ARG:HH11	15:AO:64:ARG:HB3	1.70	0.56
18:AR:56:THR:HB	18:AR:58:LEU:HD23	1.87	0.56
25:BA:2825:C:H5'	51:B5:29:THR:HG21	1.87	0.56
25:BA:1428:G:N7	61:BA:5233:HOH:O	2.33	0.56
29:BF:157:VAL:HB	29:BF:194:MET:HG2	1.88	0.56
36:BQ:111:GLU:OE1	36:BQ:133:ARG:NH2	2.38	0.56
1:CA:201:C:N4	1:CA:216:G:H1	2.04	0.56
1:CA:685:G:N1	1:CA:686:U:O4	2.39	0.56
9:CI:18:PHE:HD2	9:CI:62:TYR:HD2	1.52	0.56
14:CN:12:ARG:HE	14:CN:14:PRO:HB3	1.71	0.56
23:CW:23:A:H2'	23:CW:24:G:C8	2.40	0.56
25:DA:2611:U:H5'	25:DA:2611:U:H6	1.71	0.56
30:DG:43:LEU:HD11	30:DG:153:ARG:HG2	1.86	0.56
23:AW:4:C:H2'	23:AW:5:G:H8	1.71	0.56
1:CA:1014:A:OP1	19:CS:18:LYS:NZ	2.30	0.56
18:CR:32:ARG:HA	18:CR:69:THR:HG21	1.86	0.56
36:DQ:111:GLU:O	36:DQ:115:MET:HG2	2.05	0.56
1:AA:924:C:O2'	1:AA:1502:A:N6	2.37	0.56
23:AY:19:G:H3'	23:AY:20:U:C6	2.39	0.56
25:BA:1084:C:H42	25:BA:1163:G:H1	1.54	0.56
19:CS:22:LEU:HD22	19:CS:31:ILE:HD11	1.86	0.56
25:DA:1203:G:OP2	25:DA:1204:A:O2'	2.20	0.56
25:DA:131:G:OP1	61:DA:4106:HOH:O	2.18	0.56
29:DF:167:ALA:HB1	29:DF:173:VAL:HG11	1.87	0.56
25:DA:1226:A:OP1	41:DV:84:LYS:HE2	2.05	0.56
52:B6:35:GLU:OE2	52:B6:50:ARG:NH1	2.39	0.56
25:BA:2289:G:OP2	46:B0:10:THR:HG21	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BE:24:THR:HG22	28:BE:186:GLY:O	2.06	0.56
2:CB:87:ARG:HH12	2:CB:230:VAL:HG11	1.70	0.56
11:CK:81:ASP:OD1	11:CK:107:SER:OG	2.21	0.56
23:CW:39:PSU:H2'	23:CW:40:C:H6	1.71	0.56
25:DA:649:G:H4'	54:D8:46:ARG:HH22	1.70	0.56
25:DA:1414:G:N2	25:DA:1588:C:O2	2.37	0.56
28:DE:72:VAL:HA	28:DE:73:GLU:HB3	1.88	0.56
37:DR:56:LYS:NZ	37:DR:90:ARG:O	2.39	0.56
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.88	0.56
23:AW:8:4SU:H6	23:AW:8:4SU:O5'	2.06	0.56
25:BA:2157:A:N1	25:BA:2178:G:O2'	2.32	0.56
25:BA:796:C:OP2	61:BA:5333:HOH:O	2.18	0.56
29:BF:125:LEU:HD12	29:BF:194:MET:HB2	1.88	0.56
38:BS:14:VAL:O	38:BS:18:ILE:HG12	2.06	0.56
1:CA:1029:C:C4	1:CA:1033:G:C6	2.94	0.56
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.41	0.56
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.88	0.56
13:CM:92:HIS:CE1	13:CM:98:VAL:HG21	2.41	0.56
25:DA:1721:G:N1	25:DA:1739:U:OP2	2.39	0.56
25:DA:1798:U:OP2	27:DD:274:ARG:NH2	2.39	0.56
25:DA:2303:G:O2'	30:DG:132:ASN:HB2	2.06	0.56
45:DZ:120:ILE:HG13	45:DZ:173:ALA:HB3	1.88	0.56
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.74	0.55
3:AC:17:ASP:O	3:AC:54:ARG:NH2	2.40	0.55
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.87	0.55
25:BA:795:G:H2'	25:BA:797:A:OP2	2.06	0.55
1:CA:1051:C:H2'	1:CA:1052:U:C6	2.41	0.55
1:CA:1442(A):G:C8	39:DT:118:ARG:HG2	2.41	0.55
1:CA:45:U:H2'	1:CA:46:G:C8	2.42	0.55
1:CA:1073:U:O2	2:CB:104:ASN:ND2	2.38	0.55
2:CB:189:ASP:N	2:CB:189:ASP:OD1	2.34	0.55
45:DZ:33:LEU:HD11	45:DZ:90:VAL:HG21	1.87	0.55
1:AA:60:A:H4'	1:AA:61:G:H5'	1.88	0.55
32:BI:72:LEU:O	32:BI:74:ASN:N	2.39	0.55
1:CA:1122:U:N3	1:CA:1123:A:N7	2.55	0.55
11:CK:92:GLU:HB3	11:CK:96:ARG:HH21	1.72	0.55
25:DA:1300:U:H4'	25:DA:1301:A:C5'	2.37	0.55
25:DA:27:G:N2	25:DA:512:G:H1'	2.20	0.55
27:DD:242:ARG:N	27:DD:242:ARG:HD3	2.20	0.55
25:BA:559:U:H2'	25:BA:560:C:C6	2.42	0.55
37:BR:96:ARG:NH1	37:BR:118:GLU:OE2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:352:C:OP2	61:CA:4054:HOH:O	2.17	0.55
1:CA:838:G:N2	1:CA:848:C:N3	2.52	0.55
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	1.88	0.55
19:CS:41:VAL:HG12	19:CS:43:GLU:H	1.71	0.55
20:CT:43:LEU:O	20:CT:47:GLY:N	2.39	0.55
25:DA:1406:U:H2'	25:DA:1407:C:C6	2.41	0.55
25:DA:2177:C:H2'	25:DA:2178:C:O4'	2.06	0.55
25:DA:330:A:HO2'	25:DA:331:A:H8	1.53	0.55
25:DA:878:A:N6	25:DA:899:A:O2'	2.39	0.55
27:DD:218:ARG:HB3	27:DD:219:PRO:HD2	1.88	0.55
36:DQ:37:LEU:HD21	36:DQ:130:LYS:HE2	1.89	0.55
1:AA:1392:G:N2	1:AA:1502:A:C8	2.74	0.55
25:BA:431:C:H4'	25:BA:432:U:H5'	1.87	0.55
25:BA:641:G:OP1	29:BF:40:GLN:HG2	2.07	0.55
1:CA:1469:G:H2'	1:CA:1470:G:C8	2.42	0.55
2:CB:98:LEU:H	2:CB:98:LEU:HD22	1.71	0.55
8:CH:69:ARG:NH2	8:CH:75:ARG:O	2.39	0.55
25:DA:2273:A:H2'	25:DA:2274:A:C8	2.41	0.55
1:AA:356:A:N3	1:AA:368:U:O2'	2.33	0.55
1:AA:715:A:H2'	1:AA:716:A:C8	2.41	0.55
1:AA:975:A:H8	1:AA:975:A:H5'	1.70	0.55
9:AI:22:GLY:N	9:AI:58:HIS:O	2.31	0.55
25:BA:1735:U:O2	25:BA:1747:A:H5'	2.06	0.55
25:BA:661:G:OP1	35:BP:132:LYS:HE2	2.07	0.55
25:DA:1266:G:O2'	25:DA:2012:G:O6	2.20	0.55
35:DP:38:GLN:O	35:DP:39:LYS:HB3	2.05	0.55
25:DA:2296:U:OP2	38:DS:9:ARG:NH2	2.39	0.55
1:AA:165:C:H2'	1:AA:166:G:C8	2.42	0.55
1:AA:509:A:O2'	1:AA:510:A:OP1	2.18	0.55
6:AF:91:VAL:HG11	18:AR:72:ARG:NH1	2.20	0.55
47:B1:89:GLU:O	47:B1:93:GLU:HG2	2.07	0.55
25:BA:333:G:N3	25:BA:353:G:O2'	2.36	0.55
32:BI:93:THR:OG1	32:BI:96:ASP:OD1	2.16	0.55
61:BA:5082:HOH:O	35:BP:39:LYS:HE3	2.06	0.55
1:CA:1006:C:H2'	1:CA:1007:C:C6	2.41	0.55
1:CA:677:U:H3	1:CA:713:G:H22	1.53	0.55
25:DA:143:G:H4'	43:DX:35:THR:HG21	1.87	0.55
31:DH:30:LYS:HG3	31:DH:80:SER:O	2.06	0.55
25:BA:1222:A:H2'	25:BA:1222:A:N3	2.21	0.55
25:BA:906:G:O2'	25:BA:962:G:O6	2.21	0.55
1:CA:1469:G:H2'	1:CA:1470:G:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:814:A:H2'	1:CA:816:A:H5''	1.87	0.55
23:CW:29:G:H2'	23:CW:30:G:H8	1.72	0.55
1:AA:1025:U:C2	1:AA:1036:G:O6	2.59	0.55
1:AA:407:G:OP1	4:AD:115:ARG:NH2	2.39	0.55
4:AD:190:ASP:HB2	4:AD:193:ASP:OD2	2.07	0.55
25:BA:206:G:OP2	61:BA:5143:HOH:O	2.18	0.55
26:BB:66:A:H61	26:BB:109:C:H5'	1.71	0.55
1:CA:1010:G:H2'	1:CA:1011:G:H8	1.71	0.55
3:CC:37:GLN:HE22	3:CC:40:ARG:HD2	1.72	0.55
14:CN:23:ARG:NH1	14:CN:30:ALA:HB2	2.21	0.55
24:CX:19:G:H4'	24:CX:20:U:OP2	2.07	0.55
25:DA:1579:A:H2'	25:DA:1580:A:C8	2.42	0.55
25:DA:2022:U:O2'	25:DA:2617:C:H5'	2.07	0.55
25:DA:2683:C:P	39:DT:53:ARG:HH22	2.30	0.55
1:AA:1414:U:H3	1:AA:1486:G:H1	1.54	0.55
50:B4:63:TYR:N	50:B4:64:GLY:HA2	2.20	0.55
25:BA:139:A:H8	25:BA:1454:C:O2'	1.90	0.55
25:BA:272:U:OP1	32:BI:50:ARG:NH1	2.40	0.55
25:BA:479:C:O2	25:BA:483:A:O2'	2.23	0.55
25:BA:704:U:H2'	25:BA:705:C:C6	2.42	0.55
1:CA:1370:G:O6	61:CA:4006:HOH:O	2.16	0.55
3:CC:7:PRO:O	3:CC:11:ARG:NH1	2.38	0.55
25:DA:191:A:H2'	25:DA:192:C:C6	2.41	0.55
25:DA:674:G:H1'	29:DF:74:ARG:HD3	1.89	0.55
42:DW:4:LYS:HB2	42:DW:106:ILE:HG12	1.89	0.55
43:DX:31:HIS:CD2	43:DX:33:LYS:H	2.24	0.55
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.30	0.55
5:AE:151:LEU:HD11	8:AH:77:GLU:HG2	1.88	0.55
5:AE:91:LEU:HG	5:AE:118:ILE:HD11	1.89	0.55
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.39	0.55
20:AT:36:LEU:HD13	20:AT:58:LYS:HG3	1.88	0.55
25:BA:1873:G:O2'	27:BD:253:GLN:NE2	2.39	0.55
33:BN:15:LEU:HD12	33:BN:137:LYS:HG3	1.89	0.55
1:CA:1121:U:C4	1:CA:1122:U:C4	2.96	0.55
3:CC:134:ILE:HG23	3:CC:151:VAL:HB	1.88	0.55
9:CI:23:ASN:HD22	9:CI:25:LYS:HG2	1.72	0.55
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HB3	1.89	0.55
50:D4:59:PHE:HA	50:D4:60:GLN:C	2.27	0.55
25:DA:2641:G:H5''	33:DN:76:SER:HB3	1.88	0.55
25:DA:829:A:N7	25:DA:2247:A:O2'	2.37	0.55
40:DU:49:HIS:HA	40:DU:52:ARG:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DX:8:ILE:O	48:D2:36:ARG:NH2	2.40	0.55
1:AA:1007:C:H2'	1:AA:1008:C:H5''	1.88	0.54
9:AI:21:PRO:HA	9:AI:59:PHE:HA	1.90	0.54
1:CA:76:C:H42	1:CA:93:G:H1	1.55	0.54
25:DA:2666:C:N4	31:DH:108:GLY:O	2.39	0.54
31:DH:80:SER:OG	31:DH:81:GLU:N	2.40	0.54
1:AA:69:G:H2'	1:AA:70:G:C8	2.42	0.54
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.89	0.54
3:AC:164:ARG:NH1	3:AC:166:GLU:OE1	2.40	0.54
24:AX:19:G:H4'	24:AX:20:U:OP2	2.07	0.54
23:AY:40:C:H2'	23:AY:41:C:H6	1.72	0.54
29:BF:14:PRO:HD2	29:BF:127:GLU:OE2	2.07	0.54
34:BO:104:ARG:CZ	39:BT:34:VAL:HG21	2.37	0.54
34:BO:64:ARG:NH1	34:BO:81:ASP:OD1	2.40	0.54
35:BP:1:MET:HE3	35:BP:5:ASP:HB3	1.89	0.54
23:CW:51:U:H2'	23:CW:52:G:H8	1.72	0.54
23:CY:67:C:H2'	23:CY:68:C:C6	2.42	0.54
23:CY:9:A:O3'	23:CY:45:U:O2'	2.25	0.54
25:DA:829:A:N7	25:DA:2248:C:H5'	2.22	0.54
26:DB:19:G:H2'	26:DB:20:C:O4'	2.06	0.54
25:DA:896:A:H62	45:DZ:146:ILE:HD13	1.72	0.54
1:AA:153:C:H2'	1:AA:154:C:C6	2.42	0.54
1:AA:165:C:H2'	1:AA:166:G:H8	1.72	0.54
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.41	0.54
25:BA:714:U:O2	54:B8:2:PRO:HD2	2.06	0.54
39:BT:112:ARG:HG3	39:BT:115:ARG:NH2	2.23	0.54
1:CA:664:G:H22	1:CA:741:G:H1	1.53	0.54
25:DA:807:U:O2'	25:DA:2060:A:N1	2.40	0.54
26:DB:66:A:N6	26:DB:109:C:H5'	2.14	0.54
1:AA:1112:C:H1'	3:AC:179:ARG:HG2	1.88	0.54
1:AA:637:G:H2'	1:AA:638:G:H8	1.71	0.54
1:AA:749:C:H2'	1:AA:750:G:H8	1.72	0.54
1:AA:731:G:H5'	1:AA:766:A:H4'	1.89	0.54
4:AD:98:GLU:HG2	4:AD:189:PRO:HG2	1.88	0.54
25:BA:2146:G:H1	25:BA:2196:C:N4	2.05	0.54
34:BO:80:ASP:OD1	39:BT:64:ARG:NH2	2.40	0.54
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.23	0.54
1:CA:1183:A:O2'	1:CA:1184:G:OP1	2.22	0.54
1:CA:976:G:H5'	1:CA:1358:U:O2'	2.07	0.54
23:CW:51:U:H2'	23:CW:52:G:C8	2.42	0.54
25:DA:1889:A:H2'	25:DA:1890:A:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2167:U:H2'	25:DA:2168:G:H21	1.73	0.54
25:DA:2183:C:H2'	25:DA:2184:G:H8	1.72	0.54
25:DA:2430:A:H2'	25:DA:2430:A:N3	2.22	0.54
25:DA:864:G:H21	25:DA:866:A:H61	1.54	0.54
2:AB:83:MET:HB3	2:AB:234:PRO:HG2	1.88	0.54
50:B4:53:GLU:HG3	50:B4:55:ARG:H	1.72	0.54
25:BA:2298:A:H4'	25:BA:2299:A:O4'	2.07	0.54
25:BA:602:G:H2'	25:BA:603:C:C6	2.43	0.54
32:BI:72:LEU:C	32:BI:74:ASN:H	2.08	0.54
40:BU:108:GLU:O	40:BU:112:ARG:HG2	2.07	0.54
1:CA:448:A:O5'	1:CA:485:G:N2	2.40	0.54
7:CG:32:ARG:HH12	7:CG:109:ASN:ND2	2.05	0.54
15:CO:5:LYS:NZ	15:CO:5:LYS:H	2.06	0.54
1:CA:1456:G:O3'	20:CT:39:LYS:NZ	2.40	0.54
25:DA:2721:A:OP1	61:DA:4147:HOH:O	2.18	0.54
28:DE:116:VAL:HG13	28:DE:122:PHE:HB2	1.90	0.54
45:DZ:70:LEU:O	45:DZ:89:PHE:N	2.38	0.54
23:AY:76:A:N6	25:BA:2434:A:O4'	2.40	0.54
25:BA:552:C:H5	61:BA:4972:HOH:O	1.90	0.54
33:BN:4:TYR:CD2	40:BU:100:VAL:HG11	2.42	0.54
4:CD:162:LEU:HD13	4:CD:181:MET:HG2	1.90	0.54
25:DA:2447:G:N2	25:DA:2450:A:OP2	2.40	0.54
28:DE:73:GLU:HG3	28:DE:73:GLU:O	2.06	0.54
45:DZ:117:LEU:HD12	45:DZ:174:VAL:HG22	1.89	0.54
1:AA:376:G:O3'	16:AP:5:ARG:HD2	2.07	0.54
6:AF:8:ILE:HD11	6:AF:79:LEU:HD13	1.89	0.54
25:BA:2227:G:O2'	25:BA:2228:G:OP1	2.24	0.54
25:BA:2373:A:OP1	54:B8:27:THR:OG1	2.18	0.54
2:CB:201:ILE:HG21	2:CB:214:ILE:HG21	1.89	0.54
19:CS:52:TYR:HB2	19:CS:57:HIS:CE1	2.42	0.54
25:DA:303:U:H2'	25:DA:304:G:C8	2.42	0.54
1:AA:532:A:O2'	1:AA:533:A:OP1	2.22	0.54
2:AB:162:ILE:O	2:AB:185:ILE:HG12	2.07	0.54
3:AC:181:ASN:HD21	3:AC:204:LEU:HD12	1.73	0.54
4:AD:168:ARG:H	4:AD:168:ARG:CD	2.21	0.54
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.89	0.54
23:AY:55:PSU:C2	23:AY:57:G:H5'	2.43	0.54
25:BA:2255:U:H2'	25:BA:2256:U:C6	2.43	0.54
25:BA:310:C:H2'	25:BA:311:C:H6	1.72	0.54
29:BF:184:TYR:CE2	29:BF:188:ARG:HD2	2.43	0.54
44:BY:20:TYR:CE1	44:BY:43:ASN:HA	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.43	0.54
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.90	0.54
23:CW:27:G:H2'	23:CW:28:G:C8	2.43	0.54
25:DA:323:G:HO2'	25:DA:1205:U:H3	0.67	0.54
25:DA:2659:G:H4'	31:DH:175:LYS:HD3	1.88	0.54
28:DE:38:THR:HG23	28:DE:41:LYS:HB3	1.90	0.54
1:CA:1003:G:H1	1:CA:1035:A:N6	2.06	0.54
23:CW:21:A:N6	23:CW:46:7MG:N3	2.56	0.54
39:DT:64:ARG:HB2	39:DT:73:GLU:HG2	1.89	0.54
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.43	0.54
1:AA:676:A:H1'	11:AK:115:PRO:HB3	1.88	0.54
47:B1:85:LEU:HD22	47:B1:89:GLU:HG3	1.90	0.54
25:BA:2178:G:H2'	25:BA:2179:G:C4	2.42	0.54
25:BA:2227:G:H3'	25:BA:2228:G:C8	2.42	0.54
30:BG:72:ARG:NH1	30:BG:87:PRO:HG3	2.23	0.54
31:BH:56:SER:OG	31:BH:57:ASP:N	2.41	0.54
1:CA:1028:C:O2	1:CA:1033:G:N1	2.41	0.54
1:CA:160:A:H1'	1:CA:344:A:N7	2.23	0.54
1:CA:41:G:H2'	1:CA:42:G:C8	2.43	0.54
1:CA:41:G:H2'	1:CA:42:G:H8	1.73	0.54
1:CA:35:G:O2'	12:CL:118:SER:O	2.19	0.54
15:CO:70:LEU:HD11	15:CO:77:ARG:HB2	1.89	0.54
25:DA:319:C:H2'	25:DA:320:A:O4'	2.08	0.54
32:DI:57:ARG:HA	32:DI:61:ARG:HH21	1.72	0.54
36:DQ:16:ARG:HG2	36:DQ:18:LYS:HE2	1.89	0.54
37:DR:21:TYR:CZ	37:DR:43:GLU:HG2	2.43	0.54
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.56	0.53
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.90	0.53
25:BA:1653:C:H4'	25:BA:1654:A:O5'	2.07	0.53
25:BA:2549:U:H2'	25:BA:2550:C:C6	2.43	0.53
13:AM:93:ARG:HD2	25:BA:935:C:OP1	2.08	0.53
34:BO:16:ALA:HB2	34:BO:52:VAL:HG21	1.89	0.53
1:CA:158:G:N2	1:CA:163:C:O2	2.41	0.53
25:DA:2141:G:O4'	25:DA:2151:G:N2	2.41	0.53
25:DA:770:G:OP2	61:DA:4559:HOH:O	2.19	0.53
27:DD:132:PRO:HD3	27:DD:190:TYR:CZ	2.42	0.53
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.74	0.53
48:B2:24:LEU:HD23	48:B2:60:LEU:HD21	1.89	0.53
25:BA:354:A:H2	25:BA:1255:A:C2'	2.21	0.53
1:AA:1494:G:O2'	25:BA:1934:A:O2'	2.27	0.53
25:BA:718:C:N4	61:BA:5006:HOH:O	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BD:145:VAL:HG12	27:BD:146:GLU:O	2.07	0.53
25:BA:1740:U:O2'	27:BD:14:ARG:NH2	2.41	0.53
1:CA:21:G:H2'	1:CA:22:G:C8	2.43	0.53
30:DG:113:ARG:NH1	30:DG:139:LEU:O	2.37	0.53
31:DH:9:ILE:HG12	31:DH:69:ARG:HD2	1.90	0.53
1:AA:110:C:H2'	1:AA:111:G:O4'	2.07	0.53
1:AA:933:G:O6	7:AG:3:ARG:NH2	2.39	0.53
13:AM:37:THR:O	13:AM:55:ARG:NH1	2.42	0.53
25:BA:794:U:O2	25:BA:2036:A:H1'	2.07	0.53
25:BA:236:G:H4'	25:BA:413:G:C5	2.42	0.53
25:BA:968:U:H2'	25:BA:969:C:C6	2.44	0.53
45:BZ:117:LEU:HD21	45:BZ:144:LEU:HD13	1.89	0.53
1:CA:187:C:O2'	20:CT:89:ARG:NH2	2.39	0.53
1:CA:788:U:O2'	57:CA:3178:PCY:O14	2.20	0.53
1:CA:692:U:O2'	1:CA:694:A:N7	2.30	0.53
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.40	0.53
15:CO:26:GLU:OE2	15:CO:77:ARG:NH2	2.35	0.53
19:CS:27:GLU:HG2	19:CS:47:HIS:CE1	2.43	0.53
23:CW:52:G:H2'	23:CW:53:G:O4'	2.08	0.53
23:CY:8:4SU:H6	23:CY:8:4SU:H5''	1.91	0.53
25:DA:709:U:H2'	25:DA:710:G:C8	2.44	0.53
31:DH:90:LYS:HD3	31:DH:159:GLU:HG2	1.91	0.53
35:DP:84:ASN:OD1	35:DP:117:GLU:HB2	2.08	0.53
41:DV:6:LYS:HB2	41:DV:38:LEU:HD21	1.90	0.53
1:AA:1001:A:H2'	1:AA:1001(A):G:C8	2.43	0.53
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.72	0.53
1:AA:1494:G:HO2'	25:BA:1934:A:HO2'	1.56	0.53
4:AD:101:LEU:HB2	4:AD:138:TYR:HB3	1.90	0.53
25:BA:1067:A:H3'	25:BA:1067:A:C8	2.43	0.53
25:BA:927:G:H2'	25:BA:928:G:H8	1.74	0.53
25:BA:1000:C:OP1	36:BQ:87:LYS:HE3	2.08	0.53
39:BT:23:ARG:HG3	39:BT:120:ARG:NH1	2.23	0.53
25:DA:2206:G:H3'	25:DA:2207:G:N7	2.22	0.53
25:DA:811:U:OP2	35:DP:29:LYS:N	2.35	0.53
25:DA:660:G:H5'	29:DF:99:TYR:CE2	2.43	0.53
31:DH:113:VAL:HG11	31:DH:151:ILE:HD13	1.89	0.53
31:DH:103:LEU:HB3	31:DH:115:VAL:HB	1.89	0.53
1:AA:1027:C:N4	1:AA:1033:G:O6	2.42	0.53
1:AA:1124:G:N7	1:AA:1145:C:O2'	2.40	0.53
10:AJ:5:ARG:NH2	10:AJ:73:ASP:OD2	2.32	0.53
23:AW:4:C:N3	23:AW:69:G:O6	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1058:U:C5	33:BN:28:THR:HG21	2.44	0.53
1:CA:142:G:H2'	1:CA:143:A:C8	2.44	0.53
1:CA:254:G:OP1	17:CQ:66:SER:OG	2.21	0.53
15:CO:16:ALA:HB1	15:CO:21:ASP:HB3	1.89	0.53
25:DA:1292:U:H2'	25:DA:1293:C:C6	2.44	0.53
25:DA:247:G:H4'	25:DA:386:G:C5	2.44	0.53
25:DA:2483:C:H2'	25:DA:2484:G:O4'	2.07	0.53
26:DB:17:C:H2'	26:DB:18:G:O4'	2.09	0.53
26:DB:6:C:H2'	26:DB:7:G:H5''	1.89	0.53
29:DF:129:PHE:CD2	29:DF:163:VAL:HG21	2.44	0.53
36:DQ:14:ARG:HG2	36:DQ:41:TRP:HH2	1.73	0.53
40:DU:76:TYR:HH	40:DU:92:ARG:HH11	1.56	0.53
1:AA:1004:A:H5''	1:AA:1025:U:C5	2.43	0.53
1:AA:954:G:H21	1:AA:1227:A:H62	1.56	0.53
9:AI:86:VAL:HG13	9:AI:96:LEU:HD12	1.91	0.53
23:AW:26:A:H61	23:AW:44:G:H1	1.55	0.53
23:AY:67:C:H2'	23:AY:68:C:H6	1.71	0.53
51:B5:16:ARG:NH1	51:B5:17:ASP:OD1	2.41	0.53
25:BA:238:C:O2	54:B8:12:LYS:NZ	2.33	0.53
25:BA:2798:C:OP1	28:BE:41:LYS:NZ	2.39	0.53
27:BD:77:ALA:HB2	27:BD:97:TYR:CD2	2.44	0.53
28:BE:28:ALA:HB3	28:BE:93:VAL:HG12	1.91	0.53
1:CA:91:C:H2'	1:CA:92:C:C6	2.43	0.53
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.42	0.53
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	2.08	0.53
27:DD:26:LYS:HE2	27:DD:28:GLU:O	2.08	0.53
36:DQ:85:LYS:HG2	46:D0:7:LEU:HB3	1.90	0.53
1:AA:1176:A:H2'	1:AA:1177:G:C8	2.43	0.53
15:AO:82:ILE:O	15:AO:86:GLY:N	2.41	0.53
25:BA:239:G:OP2	54:B8:13:ARG:NH2	2.42	0.53
25:BA:2589:A:H5''	25:BA:2590:G:H5'	1.90	0.53
44:BY:54:LYS:H	44:BY:56:PRO:HD3	1.73	0.53
45:BZ:11:GLU:O	45:BZ:36:LYS:NZ	2.31	0.53
1:CA:1077:G:N2	1:CA:1080:A:OP2	2.42	0.53
1:CA:49:U:O4	1:CA:365:U:H5	1.89	0.53
3:CC:37:GLN:NE2	3:CC:40:ARG:HD2	2.23	0.53
25:DA:403:U:H4'	25:DA:404:C:H5'	1.89	0.53
25:DA:774:A:H2'	25:DA:774:A:N3	2.24	0.53
25:DA:1247:A:OP1	29:DF:95:ARG:NH2	2.40	0.53
40:DU:79:PHE:CZ	40:DU:83:LEU:HD21	2.43	0.53
8:AH:4:ASP:OD2	8:AH:85:ARG:NH1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.24	0.53
1:CA:396:G:O2'	1:CA:398:C:OP1	2.09	0.53
16:CP:9:PHE:CE1	16:CP:18:ARG:HD2	2.44	0.53
25:DA:1496:A:N3	25:DA:1577:C:O2'	2.40	0.53
25:DA:2567:G:H2'	25:DA:2568:C:C6	2.43	0.53
25:DA:956:G:N2	25:DA:959:A:H3'	2.24	0.53
25:DA:993:G:H21	41:DV:89:GLN:NE2	2.06	0.53
42:DW:86:LEU:HD22	42:DW:96:ILE:HD11	1.91	0.53
6:AF:68:PRO:HB2	6:AF:71:ARG:HG3	1.90	0.53
23:AY:40:C:H2'	23:AY:41:C:C6	2.44	0.53
25:BA:1154:U:O2'	25:BA:1155:C:O4'	2.27	0.53
25:BA:1338:U:H2'	25:BA:1339:C:C6	2.44	0.53
38:BS:34:HIS:O	38:BS:97:ARG:NH2	2.41	0.53
44:BY:6:HIS:H	44:BY:6:HIS:CD2	2.26	0.53
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.44	0.53
1:CA:428:G:OP2	4:CD:10:ARG:NH1	2.42	0.53
25:DA:39:C:H2'	25:DA:40:C:C6	2.44	0.53
25:DA:455:C:N3	25:DA:472:A:H2'	2.24	0.53
26:DB:105:A:OP1	45:DZ:72:ARG:NH1	2.42	0.53
25:DA:323:G:C8	29:DF:171:PRO:HG3	2.44	0.53
30:DG:115:ARG:HD2	30:DG:136:ARG:HH21	1.73	0.53
30:DG:16:ARG:O	30:DG:20:ILE:HG13	2.07	0.53
40:DU:92:ARG:HA	40:DU:95:LEU:HB2	1.90	0.53
1:AA:1149:C:P	9:AI:9:ARG:HH21	2.32	0.53
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.91	0.53
1:AA:78:G:C2	1:AA:91:C:N3	2.77	0.53
8:AH:112:LEU:HA	8:AH:134:ILE:HG12	1.91	0.53
25:BA:1634:C:H2'	25:BA:1635:C:H6	1.74	0.53
25:BA:2346:G:H5'	38:BS:9:ARG:HG2	1.90	0.53
25:BA:2604:G:OP1	61:BA:4863:HOH:O	2.18	0.53
39:BT:64:ARG:HB2	39:BT:73:GLU:HG2	1.90	0.53
5:CE:60:TYR:OH	5:CE:64:ARG:NH2	2.41	0.53
25:DA:1405:U:H2'	25:DA:1406:U:C6	2.43	0.53
25:DA:2881:C:H2'	25:DA:2882:A:O4'	2.09	0.53
29:DF:117:ARG:HH12	35:DP:1:MET:H2	1.55	0.53
1:AA:253:U:OP1	17:AQ:67:LYS:NZ	2.42	0.52
1:AA:67:C:H2'	1:AA:68:G:C8	2.44	0.52
23:AW:20:U:H4'	23:AW:20:U:OP1	2.07	0.52
49:B3:8:LEU:HD13	49:B3:31:LEU:HD23	1.91	0.52
50:B4:15:ILE:O	50:B4:33:VAL:N	2.40	0.52
25:BA:1159:U:H2'	25:BA:1160:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1634:C:H2'	25:BA:1635:C:C6	2.44	0.52
25:BA:2364:A:N6	25:BA:2377:G:O2'	2.42	0.52
25:BA:2490:A:H5'	55:B9:31:LYS:HE2	1.92	0.52
39:BT:51:ARG:HG3	39:BT:98:LYS:HD2	1.91	0.52
1:CA:179:A:H2'	1:CA:180:U:C6	2.44	0.52
25:DA:918:A:H5''	26:DB:98:G:O2'	2.09	0.52
25:DA:1278:A:OP1	37:DR:36:THR:HG23	2.08	0.52
4:AD:173:TRP:HE1	4:AD:193:ASP:HB3	1.74	0.52
20:AT:90:GLN:O	20:AT:93:GLU:HB3	2.09	0.52
25:BA:1346:U:H4'	25:BA:1347:A:H5'	1.91	0.52
25:BA:2169:G:H2'	25:BA:2170:G:O4'	2.09	0.52
25:BA:599:U:H2'	25:BA:600:G:C8	2.44	0.52
26:BB:83:G:OP1	49:B3:19:GLN:NE2	2.41	0.52
32:BI:65:ALA:HB1	32:BI:136:VAL:HG11	1.91	0.52
35:BP:82:GLY:HA2	35:BP:113:LYS:O	2.09	0.52
43:BX:53:LYS:HB3	43:BX:82:GLN:HB3	1.90	0.52
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.09	0.52
1:CA:165:C:H2'	1:CA:166:G:C8	2.44	0.52
3:CC:54:ARG:NH1	3:CC:56:ASP:OD1	2.42	0.52
6:CF:91:VAL:HG11	18:CR:72:ARG:NH1	2.24	0.52
8:CH:73:ASP:OD1	8:CH:75:ARG:HD3	2.10	0.52
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.08	0.52
36:DQ:85:LYS:HD3	46:D0:7:LEU:HG	1.92	0.52
25:DA:2836:U:H2'	25:DA:2837:G:C8	2.44	0.52
25:DA:937:U:H2'	25:DA:938:G:O4'	2.08	0.52
28:DE:170:LEU:HB3	28:DE:184:VAL:HG22	1.91	0.52
31:DH:89:ILE:O	31:DH:129:THR:HG23	2.09	0.52
40:DU:104:GLN:OE1	40:DU:105:VAL:N	2.39	0.52
1:AA:1179:A:H4'	9:AI:103:THR:HA	1.90	0.52
1:AA:741:G:H2'	1:AA:742:G:O4'	2.09	0.52
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.89	0.52
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.74	0.52
11:AK:32:ILE:HG13	11:AK:72:ALA:HB2	1.91	0.52
25:BA:2228:G:O2'	25:BA:2229:A:OP1	2.25	0.52
25:BA:2603:C:H2'	25:BA:2604:G:C8	2.44	0.52
25:BA:934:A:H2	25:BA:936:C:H2'	1.74	0.52
29:BF:143:ALA:HB1	29:BF:148:LEU:HB2	1.91	0.52
43:BX:43:VAL:HG21	43:BX:81:VAL:HG11	1.91	0.52
1:CA:1325:C:OP1	21:CU:15:ARG:NE	2.40	0.52
1:CA:833:U:H2'	1:CA:834:C:H6	1.73	0.52
25:DA:1149:G:H2'	25:DA:1150:C:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:220:G:O2'	25:DA:233:A:N3	2.39	0.52
42:DW:14:PRO:HG2	42:DW:78:GLU:HG2	1.92	0.52
43:DX:84:ALA:HB3	43:DX:87:GLN:NE2	2.24	0.52
1:AA:1442(B):A:N3	39:BT:118:ARG:NH2	2.57	0.52
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.29	0.52
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.91	0.52
23:AY:18:G:H1	23:AY:55:PSU:H1'	1.74	0.52
51:B5:16:ARG:HG2	51:B5:16:ARG:HH11	1.74	0.52
52:B6:34:LEU:HB2	52:B6:51:GLU:HB2	1.91	0.52
25:BA:469:A:H1'	25:BA:1246:C:O4'	2.08	0.52
25:BA:1405:A:H2'	25:BA:1406:A:H5'	1.90	0.52
25:BA:957:A:H2'	36:BQ:9:TYR:OH	2.10	0.52
36:BQ:32:TYR:OH	36:BQ:111:GLU:OE1	2.22	0.52
1:CA:1111:A:N1	3:CC:177:THR:OG1	2.33	0.52
1:CA:642:A:N3	8:CH:113:SER:OG	2.43	0.52
1:CA:735:C:H2'	1:CA:736:C:H6	1.73	0.52
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.92	0.52
1:CA:185:A:N3	20:CT:81:LYS:NZ	2.58	0.52
25:DA:1913:A:H4'	25:DA:1914:C:O5'	2.09	0.52
25:DA:2136:C:O2'	25:DA:2137:C:O5'	2.23	0.52
25:DA:2712:U:H2'	25:DA:2714:G:H5''	1.91	0.52
41:DV:35:LEU:HB2	41:DV:57:VAL:HG22	1.91	0.52
3:AC:16:ARG:NH2	3:AC:183:ASP:OD1	2.36	0.52
1:AA:438:G:H4'	4:AD:123:HIS:ND1	2.24	0.52
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.92	0.52
25:BA:1094:A:N1	25:BA:1158:G:O2'	2.36	0.52
25:BA:153:C:OP2	47:B1:92:LYS:NZ	2.43	0.52
25:BA:847:A:OP1	25:BA:847:A:H8	1.92	0.52
25:BA:924:U:H3	25:BA:945:A:H2	1.56	0.52
33:BN:14:VAL:HG11	33:BN:138:LEU:HD12	1.91	0.52
1:CA:1192:C:OP2	3:CC:4:LYS:NZ	2.36	0.52
57:CA:3178:PCY:H381	7:CG:82:GLY:O	2.10	0.52
1:CA:992:U:OP1	1:CA:992:U:H3'	2.08	0.52
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.90	0.52
6:CF:76:ALA:O	6:CF:80:ARG:HG3	2.09	0.52
10:CJ:30:SER:HB2	10:CJ:80:LYS:CB	2.39	0.52
25:DA:1971:A:OP2	27:DD:242:ARG:NH2	2.42	0.52
25:DA:361:G:O2'	25:DA:362:U:H5'	2.09	0.52
25:DA:590:A:OP1	29:DF:95:ARG:NH1	2.43	0.52
33:DN:34:LEU:O	33:DN:49:GLY:HA3	2.09	0.52
36:DQ:34:LEU:HB2	36:DQ:118:LEU:HD22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DR:44:LEU:HD22	37:DR:48:VAL:HG23	1.91	0.52
1:AA:1320:C:O2	19:AS:36:ARG:NH2	2.38	0.52
1:AA:346:G:C2	1:AA:347:G:H1'	2.44	0.52
1:AA:347:G:H2'	1:AA:348:G:C8	2.44	0.52
1:AA:76:C:H2'	1:AA:77:G:C8	2.44	0.52
1:CA:1002:G:H1	1:CA:1038:C:N4	2.07	0.52
1:CA:97:G:O2'	1:CA:98:G:H8	1.93	0.52
25:DA:1324:G:C2	25:DA:1331:A:C2	2.97	0.52
25:DA:1607:C:H4'	25:DA:1608:A:O5'	2.10	0.52
28:DE:7:VAL:HG12	28:DE:27:LEU:HB3	1.90	0.52
38:DS:77:ALA:HB1	38:DS:82:ILE:HB	1.91	0.52
45:DZ:100:VAL:HG21	45:DZ:134:PRO:HG2	1.91	0.52
1:AA:1158:C:H5	1:AA:1181:G:N1	2.02	0.52
1:AA:946:A:H2'	1:AA:947:G:C8	2.44	0.52
13:AM:3:ARG:HG3	13:AM:8:GLU:HA	1.92	0.52
18:AR:26:LEU:HD23	18:AR:29:PHE:CE2	2.45	0.52
47:B1:3:LYS:HB2	47:B1:61:ARG:HH12	1.75	0.52
25:BA:1699:A:OP1	37:BR:8:ARG:NH1	2.36	0.52
33:BN:73:THR:HG23	33:BN:82:LEU:HD11	1.91	0.52
25:BA:2331:G:H22	38:BS:3:ARG:CZ	2.23	0.52
1:CA:1117:G:N2	1:CA:1180:A:O2'	2.42	0.52
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.91	0.52
8:CH:39:LEU:HD12	8:CH:44:PHE:HB2	1.91	0.52
47:D1:89:GLU:O	47:D1:93:GLU:HG2	2.10	0.52
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.45	0.52
1:AA:1499:A:H1'	1:AA:1520:G:H5'	1.90	0.52
25:BA:2148:A:N6	25:BA:2184:G:O2'	2.43	0.52
25:BA:2797:C:H1'	28:BE:37:ARG:NH1	2.25	0.52
25:BA:482:C:H4'	61:BA:4038:HOH:O	2.09	0.52
38:BS:10:ARG:O	38:BS:14:VAL:HG13	2.09	0.52
1:CA:1222:G:OP1	19:CS:77:THR:HG21	2.10	0.52
1:CA:353:A:C8	1:CA:353:A:H5'	2.40	0.52
6:CF:8:ILE:HD11	6:CF:79:LEU:HD13	1.91	0.52
23:CY:52:G:N1	23:CY:62:C:O2	2.33	0.52
25:DA:1786:A:H1'	25:DA:1938:A:N6	2.24	0.52
25:DA:190:A:OP2	47:D1:39:LYS:HE3	2.09	0.52
25:DA:2143:C:H2'	25:DA:2144:U:O4'	2.10	0.52
25:DA:492:A:H2'	25:DA:493:G:O4'	2.09	0.52
31:DH:90:LYS:HD2	31:DH:163:TYR:CE1	2.45	0.52
8:AH:51:VAL:HG12	8:AH:52:ASP:H	1.75	0.52
26:BB:105:A:OP1	45:BZ:72:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BO:2:ILE:HD12	34:BO:6:THR:HG21	1.92	0.52
43:BX:54:VAL:HG22	43:BX:81:VAL:HG12	1.92	0.52
2:CB:122:PHE:HD1	2:CB:123:ALA:H	1.56	0.52
2:CB:87:ARG:NH2	2:CB:220:ASP:OD1	2.43	0.52
23:CY:13:C:O2	23:CY:22:G:N1	2.33	0.52
1:AA:189(I):G:H2'	1:AA:189(J):G:H5''	1.92	0.52
15:AO:26:GLU:OE2	15:AO:77:ARG:NE	2.31	0.52
25:BA:1804:A:OP2	61:BA:4855:HOH:O	2.19	0.52
25:BA:310:C:H2'	25:BA:311:C:C6	2.45	0.52
25:BA:427:G:O6	61:BA:5098:HOH:O	2.16	0.52
45:BZ:55:HIS:CE1	45:BZ:135:GLU:HG3	2.45	0.52
1:CA:110:C:H2'	1:CA:111:G:O4'	2.10	0.52
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.45	0.52
25:DA:1859:A:N6	25:DA:1883:G:O2'	2.42	0.52
25:DA:1939:U:OP1	25:DA:2604:U:O2'	2.27	0.52
25:DA:242:G:C8	54:D8:5:LYS:HG2	2.45	0.52
25:DA:2820:A:O2'	25:DA:2821:A:OP1	2.27	0.52
44:DY:23:ARG:HG2	44:DY:42:VAL:HG22	1.91	0.52
45:DZ:117:LEU:HD23	45:DZ:119:GLU:HG2	1.92	0.52
1:AA:309:G:O2'	1:AA:607:A:N1	2.42	0.51
25:BA:2339:A:H2'	25:BA:2340:A:C8	2.45	0.51
43:BX:31:HIS:CD2	43:BX:33:LYS:HB2	2.45	0.51
1:CA:1120:G:C6	1:CA:1121:U:C4	2.98	0.51
1:CA:1512:U:H2'	1:CA:1513:A:C8	2.46	0.51
2:CB:71:VAL:HB	2:CB:164:VAL:HA	1.91	0.51
13:CM:3:ARG:N	50:D4:34:GLU:OE1	2.43	0.51
17:CQ:78:GLU:OE2	17:CQ:81:ARG:NH1	2.41	0.51
25:DA:1028:A:N6	25:DA:1125:G:H2'	2.24	0.51
25:DA:1386:C:H2'	25:DA:1387:C:C6	2.45	0.51
25:DA:812:C:H2'	25:DA:813:U:H6	1.74	0.51
25:DA:911:A:H2'	36:DQ:9:TYR:OH	2.10	0.51
29:DF:20:LEU:HD12	29:DF:125:LEU:HD13	1.92	0.51
37:DR:36:THR:HG22	37:DR:37:THR:H	1.75	0.51
34:DO:80:ASP:OD1	39:DT:64:ARG:NH2	2.43	0.51
1:AA:250:A:H4'	1:AA:251:G:O5'	2.10	0.51
1:AA:583:A:OP2	61:AA:4025:HOH:O	2.19	0.51
13:AM:19:LEU:HD21	13:AM:56:LEU:HD11	1.91	0.51
24:AX:59:A:C2'	24:AX:60:U:H5'	2.40	0.51
25:BA:595:A:OP2	41:BV:78:LYS:NZ	2.43	0.51
27:BD:242:ARG:HD3	27:BD:242:ARG:N	2.25	0.51
25:BA:572:A:N6	41:BV:19:LYS:H	2.07	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1312:G:H1	1:CA:1325:C:N4	2.07	0.51
2:CB:185:ILE:HG22	2:CB:199:TYR:CD2	2.45	0.51
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.91	0.51
51:D5:16:ARG:HG2	51:D5:16:ARG:HH11	1.74	0.51
25:DA:938:G:OP1	54:D8:52:LYS:HD2	2.10	0.51
25:DA:1429:G:H2'	25:DA:1430:C:C6	2.45	0.51
25:DA:2683:C:O2	34:DO:70:LYS:NZ	2.39	0.51
25:DA:668:G:H5'	25:DA:669:G:OP2	2.11	0.51
1:AA:28:G:O2'	1:AA:296:U:OP1	2.26	0.51
2:AB:77:ALA:HB2	2:AB:165:VAL:HG11	1.92	0.51
7:AG:48:LYS:O	7:AG:52:GLU:HG2	2.11	0.51
20:AT:54:LYS:HB2	20:AT:100:ILE:HD11	1.93	0.51
25:BA:1604:C:OP2	25:BA:1605:A:O2'	2.22	0.51
25:BA:2623:U:C4	51:B5:3:LYS:HG2	2.44	0.51
28:BE:105:THR:OG1	28:BE:199:ARG:NH2	2.43	0.51
7:CG:138:LYS:NZ	7:CG:142:GLU:OE1	2.42	0.51
7:CG:50:ILE:HD11	7:CG:58:PRO:HA	1.93	0.51
6:CF:41:GLU:OE1	18:CR:35:ARG:NH2	2.42	0.51
23:CW:4:C:N4	23:CW:69:G:C6	2.77	0.51
25:DA:330:A:H2	25:DA:1210:A:O2'	1.93	0.51
1:AA:1036:G:H3'	1:AA:1037:C:C6	2.45	0.51
9:AI:77:ILE:O	9:AI:81:ILE:HG22	2.10	0.51
23:AY:34:G:H2'	23:AY:35:A:C8	2.45	0.51
25:BA:1212:C:O2'	61:BA:4755:HOH:O	2.19	0.51
25:BA:489:G:O6	61:BA:4635:HOH:O	2.18	0.51
37:BR:21:TYR:OH	37:BR:43:GLU:HG2	2.10	0.51
1:CA:1014:A:C2	1:CA:1219:U:H1'	2.45	0.51
54:D8:63:PRO:HG2	54:D8:64:TYR:CD2	2.44	0.51
25:DA:1005:C:H2'	25:DA:1006:C:C6	2.44	0.51
42:DW:12:ILE:HD13	42:DW:17:VAL:HG13	1.93	0.51
45:DZ:97:GLU:HB2	45:DZ:125:LEU:HD11	1.92	0.51
1:AA:49:U:O4	1:AA:365:U:H5	1.94	0.51
9:AI:93:ARG:HB2	9:AI:93:ARG:HH11	1.75	0.51
25:BA:1091:A:OP1	25:BA:1091:A:H4'	2.10	0.51
25:BA:2143:G:H1	25:BA:2199:C:N4	2.08	0.51
25:BA:2797:C:H1'	28:BE:37:ARG:HH12	1.74	0.51
26:BB:2:C:H2'	26:BB:3:C:C6	2.45	0.51
38:BS:15:ARG:O	38:BS:19:LYS:HG2	2.09	0.51
1:CA:1053:G:N7	1:CA:1200:C:H5''	2.26	0.51
1:CA:142:G:H2'	1:CA:143:A:H8	1.75	0.51
1:CA:920:U:H2'	1:CA:921:U:H6	1.72	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:121:ALA:O	3:CC:125:GLU:HG3	2.11	0.51
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.41	0.51
18:CR:24:ALA:O	18:CR:26:LEU:N	2.39	0.51
25:DA:1771:C:OP1	61:DA:4530:HOH:O	2.19	0.51
25:DA:580:C:H2'	25:DA:581:C:H6	1.74	0.51
25:DA:637:A:H5''	35:DP:117:GLU:HG2	1.92	0.51
26:DB:14:U:OP2	26:DB:70:C:O2'	2.25	0.51
28:DE:72:VAL:HA	28:DE:73:GLU:CB	2.41	0.51
25:DA:2727:G:O2'	34:DO:70:LYS:NZ	2.42	0.51
38:BS:15:ARG:NE	38:BS:88:ASP:OD2	2.37	0.51
44:BY:92:ASN:N	44:BY:93:GLY:HA2	2.26	0.51
1:CA:1132:C:H2'	1:CA:1133:G:C8	2.45	0.51
1:CA:1512:U:H2'	1:CA:1513:A:H8	1.76	0.51
1:CA:56:U:H2'	1:CA:57:G:C8	2.45	0.51
25:DA:2640:G:N7	61:DA:4154:HOH:O	2.34	0.51
25:DA:852:G:H2'	25:DA:853:G:C8	2.45	0.51
29:DF:156:LEU:HD21	29:DF:163:VAL:HG12	1.92	0.51
29:DF:24:LEU:HD21	29:DF:114:VAL:HG12	1.92	0.51
31:DH:80:SER:OG	31:DH:81:GLU:OE1	2.26	0.51
40:DU:66:ASN:O	40:DU:70:ARG:HG3	2.10	0.51
1:AA:757:U:H2'	1:AA:758:G:O4'	2.11	0.51
6:AF:70:ASP:OD1	6:AF:70:ASP:N	2.36	0.51
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.25	0.51
15:AO:21:ASP:OD2	15:AO:24:SER:HB3	2.10	0.51
1:AA:581:G:OP1	15:AO:65:ARG:NH2	2.43	0.51
16:AP:71:ARG:HG3	16:AP:80:PHE:HE2	1.75	0.51
25:BA:1223:C:H2'	25:BA:1224:C:C6	2.45	0.51
28:BE:9:VAL:HB	39:BT:3:ARG:HG2	1.93	0.51
3:CC:3:ASN:N	3:CC:3:ASN:OD1	2.41	0.51
9:CI:3:GLN:OE1	9:CI:20:ARG:NH2	2.43	0.51
25:DA:2299:G:N1	25:DA:2318:G:N7	2.59	0.51
25:DA:625:G:O6	35:DP:107:LYS:NZ	2.35	0.51
33:DN:19:GLU:HA	33:DN:59:LYS:HB2	1.93	0.51
35:DP:44:GLY:CA	35:DP:45:LEU:HB2	2.40	0.51
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.43	0.51
1:AA:381:C:H2'	1:AA:382:A:O4'	2.10	0.51
2:AB:21:ARG:HH21	2:AB:21:ARG:H	1.59	0.51
23:AW:18:G:N2	23:AW:57:G:H2'	2.25	0.51
23:AW:18:G:H4'	23:AW:60:U:C5	2.46	0.51
54:B8:23:VAL:HG11	54:B8:47:LYS:HD3	1.93	0.51
25:BA:720:C:OP1	29:BF:54:ARG:NH1	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.21	0.51
1:CA:833:U:H2'	1:CA:834:C:C6	2.46	0.51
25:DA:1507:A:O2'	25:DA:1508:A:O5'	2.28	0.51
25:DA:1530:C:H42	25:DA:1539:G:H1	1.58	0.51
25:DA:2630:G:H2'	25:DA:2631:G:C8	2.45	0.51
25:DA:362:U:O2'	25:DA:363:G:H5''	2.11	0.51
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.10	0.51
1:AA:1318:A:H5''	19:AS:3:ARG:NH1	2.26	0.51
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.93	0.51
19:AS:65:ASN:HD22	19:AS:65:ASN:N	2.07	0.51
47:B1:85:LEU:HB3	47:B1:89:GLU:HG3	1.93	0.51
25:BA:704:U:H2'	25:BA:705:C:H6	1.76	0.51
28:BE:12:THR:HG22	28:BE:13:ARG:H	1.76	0.51
28:BE:11:MET:HG2	28:BE:24:THR:HB	1.93	0.51
37:BR:57:ARG:NE	37:BR:59:ASP:OD1	2.44	0.51
2:CB:95:GLN:HB2	2:CB:148:TYR:HD1	1.76	0.51
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.26	0.51
25:DA:2193:G:H2'	25:DA:2194:G:C8	2.46	0.51
25:DA:608:A:H2'	25:DA:609:A:C8	2.45	0.51
39:DT:16:ARG:NH2	39:DT:83:ILE:O	2.43	0.51
6:AF:37:VAL:HA	6:AF:65:VAL:HG12	1.92	0.51
25:BA:2044:U:O2'	25:BA:2629:C:H5'	2.11	0.51
25:BA:771:U:H2'	25:BA:772:G:O4'	2.11	0.51
25:BA:865:G:O6	61:BA:4412:HOH:O	2.19	0.51
32:BI:81:VAL:O	32:BI:146:ALA:HA	2.10	0.51
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.25	0.51
1:CA:748:C:H4'	1:CA:749:C:O5'	2.11	0.51
2:CB:134:GLU:O	2:CB:138:LEU:HG	2.10	0.51
30:DG:5:VAL:HG22	30:DG:8:LYS:H	1.76	0.51
31:DH:20:ALA:HB1	31:DH:21:PRO:HD2	1.92	0.51
45:DZ:52:SER:OG	45:DZ:53:ILE:N	2.43	0.51
1:AA:1001:A:H2'	1:AA:1001(A):G:H8	1.76	0.50
1:AA:174:C:H2'	1:AA:175:C:H6	1.77	0.50
1:AA:92:C:H2'	1:AA:93:G:C8	2.46	0.50
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.46	0.50
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.93	0.50
12:AL:117:ARG:HB3	12:AL:122:THR:HB	1.93	0.50
13:AM:11:ARG:HA	13:AM:45:VAL:HB	1.92	0.50
25:BA:407:U:OP1	61:BA:4339:HOH:O	2.19	0.50
27:BD:85:ASP:OD2	27:BD:88:ARG:NH1	2.39	0.50
1:CA:953:G:H5'	1:CA:965:A:N6	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:986:A:H2'	1:CA:987:G:C8	2.47	0.50
2:CB:15:VAL:HG13	2:CB:209:ARG:HB3	1.93	0.50
25:DA:1025:G:C4	25:DA:1135:C:H1'	2.46	0.50
25:DA:2183:C:H2'	25:DA:2184:G:C8	2.46	0.50
25:DA:2819:G:N7	61:DA:4376:HOH:O	2.34	0.50
27:DD:17:THR:O	27:DD:211:ARG:NH2	2.41	0.50
3:AC:164:ARG:HG2	3:AC:165:THR:H	1.76	0.50
17:AQ:67:LYS:HA	17:AQ:70:ARG:HH12	1.76	0.50
57:AA:3231:PCY:H40	23:AY:35:A:C2	2.45	0.50
25:BA:1040:C:OP1	40:BU:53:ARG:NH2	2.44	0.50
25:BA:801:C:H2'	25:BA:802:C:C6	2.46	0.50
26:BB:82:G:N7	61:BB:3110:HOH:O	2.34	0.50
30:BG:16:ARG:HH21	30:BG:31:VAL:HG11	1.75	0.50
30:BG:75:LYS:HA	30:BG:84:LYS:HE2	1.92	0.50
40:BU:76:TYR:CZ	40:BU:80:ILE:HG13	2.46	0.50
2:CB:47:THR:O	2:CB:51:LEU:N	2.44	0.50
15:CO:87:ILE:HG22	15:CO:88:ARG:N	2.23	0.50
23:CW:4:C:N4	23:CW:69:G:H1	2.10	0.50
25:DA:2846:G:H2'	25:DA:2847:U:O4'	2.11	0.50
31:DH:56:SER:OG	31:DH:57:ASP:N	2.43	0.50
37:DR:29:LEU:HB3	37:DR:75:LEU:HD11	1.93	0.50
2:AB:231:GLU:HB3	2:AB:232:PRO:HD3	1.93	0.50
23:AY:6:G:O6	23:AY:7:A:N6	2.45	0.50
25:BA:1002:A:H5'	36:BQ:76:LYS:HG3	1.92	0.50
25:BA:1269:G:N2	25:BA:1272:A:OP2	2.36	0.50
25:BA:510:C:H2'	25:BA:511:C:C6	2.47	0.50
45:BZ:52:SER:OG	45:BZ:53:ILE:N	2.45	0.50
1:CA:1035:A:H2'	1:CA:1036:G:H8	1.77	0.50
1:CA:78:G:C2'	1:CA:79:G:H5''	2.37	0.50
3:CC:54:ARG:HH12	3:CC:56:ASP:CG	2.14	0.50
23:CW:8:4SU:O2'	23:CW:21:A:N6	2.41	0.50
52:D6:34:LEU:HB2	52:D6:51:GLU:HB2	1.92	0.50
25:DA:1448:G:H4'	25:DA:1542:A:OP1	2.10	0.50
25:DA:531:C:H4'	25:DA:532:A:H5''	1.94	0.50
9:AI:50:LEU:HD23	9:AI:81:ILE:HD11	1.94	0.50
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.93	0.50
23:CY:2:C:H2'	23:CY:3:C:C6	2.46	0.50
25:DA:76:C:O3'	48:D2:59:ARG:HG3	2.11	0.50
25:DA:443:A:H1'	25:DA:1201:C:O4'	2.10	0.50
4:AD:127:THR:HA	4:AD:132:ARG:HA	1.93	0.50
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1254:C:H41	10:AJ:43:ARG:HH12	1.58	0.50
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.42	0.50
25:BA:2148:A:N6	25:BA:2184:G:HO2'	2.09	0.50
25:BA:385:G:N1	25:BA:386:U:O4	2.44	0.50
25:BA:721:G:O2'	29:BF:74:ARG:HD3	2.10	0.50
6:CF:70:ASP:OD1	6:CF:70:ASP:N	2.27	0.50
1:CA:1179:A:H4'	9:CI:103:THR:HA	1.93	0.50
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.12	0.50
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.77	0.50
17:CQ:95:TYR:HA	17:CQ:98:LEU:HD22	1.94	0.50
25:DA:1946:U:H2'	25:DA:1947:C:C6	2.45	0.50
25:DA:2334:G:H5'	38:DS:9:ARG:HG2	1.93	0.50
25:DA:2830:G:OP1	28:DE:76:ARG:NH2	2.45	0.50
30:DG:23:PHE:HB2	30:DG:25:TYR:CZ	2.47	0.50
31:DH:144:VAL:O	31:DH:148:ILE:HG12	2.12	0.50
1:AA:93:G:H2'	1:AA:96:U:O4'	2.12	0.50
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.94	0.50
20:AT:34:LYS:HZ2	20:AT:80:ARG:HH12	1.59	0.50
23:AY:5:G:H1'	23:AY:69:G:N2	2.25	0.50
25:BA:1744:G:OP2	25:BA:1745:A:O2'	2.13	0.50
25:BA:2132:G:C2	25:BA:2142:G:H1'	2.47	0.50
25:BA:470:C:H5''	61:BA:4091:HOH:O	2.10	0.50
41:BV:40:LEU:HB2	41:BV:46:VAL:HG13	1.93	0.50
1:CA:297:G:N2	1:CA:300:A:OP2	2.45	0.50
1:CA:9:G:H2'	1:CA:10:A:H8	1.77	0.50
2:CB:224:GLN:HG2	2:CB:225:ALA:N	2.27	0.50
8:CH:82:HIS:N	8:CH:138:TRP:O	2.42	0.50
25:DA:2655:G:O2'	25:DA:2664:G:O6	2.28	0.50
28:DE:111:ARG:HG3	28:DE:160:TYR:CD2	2.46	0.50
30:DG:48:GLU:O	30:DG:51:ARG:HG3	2.12	0.50
35:DP:81:GLN:NE2	35:DP:105:LEU:O	2.44	0.50
1:AA:1027:C:N3	1:AA:1034:G:C6	2.80	0.50
1:AA:1027:C:O2	1:AA:1034:G:C2	2.65	0.50
1:AA:1318:A:H5''	19:AS:3:ARG:HH12	1.77	0.50
1:AA:69:G:H2'	1:AA:70:G:H8	1.76	0.50
1:AA:833:U:H2'	1:AA:834:C:C6	2.47	0.50
1:AA:96:U:O2'	1:AA:97:G:H5'	2.11	0.50
1:AA:8:A:H5'	5:AE:101:ILE:HG22	1.93	0.50
11:AK:45:GLY:O	11:AK:50:TYR:HB2	2.11	0.50
25:BA:2235:G:OP1	27:BD:172:TYR:OH	2.24	0.50
25:BA:2389:A:H2'	25:BA:2390:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:56:C:P	25:BA:943:C:H5'	2.52	0.50
25:BA:2885:C:O2'	39:BT:2:ASN:OD1	2.26	0.50
1:CA:1310:G:H5'	13:CM:77:ASN:ND2	2.26	0.50
1:CA:1399:C:H4'	1:CA:1400:C:O5'	2.12	0.50
1:CA:909:A:N3	1:CA:1413:A:O2'	2.32	0.50
23:CY:26:A:N1	23:CY:44:G:C6	2.79	0.50
26:DB:9:G:H1	26:DB:112:U:H3	1.58	0.50
39:DT:85:LYS:NZ	39:DT:87:ASP:OD2	2.43	0.50
1:AA:21:G:OP1	61:AA:4120:HOH:O	2.19	0.50
2:AB:109:SER:HA	2:AB:112:VAL:HG13	1.94	0.50
25:BA:1298:G:OP1	40:BU:36:ARG:NH2	2.45	0.50
25:BA:2155:G:H21	25:BA:2180:A:H62	1.58	0.50
25:BA:555:G:O4'	25:BA:555:G:N3	2.43	0.50
33:BN:62:VAL:HG22	33:BN:66:LYS:HD2	1.92	0.50
44:BY:55:TYR:CD2	44:BY:55:TYR:N	2.80	0.50
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.27	0.50
1:CA:222:U:H2'	1:CA:223:U:C6	2.46	0.50
25:DA:1009:A:H5'	40:DU:59:ARG:HG2	1.92	0.50
1:AA:97:G:HO2'	1:AA:98:G:H8	1.60	0.50
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.76	0.50
25:BA:489:G:OP2	61:BA:5265:HOH:O	2.20	0.50
25:BA:2116:G:P	32:BI:22:LYS:HD2	2.52	0.50
35:BP:59:LEU:HD22	54:B8:13:ARG:HD2	1.94	0.50
40:BU:86:ALA:O	41:BV:49:THR:HG23	2.12	0.50
1:CA:1004:A:H5''	1:CA:1025:U:C5	2.47	0.50
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.27	0.50
1:CA:349:A:C2'	1:CA:350:G:H5''	2.38	0.50
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.77	0.50
4:CD:149:ALA:HB3	4:CD:152:SER:HB2	1.94	0.50
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.45	0.50
6:CF:45:LEU:HD12	6:CF:59:TYR:CD2	2.46	0.50
9:CI:121:ARG:NH1	9:CI:122:ALA:O	2.44	0.50
23:CY:8:4SU:S4	23:CY:14:A:N7	2.85	0.50
25:DA:274:G:H2'	25:DA:275:G:C8	2.46	0.50
45:DZ:111:VAL:HG13	45:DZ:117:LEU:H	1.77	0.50
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.95	0.49
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.12	0.49
50:B4:56:VAL:O	50:B4:60:GLN:HG3	2.12	0.49
25:BA:2495:C:N3	36:BQ:124:LYS:NZ	2.58	0.49
32:BI:66:GLU:HA	32:BI:69:LYS:HB3	1.94	0.49
38:BS:34:HIS:ND1	38:BS:53:SER:OG	2.35	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1123:A:O3'	10:CJ:36:GLY:HA3	2.12	0.49
1:CA:811:C:O2'	1:CA:901:A:N1	2.41	0.49
1:CA:947:G:H1	1:CA:1234:C:N4	2.09	0.49
15:CO:15:PHE:CE2	15:CO:84:LYS:HD3	2.47	0.49
20:CT:77:ALA:O	20:CT:81:LYS:HG3	2.11	0.49
25:DA:1155:A:H3'	61:DA:4617:HOH:O	2.11	0.49
25:DA:2124:G:N2	25:DA:2174:C:N3	2.58	0.49
25:DA:2502:G:H5''	25:DA:2503:A:H5''	1.94	0.49
25:DA:2741:A:H2'	25:DA:2742:C:O4'	2.12	0.49
28:DE:174:ASP:OD1	28:DE:175:VAL:N	2.45	0.49
25:DA:2313:C:H4'	30:DG:91:ARG:HG3	1.94	0.49
25:DA:587:C:OP2	35:DP:21:ARG:NH2	2.45	0.49
42:DW:71:VAL:HA	42:DW:107:LEU:HD12	1.94	0.49
1:AA:174:C:H2'	1:AA:175:C:C6	2.47	0.49
1:AA:524:G:H2'	1:AA:525:C:C6	2.47	0.49
1:AA:590:C:O2	1:AA:649:G:N2	2.30	0.49
1:AA:922:G:C6	1:AA:923:A:C6	3.00	0.49
2:AB:231:GLU:HB3	2:AB:232:PRO:CD	2.42	0.49
25:BA:1517:G:H5''	25:BA:1518:A:OP1	2.12	0.49
25:BA:484:G:O2'	25:BA:495:G:O6	2.29	0.49
30:BG:131:TYR:HB3	30:BG:159:VAL:HG13	1.93	0.49
31:BH:154:PRO:HB3	31:BH:163:TYR:CZ	2.47	0.49
1:CA:1035:A:H2'	1:CA:1036:G:C8	2.47	0.49
1:CA:973:G:H3'	1:CA:974:A:H5''	1.94	0.49
7:CG:111:ARG:NH2	7:CG:126:ASP:OD2	2.45	0.49
24:CX:76:A:H3'	25:DA:2585:U:C5	2.47	0.49
25:DA:1639:U:H4'	25:DA:2699:C:H4'	1.93	0.49
25:DA:2148:G:H2'	25:DA:2149:G:C8	2.47	0.49
36:DQ:108:GLY:HA3	45:DZ:116:VAL:HG13	1.93	0.49
38:DS:93:LYS:CD	38:DS:95:HIS:HB2	2.42	0.49
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.48	0.49
3:AC:87:LEU:O	3:AC:91:LEU:N	2.36	0.49
25:BA:1155:C:H5'	25:BA:1156:G:OP2	2.11	0.49
32:BI:106:GLY:HA2	32:BI:107:VAL:O	2.12	0.49
1:CA:532:A:H2	1:CA:1206:G:H21	1.60	0.49
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.26	0.49
23:CW:25:C:H2'	23:CW:26:A:H8	1.76	0.49
30:DG:108:ASN:HB3	50:D4:22:ILE:HD13	1.95	0.49
25:DA:921:G:H4'	25:DA:2269:A:C5	2.47	0.49
38:DS:78:LEU:HD11	38:DS:108:GLY:O	2.12	0.49
23:AW:4:C:H2'	23:AW:5:G:C8	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1067:A:H3'	25:BA:1067:A:H8	1.77	0.49
25:BA:2357:G:H4'	25:BA:2358:A:H5''	1.94	0.49
25:BA:2710:U:H2'	25:BA:2711:C:C6	2.47	0.49
28:BE:170:LEU:HB3	28:BE:184:VAL:HG22	1.93	0.49
31:BH:164:TYR:N	31:BH:167:GLU:OE1	2.42	0.49
32:BI:77:LEU:HB3	32:BI:142:VAL:HG12	1.94	0.49
1:CA:1178:G:N2	1:CA:1180:A:H3'	2.28	0.49
1:CA:185:A:H5'	20:CT:74:LYS:HE2	1.94	0.49
2:CB:185:ILE:HG22	2:CB:199:TYR:HD2	1.77	0.49
5:CE:38:GLN:HE21	5:CE:38:GLN:N	2.10	0.49
25:DA:1589:C:H2'	25:DA:1590:U:H6	1.77	0.49
25:DA:2529:G:H5''	25:DA:2530:A:H5''	1.94	0.49
25:DA:2537:U:H2'	25:DA:2538:C:C6	2.47	0.49
25:DA:276:A:H5''	25:DA:277:C:H5'	1.94	0.49
25:DA:657:U:H2'	25:DA:658:C:C6	2.46	0.49
31:DH:4:ILE:HG22	31:DH:69:ARG:HG2	1.94	0.49
32:DI:130:TYR:HD2	32:DI:138:ILE:HD12	1.78	0.49
1:AA:1399:C:C2	1:AA:1502:A:N6	2.81	0.49
2:AB:17:PHE:HB2	2:AB:44:LEU:HD21	1.94	0.49
2:AB:59:GLU:HB2	2:AB:221:LEU:HG	1.94	0.49
19:AS:3:ARG:HE	19:AS:7:LYS:HB2	1.78	0.49
48:B2:16:LEU:O	48:B2:67:LYS:NZ	2.46	0.49
53:B7:12:ARG:NH2	53:B7:44:PRO:HB3	2.27	0.49
25:BA:125:A:H5''	25:BA:126:C:C6	2.48	0.49
25:BA:2626:A:OP1	61:BA:4516:HOH:O	2.19	0.49
25:BA:739:C:O2'	27:BD:38:LYS:NZ	2.46	0.49
32:BI:129:THR:HG22	32:BI:139:GLN:HE22	1.76	0.49
1:CA:184:G:H2'	1:CA:185:A:H8	1.77	0.49
1:CA:193:C:H2'	1:CA:194:C:C6	2.47	0.49
1:CA:787:A:C2	57:CA:3178:PCY:H111	2.48	0.49
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	1.94	0.49
18:CR:53:ARG:HH21	18:CR:59:SER:HA	1.77	0.49
47:D1:24:ALA:HA	47:D1:32:LYS:HD2	1.95	0.49
25:DA:2125:G:H1	25:DA:2172:U:P	2.35	0.49
25:DA:839:U:H2'	25:DA:840:C:C6	2.46	0.49
29:DF:165:ARG:HG2	29:DF:168:ARG:NH2	2.28	0.49
39:DT:19:LEU:HD22	39:DT:86:ILE:HG13	1.93	0.49
1:AA:1025:U:O2	1:AA:1036:G:C6	2.62	0.49
1:AA:1034:G:H2'	1:AA:1035:A:H8	1.72	0.49
4:AD:175:SER:HB3	4:AD:186:LEU:HD11	1.93	0.49
5:AE:85:GLY:C	5:AE:87:SER:H	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1553:A:O2'	25:BA:1554:A:O4'	2.30	0.49
25:BA:1589:A:O2'	61:BA:5331:HOH:O	2.20	0.49
25:BA:630:U:OP1	29:BF:102:PRO:HA	2.12	0.49
25:BA:779:C:OP1	61:BA:4829:HOH:O	2.19	0.49
25:BA:801:C:H2'	25:BA:802:C:H6	1.78	0.49
27:BD:107:ALA:O	61:BD:416:HOH:O	2.20	0.49
29:BF:89:VAL:HG12	29:BF:90:PHE:CD2	2.48	0.49
44:BY:35:TYR:CE2	44:BY:69:ALA:HB3	2.47	0.49
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.12	0.49
1:CA:1030:C:N4	1:CA:1032:G:O6	2.45	0.49
1:CA:153:C:H2'	1:CA:154:C:C6	2.47	0.49
57:CA:3178:PCY:O36	57:CA:3178:PCY:O21	2.29	0.49
4:CD:111:ALA:HB1	4:CD:116:GLN:HB3	1.94	0.49
8:CH:64:LYS:HD2	8:CH:79:VAL:HG11	1.94	0.49
21:CU:13:ILE:HG12	21:CU:22:ARG:NH2	2.28	0.49
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.94	0.49
24:CX:47:U:N3	24:CX:50:U:OP1	2.45	0.49
25:DA:1006:C:C2	25:DA:1138:G:N2	2.81	0.49
25:DA:184:C:H2'	25:DA:185:U:C6	2.47	0.49
25:DA:271(O):C:H2'	25:DA:271(P):C:C6	2.48	0.49
45:DZ:52:SER:OG	45:DZ:54:HIS:ND1	2.42	0.49
45:DZ:53:ILE:HD13	45:DZ:99:TYR:HB2	1.94	0.49
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.13	0.49
1:AA:131:C:H2'	1:AA:132:C:C6	2.48	0.49
52:B6:6:ARG:NH1	52:B6:26:ASN:HB2	2.27	0.49
25:BA:2348:A:H61	46:B0:43:THR:HG22	1.78	0.49
27:BD:12:SER:HB3	27:BD:208:LYS:HB3	1.94	0.49
27:BD:2:ALA:HA	27:BD:200:ASP:OD2	2.12	0.49
39:BT:11:GLU:OE1	39:BT:57:PHE:HB3	2.13	0.49
1:CA:1149:C:H2'	1:CA:1150:U:C6	2.48	0.49
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.45	0.49
1:CA:519:C:OP2	12:CL:50:SER:OG	2.31	0.49
25:DA:298:G:H5''	25:DA:299:A:OP1	2.13	0.49
25:DA:576:U:OP1	61:DA:4464:HOH:O	2.19	0.49
31:DH:3:ARG:HD3	31:DH:54:ARG:HH12	1.76	0.49
3:AC:11:ARG:HB3	3:AC:15:THR:HB	1.94	0.49
17:AQ:62:SER:HB3	17:AQ:72:ARG:HD2	1.94	0.49
24:AX:8:4SU:H6	24:AX:8:4SU:O5'	2.13	0.49
25:BA:1424:A:OP1	53:B7:10:ARG:NH2	2.46	0.49
25:BA:2856:G:H2'	25:BA:2857:U:O4'	2.13	0.49
25:BA:860:U:H2'	25:BA:861:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BE:59:VAL:HG21	28:BE:74:PRO:HB3	1.93	0.49
29:BF:53:THR:CG2	29:BF:55:GLY:H	2.25	0.49
25:BA:709:G:H5''	35:BP:16:ARG:HG2	1.93	0.49
1:CA:1028:C:C2	1:CA:1033:G:C6	3.00	0.49
2:CB:48:MET:HA	2:CB:51:LEU:HB2	1.95	0.49
25:DA:2137:C:H2'	25:DA:2138:C:C6	2.47	0.49
25:DA:2650:U:H2'	25:DA:2651:C:C6	2.47	0.49
26:DB:75:G:HO2'	45:DZ:85:HIS:CE1	2.27	0.49
25:DA:2784:C:H1'	28:DE:37:ARG:HH12	1.77	0.49
35:DP:95:VAL:HG13	35:DP:125:VAL:HG12	1.94	0.49
36:DQ:37:LEU:HD11	36:DQ:130:LYS:HB2	1.94	0.49
37:DR:2:ARG:NH1	37:DR:5:LYS:O	2.46	0.49
50:B4:63:TYR:CD1	50:B4:63:TYR:N	2.78	0.49
25:BA:2245:U:H2'	25:BA:2246:G:C8	2.47	0.49
25:BA:2784:C:H2'	25:BA:2785:C:C6	2.48	0.49
25:BA:2880:C:H2'	25:BA:2881:C:O4'	2.13	0.49
1:CA:1009:G:H22	1:CA:1021:G:H1'	1.75	0.49
1:CA:946:A:H2'	1:CA:947:G:C8	2.48	0.49
2:CB:17:PHE:HB2	2:CB:44:LEU:HD11	1.95	0.49
1:CA:1106:G:H5''	3:CC:172:ARG:HG2	1.94	0.49
10:CJ:42:THR:HG23	10:CJ:68:HIS:HA	1.94	0.49
19:CS:49:ILE:HD13	19:CS:62:ILE:HD13	1.95	0.49
25:DA:146:G:O6	61:DA:4857:HOH:O	2.17	0.49
25:DA:2078:C:C4	25:DA:2079:U:C4	3.01	0.49
25:DA:2647:U:H2'	25:DA:2648:C:C6	2.48	0.49
25:DA:71:A:N7	43:DX:31:HIS:HE1	2.11	0.49
26:DB:13:A:O2'	26:DB:14:U:H3'	2.12	0.49
38:DS:15:ARG:O	38:DS:19:LYS:HG2	2.12	0.49
2:AB:128:GLU:HB2	2:AB:135:GLN:NE2	2.28	0.49
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.46	0.49
17:AQ:45:HIS:NE2	17:AQ:47:PRO:HG3	2.28	0.49
1:AA:1244:C:OP1	21:AU:9:ARG:HB2	2.13	0.49
25:BA:354:A:H2	25:BA:1255:A:HO2'	1.61	0.49
25:BA:956:A:N1	25:BA:2289:G:H1'	2.28	0.49
29:BF:51:THR:O	29:BF:93:LYS:HE2	2.13	0.49
44:BY:86:ARG:HH11	44:BY:100:ALA:HB1	1.78	0.49
1:CA:1000:U:H3	1:CA:1041:A:N6	2.05	0.49
1:CA:202:U:O2'	1:CA:203:U:O5'	2.26	0.49
1:CA:662:G:H2'	1:CA:663:A:C8	2.48	0.49
2:CB:52:GLU:HG2	2:CB:56:ARG:HH22	1.78	0.49
11:CK:45:GLY:O	11:CK:50:TYR:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1168:G:H2'	25:DA:1169:G:C8	2.48	0.49
25:DA:2116:G:H5'	25:DA:2117:A:OP2	2.13	0.49
25:DA:2156:G:H2'	25:DA:2157:G:C2	2.48	0.49
25:DA:861:A:N3	26:DB:79:C:O2'	2.41	0.49
26:DB:24:G:H4'	26:DB:25:A:C8	2.47	0.49
30:DG:68:PRO:HB3	30:DG:92:VAL:HB	1.95	0.49
44:DY:5:MET:HE1	44:DY:32:PRO:HA	1.95	0.49
45:DZ:126:VAL:CG1	45:DZ:161:VAL:HG23	2.40	0.49
1:AA:972:C:OP2	10:AJ:57:LYS:NZ	2.42	0.48
2:AB:32:ILE:HD13	2:AB:40:HIS:CD2	2.48	0.48
23:AY:48:C:C2	23:AY:59:U:H1'	2.48	0.48
25:BA:1815:A:OP2	61:BA:4831:HOH:O	2.20	0.48
25:BA:625:G:O2'	25:BA:702:A:N6	2.46	0.48
28:BE:31:CYS:HB3	28:BE:49:LEU:HG	1.95	0.48
29:BF:185:ASP:HA	29:BF:188:ARG:HD3	1.95	0.48
34:BO:87:ILE:HD12	34:BO:91:LEU:HA	1.94	0.48
1:CA:189(F):U:O2	17:CQ:63:ARG:NH2	2.46	0.48
1:CA:434:U:H2'	1:CA:435:C:C6	2.47	0.48
25:DA:1430:C:H2'	25:DA:1431:U:H6	1.76	0.48
25:DA:1507:A:O2'	25:DA:1508:A:O4'	2.31	0.48
25:DA:2756:U:H1'	25:DA:2757:A:H5''	1.95	0.48
25:DA:897:C:H3'	25:DA:898:C:C6	2.46	0.48
25:DA:947:G:H2'	25:DA:948:G:C8	2.48	0.48
30:DG:72:ARG:NH1	30:DG:87:PRO:HG3	2.28	0.48
25:DA:2820:A:O5'	37:DR:4:LEU:HD23	2.13	0.48
1:AA:1236:A:H4'	1:AA:1304:G:H4'	1.94	0.48
1:AA:346:G:H3'	1:AA:347:G:H4'	1.94	0.48
25:BA:1733:C:H2'	25:BA:1734:G:O4'	2.13	0.48
25:BA:2203:G:O2'	25:BA:2204:G:OP1	2.26	0.48
25:BA:2073:A:H5'	25:BA:2590:G:O4'	2.13	0.48
1:CA:1316:G:N1	1:CA:1319:A:OP2	2.46	0.48
1:CA:194:C:O3'	20:CT:68:LYS:HD2	2.13	0.48
1:CA:26:A:N6	1:CA:558:G:O2'	2.43	0.48
5:CE:78:HIS:HA	8:CH:105:ARG:HG3	1.96	0.48
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.13	0.48
19:CS:20:LEU:HD23	19:CS:23:ASN:HD22	1.77	0.48
23:CW:34:G:H2'	23:CW:35:A:C8	2.47	0.48
54:D8:31:HIS:ND1	54:D8:32:LEU:HD13	2.28	0.48
25:DA:2365:G:O6	54:D8:39:LYS:HE3	2.12	0.48
25:DA:1231:G:H2'	25:DA:1232:G:H8	1.78	0.48
25:DA:1641:A:H2'	25:DA:1642:G:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:307:G:H21	25:DA:330:A:H62	1.61	0.48
25:DA:819:A:OP2	25:DA:1187:G:N2	2.31	0.48
25:DA:1335:U:OP1	43:DX:65:ARG:NH2	2.46	0.48
45:DZ:110:GLY:O	45:DZ:174:VAL:HG11	2.13	0.48
1:AA:1298:C:H4'	1:AA:1299:A:O4'	2.13	0.48
1:AA:347:G:H3'	1:AA:348:G:H5''	1.96	0.48
1:AA:473:G:H2'	1:AA:474:G:H8	1.78	0.48
10:AJ:11:PHE:HB3	14:AN:55:GLY:HA3	1.95	0.48
14:AN:6:LEU:HB3	14:AN:23:ARG:NH2	2.28	0.48
25:BA:933:C:H4'	25:BA:933:C:OP1	2.13	0.48
27:BD:39:LYS:NZ	27:BD:57:GLY:O	2.44	0.48
35:BP:121:LYS:HB3	35:BP:123:LEU:HG	1.95	0.48
42:BW:71:VAL:HA	42:BW:107:LEU:HD12	1.96	0.48
42:BW:79:GLY:HA3	42:BW:100:THR:HG22	1.94	0.48
1:CA:1004:A:H2'	1:CA:1038:C:H1'	1.95	0.48
1:CA:1228:C:H2'	1:CA:1229:A:H8	1.78	0.48
1:CA:337:C:H2'	1:CA:338:A:C8	2.48	0.48
1:CA:1457:G:H5''	20:CT:35:THR:HG21	1.95	0.48
23:CW:76:A:H4'	25:DA:2506:U:O2'	2.12	0.48
25:DA:1778:U:H2'	25:DA:1784:A:N6	2.27	0.48
25:DA:2128:C:H1'	25:DA:2173:A:O2'	2.12	0.48
25:DA:443:A:N7	29:DF:45:ARG:HG2	2.28	0.48
28:DE:119:ARG:HB3	28:DE:120:TRP:CD1	2.48	0.48
28:DE:11:MET:HG2	28:DE:24:THR:HB	1.96	0.48
28:DE:9:VAL:HG22	28:DE:25:VAL:HB	1.95	0.48
1:AA:447:G:H2'	1:AA:485:G:N2	2.28	0.48
1:AA:620:C:H2'	1:AA:621:A:O4'	2.14	0.48
8:AH:82:HIS:N	8:AH:138:TRP:O	2.47	0.48
23:AW:62:C:H2'	23:AW:63:G:H8	1.79	0.48
25:BA:2033:U:OP1	42:BW:42:ARG:NH1	2.43	0.48
25:BA:2486:C:H5''	25:BA:2487:C:OP2	2.13	0.48
30:BG:7:LEU:HD11	30:BG:107:LEU:HD12	1.96	0.48
32:BI:116:LEU:HD21	32:BI:119:PRO:HA	1.96	0.48
25:BA:63:A:H1'	43:BX:66:LEU:HB2	1.94	0.48
1:CA:1002:G:C5	1:CA:1003:G:C8	3.02	0.48
1:CA:1126:U:H3	10:CJ:40:LEU:HD11	1.78	0.48
5:CE:24:ARG:NH1	22:CV:24:A:OP2	2.46	0.48
6:CF:2:ARG:NE	6:CF:69:GLU:HG2	2.28	0.48
1:CA:1317:C:OP2	14:CN:17:LYS:HE3	2.13	0.48
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.42	0.48
25:DA:323:G:O2'	25:DA:1205:U:N3	2.23	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:5:LYS:HD2	15:AO:5:LYS:H	1.78	0.48
23:AY:33:U:H3'	23:AY:34:G:H5''	1.95	0.48
25:BA:390:G:H2'	25:BA:391:G:C8	2.49	0.48
25:BA:2482:G:OP1	36:BQ:56:ARG:NH2	2.47	0.48
42:BW:25:ARG:NH2	42:BW:74:ALA:O	2.28	0.48
1:CA:1002:G:C4	1:CA:1003:G:C8	2.99	0.48
1:CA:1316:G:H22	1:CA:1319:A:H5''	1.79	0.48
1:CA:601:C:H2'	1:CA:602:A:C8	2.49	0.48
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.95	0.48
9:CI:23:ASN:HB2	9:CI:25:LYS:HE3	1.94	0.48
25:DA:143:G:C2	25:DA:143(A):C:C2	3.02	0.48
30:DG:179:PRO:HB2	50:D4:42:PHE:HE1	1.78	0.48
1:AA:1029:C:N3	1:AA:1032:G:O6	2.46	0.48
1:AA:486:U:H2'	1:AA:487:A:H8	1.77	0.48
1:AA:628:G:H2'	1:AA:629:G:C8	2.49	0.48
13:AM:79:LYS:HA	13:AM:82:MET:HE2	1.95	0.48
25:BA:1093:G:H2'	25:BA:1156:G:H22	1.77	0.48
42:BW:48:ALA:O	42:BW:52:GLU:HB2	2.13	0.48
1:CA:1008:C:H2'	1:CA:1009:G:O4'	2.13	0.48
1:CA:174:C:H2'	1:CA:175:C:H6	1.79	0.48
1:CA:522:C:OP2	12:CL:69:TYR:OH	2.25	0.48
1:CA:73:G:C6	1:CA:97:G:C6	3.02	0.48
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.47	0.48
7:CG:113:GLU:CG	7:CG:119:ARG:HG2	2.44	0.48
11:CK:15:ALA:HA	11:CK:76:GLY:O	2.13	0.48
25:DA:1354:A:H2'	25:DA:1355:G:O4'	2.13	0.48
25:DA:1358:G:O2'	25:DA:1359:A:H5''	2.14	0.48
25:DA:1991:U:H2'	25:DA:1992:G:H5''	1.95	0.48
25:DA:2042:A:OP1	61:DA:4181:HOH:O	2.20	0.48
1:AA:1292:U:OP2	7:AG:41:ARG:NH2	2.47	0.48
1:AA:738:C:H2'	1:AA:739:C:H6	1.78	0.48
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.60	0.48
7:AG:153:HIS:HA	7:AG:155:ARG:NH2	2.29	0.48
25:BA:1845:G:H4'	27:BD:51:VAL:HG21	1.96	0.48
25:BA:185:A:H2'	25:BA:185:A:N3	2.29	0.48
25:BA:2760:G:O6	25:BA:2768:C:H5''	2.13	0.48
25:BA:2802:C:O2'	25:BA:2803:A:H4'	2.14	0.48
25:BA:671:A:H2'	25:BA:672:G:O4'	2.13	0.48
25:BA:821:A:H2'	25:BA:821:A:N3	2.29	0.48
26:BB:7:G:H5''	26:BB:7:G:H8	1.78	0.48
43:BX:60:ARG:HA	43:BX:75:ASP:OD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1051:C:H2'	1:CA:1052:U:H6	1.79	0.48
1:CA:1129:C:H1'	1:CA:1130:A:N7	2.28	0.48
1:CA:1064:G:O6	1:CA:1191:A:N6	2.46	0.48
1:CA:171:A:H2'	1:CA:172:A:C8	2.49	0.48
24:CX:59:A:H2'	24:CX:60:U:H5'	1.95	0.48
25:DA:1204:A:H61	25:DA:1240:U:H2'	1.79	0.48
25:DA:2059:A:O2'	29:DF:69:HIS:HD2	1.97	0.48
25:DA:322:A:H5'	25:DA:340:A:H1'	1.95	0.48
25:DA:997:G:OP1	40:DU:92:ARG:HG2	2.12	0.48
33:DN:82:LEU:HD23	33:DN:84:LYS:HE2	1.96	0.48
39:DT:11:GLU:O	39:DT:15:VAL:HG23	2.14	0.48
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.49	0.48
3:AC:181:ASN:HD22	3:AC:204:LEU:HB2	1.77	0.48
50:B4:53:GLU:HG3	50:B4:55:ARG:N	2.29	0.48
35:BP:59:LEU:HD21	54:B8:10:ALA:HA	1.95	0.48
25:BA:2627:U:H2'	25:BA:2628:C:H6	1.79	0.48
29:BF:164:ARG:O	29:BF:168:ARG:HB2	2.14	0.48
36:BQ:135:ASP:N	36:BQ:138:ASP:OD2	2.34	0.48
45:BZ:65:GLN:HB3	45:BZ:67:LEU:HD21	1.95	0.48
4:CD:150:GLU:HA	4:CD:153:ARG:HE	1.79	0.48
7:CG:132:GLY:O	7:CG:136:LYS:HG2	2.14	0.48
9:CI:24:GLY:HA2	9:CI:59:PHE:O	2.14	0.48
1:AA:1053:G:H4'	1:AA:1054:C:H5'	1.94	0.48
1:AA:486:U:H2'	1:AA:487:A:C8	2.49	0.48
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.14	0.48
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.14	0.48
19:AS:51:VAL:O	19:AS:58:VAL:N	2.43	0.48
50:B4:24:THR:OG1	50:B4:25:TYR:N	2.45	0.48
25:BA:2327:G:H2'	25:BA:2328:C:C6	2.49	0.48
42:BW:14:PRO:HG2	42:BW:78:GLU:CG	2.43	0.48
44:BY:99:CYS:HB2	44:BY:106:LEU:HD21	1.95	0.48
45:BZ:111:VAL:C	45:BZ:113:ALA:H	2.17	0.48
1:CA:1060:C:H5'	10:CJ:51:ARG:HB3	1.96	0.48
1:CA:757:U:H2'	1:CA:758:G:O4'	2.13	0.48
1:CA:976:G:C8	1:CA:1358:U:C2	3.02	0.48
2:CB:16:HIS:HB2	2:CB:204:ASN:CB	2.43	0.48
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.14	0.48
23:CY:38:A:H2'	23:CY:39:PSU:O4'	2.13	0.48
25:DA:2029:G:H2'	25:DA:2031:A:OP1	2.14	0.48
25:DA:2334:G:O6	46:D0:74:ARG:NH2	2.46	0.48
25:DA:322:A:OP1	29:DF:168:ARG:HD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DE:24:THR:HG23	28:DE:184:VAL:HG12	1.96	0.48
29:DF:164:ARG:O	29:DF:168:ARG:HB2	2.14	0.48
31:DH:90:LYS:HD2	31:DH:163:TYR:CD1	2.49	0.48
2:AB:95:GLN:HG3	2:AB:147:LYS:HD3	1.96	0.48
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.14	0.48
7:AG:72:ARG:HG2	7:AG:72:ARG:H	1.42	0.48
13:AM:23:TYR:HB3	13:AM:67:GLU:HA	1.95	0.48
29:BF:33:LEU:HD22	29:BF:112:MET:HE3	1.96	0.48
31:BH:4:ILE:O	31:BH:69:ARG:HG2	2.14	0.48
1:CA:12:U:H4'	1:CA:526:C:O2'	2.13	0.48
1:CA:1388:C:H2'	1:CA:1389:C:C6	2.49	0.48
1:CA:275:G:H5'	17:CQ:14:LYS:HB3	1.96	0.48
1:CA:299:G:H2'	1:CA:300:A:C8	2.49	0.48
1:CA:779:C:H2'	1:CA:780:A:O4'	2.13	0.48
3:CC:164:ARG:HG2	3:CC:165:THR:H	1.79	0.48
3:CC:39:ILE:HG23	3:CC:91:LEU:HD11	1.96	0.48
4:CD:173:TRP:CZ3	4:CD:193:ASP:HB3	2.49	0.48
25:DA:534:U:H2'	25:DA:535:C:C6	2.49	0.48
32:DI:57:ARG:HA	32:DI:61:ARG:NH2	2.28	0.48
25:DA:910:A:C5	36:DQ:13:GLN:HG3	2.48	0.48
41:DV:29:PRO:HG3	41:DV:63:GLY:HA2	1.95	0.48
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.49	0.47
1:AA:1399:C:H4'	1:AA:1400:C:O5'	2.14	0.47
1:AA:56:U:H2'	1:AA:57:G:C8	2.49	0.47
2:AB:115:LEU:O	2:AB:119:GLU:HG2	2.14	0.47
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.14	0.47
5:AE:38:GLN:HB2	5:AE:38:GLN:HE21	1.55	0.47
10:AJ:8:LEU:HD22	10:AJ:96:ILE:HG12	1.95	0.47
25:BA:1938:A:H2'	25:BA:1939:U:O4'	2.13	0.47
31:BH:3:ARG:CG	31:BH:6:ARG:HG2	2.44	0.47
1:CA:1176:A:H2'	1:CA:1177:G:O4'	2.14	0.47
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.49	0.47
1:CA:96:U:O2'	1:CA:97:G:H5'	2.14	0.47
1:CA:921:U:O2	5:CE:19:MET:HB2	2.13	0.47
1:CA:376:G:H4'	16:CP:5:ARG:HD3	1.96	0.47
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.49	0.47
25:DA:1257:C:H4'	29:DF:83:PHE:CD2	2.49	0.47
25:DA:623:G:H2'	25:DA:624:C:C6	2.49	0.47
26:DB:41:U:H5	30:DG:70:VAL:H	1.60	0.47
38:DS:105:ALA:O	38:DS:110:LEU:HB2	2.14	0.47
1:AA:1057:G:OP2	61:AA:4034:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:659:C:H2'	25:BA:660:C:C6	2.48	0.47
31:BH:90:LYS:HD3	31:BH:159:GLU:HG2	1.96	0.47
1:CA:1239:A:H62	1:CA:1299:A:H62	1.62	0.47
1:CA:646:U:H2'	1:CA:647:C:H6	1.78	0.47
1:CA:865:A:H5'	1:CA:1078:U:C5	2.49	0.47
13:CM:50:GLU:HA	13:CM:53:VAL:HB	1.96	0.47
23:CW:9:A:O2'	23:CW:10:G:N7	2.47	0.47
25:DA:1263:U:C4	25:DA:1264:G:C6	3.02	0.47
25:DA:2331:G:O2'	46:D0:43:THR:HG22	2.14	0.47
25:DA:315:G:H2'	25:DA:316:C:C6	2.49	0.47
25:DA:851:U:O2'	49:D3:42:ALA:O	2.32	0.47
13:AM:11:ARG:C	13:AM:13:LYS:H	2.17	0.47
25:BA:1513:G:H2'	25:BA:1594:C:H41	1.80	0.47
25:BA:1882:U:H2'	25:BA:1883:C:O4'	2.14	0.47
28:BE:101:ARG:CZ	28:BE:171:GLU:HB2	2.44	0.47
25:BA:346:A:OP2	29:BF:169:ASN:HB2	2.14	0.47
29:BF:18:ARG:NH2	29:BF:127:GLU:OE1	2.46	0.47
30:BG:126:ASP:OD2	30:BG:130:ASN:ND2	2.38	0.47
25:BA:185:A:H62	35:BP:38:GLN:HE22	1.62	0.47
1:CA:9:G:H2'	1:CA:10:A:C8	2.49	0.47
3:CC:32:LEU:H	3:CC:32:LEU:HD22	1.79	0.47
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.96	0.47
13:CM:122:LYS:CD	13:CM:123:ALA:H	2.27	0.47
23:CW:46:7MG:O2'	23:CW:47:U:O5'	2.29	0.47
25:DA:1685:C:H2'	25:DA:1686:C:C6	2.49	0.47
25:DA:2127:G:N2	25:DA:2161:C:N3	2.63	0.47
25:DA:2651:C:C2'	25:DA:2652:C:H5'	2.45	0.47
25:DA:2651:C:H2'	25:DA:2652:C:H5'	1.97	0.47
45:DZ:156:LYS:HG2	45:DZ:158:PRO:HD3	1.97	0.47
45:DZ:53:ILE:HG22	45:DZ:71:VAL:O	2.14	0.47
1:AA:342:C:C2	1:AA:348:G:N2	2.82	0.47
1:AA:833:U:H2'	1:AA:834:C:H6	1.79	0.47
4:AD:166:LYS:HB2	4:AD:168:ARG:NH2	2.30	0.47
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.14	0.47
1:AA:642:A:N3	8:AH:113:SER:OG	2.46	0.47
13:AM:96:LEU:O	13:AM:110:ARG:NH1	2.32	0.47
15:AO:16:ALA:HB1	15:AO:21:ASP:HB3	1.97	0.47
49:B3:23:LEU:HD13	49:B3:50:VAL:HG11	1.96	0.47
25:BA:211:A:H3'	25:BA:448:U:H5'	1.96	0.47
25:BA:2139:A:O2'	25:BA:2140:U:H5''	2.14	0.47
25:BA:2163:G:H1	25:BA:2171:G:N2	2.12	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2138:G:N1	25:BA:2184:G:OP1	2.31	0.47
25:BA:2658:C:H2'	25:BA:2659:U:O4'	2.14	0.47
44:BY:86:ARG:NH1	44:BY:100:ALA:HB1	2.29	0.47
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.13	0.47
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.78	0.47
23:CW:23:A:H2'	23:CW:24:G:H8	1.80	0.47
25:DA:1011:G:OP2	40:DU:70:ARG:NH2	2.48	0.47
25:DA:1503:U:H2'	25:DA:1504:C:C6	2.50	0.47
25:DA:2532:G:H1'	25:DA:2663:G:N2	2.29	0.47
25:DA:2849:U:H4'	25:DA:2868:A:C2	2.49	0.47
25:DA:2886:G:N7	61:DA:4437:HOH:O	2.35	0.47
25:DA:852:G:H2'	25:DA:853:G:H8	1.77	0.47
31:DH:126:PRO:HG2	31:DH:130:ARG:HD2	1.96	0.47
31:DH:18:GLU:HG2	31:DH:19:VAL:N	2.29	0.47
32:DI:40:THR:O	32:DI:44:LEU:HB2	2.14	0.47
33:DN:123:TYR:HH	33:DN:130:HIS:CD2	2.28	0.47
25:DA:2684:U:O2'	34:DO:68:GLU:OE1	2.32	0.47
1:AA:1370:G:O6	61:AA:4100:HOH:O	2.20	0.47
1:AA:184:G:H2'	1:AA:185:A:C8	2.50	0.47
1:AA:625:G:H2'	1:AA:626:U:C6	2.50	0.47
12:AL:7:ILE:O	12:AL:11:VAL:HG23	2.14	0.47
25:BA:1153:G:N3	25:BA:1153:G:H2'	2.29	0.47
25:BA:211:A:H5''	25:BA:448:U:OP1	2.14	0.47
30:BG:43:LEU:HD11	30:BG:153:ARG:HG2	1.95	0.47
31:BH:90:LYS:HD2	31:BH:163:TYR:CD1	2.49	0.47
38:BS:11:LYS:O	38:BS:15:ARG:HG3	2.14	0.47
1:CA:1399:C:C2	1:CA:1502:A:N6	2.83	0.47
1:CA:232:G:H1'	1:CA:262:A:N1	2.29	0.47
1:CA:250:A:H4'	1:CA:251:G:O5'	2.13	0.47
5:CE:84:PHE:N	5:CE:87:SER:O	2.48	0.47
9:CI:23:ASN:ND2	9:CI:23:ASN:H	2.12	0.47
19:CS:51:VAL:O	19:CS:58:VAL:N	2.40	0.47
25:DA:194:G:H2'	25:DA:195:A:O4'	2.14	0.47
25:DA:2320:A:N3	25:DA:2320:A:H2'	2.28	0.47
25:DA:2336:A:H61	46:D0:43:THR:HG22	1.79	0.47
25:DA:2461:C:H2'	25:DA:2462:U:C6	2.50	0.47
25:DA:2704:C:H2'	25:DA:2705:A:O4'	2.15	0.47
1:AA:1004:A:H5''	1:AA:1025:U:H5	1.79	0.47
1:AA:1029:C:N4	1:AA:1030:C:H41	2.13	0.47
1:AA:6:G:H4'	1:AA:298:A:H4'	1.97	0.47
1:AA:438:G:H4'	4:AD:123:HIS:HD1	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:501:C:H2'	1:AA:502:G:C8	2.50	0.47
1:AA:695:A:H2'	1:AA:696:A:C8	2.49	0.47
4:AD:162:LEU:CD1	4:AD:181:MET:HG2	2.45	0.47
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.80	0.47
25:BA:898:U:O2'	49:B3:42:ALA:O	2.30	0.47
50:B4:44:THR:O	50:B4:46:GLN:N	2.47	0.47
25:BA:2096:U:H2'	25:BA:2097:U:C6	2.49	0.47
25:BA:2175:G:N3	25:BA:2175:G:H2'	2.29	0.47
25:BA:274:U:H3'	25:BA:275:C:C5'	2.44	0.47
27:BD:26:LYS:HE2	27:BD:28:GLU:O	2.14	0.47
39:BT:112:ARG:HG3	39:BT:115:ARG:HH21	1.78	0.47
40:BU:66:ASN:O	40:BU:70:ARG:HG3	2.15	0.47
45:BZ:105:VAL:O	45:BZ:140:ASP:HA	2.14	0.47
45:BZ:126:VAL:CG1	45:BZ:161:VAL:HG23	2.43	0.47
1:CA:109:A:C6	1:CA:326:G:C6	3.03	0.47
1:CA:1378:C:H5	1:CA:1379:G:H1'	1.79	0.47
1:CA:1391:U:H2'	1:CA:1392:G:C8	2.50	0.47
1:CA:1392:G:N2	1:CA:1502:A:H8	2.12	0.47
19:CS:27:GLU:HB2	19:CS:28:LYS:NZ	2.28	0.47
47:D1:54:ALA:HB1	47:D1:83:GLU:HG3	1.96	0.47
25:DA:1386:C:H2'	25:DA:1387:C:H6	1.79	0.47
25:DA:1667:G:O2'	25:DA:1991:U:O4	2.26	0.47
25:DA:2299:G:H2'	25:DA:2300:G:C8	2.47	0.47
29:DF:12:LEU:HB2	29:DF:124:LEU:HD11	1.96	0.47
25:DA:2748:A:H5'	31:DH:4:ILE:HD12	1.96	0.47
33:DN:67:LEU:HB3	33:DN:88:GLU:HG3	1.97	0.47
43:DX:54:VAL:HG22	43:DX:81:VAL:HG12	1.95	0.47
1:AA:193:C:H2'	1:AA:194:C:C6	2.49	0.47
9:AI:26:VAL:HG13	9:AI:61:ALA:HB3	1.96	0.47
10:AJ:76:ASN:HA	10:AJ:77:PRO:HD2	1.68	0.47
23:AW:7:A:N6	23:AW:66:U:H3	2.10	0.47
25:BA:1756:U:H2'	25:BA:1757:C:C6	2.50	0.47
25:BA:1814:A:N7	61:BA:5150:HOH:O	2.35	0.47
25:BA:1993:A:OP2	27:BD:242:ARG:NH2	2.48	0.47
1:CA:1132:C:N4	1:CA:1142:G:H1	2.12	0.47
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.95	0.47
1:CA:408:A:H4'	4:CD:112:VAL:HG21	1.97	0.47
1:CA:886:G:O6	61:CA:4005:HOH:O	2.18	0.47
2:CB:17:PHE:HB2	2:CB:44:LEU:HD21	1.96	0.47
2:CB:207:ALA:HB3	2:CB:210:SER:HB3	1.95	0.47
3:CC:19:GLU:HB3	3:CC:40:ARG:NH2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:34:ARG:HG3	12:CL:105:TYR:CE2	2.50	0.47
25:DA:116:C:H2'	25:DA:117:G:O4'	2.15	0.47
25:DA:1297:C:OP1	25:DA:2710:C:H4'	2.14	0.47
25:DA:2635:C:H5''	28:DE:78:LEU:O	2.15	0.47
31:DH:46:GLU:HB2	31:DH:49:VAL:HG13	1.97	0.47
38:DS:80:LEU:HA	38:DS:80:LEU:HD12	1.76	0.47
39:DT:117:ASP:OD2	39:DT:120:ARG:NE	2.39	0.47
1:AA:164:U:H2'	1:AA:165:C:C6	2.50	0.47
1:AA:841:U:C5	1:AA:848:C:H1'	2.49	0.47
52:B6:10:LEU:HG	52:B6:54:ILE:HG13	1.97	0.47
25:BA:1640:G:H2'	25:BA:1641:G:O4'	2.14	0.47
25:BA:2641:A:H1'	25:BA:2642:G:H5''	1.95	0.47
25:BA:2021:C:H5''	25:BA:2736:C:O2'	2.15	0.47
25:BA:2745:G:OP1	28:BE:203:LYS:NZ	2.43	0.47
25:BA:670:C:H5'	25:BA:671:A:OP2	2.15	0.47
31:BH:20:ALA:HB1	31:BH:21:PRO:HD2	1.96	0.47
37:BR:118:GLU:H	37:BR:118:GLU:CD	2.18	0.47
39:BT:33:LYS:O	39:BT:82:LEU:HD23	2.15	0.47
45:BZ:145:GLU:H	45:BZ:148:ASP:HB2	1.79	0.47
1:CA:538:G:H5''	12:CL:114:LYS:HB2	1.96	0.47
2:CB:19:HIS:ND1	2:CB:20:GLU:HG2	2.29	0.47
2:CB:48:MET:O	2:CB:52:GLU:N	2.48	0.47
2:CB:87:ARG:HD3	2:CB:234:PRO:HD2	1.97	0.47
7:CG:103:TRP:CH2	7:CG:141:VAL:HG21	2.50	0.47
1:CA:1187:G:P	9:CI:113:LYS:HZ1	2.38	0.47
24:CX:47:U:H5'	24:CX:48:C:H5'	1.97	0.47
25:DA:1926:U:O2'	25:DA:1928:A:N7	2.37	0.47
28:DE:5:LEU:HD11	28:DE:79:ARG:HB2	1.96	0.47
25:DA:2316:C:H1'	30:DG:128:ARG:HH21	1.79	0.47
31:DH:11:VAL:HG13	31:DH:15:VAL:HG13	1.96	0.47
36:DQ:77:LYS:NZ	36:DQ:86:GLY:O	2.46	0.47
41:DV:60:GLU:HB3	41:DV:95:LEU:HB3	1.97	0.47
41:DV:16:PRO:HD3	41:DV:99:ILE:HD11	1.95	0.47
1:AA:920:U:H2'	1:AA:921:U:C6	2.49	0.47
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.15	0.47
19:AS:27:GLU:CD	19:AS:27:GLU:H	2.18	0.47
20:AT:77:ALA:O	20:AT:81:LYS:HG3	2.14	0.47
23:AY:54:5MU:O2	23:AY:58:A:N7	2.48	0.47
25:BA:2141:A:C2	25:BA:2192:A:H2'	2.50	0.47
26:BB:75:G:H8	26:BB:75:G:H5''	1.79	0.47
1:CA:997:U:H3	1:CA:1044:A:H61	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1245:A:N6	1:CA:1292:U:H3	2.13	0.47
1:CA:741:G:H2'	1:CA:742:G:O4'	2.15	0.47
1:CA:955:U:O2'	19:CS:83:HIS:HD2	1.98	0.47
8:CH:51:VAL:HG11	8:CH:60:ARG:HH12	1.79	0.47
8:CH:51:VAL:HG12	8:CH:52:ASP:H	1.80	0.47
1:CA:1054:C:C5	23:CW:34:G:H1'	2.49	0.47
25:DA:1019:U:H2'	25:DA:1020:A:H8	1.79	0.47
25:DA:2080:G:H2'	25:DA:2081:C:C6	2.49	0.47
25:DA:2114:A:H8	25:DA:2168:G:HO2'	1.63	0.47
25:DA:271(D):G:H2'	25:DA:271(E):U:C6	2.50	0.47
25:DA:889:C:O2'	25:DA:890:A:O5'	2.29	0.47
32:DI:4:ILE:HG12	32:DI:18:VAL:HG22	1.97	0.47
45:DZ:45:ASP:OD2	45:DZ:49:ARG:HD2	2.15	0.47
2:AB:61:LEU:HD23	2:AB:68:ILE:HD11	1.97	0.47
18:AR:38:GLU:HA	18:AR:41:LYS:HD2	1.97	0.47
23:AW:51:U:H2'	23:AW:52:G:H8	1.75	0.47
23:AY:2:C:N4	23:AY:71:G:N1	2.39	0.47
25:BA:1537:G:O2'	27:BD:101:GLU:HB2	2.15	0.47
25:BA:1694:G:OP1	61:BA:5334:HOH:O	2.20	0.47
25:BA:2230:U:O2	47:B1:52:ARG:NH2	2.48	0.47
25:BA:2398:C:O2'	61:BA:5405:HOH:O	2.20	0.47
34:BO:107:ARG:CZ	39:BT:36:GLU:HG2	2.45	0.47
34:BO:68:GLU:HB3	34:BO:78:ARG:HB2	1.96	0.47
39:BT:118:ARG:HD2	39:BT:118:ARG:HA	1.66	0.47
1:CA:1262:C:H2'	1:CA:1263:C:C6	2.49	0.47
1:CA:685:G:C2	1:CA:686:U:C4	3.03	0.47
7:CG:114:ARG:HB2	7:CG:115:ARG:HH21	1.80	0.47
15:CO:48:LYS:HD3	15:CO:48:LYS:HA	1.69	0.47
23:CW:39:PSU:H2'	23:CW:40:C:C6	2.50	0.47
25:DA:1471:A:H3'	25:DA:1472:A:H8	1.79	0.47
25:DA:1786:A:OP1	25:DA:1980:G:N2	2.39	0.47
25:DA:2124:G:H1	25:DA:2174:C:H42	1.59	0.47
25:DA:2390:U:OP2	54:D8:35:GLN:NE2	2.32	0.47
25:DA:271(E):U:H2'	25:DA:271(F):C:C6	2.50	0.47
25:DA:493:G:H2'	25:DA:494:G:O4'	2.14	0.47
1:AA:1028:C:H2'	1:AA:1029:C:H4'	1.97	0.47
1:AA:748:C:H4'	1:AA:749:C:O5'	2.15	0.47
2:AB:145:LEU:O	2:AB:149:LEU:HB2	2.14	0.47
6:AF:75:LEU:O	6:AF:79:LEU:HG	2.15	0.47
13:AM:11:ARG:O	13:AM:13:LYS:N	2.46	0.47
25:BA:905:U:O2	25:BA:2280:A:H2'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2527:C:O2'	25:BA:2528:G:H5'	2.15	0.47
39:BT:127:ALA:O	39:BT:128:GLU:HB2	2.15	0.47
1:CA:784:C:H4'	25:DA:1837:C:OP1	2.15	0.47
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.97	0.47
3:CC:70:VAL:O	3:CC:106:VAL:N	2.48	0.47
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.50	0.47
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.49	0.47
1:CA:750:G:H1'	15:CO:22:THR:OG1	2.15	0.47
13:CM:65:LYS:HA	50:D4:50:VAL:HG11	1.97	0.47
25:DA:2584:U:H2'	25:DA:2585:U:H2'	1.97	0.47
25:DA:2631:G:N2	25:DA:2787:C:O2	2.38	0.47
25:DA:286:C:H2'	25:DA:287:C:C6	2.50	0.47
26:DB:78:A:C2	26:DB:100:A:C4	3.03	0.47
25:DA:2572:A:C8	28:DE:144:ARG:HD2	2.50	0.47
1:AA:473:G:H2'	1:AA:474:G:C8	2.50	0.46
24:AX:13:C:O2'	25:BA:1946:C:H4'	2.15	0.46
29:BF:129:PHE:CD2	29:BF:163:VAL:HG21	2.50	0.46
31:BH:33:LEU:HD21	31:BH:136:ILE:HG13	1.97	0.46
32:BI:60:GLU:HG3	32:BI:61:ARG:HD2	1.97	0.46
1:CA:1227:A:P	13:CM:111:LYS:HZ1	2.38	0.46
11:CK:99:GLN:HG2	11:CK:105:VAL:HG21	1.96	0.46
14:CN:47:LEU:O	14:CN:51:GLY:N	2.48	0.46
35:DP:68:GLN:HG3	54:D8:12:LYS:HG2	1.97	0.46
25:DA:2271:G:C5	25:DA:2272:U:C5	3.03	0.46
25:DA:221:A:C8	25:DA:266:G:C6	3.03	0.46
25:DA:478:A:N1	25:DA:500:G:H4'	2.30	0.46
25:DA:963:U:OP1	61:DA:4058:HOH:O	2.21	0.46
26:DB:80:U:H2'	26:DB:81:G:C8	2.49	0.46
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.49	0.46
1:AA:662:G:H2'	1:AA:663:A:C8	2.49	0.46
2:AB:32:ILE:HG21	2:AB:40:HIS:HD2	1.79	0.46
4:AD:133:VAL:HG12	4:AD:135:LEU:H	1.79	0.46
16:AP:19:ILE:HG22	16:AP:37:GLY:C	2.36	0.46
25:BA:1475:G:H2'	25:BA:1476:C:H6	1.79	0.46
25:BA:1891:G:H2'	25:BA:1892:G:O4'	2.15	0.46
25:BA:2561:G:O6	61:BA:4141:HOH:O	2.20	0.46
25:BA:2720:G:H1'	37:BR:71:GLN:NE2	2.26	0.46
25:BA:2834:C:H5	61:BA:4097:HOH:O	1.98	0.46
1:CA:1039:C:C4	1:CA:1040:U:C4	3.03	0.46
1:CA:1118:C:H2'	1:CA:1119:C:C6	2.42	0.46
1:CA:1133:G:C4	1:CA:1134:G:C8	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:113:ALA:HB2	3:CC:202:ILE:HG13	1.97	0.46
9:CI:23:ASN:ND2	9:CI:25:LYS:HG2	2.30	0.46
25:DA:1015:G:H2'	25:DA:1016:G:H8	1.80	0.46
25:DA:392:C:H5''	25:DA:409:C:H5''	1.97	0.46
25:DA:223:A:O2'	25:DA:420:C:O2	2.29	0.46
25:DA:900:A:O2'	25:DA:901:A:OP1	2.33	0.46
25:DA:955:C:OP1	36:DQ:87:LYS:HE3	2.16	0.46
43:DX:9:LEU:HA	48:D2:36:ARG:HH21	1.80	0.46
25:DA:300:A:P	44:DY:86:ARG:HH22	2.38	0.46
1:AA:76:C:O2	1:AA:93:G:N1	2.32	0.46
2:AB:62:ALA:HB3	2:AB:225:ALA:HB3	1.97	0.46
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.96	0.46
1:AA:376:G:P	16:AP:67:THR:HG21	2.56	0.46
1:AA:236:G:H5''	17:AQ:42:TYR:OH	2.15	0.46
24:AX:8:4SU:O2	24:AX:21:A:H2	1.98	0.46
23:AY:19:G:H1	23:AY:56:C:N4	2.09	0.46
47:B1:86:SER:OG	47:B1:89:GLU:OE1	2.24	0.46
13:AM:57:ARG:CZ	50:B4:34:GLU:HB3	2.45	0.46
25:BA:733:G:C4	53:B7:11:LYS:HG2	2.50	0.46
53:B7:30:VAL:O	53:B7:34:ARG:HG3	2.15	0.46
32:BI:96:ASP:OD1	32:BI:96:ASP:N	2.47	0.46
40:BU:104:GLN:H	40:BU:104:GLN:CD	2.18	0.46
1:CA:1057:G:H2'	1:CA:1058:G:O4'	2.16	0.46
1:CA:735:C:H2'	1:CA:736:C:C6	2.50	0.46
7:CG:48:LYS:O	7:CG:52:GLU:HG2	2.16	0.46
7:CG:79:ARG:HB3	7:CG:79:ARG:CZ	2.45	0.46
26:DB:12:C:O2'	46:D0:74:ARG:HG2	2.15	0.46
25:DA:144:C:H2'	25:DA:145:G:H8	1.80	0.46
25:DA:1857:G:C6	25:DA:1858:G:C6	3.03	0.46
25:DA:1151:G:H4'	40:DU:81:HIS:CG	2.51	0.46
44:DY:20:TYR:CE1	44:DY:43:ASN:HA	2.50	0.46
45:DZ:3:TYR:O	45:DZ:57:ILE:HA	2.16	0.46
19:AS:3:ARG:HH21	19:AS:7:LYS:HB3	1.79	0.46
23:AY:3:C:H42	23:AY:70:G:H1	1.64	0.46
25:BA:876:A:N7	25:BA:2260:C:H5'	2.31	0.46
25:BA:2331:G:N2	38:BS:3:ARG:HA	2.31	0.46
25:BA:2541:G:H5''	25:BA:2542:A:H5''	1.98	0.46
25:BA:305:G:O2'	25:BA:383:A:N6	2.45	0.46
41:BV:52:VAL:HG22	41:BV:55:ALA:HB3	1.98	0.46
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.14	0.46
1:CA:918:A:H2'	1:CA:919:A:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:54:THR:HG21	2:CB:201:ILE:HD11	1.97	0.46
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.97	0.46
8:CH:91:ARG:NH1	17:CQ:33:GLY:HA3	2.30	0.46
19:CS:51:VAL:HB	19:CS:75:ALA:HB2	1.97	0.46
23:CW:75:C:H2'	23:CW:76:A:C4	2.50	0.46
48:D2:16:LEU:O	48:D2:67:LYS:NZ	2.49	0.46
25:DA:477:A:H2'	25:DA:478:A:C8	2.51	0.46
25:DA:1803:A:H4'	27:DD:259:THR:HG23	1.98	0.46
1:AA:870:U:H4'	1:AA:871:U:H5''	1.97	0.46
5:AE:121:LYS:HG3	5:AE:123:LEU:HG	1.98	0.46
12:AL:84:LEU:HB2	12:AL:105:TYR:CE2	2.50	0.46
25:BA:1221:G:H21	25:BA:1222:A:H4'	1.80	0.46
25:BA:1496:A:H5'	25:BA:1497:G:OP2	2.15	0.46
25:BA:2285:A:H2'	25:BA:2286:A:C8	2.49	0.46
25:BA:2504:U:H2'	25:BA:2505:U:C6	2.51	0.46
25:BA:2660:C:H2'	25:BA:2661:U:C6	2.50	0.46
25:BA:864:C:H4'	25:BA:977:G:C5	2.51	0.46
1:CA:1202:G:O4'	14:CN:29:ARG:NH1	2.49	0.46
1:CA:1243:C:H42	1:CA:1294:G:H1	1.63	0.46
1:CA:407:G:OP1	4:CD:115:ARG:HD2	2.16	0.46
2:CB:201:ILE:O	2:CB:203:GLY:N	2.48	0.46
2:CB:35:GLU:OE2	2:CB:38:GLY:HA2	2.16	0.46
1:CA:1187:G:OP1	9:CI:113:LYS:NZ	2.49	0.46
17:CQ:9:VAL:HG13	17:CQ:56:VAL:HG22	1.97	0.46
23:CW:29:G:H2'	23:CW:30:G:C8	2.51	0.46
47:D1:83:GLU:HA	47:D1:84:GLY:HA2	1.64	0.46
25:DA:1434:A:H61	25:DA:1558:A:N6	2.14	0.46
23:CY:71:G:H4'	25:DA:1851:U:H4'	1.97	0.46
25:DA:521:G:H2'	25:DA:522:G:H8	1.80	0.46
26:DB:33:G:C2	26:DB:50:G:C2	3.04	0.46
27:DD:108:PRO:HB3	27:DD:143:HIS:CE1	2.50	0.46
29:DF:187:VAL:HG11	35:DP:6:LEU:HD11	1.97	0.46
35:DP:47:ASP:OD2	35:DP:50:ARG:HD3	2.16	0.46
1:AA:1278:U:H6	1:AA:1278:U:H3'	1.81	0.46
1:AA:202:U:O2'	1:AA:203:U:O5'	2.29	0.46
1:AA:614:A:H2'	1:AA:615:C:O4'	2.15	0.46
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.30	0.46
4:AD:53:ASP:O	4:AD:57:ARG:HG3	2.16	0.46
9:AI:4:TYR:CE1	9:AI:88:TYR:HD1	2.34	0.46
25:BA:1093:G:HO2'	25:BA:1094:A:H8	1.64	0.46
25:BA:1289:G:O2'	35:BP:7:ARG:NH2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2160:C:H2'	25:BA:2160:C:O2	2.15	0.46
25:BA:2209:G:H2'	25:BA:2210:C:O4'	2.15	0.46
42:BW:18:ARG:NH1	42:BW:76:VAL:O	2.49	0.46
1:CA:1006:C:OP1	1:CA:1037:C:O2'	2.33	0.46
1:CA:573:A:N3	1:CA:883:C:O2'	2.45	0.46
3:CC:11:ARG:HB3	3:CC:15:THR:HB	1.97	0.46
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.98	0.46
24:CX:23:C:H2'	24:CX:24:U:C6	2.50	0.46
24:CX:59:A:C2'	24:CX:60:U:H5'	2.46	0.46
23:CY:51:U:O4	23:CY:63:G:O6	2.33	0.46
23:CY:71:G:H2'	23:CY:72:C:C6	2.51	0.46
49:D3:6:VAL:HG13	49:D3:56:VAL:HG22	1.97	0.46
50:D4:26:SER:OG	50:D4:27:THR:N	2.49	0.46
25:DA:1378:A:OP1	53:D7:10:ARG:NH2	2.49	0.46
25:DA:740:U:H2'	25:DA:741:G:C8	2.51	0.46
25:DA:989:G:H4'	25:DA:990:A:OP1	2.15	0.46
34:DO:15:GLY:O	34:DO:47:ILE:HG12	2.14	0.46
24:CX:64:G:H4'	36:DQ:10:ARG:NH1	2.27	0.46
1:AA:189(D):C:H2'	1:AA:189(E):U:O4'	2.16	0.46
1:AA:345:C:O5'	1:AA:345:C:H6	1.98	0.46
1:AA:600:C:H5'	8:AH:129:VAL:HA	1.98	0.46
2:AB:17:PHE:CB	2:AB:44:LEU:HD21	2.46	0.46
9:AI:5:TYR:O	9:AI:87:GLN:NE2	2.49	0.46
13:AM:65:LYS:NZ	13:AM:73:GLU:HG3	2.31	0.46
19:AS:80:TYR:CZ	19:AS:82:GLY:HA2	2.51	0.46
25:BA:1258:A:N3	25:BA:1284:G:O2'	2.41	0.46
25:BA:139:A:C8	25:BA:1454:C:O2'	2.67	0.46
25:BA:2297:C:OP2	52:B6:6:ARG:NH1	2.49	0.46
25:BA:2325:C:H4'	30:BG:91:ARG:HG3	1.96	0.46
25:BA:932:C:H3'	25:BA:933:C:C5'	2.44	0.46
27:BD:142:VAL:HG13	27:BD:191:ALA:HB1	1.98	0.46
29:BF:126:VAL:HG21	29:BF:129:PHE:CZ	2.50	0.46
29:BF:195:ASP:HB3	29:BF:198:ALA:H	1.81	0.46
42:BW:4:LYS:HB2	42:BW:106:ILE:HG12	1.96	0.46
1:CA:1128:C:C2'	1:CA:1129:C:H5''	2.46	0.46
1:CA:1161:C:H2'	1:CA:1162:C:C6	2.51	0.46
1:CA:1327:C:H2'	1:CA:1328:C:C6	2.51	0.46
1:CA:1442:G:HO2'	1:CA:1442(A):G:P	2.37	0.46
57:CA:3178:PCY:N16	57:CA:3178:PCY:O5	2.45	0.46
12:CL:34:ARG:HB3	12:CL:34:ARG:HE	1.44	0.46
15:CO:17:ARG:HG3	15:CO:17:ARG:HH11	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1292:U:H2'	25:DA:1293:C:H6	1.79	0.46
25:DA:1336:A:H2'	25:DA:1337:G:C8	2.51	0.46
25:DA:2112:G:H2'	25:DA:2113:U:O4'	2.15	0.46
29:DF:120:GLU:HB2	29:DF:122:LYS:HG2	1.97	0.46
30:DG:114:ILE:HG23	30:DG:136:ARG:NH2	2.30	0.46
30:DG:49:ASP:N	30:DG:49:ASP:OD1	2.45	0.46
31:DH:124:GLU:OE1	31:DH:132:ARG:HD2	2.15	0.46
35:DP:101:VAL:HA	35:DP:106:LEU:O	2.16	0.46
45:DZ:52:SER:HG	45:DZ:54:HIS:HD1	1.58	0.46
1:AA:184:G:H2'	1:AA:185:A:H8	1.81	0.46
12:AL:33:ARG:HH11	12:AL:62:SER:HB3	1.81	0.46
23:AW:2:C:H2'	23:AW:3:C:C6	2.51	0.46
23:AY:26:A:N6	23:AY:44:G:N1	2.42	0.46
50:B4:15:ILE:HD12	50:B4:21:VAL:HG22	1.98	0.46
25:BA:2018:C:H4'	25:BA:2019:G:OP1	2.15	0.46
25:BA:231:G:C8	54:B8:5:LYS:HG2	2.50	0.46
25:BA:2486:C:OP2	25:BA:2487:C:N4	2.41	0.46
38:BS:39:ILE:HB	38:BS:49:VAL:HG13	1.98	0.46
45:BZ:145:GLU:O	45:BZ:147:GLY:HA2	2.16	0.46
1:CA:1307:U:H2'	1:CA:1308:U:C6	2.51	0.46
1:CA:1410:G:H2'	1:CA:1411:C:C6	2.51	0.46
1:CA:23:C:H5	1:CA:561:U:O4	1.98	0.46
1:CA:447:G:O6	1:CA:485:G:O2'	2.29	0.46
2:CB:125:PRO:O	2:CB:127:ILE:N	2.49	0.46
5:CE:57:LYS:HG2	5:CE:61:TYR:CE2	2.51	0.46
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.16	0.46
23:CW:33:U:N3	23:CW:36:A:OP2	2.46	0.46
25:DA:1029:A:N1	25:DA:2465:C:O2'	2.36	0.46
25:DA:1325:G:OP1	25:DA:1647:G:O2'	2.21	0.46
25:DA:2170:A:H2'	25:DA:2171:A:H5'	1.98	0.46
25:DA:2203:U:H4'	27:DD:151:LYS:HG2	1.96	0.46
25:DA:981:A:N1	25:DA:2027:G:O2'	2.39	0.46
31:DH:117:PRO:HG3	31:DH:123:PHE:CD2	2.51	0.46
32:DI:101:LEU:HD12	32:DI:105:HIS:HD2	1.81	0.46
39:DT:27:THR:HB	39:DT:89:VAL:HG22	1.97	0.46
45:DZ:97:GLU:HA	45:DZ:126:VAL:O	2.16	0.46
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.16	0.46
1:AA:573:A:OP2	61:AA:4006:HOH:O	2.20	0.46
4:AD:98:GLU:O	4:AD:103:ASN:ND2	2.48	0.46
8:AH:101:PRO:HG3	8:AH:133:LEU:HD11	1.98	0.46
15:AO:7:GLU:O	15:AO:11:VAL:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.16	0.46
23:AW:9:A:O2'	23:AW:10:G:N7	2.49	0.46
47:B1:72:GLU:O	47:B1:76:ARG:HG3	2.16	0.46
50:B4:46:GLN:HB3	50:B4:46:GLN:HE21	1.60	0.46
25:BA:1535:U:HO2'	25:BA:1536:A:H8	1.63	0.46
25:BA:2021:C:H4'	25:BA:2736:C:O2	2.15	0.46
25:BA:2135:U:O4	25:BA:2136:A:N6	2.46	0.46
25:BA:2697:G:H5'	34:BO:68:GLU:OE1	2.16	0.46
25:BA:397:G:OP2	25:BA:397:G:H8	1.99	0.46
31:BH:126:PRO:HB2	31:BH:130:ARG:HH21	1.81	0.46
35:BP:138:LEU:HD23	35:BP:145:PRO:HG3	1.98	0.46
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.79	0.46
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.16	0.46
1:CA:1194:U:H2'	1:CA:1195:C:C6	2.51	0.46
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.50	0.46
1:CA:943:U:H2'	1:CA:944:G:H5'	1.97	0.46
3:CC:83:ARG:O	3:CC:87:LEU:HG	2.16	0.46
1:CA:1118:C:OP1	9:CI:9:ARG:HD2	2.16	0.46
12:CL:83:VAL:HG23	12:CL:107:ALA:HB2	1.98	0.46
17:CQ:5:VAL:HG22	17:CQ:60:ILE:HG13	1.97	0.46
55:D9:10:ILE:HD12	55:D9:32:HIS:HA	1.97	0.46
25:DA:1449:A:H8	25:DA:1449:A:OP2	1.98	0.46
25:DA:747:U:O2	25:DA:2014:A:H1'	2.14	0.46
25:DA:2179:C:C2'	25:DA:2180:U:H5'	2.46	0.46
25:DA:2815:C:H5'	51:D5:29:THR:HG21	1.98	0.46
25:DA:479:A:H4'	25:DA:480:A:OP1	2.15	0.46
25:DA:639:U:H2'	25:DA:640:C:H6	1.80	0.46
30:DG:70:VAL:HA	30:DG:90:LEU:HD23	1.97	0.46
40:DU:16:LYS:HB3	40:DU:16:LYS:HE2	1.69	0.46
1:AA:197:A:C6	1:AA:221:C:H4'	2.51	0.46
1:AA:38:G:H22	1:AA:397:A:H5''	1.81	0.46
1:AA:922:G:H2'	1:AA:923:A:C8	2.51	0.46
2:AB:166:ASP:OD2	2:AB:169:LYS:HB2	2.16	0.46
7:AG:113:GLU:HG3	7:AG:118:VAL:HG12	1.98	0.46
7:AG:15:ASP:OD1	7:AG:20:ASP:N	2.40	0.46
20:AT:10:LEU:HD13	20:AT:12:ALA:HB2	1.98	0.46
35:BP:62:LEU:O	54:B8:13:ARG:HD3	2.15	0.46
27:BD:95:LEU:HD11	27:BD:105:ILE:HD13	1.97	0.46
36:BQ:85:LYS:HG2	46:B0:7:LEU:HB3	1.98	0.46
25:BA:63:A:O3'	43:BX:71:GLY:HA3	2.16	0.46
1:CA:1004:A:C2	1:CA:1038:C:C4	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1318:A:OP1	19:CS:3:ARG:NH2	2.43	0.46
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.56	0.46
1:CA:544:G:P	4:CD:62:GLN:HE21	2.37	0.46
10:CJ:27:ALA:HA	10:CJ:81:THR:HG22	1.97	0.46
12:CL:7:ILE:O	12:CL:11:VAL:HG23	2.16	0.46
50:D4:16:CYS:SG	50:D4:17:GLY:N	2.89	0.46
25:DA:2336:A:H61	46:D0:43:THR:CG2	2.29	0.46
25:DA:2552:U:C2	25:DA:2554:U:H5''	2.51	0.46
25:DA:887:A:H5'	25:DA:888:C:OP1	2.16	0.46
25:DA:896:A:H61	45:DZ:114:GLY:HA3	1.81	0.46
31:DH:2:SER:O	31:DH:3:ARG:HG2	2.15	0.46
41:DV:62:LEU:HD21	41:DV:95:LEU:HB2	1.97	0.46
57:AA:3231:PCY:O21	57:AA:3231:PCY:N20	2.49	0.45
1:AA:707:C:OP1	11:AK:85:ARG:NH1	2.48	0.45
7:AG:15:ASP:O	7:AG:19:GLY:HA2	2.16	0.45
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.51	0.45
25:BA:1987:C:OP1	25:BA:1988:A:O2'	2.30	0.45
25:BA:265:U:H2'	25:BA:266:C:H6	1.80	0.45
25:BA:439:A:H8	25:BA:439:A:O5'	1.99	0.45
25:BA:505:A:N3	25:BA:507:G:H5''	2.31	0.45
31:BH:13:LYS:HA	31:BH:14:GLY:HA2	1.54	0.45
1:CA:583:A:H2'	1:CA:584:G:O4'	2.16	0.45
1:CA:713:G:H2'	1:CA:714:G:C8	2.51	0.45
1:CA:865:A:H2	1:CA:918:A:H4'	1.81	0.45
4:CD:112:VAL:HG13	4:CD:161:ASN:OD1	2.15	0.45
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.28	0.45
50:D4:15:ILE:HG23	50:D4:21:VAL:HG22	1.96	0.45
25:DA:1669:A:H5''	25:DA:2550:G:OP1	2.16	0.45
25:DA:265:A:H1'	25:DA:266:G:O4'	2.16	0.45
25:DA:2712:U:OP1	25:DA:2714:G:H4'	2.17	0.45
25:DA:305:U:H2'	25:DA:306:U:C6	2.51	0.45
25:DA:588:U:H2'	25:DA:589:C:C6	2.51	0.45
25:DA:695:G:OP1	25:DA:1380:G:O2'	2.32	0.45
28:DE:112:GLY:O	28:DE:159:HIS:HA	2.16	0.45
25:DA:2666:C:N4	31:DH:109:PHE:HA	2.31	0.45
41:DV:15:GLU:O	41:DV:18:LEU:HB2	2.16	0.45
1:AA:204:U:H4'	1:AA:216:G:O5'	2.15	0.45
19:AS:3:ARG:NH2	19:AS:7:LYS:HE2	2.31	0.45
23:AY:28:G:H1	23:AY:42:C:H42	1.64	0.45
46:B0:10:THR:HG22	46:B0:12:ASN:N	2.20	0.45
47:B1:3:LYS:HB3	47:B1:4:VAL:H	1.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2430:A:H2'	25:BA:2431:U:C6	2.51	0.45
25:BA:549:U:H2'	25:BA:550:U:C6	2.51	0.45
28:BE:73:GLU:HG3	28:BE:73:GLU:H	1.55	0.45
33:BN:75:TYR:CE2	33:BN:77:GLY:HA2	2.51	0.45
36:BQ:18:LYS:O	36:BQ:98:LYS:NZ	2.31	0.45
1:CA:1066:C:O2'	1:CA:1067:A:H5'	2.15	0.45
1:CA:1186:G:H21	14:CN:61:TRP:C	2.20	0.45
1:CA:62:U:H2'	1:CA:63:C:C6	2.51	0.45
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.80	0.45
10:CJ:32:ALA:CB	10:CJ:33:GLN:HA	2.43	0.45
23:CW:2:C:H2'	23:CW:3:C:H6	1.81	0.45
50:D4:49:PHE:HB3	50:D4:50:VAL:H	1.52	0.45
25:DA:2191:G:H2'	25:DA:2192:G:O4'	2.16	0.45
25:DA:1782:C:H1'	25:DA:2609:U:H5''	1.98	0.45
31:DH:4:ILE:O	31:DH:69:ARG:HG2	2.17	0.45
44:DY:9:LYS:HA	44:DY:10:GLY:HA2	1.57	0.45
1:AA:434:U:H2'	1:AA:435:C:C6	2.51	0.45
1:AA:455:C:H6	1:AA:455:C:O5'	2.00	0.45
1:AA:738:C:H2'	1:AA:739:C:C6	2.50	0.45
2:AB:80:ILE:HD13	2:AB:211:ILE:HG22	1.98	0.45
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.99	0.45
7:AG:76:ARG:HB3	7:AG:156:TRP:HH2	1.82	0.45
23:AY:48:C:OP1	23:AY:48:C:H2'	2.17	0.45
49:B3:5:LYS:HE3	49:B3:55:ARG:HH12	1.82	0.45
50:B4:26:SER:OG	50:B4:27:THR:N	2.49	0.45
25:BA:2168:C:H4'	25:BA:2169:G:N3	2.31	0.45
25:BA:2357:G:N3	25:BA:2393:C:H2'	2.31	0.45
25:BA:555:G:C5	25:BA:2044:U:H5''	2.51	0.45
25:BA:581:G:OP1	33:BN:111:PRO:HD2	2.17	0.45
25:BA:942:A:N7	45:BZ:146:ILE:HD12	2.31	0.45
1:CA:1022:G:H4'	1:CA:1022:G:OP1	2.16	0.45
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.81	0.45
1:CA:1388:C:H2'	1:CA:1389:C:H6	1.81	0.45
1:CA:50:A:H1'	1:CA:52:G:C8	2.52	0.45
1:CA:529:G:O6	12:CL:49:ASN:HA	2.16	0.45
1:CA:630:G:O2'	1:CA:631:G:H5'	2.16	0.45
5:CE:57:LYS:HG2	5:CE:61:TYR:HE2	1.82	0.45
47:D1:53:VAL:HG22	47:D1:74:VAL:HG13	1.97	0.45
25:DA:1187:G:H5'	41:DV:81:TYR:CE1	2.51	0.45
25:DA:2080:G:H2'	25:DA:2081:C:H6	1.81	0.45
25:DA:2127:G:N1	25:DA:2161:C:N4	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2519:U:C6	25:DA:2542:A:N6	2.84	0.45
25:DA:2728:U:H2'	25:DA:2729:G:C8	2.51	0.45
25:DA:892:G:H2'	25:DA:893:C:C4'	2.46	0.45
29:DF:37:VAL:O	29:DF:41:LEU:HG	2.17	0.45
34:DO:16:ALA:HB2	34:DO:52:VAL:HG21	1.98	0.45
43:DX:44:GLU:O	43:DX:48:LYS:N	2.49	0.45
1:AA:872:A:C8	1:AA:874:G:C8	3.05	0.45
4:AD:164:ALA:O	4:AD:168:ARG:HD3	2.16	0.45
23:AW:19:G:H1	23:AW:56:C:N4	2.10	0.45
26:BB:12:C:H2'	46:B0:73:GLY:HA3	1.97	0.45
25:BA:1170:C:H1'	55:B9:36:GLN:NE2	2.31	0.45
25:BA:1834:A:H4'	27:BD:259:THR:HG23	1.97	0.45
25:BA:266:C:H2'	25:BA:267:C:O4'	2.16	0.45
25:BA:2745:G:H3'	25:BA:2746:A:O4'	2.16	0.45
35:BP:50:ARG:HD3	54:B8:7:HIS:CD2	2.51	0.45
45:BZ:138:GLU:N	45:BZ:156:LYS:HD3	2.30	0.45
1:CA:1128:C:H2'	1:CA:1129:C:H5''	1.99	0.45
1:CA:200:G:H2'	1:CA:201:C:O4'	2.15	0.45
3:CC:148:GLY:HA3	3:CC:172:ARG:O	2.16	0.45
5:CE:68:GLU:OE1	5:CE:70:PRO:HG3	2.16	0.45
25:DA:196:A:H62	35:DP:38:GLN:HE22	1.63	0.45
28:DE:24:THR:HG22	28:DE:186:GLY:O	2.16	0.45
29:DF:126:VAL:HG21	29:DF:129:PHE:CZ	2.52	0.45
31:DH:6:ARG:HH22	31:DH:54:ARG:NH2	2.14	0.45
33:DN:73:THR:HA	33:DN:83:LYS:O	2.16	0.45
37:DR:44:LEU:HD23	37:DR:44:LEU:HA	1.74	0.45
1:AA:1131:G:C2'	1:AA:1132:C:H5'	2.47	0.45
1:AA:390:C:H2'	1:AA:391:G:C8	2.51	0.45
4:AD:23:GLY:HA3	4:AD:112:VAL:CG1	2.46	0.45
9:AI:121:ARG:NH1	9:AI:122:ALA:O	2.50	0.45
17:AQ:67:LYS:O	17:AQ:68:ARG:HB3	2.16	0.45
51:B5:17:ASP:OD2	61:B5:205:HOH:O	2.21	0.45
25:BA:1199:C:H2'	25:BA:1200:G:O4'	2.16	0.45
25:BA:2119:C:H2'	25:BA:2120:U:O4'	2.16	0.45
25:BA:2162:C:O2'	25:BA:2174:G:N2	2.49	0.45
25:BA:843:C:H2'	25:BA:844:C:C6	2.50	0.45
25:BA:904:C:N4	25:BA:905:U:O4	2.49	0.45
36:BQ:16:ARG:HG3	36:BQ:17:LEU:H	1.81	0.45
1:CA:1073:U:H2'	1:CA:1074:G:H8	1.82	0.45
1:CA:1122:U:C4	1:CA:1123:A:N7	2.84	0.45
1:CA:67:C:H2'	1:CA:68:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:75:HIS:HA	12:CL:102:ARG:HH22	1.80	0.45
12:CL:117:ARG:NH2	12:CL:124:LYS:HB2	2.31	0.45
23:CW:47:U:O2'	23:CW:48:C:OP1	2.33	0.45
23:CY:57:G:H2'	23:CY:57:G:N3	2.32	0.45
23:CY:69:G:H2'	23:CY:70:G:O4'	2.17	0.45
50:D4:46:GLN:C	50:D4:48:ARG:H	2.20	0.45
25:DA:1703:G:H2'	25:DA:1704:G:C8	2.51	0.45
25:DA:1857:G:C6	25:DA:1858:G:N1	2.84	0.45
25:DA:2792:G:N3	25:DA:2792:G:H2'	2.32	0.45
25:DA:38:A:H2'	25:DA:39:C:C6	2.51	0.45
25:DA:500:G:N1	25:DA:503:A:OP2	2.50	0.45
27:DD:182:LEU:HA	27:DD:182:LEU:HD23	1.81	0.45
30:DG:137:GLU:HG2	30:DG:152:LEU:HD23	1.99	0.45
31:DH:35:VAL:O	31:DH:37:VAL:HG23	2.17	0.45
44:DY:88:LYS:NZ	44:DY:89:PHE:O	2.38	0.45
1:AA:130:A:O2'	1:AA:131:C:O5'	2.30	0.45
1:AA:626:U:C2	1:AA:627:G:C8	3.04	0.45
3:AC:121:ALA:O	3:AC:125:GLU:HG3	2.17	0.45
3:AC:82:GLU:HG2	3:AC:85:ARG:NH2	2.32	0.45
4:AD:164:ALA:C	4:AD:168:ARG:HH11	2.19	0.45
54:B8:23:VAL:CG1	54:B8:47:LYS:HD3	2.46	0.45
25:BA:2699:U:OP2	61:BA:4975:HOH:O	2.21	0.45
25:BA:940:C:H2'	25:BA:941:U:O4'	2.16	0.45
29:BF:170:LEU:HG	29:BF:172:TRP:NE1	2.32	0.45
35:BP:101:VAL:HA	35:BP:106:LEU:O	2.16	0.45
44:BY:92:ASN:OD1	44:BY:94:LYS:HG3	2.16	0.45
2:CB:16:HIS:CD2	2:CB:204:ASN:HB3	2.51	0.45
2:CB:63:MET:CG	2:CB:225:ALA:HB1	2.47	0.45
1:CA:264:U:H4'	17:CQ:63:ARG:HD2	1.99	0.45
23:CW:21:A:N6	23:CW:46:7MG:C4	2.85	0.45
25:DA:117:G:C6	25:DA:119:A:C6	3.05	0.45
25:DA:2514:U:H2'	25:DA:2515:C:C6	2.52	0.45
25:DA:2724:C:OP1	28:DE:118:LYS:NZ	2.44	0.45
25:DA:1709:U:H1'	25:DA:2860:A:N3	2.32	0.45
25:DA:433:C:H2'	25:DA:434:U:C6	2.51	0.45
25:DA:656:G:H2'	25:DA:657:U:O4'	2.17	0.45
27:DD:71:ASP:CB	27:DD:103:ARG:HH22	2.28	0.45
30:DG:41:GLN:NE2	30:DG:153:ARG:HB3	2.32	0.45
33:DN:39:ARG:HA	33:DN:40:PRO:HD3	1.78	0.45
1:AA:171:A:H2'	1:AA:172:A:C8	2.52	0.45
1:AA:691:G:H2'	1:AA:692:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:157:LEU:HD22	4:AD:161:ASN:HD21	1.81	0.45
11:AK:34:ASP:HB3	11:AK:40:ILE:HD11	1.99	0.45
11:AK:20:TYR:CZ	11:AK:83:ILE:HD12	2.52	0.45
14:AN:6:LEU:HD12	14:AN:6:LEU:HA	1.88	0.45
1:AA:277:C:H5'	17:AQ:68:ARG:NH2	2.31	0.45
25:BA:1213:U:H2'	25:BA:1214:G:C8	2.52	0.45
25:BA:939:C:H2'	25:BA:940:C:C6	2.51	0.45
34:BO:120:GLU:OE1	39:BT:67:SER:OG	2.19	0.45
36:BQ:37:LEU:HD21	36:BQ:130:LYS:HE2	1.98	0.45
38:BS:3:ARG:HA	38:BS:3:ARG:HE	1.82	0.45
1:CA:1230:C:H2'	1:CA:1231:G:H8	1.82	0.45
1:CA:130:A:O2'	1:CA:131:C:O5'	2.35	0.45
1:CA:256:U:H2'	1:CA:257:G:C8	2.51	0.45
2:CB:13:ALA:C	2:CB:15:VAL:H	2.20	0.45
2:CB:219:VAL:HA	2:CB:222:ILE:CG1	2.47	0.45
23:CW:61:C:O2'	23:CW:62:C:H6	1.99	0.45
24:CX:72:A:H2'	24:CX:73:A:C8	2.52	0.45
23:CY:59:U:O5'	23:CY:59:U:H6	1.99	0.45
49:D3:7:LYS:HB2	49:D3:34:GLU:HG2	1.98	0.45
25:DA:1227:G:N2	25:DA:1228:G:H1'	2.32	0.45
25:DA:1218:C:N4	25:DA:1231:G:H1	2.13	0.45
25:DA:1417:C:H2'	25:DA:1418:G:O4'	2.16	0.45
25:DA:724:U:H2'	25:DA:725:G:O4'	2.17	0.45
35:DP:59:LEU:HD23	54:D8:58:ILE:HD13	1.98	0.45
36:DQ:35:VAL:HG12	36:DQ:130:LYS:O	2.16	0.45
42:DW:83:LYS:HE2	42:DW:97:LYS:HD3	1.99	0.45
1:AA:119:A:H4'	1:AA:120:A:C8	2.52	0.45
2:AB:103:THR:HA	2:AB:180:LEU:HD11	1.99	0.45
2:AB:215:LEU:O	2:AB:219:VAL:HG23	2.17	0.45
43:BX:66:LEU:HD23	43:BX:66:LEU:HA	1.68	0.45
45:BZ:152:ALA:HA	45:BZ:155:LEU:HD22	1.98	0.45
1:CA:1154:G:H8	1:CA:1154:G:H3'	1.81	0.45
1:CA:1359:C:H1'	1:CA:1362:C:H41	1.82	0.45
1:CA:258:G:O6	61:CA:4159:HOH:O	2.21	0.45
2:CB:63:MET:HG3	2:CB:225:ALA:HB1	1.99	0.45
4:CD:166:LYS:HD3	4:CD:178:VAL:HG11	1.99	0.45
14:CN:21:TYR:HE2	14:CN:23:ARG:NE	2.15	0.45
19:CS:27:GLU:HG2	19:CS:47:HIS:HE2	1.81	0.45
25:DA:1341:U:O2	43:DX:80:ILE:HD12	2.16	0.45
25:DA:2120:G:H2'	25:DA:2121:G:H8	1.82	0.45
25:DA:2275:C:H5'	25:DA:2275:C:H6	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2518:A:OP2	61:DA:4302:HOH:O	2.21	0.45
25:DA:30:G:H2'	25:DA:31:C:C6	2.52	0.45
25:DA:572:A:OP2	41:DV:78:LYS:NZ	2.50	0.45
27:DD:10:THR:OG1	27:DD:13:ARG:HG2	2.17	0.45
35:DP:100:LEU:HD12	35:DP:112:LEU:HD11	1.97	0.45
45:DZ:6:LYS:HD2	45:DZ:8:TYR:OH	2.16	0.45
1:AA:1002:G:O6	1:AA:1003:G:N2	2.50	0.45
1:AA:1128:C:H2'	1:AA:1129:C:H5'	1.98	0.45
1:AA:1145:C:H4'	1:AA:1146:A:H5''	1.98	0.45
1:AA:149:A:H2'	1:AA:150:C:C6	2.52	0.45
23:AY:50:U:N3	23:AY:64:A:C2	2.77	0.45
25:BA:2149:G:H1	25:BA:2183:C:N4	2.15	0.45
25:BA:2545:A:H2'	25:BA:2546:A:O4'	2.16	0.45
25:BA:274:U:H3'	25:BA:275:C:H5'	1.99	0.45
25:BA:327:U:H2'	25:BA:328:G:H8	1.81	0.45
25:BA:909:G:H2'	25:BA:910:A:O4'	2.17	0.45
37:BR:41:ALA:HB1	37:BR:114:VAL:HG22	1.99	0.45
38:BS:3:ARG:CA	38:BS:3:ARG:HE	2.30	0.45
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.52	0.45
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.43	0.45
1:CA:715:A:H2'	1:CA:716:A:C8	2.52	0.45
3:CC:131:ARG:HH21	3:CC:166:GLU:HB3	1.82	0.45
3:CC:179:ARG:NH1	3:CC:206:GLU:OE1	2.50	0.45
8:CH:86:ILE:HG12	8:CH:135:CYS:HA	1.99	0.45
15:CO:4:THR:OG1	15:CO:7:GLU:OE1	2.20	0.45
23:CY:51:U:H2'	23:CY:52:G:O4'	2.17	0.45
46:D0:38:VAL:HG12	46:D0:40:GLN:HG2	1.99	0.45
25:DA:83:G:N1	25:DA:102:G:O2'	2.31	0.45
25:DA:1152:C:H2'	25:DA:1153:C:C6	2.51	0.45
25:DA:1529:G:C6	25:DA:1530:C:N4	2.85	0.45
25:DA:1826:G:H4'	27:DD:242:ARG:CZ	2.47	0.45
25:DA:2149:G:H3'	25:DA:2150:U:H6	1.82	0.45
25:DA:2317:C:N3	25:DA:2318:G:N7	2.65	0.45
25:DA:2399:G:H2'	25:DA:2400:G:O4'	2.16	0.45
25:DA:2693:A:H2'	25:DA:2694:G:H8	1.81	0.45
25:DA:463:G:N2	25:DA:466:A:OP2	2.46	0.45
1:AA:1151:A:O4'	10:AJ:39:PRO:HB2	2.17	0.45
1:AA:1286:A:H2	21:AU:18:TYR:OH	2.00	0.45
1:AA:345:C:H4'	1:AA:346:G:N3	2.31	0.45
23:AW:37:MIA:H162	23:AW:37:MIA:H122	1.87	0.45
47:B1:2:SER:HB3	47:B1:46:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2054:G:O2'	28:BE:145:LYS:HE3	2.17	0.45
25:BA:553:A:H3'	25:BA:553:A:C8	2.52	0.45
29:BF:197:ASP:OD1	29:BF:197:ASP:N	2.49	0.45
30:BG:41:GLN:HE22	30:BG:153:ARG:HB3	1.82	0.45
44:BY:1:MET:HB2	44:BY:2:ARG:H	1.65	0.45
10:CJ:6:ILE:HG12	10:CJ:98:ILE:HG13	1.99	0.45
13:CM:122:LYS:HD3	13:CM:123:ALA:H	1.82	0.45
23:CW:4:C:N3	23:CW:69:G:C2	2.84	0.45
25:DA:1007:C:P	33:DN:37:LYS:HZ1	2.40	0.45
25:DA:224:G:H2'	25:DA:225:A:O4'	2.17	0.45
25:DA:2526:G:H5'	25:DA:2742:C:O2'	2.17	0.45
27:DD:166:GLN:HB2	27:DD:174:ILE:HG22	1.99	0.45
29:DF:125:LEU:HD22	29:DF:199:TRP:HB2	1.99	0.45
31:DH:13:LYS:HA	31:DH:14:GLY:HA2	1.61	0.45
31:DH:44:VAL:O	31:DH:50:VAL:HA	2.16	0.45
35:DP:63:PRO:HD3	54:D8:27:THR:HG22	1.97	0.45
1:AA:1036:G:H5''	1:AA:1037:C:C5	2.52	0.44
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.82	0.44
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.39	0.44
1:AA:198:G:H2'	1:AA:199:G:H8	1.83	0.44
25:BA:1639:G:H2'	25:BA:1640:G:C8	2.53	0.44
25:BA:2023:A:H2'	25:BA:2024:G:C8	2.51	0.44
25:BA:997:G:OP1	36:BQ:16:ARG:NH2	2.48	0.44
25:BA:2799:U:O2'	28:BE:62:PRO:O	2.29	0.44
37:BR:83:ILE:O	37:BR:86:ARG:HG2	2.17	0.44
45:BZ:7:ALA:HB3	45:BZ:61:LEU:HD12	1.99	0.44
1:CA:1010:G:H2'	1:CA:1011:G:C8	2.50	0.44
1:CA:357:G:OP1	1:CA:367:U:H5''	2.17	0.44
1:CA:532:A:H2	1:CA:1206:G:N2	2.14	0.44
2:CB:95:GLN:HB2	2:CB:148:TYR:CD1	2.52	0.44
46:D0:68:GLU:OE1	46:D0:82:ARG:HD2	2.17	0.44
54:D8:63:PRO:HG2	54:D8:64:TYR:CE2	2.53	0.44
25:DA:2168:G:H2'	25:DA:2169:A:C8	2.52	0.44
25:DA:383:U:H2'	25:DA:385:C:H5	1.81	0.44
25:DA:646:A:H2'	25:DA:647:G:O4'	2.17	0.44
25:DA:864:G:H2'	25:DA:865:C:C6	2.53	0.44
25:DA:93:G:H2'	25:DA:94:C:C6	2.52	0.44
27:DD:169:GLU:HG3	27:DD:169:GLU:O	2.17	0.44
29:DF:7:TYR:O	29:DF:22:ALA:N	2.50	0.44
35:DP:122:PRO:HB3	35:DP:141:ALA:O	2.17	0.44
40:DU:65:ILE:HD11	40:DU:95:LEU:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:DV:72:VAL:CG1	41:DV:85:LYS:HD2	2.47	0.44
43:DX:47:PHE:O	43:DX:49:VAL:HG13	2.18	0.44
1:AA:1054:C:C4	23:AW:34:G:H1'	2.52	0.44
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.52	0.44
1:AA:1262:C:H2'	1:AA:1263:C:C6	2.53	0.44
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.17	0.44
1:AA:262:A:H2'	1:AA:263:A:C8	2.52	0.44
1:AA:371:G:H2'	1:AA:372:C:O4'	2.17	0.44
1:AA:673:G:H2'	1:AA:674:G:C8	2.52	0.44
7:AG:26:PHE:CE2	7:AG:30:ILE:HD11	2.53	0.44
2:AB:178:ARG:HH22	8:AH:68:ARG:HH22	1.66	0.44
25:BA:1320:A:N3	25:BA:1343:C:H1'	2.32	0.44
25:BA:2735:G:H2'	25:BA:2736:C:C6	2.52	0.44
27:BD:223:GLY:HA3	27:BD:231:HIS:CE1	2.52	0.44
28:BE:174:ASP:OD1	28:BE:175:VAL:N	2.50	0.44
33:BN:67:LEU:HD13	33:BN:87:LEU:HD13	1.98	0.44
39:BT:6:LEU:O	39:BT:10:VAL:HG23	2.18	0.44
44:BY:92:ASN:HB3	44:BY:94:LYS:N	2.30	0.44
1:CA:1136:U:H5''	1:CA:1137:C:C5	2.52	0.44
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.18	0.44
1:CA:1530:G:H2'	1:CA:1531:A:O4'	2.18	0.44
1:CA:664:G:N2	1:CA:741:G:H1	2.14	0.44
1:CA:944:G:O2'	1:CA:1339:A:N6	2.49	0.44
25:DA:1019:U:H2'	25:DA:1020:A:C8	2.51	0.44
25:DA:1127:A:C2'	25:DA:1128:A:H5''	2.48	0.44
25:DA:1165:U:H2'	25:DA:1166:C:C6	2.52	0.44
25:DA:212:G:H5'	25:DA:213:A:OP2	2.17	0.44
25:DA:2268:A:OP1	61:DA:4433:HOH:O	2.21	0.44
25:DA:479:A:HO2'	25:DA:481:G:H8	1.64	0.44
25:DA:848:G:N9	25:DA:933:A:H8	2.15	0.44
26:DB:24:G:N3	26:DB:26:A:N6	2.65	0.44
33:DN:67:LEU:O	33:DN:88:GLU:HG3	2.17	0.44
42:DW:34:ASN:OD1	42:DW:37:ARG:NH1	2.40	0.44
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.18	0.44
1:AA:161:A:H2'	1:AA:162:A:C8	2.52	0.44
1:AA:192:U:H2'	1:AA:193:C:C6	2.52	0.44
1:AA:767:A:H2'	1:AA:768:A:O4'	2.17	0.44
1:AA:973:G:H3'	1:AA:974:A:H5''	1.99	0.44
1:AA:98:G:H5'	1:AA:99:U:OP2	2.17	0.44
4:AD:163:GLU:C	4:AD:165:MET:H	2.21	0.44
4:AD:168:ARG:H	4:AD:168:ARG:NE	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:19:G:H4'	23:AY:57:G:H22	1.82	0.44
23:AY:69:G:H2'	23:AY:70:G:O4'	2.17	0.44
48:B2:1:MET:HG2	48:B2:5:GLU:OE1	2.17	0.44
25:BA:1324:A:OP1	37:BR:36:THR:HG23	2.17	0.44
25:BA:174:U:H2'	25:BA:175:G:C8	2.52	0.44
25:BA:2123:G:H1	25:BA:2210:C:H42	1.65	0.44
25:BA:831:A:C8	25:BA:839:G:C5	3.05	0.44
34:BO:36:GLY:HA3	34:BO:109:LYS:HD2	1.99	0.44
39:BT:37:GLY:HA2	39:BT:38:ASN:HA	1.67	0.44
45:BZ:155:LEU:HD12	45:BZ:156:LYS:H	1.82	0.44
1:CA:1315:U:H2'	1:CA:1316:G:O4'	2.17	0.44
1:CA:203:U:OP2	1:CA:203:U:H2'	2.17	0.44
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	1.98	0.44
2:CB:7:VAL:HB	2:CB:8:LYS:H	1.55	0.44
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.99	0.44
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.52	0.44
25:DA:1184:G:OP1	49:D3:30:ARG:HD2	2.17	0.44
51:D5:16:ARG:HD2	51:D5:20:ARG:NH1	2.33	0.44
52:D6:18:ARG:HD2	52:D6:42:TRP:CE2	2.52	0.44
25:DA:1900:A:N1	25:DA:1970:A:C6	2.85	0.44
25:DA:2108:C:H2'	25:DA:2109:U:H6	1.82	0.44
25:DA:2141:G:O6	25:DA:2150:U:C2	2.70	0.44
25:DA:2648:C:H2'	25:DA:2649:U:C6	2.52	0.44
25:DA:286:C:H2'	25:DA:287:C:H6	1.83	0.44
25:DA:422:A:OP2	61:DA:4103:HOH:O	2.21	0.44
25:DA:910:A:N1	25:DA:2277:G:H1'	2.33	0.44
28:DE:101:ARG:NH1	28:DE:169:ASN:O	2.43	0.44
29:DF:150:GLY:HA2	29:DF:172:TRP:CD2	2.52	0.44
32:DI:38:LEU:HD12	32:DI:38:LEU:H	1.82	0.44
39:DT:99:LEU:HD22	39:DT:101:PHE:HE1	1.81	0.44
43:DX:31:HIS:HD2	43:DX:33:LYS:H	1.65	0.44
45:DZ:138:GLU:H	45:DZ:156:LYS:HD3	1.82	0.44
1:AA:1270:C:OP2	21:AU:24:ARG:NH2	2.51	0.44
1:AA:664:G:OP1	18:AR:64:ARG:NE	2.46	0.44
2:AB:170:GLU:O	2:AB:174:VAL:HG23	2.18	0.44
48:B2:21:LEU:HB2	48:B2:64:LEU:HD23	2.00	0.44
50:B4:57:GLU:HA	50:B4:58:ARG:HA	1.61	0.44
37:BR:33:ARG:NH2	51:B5:57:VAL:O	2.46	0.44
25:BA:1360:C:OP1	61:BA:4775:HOH:O	2.21	0.44
25:BA:2221:A:OP2	25:BA:2222:C:H5	2.00	0.44
25:BA:2453:C:OP2	25:BA:2598:C:O2'	2.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2661:U:H2'	25:BA:2662:U:C6	2.52	0.44
25:BA:2574:U:H1'	34:BO:23:ARG:HD3	2.00	0.44
43:BX:31:HIS:HD2	43:BX:33:LYS:HB2	1.83	0.44
1:CA:779:C:O2'	11:CK:120:ARG:HD3	2.17	0.44
2:CB:19:HIS:NE2	2:CB:206:ASP:HB2	2.32	0.44
4:CD:58:LEU:HD22	4:CD:62:GLN:HG2	1.98	0.44
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.99	0.44
19:CS:28:LYS:HB3	19:CS:28:LYS:HZ3	1.83	0.44
52:D6:11:LEU:HB2	52:D6:21:TYR:HB2	1.99	0.44
25:DA:1015:G:H2'	25:DA:1016:G:C8	2.53	0.44
25:DA:2331:G:O2'	25:DA:2336:A:N1	2.37	0.44
25:DA:2532:G:H1'	25:DA:2663:G:H22	1.83	0.44
25:DA:2871:C:N4	61:DA:4551:HOH:O	2.51	0.44
25:DA:307:G:H22	25:DA:310:A:P	2.39	0.44
31:DH:25:LYS:HE2	31:DH:34:GLU:OE2	2.17	0.44
25:DA:908:C:OP1	36:DQ:22:LYS:HB3	2.18	0.44
1:AA:1131:G:O2'	1:AA:1132:C:H5'	2.18	0.44
1:AA:1169:A:C6	1:AA:1170:A:C6	3.06	0.44
1:AA:154:C:C2'	1:AA:155:C:H5'	2.48	0.44
1:AA:257:G:C6	1:AA:258:G:C5	3.05	0.44
1:AA:1073:U:O2'	2:AB:104:ASN:OD1	2.28	0.44
4:AD:155:LEU:HB3	4:AD:158:ILE:HD11	1.99	0.44
13:AM:84:ILE:HD12	19:AS:74:PHE:CE2	2.53	0.44
16:AP:14:ASN:OD1	16:AP:42:ARG:NH2	2.50	0.44
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.17	0.44
23:AW:31:A:H2'	23:AW:32:PSU:O4'	2.17	0.44
23:AY:25:C:H2'	23:AY:26:A:H8	1.82	0.44
23:AY:19:G:C2	23:AY:56:C:N3	2.86	0.44
54:B8:6:THR:HG23	54:B8:64:TYR:HD2	1.83	0.44
25:BA:1552:C:O2'	25:BA:1553:A:H5'	2.17	0.44
25:BA:1727:U:O2'	25:BA:1794:G:N7	2.40	0.44
25:BA:2707:C:H2'	25:BA:2708:U:C6	2.52	0.44
25:BA:2707:C:H2'	25:BA:2708:U:H6	1.82	0.44
25:BA:270:C:H4'	25:BA:271:U:OP1	2.18	0.44
35:BP:135:LEU:HD23	35:BP:135:LEU:HA	1.70	0.44
38:BS:26:LEU:HB2	38:BS:85:VAL:HG21	1.99	0.44
1:CA:1244:C:H42	1:CA:1293:G:H1	1.65	0.44
1:CA:564:C:C4	1:CA:565:U:C4	3.06	0.44
2:CB:112:VAL:O	2:CB:116:GLU:HB2	2.18	0.44
7:CG:79:ARG:NE	7:CG:80:VAL:H	2.16	0.44
23:CW:24:G:C2'	23:CW:25:C:H5'	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DP:63:PRO:HG2	54:D8:25:MET:HB2	2.00	0.44
55:D9:29:ASN:HD22	55:D9:32:HIS:CE1	2.35	0.44
25:DA:2872:G:O2'	25:DA:2873:A:H5'	2.18	0.44
25:DA:510:C:H2'	25:DA:511:U:O4'	2.18	0.44
25:DA:57:C:H2'	25:DA:58:G:O4'	2.18	0.44
25:DA:887:A:H4'	25:DA:888:C:C5	2.51	0.44
28:DE:163:GLU:HG2	28:DE:164:ARG:N	2.33	0.44
36:DQ:18:LYS:HE3	36:DQ:18:LYS:HB2	1.74	0.44
1:AA:1124:G:O2'	1:AA:1145:C:C4	2.71	0.44
1:AA:376:G:OP2	16:AP:67:THR:HG21	2.17	0.44
1:AA:652:U:O4	1:AA:752:G:O2'	2.24	0.44
1:AA:964:A:N3	1:AA:969:A:O2'	2.40	0.44
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	1.99	0.44
5:AE:8:GLU:OE2	5:AE:63:ARG:NH2	2.49	0.44
1:AA:1226:C:H4'	19:AS:80:TYR:OH	2.17	0.44
20:AT:100:ILE:HB	20:AT:101:GLY:H	1.63	0.44
20:AT:92:LEU:O	20:AT:96:GLY:HA2	2.18	0.44
19:AS:68:GLY:N	50:B4:58:ARG:HH12	2.13	0.44
25:BA:1809:U:H2'	25:BA:1815:A:N6	2.33	0.44
25:BA:2062:C:H2'	25:BA:2063:U:O4'	2.18	0.44
25:BA:2376:C:H2'	25:BA:2377:G:O4'	2.18	0.44
25:BA:934:A:O2'	25:BA:935:C:OP2	2.31	0.44
35:BP:76:LYS:HE3	35:BP:76:LYS:HB3	1.78	0.44
1:CA:532:A:O2'	1:CA:533:A:P	2.75	0.44
2:CB:62:ALA:HB1	2:CB:225:ALA:HB3	2.00	0.44
3:CC:113:ALA:N	3:CC:183:ASP:OD2	2.45	0.44
3:CC:32:LEU:O	3:CC:36:ASP:HB2	2.17	0.44
9:CI:53:VAL:HG21	9:CI:92:TYR:CE1	2.53	0.44
23:CY:33:U:OP2	23:CY:33:U:H6	2.00	0.44
49:D3:26:LEU:O	49:D3:35:ARG:HD3	2.18	0.44
25:DA:1557:C:H5''	25:DA:1558:A:OP2	2.17	0.44
25:DA:2557:G:H2'	25:DA:2558:C:C6	2.52	0.44
25:DA:416:C:H2'	25:DA:417:C:O4'	2.17	0.44
25:DA:528:A:N1	25:DA:2042:A:H2'	2.33	0.44
25:DA:583:G:OP2	40:DU:10:ARG:HD2	2.17	0.44
25:DA:973:A:H5'	25:DA:1188:U:H1'	1.99	0.44
25:DA:2094:G:OP1	32:DI:22:LYS:HD2	2.18	0.44
42:DW:68:ARG:HH11	42:DW:111:HIS:HA	1.81	0.44
1:AA:1006:C:H2'	1:AA:1007:C:C6	2.53	0.44
1:AA:1004:A:H5'	1:AA:1024:G:O6	2.17	0.44
1:AA:1047:G:H5''	14:AN:4:LYS:HD2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:555:C:H2'	1:AA:556:C:C6	2.53	0.44
6:AF:19:LEU:HD21	6:AF:59:TYR:CE1	2.53	0.44
19:AS:66:MET:HB2	19:AS:74:PHE:CZ	2.53	0.44
24:AX:20:U:H5''	24:AX:21:A:OP2	2.18	0.44
23:AY:9:A:O3'	23:AY:45:U:O2'	2.26	0.44
25:BA:1343:C:OP1	25:BA:2722:C:H4'	2.18	0.44
25:BA:2295:C:H2'	25:BA:2296:C:O4'	2.17	0.44
25:BA:895:G:H2'	25:BA:896:A:C8	2.53	0.44
31:BH:167:GLU:HA	31:BH:168:PRO:HD3	1.83	0.44
32:BI:110:ASP:HA	32:BI:111:PRO:HD2	1.67	0.44
1:CA:390:C:H2'	1:CA:391:G:C8	2.53	0.44
1:CA:91:C:H2'	1:CA:92:C:H6	1.83	0.44
47:D1:94:LEU:HD23	47:D1:94:LEU:HA	1.76	0.44
25:DA:1239:G:H2'	25:DA:1240:U:O4'	2.18	0.44
25:DA:1632:A:H8	25:DA:1632:A:O5'	1.99	0.44
25:DA:2207:G:H3'	25:DA:2208:A:H5''	1.99	0.44
25:DA:2340:G:H2'	25:DA:2341:G:H8	1.82	0.44
25:DA:2818:G:OP2	37:DR:42:LYS:NZ	2.46	0.44
25:DA:2849:U:OP2	39:DT:95:ARG:NH1	2.51	0.44
25:DA:309:G:N3	25:DA:329:G:O2'	2.47	0.44
25:DA:903:C:H2'	25:DA:904:C:C6	2.52	0.44
29:DF:51:THR:HG23	29:DF:92:PRO:HG2	1.99	0.44
30:DG:86:MET:HA	30:DG:87:PRO:HD3	1.89	0.44
45:DZ:110:GLY:HA3	45:DZ:144:LEU:O	2.18	0.44
1:AA:1286:A:C8	1:AA:1287:A:H4'	2.53	0.44
57:AA:3231:PCY:H37	23:AY:34:G:O6	2.17	0.44
1:AA:376:G:H5''	16:AP:5:ARG:CG	2.38	0.44
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	2.00	0.44
13:AM:115:LYS:HE2	13:AM:115:LYS:HB2	1.84	0.44
25:BA:1210:G:H2'	25:BA:1211:U:C6	2.53	0.44
25:BA:2343:G:O2'	46:B0:43:THR:HG22	2.18	0.44
29:BF:33:LEU:HB3	35:BP:6:LEU:HD21	2.00	0.44
31:BH:11:VAL:HG21	31:BH:50:VAL:HG23	1.99	0.44
1:CA:1068:G:H8	1:CA:1068:G:OP2	2.01	0.44
1:CA:1105:A:H2'	1:CA:1106:G:H8	1.83	0.44
1:CA:1327:C:H2'	1:CA:1328:C:H6	1.83	0.44
1:CA:160:A:H1'	1:CA:344:A:C8	2.53	0.44
1:CA:603:U:H2'	1:CA:604:G:H8	1.83	0.44
1:CA:936:C:H2'	1:CA:937:A:O4'	2.18	0.44
4:CD:184:LYS:HE3	4:CD:186:LEU:HD23	2.00	0.44
49:D3:7:LYS:NZ	49:D3:32:GLN:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1449:A:O2'	25:DA:1529:G:N2	2.23	0.44
25:DA:1450(A):C:N4	25:DA:1451:C:H41	2.15	0.44
25:DA:2023:G:H4'	25:DA:2617:C:O3'	2.18	0.44
25:DA:2591:C:H2'	25:DA:2592:G:C8	2.53	0.44
25:DA:885:C:H2'	25:DA:886:C:H4'	1.98	0.44
26:DB:24:G:N2	26:DB:27:C:N3	2.47	0.44
37:DR:63:ARG:O	37:DR:67:LEU:HB2	2.18	0.44
1:AA:1003:G:C2	1:AA:1004:A:N3	2.86	0.44
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.53	0.44
1:AA:1353:G:H2'	1:AA:1354:C:H6	1.83	0.44
1:AA:840:C:H4'	1:AA:841:U:OP1	2.18	0.44
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.99	0.44
25:BA:1822:A:H8	25:BA:1822:A:OP2	2.00	0.44
25:BA:2148:A:H4'	25:BA:2149:G:H5'	2.00	0.44
25:BA:2371:C:H2'	25:BA:2372:A:O4'	2.18	0.44
25:BA:280:C:H2'	25:BA:281:G:H8	1.83	0.44
25:BA:537:G:OP1	25:BA:1280:U:O2'	2.23	0.44
25:BA:664:U:H2'	25:BA:665:C:C6	2.53	0.44
25:BA:2762:A:P	31:BH:3:ARG:HH21	2.39	0.44
38:BS:110:LEU:HD12	38:BS:110:LEU:HA	1.73	0.44
25:BA:2695:C:OP1	39:BT:53:ARG:NH2	2.51	0.44
43:BX:50:LYS:N	43:BX:87:GLN:OE1	2.47	0.44
1:CA:1005:A:H3'	1:CA:1006:C:O4'	2.17	0.44
1:CA:1256:A:OP2	3:CC:26:LYS:NZ	2.51	0.44
2:CB:19:HIS:HD1	2:CB:20:GLU:HG2	1.83	0.44
6:CF:3:ARG:HD3	6:CF:64:GLN:NE2	2.32	0.44
7:CG:27:ILE:HD11	7:CG:43:PHE:HB3	2.00	0.44
12:CL:71:PRO:O	12:CL:102:ARG:HD2	2.18	0.44
23:CY:8:4SU:H5'	23:CY:49:C:H5''	2.00	0.44
25:DA:528:A:C2'	25:DA:529:A:H5''	2.48	0.44
25:DA:721:C:H2'	25:DA:722:A:C8	2.53	0.44
35:DP:2:LYS:HG2	35:DP:5:ASP:CG	2.38	0.44
45:DZ:29:TYR:HB3	45:DZ:34:ASN:HD22	1.83	0.44
1:AA:1008:C:H2'	1:AA:1009:G:O4'	2.17	0.43
1:AA:167:G:H2'	1:AA:168:G:H8	1.82	0.43
1:AA:736:C:H2'	1:AA:737:A:C8	2.53	0.43
3:AC:82:GLU:HA	3:AC:85:ARG:CZ	2.48	0.43
4:AD:170:VAL:CG1	4:AD:174:LEU:HB2	2.48	0.43
4:AD:174:LEU:HD23	4:AD:185:PHE:HA	2.00	0.43
23:AY:34:G:C6	23:AY:35:A:C6	3.06	0.43
23:AY:46:7MG:H2'	23:AY:46:7MG:H81	1.75	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:831:A:C6	27:BD:229:VAL:HG11	2.52	0.43
25:BA:1836:U:O2	27:BD:50:THR:HB	2.17	0.43
45:BZ:152:ALA:O	45:BZ:155:LEU:HB2	2.18	0.43
4:CD:64:LEU:HD22	4:CD:198:VAL:HG11	1.99	0.43
6:CF:35:ALA:HA	6:CF:67:MET:HB3	2.00	0.43
25:DA:1013:C:O2'	25:DA:1014:U:H5'	2.18	0.43
27:DD:68:LYS:O	27:DD:69:ARG:HB2	2.18	0.43
25:DA:2572:A:N7	28:DE:145:LYS:HB2	2.33	0.43
30:DG:43:LEU:HD12	30:DG:43:LEU:HA	1.85	0.43
36:DQ:56:ARG:O	36:DQ:56:ARG:HD3	2.18	0.43
42:DW:84:ARG:O	42:DW:96:ILE:N	2.50	0.43
45:DZ:150:LEU:HD12	45:DZ:150:LEU:HA	1.80	0.43
1:AA:109:A:H2'	1:AA:326:G:N2	2.33	0.43
1:AA:1129:C:H5''	9:AI:16:ARG:NH1	2.29	0.43
1:AA:429:U:H4'	1:AA:430:A:O5'	2.18	0.43
1:AA:72:C:H2'	1:AA:73:G:O4'	2.17	0.43
7:AG:65:ALA:O	7:AG:69:VAL:HG23	2.17	0.43
10:AJ:11:PHE:CE1	10:AJ:67:THR:HG22	2.53	0.43
46:B0:38:VAL:HG12	46:B0:40:GLN:HG2	1.99	0.43
30:BG:179:PRO:HG3	50:B4:43:TYR:OH	2.18	0.43
25:BA:1086:C:H2'	25:BA:1087:C:O4'	2.17	0.43
25:BA:1218:G:H2'	25:BA:1218:G:OP2	2.18	0.43
25:BA:2173:G:C2	25:BA:2174:G:C6	3.06	0.43
41:BV:49:THR:HG22	41:BV:49:THR:O	2.19	0.43
45:BZ:100:VAL:HG21	45:BZ:134:PRO:HG2	2.00	0.43
45:BZ:125:LEU:HG	45:BZ:164:ALA:HB3	2.00	0.43
1:CA:1121:U:H2'	1:CA:1122:U:O4'	2.18	0.43
1:CA:1210:C:H2'	1:CA:1211:U:H5''	1.99	0.43
1:CA:1353:G:OP1	21:CU:10:ARG:NH1	2.51	0.43
1:CA:184:G:H2'	1:CA:185:A:C8	2.53	0.43
3:CC:155:GLY:O	3:CC:157:ILE:N	2.48	0.43
4:CD:81:GLU:O	4:CD:85:LYS:HB2	2.18	0.43
6:CF:100:ASN:HB2	18:CR:28:GLU:HA	2.00	0.43
7:CG:99:LEU:HD22	7:CG:103:TRP:CZ2	2.54	0.43
8:CH:82:HIS:CE1	8:CH:84:ARG:HG2	2.53	0.43
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	2.00	0.43
14:CN:3:ARG:O	14:CN:7:ILE:HG23	2.17	0.43
16:CP:49:LEU:HD22	16:CP:73:LEU:HD22	1.99	0.43
17:CQ:27:PHE:CE2	17:CQ:36:ILE:HD11	2.52	0.43
25:DA:2474:C:H5''	25:DA:2475:C:OP2	2.17	0.43
25:DA:528:A:H2'	25:DA:529:A:H5''	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:848:G:C4	25:DA:933:A:H8	2.36	0.43
38:DS:25:ARG:HD3	38:DS:42:ASP:OD2	2.17	0.43
38:DS:30:ARG:HG3	38:DS:35:ILE:HD12	2.00	0.43
39:DT:78:LEU:HD12	39:DT:79:HIS:NE2	2.33	0.43
44:DY:83:THR:HG21	44:DY:99:CYS:HB2	2.01	0.43
45:DZ:146:ILE:H	45:DZ:146:ILE:HD12	1.83	0.43
45:DZ:158:PRO:HA	45:DZ:159:PRO:HD3	1.90	0.43
45:DZ:166:SER:O	45:DZ:169:GLU:HB2	2.18	0.43
1:AA:532:A:N6	1:AA:1206:G:O2'	2.52	0.43
2:AB:155:LEU:HD11	2:AB:159:PRO:HD3	2.00	0.43
10:AJ:13:HIS:HB3	10:AJ:68:HIS:CE1	2.54	0.43
25:BA:1476:C:H2'	25:BA:1477:U:C6	2.52	0.43
25:BA:2651:A:OP2	61:BA:4267:HOH:O	2.21	0.43
25:BA:692:C:H2'	25:BA:693:G:O4'	2.18	0.43
25:BA:1547:C:O4'	27:BD:100:GLY:HA2	2.17	0.43
30:BG:16:ARG:HB2	30:BG:17:PRO:HD3	1.99	0.43
25:BA:956:A:C5	36:BQ:13:GLN:HG3	2.53	0.43
45:BZ:19:ARG:NH1	45:BZ:84:GLU:O	2.51	0.43
1:CA:1040:U:H2'	1:CA:1041:A:H5''	2.00	0.43
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.52	0.43
1:CA:875:C:H1'	8:CH:15:ASN:HD21	1.82	0.43
3:CC:130:VAL:O	3:CC:134:ILE:HG12	2.18	0.43
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.54	0.43
1:CA:393:A:OP2	16:CP:12:LYS:HD2	2.17	0.43
16:CP:8:ARG:HB3	16:CP:28:ARG:NH1	2.32	0.43
23:CY:5:G:H1	23:CY:68:C:N4	2.12	0.43
25:DA:1038:C:C4	25:DA:1039:G:N7	2.86	0.43
25:DA:1157:G:C2	25:DA:1158:C:C2	3.06	0.43
25:DA:11:G:N7	61:DA:4572:HOH:O	2.36	0.43
25:DA:141:A:C8	25:DA:1408:C:O2'	2.70	0.43
25:DA:182:A:N3	25:DA:433:C:O2'	2.45	0.43
25:DA:2133:G:HO2'	25:DA:2134:A:P	2.42	0.43
25:DA:2135:A:C6	25:DA:2136:C:N4	2.86	0.43
25:DA:2538:C:H2'	25:DA:2539:C:H6	1.83	0.43
25:DA:468:G:H5''	29:DF:60:SER:HB2	2.00	0.43
25:DA:662:G:H5''	35:DP:16:ARG:HG2	2.00	0.43
25:DA:2590:A:OP2	27:DD:238:GLY:HA2	2.18	0.43
29:DF:116:ASP:OD2	35:DP:1:MET:N	2.40	0.43
41:DV:55:ALA:HA	41:DV:100:ARG:O	2.18	0.43
1:AA:1317:C:N3	19:AS:37:ARG:NH2	2.65	0.43
1:AA:159:G:N2	1:AA:161:A:H3'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:44:G:C2	1:AA:45:U:H1'	2.53	0.43
1:AA:7:G:H5'	1:AA:298:A:O4'	2.18	0.43
8:AH:72:PRO:O	8:AH:74:PRO:HD3	2.19	0.43
12:AL:39:VAL:HG11	12:AL:41:ARG:NH1	2.33	0.43
14:AN:24:CYS:HB2	14:AN:40:CYS:HB3	1.99	0.43
16:AP:48:TRP:HH2	16:AP:76:GLN:HE22	1.65	0.43
49:B3:19:GLN:OE1	49:B3:52:HIS:NE2	2.48	0.43
50:B4:40:HIS:HA	50:B4:41:PRO:HD2	1.70	0.43
54:B8:62:LEU:HB3	54:B8:65:GLU:HG2	2.00	0.43
25:BA:1501:U:O2'	25:BA:1502:G:N7	2.51	0.43
25:BA:201:G:H2'	25:BA:202:A:O4'	2.19	0.43
25:BA:2879:G:H2'	25:BA:2880:C:O4'	2.19	0.43
25:BA:645:G:H5'	25:BA:645:G:N3	2.33	0.43
1:CA:60:A:N6	1:CA:110:C:N3	2.64	0.43
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.33	0.43
4:CD:88:VAL:HA	5:CE:97:GLY:HA3	1.99	0.43
12:CL:11:VAL:HG11	17:CQ:36:ILE:HG21	2.00	0.43
15:CO:82:ILE:HB	15:CO:87:ILE:HB	2.00	0.43
17:CQ:81:ARG:NH2	17:CQ:84:LEU:HD21	2.32	0.43
20:CT:63:ILE:HD13	20:CT:80:ARG:HB3	1.99	0.43
23:CW:32:PSU:H2'	23:CW:32:PSU:O4	2.18	0.43
19:CS:64:GLU:HB2	50:D4:59:PHE:CE1	2.53	0.43
25:DA:196:A:H2'	25:DA:196:A:N3	2.33	0.43
25:DA:2018:G:H2'	25:DA:2019:A:O4'	2.18	0.43
25:DA:207:A:H2'	25:DA:208:C:O4'	2.18	0.43
25:DA:2753:A:N3	55:D9:15:LYS:NZ	2.64	0.43
25:DA:614(B):G:H2'	29:DF:44:ARG:HH11	1.82	0.43
25:DA:94(A):G:C6	25:DA:95:G:C5	3.06	0.43
36:DQ:16:ARG:HG3	36:DQ:17:LEU:H	1.82	0.43
38:DS:5:THR:OG1	38:DS:8:GLU:OE2	2.23	0.43
44:DY:35:TYR:CE2	44:DY:69:ALA:HB3	2.54	0.43
1:AA:1346:A:N6	1:AA:1375:A:OP2	2.51	0.43
1:AA:1493:A:H5''	1:AA:1494:G:OP2	2.19	0.43
1:AA:481:G:O2'	1:AA:483:C:N4	2.48	0.43
1:AA:814:A:H2'	1:AA:816:A:H5''	2.00	0.43
6:AF:2:ARG:NE	6:AF:69:GLU:HG2	2.33	0.43
10:AJ:40:LEU:HB2	10:AJ:69:ASN:HB2	2.00	0.43
11:AK:34:ASP:OD2	11:AK:38:ASN:HB2	2.18	0.43
11:AK:48:ILE:O	11:AK:50:TYR:N	2.46	0.43
19:AS:30:LEU:HG	19:AS:31:ILE:N	2.33	0.43
25:BA:1490:G:N2	25:BA:1595:C:C2	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1921:G:H2'	25:BA:1921:G:N3	2.33	0.43
26:BB:13:A:N1	26:BB:69:G:O2'	2.40	0.43
26:BB:114:C:H4'	38:BS:46:VAL:HG22	2.00	0.43
1:CA:1134:G:N3	1:CA:1134:G:H2'	2.33	0.43
1:CA:552:U:O3'	12:CL:87:GLY:HA3	2.19	0.43
25:DA:1359:A:N1	25:DA:1372:U:O4	2.52	0.43
25:DA:140:G:N2	25:DA:1596:A:H4'	2.34	0.43
25:DA:1886:C:H2'	25:DA:1887:C:H6	1.84	0.43
25:DA:2096:U:H2'	25:DA:2097:C:C6	2.54	0.43
25:DA:2243:U:H2'	25:DA:2244:U:C6	2.54	0.43
25:DA:2391:G:O6	25:DA:2425:A:H8	2.02	0.43
25:DA:2507:C:H2'	25:DA:2508:G:O4'	2.18	0.43
25:DA:2854:G:H2'	25:DA:2855:C:C6	2.53	0.43
25:DA:616:G:OP2	29:DF:106:ARG:NE	2.40	0.43
25:DA:866:A:C2	25:DA:867:C:C5	3.06	0.43
25:DA:974:G:N2	25:DA:989:G:HI1'	2.34	0.43
29:DF:178:PRO:HB3	29:DF:198:ALA:HA	2.00	0.43
1:AA:269:C:H2'	1:AA:270:A:C8	2.54	0.43
2:AB:170:GLU:HB3	2:AB:173:ALA:HB3	2.01	0.43
2:AB:87:ARG:NE	2:AB:233:SER:HB3	2.33	0.43
4:AD:107:ARG:HD2	4:AD:107:ARG:HA	1.88	0.43
5:AE:31:LEU:HD23	5:AE:31:LEU:HA	1.91	0.43
8:AH:25:ASP:OD1	8:AH:60:ARG:HG3	2.18	0.43
25:BA:180:A:H2'	25:BA:181:C:C6	2.53	0.43
25:BA:2334:A:H2'	25:BA:2335:G:O4'	2.19	0.43
25:BA:2346:G:H4'	25:BA:2347:A:OP2	2.19	0.43
26:BB:7:G:C5'	26:BB:7:G:H8	2.32	0.43
28:BE:51:PHE:O	28:BE:77:ILE:HD12	2.18	0.43
30:BG:11:TYR:CZ	30:BG:16:ARG:HD3	2.54	0.43
41:BV:21:ARG:HG2	41:BV:91:TYR:CD1	2.54	0.43
43:BX:92:LEU:HA	43:BX:92:LEU:HD12	1.79	0.43
1:CA:189(D):C:H2'	1:CA:189(E):U:O4'	2.19	0.43
1:CA:694:A:N1	1:CA:787:A:O2'	2.52	0.43
1:CA:979:C:H2'	1:CA:980:C:H5'	2.01	0.43
2:CB:76:GLN:HG3	2:CB:206:ASP:O	2.18	0.43
3:CC:109:PRO:C	3:CC:111:LEU:H	2.22	0.43
4:CD:166:LYS:HD3	4:CD:166:LYS:HA	1.73	0.43
7:CG:15:ASP:O	7:CG:19:GLY:HA2	2.18	0.43
7:CG:15:ASP:OD1	7:CG:20:ASP:N	2.43	0.43
10:CJ:16:LEU:HA	10:CJ:16:LEU:HD23	1.85	0.43
13:CM:115:LYS:HB2	13:CM:115:LYS:HE2	1.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:19:LEU:HD21	13:CM:56:LEU:HD11	2.00	0.43
17:CQ:13:ASP:C	17:CQ:15:MET:H	2.20	0.43
17:CQ:54:GLY:O	17:CQ:81:ARG:N	2.46	0.43
51:D5:16:ARG:HG2	51:D5:16:ARG:NH1	2.34	0.43
25:DA:1693:U:O2'	25:DA:1695:G:O6	2.32	0.43
25:DA:1833:U:O2'	25:DA:1969:A:N1	2.45	0.43
25:DA:253:C:OP2	54:D8:5:LYS:NZ	2.38	0.43
25:DA:2572:A:N7	28:DE:144:ARG:HD2	2.33	0.43
25:DA:2693:A:H2'	25:DA:2694:G:C8	2.54	0.43
25:DA:456:C:H4'	61:DA:4011:HOH:O	2.18	0.43
25:DA:658:C:H2'	25:DA:659:C:C6	2.53	0.43
25:DA:699:A:H2'	25:DA:700:G:O4'	2.17	0.43
25:DA:763:G:H1'	25:DA:765:G:O4'	2.18	0.43
25:DA:567:A:H4'	25:DA:808:G:OP1	2.19	0.43
25:DA:820:A:N3	25:DA:943:U:H4'	2.33	0.43
32:DI:88:ILE:O	32:DI:121:LYS:NZ	2.34	0.43
25:DA:637:A:H8	35:DP:117:GLU:HG3	1.84	0.43
25:DA:2685:G:P	39:DT:51:ARG:HH12	2.42	0.43
25:DA:1155:A:H5''	40:DU:55:ARG:HD3	2.00	0.43
1:AA:232:G:H1'	1:AA:262:A:N1	2.33	0.43
1:AA:664:G:N2	1:AA:741:G:H1	2.11	0.43
1:AA:890:G:O2'	1:AA:906:G:O6	2.18	0.43
1:AA:936:C:H2'	1:AA:937:A:O4'	2.18	0.43
4:AD:173:TRP:CZ3	4:AD:174:LEU:HG	2.53	0.43
8:AH:64:LYS:HG2	8:AH:79:VAL:HG21	1.99	0.43
13:AM:15:VAL:HG22	13:AM:43:THR:O	2.18	0.43
25:BA:1810:U:H2'	61:BA:5150:HOH:O	2.17	0.43
25:BA:1994:A:H2'	25:BA:1995:G:H8	1.83	0.43
25:BA:2168:C:H4'	25:BA:2169:G:C4	2.54	0.43
25:BA:2627:U:H2'	25:BA:2628:C:C6	2.54	0.43
25:BA:313:A:N6	25:BA:375:G:O2'	2.52	0.43
25:BA:609:A:N1	25:BA:856:G:O2'	2.44	0.43
25:BA:9:U:O4	25:BA:2641:A:H2	2.02	0.43
29:BF:164:ARG:HD2	29:BF:175:THR:HG23	2.00	0.43
30:BG:121:ASN:HA	30:BG:122:PRO:HD3	1.90	0.43
1:CA:1004:A:N6	1:CA:1037:C:N3	2.66	0.43
1:CA:1150:U:C2'	1:CA:1151:A:H5'	2.48	0.43
1:CA:1297:C:H1'	1:CA:1298:C:H5	1.83	0.43
1:CA:1410:G:H2'	1:CA:1411:C:H6	1.83	0.43
1:CA:308:C:H2'	1:CA:309:G:C8	2.54	0.43
1:CA:580:U:H5''	15:CO:58:MET:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:603:U:H2'	1:CA:604:G:C8	2.53	0.43
2:CB:219:VAL:HA	2:CB:222:ILE:HG12	2.01	0.43
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.19	0.43
23:CY:56:C:H2'	23:CY:57:G:C8	2.35	0.43
50:D4:40:HIS:HA	50:D4:41:PRO:HD2	1.79	0.43
52:D6:10:LEU:HG	52:D6:54:ILE:HG13	2.00	0.43
53:D7:1:MET:HB2	53:D7:1:MET:HE2	1.88	0.43
25:DA:1371:G:H2'	25:DA:1372:U:H5	1.83	0.43
25:DA:1608:A:H1'	25:DA:1610:A:OP2	2.19	0.43
25:DA:1688:U:O2	25:DA:1700:A:H5'	2.19	0.43
25:DA:244:A:C2	25:DA:255:A:C4	3.07	0.43
25:DA:2802:G:H2'	25:DA:2803:C:O4'	2.19	0.43
25:DA:812:C:H1'	25:DA:1250:G:C2	2.53	0.43
29:DF:64:ILE:HG21	29:DF:78:ILE:HG23	1.99	0.43
29:DF:117:ARG:HH12	35:DP:1:MET:N	2.16	0.43
39:DT:60:THR:HG22	39:DT:77:PRO:HA	2.00	0.43
45:DZ:111:VAL:CG2	45:DZ:117:LEU:HB2	2.49	0.43
1:AA:1149:C:H2'	1:AA:1150:U:C6	2.53	0.43
1:AA:1164:G:H2'	1:AA:1165:C:C6	2.53	0.43
1:AA:1302:U:C5	13:AM:17:VAL:HG21	2.53	0.43
1:AA:456:C:H2'	1:AA:457:C:C6	2.53	0.43
1:AA:974:A:OP1	1:AA:974:A:H8	2.01	0.43
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.34	0.43
4:AD:99:SER:O	4:AD:140:VAL:HG23	2.19	0.43
4:AD:157:LEU:HD22	4:AD:161:ASN:ND2	2.34	0.43
23:AY:25:C:H2'	23:AY:26:A:C8	2.54	0.43
23:AY:71:G:H2'	23:AY:72:C:C6	2.54	0.43
52:B6:40:CYS:HA	52:B6:41:PRO:HD3	1.84	0.43
25:BA:1587:U:H2'	25:BA:1588:G:O4'	2.18	0.43
25:BA:2102:G:OP1	47:B1:35:THR:HG21	2.18	0.43
25:BA:2284:U:H5''	25:BA:2285:A:OP1	2.18	0.43
25:BA:561:A:H2'	25:BA:562:C:C6	2.54	0.43
25:BA:964:A:H5''	26:BB:98:G:O2'	2.19	0.43
27:BD:145:VAL:HB	27:BD:155:LEU:HB2	2.00	0.43
29:BF:150:GLY:HA2	29:BF:172:TRP:CE3	2.53	0.43
30:BG:49:ASP:O	30:BG:51:ARG:N	2.51	0.43
32:BI:93:THR:O	32:BI:97:ILE:HG13	2.19	0.43
33:BN:34:LEU:HD21	33:BN:120:LEU:HB2	2.01	0.43
34:BO:115:VAL:HG13	34:BO:121:VAL:HG21	2.01	0.43
36:BQ:16:ARG:HG2	36:BQ:18:LYS:HE2	2.00	0.43
38:BS:15:ARG:HE	38:BS:88:ASP:CG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BT:60:THR:HG22	39:BT:77:PRO:HA	1.99	0.43
41:BV:62:LEU:HD21	41:BV:95:LEU:HB2	2.01	0.43
44:BY:14:LEU:HB2	44:BY:75:ILE:HD11	2.01	0.43
45:BZ:151:HIS:O	45:BZ:153:SER:N	2.49	0.43
1:CA:130:A:H1'	1:CA:263:A:O2'	2.18	0.43
1:CA:707:C:H2'	1:CA:708:C:C6	2.53	0.43
1:CA:788:U:O3'	57:CA:3178:PCY:H25	2.18	0.43
2:CB:42:ILE:HG21	2:CB:202:PRO:O	2.19	0.43
11:CK:80:VAL:HG13	11:CK:103:LEU:HD12	1.99	0.43
19:CS:66:MET:HB2	19:CS:74:PHE:CZ	2.54	0.43
25:DA:1528(A):A:H2'	25:DA:1529:G:O4'	2.19	0.43
25:DA:1418:G:OP1	25:DA:1588:C:H4'	2.19	0.43
25:DA:2238:G:H2'	25:DA:2238:G:N3	2.33	0.43
25:DA:2432:A:C6	25:DA:2433:A:C6	3.07	0.43
25:DA:2487:G:H2'	25:DA:2488:A:C8	2.53	0.43
25:DA:2722:G:H2'	25:DA:2723:C:C6	2.53	0.43
25:DA:2729:G:C6	25:DA:2730:C:C4	3.06	0.43
25:DA:686:G:N2	25:DA:788:A:H61	2.17	0.43
25:DA:892:G:H2'	25:DA:893:C:O4'	2.19	0.43
27:DD:80:ALA:HB3	27:DD:94:LEU:HB3	2.01	0.43
31:DH:8:PRO:HA	31:DH:51:ARG:HG2	2.00	0.43
35:DP:138:LEU:HD23	35:DP:145:PRO:HG3	2.01	0.43
37:DR:97:VAL:CG2	37:DR:114:VAL:HG13	2.49	0.43
38:DS:93:LYS:HD3	38:DS:95:HIS:HB2	1.99	0.43
45:DZ:108:PRO:HG3	45:DZ:141:VAL:HB	2.00	0.43
1:AA:1316:G:H22	1:AA:1319:A:H5''	1.84	0.43
2:AB:196:LEU:HA	2:AB:196:LEU:HD12	1.80	0.43
3:AC:45:LYS:HG3	3:AC:46:GLU:N	2.34	0.43
5:AE:145:LYS:O	5:AE:149:GLU:HG2	2.19	0.43
1:AA:1240:U:O2'	7:AG:32:ARG:NH2	2.51	0.43
13:AM:2:ALA:N	13:AM:8:GLU:OE1	2.52	0.43
18:AR:32:ARG:HA	18:AR:69:THR:HG21	2.01	0.43
23:AW:62:C:H2'	23:AW:63:G:C8	2.54	0.43
25:BA:1440:U:H2'	25:BA:1441:A:O4'	2.19	0.43
25:BA:200:A:H2'	25:BA:201:G:O4'	2.18	0.43
25:BA:212:A:O4'	25:BA:449:A:H5'	2.19	0.43
25:BA:2250:G:H2'	25:BA:2250:G:N3	2.34	0.43
25:BA:2398:C:H2'	25:BA:2399:U:C6	2.54	0.43
25:BA:2897:U:H2'	25:BA:2898:C:C6	2.54	0.43
28:BE:40:GLU:CD	28:BE:40:GLU:H	2.22	0.43
42:BW:4:LYS:HE2	42:BW:6:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1054:C:C4	23:CW:34:G:H1'	2.54	0.43
1:CA:228:A:H2'	1:CA:229:U:O4'	2.19	0.43
1:CA:789:U:H2'	1:CA:791:G:OP2	2.19	0.43
3:CC:180:ALA:O	3:CC:181:ASN:C	2.56	0.43
9:CI:5:TYR:OH	9:CI:16:ARG:HG2	2.19	0.43
11:CK:38:ASN:HA	11:CK:39:PRO:HD3	1.77	0.43
12:CL:113:ARG:NE	12:CL:115:LYS:O	2.43	0.43
20:CT:50:GLU:O	20:CT:100:ILE:HD11	2.18	0.43
25:DA:1164:G:H2'	25:DA:1165:U:C6	2.54	0.43
25:DA:1363:C:H2'	25:DA:1364:G:H8	1.82	0.43
25:DA:1533:G:H22	25:DA:1536:C:H1'	1.82	0.43
25:DA:1741:A:H2'	25:DA:1742:G:O4'	2.18	0.43
25:DA:2026:C:H2'	25:DA:2027:G:O4'	2.19	0.43
25:DA:2443:C:H2'	25:DA:2444:G:H8	1.84	0.43
25:DA:2787:C:H1'	28:DE:62:PRO:HG3	2.01	0.43
25:DA:576:U:H2'	25:DA:577:G:C8	2.54	0.43
25:DA:2683:C:H4'	28:DE:13:ARG:CZ	2.49	0.43
28:DE:1:MET:HE1	28:DE:199:ARG:HD2	2.00	0.43
28:DE:9:VAL:HG13	28:DE:25:VAL:O	2.19	0.43
29:DF:93:LYS:HD3	29:DF:93:LYS:HA	1.79	0.43
37:DR:2:ARG:HG2	37:DR:5:LYS:HB2	2.01	0.43
25:DA:2875:C:OP1	39:DT:3:ARG:NH2	2.51	0.43
44:DY:43:ASN:OD1	44:DY:65:ALA:HB3	2.19	0.43
36:DQ:135:ASP:OD2	45:DZ:49:ARG:NH2	2.51	0.43
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.53	0.43
1:AA:1315:U:H2'	1:AA:1316:G:O4'	2.19	0.43
1:AA:411:A:OP2	4:AD:30:LYS:HD2	2.19	0.43
1:AA:955:U:O2'	19:AS:83:HIS:HD2	2.01	0.43
6:AF:81:ILE:HD11	27:BD:125:ILE:HB	2.00	0.43
11:AK:99:GLN:HE21	11:AK:108:ILE:HD11	1.83	0.43
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.19	0.43
23:AY:54:5MU:C4	23:AY:55:PSU:C2	3.07	0.43
25:BA:1566:U:H2'	25:BA:1567:G:O4'	2.19	0.43
25:BA:596:G:N1	25:BA:2053:A:OP2	2.38	0.43
25:BA:323:A:N1	25:BA:346:A:O2'	2.43	0.43
25:BA:343:C:H2'	25:BA:344:A:O4'	2.19	0.43
27:BD:5:LYS:HE3	27:BD:5:LYS:HB3	1.80	0.43
28:BE:119:ARG:HD2	28:BE:120:TRP:CE2	2.54	0.43
44:BY:6:HIS:HE1	44:BY:72:VAL:O	2.02	0.43
1:CA:1236:A:H2'	1:CA:1237:C:C6	2.54	0.43
1:CA:1258:G:O2'	1:CA:1259:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:347:G:H8	1:CA:347:G:OP2	2.01	0.43
2:CB:98:LEU:HB2	2:CB:101:MET:HG3	2.01	0.43
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.18	0.43
8:CH:119:LEU:HB3	8:CH:123:GLU:HB3	2.01	0.43
12:CL:39:VAL:HG11	12:CL:41:ARG:NH1	2.34	0.43
49:D3:7:LYS:HE3	49:D3:32:GLN:NE2	2.34	0.43
25:DA:2086:U:H2'	25:DA:2087:G:C8	2.54	0.43
25:DA:2141:G:C8	25:DA:2151:G:N2	2.86	0.43
25:DA:845:G:N2	25:DA:845:G:OP2	2.41	0.43
27:DD:5:LYS:HE3	27:DD:5:LYS:HB3	1.81	0.43
31:DH:116:GLU:HA	31:DH:117:PRO:HD3	1.79	0.43
44:DY:86:ARG:NH1	44:DY:100:ALA:HB1	2.34	0.43
1:AA:113:G:H2'	1:AA:114:U:C6	2.54	0.42
1:AA:154:C:N3	1:AA:168:G:C2	2.87	0.42
1:AA:448:A:O5'	1:AA:485:G:N2	2.45	0.42
1:AA:553:A:H2'	1:AA:554:C:C6	2.54	0.42
2:AB:73:THR:OG1	2:AB:170:GLU:OE1	2.31	0.42
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.66	0.42
5:AE:152:ARG:NH2	8:AH:107:LEU:O	2.52	0.42
13:AM:84:ILE:HD12	19:AS:74:PHE:CZ	2.54	0.42
52:B6:37:ARG:O	52:B6:38:LYS:HD2	2.19	0.42
25:BA:1087:C:H42	25:BA:1160:G:H1	1.67	0.42
24:AX:12:G:H4'	25:BA:1930:C:O2	2.19	0.42
25:BA:2724:U:OP1	25:BA:2727:G:H4'	2.19	0.42
25:BA:1831:C:OP2	27:BD:183:ARG:NH2	2.51	0.42
31:BH:97:ARG:NE	31:BH:104:GLU:OE1	2.40	0.42
44:BY:98:VAL:HG12	44:BY:105:ALA:HA	2.00	0.42
44:BY:19:LYS:HB3	44:BY:19:LYS:HE2	1.90	0.42
1:CA:1005:A:H5''	1:CA:1006:C:C5	2.54	0.42
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.53	0.42
1:CA:1236:A:O2'	1:CA:1304:G:H4'	2.19	0.42
1:CA:1432:G:O6	61:CA:4070:HOH:O	2.21	0.42
1:CA:170:U:O2'	1:CA:171:A:H5'	2.19	0.42
2:CB:67:THR:HG22	2:CB:90:MET:HE2	2.01	0.42
4:CD:112:VAL:HG22	4:CD:116:GLN:OE1	2.18	0.42
10:CJ:8:LEU:CD2	10:CJ:96:ILE:HG12	2.49	0.42
1:CA:376:G:H5''	16:CP:5:ARG:HB2	2.00	0.42
21:CU:9:ARG:O	21:CU:13:ILE:HG13	2.18	0.42
25:DA:152:G:H2'	25:DA:153:C:C6	2.54	0.42
25:DA:2161:C:H2'	25:DA:2162:G:C8	2.54	0.42
25:DA:2350:C:H2'	25:DA:2351:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2543:G:H2'	25:DA:2544:G:C8	2.54	0.42
25:DA:265:A:C8	25:DA:266:G:H1'	2.54	0.42
25:DA:271(H):G:O6	25:DA:271(Q):G:C6	2.72	0.42
25:DA:446:G:OP1	40:DU:3:ARG:NH1	2.52	0.42
25:DA:511:U:O4	25:DA:512:G:N1	2.51	0.42
25:DA:775:G:N3	61:DA:4545:HOH:O	2.37	0.42
25:DA:959:A:N3	25:DA:2457:U:O2'	2.43	0.42
26:DB:80:U:H2'	26:DB:81:G:N7	2.34	0.42
31:DH:56:SER:HB3	31:DH:61:HIS:ND1	2.33	0.42
32:DI:12:LEU:HD22	32:DI:19:VAL:HG21	2.01	0.42
35:DP:82:GLY:HA2	35:DP:113:LYS:O	2.19	0.42
41:DV:28:GLU:HG2	41:DV:28:GLU:H	1.58	0.42
1:AA:1446:U:O2'	1:AA:1447:A:O5'	2.37	0.42
1:AA:149:A:H2'	1:AA:150:C:H6	1.84	0.42
1:AA:993:G:H2'	1:AA:995:C:H41	1.84	0.42
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.55	0.42
3:AC:35:GLU:CD	3:AC:59:ARG:HH22	2.22	0.42
3:AC:6:HIS:CD2	3:AC:8:ILE:HB	2.54	0.42
13:AM:96:LEU:C	13:AM:110:ARG:HG2	2.39	0.42
25:BA:1846:A:OP1	25:BA:1846:A:H8	2.02	0.42
25:BA:239:G:C6	25:BA:240:A:C6	3.08	0.42
25:BA:2724:U:H2'	25:BA:2727:G:H5''	2.00	0.42
38:BS:59:LYS:CD	38:BS:60:GLY:H	2.30	0.42
1:CA:581:G:O2'	1:CA:582:U:H5'	2.19	0.42
1:CA:859:A:H2'	1:CA:860:A:O4'	2.19	0.42
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.87	0.42
1:CA:619:U:N3	4:CD:134:ASP:OD1	2.45	0.42
25:DA:1010:A:N3	25:DA:1153:C:H1'	2.35	0.42
25:DA:1012:U:O2	33:DN:25:ARG:NH2	2.50	0.42
25:DA:117:G:C6	25:DA:119:A:N6	2.87	0.42
25:DA:1255:U:O5'	25:DA:1256:G:H5''	2.20	0.42
25:DA:1268:A:C2	25:DA:2013:A:C4	3.06	0.42
25:DA:2184:G:H2'	25:DA:2185:C:C6	2.54	0.42
25:DA:1027:A:C2	25:DA:2488:A:H5'	2.54	0.42
25:DA:2648:C:H2'	25:DA:2649:U:H6	1.83	0.42
25:DA:2820:A:OP1	37:DR:2:ARG:NH2	2.51	0.42
27:DD:132:PRO:HG2	27:DD:135:PHE:HD2	1.80	0.42
25:DA:2203:U:O4'	27:DD:151:LYS:HE2	2.19	0.42
25:DA:1903:G:OP1	27:DD:241:PRO:HB2	2.19	0.42
30:DG:33:ARG:O	30:DG:161:THR:HG23	2.19	0.42
29:DF:31:HIS:HB2	35:DP:9:ASN:OD1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DS:10:ARG:O	38:DS:14:VAL:HG13	2.19	0.42
44:DY:52:SER:HB2	44:DY:53:PRO:HD2	2.02	0.42
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.54	0.42
2:AB:88:ALA:O	2:AB:226:ARG:NH1	2.52	0.42
2:AB:76:GLN:H	2:AB:76:GLN:CD	2.21	0.42
6:AF:6:VAL:HG13	6:AF:90:VAL:HG22	2.01	0.42
13:AM:80:ARG:HH21	19:AS:69:HIS:HE1	1.66	0.42
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.19	0.42
23:AY:51:U:O2	23:AY:63:G:N2	2.47	0.42
25:BA:1081:U:H2'	25:BA:1082:G:C8	2.53	0.42
25:BA:1093:G:H2'	25:BA:1156:G:N2	2.34	0.42
25:BA:1857:G:H2'	25:BA:1858:C:O4'	2.18	0.42
25:BA:302:A:HO2'	25:BA:303:C:P	2.40	0.42
27:BD:228:PRO:HD3	27:BD:235:GLY:CA	2.49	0.42
30:BG:67:LYS:HE3	30:BG:68:PRO:O	2.19	0.42
33:BN:108:PRO:O	33:BN:113:GLY:HA3	2.18	0.42
35:BP:98:GLU:OE1	35:BP:102:ARG:NH1	2.53	0.42
45:BZ:150:LEU:HA	45:BZ:150:LEU:HD12	1.86	0.42
1:CA:1005:A:H5''	1:CA:1006:C:C6	2.53	0.42
1:CA:1142:G:H2'	1:CA:1143:G:O4'	2.18	0.42
1:CA:1241:G:H2'	1:CA:1242:C:C6	2.54	0.42
1:CA:978:A:O2'	1:CA:1322:C:N3	2.40	0.42
1:CA:1494:G:HO2'	25:DA:1912:A:HO2'	1.66	0.42
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.54	0.42
1:CA:300:A:H1'	1:CA:565:U:O2	2.19	0.42
1:CA:828:A:H5''	1:CA:859:A:C2	2.54	0.42
1:CA:93:G:O2'	1:CA:96:U:H5'	2.19	0.42
1:CA:97:G:HO2'	1:CA:98:G:P	2.42	0.42
5:CE:91:LEU:HG	5:CE:118:ILE:HD11	2.02	0.42
7:CG:59:LEU:HD11	7:CG:63:LYS:HE2	2.00	0.42
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.54	0.42
9:CI:89:ASN:O	9:CI:92:TYR:HB2	2.19	0.42
25:DA:1308:A:H2'	25:DA:1309:G:O4'	2.19	0.42
25:DA:1668:A:O2'	25:DA:1674:G:N7	2.43	0.42
25:DA:208:C:H2'	25:DA:209:C:C6	2.54	0.42
25:DA:39:C:H2'	25:DA:40:C:H6	1.82	0.42
25:DA:411:G:C5	35:DP:72:PRO:HB3	2.54	0.42
25:DA:529:A:H62	25:DA:2041:U:H3	1.67	0.42
25:DA:566:U:H5''	35:DP:29:LYS:HE3	2.01	0.42
25:DA:580:C:H2'	25:DA:581:C:C6	2.53	0.42
25:DA:784:A:C8	25:DA:792:G:C5	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DF:13:SER:OG	29:DF:16:GLY:O	2.23	0.42
31:DH:38:SER:HA	31:DH:39:PRO:HD3	1.83	0.42
31:DH:44:VAL:HG12	31:DH:46:GLU:HG2	2.00	0.42
31:DH:3:ARG:CZ	31:DH:5:GLY:H	2.32	0.42
35:DP:88:LEU:HD11	35:DP:114:ILE:HD12	2.01	0.42
35:DP:45:LEU:HD22	35:DP:45:LEU:HA	1.61	0.42
36:DQ:111:GLU:CD	36:DQ:133:ARG:HH21	2.18	0.42
44:DY:38:ILE:HD11	44:DY:66:PRO:HG3	2.00	0.42
1:AA:975:A:C8	1:AA:975:A:H5'	2.53	0.42
3:AC:142:MET:HG3	3:AC:170:GLN:HB3	2.00	0.42
4:AD:170:VAL:HG12	4:AD:174:LEU:HB2	2.01	0.42
5:AE:36:ASP:OD2	5:AE:40:ARG:HB2	2.19	0.42
5:AE:148:VAL:HG21	8:AH:107:LEU:HB3	2.00	0.42
15:AO:26:GLU:HG2	15:AO:26:GLU:H	1.38	0.42
1:AA:377:G:OP1	16:AP:3:LYS:HD2	2.19	0.42
19:AS:63:THR:O	19:AS:66:MET:HG2	2.18	0.42
48:B2:32:LEU:HD13	48:B2:36:ARG:HH11	1.84	0.42
53:B7:11:LYS:HE3	53:B7:15:THR:OG1	2.18	0.42
25:BA:605:G:H2'	25:BA:606:G:C8	2.54	0.42
27:BD:242:ARG:HG2	27:BD:246:PRO:HG3	2.01	0.42
25:BA:1700:G:O3'	37:BR:2:ARG:HB2	2.18	0.42
25:BA:1199:C:OP1	40:BU:92:ARG:NH1	2.52	0.42
1:CA:1022:G:C6	1:CA:1023:G:C6	3.07	0.42
1:CA:1262:C:H2'	1:CA:1263:C:H6	1.83	0.42
1:CA:1353:G:C2	1:CA:1370:G:C2	3.07	0.42
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.54	0.42
2:CB:82:ARG:HB3	2:CB:94:ASN:OD1	2.20	0.42
1:CA:1227:A:OP2	13:CM:111:LYS:HE3	2.19	0.42
23:CW:68:C:H2'	23:CW:69:G:H8	1.85	0.42
23:CY:12:U:C2	23:CY:13:C:H1'	2.53	0.42
25:DA:1473:G:C6	25:DA:1474:C:C4	3.07	0.42
25:DA:1618:A:H5'	61:DA:4351:HOH:O	2.19	0.42
25:DA:2328:A:H2'	25:DA:2329:G:C8	2.55	0.42
25:DA:2740:A:C6	25:DA:2764:A:C8	3.07	0.42
25:DA:2847:U:OP1	39:DT:98:LYS:HE3	2.19	0.42
25:DA:598:G:C6	25:DA:599:G:C5	3.07	0.42
25:DA:995:C:N3	33:DN:2:LYS:HA	2.34	0.42
26:DB:89:G:C6	26:DB:90:A:C6	3.07	0.42
31:DH:106:THR:HG23	31:DH:112:PRO:HB3	2.01	0.42
1:AA:1219:U:OP1	14:AN:19:ARG:NH2	2.47	0.42
1:AA:922:G:N3	1:AA:1398:A:H2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:138:TYR:HE1	4:AD:140:VAL:HA	1.83	0.42
10:AJ:70:ARG:HA	10:AJ:70:ARG:HD3	1.71	0.42
12:AL:28:LYS:HE2	12:AL:64:TYR:CE1	2.54	0.42
48:B2:22:GLU:OE2	48:B2:68:ARG:NH2	2.53	0.42
25:BA:1549:U:H2'	25:BA:1550:C:C6	2.54	0.42
25:BA:1644:C:H2'	25:BA:1645:C:H6	1.85	0.42
25:BA:1683:C:H2'	25:BA:1684:A:C8	2.54	0.42
25:BA:2699:U:H2'	25:BA:2700:U:O4'	2.20	0.42
25:BA:746:A:H2'	25:BA:747:G:O4'	2.20	0.42
28:BE:116:VAL:HG13	28:BE:122:PHE:HB2	2.00	0.42
28:BE:143:ASN:HD22	28:BE:147:PRO:CD	2.31	0.42
45:BZ:111:VAL:HG13	45:BZ:117:LEU:H	1.84	0.42
1:CA:1003:G:H2'	1:CA:1004:A:H1'	2.01	0.42
1:CA:1319:A:H61	1:CA:1361:G:H21	1.67	0.42
1:CA:189(C):C:H2'	1:CA:189(D):C:O4'	2.20	0.42
1:CA:241:C:C2	1:CA:286:G:C2	3.08	0.42
1:CA:381:C:H2'	1:CA:382:A:O4'	2.19	0.42
1:CA:429:U:H4'	1:CA:430:A:O5'	2.19	0.42
1:CA:519:C:H2'	1:CA:520:A:O4'	2.19	0.42
1:CA:532:A:HO2'	1:CA:533:A:P	2.37	0.42
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.92	0.42
4:CD:58:LEU:O	4:CD:62:GLN:HG2	2.19	0.42
1:CA:8:A:H5'	5:CE:101:ILE:HG22	2.01	0.42
10:CJ:7:LYS:HB2	10:CJ:97:GLU:HB2	2.01	0.42
11:CK:93:GLN:CA	11:CK:93:GLN:HE21	2.28	0.42
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.20	0.42
24:CX:10:G:C2	24:CX:26:G:H1'	2.54	0.42
25:DA:2271:G:OP1	46:D0:18:ALA:HB1	2.20	0.42
25:DA:1171:G:H1	25:DA:1178:C:N4	2.06	0.42
25:DA:1264:G:H2'	25:DA:2014:A:N6	2.33	0.42
25:DA:570:G:H2'	25:DA:2030:A:N7	2.35	0.42
25:DA:2134:A:O2'	25:DA:2135:A:OP1	2.37	0.42
25:DA:2136:C:O2'	25:DA:2137:C:H6	2.02	0.42
25:DA:2659:G:H2'	25:DA:2661:G:OP2	2.19	0.42
25:DA:856:C:O4'	46:D0:27:GLU:HB3	2.19	0.42
25:DA:2723:C:OP2	28:DE:109:LYS:NZ	2.52	0.42
25:DA:444:C:H4'	29:DF:49:ALA:HB2	2.01	0.42
31:DH:40:GLU:O	31:DH:55:PRO:HG3	2.20	0.42
31:DH:11:VAL:HG21	31:DH:50:VAL:HG23	2.02	0.42
33:DN:123:TYR:OH	33:DN:130:HIS:NE2	2.18	0.42
35:DP:21:ARG:HA	35:DP:21:ARG:HD3	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DR:29:LEU:HA	37:DR:29:LEU:HD12	1.81	0.42
41:DV:8:GLY:O	41:DV:10:LYS:NZ	2.50	0.42
1:AA:1030(A):G:O2'	1:AA:1030(C):G:N7	2.53	0.42
1:AA:123:C:OP1	1:AA:311:C:O2'	2.32	0.42
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.54	0.42
1:AA:598:U:O4	61:AA:4079:HOH:O	2.21	0.42
2:AB:211:ILE:HG22	2:AB:215:LEU:HD12	2.00	0.42
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.55	0.42
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.55	0.42
47:B1:50:ARG:HG2	47:B1:59:THR:HB	2.02	0.42
25:BA:2418:U:H6	25:BA:2418:U:H2'	1.70	0.42
25:BA:2576:A:C2	25:BA:2659:U:H4'	2.54	0.42
29:BF:132:VAL:HA	29:BF:138:GLU:HB3	2.01	0.42
39:BT:33:LYS:HA	39:BT:42:ILE:HD13	2.00	0.42
1:CA:1064:G:H4'	1:CA:1065:U:O5'	2.20	0.42
1:CA:273:A:N6	1:CA:274:A:C6	2.87	0.42
1:CA:114:U:H1'	1:CA:353:A:H1'	2.02	0.42
1:CA:767:A:H2'	1:CA:768:A:O4'	2.20	0.42
2:CB:210:SER:OG	2:CB:211:ILE:N	2.52	0.42
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.20	0.42
2:CB:91:PRO:HA	2:CB:151:GLY:O	2.19	0.42
4:CD:158:ILE:HG22	4:CD:162:LEU:HD12	2.02	0.42
8:CH:9:MET:SD	8:CH:32:LYS:HD3	2.59	0.42
9:CI:111:ARG:O	9:CI:113:LYS:HD2	2.19	0.42
14:CN:24:CYS:HB2	14:CN:40:CYS:HB3	2.01	0.42
23:CW:61:C:OP2	23:CW:61:C:H2'	2.20	0.42
50:D4:33:VAL:HG12	50:D4:34:GLU:H	1.85	0.42
25:DA:1027:A:N6	25:DA:1126:A:C4	2.87	0.42
25:DA:141:A:H8	25:DA:1408:C:O2'	2.01	0.42
25:DA:1992:G:O5'	25:DA:1992:G:C8	2.73	0.42
25:DA:2393:A:H2'	25:DA:2394:C:O4'	2.19	0.42
25:DA:800:A:OP1	25:DA:800:A:H8	2.03	0.42
29:DF:150:GLY:HA2	29:DF:172:TRP:CE3	2.54	0.42
29:DF:64:ILE:HG13	29:DF:65:TRP:N	2.34	0.42
31:DH:121:ILE:HD11	31:DH:140:LYS:HG2	1.99	0.42
31:DH:69:ARG:HG3	31:DH:70:THR:N	2.33	0.42
1:AA:1169:A:H2'	1:AA:1170:A:C8	2.54	0.42
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.49	0.42
1:AA:262:A:C6	1:AA:263:A:C6	3.08	0.42
1:AA:757:U:O2'	1:AA:879:C:O2	2.34	0.42
2:AB:69:LEU:HD12	2:AB:91:PRO:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.85	0.42
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.84	0.42
19:AS:36:ARG:HB3	19:AS:72:GLY:HA3	2.02	0.42
25:BA:1405:A:C2	25:BA:1418:U:O4	2.72	0.42
25:BA:1527:G:C6	25:BA:1528:U:C4	3.08	0.42
25:BA:1495:G:H1'	25:BA:1574:A:N1	2.34	0.42
29:BF:93:LYS:HD3	29:BF:93:LYS:HA	1.79	0.42
32:BI:57:ARG:O	32:BI:61:ARG:HD3	2.20	0.42
37:BR:96:ARG:HD2	37:BR:115:GLU:OE1	2.20	0.42
42:BW:9:TYR:HA	42:BW:100:THR:HG23	2.01	0.42
45:BZ:111:VAL:O	45:BZ:113:ALA:N	2.49	0.42
1:CA:189(D):C:H6	1:CA:189(D):C:O5'	2.03	0.42
57:CA:3178:PCY:H24	57:CA:3178:PCY:H17	1.67	0.42
1:CA:890:G:O2'	1:CA:906:G:O6	2.27	0.42
3:CC:112:SER:O	3:CC:116:VAL:HG23	2.20	0.42
4:CD:150:GLU:CD	4:CD:151:LYS:H	2.22	0.42
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	2.02	0.42
9:CI:16:ARG:HD3	9:CI:64:THR:HG21	2.01	0.42
20:CT:65:LYS:HA	20:CT:68:LYS:HD3	2.00	0.42
47:D1:78:LYS:HE3	47:D1:78:LYS:HB2	1.86	0.42
49:D3:7:LYS:HZ3	49:D3:34:GLU:HG3	1.84	0.42
25:DA:1356:G:OP1	61:DA:4817:HOH:O	2.21	0.42
25:DA:1794:U:H2'	25:DA:1795:C:C6	2.55	0.42
25:DA:2004:G:H2'	25:DA:2005:A:O4'	2.20	0.42
25:DA:2805:G:H2'	25:DA:2807:G:C8	2.54	0.42
25:DA:807:U:OP2	35:DP:41:ARG:NH2	2.52	0.42
31:DH:3:ARG:HB3	31:DH:6:ARG:HG2	2.01	0.42
31:DH:8:PRO:O	31:DH:69:ARG:NH1	2.53	0.42
32:DI:93:THR:HG22	32:DI:119:PRO:HB3	2.01	0.42
1:CA:1423:G:P	34:DO:49:ARG:HH12	2.42	0.42
35:DP:2:LYS:HG2	35:DP:5:ASP:OD2	2.20	0.42
40:DU:97:ASP:OD1	40:DU:101:ARG:HD2	2.20	0.42
45:DZ:24:LEU:N	45:DZ:39:VAL:O	2.50	0.42
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.54	0.42
1:AA:918:A:H2'	1:AA:919:A:O4'	2.19	0.42
5:AE:145:LYS:HB3	5:AE:145:LYS:HE2	1.82	0.42
18:AR:47:THR:HG23	18:AR:49:LYS:HG3	2.02	0.42
20:AT:13:LEU:HD12	20:AT:14:LYS:N	2.35	0.42
25:BA:1553:A:O2'	25:BA:1554:A:O5'	2.25	0.42
25:BA:1821:C:H5''	25:BA:1822:A:OP1	2.20	0.42
25:BA:2108:U:H2'	25:BA:2109:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:495:G:O6	53:B7:37:LYS:HE2	2.20	0.42
25:BA:886:U:H1'	25:BA:1236:G:H1'	2.02	0.42
34:BO:6:THR:HG22	34:BO:8:LEU:HD22	2.01	0.42
1:CA:1018:C:H2'	1:CA:1019:C:O4'	2.20	0.42
1:CA:1278:U:H5'	1:CA:1279:A:C5'	2.50	0.42
1:CA:431:A:OP2	61:CA:4140:HOH:O	2.21	0.42
1:CA:457:C:H2'	1:CA:458:C:C6	2.54	0.42
1:CA:736:C:H2'	1:CA:737:A:C8	2.55	0.42
2:CB:58:ILE:HD13	2:CB:58:ILE:HA	1.83	0.42
5:CE:93:PRO:HG2	8:CH:105:ARG:HE	1.85	0.42
9:CI:105:ASP:HB2	9:CI:107:ARG:HG3	2.02	0.42
13:CM:65:LYS:N	50:D4:50:VAL:HG21	2.35	0.42
25:DA:1364:G:C5	47:D1:3:LYS:HE2	2.55	0.42
47:D1:3:LYS:HB3	47:D1:4:VAL:H	1.58	0.42
53:D7:34:ARG:NH2	61:D7:203:HOH:O	2.53	0.42
25:DA:141:A:H8	25:DA:1408:C:HO2'	1.57	0.42
25:DA:1983:C:H4'	25:DA:2606:C:H4'	2.00	0.42
25:DA:2061:G:H5''	25:DA:2503:A:C2	2.54	0.42
25:DA:262:A:H2'	25:DA:263:C:O4'	2.20	0.42
25:DA:471:A:H2'	25:DA:472:A:O4'	2.20	0.42
25:DA:796:C:H2'	25:DA:797:C:H6	1.80	0.42
25:DA:921:G:H2'	25:DA:922:U:H6	1.85	0.42
25:DA:568:U:H5'	25:DA:945:A:N1	2.34	0.42
29:DF:9:ILE:HA	29:DF:10:PRO:HD3	1.79	0.42
30:DG:106:LEU:HA	30:DG:110:ALA:HB3	2.01	0.42
35:DP:85:LEU:HD13	35:DP:120:ALA:HB2	2.02	0.42
37:DR:98:LEU:HB2	37:DR:113:LEU:HD11	2.02	0.42
45:DZ:111:VAL:HG22	45:DZ:174:VAL:HG22	2.02	0.42
45:DZ:28:MET:HE3	45:DZ:35:ARG:HB2	2.02	0.42
1:AA:1002:G:C5	1:AA:1003:G:H1'	2.54	0.42
1:AA:1530:G:H4'	1:AA:1530:G:OP1	2.19	0.42
1:AA:501:C:H2'	1:AA:502:G:H8	1.84	0.42
4:AD:22:LYS:HB2	4:AD:26:CYS:SG	2.60	0.42
1:AA:1291:G:O2'	9:AI:38:GLN:OE1	2.30	0.42
48:B2:35:LEU:HA	48:B2:35:LEU:HD23	1.84	0.42
50:B4:55:ARG:HA	50:B4:55:ARG:HD2	1.83	0.42
50:B4:53:GLU:HG2	50:B4:55:ARG:HD2	2.02	0.42
25:BA:2086:C:H2'	25:BA:2087:C:C6	2.55	0.42
25:BA:669:A:H4'	25:BA:670:C:H5	1.85	0.42
25:BA:895:G:O6	25:BA:974:G:H2'	2.20	0.42
26:BB:2:C:H2'	26:BB:3:C:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BD:143:HIS:ND1	27:BD:194:GLY:O	2.43	0.42
32:BI:131:LYS:H	32:BI:138:ILE:H	1.67	0.42
41:BV:72:VAL:HG11	41:BV:85:LYS:HD2	2.01	0.42
45:BZ:7:ALA:O	45:BZ:62:PRO:HD3	2.20	0.42
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.54	0.42
1:CA:769:G:H4'	1:CA:1513:A:H4'	2.02	0.42
1:CA:324:G:N2	1:CA:326:G:H3'	2.35	0.42
2:CB:52:GLU:HG2	2:CB:56:ARG:NH2	2.34	0.42
3:CC:181:ASN:ND2	3:CC:204:LEU:HD12	2.30	0.42
6:CF:22:GLU:O	6:CF:26:ILE:HG13	2.20	0.42
11:CK:93:GLN:NE2	11:CK:93:GLN:HA	2.29	0.42
23:CW:25:C:H2'	23:CW:26:A:C8	2.54	0.42
23:CW:29:G:N2	23:CW:41:C:N3	2.67	0.42
52:D6:37:ARG:O	52:D6:38:LYS:HD2	2.20	0.42
25:DA:667:U:O2	54:D8:2:PRO:HD2	2.20	0.42
25:DA:1187:G:OP2	25:DA:1187:G:H8	2.02	0.42
25:DA:1796:U:H2'	25:DA:1797:C:H6	1.84	0.42
25:DA:2335:A:C8	25:DA:2337:G:C5	3.08	0.42
25:DA:2419:U:H2'	25:DA:2420:C:C6	2.55	0.42
25:DA:2646:C:O5'	25:DA:2646:C:H6	2.03	0.42
25:DA:2652:C:O2	25:DA:2668:G:N2	2.32	0.42
30:DG:111:LEU:HB3	30:DG:117:PHE:CE2	2.55	0.42
36:DQ:79:LEU:HA	36:DQ:79:LEU:HD23	1.94	0.42
1:AA:107:G:H2'	1:AA:108:G:O4'	2.20	0.42
1:AA:431:A:H2'	1:AA:432:A:O4'	2.20	0.42
2:AB:220:ASP:O	2:AB:224:GLN:HG3	2.20	0.42
2:AB:230:VAL:HG22	2:AB:231:GLU:H	1.84	0.42
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.27	0.42
8:AH:29:SER:HB3	8:AH:32:LYS:HG3	2.02	0.42
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.35	0.42
25:BA:1091:A:O2'	25:BA:1093:G:C4	2.66	0.42
25:BA:1405:A:H61	25:BA:1418:U:H3	1.68	0.42
25:BA:1945:U:H2'	25:BA:1946:C:C6	2.54	0.42
25:BA:196:A:H2'	25:BA:197:C:O4'	2.18	0.42
25:BA:213:G:H2'	25:BA:214:A:O4'	2.19	0.42
25:BA:329:U:H2'	25:BA:330:U:C6	2.55	0.42
25:BA:316:C:C2	25:BA:373:G:C2	3.08	0.42
29:BF:32:LEU:HB3	29:BF:112:MET:HE1	2.02	0.42
30:BG:163:ALA:HB1	30:BG:168:GLU:HB2	2.01	0.42
32:BI:40:THR:O	32:BI:44:LEU:HB2	2.19	0.42
35:BP:100:LEU:HA	35:BP:100:LEU:HD23	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BP:99:LEU:HD22	35:BP:102:ARG:NH2	2.35	0.42
41:BV:18:LEU:HD13	41:BV:20:LEU:HB2	2.02	0.42
43:BX:92:LEU:O	43:BX:94:GLY:N	2.44	0.42
1:CA:1111:A:H2'	1:CA:1112:C:C6	2.54	0.42
1:CA:1120:G:O6	1:CA:1154:G:N2	2.53	0.42
1:CA:397:A:H3'	1:CA:397:A:N3	2.34	0.42
1:CA:625:G:H2'	1:CA:626:U:C6	2.55	0.42
1:CA:714:G:H2'	1:CA:715:A:C8	2.55	0.42
1:CA:737:A:H2'	1:CA:738:C:C6	2.55	0.42
6:CF:82:ARG:HA	6:CF:82:ARG:HD2	1.90	0.42
8:CH:73:ASP:OD2	8:CH:75:ARG:NH1	2.53	0.42
10:CJ:37:PRO:HA	10:CJ:72:VAL:HG12	2.02	0.42
25:DA:1027:A:C6	25:DA:1126:A:C4	3.07	0.42
25:DA:1171:G:H8	25:DA:1171:G:OP2	2.03	0.42
25:DA:1913:A:H4'	25:DA:1914:C:C5'	2.50	0.42
25:DA:2149:G:H3'	25:DA:2150:U:C6	2.55	0.42
25:DA:2135:A:N6	25:DA:2157:G:H21	2.12	0.42
25:DA:2514:U:H2'	25:DA:2515:C:H6	1.84	0.42
25:DA:2787:C:H2'	25:DA:2788:C:C6	2.55	0.42
25:DA:848:G:H2'	25:DA:849:A:C8	2.54	0.42
26:DB:14:U:H1'	26:DB:108:U:O2'	2.20	0.42
27:DD:118:VAL:HG22	27:DD:119:ALA:H	1.85	0.42
28:DE:31:CYS:HA	28:DE:32:PRO:HD2	1.86	0.42
30:DG:165:THR:OG1	30:DG:168:GLU:HG3	2.20	0.42
37:DR:55:ALA:HB2	37:DR:79:LEU:HD13	2.02	0.42
43:DX:12:VAL:HG22	43:DX:29:TRP:CE2	2.55	0.42
43:DX:92:LEU:C	43:DX:94:GLY:H	2.23	0.42
1:AA:1106:G:C6	1:AA:1107:C:C4	3.08	0.41
1:AA:31:G:O2'	1:AA:48:C:N4	2.53	0.41
1:AA:50:A:H1'	1:AA:52:G:C8	2.55	0.41
2:AB:133:LYS:O	2:AB:137:ARG:HG3	2.19	0.41
5:AE:36:ASP:OD1	5:AE:38:GLN:N	2.41	0.41
5:AE:41:VAL:HG11	5:AE:109:ILE:O	2.20	0.41
8:AH:19:VAL:HG23	8:AH:21:LYS:HD3	2.02	0.41
8:AH:56:LYS:HD3	8:AH:56:LYS:HA	1.87	0.41
1:AA:1368:G:OP2	9:AI:112:LYS:HG3	2.19	0.41
10:AJ:90:LEU:HA	10:AJ:91:PRO:HD3	1.95	0.41
11:AK:81:ASP:OD1	11:AK:107:SER:OG	2.25	0.41
12:AL:92:ASP:O	12:AL:94:PRO:HD3	2.19	0.41
20:AT:48:LYS:HD3	20:AT:48:LYS:HA	1.85	0.41
23:AW:26:A:N6	23:AW:44:G:H1	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2348:A:H61	46:B0:43:THR:CG2	2.33	0.41
25:BA:2815:C:H2'	25:BA:2816:G:C8	2.55	0.41
25:BA:354:A:H2	25:BA:1255:A:O2'	2.03	0.41
25:BA:553:A:C2	25:BA:2065:C:H4'	2.55	0.41
25:BA:766:C:H2'	25:BA:767:C:C6	2.54	0.41
25:BA:1855:G:O3'	27:BD:249:PRO:HD3	2.20	0.41
31:BH:144:VAL:O	31:BH:148:ILE:HG13	2.20	0.41
39:BT:118:ARG:HH11	39:BT:118:ARG:HG3	1.85	0.41
45:BZ:146:ILE:HA	45:BZ:147:GLY:HA2	1.77	0.41
1:CA:620:C:H2'	1:CA:621:A:O4'	2.20	0.41
1:CA:718:G:H5'	11:CK:117:ASN:ND2	2.35	0.41
2:CB:229:VAL:HG12	2:CB:230:VAL:N	2.35	0.41
5:CE:13:ILE:HA	5:CE:29:GLY:O	2.19	0.41
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	2.01	0.41
8:CH:39:LEU:HA	8:CH:39:LEU:HD13	1.85	0.41
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.19	0.41
13:CM:64:TRP:HB2	13:CM:66:LEU:HD21	2.00	0.41
16:CP:43:LYS:HB3	16:CP:48:TRP:CD1	2.55	0.41
17:CQ:94:ASN:O	17:CQ:98:LEU:HD13	2.20	0.41
25:DA:1213:A:H1'	25:DA:1238:G:N3	2.35	0.41
25:DA:2114:A:H2'	25:DA:2114:A:N3	2.35	0.41
25:DA:25:U:H2'	25:DA:26:G:O4'	2.20	0.41
30:DG:131:TYR:HB3	30:DG:159:VAL:CG2	2.50	0.41
33:DN:4:TYR:HB2	40:DU:101:ARG:NH1	2.35	0.41
1:AA:1292:U:H5'	9:AI:38:GLN:OE1	2.19	0.41
2:AB:134:GLU:O	2:AB:138:LEU:HG	2.20	0.41
9:AI:93:ARG:HB2	9:AI:93:ARG:NH1	2.35	0.41
16:AP:52:ASP:HB3	16:AP:55:ARG:HB2	2.02	0.41
50:B4:47:GLN:HG2	50:B4:49:PHE:H	1.85	0.41
25:BA:1506:G:C6	25:BA:1508:G:C5	3.08	0.41
25:BA:1506:G:H5''	25:BA:1507:A:OP2	2.20	0.41
25:BA:2126:G:H2'	25:BA:2127:C:H6	1.82	0.41
25:BA:239:G:P	54:B8:13:ARG:HH22	2.43	0.41
25:BA:327:U:H2'	25:BA:328:G:C8	2.54	0.41
28:BE:7:VAL:HG12	28:BE:27:LEU:HB3	2.02	0.41
37:BR:21:TYR:CZ	37:BR:43:GLU:HG2	2.55	0.41
45:BZ:54:HIS:HD2	45:BZ:99:TYR:O	2.03	0.41
1:CA:344:A:H4'	1:CA:345:C:OP2	2.21	0.41
1:CA:399:G:H2'	1:CA:400:C:C6	2.54	0.41
1:CA:407:G:H5''	4:CD:115:ARG:HB3	2.02	0.41
1:CA:7:G:H5'	1:CA:298:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:65:ARG:HD3	4:CD:70:ILE:O	2.20	0.41
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.37	0.41
5:CE:51:VAL:HG23	5:CE:52:PRO:HD3	2.01	0.41
9:CI:19:LEU:HA	9:CI:19:LEU:HD23	1.89	0.41
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	2.01	0.41
15:CO:32:LEU:HD13	15:CO:63:ARG:HB2	2.02	0.41
15:CO:36:ILE:HG23	15:CO:56:LEU:HD11	2.02	0.41
23:CY:2:C:H2'	23:CY:3:C:H6	1.85	0.41
25:DA:1274:A:N3	25:DA:1297:C:H1'	2.35	0.41
25:DA:1336:A:H2'	25:DA:1337:G:H8	1.84	0.41
25:DA:1404:C:O2'	25:DA:1405:U:H5'	2.20	0.41
25:DA:1848:A:C4	25:DA:1849:G:C8	3.09	0.41
25:DA:2144:U:O2	25:DA:2148:G:N1	2.54	0.41
25:DA:2526:G:H2'	25:DA:2527:C:H6	1.85	0.41
25:DA:2769:C:H2'	25:DA:2770:G:O4'	2.20	0.41
26:DB:4:C:N4	26:DB:117:G:H1	2.15	0.41
26:DB:61:G:C6	26:DB:62:C:C4	3.08	0.41
27:DD:79:VAL:O	27:DD:113:VAL:HG23	2.19	0.41
27:DD:164:GLN:NE2	27:DD:176:ARG:HH22	2.17	0.41
28:DE:51:PHE:O	28:DE:77:ILE:HD12	2.20	0.41
30:DG:47:LYS:HB3	30:DG:48:GLU:H	1.58	0.41
31:DH:27:LYS:NZ	31:DH:32:GLU:OE2	2.45	0.41
34:DO:66:LYS:HA	34:DO:79:PHE:O	2.21	0.41
35:DP:97:PRO:HG3	35:DP:112:LEU:HD12	2.02	0.41
1:AA:1022:G:H4'	1:AA:1022:G:OP1	2.21	0.41
1:AA:1278:U:H5'	1:AA:1279:A:C5'	2.50	0.41
1:AA:266:G:O2'	1:AA:267:C:OP2	2.33	0.41
1:AA:92:C:H2'	1:AA:93:G:H8	1.84	0.41
3:AC:130:VAL:O	3:AC:134:ILE:HG13	2.20	0.41
4:AD:166:LYS:HB2	4:AD:168:ARG:CZ	2.50	0.41
24:AX:21:A:H61	24:AX:46:G:H2'	1.84	0.41
23:AY:69:G:C2	23:AY:70:G:H1'	2.55	0.41
25:BA:1249:A:N6	25:BA:1286:U:H2'	2.36	0.41
25:BA:1686:U:O2'	25:BA:1687:C:H5'	2.20	0.41
25:BA:2122:G:H2'	25:BA:2123:G:C8	2.56	0.41
25:BA:18:C:O2'	25:BA:577:U:OP1	2.33	0.41
25:BA:2584:A:C8	28:BE:144:ARG:HD2	2.55	0.41
31:BH:104:GLU:HG3	31:BH:114:VAL:HG22	2.03	0.41
38:BS:19:LYS:HE3	38:BS:42:ASP:OD1	2.20	0.41
43:BX:84:ALA:HB3	43:BX:87:GLN:NE2	2.35	0.41
1:CA:984:C:O5'	1:CA:984:C:H6	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.88	0.41
4:CD:45:GLN:HB2	4:CD:46:LYS:H	1.73	0.41
5:CE:33:VAL:HA	5:CE:42:GLY:O	2.20	0.41
7:CG:108:ALA:HA	7:CG:111:ARG:HD2	2.02	0.41
9:CI:100:GLY:O	9:CI:103:THR:HG22	2.20	0.41
9:CI:5:TYR:CE2	9:CI:7:THR:HG23	2.55	0.41
1:CA:552:U:H4'	12:CL:86:ARG:HD2	2.02	0.41
12:CL:24:VAL:HG12	12:CL:98:TYR:CE1	2.56	0.41
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.21	0.41
15:CO:74:ASP:OD1	15:CO:76:GLU:HB2	2.20	0.41
25:DA:2097:C:H2'	25:DA:2098:U:O4'	2.20	0.41
25:DA:2135:A:H2'	25:DA:2136:C:C6	2.55	0.41
25:DA:2156:G:H2'	25:DA:2157:G:N3	2.35	0.41
30:DG:115:ARG:HH11	30:DG:115:ARG:H	1.68	0.41
30:DG:179:PRO:HG3	50:D4:43:TYR:OH	2.20	0.41
39:DT:88:ILE:HG13	39:DT:91:ARG:NH2	2.35	0.41
25:DA:1614:A:C2	42:DW:93:ALA:HB2	2.54	0.41
44:DY:90:LEU:HD11	44:DY:96:ILE:HG23	2.02	0.41
1:AA:1028:C:N3	1:AA:1029:C:H1'	2.35	0.41
57:AA:3231:PCY:H40	23:AY:35:A:N1	2.36	0.41
1:AA:362:G:O3'	12:AL:33:ARG:NH2	2.53	0.41
1:AA:601:C:H2'	1:AA:602:A:H8	1.84	0.41
1:AA:658:G:H2'	1:AA:659:U:C6	2.55	0.41
1:AA:865:A:H2	1:AA:918:A:H4'	1.85	0.41
1:AA:911:U:OP1	12:AL:95:GLY:HA2	2.20	0.41
5:AE:83:GLU:HG2	5:AE:88:LYS:HB2	2.02	0.41
7:AG:14:PRO:HG3	7:AG:21:VAL:HG13	2.02	0.41
14:AN:13:THR:HA	14:AN:14:PRO:HD3	1.95	0.41
18:AR:59:SER:OG	18:AR:62:GLU:HG2	2.20	0.41
23:AW:1:G:H2'	23:AW:1:G:N3	2.34	0.41
25:BA:1074:A:N6	25:BA:1171:G:H2'	2.36	0.41
25:BA:1091:A:C8	25:BA:1093:G:N2	2.88	0.41
25:BA:1221:G:H1'	25:BA:1222:A:O5'	2.21	0.41
25:BA:2186:C:H5	25:BA:2187:G:C4	2.37	0.41
25:BA:2574:U:H1'	34:BO:23:ARG:HH11	1.86	0.41
25:BA:288:U:O2'	25:BA:289:G:P	2.79	0.41
25:BA:543:G:H2'	25:BA:544:U:C6	2.55	0.41
27:BD:132:PRO:HG3	27:BD:190:TYR:CE1	2.55	0.41
30:BG:56:ALA:HA	30:BG:153:ARG:HH21	1.85	0.41
34:BO:118:ALA:HA	34:BO:119:PRO:HD2	1.80	0.41
25:BA:2849:G:C5'	37:BR:46:GLY:HA2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:BU:83:LEU:HD13	40:BU:113:ALA:HB2	2.01	0.41
1:CA:1313:U:P	19:CS:5:LEU:HG	2.60	0.41
1:CA:1441:G:O5'	1:CA:1441:G:H8	2.04	0.41
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.55	0.41
2:CB:16:HIS:HB3	2:CB:210:SER:HB3	2.03	0.41
4:CD:15:GLU:OE1	4:CD:63:LYS:HG3	2.21	0.41
10:CJ:5:ARG:HA	10:CJ:73:ASP:OD1	2.19	0.41
11:CK:85:ARG:HG2	11:CK:112:THR:HA	2.02	0.41
23:CY:3:C:O5'	23:CY:3:C:H6	2.04	0.41
25:DA:2001:A:H2'	25:DA:2002:G:C8	2.55	0.41
25:DA:271(H):G:N3	25:DA:271(I):G:C8	2.88	0.41
25:DA:2815:C:H2'	25:DA:2816:C:H6	1.85	0.41
26:DB:66:A:N6	26:DB:108:U:H3'	2.34	0.41
27:DD:3:VAL:HG13	27:DD:17:THR:HB	2.02	0.41
28:DE:28:ALA:HB3	28:DE:93:VAL:HG12	2.02	0.41
30:DG:61:ALA:O	50:D4:7:PRO:HG2	2.21	0.41
32:DI:93:THR:O	32:DI:97:ILE:HG13	2.20	0.41
33:DN:110:GLY:O	33:DN:114:ARG:HG3	2.20	0.41
33:DN:15:LEU:HB2	33:DN:135:PRO:CB	2.49	0.41
33:DN:67:LEU:C	33:DN:88:GLU:HG3	2.41	0.41
37:DR:87:TYR:OH	37:DR:116:LEU:HB3	2.20	0.41
39:DT:91:ARG:HD2	39:DT:120:ARG:NH1	2.36	0.41
28:DE:27:LEU:HD22	39:DT:1:MET:HE1	2.02	0.41
45:DZ:97:GLU:HG2	45:DZ:97:GLU:H	1.61	0.41
1:AA:1001(A):G:C6	1:AA:1002:G:N7	2.89	0.41
1:AA:892:A:O2'	1:AA:1415:G:H4'	2.20	0.41
1:AA:1516:G:H2'	1:AA:1518:A:OP2	2.21	0.41
1:AA:691:G:OP2	11:AK:26:ASN:ND2	2.43	0.41
3:AC:131:ARG:NE	3:AC:166:GLU:OE2	2.53	0.41
3:AC:152:ILE:HG23	3:AC:167:TRP:HB3	2.02	0.41
1:AA:1125:U:H4'	10:AJ:5:ARG:HH22	1.83	0.41
1:AA:1049:U:OP1	14:AN:3:ARG:HB2	2.20	0.41
50:B4:58:ARG:HB3	50:B4:58:ARG:CZ	2.49	0.41
25:BA:1183:G:H2'	25:BA:1184:G:O4'	2.20	0.41
25:BA:2195:A:H2'	25:BA:2195:A:N3	2.35	0.41
25:BA:2827:G:OP1	37:BR:99:LYS:HE2	2.21	0.41
42:BW:68:ARG:NH1	42:BW:112:GLY:H	2.19	0.41
1:CA:1023:G:C5	1:CA:1024:G:C8	3.08	0.41
1:CA:1360:A:H2'	1:CA:1361:G:O4'	2.21	0.41
1:CA:1414:U:H3	1:CA:1486:G:H1	1.68	0.41
1:CA:89:C:H2'	1:CA:90:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:982:U:O2	1:CA:1222:G:N1	2.39	0.41
2:CB:133:LYS:O	2:CB:137:ARG:HG3	2.20	0.41
11:CK:120:ARG:HA	11:CK:121:PRO:HD3	1.95	0.41
24:CX:15:G:H2'	24:CX:59:A:N1	2.35	0.41
50:D4:68:ARG:O	50:D4:69:LYS:HB3	2.20	0.41
25:DA:1005:C:H4'	25:DA:1012:U:C6	2.55	0.41
25:DA:1127:A:H2'	25:DA:1128:A:H5''	2.02	0.41
25:DA:1131:G:N2	25:DA:1132:A:N3	2.68	0.41
25:DA:1159:U:O2'	25:DA:1160:G:H5'	2.20	0.41
25:DA:1270:C:H5''	25:DA:1271:G:O5'	2.20	0.41
25:DA:1707:G:C5	25:DA:1756:G:C6	3.08	0.41
25:DA:1706:U:O2	25:DA:1757:U:H5'	2.20	0.41
25:DA:1817:G:H2'	25:DA:1818:U:H5'	2.03	0.41
25:DA:2319:G:N2	38:DS:3:ARG:HA	2.35	0.41
25:DA:2356:C:O3'	46:D0:20:ARG:HD3	2.21	0.41
25:DA:248:G:C2	25:DA:2431:U:H4'	2.55	0.41
25:DA:2758:A:H2'	25:DA:2759:G:O4'	2.21	0.41
25:DA:579:G:H2'	25:DA:580:C:C6	2.56	0.41
25:DA:930:U:O4'	25:DA:931:G:C2	2.74	0.41
31:DH:9:ILE:HD13	31:DH:72:ILE:HG21	2.03	0.41
38:DS:11:LYS:O	38:DS:15:ARG:HG3	2.20	0.41
40:DU:79:PHE:CE2	40:DU:83:LEU:HD21	2.55	0.41
43:DX:43:VAL:HG21	43:DX:81:VAL:HG11	2.03	0.41
45:DZ:44:PHE:CZ	45:DZ:86:VAL:HG11	2.56	0.41
45:DZ:8:TYR:HB2	45:DZ:38:TYR:CE2	2.55	0.41
1:AA:1145:C:H4'	1:AA:1146:A:C5'	2.51	0.41
4:AD:163:GLU:O	4:AD:166:LYS:HG2	2.20	0.41
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.20	0.41
16:AP:27:LYS:HE3	16:AP:27:LYS:HB2	1.72	0.41
25:BA:2162:C:H1'	25:BA:2174:G:H22	1.85	0.41
25:BA:2591:C:H6	25:BA:2591:C:O5'	2.04	0.41
25:BA:308:U:H2'	25:BA:309:C:C6	2.55	0.41
25:BA:80:G:HO2'	25:BA:319:G:HO2'	1.66	0.41
25:BA:982:U:H2'	25:BA:983:G:O4'	2.21	0.41
39:BT:53:ARG:NH1	39:BT:53:ARG:HB3	2.35	0.41
45:BZ:107:THR:HA	45:BZ:108:PRO:HD3	1.63	0.41
45:BZ:136:PHE:O	45:BZ:137:ILE:HG13	2.20	0.41
1:CA:164:U:H2'	1:CA:165:C:C6	2.56	0.41
1:CA:542:G:P	4:CD:10:ARG:HH22	2.43	0.41
5:CE:84:PHE:CE2	5:CE:133:TYR:HD2	2.39	0.41
9:CI:18:PHE:CD2	9:CI:62:TYR:HD2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CT:16:HIS:O	20:CT:19:SER:OG	2.27	0.41
46:D0:56:ASP:O	46:D0:57:PHE:HB2	2.20	0.41
46:D0:50:ASN:HA	46:D0:62:LEU:HD12	2.03	0.41
50:D4:14:ILE:HB	50:D4:22:ILE:HB	2.03	0.41
50:D4:28:LYS:HA	50:D4:29:PRO:HD3	1.93	0.41
53:D7:26:GLY:O	53:D7:30:VAL:HG23	2.21	0.41
55:D9:17:ILE:HD12	55:D9:17:ILE:HA	1.82	0.41
25:DA:1593:G:H2'	25:DA:1594:G:C8	2.55	0.41
25:DA:1810:A:H2'	25:DA:1811:G:O4'	2.20	0.41
25:DA:263:C:H2'	25:DA:264:C:O4'	2.21	0.41
25:DA:271(H):G:O2'	25:DA:271(I):G:C8	2.69	0.41
25:DA:42:G:H2'	25:DA:43:A:O4'	2.19	0.41
28:DE:48:GLN:HA	28:DE:80:GLU:HA	2.03	0.41
36:DQ:42:ILE:HD13	36:DQ:97:VAL:HB	2.02	0.41
41:DV:24:LYS:HA	41:DV:92:THR:OG1	2.21	0.41
44:DY:94:LYS:HA	44:DY:94:LYS:HD2	1.84	0.41
45:DZ:156:LYS:HE2	45:DZ:158:PRO:HB3	2.02	0.41
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.20	0.41
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.53	0.41
14:AN:33:VAL:HA	14:AN:40:CYS:HA	2.03	0.41
25:BA:1065:U:H3	25:BA:1188:A:H62	1.66	0.41
25:BA:715:G:H5'	25:BA:716:G:OP2	2.20	0.41
26:BB:17:C:H2'	26:BB:18:G:O4'	2.21	0.41
37:BR:1:MET:HB2	37:BR:2:ARG:H	1.74	0.41
1:CA:1028:C:O2	1:CA:1034:G:H1'	2.20	0.41
1:CA:1055:A:C5	1:CA:1206:G:C2	3.09	0.41
1:CA:302:G:N3	1:CA:556:C:H4'	2.35	0.41
1:CA:583:A:N6	1:CA:758:G:O2'	2.54	0.41
2:CB:16:HIS:CB	2:CB:204:ASN:HB3	2.50	0.41
2:CB:80:ILE:HD11	2:CB:212:GLN:CA	2.51	0.41
1:CA:411:A:OP2	4:CD:25:ARG:NH2	2.54	0.41
4:CD:92:VAL:O	4:CD:96:LEU:HD22	2.21	0.41
13:CM:87:TYR:O	13:CM:91:ARG:HG2	2.21	0.41
14:CN:13:THR:HA	14:CN:14:PRO:HD3	1.88	0.41
20:CT:89:ARG:O	20:CT:93:GLU:HB2	2.20	0.41
24:CX:67:C:H2'	24:CX:68:C:H5'	2.03	0.41
25:DA:1316:U:H2'	25:DA:1317:A:C8	2.55	0.41
25:DA:1379:A:H4'	25:DA:1380:G:OP2	2.21	0.41
25:DA:1494:A:C6	25:DA:1495:A:C6	3.09	0.41
25:DA:2489:G:C2'	25:DA:2490:G:H5'	2.51	0.41
25:DA:2516:G:C6	25:DA:2517:C:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2643:G:H2'	25:DA:2644:G:O4'	2.21	0.41
25:DA:673:C:H5''	29:DF:81:PRO:HD2	2.02	0.41
29:DF:64:ILE:HD11	29:DF:75:HIS:HB2	2.02	0.41
44:DY:86:ARG:HH11	44:DY:100:ALA:HB1	1.85	0.41
45:DZ:129:SER:HA	45:DZ:130:PRO:HD3	1.92	0.41
1:AA:1261:A:H3'	1:AA:1262:C:C6	2.56	0.41
1:AA:674:G:H2'	1:AA:675:A:C8	2.56	0.41
6:AF:44:GLY:HA2	6:AF:59:TYR:CE2	2.56	0.41
6:AF:91:VAL:HG11	18:AR:72:ARG:HH12	1.86	0.41
16:AP:69:THR:O	16:AP:73:LEU:HG	2.21	0.41
17:AQ:45:HIS:O	17:AQ:73:VAL:HG23	2.21	0.41
20:AT:8:ARG:O	20:AT:9:ASN:HB2	2.21	0.41
23:AY:64:A:H2'	23:AY:65:G:C8	2.56	0.41
50:B4:40:HIS:HB3	50:B4:43:TYR:CD2	2.55	0.41
25:BA:1076:G:OP2	36:BQ:128:LYS:NZ	2.49	0.41
25:BA:1334:U:C4	25:BA:1373:C:H1'	2.56	0.41
25:BA:2159:C:H2'	25:BA:2160:C:C6	2.56	0.41
25:BA:2141:A:N1	25:BA:2192:A:H2'	2.36	0.41
25:BA:2853:G:N7	61:BA:4892:HOH:O	2.37	0.41
25:BA:492:A:N3	25:BA:730:C:H1'	2.35	0.41
37:BR:61:HIS:O	37:BR:65:LEU:HD22	2.21	0.41
39:BT:127:ALA:C	39:BT:129:ARG:H	2.24	0.41
1:CA:1029:C:N4	1:CA:1032:G:C2	2.87	0.41
1:CA:109:A:H5'	1:CA:110:C:C5	2.56	0.41
1:CA:1116:C:C2'	1:CA:1117:G:H5''	2.46	0.41
1:CA:1424:C:H2'	1:CA:1425:U:O4'	2.21	0.41
1:CA:788:U:O2	1:CA:795:C:N4	2.53	0.41
2:CB:94:ASN:HD22	2:CB:94:ASN:HA	1.54	0.41
3:CC:120:VAL:HA	3:CC:123:GLN:NE2	2.25	0.41
9:CI:55:ALA:HA	9:CI:58:HIS:HD2	1.86	0.41
9:CI:70:LYS:O	9:CI:74:ILE:HG13	2.21	0.41
1:CA:657:G:H4'	15:CO:28:GLN:HG2	2.02	0.41
15:CO:80:ALA:O	15:CO:83:GLU:HB3	2.21	0.41
49:D3:31:LEU:HA	49:D3:31:LEU:HD23	1.92	0.41
54:D8:10:ALA:HB3	54:D8:62:LEU:HD21	2.02	0.41
25:DA:1794:U:H2'	25:DA:1795:C:H6	1.86	0.41
25:DA:2120:G:H2'	25:DA:2121:G:C8	2.56	0.41
25:DA:2153:G:H2'	25:DA:2154:G:C8	2.55	0.41
25:DA:247:G:H4'	25:DA:386:G:C6	2.55	0.41
25:DA:746:A:H2'	25:DA:2612:C:H5''	2.03	0.41
25:DA:861:A:C2	25:DA:917:A:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:784:A:O4'	27:DD:227:ASN:ND2	2.53	0.41
31:DH:154:PRO:HB3	31:DH:163:TYR:CZ	2.54	0.41
31:DH:59:ARG:O	31:DH:63:SER:OG	2.29	0.41
31:DH:98:LEU:HA	31:DH:98:LEU:HD12	1.85	0.41
25:DA:636:G:OP1	35:DP:132:LYS:HE2	2.21	0.41
40:DU:49:HIS:O	40:DU:53:ARG:N	2.54	0.41
45:DZ:107:THR:HA	45:DZ:108:PRO:HD3	1.81	0.41
1:AA:1261:A:H5'	1:AA:1262:C:OP2	2.21	0.41
1:AA:189:G:H1	1:AA:189(K):U:H3	1.68	0.41
57:AA:3231:PCY:H17	57:AA:3231:PCY:H24	1.77	0.41
1:AA:621:A:H2'	1:AA:622:A:C8	2.56	0.41
1:AA:974:A:OP2	14:AN:29:ARG:NH2	2.53	0.41
2:AB:105:PHE:CZ	2:AB:155:LEU:HD12	2.56	0.41
2:AB:223:ILE:HD12	2:AB:230:VAL:HG12	2.03	0.41
1:AA:1223:C:P	19:AS:78:ARG:HH21	2.43	0.41
23:AY:44:G:H3'	23:AY:45:U:C6	2.56	0.41
25:BA:142:G:H4'	43:BX:35:THR:HG21	2.01	0.41
25:BA:1466:U:O2'	25:BA:1467:G:OP1	2.33	0.41
25:BA:1481:G:H2'	25:BA:1482:G:O4'	2.20	0.41
25:BA:119:G:H4'	25:BA:149:A:H5'	2.03	0.41
25:BA:70:A:N7	43:BX:31:HIS:HE1	2.18	0.41
27:BD:26:LYS:HB3	27:BD:83:GLU:HG2	2.02	0.41
28:BE:36:ARG:NH2	28:BE:88:GLY:O	2.54	0.41
25:BA:2418:U:N3	35:BP:73:GLY:O	2.37	0.41
25:BA:798:A:H5'	42:BW:90:ARG:HA	2.03	0.41
43:BX:31:HIS:HA	43:BX:32:PRO:HD3	1.93	0.41
1:CA:269:C:H2'	1:CA:270:A:C8	2.56	0.41
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.60	0.41
1:CA:993:G:H2'	1:CA:993:G:N3	2.36	0.41
7:CG:52:GLU:H	7:CG:52:GLU:HG2	1.47	0.41
9:CI:85:LEU:HB3	9:CI:92:TYR:CD2	2.56	0.41
1:CA:718:G:H5'	11:CK:117:ASN:CG	2.41	0.41
54:D8:37:SER:OG	54:D8:39:LYS:HB3	2.21	0.41
25:DA:1149:G:H2'	25:DA:1150:C:H6	1.85	0.41
25:DA:1207:C:H2'	25:DA:1208:C:C6	2.56	0.41
25:DA:1899:G:N3	25:DA:1899:G:H2'	2.36	0.41
25:DA:2070:G:H2'	25:DA:2071:A:O4'	2.21	0.41
25:DA:2356:C:P	46:D0:24:LYS:HZ1	2.44	0.41
25:DA:2365:G:H4'	46:D0:60:PHE:CZ	2.56	0.41
25:DA:311:A:C6	25:DA:328:U:C4	3.09	0.41
25:DA:483:A:O2'	44:DY:59:GLY:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:715:G:H2'	25:DA:716:A:O4'	2.21	0.41
25:DA:816:C:O2'	25:DA:932:G:O6	2.31	0.41
25:DA:97:C:O3'	48:D2:2:LYS:HA	2.20	0.41
26:DB:5:C:H42	26:DB:116:G:H1	1.69	0.41
28:DE:27:LEU:HD22	39:DT:1:MET:CE	2.51	0.41
29:DF:53:THR:HG23	29:DF:55:GLY:N	2.23	0.41
31:DH:17:VAL:HG11	31:DH:50:VAL:HG21	2.03	0.41
31:DH:18:GLU:OE2	31:DH:25:LYS:HD3	2.21	0.41
32:DI:102:SER:O	32:DI:106:GLY:N	2.54	0.41
35:DP:2:LYS:HG3	35:DP:4:SER:OG	2.21	0.41
40:DU:92:ARG:H	40:DU:92:ARG:HG2	1.56	0.41
45:DZ:8:TYR:HB2	45:DZ:38:TYR:CZ	2.56	0.41
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.45	0.41
1:AA:1121:U:H2'	1:AA:1122:U:O4'	2.21	0.41
1:AA:1191:A:OP1	3:AC:4:LYS:NZ	2.45	0.41
1:AA:216:G:C2	1:AA:217:C:C4	3.08	0.41
1:AA:308:C:H2'	1:AA:309:G:C8	2.56	0.41
1:AA:826:C:H4'	8:AH:12:ARG:HG2	2.02	0.41
5:AE:110:LEU:HD13	5:AE:118:ILE:HD13	2.02	0.41
6:AF:2:ARG:HG3	6:AF:69:GLU:HG3	2.03	0.41
8:AH:49:GLU:HG2	8:AH:62:TYR:HE1	1.86	0.41
10:AJ:35:SER:N	10:AJ:73:ASP:O	2.38	0.41
13:AM:3:ARG:HD3	13:AM:4:ILE:HG22	2.02	0.41
25:BA:2283:G:OP1	46:B0:18:ALA:HB1	2.21	0.41
25:BA:2132:G:OP1	25:BA:2140:U:N3	2.51	0.41
25:BA:2205:C:C2	25:BA:2206:G:C8	3.09	0.41
25:BA:2664:C:H2'	25:BA:2665:U:O4'	2.21	0.41
25:BA:776:G:C6	27:BD:208:LYS:HB2	2.56	0.41
25:BA:722:A:C8	25:BA:851:A:C6	3.09	0.41
25:BA:904:C:H1'	46:B0:26:TYR:CE2	2.56	0.41
27:BD:182:LEU:HA	27:BD:182:LEU:HD23	1.77	0.41
28:BE:101:ARG:HA	28:BE:170:LEU:O	2.21	0.41
1:CA:100:C:H2'	1:CA:101:A:O4'	2.20	0.41
1:CA:175:C:H2'	1:CA:176:C:C6	2.56	0.41
1:CA:309:G:H1'	1:CA:608:A:C2	2.56	0.41
1:CA:866:C:O2'	1:CA:919:A:OP1	2.26	0.41
1:CA:976:G:H22	1:CA:1363:C:H5''	1.86	0.41
2:CB:118:LEU:HD13	2:CB:142:LEU:HB2	2.03	0.41
3:CC:45:LYS:HG3	3:CC:46:GLU:N	2.36	0.41
4:CD:196:LEU:O	4:CD:198:VAL:N	2.48	0.41
10:CJ:16:LEU:HD23	10:CJ:94:VAL:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CK:16:SER:O	11:CK:35:PRO:HD3	2.21	0.41
25:DA:1151:G:C6	25:DA:1152:C:N3	2.89	0.41
25:DA:1379:A:O5'	25:DA:1379:A:H8	2.04	0.41
25:DA:2323:G:C6	25:DA:2324:C:C4	3.09	0.41
25:DA:2364:C:H2'	25:DA:2365:G:O4'	2.21	0.41
25:DA:2418:A:C2	25:DA:2419:U:C2	3.09	0.41
25:DA:2671:A:H2'	25:DA:2672:G:O4'	2.21	0.41
25:DA:299:A:N3	25:DA:319:C:O2'	2.51	0.41
25:DA:464:U:H2'	25:DA:465:G:O4'	2.21	0.41
26:DB:95:C:H2'	26:DB:96:U:C6	2.56	0.41
30:DG:43:LEU:HB3	30:DG:44:GLY:H	1.53	0.41
30:DG:91:ARG:HB3	30:DG:91:ARG:HE	1.60	0.41
35:DP:90:ARG:HG2	35:DP:91:PHE:CD1	2.55	0.41
39:DT:6:LEU:O	39:DT:10:VAL:HG23	2.21	0.41
42:DW:18:ARG:NH1	42:DW:76:VAL:O	2.54	0.41
44:DY:6:HIS:CD2	44:DY:6:HIS:H	2.39	0.41
1:AA:193:C:H2'	1:AA:194:C:H6	1.85	0.41
1:AA:601:C:H2'	1:AA:602:A:C8	2.56	0.41
1:AA:61:G:H2'	1:AA:62:U:O4'	2.21	0.41
2:AB:189:ASP:HB2	2:AB:190:THR:H	1.73	0.41
3:AC:108:ASN:HB3	3:AC:111:LEU:HD12	2.03	0.41
3:AC:65:ALA:HA	3:AC:100:ALA:HB3	2.03	0.41
4:AD:134:ASP:O	4:AD:136:PRO:HD3	2.21	0.41
1:AA:542:G:H5'	4:AD:41:GLY:HA3	2.03	0.41
10:AJ:35:SER:CB	10:AJ:73:ASP:HB2	2.49	0.41
19:AS:20:LEU:HD23	19:AS:23:ASN:ND2	2.23	0.41
20:AT:99:LEU:HA	20:AT:100:ILE:O	2.21	0.41
25:BA:1073:A:C6	25:BA:1172:A:C4	3.09	0.41
25:BA:2148:A:N6	25:BA:2185:C:O4'	2.54	0.41
25:BA:223:C:H2'	25:BA:224:U:H6	1.85	0.41
25:BA:2304:C:H2'	25:BA:2305:C:C6	2.56	0.41
25:BA:251:A:N3	25:BA:457:G:O2'	2.48	0.41
25:BA:331:G:H21	25:BA:354:A:H62	1.69	0.41
25:BA:865:G:H4'	25:BA:885:C:O3'	2.21	0.41
34:BO:2:ILE:HG23	34:BO:6:THR:HG21	2.02	0.41
40:BU:50:ARG:HH12	41:BV:72:VAL:HA	1.85	0.41
45:BZ:44:PHE:CZ	45:BZ:86:VAL:HG11	2.56	0.41
1:CA:1002:G:C5	1:CA:1003:G:H8	2.39	0.41
1:CA:1129:C:O2'	1:CA:1139:G:O6	2.31	0.41
1:CA:461:A:O2'	1:CA:471:G:N7	2.42	0.41
1:CA:790:A:C6	1:CA:791:G:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:54:ARG:NH1	3:CC:54:ARG:HB3	2.29	0.41
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.56	0.41
5:CE:31:LEU:HA	5:CE:31:LEU:HD23	1.93	0.41
11:CK:84:VAL:HG21	11:CK:95:ILE:HD11	2.03	0.41
25:DA:108:U:OP1	25:DA:293:U:O2'	2.36	0.41
25:DA:127:A:H5''	25:DA:128:C:C6	2.55	0.41
25:DA:1374:G:H2'	25:DA:1375:C:C6	2.56	0.41
25:DA:530:G:N3	25:DA:530:G:O4'	2.53	0.41
25:DA:582:G:H2'	25:DA:583:G:C8	2.56	0.41
25:DA:79:G:C6	25:DA:80:G:C5	3.09	0.41
25:DA:974:G:OP1	25:DA:1187:G:O2'	2.21	0.41
26:DB:76:G:N2	26:DB:101:G:O6	2.42	0.41
27:DD:73:VAL:HG13	27:DD:120:GLY:HA3	2.03	0.41
27:DD:29:PRO:HA	27:DD:83:GLU:OE1	2.20	0.41
43:DX:94:GLY:N	43:DX:95:LEU:HA	2.36	0.41
45:DZ:145:GLU:HG3	45:DZ:146:ILE:N	2.36	0.41
1:AA:1003:G:O3'	1:AA:1004:A:H4'	2.22	0.40
1:AA:1263:C:H5''	1:AA:1264:C:OP2	2.21	0.40
2:AB:19:HIS:HE1	2:AB:189:ASP:HB3	1.86	0.40
19:AS:22:LEU:C	19:AS:27:GLU:HG3	2.41	0.40
23:AW:54:5MU:H73	23:AW:55:PSU:O2	2.22	0.40
23:AY:35:A:H2'	23:AY:36:A:C8	2.57	0.40
47:B1:80:LEU:HD22	47:B1:97:LEU:HD11	2.03	0.40
47:B1:86:SER:O	47:B1:89:GLU:HG2	2.20	0.40
50:B4:69:LYS:HE3	50:B4:69:LYS:HB3	1.83	0.40
25:BA:1314:A:C2	25:BA:2035:A:C4	3.09	0.40
25:BA:2163:G:N1	25:BA:2164:C:O2	2.55	0.40
25:BA:2353:G:H2'	25:BA:2354:C:C6	2.57	0.40
27:BD:68:LYS:O	27:BD:69:ARG:HB2	2.21	0.40
31:BH:24:VAL:HG22	31:BH:35:VAL:HB	2.03	0.40
33:BN:39:ARG:HA	33:BN:40:PRO:HD3	1.91	0.40
45:BZ:158:PRO:HA	45:BZ:159:PRO:HD3	1.85	0.40
1:CA:1005:A:N6	1:CA:1024:G:O2'	2.54	0.40
1:CA:1201:A:H4'	1:CA:1202:G:O5'	2.21	0.40
1:CA:1358:U:H2'	1:CA:1359:C:O4'	2.21	0.40
1:CA:865:A:C2	1:CA:918:A:H4'	2.56	0.40
4:CD:174:LEU:HD23	4:CD:185:PHE:HA	2.03	0.40
5:CE:53:LEU:O	5:CE:57:LYS:HB2	2.21	0.40
23:CW:9:A:H5'	23:CW:46:7MG:N2	2.34	0.40
24:CX:13:C:O2'	25:DA:1924:C:H4'	2.21	0.40
24:CX:9:G:H21	24:CX:45:G:H3'	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CY:8:4SU:S4	23:CY:14:A:C8	3.14	0.40
25:DA:1171:G:N2	25:DA:1178:C:N3	2.50	0.40
25:DA:144:C:H2'	25:DA:145:G:C8	2.56	0.40
25:DA:1495:A:H2'	25:DA:1496:A:C8	2.56	0.40
25:DA:1790:C:H5''	25:DA:1791:A:OP1	2.20	0.40
25:DA:1877:A:OP2	25:DA:1877:A:H8	2.04	0.40
25:DA:19:C:H2'	25:DA:20:C:C6	2.55	0.40
25:DA:2108:C:H2'	25:DA:2109:U:C6	2.55	0.40
25:DA:2320:A:H1'	25:DA:2321:G:C2	2.56	0.40
25:DA:314:A:H2'	25:DA:315:G:C8	2.57	0.40
25:DA:643:A:N1	25:DA:2369:A:O2'	2.43	0.40
25:DA:566:U:O2'	25:DA:809:G:OP2	2.27	0.40
25:DA:84:A:N1	25:DA:98:G:O2'	2.46	0.40
25:DA:912:C:N4	25:DA:913:U:O4	2.54	0.40
25:DA:1140:C:O3'	33:DN:25:ARG:NH1	2.53	0.40
33:DN:71:ILE:HA	33:DN:86:PRO:HA	2.02	0.40
43:DX:92:LEU:HA	43:DX:92:LEU:HD12	1.91	0.40
1:AA:1007:C:N3	1:AA:1022:G:C6	2.89	0.40
1:AA:1128:C:C2'	1:AA:1129:C:H5'	2.51	0.40
1:AA:179:A:C5	1:AA:180:U:C4	3.09	0.40
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	2.03	0.40
5:AE:82:VAL:HG21	5:AE:138:ALA:HA	2.03	0.40
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	2.03	0.40
19:AS:65:ASN:ND2	19:AS:65:ASN:N	2.68	0.40
23:AW:43:C:H2'	23:AW:44:G:C8	2.56	0.40
48:B2:65:ASN:OD1	48:B2:69:ARG:HD3	2.22	0.40
55:B9:17:ILE:HD12	55:B9:17:ILE:HA	1.90	0.40
25:BA:12:U:O2	25:BA:12:U:H2'	2.21	0.40
25:BA:1408:C:O2'	25:BA:1841:A:O2'	2.35	0.40
25:BA:2331:G:C2	38:BS:3:ARG:HA	2.56	0.40
25:BA:2332:A:H2'	25:BA:2332:A:N3	2.37	0.40
25:BA:2624:C:OP2	51:B5:2:ALA:N	2.54	0.40
25:BA:2672:A:N7	31:BH:175:LYS:NZ	2.68	0.40
25:BA:2812:A:N3	25:BA:2904:U:H1'	2.37	0.40
25:BA:624:C:O2'	25:BA:628:C:H5''	2.21	0.40
36:BQ:85:LYS:HD3	46:B0:7:LEU:HG	2.02	0.40
38:BS:59:LYS:H	38:BS:59:LYS:HG3	1.77	0.40
1:CA:1060:C:N4	3:CC:2:GLY:HA2	2.36	0.40
1:CA:174:C:H2'	1:CA:175:C:C6	2.56	0.40
1:CA:560:U:H5'	1:CA:566:G:N2	2.36	0.40
1:CA:683:G:O6	61:CA:4133:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:69:G:H2'	1:CA:70:G:C8	2.56	0.40
2:CB:33:TYR:HB2	2:CB:43:ASP:HB2	2.02	0.40
3:CC:16:ARG:HD2	3:CC:16:ARG:HA	1.96	0.40
10:CJ:40:LEU:HA	10:CJ:40:LEU:HD23	1.93	0.40
15:CO:87:ILE:CG2	15:CO:88:ARG:H	2.26	0.40
25:DA:2529:G:O6	55:D9:31:LYS:NZ	2.54	0.40
25:DA:815:C:N3	25:DA:1193:G:C2	2.89	0.40
25:DA:1288:U:C2	25:DA:1327:C:O2	2.74	0.40
25:DA:1668:A:H4'	25:DA:1669:A:O5'	2.21	0.40
25:DA:1711:C:H2'	25:DA:1712:C:H6	1.85	0.40
25:DA:1777:U:O2'	25:DA:1778:U:H5'	2.21	0.40
25:DA:1782:C:O2	25:DA:2608:G:O2'	2.31	0.40
25:DA:1971:A:OP1	61:DA:4260:HOH:O	2.21	0.40
25:DA:2679:A:C2	25:DA:2729:G:C2	3.09	0.40
25:DA:2684:U:H1'	34:DO:70:LYS:HD2	2.03	0.40
25:DA:660:G:C6	25:DA:661:C:C4	3.10	0.40
27:DD:264:LYS:HA	27:DD:265:PRO:HD3	1.95	0.40
29:DF:154:VAL:HG22	29:DF:191:ARG:HB2	2.03	0.40
29:DF:78:ILE:HA	29:DF:83:PHE:CE1	2.56	0.40
31:DH:85:LYS:O	31:DH:132:ARG:HA	2.21	0.40
31:DH:137:ASP:O	31:DH:141:VAL:HG23	2.21	0.40
32:DI:47:LEU:O	32:DI:51:ILE:HG13	2.21	0.40
38:DS:105:ALA:HB1	38:DS:110:LEU:HD23	2.02	0.40
39:DT:65:LYS:O	39:DT:72:VAL:N	2.47	0.40
43:DX:31:HIS:HB3	43:DX:34:ALA:HB2	2.03	0.40
45:DZ:67:LEU:HA	45:DZ:68:PRO:HD3	1.77	0.40
1:AA:1068:G:N2	1:AA:1191:A:N3	2.60	0.40
1:AA:769:G:H4'	1:AA:1513:A:H4'	2.04	0.40
1:AA:374:A:C6	1:AA:375:U:C4	3.09	0.40
1:AA:461:A:O2'	1:AA:470:C:H5'	2.22	0.40
4:AD:63:LYS:HG3	4:AD:64:LEU:H	1.87	0.40
7:AG:8:GLU:HG3	7:AG:8:GLU:H	1.63	0.40
16:AP:4:ILE:HB	16:AP:66:PRO:HA	2.03	0.40
17:AQ:66:SER:OG	17:AQ:69:LYS:HB2	2.22	0.40
20:AT:10:LEU:HD22	20:AT:11:SER:H	1.86	0.40
25:BA:2236:G:H4'	25:BA:2238:C:C2	2.56	0.40
25:BA:2359:C:H2'	25:BA:2360:U:C6	2.56	0.40
25:BA:34:C:H5''	25:BA:35:G:OP2	2.22	0.40
25:BA:866:A:C4	25:BA:1234:A:C2	3.09	0.40
26:BB:16:G:C6	26:BB:69:G:C2	3.09	0.40
27:BD:136:ILE:HA	27:BD:137:PRO:HD3	1.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BE:162:ALA:HB3	61:BE:409:HOH:O	2.21	0.40
30:BG:106:LEU:HA	30:BG:110:ALA:HB3	2.01	0.40
32:BI:10:GLU:O	32:BI:12:LEU:N	2.54	0.40
43:BX:41:ASN:O	43:BX:45:THR:HG23	2.21	0.40
1:CA:1158:C:O3'	2:CB:133:LYS:NZ	2.54	0.40
1:CA:1381:U:H1'	7:CG:79:ARG:HD3	2.03	0.40
1:CA:486:U:H2'	1:CA:487:A:C8	2.57	0.40
1:CA:731:G:OP1	1:CA:766:A:H1'	2.22	0.40
3:CC:6:HIS:HA	3:CC:7:PRO:HD3	1.84	0.40
5:CE:106:PRO:O	5:CE:110:LEU:HG	2.21	0.40
8:CH:51:VAL:CG2	8:CH:60:ARG:HB2	2.51	0.40
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.56	0.40
15:CO:5:LYS:HD3	15:CO:5:LYS:N	2.36	0.40
16:CP:57:ARG:HH21	16:CP:79:VAL:HA	1.85	0.40
18:CR:66:LEU:O	18:CR:70:ILE:HG13	2.21	0.40
54:D8:50:LEU:HD23	54:D8:50:LEU:HA	1.86	0.40
25:DA:1344:G:C2	25:DA:1385:G:C8	3.09	0.40
25:DA:1434:A:H2'	25:DA:1435:G:C8	2.56	0.40
25:DA:1446:C:H42	25:DA:1465:G:H1	1.69	0.40
25:DA:1692:U:O2'	25:DA:1693:U:H2'	2.21	0.40
25:DA:1789:A:H2'	25:DA:1790:C:O4'	2.21	0.40
25:DA:1866:C:H6	25:DA:1866:C:O5'	2.05	0.40
25:DA:2140:C:H2'	25:DA:2140:C:O2	2.22	0.40
25:DA:41:C:H2'	25:DA:42:G:H8	1.86	0.40
25:DA:857:C:H2'	25:DA:858:U:C6	2.56	0.40
29:DF:27:GLU:HA	29:DF:27:GLU:OE2	2.20	0.40
30:DG:67:LYS:HG2	30:DG:68:PRO:HD2	2.04	0.40
25:DA:2666:C:H42	31:DH:109:PHE:HA	1.86	0.40
31:DH:105:LEU:N	31:DH:113:VAL:O	2.45	0.40
32:DI:101:LEU:HG	32:DI:107:VAL:HB	2.03	0.40
36:DQ:43:THR:OG1	36:DQ:45:GLN:HG2	2.22	0.40
37:DR:22:ARG:O	37:DR:26:LYS:HG3	2.21	0.40
39:DT:109:GLU:HG2	39:DT:112:ARG:NH2	2.36	0.40
1:AA:1035:A:H2	1:AA:1036:G:C5	2.39	0.40
2:AB:15:VAL:O	2:AB:16:HIS:HB3	2.22	0.40
11:AK:38:ASN:HA	11:AK:39:PRO:HD3	1.79	0.40
13:AM:13:LYS:O	13:AM:44:ARG:HA	2.22	0.40
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	2.03	0.40
23:AW:63:G:H2'	23:AW:64:A:O4'	2.21	0.40
25:BA:1271:G:OP1	41:BV:69:LYS:NZ	2.45	0.40
25:BA:155:C:O5'	25:BA:155:C:H6	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:174:U:H2'	25:BA:175:G:H8	1.85	0.40
25:BA:1857:G:H4'	27:BD:242:ARG:CZ	2.51	0.40
25:BA:207:A:C2	25:BA:224:U:H4'	2.57	0.40
25:BA:2155:G:H21	25:BA:2180:A:N6	2.19	0.40
25:BA:2162:C:O2	25:BA:2162:C:H2'	2.21	0.40
25:BA:2520:G:H2'	25:BA:2521:G:O4'	2.22	0.40
25:BA:2765:C:O5'	25:BA:2765:C:H6	2.05	0.40
30:BG:45:GLU:HG2	30:BG:45:GLU:H	1.53	0.40
30:BG:67:LYS:HG2	30:BG:68:PRO:HD2	2.03	0.40
31:BH:69:ARG:HG3	31:BH:70:THR:N	2.35	0.40
1:CA:617:G:H4'	16:CP:44:THR:O	2.22	0.40
2:CB:16:HIS:O	2:CB:18:GLY:N	2.55	0.40
2:CB:84:GLU:OE1	2:CB:216:SER:HA	2.21	0.40
4:CD:162:LEU:HA	4:CD:162:LEU:HD23	1.89	0.40
7:CG:76:ARG:HG2	7:CG:156:TRP:CH2	2.55	0.40
10:CJ:74:ILE:HG22	61:CJ:5101:HOH:O	2.20	0.40
24:CX:43:A:H2'	24:CX:44:A:C8	2.56	0.40
46:D0:18:ALA:HB3	46:D0:20:ARG:HH21	1.87	0.40
25:DA:1000:A:C6	25:DA:1155:A:C8	3.09	0.40
25:DA:1116:C:H2'	25:DA:1117:G:C8	2.57	0.40
25:DA:1653:G:C4	37:DR:9:LYS:HD2	2.56	0.40
25:DA:1786:A:C4	25:DA:1938:A:C6	3.09	0.40
25:DA:1922:G:H2'	25:DA:1923:U:O4'	2.21	0.40
25:DA:2176:A:H2'	25:DA:2177:C:C5	2.56	0.40
25:DA:2461:C:H2'	25:DA:2462:U:H6	1.85	0.40
25:DA:2550:G:C6	25:DA:2551:C:C4	3.09	0.40
25:DA:2699:C:H2'	25:DA:2700:C:O4'	2.21	0.40
25:DA:875:G:N2	25:DA:903:C:C2	2.89	0.40
25:DA:921:G:H2'	25:DA:922:U:C6	2.57	0.40
25:DA:90:U:H1'	25:DA:92:A:C8	2.56	0.40
30:DG:106:LEU:O	30:DG:110:ALA:HB3	2.21	0.40
30:DG:97:ASP:HA	30:DG:100:TRP:HD1	1.86	0.40
34:DO:22:ILE:HD11	34:DO:40:VAL:HG12	2.03	0.40
35:DP:65:ARG:HG3	54:D8:25:MET:CG	2.52	0.40
36:DQ:137:TYR:HB3	45:DZ:76:LEU:HD21	2.04	0.40
1:AA:1288:A:H2'	1:AA:1289:A:C8	2.57	0.40
1:AA:355:C:C4	1:AA:356:A:N7	2.89	0.40
1:AA:580:U:H5''	15:AO:58:MET:HG2	2.03	0.40
24:AX:4:G:H2'	24:AX:5:G:C8	2.55	0.40
23:AY:57:G:N3	23:AY:57:G:H2'	2.35	0.40
54:B8:54:GLU:O	54:B8:58:ILE:HG13	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1790:A:H1'	25:BA:2723:A:C2	2.57	0.40
25:BA:831:A:O4'	27:BD:227:ASN:ND2	2.54	0.40
28:BE:56:PRO:HG3	28:BE:74:PRO:HG2	2.04	0.40
61:BA:4080:HOH:O	33:BN:28:THR:HG23	2.21	0.40
43:BX:61:GLY:HA3	43:BX:73:ARG:O	2.22	0.40
1:CA:1004:A:H5''	1:CA:1024:G:H22	1.87	0.40
1:CA:1133:G:H2'	1:CA:1134:G:O4'	2.22	0.40
1:CA:1368:G:OP2	9:CI:112:LYS:NZ	2.50	0.40
1:CA:1427:U:H2'	1:CA:1428:A:C8	2.56	0.40
1:CA:634:C:H2'	1:CA:635:G:H8	1.86	0.40
2:CB:110:GLN:O	2:CB:110:GLN:HG2	2.21	0.40
2:CB:20:GLU:HB2	2:CB:190:THR:OG1	2.22	0.40
4:CD:128:VAL:N	4:CD:131:ARG:O	2.51	0.40
5:CE:33:VAL:HG21	5:CE:109:ILE:HA	2.02	0.40
8:CH:56:LYS:HD3	8:CH:56:LYS:HA	1.82	0.40
15:CO:11:VAL:O	15:CO:15:PHE:HD1	2.04	0.40
1:CA:1327:C:OP1	21:CU:20:LYS:N	2.55	0.40
21:CU:13:ILE:HG12	21:CU:22:ARG:CZ	2.51	0.40
23:CW:53:G:H1	23:CW:61:C:H42	1.69	0.40
24:CX:38:A:O5'	24:CX:38:A:H8	2.04	0.40
23:CY:58:A:H1'	23:CY:60:U:O2	2.22	0.40
50:D4:15:ILE:HB	50:D4:32:TYR:CD1	2.56	0.40
25:DA:2055:C:H5'	25:DA:2056:G:O5'	2.22	0.40
25:DA:2126:A:H4'	25:DA:2127:G:OP1	2.20	0.40
25:DA:2133:G:O2'	25:DA:2134:A:P	2.79	0.40
25:DA:2359:C:H2'	25:DA:2360:A:O4'	2.21	0.40
25:DA:858:U:O2	25:DA:2268:A:H2'	2.21	0.40
25:DA:947:G:H2'	25:DA:948:G:H8	1.87	0.40
26:DB:75:G:H21	45:DZ:85:HIS:HD1	1.68	0.40
30:DG:113:ARG:HD2	30:DG:140:ILE:O	2.21	0.40
30:DG:167:GLU:H	30:DG:167:GLU:CD	2.25	0.40
30:DG:31:VAL:HA	30:DG:32:PRO:HD2	1.78	0.40
32:DI:26:ALA:O	32:DI:31:LEU:HB2	2.22	0.40
40:DU:85:LYS:HE2	40:DU:85:LYS:HB3	1.82	0.40
41:DV:58:VAL:HG21	41:DV:100:ARG:HH11	1.87	0.40
44:DY:12:THR:OG1	44:DY:26:LYS:HE2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	229/256 (90%)	200 (87%)	19 (8%)	10 (4%)	2	1
2	CB	229/256 (90%)	195 (85%)	24 (10%)	10 (4%)	2	1
3	AC	204/239 (85%)	184 (90%)	17 (8%)	3 (2%)	10	14
3	CC	204/239 (85%)	180 (88%)	22 (11%)	2 (1%)	15	22
4	AD	206/209 (99%)	192 (93%)	12 (6%)	2 (1%)	15	22
4	CD	206/209 (99%)	189 (92%)	16 (8%)	1 (0%)	29	40
5	AE	146/162 (90%)	134 (92%)	9 (6%)	3 (2%)	7	7
5	CE	146/162 (90%)	138 (94%)	7 (5%)	1 (1%)	22	30
6	AF	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
6	CF	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
7	AG	153/156 (98%)	143 (94%)	8 (5%)	2 (1%)	12	16
7	CG	153/156 (98%)	140 (92%)	9 (6%)	4 (3%)	5	5
8	AH	135/138 (98%)	129 (96%)	6 (4%)	0	100	100
8	CH	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	22	30
9	AI	125/128 (98%)	111 (89%)	11 (9%)	3 (2%)	6	5
9	CI	125/128 (98%)	114 (91%)	8 (6%)	3 (2%)	6	5
10	AJ	95/105 (90%)	83 (87%)	9 (10%)	3 (3%)	4	3
10	CJ	94/105 (90%)	81 (86%)	10 (11%)	3 (3%)	4	3
11	AK	112/129 (87%)	106 (95%)	4 (4%)	2 (2%)	8	10
11	CK	112/129 (87%)	107 (96%)	3 (3%)	2 (2%)	8	10
12	AL	120/132 (91%)	115 (96%)	5 (4%)	0	100	100
12	CL	120/132 (91%)	116 (97%)	4 (3%)	0	100	100
13	AM	121/126 (96%)	110 (91%)	9 (7%)	2 (2%)	9	11
13	CM	120/126 (95%)	108 (90%)	9 (8%)	3 (2%)	5	5
14	AN	58/61 (95%)	54 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	CN	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
15	AO	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
15	CO	86/89 (97%)	80 (93%)	4 (5%)	2 (2%)	6	6
16	AP	80/88 (91%)	78 (98%)	2 (2%)	0	100	100
16	CP	80/88 (91%)	77 (96%)	2 (2%)	1 (1%)	12	16
17	AQ	97/105 (92%)	90 (93%)	7 (7%)	0	100	100
17	CQ	97/105 (92%)	91 (94%)	5 (5%)	1 (1%)	15	22
18	AR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
18	CR	66/88 (75%)	65 (98%)	0	1 (2%)	10	14
19	AS	81/93 (87%)	72 (89%)	9 (11%)	0	100	100
19	CS	81/93 (87%)	71 (88%)	10 (12%)	0	100	100
20	AT	94/106 (89%)	84 (89%)	3 (3%)	7 (7%)	1	0
20	CT	94/106 (89%)	84 (89%)	5 (5%)	5 (5%)	2	0
21	AU	21/27 (78%)	18 (86%)	3 (14%)	0	100	100
21	CU	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	2	1
27	BD	273/276 (99%)	257 (94%)	15 (6%)	1 (0%)	34	46
27	DD	273/276 (99%)	258 (94%)	13 (5%)	2 (1%)	22	30
28	BE	202/206 (98%)	193 (96%)	8 (4%)	1 (0%)	29	40
28	DE	202/206 (98%)	191 (95%)	9 (4%)	2 (1%)	15	22
29	BF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	29	40
29	DF	201/210 (96%)	195 (97%)	4 (2%)	2 (1%)	15	22
30	BG	179/182 (98%)	167 (93%)	7 (4%)	5 (3%)	5	4
30	DG	179/182 (98%)	165 (92%)	7 (4%)	7 (4%)	3	1
31	BH	172/180 (96%)	159 (92%)	12 (7%)	1 (1%)	25	34
31	DH	172/180 (96%)	157 (91%)	13 (8%)	2 (1%)	13	17
32	BI	144/148 (97%)	123 (85%)	16 (11%)	5 (4%)	3	2
32	DI	144/148 (97%)	126 (88%)	17 (12%)	1 (1%)	22	30
33	BN	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
33	DN	138/140 (99%)	133 (96%)	4 (3%)	1 (1%)	22	30
34	BO	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
34	DO	120/122 (98%)	115 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	BP	147/150 (98%)	138 (94%)	8 (5%)	1 (1%)	22	30
35	DP	147/150 (98%)	135 (92%)	10 (7%)	2 (1%)	11	15
36	BQ	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
36	DQ	139/141 (99%)	129 (93%)	8 (6%)	2 (1%)	11	15
37	BR	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
37	DR	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
38	BS	108/112 (96%)	102 (94%)	6 (6%)	0	100	100
38	DS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	17	24
39	BT	129/146 (88%)	121 (94%)	7 (5%)	1 (1%)	19	27
39	DT	129/146 (88%)	123 (95%)	5 (4%)	1 (1%)	19	27
40	BU	114/118 (97%)	114 (100%)	0	0	100	100
40	DU	114/118 (97%)	114 (100%)	0	0	100	100
41	BV	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	15	22
41	DV	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	15	22
42	BW	110/113 (97%)	108 (98%)	2 (2%)	0	100	100
42	DW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
43	BX	93/96 (97%)	90 (97%)	1 (1%)	2 (2%)	6	7
43	DX	93/96 (97%)	90 (97%)	2 (2%)	1 (1%)	14	19
44	BY	105/110 (96%)	96 (91%)	9 (9%)	0	100	100
44	DY	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
45	BZ	169/206 (82%)	143 (85%)	24 (14%)	2 (1%)	13	17
45	DZ	172/206 (84%)	149 (87%)	22 (13%)	1 (1%)	25	34
46	B0	81/85 (95%)	77 (95%)	3 (4%)	1 (1%)	13	17
46	D0	81/85 (95%)	75 (93%)	6 (7%)	0	100	100
47	B1	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
47	D1	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
48	B2	68/72 (94%)	68 (100%)	0	0	100	100
48	D2	68/72 (94%)	68 (100%)	0	0	100	100
49	B3	57/60 (95%)	57 (100%)	0	0	100	100
49	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
50	B4	67/71 (94%)	50 (75%)	11 (16%)	6 (9%)	1	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	D4	67/71 (94%)	51 (76%)	12 (18%)	4 (6%)	1	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%)	2 (4%)	0	100	100
52	D6	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
53	B7	46/49 (94%)	46 (100%)	0	0	100	100
53	D7	46/49 (94%)	45 (98%)	0	1 (2%)	6	7
54	B8	62/65 (95%)	62 (100%)	0	0	100	100
54	D8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
55	B9	35/37 (95%)	35 (100%)	0	0	100	100
55	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11409/12128 (94%)	10643 (93%)	629 (6%)	137 (1%)	13	17

All (137) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	9	GLU
2	AB	15	VAL
2	AB	16	HIS
2	AB	17	PHE
2	AB	126	GLU
2	AB	231	GLU
3	AC	65	ALA
9	AI	44	VAL
9	AI	54	ASP
10	AJ	77	PRO
20	AT	47	GLY
27	BD	275	LYS
29	BF	130	ALA
30	BG	50	ALA
50	B4	55	ARG
50	B4	57	GLU
2	CB	16	HIS
2	CB	17	PHE
2	CB	126	GLU
7	CG	7	ALA
9	CI	44	VAL
9	CI	54	ASP

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Mol	Chain	Res	Type
10	CJ	79	ARG
13	CM	107	ALA
20	CT	10	LEU
29	DF	21	ALA
29	DF	130	ALA
30	DG	47	LYS
30	DG	81	LYS
31	DH	29	PRO
31	DH	126	PRO
32	DI	10	GLU
35	DP	45	LEU
50	D4	45	GLY
50	D4	51	ASP
50	D4	62	ARG
53	D7	46	VAL
3	AC	66	VAL
5	AE	85	GLY
5	AE	86	ALA
9	AI	43	ALA
10	AJ	31	GLY
10	AJ	91	PRO
11	AK	49	GLY
30	BG	43	LEU
30	BG	126	ASP
31	BH	126	PRO
32	BI	11	ASN
32	BI	106	GLY
41	BV	79	VAL
45	BZ	152	ALA
45	BZ	159	PRO
50	B4	45	GLY
50	B4	54	GLY
50	B4	68	ARG
2	CB	10	LEU
3	CC	181	ASN
7	CG	81	GLY
10	CJ	77	PRO
11	CK	49	GLY
13	CM	106	ASN
15	CO	23	GLY
16	CP	53	VAL
20	CT	47	GLY

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Mol	Chain	Res	Type
28	DE	73	GLU
30	DG	43	LEU
30	DG	51	ARG
30	DG	126	ASP
41	DV	79	VAL
45	DZ	117	LEU
2	AB	150	SER
4	AD	166	LYS
4	AD	173	TRP
13	AM	12	ASN
20	AT	9	ASN
20	AT	10	LEU
20	AT	94	ALA
20	AT	100	ILE
20	AT	102	GLY
28	BE	52	LEU
46	B0	13	GLY
2	CB	8	LYS
2	CB	150	SER
4	CD	45	GLN
5	CE	69	VAL
8	CH	73	ASP
9	CI	11	LYS
20	CT	99	LEU
27	DD	3	VAL
28	DE	52	LEU
33	DN	2	LYS
36	DQ	28	ALA
38	DS	84	GLN
2	AB	10	LEU
3	AC	107	GLN
5	AE	69	VAL
7	AG	80	VAL
13	AM	11	ARG
30	BG	32	PRO
30	BG	51	ARG
32	BI	73	GLU
39	BT	55	ASN
43	BX	93	GLU
15	CO	88	ARG
17	CQ	14	LYS
27	DD	239	ARG

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Mol	Chain	Res	Type
30	DG	32	PRO
39	DT	55	ASN
43	DX	2	LYS
50	D4	55	ARG
2	AB	124	SER
11	AK	105	VAL
20	AT	95	ALA
32	BI	107	VAL
35	BP	29	LYS
50	B4	44	THR
2	CB	120	ALA
2	CB	234	PRO
3	CC	156	ARG
7	CG	55	GLY
18	CR	25	THR
20	CT	102	GLY
30	DG	50	ALA
2	AB	202	PRO
2	CB	202	PRO
2	CB	232	PRO
20	CT	100	ILE
35	DP	29	LYS
43	BX	94	GLY
11	CK	105	VAL
7	AG	17	VAL
10	CJ	91	PRO
21	CU	23	PRO
7	CG	80	VAL
13	CM	4	ILE
36	DQ	27	VAL
32	BI	131	LYS

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	192/220 (87%)	169 (88%)	23 (12%)	5	5
2	CB	187/220 (85%)	168 (90%)	19 (10%)	7	8
3	AC	143/188 (76%)	132 (92%)	11 (8%)	13	16
3	CC	140/188 (74%)	127 (91%)	13 (9%)	9	10
4	AD	170/181 (94%)	155 (91%)	15 (9%)	10	12
4	CD	173/181 (96%)	160 (92%)	13 (8%)	13	17
5	AE	113/123 (92%)	106 (94%)	7 (6%)	18	24
5	CE	114/123 (93%)	105 (92%)	9 (8%)	12	15
6	AF	83/90 (92%)	77 (93%)	6 (7%)	14	18
6	CF	85/90 (94%)	81 (95%)	4 (5%)	26	35
7	AG	119/127 (94%)	106 (89%)	13 (11%)	6	6
7	CG	120/127 (94%)	111 (92%)	9 (8%)	13	17
8	AH	114/119 (96%)	107 (94%)	7 (6%)	18	24
8	CH	114/119 (96%)	104 (91%)	10 (9%)	10	12
9	AI	90/99 (91%)	82 (91%)	8 (9%)	9	12
9	CI	89/99 (90%)	73 (82%)	16 (18%)	1	1
10	AJ	66/92 (72%)	62 (94%)	4 (6%)	18	24
10	CJ	69/92 (75%)	66 (96%)	3 (4%)	29	39
11	AK	82/99 (83%)	76 (93%)	6 (7%)	14	18
11	CK	83/99 (84%)	77 (93%)	6 (7%)	14	18
12	AL	97/109 (89%)	93 (96%)	4 (4%)	30	41
12	CL	97/109 (89%)	92 (95%)	5 (5%)	23	30
13	AM	93/101 (92%)	83 (89%)	10 (11%)	6	6
13	CM	92/101 (91%)	83 (90%)	9 (10%)	8	9
14	AN	49/50 (98%)	43 (88%)	6 (12%)	5	4
14	CN	49/50 (98%)	43 (88%)	6 (12%)	5	4
15	AO	78/80 (98%)	67 (86%)	11 (14%)	3	3
15	CO	78/80 (98%)	70 (90%)	8 (10%)	7	7
16	AP	69/74 (93%)	62 (90%)	7 (10%)	7	8
16	CP	68/74 (92%)	63 (93%)	5 (7%)	13	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	AQ	94/97 (97%)	91 (97%)	3 (3%)	39	53
17	CQ	94/97 (97%)	88 (94%)	6 (6%)	17	23
18	AR	59/77 (77%)	56 (95%)	3 (5%)	24	32
18	CR	59/77 (77%)	54 (92%)	5 (8%)	10	13
19	AS	69/80 (86%)	66 (96%)	3 (4%)	29	39
19	CS	67/80 (84%)	57 (85%)	10 (15%)	3	2
20	AT	70/82 (85%)	64 (91%)	6 (9%)	10	13
20	CT	70/82 (85%)	64 (91%)	6 (9%)	10	13
21	AU	18/22 (82%)	16 (89%)	2 (11%)	6	6
21	CU	18/22 (82%)	16 (89%)	2 (11%)	6	6
27	BD	215/218 (99%)	200 (93%)	15 (7%)	15	19
27	DD	215/218 (99%)	202 (94%)	13 (6%)	19	25
28	BE	164/166 (99%)	147 (90%)	17 (10%)	7	7
28	DE	164/166 (99%)	145 (88%)	19 (12%)	5	5
29	BF	160/166 (96%)	142 (89%)	18 (11%)	6	5
29	DF	159/166 (96%)	142 (89%)	17 (11%)	6	7
30	BG	143/156 (92%)	130 (91%)	13 (9%)	9	11
30	DG	142/156 (91%)	128 (90%)	14 (10%)	8	9
31	BH	144/148 (97%)	136 (94%)	8 (6%)	21	28
31	DH	144/148 (97%)	133 (92%)	11 (8%)	13	17
32	BI	110/124 (89%)	92 (84%)	18 (16%)	2	2
32	DI	104/124 (84%)	93 (89%)	11 (11%)	6	7
33	BN	118/119 (99%)	103 (87%)	15 (13%)	4	4
33	DN	118/119 (99%)	107 (91%)	11 (9%)	9	10
34	BO	100/100 (100%)	97 (97%)	3 (3%)	41	55
34	DO	100/100 (100%)	96 (96%)	4 (4%)	31	43
35	BP	115/116 (99%)	107 (93%)	8 (7%)	15	19
35	DP	115/116 (99%)	103 (90%)	12 (10%)	7	7
36	BQ	111/111 (100%)	97 (87%)	14 (13%)	4	4
36	DQ	111/111 (100%)	101 (91%)	10 (9%)	9	11
37	BR	101/101 (100%)	84 (83%)	17 (17%)	2	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	DR	101/101 (100%)	86 (85%)	15 (15%)	3	2
38	BS	87/88 (99%)	78 (90%)	9 (10%)	7	7
38	DS	85/88 (97%)	78 (92%)	7 (8%)	11	14
39	BT	115/127 (91%)	109 (95%)	6 (5%)	23	30
39	DT	113/127 (89%)	106 (94%)	7 (6%)	18	24
40	BU	93/94 (99%)	86 (92%)	7 (8%)	13	17
40	DU	93/94 (99%)	88 (95%)	5 (5%)	22	29
41	BV	80/82 (98%)	72 (90%)	8 (10%)	7	8
41	DV	80/82 (98%)	71 (89%)	9 (11%)	6	5
42	BW	90/92 (98%)	82 (91%)	8 (9%)	9	12
42	DW	90/92 (98%)	84 (93%)	6 (7%)	16	21
43	BX	77/78 (99%)	72 (94%)	5 (6%)	17	23
43	DX	77/78 (99%)	72 (94%)	5 (6%)	17	23
44	BY	85/91 (93%)	80 (94%)	5 (6%)	19	25
44	DY	85/91 (93%)	82 (96%)	3 (4%)	36	49
45	BZ	145/179 (81%)	131 (90%)	14 (10%)	8	9
45	DZ	145/179 (81%)	132 (91%)	13 (9%)	9	11
46	B0	65/67 (97%)	63 (97%)	2 (3%)	40	54
46	D0	65/67 (97%)	63 (97%)	2 (3%)	40	54
47	B1	80/83 (96%)	75 (94%)	5 (6%)	18	23
47	D1	80/83 (96%)	73 (91%)	7 (9%)	10	12
48	B2	65/67 (97%)	61 (94%)	4 (6%)	18	24
48	D2	65/67 (97%)	64 (98%)	1 (2%)	65	77
49	B3	51/52 (98%)	47 (92%)	4 (8%)	12	16
49	D3	50/52 (96%)	45 (90%)	5 (10%)	7	8
50	B4	60/63 (95%)	52 (87%)	8 (13%)	4	3
50	D4	53/63 (84%)	47 (89%)	6 (11%)	6	5
51	B5	50/52 (96%)	47 (94%)	3 (6%)	19	25
51	D5	50/52 (96%)	45 (90%)	5 (10%)	7	8
52	B6	51/52 (98%)	46 (90%)	5 (10%)	8	9
52	D6	50/52 (96%)	48 (96%)	2 (4%)	31	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	B7	41/42 (98%)	38 (93%)	3 (7%)	14	18
53	D7	41/42 (98%)	40 (98%)	1 (2%)	49	64
54	B8	53/55 (96%)	50 (94%)	3 (6%)	20	27
54	D8	54/55 (98%)	51 (94%)	3 (6%)	21	28
55	B9	34/34 (100%)	34 (100%)	0	100	100
55	D9	34/34 (100%)	34 (100%)	0	100	100
All	All	9320/10066 (93%)	8532 (92%)	788 (8%)	10	13

All (788) 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	16	HIS
2	AB	17	PHE
2	AB	21	ARG
2	AB	24	TRP
2	AB	64	ARG
2	AB	76	GLN
2	AB	94	ASN
2	AB	114	ARG
2	AB	127	ILE
2	AB	144	ARG
2	AB	145	LEU
2	AB	155	LEU
2	AB	157	ARG
2	AB	189	ASP
2	AB	196	LEU
2	AB	200	ILE
2	AB	209	ARG
2	AB	213	LEU
2	AB	217	ARG
2	AB	221	LEU
3	AC	3	ASN
3	AC	8	ILE
3	AC	21	ARG
3	AC	28	GLN
3	AC	37	GLN
3	AC	40	ARG

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Mol	Chain	Res	Type
3	AC	45	LYS
3	AC	89	GLU
3	AC	119	ARG
3	AC	131	ARG
3	AC	150	LYS
4	AD	5	ILE
4	AD	15	GLU
4	AD	19	LEU
4	AD	31	CYS
4	AD	49	ARG
4	AD	58	LEU
4	AD	115	ARG
4	AD	127	THR
4	AD	135	LEU
4	AD	140	VAL
4	AD	141	ARG
4	AD	150	GLU
4	AD	157	LEU
4	AD	158	ILE
4	AD	168	ARG
5	AE	31	LEU
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	51	VAL
5	AE	73	ASN
5	AE	151	LEU
6	AF	36	ARG
6	AF	55	ASP
6	AF	70	ASP
6	AF	74	ASP
6	AF	75	LEU
6	AF	82	ARG
7	AG	8	GLU
7	AG	13	GLN
7	AG	50	ILE
7	AG	51	GLN
7	AG	52	GLU
7	AG	72	ARG
7	AG	76	ARG
7	AG	79	ARG
7	AG	104	LEU

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Mol	Chain	Res	Type
7	AG	113	GLU
7	AG	114	ARG
7	AG	138	LYS
7	AG	155	ARG
8	AH	21	LYS
8	AH	52	ASP
8	AH	75	ARG
8	AH	78	GLN
8	AH	91	ARG
8	AH	95	VAL
8	AH	97	VAL
9	AI	14	VAL
9	AI	23	ASN
9	AI	65	VAL
9	AI	86	VAL
9	AI	89	ASN
9	AI	108	VAL
9	AI	127	LYS
9	AI	128	ARG
10	AJ	5	ARG
10	AJ	23	ILE
10	AJ	55	LYS
10	AJ	84	GLN
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	96	ARG
11	AK	104	GLN
11	AK	114	VAL
12	AL	24	VAL
12	AL	33	ARG
12	AL	53	ARG
12	AL	60	LEU
13	AM	3	ARG
13	AM	4	ILE
13	AM	15	VAL
13	AM	19	LEU
13	AM	43	THR
13	AM	56	LEU
13	AM	70	LEU
13	AM	73	GLU
13	AM	102	ARG

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Mol	Chain	Res	Type
13	AM	110	ARG
14	AN	3	ARG
14	AN	7	ILE
14	AN	18	VAL
14	AN	23	ARG
14	AN	33	VAL
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	22	THR
15	AO	24	SER
15	AO	26	GLU
15	AO	38	ARG
15	AO	39	LEU
15	AO	41	GLU
15	AO	47	LYS
15	AO	64	ARG
15	AO	76	GLU
16	AP	19	ILE
16	AP	20	VAL
16	AP	27	LYS
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	62	VAL
17	AQ	14	LYS
17	AQ	74	LEU
17	AQ	83	ASP
18	AR	31	LEU
18	AR	46	GLU
18	AR	76	LEU
19	AS	28	LYS
19	AS	37	ARG
19	AS	65	ASN
20	AT	8	ARG
20	AT	13	LEU
20	AT	30	LYS
20	AT	45	GLN
20	AT	56	MET
20	AT	62	LEU
21	AU	9	ARG
21	AU	10	ARG

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Mol	Chain	Res	Type
27	BD	3	VAL
27	BD	61	LEU
27	BD	71	ASP
27	BD	94	LEU
27	BD	99	ASP
27	BD	113	VAL
27	BD	116	GLN
27	BD	126	GLN
27	BD	142	VAL
27	BD	211	ARG
27	BD	221	VAL
27	BD	229	VAL
27	BD	242	ARG
27	BD	259	THR
27	BD	260	ARG
28	BE	12	THR
28	BE	21	VAL
28	BE	24	THR
28	BE	40	GLU
28	BE	73	GLU
28	BE	77	ILE
28	BE	78	LEU
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	154	LYS
28	BE	163	GLU
28	BE	175	VAL
29	BF	19	GLU
29	BF	20	LEU
29	BF	23	ASP
29	BF	27	GLU
29	BF	33	LEU
29	BF	38	ARG
29	BF	53	THR
29	BF	57	VAL
29	BF	106	ARG
29	BF	110	LEU

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Mol	Chain	Res	Type
29	BF	125	LEU
29	BF	158	THR
29	BF	170	LEU
29	BF	175	THR
29	BF	192	LEU
29	BF	195	ASP
29	BF	197	ASP
29	BF	200	GLU
30	BG	43	LEU
30	BG	45	GLU
30	BG	60	LEU
30	BG	78	SER
30	BG	81	LYS
30	BG	91	ARG
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	3	ARG
31	BH	41	MET
31	BH	45	VAL
31	BH	59	ARG
31	BH	69	ARG
31	BH	71	LEU
31	BH	116	GLU
31	BH	130	ARG
32	BI	5	LEU
32	BI	10	GLU
32	BI	20	ASP
32	BI	38	LEU
32	BI	43	ASN
32	BI	47	LEU
32	BI	50	ARG
32	BI	57	ARG
32	BI	60	GLU
32	BI	66	GLU
32	BI	77	LEU
32	BI	92	VAL
32	BI	96	ASP

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Mol	Chain	Res	Type
32	BI	101	LEU
32	BI	109	ILE
32	BI	140	LEU
32	BI	142	VAL
32	BI	144	VAL
33	BN	5	VAL
33	BN	12	ARG
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	68	GLU
33	BN	87	LEU
33	BN	97	ARG
33	BN	99	LEU
33	BN	120	LEU
33	BN	133	GLN
34	BO	8	LEU
34	BO	23	ARG
34	BO	108	GLU
35	BP	55	ARG
35	BP	59	LEU
35	BP	65	ARG
35	BP	70	GLN
35	BP	83	VAL
35	BP	106	LEU
35	BP	112	LEU
35	BP	135	LEU
36	BQ	1	MET
36	BQ	2	LEU
36	BQ	5	ARG
36	BQ	7	MET
36	BQ	8	LYS
36	BQ	16	ARG
36	BQ	21	THR
36	BQ	35	VAL
36	BQ	45	GLN
36	BQ	54	MET
36	BQ	59	ARG

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Mol	Chain	Res	Type
36	BQ	60	ARG
36	BQ	75	THR
36	BQ	110	THR
37	BR	1	MET
37	BR	6	SER
37	BR	15	SER
37	BR	18	LEU
37	BR	28	LEU
37	BR	29	LEU
37	BR	33	ARG
37	BR	36	THR
37	BR	44	LEU
37	BR	54	LEU
37	BR	60	LEU
37	BR	65	LEU
37	BR	67	LEU
37	BR	79	LEU
37	BR	100	LEU
37	BR	111	LEU
37	BR	114	VAL
38	BS	14	VAL
38	BS	20	ARG
38	BS	49	VAL
38	BS	50	SER
38	BS	57	LYS
38	BS	59	LYS
38	BS	69	VAL
38	BS	78	LEU
38	BS	110	LEU
39	BT	6	LEU
39	BT	28	VAL
39	BT	49	VAL
39	BT	53	ARG
39	BT	96	ARG
39	BT	118	ARG
40	BU	8	VAL
40	BU	36	ARG
40	BU	59	ARG
40	BU	74	LEU
40	BU	83	LEU
40	BU	95	LEU
40	BU	104	GLN

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Mol	Chain	Res	Type
41	BV	18	LEU
41	BV	28	GLU
41	BV	32	THR
41	BV	46	VAL
41	BV	52	VAL
41	BV	62	LEU
41	BV	95	LEU
41	BV	100	ARG
42	BW	4	LYS
42	BW	11	ARG
42	BW	17	VAL
42	BW	19	LEU
42	BW	51	LEU
42	BW	52	GLU
42	BW	67	ASP
42	BW	107	LEU
43	BX	23	GLU
43	BX	35	THR
43	BX	57	LEU
43	BX	65	ARG
43	BX	66	LEU
44	BY	23	ARG
44	BY	55	TYR
44	BY	73	ARG
44	BY	90	LEU
44	BY	99	CYS
45	BZ	5	LEU
45	BZ	6	LYS
45	BZ	18	LEU
45	BZ	33	LEU
45	BZ	61	LEU
45	BZ	91	LEU
45	BZ	111	VAL
45	BZ	117	LEU
45	BZ	121	HIS
45	BZ	136	PHE
45	BZ	153	SER
45	BZ	154	ASP
45	BZ	155	LEU
45	BZ	171	ILE
46	B0	14	ARG
46	B0	20	ARG

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Mol	Chain	Res	Type
47	B1	40	ARG
47	B1	59	THR
47	B1	75	GLU
47	B1	78	LYS
47	B1	95	LEU
48	B2	30	ARG
48	B2	40	SER
48	B2	52	ASP
48	B2	70	GLN
49	B3	8	LEU
49	B3	23	LEU
49	B3	54	VAL
49	B3	60	GLU
50	B4	34	GLU
50	B4	46	GLN
50	B4	49	PHE
50	B4	58	ARG
50	B4	63	TYR
50	B4	67	TYR
50	B4	68	ARG
50	B4	69	LYS
51	B5	6	VAL
51	B5	29	THR
51	B5	40	LYS
52	B6	4	GLU
52	B6	14	THR
52	B6	28	ARG
52	B6	38	LYS
52	B6	52	VAL
53	B7	1	MET
53	B7	24	THR
53	B7	43	THR
54	B8	14	VAL
54	B8	31	HIS
54	B8	32	LEU
2	CB	8	LYS
2	CB	11	LEU
2	CB	23	ARG
2	CB	24	TRP
2	CB	47	THR
2	CB	48	MET
2	CB	76	GLN

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Mol	Chain	Res	Type
2	CB	94	ASN
2	CB	96	ARG
2	CB	115	LEU
2	CB	126	GLU
2	CB	133	LYS
2	CB	155	LEU
2	CB	163	PHE
2	CB	185	ILE
2	CB	189	ASP
2	CB	213	LEU
2	CB	217	ARG
2	CB	224	GLN
3	CC	3	ASN
3	CC	21	ARG
3	CC	28	GLN
3	CC	30	ARG
3	CC	54	ARG
3	CC	105	GLU
3	CC	115	LEU
3	CC	118	GLN
3	CC	119	ARG
3	CC	131	ARG
3	CC	152	ILE
3	CC	162	GLN
3	CC	196	LEU
4	CD	31	CYS
4	CD	34	GLU
4	CD	47	ARG
4	CD	58	LEU
4	CD	61	LYS
4	CD	96	LEU
4	CD	108	LEU
4	CD	135	LEU
4	CD	141	ARG
4	CD	150	GLU
4	CD	155	LEU
4	CD	157	LEU
4	CD	194	LEU
5	CE	24	ARG
5	CE	31	LEU
5	CE	38	GLN
5	CE	41	VAL

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Mol	Chain	Res	Type
5	CE	47	LYS
5	CE	51	VAL
5	CE	64	ARG
5	CE	78	HIS
5	CE	79	GLU
6	CF	10	LEU
6	CF	28	ARG
6	CF	70	ASP
6	CF	75	LEU
7	CG	10	ARG
7	CG	11	GLN
7	CG	12	LEU
7	CG	32	ARG
7	CG	51	GLN
7	CG	52	GLU
7	CG	104	LEU
7	CG	114	ARG
7	CG	155	ARG
8	CH	18	ARG
8	CH	29	SER
8	CH	39	LEU
8	CH	75	ARG
8	CH	84	ARG
8	CH	91	ARG
8	CH	95	VAL
8	CH	97	VAL
8	CH	98	LYS
8	CH	127	LEU
9	CI	7	THR
9	CI	14	VAL
9	CI	17	VAL
9	CI	23	ASN
9	CI	27	THR
9	CI	50	LEU
9	CI	56	LEU
9	CI	64	THR
9	CI	65	VAL
9	CI	81	ILE
9	CI	89	ASN
9	CI	102	LEU
9	CI	108	VAL
9	CI	113	LYS

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Mol	Chain	Res	Type
9	CI	127	LYS
9	CI	128	ARG
10	CJ	21	GLN
10	CJ	46	ARG
10	CJ	67	THR
11	CK	14	VAL
11	CK	54	ARG
11	CK	93	GLN
11	CK	96	ARG
11	CK	104	GLN
11	CK	114	VAL
12	CL	24	VAL
12	CL	33	ARG
12	CL	50	SER
12	CL	53	ARG
12	CL	79	GLU
13	CM	3	ARG
13	CM	15	VAL
13	CM	19	LEU
13	CM	47	ASP
13	CM	56	LEU
13	CM	70	LEU
13	CM	102	ARG
13	CM	110	ARG
13	CM	121	LYS
14	CN	3	ARG
14	CN	7	ILE
14	CN	12	ARG
14	CN	15	LYS
14	CN	23	ARG
14	CN	33	VAL
15	CO	3	ILE
15	CO	5	LYS
15	CO	26	GLU
15	CO	38	ARG
15	CO	39	LEU
15	CO	41	GLU
15	CO	54	ARG
15	CO	64	ARG
16	CP	5	ARG
16	CP	20	VAL
16	CP	27	LYS

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Mol	Chain	Res	Type
16	CP	62	VAL
16	CP	67	THR
17	CQ	9	VAL
17	CQ	14	LYS
17	CQ	36	ILE
17	CQ	74	LEU
17	CQ	83	ASP
17	CQ	96	GLU
18	CR	26	LEU
18	CR	41	LYS
18	CR	42	ARG
18	CR	46	GLU
18	CR	76	LEU
19	CS	16	LEU
19	CS	27	GLU
19	CS	28	LYS
19	CS	30	LEU
19	CS	37	ARG
19	CS	56	GLN
19	CS	65	ASN
19	CS	71	LEU
19	CS	77	THR
19	CS	78	ARG
20	CT	36	LEU
20	CT	45	GLN
20	CT	56	MET
20	CT	62	LEU
20	CT	80	ARG
20	CT	99	LEU
21	CU	10	ARG
21	CU	24	ARG
27	DD	61	LEU
27	DD	71	ASP
27	DD	94	LEU
27	DD	99	ASP
27	DD	106	ILE
27	DD	109	ASP
27	DD	113	VAL
27	DD	116	GLN
27	DD	211	ARG
27	DD	221	VAL
27	DD	242	ARG

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Mol	Chain	Res	Type
27	DD	259	THR
27	DD	260	ARG
28	DE	9	VAL
28	DE	12	THR
28	DE	21	VAL
28	DE	24	THR
28	DE	34	VAL
28	DE	38	THR
28	DE	52	LEU
28	DE	73	GLU
28	DE	75	VAL
28	DE	77	ILE
28	DE	78	LEU
28	DE	82	ARG
28	DE	111	ARG
28	DE	116	VAL
28	DE	119	ARG
28	DE	144	ARG
28	DE	154	LYS
28	DE	163	GLU
28	DE	175	VAL
29	DF	17	ARG
29	DF	19	GLU
29	DF	20	LEU
29	DF	27	GLU
29	DF	33	LEU
29	DF	38	ARG
29	DF	53	THR
29	DF	57	VAL
29	DF	106	ARG
29	DF	107	LYS
29	DF	108	LYS
29	DF	110	LEU
29	DF	158	THR
29	DF	170	LEU
29	DF	175	THR
29	DF	192	LEU
29	DF	200	GLU
30	DG	16	ARG
30	DG	43	LEU
30	DG	45	GLU
30	DG	47	LYS

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Mol	Chain	Res	Type
30	DG	49	ASP
30	DG	60	LEU
30	DG	91	ARG
30	DG	115	ARG
30	DG	136	ARG
30	DG	140	ILE
30	DG	143	GLU
30	DG	148	MET
30	DG	170	ARG
30	DG	175	LEU
31	DH	3	ARG
31	DH	33	LEU
31	DH	63	SER
31	DH	69	ARG
31	DH	72	ILE
31	DH	95	ARG
31	DH	105	LEU
31	DH	106	THR
31	DH	136	ILE
31	DH	139	GLN
31	DH	175	LYS
32	DI	5	LEU
32	DI	9	LEU
32	DI	20	ASP
32	DI	38	LEU
32	DI	43	ASN
32	DI	47	LEU
32	DI	57	ARG
32	DI	61	ARG
32	DI	73	GLU
32	DI	77	LEU
32	DI	140	LEU
33	DN	28	THR
33	DN	33	LEU
33	DN	34	LEU
33	DN	46	VAL
33	DN	58	ASP
33	DN	62	VAL
33	DN	85	ILE
33	DN	87	LEU
33	DN	97	ARG
33	DN	120	LEU

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Mol	Chain	Res	Type
33	DN	138	LEU
34	DO	8	LEU
34	DO	23	ARG
34	DO	69	ILE
34	DO	108	GLU
35	DP	2	LYS
35	DP	15	ARG
35	DP	45	LEU
35	DP	50	ARG
35	DP	55	ARG
35	DP	65	ARG
35	DP	77	ARG
35	DP	83	VAL
35	DP	95	VAL
35	DP	106	LEU
35	DP	112	LEU
35	DP	135	LEU
36	DQ	1	MET
36	DQ	16	ARG
36	DQ	21	THR
36	DQ	45	GLN
36	DQ	48	GLU
36	DQ	54	MET
36	DQ	56	ARG
36	DQ	60	ARG
36	DQ	75	THR
36	DQ	110	THR
37	DR	1	MET
37	DR	6	SER
37	DR	18	LEU
37	DR	24	GLN
37	DR	28	LEU
37	DR	29	LEU
37	DR	33	ARG
37	DR	36	THR
37	DR	44	LEU
37	DR	54	LEU
37	DR	60	LEU
37	DR	65	LEU
37	DR	67	LEU
37	DR	79	LEU
37	DR	100	LEU

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Mol	Chain	Res	Type
38	DS	20	ARG
38	DS	50	SER
38	DS	67	ARG
38	DS	75	GLU
38	DS	80	LEU
38	DS	83	LYS
38	DS	110	LEU
39	DT	16	ARG
39	DT	17	THR
39	DT	28	VAL
39	DT	38	ASN
39	DT	49	VAL
39	DT	96	ARG
39	DT	118	ARG
40	DU	36	ARG
40	DU	74	LEU
40	DU	92	ARG
40	DU	104	GLN
40	DU	108	GLU
41	DV	15	GLU
41	DV	18	LEU
41	DV	28	GLU
41	DV	32	THR
41	DV	51	VAL
41	DV	52	VAL
41	DV	79	VAL
41	DV	85	LYS
41	DV	95	LEU
42	DW	4	LYS
42	DW	11	ARG
42	DW	17	VAL
42	DW	51	LEU
42	DW	67	ASP
42	DW	107	LEU
43	DX	1	MET
43	DX	23	GLU
43	DX	35	THR
43	DX	57	LEU
43	DX	70	LEU
44	DY	23	ARG
44	DY	72	VAL
44	DY	99	CYS

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Mol	Chain	Res	Type
45	DZ	5	LEU
45	DZ	18	LEU
45	DZ	33	LEU
45	DZ	41	LEU
45	DZ	61	LEU
45	DZ	111	VAL
45	DZ	119	GLU
45	DZ	121	HIS
45	DZ	131	ARG
45	DZ	136	PHE
45	DZ	153	SER
45	DZ	154	ASP
45	DZ	155	LEU
46	D0	20	ARG
46	D0	24	LYS
47	D1	3	LYS
47	D1	32	LYS
47	D1	40	ARG
47	D1	52	ARG
47	D1	59	THR
47	D1	95	LEU
47	D1	97	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	5	ILE
50	D4	13	ARG
50	D4	33	VAL
50	D4	34	GLU
50	D4	58	ARG
50	D4	68	ARG
51	D5	6	VAL
51	D5	29	THR
51	D5	40	LYS
51	D5	48	GLU
51	D5	59	GLU
52	D6	14	THR
52	D6	28	ARG
53	D7	1	MET

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Mol	Chain	Res	Type
54	D8	14	VAL
54	D8	32	LEU
54	D8	37	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (122) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	16	HIS
2	AB	19	HIS
2	AB	40	HIS
2	AB	94	ASN
3	AC	6	HIS
3	AC	28	GLN
3	AC	37	GLN
3	AC	98	ASN
3	AC	102	ASN
3	AC	104	GLN
3	AC	123	GLN
3	AC	136	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	45	GLN
4	AD	77	ASN
4	AD	125	HIS
5	AE	38	GLN
5	AE	141	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	97	GLN
9	AI	23	ASN
9	AI	58	HIS
10	AJ	56	HIS
11	AK	99	GLN
11	AK	104	GLN
12	AL	78	GLN
12	AL	99	HIS
15	AO	28	GLN
17	AQ	16	GLN
19	AS	23	ASN
19	AS	65	ASN
19	AS	69	HIS
19	AS	83	HIS

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Mol	Chain	Res	Type
20	AT	42	GLN
20	AT	45	GLN
27	BD	87	ASN
27	BD	253	GLN
28	BE	85	ASN
28	BE	143	ASN
29	BF	69	HIS
29	BF	169	ASN
29	BF	203	GLN
30	BG	26	GLN
32	BI	43	ASN
32	BI	74	ASN
35	BP	38	GLN
36	BQ	12	GLN
36	BQ	57	HIS
37	BR	71	GLN
39	BT	43	GLN
39	BT	123	GLN
40	BU	94	ASN
43	BX	31	HIS
43	BX	82	GLN
44	BY	6	HIS
45	BZ	34	ASN
45	BZ	55	HIS
45	BZ	118	GLN
48	B2	70	GLN
49	B3	32	GLN
50	B4	46	GLN
55	B9	36	GLN
2	CB	135	GLN
2	CB	224	GLN
3	CC	6	HIS
3	CC	28	GLN
3	CC	37	GLN
3	CC	104	GLN
3	CC	123	GLN
3	CC	136	GLN
4	CD	77	ASN
4	CD	125	HIS
5	CE	38	GLN
5	CE	73	ASN
5	CE	141	GLN

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Mol	Chain	Res	Type
6	CF	73	ASN
6	CF	100	ASN
7	CG	51	GLN
7	CG	97	GLN
8	CH	15	ASN
9	CI	23	ASN
9	CI	31	GLN
9	CI	58	HIS
9	CI	87	GLN
9	CI	89	ASN
9	CI	124	GLN
10	CJ	13	HIS
10	CJ	21	GLN
11	CK	93	GLN
12	CL	78	GLN
12	CL	99	HIS
13	CM	77	ASN
15	CO	28	GLN
19	CS	23	ASN
19	CS	65	ASN
19	CS	69	HIS
19	CS	83	HIS
20	CT	90	GLN
27	DD	164	GLN
27	DD	253	GLN
29	DF	69	HIS
29	DF	169	ASN
29	DF	203	GLN
30	DG	26	GLN
30	DG	40	ASN
32	DI	105	HIS
34	DO	89	ASN
35	DP	38	GLN
36	DQ	45	GLN
36	DQ	57	HIS
37	DR	13	HIS
38	DS	68	GLN
39	DT	123	GLN
41	DV	64	HIS
41	DV	89	GLN
42	DW	60	ASN
43	DX	31	HIS

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Mol	Chain	Res	Type
43	DX	82	GLN
45	DZ	55	HIS
55	D9	36	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1521 (98%)	306 (20%)	21 (1%)
1	CA	1501/1521 (98%)	310 (20%)	23 (1%)
22	AV	12/24 (50%)	3 (25%)	0
22	CV	12/24 (50%)	3 (25%)	0
23	AW	71/76 (93%)	30 (42%)	2 (2%)
23	AY	71/76 (93%)	33 (46%)	1 (1%)
23	CW	68/76 (89%)	30 (44%)	3 (4%)
23	CY	69/76 (90%)	28 (40%)	0
24	AX	75/77 (97%)	18 (24%)	1 (1%)
24	CX	75/77 (97%)	19 (25%)	0
25	BA	2811/2915 (96%)	433 (15%)	27 (0%)
25	DA	2791/2915 (95%)	499 (17%)	33 (1%)
26	BB	119/121 (98%)	13 (10%)	0
26	DB	119/121 (98%)	17 (14%)	0
All	All	9289/9620 (96%)	1742 (18%)	111 (1%)

All (1742) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	9	G
1	AA	22	G
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	54	C
1	AA	61	G
1	AA	65	U
1	AA	70	G
1	AA	73	G
1	AA	78	G
1	AA	79	G

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Mol	Chain	Res	Type
1	AA	96	U
1	AA	97	G
1	AA	98	G
1	AA	111	G
1	AA	116	A
1	AA	121	C
1	AA	129(A)	G
1	AA	131	C
1	AA	145	G
1	AA	146	G
1	AA	155	C
1	AA	156	G
1	AA	163	C
1	AA	166	G
1	AA	171	A
1	AA	174	C
1	AA	180	U
1	AA	182	U
1	AA	189(C)	C
1	AA	189(E)	U
1	AA	189(F)	U
1	AA	189(I)	G
1	AA	189(J)	G
1	AA	189(K)	U
1	AA	190	U
1	AA	194	C
1	AA	195	A
1	AA	197	A
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	217	C
1	AA	220	G
1	AA	247	G
1	AA	251	G
1	AA	253	U
1	AA	258	G
1	AA	262	A
1	AA	266	G
1	AA	267	C

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Mol	Chain	Res	Type
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	332	G
1	AA	341	C
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	382	A
1	AA	384	G
1	AA	388	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	412	A
1	AA	413	G
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	439	A
1	AA	442	C
1	AA	443	C
1	AA	449	C
1	AA	452	A
1	AA	455	C
1	AA	457	C
1	AA	461	A
1	AA	470	C
1	AA	475	G
1	AA	477	A
1	AA	485	G
1	AA	496	A
1	AA	498	U

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Mol	Chain	Res	Type
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	521	G
1	AA	524	G
1	AA	527	G
1	AA	528	C
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	547	A
1	AA	559	A
1	AA	561	U
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	577	G
1	AA	581	G
1	AA	590	C
1	AA	596	C
1	AA	619	U
1	AA	630	G
1	AA	653	A
1	AA	657	G
1	AA	660	G
1	AA	665	A
1	AA	671	G
1	AA	673	G
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	695	A
1	AA	703	G
1	AA	723	U
1	AA	731	G
1	AA	733	A
1	AA	749	C
1	AA	752	G
1	AA	755	G

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Mol	Chain	Res	Type
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	815	A
1	AA	817	C
1	AA	821	G
1	AA	827	U
1	AA	828	A
1	AA	829	G
1	AA	833	U
1	AA	834	C
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	874	G
1	AA	902	G
1	AA	914	A
1	AA	926	G
1	AA	927	G
1	AA	934	C
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	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	991	U
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	997	U
1	AA	998	G

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Mol	Chain	Res	Type
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1006	C
1	AA	1008	C
1	AA	1014	A
1	AA	1020	U
1	AA	1021	G
1	AA	1022	G
1	AA	1023	G
1	AA	1024	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1033	G
1	AA	1035	A
1	AA	1037	C
1	AA	1039	C
1	AA	1054	C
1	AA	1060	C
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1088	G
1	AA	1089	G
1	AA	1094	G
1	AA	1095	U
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1110	A
1	AA	1122	U
1	AA	1123	A
1	AA	1124	G

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Mol	Chain	Res	Type
1	AA	1125	U
1	AA	1126	U
1	AA	1130	A
1	AA	1132	C
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	1141	C
1	AA	1145	C
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1157	A
1	AA	1158	C
1	AA	1159	U
1	AA	1175	G
1	AA	1183	A
1	AA	1184	G
1	AA	1191	A
1	AA	1196	U
1	AA	1197	G
1	AA	1202	G
1	AA	1212	U
1	AA	1213	A
1	AA	1227	A
1	AA	1228	C
1	AA	1236	A
1	AA	1238	A
1	AA	1250	A
1	AA	1255	G
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1263	C
1	AA	1270	C
1	AA	1272	G
1	AA	1273	G
1	AA	1278	U

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Mol	Chain	Res	Type
1	AA	1279	A
1	AA	1280	A
1	AA	1281	U
1	AA	1286	A
1	AA	1287	A
1	AA	1297	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1317	C
1	AA	1319	A
1	AA	1320	C
1	AA	1338	G
1	AA	1340	A
1	AA	1346	A
1	AA	1347	G
1	AA	1358	U
1	AA	1363	C
1	AA	1370	G
1	AA	1397	C
1	AA	1419	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1456	G
1	AA	1492	A
1	AA	1493	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	13	A
22	AV	14	A
22	AV	24	A

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Mol	Chain	Res	Type
23	AW	2	C
23	AW	3	C
23	AW	6	G
23	AW	8	4SU
23	AW	11	C
23	AW	13	C
23	AW	14	A
23	AW	19	G
23	AW	20	U
23	AW	21	A
23	AW	22	G
23	AW	23	A
23	AW	26	A
23	AW	34	G
23	AW	42	C
23	AW	44	G
23	AW	45	U
23	AW	46	7MG
23	AW	47	U
23	AW	48	C
23	AW	49	C
23	AW	61	C
23	AW	63	G
23	AW	64	A
23	AW	68	C
23	AW	70	G
23	AW	73	A
23	AW	74	C
23	AW	75	C
23	AW	76	A
24	AX	3	C
24	AX	9	G
24	AX	18	G
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	31	G
24	AX	42	G
24	AX	47	U
24	AX	48	C
24	AX	60	U
24	AX	61	C

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Mol	Chain	Res	Type
24	AX	62	C
24	AX	65	C
24	AX	67	C
24	AX	68	C
24	AX	70	G
24	AX	76	A
23	AY	2	C
23	AY	3	C
23	AY	5	G
23	AY	9	A
23	AY	13	C
23	AY	14	A
23	AY	15	G
23	AY	19	G
23	AY	20	U
23	AY	21	A
23	AY	22	G
23	AY	30	G
23	AY	31	A
23	AY	33	U
23	AY	34	G
23	AY	35	A
23	AY	39	PSU
23	AY	44	G
23	AY	45	U
23	AY	46	7MG
23	AY	47	U
23	AY	48	C
23	AY	49	C
23	AY	51	U
23	AY	53	G
23	AY	56	C
23	AY	57	G
23	AY	58	A
23	AY	62	C
23	AY	65	G
23	AY	67	C
23	AY	70	G
23	AY	73	A
25	BA	11	G
25	BA	12	U
25	BA	13	A

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Mol	Chain	Res	Type
25	BA	34	C
25	BA	45	C
25	BA	54	G
25	BA	60	G
25	BA	63	A
25	BA	70	A
25	BA	71	U
25	BA	73	A
25	BA	74	G
25	BA	82	G
25	BA	83	A
25	BA	94	G
25	BA	95	G
25	BA	116	A
25	BA	117	A
25	BA	118	U
25	BA	170	A
25	BA	185	A
25	BA	188	A
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	212	A
25	BA	218	A
25	BA	219	U
25	BA	222	A
25	BA	237	G
25	BA	256	C
25	BA	265	U
25	BA	269	G
25	BA	271	U
25	BA	272	U
25	BA	273	G
25	BA	274	U
25	BA	275	C
25	BA	276	C
25	BA	279	G
25	BA	289	G
25	BA	294	C

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Mol	Chain	Res	Type
25	BA	303	C
25	BA	307	A
25	BA	335	A
25	BA	353	G
25	BA	354	A
25	BA	376	G
25	BA	387	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	433	G
25	BA	438	G
25	BA	448	U
25	BA	455	A
25	BA	469	A
25	BA	470	C
25	BA	474	U
25	BA	477	C
25	BA	481	C
25	BA	482	C
25	BA	496	A
25	BA	497	A
25	BA	507	G
25	BA	526	A
25	BA	529	U
25	BA	530	A
25	BA	534	C
25	BA	553	A
25	BA	555	G
25	BA	556	C
25	BA	557	A
25	BA	558	G
25	BA	569	G
25	BA	573	G
25	BA	585	U
25	BA	586	G
25	BA	596	G
25	BA	598	A
25	BA	609	A

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Mol	Chain	Res	Type
25	BA	626	A
25	BA	627	G
25	BA	630	U
25	BA	638	U
25	BA	639	G
25	BA	640	A
25	BA	641	G
25	BA	652	A
25	BA	662	A
25	BA	670	C
25	BA	671	A
25	BA	678	A
25	BA	693	G
25	BA	694	G
25	BA	697	C
25	BA	698	G
25	BA	716	G
25	BA	724	A
25	BA	733	G
25	BA	777	C
25	BA	795	G
25	BA	796	C
25	BA	811	A
25	BA	812	G
25	BA	822	G
25	BA	823	G
25	BA	829	A
25	BA	830	A
25	BA	831	A
25	BA	832	G
25	BA	836	A
25	BA	839	G
25	BA	852	G
25	BA	859	C
25	BA	866	A
25	BA	874	U
25	BA	875	U
25	BA	877	G
25	BA	906	G
25	BA	908	A
25	BA	913	A
25	BA	924	U

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Mol	Chain	Res	Type
25	BA	926	G
25	BA	927	G
25	BA	929	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	941	U
25	BA	942	A
25	BA	943	C
25	BA	944	C
25	BA	945	A
25	BA	953	U
25	BA	956	A
25	BA	977	G
25	BA	986	A
25	BA	990	A
25	BA	991	G
25	BA	998	A
25	BA	1004	A
25	BA	1006	C
25	BA	1019	G
25	BA	1020	C
25	BA	1029	A
25	BA	1042	A
25	BA	1051	C
25	BA	1058	U
25	BA	1059	C
25	BA	1068	G
25	BA	1072	U
25	BA	1079	U
25	BA	1084	C
25	BA	1087	C
25	BA	1088	G
25	BA	1091	A
25	BA	1092	A
25	BA	1093	G
25	BA	1097	G

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Mol	Chain	Res	Type
25	BA	1153	G
25	BA	1154	U
25	BA	1156	G
25	BA	1158	G
25	BA	1174	A
25	BA	1180	C
25	BA	1181	G
25	BA	1184	G
25	BA	1217	G
25	BA	1218	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1222	A
25	BA	1223	C
25	BA	1250	U
25	BA	1255	A
25	BA	1256	U
25	BA	1263	C
25	BA	1265	A
25	BA	1299	A
25	BA	1302	G
25	BA	1317	G
25	BA	1318	A
25	BA	1346	U
25	BA	1347	A
25	BA	1349	G
25	BA	1360	C
25	BA	1365	G
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

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Mol	Chain	Res	Type
25	BA	1483	C
25	BA	1491	A
25	BA	1496	A
25	BA	1497	G
25	BA	1502	G
25	BA	1506	G
25	BA	1508	G
25	BA	1514	C
25	BA	1518	A
25	BA	1525	G
25	BA	1529	G
25	BA	1539	C
25	BA	1540	A
25	BA	1553	A
25	BA	1554	A
25	BA	1555	C
25	BA	1556	A
25	BA	1578	C
25	BA	1589	A
25	BA	1605	A
25	BA	1613	A
25	BA	1616	A
25	BA	1625	U
25	BA	1628	G
25	BA	1629	C
25	BA	1631	C
25	BA	1632	A
25	BA	1654	A
25	BA	1655	A
25	BA	1656	A
25	BA	1695	C
25	BA	1701	A
25	BA	1708	G
25	BA	1721	G
25	BA	1743	G
25	BA	1747	A
25	BA	1748	A
25	BA	1766	G
25	BA	1767	A
25	BA	1787	G
25	BA	1794	G
25	BA	1795	G

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Mol	Chain	Res	Type
25	BA	1804	A
25	BA	1811	A
25	BA	1813	C
25	BA	1822	A
25	BA	1831	C
25	BA	1847	G
25	BA	1848	G
25	BA	1860	A
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	1922	A
25	BA	1928	G
25	BA	1937	U
25	BA	1941	A
25	BA	1949	A
25	BA	1951	G
25	BA	1952	G
25	BA	1953	U
25	BA	1959	A
25	BA	1960	A
25	BA	1977	U
25	BA	1985	U
25	BA	1987	C
25	BA	1989	C
25	BA	1992	A
25	BA	1993	A
25	BA	1994	A
25	BA	2014	G
25	BA	2015	U
25	BA	2019	G
25	BA	2042	A
25	BA	2045	G
25	BA	2053	A
25	BA	2054	G
25	BA	2055	A
25	BA	2061	C
25	BA	2065	C
25	BA	2077	C

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Mol	Chain	Res	Type
25	BA	2078	G
25	BA	2082	A
25	BA	2083	G
25	BA	2084	A
25	BA	2091	G
25	BA	2118	U
25	BA	2120	U
25	BA	2132	G
25	BA	2135	U
25	BA	2138	G
25	BA	2141	A
25	BA	2142	G
25	BA	2144	U
25	BA	2147	G
25	BA	2149	G
25	BA	2151	C
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	2164	C
25	BA	2165	C
25	BA	2168	C
25	BA	2170	G
25	BA	2175	G
25	BA	2179	G
25	BA	2180	A
25	BA	2181	G
25	BA	2182	G
25	BA	2188	G
25	BA	2189	U
25	BA	2190	G
25	BA	2193	A
25	BA	2194	U
25	BA	2195	A
25	BA	2196	C
25	BA	2197	C
25	BA	2200	C
25	BA	2203	G
25	BA	2204	G

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Mol	Chain	Res	Type
25	BA	2206	G
25	BA	2207	C
25	BA	2208	G
25	BA	2210	C
25	BA	2212	G
25	BA	2214	G
25	BA	2220	A
25	BA	2221	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	2287	C
25	BA	2295	C
25	BA	2299	A
25	BA	2301	G
25	BA	2317	A
25	BA	2320	G
25	BA	2332	A
25	BA	2337	G
25	BA	2346	G
25	BA	2348	A
25	BA	2355	C
25	BA	2359	C
25	BA	2366	G
25	BA	2373	A
25	BA	2395	G
25	BA	2397	C
25	BA	2418	U
25	BA	2435	U
25	BA	2436	C
25	BA	2437	A
25	BA	2441	G
25	BA	2442	A
25	BA	2446	A
25	BA	2447	A
25	BA	2451	A
25	BA	2453	C

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Mol	Chain	Res	Type
25	BA	2460	A
25	BA	2461	U
25	BA	2480	G
25	BA	2481	A
25	BA	2486	C
25	BA	2488	A
25	BA	2490	A
25	BA	2514	G
25	BA	2517	G
25	BA	2530	A
25	BA	2541	G
25	BA	2561	G
25	BA	2566	U
25	BA	2578	A
25	BA	2579	G
25	BA	2585	C
25	BA	2590	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	2653	G
25	BA	2666	A
25	BA	2682	A
25	BA	2701	U
25	BA	2702	C
25	BA	2703	C
25	BA	2715	C
25	BA	2725	A
25	BA	2726	A
25	BA	2727	G
25	BA	2739	U
25	BA	2746	A
25	BA	2771	A
25	BA	2777	A
25	BA	2778	A
25	BA	2782	C
25	BA	2791	A
25	BA	2803	A
25	BA	2813	G

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Mol	Chain	Res	Type
25	BA	2828	G
25	BA	2830	A
25	BA	2831	A
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	7	G
26	BB	15	A
26	BB	20	C
26	BB	25	A
26	BB	42	C
26	BB	56	G
26	BB	73	A
26	BB	75	G
26	BB	85	G
26	BB	98	G
26	BB	106	G
26	BB	110	G
1	CA	5	U
1	CA	6	G
1	CA	9	G
1	CA	22	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	54	C
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	96	U

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Mol	Chain	Res	Type
1	CA	97	G
1	CA	98	G
1	CA	111	G
1	CA	112	G
1	CA	116	A
1	CA	121	C
1	CA	129(A)	G
1	CA	131	C
1	CA	143	A
1	CA	155	C
1	CA	156	G
1	CA	163	C
1	CA	166	G
1	CA	171	A
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(C)	C
1	CA	189(E)	U
1	CA	189(F)	U
1	CA	189(I)	G
1	CA	189(K)	U
1	CA	190	U
1	CA	194	C
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	202	U
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	220	G
1	CA	247	G
1	CA	251	G
1	CA	253	U
1	CA	258	G
1	CA	262	A
1	CA	266	G
1	CA	267	C
1	CA	289	G
1	CA	301	G
1	CA	321	A

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Mol	Chain	Res	Type
1	CA	328	C
1	CA	329	A
1	CA	332	G
1	CA	341	C
1	CA	343	U
1	CA	344	A
1	CA	346	G
1	CA	350	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	382	A
1	CA	384	G
1	CA	388	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	412	A
1	CA	413	G
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	439	A
1	CA	442	C
1	CA	443	C
1	CA	449	C
1	CA	452	A
1	CA	455	C
1	CA	457	C
1	CA	461	A
1	CA	470	C
1	CA	475	G
1	CA	477	A
1	CA	485	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A

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Mol	Chain	Res	Type
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	521	G
1	CA	524	G
1	CA	528	C
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	547	A
1	CA	559	A
1	CA	561	U
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	577	G
1	CA	581	G
1	CA	590	C
1	CA	596	C
1	CA	619	U
1	CA	630	G
1	CA	653	A
1	CA	657	G
1	CA	660	G
1	CA	665	A
1	CA	671	G
1	CA	673	G
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	695	A
1	CA	702	A
1	CA	723	U
1	CA	731	G
1	CA	749	C
1	CA	752	G
1	CA	755	G
1	CA	773	G
1	CA	774	G
1	CA	777	A
1	CA	792	A

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Mol	Chain	Res	Type
1	CA	793	U
1	CA	794	A
1	CA	815	A
1	CA	817	C
1	CA	821	G
1	CA	827	U
1	CA	828	A
1	CA	829	G
1	CA	833	U
1	CA	834	C
1	CA	840	C
1	CA	841	U
1	CA	848	C
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	874	G
1	CA	902	G
1	CA	914	A
1	CA	926	G
1	CA	927	G
1	CA	932	C
1	CA	934	C
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	972	C
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	991	U
1	CA	992	U
1	CA	993	G
1	CA	996	A
1	CA	997	U
1	CA	998	G
1	CA	1002	G
1	CA	1003	G
1	CA	1004	A

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Mol	Chain	Res	Type
1	CA	1005	A
1	CA	1006	C
1	CA	1014	A
1	CA	1020	U
1	CA	1021	G
1	CA	1022	G
1	CA	1023	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1029	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1030(D)	A
1	CA	1031	G
1	CA	1033	G
1	CA	1035	A
1	CA	1037	C
1	CA	1039	C
1	CA	1041	A
1	CA	1054	C
1	CA	1060	C
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1088	G
1	CA	1089	G
1	CA	1094	G
1	CA	1095	U
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1110	A
1	CA	1117	G
1	CA	1122	U
1	CA	1125	U
1	CA	1126	U
1	CA	1129	C

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Mol	Chain	Res	Type
1	CA	1130	A
1	CA	1132	C
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1141	C
1	CA	1145	C
1	CA	1146	A
1	CA	1152	A
1	CA	1154	G
1	CA	1157	A
1	CA	1158	C
1	CA	1159	U
1	CA	1175	G
1	CA	1182	G
1	CA	1183	A
1	CA	1184	G
1	CA	1191	A
1	CA	1196	U
1	CA	1197	G
1	CA	1201	A
1	CA	1202	G
1	CA	1212	U
1	CA	1213	A
1	CA	1227	A
1	CA	1228	C
1	CA	1236	A
1	CA	1238	A
1	CA	1250	A
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1263	C
1	CA	1270	C
1	CA	1272	G
1	CA	1273	G
1	CA	1278	U
1	CA	1279	A

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Mol	Chain	Res	Type
1	CA	1280	A
1	CA	1281	U
1	CA	1286	A
1	CA	1287	A
1	CA	1297	C
1	CA	1299	A
1	CA	1300	G
1	CA	1305	G
1	CA	1317	C
1	CA	1319	A
1	CA	1320	C
1	CA	1338	G
1	CA	1340	A
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1358	U
1	CA	1363	C
1	CA	1370	G
1	CA	1397	C
1	CA	1419	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1446	U
1	CA	1447	A
1	CA	1452	C
1	CA	1456	G
1	CA	1492	A
1	CA	1493	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1517	G
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	13	A
22	CV	14	A
22	CV	24	A

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Mol	Chain	Res	Type
23	CW	3	C
23	CW	5	G
23	CW	6	G
23	CW	7	A
23	CW	8	4SU
23	CW	9	A
23	CW	12	U
23	CW	13	C
23	CW	14	A
23	CW	19	G
23	CW	22	G
23	CW	25	C
23	CW	27	G
23	CW	28	G
23	CW	44	G
23	CW	46	7MG
23	CW	47	U
23	CW	48	C
23	CW	59	U
23	CW	61	C
23	CW	62	C
23	CW	63	G
23	CW	64	A
23	CW	66	U
23	CW	67	C
23	CW	70	G
23	CW	73	A
23	CW	74	C
23	CW	75	C
23	CW	76	A
24	CX	3	C
24	CX	9	G
24	CX	13	C
24	CX	18	G
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	31	G
24	CX	42	G
24	CX	47	U
24	CX	48	C
24	CX	60	U

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Mol	Chain	Res	Type
24	CX	61	C
24	CX	62	C
24	CX	65	C
24	CX	67	C
24	CX	68	C
24	CX	70	G
24	CX	76	A
23	CY	2	C
23	CY	3	C
23	CY	8	4SU
23	CY	13	C
23	CY	14	A
23	CY	15	G
23	CY	19	G
23	CY	22	G
23	CY	30	G
23	CY	31	A
23	CY	33	U
23	CY	34	G
23	CY	35	A
23	CY	39	PSU
23	CY	45	U
23	CY	46	7MG
23	CY	47	U
23	CY	49	C
23	CY	51	U
23	CY	52	G
23	CY	56	C
23	CY	57	G
23	CY	58	A
23	CY	62	C
23	CY	65	G
23	CY	67	C
23	CY	70	G
23	CY	73	A
25	DA	11	G
25	DA	12	U
25	DA	15	G
25	DA	34	C
25	DA	35	G
25	DA	45	C
25	DA	59	U

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Mol	Chain	Res	Type
25	DA	71	A
25	DA	74	A
25	DA	75	G
25	DA	84	A
25	DA	95	G
25	DA	118	A
25	DA	119	A
25	DA	120	U
25	DA	141	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	213	A
25	DA	214	G
25	DA	215	G
25	DA	216	A
25	DA	221	A
25	DA	222	A
25	DA	229	A
25	DA	230	U
25	DA	233	A
25	DA	248	G
25	DA	269	U
25	DA	271(A)	A
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(S)	G
25	DA	272(A)	U
25	DA	272(B)	G
25	DA	274	G
25	DA	277	C
25	DA	278	A
25	DA	283	A
25	DA	292	C

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Mol	Chain	Res	Type
25	DA	311	A
25	DA	312	G
25	DA	327	G
25	DA	329	G
25	DA	330	A
25	DA	342	G
25	DA	352	G
25	DA	363	G
25	DA	380	U
25	DA	386	G
25	DA	396	G
25	DA	405	U
25	DA	411	G
25	DA	412	A
25	DA	418	G
25	DA	422	A
25	DA	428	A
25	DA	442	G
25	DA	443	A
25	DA	444	C
25	DA	455	C
25	DA	457	A
25	DA	481	G
25	DA	494	G
25	DA	504	U
25	DA	505	A
25	DA	507	A
25	DA	508	G
25	DA	509	C
25	DA	530	G
25	DA	531	C
25	DA	532	A
25	DA	533	G
25	DA	545	G
25	DA	555	U
25	DA	556	G
25	DA	563	G
25	DA	568	U
25	DA	573	G
25	DA	575	A
25	DA	588	U
25	DA	599	G

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Mol	Chain	Res	Type
25	DA	603	A
25	DA	604	G
25	DA	607	U
25	DA	614(B)	G
25	DA	615	G
25	DA	627	A
25	DA	637	A
25	DA	645	C
25	DA	652(B)	A
25	DA	652(C)	G
25	DA	653	A
25	DA	655	A
25	DA	669	G
25	DA	686	G
25	DA	701	G
25	DA	730	C
25	DA	753	C
25	DA	775	G
25	DA	776	G
25	DA	782	A
25	DA	784	A
25	DA	785	G
25	DA	790	C
25	DA	792	G
25	DA	805	G
25	DA	812	C
25	DA	819	A
25	DA	827	U
25	DA	828	U
25	DA	849	A
25	DA	857	C
25	DA	859	G
25	DA	866	A
25	DA	874	G
25	DA	878	A
25	DA	879	G
25	DA	882	G
25	DA	884	C
25	DA	886	C
25	DA	887	A
25	DA	888	C
25	DA	889	C

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Mol	Chain	Res	Type
25	DA	890	A
25	DA	893	C
25	DA	895	U
25	DA	896	A
25	DA	897	C
25	DA	900	A
25	DA	901	A
25	DA	903	C
25	DA	907	U
25	DA	910	A
25	DA	915	C
25	DA	917	A
25	DA	932	G
25	DA	938	G
25	DA	941	A
25	DA	945	A
25	DA	946	G
25	DA	953	A
25	DA	958	U
25	DA	959	A
25	DA	961	C
25	DA	974	G
25	DA	975	C
25	DA	983	A
25	DA	996	A
25	DA	1003	G
25	DA	1006	C
25	DA	1012	U
25	DA	1013	C
25	DA	1017	G
25	DA	1022	G
25	DA	1025	G
25	DA	1026	U
25	DA	1027	A
25	DA	1033	U
25	DA	1038	C
25	DA	1039	G
25	DA	1040	C
25	DA	1042	G
25	DA	1043	C
25	DA	1113	U
25	DA	1116	C

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Mol	Chain	Res	Type
25	DA	1128	A
25	DA	1129	A
25	DA	1130	U
25	DA	1135	C
25	DA	1136	G
25	DA	1138	G
25	DA	1139	G
25	DA	1142	U
25	DA	1143	A
25	DA	1144	G
25	DA	1168	G
25	DA	1170	G
25	DA	1171	G
25	DA	1188	U
25	DA	1206	G
25	DA	1211	U
25	DA	1219	G
25	DA	1220	A
25	DA	1229	G
25	DA	1237	A
25	DA	1241	A
25	DA	1244	G
25	DA	1248	G
25	DA	1253	A
25	DA	1256	G
25	DA	1271	G
25	DA	1272	A
25	DA	1284	A
25	DA	1286	A
25	DA	1287	A
25	DA	1300	U
25	DA	1301	A
25	DA	1303	G
25	DA	1305	C
25	DA	1314	C
25	DA	1345	C
25	DA	1352	U
25	DA	1359	A
25	DA	1360	A
25	DA	1365	A
25	DA	1370	C
25	DA	1384	A

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Mol	Chain	Res	Type
25	DA	1385	G
25	DA	1408	C
25	DA	1416	G
25	DA	1417	C
25	DA	1419	A
25	DA	1420	U
25	DA	1421	G
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	1459	G
25	DA	1461	G
25	DA	1467	C
25	DA	1471	A
25	DA	1482	G
25	DA	1487	G
25	DA	1490	A
25	DA	1493	C
25	DA	1494	A
25	DA	1496	A
25	DA	1497	U
25	DA	1505	C
25	DA	1508	A
25	DA	1509	C
25	DA	1509(A)	A
25	DA	1531	C
25	DA	1533	G
25	DA	1541	G
25	DA	1542	A
25	DA	1545	A
25	DA	1547	C
25	DA	1558	A
25	DA	1559	G
25	DA	1566	A
25	DA	1569	A
25	DA	1578	U
25	DA	1580	A
25	DA	1583	A
25	DA	1584	C

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Mol	Chain	Res	Type
25	DA	1586	A
25	DA	1598	C
25	DA	1608	A
25	DA	1610	A
25	DA	1616	A
25	DA	1639	U
25	DA	1640	C
25	DA	1648	C
25	DA	1654	A
25	DA	1664	A
25	DA	1674	G
25	DA	1696	G
25	DA	1700	A
25	DA	1701	A
25	DA	1721	G
25	DA	1722	A
25	DA	1740	G
25	DA	1756	G
25	DA	1762	A
25	DA	1763	G
25	DA	1764	G
25	DA	1773	A
25	DA	1780	A
25	DA	1782	C
25	DA	1791	A
25	DA	1797	C
25	DA	1800	C
25	DA	1801	G
25	DA	1816	G
25	DA	1829	A
25	DA	1835	G
25	DA	1847	A
25	DA	1848	A
25	DA	1877	A
25	DA	1878	G
25	DA	1896	G
25	DA	1900	A
25	DA	1906	G
25	DA	1913	A
25	DA	1914	C
25	DA	1929	G
25	DA	1930	G

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Mol	Chain	Res	Type
25	DA	1937	A
25	DA	1938	A
25	DA	1955	U
25	DA	1963	U
25	DA	1967	C
25	DA	1970	A
25	DA	1971	A
25	DA	1972	A
25	DA	1993	U
25	DA	1995	U
25	DA	1996	C
25	DA	1997	G
25	DA	2005	A
25	DA	2023	G
25	DA	2031	A
25	DA	2032	G
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
25	DA	2070	G
25	DA	2082	A
25	DA	2099	U
25	DA	2103	C
25	DA	2107	C
25	DA	2110	G
25	DA	2111	C
25	DA	2113	U
25	DA	2115	G
25	DA	2116	G
25	DA	2117	A
25	DA	2119	A
25	DA	2122	U
25	DA	2124	G
25	DA	2126	A
25	DA	2127	G
25	DA	2129	C

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Mol	Chain	Res	Type
25	DA	2132	U
25	DA	2133	G
25	DA	2134	A
25	DA	2135	A
25	DA	2136	C
25	DA	2137	C
25	DA	2141	G
25	DA	2142	C
25	DA	2145	C
25	DA	2146	C
25	DA	2148	G
25	DA	2153	G
25	DA	2154	G
25	DA	2156	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
25	DA	2172	U
25	DA	2173	A
25	DA	2175	C
25	DA	2176	A
25	DA	2177	C
25	DA	2178	C
25	DA	2180	U
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	2225	A
25	DA	2238	G
25	DA	2268	A

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Mol	Chain	Res	Type
25	DA	2272	U
25	DA	2275	C
25	DA	2279	G
25	DA	2283	C
25	DA	2287	A
25	DA	2289	G
25	DA	2302	G
25	DA	2303	G
25	DA	2305	A
25	DA	2308	G
25	DA	2312	U
25	DA	2318	G
25	DA	2319	G
25	DA	2320	A
25	DA	2325	G
25	DA	2327	A
25	DA	2334	G
25	DA	2336	A
25	DA	2343	C
25	DA	2347	C
25	DA	2350	C
25	DA	2354	G
25	DA	2355	C
25	DA	2376	A
25	DA	2383	G
25	DA	2385	C
25	DA	2393	A
25	DA	2406	U
25	DA	2410	G
25	DA	2414	G
25	DA	2422	A
25	DA	2423	U
25	DA	2425	A
25	DA	2428	G
25	DA	2429	G
25	DA	2430	A
25	DA	2431	U
25	DA	2434	A
25	DA	2435	A
25	DA	2439	A
25	DA	2441	C
25	DA	2448	A

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Mol	Chain	Res	Type
25	DA	2453	A
25	DA	2469	A
25	DA	2474	C
25	DA	2476	A
25	DA	2478	A
25	DA	2487	G
25	DA	2490	G
25	DA	2494	G
25	DA	2502	G
25	DA	2505	G
25	DA	2506	U
25	DA	2507	C
25	DA	2518	A
25	DA	2529	G
25	DA	2554	U
25	DA	2556	C
25	DA	2566	A
25	DA	2567	G
25	DA	2573	C
25	DA	2602	A
25	DA	2611	U
25	DA	2612	C
25	DA	2615	U
25	DA	2629	A
25	DA	2630	G
25	DA	2647	U
25	DA	2652	C
25	DA	2654	A
25	DA	2663	G
25	DA	2681	C
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	2726	U
25	DA	2733	A
25	DA	2744	G
25	DA	2748	A
25	DA	2751	G

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Mol	Chain	Res	Type
25	DA	2752	C
25	DA	2754	U
25	DA	2757	A
25	DA	2758	A
25	DA	2761	G
25	DA	2764	A
25	DA	2765	A
25	DA	2766	G
25	DA	2778	A
25	DA	2789	C
25	DA	2793	G
25	DA	2794	C
25	DA	2802	G
25	DA	2807	G
25	DA	2808	U
25	DA	2818	G
25	DA	2820	A
25	DA	2821	A
25	DA	2833	G
25	DA	2835	A
25	DA	2872	G
25	DA	2873	A
25	DA	2876	G
25	DA	2879	C
25	DA	2880	C
25	DA	2892	A
25	DA	2894	G
25	DA	2895	U
25	DA	2896	C
25	DA	2897	U
26	DB	2	C
26	DB	5	C
26	DB	7	G
26	DB	8	U
26	DB	15	A
26	DB	20	C
26	DB	25	A
26	DB	42	C
26	DB	56	G
26	DB	73	A
26	DB	75	G
26	DB	85	G

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Mol	Chain	Res	Type
26	DB	98	G
26	DB	106	G
26	DB	108	U
26	DB	110	G
26	DB	112	U

All (111) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	97	G
1	AA	115	G
1	AA	266	G
1	AA	429	U
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1036	G
1	AA	1065	U
1	AA	1067	A
1	AA	1190	G
1	AA	1201	A
1	AA	1285	A
1	AA	1299	A
1	AA	1442	G
1	AA	1492	A
23	AW	13	C
23	AW	22	G
24	AX	47	U
23	AY	44	G
25	BA	70	A
25	BA	184	A
25	BA	185	A
25	BA	270	C
25	BA	271	U
25	BA	273	G
25	BA	288	U
25	BA	302	A

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Mol	Chain	Res	Type
25	BA	732	A
25	BA	793	A
25	BA	795	G
25	BA	811	A
25	BA	1019	G
25	BA	1188	A
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1255	A
25	BA	1346	U
25	BA	1425	A
25	BA	1466	U
25	BA	1700	G
25	BA	1793	A
25	BA	2014	G
25	BA	2203	G
25	BA	2418	U
25	BA	2701	U
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	913	A
1	CA	991	U
1	CA	992	U
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1183	A
1	CA	1190	G
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1442	G
1	CA	1492	A

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Mol	Chain	Res	Type
23	CW	4	C
23	CW	13	C
23	CW	75	C
25	DA	195	A
25	DA	196	A
25	DA	228	A
25	DA	271(K)	U
25	DA	271(M)	G
25	DA	277	C
25	DA	587	C
25	DA	752	A
25	DA	764	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	1240	U
25	DA	1300	U
25	DA	1420	U
25	DA	1427	A
25	DA	1493	C
25	DA	1530	C
25	DA	1558	A
25	DA	1653	G
25	DA	1663	C
25	DA	1913	A
25	DA	1992	G
25	DA	2110	G
25	DA	2116	G
25	DA	2335	A
25	DA	2406	U
25	DA	2430	A
25	DA	2689	U
25	DA	2756	U

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

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	PSU	CY	55	23	17,21,22	1.50	3 (17%)	20,30,33	3.01	6 (30%)
23	MIA	AY	37	23	18,24,32	1.15	2 (11%)	18,35,47	1.23	2 (11%)
23	7MG	AW	46	23	22,26,27	1.80	4 (18%)	28,39,42	2.84	9 (32%)
24	5MC	AX	32	24	15,22,23	1.32	1 (6%)	19,32,35	1.40	3 (15%)
24	4SU	AX	8	24	14,21,22	1.46	2 (14%)	15,30,33	2.87	2 (13%)
23	5MU	CY	54	23	15,22,23	1.14	1 (6%)	16,32,35	2.10	1 (6%)
23	MIA	AW	37	23	24,31,32	2.28	3 (12%)	26,44,47	2.40	8 (30%)
24	PSU	AX	55	24	17,21,22	1.69	3 (17%)	20,30,33	3.19	6 (30%)
23	PSU	CY	32	23	17,21,22	1.39	2 (11%)	20,30,33	3.17	6 (30%)
23	7MG	CW	46	23	22,26,27	1.77	3 (13%)	28,39,42	2.75	8 (28%)
23	4SU	AY	8	23	14,21,22	1.20	1 (7%)	15,30,33	1.94	2 (13%)
23	PSU	AW	55	23	17,21,22	1.49	2 (11%)	20,30,33	3.34	6 (30%)
23	5MU	CW	54	23	15,22,23	1.08	1 (6%)	16,32,35	1.97	1 (6%)
23	4SU	CY	8	23	14,21,22	1.28	1 (7%)	15,30,33	1.54	2 (13%)
23	PSU	CY	39	23	17,21,22	1.65	3 (17%)	20,30,33	3.28	7 (35%)
24	5MC	CX	32	24	15,22,23	1.30	1 (6%)	19,32,35	1.53	4 (21%)
24	5MU	AX	54	24,56	15,22,23	1.13	2 (13%)	16,32,35	1.92	2 (12%)
23	PSU	CW	39	23	17,21,22	1.46	3 (17%)	20,30,33	3.52	6 (30%)
23	MIA	CW	37	23	18,24,32	1.07	2 (11%)	18,35,47	1.38	2 (11%)
23	7MG	AY	46	23	22,26,27	1.85	3 (13%)	28,39,42	2.92	10 (35%)
24	PSU	CX	55	24	17,21,22	1.36	2 (11%)	20,30,33	3.09	5 (25%)
23	PSU	AW	39	23	17,21,22	1.53	2 (11%)	20,30,33	3.07	6 (30%)
24	5MU	CX	54	24	15,22,23	1.14	1 (6%)	16,32,35	1.80	1 (6%)
23	4SU	AW	8	23	14,21,22	1.23	1 (7%)	15,30,33	1.73	2 (13%)
23	PSU	CW	32	23	17,21,22	1.43	3 (17%)	20,30,33	3.21	6 (30%)
23	PSU	AY	32	23	17,21,22	1.56	2 (11%)	20,30,33	3.16	6 (30%)
23	PSU	AY	39	23	17,21,22	1.53	3 (17%)	20,30,33	3.61	6 (30%)
23	PSU	CW	55	23	17,21,22	1.42	2 (11%)	20,30,33	3.24	6 (30%)
24	4SU	CX	8	24	14,21,22	1.25	2 (14%)	15,30,33	2.71	2 (13%)
23	5MU	AW	54	23	15,22,23	1.09	2 (13%)	16,32,35	2.25	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	5MU	AY	54	23	15,22,23	1.07	1 (6%)	16,32,35	2.40	1 (6%)
23	4SU	CW	8	56,23	14,21,22	1.24	1 (7%)	15,30,33	1.57	2 (13%)
23	7MG	CY	46	23	22,26,27	1.80	4 (18%)	28,39,42	2.86	10 (35%)
23	PSU	AW	32	56,23	17,21,22	1.52	3 (17%)	20,30,33	3.33	6 (30%)
23	PSU	AY	55	23	17,21,22	1.44	2 (11%)	20,30,33	3.13	6 (30%)
23	MIA	CY	37	23	18,24,32	1.16	2 (11%)	18,35,47	1.28	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	PSU	CY	55	23	-	2/7/25/26	0/2/2/2
23	MIA	AY	37	23	-	1/3/25/34	0/3/3/3
23	7MG	AW	46	23	-	3/7/37/38	0/3/3/3
24	5MC	AX	32	24	-	0/5/25/26	0/2/2/2
24	4SU	AX	8	24	-	0/5/25/26	0/2/2/2
23	5MU	CY	54	23	-	1/5/25/26	0/2/2/2
23	MIA	AW	37	23	-	1/11/33/34	0/3/3/3
24	PSU	AX	55	24	-	0/7/25/26	0/2/2/2
23	PSU	CY	32	23	-	1/7/25/26	0/2/2/2
23	7MG	CW	46	23	-	3/7/37/38	0/3/3/3
23	4SU	AY	8	23	-	1/5/25/26	0/2/2/2
23	PSU	AW	55	23	-	0/7/25/26	0/2/2/2
23	5MU	CW	54	23	-	0/5/25/26	0/2/2/2
23	4SU	CY	8	23	-	2/5/25/26	0/2/2/2
23	PSU	CY	39	23	-	2/7/25/26	0/2/2/2
24	5MC	CX	32	24	-	2/5/25/26	0/2/2/2
24	5MU	AX	54	24,56	-	0/5/25/26	0/2/2/2
23	PSU	CW	39	23	-	0/7/25/26	0/2/2/2
23	MIA	CW	37	23	-	0/3/25/34	0/3/3/3
23	7MG	AY	46	23	-	3/7/37/38	0/3/3/3
24	PSU	CX	55	24	-	0/7/25/26	0/2/2/2
23	PSU	AW	39	23	-	0/7/25/26	0/2/2/2
24	5MU	CX	54	24	-	0/5/25/26	0/2/2/2
23	4SU	AW	8	23	-	0/5/25/26	0/2/2/2
23	PSU	CW	32	23	-	2/7/25/26	0/2/2/2
23	PSU	AY	32	23	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	PSU	AY	39	23	-	3/7/25/26	0/2/2/2
23	PSU	CW	55	23	-	0/7/25/26	0/2/2/2
24	4SU	CX	8	24	-	0/5/25/26	0/2/2/2
23	5MU	AW	54	23	-	0/5/25/26	0/2/2/2
23	5MU	AY	54	23	-	0/5/25/26	0/2/2/2
23	4SU	CW	8	56,23	-	0/5/25/26	0/2/2/2
23	7MG	CY	46	23	-	2/7/37/38	0/3/3/3
23	PSU	AW	32	56,23	-	0/7/25/26	0/2/2/2
23	PSU	AY	55	23	-	1/7/25/26	0/2/2/2
23	MIA	CY	37	23	-	3/3/25/34	0/3/3/3

All (76) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C2-S10	-7.27	1.69	1.75
23	AW	37	MIA	C13-C14	7.14	1.52	1.32
23	AY	46	7MG	C5-C4	5.02	1.49	1.39
23	AW	46	7MG	C6-C5	5.02	1.48	1.41
24	AX	55	PSU	C5-C1'	-5.00	1.48	1.52
23	AY	46	7MG	C6-C5	4.99	1.48	1.41
23	CY	46	7MG	C6-C5	4.92	1.48	1.41
23	CW	46	7MG	C6-C5	4.91	1.48	1.41
24	AX	32	5MC	C5-C4	4.70	1.48	1.41
23	CY	46	7MG	C5-C4	4.63	1.48	1.39
23	AW	46	7MG	C5-C4	4.56	1.48	1.39
24	CX	32	5MC	C5-C4	4.55	1.48	1.41
23	CW	46	7MG	C5-C4	4.48	1.47	1.39
23	CY	39	PSU	C5-C1'	-4.30	1.48	1.52
23	AY	32	PSU	C5-C1'	-4.21	1.48	1.52
23	CW	32	PSU	C4-C5	4.18	1.50	1.41
23	AY	55	PSU	C5-C1'	-4.15	1.48	1.52
23	CY	8	4SU	C4-S4	-4.12	1.60	1.67
23	AW	39	PSU	C5-C1'	-3.93	1.48	1.52
23	AW	8	4SU	C4-S4	-3.87	1.60	1.67
23	AW	32	PSU	C5-C1'	-3.86	1.49	1.52
23	AW	55	PSU	C5-C1'	-3.85	1.49	1.52
23	CY	55	PSU	C5-C1'	-3.78	1.49	1.52
24	AX	8	4SU	C2-N3	-3.70	1.30	1.38
24	AX	8	4SU	C4-S4	-3.69	1.60	1.67
23	CW	8	4SU	C4-S4	-3.68	1.60	1.67
24	CX	55	PSU	C4-C5	3.64	1.49	1.41
23	AY	8	4SU	C4-S4	-3.60	1.60	1.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CX	54	5MU	C4-C5	3.58	1.49	1.41
23	CY	54	5MU	C4-C5	3.58	1.49	1.41
23	AW	32	PSU	C4-C5	3.58	1.49	1.41
23	AY	39	PSU	C5-C1'	-3.55	1.49	1.52
23	AY	32	PSU	C4-C5	3.55	1.49	1.41
23	CW	46	7MG	C5-N7	-3.52	1.33	1.39
23	CW	39	PSU	C5-C1'	-3.52	1.49	1.52
23	CW	55	PSU	C4-C5	3.52	1.49	1.41
24	CX	8	4SU	C4-S4	-3.51	1.61	1.67
23	CY	32	PSU	C4-C5	3.48	1.48	1.41
23	AY	54	5MU	C4-C5	3.45	1.48	1.41
23	CW	54	5MU	C4-C5	3.44	1.48	1.41
23	CW	55	PSU	C5-C1'	-3.42	1.49	1.52
23	CW	39	PSU	C4-C5	3.42	1.48	1.41
23	AW	46	7MG	C5-N7	-3.42	1.34	1.39
24	AX	54	5MU	C4-C5	3.38	1.48	1.41
23	AW	54	5MU	C4-C5	3.36	1.48	1.41
23	CY	39	PSU	C4-C5	3.35	1.48	1.41
23	CY	55	PSU	C4-C5	3.33	1.48	1.41
23	AW	55	PSU	C4-C5	3.28	1.48	1.41
23	CY	46	7MG	C5-N7	-3.28	1.34	1.39
23	AY	46	7MG	C5-N7	-3.27	1.34	1.39
23	AW	39	PSU	C4-C5	3.25	1.48	1.41
24	AX	55	PSU	C4-C5	3.22	1.48	1.41
23	AY	39	PSU	C4-C5	3.18	1.48	1.41
23	CY	32	PSU	C5-C1'	-3.17	1.49	1.52
23	CY	37	MIA	C5-C4	2.84	1.48	1.40
23	AY	55	PSU	C4-C5	2.84	1.47	1.41
23	AY	37	MIA	C5-C4	2.83	1.48	1.40
24	CX	8	4SU	C2-N3	-2.71	1.32	1.38
24	CX	55	PSU	C5-C1'	-2.70	1.49	1.52
23	AY	39	PSU	O4'-C1'	-2.67	1.40	1.44
23	CY	37	MIA	C2-N3	2.67	1.36	1.32
23	AY	37	MIA	C2-N3	2.66	1.36	1.32
23	CW	37	MIA	C2-N3	2.60	1.36	1.32
23	CW	37	MIA	C5-C4	2.51	1.47	1.40
23	CY	39	PSU	O4'-C1'	-2.48	1.40	1.44
23	AW	37	MIA	C5-C4	2.41	1.47	1.40
23	CW	32	PSU	C5-C1'	-2.40	1.50	1.52
23	CY	46	7MG	C4-N9	-2.37	1.33	1.38
23	AW	54	5MU	C2-N3	-2.14	1.33	1.38
23	CY	55	PSU	O4'-C1'	-2.14	1.41	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AX	54	5MU	C2-N3	-2.13	1.34	1.38
23	AW	32	PSU	C2-N3	-2.07	1.34	1.38
23	AW	46	7MG	C4-N9	-2.06	1.34	1.38
23	CW	39	PSU	O4'-C1'	-2.02	1.41	1.44
23	CW	32	PSU	C2-N3	-2.02	1.34	1.38
24	AX	55	PSU	O4'-C1'	-2.01	1.41	1.44

All (161) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CW	39	PSU	N1-C2-N3	-9.98	120.50	128.43
23	AY	39	PSU	N1-C2-N3	-9.84	120.61	128.43
24	AX	8	4SU	C2-N3-C4	9.74	129.28	115.15
23	AY	46	7MG	N3-C4-N9	9.48	139.09	126.91
23	AW	46	7MG	N3-C4-N9	9.38	138.96	126.91
23	AY	54	5MU	C4-N3-C2	9.24	122.94	115.14
23	CW	46	7MG	N3-C4-N9	9.15	138.66	126.91
23	CW	32	PSU	N1-C2-N3	-9.09	121.21	128.43
24	CX	55	PSU	N1-C2-N3	-9.04	121.24	128.43
23	AY	39	PSU	C4-N3-C2	9.03	122.76	115.14
23	AW	32	PSU	N1-C2-N3	-8.95	121.31	128.43
23	CY	46	7MG	N3-C4-N9	8.93	138.38	126.91
24	CX	8	4SU	C2-N3-C4	8.89	128.04	115.15
23	CY	32	PSU	N1-C2-N3	-8.81	121.42	128.43
23	AY	55	PSU	N1-C2-N3	-8.66	121.55	128.43
23	AW	54	5MU	C4-N3-C2	8.55	122.36	115.14
23	AW	39	PSU	N1-C2-N3	-8.54	121.64	128.43
24	AX	55	PSU	N1-C2-N3	-8.53	121.65	128.43
23	CY	39	PSU	N1-C2-N3	-8.49	121.68	128.43
23	CW	39	PSU	C4-N3-C2	8.46	122.28	115.14
23	AW	55	PSU	N1-C2-N3	-8.41	121.75	128.43
23	CY	55	PSU	N1-C2-N3	-8.14	121.96	128.43
23	AY	32	PSU	N1-C2-N3	-8.14	121.96	128.43
23	CW	55	PSU	N1-C2-N3	-7.90	122.15	128.43
23	CY	54	5MU	C4-N3-C2	7.87	121.79	115.14
23	AW	37	MIA	C12-C13-C14	-7.69	112.17	127.14
23	CY	39	PSU	C4-N3-C2	7.65	121.60	115.14
23	CW	54	5MU	C4-N3-C2	7.48	121.46	115.14
23	AW	32	PSU	C4-N3-C2	7.48	121.46	115.14
23	CY	32	PSU	C4-N3-C2	7.20	121.22	115.14
23	CW	32	PSU	C4-N3-C2	7.14	121.17	115.14
24	AX	55	PSU	C4-N3-C2	6.86	120.93	115.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	54	5MU	C4-N3-C2	6.81	120.89	115.14
23	AW	55	PSU	C4-N3-C2	6.73	120.82	115.14
23	CW	55	PSU	C4-N3-C2	6.71	120.81	115.14
23	CY	55	PSU	C4-N3-C2	6.68	120.78	115.14
24	CX	54	5MU	C4-N3-C2	6.65	120.76	115.14
23	AW	39	PSU	C4-N3-C2	6.56	120.68	115.14
23	AY	55	PSU	C4-N3-C2	6.42	120.56	115.14
23	AY	32	PSU	C4-N3-C2	6.38	120.53	115.14
24	CX	55	PSU	C4-N3-C2	6.17	120.35	115.14
23	AY	8	4SU	C2-N3-C4	6.06	123.94	115.15
23	CY	39	PSU	C5-C4-N3	-6.01	117.61	125.36
23	AW	55	PSU	C5-C1'-C2'	-5.86	104.87	115.32
23	AY	39	PSU	C5-C4-N3	-5.77	117.92	125.36
24	AX	55	PSU	C5-C4-N3	-5.76	117.94	125.36
23	CW	46	7MG	C5-C4-N3	-5.70	117.19	126.49
23	CW	39	PSU	C5-C4-N3	-5.57	118.19	125.36
23	AW	8	4SU	C2-N3-C4	5.56	123.21	115.15
23	CW	55	PSU	C5-C4-N3	-5.50	118.28	125.36
23	CY	55	PSU	C5-C4-N3	-5.44	118.35	125.36
23	AY	46	7MG	C6-N1-C2	5.40	124.50	115.93
23	AW	32	PSU	C5-C4-N3	-5.35	118.47	125.36
23	CY	32	PSU	C5-C4-N3	-5.33	118.49	125.36
23	CW	55	PSU	C5-C1'-C2'	-5.30	105.86	115.32
23	AY	32	PSU	C5-C4-N3	-5.27	118.57	125.36
23	CY	46	7MG	C6-N1-C2	5.26	124.29	115.93
23	AY	55	PSU	C5-C4-N3	-5.24	118.61	125.36
23	AW	46	7MG	N7-C8-N9	-5.22	95.92	103.38
23	AW	46	7MG	C5-C4-N3	-5.19	118.01	126.49
23	CY	46	7MG	N7-C8-N9	-5.19	95.96	103.38
23	AY	46	7MG	C5-C4-N3	-5.17	118.04	126.49
23	AW	55	PSU	C5-C4-N3	-5.08	118.82	125.36
23	AW	39	PSU	C5-C4-N3	-5.05	118.86	125.36
24	CX	8	4SU	C5-C4-N3	-4.98	117.16	123.83
23	CW	32	PSU	C5-C4-N3	-4.97	118.95	125.36
23	CY	46	7MG	C5-C4-N3	-4.88	118.53	126.49
23	CW	46	7MG	N7-C8-N9	-4.85	96.45	103.38
24	AX	8	4SU	C5-C4-N3	-4.84	117.35	123.83
23	AW	46	7MG	C6-N1-C2	4.71	123.41	115.93
23	AY	46	7MG	N7-C8-N9	-4.67	96.71	103.38
23	AY	32	PSU	C5-C1'-C2'	-4.61	107.09	115.32
24	CX	55	PSU	C6-N1-C2	4.58	122.92	115.36
23	CY	8	4SU	C2-N3-C4	4.49	121.66	115.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AY	55	PSU	C5-C6-N1	-4.48	118.94	124.44
24	CX	55	PSU	C5-C6-N1	-4.46	118.96	124.44
23	CW	46	7MG	C6-C5-C4	4.46	119.99	115.20
23	CW	8	4SU	C2-N3-C4	4.45	121.60	115.15
23	AY	46	7MG	C6-C5-C4	4.39	119.92	115.20
23	AW	46	7MG	C6-C5-C4	4.35	119.87	115.20
24	CX	55	PSU	C5-C4-N3	-4.26	119.87	125.36
23	AY	39	PSU	O4'-C1'-C5	-4.26	103.34	109.93
23	AY	32	PSU	C5-C6-N1	-4.24	119.22	124.44
23	AW	37	MIA	C15-C14-C13	-4.22	110.44	122.65
23	AW	32	PSU	C5-C1'-C2'	-4.22	107.79	115.32
24	AX	55	PSU	C5-C6-N1	-4.21	119.26	124.44
23	CW	32	PSU	C6-N1-C2	4.19	122.28	115.36
23	AW	39	PSU	C6-N1-C2	4.19	122.27	115.36
23	CW	39	PSU	C6-N1-C2	4.16	122.22	115.36
23	AW	39	PSU	C5-C6-N1	-4.14	119.36	124.44
23	AW	37	MIA	C5-C6-N1	-4.11	117.40	120.81
23	AY	55	PSU	C6-N1-C2	4.10	122.13	115.36
23	AY	46	7MG	C5-C6-N1	-4.10	114.72	123.14
23	AW	37	MIA	C16-C14-C13	-4.10	110.80	122.65
24	AX	55	PSU	C6-N1-C2	4.10	122.12	115.36
23	CW	55	PSU	C5-C6-N1	-4.09	119.42	124.44
23	AY	32	PSU	C6-N1-C2	4.05	122.04	115.36
23	AW	32	PSU	C6-N1-C2	4.03	122.02	115.36
23	AW	55	PSU	C6-N1-C2	4.00	121.97	115.36
23	CY	46	7MG	C5-C6-N1	-4.00	114.93	123.14
23	CY	32	PSU	C6-N1-C2	3.98	121.93	115.36
23	AW	55	PSU	C5-C6-N1	-3.95	119.58	124.44
23	CY	46	7MG	C6-C5-C4	3.93	119.41	115.20
23	AW	37	MIA	C2-N3-C4	3.92	120.73	115.32
23	CW	37	MIA	N3-C2-N1	-3.92	122.55	128.68
23	AY	8	4SU	C5-C4-N3	-3.91	118.60	123.83
23	CW	55	PSU	C6-N1-C2	3.86	121.72	115.36
23	CY	55	PSU	C6-N1-C2	3.84	121.69	115.36
23	CW	46	7MG	C6-N1-C2	3.83	122.02	115.93
23	AW	46	7MG	C5-C6-N1	-3.79	115.35	123.14
23	CY	32	PSU	C5-C6-N1	-3.75	119.83	124.44
23	AW	32	PSU	C5-C6-N1	-3.74	119.84	124.44
23	CW	39	PSU	C5-C6-N1	-3.68	119.91	124.44
24	CX	32	5MC	C2-N3-C4	3.67	120.44	116.02
23	CY	55	PSU	C5-C6-N1	-3.61	120.00	124.44
23	CY	39	PSU	C6-N1-C2	3.60	121.30	115.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AY	39	PSU	C6-N1-C2	3.57	121.24	115.36
23	AY	37	MIA	N3-C2-N1	-3.44	123.30	128.68
23	CY	37	MIA	N3-C2-N1	-3.43	123.32	128.68
23	CW	46	7MG	C5-C6-N1	-3.39	116.17	123.14
23	CW	8	4SU	C5-C4-N3	-3.38	119.31	123.83
23	CY	39	PSU	C5-C6-N1	-3.31	120.37	124.44
23	CW	32	PSU	C5-C6-N1	-3.20	120.51	124.44
23	AW	8	4SU	C5-C4-N3	-3.12	119.65	123.83
24	AX	32	5MC	C2-N3-C4	3.06	119.71	116.02
24	AX	32	5MC	C5-C6-N1	-2.96	119.00	122.19
23	CW	32	PSU	C4-C5-C1'	2.95	126.67	121.12
24	AX	55	PSU	C5-C1'-C2'	-2.94	110.08	115.32
23	CY	39	PSU	C5-C1'-C2'	-2.90	110.15	115.32
23	CY	39	PSU	O4'-C1'-C5	-2.89	105.46	109.93
24	AX	32	5MC	N4-C4-N3	2.87	121.09	117.03
23	AW	37	MIA	C2-N1-C6	2.87	122.32	117.19
23	CW	37	MIA	C4-C5-N7	-2.83	106.45	109.40
24	AX	54	5MU	C5-C6-N1	-2.78	119.20	122.19
24	CX	32	5MC	CM5-C5-C4	-2.70	118.99	121.72
23	AY	39	PSU	C5-C6-N1	-2.67	121.15	124.44
23	CW	46	7MG	C8-N7-C5	2.67	115.89	108.94
24	CX	32	5MC	N4-C4-N3	2.66	120.79	117.03
23	AW	46	7MG	C8-N7-C5	2.64	115.81	108.94
23	CY	8	4SU	C5-C4-N3	-2.63	120.30	123.83
23	AY	46	7MG	C5-C4-N9	-2.56	102.86	106.44
23	CY	46	7MG	C8-N7-C5	2.55	115.58	108.94
23	CY	46	7MG	O4'-C1'-N9	-2.53	105.93	109.35
23	CW	39	PSU	C5-C1'-C2'	-2.50	110.86	115.32
23	AY	46	7MG	C8-N7-C5	2.46	115.33	108.94
24	CX	32	5MC	C5-C6-N1	-2.44	119.57	122.19
23	AW	46	7MG	C5-C4-N9	-2.44	103.03	106.44
23	CY	46	7MG	C5-C4-N9	-2.41	103.06	106.44
23	AY	37	MIA	C4-C5-N7	-2.41	106.89	109.40
23	CW	46	7MG	C2-N3-C4	2.39	120.50	113.89
23	CY	37	MIA	C4-C5-N7	-2.30	107.00	109.40
23	CY	55	PSU	C5-C1'-C2'	-2.29	111.24	115.32
23	CY	32	PSU	C5-C1'-C2'	-2.26	111.28	115.32
23	AW	37	MIA	N3-C2-N1	-2.24	122.87	126.98
23	AW	39	PSU	C5-C1'-C2'	-2.21	111.37	115.32
23	CY	46	7MG	C2-N3-C4	2.16	119.87	113.89
23	AW	46	7MG	C2-N3-C4	2.14	119.80	113.89
23	AW	37	MIA	C4-C5-N7	-2.14	107.17	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AY	55	PSU	O4'-C1'-C2'	2.08	108.03	104.66
23	AY	46	7MG	C2-N3-C4	2.06	119.58	113.89
23	AY	46	7MG	CM7-N7-C5	2.03	131.81	124.01

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	CY	54	5MU	C2'-C1'-N1-C6
23	AW	37	MIA	C12-C13-C14-C16
23	AY	8	4SU	C2'-C1'-N1-C6
23	CY	8	4SU	O4'-C4'-C5'-O5'
23	CY	39	PSU	C3'-C4'-C5'-O5'
24	CX	32	5MC	O4'-C1'-N1-C6
24	CX	32	5MC	C2'-C1'-N1-C6
23	AY	46	7MG	C4'-C5'-O5'-P
23	CW	32	PSU	C2'-C1'-C5-C4
23	CW	32	PSU	C2'-C1'-C5-C6
23	AY	39	PSU	C3'-C4'-C5'-O5'
23	CY	37	MIA	C3'-C4'-C5'-O5'
23	CY	46	7MG	O4'-C4'-C5'-O5'
23	CY	39	PSU	O4'-C4'-C5'-O5'
23	AY	39	PSU	O4'-C4'-C5'-O5'
23	CY	46	7MG	C3'-C4'-C5'-O5'
23	CY	37	MIA	O4'-C4'-C5'-O5'
23	AY	55	PSU	O4'-C1'-C5-C4
23	CW	46	7MG	C2'-C1'-N9-C8
23	AY	46	7MG	C2'-C1'-N9-C8
23	CY	55	PSU	C3'-C4'-C5'-O5'
23	AW	46	7MG	C3'-C4'-C5'-O5'
23	AY	37	MIA	C4'-C5'-O5'-P
23	AW	46	7MG	O4'-C4'-C5'-O5'
23	CY	37	MIA	C4'-C5'-O5'-P
23	CY	55	PSU	O4'-C1'-C5-C4
23	AY	39	PSU	C2'-C1'-C5-C6
23	CY	32	PSU	O4'-C4'-C5'-O5'
23	CW	46	7MG	C2'-C1'-N9-C4
23	AY	46	7MG	O4'-C1'-N9-C8
23	CY	8	4SU	C3'-C4'-C5'-O5'
23	CW	46	7MG	O4'-C1'-N9-C8
23	AW	46	7MG	C4'-C5'-O5'-P

There are no ring outliers.

19 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	AX	8	4SU	2	0
23	AW	37	MIA	1	0
23	CW	46	7MG	5	0
23	AY	8	4SU	1	0
23	AW	55	PSU	1	0
23	CY	8	4SU	4	0
23	CY	39	PSU	2	0
23	CW	39	PSU	2	0
23	AY	46	7MG	1	0
23	AW	8	4SU	1	0
23	CW	32	PSU	1	0
24	CX	8	4SU	1	0
23	AW	54	5MU	1	0
23	AY	54	5MU	2	0
23	CW	8	4SU	1	0
23	CY	46	7MG	1	0
23	AW	32	PSU	1	0
23	AY	55	PSU	3	0
23	CY	37	MIA	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2152 ligands modelled in this entry, 2148 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	PCY	AA	3231	-	36,42,42	1.68	5 (13%)	41,65,65	1.42	8 (19%)
57	PCY	CA	3178	-	36,42,42	1.63	4 (11%)	41,65,65	1.17	4 (9%)

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	-	-		
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
57	PCY	AA	3231	-	-	5/33/67/67	0/3/3/3
57	PCY	CA	3178	-	-	9/33/67/67	0/3/3/3
58	SF4	CD	501	4	-	-	0/6/5/5
58	SF4	AD	501	4	-	-	0/6/5/5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	CA	3178	PCY	C28-C32	-5.59	1.39	1.49
57	AA	3231	PCY	C28-C32	-5.44	1.39	1.49
57	AA	3231	PCY	C34-C30	-5.24	1.40	1.51
57	CA	3178	PCY	C34-C30	-5.21	1.40	1.51
57	AA	3231	PCY	C27-C23	-4.06	1.40	1.50
57	CA	3178	PCY	C27-C23	-3.63	1.41	1.50
57	CA	3178	PCY	C22-N20	-3.21	1.33	1.39
57	AA	3231	PCY	C22-N20	-2.92	1.34	1.39
57	AA	3231	PCY	C17-N20	2.26	1.48	1.45

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	AA	3231	PCY	C18-O21-C23	-4.75	107.00	116.57
57	CA	3178	PCY	C18-O21-C23	-3.62	109.27	116.57
57	AA	3231	PCY	O21-C23-C27	3.01	119.12	112.33
57	AA	3231	PCY	O21-C18-C15	2.78	112.92	107.79
57	AA	3231	PCY	O36-C31-C27	-2.26	116.91	121.14
57	AA	3231	PCY	C34-C30-C35	-2.17	116.08	120.31
57	AA	3231	PCY	C30-C27-C23	2.15	126.64	120.47
57	AA	3231	PCY	C34-C30-C27	2.14	124.53	121.67
57	CA	3178	PCY	C10-N4-C9	2.12	122.35	115.77
57	AA	3231	PCY	C10-N4-C9	2.08	122.22	115.77
57	CA	3178	PCY	C34-C30-C35	-2.04	116.32	120.31
57	CA	3178	PCY	C38-C32-C28	-2.03	115.07	119.24

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	AA	3231	PCY	N2-C3-C6-C11
57	AA	3231	PCY	C7-C3-C6-C11
57	AA	3231	PCY	C7-C15-C18-O21
57	AA	3231	PCY	C17-C15-C18-O21
57	AA	3231	PCY	O19-C15-C18-O21
57	CA	3178	PCY	N2-C3-C6-C11
57	CA	3178	PCY	N2-C3-C6-O12
57	CA	3178	PCY	C7-C3-C6-C11
57	CA	3178	PCY	C7-C3-C6-O12
57	CA	3178	PCY	O26-C23-C27-C30
57	CA	3178	PCY	O21-C23-C27-C30
57	CA	3178	PCY	O26-C23-C27-C31
57	CA	3178	PCY	O21-C23-C27-C31
57	CA	3178	PCY	C8-C3-C6-C11

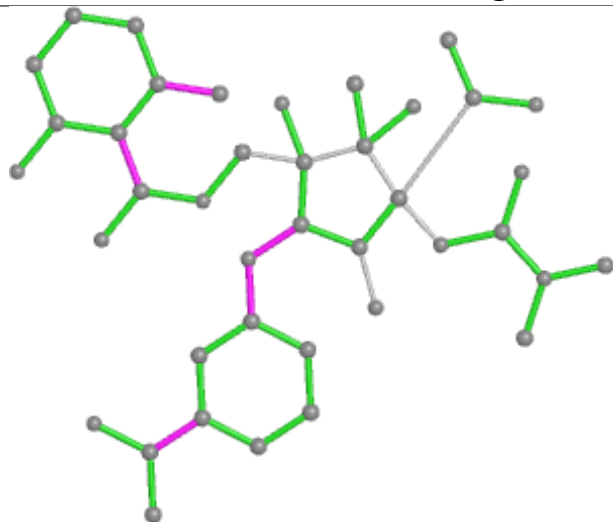
There are no ring outliers.

2 monomers are involved in 16 short contacts:

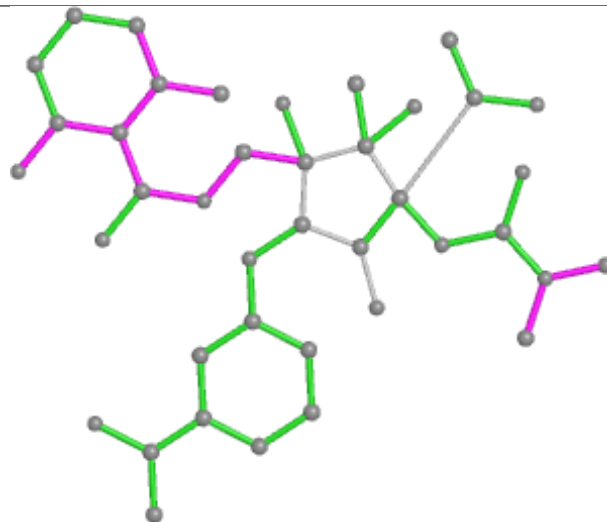
Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	AA	3231	PCY	7	0
57	CA	3178	PCY	9	0

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.

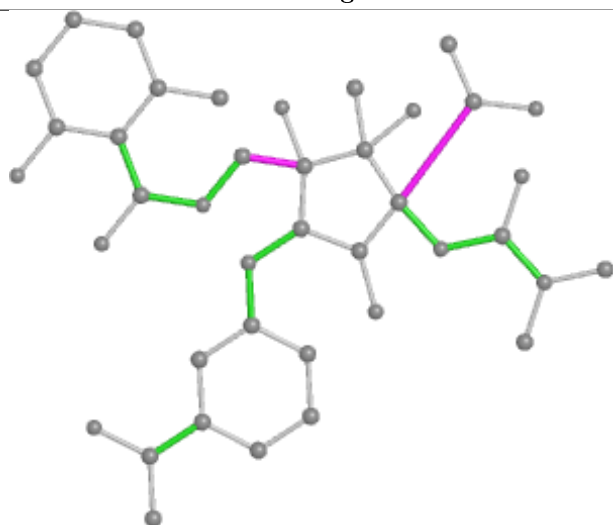
Ligand PCY AA 3231



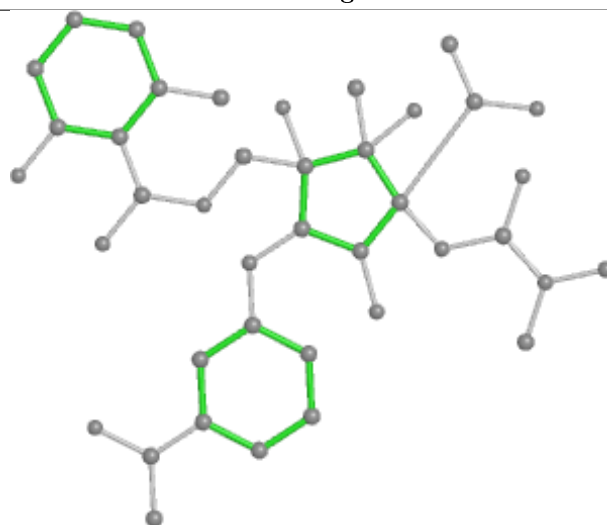
Bond lengths



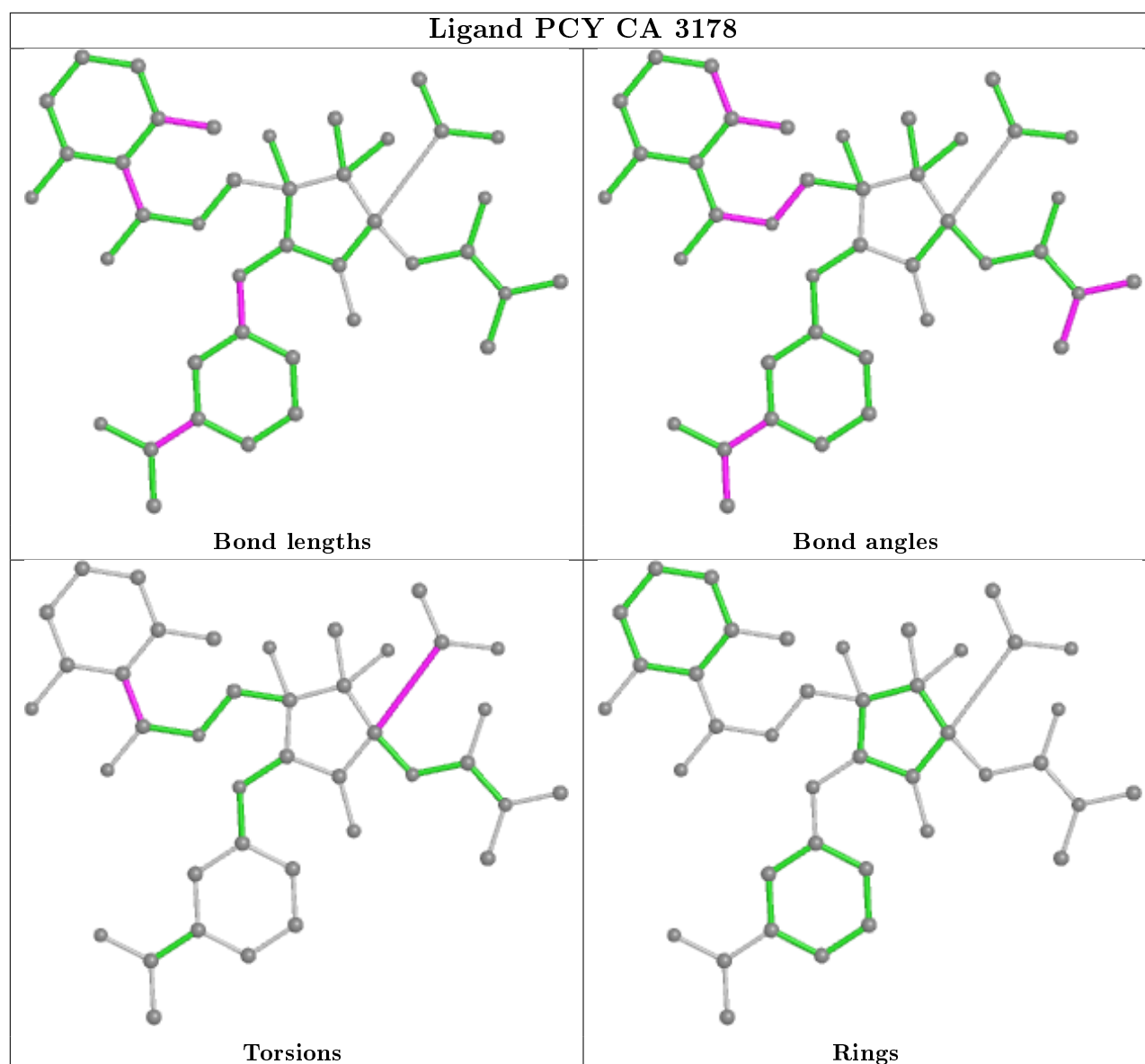
Bond angles



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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1498/1521 (98%)	0.22	56 (3%) 41 48	40, 67, 92, 106	0
1	CA	1503/1521 (98%)	0.11	52 (3%) 44 51	43, 69, 92, 106	0
2	AB	231/256 (90%)	1.20	44 (19%) 1 1	63, 80, 90, 94	0
2	CB	231/256 (90%)	1.47	68 (29%) 0 0	64, 82, 89, 96	0
3	AC	206/239 (86%)	1.09	30 (14%) 2 3	61, 74, 84, 92	0
3	CC	206/239 (86%)	1.76	83 (40%) 0 0	64, 76, 86, 92	0
4	AD	208/209 (99%)	0.47	6 (2%) 51 59	56, 68, 79, 87	0
4	CD	208/209 (99%)	1.06	29 (13%) 2 3	57, 68, 78, 87	0
5	AE	148/162 (91%)	0.78	9 (6%) 21 25	56, 67, 77, 91	0
5	CE	148/162 (91%)	0.89	17 (11%) 4 6	57, 69, 79, 92	0
6	AF	100/101 (99%)	0.40	1 (1%) 82 86	53, 66, 76, 82	0
6	CF	100/101 (99%)	0.30	1 (1%) 82 86	54, 66, 76, 82	0
7	AG	155/156 (99%)	0.86	16 (10%) 6 8	61, 71, 83, 93	0
7	CG	155/156 (99%)	0.94	15 (9%) 7 9	62, 73, 84, 96	0
8	AH	137/138 (99%)	0.81	12 (8%) 10 11	57, 69, 75, 83	0
8	CH	137/138 (99%)	1.05	19 (13%) 2 3	59, 71, 77, 84	0
9	AI	127/128 (99%)	1.50	33 (25%) 0 0	56, 78, 85, 90	0
9	CI	127/128 (99%)	2.04	57 (44%) 0 0	62, 79, 86, 89	0
10	AJ	97/105 (92%)	1.46	29 (29%) 0 0	57, 78, 90, 91	0
10	CJ	96/105 (91%)	1.85	39 (40%) 0 0	60, 80, 91, 93	0
11	AK	114/129 (88%)	0.88	9 (7%) 12 16	47, 67, 80, 83	0
11	CK	114/129 (88%)	0.39	2 (1%) 68 74	47, 67, 79, 83	0
12	AL	122/132 (92%)	0.52	2 (1%) 72 78	42, 56, 69, 75	0
12	CL	122/132 (92%)	0.94	16 (13%) 3 4	45, 58, 71, 75	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	123/126 (97%)	0.57	6 (4%) 29 35	42, 63, 75, 80	0
13	CM	122/126 (96%)	1.59	42 (34%) 0 0	66, 79, 86, 90	0
14	AN	60/61 (98%)	1.13	8 (13%) 3 4	60, 70, 77, 81	0
14	CN	60/61 (98%)	2.77	43 (71%) 0 0	64, 73, 80, 83	0
15	AO	88/89 (98%)	0.34	2 (2%) 60 67	50, 66, 76, 82	0
15	CO	88/89 (98%)	0.56	2 (2%) 60 67	53, 68, 77, 82	0
16	AP	82/88 (93%)	1.03	11 (13%) 3 4	52, 68, 76, 80	0
16	CP	82/88 (93%)	1.08	12 (14%) 2 3	51, 68, 76, 79	0
17	AQ	99/105 (94%)	0.66	4 (4%) 38 45	55, 68, 77, 79	0
17	CQ	99/105 (94%)	1.53	32 (32%) 0 0	57, 69, 77, 80	0
18	AR	68/88 (77%)	0.80	5 (7%) 14 18	58, 66, 76, 80	0
18	CR	68/88 (77%)	0.53	3 (4%) 34 41	59, 68, 77, 80	0
19	AS	83/93 (89%)	0.81	4 (4%) 30 37	63, 73, 81, 91	0
19	CS	83/93 (89%)	1.99	38 (45%) 0 0	66, 76, 84, 92	0
20	AT	96/106 (90%)	1.72	38 (39%) 0 0	57, 68, 80, 86	0
20	CT	96/106 (90%)	1.69	39 (40%) 0 0	58, 68, 82, 87	0
21	AU	23/27 (85%)	1.29	4 (17%) 1 1	63, 66, 72, 75	0
21	CU	23/27 (85%)	1.58	9 (39%) 0 0	65, 68, 74, 77	0
22	AV	13/24 (54%)	0.99	1 (7%) 13 17	52, 64, 82, 98	0
22	CV	13/24 (54%)	0.49	2 (15%) 2 2	56, 67, 85, 99	0
23	AW	67/76 (88%)	1.00	7 (10%) 6 8	47, 84, 97, 104	0
23	AY	67/76 (88%)	1.04	10 (14%) 2 2	38, 97, 101, 104	0
23	CW	65/76 (85%)	0.97	11 (16%) 1 1	68, 91, 102, 104	0
23	CY	66/76 (86%)	1.54	26 (39%) 0 0	43, 97, 101, 104	0
24	AX	72/77 (93%)	0.57	2 (2%) 53 60	39, 68, 85, 93	0
24	CX	72/77 (93%)	-0.04	0 100 100	43, 71, 86, 94	0
25	BA	2819/2915 (96%)	0.43	64 (2%) 60 67	23, 42, 88, 104	0
25	DA	2800/2915 (96%)	-0.09	84 (3%) 50 57	27, 47, 89, 108	0
26	BB	120/121 (99%)	-0.04	0 100 100	35, 56, 70, 86	0
26	DB	120/121 (99%)	-0.03	0 100 100	42, 62, 73, 87	0
27	BD	275/276 (99%)	0.72	3 (1%) 80 85	23, 40, 55, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
27	DD	275/276 (99%)	0.40	3 (1%) 80 85	26, 42, 56, 77	0
28	BE	204/206 (99%)	0.67	3 (1%) 73 79	22, 47, 66, 76	0
28	DE	204/206 (99%)	0.21	3 (1%) 73 79	28, 50, 67, 77	0
29	BF	203/210 (96%)	0.72	12 (5%) 22 26	23, 49, 73, 88	0
29	DF	203/210 (96%)	0.81	25 (12%) 4 5	27, 55, 75, 88	0
30	BG	181/182 (99%)	0.50	10 (5%) 25 30	44, 64, 78, 90	0
30	DG	181/182 (99%)	1.27	41 (22%) 0 0	50, 67, 80, 90	0
31	BH	174/180 (96%)	0.43	3 (1%) 70 76	51, 65, 76, 85	0
31	DH	174/180 (96%)	2.63	106 (60%) 0 0	57, 70, 80, 86	0
32	BI	146/148 (98%)	0.90	16 (10%) 5 7	50, 71, 82, 86	0
32	DI	146/148 (98%)	0.48	8 (5%) 25 30	53, 71, 82, 85	0
33	BN	140/140 (100%)	0.53	1 (0%) 87 90	32, 47, 68, 75	0
33	DN	140/140 (100%)	0.65	6 (4%) 35 42	36, 52, 70, 77	0
34	BO	122/122 (100%)	0.35	0 100 100	25, 38, 59, 65	0
34	DO	122/122 (100%)	0.49	0 100 100	47, 59, 74, 79	0
35	BP	149/150 (99%)	0.46	1 (0%) 87 90	24, 55, 74, 81	0
35	DP	149/150 (99%)	0.87	24 (16%) 1 2	29, 59, 76, 82	0
36	BQ	141/141 (100%)	0.77	3 (2%) 63 70	31, 50, 66, 77	0
36	DQ	141/141 (100%)	0.85	18 (12%) 3 4	38, 54, 69, 80	0
37	BR	118/118 (100%)	0.28	0 100 100	21, 32, 50, 58	0
37	DR	118/118 (100%)	0.24	0 100 100	38, 53, 64, 74	0
38	BS	110/112 (98%)	0.44	1 (0%) 84 88	32, 48, 64, 67	0
38	DS	110/112 (98%)	1.47	29 (26%) 0 0	58, 69, 80, 85	0
39	BT	131/146 (89%)	0.20	1 (0%) 86 89	31, 42, 68, 89	0
39	DT	131/146 (89%)	0.29	1 (0%) 86 89	51, 64, 78, 84	0
40	BU	116/118 (98%)	0.26	0 100 100	17, 28, 47, 65	0
40	DU	116/118 (98%)	0.55	7 (6%) 21 25	40, 62, 76, 82	0
41	BV	101/101 (100%)	0.15	0 100 100	15, 35, 54, 67	0
41	DV	101/101 (100%)	1.02	17 (16%) 1 1	39, 74, 81, 88	0
42	BW	112/113 (99%)	0.32	1 (0%) 84 88	17, 28, 53, 79	0
42	DW	112/113 (99%)	0.55	1 (0%) 84 88	38, 51, 68, 86	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
43	BX	95/96 (98%)	0.32	1 (1%) 80 85	21, 35, 60, 75	0
43	DX	95/96 (98%)	0.99	11 (11%) 4 6	38, 56, 76, 85	0
44	BY	107/110 (97%)	0.20	2 (1%) 66 73	30, 46, 65, 83	0
44	DY	107/110 (97%)	1.34	28 (26%) 0 0	57, 71, 83, 86	0
45	BZ	171/206 (83%)	1.66	43 (25%) 0 0	35, 67, 94, 105	0
45	DZ	174/206 (84%)	2.79	87 (50%) 0 0	65, 83, 97, 103	0
46	B0	83/85 (97%)	0.42	4 (4%) 30 37	20, 36, 57, 76	0
46	D0	83/85 (97%)	1.09	12 (14%) 2 3	44, 64, 74, 79	0
47	B1	97/98 (98%)	0.49	3 (3%) 49 56	24, 45, 70, 73	0
47	D1	97/98 (98%)	0.68	5 (5%) 27 32	37, 56, 75, 86	0
48	B2	70/72 (97%)	0.46	1 (1%) 75 81	30, 45, 58, 78	0
48	D2	70/72 (97%)	0.58	2 (2%) 51 59	53, 66, 78, 82	0
49	B3	59/60 (98%)	0.18	0 100 100	19, 31, 58, 75	0
49	D3	59/60 (98%)	0.85	7 (11%) 4 5	54, 66, 78, 88	0
50	B4	69/71 (97%)	0.60	8 (11%) 4 6	51, 70, 89, 99	0
50	D4	69/71 (97%)	2.02	33 (47%) 0 0	72, 82, 92, 93	0
51	B5	59/60 (98%)	0.36	1 (1%) 70 76	17, 27, 43, 54	0
51	D5	59/60 (98%)	0.38	1 (1%) 70 76	35, 50, 66, 74	0
52	B6	53/54 (98%)	0.18	0 100 100	28, 39, 56, 67	0
52	D6	53/54 (98%)	0.70	4 (7%) 14 17	48, 59, 71, 76	0
53	B7	48/49 (97%)	0.62	2 (4%) 36 42	18, 26, 62, 72	0
53	D7	48/49 (97%)	0.90	3 (6%) 20 23	30, 41, 61, 78	0
54	B8	64/65 (98%)	0.19	0 100 100	19, 31, 40, 63	0
54	D8	64/65 (98%)	0.77	2 (3%) 49 56	44, 54, 65, 71	0
55	B9	37/37 (100%)	0.61	1 (2%) 54 61	26, 47, 63, 70	0
55	D9	37/37 (100%)	1.30	7 (18%) 1 1	45, 57, 68, 75	0
All	All	20900/21748 (96%)	0.58	1766 (8%) 11 13	15, 61, 87, 108	0

All (1766) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	BZ	108	PRO	15.6
45	DZ	116	VAL	13.2

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Mol	Chain	Res	Type	RSRZ
45	DZ	115	GLY	12.4
45	DZ	107	THR	11.0
45	DZ	114	GLY	11.0
45	BZ	111	VAL	11.0
45	DZ	144	LEU	10.8
7	CG	82	GLY	10.8
45	DZ	108	PRO	10.4
45	BZ	115	GLY	9.8
45	DZ	113	ALA	9.6
45	DZ	171	ILE	9.0
45	BZ	114	GLY	8.9
45	BZ	113	ALA	8.9
45	DZ	112	ARG	8.7
25	DA	888	C	8.6
45	BZ	116	VAL	8.5
25	BA	942	A	8.4
45	DZ	155	LEU	8.3
25	DA	883	G	8.2
25	DA	896	A	8.0
23	AW	71	G	8.0
45	DZ	149	SER	7.9
45	DZ	147	GLY	7.9
25	DA	229	A	7.7
25	BA	931	C	7.7
1	CA	1030(B)	C	7.6
45	DZ	141	VAL	7.5
45	DZ	170	THR	7.5
50	D4	49	PHE	7.4
43	DX	92	LEU	7.3
25	DA	2802	G	7.3
13	AM	124	PRO	7.3
1	AA	1030(B)	C	7.3
31	DH	48	GLY	7.3
25	DA	884	C	7.3
3	CC	198	VAL	7.2
14	CN	39	LEU	7.2
45	BZ	106	GLY	7.1
7	AG	79	ARG	7.1
45	BZ	141	VAL	7.0
13	CM	124	PRO	7.0
13	CM	123	ALA	6.9
44	DY	1	MET	6.8

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Mol	Chain	Res	Type	RSRZ
36	DQ	109	VAL	6.7
25	BA	932	C	6.7
10	CJ	10	GLY	6.7
14	CN	37	PHE	6.6
23	CY	36	A	6.6
10	CJ	47	PHE	6.5
23	AW	20	U	6.5
45	DZ	111	VAL	6.5
45	BZ	112	ARG	6.4
10	CJ	85	LEU	6.4
45	BZ	143	GLY	6.4
23	AY	36	A	6.4
31	DH	76	VAL	6.3
25	BA	934	A	6.3
1	AA	1532	U	6.3
45	DZ	156	LYS	6.3
31	DH	82	GLY	6.2
9	CI	8	GLY	6.2
45	DZ	139	VAL	6.2
23	CW	71	G	6.2
2	CB	165	VAL	6.2
45	BZ	144	LEU	6.2
25	BA	943	C	6.1
23	AW	44	G	6.1
25	DA	885	C	6.1
25	BA	2153	G	6.1
31	DH	44	VAL	6.1
25	BA	930	G	6.0
14	CN	34	TYR	6.0
31	DH	25	LYS	6.0
2	AB	232	PRO	6.0
44	DY	65	ALA	5.9
45	DZ	173	ALA	5.9
50	D4	59	PHE	5.9
2	CB	207	ALA	5.9
23	AY	34	G	5.8
31	DH	45	VAL	5.8
14	CN	38	GLY	5.8
45	DZ	172	ALA	5.8
9	CI	4	TYR	5.8
14	CN	25	VAL	5.8
1	CA	1030(A)	G	5.7

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Mol	Chain	Res	Type	RSRZ
7	CG	16	LEU	5.7
31	DH	24	VAL	5.7
31	DH	49	VAL	5.6
7	AG	84	ASN	5.6
1	AA	1030(C)	G	5.5
1	CA	1001(A)	G	5.5
3	CC	182	ILE	5.5
25	DA	2145	C	5.5
25	DA	2160	G	5.5
47	B1	2	SER	5.5
10	CJ	63	PHE	5.4
19	CS	80	TYR	5.4
31	DH	32	GLU	5.4
31	DH	47	GLU	5.4
31	DH	51	ARG	5.4
45	DZ	174	VAL	5.4
45	DZ	4	ARG	5.3
3	CC	145	GLY	5.3
45	BZ	110	GLY	5.3
14	CN	51	GLY	5.3
45	BZ	146	ILE	5.3
50	D4	50	VAL	5.3
30	BG	146	TYR	5.3
45	DZ	146	ILE	5.3
45	BZ	107	THR	5.3
45	DZ	145	GLU	5.3
2	CB	34	ALA	5.3
7	CG	156	TRP	5.3
25	DA	887	A	5.2
25	DA	2146	C	5.2
1	AA	1257	U	5.2
1	CA	1257	U	5.2
13	AM	123	ALA	5.2
25	DA	2125	G	5.2
9	AI	15	ALA	5.2
45	DZ	9	TYR	5.2
23	AY	13	C	5.2
25	BA	936	C	5.2
31	DH	43	VAL	5.2
31	DH	105	LEU	5.1
29	DF	208	GLY	5.1
45	DZ	96	VAL	5.1

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Mol	Chain	Res	Type	RSRZ
3	AC	80	GLY	5.1
45	BZ	104	PHE	5.1
31	DH	20	ALA	5.1
23	CY	34	G	5.0
30	DG	115	ARG	5.0
1	AA	163	C	5.0
1	CA	1034	G	5.0
25	BA	2806	G	5.0
45	BZ	120	ILE	5.0
13	CM	68	GLY	5.0
2	CB	51	LEU	5.0
44	DY	45	VAL	5.0
7	CG	83	ALA	4.9
19	CS	16	LEU	4.9
1	AA	204	U	4.9
3	AC	65	ALA	4.9
45	DZ	51	ALA	4.9
1	AA	1446	U	4.9
45	DZ	47	VAL	4.9
12	CL	39	VAL	4.9
20	CT	9	ASN	4.9
1	CA	1030(C)	G	4.9
3	CC	39	ILE	4.9
31	DH	52	VAL	4.9
20	AT	55	ILE	4.9
25	BA	929	G	4.9
31	DH	7	LEU	4.9
31	DH	79	VAL	4.8
1	AA	1031	G	4.8
25	BA	938	G	4.8
31	DH	18	GLU	4.8
7	AG	82	GLY	4.8
45	DZ	57	ILE	4.8
9	CI	19	LEU	4.8
14	CN	35	ARG	4.8
45	DZ	118	GLN	4.8
45	DZ	120	ILE	4.8
2	CB	92	TYR	4.8
2	AB	227	GLY	4.7
31	DH	8	PRO	4.7
1	CA	1036	G	4.7
30	DG	139	LEU	4.7

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Mol	Chain	Res	Type	RSRZ
25	BA	2154	U	4.7
25	DA	2133	G	4.7
9	CI	106	ALA	4.7
9	CI	90	PRO	4.7
25	BA	2180	A	4.7
25	DA	2159	G	4.7
25	BA	935	C	4.7
3	CC	60	ALA	4.7
25	DA	2794	C	4.7
3	CC	157	ILE	4.7
25	BA	1221	G	4.6
2	CB	32	ILE	4.6
9	CI	56	LEU	4.6
13	CM	87	TYR	4.6
25	BA	1555	C	4.6
31	DH	35	VAL	4.6
46	D0	42	GLY	4.6
46	D0	2	ALA	4.6
38	DS	58	LEU	4.6
25	BA	2162	C	4.6
2	CB	123	ALA	4.6
45	DZ	50	GLN	4.6
3	CC	186	PHE	4.6
25	BA	2168	C	4.6
25	DA	2128	C	4.6
45	BZ	149	SER	4.6
1	AA	1030(D)	A	4.6
9	CI	15	ALA	4.5
14	CN	61	TRP	4.5
25	DA	2793	G	4.5
31	DH	123	PHE	4.5
9	CI	80	GLY	4.5
45	BZ	147	GLY	4.5
45	DZ	148	ASP	4.5
25	DA	886	C	4.5
30	DG	182	LYS	4.5
9	AI	19	LEU	4.5
19	CS	63	THR	4.5
31	DH	106	THR	4.5
25	BA	941	U	4.5
3	CC	64	VAL	4.5
25	DA	882	G	4.5

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Mol	Chain	Res	Type	RSRZ
31	DH	128	PRO	4.5
23	CW	44	G	4.4
23	CY	52	G	4.4
50	B4	59	PHE	4.4
7	AG	156	TRP	4.4
9	CI	9	ARG	4.4
33	DN	140	VAL	4.4
3	CC	91	LEU	4.4
1	AA	841	U	4.4
50	D4	18	CYS	4.4
3	AC	87	LEU	4.4
19	CS	71	LEU	4.4
44	DY	5	MET	4.4
10	CJ	74	ILE	4.4
25	DA	652(B)	A	4.4
31	DH	71	LEU	4.4
3	CC	101	LEU	4.4
30	DG	136	ARG	4.4
31	DH	13	LYS	4.4
1	AA	1036	G	4.4
25	DA	2154	G	4.4
45	DZ	42	VAL	4.3
7	AG	83	ALA	4.3
13	CM	4	ILE	4.3
23	CY	47	U	4.3
1	AA	1447	A	4.3
12	CL	55	VAL	4.3
51	D5	60	VAL	4.3
31	DH	31	GLY	4.3
9	AI	90	PRO	4.3
13	CM	90	LEU	4.3
31	DH	17	VAL	4.3
2	AB	228	GLY	4.3
9	CI	27	THR	4.3
9	CI	76	ALA	4.3
25	BA	933	C	4.2
14	CN	36	PHE	4.2
21	CU	16	GLY	4.2
20	CT	26	ASN	4.2
10	AJ	90	LEU	4.2
19	CS	13	ASP	4.2
41	DV	30	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
44	DY	61	ILE	4.2
8	CH	133	LEU	4.2
20	AT	43	LEU	4.2
25	DA	2155	G	4.2
25	DA	2161	C	4.2
9	AI	65	VAL	4.2
23	AY	35	A	4.2
1	CA	1002	G	4.2
45	BZ	164	ALA	4.2
29	DF	196	LEU	4.2
9	CI	103	THR	4.2
45	BZ	109	ALA	4.2
2	CB	232	PRO	4.2
25	DA	897	C	4.2
9	CI	36	TYR	4.2
45	DZ	89	PHE	4.2
31	DH	36	PRO	4.1
31	DH	141	VAL	4.1
1	AA	1027	C	4.1
25	DA	2896	C	4.1
50	D4	43	TYR	4.1
2	AB	222	ILE	4.1
44	DY	75	ILE	4.1
3	CC	87	LEU	4.1
23	CW	70	G	4.1
50	D4	52	THR	4.1
15	CO	60	VAL	4.1
17	CQ	23	VAL	4.1
31	DH	73	ALA	4.1
12	CL	95	GLY	4.1
19	CS	40	ILE	4.1
45	DZ	3	TYR	4.1
9	CI	52	ALA	4.1
12	CL	18	VAL	4.1
31	DH	11	VAL	4.1
9	CI	62	TYR	4.1
31	DH	75	ALA	4.1
20	CT	47	GLY	4.1
23	CW	45	U	4.1
13	CM	7	VAL	4.1
1	CA	1021	G	4.0
3	CC	57	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
8	CH	2	LEU	4.0
9	AI	81	ILE	4.0
7	CG	7	ALA	4.0
1	CA	1030(D)	A	4.0
45	DZ	58	VAL	4.0
31	DH	16	SER	4.0
45	BZ	118	GLN	4.0
9	AI	82	ALA	4.0
44	DY	43	ASN	4.0
45	DZ	109	ALA	4.0
9	AI	26	VAL	4.0
17	AQ	27	PHE	4.0
9	AI	80	GLY	4.0
23	AY	47	U	4.0
20	CT	59	ALA	4.0
31	DH	159	GLU	4.0
1	CA	1001	A	4.0
14	CN	53	LEU	4.0
14	CN	55	GLY	4.0
12	CL	64	TYR	4.0
9	AI	14	VAL	4.0
3	AC	81	GLY	4.0
45	DZ	163	LEU	4.0
31	DH	46	GLU	4.0
1	AA	202	U	3.9
25	BA	2181	G	3.9
50	D4	44	THR	3.9
9	CI	28	VAL	3.9
13	CM	15	VAL	3.9
29	DF	15	SER	3.9
31	DH	14	GLY	3.9
3	CC	134	ILE	3.9
1	AA	1024	G	3.9
23	CY	53	G	3.9
14	CN	42	ILE	3.9
9	AI	76	ALA	3.9
25	DA	2167	U	3.9
1	CA	1035	A	3.9
31	DH	10	PRO	3.9
29	DF	12	LEU	3.9
45	DZ	117	LEU	3.9
9	CI	81	ILE	3.9

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Mol	Chain	Res	Type	RSRZ
14	AN	2	ALA	3.9
4	CD	188	LEU	3.9
9	AI	47	LEU	3.9
53	B7	48	LYS	3.9
23	CY	1	G	3.9
25	DA	2127	G	3.9
31	DH	72	ILE	3.9
1	CA	1030	C	3.9
9	CI	109	VAL	3.9
10	CJ	90	LEU	3.9
31	DH	6	ARG	3.9
31	DH	98	LEU	3.9
20	CT	63	ILE	3.9
25	BA	271	U	3.9
25	DA	2138	C	3.9
11	AK	14	VAL	3.9
2	CB	187	LEU	3.9
2	CB	211	ILE	3.8
3	AC	52	LEU	3.8
19	AS	71	LEU	3.8
39	BT	38	ASN	3.8
17	AQ	36	ILE	3.8
45	BZ	170	THR	3.8
36	DQ	114	ALA	3.8
1	AA	1003	G	3.8
4	CD	135	LEU	3.8
3	CC	202	ILE	3.8
45	DZ	152	ALA	3.8
47	D1	2	SER	3.8
45	DZ	93	ASP	3.8
9	CI	17	VAL	3.8
45	BZ	169	GLU	3.8
29	BF	16	GLY	3.8
13	AM	90	LEU	3.8
35	DP	91	PHE	3.8
25	BA	926	G	3.8
40	DU	88	ILE	3.8
3	CC	197	GLY	3.8
13	CM	88	ARG	3.8
14	CN	7	ILE	3.8
25	BA	2167	C	3.8
16	CP	59	TRP	3.8

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Mol	Chain	Res	Type	RSRZ
5	CE	12	LEU	3.8
45	BZ	1	MET	3.7
31	DH	2	SER	3.7
38	DS	20	ARG	3.7
31	DH	34	GLU	3.7
45	DZ	99	TYR	3.7
25	BA	2183	C	3.7
7	AG	80	VAL	3.7
31	DH	142	GLY	3.7
31	DH	145	ALA	3.7
23	CW	72	C	3.7
3	AC	101	LEU	3.7
1	CA	485	G	3.7
1	AA	162	A	3.7
19	CS	14	HIS	3.7
7	CG	4	ARG	3.7
44	DY	55	TYR	3.7
2	CB	228	GLY	3.7
3	CC	28	GLN	3.7
31	DH	29	PRO	3.7
45	DZ	121	HIS	3.7
20	AT	100	ILE	3.7
27	BD	276	LYS	3.7
2	AB	61	LEU	3.7
45	DZ	157	LEU	3.7
25	DA	2144	U	3.7
10	CJ	71	LEU	3.7
17	AQ	98	LEU	3.7
36	DQ	106	VAL	3.7
23	AY	12	U	3.6
3	CC	184	TYR	3.6
46	D0	3	HIS	3.6
5	CE	11	ILE	3.6
30	DG	39	ILE	3.6
45	DZ	133	ILE	3.6
20	AT	74	LYS	3.6
53	D7	46	VAL	3.6
1	AA	1030(A)	G	3.6
2	CB	17	PHE	3.6
10	AJ	4	ILE	3.6
30	DG	42	GLY	3.6
41	DV	17	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
4	CD	152	SER	3.6
7	CG	154	TYR	3.6
21	AU	14	TRP	3.6
9	CI	61	ALA	3.6
23	CY	62	C	3.6
10	CJ	91	PRO	3.6
3	CC	18	TRP	3.6
31	DH	95	ARG	3.6
53	D7	48	LYS	3.6
35	DP	1	MET	3.6
4	CD	87	GLY	3.6
25	DA	2153	G	3.6
20	CT	83	ARG	3.6
25	BA	2814	C	3.6
32	BI	72	LEU	3.6
19	CS	52	TYR	3.6
45	DZ	128	VAL	3.6
32	DI	74	ASN	3.6
2	CB	208	ILE	3.6
18	AR	31	LEU	3.6
25	BA	2155	G	3.6
5	CE	99	GLY	3.6
36	DQ	33	GLY	3.6
41	DV	92	THR	3.6
2	CB	37	ASN	3.5
25	BA	2151	C	3.5
45	DZ	140	ASP	3.5
3	AC	179	ARG	3.5
29	BF	21	ALA	3.5
25	BA	944	C	3.5
3	AC	184	TYR	3.5
1	AA	216	G	3.5
25	DA	2792	G	3.5
8	CH	134	ILE	3.5
31	DH	92	ILE	3.5
1	CA	202	U	3.5
24	AX	47	U	3.5
3	CC	188	LEU	3.5
49	D3	29	ARG	3.5
35	DP	92	GLU	3.5
31	DH	15	VAL	3.5
17	CQ	80	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
46	D0	37	LEU	3.5
2	AB	123	ALA	3.5
3	CC	193	TYR	3.5
8	CH	65	TYR	3.5
43	DX	94	GLY	3.5
45	DZ	106	GLY	3.5
23	CW	47	U	3.5
4	CD	196	LEU	3.5
20	AT	72	LEU	3.5
23	CY	63	G	3.5
12	CL	30	ALA	3.5
14	CN	2	ALA	3.5
5	AE	10	MET	3.5
10	AJ	72	VAL	3.5
35	DP	102	ARG	3.5
19	CS	68	GLY	3.5
40	DU	73	GLY	3.5
31	DH	30	LYS	3.5
44	DY	106	LEU	3.5
16	CP	48	TRP	3.5
44	DY	91	GLU	3.4
2	AB	196	LEU	3.4
31	DH	103	LEU	3.4
21	CU	17	THR	3.4
30	DG	116	ASP	3.4
31	DH	102	ALA	3.4
14	CN	4	LYS	3.4
13	CM	119	GLY	3.4
10	CJ	72	VAL	3.4
23	AY	24	G	3.4
4	AD	110	PHE	3.4
10	AJ	96	ILE	3.4
30	DG	140	ILE	3.4
25	DA	2139	C	3.4
50	D4	54	GLY	3.4
32	BI	136	VAL	3.4
1	AA	1001(A)	G	3.4
25	DA	2173	A	3.4
3	CC	187	ALA	3.4
10	CJ	15	THR	3.4
25	DA	2140	C	3.4
19	CS	41	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
19	CS	51	VAL	3.4
13	CM	64	TRP	3.4
2	AB	70	PHE	3.4
19	CS	69	HIS	3.4
1	CA	1446	U	3.4
4	CD	157	LEU	3.4
8	CH	94	TYR	3.4
9	CI	114	TYR	3.4
18	CR	66	LEU	3.4
18	AR	25	THR	3.4
2	AB	125	PRO	3.4
24	AX	67	C	3.4
36	DQ	63	LYS	3.4
45	DZ	169	GLU	3.4
10	CJ	88	LEU	3.4
38	DS	56	LEU	3.4
3	CC	129	ALA	3.4
31	DH	27	LYS	3.4
35	DP	79	ARG	3.4
31	DH	41	MET	3.4
2	AB	215	LEU	3.4
2	CB	69	LEU	3.4
18	CR	85	LEU	3.4
45	DZ	125	LEU	3.4
13	CM	76	ALA	3.4
43	DX	91	ALA	3.4
25	BA	2163	G	3.4
25	BA	2176	G	3.4
31	DH	50	VAL	3.4
3	CC	179	ARG	3.4
20	AT	22	ARG	3.4
53	D7	47	ARG	3.4
19	CS	30	LEU	3.3
20	AT	41	ILE	3.3
30	DG	3	LEU	3.3
35	DP	94	GLU	3.3
43	DX	18	TYR	3.3
12	CL	28	LYS	3.3
31	DH	26	VAL	3.3
5	CE	114	GLY	3.3
29	BF	15	SER	3.3
3	CC	204	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
20	AT	84	LEU	3.3
29	BF	17	ARG	3.3
45	DZ	1	MET	3.3
8	CH	93	VAL	3.3
23	CW	4	C	3.3
2	CB	201	ILE	3.3
19	AS	40	ILE	3.3
45	BZ	102	LEU	3.3
45	DZ	5	LEU	3.3
20	CT	86	ARG	3.3
25	DA	2156	G	3.3
28	DE	71	GLY	3.3
10	CJ	59	SER	3.3
45	DZ	153	SER	3.3
25	BA	939	C	3.3
31	DH	69	ARG	3.3
50	D4	48	ARG	3.3
16	CP	19	ILE	3.3
3	CC	170	GLN	3.3
2	CB	33	TYR	3.3
31	DH	37	VAL	3.3
4	CD	158	ILE	3.3
9	CI	18	PHE	3.3
19	CS	79	THR	3.3
31	DH	89	ILE	3.3
1	AA	1028	C	3.3
25	DA	2164	C	3.3
25	DA	2803	C	3.3
3	CC	6	HIS	3.3
46	D0	4	LYS	3.3
50	B4	54	GLY	3.3
31	DH	94	TYR	3.3
1	CA	1033	G	3.3
25	DA	1039	G	3.3
41	DV	14	VAL	3.3
31	DH	12	PRO	3.3
3	AC	196	LEU	3.3
17	CQ	36	ILE	3.3
25	BA	925	A	3.3
43	DX	68	ARG	3.3
9	CI	86	VAL	3.3
23	AW	70	G	3.2

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Mol	Chain	Res	Type	RSRZ
25	DA	2123	G	3.2
3	AC	39	ILE	3.2
9	CI	30	GLY	3.2
9	CI	33	PHE	3.2
45	DZ	110	GLY	3.2
3	AC	201	TYR	3.2
10	CJ	44	VAL	3.2
13	CM	70	LEU	3.2
2	CB	122	PHE	3.2
14	CN	10	ALA	3.2
20	CT	44	ALA	3.2
32	BI	65	ALA	3.2
32	BI	103	ARG	3.2
33	DN	57	ALA	3.2
52	D6	50	ARG	3.2
1	AA	1030	C	3.2
38	DS	36	TYR	3.2
2	CB	229	VAL	3.2
9	CI	14	VAL	3.2
31	DH	19	VAL	3.2
45	BZ	100	VAL	3.2
14	CN	58	LYS	3.2
3	CC	22	TRP	3.2
36	DQ	65	PHE	3.2
50	D4	42	PHE	3.2
1	AA	93	G	3.2
10	AJ	97	GLU	3.2
25	DA	892	G	3.2
10	CJ	66	ARG	3.2
17	CQ	42	TYR	3.2
16	AP	2	VAL	3.2
25	BA	2157	A	3.2
1	CA	204	U	3.2
25	DA	2897	U	3.2
36	DQ	59	ARG	3.2
3	CC	41	GLY	3.2
14	AN	51	GLY	3.2
2	CB	81	VAL	3.2
25	BA	2905	C	3.2
30	DG	146	TYR	3.2
31	DH	53	GLU	3.2
45	BZ	165	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
17	CQ	74	LEU	3.2
30	DG	145	THR	3.2
10	AJ	47	PHE	3.2
10	CJ	98	ILE	3.2
19	CS	49	ILE	3.2
20	AT	63	ILE	3.2
4	CD	134	ASP	3.2
3	CC	13	GLY	3.2
4	CD	23	GLY	3.2
9	AI	17	VAL	3.2
13	CM	60	VAL	3.2
45	DZ	161	VAL	3.2
9	CI	79	LEU	3.2
14	CN	44	LEU	3.2
25	DA	894	C	3.2
31	DH	33	LEU	3.2
1	CA	161	A	3.2
20	CT	55	ILE	3.2
7	CG	81	GLY	3.2
29	DF	131	GLY	3.2
30	DG	29	TRP	3.2
31	DH	93	GLY	3.2
9	CI	49	PRO	3.2
13	CM	65	LYS	3.2
38	DS	83	LYS	3.2
14	CN	31	ARG	3.2
19	CS	67	VAL	3.2
3	CC	189	ALA	3.1
7	AG	85	TYR	3.1
1	CA	1028	C	3.1
25	BA	2807	C	3.1
45	DZ	104	PHE	3.1
50	D4	51	ASP	3.1
45	DZ	130	PRO	3.1
36	BQ	59	ARG	3.1
2	AB	12	GLU	3.1
3	CC	44	GLU	3.1
2	AB	73	THR	3.1
9	AI	28	VAL	3.1
10	CJ	87	THR	3.1
32	BI	68	LEU	3.1
44	DY	51	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1149	C	3.1
17	CQ	27	PHE	3.1
17	CQ	59	ILE	3.1
10	CJ	56	HIS	3.1
25	DA	2115	G	3.1
23	CY	64	A	3.1
6	AF	46	ARG	3.1
30	DG	2	PRO	3.1
11	AK	42	TRP	3.1
18	AR	79	LEU	3.1
9	CI	57	GLY	3.1
45	BZ	166	SER	3.1
20	CT	41	ILE	3.1
10	CJ	39	PRO	3.1
23	CY	61	C	3.1
30	DG	35	GLU	3.1
1	CA	1024	G	3.1
25	BA	2803	A	3.1
25	DA	2157	G	3.1
25	DA	2158	A	3.1
25	DA	2801(A)	A	3.1
45	DZ	46	LYS	3.1
3	CC	111	LEU	3.1
20	CT	53	LEU	3.1
50	B4	45	GLY	3.1
9	CI	92	TYR	3.1
25	DA	1509	C	3.1
9	CI	75	ASP	3.1
23	AY	23	A	3.1
1	AA	78	G	3.1
1	CA	998	G	3.1
23	CY	19	G	3.1
25	BA	927	G	3.1
7	CG	117	ALA	3.1
16	AP	21	VAL	3.1
14	CN	14	PRO	3.1
45	DZ	62	PRO	3.1
45	DZ	124	ILE	3.1
55	D9	12	ASP	3.1
16	AP	78	GLY	3.1
16	CP	74	LEU	3.1
50	D4	45	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
9	AI	113	LYS	3.1
9	CI	71	SER	3.1
2	CB	31	TYR	3.1
3	CC	19	GLU	3.1
29	DF	127	GLU	3.1
50	D4	62	ARG	3.1
2	AB	213	LEU	3.1
45	BZ	152	ALA	3.1
16	CP	79	VAL	3.1
19	CS	58	VAL	3.1
25	DA	2126	A	3.0
10	CJ	89	ASP	3.0
35	DP	110	TYR	3.0
8	CH	55	GLY	3.0
10	CJ	13	HIS	3.0
20	AT	62	LEU	3.0
23	AW	72	C	3.0
29	DF	21	ALA	3.0
2	AB	165	VAL	3.0
13	CM	17	VAL	3.0
20	AT	23	ARG	3.0
29	BF	23	ASP	3.0
1	CA	1447	A	3.0
18	AR	29	PHE	3.0
25	BA	2173	G	3.0
50	D4	53	GLU	3.0
17	CQ	22	LEU	3.0
35	DP	147	LEU	3.0
2	AB	229	VAL	3.0
25	DA	889	C	3.0
25	DA	2129	C	3.0
8	AH	35	ILE	3.0
3	CC	159	GLY	3.0
2	AB	95	GLN	3.0
20	AT	45	GLN	3.0
36	DQ	113	GLN	3.0
8	CH	122	ARG	3.0
20	AT	40	ALA	3.0
25	BA	2816	G	3.0
9	CI	108	VAL	3.0
25	DA	1043	C	3.0
2	CB	48	MET	3.0

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Mol	Chain	Res	Type	RSRZ
2	AB	78	GLN	3.0
13	CM	120	LYS	3.0
3	CC	23	TYR	3.0
3	AC	18	TRP	3.0
14	CN	13	THR	3.0
20	CT	49	ALA	3.0
27	DD	2	ALA	3.0
4	CD	198	VAL	3.0
31	DH	131	VAL	3.0
35	DP	101	VAL	3.0
1	CA	1027	C	3.0
2	AB	200	ILE	3.0
4	CD	5	ILE	3.0
13	AM	25	ILE	3.0
30	BG	80	PHE	3.0
20	CT	16	HIS	3.0
9	CI	50	LEU	3.0
10	AJ	8	LEU	3.0
29	DF	115	ALA	3.0
29	DF	167	ALA	3.0
38	DS	45	GLY	3.0
50	B4	50	VAL	3.0
25	DA	1042	G	3.0
2	CB	152	PHE	3.0
25	BA	940	C	3.0
10	AJ	85	LEU	3.0
20	AT	95	ALA	3.0
25	BA	937	A	3.0
19	CS	81	ARG	3.0
17	CQ	5	VAL	2.9
31	DH	9	ILE	2.9
1	AA	1002	G	2.9
14	CN	30	ALA	2.9
35	DP	140	ALA	2.9
46	D0	76	GLY	2.9
2	AB	117	GLU	2.9
32	DI	41	GLU	2.9
10	CJ	55	LYS	2.9
3	CC	124	ILE	2.9
2	CB	216	SER	2.9
9	AI	59	PHE	2.9
3	CC	160	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
12	CL	61	THR	2.9
13	CM	6	GLY	2.9
7	CG	85	TYR	2.9
20	AT	13	LEU	2.9
25	BA	2805	G	2.9
30	DG	161	THR	2.9
1	CA	1286	A	2.9
8	CH	95	VAL	2.9
10	AJ	24	VAL	2.9
38	DS	14	VAL	2.9
31	DH	23	ARG	2.9
3	CC	8	ILE	2.9
43	DX	89	ILE	2.9
2	CB	47	THR	2.9
3	CC	61	ALA	2.9
29	DF	113	ALA	2.9
38	DS	80	LEU	2.9
43	DX	69	TYR	2.9
17	CQ	19	VAL	2.9
52	D6	52	VAL	2.9
31	DH	80	SER	2.9
9	CI	37	PHE	2.9
21	AU	2	GLY	2.9
2	CB	120	ALA	2.9
19	CS	59	PRO	2.9
4	CD	19	LEU	2.9
2	AB	50	GLU	2.9
14	CN	52	GLN	2.9
3	CC	80	GLY	2.9
10	AJ	50	ILE	2.9
19	CS	31	ILE	2.9
23	CY	21	A	2.9
10	AJ	20	ALA	2.9
13	CM	42	ALA	2.9
14	CN	23	ARG	2.9
13	CM	23	TYR	2.9
50	D4	32	TYR	2.9
50	D4	63	TYR	2.9
17	CQ	21	VAL	2.9
44	DY	58	GLY	2.9
25	DA	2132	U	2.9
46	D0	45	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
23	CY	35	A	2.9
3	CC	53	ALA	2.9
2	CB	8	LYS	2.9
10	CJ	68	HIS	2.9
12	CL	60	LEU	2.9
43	DX	95	LEU	2.9
1	AA	91	C	2.8
10	AJ	73	ASP	2.8
20	AT	9	ASN	2.8
25	BA	696	C	2.8
2	CB	222	ILE	2.8
13	CM	78	ILE	2.8
17	CQ	65	ILE	2.8
50	B4	49	PHE	2.8
11	AK	60	ALA	2.8
23	CY	22	G	2.8
3	CC	63	ASN	2.8
7	CG	32	ARG	2.8
2	AB	207	ALA	2.8
2	CB	218	ALA	2.8
3	CC	71	ALA	2.8
48	D2	44	LEU	2.8
9	CI	54	ASP	2.8
1	AA	1033	G	2.8
1	CA	1031	G	2.8
23	CW	73	A	2.8
3	CC	194	GLY	2.8
20	AT	80	ARG	2.8
27	BD	275	LYS	2.8
5	AE	51	VAL	2.8
12	CL	69	TYR	2.8
20	AT	42	GLN	2.8
45	DZ	98	MET	2.8
31	DH	113	VAL	2.8
44	DY	3	VAL	2.8
50	B4	56	VAL	2.8
52	D6	5	VAL	2.8
2	AB	182	ILE	2.8
16	CP	9	PHE	2.8
11	AK	89	ALA	2.8
2	CB	215	LEU	2.8
17	CQ	6	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
36	DQ	6	ARG	2.8
50	B4	55	ARG	2.8
38	DS	60	GLY	2.8
1	CA	1004	A	2.8
23	CW	76	A	2.8
3	CC	142	MET	2.8
2	AB	15	VAL	2.8
25	DA	614(B)	G	2.8
55	D9	16	VAL	2.8
9	CI	5	TYR	2.8
31	DH	164	TYR	2.8
50	D4	67	TYR	2.8
25	BA	2906	U	2.8
2	CB	55	PHE	2.8
9	CI	42	ARG	2.8
14	CN	29	ARG	2.8
2	CB	115	LEU	2.8
41	DV	29	PRO	2.8
45	BZ	159	PRO	2.8
23	CY	65	G	2.8
25	BA	2178	G	2.8
31	DH	57	ASP	2.8
55	D9	17	ILE	2.8
2	CB	94	ASN	2.8
8	AH	39	LEU	2.8
13	CM	12	ASN	2.8
20	AT	69	GLY	2.8
20	AT	91	LEU	2.8
31	DH	86	GLU	2.8
41	DV	62	LEU	2.8
49	D3	23	LEU	2.8
2	CB	220	ASP	2.8
5	AE	69	VAL	2.8
32	BI	117	GLU	2.8
10	CJ	48	THR	2.8
31	DH	166	GLY	2.8
44	DY	25	GLY	2.8
1	AA	79	G	2.8
45	DZ	91	LEU	2.8
3	CC	36	ASP	2.8
10	AJ	10	GLY	2.7
11	AK	25	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
2	CB	214	ILE	2.7
10	CJ	20	ALA	2.7
29	DF	198	ALA	2.7
30	DG	163	ALA	2.7
44	DY	44	ILE	2.7
45	DZ	21	ALA	2.7
30	BG	139	LEU	2.7
32	BI	75	LEU	2.7
3	CC	190	ARG	2.7
29	DF	174	VAL	2.7
31	DH	115	VAL	2.7
9	CI	13	ALA	2.7
10	AJ	98	ILE	2.7
35	DP	96	THR	2.7
30	DG	152	LEU	2.7
3	AC	206	GLU	2.7
19	CS	47	HIS	2.7
38	DS	84	GLN	2.7
32	BI	111	PRO	2.7
48	D2	1	MET	2.7
1	AA	144	G	2.7
36	DQ	5	ARG	2.7
5	CE	8	GLU	2.7
13	CM	18	ALA	2.7
25	DA	895	U	2.7
50	D4	57	GLU	2.7
5	CE	6	PHE	2.7
12	CL	62	SER	2.7
20	AT	24	LEU	2.7
31	DH	38	SER	2.7
3	AC	148	GLY	2.7
9	CI	110	GLU	2.7
10	AJ	9	ARG	2.7
23	CW	3	C	2.7
19	CS	50	ALA	2.7
19	CS	35	SER	2.7
20	CT	24	LEU	2.7
30	DG	60	LEU	2.7
31	BH	2	SER	2.7
9	AI	117	HIS	2.7
2	AB	231	GLU	2.7
3	CC	35	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
9	AI	8	GLY	2.7
10	AJ	36	GLY	2.7
10	CJ	78	ASN	2.7
50	D4	19	GLY	2.7
41	DV	5	VAL	2.7
55	D9	25	VAL	2.7
45	DZ	164	ALA	2.7
1	CA	1003	G	2.7
5	CE	13	ILE	2.7
20	AT	20	LEU	2.7
23	CY	18	G	2.7
36	DQ	104	PHE	2.7
31	DH	81	GLU	2.7
36	DQ	32	TYR	2.7
20	CT	98	PRO	2.7
45	BZ	148	ASP	2.7
3	CC	20	SER	2.7
25	DA	898	C	2.7
2	CB	223	ILE	2.7
3	AC	12	LEU	2.7
16	CP	73	LEU	2.7
46	D0	7	LEU	2.7
13	AM	26	GLY	2.7
13	CM	13	LYS	2.7
31	DH	157	TYR	2.7
44	DY	47	LYS	2.7
29	DF	14	PRO	2.7
3	CC	183	ASP	2.7
23	CY	23	A	2.6
25	BA	945	A	2.6
25	DA	6	A	2.6
3	AC	60	ALA	2.6
9	AI	93	ARG	2.6
20	AT	59	ALA	2.6
20	AT	61	SER	2.6
31	DH	99	VAL	2.6
31	DH	144	VAL	2.6
36	DQ	27	VAL	2.6
20	AT	76	ALA	2.6
17	CQ	60	ILE	2.6
28	BE	195	LEU	2.6
52	D6	11	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
44	BY	1	MET	2.6
54	D8	29	LYS	2.6
22	CV	24	A	2.6
4	AD	16	GLY	2.6
4	CD	161	ASN	2.6
20	CT	43	LEU	2.6
25	BA	1220	U	2.6
25	BA	2152	U	2.6
25	DA	1113	U	2.6
45	BZ	123	ASP	2.6
4	CD	168	ARG	2.6
14	CN	12	ARG	2.6
19	CS	28	LYS	2.6
3	CC	154	SER	2.6
2	CB	164	VAL	2.6
17	CQ	77	VAL	2.6
45	BZ	160	GLY	2.6
1	AA	203	U	2.6
1	CA	1150	U	2.6
2	CB	121	LEU	2.6
12	CL	93	LEU	2.6
25	BA	218	A	2.6
47	B1	98	LEU	2.6
5	CE	109	ILE	2.6
10	AJ	75	ILE	2.6
14	CN	54	PRO	2.6
17	CQ	30	PRO	2.6
31	DH	21	PRO	2.6
3	CC	88	ARG	2.6
30	BG	51	ARG	2.6
50	D4	68	ARG	2.6
1	CA	91	C	2.6
2	AB	19	HIS	2.6
2	CB	136	VAL	2.6
9	CI	6	GLY	2.6
19	CS	9	VAL	2.6
41	DV	101	GLY	2.6
50	B4	4	GLY	2.6
1	AA	146	G	2.6
10	CJ	29	ARG	2.6
25	DA	881	G	2.6
16	AP	66	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
45	DZ	137	ILE	2.6
23	CY	56	C	2.6
25	DA	1041	C	2.6
55	D9	20	HIS	2.6
3	CC	51	GLY	2.6
2	CB	161	ALA	2.6
3	AC	100	ALA	2.6
11	AK	68	ALA	2.6
14	CN	56	VAL	2.6
32	BI	86	THR	2.6
44	DY	42	VAL	2.6
23	AW	45	U	2.6
9	CI	63	ILE	2.6
29	DF	145	GLU	2.6
1	AA	1035	A	2.6
20	CT	45	GLN	2.6
1	AA	150	C	2.6
3	AC	205	GLY	2.6
5	CE	59	GLY	2.6
16	CP	58	TYR	2.6
20	AT	70	SER	2.6
9	CI	105	ASP	2.6
14	CN	40	CYS	2.6
20	AT	79	ARG	2.6
9	AI	55	ALA	2.6
20	CT	40	ALA	2.6
10	CJ	65	LEU	2.6
14	CN	6	LEU	2.6
19	CS	15	LEU	2.6
41	DV	94	LEU	2.6
13	CM	39	ILE	2.6
14	AN	16	PHE	2.6
29	BF	9	ILE	2.6
20	CT	30	LYS	2.6
29	DF	172	TRP	2.6
10	AJ	35	SER	2.6
21	CU	24	ARG	2.6
25	BA	1878	A	2.6
25	DA	2162	G	2.6
50	D4	66	SER	2.6
4	AD	138	TYR	2.6
1	AA	76	C	2.6

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Mol	Chain	Res	Type	RSRZ
9	CI	82	ALA	2.5
25	DA	2137	C	2.6
2	AB	230	VAL	2.5
19	CS	48	THR	2.5
2	AB	138	LEU	2.5
17	CQ	28	PRO	2.5
46	B0	7	LEU	2.5
9	CI	77	ILE	2.5
10	AJ	63	PHE	2.5
30	DG	178	PHE	2.5
3	CC	81	GLY	2.5
44	DY	80	GLY	2.5
1	AA	161	A	2.5
1	AA	1503	A	2.5
1	AA	1023	G	2.5
3	CC	138	VAL	2.5
9	AI	56	LEU	2.5
33	DN	46	VAL	2.5
45	DZ	150	LEU	2.5
53	B7	46	VAL	2.5
13	CM	84	ILE	2.5
14	CN	16	PHE	2.5
32	BI	109	ILE	2.5
50	D4	40	HIS	2.5
2	AB	233	SER	2.5
2	CB	139	LYS	2.5
13	CM	121	LYS	2.5
9	CI	125	TYR	2.5
20	AT	18	GLN	2.5
29	DF	171	PRO	2.5
1	AA	1032	G	2.5
2	AB	221	LEU	2.5
4	AD	88	VAL	2.5
8	CH	129	VAL	2.5
38	DS	3	ARG	2.5
25	DA	2147	G	2.5
31	DH	40	GLU	2.5
45	DZ	60	GLU	2.5
55	B9	26	ILE	2.5
29	BF	13	SER	2.5
20	CT	8	ARG	2.5
9	AI	4	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
9	CI	21	PRO	2.5
12	CL	25	PRO	2.5
30	DG	169	ALA	2.5
31	DH	96	ALA	2.5
47	B1	93	GLU	2.5
10	CJ	40	LEU	2.5
14	AN	33	VAL	2.5
45	DZ	126	VAL	2.5
1	AA	1025	U	2.5
2	AB	16	HIS	2.5
2	CB	39	ILE	2.5
23	AY	22	G	2.5
31	DH	148	ILE	2.5
38	DS	12	PHE	2.5
18	AR	42	ARG	2.5
31	DH	101	ARG	2.5
2	AB	234	PRO	2.5
10	CJ	92	THR	2.5
20	CT	77	ALA	2.5
35	DP	141	ALA	2.5
38	DS	33	LYS	2.5
4	CD	94	LEU	2.5
13	CM	53	VAL	2.5
41	DV	42	GLY	2.5
41	DV	47	VAL	2.5
41	DV	63	GLY	2.5
41	DV	95	LEU	2.5
49	D3	47	VAL	2.5
2	AB	211	ILE	2.5
13	CM	71	ARG	2.5
36	DQ	1	MET	2.5
36	DQ	60	ARG	2.5
1	AA	1034	G	2.5
35	DP	76	LYS	2.5
3	AC	71	ALA	2.5
7	CG	40	ALA	2.5
38	DS	66	ALA	2.5
2	CB	145	LEU	2.5
8	AH	93	VAL	2.5
16	AP	59	TRP	2.5
17	CQ	73	VAL	2.5
20	CT	91	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
31	DH	133	VAL	2.5
31	DH	169	VAL	2.5
45	DZ	65	GLN	2.5
17	CQ	12	SER	2.5
31	DH	54	ARG	2.5
31	DH	56	SER	2.5
45	DZ	49	ARG	2.5
2	CB	70	PHE	2.5
2	CB	185	ILE	2.5
13	CM	9	ILE	2.5
15	CO	15	PHE	2.5
38	DS	35	ILE	2.5
1	CA	1452	C	2.5
3	CC	149	ALA	2.5
23	CY	5	G	2.5
29	DF	161	GLU	2.5
43	BX	94	GLY	2.5
50	D4	64	GLY	2.5
38	DS	34	HIS	2.4
3	CC	178	LEU	2.4
8	AH	122	ARG	2.4
13	CM	66	LEU	2.4
47	D1	98	LEU	2.4
4	CD	140	VAL	2.4
31	DH	85	LYS	2.4
44	DY	34	LYS	2.4
2	AB	122	PHE	2.4
2	CB	200	ILE	2.4
10	CJ	11	PHE	2.4
46	D0	57	PHE	2.4
25	BA	2815	C	2.4
45	DZ	119	GLU	2.4
19	AS	68	GLY	2.4
20	CT	42	GLN	2.4
32	BI	98	ALA	2.4
25	DA	1114	G	2.4
41	DV	35	LEU	2.4
2	CB	124	SER	2.4
17	CQ	9	VAL	2.4
45	DZ	92	SER	2.4
36	BQ	41	TRP	2.4
3	CC	128	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
50	D4	22	ILE	2.4
39	DT	1	MET	2.4
14	CN	57	ARG	2.4
25	DA	2135	A	2.4
35	DP	97	PRO	2.4
1	AA	217	C	2.4
1	CA	1116	C	2.4
9	CI	7	THR	2.4
29	DF	118	ALA	2.4
3	AC	204	LEU	2.4
3	CC	196	LEU	2.4
32	DI	68	LEU	2.4
49	D3	26	LEU	2.4
4	CD	34	GLU	2.4
2	AB	133	LYS	2.4
2	CB	97	TRP	2.4
3	CC	40	ARG	2.4
14	AN	61	TRP	2.4
50	D4	13	ARG	2.4
17	CQ	33	GLY	2.4
35	DP	93	GLY	2.4
17	CQ	47	PRO	2.4
3	AC	169	ALA	2.4
5	CE	17	ALA	2.4
13	AM	2	ALA	2.4
30	DG	110	ALA	2.4
1	AA	840	C	2.4
35	DP	144	GLU	2.4
2	AB	149	LEU	2.4
17	CQ	84	LEU	2.4
35	DP	100	LEU	2.4
3	CC	207	VAL	2.4
14	CN	11	LYS	2.4
3	AC	193	TYR	2.4
3	CC	155	GLY	2.4
9	AI	33	PHE	2.4
16	AP	80	PHE	2.4
19	CS	84	GLY	2.4
1	AA	73	G	2.4
25	DA	2166	G	2.4
31	DH	126	PRO	2.4
35	DP	122	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
45	DZ	54	HIS	2.4
9	CI	78	LYS	2.4
1	CA	1005	A	2.4
30	BG	43	LEU	2.4
30	DG	133	LEU	2.4
44	DY	90	LEU	2.4
3	CC	21	ARG	2.4
14	AN	12	ARG	2.4
20	CT	23	ARG	2.4
44	DY	50	ARG	2.4
30	DG	109	VAL	2.4
10	CJ	31	GLY	2.4
31	DH	28	GLY	2.4
31	DH	78	GLY	2.4
40	DU	66	ASN	2.4
42	BW	112	GLY	2.4
2	CB	231	GLU	2.4
13	CM	69	GLU	2.4
44	DY	35	TYR	2.4
25	BA	2179	G	2.4
4	CD	47	ARG	2.4
14	CN	19	ARG	2.4
17	CQ	75	ARG	2.4
2	CB	44	LEU	2.4
8	AH	112	LEU	2.4
10	AJ	16	LEU	2.4
5	CE	90	VAL	2.4
29	BF	11	VAL	2.4
30	DG	38	VAL	2.4
38	DS	46	VAL	2.4
40	DU	89	GLU	2.4
46	B0	6	GLY	2.4
10	CJ	41	PRO	2.4
30	DG	114	ILE	2.4
33	DN	44	PRO	2.4
50	D4	15	ILE	2.4
5	CE	146	ALA	2.4
10	AJ	5	ARG	2.4
16	AP	22	THR	2.4
31	DH	124	GLU	2.4
45	BZ	70	LEU	2.4
1	CA	79	G	2.3

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Mol	Chain	Res	Type	RSRZ
1	CA	220	G	2.3
38	DS	76	LYS	2.3
55	D9	13	LYS	2.3
17	CQ	11	VAL	2.3
5	CE	131	ILE	2.3
9	AI	98	PRO	2.3
30	DG	142	PRO	2.3
45	DZ	68	PRO	2.3
47	D1	58	ILE	2.3
5	AE	132	ALA	2.3
7	AG	127	ALA	2.3
14	CN	46	GLU	2.3
19	CS	24	ALA	2.3
20	AT	71	THR	2.3
43	DX	14	SER	2.3
28	DE	52	LEU	2.3
31	DH	88	LEU	2.3
45	DZ	70	LEU	2.3
49	D3	53	LEU	2.3
7	AG	20	ASP	2.3
20	AT	86	ARG	2.3
23	CY	66	U	2.3
25	DA	2165	G	2.3
45	BZ	140	ASP	2.3
45	DZ	122	ARG	2.3
4	AD	70	ILE	2.3
4	CD	146	ILE	2.3
21	AU	13	ILE	2.3
25	DA	2169	A	2.3
30	DG	137	GLU	2.3
20	AT	77	ALA	2.3
14	CN	22	THR	2.3
55	D9	29	ASN	2.3
17	CQ	98	LEU	2.3
29	DF	199	TRP	2.3
3	CC	120	VAL	2.3
40	DU	117	GLN	2.3
38	DS	11	LYS	2.3
15	AO	87	ILE	2.3
19	CS	10	PHE	2.3
31	DH	165	ALA	2.3
44	DY	48	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
35	DP	118	GLY	2.3
2	AB	114	ARG	2.3
3	AC	47	LEU	2.3
13	CM	19	LEU	2.3
20	CT	13	LEU	2.3
29	DF	20	LEU	2.3
46	D0	77	ARG	2.3
14	CN	50	LYS	2.3
46	D0	5	LYS	2.3
2	AB	197	VAL	2.3
9	CI	53	VAL	2.3
30	DG	149	VAL	2.3
20	CT	100	ILE	2.3
1	AA	219	C	2.3
2	CB	35	GLU	2.3
1	AA	1286	A	2.3
9	AI	88	TYR	2.3
23	CY	14	A	2.3
4	CD	78	LEU	2.3
16	CP	29	ASP	2.3
20	CT	72	LEU	2.3
35	DP	123	LEU	2.3
46	B0	5	LYS	2.3
2	CB	24	TRP	2.3
16	AP	1	MET	2.3
32	BI	74	ASN	2.3
4	CD	69	GLY	2.3
8	CH	131	GLY	2.3
2	CB	188	ALA	2.3
12	CL	26	ALA	2.3
10	AJ	21	GLN	2.3
11	AK	36	ASP	2.3
36	BQ	141	GLN	2.3
1	AA	92	C	2.3
25	DA	645	C	2.3
20	AT	16	HIS	2.3
25	DA	652(U)	G	2.3
3	CC	174	PRO	2.3
33	DN	126	PRO	2.3
45	BZ	158	PRO	2.3
2	CB	71	VAL	2.3
1	CA	1020	U	2.3

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Mol	Chain	Res	Type	RSRZ
13	CM	110	ARG	2.3
30	DG	51	ARG	2.3
30	DG	181	ARG	2.3
31	DH	132	ARG	2.3
45	DZ	72	ARG	2.3
2	CB	101	MET	2.3
17	CQ	100	LYS	2.3
29	DF	160	ASN	2.3
31	DH	74	ASN	2.3
3	CC	185	GLY	2.3
12	AL	29	GLY	2.3
10	AJ	11	PHE	2.3
38	BS	77	ALA	2.3
13	CM	63	THR	2.3
3	CC	32	LEU	2.3
9	AI	92	TYR	2.3
9	CI	88	TYR	2.3
14	CN	24	CYS	2.3
19	CS	27	GLU	2.3
19	CS	43	GLU	2.3
20	AT	53	LEU	2.3
8	AH	84	ARG	2.2
17	CQ	25	ARG	2.2
1	CA	1026	G	2.2
25	BA	2813	G	2.2
9	CI	24	GLY	2.2
10	AJ	34	VAL	2.2
23	AY	20	U	2.2
31	BH	174	GLY	2.2
32	BI	106	GLY	2.2
38	DS	109	GLY	2.2
41	DV	22	VAL	2.2
38	DS	52	SER	2.2
7	CG	26	PHE	2.2
21	CU	14	TRP	2.2
43	DX	93	GLU	2.2
2	CB	132	LYS	2.2
8	AH	127	LEU	2.2
9	CI	85	LEU	2.2
14	CN	47	LEU	2.2
20	CT	25	ARG	2.2
30	DG	173	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
32	BI	140	LEU	2.2
32	DI	38	LEU	2.2
4	CD	20	TYR	2.2
1	AA	171	A	2.2
30	DG	92	VAL	2.2
1	CA	4	U	2.2
25	BA	2177	G	2.2
13	CM	20	THR	2.2
7	AG	32	ARG	2.2
7	CG	6	ARG	2.2
31	BH	21	PRO	2.2
45	DZ	158	PRO	2.2
10	CJ	33	GLN	2.2
25	DA	2174	C	2.2
25	DA	2804	C	2.2
30	DG	48	GLU	2.2
45	DZ	162	GLU	2.2
9	CI	65	VAL	2.2
11	CK	109	VAL	2.2
1	AA	170	U	2.2
20	AT	38	LYS	2.2
3	CC	59	ARG	2.2
9	AI	52	ALA	2.2
13	CM	93	ARG	2.2
21	CU	8	THR	2.2
1	AA	104	G	2.2
1	CA	97	G	2.2
9	AI	40	LEU	2.2
9	CI	102	LEU	2.2
3	CC	89	GLU	2.2
13	CM	41	PRO	2.2
18	CR	58	LEU	2.2
30	DG	17	PRO	2.2
38	DS	54	LEU	2.2
16	AP	48	TRP	2.2
15	AO	78	TYR	2.2
20	CT	22	ARG	2.2
45	BZ	52	SER	2.2
1	AA	201	C	2.2
7	AG	141	VAL	2.2
45	DZ	56	VAL	2.2
7	AG	153	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
20	CT	12	ALA	2.2
31	DH	122	THR	2.2
2	AB	134	GLU	2.2
5	CE	81	GLU	2.2
8	CH	136	GLU	2.2
2	CB	155	LEU	2.2
3	CC	43	LEU	2.2
14	CN	15	LYS	2.2
31	DH	77	LYS	2.2
25	BA	2182	G	2.2
3	AC	21	ARG	2.2
4	CD	115	ARG	2.2
29	DF	7	TYR	2.2
30	BG	181	ARG	2.2
45	BZ	122	ARG	2.2
4	CD	33	MET	2.2
45	DZ	55	HIS	2.2
3	CC	107	GLN	2.2
29	DF	177	ALA	2.2
45	DZ	2	GLU	2.2
50	D4	31	ILE	2.2
13	CM	16	ASP	2.2
7	AG	16	LEU	2.2
8	AH	10	LEU	2.2
19	CS	26	GLY	2.2
33	DN	116	LEU	2.2
7	AG	78	ARG	2.2
20	AT	8	ARG	2.2
3	CC	105	GLU	2.2
23	AW	69	G	2.2
25	BA	2184	G	2.2
25	DA	2116	G	2.2
48	B2	5	GLU	2.2
9	AI	70	LYS	2.2
17	CQ	56	VAL	2.2
20	CT	38	LYS	2.2
32	DI	107	VAL	2.2
2	CB	29	ALA	2.2
13	CM	72	ALA	2.2
8	CH	86	ILE	2.2
10	CJ	38	ILE	2.2
23	CY	13	C	2.2

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Mol	Chain	Res	Type	RSRZ
29	DF	189	THR	2.2
20	CT	57	ARG	2.2
27	DD	238	GLY	2.2
29	BF	131	GLY	2.2
38	DS	97	ARG	2.2
2	AB	121	LEU	2.2
32	DI	72	LEU	2.2
45	DZ	102	LEU	2.2
20	CT	18	GLN	2.1
20	CT	31	SER	2.2
38	DS	31	SER	2.2
2	CB	19	HIS	2.1
1	CA	1023	G	2.1
4	CD	56	VAL	2.1
23	CY	57	G	2.1
29	BF	89	VAL	2.1
49	D3	59	VAL	2.1
50	D4	10	VAL	2.1
3	AC	189	ALA	2.1
20	AT	83	ARG	2.1
2	CB	41	ILE	2.1
3	CC	14	ILE	2.1
8	AH	117	GLY	2.1
35	DP	15	ARG	2.1
45	DZ	20	ARG	2.1
29	BF	206	ILE	2.1
42	DW	30	GLU	2.1
9	AI	126	SER	2.1
25	DA	890	A	2.1
46	B0	3	HIS	2.1
21	AU	18	TYR	2.1
21	CU	21	TYR	2.1
2	CB	219	VAL	2.1
12	AL	55	VAL	2.1
14	AN	18	VAL	2.1
50	D4	55	ARG	2.1
19	CS	75	ALA	2.1
23	CY	45	U	2.1
25	DA	2113	U	2.1
49	D3	60	GLU	2.1
8	CH	120	THR	2.1
11	AK	48	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
44	DY	82	PRO	2.1
2	AB	180	LEU	2.1
3	CC	33	LEU	2.1
9	AI	31	GLN	2.1
12	CL	27	LEU	2.1
16	AP	73	LEU	2.1
1	AA	100	C	2.1
14	CN	8	GLU	2.1
22	CV	12	A	2.1
25	BA	2195	A	2.1
5	AE	95	ALA	2.1
10	AJ	44	VAL	2.1
17	CQ	51	TYR	2.1
19	CS	60	VAL	2.1
30	DG	67	LYS	2.1
25	BA	924	U	2.1
31	DH	125	VAL	2.1
32	BI	19	VAL	2.1
35	DP	124	LYS	2.1
38	DS	37	ALA	2.1
2	CB	67	THR	2.1
2	CB	131	PRO	2.1
9	CI	74	ILE	2.1
16	CP	36	ILE	2.1
50	D4	46	GLN	2.1
3	AC	128	PHE	2.1
4	CD	110	PHE	2.1
4	AD	21	LEU	2.1
30	DG	111	LEU	2.1
45	BZ	117	LEU	2.1
1	CA	1202	G	2.1
1	CA	217	C	2.1
1	CA	218	C	2.1
2	AB	193	ASP	2.1
3	AC	126	ARG	2.1
23	CY	6	G	2.1
25	DA	880	G	2.1
31	DH	3	ARG	2.1
45	BZ	168	GLU	2.1
2	CB	227	GLY	2.1
5	CE	22	GLY	2.1
30	DG	85	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
36	DQ	61	GLY	2.1
41	DV	1	MET	2.1
11	AK	15	ALA	2.1
11	CK	84	VAL	2.1
20	CT	76	ALA	2.1
28	BE	175	VAL	2.1
38	DS	65	VAL	2.1
40	DU	116	ALA	2.1
5	AE	96	PRO	2.1
21	CU	13	ILE	2.1
5	CE	110	LEU	2.1
8	AH	18	ARG	2.1
12	CL	32	PHE	2.1
13	CM	80	ARG	2.1
44	BY	91	GLU	2.1
3	CC	4	LYS	2.1
27	DD	38	LYS	2.1
45	DZ	52	SER	2.1
6	CF	100	ASN	2.1
1	CA	1037	C	2.1
23	CW	19	G	2.1
25	DA	2805	G	2.1
3	CC	180	ALA	2.1
3	AC	19	GLU	2.1
21	CU	23	PRO	2.1
23	CY	58	A	2.1
25	BA	1092	A	2.1
27	BD	221	VAL	2.1
29	DF	200	GLU	2.1
50	D4	56	VAL	2.1
51	B5	60	VAL	2.1
9	CI	20	ARG	2.1
10	CJ	79	ARG	2.1
31	DH	83	TYR	2.1
32	BI	57	ARG	2.1
50	D4	25	TYR	2.1
19	CS	62	ILE	2.1
30	BG	88	ILE	2.1
17	CQ	31	LEU	2.1
30	BG	82	LEU	2.1
32	DI	140	LEU	2.1
45	DZ	136	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
2	CB	72	GLY	2.1
19	CS	82	GLY	2.1
1	AA	1452	C	2.1
10	AJ	95	GLU	2.1
25	DA	652(V)	C	2.1
31	DH	167	GLU	2.1
4	CD	86	LYS	2.1
4	CD	122	ARG	2.1
10	AJ	18	ALA	2.1
19	CS	36	ARG	2.1
3	CC	55	VAL	2.1
10	CJ	34	VAL	2.1
13	CM	97	PRO	2.1
44	DY	88	LYS	2.1
8	AH	111	ILE	2.1
44	DY	31	LEU	2.1
3	CC	206	GLU	2.1
4	CD	167	GLY	2.1
9	AI	67	GLY	2.1
14	CN	43	CYS	2.1
30	BG	42	GLY	2.1
47	D1	26	ARG	2.1
5	AE	136	MET	2.0
30	DG	148	MET	2.0
1	CA	999	C	2.0
1	CA	1006	C	2.0
3	CC	62	ASP	2.0
25	BA	2150	C	2.0
25	BA	2161	C	2.0
16	CP	20	VAL	2.0
16	CP	62	VAL	2.0
28	DE	104	VAL	2.0
33	BN	9	VAL	2.0
41	DV	46	VAL	2.0
1	CA	630	G	2.0
10	CJ	62	HIS	2.0
2	AB	31	TYR	2.0
25	DA	1170	G	2.0
2	AB	126	GLU	2.0
2	CB	12	GLU	2.0
3	AC	14	ILE	2.0
8	AH	38	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
8	CH	45	ILE	2.0
8	CH	83	ILE	2.0
10	AJ	38	ILE	2.0
36	DQ	66	ILE	2.0
45	BZ	66	SER	2.0
25	DA	899	A	2.0
30	DG	138	GLN	2.0
44	DY	89	PHE	2.0
45	DZ	67	LEU	2.0
47	D1	28	GLY	2.0
20	CT	29	LYS	2.0
50	D4	38	LYS	2.0
10	CJ	46	ARG	2.0
14	CN	41	ARG	2.0
3	CC	167	TRP	2.0
54	D8	34	TRP	2.0
3	CC	24	ALA	2.0
30	DG	73	ALA	2.0
45	BZ	51	ALA	2.0
3	AC	64	VAL	2.0
3	CC	58	GLU	2.0
20	CT	14	LYS	2.0
38	DS	50	SER	2.0
2	CB	236	TYR	2.0
10	CJ	96	ILE	2.0
14	AN	7	ILE	2.0
16	AP	19	ILE	2.0
3	CC	79	ARG	2.0
5	AE	53	LEU	2.0
5	AE	89	ILE	2.0
7	AG	154	TYR	2.0
8	CH	36	LEU	2.0
21	CU	18	TYR	2.0
32	DI	71	ILE	2.0
35	DP	138	LEU	2.0
45	BZ	124	ILE	2.0
8	CH	104	ARG	2.0
9	AI	16	ARG	2.0
1	AA	77	G	2.0
1	CA	156	G	2.0
25	DA	1112	G	2.0
25	DA	2131	G	2.0

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Mol	Chain	Res	Type	RSRZ
1	AA	143	A	2.0
1	CA	162	A	2.0
22	AV	15	A	2.0
25	BA	2812	A	2.0
30	BG	49	ASP	2.0
44	DY	107	ASP	2.0
46	D0	64	ASP	2.0
7	AG	8	GLU	2.0
10	AJ	41	PRO	2.0
17	AQ	28	PRO	2.0
19	AS	27	GLU	2.0
20	CT	60	GLU	2.0
9	AI	64	THR	2.0
17	CQ	18	THR	2.0
20	AT	14	LYS	2.0
29	BF	166	ALA	2.0
35	BP	12	ALA	2.0
36	DQ	107	ALA	2.0
43	DX	3	THR	2.0
7	CG	66	VAL	2.0
1	AA	1029	C	2.0
1	CA	1007	C	2.0
2	CB	203	GLY	2.0
30	DG	78	SER	2.0
25	BA	2130	C	2.0
38	DS	104	GLY	2.0
28	BE	77	ILE	2.0
31	DH	121	ILE	2.0
31	DH	163	TYR	2.0
31	DH	137	ASP	2.0
35	DP	98	GLU	2.0
38	DS	8	GLU	2.0
1	AA	145	G	2.0
1	CA	1041	A	2.0
20	CT	48	LYS	2.0
25	DA	2148	G	2.0
25	DA	2176	A	2.0
2	AB	167	PRO	2.0
5	CE	10	MET	2.0
8	CH	67	PRO	2.0
20	AT	85	MET	2.0
40	DU	2	PRO	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	MIA	CY	37	22/30	0.68	0.33	82,93,117,140	0
23	PSU	AY	55	20/21	0.69	0.28	93,99,105,118	0
23	5MU	CY	54	21/22	0.69	0.40	78,92,113,136	0
23	4SU	CY	8	20/21	0.70	0.19	83,99,114,124	0
23	7MG	AY	46	24/25	0.72	0.24	80,94,107,121	0
23	4SU	CW	8	20/21	0.75	0.24	88,94,105,122	0
23	7MG	CY	46	24/25	0.77	0.18	86,95,102,125	0
23	PSU	CY	32	20/21	0.79	0.20	83,92,99,105	0
23	7MG	CW	46	24/25	0.80	0.30	85,98,110,126	0
23	5MU	AY	54	21/22	0.81	0.23	81,91,102,125	0
23	4SU	AY	8	20/21	0.82	0.20	92,98,108,126	0
23	MIA	AY	37	22/30	0.82	0.25	72,87,104,128	0
23	PSU	CW	55	20/21	0.83	0.20	61,83,94,94	0
23	PSU	CY	55	20/21	0.83	0.29	92,98,105,119	0
23	7MG	AW	46	24/25	0.83	0.22	70,83,111,120	0
23	PSU	AY	32	20/21	0.85	0.24	83,91,98,100	0
23	PSU	CY	39	20/21	0.87	0.19	80,88,99,111	0
23	5MU	CW	54	21/22	0.90	0.17	60,72,84,86	0
23	PSU	AY	39	20/21	0.90	0.21	77,86,97,100	0
24	PSU	CX	55	20/21	0.90	0.16	63,69,89,97	0
23	PSU	CW	32	20/21	0.90	0.19	70,85,92,95	0
23	4SU	AW	8	20/21	0.91	0.17	73,85,96,105	0
23	MIA	CW	37	22/30	0.91	0.16	55,66,75,81	0
24	5MU	CX	54	21/22	0.92	0.23	71,80,88,94	0
24	4SU	CX	8	20/21	0.93	0.17	54,78,85,86	0
23	PSU	AW	55	20/21	0.93	0.20	50,70,80,81	0
24	5MU	AX	54	21/22	0.94	0.18	58,65,74,81	0
24	PSU	AX	55	20/21	0.94	0.18	60,67,93,94	0
23	PSU	AW	32	20/21	0.95	0.16	50,60,69,69	0
23	5MU	AW	54	21/22	0.95	0.16	42,58,69,76	0
24	5MC	CX	32	21/22	0.95	0.16	66,71,81,83	0
23	PSU	CW	39	20/21	0.96	0.17	63,72,81,82	0
23	PSU	AW	39	20/21	0.96	0.20	49,59,65,65	0
24	4SU	AX	8	20/21	0.96	0.18	51,64,80,88	0
23	MIA	AW	37	29/30	0.96	0.21	40,49,63,75	0
24	5MC	AX	32	21/22	0.97	0.19	48,54,58,72	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	BA	3571	1/1	0.29	0.10	66,66,66,66	0
56	MG	DA	3565	1/1	0.51	0.18	70,70,70,70	0
56	MG	CJ	5001	1/1	0.53	0.14	76,76,76,76	0
56	MG	AA	3192	1/1	0.56	0.30	69,69,69,69	0
56	MG	AA	3098	1/1	0.57	0.17	68,68,68,68	0
56	MG	DA	3419	1/1	0.59	0.17	44,44,44,44	0
56	MG	BA	3224	1/1	0.60	0.18	64,64,64,64	0
56	MG	BA	3677	1/1	0.61	0.12	62,62,62,62	0
56	MG	DA	3182	1/1	0.63	0.30	64,64,64,64	0
56	MG	BA	3712	1/1	0.63	0.13	64,64,64,64	0
56	MG	DA	3241	1/1	0.64	0.20	50,50,50,50	0
56	MG	CA	3051	1/1	0.64	0.11	66,66,66,66	0
56	MG	BA	3683	1/1	0.64	0.15	61,61,61,61	0
56	MG	DB	3005	1/1	0.65	0.28	64,64,64,64	0
56	MG	DA	3596	1/1	0.65	0.44	63,63,63,63	0
56	MG	BA	3726	1/1	0.65	0.23	70,70,70,70	0
56	MG	DA	3109	1/1	0.65	0.20	66,66,66,66	0
56	MG	AA	3110	1/1	0.66	0.22	61,61,61,61	0
56	MG	BA	3804	1/1	0.66	0.10	58,58,58,58	0
56	MG	CA	3064	1/1	0.67	0.11	57,57,57,57	0
56	MG	DA	3607	1/1	0.68	0.34	53,53,53,53	0
56	MG	DA	3505	1/1	0.68	0.12	66,66,66,66	0
56	MG	DA	3051	1/1	0.68	0.20	56,56,56,56	0
56	MG	BR	202	1/1	0.68	0.41	53,53,53,53	0
56	MG	BA	3527	1/1	0.68	0.11	52,52,52,52	0
56	MG	DA	3504	1/1	0.69	0.13	60,60,60,60	0
56	MG	BA	3725	1/1	0.69	0.22	67,67,67,67	0
56	MG	BA	3446	1/1	0.70	0.27	52,52,52,52	0
56	MG	AX	3003	1/1	0.70	0.16	66,66,66,66	0
56	MG	BA	3249	1/1	0.70	0.29	74,74,74,74	0
56	MG	BA	3639	1/1	0.70	0.29	59,59,59,59	0
56	MG	CX	3006	1/1	0.70	0.50	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3728	1/1	0.70	0.10	72,72,72,72	0
56	MG	CA	3049	1/1	0.70	0.23	68,68,68,68	0
56	MG	CA	3027	1/1	0.71	0.51	70,70,70,70	0
56	MG	BA	3431	1/1	0.71	0.27	55,55,55,55	0
56	MG	BA	3030	1/1	0.71	0.19	50,50,50,50	0
56	MG	BA	3470	1/1	0.72	0.16	48,48,48,48	0
56	MG	BA	3079	1/1	0.72	0.32	57,57,57,57	0
56	MG	BA	3734	1/1	0.72	0.35	60,60,60,60	0
56	MG	AA	3082	1/1	0.72	0.26	68,68,68,68	0
56	MG	DA	3041	1/1	0.72	0.18	55,55,55,55	0
56	MG	DA	3466	1/1	0.72	0.17	62,62,62,62	0
56	MG	DA	3448	1/1	0.73	0.14	41,41,41,41	0
56	MG	BA	3807	1/1	0.73	0.11	67,67,67,67	0
56	MG	DA	3538	1/1	0.73	0.27	56,56,56,56	0
56	MG	DA	3098	1/1	0.73	0.21	43,43,43,43	0
56	MG	DA	3541	1/1	0.73	0.08	54,54,54,54	0
56	MG	B8	101	1/1	0.73	0.14	42,42,42,42	0
56	MG	DA	3238	1/1	0.73	0.24	61,61,61,61	0
56	MG	AA	3095	1/1	0.73	0.28	68,68,68,68	0
56	MG	AA	3204	1/1	0.73	0.19	71,71,71,71	0
56	MG	AA	3004	1/1	0.73	0.14	67,67,67,67	0
56	MG	BA	3434	1/1	0.74	0.20	34,34,34,34	0
56	MG	DA	3028	1/1	0.74	0.17	70,70,70,70	0
56	MG	BA	3221	1/1	0.74	0.20	54,54,54,54	0
56	MG	BA	3605	1/1	0.74	0.13	61,61,61,61	0
56	MG	BA	3333	1/1	0.74	0.11	61,61,61,61	0
56	MG	DA	3312	1/1	0.74	0.14	52,52,52,52	0
56	MG	BA	3689	1/1	0.75	0.22	57,57,57,57	0
56	MG	BA	3020	1/1	0.75	0.20	61,61,61,61	0
56	MG	DA	3452	1/1	0.75	0.24	61,61,61,61	0
56	MG	DA	3066	1/1	0.75	0.13	65,65,65,65	0
56	MG	DA	3251	1/1	0.75	0.27	51,51,51,51	0
56	MG	BB	3015	1/1	0.75	0.10	51,51,51,51	0
56	MG	BA	3560	1/1	0.75	0.23	35,35,35,35	0
56	MG	CA	3055	1/1	0.76	0.12	53,53,53,53	0
56	MG	AA	3038	1/1	0.76	0.14	51,51,51,51	0
56	MG	DA	3521	1/1	0.76	0.17	51,51,51,51	0
56	MG	DA	3209	1/1	0.76	0.24	52,52,52,52	0
56	MG	BA	3315	1/1	0.76	0.14	56,56,56,56	0
56	MG	DA	3632	1/1	0.76	0.16	58,58,58,58	0
56	MG	DA	3436	1/1	0.77	0.13	54,54,54,54	0
56	MG	DA	3286	1/1	0.77	0.14	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	3663	1/1	0.77	0.14	50,50,50,50	0
56	MG	AA	3042	1/1	0.77	0.21	57,57,57,57	0
56	MG	CA	3069	1/1	0.77	0.12	68,68,68,68	0
56	MG	DA	3604	1/1	0.77	0.13	57,57,57,57	0
56	MG	CA	3025	1/1	0.77	0.14	61,61,61,61	0
56	MG	BA	3229	1/1	0.78	0.31	51,51,51,51	0
56	MG	BA	3204	1/1	0.78	0.33	66,66,66,66	0
56	MG	DA	3404	1/1	0.78	0.20	51,51,51,51	0
56	MG	DA	3542	1/1	0.78	0.20	63,63,63,63	0
56	MG	DW	3002	1/1	0.78	0.39	65,65,65,65	0
56	MG	DA	3487	1/1	0.78	0.24	65,65,65,65	0
56	MG	BA	3241	1/1	0.78	0.22	52,52,52,52	0
56	MG	DA	3199	1/1	0.78	0.41	52,52,52,52	0
56	MG	BA	3377	1/1	0.78	0.23	30,30,30,30	0
56	MG	DA	3445	1/1	0.78	0.23	72,72,72,72	0
56	MG	DA	3614	1/1	0.78	0.14	50,50,50,50	0
56	MG	AW	3001	1/1	0.78	0.09	55,55,55,55	0
56	MG	DA	3127	1/1	0.78	0.27	38,38,38,38	0
56	MG	DA	3605	1/1	0.79	0.15	52,52,52,52	0
56	MG	AA	3114	1/1	0.79	0.34	51,51,51,51	0
56	MG	AA	3072	1/1	0.79	0.19	68,68,68,68	0
56	MG	BA	3699	1/1	0.79	0.18	42,42,42,42	0
56	MG	CA	3026	1/1	0.79	0.29	64,64,64,64	0
56	MG	CA	3169	1/1	0.79	0.21	65,65,65,65	0
56	MG	BA	3162	1/1	0.79	0.26	46,46,46,46	0
56	MG	BB	3009	1/1	0.79	0.27	58,58,58,58	0
56	MG	DA	3325	1/1	0.79	0.25	57,57,57,57	0
56	MG	DA	3547	1/1	0.79	0.17	65,65,65,65	0
56	MG	B1	102	1/1	0.79	0.41	68,68,68,68	0
56	MG	BA	3367	1/1	0.79	0.33	53,53,53,53	0
56	MG	DA	3508	1/1	0.79	0.10	59,59,59,59	0
56	MG	BA	3347	1/1	0.79	0.26	48,48,48,48	0
56	MG	DA	3224	1/1	0.79	0.35	48,48,48,48	0
56	MG	DA	3105	1/1	0.79	0.19	60,60,60,60	0
56	MG	BA	3028	1/1	0.79	0.14	59,59,59,59	0
56	MG	CA	3065	1/1	0.79	0.07	65,65,65,65	0
56	MG	BA	3720	1/1	0.79	0.23	46,46,46,46	0
56	MG	DA	3645	1/1	0.80	0.20	44,44,44,44	0
56	MG	AA	3040	1/1	0.80	0.16	59,59,59,59	0
56	MG	CA	3020	1/1	0.80	0.13	73,73,73,73	0
56	MG	BA	3585	1/1	0.80	0.39	55,55,55,55	0
56	MG	DA	3509	1/1	0.80	0.18	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	3277	1/1	0.80	0.19	54,54,54,54	0
56	MG	BQ	3005	1/1	0.80	0.30	50,50,50,50	0
56	MG	AA	3091	1/1	0.80	0.10	70,70,70,70	0
56	MG	BA	3095	1/1	0.80	0.30	53,53,53,53	0
56	MG	BA	3583	1/1	0.80	0.12	45,45,45,45	0
56	MG	CA	3061	1/1	0.80	0.22	56,56,56,56	0
56	MG	AW	3002	1/1	0.80	0.17	69,69,69,69	0
56	MG	CA	3034	1/1	0.80	0.13	61,61,61,61	0
56	MG	DA	3170	1/1	0.80	0.09	50,50,50,50	0
56	MG	DA	3513	1/1	0.80	0.17	50,50,50,50	0
56	MG	BA	3595	1/1	0.80	0.21	32,32,32,32	0
56	MG	BA	3070	1/1	0.80	0.26	55,55,55,55	0
56	MG	BA	3516	1/1	0.81	0.22	65,65,65,65	0
56	MG	DA	3309	1/1	0.81	0.14	42,42,42,42	0
56	MG	DA	3213	1/1	0.81	0.23	61,61,61,61	0
56	MG	BA	3831	1/1	0.81	0.95	52,52,52,52	0
56	MG	BA	3409	1/1	0.81	0.23	62,62,62,62	0
56	MG	DA	3037	1/1	0.81	0.16	54,54,54,54	0
56	MG	AA	3062	1/1	0.81	0.14	60,60,60,60	0
56	MG	AA	3153	1/1	0.81	0.18	55,55,55,55	0
56	MG	DA	3121	1/1	0.81	0.28	41,41,41,41	0
56	MG	DA	3540	1/1	0.81	0.18	67,67,67,67	0
56	MG	DA	3566	1/1	0.81	0.17	48,48,48,48	0
56	MG	DA	3115	1/1	0.81	0.18	41,41,41,41	0
56	MG	DA	3393	1/1	0.81	0.10	52,52,52,52	0
56	MG	BB	3011	1/1	0.81	0.06	59,59,59,59	0
56	MG	BA	3472	1/1	0.81	0.23	70,70,70,70	0
56	MG	AA	3087	1/1	0.81	0.34	52,52,52,52	0
56	MG	BA	3022	1/1	0.81	0.26	40,40,40,40	0
56	MG	DA	3468	1/1	0.81	0.20	44,44,44,44	0
56	MG	CA	3070	1/1	0.81	0.14	71,71,71,71	0
56	MG	BA	3317	1/1	0.82	0.19	64,64,64,64	0
56	MG	CA	3081	1/1	0.82	0.18	58,58,58,58	0
56	MG	BA	3101	1/1	0.82	0.25	60,60,60,60	0
56	MG	BA	3413	1/1	0.82	0.19	41,41,41,41	0
56	MG	DA	3429	1/1	0.82	0.26	40,40,40,40	0
56	MG	AA	3068	1/1	0.82	0.17	60,60,60,60	0
56	MG	BA	3603	1/1	0.82	0.11	54,54,54,54	0
56	MG	CA	3122	1/1	0.82	0.15	70,70,70,70	0
56	MG	DA	3305	1/1	0.82	0.18	28,28,28,28	0
56	MG	DA	3214	1/1	0.82	0.34	47,47,47,47	0
56	MG	AA	3190	1/1	0.82	0.11	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3408	1/1	0.82	0.20	55,55,55,55	0
56	MG	DA	3568	1/1	0.82	0.12	54,54,54,54	0
56	MG	BA	3590	1/1	0.82	0.23	32,32,32,32	0
56	MG	AA	3145	1/1	0.82	0.16	58,58,58,58	0
56	MG	AA	3125	1/1	0.82	0.11	71,71,71,71	0
56	MG	DA	3493	1/1	0.82	0.27	58,58,58,58	0
56	MG	BA	3005	1/1	0.82	0.21	51,51,51,51	0
56	MG	BR	203	1/1	0.82	0.20	44,44,44,44	0
56	MG	DA	3583	1/1	0.82	0.25	60,60,60,60	0
56	MG	BB	3008	1/1	0.83	0.30	54,54,54,54	0
56	MG	CX	3002	1/1	0.83	0.20	81,81,81,81	0
56	MG	BA	3289	1/1	0.83	0.26	55,55,55,55	0
56	MG	BA	3064	1/1	0.83	0.36	61,61,61,61	0
56	MG	AA	3170	1/1	0.83	0.13	57,57,57,57	0
56	MG	BA	3659	1/1	0.83	0.27	53,53,53,53	0
56	MG	BA	3442	1/1	0.83	0.11	59,59,59,59	0
56	MG	BA	3295	1/1	0.83	0.26	42,42,42,42	0
56	MG	BA	3553	1/1	0.83	0.16	42,42,42,42	0
56	MG	DA	3078	1/1	0.83	0.11	45,45,45,45	0
56	MG	BA	3002	1/1	0.83	0.37	62,62,62,62	0
56	MG	DA	3620	1/1	0.83	0.17	62,62,62,62	0
56	MG	DA	3234	1/1	0.83	0.19	45,45,45,45	0
56	MG	AA	3073	1/1	0.83	0.24	58,58,58,58	0
56	MG	AA	3175	1/1	0.83	0.20	54,54,54,54	0
56	MG	AA	3085	1/1	0.83	0.15	55,55,55,55	0
56	MG	BA	3705	1/1	0.83	0.17	54,54,54,54	0
56	MG	BQ	3003	1/1	0.83	0.15	54,54,54,54	0
56	MG	DA	3410	1/1	0.83	0.15	62,62,62,62	0
56	MG	CA	3037	1/1	0.83	0.25	55,55,55,55	0
56	MG	BA	3291	1/1	0.83	0.21	71,71,71,71	0
56	MG	CA	3023	1/1	0.83	0.22	55,55,55,55	0
56	MG	BA	3393	1/1	0.83	0.26	54,54,54,54	0
56	MG	BA	3706	1/1	0.83	0.23	50,50,50,50	0
56	MG	BA	3407	1/1	0.83	0.19	37,37,37,37	0
56	MG	DA	3155	1/1	0.83	0.29	40,40,40,40	0
56	MG	AA	3205	1/1	0.83	0.12	51,51,51,51	0
56	MG	BA	3758	1/1	0.83	0.14	34,34,34,34	0
56	MG	DA	3451	1/1	0.83	0.30	56,56,56,56	0
56	MG	BA	3365	1/1	0.83	0.13	49,49,49,49	0
56	MG	BA	3227	1/1	0.83	0.26	57,57,57,57	0
56	MG	BA	3742	1/1	0.83	0.17	51,51,51,51	0
56	MG	CA	3011	1/1	0.83	0.17	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	BA	3220	1/1	0.83	0.20	55,55,55,55	0
56	MG	BA	3322	1/1	0.83	0.16	32,32,32,32	0
56	MG	DA	3387	1/1	0.83	0.22	56,56,56,56	0
56	MG	DA	3110	1/1	0.83	0.13	50,50,50,50	0
56	MG	BA	3238	1/1	0.83	0.25	43,43,43,43	0
56	MG	DA	3611	1/1	0.83	0.32	55,55,55,55	0
56	MG	AA	3113	1/1	0.84	0.20	59,59,59,59	0
56	MG	DA	3319	1/1	0.84	0.30	43,43,43,43	0
56	MG	BA	3629	1/1	0.84	0.14	56,56,56,56	0
56	MG	BA	3402	1/1	0.84	0.19	30,30,30,30	0
56	MG	DA	3231	1/1	0.84	0.32	57,57,57,57	0
56	MG	AA	3165	1/1	0.84	0.25	60,60,60,60	0
56	MG	BA	3514	1/1	0.84	0.25	41,41,41,41	0
56	MG	BA	3481	1/1	0.84	0.29	45,45,45,45	0
56	MG	BA	3152	1/1	0.84	0.18	43,43,43,43	0
56	MG	AX	3009	1/1	0.84	0.25	71,71,71,71	0
56	MG	DA	3423	1/1	0.84	0.14	51,51,51,51	0
56	MG	CA	3147	1/1	0.84	0.18	72,72,72,72	0
56	MG	DA	3192	1/1	0.84	0.18	51,51,51,51	0
56	MG	BA	3692	1/1	0.84	0.28	57,57,57,57	0
56	MG	DV	3002	1/1	0.84	0.43	57,57,57,57	0
56	MG	CA	3087	1/1	0.84	0.15	63,63,63,63	0
56	MG	AN	502	1/1	0.84	0.13	52,52,52,52	0
56	MG	DA	3580	1/1	0.84	0.19	64,64,64,64	0
56	MG	BA	3693	1/1	0.84	0.13	70,70,70,70	0
56	MG	CA	3121	1/1	0.84	0.23	75,75,75,75	0
56	MG	DA	3591	1/1	0.84	0.20	56,56,56,56	0
56	MG	BA	3736	1/1	0.84	0.17	56,56,56,56	0
56	MG	CA	3152	1/1	0.84	0.36	79,79,79,79	0
56	MG	BA	3716	1/1	0.84	0.24	54,54,54,54	0
56	MG	BA	3196	1/1	0.84	0.23	51,51,51,51	0
56	MG	BA	3192	1/1	0.84	0.25	48,48,48,48	0
56	MG	BA	3467	1/1	0.84	0.20	39,39,39,39	0
56	MG	DA	3549	1/1	0.84	0.18	57,57,57,57	0
56	MG	DA	3343	1/1	0.84	0.20	40,40,40,40	0
56	MG	BA	3181	1/1	0.84	0.24	41,41,41,41	0
56	MG	DA	3674	1/1	0.84	0.40	73,73,73,73	0
56	MG	AA	3161	1/1	0.84	0.26	46,46,46,46	0
56	MG	DA	3642	1/1	0.84	0.15	49,49,49,49	0
56	MG	DA	3176	1/1	0.85	0.12	52,52,52,52	0
56	MG	DA	3168	1/1	0.85	0.29	53,53,53,53	0
56	MG	DA	3359	1/1	0.85	0.13	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	CA	3072	1/1	0.85	0.14	62,62,62,62	0
56	MG	BA	3798	1/1	0.85	0.14	61,61,61,61	0
56	MG	CA	3133	1/1	0.85	0.20	65,65,65,65	0
56	MG	AA	3136	1/1	0.85	0.08	53,53,53,53	0
56	MG	AA	3181	1/1	0.85	0.19	75,75,75,75	0
56	MG	DA	3102	1/1	0.85	0.12	57,57,57,57	0
56	MG	BA	3100	1/1	0.85	0.14	45,45,45,45	0
56	MG	AA	3112	1/1	0.85	0.14	57,57,57,57	0
56	MG	AA	3100	1/1	0.85	0.08	68,68,68,68	0
56	MG	CA	3137	1/1	0.85	0.19	52,52,52,52	0
56	MG	AW	3005	1/1	0.85	0.39	68,68,68,68	0
56	MG	DA	3665	1/1	0.85	0.17	58,58,58,58	0
56	MG	BA	3371	1/1	0.85	0.13	54,54,54,54	0
56	MG	BA	3634	1/1	0.85	0.16	64,64,64,64	0
56	MG	CA	3084	1/1	0.85	0.31	69,69,69,69	0
56	MG	DA	3403	1/1	0.85	0.15	57,57,57,57	0
56	MG	BA	3138	1/1	0.85	0.16	48,48,48,48	0
56	MG	CA	3031	1/1	0.85	0.14	53,53,53,53	0
56	MG	DA	3569	1/1	0.85	0.21	57,57,57,57	0
56	MG	DA	3671	1/1	0.85	0.22	59,59,59,59	0
56	MG	BA	3170	1/1	0.85	0.23	48,48,48,48	0
56	MG	DA	3086	1/1	0.85	0.19	62,62,62,62	0
56	MG	AA	3071	1/1	0.85	0.25	62,62,62,62	0
56	MG	DA	3144	1/1	0.85	0.14	63,63,63,63	0
56	MG	BA	3802	1/1	0.85	0.13	56,56,56,56	0
56	MG	BA	3673	1/1	0.85	0.17	47,47,47,47	0
56	MG	AA	3142	1/1	0.85	0.23	62,62,62,62	0
56	MG	BA	3171	1/1	0.85	0.33	53,53,53,53	0
59	ZN	D4	501	1/1	0.85	0.08	119,119,119,119	0
57	PCY	CA	3178	40/40	0.85	0.35	58,78,89,91	0
56	MG	BA	3225	1/1	0.85	0.35	42,42,42,42	0
56	MG	AA	3226	1/1	0.85	0.26	58,58,58,58	0
56	MG	BA	3017	1/1	0.85	0.22	50,50,50,50	0
56	MG	AA	3116	1/1	0.85	0.27	61,61,61,61	0
56	MG	DA	3103	1/1	0.85	0.22	50,50,50,50	0
56	MG	AA	3059	1/1	0.85	0.29	59,59,59,59	0
56	MG	AA	3199	1/1	0.85	0.24	59,59,59,59	0
56	MG	CA	3028	1/1	0.86	0.19	60,60,60,60	0
56	MG	BA	3674	1/1	0.86	0.11	47,47,47,47	0
56	MG	DA	3366	1/1	0.86	0.13	50,50,50,50	0
56	MG	CA	3053	1/1	0.86	0.07	74,74,74,74	0
56	MG	DA	3287	1/1	0.86	0.16	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	CA	3083	1/1	0.86	0.09	58,58,58,58	0
56	MG	AA	3159	1/1	0.86	0.09	59,59,59,59	0
56	MG	CA	3019	1/1	0.86	0.39	58,58,58,58	0
56	MG	BA	3757	1/1	0.86	0.16	25,25,25,25	0
56	MG	DA	3053	1/1	0.86	0.09	45,45,45,45	0
56	MG	BA	3618	1/1	0.86	0.18	63,63,63,63	0
56	MG	BA	3567	1/1	0.86	0.18	50,50,50,50	0
56	MG	CA	3018	1/1	0.86	0.18	45,45,45,45	0
56	MG	BA	3747	1/1	0.86	0.27	42,42,42,42	0
56	MG	DA	3184	1/1	0.86	0.30	49,49,49,49	0
56	MG	DA	3453	1/1	0.86	0.23	45,45,45,45	0
56	MG	DA	3628	1/1	0.86	0.14	56,56,56,56	0
56	MG	CA	3007	1/1	0.86	0.18	69,69,69,69	0
56	MG	BA	3357	1/1	0.86	0.19	46,46,46,46	0
56	MG	DA	3179	1/1	0.86	0.08	46,46,46,46	0
56	MG	BA	3180	1/1	0.86	0.12	58,58,58,58	0
56	MG	DA	3424	1/1	0.86	0.24	63,63,63,63	0
56	MG	DA	3246	1/1	0.86	0.12	39,39,39,39	0
56	MG	BA	3278	1/1	0.86	0.10	55,55,55,55	0
56	MG	BA	3392	1/1	0.86	0.19	46,46,46,46	0
56	MG	DA	3186	1/1	0.86	0.23	40,40,40,40	0
56	MG	BA	3444	1/1	0.86	0.18	48,48,48,48	0
56	MG	BA	3014	1/1	0.86	0.23	33,33,33,33	0
56	MG	BA	3218	1/1	0.86	0.18	44,44,44,44	0
56	MG	BE	307	1/1	0.86	0.20	70,70,70,70	0
56	MG	CA	3005	1/1	0.86	0.10	58,58,58,58	0
56	MG	BA	3203	1/1	0.86	0.15	39,39,39,39	0
56	MG	DA	3397	1/1	0.86	0.17	49,49,49,49	0
56	MG	BA	3748	1/1	0.86	0.17	63,63,63,63	0
56	MG	DA	3002	1/1	0.86	0.17	68,68,68,68	0
56	MG	BA	3197	1/1	0.86	0.31	36,36,36,36	0
56	MG	BA	3311	1/1	0.86	0.20	37,37,37,37	0
56	MG	BA	3266	1/1	0.86	0.24	64,64,64,64	0
56	MG	DA	3306	1/1	0.86	0.13	42,42,42,42	0
56	MG	CA	3016	1/1	0.86	0.10	61,61,61,61	0
56	MG	DA	3079	1/1	0.86	0.17	48,48,48,48	0
56	MG	DA	3057	1/1	0.86	0.08	47,47,47,47	0
56	MG	BA	3782	1/1	0.86	0.11	51,51,51,51	0
56	MG	AA	3228	1/1	0.86	0.10	68,68,68,68	0
56	MG	BA	3695	1/1	0.86	0.22	48,48,48,48	0
56	MG	BA	3102	1/1	0.86	0.27	54,54,54,54	0
56	MG	AA	3130	1/1	0.86	0.16	43,43,43,43	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	0.18	61,61,61,61	0
56	MG	DA	3507	1/1	0.86	0.22	60,60,60,60	0
56	MG	DA	3610	1/1	0.86	0.22	48,48,48,48	0
56	MG	BB	3004	1/1	0.86	0.11	47,47,47,47	0
56	MG	DA	3149	1/1	0.86	0.10	48,48,48,48	0
56	MG	AA	3202	1/1	0.86	0.15	57,57,57,57	0
56	MG	BA	3753	1/1	0.86	0.29	44,44,44,44	0
56	MG	BA	3670	1/1	0.86	0.20	47,47,47,47	0
56	MG	DA	3615	1/1	0.86	0.33	47,47,47,47	0
56	MG	DA	3106	1/1	0.86	0.27	61,61,61,61	0
56	MG	CA	3059	1/1	0.86	0.42	67,67,67,67	0
56	MG	BA	3637	1/1	0.86	0.20	59,59,59,59	0
56	MG	AA	3003	1/1	0.86	0.16	66,66,66,66	0
56	MG	BB	3019	1/1	0.86	0.16	49,49,49,49	0
56	MG	BA	3298	1/1	0.86	0.18	68,68,68,68	0
56	MG	CA	3054	1/1	0.86	0.16	71,71,71,71	0
56	MG	AX	3002	1/1	0.86	0.24	53,53,53,53	0
56	MG	DA	3085	1/1	0.86	0.19	52,52,52,52	0
56	MG	DA	3321	1/1	0.86	0.27	35,35,35,35	0
56	MG	BA	3717	1/1	0.86	0.19	58,58,58,58	0
56	MG	BA	3274	1/1	0.86	0.16	49,49,49,49	0
56	MG	BA	3760	1/1	0.86	0.26	68,68,68,68	0
56	MG	BA	3140	1/1	0.86	0.23	46,46,46,46	0
56	MG	DA	3060	1/1	0.86	0.23	47,47,47,47	0
56	MG	BA	3326	1/1	0.87	0.24	38,38,38,38	0
56	MG	DA	3273	1/1	0.87	0.11	45,45,45,45	0
56	MG	DA	3297	1/1	0.87	0.12	66,66,66,66	0
56	MG	BA	3752	1/1	0.87	0.18	19,19,19,19	0
56	MG	AA	3221	1/1	0.87	0.14	49,49,49,49	0
56	MG	BA	3478	1/1	0.87	0.20	59,59,59,59	0
56	MG	BA	3511	1/1	0.87	0.23	54,54,54,54	0
56	MG	DA	3068	1/1	0.87	0.17	58,58,58,58	0
56	MG	AA	3032	1/1	0.87	0.09	75,75,75,75	0
56	MG	BA	3060	1/1	0.87	0.20	56,56,56,56	0
56	MG	BA	3455	1/1	0.87	0.17	39,39,39,39	0
56	MG	DA	3324	1/1	0.87	0.29	39,39,39,39	0
56	MG	DR	5001	1/1	0.87	0.08	58,58,58,58	0
56	MG	DA	3044	1/1	0.87	0.10	58,58,58,58	0
56	MG	BA	3557	1/1	0.87	0.22	56,56,56,56	0
56	MG	BA	3523	1/1	0.87	0.15	64,64,64,64	0
56	MG	AA	3134	1/1	0.87	0.22	69,69,69,69	0
56	MG	BA	3606	1/1	0.87	0.19	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	DA	3439	1/1	0.87	0.14	50,50,50,50	0
56	MG	BF	307	1/1	0.87	0.23	39,39,39,39	0
56	MG	DA	3235	1/1	0.87	0.28	61,61,61,61	0
56	MG	BA	3668	1/1	0.87	0.18	56,56,56,56	0
56	MG	BA	3604	1/1	0.87	0.28	72,72,72,72	0
56	MG	BA	3290	1/1	0.87	0.30	58,58,58,58	0
56	MG	DA	3567	1/1	0.87	0.16	46,46,46,46	0
56	MG	BA	3594	1/1	0.87	0.23	24,24,24,24	0
56	MG	DA	3272	1/1	0.87	0.16	44,44,44,44	0
56	MG	BA	3186	1/1	0.87	0.19	51,51,51,51	0
56	MG	BA	3512	1/1	0.87	0.28	27,27,27,27	0
56	MG	BA	3586	1/1	0.87	0.16	65,65,65,65	0
56	MG	BA	3059	1/1	0.87	0.11	55,55,55,55	0
56	MG	BA	3638	1/1	0.87	0.26	38,38,38,38	0
56	MG	DB	3003	1/1	0.87	0.15	68,68,68,68	0
56	MG	BA	3313	1/1	0.87	0.15	46,46,46,46	0
56	MG	BA	3769	1/1	0.87	0.17	56,56,56,56	0
56	MG	AX	3010	1/1	0.87	0.10	62,62,62,62	0
56	MG	BA	3729	1/1	0.87	0.11	52,52,52,52	0
56	MG	DA	3480	1/1	0.87	0.14	48,48,48,48	0
56	MG	DD	303	1/1	0.87	0.25	49,49,49,49	0
56	MG	BA	3113	1/1	0.87	0.32	58,58,58,58	0
56	MG	BA	3435	1/1	0.87	0.16	57,57,57,57	0
56	MG	CA	3060	1/1	0.87	0.24	68,68,68,68	0
56	MG	DA	3623	1/1	0.87	0.15	70,70,70,70	0
56	MG	BA	3133	1/1	0.87	0.30	47,47,47,47	0
56	MG	BW	201	1/1	0.87	0.21	46,46,46,46	0
56	MG	BA	3633	1/1	0.87	0.17	45,45,45,45	0
56	MG	CA	3006	1/1	0.87	0.30	53,53,53,53	0
56	MG	BA	3588	1/1	0.87	0.17	47,47,47,47	0
56	MG	B7	102	1/1	0.87	0.24	58,58,58,58	0
56	MG	BA	3655	1/1	0.87	0.12	50,50,50,50	0
56	MG	DB	3010	1/1	0.87	0.17	55,55,55,55	0
56	MG	AA	3198	1/1	0.87	0.39	70,70,70,70	0
56	MG	DA	3657	1/1	0.87	0.10	67,67,67,67	0
56	MG	DA	3096	1/1	0.87	0.22	51,51,51,51	0
56	MG	BA	3477	1/1	0.87	0.20	55,55,55,55	0
56	MG	DA	3032	1/1	0.87	0.15	40,40,40,40	0
56	MG	BA	3779	1/1	0.87	0.12	59,59,59,59	0
56	MG	BA	3424	1/1	0.87	0.25	24,24,24,24	0
56	MG	BA	3564	1/1	0.88	0.18	41,41,41,41	0
56	MG	BZ	3001	1/1	0.88	0.22	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	DA	3514	1/1	0.88	0.12	41,41,41,41	0
56	MG	DA	3211	1/1	0.88	0.20	48,48,48,48	0
56	MG	BA	3261	1/1	0.88	0.26	44,44,44,44	0
56	MG	B6	102	1/1	0.88	0.32	55,55,55,55	0
56	MG	CA	3090	1/1	0.88	0.17	62,62,62,62	0
56	MG	D8	5001	1/1	0.88	0.23	55,55,55,55	0
56	MG	BA	3275	1/1	0.88	0.13	46,46,46,46	0
56	MG	CA	3111	1/1	0.88	0.21	61,61,61,61	0
56	MG	DD	302	1/1	0.88	0.23	49,49,49,49	0
56	MG	BA	3690	1/1	0.88	0.21	63,63,63,63	0
56	MG	BA	3574	1/1	0.88	0.12	63,63,63,63	0
56	MG	AA	3047	1/1	0.88	0.09	47,47,47,47	0
56	MG	CA	3132	1/1	0.88	0.37	70,70,70,70	0
56	MG	DA	3197	1/1	0.88	0.15	48,48,48,48	0
56	MG	BA	3179	1/1	0.88	0.19	39,39,39,39	0
56	MG	BA	3439	1/1	0.88	0.17	58,58,58,58	0
56	MG	CA	3010	1/1	0.88	0.12	53,53,53,53	0
56	MG	BA	3672	1/1	0.88	0.21	61,61,61,61	0
56	MG	DA	3437	1/1	0.88	0.25	39,39,39,39	0
56	MG	DA	3201	1/1	0.88	0.23	52,52,52,52	0
56	MG	BA	3708	1/1	0.88	0.24	63,63,63,63	0
56	MG	CA	3177	1/1	0.88	0.21	62,62,62,62	0
56	MG	DA	3194	1/1	0.88	0.23	35,35,35,35	0
56	MG	BB	3012	1/1	0.88	0.08	59,59,59,59	0
56	MG	CA	3172	1/1	0.88	0.15	64,64,64,64	0
56	MG	BA	3254	1/1	0.88	0.16	30,30,30,30	0
56	MG	BA	3127	1/1	0.88	0.17	41,41,41,41	0
56	MG	BA	3320	1/1	0.88	0.30	60,60,60,60	0
56	MG	BA	3770	1/1	0.88	0.30	37,37,37,37	0
56	MG	BA	3679	1/1	0.88	0.23	61,61,61,61	0
56	MG	BA	3451	1/1	0.88	0.11	64,64,64,64	0
56	MG	CA	3173	1/1	0.88	0.08	69,69,69,69	0
56	MG	DA	3457	1/1	0.88	0.24	47,47,47,47	0
56	MG	BA	3312	1/1	0.88	0.18	33,33,33,33	0
56	MG	BA	3112	1/1	0.88	0.34	57,57,57,57	0
56	MG	BQ	3002	1/1	0.88	0.16	37,37,37,37	0
56	MG	DA	3477	1/1	0.88	0.08	55,55,55,55	0
56	MG	CA	3085	1/1	0.88	0.20	71,71,71,71	0
56	MG	BA	3743	1/1	0.88	0.18	21,21,21,21	0
56	MG	DA	3187	1/1	0.88	0.12	56,56,56,56	0
56	MG	AA	3139	1/1	0.88	0.14	58,58,58,58	0
56	MG	CA	3153	1/1	0.88	0.16	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	DA	3600	1/1	0.88	0.08	53,53,53,53	0
56	MG	AV	101	1/1	0.88	0.28	59,59,59,59	0
56	MG	BA	3524	1/1	0.88	0.13	53,53,53,53	0
56	MG	B4	502	1/1	0.88	0.12	72,72,72,72	0
56	MG	DA	3408	1/1	0.88	0.22	48,48,48,48	0
56	MG	DA	3248	1/1	0.88	0.31	33,33,33,33	0
56	MG	DB	3004	1/1	0.88	0.15	51,51,51,51	0
56	MG	DA	3434	1/1	0.88	0.46	51,51,51,51	0
56	MG	DA	3222	1/1	0.88	0.18	54,54,54,54	0
56	MG	AA	3011	1/1	0.88	0.20	64,64,64,64	0
56	MG	DA	3145	1/1	0.88	0.32	49,49,49,49	0
56	MG	BA	3205	1/1	0.88	0.24	41,41,41,41	0
56	MG	AA	3155	1/1	0.88	0.18	53,53,53,53	0
56	MG	BA	3264	1/1	0.88	0.29	39,39,39,39	0
56	MG	DA	3495	1/1	0.88	0.09	62,62,62,62	0
56	MG	DA	3399	1/1	0.88	0.18	47,47,47,47	0
56	MG	BA	3777	1/1	0.88	0.23	49,49,49,49	0
56	MG	DA	3034	1/1	0.88	0.15	43,43,43,43	0
56	MG	AA	3018	1/1	0.88	0.10	51,51,51,51	0
56	MG	DA	3395	1/1	0.88	0.19	42,42,42,42	0
56	MG	BA	3727	1/1	0.88	0.14	39,39,39,39	0
56	MG	DA	3247	1/1	0.88	0.38	57,57,57,57	0
56	MG	CA	3029	1/1	0.88	0.38	61,61,61,61	0
56	MG	DA	3546	1/1	0.88	0.11	53,53,53,53	0
56	MG	BA	3047	1/1	0.88	0.15	27,27,27,27	0
56	MG	DA	3320	1/1	0.88	0.16	40,40,40,40	0
56	MG	BA	3114	1/1	0.88	0.36	52,52,52,52	0
56	MG	BA	3482	1/1	0.88	0.22	59,59,59,59	0
56	MG	AA	3094	1/1	0.88	0.23	44,44,44,44	0
56	MG	BE	306	1/1	0.88	0.23	25,25,25,25	0
56	MG	DA	3196	1/1	0.88	0.09	53,53,53,53	0
56	MG	BA	3198	1/1	0.88	0.17	55,55,55,55	0
56	MG	DA	3673	1/1	0.89	0.16	61,61,61,61	0
56	MG	BA	3207	1/1	0.89	0.18	38,38,38,38	0
56	MG	DA	3303	1/1	0.89	0.15	42,42,42,42	0
56	MG	CA	3015	1/1	0.89	0.12	58,58,58,58	0
56	MG	BA	3052	1/1	0.89	0.31	43,43,43,43	0
56	MG	CA	3125	1/1	0.89	0.14	64,64,64,64	0
56	MG	DA	3499	1/1	0.89	0.10	60,60,60,60	0
56	MG	BB	3001	1/1	0.89	0.20	50,50,50,50	0
56	MG	DA	3545	1/1	0.89	0.16	37,37,37,37	0
56	MG	BA	3094	1/1	0.89	0.24	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3358	1/1	0.89	0.42	64,64,64,64	0
56	MG	BA	3292	1/1	0.89	0.15	42,42,42,42	0
56	MG	AA	3197	1/1	0.89	0.14	56,56,56,56	0
56	MG	BA	3427	1/1	0.89	0.25	32,32,32,32	0
56	MG	BA	3356	1/1	0.89	0.13	55,55,55,55	0
56	MG	BA	3088	1/1	0.89	0.16	50,50,50,50	0
56	MG	DA	3516	1/1	0.89	0.09	59,59,59,59	0
56	MG	AA	3030	1/1	0.89	0.16	57,57,57,57	0
56	MG	CA	3146	1/1	0.89	0.05	69,69,69,69	0
56	MG	DA	3323	1/1	0.89	0.32	53,53,53,53	0
56	MG	DA	3602	1/1	0.89	0.34	51,51,51,51	0
56	MG	CA	3161	1/1	0.89	0.10	70,70,70,70	0
56	MG	BA	3832	1/1	0.89	0.09	37,37,37,37	0
56	MG	DA	3643	1/1	0.89	0.10	60,60,60,60	0
56	MG	BA	3328	1/1	0.89	0.16	60,60,60,60	0
56	MG	BA	3544	1/1	0.89	0.20	35,35,35,35	0
56	MG	BA	3437	1/1	0.89	0.20	28,28,28,28	0
56	MG	DA	3225	1/1	0.89	0.23	54,54,54,54	0
56	MG	B2	3001	1/1	0.89	0.17	45,45,45,45	0
56	MG	BA	3667	1/1	0.89	0.11	52,52,52,52	0
56	MG	DA	3229	1/1	0.89	0.12	55,55,55,55	0
56	MG	CA	3115	1/1	0.89	0.18	62,62,62,62	0
56	MG	DA	3132	1/1	0.89	0.43	41,41,41,41	0
56	MG	BA	3250	1/1	0.89	0.20	40,40,40,40	0
56	MG	AA	3048	1/1	0.89	0.08	51,51,51,51	0
56	MG	DA	3370	1/1	0.89	0.08	46,46,46,46	0
56	MG	BA	3703	1/1	0.89	0.23	48,48,48,48	0
56	MG	BA	3714	1/1	0.89	0.06	47,47,47,47	0
56	MG	B5	102	1/1	0.89	0.18	45,45,45,45	0
56	MG	DA	3587	1/1	0.89	0.09	61,61,61,61	0
56	MG	DA	3470	1/1	0.89	0.16	42,42,42,42	0
56	MG	AA	3051	1/1	0.89	0.17	62,62,62,62	0
56	MG	BE	302	1/1	0.89	0.17	34,34,34,34	0
56	MG	DA	3172	1/1	0.89	0.32	51,51,51,51	0
56	MG	AA	3212	1/1	0.89	0.30	59,59,59,59	0
56	MG	B3	101	1/1	0.89	0.31	48,48,48,48	0
56	MG	BA	3269	1/1	0.89	0.38	53,53,53,53	0
56	MG	BA	3723	1/1	0.89	0.16	47,47,47,47	0
56	MG	BA	3835	1/1	0.89	0.20	46,46,46,46	0
56	MG	DA	3269	1/1	0.89	0.20	32,32,32,32	0
56	MG	BA	3419	1/1	0.89	0.17	39,39,39,39	0
56	MG	BN	3002	1/1	0.89	0.12	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AX	3008	1/1	0.89	0.36	57,57,57,57	0
56	MG	BA	3491	1/1	0.89	0.23	47,47,47,47	0
56	MG	CA	3002	1/1	0.89	0.07	51,51,51,51	0
56	MG	AA	3022	1/1	0.89	0.28	55,55,55,55	0
56	MG	DA	3375	1/1	0.89	0.11	40,40,40,40	0
56	MG	AA	3230	1/1	0.89	0.18	68,68,68,68	0
56	MG	BA	3778	1/1	0.89	0.14	35,35,35,35	0
56	MG	DA	3358	1/1	0.89	0.32	45,45,45,45	0
56	MG	BA	3115	1/1	0.89	0.08	67,67,67,67	0
56	MG	BA	3508	1/1	0.89	0.09	54,54,54,54	0
56	MG	BN	3001	1/1	0.89	0.33	51,51,51,51	0
56	MG	BA	3700	1/1	0.89	0.20	54,54,54,54	0
56	MG	DA	3536	1/1	0.89	0.32	54,54,54,54	0
56	MG	BA	3255	1/1	0.89	0.26	58,58,58,58	0
56	MG	BA	3739	1/1	0.89	0.19	46,46,46,46	0
56	MG	DA	3443	1/1	0.89	0.10	51,51,51,51	0
56	MG	DA	3612	1/1	0.89	0.23	56,56,56,56	0
56	MG	BA	3004	1/1	0.89	0.24	36,36,36,36	0
56	MG	DA	3655	1/1	0.89	0.17	57,57,57,57	0
56	MG	AA	3078	1/1	0.89	0.06	48,48,48,48	0
56	MG	DA	3069	1/1	0.89	0.39	53,53,53,53	0
56	MG	DA	3454	1/1	0.89	0.28	54,54,54,54	0
56	MG	BA	3791	1/1	0.89	0.13	47,47,47,47	0
56	MG	AA	3102	1/1	0.89	0.34	51,51,51,51	0
56	MG	DA	3157	1/1	0.89	0.28	44,44,44,44	0
56	MG	DA	3107	1/1	0.89	0.19	49,49,49,49	0
56	MG	DA	3630	1/1	0.89	0.17	49,49,49,49	0
56	MG	BA	3046	1/1	0.89	0.18	43,43,43,43	0
56	MG	CX	3004	1/1	0.89	0.33	54,54,54,54	0
56	MG	DA	3396	1/1	0.89	0.13	45,45,45,45	0
56	MG	BA	3820	1/1	0.89	0.20	45,45,45,45	0
56	MG	DA	3500	1/1	0.89	0.12	45,45,45,45	0
56	MG	DA	3354	1/1	0.90	0.24	46,46,46,46	0
56	MG	AX	3012	1/1	0.90	0.23	59,59,59,59	0
56	MG	DA	3333	1/1	0.90	0.07	50,50,50,50	0
56	MG	BA	3768	1/1	0.90	0.06	56,56,56,56	0
56	MG	AA	3115	1/1	0.90	0.11	51,51,51,51	0
56	MG	DA	3181	1/1	0.90	0.30	45,45,45,45	0
56	MG	AA	3020	1/1	0.90	0.15	59,59,59,59	0
56	MG	BA	3838	1/1	0.90	0.19	50,50,50,50	0
56	MG	DA	3061	1/1	0.90	0.21	56,56,56,56	0
56	MG	AA	3057	1/1	0.90	0.20	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	BA	3464	1/1	0.90	0.21	56,56,56,56	0
56	MG	CA	3036	1/1	0.90	0.09	60,60,60,60	0
56	MG	BA	3724	1/1	0.90	0.34	44,44,44,44	0
56	MG	BA	3433	1/1	0.90	0.19	57,57,57,57	0
56	MG	BA	3149	1/1	0.90	0.13	53,53,53,53	0
56	MG	DA	3539	1/1	0.90	0.14	46,46,46,46	0
56	MG	BA	3749	1/1	0.90	0.25	45,45,45,45	0
56	MG	BA	3233	1/1	0.90	0.33	48,48,48,48	0
56	MG	AA	3035	1/1	0.90	0.07	46,46,46,46	0
56	MG	DA	3271	1/1	0.90	0.14	47,47,47,47	0
56	MG	DA	3597	1/1	0.90	0.10	51,51,51,51	0
56	MG	CA	3175	1/1	0.90	0.16	39,39,39,39	0
56	MG	BA	3139	1/1	0.90	0.09	61,61,61,61	0
56	MG	DA	3089	1/1	0.90	0.23	46,46,46,46	0
56	MG	DA	3407	1/1	0.90	0.08	46,46,46,46	0
56	MG	CA	3176	1/1	0.90	0.13	43,43,43,43	0
56	MG	AA	3089	1/1	0.90	0.27	57,57,57,57	0
56	MG	BA	3293	1/1	0.90	0.25	52,52,52,52	0
56	MG	BA	3492	1/1	0.90	0.12	55,55,55,55	0
56	MG	AA	3055	1/1	0.90	0.22	58,58,58,58	0
56	MG	AA	3086	1/1	0.90	0.20	52,52,52,52	0
56	MG	BA	3410	1/1	0.90	0.10	46,46,46,46	0
56	MG	BA	3751	1/1	0.90	0.14	45,45,45,45	0
56	MG	CA	3123	1/1	0.90	0.12	80,80,80,80	0
56	MG	BA	3504	1/1	0.90	0.19	58,58,58,58	0
56	MG	DA	3183	1/1	0.90	0.22	58,58,58,58	0
56	MG	AD	502	1/1	0.90	0.29	56,56,56,56	0
56	MG	BA	3738	1/1	0.90	0.11	58,58,58,58	0
56	MG	BA	3447	1/1	0.90	0.23	26,26,26,26	0
56	MG	DA	3533	1/1	0.90	0.30	53,53,53,53	0
56	MG	BA	3089	1/1	0.90	0.29	45,45,45,45	0
56	MG	DA	3020	1/1	0.90	0.14	50,50,50,50	0
56	MG	AA	3080	1/1	0.90	0.21	47,47,47,47	0
56	MG	BA	3143	1/1	0.90	0.25	42,42,42,42	0
56	MG	DA	3376	1/1	0.90	0.24	54,54,54,54	0
56	MG	BA	3015	1/1	0.90	0.23	47,47,47,47	0
56	MG	BA	3641	1/1	0.90	0.19	49,49,49,49	0
56	MG	DA	3087	1/1	0.90	0.21	49,49,49,49	0
56	MG	CA	3139	1/1	0.90	0.15	61,61,61,61	0
56	MG	CA	3013	1/1	0.90	0.10	63,63,63,63	0
56	MG	DB	3002	1/1	0.90	0.15	56,56,56,56	0
56	MG	BA	3228	1/1	0.90	0.22	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	3346	1/1	0.90	0.14	32,32,32,32	0
56	MG	DA	3616	1/1	0.90	0.07	45,45,45,45	0
56	MG	DA	3460	1/1	0.90	0.17	65,65,65,65	0
56	MG	DQ	3003	1/1	0.90	0.19	58,58,58,58	0
56	MG	DA	3422	1/1	0.90	0.36	43,43,43,43	0
56	MG	BA	3579	1/1	0.90	0.08	47,47,47,47	0
56	MG	DA	3355	1/1	0.90	0.10	50,50,50,50	0
56	MG	DA	3368	1/1	0.90	0.19	50,50,50,50	0
56	MG	DF	302	1/1	0.90	0.18	43,43,43,43	0
56	MG	CA	3101	1/1	0.90	0.22	54,54,54,54	0
56	MG	DA	3531	1/1	0.90	0.33	54,54,54,54	0
56	MG	BA	3828	1/1	0.90	0.20	37,37,37,37	0
56	MG	AA	3058	1/1	0.90	0.21	57,57,57,57	0
56	MG	DA	3574	1/1	0.90	0.20	51,51,51,51	0
56	MG	CA	3167	1/1	0.90	0.17	48,48,48,48	0
56	MG	DA	3648	1/1	0.90	0.12	60,60,60,60	0
56	MG	BA	3172	1/1	0.90	0.23	45,45,45,45	0
56	MG	CA	3024	1/1	0.90	0.14	63,63,63,63	0
56	MG	DA	3029	1/1	0.90	0.21	51,51,51,51	0
56	MG	BA	3718	1/1	0.90	0.20	46,46,46,46	0
56	MG	AA	3158	1/1	0.90	0.27	59,59,59,59	0
56	MG	DA	3621	1/1	0.90	0.29	45,45,45,45	0
56	MG	BO	5001	1/1	0.90	0.17	55,55,55,55	0
56	MG	BA	3283	1/1	0.90	0.12	36,36,36,36	0
56	MG	DA	3506	1/1	0.90	0.10	48,48,48,48	0
56	MG	BW	202	1/1	0.90	0.31	49,49,49,49	0
56	MG	DA	3093	1/1	0.90	0.10	57,57,57,57	0
56	MG	AA	3169	1/1	0.90	0.19	64,64,64,64	0
56	MG	BA	3566	1/1	0.90	0.23	30,30,30,30	0
56	MG	AA	3185	1/1	0.90	0.26	53,53,53,53	0
56	MG	BA	3787	1/1	0.90	0.22	59,59,59,59	0
56	MG	BA	3273	1/1	0.90	0.29	53,53,53,53	0
56	MG	BA	3248	1/1	0.90	0.15	45,45,45,45	0
56	MG	CA	3126	1/1	0.90	0.17	72,72,72,72	0
56	MG	BA	3797	1/1	0.90	0.20	52,52,52,52	0
56	MG	BA	3620	1/1	0.90	0.15	47,47,47,47	0
56	MG	CA	3017	1/1	0.90	0.17	49,49,49,49	0
56	MG	BA	3150	1/1	0.90	0.12	48,48,48,48	0
56	MG	AA	3033	1/1	0.90	0.15	57,57,57,57	0
56	MG	DA	3039	1/1	0.90	0.22	56,56,56,56	0
56	MG	AA	3017	1/1	0.90	0.12	62,62,62,62	0
56	MG	BA	3023	1/1	0.90	0.27	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	3093	1/1	0.90	0.32	38,38,38,38	0
56	MG	CA	3124	1/1	0.90	0.16	79,79,79,79	0
56	MG	CA	3067	1/1	0.90	0.10	79,79,79,79	0
56	MG	DA	3140	1/1	0.90	0.11	34,34,34,34	0
56	MG	DA	3191	1/1	0.90	0.32	44,44,44,44	0
56	MG	BA	3686	1/1	0.90	0.24	30,30,30,30	0
56	MG	CA	3040	1/1	0.90	0.12	58,58,58,58	0
56	MG	BA	3475	1/1	0.90	0.15	53,53,53,53	0
56	MG	AA	3213	1/1	0.90	0.08	69,69,69,69	0
56	MG	BA	3348	1/1	0.90	0.13	54,54,54,54	0
56	MG	DA	3178	1/1	0.90	0.12	54,54,54,54	0
56	MG	DA	3534	1/1	0.90	0.26	74,74,74,74	0
56	MG	DA	3515	1/1	0.90	0.14	57,57,57,57	0
56	MG	DA	3019	1/1	0.90	0.15	57,57,57,57	0
56	MG	DA	3310	1/1	0.90	0.22	55,55,55,55	0
56	MG	DA	3563	1/1	0.90	0.15	42,42,42,42	0
56	MG	BA	3569	1/1	0.90	0.33	57,57,57,57	0
56	MG	DA	3142	1/1	0.90	0.11	45,45,45,45	0
56	MG	DA	3221	1/1	0.90	0.17	49,49,49,49	0
56	MG	DA	3101	1/1	0.90	0.12	53,53,53,53	0
56	MG	AA	3079	1/1	0.90	0.22	47,47,47,47	0
56	MG	BA	3548	1/1	0.90	0.28	48,48,48,48	0
56	MG	CA	3164	1/1	0.90	0.07	54,54,54,54	0
56	MG	DA	3380	1/1	0.90	0.09	55,55,55,55	0
56	MG	BA	3049	1/1	0.90	0.27	37,37,37,37	0
56	MG	DA	3405	1/1	0.90	0.13	52,52,52,52	0
56	MG	DB	3006	1/1	0.90	0.18	62,62,62,62	0
56	MG	BA	3364	1/1	0.90	0.15	42,42,42,42	0
56	MG	CA	3097	1/1	0.91	0.23	57,57,57,57	0
56	MG	AW	3006	1/1	0.91	0.16	50,50,50,50	0
56	MG	CA	3134	1/1	0.91	0.14	70,70,70,70	0
56	MG	AY	3003	1/1	0.91	0.14	48,48,48,48	0
56	MG	DA	3606	1/1	0.91	0.22	54,54,54,54	0
56	MG	BA	3438	1/1	0.91	0.19	47,47,47,47	0
56	MG	DB	3011	1/1	0.91	0.09	52,52,52,52	0
56	MG	DA	3649	1/1	0.91	0.07	64,64,64,64	0
56	MG	AA	3183	1/1	0.91	0.14	71,71,71,71	0
56	MG	BA	3526	1/1	0.91	0.09	32,32,32,32	0
56	MG	DA	3072	1/1	0.91	0.09	36,36,36,36	0
56	MG	BP	202	1/1	0.91	0.20	34,34,34,34	0
56	MG	BA	3031	1/1	0.91	0.23	56,56,56,56	0
56	MG	BA	3666	1/1	0.91	0.12	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	3081	1/1	0.91	0.27	45,45,45,45	0
56	MG	DA	3581	1/1	0.91	0.19	63,63,63,63	0
56	MG	BA	3058	1/1	0.91	0.20	36,36,36,36	0
56	MG	BA	3453	1/1	0.91	0.21	42,42,42,42	0
56	MG	BA	3812	1/1	0.91	0.18	52,52,52,52	0
56	MG	DA	3418	1/1	0.91	0.22	37,37,37,37	0
56	MG	DA	3415	1/1	0.91	0.24	50,50,50,50	0
56	MG	CA	3046	1/1	0.91	0.09	56,56,56,56	0
56	MG	BA	3701	1/1	0.91	0.14	51,51,51,51	0
56	MG	BA	3342	1/1	0.91	0.18	51,51,51,51	0
56	MG	DA	3537	1/1	0.91	0.17	55,55,55,55	0
56	MG	AW	3003	1/1	0.91	0.31	59,59,59,59	0
56	MG	BA	3236	1/1	0.91	0.15	43,43,43,43	0
56	MG	DA	3223	1/1	0.91	0.29	54,54,54,54	0
56	MG	BA	3622	1/1	0.91	0.19	31,31,31,31	0
56	MG	BA	3789	1/1	0.91	0.17	39,39,39,39	0
56	MG	BA	3201	1/1	0.91	0.17	40,40,40,40	0
56	MG	BA	3090	1/1	0.91	0.20	37,37,37,37	0
56	MG	BA	3153	1/1	0.91	0.22	39,39,39,39	0
56	MG	BA	3345	1/1	0.91	0.12	44,44,44,44	0
56	MG	DA	3365	1/1	0.91	0.34	57,57,57,57	0
56	MG	DA	3402	1/1	0.91	0.27	65,65,65,65	0
56	MG	BB	3022	1/1	0.91	0.14	62,62,62,62	0
56	MG	CA	3073	1/1	0.91	0.32	48,48,48,48	0
56	MG	DA	3001	1/1	0.91	0.26	58,58,58,58	0
56	MG	DA	3328	1/1	0.91	0.15	47,47,47,47	0
56	MG	BD	306	1/1	0.91	0.36	22,22,22,22	0
56	MG	DA	3384	1/1	0.91	0.10	52,52,52,52	0
56	MG	AA	3223	1/1	0.91	0.30	59,59,59,59	0
56	MG	AA	3005	1/1	0.91	0.07	53,53,53,53	0
56	MG	AA	3106	1/1	0.91	0.17	51,51,51,51	0
56	MG	CA	3157	1/1	0.91	0.28	64,64,64,64	0
56	MG	DA	3210	1/1	0.91	0.11	44,44,44,44	0
56	MG	BA	3436	1/1	0.91	0.22	46,46,46,46	0
56	MG	BA	3360	1/1	0.91	0.09	50,50,50,50	0
56	MG	BA	3219	1/1	0.91	0.19	29,29,29,29	0
56	MG	DD	307	1/1	0.91	0.14	56,56,56,56	0
56	MG	AA	3194	1/1	0.91	0.17	58,58,58,58	0
56	MG	AA	3216	1/1	0.91	0.13	72,72,72,72	0
56	MG	BA	3065	1/1	0.91	0.12	37,37,37,37	0
56	MG	BA	3314	1/1	0.91	0.15	47,47,47,47	0
56	MG	AA	3049	1/1	0.91	0.22	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	3625	1/1	0.91	0.14	57,57,57,57	0
59	ZN	D9	501	1/1	0.91	0.07	63,63,63,63	0
56	MG	BA	3650	1/1	0.91	0.12	57,57,57,57	0
56	MG	BA	3774	1/1	0.91	0.19	43,43,43,43	0
56	MG	AA	3066	1/1	0.91	0.12	44,44,44,44	0
56	MG	BA	3613	1/1	0.91	0.13	45,45,45,45	0
56	MG	AA	3143	1/1	0.91	0.16	73,73,73,73	0
56	MG	CA	3086	1/1	0.91	0.12	61,61,61,61	0
56	MG	DA	3026	1/1	0.91	0.14	42,42,42,42	0
56	MG	DA	3351	1/1	0.91	0.12	39,39,39,39	0
56	MG	BA	3144	1/1	0.91	0.09	43,43,43,43	0
56	MG	BA	3503	1/1	0.91	0.23	58,58,58,58	0
56	MG	AA	3189	1/1	0.91	0.17	59,59,59,59	0
56	MG	BA	3763	1/1	0.91	0.27	34,34,34,34	0
56	MG	BA	3537	1/1	0.91	0.13	49,49,49,49	0
56	MG	AA	3021	1/1	0.91	0.17	45,45,45,45	0
56	MG	BA	3341	1/1	0.91	0.16	57,57,57,57	0
56	MG	DA	3131	1/1	0.91	0.15	52,52,52,52	0
56	MG	BG	203	1/1	0.91	0.07	36,36,36,36	0
56	MG	BE	305	1/1	0.91	0.22	59,59,59,59	0
56	MG	DA	3432	1/1	0.91	0.15	56,56,56,56	0
56	MG	BA	3441	1/1	0.91	0.27	46,46,46,46	0
56	MG	BA	3568	1/1	0.91	0.25	52,52,52,52	0
56	MG	BB	3003	1/1	0.91	0.12	40,40,40,40	0
56	MG	BA	3124	1/1	0.91	0.20	38,38,38,38	0
56	MG	BA	3240	1/1	0.91	0.26	45,45,45,45	0
56	MG	BA	3592	1/1	0.91	0.14	29,29,29,29	0
56	MG	DA	3595	1/1	0.91	0.18	61,61,61,61	0
56	MG	BA	3016	1/1	0.91	0.20	44,44,44,44	0
56	MG	DA	3497	1/1	0.91	0.32	51,51,51,51	0
56	MG	DA	3589	1/1	0.91	0.15	63,63,63,63	0
56	MG	BA	3251	1/1	0.91	0.32	52,52,52,52	0
56	MG	DA	3406	1/1	0.91	0.15	40,40,40,40	0
56	MG	BA	3762	1/1	0.91	0.38	40,40,40,40	0
56	MG	BA	3414	1/1	0.91	0.22	29,29,29,29	0
56	MG	BA	3062	1/1	0.91	0.25	57,57,57,57	0
56	MG	BA	3707	1/1	0.91	0.14	66,66,66,66	0
56	MG	CA	3043	1/1	0.91	0.26	54,54,54,54	0
56	MG	DA	3638	1/1	0.91	0.25	60,60,60,60	0
56	MG	BA	3815	1/1	0.91	0.28	50,50,50,50	0
56	MG	DA	3293	1/1	0.91	0.11	60,60,60,60	0
56	MG	BA	3096	1/1	0.91	0.30	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	AA	3015	1/1	0.91	0.17	60,60,60,60	0
56	MG	AA	3103	1/1	0.91	0.14	59,59,59,59	0
56	MG	BA	3352	1/1	0.91	0.26	29,29,29,29	0
56	MG	DA	3236	1/1	0.91	0.13	48,48,48,48	0
56	MG	DA	3318	1/1	0.91	0.18	42,42,42,42	0
56	MG	BA	3429	1/1	0.91	0.24	47,47,47,47	0
56	MG	BA	3756	1/1	0.91	0.21	27,27,27,27	0
56	MG	BA	3581	1/1	0.91	0.11	38,38,38,38	0
56	MG	BA	3445	1/1	0.91	0.20	32,32,32,32	0
56	MG	AA	3156	1/1	0.91	0.14	52,52,52,52	0
56	MG	CW	3001	1/1	0.91	0.32	63,63,63,63	0
56	MG	DA	3650	1/1	0.91	0.27	44,44,44,44	0
56	MG	CA	3099	1/1	0.91	0.11	62,62,62,62	0
59	ZN	CN	501	1/1	0.91	0.04	92,92,92,92	0
56	MG	BA	3702	1/1	0.91	0.07	51,51,51,51	0
56	MG	DA	3585	1/1	0.91	0.10	51,51,51,51	0
56	MG	BA	3307	1/1	0.91	0.17	37,37,37,37	0
56	MG	BA	3280	1/1	0.91	0.24	49,49,49,49	0
56	MG	BA	3500	1/1	0.91	0.18	26,26,26,26	0
56	MG	BA	3387	1/1	0.91	0.06	65,65,65,65	0
56	MG	DA	3119	1/1	0.92	0.20	62,62,62,62	0
56	MG	DA	3548	1/1	0.92	0.17	65,65,65,65	0
56	MG	B9	502	1/1	0.92	0.10	57,57,57,57	0
56	MG	AA	3050	1/1	0.92	0.10	70,70,70,70	0
56	MG	BA	3151	1/1	0.92	0.28	42,42,42,42	0
56	MG	CA	3104	1/1	0.92	0.11	64,64,64,64	0
56	MG	BA	3232	1/1	0.92	0.14	37,37,37,37	0
56	MG	BF	305	1/1	0.92	0.26	47,47,47,47	0
56	MG	BA	3411	1/1	0.92	0.13	36,36,36,36	0
56	MG	BA	3593	1/1	0.92	0.14	42,42,42,42	0
56	MG	BA	3428	1/1	0.92	0.30	38,38,38,38	0
56	MG	B5	103	1/1	0.92	0.18	44,44,44,44	0
56	MG	CA	3114	1/1	0.92	0.20	56,56,56,56	0
56	MG	BA	3375	1/1	0.92	0.15	35,35,35,35	0
56	MG	BA	3396	1/1	0.92	0.22	55,55,55,55	0
56	MG	CA	3074	1/1	0.92	0.39	55,55,55,55	0
56	MG	AA	3210	1/1	0.92	0.19	69,69,69,69	0
56	MG	DA	3661	1/1	0.92	0.20	42,42,42,42	0
56	MG	CA	3143	1/1	0.92	0.15	62,62,62,62	0
56	MG	AX	3005	1/1	0.92	0.15	44,44,44,44	0
56	MG	BA	3837	1/1	0.92	0.20	40,40,40,40	0
56	MG	BA	3522	1/1	0.92	0.28	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3618	1/1	0.92	0.26	54,54,54,54	0
56	MG	CA	3092	1/1	0.92	0.15	44,44,44,44	0
56	MG	CA	3119	1/1	0.92	0.26	58,58,58,58	0
56	MG	DA	3167	1/1	0.92	0.25	47,47,47,47	0
56	MG	DA	3367	1/1	0.92	0.08	51,51,51,51	0
56	MG	CA	3170	1/1	0.92	0.12	64,64,64,64	0
56	MG	BA	3131	1/1	0.92	0.18	38,38,38,38	0
56	MG	BA	3484	1/1	0.92	0.29	36,36,36,36	0
56	MG	B1	101	1/1	0.92	0.38	44,44,44,44	0
56	MG	BA	3520	1/1	0.92	0.32	47,47,47,47	0
57	PCY	AA	3231	40/40	0.92	0.33	45,69,81,87	0
56	MG	BA	3099	1/1	0.92	0.16	50,50,50,50	0
56	MG	BA	3765	1/1	0.92	0.17	33,33,33,33	0
56	MG	DA	3025	1/1	0.92	0.16	44,44,44,44	0
56	MG	DA	3122	1/1	0.92	0.22	36,36,36,36	0
56	MG	BA	3061	1/1	0.92	0.17	40,40,40,40	0
60	K	CX	3001	1/1	0.92	0.17	74,74,74,74	0
56	MG	DA	3220	1/1	0.92	0.19	46,46,46,46	0
56	MG	DA	3441	1/1	0.92	0.09	43,43,43,43	0
56	MG	AA	3120	1/1	0.92	0.16	59,59,59,59	0
56	MG	DA	3526	1/1	0.92	0.22	47,47,47,47	0
56	MG	DA	3208	1/1	0.92	0.10	59,59,59,59	0
56	MG	DE	304	1/1	0.92	0.22	47,47,47,47	0
56	MG	DA	3491	1/1	0.92	0.17	45,45,45,45	0
56	MG	DA	3556	1/1	0.92	0.19	64,64,64,64	0
56	MG	DA	3147	1/1	0.92	0.09	44,44,44,44	0
56	MG	BA	3063	1/1	0.92	0.17	47,47,47,47	0
56	MG	BA	3651	1/1	0.92	0.19	56,56,56,56	0
56	MG	DA	3043	1/1	0.92	0.17	48,48,48,48	0
56	MG	DA	3138	1/1	0.92	0.41	59,59,59,59	0
56	MG	BA	3825	1/1	0.92	0.18	65,65,65,65	0
56	MG	AA	3215	1/1	0.92	0.19	57,57,57,57	0
56	MG	BA	3083	1/1	0.92	0.29	47,47,47,47	0
56	MG	BA	3623	1/1	0.92	0.13	52,52,52,52	0
56	MG	DA	3391	1/1	0.92	0.09	44,44,44,44	0
56	MG	CA	3082	1/1	0.92	0.13	63,63,63,63	0
56	MG	BA	3582	1/1	0.92	0.16	44,44,44,44	0
56	MG	BA	3117	1/1	0.92	0.23	42,42,42,42	0
56	MG	DA	3523	1/1	0.92	0.14	57,57,57,57	0
56	MG	DA	3663	1/1	0.92	0.25	60,60,60,60	0
56	MG	BA	3449	1/1	0.92	0.29	60,60,60,60	0
56	MG	B3	102	1/1	0.92	0.11	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	AA	3127	1/1	0.92	0.18	48,48,48,48	0
56	MG	BA	3194	1/1	0.92	0.20	37,37,37,37	0
56	MG	DA	3483	1/1	0.92	0.38	48,48,48,48	0
56	MG	AA	3138	1/1	0.92	0.17	34,34,34,34	0
56	MG	BA	3253	1/1	0.92	0.21	40,40,40,40	0
56	MG	DA	3390	1/1	0.92	0.07	54,54,54,54	0
56	MG	AA	3150	1/1	0.92	0.44	55,55,55,55	0
56	MG	DA	3485	1/1	0.92	0.11	44,44,44,44	0
56	MG	BA	3001	1/1	0.92	0.20	43,43,43,43	0
56	MG	DA	3094	1/1	0.92	0.19	52,52,52,52	0
56	MG	BA	3376	1/1	0.92	0.11	34,34,34,34	0
56	MG	DA	3250	1/1	0.92	0.13	61,61,61,61	0
56	MG	BA	3681	1/1	0.92	0.22	53,53,53,53	0
56	MG	BA	3354	1/1	0.92	0.17	31,31,31,31	0
56	MG	BA	3259	1/1	0.92	0.40	52,52,52,52	0
56	MG	BA	3237	1/1	0.92	0.14	36,36,36,36	0
56	MG	BA	3284	1/1	0.92	0.26	51,51,51,51	0
56	MG	AA	3016	1/1	0.92	0.16	46,46,46,46	0
56	MG	DA	3635	1/1	0.92	0.15	52,52,52,52	0
56	MG	AA	3144	1/1	0.92	0.12	50,50,50,50	0
56	MG	AA	3174	1/1	0.92	0.13	60,60,60,60	0
56	MG	DA	3027	1/1	0.92	0.21	53,53,53,53	0
56	MG	DA	3672	1/1	0.92	0.28	52,52,52,52	0
56	MG	DA	3239	1/1	0.92	0.20	54,54,54,54	0
56	MG	AA	3061	1/1	0.92	0.08	54,54,54,54	0
56	MG	DA	3204	1/1	0.92	0.31	51,51,51,51	0
56	MG	CA	3148	1/1	0.92	0.11	67,67,67,67	0
56	MG	CA	3159	1/1	0.92	0.13	57,57,57,57	0
56	MG	CA	3162	1/1	0.92	0.14	67,67,67,67	0
56	MG	BA	3601	1/1	0.92	0.16	42,42,42,42	0
56	MG	DA	3335	1/1	0.92	0.19	32,32,32,32	0
56	MG	BA	3669	1/1	0.92	0.13	42,42,42,42	0
56	MG	AA	3209	1/1	0.92	0.30	51,51,51,51	0
56	MG	DA	3667	1/1	0.92	0.96	73,73,73,73	0
56	MG	BA	3597	1/1	0.92	0.20	44,44,44,44	0
56	MG	DF	301	1/1	0.92	0.15	47,47,47,47	0
56	MG	CA	3021	1/1	0.92	0.13	42,42,42,42	0
56	MG	DA	3394	1/1	0.92	0.14	49,49,49,49	0
56	MG	DA	3586	1/1	0.92	0.09	44,44,44,44	0
56	MG	BA	3740	1/1	0.92	0.21	51,51,51,51	0
56	MG	BA	3394	1/1	0.92	0.21	52,52,52,52	0
56	MG	BA	3305	1/1	0.92	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	3542	1/1	0.92	0.16	48,48,48,48	0
56	MG	BA	3182	1/1	0.92	0.31	41,41,41,41	0
56	MG	CA	3004	1/1	0.92	0.07	71,71,71,71	0
56	MG	AA	3101	1/1	0.92	0.17	54,54,54,54	0
56	MG	CA	3128	1/1	0.92	0.10	63,63,63,63	0
56	MG	DA	3636	1/1	0.92	0.24	56,56,56,56	0
56	MG	AA	3044	1/1	0.92	0.32	71,71,71,71	0
56	MG	AA	3023	1/1	0.92	0.15	37,37,37,37	0
56	MG	DA	3195	1/1	0.92	0.19	57,57,57,57	0
56	MG	BA	3351	1/1	0.92	0.17	34,34,34,34	0
56	MG	DA	3502	1/1	0.92	0.20	64,64,64,64	0
56	MG	BA	3158	1/1	0.92	0.19	44,44,44,44	0
56	MG	AA	3081	1/1	0.92	0.26	58,58,58,58	0
56	MG	BA	3344	1/1	0.92	0.14	37,37,37,37	0
56	MG	AA	3148	1/1	0.92	0.15	63,63,63,63	0
56	MG	DA	3190	1/1	0.92	0.26	45,45,45,45	0
59	ZN	DY	501	1/1	0.92	0.09	106,106,106,106	0
56	MG	DA	3295	1/1	0.92	0.17	58,58,58,58	0
56	MG	CA	3151	1/1	0.92	0.08	65,65,65,65	0
56	MG	BA	3509	1/1	0.92	0.25	39,39,39,39	0
56	MG	AA	3109	1/1	0.92	0.32	64,64,64,64	0
56	MG	DA	3378	1/1	0.92	0.13	45,45,45,45	0
56	MG	BA	3271	1/1	0.92	0.11	26,26,26,26	0
56	MG	BA	3808	1/1	0.92	0.14	34,34,34,34	0
56	MG	BA	3287	1/1	0.92	0.29	54,54,54,54	0
56	MG	BB	3020	1/1	0.92	0.16	54,54,54,54	0
56	MG	CA	3098	1/1	0.92	0.22	43,43,43,43	0
56	MG	AX	3004	1/1	0.92	0.21	70,70,70,70	0
56	MG	DA	3503	1/1	0.92	0.14	37,37,37,37	0
56	MG	DA	3288	1/1	0.92	0.16	61,61,61,61	0
56	MG	DA	3203	1/1	0.92	0.28	37,37,37,37	0
56	MG	BA	3294	1/1	0.92	0.20	45,45,45,45	0
56	MG	BA	3130	1/1	0.92	0.26	48,48,48,48	0
56	MG	CA	3117	1/1	0.92	0.10	48,48,48,48	0
56	MG	DA	3401	1/1	0.92	0.29	36,36,36,36	0
56	MG	BA	3626	1/1	0.92	0.18	49,49,49,49	0
56	MG	BA	3617	1/1	0.92	0.13	64,64,64,64	0
56	MG	BB	3018	1/1	0.92	0.15	77,77,77,77	0
56	MG	BA	3530	1/1	0.92	0.20	51,51,51,51	0
56	MG	DA	3111	1/1	0.92	0.14	33,33,33,33	0
56	MG	DA	3300	1/1	0.92	0.26	60,60,60,60	0
56	MG	BA	3019	1/1	0.92	0.32	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	3045	1/1	0.92	0.32	59,59,59,59	0
56	MG	BA	3270	1/1	0.92	0.24	57,57,57,57	0
56	MG	AA	3067	1/1	0.92	0.09	59,59,59,59	0
56	MG	DA	3133	1/1	0.92	0.29	40,40,40,40	0
56	MG	DA	3338	1/1	0.93	0.19	40,40,40,40	0
56	MG	DA	3033	1/1	0.93	0.22	31,31,31,31	0
56	MG	BA	3474	1/1	0.93	0.09	61,61,61,61	0
56	MG	BA	3636	1/1	0.93	0.10	53,53,53,53	0
56	MG	BA	3529	1/1	0.93	0.16	33,33,33,33	0
56	MG	DA	3212	1/1	0.93	0.29	44,44,44,44	0
56	MG	AA	3171	1/1	0.93	0.10	48,48,48,48	0
56	MG	BA	3721	1/1	0.93	0.18	47,47,47,47	0
56	MG	BA	3007	1/1	0.93	0.24	51,51,51,51	0
56	MG	DA	3150	1/1	0.93	0.06	41,41,41,41	0
56	MG	BA	3773	1/1	0.93	0.22	49,49,49,49	0
56	MG	AA	3222	1/1	0.93	0.24	67,67,67,67	0
56	MG	DA	3137	1/1	0.93	0.13	54,54,54,54	0
56	MG	BA	3370	1/1	0.93	0.12	60,60,60,60	0
56	MG	DA	3498	1/1	0.93	0.09	57,57,57,57	0
56	MG	BA	3412	1/1	0.93	0.20	41,41,41,41	0
56	MG	DA	3259	1/1	0.93	0.12	34,34,34,34	0
56	MG	BA	3786	1/1	0.93	0.10	37,37,37,37	0
56	MG	DA	3256	1/1	0.93	0.12	47,47,47,47	0
56	MG	CA	3003	1/1	0.93	0.24	58,58,58,58	0
56	MG	CA	3032	1/1	0.93	0.23	52,52,52,52	0
56	MG	BA	3136	1/1	0.93	0.12	58,58,58,58	0
56	MG	AA	3090	1/1	0.93	0.35	53,53,53,53	0
56	MG	BA	3252	1/1	0.93	0.24	45,45,45,45	0
56	MG	DA	3075	1/1	0.93	0.12	39,39,39,39	0
56	MG	AA	3083	1/1	0.93	0.15	52,52,52,52	0
56	MG	DA	3092	1/1	0.93	0.26	48,48,48,48	0
56	MG	BA	3805	1/1	0.93	0.16	21,21,21,21	0
56	MG	BA	3648	1/1	0.93	0.37	53,53,53,53	0
56	MG	DA	3572	1/1	0.93	0.26	28,28,28,28	0
56	MG	DA	3550	1/1	0.93	0.08	51,51,51,51	0
56	MG	BA	3310	1/1	0.93	0.20	57,57,57,57	0
56	MG	CA	3109	1/1	0.93	0.24	68,68,68,68	0
56	MG	BA	3576	1/1	0.93	0.17	48,48,48,48	0
56	MG	BA	3422	1/1	0.93	0.18	32,32,32,32	0
56	MG	BA	3337	1/1	0.93	0.17	35,35,35,35	0
56	MG	DA	3146	1/1	0.93	0.27	46,46,46,46	0
56	MG	BA	3704	1/1	0.93	0.23	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	BF	311	1/1	0.93	0.18	43,43,43,43	0
56	MG	DA	3090	1/1	0.93	0.21	45,45,45,45	0
56	MG	BA	3423	1/1	0.93	0.18	23,23,23,23	0
56	MG	DA	3180	1/1	0.93	0.14	51,51,51,51	0
56	MG	DA	3461	1/1	0.93	0.13	56,56,56,56	0
56	MG	BD	301	1/1	0.93	0.21	49,49,49,49	0
56	MG	AY	3002	1/1	0.93	0.12	68,68,68,68	0
56	MG	BA	3810	1/1	0.93	0.25	50,50,50,50	0
56	MG	DA	3609	1/1	0.93	0.16	60,60,60,60	0
56	MG	AA	3077	1/1	0.93	0.14	49,49,49,49	0
56	MG	B6	101	1/1	0.93	0.18	48,48,48,48	0
56	MG	DA	3304	1/1	0.93	0.12	40,40,40,40	0
56	MG	BA	3754	1/1	0.93	0.17	60,60,60,60	0
56	MG	CA	3076	1/1	0.93	0.19	56,56,56,56	0
56	MG	AA	3208	1/1	0.93	0.16	45,45,45,45	0
56	MG	AA	3140	1/1	0.93	0.11	71,71,71,71	0
56	MG	AA	3111	1/1	0.93	0.18	52,52,52,52	0
56	MG	BA	3145	1/1	0.93	0.26	32,32,32,32	0
56	MG	DE	302	1/1	0.93	0.20	39,39,39,39	0
56	MG	DA	3551	1/1	0.93	0.16	55,55,55,55	0
56	MG	BA	3619	1/1	0.93	0.40	51,51,51,51	0
56	MG	BA	3033	1/1	0.93	0.26	33,33,33,33	0
56	MG	BX	101	1/1	0.93	0.26	65,65,65,65	0
56	MG	BB	3005	1/1	0.93	0.19	64,64,64,64	0
56	MG	BA	3081	1/1	0.93	0.19	49,49,49,49	0
56	MG	D0	102	1/1	0.93	0.17	62,62,62,62	0
56	MG	BA	3116	1/1	0.93	0.15	29,29,29,29	0
56	MG	BA	3711	1/1	0.93	0.26	45,45,45,45	0
56	MG	AA	3218	1/1	0.93	0.25	53,53,53,53	0
56	MG	DA	3046	1/1	0.93	0.37	57,57,57,57	0
56	MG	DA	3255	1/1	0.93	0.05	59,59,59,59	0
56	MG	BA	3628	1/1	0.93	0.17	30,30,30,30	0
56	MG	AA	3002	1/1	0.93	0.08	62,62,62,62	0
56	MG	BA	3260	1/1	0.93	0.56	57,57,57,57	0
56	MG	BA	3244	1/1	0.93	0.10	63,63,63,63	0
56	MG	BA	3156	1/1	0.93	0.23	41,41,41,41	0
56	MG	BA	3304	1/1	0.93	0.20	39,39,39,39	0
56	MG	CA	3154	1/1	0.93	0.17	62,62,62,62	0
56	MG	AA	3054	1/1	0.93	0.43	52,52,52,52	0
56	MG	AA	3008	1/1	0.93	0.15	54,54,54,54	0
56	MG	BA	3199	1/1	0.93	0.09	53,53,53,53	0
56	MG	BA	3493	1/1	0.93	0.13	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3420	1/1	0.93	0.16	46,46,46,46	0
56	MG	DA	3578	1/1	0.93	0.10	55,55,55,55	0
56	MG	DA	3233	1/1	0.93	0.25	43,43,43,43	0
56	MG	DA	3135	1/1	0.93	0.11	50,50,50,50	0
56	MG	DA	3030	1/1	0.93	0.28	40,40,40,40	0
56	MG	DA	3561	1/1	0.93	0.22	48,48,48,48	0
56	MG	BA	3685	1/1	0.93	0.17	59,59,59,59	0
56	MG	DA	3442	1/1	0.93	0.15	44,44,44,44	0
56	MG	BA	3554	1/1	0.93	0.21	37,37,37,37	0
56	MG	BA	3578	1/1	0.93	0.25	47,47,47,47	0
56	MG	BA	3097	1/1	0.93	0.17	52,52,52,52	0
56	MG	DA	3383	1/1	0.93	0.24	37,37,37,37	0
56	MG	BA	3732	1/1	0.93	0.26	40,40,40,40	0
56	MG	AA	3024	1/1	0.93	0.15	58,58,58,58	0
56	MG	DA	3205	1/1	0.93	0.21	47,47,47,47	0
56	MG	CA	3038	1/1	0.93	0.19	46,46,46,46	0
56	MG	BA	3741	1/1	0.93	0.11	28,28,28,28	0
56	MG	BA	3366	1/1	0.93	0.17	45,45,45,45	0
56	MG	BA	3279	1/1	0.93	0.22	43,43,43,43	0
56	MG	BA	3323	1/1	0.93	0.22	39,39,39,39	0
56	MG	DA	3562	1/1	0.93	0.34	58,58,58,58	0
56	MG	BA	3374	1/1	0.93	0.08	37,37,37,37	0
56	MG	DA	3518	1/1	0.93	0.18	50,50,50,50	0
56	MG	BB	3002	1/1	0.93	0.18	52,52,52,52	0
56	MG	AA	3056	1/1	0.93	0.19	46,46,46,46	0
56	MG	BA	3430	1/1	0.93	0.33	32,32,32,32	0
56	MG	DA	3095	1/1	0.93	0.27	47,47,47,47	0
56	MG	DA	3070	1/1	0.93	0.23	48,48,48,48	0
56	MG	BA	3819	1/1	0.93	0.24	32,32,32,32	0
56	MG	BA	3106	1/1	0.93	0.47	50,50,50,50	0
56	MG	BA	3426	1/1	0.93	0.21	22,22,22,22	0
56	MG	DA	3613	1/1	0.93	0.14	50,50,50,50	0
56	MG	BA	3616	1/1	0.93	0.12	53,53,53,53	0
56	MG	BA	3698	1/1	0.93	0.13	48,48,48,48	0
56	MG	DU	3002	1/1	0.93	0.22	50,50,50,50	0
56	MG	BA	3235	1/1	0.93	0.16	37,37,37,37	0
56	MG	DA	3409	1/1	0.93	0.09	47,47,47,47	0
56	MG	DA	3369	1/1	0.93	0.05	61,61,61,61	0
56	MG	CA	3120	1/1	0.93	0.12	64,64,64,64	0
56	MG	DA	3675	1/1	0.93	0.28	44,44,44,44	0
56	MG	BA	3719	1/1	0.93	0.13	42,42,42,42	0
56	MG	AA	3166	1/1	0.93	0.13	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3302	1/1	0.93	0.16	35,35,35,35	0
56	MG	DA	3557	1/1	0.93	0.23	34,34,34,34	0
56	MG	AX	3006	1/1	0.93	0.18	74,74,74,74	0
56	MG	DA	3559	1/1	0.93	0.18	48,48,48,48	0
56	MG	BA	3164	1/1	0.93	0.28	43,43,43,43	0
56	MG	AA	3135	1/1	0.93	0.10	65,65,65,65	0
56	MG	DA	3577	1/1	0.93	0.14	49,49,49,49	0
56	MG	BA	3125	1/1	0.93	0.14	42,42,42,42	0
56	MG	DA	3263	1/1	0.93	0.10	61,61,61,61	0
56	MG	BW	203	1/1	0.93	0.23	34,34,34,34	0
56	MG	BA	3645	1/1	0.93	0.18	32,32,32,32	0
56	MG	DA	3474	1/1	0.93	0.07	53,53,53,53	0
56	MG	BA	3329	1/1	0.93	0.19	29,29,29,29	0
56	MG	BA	3839	1/1	0.93	0.12	38,38,38,38	0
56	MG	AA	3026	1/1	0.93	0.22	53,53,53,53	0
56	MG	AA	3105	1/1	0.93	0.20	49,49,49,49	0
56	MG	DA	3139	1/1	0.93	0.10	40,40,40,40	0
56	MG	BA	3120	1/1	0.93	0.23	32,32,32,32	0
56	MG	BA	3092	1/1	0.93	0.26	41,41,41,41	0
56	MG	CE	202	1/1	0.93	0.05	66,66,66,66	0
56	MG	DA	3374	1/1	0.93	0.18	37,37,37,37	0
56	MG	BA	3818	1/1	0.93	0.26	32,32,32,32	0
56	MG	BA	3766	1/1	0.93	0.19	31,31,31,31	0
56	MG	BA	3519	1/1	0.93	0.12	44,44,44,44	0
56	MG	BN	3005	1/1	0.93	0.39	51,51,51,51	0
56	MG	BA	3803	1/1	0.93	0.09	47,47,47,47	0
56	MG	BA	3658	1/1	0.94	0.23	45,45,45,45	0
56	MG	BA	3327	1/1	0.94	0.25	25,25,25,25	0
56	MG	BA	3286	1/1	0.94	0.32	46,46,46,46	0
56	MG	BA	3105	1/1	0.94	0.45	69,69,69,69	0
56	MG	AA	3152	1/1	0.94	0.13	45,45,45,45	0
56	MG	BA	3359	1/1	0.94	0.14	46,46,46,46	0
56	MG	CA	3105	1/1	0.94	0.14	49,49,49,49	0
56	MG	AA	3184	1/1	0.94	0.12	55,55,55,55	0
56	MG	BA	3034	1/1	0.94	0.21	28,28,28,28	0
56	MG	DA	3031	1/1	0.94	0.41	51,51,51,51	0
56	MG	DA	3243	1/1	0.94	0.17	54,54,54,54	0
56	MG	BA	3454	1/1	0.94	0.15	31,31,31,31	0
56	MG	DA	3283	1/1	0.94	0.25	46,46,46,46	0
56	MG	AA	3053	1/1	0.94	0.37	49,49,49,49	0
56	MG	AA	3029	1/1	0.94	0.28	53,53,53,53	0
56	MG	BU	208	1/1	0.94	0.13	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	3175	1/1	0.94	0.21	35,35,35,35	0
56	MG	CA	3014	1/1	0.94	0.14	47,47,47,47	0
56	MG	DA	3159	1/1	0.94	0.30	41,41,41,41	0
56	MG	D7	101	1/1	0.94	0.19	39,39,39,39	0
56	MG	CA	3068	1/1	0.94	0.40	55,55,55,55	0
56	MG	BA	3267	1/1	0.94	0.14	37,37,37,37	0
56	MG	AA	3043	1/1	0.94	0.27	26,26,26,26	0
56	MG	AA	3064	1/1	0.94	0.13	61,61,61,61	0
56	MG	DA	3511	1/1	0.94	0.11	45,45,45,45	0
56	MG	DA	3242	1/1	0.94	0.07	43,43,43,43	0
56	MG	AW	3004	1/1	0.94	0.12	51,51,51,51	0
56	MG	BA	3361	1/1	0.94	0.16	35,35,35,35	0
56	MG	CA	3094	1/1	0.94	0.18	72,72,72,72	0
56	MG	DA	3048	1/1	0.94	0.15	45,45,45,45	0
56	MG	DA	3152	1/1	0.94	0.25	42,42,42,42	0
56	MG	CX	3005	1/1	0.94	0.45	58,58,58,58	0
56	MG	BA	3296	1/1	0.94	0.19	31,31,31,31	0
56	MG	D0	101	1/1	0.94	0.08	56,56,56,56	0
56	MG	BA	3533	1/1	0.94	0.23	50,50,50,50	0
56	MG	CA	3052	1/1	0.94	0.09	65,65,65,65	0
56	MG	DA	3282	1/1	0.94	0.10	42,42,42,42	0
56	MG	BA	3750	1/1	0.94	0.21	49,49,49,49	0
56	MG	DA	3065	1/1	0.94	0.08	56,56,56,56	0
56	MG	DA	3659	1/1	0.94	0.48	67,67,67,67	0
56	MG	BA	3814	1/1	0.94	0.28	26,26,26,26	0
56	MG	BA	3276	1/1	0.94	0.29	41,41,41,41	0
56	MG	BA	3137	1/1	0.94	0.24	45,45,45,45	0
56	MG	CA	3035	1/1	0.94	0.10	60,60,60,60	0
56	MG	AA	3129	1/1	0.94	0.08	73,73,73,73	0
56	MG	BA	3021	1/1	0.94	0.17	60,60,60,60	0
56	MG	AA	3188	1/1	0.94	0.16	56,56,56,56	0
56	MG	BA	3570	1/1	0.94	0.35	30,30,30,30	0
56	MG	DA	3603	1/1	0.94	0.14	52,52,52,52	0
56	MG	AA	3052	1/1	0.94	0.32	68,68,68,68	0
56	MG	AA	3099	1/1	0.94	0.25	63,63,63,63	0
56	MG	BA	3098	1/1	0.94	0.35	26,26,26,26	0
56	MG	BA	3223	1/1	0.94	0.16	29,29,29,29	0
56	MG	DA	3270	1/1	0.94	0.22	49,49,49,49	0
56	MG	BA	3680	1/1	0.94	0.15	52,52,52,52	0
56	MG	AA	3096	1/1	0.94	0.27	48,48,48,48	0
56	MG	BA	3456	1/1	0.94	0.39	41,41,41,41	0
56	MG	BA	3662	1/1	0.94	0.32	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	BB	3010	1/1	0.94	0.11	48,48,48,48	0
56	MG	BA	3502	1/1	0.94	0.31	45,45,45,45	0
56	MG	AA	3206	1/1	0.94	0.17	47,47,47,47	0
56	MG	DA	3564	1/1	0.94	0.31	53,53,53,53	0
56	MG	BV	203	1/1	0.94	0.24	32,32,32,32	0
56	MG	DA	3156	1/1	0.94	0.12	43,43,43,43	0
56	MG	DA	3641	1/1	0.94	0.09	44,44,44,44	0
56	MG	AA	3119	1/1	0.94	0.10	58,58,58,58	0
56	MG	BA	3213	1/1	0.94	0.09	45,45,45,45	0
56	MG	BA	3745	1/1	0.94	0.17	30,30,30,30	0
56	MG	AA	3092	1/1	0.94	0.20	39,39,39,39	0
56	MG	CA	3012	1/1	0.94	0.20	68,68,68,68	0
56	MG	BA	3008	1/1	0.94	0.22	27,27,27,27	0
56	MG	DA	3100	1/1	0.94	0.24	36,36,36,36	0
56	MG	DA	3467	1/1	0.94	0.31	43,43,43,43	0
56	MG	AA	3147	1/1	0.94	0.11	55,55,55,55	0
56	MG	AA	3173	1/1	0.94	0.11	47,47,47,47	0
56	MG	AA	3162	1/1	0.94	0.28	59,59,59,59	0
56	MG	AA	3176	1/1	0.94	0.09	54,54,54,54	0
56	MG	DA	3631	1/1	0.94	0.13	56,56,56,56	0
56	MG	BA	3691	1/1	0.94	0.25	38,38,38,38	0
56	MG	BA	3505	1/1	0.94	0.12	54,54,54,54	0
56	MG	BF	306	1/1	0.94	0.31	40,40,40,40	0
56	MG	CA	3171	1/1	0.94	0.19	63,63,63,63	0
56	MG	BA	3575	1/1	0.94	0.09	64,64,64,64	0
56	MG	CA	3113	1/1	0.94	0.11	55,55,55,55	0
56	MG	DA	3440	1/1	0.94	0.18	39,39,39,39	0
56	MG	DA	3014	1/1	0.94	0.14	50,50,50,50	0
56	MG	AA	3028	1/1	0.94	0.38	56,56,56,56	0
56	MG	DA	3216	1/1	0.94	0.29	46,46,46,46	0
56	MG	DA	3478	1/1	0.94	0.18	47,47,47,47	0
56	MG	BA	3788	1/1	0.94	0.17	41,41,41,41	0
56	MG	DA	3260	1/1	0.94	0.13	41,41,41,41	0
56	MG	DA	3342	1/1	0.94	0.10	56,56,56,56	0
56	MG	AA	3041	1/1	0.94	0.26	52,52,52,52	0
56	MG	BA	3425	1/1	0.94	0.27	29,29,29,29	0
56	MG	BA	3602	1/1	0.94	0.17	46,46,46,46	0
56	MG	BA	3379	1/1	0.94	0.18	45,45,45,45	0
56	MG	AA	3084	1/1	0.94	0.17	49,49,49,49	0
56	MG	B0	101	1/1	0.94	0.20	39,39,39,39	0
56	MG	BF	310	1/1	0.94	0.25	38,38,38,38	0
56	MG	BA	3381	1/1	0.94	0.14	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	3093	1/1	0.94	0.14	50,50,50,50	0
56	MG	AX	3007	1/1	0.94	0.24	72,72,72,72	0
56	MG	BA	3550	1/1	0.94	0.20	34,34,34,34	0
56	MG	DD	305	1/1	0.94	0.24	38,38,38,38	0
56	MG	BA	3543	1/1	0.94	0.25	26,26,26,26	0
56	MG	BA	3281	1/1	0.94	0.17	49,49,49,49	0
56	MG	DA	3054	1/1	0.94	0.15	43,43,43,43	0
56	MG	DA	3160	1/1	0.94	0.20	59,59,59,59	0
56	MG	BA	3132	1/1	0.94	0.21	42,42,42,42	0
56	MG	DA	3206	1/1	0.94	0.10	39,39,39,39	0
56	MG	CA	3129	1/1	0.94	0.19	61,61,61,61	0
56	MG	BA	3457	1/1	0.94	0.21	44,44,44,44	0
56	MG	DA	3647	1/1	0.94	0.22	47,47,47,47	0
56	MG	CF	3001	1/1	0.94	0.26	38,38,38,38	0
56	MG	BA	3190	1/1	0.94	0.16	45,45,45,45	0
56	MG	AA	3107	1/1	0.94	0.25	51,51,51,51	0
56	MG	AA	3128	1/1	0.94	0.17	41,41,41,41	0
56	MG	DA	3640	1/1	0.94	0.14	52,52,52,52	0
56	MG	BA	3501	1/1	0.94	0.18	20,20,20,20	0
56	MG	DA	3162	1/1	0.94	0.34	43,43,43,43	0
56	MG	DA	3141	1/1	0.94	0.21	56,56,56,56	0
56	MG	DA	3598	1/1	0.94	0.11	63,63,63,63	0
56	MG	DA	3331	1/1	0.94	0.25	39,39,39,39	0
56	MG	DA	3592	1/1	0.94	0.17	52,52,52,52	0
56	MG	BA	3420	1/1	0.94	0.19	22,22,22,22	0
56	MG	BA	3257	1/1	0.94	0.21	41,41,41,41	0
56	MG	BA	3214	1/1	0.94	0.20	49,49,49,49	0
56	MG	AA	3036	1/1	0.94	0.12	52,52,52,52	0
56	MG	CA	3033	1/1	0.94	0.15	56,56,56,56	0
56	MG	DA	3669	1/1	0.94	0.22	49,49,49,49	0
56	MG	BA	3110	1/1	0.94	0.26	41,41,41,41	0
56	MG	BA	3676	1/1	0.94	0.28	53,53,53,53	0
56	MG	DA	3527	1/1	0.94	0.17	53,53,53,53	0
56	MG	BA	3200	1/1	0.94	0.28	56,56,56,56	0
56	MG	DA	3005	1/1	0.94	0.20	58,58,58,58	0
56	MG	BB	3013	1/1	0.94	0.14	42,42,42,42	0
56	MG	BA	3665	1/1	0.94	0.29	49,49,49,49	0
56	MG	DA	3097	1/1	0.94	0.21	43,43,43,43	0
56	MG	BA	3141	1/1	0.94	0.23	38,38,38,38	0
56	MG	BU	201	1/1	0.94	0.14	39,39,39,39	0
56	MG	BA	3416	1/1	0.94	0.17	21,21,21,21	0
56	MG	BE	304	1/1	0.94	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	CA	3095	1/1	0.94	0.10	61,61,61,61	0
56	MG	DA	3377	1/1	0.94	0.07	42,42,42,42	0
56	MG	DE	303	1/1	0.94	0.26	44,44,44,44	0
56	MG	DA	3664	1/1	0.94	0.08	38,38,38,38	0
56	MG	CT	3001	1/1	0.94	0.07	47,47,47,47	0
56	MG	DA	3398	1/1	0.94	0.18	57,57,57,57	0
56	MG	BA	3316	1/1	0.94	0.25	23,23,23,23	0
56	MG	AA	3031	1/1	0.94	0.09	44,44,44,44	0
56	MG	DA	3626	1/1	0.94	0.06	54,54,54,54	0
56	MG	BA	3256	1/1	0.94	0.32	49,49,49,49	0
56	MG	BD	308	1/1	0.94	0.28	39,39,39,39	0
56	MG	BA	3528	1/1	0.94	0.11	43,43,43,43	0
56	MG	AA	3118	1/1	0.94	0.20	53,53,53,53	0
56	MG	BX	102	1/1	0.94	0.31	41,41,41,41	0
56	MG	BA	3761	1/1	0.94	0.19	54,54,54,54	0
56	MG	BA	3448	1/1	0.94	0.22	28,28,28,28	0
56	MG	CA	3118	1/1	0.94	0.18	47,47,47,47	0
56	MG	AA	3027	1/1	0.94	0.24	54,54,54,54	0
56	MG	BA	3011	1/1	0.94	0.20	40,40,40,40	0
56	MG	CA	3071	1/1	0.94	0.09	50,50,50,50	0
56	MG	AA	3039	1/1	0.94	0.15	61,61,61,61	0
56	MG	BA	3378	1/1	0.94	0.10	34,34,34,34	0
56	MG	B5	105	1/1	0.94	0.10	49,49,49,49	0
56	MG	DA	3535	1/1	0.94	0.35	54,54,54,54	0
56	MG	DA	3458	1/1	0.94	0.11	42,42,42,42	0
56	MG	BA	3790	1/1	0.94	0.21	32,32,32,32	0
56	MG	DW	3001	1/1	0.94	0.23	43,43,43,43	0
56	MG	AA	3097	1/1	0.94	0.13	50,50,50,50	0
56	MG	CA	3080	1/1	0.94	0.28	52,52,52,52	0
56	MG	BA	3688	1/1	0.94	0.20	45,45,45,45	0
56	MG	BA	3055	1/1	0.94	0.23	31,31,31,31	0
56	MG	BA	3531	1/1	0.94	0.39	61,61,61,61	0
56	MG	BA	3399	1/1	0.94	0.16	25,25,25,25	0
56	MG	DA	3117	1/1	0.94	0.28	60,60,60,60	0
56	MG	AA	3126	1/1	0.94	0.17	46,46,46,46	0
56	MG	BA	3614	1/1	0.94	0.15	26,26,26,26	0
56	MG	BA	3306	1/1	0.94	0.18	31,31,31,31	0
56	MG	AA	3187	1/1	0.94	0.12	62,62,62,62	0
56	MG	BA	3661	1/1	0.94	0.09	53,53,53,53	0
56	MG	AA	3211	1/1	0.94	0.09	59,59,59,59	0
56	MG	DA	3035	1/1	0.94	0.24	38,38,38,38	0
56	MG	DA	3274	1/1	0.94	0.22	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	3506	1/1	0.94	0.26	51,51,51,51	0
56	MG	BR	201	1/1	0.94	0.17	44,44,44,44	0
56	MG	BY	502	1/1	0.94	0.13	50,50,50,50	0
56	MG	BA	3469	1/1	0.94	0.31	37,37,37,37	0
56	MG	DA	3449	1/1	0.94	0.19	47,47,47,47	0
56	MG	DA	3258	1/1	0.94	0.18	59,59,59,59	0
56	MG	BA	3183	1/1	0.94	0.22	40,40,40,40	0
56	MG	BA	3545	1/1	0.94	0.25	41,41,41,41	0
56	MG	DA	3348	1/1	0.94	0.27	38,38,38,38	0
56	MG	BA	3350	1/1	0.94	0.24	27,27,27,27	0
56	MG	DA	3633	1/1	0.94	0.14	61,61,61,61	0
56	MG	DA	3296	1/1	0.94	0.18	48,48,48,48	0
56	MG	DA	3278	1/1	0.94	0.21	53,53,53,53	0
56	MG	BA	3559	1/1	0.94	0.20	30,30,30,30	0
56	MG	CA	3030	1/1	0.94	0.08	59,59,59,59	0
56	MG	BA	3829	1/1	0.94	0.34	45,45,45,45	0
56	MG	DA	3073	1/1	0.94	0.17	54,54,54,54	0
56	MG	DA	3059	1/1	0.94	0.45	53,53,53,53	0
56	MG	BA	3300	1/1	0.94	0.18	22,22,22,22	0
56	MG	CA	3001	1/1	0.94	0.25	73,73,73,73	0
56	MG	BA	3654	1/1	0.94	0.15	55,55,55,55	0
56	MG	BA	3382	1/1	0.94	0.21	55,55,55,55	0
56	MG	CA	3063	1/1	0.94	0.14	59,59,59,59	0
56	MG	DA	3311	1/1	0.94	0.18	42,42,42,42	0
56	MG	DA	3484	1/1	0.94	0.05	45,45,45,45	0
56	MG	DA	3381	1/1	0.94	0.11	60,60,60,60	0
56	MG	DA	3652	1/1	0.94	0.12	49,49,49,49	0
56	MG	CA	3168	1/1	0.94	0.19	72,72,72,72	0
56	MG	CA	3041	1/1	0.94	0.16	58,58,58,58	0
56	MG	BA	3404	1/1	0.95	0.18	36,36,36,36	0
56	MG	BA	3406	1/1	0.95	0.19	32,32,32,32	0
56	MG	AA	3046	1/1	0.95	0.16	56,56,56,56	0
56	MG	BA	3077	1/1	0.95	0.20	34,34,34,34	0
56	MG	DA	3464	1/1	0.95	0.11	44,44,44,44	0
56	MG	DA	3074	1/1	0.95	0.22	50,50,50,50	0
56	MG	BA	3109	1/1	0.95	0.28	42,42,42,42	0
56	MG	BA	3206	1/1	0.95	0.21	29,29,29,29	0
56	MG	DA	3279	1/1	0.95	0.07	48,48,48,48	0
56	MG	DA	3639	1/1	0.95	0.14	64,64,64,64	0
56	MG	AA	3141	1/1	0.95	0.10	55,55,55,55	0
56	MG	DA	3285	1/1	0.95	0.20	28,28,28,28	0
56	MG	AA	3010	1/1	0.95	0.14	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	AA	3075	1/1	0.95	0.22	33,33,33,33	0
56	MG	BA	3066	1/1	0.95	0.39	51,51,51,51	0
56	MG	BA	3722	1/1	0.95	0.13	50,50,50,50	0
56	MG	DA	3008	1/1	0.95	0.21	33,33,33,33	0
56	MG	BA	3202	1/1	0.95	0.13	46,46,46,46	0
56	MG	BA	3587	1/1	0.95	0.20	44,44,44,44	0
56	MG	BA	3483	1/1	0.95	0.28	38,38,38,38	0
56	MG	CA	3103	1/1	0.95	0.10	75,75,75,75	0
56	MG	DA	3099	1/1	0.95	0.09	60,60,60,60	0
56	MG	DA	3007	1/1	0.95	0.39	54,54,54,54	0
56	MG	BA	3558	1/1	0.95	0.19	29,29,29,29	0
56	MG	BG	202	1/1	0.95	0.07	46,46,46,46	0
56	MG	AA	3149	1/1	0.95	0.21	41,41,41,41	0
56	MG	CA	3145	1/1	0.95	0.13	63,63,63,63	0
56	MG	BA	3485	1/1	0.95	0.23	46,46,46,46	0
56	MG	DA	3529	1/1	0.95	0.10	41,41,41,41	0
56	MG	DA	3601	1/1	0.95	0.19	54,54,54,54	0
56	MG	DA	3174	1/1	0.95	0.17	48,48,48,48	0
56	MG	DA	3134	1/1	0.95	0.13	49,49,49,49	0
56	MG	BA	3173	1/1	0.95	0.30	36,36,36,36	0
56	MG	CA	3022	1/1	0.95	0.10	53,53,53,53	0
56	MG	BA	3709	1/1	0.95	0.29	44,44,44,44	0
56	MG	BA	3631	1/1	0.95	0.14	43,43,43,43	0
56	MG	CA	3100	1/1	0.95	0.23	62,62,62,62	0
56	MG	DA	3372	1/1	0.95	0.15	47,47,47,47	0
56	MG	AK	201	1/1	0.95	0.14	61,61,61,61	0
56	MG	BA	3827	1/1	0.95	0.20	30,30,30,30	0
56	MG	CA	3149	1/1	0.95	0.27	65,65,65,65	0
56	MG	DA	3185	1/1	0.95	0.24	54,54,54,54	0
56	MG	CW	3002	1/1	0.95	0.16	74,74,74,74	0
56	MG	DA	3126	1/1	0.95	0.15	44,44,44,44	0
56	MG	BA	3135	1/1	0.95	0.21	35,35,35,35	0
56	MG	DA	3347	1/1	0.95	0.16	44,44,44,44	0
56	MG	BV	204	1/1	0.95	0.21	50,50,50,50	0
56	MG	BA	3532	1/1	0.95	0.27	49,49,49,49	0
56	MG	BU	205	1/1	0.95	0.22	38,38,38,38	0
56	MG	DA	3021	1/1	0.95	0.30	48,48,48,48	0
56	MG	DA	3337	1/1	0.95	0.09	43,43,43,43	0
56	MG	BA	3517	1/1	0.95	0.12	51,51,51,51	0
56	MG	BA	3794	1/1	0.95	0.20	33,33,33,33	0
56	MG	DA	3076	1/1	0.95	0.22	43,43,43,43	0
56	MG	DA	3244	1/1	0.95	0.13	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	3126	1/1	0.95	0.26	43,43,43,43	0
56	MG	CA	3160	1/1	0.95	0.16	65,65,65,65	0
56	MG	AA	3108	1/1	0.95	0.20	55,55,55,55	0
56	MG	DA	3245	1/1	0.95	0.10	62,62,62,62	0
56	MG	DA	3013	1/1	0.95	0.17	40,40,40,40	0
56	MG	BA	3834	1/1	0.95	0.13	35,35,35,35	0
56	MG	BA	3539	1/1	0.95	0.21	23,23,23,23	0
56	MG	AA	3207	1/1	0.95	0.14	68,68,68,68	0
56	MG	DA	3617	1/1	0.95	0.36	53,53,53,53	0
56	MG	BF	304	1/1	0.95	0.15	32,32,32,32	0
56	MG	DA	3426	1/1	0.95	0.17	41,41,41,41	0
56	MG	BA	3563	1/1	0.95	0.08	60,60,60,60	0
56	MG	BA	3243	1/1	0.95	0.18	44,44,44,44	0
56	MG	CA	3140	1/1	0.95	0.16	79,79,79,79	0
56	MG	BQ	3004	1/1	0.95	0.24	35,35,35,35	0
56	MG	BA	3191	1/1	0.95	0.26	40,40,40,40	0
56	MG	BA	3134	1/1	0.95	0.15	35,35,35,35	0
56	MG	CA	3107	1/1	0.95	0.10	66,66,66,66	0
56	MG	CA	3150	1/1	0.95	0.16	62,62,62,62	0
56	MG	AA	3132	1/1	0.95	0.13	22,22,22,22	0
56	MG	DA	3360	1/1	0.95	0.16	51,51,51,51	0
56	MG	DA	3077	1/1	0.95	0.18	43,43,43,43	0
56	MG	DA	3265	1/1	0.95	0.31	52,52,52,52	0
56	MG	DA	3163	1/1	0.95	0.27	49,49,49,49	0
56	MG	BA	3536	1/1	0.95	0.18	48,48,48,48	0
56	MG	AA	3191	1/1	0.95	0.24	48,48,48,48	0
56	MG	AA	3220	1/1	0.95	0.07	64,64,64,64	0
56	MG	DA	3357	1/1	0.95	0.14	44,44,44,44	0
56	MG	AA	3014	1/1	0.95	0.12	69,69,69,69	0
56	MG	DA	3575	1/1	0.95	0.10	47,47,47,47	0
56	MG	BA	3432	1/1	0.95	0.10	52,52,52,52	0
56	MG	DA	3125	1/1	0.95	0.26	45,45,45,45	0
56	MG	BA	3494	1/1	0.95	0.13	57,57,57,57	0
56	MG	DA	3327	1/1	0.95	0.19	59,59,59,59	0
56	MG	DA	3417	1/1	0.95	0.22	33,33,33,33	0
56	MG	DA	3226	1/1	0.95	0.15	54,54,54,54	0
56	MG	AA	3009	1/1	0.95	0.26	46,46,46,46	0
56	MG	AA	3034	1/1	0.95	0.26	48,48,48,48	0
56	MG	BA	3580	1/1	0.95	0.22	42,42,42,42	0
56	MG	DA	3593	1/1	0.95	0.24	39,39,39,39	0
56	MG	BA	3463	1/1	0.95	0.20	37,37,37,37	0
56	MG	BA	3486	1/1	0.95	0.23	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	DA	3488	1/1	0.95	0.13	37,37,37,37	0
56	MG	AA	3012	1/1	0.95	0.23	33,33,33,33	0
56	MG	BU	206	1/1	0.95	0.34	43,43,43,43	0
56	MG	DA	3462	1/1	0.95	0.28	43,43,43,43	0
56	MG	AA	3163	1/1	0.95	0.15	37,37,37,37	0
56	MG	BA	3216	1/1	0.95	0.21	34,34,34,34	0
56	MG	AA	3124	1/1	0.95	0.20	53,53,53,53	0
56	MG	BA	3362	1/1	0.95	0.25	19,19,19,19	0
56	MG	BA	3598	1/1	0.95	0.15	47,47,47,47	0
56	MG	BA	3608	1/1	0.95	0.21	60,60,60,60	0
56	MG	BA	3800	1/1	0.95	0.15	39,39,39,39	0
56	MG	DF	303	1/1	0.95	0.07	46,46,46,46	0
56	MG	BA	3343	1/1	0.95	0.18	33,33,33,33	0
56	MG	BA	3339	1/1	0.95	0.15	40,40,40,40	0
56	MG	BA	3309	1/1	0.95	0.07	55,55,55,55	0
56	MG	DA	3584	1/1	0.95	0.40	58,58,58,58	0
56	MG	BA	3611	1/1	0.95	0.13	42,42,42,42	0
56	MG	BA	3187	1/1	0.95	0.16	36,36,36,36	0
56	MG	BB	3021	1/1	0.95	0.13	54,54,54,54	0
56	MG	DE	301	1/1	0.95	0.29	45,45,45,45	0
56	MG	BA	3652	1/1	0.95	0.13	46,46,46,46	0
56	MG	BA	3230	1/1	0.95	0.14	62,62,62,62	0
56	MG	DA	3154	1/1	0.95	0.32	52,52,52,52	0
56	MG	CA	3136	1/1	0.95	0.18	65,65,65,65	0
56	MG	DA	3553	1/1	0.95	0.14	54,54,54,54	0
56	MG	BA	3268	1/1	0.95	0.28	58,58,58,58	0
56	MG	DA	3326	1/1	0.95	0.18	46,46,46,46	0
56	MG	DA	3400	1/1	0.95	0.34	39,39,39,39	0
56	MG	BA	3169	1/1	0.95	0.25	47,47,47,47	0
56	MG	DA	3123	1/1	0.95	0.12	47,47,47,47	0
56	MG	DA	3353	1/1	0.95	0.14	37,37,37,37	0
56	MG	DA	3634	1/1	0.95	0.14	53,53,53,53	0
56	MG	BA	3687	1/1	0.95	0.23	36,36,36,36	0
56	MG	BA	3037	1/1	0.95	0.16	37,37,37,37	0
56	MG	BA	3792	1/1	0.95	0.16	32,32,32,32	0
56	MG	BA	3647	1/1	0.95	0.16	45,45,45,45	0
56	MG	DA	3067	1/1	0.95	0.25	49,49,49,49	0
56	MG	BA	3388	1/1	0.95	0.13	52,52,52,52	0
56	MG	DV	3001	1/1	0.95	0.35	71,71,71,71	0
56	MG	DA	3188	1/1	0.95	0.38	50,50,50,50	0
56	MG	DA	3496	1/1	0.95	0.06	48,48,48,48	0
56	MG	DA	3148	1/1	0.95	0.23	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3112	1/1	0.95	0.15	59,59,59,59	0
56	MG	DA	3475	1/1	0.95	0.13	42,42,42,42	0
56	MG	BA	3799	1/1	0.95	0.22	47,47,47,47	0
56	MG	BA	3833	1/1	0.95	0.20	43,43,43,43	0
56	MG	BA	3262	1/1	0.95	0.31	47,47,47,47	0
56	MG	DA	3052	1/1	0.95	0.12	38,38,38,38	0
56	MG	DA	3330	1/1	0.95	0.17	46,46,46,46	0
56	MG	DA	3267	1/1	0.95	0.26	38,38,38,38	0
56	MG	DA	3058	1/1	0.95	0.21	46,46,46,46	0
56	MG	BA	3177	1/1	0.95	0.30	44,44,44,44	0
56	MG	DA	3302	1/1	0.95	0.12	33,33,33,33	0
56	MG	CV	3001	1/1	0.95	0.19	58,58,58,58	0
56	MG	BA	3488	1/1	0.95	0.10	50,50,50,50	0
56	MG	BA	3671	1/1	0.95	0.14	45,45,45,45	0
56	MG	BA	3796	1/1	0.95	0.13	40,40,40,40	0
56	MG	DA	3268	1/1	0.95	0.04	60,60,60,60	0
56	MG	DA	3489	1/1	0.95	0.16	37,37,37,37	0
56	MG	BF	301	1/1	0.95	0.26	38,38,38,38	0
56	MG	DA	3084	1/1	0.95	0.27	27,27,27,27	0
56	MG	DA	3555	1/1	0.95	0.08	54,54,54,54	0
56	MG	DA	3264	1/1	0.95	0.13	31,31,31,31	0
56	MG	BA	3577	1/1	0.95	0.19	60,60,60,60	0
56	MG	DA	3130	1/1	0.95	0.25	47,47,47,47	0
56	MG	CA	3165	1/1	0.95	0.08	56,56,56,56	0
56	MG	BA	3471	1/1	0.95	0.06	45,45,45,45	0
56	MG	BA	3222	1/1	0.95	0.36	27,27,27,27	0
56	MG	DB	3007	1/1	0.95	0.09	59,59,59,59	0
56	MG	DA	3232	1/1	0.95	0.28	53,53,53,53	0
56	MG	DA	3040	1/1	0.95	0.11	53,53,53,53	0
56	MG	BA	3263	1/1	0.95	0.18	32,32,32,32	0
56	MG	BA	3635	1/1	0.95	0.28	62,62,62,62	0
56	MG	AA	3069	1/1	0.95	0.21	67,67,67,67	0
56	MG	DA	3082	1/1	0.95	0.22	34,34,34,34	0
59	ZN	B4	501	1/1	0.95	0.12	73,73,73,73	0
56	MG	DB	3008	1/1	0.95	0.14	68,68,68,68	0
56	MG	BA	3499	1/1	0.95	0.24	33,33,33,33	0
56	MG	DA	3202	1/1	0.95	0.33	50,50,50,50	0
56	MG	CA	3075	1/1	0.95	0.10	44,44,44,44	0
56	MG	DA	3379	1/1	0.95	0.20	59,59,59,59	0
56	MG	DA	3414	1/1	0.95	0.16	41,41,41,41	0
56	MG	BA	3324	1/1	0.95	0.17	34,34,34,34	0
56	MG	BA	3401	1/1	0.95	0.14	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	AA	3074	1/1	0.95	0.17	47,47,47,47	0
56	MG	BA	3600	1/1	0.95	0.10	56,56,56,56	0
56	MG	CA	3056	1/1	0.95	0.23	60,60,60,60	0
56	MG	BA	3715	1/1	0.95	0.24	53,53,53,53	0
56	MG	BA	3642	1/1	0.95	0.09	37,37,37,37	0
56	MG	AA	3019	1/1	0.95	0.15	48,48,48,48	0
56	MG	DA	3083	1/1	0.95	0.18	51,51,51,51	0
56	MG	AA	3219	1/1	0.95	0.21	65,65,65,65	0
56	MG	BA	3783	1/1	0.95	0.19	53,53,53,53	0
56	MG	BA	3584	1/1	0.95	0.24	27,27,27,27	0
56	MG	DA	3169	1/1	0.95	0.13	49,49,49,49	0
56	MG	BA	3385	1/1	0.95	0.15	39,39,39,39	0
56	MG	AA	3180	1/1	0.95	0.14	57,57,57,57	0
56	MG	DA	3525	1/1	0.95	0.17	41,41,41,41	0
56	MG	BA	3696	1/1	0.95	0.16	33,33,33,33	0
56	MG	DA	3625	1/1	0.95	0.20	53,53,53,53	0
56	MG	AK	202	1/1	0.95	0.26	38,38,38,38	0
56	MG	DA	3413	1/1	0.95	0.20	36,36,36,36	0
56	MG	BA	3403	1/1	0.95	0.28	31,31,31,31	0
56	MG	DA	3240	1/1	0.95	0.17	51,51,51,51	0
56	MG	BA	3067	1/1	0.95	0.23	49,49,49,49	0
56	MG	DA	3042	1/1	0.95	0.15	41,41,41,41	0
56	MG	BA	3051	1/1	0.95	0.23	25,25,25,25	0
56	MG	DA	3362	1/1	0.95	0.22	43,43,43,43	0
56	MG	DA	3063	1/1	0.95	0.14	46,46,46,46	0
56	MG	BA	3380	1/1	0.95	0.12	60,60,60,60	0
56	MG	BD	310	1/1	0.95	0.15	31,31,31,31	0
56	MG	AA	3178	1/1	0.95	0.12	54,54,54,54	0
56	MG	DA	3023	1/1	0.95	0.14	30,30,30,30	0
56	MG	BA	3318	1/1	0.95	0.27	37,37,37,37	0
56	MG	BA	3163	1/1	0.95	0.22	45,45,45,45	0
56	MG	BA	3480	1/1	0.95	0.15	56,56,56,56	0
56	MG	DN	5001	1/1	0.95	0.07	62,62,62,62	0
56	MG	BP	203	1/1	0.95	0.12	32,32,32,32	0
56	MG	BA	3390	1/1	0.95	0.21	52,52,52,52	0
56	MG	BF	302	1/1	0.96	0.22	39,39,39,39	0
56	MG	CY	3001	1/1	0.96	0.27	58,58,58,58	0
56	MG	BA	3417	1/1	0.96	0.22	33,33,33,33	0
56	MG	BA	3573	1/1	0.96	0.09	32,32,32,32	0
56	MG	BA	3386	1/1	0.96	0.22	42,42,42,42	0
56	MG	BA	3538	1/1	0.96	0.20	45,45,45,45	0
56	MG	DA	3576	1/1	0.96	0.16	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	CA	3079	1/1	0.96	0.15	54,54,54,54	0
56	MG	BQ	3001	1/1	0.96	0.23	40,40,40,40	0
56	MG	AA	3182	1/1	0.96	0.20	52,52,52,52	0
56	MG	DA	3519	1/1	0.96	0.17	24,24,24,24	0
56	MG	DA	3416	1/1	0.96	0.34	40,40,40,40	0
56	MG	AA	3122	1/1	0.96	0.19	60,60,60,60	0
56	MG	CX	3003	1/1	0.96	0.38	50,50,50,50	0
56	MG	BA	3245	1/1	0.96	0.28	29,29,29,29	0
56	MG	BE	303	1/1	0.96	0.16	27,27,27,27	0
56	MG	BA	3349	1/1	0.96	0.19	34,34,34,34	0
56	MG	DA	3512	1/1	0.96	0.22	46,46,46,46	0
56	MG	DA	3177	1/1	0.96	0.17	54,54,54,54	0
56	MG	AX	3013	1/1	0.96	0.30	39,39,39,39	0
56	MG	BA	3146	1/1	0.96	0.19	42,42,42,42	0
56	MG	DA	3332	1/1	0.96	0.20	41,41,41,41	0
56	MG	DA	3450	1/1	0.96	0.16	36,36,36,36	0
56	MG	DF	305	1/1	0.96	0.17	43,43,43,43	0
56	MG	DA	3364	1/1	0.96	0.14	38,38,38,38	0
56	MG	BA	3247	1/1	0.96	0.30	28,28,28,28	0
56	MG	CA	3057	1/1	0.96	0.17	58,58,58,58	0
56	MG	B5	101	1/1	0.96	0.14	31,31,31,31	0
56	MG	DA	3431	1/1	0.96	0.17	25,25,25,25	0
56	MG	BA	3189	1/1	0.96	0.16	30,30,30,30	0
56	MG	BA	3468	1/1	0.96	0.23	49,49,49,49	0
56	MG	DA	3277	1/1	0.96	0.10	56,56,56,56	0
56	MG	BA	3085	1/1	0.96	0.13	31,31,31,31	0
56	MG	BA	3242	1/1	0.96	0.33	42,42,42,42	0
56	MG	DA	3080	1/1	0.96	0.22	45,45,45,45	0
56	MG	DA	3579	1/1	0.96	0.07	55,55,55,55	0
56	MG	AA	3060	1/1	0.96	0.21	59,59,59,59	0
56	MG	DA	3666	1/1	0.96	0.22	41,41,41,41	0
56	MG	DA	3490	1/1	0.96	0.18	39,39,39,39	0
56	MG	BA	3552	1/1	0.96	0.26	34,34,34,34	0
56	MG	BA	3258	1/1	0.96	0.28	41,41,41,41	0
56	MG	BA	3040	1/1	0.96	0.14	47,47,47,47	0
56	MG	DW	3003	1/1	0.96	0.34	47,47,47,47	0
56	MG	BA	3325	1/1	0.96	0.28	56,56,56,56	0
56	MG	BA	3612	1/1	0.96	0.10	62,62,62,62	0
56	MG	DA	3492	1/1	0.96	0.12	47,47,47,47	0
56	MG	DA	3373	1/1	0.96	0.10	31,31,31,31	0
56	MG	BA	3184	1/1	0.96	0.12	30,30,30,30	0
56	MG	DA	3262	1/1	0.96	0.12	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
59	ZN	D6	501	1/1	0.96	0.11	73,73,73,73	0
56	MG	CA	3110	1/1	0.96	0.11	48,48,48,48	0
56	MG	AA	3006	1/1	0.96	0.14	37,37,37,37	0
56	MG	BA	3389	1/1	0.96	0.28	37,37,37,37	0
56	MG	BA	3498	1/1	0.96	0.07	54,54,54,54	0
56	MG	BF	312	1/1	0.96	0.14	47,47,47,47	0
56	MG	DA	3088	1/1	0.96	0.18	42,42,42,42	0
56	MG	BA	3459	1/1	0.96	0.17	48,48,48,48	0
56	MG	BA	3521	1/1	0.96	0.13	36,36,36,36	0
56	MG	BA	3159	1/1	0.96	0.22	30,30,30,30	0
56	MG	BA	3027	1/1	0.96	0.20	42,42,42,42	0
56	MG	BA	3297	1/1	0.96	0.55	55,55,55,55	0
56	MG	BD	311	1/1	0.96	0.21	51,51,51,51	0
56	MG	BA	3660	1/1	0.96	0.18	51,51,51,51	0
56	MG	AA	3121	1/1	0.96	0.15	66,66,66,66	0
56	MG	CA	3096	1/1	0.96	0.15	61,61,61,61	0
56	MG	DA	3315	1/1	0.96	0.17	41,41,41,41	0
56	MG	BA	3398	1/1	0.96	0.20	42,42,42,42	0
56	MG	DV	3003	1/1	0.96	0.12	52,52,52,52	0
56	MG	DA	3411	1/1	0.96	0.17	46,46,46,46	0
56	MG	BA	3038	1/1	0.96	0.30	47,47,47,47	0
56	MG	DA	3463	1/1	0.96	0.15	37,37,37,37	0
56	MG	BA	3075	1/1	0.96	0.20	27,27,27,27	0
56	MG	AA	3133	1/1	0.96	0.23	30,30,30,30	0
56	MG	DA	3230	1/1	0.96	0.15	33,33,33,33	0
56	MG	BA	3299	1/1	0.96	0.15	32,32,32,32	0
56	MG	BA	3068	1/1	0.96	0.26	51,51,51,51	0
56	MG	B0	102	1/1	0.96	0.12	68,68,68,68	0
56	MG	AX	3011	1/1	0.96	0.16	50,50,50,50	0
56	MG	BA	3308	1/1	0.96	0.21	39,39,39,39	0
56	MG	BA	3025	1/1	0.96	0.15	38,38,38,38	0
56	MG	BA	3643	1/1	0.96	0.20	30,30,30,30	0
56	MG	BA	3397	1/1	0.96	0.23	53,53,53,53	0
56	MG	DA	3128	1/1	0.96	0.07	45,45,45,45	0
56	MG	BA	3746	1/1	0.96	0.33	25,25,25,25	0
56	MG	DA	3266	1/1	0.96	0.10	47,47,47,47	0
56	MG	DA	3129	1/1	0.96	0.12	45,45,45,45	0
56	MG	DA	3558	1/1	0.96	0.25	34,34,34,34	0
56	MG	BA	3515	1/1	0.96	0.21	20,20,20,20	0
56	MG	BA	3176	1/1	0.96	0.29	55,55,55,55	0
56	MG	CA	3116	1/1	0.96	0.06	55,55,55,55	0
56	MG	BA	3452	1/1	0.96	0.30	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3198	1/1	0.96	0.08	51,51,51,51	0
56	MG	BA	3596	1/1	0.96	0.32	45,45,45,45	0
56	MG	BA	3084	1/1	0.96	0.18	45,45,45,45	0
56	MG	BA	3784	1/1	0.96	0.22	52,52,52,52	0
56	MG	CA	3048	1/1	0.96	0.27	52,52,52,52	0
56	MG	AA	3168	1/1	0.96	0.08	62,62,62,62	0
56	MG	AA	3104	1/1	0.96	0.20	50,50,50,50	0
56	MG	CA	3009	1/1	0.96	0.22	50,50,50,50	0
56	MG	CA	3174	1/1	0.96	0.25	46,46,46,46	0
56	MG	DA	3217	1/1	0.96	0.14	50,50,50,50	0
56	MG	DA	3486	1/1	0.96	0.22	44,44,44,44	0
56	MG	BP	201	1/1	0.96	0.39	41,41,41,41	0
56	MG	DA	3522	1/1	0.96	0.29	25,25,25,25	0
56	MG	BA	3239	1/1	0.96	0.15	31,31,31,31	0
56	MG	BA	3461	1/1	0.96	0.19	31,31,31,31	0
56	MG	BA	3764	1/1	0.96	0.12	58,58,58,58	0
56	MG	BA	3826	1/1	0.96	0.22	33,33,33,33	0
56	MG	CA	3135	1/1	0.96	0.11	53,53,53,53	0
56	MG	BA	3630	1/1	0.96	0.08	30,30,30,30	0
56	MG	BA	3338	1/1	0.96	0.16	41,41,41,41	0
56	MG	CA	3062	1/1	0.96	0.23	44,44,44,44	0
56	MG	DA	3136	1/1	0.96	0.22	44,44,44,44	0
56	MG	DA	3590	1/1	0.96	0.19	60,60,60,60	0
56	MG	DA	3298	1/1	0.96	0.17	33,33,33,33	0
56	MG	BD	305	1/1	0.96	0.14	37,37,37,37	0
56	MG	BA	3147	1/1	0.96	0.13	30,30,30,30	0
56	MG	DB	3001	1/1	0.96	0.04	73,73,73,73	0
56	MG	CA	3102	1/1	0.96	0.09	54,54,54,54	0
56	MG	BA	3161	1/1	0.96	0.23	37,37,37,37	0
56	MG	BA	3555	1/1	0.96	0.29	33,33,33,33	0
56	MG	DA	3341	1/1	0.96	0.21	31,31,31,31	0
56	MG	DA	3166	1/1	0.96	0.17	46,46,46,46	0
56	MG	DA	3299	1/1	0.96	0.24	43,43,43,43	0
56	MG	DA	3481	1/1	0.96	0.18	30,30,30,30	0
56	MG	BA	3209	1/1	0.96	0.12	41,41,41,41	0
56	MG	AA	3217	1/1	0.96	0.16	55,55,55,55	0
56	MG	BA	3627	1/1	0.96	0.17	45,45,45,45	0
56	MG	BA	3148	1/1	0.96	0.27	15,15,15,15	0
56	MG	BA	3785	1/1	0.96	0.16	41,41,41,41	0
56	MG	DA	3472	1/1	0.96	0.06	33,33,33,33	0
56	MG	DA	3662	1/1	0.96	0.09	27,27,27,27	0
56	MG	DA	3386	1/1	0.96	0.17	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	AA	3025	1/1	0.96	0.12	43,43,43,43	0
56	MG	BA	3301	1/1	0.96	0.14	26,26,26,26	0
56	MG	CE	201	1/1	0.96	0.19	50,50,50,50	0
56	MG	BA	3540	1/1	0.96	0.17	44,44,44,44	0
56	MG	DA	3412	1/1	0.96	0.16	63,63,63,63	0
56	MG	BA	3285	1/1	0.96	0.37	49,49,49,49	0
56	MG	CA	3141	1/1	0.96	0.17	49,49,49,49	0
56	MG	AA	3203	1/1	0.96	0.34	57,57,57,57	0
56	MG	DA	3629	1/1	0.96	0.22	52,52,52,52	0
56	MG	BA	3082	1/1	0.96	0.11	59,59,59,59	0
56	MG	DA	3627	1/1	0.96	0.04	48,48,48,48	0
56	MG	DA	3257	1/1	0.96	0.20	34,34,34,34	0
56	MG	DA	3471	1/1	0.96	0.15	50,50,50,50	0
56	MG	CA	3155	1/1	0.96	0.14	50,50,50,50	0
56	MG	BA	3507	1/1	0.96	0.12	39,39,39,39	0
56	MG	BA	3733	1/1	0.96	0.26	41,41,41,41	0
56	MG	DA	3016	1/1	0.96	0.12	53,53,53,53	0
56	MG	DA	3010	1/1	0.96	0.07	43,43,43,43	0
56	MG	DA	3164	1/1	0.96	0.26	33,33,33,33	0
56	MG	CA	3156	1/1	0.96	0.10	68,68,68,68	0
56	MG	BA	3490	1/1	0.96	0.22	44,44,44,44	0
56	MG	DB	3009	1/1	0.96	0.19	47,47,47,47	0
56	MG	DA	3307	1/1	0.96	0.08	45,45,45,45	0
56	MG	DA	3352	1/1	0.96	0.15	35,35,35,35	0
56	MG	BA	3684	1/1	0.96	0.20	49,49,49,49	0
56	MG	DA	3062	1/1	0.96	0.18	53,53,53,53	0
56	MG	BA	3006	1/1	0.96	0.15	52,52,52,52	0
56	MG	AA	3177	1/1	0.96	0.14	57,57,57,57	0
56	MG	BA	3208	1/1	0.96	0.32	48,48,48,48	0
56	MG	BA	3473	1/1	0.96	0.28	57,57,57,57	0
56	MG	AM	201	1/1	0.96	0.05	50,50,50,50	0
56	MG	DA	3658	1/1	0.96	0.39	37,37,37,37	0
56	MG	DA	3517	1/1	0.96	0.10	47,47,47,47	0
56	MG	BB	3014	1/1	0.96	0.14	69,69,69,69	0
56	MG	CA	3130	1/1	0.96	0.12	60,60,60,60	0
56	MG	BA	3541	1/1	0.96	0.14	29,29,29,29	0
56	MG	DA	3151	1/1	0.96	0.26	44,44,44,44	0
56	MG	BA	3562	1/1	0.96	0.18	35,35,35,35	0
56	MG	DA	3091	1/1	0.96	0.18	43,43,43,43	0
56	MG	DF	304	1/1	0.96	0.22	39,39,39,39	0
56	MG	BA	3073	1/1	0.96	0.17	41,41,41,41	0
56	MG	BE	308	1/1	0.96	0.17	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3534	1/1	0.96	0.30	31,31,31,31	0
56	MG	DA	3455	1/1	0.96	0.18	27,27,27,27	0
56	MG	AA	3001	1/1	0.96	0.18	34,34,34,34	0
56	MG	BA	3103	1/1	0.96	0.33	48,48,48,48	0
56	MG	DA	3004	1/1	0.96	0.19	42,42,42,42	0
56	MG	DA	3421	1/1	0.96	0.21	53,53,53,53	0
56	MG	DA	3494	1/1	0.96	0.18	30,30,30,30	0
56	MG	B3	103	1/1	0.96	0.07	45,45,45,45	0
56	MG	DA	3049	1/1	0.96	0.22	24,24,24,24	0
56	MG	BA	3167	1/1	0.96	0.19	50,50,50,50	0
56	MG	DA	3289	1/1	0.96	0.36	42,42,42,42	0
56	MG	AE	3001	1/1	0.96	0.06	66,66,66,66	0
56	MG	DA	3193	1/1	0.96	0.33	40,40,40,40	0
56	MG	BA	3215	1/1	0.96	0.30	45,45,45,45	0
56	MG	DA	3276	1/1	0.96	0.08	33,33,33,33	0
56	MG	DA	3501	1/1	0.96	0.15	59,59,59,59	0
56	MG	BA	3710	1/1	0.96	0.19	28,28,28,28	0
56	MG	DA	3284	1/1	0.96	0.18	40,40,40,40	0
56	MG	DA	3153	1/1	0.96	0.15	44,44,44,44	0
56	MG	AY	3001	1/1	0.96	0.31	70,70,70,70	0
56	MG	CA	3163	1/1	0.96	0.17	53,53,53,53	0
56	MG	AA	3007	1/1	0.96	0.26	65,65,65,65	0
56	MG	BA	3755	1/1	0.96	0.19	52,52,52,52	0
56	MG	BA	3086	1/1	0.96	0.28	41,41,41,41	0
56	MG	CA	3166	1/1	0.96	0.13	66,66,66,66	0
56	MG	DA	3594	1/1	0.96	0.07	44,44,44,44	0
56	MG	CA	3093	1/1	0.96	0.17	34,34,34,34	0
56	MG	BA	3744	1/1	0.96	0.13	20,20,20,20	0
56	MG	DA	3143	1/1	0.96	0.23	50,50,50,50	0
56	MG	BA	3713	1/1	0.96	0.23	54,54,54,54	0
56	MG	AA	3146	1/1	0.96	0.11	53,53,53,53	0
56	MG	DA	3349	1/1	0.96	0.11	44,44,44,44	0
56	MG	AA	3196	1/1	0.97	0.13	32,32,32,32	0
56	MG	BA	3154	1/1	0.97	0.28	29,29,29,29	0
56	MG	DA	3543	1/1	0.97	0.23	55,55,55,55	0
56	MG	BA	3450	1/1	0.97	0.28	34,34,34,34	0
56	MG	DA	3336	1/1	0.97	0.09	47,47,47,47	0
56	MG	AW	3007	1/1	0.97	0.05	64,64,64,64	0
56	MG	BA	3816	1/1	0.97	0.19	21,21,21,21	0
56	MG	BA	3336	1/1	0.97	0.13	35,35,35,35	0
56	MG	BA	3384	1/1	0.97	0.23	30,30,30,30	0
56	MG	DA	3124	1/1	0.97	0.19	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	3767	1/1	0.97	0.11	29,29,29,29	0
56	MG	AA	3167	1/1	0.97	0.21	47,47,47,47	0
56	MG	BA	3168	1/1	0.97	0.19	27,27,27,27	0
56	MG	BA	3123	1/1	0.97	0.16	35,35,35,35	0
56	MG	BA	3072	1/1	0.97	0.14	30,30,30,30	0
56	MG	BA	3303	1/1	0.97	0.17	35,35,35,35	0
56	MG	BA	3546	1/1	0.97	0.26	30,30,30,30	0
56	MG	DA	3275	1/1	0.97	0.09	52,52,52,52	0
56	MG	BA	3551	1/1	0.97	0.19	33,33,33,33	0
56	MG	DA	3346	1/1	0.97	0.15	35,35,35,35	0
56	MG	BA	3565	1/1	0.97	0.24	42,42,42,42	0
56	MG	DY	502	1/1	0.97	0.12	52,52,52,52	0
56	MG	AA	3160	1/1	0.97	0.14	57,57,57,57	0
56	MG	DA	3654	1/1	0.97	0.11	55,55,55,55	0
56	MG	DA	3599	1/1	0.97	0.24	38,38,38,38	0
56	MG	BA	3111	1/1	0.97	0.23	47,47,47,47	0
56	MG	DQ	3002	1/1	0.97	0.17	42,42,42,42	0
56	MG	BA	3465	1/1	0.97	0.19	42,42,42,42	0
56	MG	BA	3048	1/1	0.97	0.25	28,28,28,28	0
56	MG	DA	3253	1/1	0.97	0.22	38,38,38,38	0
56	MG	BA	3443	1/1	0.97	0.12	25,25,25,25	0
56	MG	BA	3624	1/1	0.97	0.18	29,29,29,29	0
56	MG	DA	3189	1/1	0.97	0.25	48,48,48,48	0
56	MG	BA	3076	1/1	0.97	0.29	23,23,23,23	0
56	MG	AA	3076	1/1	0.97	0.17	55,55,55,55	0
56	MG	AA	3070	1/1	0.97	0.23	49,49,49,49	0
56	MG	BR	204	1/1	0.97	0.36	42,42,42,42	0
56	MG	BA	3029	1/1	0.97	0.31	46,46,46,46	0
56	MG	DA	3644	1/1	0.97	0.49	55,55,55,55	0
56	MG	BA	3561	1/1	0.97	0.15	27,27,27,27	0
56	MG	BA	3811	1/1	0.97	0.31	38,38,38,38	0
56	MG	DA	3651	1/1	0.97	0.16	47,47,47,47	0
56	MG	DA	3428	1/1	0.97	0.10	61,61,61,61	0
56	MG	BA	3822	1/1	0.97	0.20	21,21,21,21	0
56	MG	DA	3344	1/1	0.97	0.09	44,44,44,44	0
56	MG	DQ	3001	1/1	0.97	0.11	48,48,48,48	0
56	MG	BA	3615	1/1	0.97	0.28	35,35,35,35	0
56	MG	DA	3314	1/1	0.97	0.18	33,33,33,33	0
56	MG	DA	3249	1/1	0.97	0.27	41,41,41,41	0
56	MG	BA	3012	1/1	0.97	0.21	26,26,26,26	0
56	MG	DA	3047	1/1	0.97	0.21	49,49,49,49	0
56	MG	BA	3656	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	3660	1/1	0.97	0.19	40,40,40,40	0
56	MG	BA	3775	1/1	0.97	0.17	43,43,43,43	0
56	MG	DA	3114	1/1	0.97	0.13	28,28,28,28	0
56	MG	DA	3624	1/1	0.97	0.07	47,47,47,47	0
56	MG	DA	3427	1/1	0.97	0.08	38,38,38,38	0
56	MG	D7	102	1/1	0.97	0.22	43,43,43,43	0
56	MG	BA	3026	1/1	0.97	0.14	19,19,19,19	0
56	MG	DA	3552	1/1	0.97	0.07	43,43,43,43	0
56	MG	BD	302	1/1	0.97	0.16	23,23,23,23	0
56	MG	BA	3036	1/1	0.97	0.18	26,26,26,26	0
56	MG	BA	3118	1/1	0.97	0.34	38,38,38,38	0
56	MG	CA	3131	1/1	0.97	0.18	55,55,55,55	0
56	MG	DA	3118	1/1	0.97	0.25	52,52,52,52	0
56	MG	BA	3607	1/1	0.97	0.26	40,40,40,40	0
56	MG	BA	3335	1/1	0.97	0.17	50,50,50,50	0
56	MG	B8	103	1/1	0.97	0.22	48,48,48,48	0
56	MG	BA	3054	1/1	0.97	0.17	30,30,30,30	0
56	MG	DA	3371	1/1	0.97	0.17	55,55,55,55	0
56	MG	DA	3582	1/1	0.97	0.11	39,39,39,39	0
56	MG	AA	3227	1/1	0.97	0.18	48,48,48,48	0
56	MG	DA	3200	1/1	0.97	0.35	43,43,43,43	0
56	MG	DA	3290	1/1	0.97	0.17	44,44,44,44	0
56	MG	DA	3045	1/1	0.97	0.12	47,47,47,47	0
56	MG	BA	3044	1/1	0.97	0.25	49,49,49,49	0
56	MG	AA	3179	1/1	0.97	0.35	79,79,79,79	0
56	MG	DA	3120	1/1	0.97	0.19	45,45,45,45	0
56	MG	BA	3556	1/1	0.97	0.11	45,45,45,45	0
56	MG	DA	3340	1/1	0.97	0.21	42,42,42,42	0
56	MG	BA	3653	1/1	0.97	0.28	49,49,49,49	0
56	MG	DA	3108	1/1	0.97	0.22	30,30,30,30	0
56	MG	DA	3385	1/1	0.97	0.14	55,55,55,55	0
56	MG	BA	3372	1/1	0.97	0.22	24,24,24,24	0
56	MG	BA	3122	1/1	0.97	0.18	26,26,26,26	0
56	MG	DD	301	1/1	0.97	0.37	39,39,39,39	0
56	MG	DA	3012	1/1	0.97	0.18	39,39,39,39	0
56	MG	DA	3425	1/1	0.97	0.07	45,45,45,45	0
56	MG	CA	3008	1/1	0.97	0.12	50,50,50,50	0
56	MG	BB	3023	1/1	0.97	0.11	46,46,46,46	0
56	MG	DG	3001	1/1	0.97	0.04	56,56,56,56	0
56	MG	BA	3535	1/1	0.97	0.25	18,18,18,18	0
56	MG	AA	3088	1/1	0.97	0.30	56,56,56,56	0
56	MG	B8	102	1/1	0.97	0.08	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	3795	1/1	0.97	0.16	53,53,53,53	0
56	MG	BA	3497	1/1	0.97	0.21	41,41,41,41	0
56	MG	BA	3009	1/1	0.97	0.17	25,25,25,25	0
56	MG	DA	3207	1/1	0.97	0.29	57,57,57,57	0
56	MG	BA	3042	1/1	0.97	0.18	40,40,40,40	0
56	MG	DU	3001	1/1	0.97	0.25	50,50,50,50	0
56	MG	AA	3214	1/1	0.97	0.15	44,44,44,44	0
56	MG	DA	3571	1/1	0.97	0.16	57,57,57,57	0
56	MG	DA	3071	1/1	0.97	0.37	44,44,44,44	0
56	MG	BA	3069	1/1	0.97	0.14	31,31,31,31	0
56	MG	AA	3164	1/1	0.97	0.24	50,50,50,50	0
56	MG	DA	3009	1/1	0.97	0.19	38,38,38,38	0
56	MG	AA	3037	1/1	0.97	0.24	44,44,44,44	0
56	MG	BA	3217	1/1	0.97	0.21	20,20,20,20	0
56	MG	BA	3824	1/1	0.97	0.12	43,43,43,43	0
56	MG	BA	3395	1/1	0.97	0.19	44,44,44,44	0
56	MG	BA	3043	1/1	0.97	0.30	39,39,39,39	0
56	MG	BA	3678	1/1	0.97	0.22	58,58,58,58	0
56	MG	BB	3006	1/1	0.97	0.14	38,38,38,38	0
56	MG	BA	3547	1/1	0.97	0.19	41,41,41,41	0
56	MG	CA	3158	1/1	0.97	0.19	53,53,53,53	0
56	MG	DA	3479	1/1	0.97	0.17	50,50,50,50	0
56	MG	DA	3573	1/1	0.97	0.31	46,46,46,46	0
56	MG	DA	3024	1/1	0.97	0.44	40,40,40,40	0
56	MG	CA	3078	1/1	0.97	0.16	48,48,48,48	0
56	MG	BD	304	1/1	0.97	0.20	48,48,48,48	0
56	MG	DA	3006	1/1	0.97	0.15	43,43,43,43	0
56	MG	BA	3391	1/1	0.97	0.14	41,41,41,41	0
56	MG	DA	3175	1/1	0.97	0.08	53,53,53,53	0
56	MG	BA	3644	1/1	0.97	0.10	36,36,36,36	0
56	MG	DA	3668	1/1	0.97	0.15	79,79,79,79	0
56	MG	BA	3737	1/1	0.97	0.11	36,36,36,36	0
56	MG	BA	3793	1/1	0.97	0.20	38,38,38,38	0
56	MG	BA	3195	1/1	0.97	0.27	50,50,50,50	0
56	MG	CA	3045	1/1	0.97	0.36	58,58,58,58	0
56	MG	AA	3172	1/1	0.97	0.16	47,47,47,47	0
56	MG	DA	3322	1/1	0.97	0.29	43,43,43,43	0
56	MG	CA	3108	1/1	0.97	0.14	51,51,51,51	0
56	MG	CA	3089	1/1	0.97	0.07	58,58,58,58	0
56	MG	DA	3459	1/1	0.97	0.07	57,57,57,57	0
56	MG	DA	3456	1/1	0.97	0.20	49,49,49,49	0
56	MG	BA	3518	1/1	0.97	0.20	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3010	1/1	0.97	0.13	29,29,29,29	0
56	MG	BA	3332	1/1	0.97	0.17	30,30,30,30	0
56	MG	BA	3024	1/1	0.97	0.27	22,22,22,22	0
56	MG	BA	3776	1/1	0.97	0.14	49,49,49,49	0
56	MG	BA	3121	1/1	0.97	0.36	41,41,41,41	0
56	MG	BA	3373	1/1	0.97	0.18	38,38,38,38	0
56	MG	BA	3421	1/1	0.97	0.22	33,33,33,33	0
56	MG	DA	3530	1/1	0.97	0.23	55,55,55,55	0
56	MG	BA	3013	1/1	0.97	0.28	34,34,34,34	0
56	MG	AA	3200	1/1	0.97	0.22	45,45,45,45	0
56	MG	DA	3334	1/1	0.97	0.17	32,32,32,32	0
56	MG	DA	3345	1/1	0.97	0.18	35,35,35,35	0
56	MG	B0	103	1/1	0.97	0.06	54,54,54,54	0
56	MG	BA	3340	1/1	0.97	0.13	45,45,45,45	0
56	MG	BA	3155	1/1	0.97	0.12	54,54,54,54	0
56	MG	BA	3415	1/1	0.97	0.20	29,29,29,29	0
56	MG	DA	3055	1/1	0.97	0.24	36,36,36,36	0
56	MG	DA	3435	1/1	0.97	0.16	44,44,44,44	0
56	MG	BA	3836	1/1	0.97	0.29	45,45,45,45	0
56	MG	BA	3489	1/1	0.97	0.11	44,44,44,44	0
56	MG	BA	3610	1/1	0.97	0.16	64,64,64,64	0
56	MG	BA	3363	1/1	0.97	0.19	50,50,50,50	0
56	MG	AA	3013	1/1	0.97	0.07	51,51,51,51	0
56	MG	BA	3108	1/1	0.97	0.19	24,24,24,24	0
56	MG	DA	3113	1/1	0.97	0.29	44,44,44,44	0
56	MG	DA	3520	1/1	0.97	0.05	48,48,48,48	0
56	MG	DA	3003	1/1	0.97	0.26	20,20,20,20	0
56	MG	BA	3211	1/1	0.97	0.28	36,36,36,36	0
56	MG	BA	3178	1/1	0.97	0.25	38,38,38,38	0
56	MG	BA	3513	1/1	0.97	0.15	34,34,34,34	0
56	MG	DA	3313	1/1	0.97	0.20	23,23,23,23	0
56	MG	BA	3035	1/1	0.97	0.14	31,31,31,31	0
56	MG	BA	3319	1/1	0.97	0.29	20,20,20,20	0
56	MG	BA	3549	1/1	0.97	0.19	37,37,37,37	0
56	MG	BA	3495	1/1	0.97	0.24	34,34,34,34	0
56	MG	DA	3446	1/1	0.97	0.32	47,47,47,47	0
56	MG	BA	3056	1/1	0.97	0.28	33,33,33,33	0
56	MG	BA	3032	1/1	0.97	0.21	38,38,38,38	0
56	MG	DA	3447	1/1	0.97	0.27	35,35,35,35	0
56	MG	BB	3007	1/1	0.97	0.09	36,36,36,36	0
56	MG	DA	3317	1/1	0.97	0.15	55,55,55,55	0
56	MG	DA	3237	1/1	0.97	0.07	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	BA	3781	1/1	0.97	0.21	52,52,52,52	0
56	MG	BA	3166	1/1	0.97	0.22	40,40,40,40	0
56	MG	DA	3022	1/1	0.97	0.21	40,40,40,40	0
56	MG	DA	3622	1/1	0.97	0.18	53,53,53,53	0
56	MG	DA	3570	1/1	0.97	0.10	49,49,49,49	0
56	MG	DA	3528	1/1	0.97	0.09	57,57,57,57	0
56	MG	AA	3123	1/1	0.97	0.17	57,57,57,57	0
56	MG	DA	3308	1/1	0.97	0.16	45,45,45,45	0
56	MG	BA	3525	1/1	0.97	0.18	52,52,52,52	0
56	MG	BE	301	1/1	0.97	0.20	23,23,23,23	0
56	MG	AA	3063	1/1	0.97	0.07	63,63,63,63	0
56	MG	BA	3087	1/1	0.97	0.12	37,37,37,37	0
56	MG	DA	3056	1/1	0.97	0.25	44,44,44,44	0
56	MG	BA	3806	1/1	0.97	0.17	51,51,51,51	0
56	MG	BA	3074	1/1	0.97	0.24	32,32,32,32	0
56	MG	AA	3117	1/1	0.97	0.16	48,48,48,48	0
56	MG	DA	3532	1/1	0.97	0.14	57,57,57,57	0
56	MG	BA	3823	1/1	0.97	0.08	53,53,53,53	0
56	MG	BA	3331	1/1	0.97	0.14	32,32,32,32	0
56	MG	BG	201	1/1	0.97	0.09	57,57,57,57	0
56	MG	BA	3119	1/1	0.97	0.19	36,36,36,36	0
56	MG	DA	3469	1/1	0.97	0.13	54,54,54,54	0
56	MG	DA	3392	1/1	0.97	0.15	36,36,36,36	0
56	MG	BA	3234	1/1	0.97	0.25	48,48,48,48	0
60	K	AX	3001	1/1	0.97	0.22	57,57,57,57	0
56	MG	CA	3050	1/1	0.97	0.14	60,60,60,60	0
56	MG	BR	205	1/1	0.97	0.15	29,29,29,29	0
56	MG	CA	3042	1/1	0.97	0.12	58,58,58,58	0
56	MG	DA	3588	1/1	0.97	0.16	39,39,39,39	0
56	MG	BA	3165	1/1	0.97	0.26	40,40,40,40	0
56	MG	DA	3382	1/1	0.97	0.12	44,44,44,44	0
56	MG	BA	3694	1/1	0.97	0.23	27,27,27,27	0
56	MG	DA	3510	1/1	0.97	0.24	50,50,50,50	0
56	MG	AA	3201	1/1	0.97	0.07	59,59,59,59	0
56	MG	DA	3038	1/1	0.97	0.43	47,47,47,47	0
56	MG	CA	3127	1/1	0.97	0.17	44,44,44,44	0
56	MG	BA	3591	1/1	0.97	0.21	23,23,23,23	0
56	MG	AA	3195	1/1	0.98	0.15	59,59,59,59	0
56	MG	AA	3154	1/1	0.98	0.14	59,59,59,59	0
56	MG	BA	3632	1/1	0.98	0.17	55,55,55,55	0
56	MG	DA	3482	1/1	0.98	0.17	50,50,50,50	0
58	SF4	CD	501	8/8	0.98	0.10	54,64,76,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3405	1/1	0.98	0.18	33,33,33,33	0
56	MG	DA	3158	1/1	0.98	0.26	40,40,40,40	0
56	MG	DA	3292	1/1	0.98	0.12	37,37,37,37	0
56	MG	AA	3131	1/1	0.98	0.32	63,63,63,63	0
56	MG	BA	3107	1/1	0.98	0.19	20,20,20,20	0
56	MG	B7	101	1/1	0.98	0.14	33,33,33,33	0
56	MG	BA	3174	1/1	0.98	0.16	34,34,34,34	0
56	MG	BA	3288	1/1	0.98	0.38	40,40,40,40	0
56	MG	CA	3044	1/1	0.98	0.23	55,55,55,55	0
56	MG	BA	3080	1/1	0.98	0.10	24,24,24,24	0
56	MG	DA	3524	1/1	0.98	0.06	38,38,38,38	0
56	MG	BA	3649	1/1	0.98	0.10	43,43,43,43	0
56	MG	DA	3171	1/1	0.98	0.28	38,38,38,38	0
56	MG	DA	3670	1/1	0.98	0.13	38,38,38,38	0
56	MG	DO	5001	1/1	0.98	0.16	51,51,51,51	0
56	MG	AA	3151	1/1	0.98	0.16	41,41,41,41	0
56	MG	BA	3185	1/1	0.98	0.20	32,32,32,32	0
56	MG	DA	3560	1/1	0.98	0.19	34,34,34,34	0
56	MG	DA	3165	1/1	0.98	0.29	33,33,33,33	0
56	MG	BA	3780	1/1	0.98	0.12	41,41,41,41	0
56	MG	BA	3018	1/1	0.98	0.25	34,34,34,34	0
56	MG	BA	3226	1/1	0.98	0.24	41,41,41,41	0
56	MG	BA	3466	1/1	0.98	0.17	28,28,28,28	0
56	MG	BN	3004	1/1	0.98	0.20	50,50,50,50	0
56	MG	DA	3363	1/1	0.98	0.38	54,54,54,54	0
56	MG	DA	3015	1/1	0.98	0.26	31,31,31,31	0
56	MG	BA	3193	1/1	0.98	0.28	57,57,57,57	0
56	MG	BN	3003	1/1	0.98	0.15	38,38,38,38	0
56	MG	DA	3361	1/1	0.98	0.36	55,55,55,55	0
56	MG	BF	309	1/1	0.98	0.16	30,30,30,30	0
56	MG	DA	3227	1/1	0.98	0.21	38,38,38,38	0
56	MG	CA	3047	1/1	0.98	0.24	35,35,35,35	0
56	MG	DA	3329	1/1	0.98	0.21	29,29,29,29	0
56	MG	BA	3675	1/1	0.98	0.17	37,37,37,37	0
56	MG	DA	3161	1/1	0.98	0.20	49,49,49,49	0
56	MG	DA	3215	1/1	0.98	0.20	37,37,37,37	0
56	MG	DA	3653	1/1	0.98	0.15	58,58,58,58	0
56	MG	CA	3039	1/1	0.98	0.23	50,50,50,50	0
56	MG	BA	3282	1/1	0.98	0.30	24,24,24,24	0
56	MG	BA	3487	1/1	0.98	0.24	25,25,25,25	0
56	MG	BA	3730	1/1	0.98	0.13	27,27,27,27	0
56	MG	BA	3160	1/1	0.98	0.17	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	BA	3353	1/1	0.98	0.10	49,49,49,49	0
56	MG	BA	3091	1/1	0.98	0.32	38,38,38,38	0
56	MG	DA	3430	1/1	0.98	0.21	28,28,28,28	0
59	ZN	BY	501	1/1	0.98	0.11	58,58,58,58	0
56	MG	DA	3112	1/1	0.98	0.26	42,42,42,42	0
56	MG	BA	3078	1/1	0.98	0.19	17,17,17,17	0
56	MG	DA	3252	1/1	0.98	0.20	29,29,29,29	0
56	MG	BA	3418	1/1	0.98	0.16	32,32,32,32	0
56	MG	BA	3813	1/1	0.98	0.19	4,4,4,4	0
56	MG	BA	3476	1/1	0.98	0.21	24,24,24,24	0
56	MG	CA	3138	1/1	0.98	0.14	59,59,59,59	0
56	MG	CA	3058	1/1	0.98	0.14	70,70,70,70	0
56	MG	BA	3369	1/1	0.98	0.17	55,55,55,55	0
56	MG	BU	207	1/1	0.98	0.14	29,29,29,29	0
56	MG	BA	3265	1/1	0.98	0.27	29,29,29,29	0
56	MG	BA	3821	1/1	0.98	0.17	50,50,50,50	0
56	MG	BA	3104	1/1	0.98	0.19	27,27,27,27	0
56	MG	BA	3817	1/1	0.98	0.17	47,47,47,47	0
56	MG	DA	3294	1/1	0.98	0.26	42,42,42,42	0
56	MG	BA	3646	1/1	0.98	0.19	38,38,38,38	0
56	MG	DA	3473	1/1	0.98	0.06	49,49,49,49	0
56	MG	AF	3001	1/1	0.98	0.26	40,40,40,40	0
56	MG	DA	3389	1/1	0.98	0.06	53,53,53,53	0
56	MG	BD	303	1/1	0.98	0.15	44,44,44,44	0
56	MG	DA	3316	1/1	0.98	0.06	44,44,44,44	0
56	MG	DA	3116	1/1	0.98	0.10	57,57,57,57	0
56	MG	BA	3142	1/1	0.98	0.14	34,34,34,34	0
56	MG	DA	3064	1/1	0.98	0.10	64,64,64,64	0
56	MG	AA	3224	1/1	0.98	0.15	33,33,33,33	0
59	ZN	AN	501	1/1	0.98	0.12	58,58,58,58	0
56	MG	BA	3041	1/1	0.98	0.25	18,18,18,18	0
56	MG	BA	3479	1/1	0.98	0.14	37,37,37,37	0
56	MG	BA	3510	1/1	0.98	0.08	48,48,48,48	0
56	MG	BF	308	1/1	0.98	0.11	36,36,36,36	0
56	MG	BA	3640	1/1	0.98	0.19	39,39,39,39	0
56	MG	DA	3388	1/1	0.98	0.14	35,35,35,35	0
56	MG	AA	3193	1/1	0.98	0.09	43,43,43,43	0
56	MG	BA	3664	1/1	0.98	0.14	43,43,43,43	0
59	ZN	B9	501	1/1	0.98	0.17	49,49,49,49	0
56	MG	BF	303	1/1	0.98	0.22	42,42,42,42	0
56	MG	BA	3772	1/1	0.98	0.17	31,31,31,31	0
56	MG	BA	3771	1/1	0.98	0.20	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	3830	1/1	0.98	0.18	21,21,21,21	0
56	MG	BD	309	1/1	0.98	0.20	37,37,37,37	0
56	MG	DA	3646	1/1	0.98	0.08	49,49,49,49	0
56	MG	DA	3608	1/1	0.98	0.13	53,53,53,53	0
56	MG	DA	3291	1/1	0.98	0.18	42,42,42,42	0
56	MG	BA	3809	1/1	0.98	0.14	29,29,29,29	0
56	MG	BA	3801	1/1	0.98	0.10	53,53,53,53	0
56	MG	CA	3106	1/1	0.98	0.16	50,50,50,50	0
56	MG	BA	3157	1/1	0.98	0.17	36,36,36,36	0
56	MG	AA	3229	1/1	0.98	0.35	62,62,62,62	0
56	MG	BA	3330	1/1	0.98	0.17	29,29,29,29	0
56	MG	DD	304	1/1	0.98	0.39	31,31,31,31	0
56	MG	BA	3383	1/1	0.98	0.23	24,24,24,24	0
56	MG	DA	3444	1/1	0.98	0.18	30,30,30,30	0
56	MG	DA	3433	1/1	0.98	0.20	61,61,61,61	0
56	MG	BA	3657	1/1	0.98	0.20	47,47,47,47	0
56	MG	BU	204	1/1	0.98	0.21	38,38,38,38	0
56	MG	BA	3735	1/1	0.98	0.14	35,35,35,35	0
56	MG	DA	3554	1/1	0.98	0.18	23,23,23,23	0
56	MG	DA	3637	1/1	0.98	0.06	44,44,44,44	0
56	MG	AA	3065	1/1	0.98	0.17	58,58,58,58	0
56	MG	BU	202	1/1	0.98	0.22	40,40,40,40	0
56	MG	DA	3011	1/1	0.98	0.09	40,40,40,40	0
56	MG	DA	3219	1/1	0.98	0.27	54,54,54,54	0
56	MG	DA	3104	1/1	0.98	0.15	46,46,46,46	0
56	MG	DA	3173	1/1	0.98	0.17	30,30,30,30	0
56	MG	BA	3057	1/1	0.98	0.20	53,53,53,53	0
56	MG	BA	3496	1/1	0.98	0.24	39,39,39,39	0
56	MG	DQ	3004	1/1	0.98	0.16	51,51,51,51	0
56	MG	BB	3017	1/1	0.98	0.20	33,33,33,33	0
56	MG	DA	3261	1/1	0.98	0.07	44,44,44,44	0
56	MG	DA	3356	1/1	0.98	0.26	20,20,20,20	0
56	MG	DA	3476	1/1	0.98	0.24	45,45,45,45	0
56	MG	D3	3001	1/1	0.98	0.16	58,58,58,58	0
56	MG	DA	3281	1/1	0.98	0.23	33,33,33,33	0
56	MG	BA	3212	1/1	0.98	0.20	42,42,42,42	0
56	MG	CA	3066	1/1	0.98	0.14	66,66,66,66	0
56	MG	CA	3091	1/1	0.98	0.15	48,48,48,48	0
56	MG	BA	3210	1/1	0.98	0.20	31,31,31,31	0
56	MG	BA	3599	1/1	0.98	0.20	23,23,23,23	0
56	MG	DA	3465	1/1	0.98	0.07	55,55,55,55	0
56	MG	BA	3589	1/1	0.98	0.18	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3045	1/1	0.98	0.20	42,42,42,42	0
56	MG	DA	3339	1/1	0.98	0.10	52,52,52,52	0
56	MG	BA	3128	1/1	0.98	0.24	27,27,27,27	0
56	MG	DA	3301	1/1	0.98	0.23	48,48,48,48	0
56	MG	BA	3572	1/1	0.98	0.27	63,63,63,63	0
56	MG	BA	3321	1/1	0.98	0.08	54,54,54,54	0
56	MG	BA	3460	1/1	0.98	0.23	35,35,35,35	0
59	ZN	B6	103	1/1	0.98	0.13	29,29,29,29	0
56	MG	DA	3544	1/1	0.98	0.14	37,37,37,37	0
56	MG	CA	3144	1/1	0.98	0.18	59,59,59,59	0
56	MG	BA	3246	1/1	0.99	0.10	27,27,27,27	0
56	MG	DA	3619	1/1	0.99	0.03	58,58,58,58	0
56	MG	DA	3017	1/1	0.99	0.21	28,28,28,28	0
59	ZN	D5	501	1/1	0.99	0.15	53,53,53,53	0
56	MG	BA	3368	1/1	0.99	0.19	12,12,12,12	0
56	MG	CA	3088	1/1	0.99	0.41	53,53,53,53	0
56	MG	BA	3050	1/1	0.99	0.17	31,31,31,31	0
56	MG	AA	3225	1/1	0.99	0.11	26,26,26,26	0
56	MG	BA	3697	1/1	0.99	0.12	35,35,35,35	0
56	MG	DA	3280	1/1	0.99	0.14	43,43,43,43	0
56	MG	BA	3053	1/1	0.99	0.27	22,22,22,22	0
56	MG	BA	3731	1/1	0.99	0.12	23,23,23,23	0
58	SF4	AD	501	8/8	0.99	0.14	56,62,64,76	0
56	MG	BA	3334	1/1	0.99	0.25	30,30,30,30	0
56	MG	BA	3355	1/1	0.99	0.15	24,24,24,24	0
56	MG	BA	3039	1/1	0.99	0.28	47,47,47,47	0
56	MG	DA	3350	1/1	0.99	0.30	29,29,29,29	0
56	MG	BA	3231	1/1	0.99	0.24	37,37,37,37	0
56	MG	BD	307	1/1	0.99	0.21	35,35,35,35	0
56	MG	DA	3036	1/1	0.99	0.15	29,29,29,29	0
56	MG	DA	3050	1/1	0.99	0.23	40,40,40,40	0
56	MG	BV	202	1/1	0.99	0.13	26,26,26,26	0
56	MG	AA	3186	1/1	0.99	0.16	52,52,52,52	0
56	MG	BA	3458	1/1	0.99	0.25	19,19,19,19	0
56	MG	BA	3759	1/1	0.99	0.15	9,9,9,9	0
56	MG	DA	3254	1/1	0.99	0.25	21,21,21,21	0
56	MG	BU	209	1/1	0.99	0.19	27,27,27,27	0
56	MG	BA	3621	1/1	0.99	0.23	52,52,52,52	0
56	MG	BA	3682	1/1	0.99	0.13	50,50,50,50	0
56	MG	DA	3018	1/1	0.99	0.18	41,41,41,41	0
56	MG	AA	3137	1/1	0.99	0.19	42,42,42,42	0
56	MG	BB	3016	1/1	0.99	0.16	43,43,43,43	0

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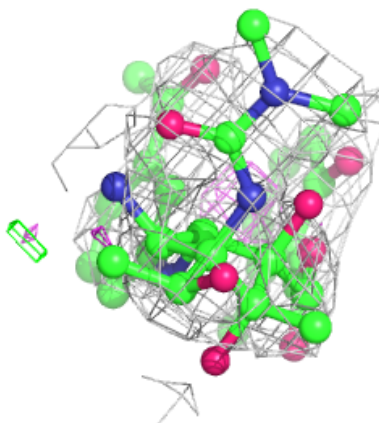
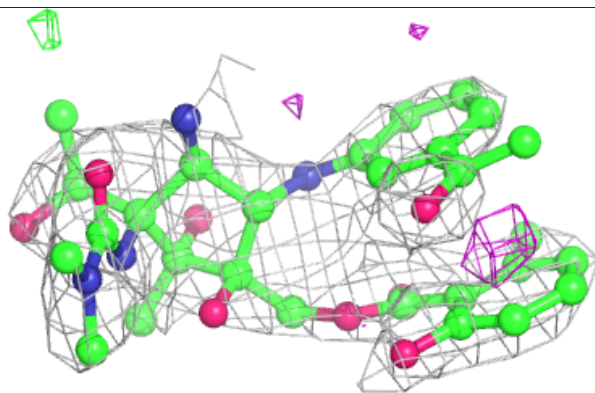
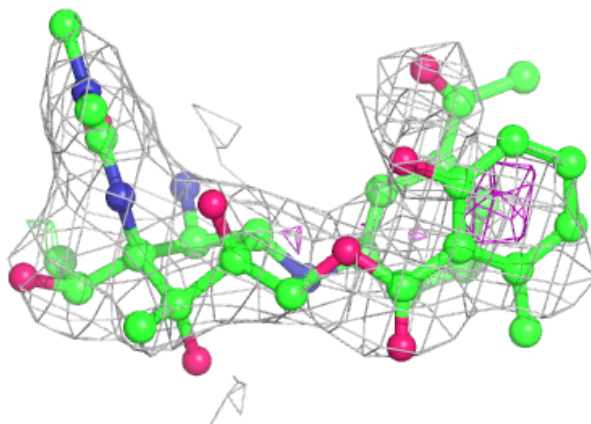
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3071	1/1	0.99	0.33	42,42,42,42	0
56	MG	DA	3218	1/1	0.99	0.16	47,47,47,47	0
56	MG	CA	3077	1/1	0.99	0.06	48,48,48,48	0
56	MG	BA	3609	1/1	0.99	0.26	20,20,20,20	0
56	MG	BA	3003	1/1	0.99	0.26	20,20,20,20	0
56	MG	BA	3462	1/1	0.99	0.13	11,11,11,11	0
56	MG	BV	205	1/1	0.99	0.12	32,32,32,32	0
56	MG	BU	203	1/1	0.99	0.14	31,31,31,31	0
56	MG	BA	3400	1/1	0.99	0.17	25,25,25,25	0
56	MG	DA	3228	1/1	0.99	0.05	42,42,42,42	0
56	MG	BA	3188	1/1	0.99	0.24	19,19,19,19	0
56	MG	BA	3129	1/1	0.99	0.22	36,36,36,36	0
56	MG	DD	306	1/1	0.99	0.26	44,44,44,44	0
56	MG	BA	3440	1/1	0.99	0.27	29,29,29,29	0
56	MG	AA	3157	1/1	0.99	0.19	46,46,46,46	0
56	MG	DA	3656	1/1	0.99	0.17	62,62,62,62	0
56	MG	BV	201	1/1	0.99	0.22	29,29,29,29	0
56	MG	DA	3438	1/1	0.99	0.10	60,60,60,60	0
56	MG	BA	3272	1/1	1.00	0.28	11,11,11,11	0
59	ZN	B5	104	1/1	1.00	0.15	38,38,38,38	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.

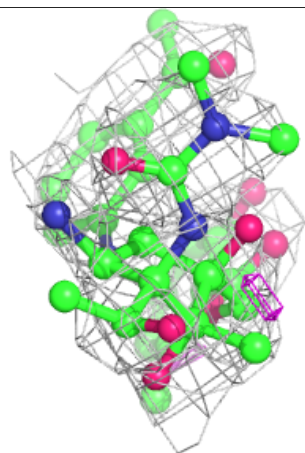
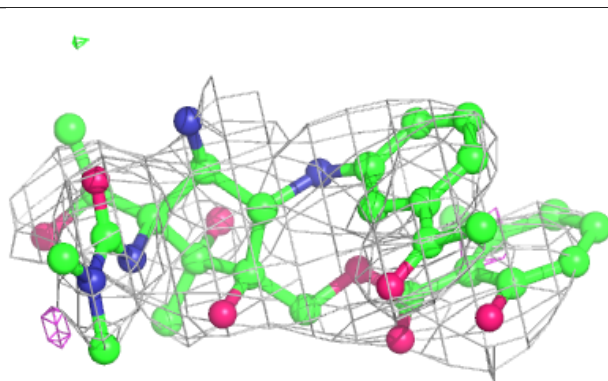
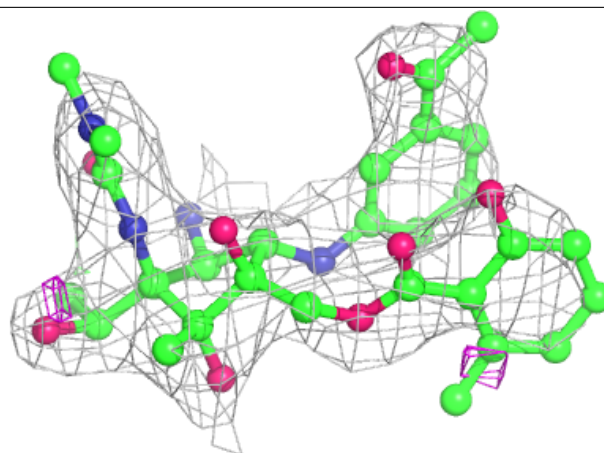
Electron density around PCY CA 3178:

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



Electron density around PCY AA 3231:

$2mF_o - DF_c$ (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.