



Full wwPDB X-ray Structure Validation Report i

Sep 11, 2014 – 03:48 AM EDT

PDB ID : 1VY6
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in the pre-attack state of peptide bond formation containing short substrate-mimic Cytidine-Puromycin in the A site and acylated tRNA in the P site.
Authors : Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on : 2014-05-13
Resolution : 2.90 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

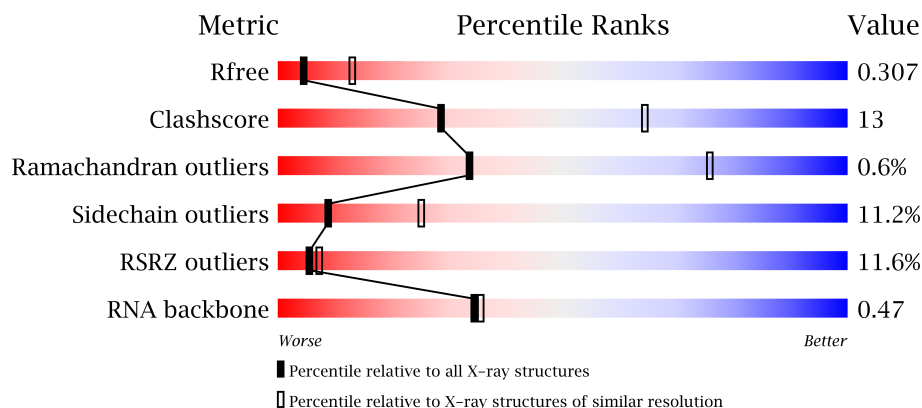
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable23489
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (2.90-2.90)
RNA backbone	1838	1055 (3.40-2.40)

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

Mol	Chain	Length	Quality of chain
1	AA	1521	
1	CA	1521	
2	AB	256	
2	CB	256	
3	AC	239	
3	CC	239	
4	AD	209	
4	CD	209	
5	AE	162	
5	CE	162	
6	AF	101	

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Mol	Chain	Length	Quality of chain
6	CF	101	
7	AG	156	
7	CG	156	
8	AH	138	
8	CH	138	
9	AI	128	
9	CI	128	
10	AJ	105	
10	CJ	105	
11	AK	129	
11	CK	129	
12	AL	132	
12	CL	132	
13	AM	126	
13	CM	126	
14	AN	61	
14	CN	61	
15	AO	89	
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AW	2	
23	CW	2	
24	AX	77	
24	CX	77	
25	BA	2915	
25	DA	2915	
26	BB	121	
26	DB	121	
27	BD	276	

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Mol	Chain	Length	Quality of chain
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	
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	

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

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 289646 atoms, of which 0 are hydrogen and 0 are deuterium.

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1659	1040	326	286	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1670	1047	332	284	7			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
22	CV	12	Total	C	N	O	P	0	0	0
			252	115	46	80	11			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AW	2	Total	C	N	O	P	0	0	0
			54	31	10	12	1			
23	CW	2	Total	C	N	O	P	0	0	0
			54	31	10	12	1			

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

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

- Molecule 25 is a RNA chain called 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			

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

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

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

- Molecule 33 is a protein called 50S ribosomal protein L13.

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

- Molecule 34 is a protein called 50S ribosomal protein L14.

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

- Molecule 35 is a protein called 50S ribosomal protein L15.

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

- Molecule 36 is a protein called 50S ribosomal protein L16.

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

- Molecule 37 is a protein called 50S ribosomal protein L17.

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

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BS	110	Total	C	N	O		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			

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

- Molecule 43 is a protein called 50S ribosomal protein L23.

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

- Molecule 44 is a protein called 50S ribosomal protein L24.

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

- Molecule 45 is a protein called 50S ribosomal protein L25.

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

- Molecule 46 is a protein called 50S ribosomal protein L27.

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

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

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

- Molecule 49 is a protein called 50S ribosomal protein L30.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B4	69	Total	C	N	O	S	0	0	0
			552	349	99	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	675	Total	Mg	0	0
			675	675		
56	AK	1	Total	Mg	0	0
			1	1		
56	DQ	3	Total	Mg	0	0
			3	3		
56	D3	1	Total	Mg	0	0
			1	1		
56	DF	3	Total	Mg	0	0
			3	3		
56	B8	1	Total	Mg	0	0
			1	1		
56	BE	6	Total	Mg	0	0
			6	6		
56	DU	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AN	1	Total 1	Mg 1	0	0
56	BP	4	Total 4	Mg 4	0	0
56	AX	7	Total 7	Mg 7	0	0
56	DN	1	Total 1	Mg 1	0	0
56	CA	154	Total 154	Mg 154	0	0
56	B5	2	Total 2	Mg 2	0	0
56	BB	18	Total 18	Mg 18	0	0
56	AE	2	Total 2	Mg 2	0	0
56	DG	1	Total 1	Mg 1	0	0
56	CF	1	Total 1	Mg 1	0	0
56	B9	1	Total 1	Mg 1	0	0
56	BF	5	Total 5	Mg 5	0	0
56	BX	3	Total 3	Mg 3	0	0
56	D8	2	Total 2	Mg 2	0	0
56	AA	187	Total 187	Mg 187	0	0
56	BQ	3	Total 3	Mg 3	0	0
56	D7	1	Total 1	Mg 1	0	0
56	CX	1	Total 1	Mg 1	0	0
56	DV	2	Total 2	Mg 2	0	0
56	AM	1	Total 1	Mg 1	0	0
56	BU	5	Total 5	Mg 5	0	0

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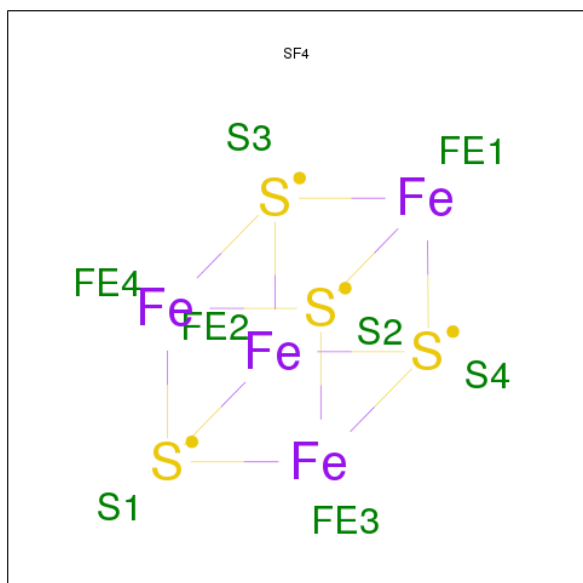
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	DR	2	Total 2	Mg 2	0	0
56	AD	1	Total 1	Mg 1	0	0
56	BN	2	Total 2	Mg 2	0	0
56	CT	1	Total 1	Mg 1	0	0
56	D0	1	Total 1	Mg 1	0	0
56	BG	3	Total 3	Mg 3	0	0
56	BY	2	Total 2	Mg 2	0	0
56	DE	5	Total 5	Mg 5	0	0
56	B3	2	Total 2	Mg 2	0	0
56	CJ	1	Total 1	Mg 1	0	0
56	BR	3	Total 3	Mg 3	0	0
56	DA	595	Total 595	Mg 595	0	0
56	DP	1	Total 1	Mg 1	0	0
56	DW	2	Total 2	Mg 2	0	0
56	B7	4	Total 4	Mg 4	0	0
56	AL	1	Total 1	Mg 1	0	0
56	BV	3	Total 3	Mg 3	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	D5	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	BD	8	Total	Mg	0	0
			8	8		
56	DT	1	Total	Mg	0	0
			1	1		
56	B0	5	Total	Mg	0	0
			5	5		
56	CE	2	Total	Mg	0	0
			2	2		
56	BW	4	Total	Mg	0	0
			4	4		
56	DB	12	Total	Mg	0	0
			12	12		
56	DD	2	Total	Mg	0	0
			2	2		
56	CK	1	Total	Mg	0	0
			1	1		
56	AF	1	Total	Mg	0	0
			1	1		
56	BH	1	Total	Mg	0	0
			1	1		

- Molecule 57 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



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

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

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	B5	1	Total	Zn	0	0
			1	1		
58	B4	1	Total	Zn	0	0
			1	1		
58	CN	1	Total	Zn	0	0
			1	1		
58	BY	1	Total	Zn	0	0
			1	1		
58	B9	1	Total	Zn	0	0
			1	1		
58	DY	1	Total	Zn	0	0
			1	1		
58	D5	1	Total	Zn	0	0
			1	1		
58	D4	1	Total	Zn	0	0
			1	1		
58	AN	1	Total	Zn	0	0
			1	1		
58	D6	1	Total	Zn	0	0
			1	1		
58	D9	1	Total	Zn	0	0
			1	1		
58	B6	1	Total	Zn	0	0
			1	1		

- Molecule 59 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	AX	1	Total	K	0	0
			1	1		
59	DA	1	Total	K	0	0
			1	1		

- Molecule 60 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	AA	165	Total O 165 165	0	0
60	AJ	1	Total O 1 1	0	0
60	AL	3	Total O 3 3	0	0
60	AP	1	Total O 1 1	0	0
60	AU	1	Total O 1 1	0	0
60	AV	2	Total O 2 2	0	0
60	AW	3	Total O 3 3	0	0
60	BA	924	Total O 924 924	0	0
60	BB	27	Total O 27 27	0	0
60	BD	6	Total O 6 6	0	0
60	BE	8	Total O 8 8	0	0
60	BF	6	Total O 6 6	0	0
60	BG	1	Total O 1 1	0	0
60	BH	1	Total O 1 1	0	0
60	BN	3	Total O 3 3	0	0
60	BO	1	Total O 1 1	0	0
60	BP	14	Total O 14 14	0	0
60	BQ	2	Total O 2 2	0	0
60	BS	1	Total O 1 1	0	0
60	BT	4	Total O 4 4	0	0
60	BU	2	Total O 2 2	0	0
60	BV	5	Total O 5 5	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	BW	1	Total O 1 1	0	0
60	BX	2	Total O 2 2	0	0
60	BZ	1	Total O 1 1	0	0
60	B0	4	Total O 4 4	0	0
60	B1	2	Total O 2 2	0	0
60	B2	1	Total O 1 1	0	0
60	B3	1	Total O 1 1	0	0
60	B5	2	Total O 2 2	0	0
60	B7	2	Total O 2 2	0	0
60	B8	8	Total O 8 8	0	0
60	CA	113	Total O 113 113	0	0
60	CE	2	Total O 2 2	0	0
60	CJ	2	Total O 2 2	0	0
60	CL	1	Total O 1 1	0	0
60	CO	1	Total O 1 1	0	0
60	CW	1	Total O 1 1	0	0
60	CX	1	Total O 1 1	0	0
60	DA	689	Total O 689 689	0	0
60	DB	9	Total O 9 9	0	0
60	DD	11	Total O 11 11	0	0
60	DE	5	Total O 5 5	0	0

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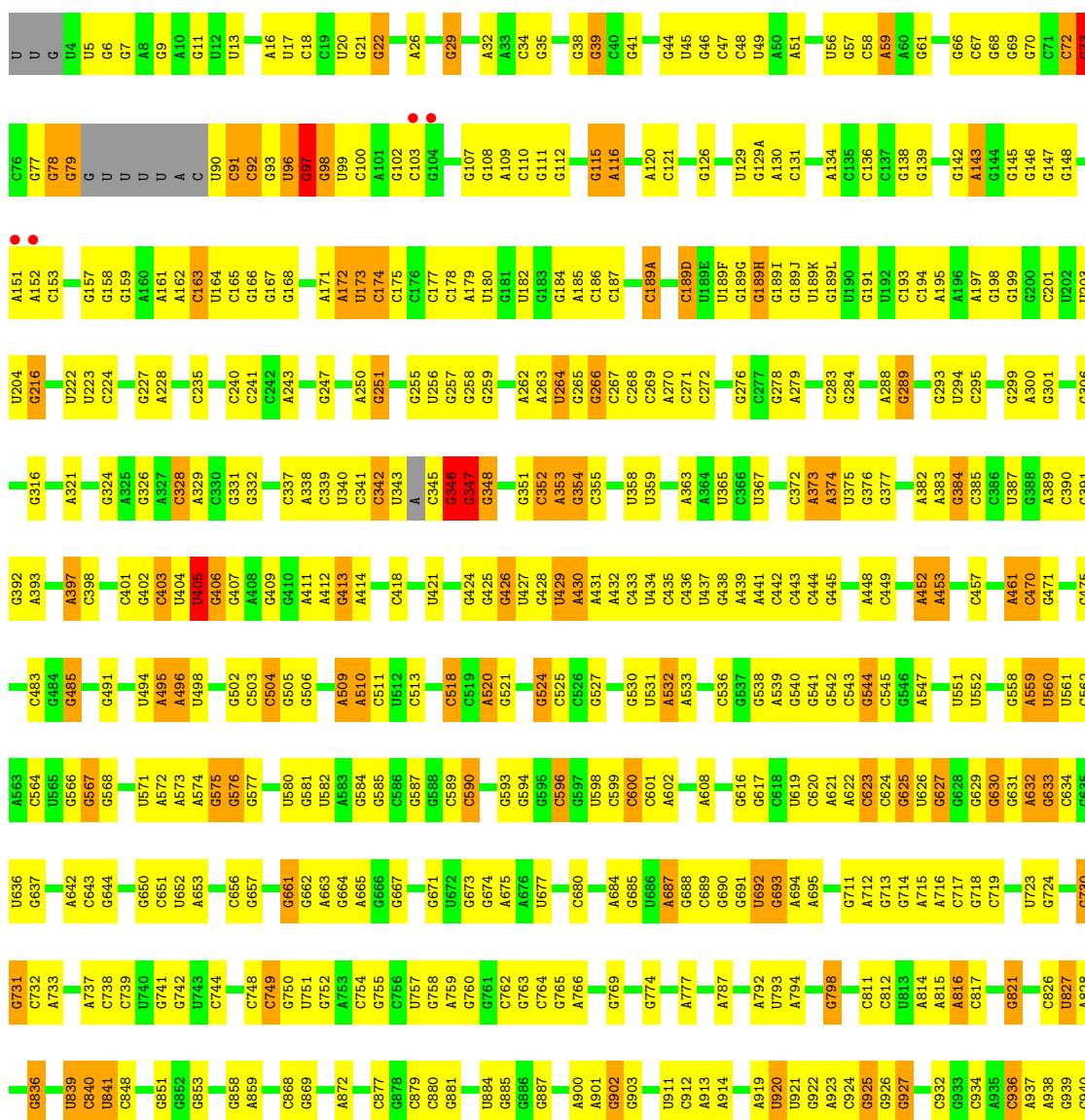
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	DF	6	Total 6	O 6	0	0
60	DO	1	Total 1	O 1	0	0
60	DP	6	Total 6	O 6	0	0
60	DU	3	Total 3	O 3	0	0
60	DV	1	Total 1	O 1	0	0
60	DW	1	Total 1	O 1	0	0
60	DX	3	Total 3	O 3	0	0
60	D0	5	Total 5	O 5	0	0
60	D1	1	Total 1	O 1	0	0
60	D3	1	Total 1	O 1	0	0
60	D8	3	Total 3	O 3	0	0

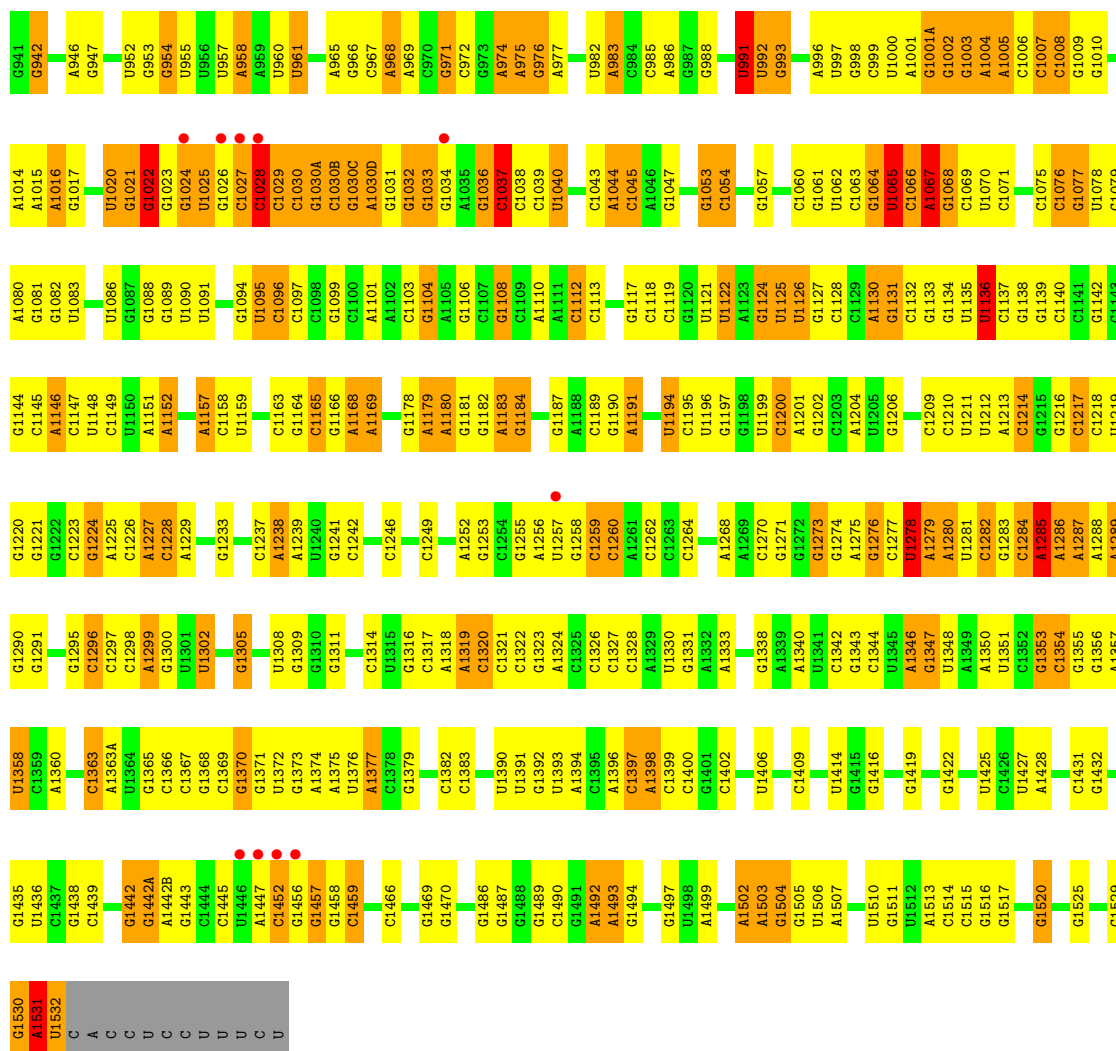
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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

Chain AA: 

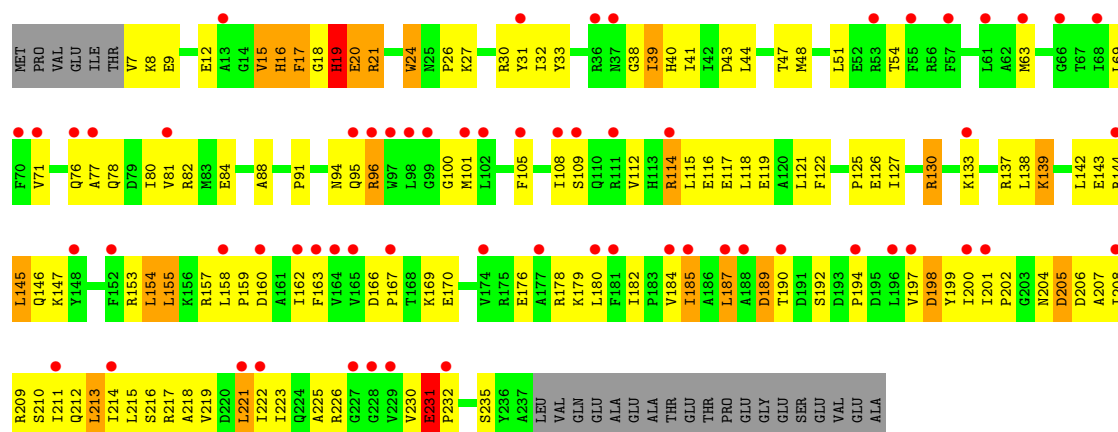




G1487	G1488	G1489	C1490	G1491	A1492	A1493	A1398	A1399	G1400	G1401	C1402	C1501	A1502	A1503	G1504	G1505	G1506	C1509	G1510	G1511	A1512	A1513	A1514	G1515	G1516	G1517	A1518	A1519	G1520	G1523	G1529	G1530	A1531	C	A	A	C	C	C	G1442	G1442A	C1442B	G1443	C1444	A1447	C1452	G1456	G1457	G1458	C1459	G1464	A1468	G1469	G1470																																																																																																																																																																																																																																																																																																																																																																																																																																																												
G1325	C1326	C1327	C1328	A1329	U1330	G1331	A1332	A1333	G1338	A1339	A1340	U1341	G1342	G1343	G1344	U1345	A1346	G1347	U1348	A1349	G1422	G1423	A1424	U1425	G1426	U1427	A1428	C1429	C1430	G1361	C1362	A1363	G1366	C1367	G1368	C1369	G1370	G1371	U1372	G1373	A1374	A1375	U1376	A1377	C1378	G1379	U1380	U1381	C1382	C1383	G1384	G1385	G1386	G1387	C1388	C1389																																																																																																																																																																																																																																																																																																																																																																																																																																																										
C1264	U1199	C1267	A1268	A1269	C1270	A1204	U1205	G1206	C1209	A1210	U1211	U1212	A1213	A1280	U1281	C1282	G1283	C1284	A1285	A1286	A1287	A1288	A1289	G1290	G1291	U1292	G1293	G1294	G1295	C1296	C1297	C1298	A1299	G1300	U1301	U1302	C1303	G1304	G1305	A1306	U1307	U1308	G1309	G1310	G1311	G1312	U1313	C1314	U1315	G1316	C1317	A1318	A1319	C1320	C1321	C1322	A1323	A1324																																																																																																																																																																																																																																																																																																																																																																																																																																																								
G1198	U1199	C1200	A1201	C1202	C1203	A1204	U1205	G1206	C1209	A1210	U1211	U1212	A1213	A1280	U1281	C1282	G1283	C1284	A1285	A1286	A1287	A1288	A1289	G1290	G1291	U1292	G1293	G1294	G1295	C1296	C1297	C1298	A1299	G1300	U1301	U1302	C1303	G1304	G1305	A1306	U1307	U1308	G1309	G1310	G1311	G1312	U1313	C1314	U1315	G1316	C1317	A1318	A1319	C1320	C1321	C1322	A1323	A1324																																																																																																																																																																																																																																																																																																																																																																																																																																																								
G1133	G1134	U1135	U1136	C1137	G1138	C1139	G1140	C1141	G1142	G1143	C1144	C1145	A1146	C1147	U1148	C1149	U1150	A1151	A1152	C1153	G1154	G1155	G1156	A1157	C1158	U1159	C1162	C1163	G1164	C1165	G1166	A1168	A1169	A1170	G1171	C1172	G1173	G1174	A1179	A1180	G1181	G1182	A1183	G1184	G1185	G1186	G1187	A1188	C1189	G1190	A1191	U1192	A1193	G1194	C1195	U1196	G1197																																																																																																																																																																																																																																																																																																																																																																																																																																																									
G1068	C1069	U1070	U1071	U1072	G1073	G1074	C1075	C1076	U1077	U1078	G1079	A1080	G1081	U1082	U1083	U1084	U1085	U1086	U1087	U1088	U1089	U1090	U1091	A1092	U1093	U1094	U1095	U1096	U1097	U1098	U1099	U1100	U1101	A1102	U1103	U1104	U1105	U1106	U1107	U1108	U1112	U1113	U1114	U1117	U1118	U1119	U1120	U1121	U1122	U1123	U1124	U1125	U1126	U1127	U1128	U1129	U1130	U1131	U1132																																																																																																																																																																																																																																																																																																																																																																																																																																																							
G1009	G1010	U1011	U1012	G1013	A1014	U1015	U1016	G1017	C1018	C1019	U1020	U1021	G1022	G1023	G1024	U1025	G1026	C1027	C1028	C1029	C1030	C1031	C1032	G1033	G1034	U1035	C1036	C1037	C1038	C1039	U1040	U1041	G1042	C1043	C1044	C1045	C1046	G1047	U1048	G1053	C1054	A1055	U1056	G1057	G1058	C1059	G1060	U1061	U1062	U1063	U1064	U1065	U1066	A1067																																																																																																																																																																																																																																																																																																																																																																																																																																																												
C945	A946	C947	C948	C949	C950	C951	U952	G953	C954	U955	A956	A957	U958	U959	U960	U961	A965	G966	C967	C968	C969	C970	C971	C972	C973	A974	C975	U981	U982	A983	C984	C985	A986	C989	C990	U991	U992	C993	A994	C995	A996	U997	G998	C999	U1000	A1001	U1002	U1003	U1004	A1005	U1006	C1007	C1008																																																																																																																																																																																																																																																																																																																																																																																																																																																													
G853	G854	G855	G856	C857	C858	C859	A860	A861	C862	U863	A864	A865	C866	C867	U868	U869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	U884	A885	C886	C887	C888	C889	C890	C891	A900	A901	C902	G906	A913	A914	A915	A916	C917	C921	C922	C923	C924	C925	C926	C927	C932	C933	C934	A935	C936	A937	C938	C939	C940	C941	C942	C943	C944																																																																																																																																																																																																																																																																																																																																																																																																																																																		
G758	A759	G760	U761	C762	C763	C764	C765	A766	A767	C768	G769	G774	A775	C776	A777	A778	A779	C780	C781	C782	C783	C784	C785	C786	C787	C788	U884	A885	C886	C887	C888	C889	C890	C891	A900	A901	C902	G906	A913	A914	A915	A916	C917	C921	C922	C923	C924	C925	C926	C927	C932	C933	C934	A935	C936	A937	C938	C939	C940	C941	C942	C943	C944																																																																																																																																																																																																																																																																																																																																																																																																																																																			
G680	G681	U682	C683	C684	C685	C686	C687	C688	C689	C690	C691	A692	A693	A694	A695	A696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758																																																																																																																																																																																																																																																																																																																																																																																																																																				
A510	C511	U512	C513	C514	C515	C516	C517	C518	C519	A520	C521	C522	A523	C524	C525	C526	C527	C528	C529	C530	C531	A532	A533	C534	C535	C536	C537	C538	A539	G540	A541	C542	C543	C544	C545	C546	A547	C548	C549	C550	C551	C552	C553	C554	C555	C556	C557	C558	C559	C560	C561	C562	C563	C564	C565	C566	C567	C568	C569	C570	C571	C572	C573	C574	C575	C576	C577	C578	C579	C580	C581	C582	C583	C584	C585	C586	C587	A588	C589	C590	C591	C592	C593	C594	C595	C596	C597	C598	C599	C600	C601	C602	C603	C604	C605	C606	C607	C608	C609	C610	C611	C612	C613	C614	C615	C616	C617	C618	C619	C620	C621	C622	C623	C624	C625	C626	C627	C628	C629	C630	C631	C632	C633	C634	C635	C636	C637	C638	C639	C640	C641	C642	C643	C644	C645	C646	C647	C648	C649	C650	C651	C652	C653	C654	C655	C656	C657	C658	C659	C660	C661	C662	C663	C664	C665	C666	C667	C668	C669	C670	C671	C672	C673	C674	C675	C676	C677	C678	C679	C680	C681	C682	C683	C684	C685	C686	C687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008

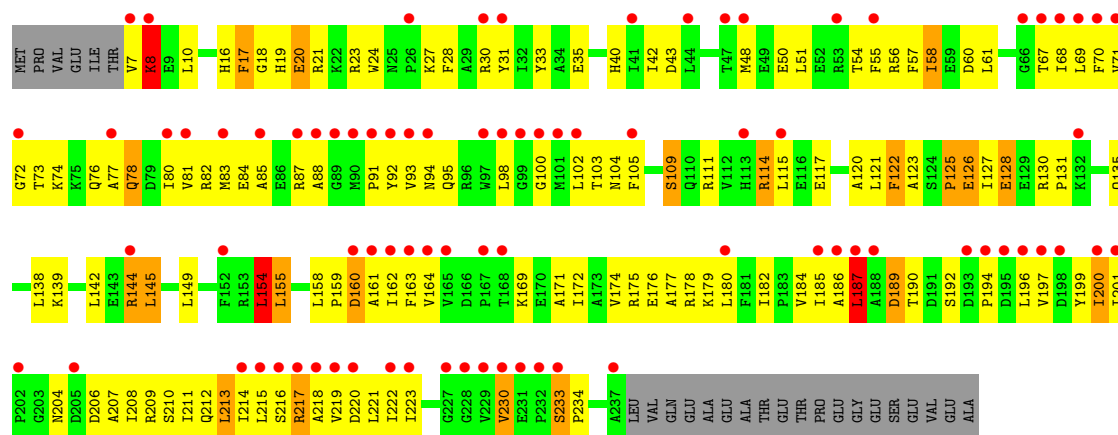
- Molecule 2: 30S ribosomal protein S2

Chain AB:



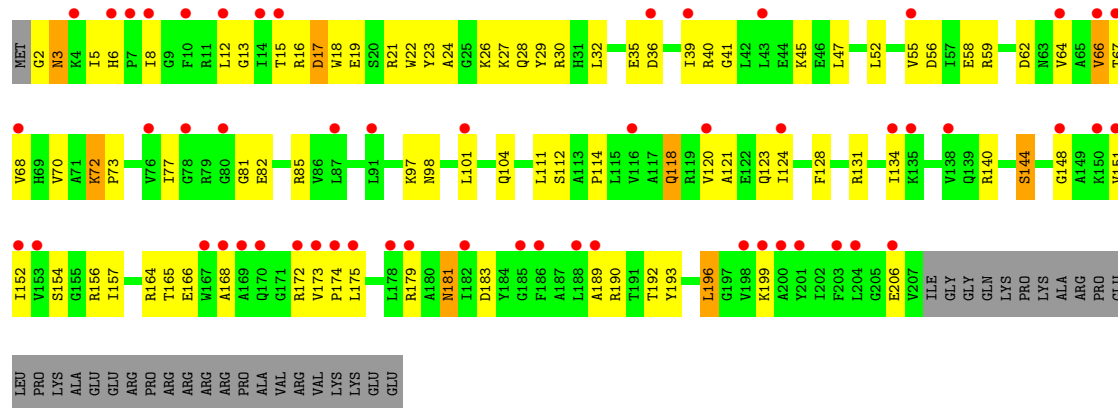
- Molecule 2: 30S ribosomal protein S2

Chain CB:

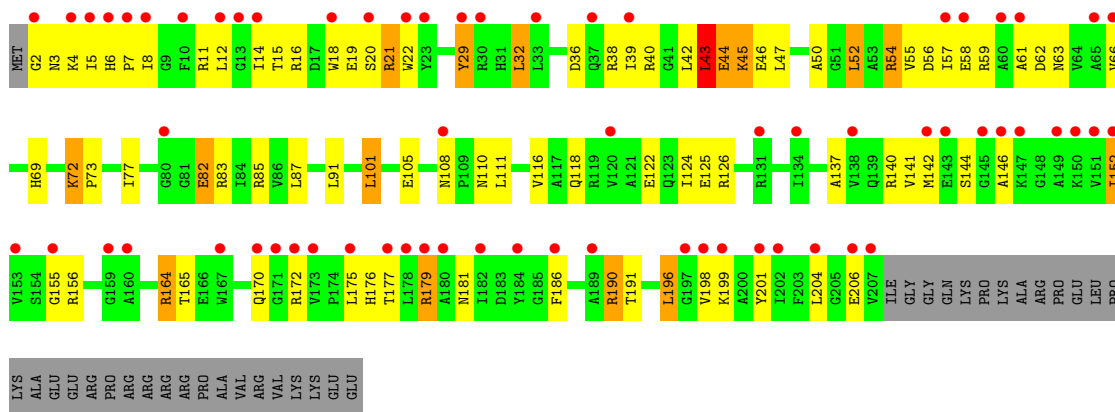


- Molecule 3: 30S ribosomal protein S3

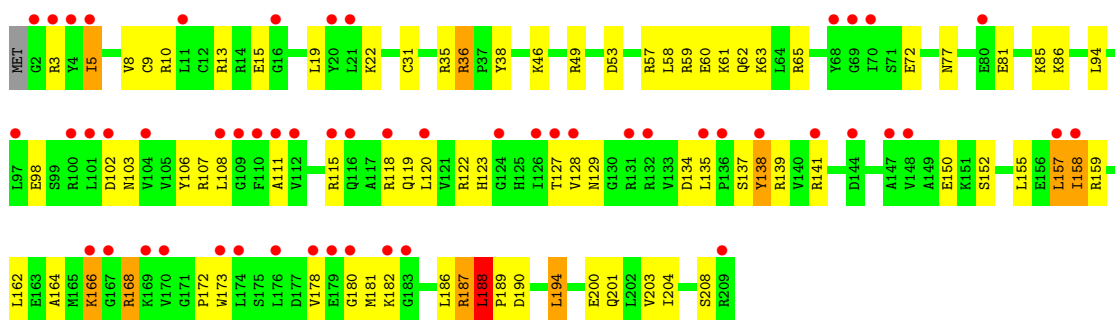
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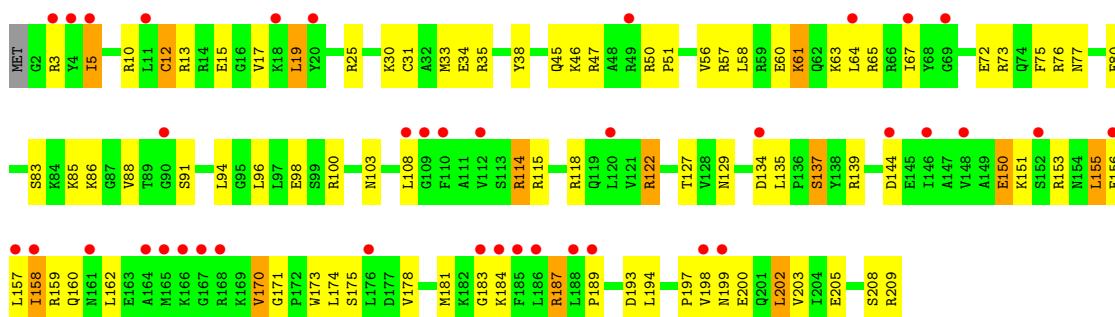
- Molecule 3: 30S ribosomal protein S3

Chain CC: 

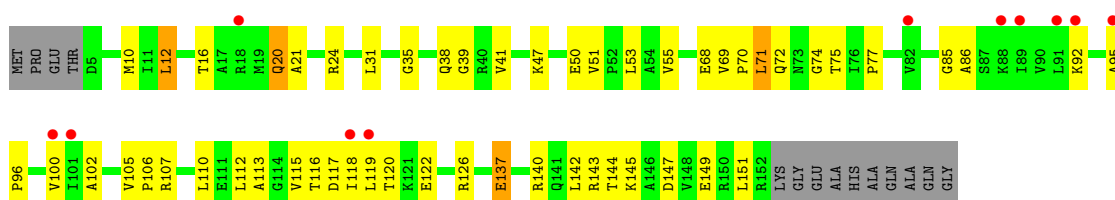
- Molecule 4: 30S ribosomal protein S4

Chain AD: 

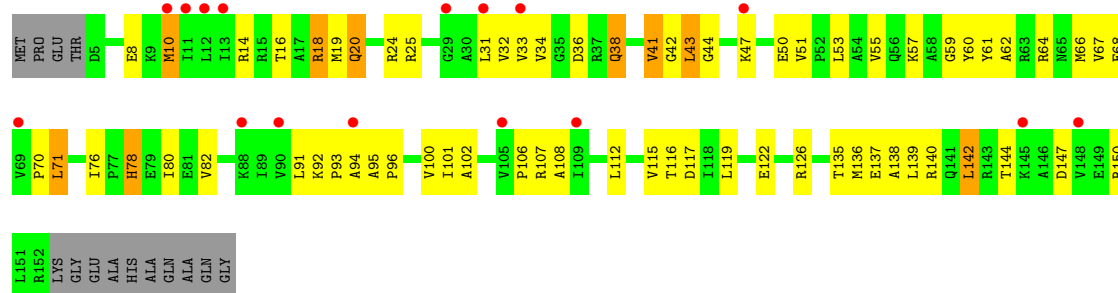
- Molecule 4: 30S ribosomal protein S4

Chain CD: 

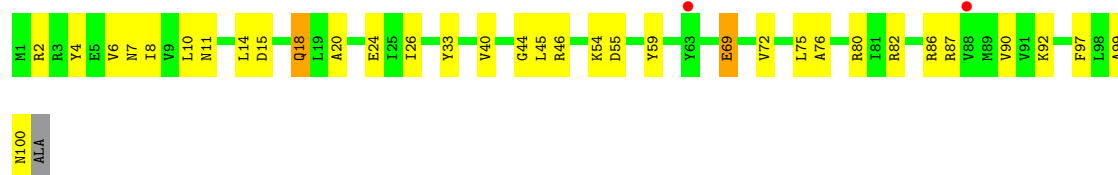
- Molecule 5: 30S ribosomal protein S5

Chain AE: 

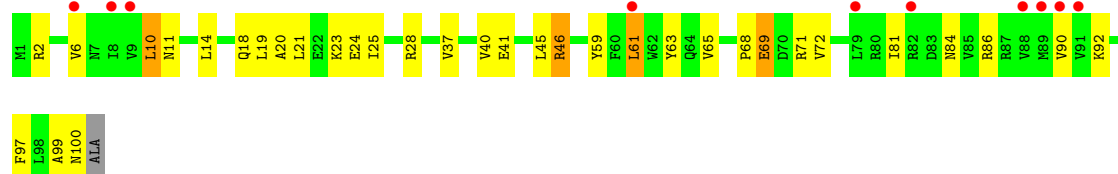
- Molecule 5: 30S ribosomal protein S5

Chain CE: 

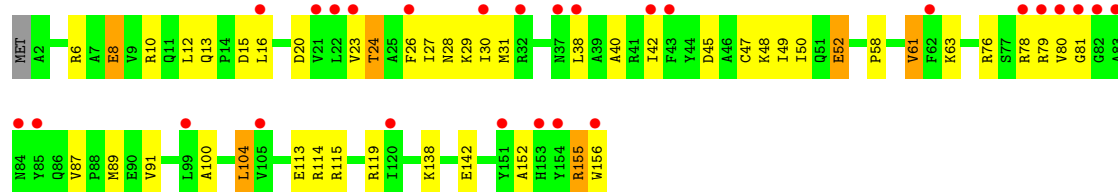
- Molecule 6: 30S ribosomal protein S6

Chain AF: 

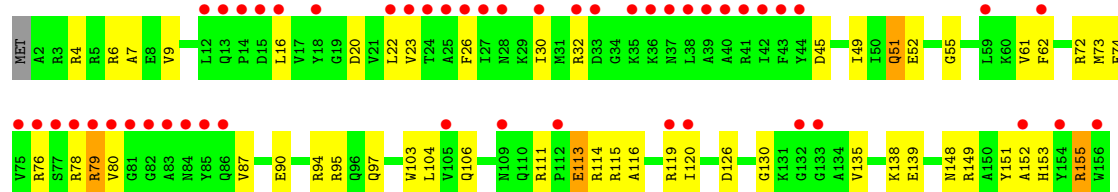
- Molecule 6: 30S ribosomal protein S6

Chain CF: 

- Molecule 7: 30S ribosomal protein S7

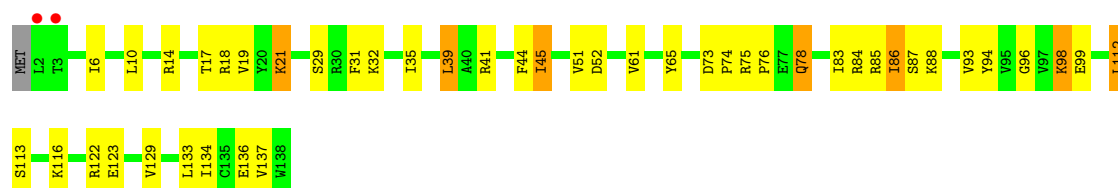
Chain AG: 

- Molecule 7: 30S ribosomal protein S7

Chain CG: 

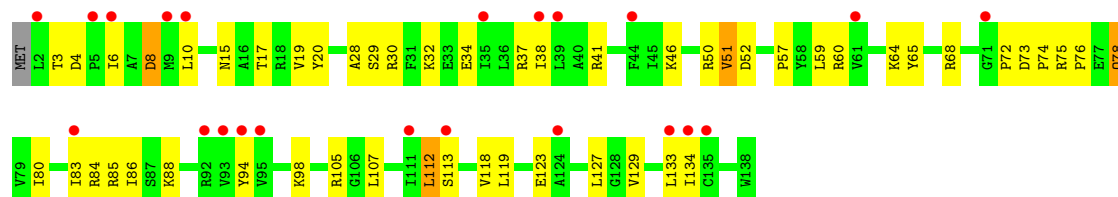
- Molecule 8: 30S ribosomal protein S8

Chain AH:



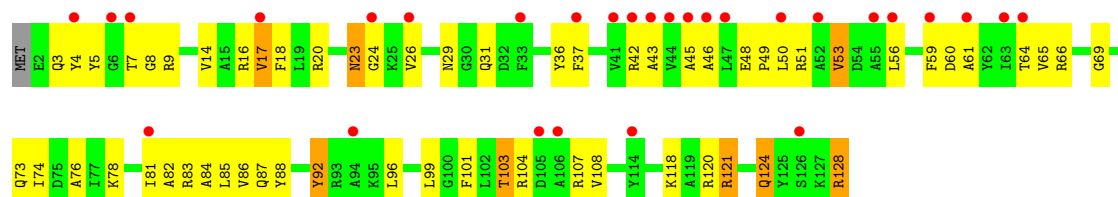
- Molecule 8: 30S ribosomal protein S8

Chain CH:



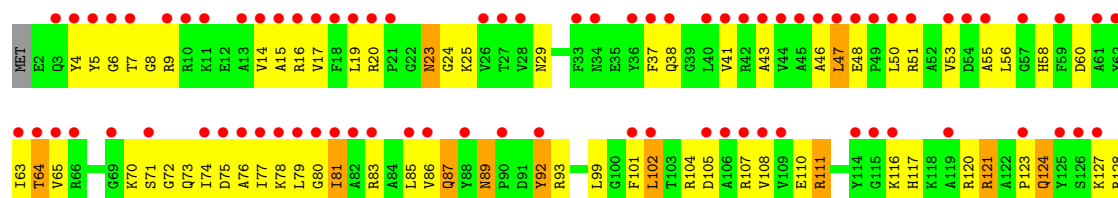
- Molecule 9: 30S ribosomal protein S9

Chain AI:



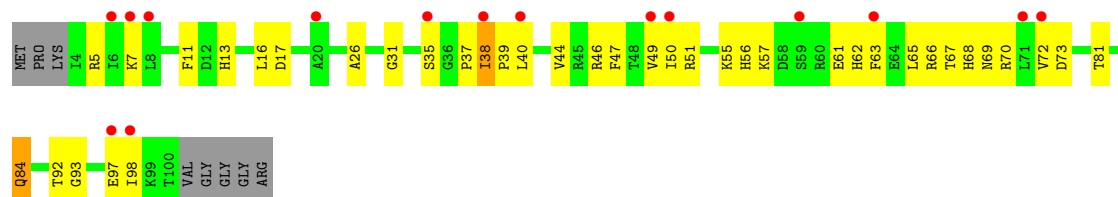
- Molecule 9: 30S ribosomal protein S9

Chain CI:



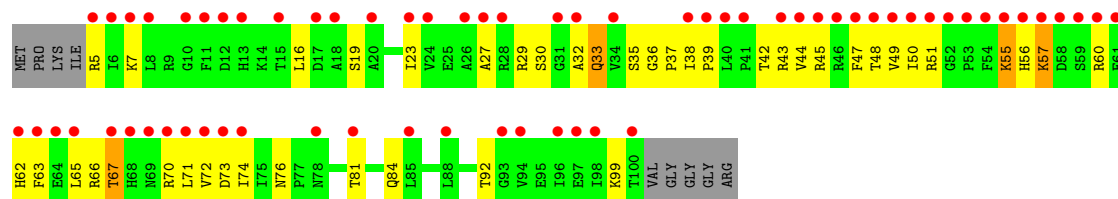
- Molecule 10: 30S ribosomal protein S10

Chain AJ:



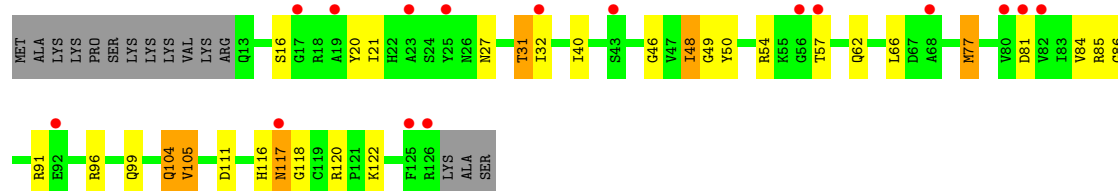
- Molecule 10: 30S ribosomal protein S10

Chain CJ: 



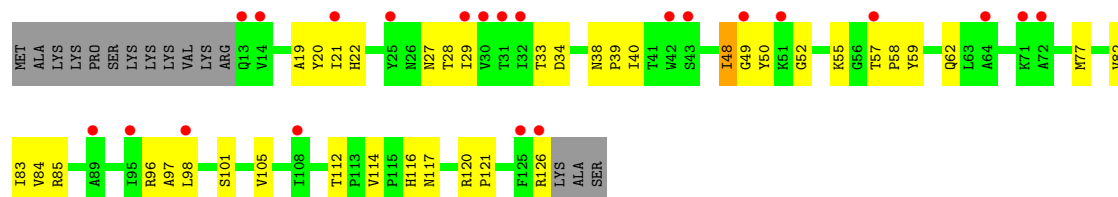
- Molecule 11: 30S ribosomal protein S11

Chain AK: 



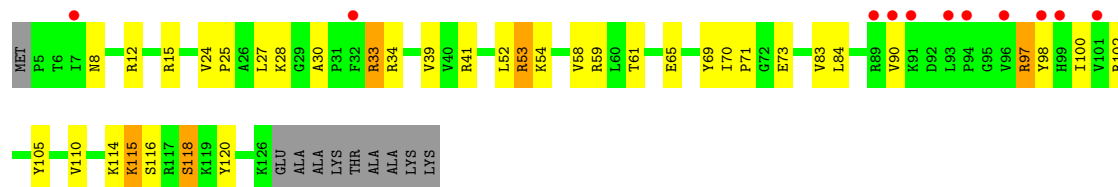
- Molecule 11: 30S ribosomal protein S11

Chain CK: 



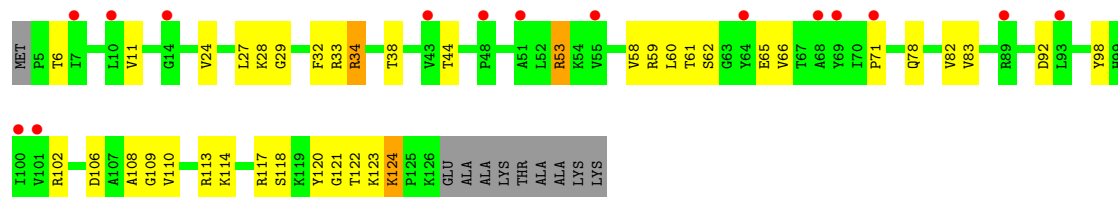
- Molecule 12: 30S ribosomal protein S12

Chain AL: 



- Molecule 12: 30S ribosomal protein S12

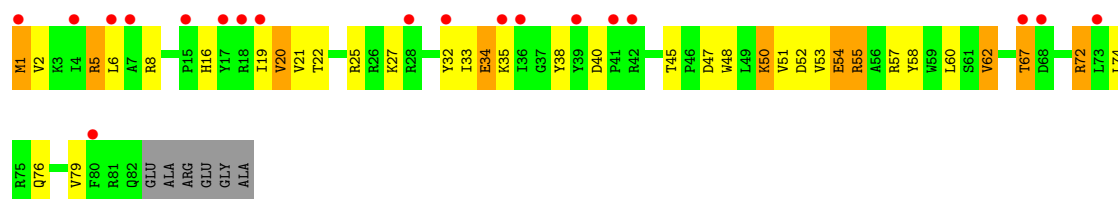
Chain CL: 



- Molecule 13: 30S ribosomal protein S13

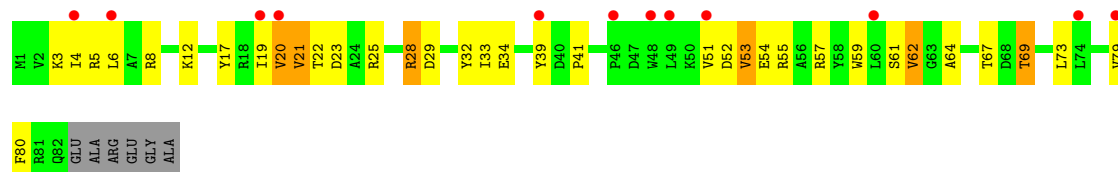
Chain AM: 





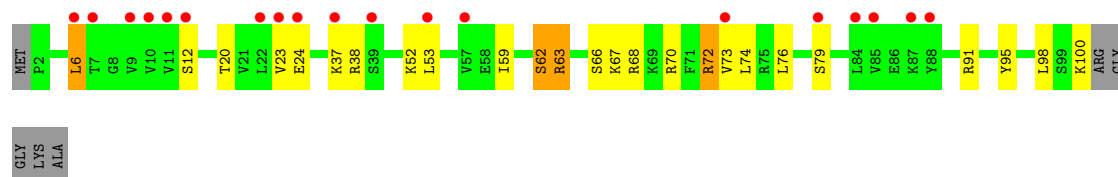
- Molecule 16: 30S ribosomal protein S16

Chain CP:



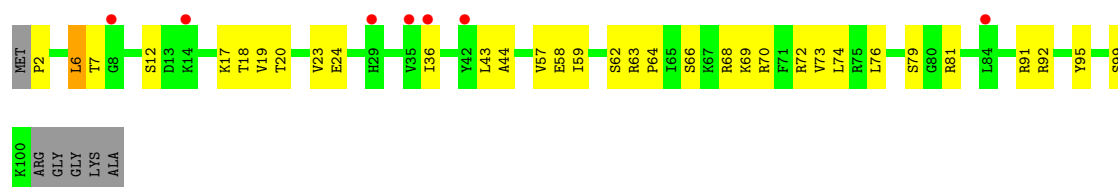
- Molecule 17: 30S ribosomal protein S17

Chain AQ:



- Molecule 17: 30S ribosomal protein S17

Chain CQ:



- Molecule 18: 30S ribosomal protein S18

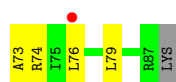
Chain AR:



- Molecule 18: 30S ribosomal protein S18

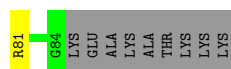
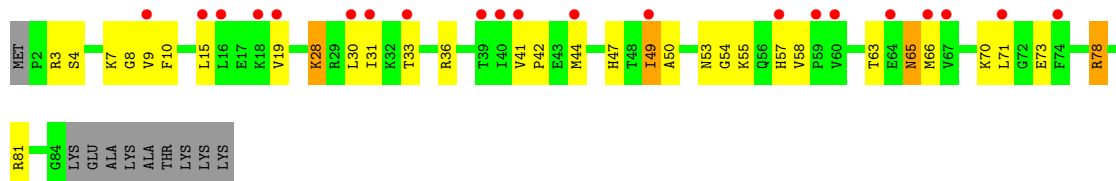
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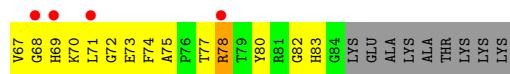
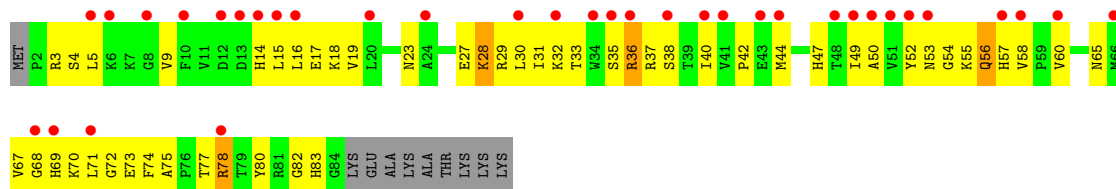
- Molecule 19: 30S ribosomal protein S19

Chain AS:



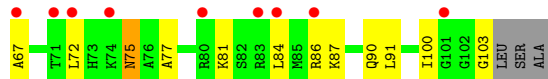
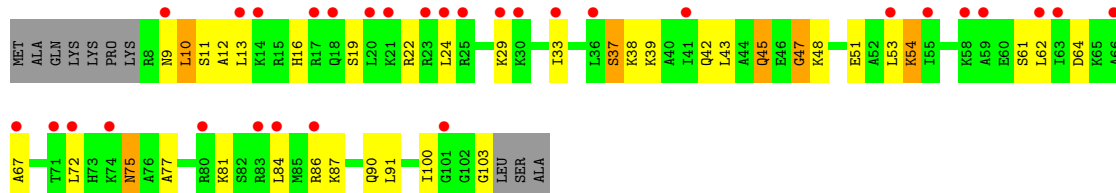
- Molecule 19: 30S ribosomal protein S19

Chain CS:



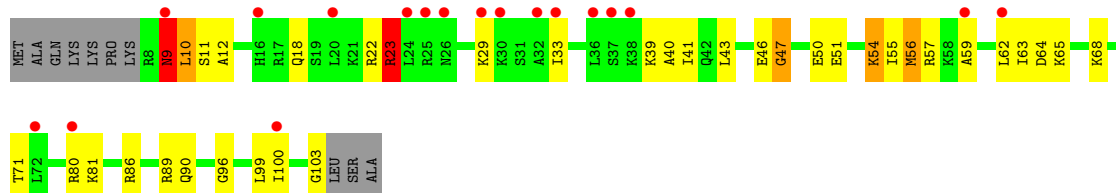
- Molecule 20: 30S ribosomal protein S20

Chain AT:



- Molecule 20: 30S ribosomal protein S20

Chain CT:



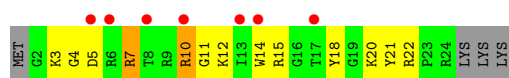
- Molecule 21: 30S ribosomal protein Thx

Chain AU:



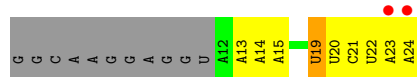
- Molecule 21: 30S ribosomal protein Thx

Chain CU:



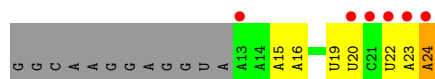
- Molecule 22: mRNA

Chain AV:



- Molecule 22: mRNA

Chain CV:



- Molecule 23: Cytidine-Puromycin

Chain AW:



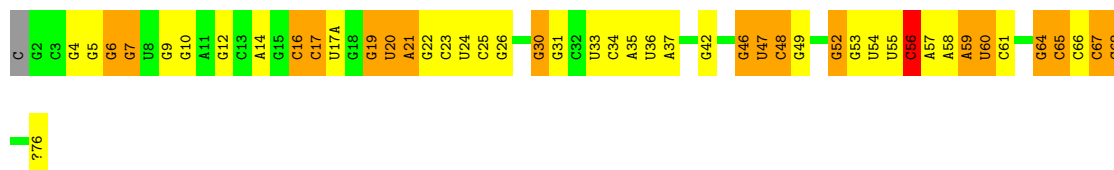
- Molecule 23: Cytidine-Puromycin

Chain CW:



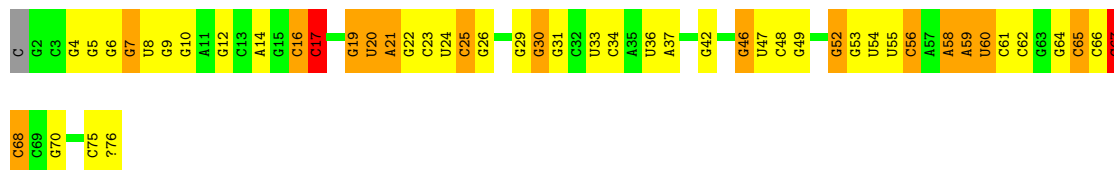
- Molecule 24: P-site tRNA

Chain AX:



- Molecule 24: P-site tRNA

Chain CX:



- Molecule 25: 23S Ribosomal RNA

Chain BA:

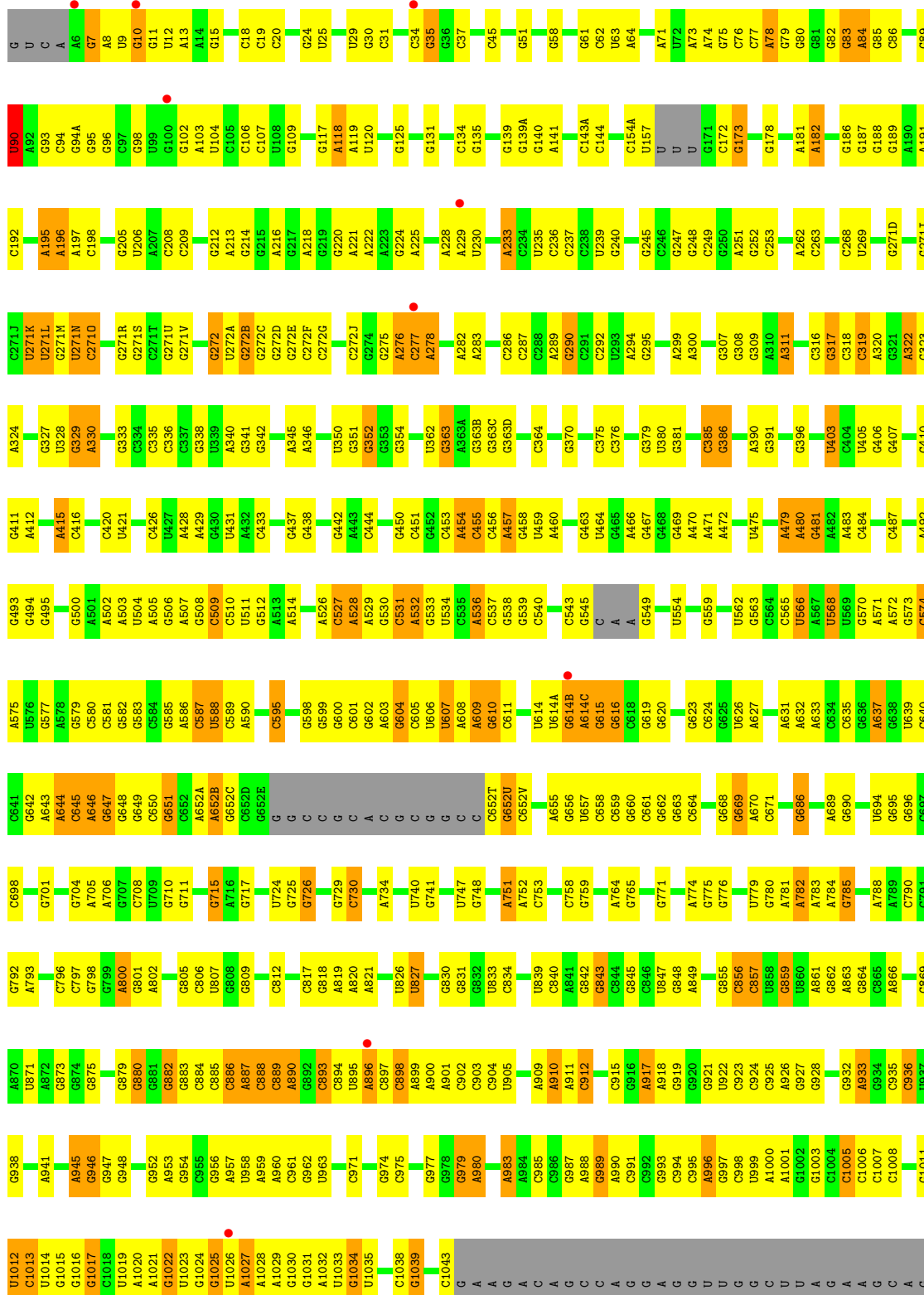
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		A1332	G1082		A990	A990	G892	A799	G			G390	C292	G204	
		U1333	G1083		A991	A991	C893		C			A393	C293	U102	
		U1334	C1084		G992	G992	U894	A811	C				C294	A205	
			G1085		G993	G993	U896		G						
		U1338	C1086				A896								

WORLDWIDE
PDB
PROTEIN DATA BANK

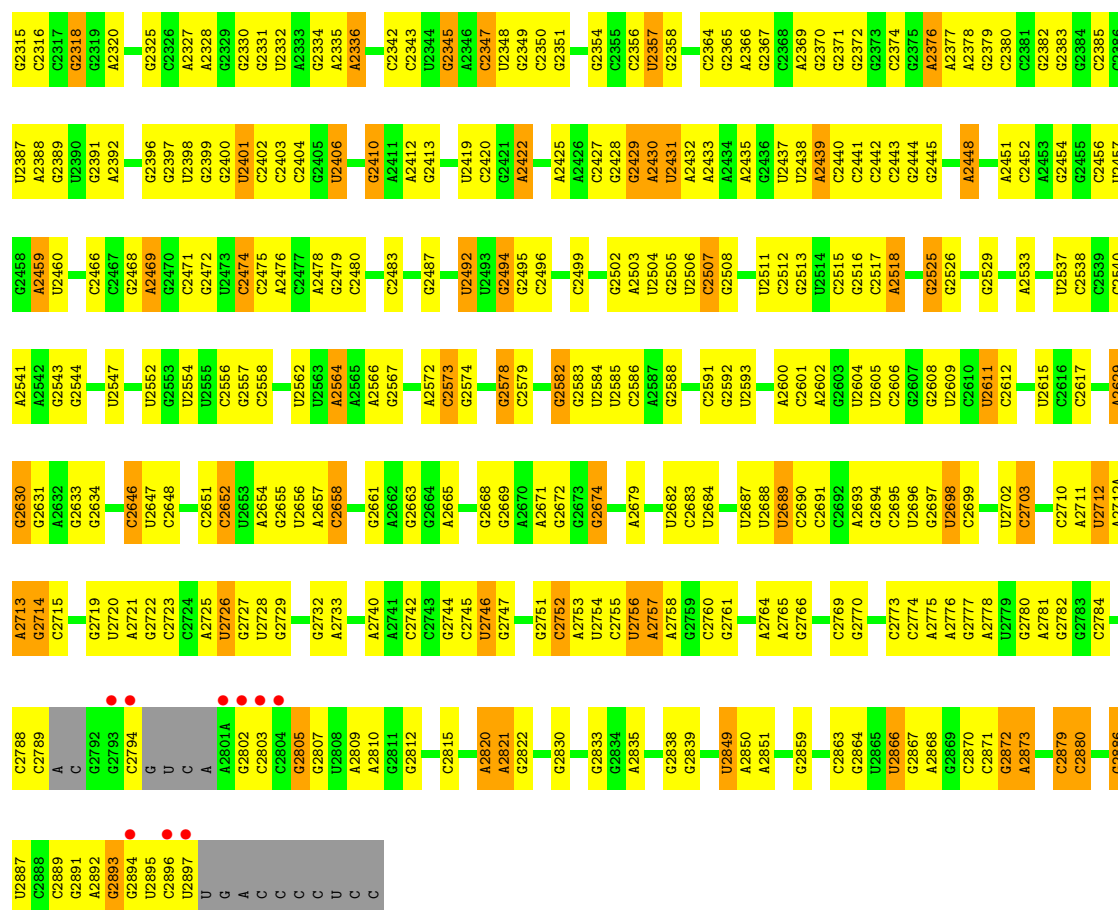
U U D U U

- Molecule 25: 23S Ribosomal RNA

Chain DA:

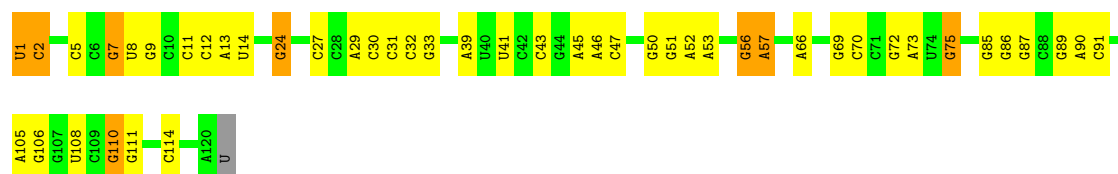


G2235	G2156	G2093	U2017	C1908	G1799	G1695	G1622	C1548	C1474	C1293	A1220	C1140	C
G2238	A2157	U2096	G2018	A1913	C1800	A1698	G1623	C1549	G1475	C1298	C1221	U1141	C
G2239	A2159	U2096	A2019	C1914	A1801	G1699	G1624	C1550	G1479	A1395	C1221A	U1142	A
G2240	G2160	U2099	C2021	U1915	A1802	G1699	G1625	C1551	G1480	U1405	C1224	A1143	U
G2242	C2161	U2022	A1916	C1806	A1803	A1700	G1626	A1554	U1481	U1405	G1225	G1144	C
U2243	G2162	G2023	U1917	C1806	C1918	G1703	G1630	C1557	G1482	U1406	G1227	G1145	U
U2249	C2163	C2103	G2027	A1919	G1811	C1710	G1631	C1558	A1486	C1408	A1226	C1146	U
G2252	G2165	C2105	U2028	A1919	A1812	C1711	G1633	G1559	A1486	C1409	G1228	G1149	A
G2253	G2166	G2106	G2029	G1813	G1814	G1721	G1633	G1560	A1487	G1410	C1230	C1150	A
G2254	U2167	C2107	A2030	C1925	G1814	G1721	A1834	G1561	A1490	C1411	G1231	G1151	A
C2261	A2169	U2109	G2032	U1926	A1915	A1722	G1835	G1562	G1491	A1412	G1232	C1152	G
U2262	A2170	G2110	A2033	A1927	G1816	U1739	G1636	G1492	C1314	G1413	C1233	G1153	A
A2171	C2171	C2110	U2034	G1928	A1637	G1740	A1637	C1565	C1493	G1413	U1234	G1154	G
U2172	G2172	C2112	G2035	G1929	U1818	A1741	C1638	A1494	G1416	U1316	G1235	A1155	U
A2173	C2173	U2113	G2036	G1930	A1819	G1742	U1639	A1567	A1495	C1417	G1239	G1160	C
C2174	C2174	A2114	A2037	A1936	G1823	C1743	C1640	G1568	A1496	C1318	U1240	C1161	C
C2175	C2175	G2115	G2038	A1937	G1824	C1744	A1641	U1497	U1420	G1319	U1241	G1162	G
A2176	G2176	G2116	C2039	A1938	G1826	C1745	G1642	A1569	G1421	C1320	A1241	G1163	U
C2177	C2040	A2117	G2040	U1939	C1827	G1746	G1643	C1498	G1422	A1321	G1242	G1164	A
C2178	U2041	U2118	U2041	G1828	G1828	G1763	G1645	U1503	G1423	A1322	G1243	G1164	A
C2179	A2042	A2119	A2042	U1985	G1828	G1763	G1646	C1577	C1505	U1504	G1244	U1165	U
U2180	C2043	G2120	C2043	U1985	U1833	A1763	G1647	C1578	C1506	A1504	G1245	C1166	A
G2181	G2121	U2122	G2049	G1959	U1834	G1756	C1648	A1579	C1506	U1427	A1246	U1167	G
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C2183	G2123	C2051	A2051	G1963	C1836	G1758	G1651	A1581	A1508	G1429	G1248	G1169	U
G2184	G2124	C2051	A2051	G1964	C1837	A1759	A1652	C1582	C1509	C1430	U1249	G1170	C
C2185	G2125	C2051	C2055	C1965	C1838	A1762	G1653	A1583	A1509A	U1431	G1250	G1171	A
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C2190	U2130	A2059	A2059	A1971	A1848	G1774	C1658	C1589	C1443	A	U1255	A	C
G2191	G2131	A2060	A2060	A1972	A1848	C1774	U1659	U1590	G1444	C1178	G1256	C1179	C
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C2194	C2063	C2063	C2063	C1979	G1866	U1777	G1661	G1593	C1446	U1113	U1263	G1185	G1113
C2195	G2064	C2064	C2064	G1980	G1866	U1778	A1664	G1594	G1447	G1185	U1264	G1186	G1115
A2196	C2136	U2191	A1981	A1877	A1876	U1779	A1665	G1595	G1448	G1186	G1264	G1187	C1116
C2197	C2137	G2078	G2078	C1982	G1878	A1780	A1665	A1596	G1449	U1188	G1266	G1188	G1117
A2198	C2138	U2068	U2068	C1983	G1879	A1780	C1670	C1597	G1529	G1364	A1269	G1192	G1120
C2199	C2139	G2069	G2069	G1984	C1880	C1781	C1670	C1598	C1530	G1366	G1270	G1193	G1121
C2200	C2140	G1985	G1985	C1881	A1783	G1782	G1674	C1600	C1532	A1366	A1271	G1194	C1121
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C2205	C2142	C2072	G2072	G1982	A1889	A1786	A1677	U	A	G1368	A1273	G1195	G1123
C2206	C2143	C2073	C2073	G1982	A1890	A1787	G1677	C1536	C1462	C1370	A1274	A1204	C1124
G2207	U2144	U2074	U2074	U1993	A1890	A1787	G1682	C1537	C1463	G1371	G1275	A1205	A1126
C2208	C2145	U2075	U2075	G1984	C1894	A1788	G1685	A1610	G1464	C1372	A1276	G1206	A1127
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G2214	G2147	U2079	U2079	G1989	C1895	A1791	C1687	G1612	U1540	A1373	A1278	C1207	A1129
A2215	G2148	G2080	G2080	A2001	G1899	G1792	G1687	G1613	G1541	C1457	A1278	A1210	U1130
C2216	G2149	C2081	C2081	G2002	A1900	C1793	U1688	A1542	G1379	A1379	U1288	U1211	U1130
G2224	U2150	G2086	G2086	A2013	C1901	U1794	C1689	A1543	A1469	G1380	U1288	G1216	G1136
A2225	G2151	G2087	G2087	G2012	C1902	C1795	A1614	A1544	A1471	A1384	C1289	G1216	G1136
C2226	G2152	G2087	G2087	A2014	G1906	U1796	U1692	A1545	A1471	A1384	C1290	G1216	G1136
G2230	G2153	G2087	G2087	A2014	G1906	U1796	U1692	C1617	A1472	A1384	C1290	G1216	G1136
C2231	G2154	G2087	G2087	A2014	G1906	U1796	U1692	C1617	A1472	A1384	C1290	G1216	G1136
C2232	G2155	G2087	G2087	A2014	G1906	U1796	U1692	C1617	A1472	A1384	C1290	G1216	G1136
C2233	G2156	G2087	G2087	A2014	G1906	U1796	U1692	C1617	A1472	A1384	C1290	G1216	G1136
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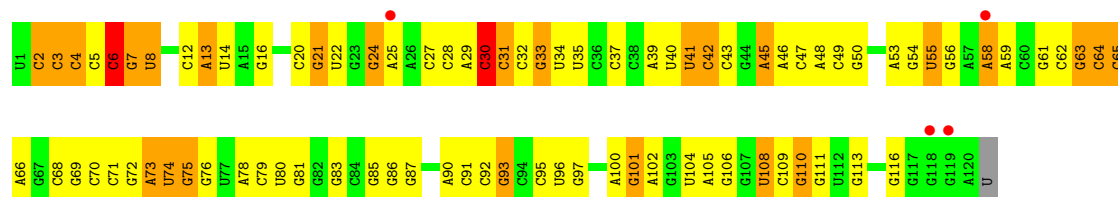
- Molecule 26: 5S Ribosomal RNA

Chain BB:



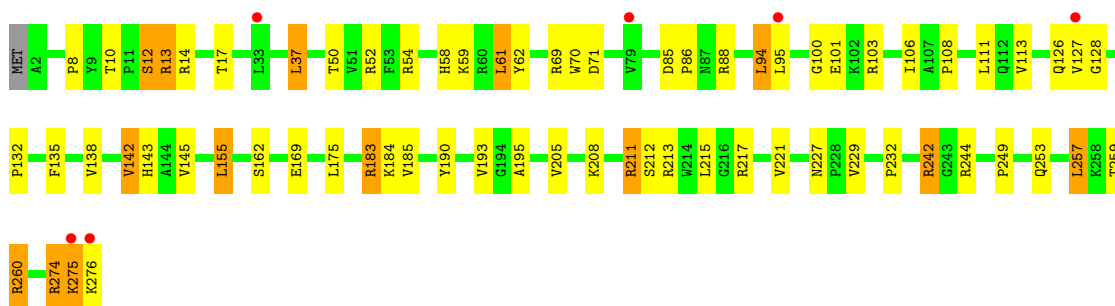
- Molecule 26: 5S Ribosomal RNA

Chain DB:



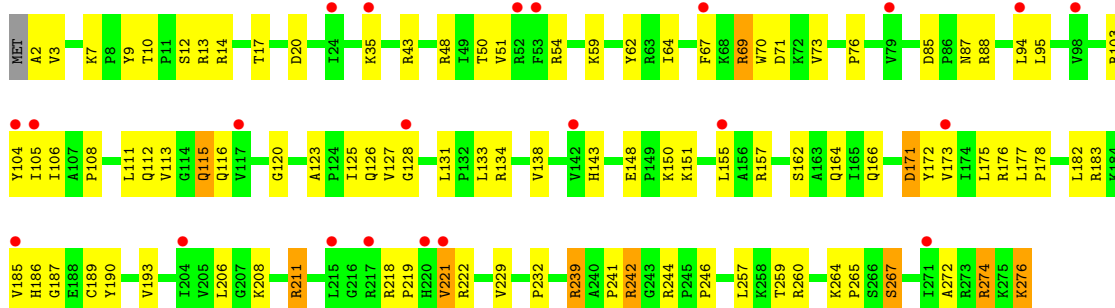
- Molecule 27: 50S ribosomal protein L2

Chain BD:



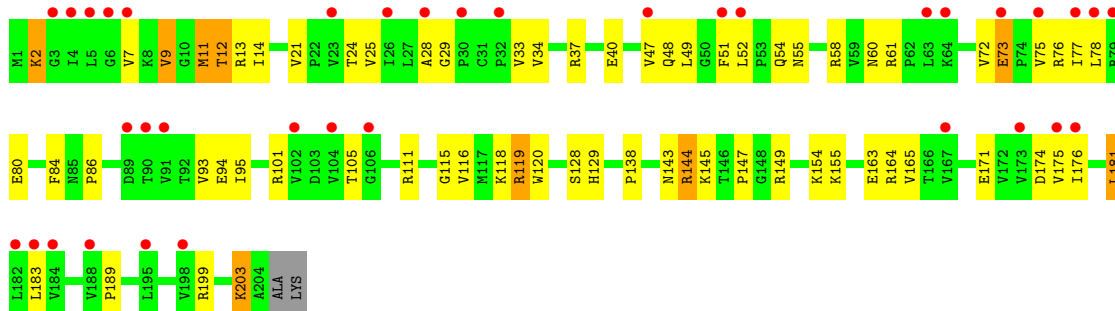
- Molecule 27: 50S ribosomal protein L2

Chain DD:



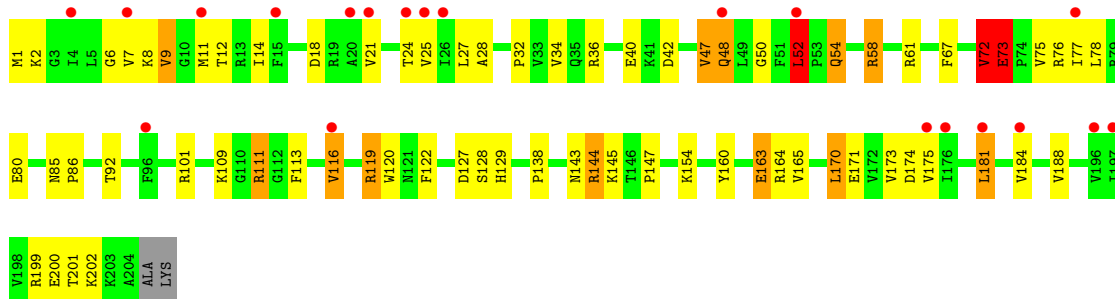
- Molecule 28: 50S ribosomal protein L3

Chain BE:



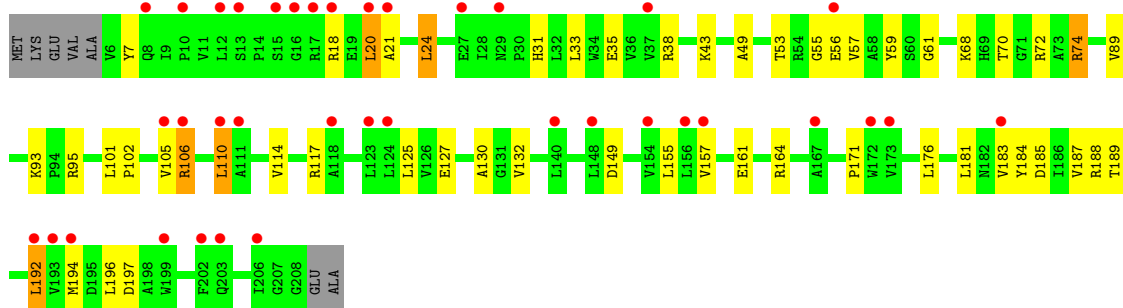
- Molecule 28: 50S ribosomal protein L3

Chain DE:



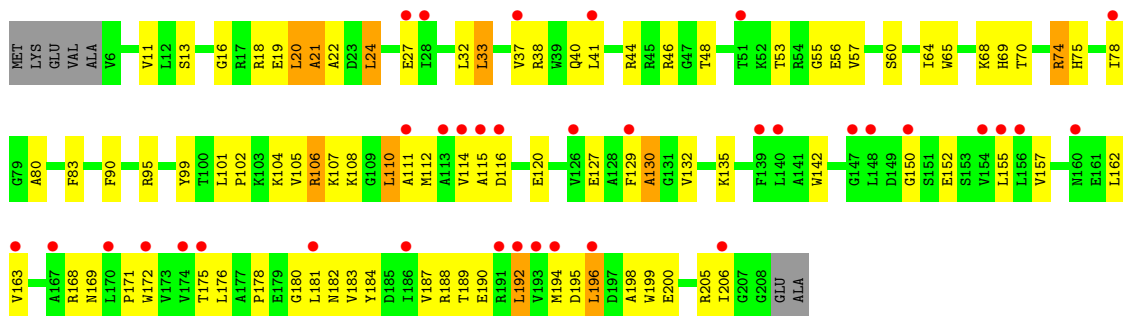
- Molecule 29: 50S ribosomal protein L4

Chain BF:



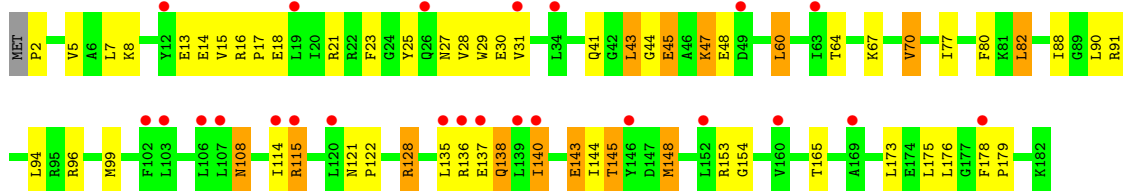
- Molecule 29: 50S ribosomal protein L4

Chain DF:



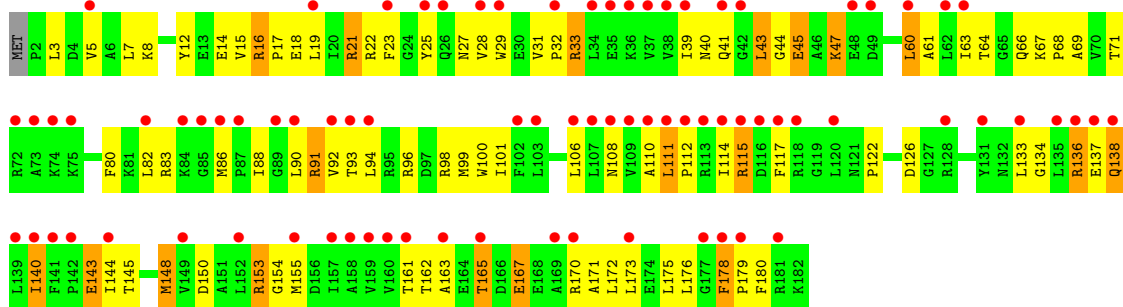
- Molecule 30: 50S ribosomal protein L5

Chain BG:



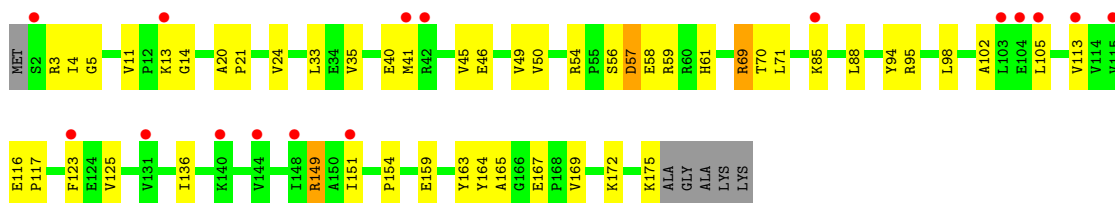
- Molecule 30: 50S ribosomal protein L5

Chain DG:



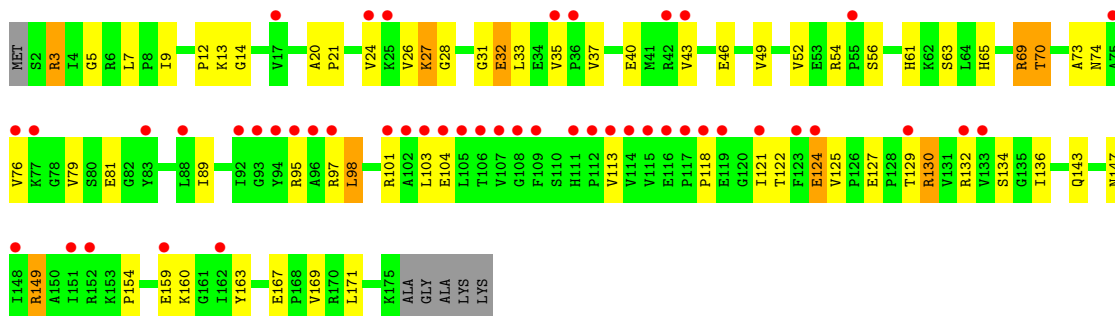
- Molecule 31: 50S ribosomal protein L6

Chain BH:



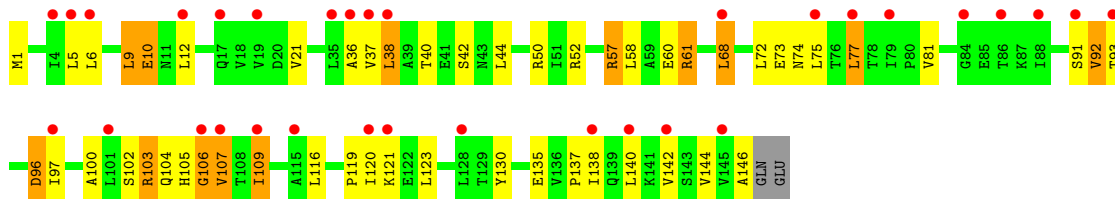
• Molecule 31: 50S ribosomal protein L6

Chain DH:



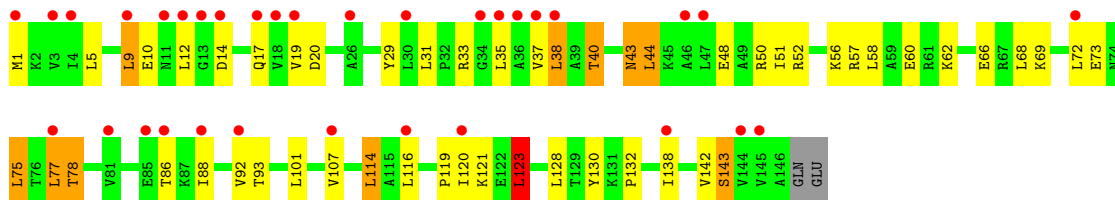
• Molecule 32: 50S ribosomal protein L9

Chain BI:



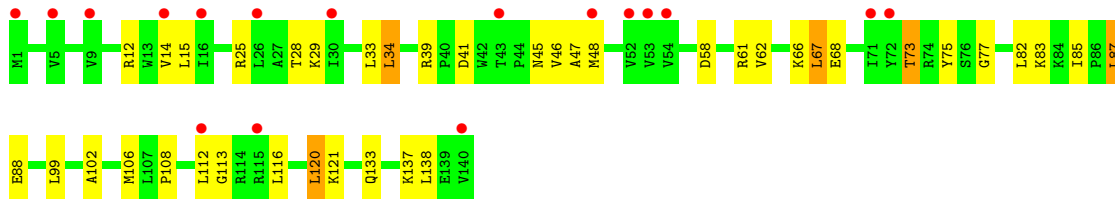
• Molecule 32: 50S ribosomal protein L9

Chain DI:

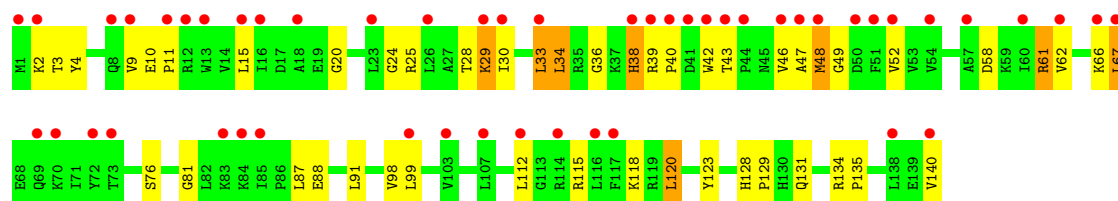


• Molecule 33: 50S ribosomal protein L13

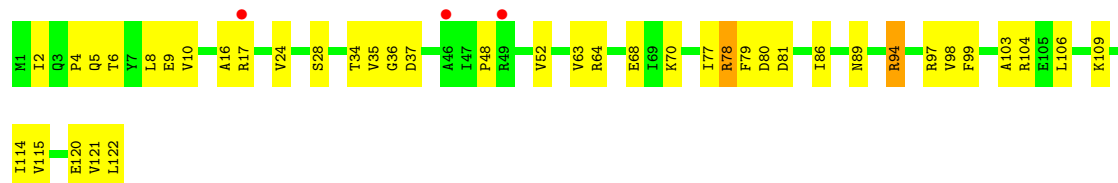
Chain BN:



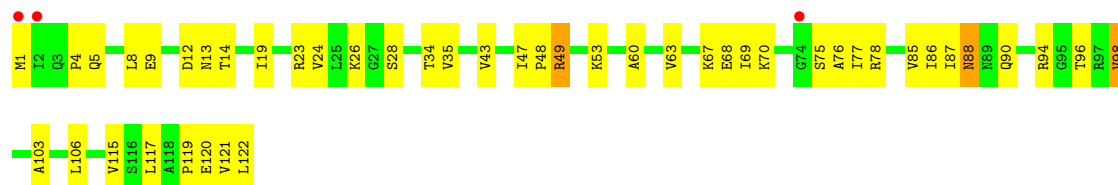
• Molecule 33: 50S ribosomal protein L13

Chain DN: 

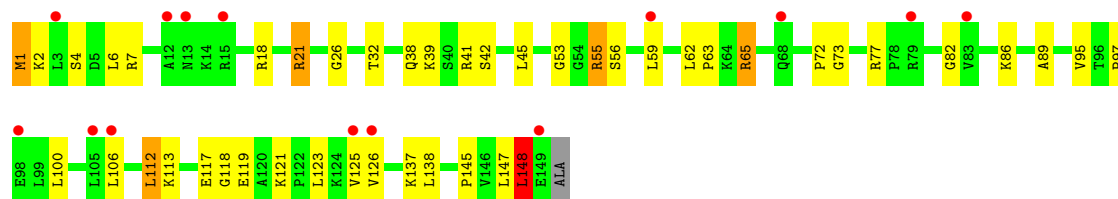
- Molecule 34: 50S ribosomal protein L14

Chain BO: 

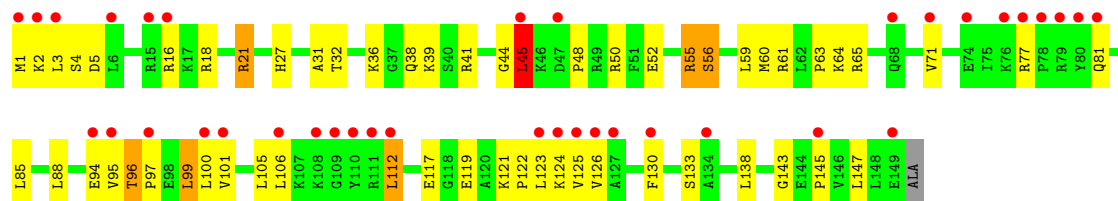
- Molecule 34: 50S ribosomal protein L14

Chain DO: 

- Molecule 35: 50S ribosomal protein L15

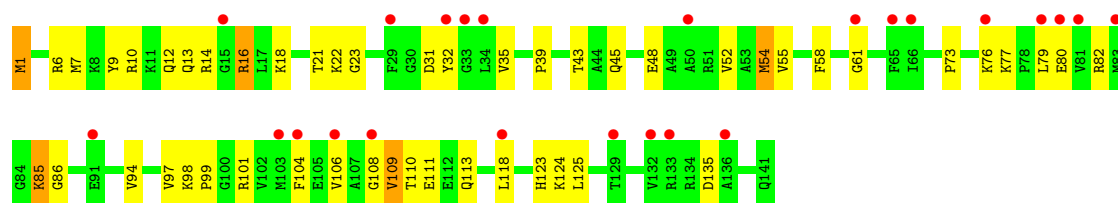
Chain BP: 

- Molecule 35: 50S ribosomal protein L15

Chain DP: 

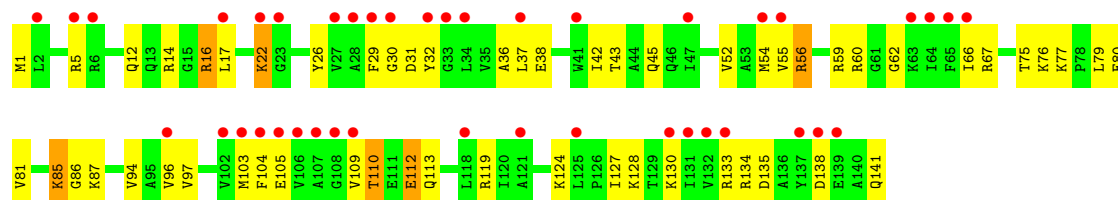
- Molecule 36: 50S ribosomal protein L16

Chain BQ: 



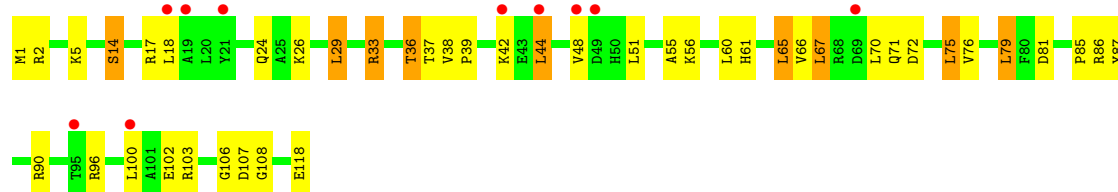
• Molecule 36: 50S ribosomal protein L16

Chain DQ:



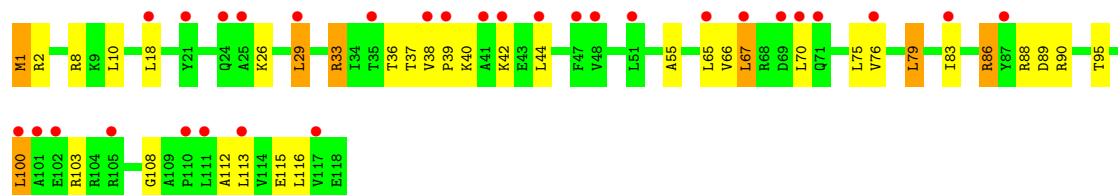
• Molecule 37: 50S ribosomal protein L17

Chain BR:



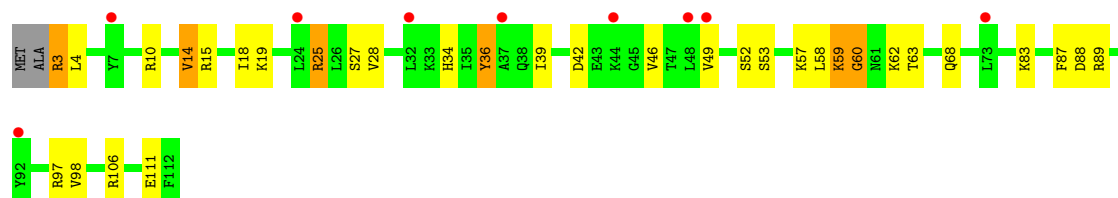
• Molecule 37: 50S ribosomal protein L17

Chain DR:



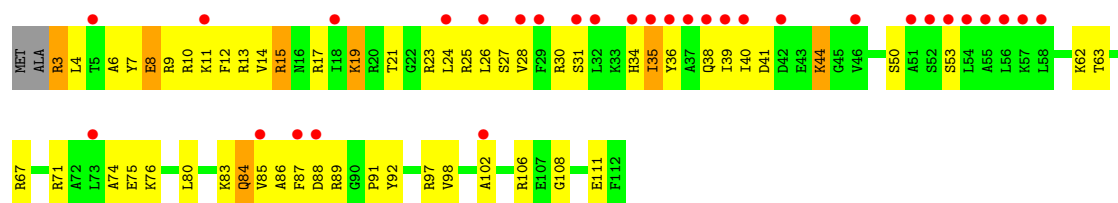
• Molecule 38: 50S ribosomal protein L18

Chain BS:



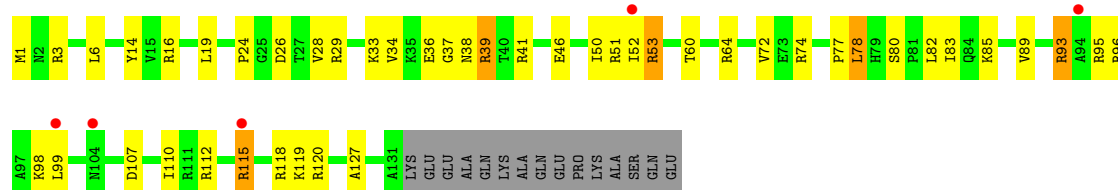
• Molecule 38: 50S ribosomal protein L18

Chain DS:



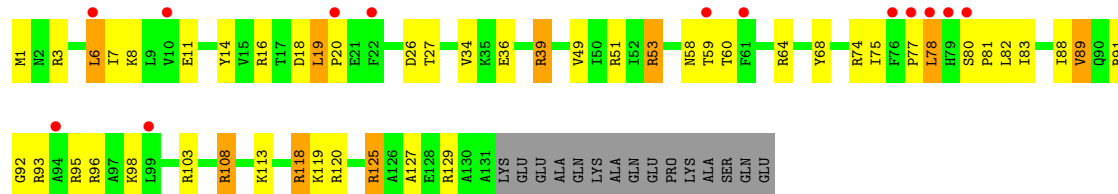
- Molecule 39: 50S ribosomal protein L19

Chain BT:



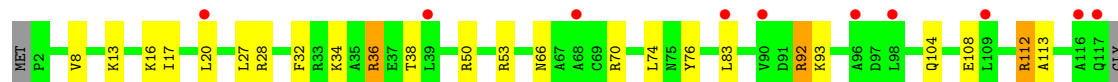
- Molecule 39: 50S ribosomal protein L19

Chain DT:



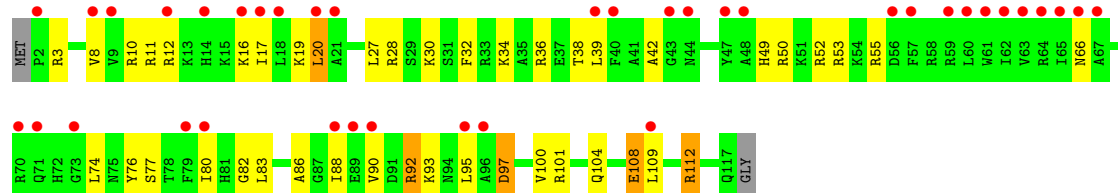
- Molecule 40: 50S ribosomal protein L20

Chain BU:



- Molecule 40: 50S ribosomal protein L20

Chain DU:



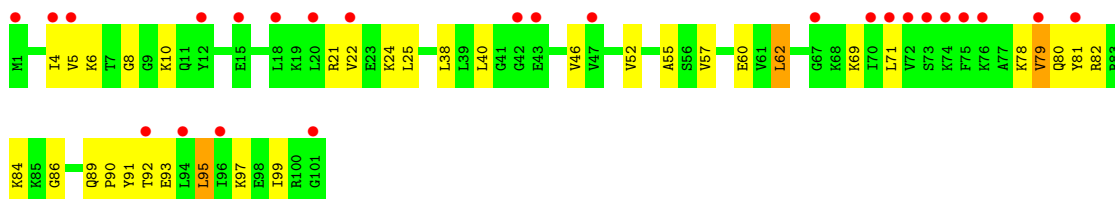
- Molecule 41: 50S ribosomal protein L21

Chain BV:



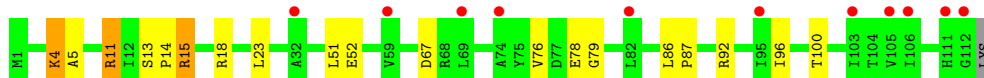
- Molecule 41: 50S ribosomal protein L21

Chain DV: 



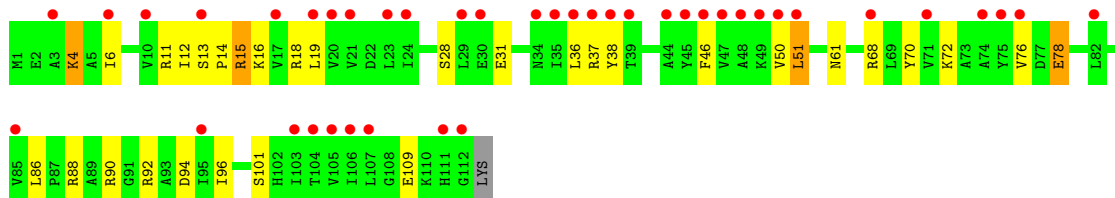
- Molecule 42: 50S ribosomal protein L22

Chain BW: 



- Molecule 42: 50S ribosomal protein L22

Chain DW: 



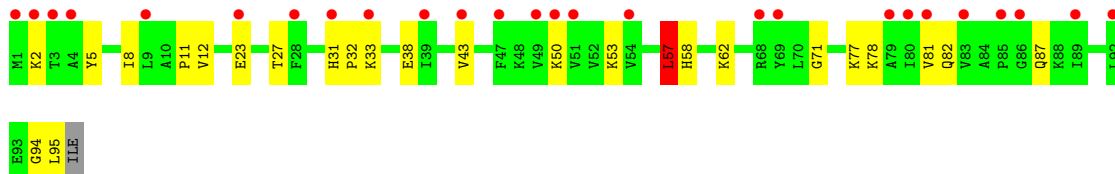
- Molecule 43: 50S ribosomal protein L23

Chain BX: 



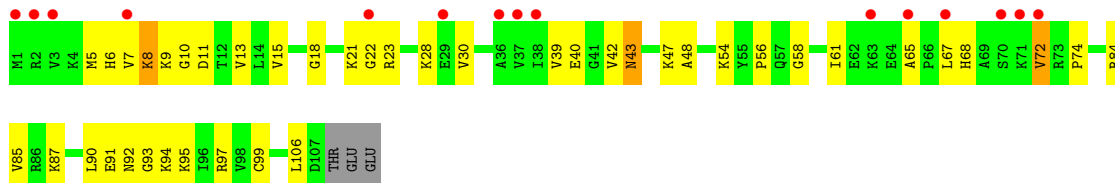
- Molecule 43: 50S ribosomal protein L23

Chain DX: 



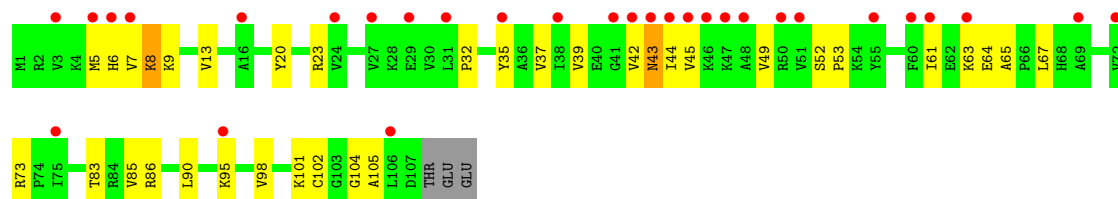
- Molecule 44: 50S ribosomal protein L24

Chain BY: 



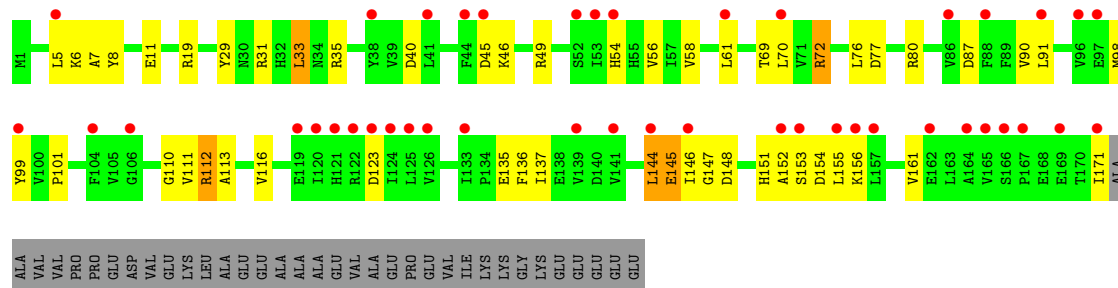
- Molecule 44: 50S ribosomal protein L24

Chain DY: 



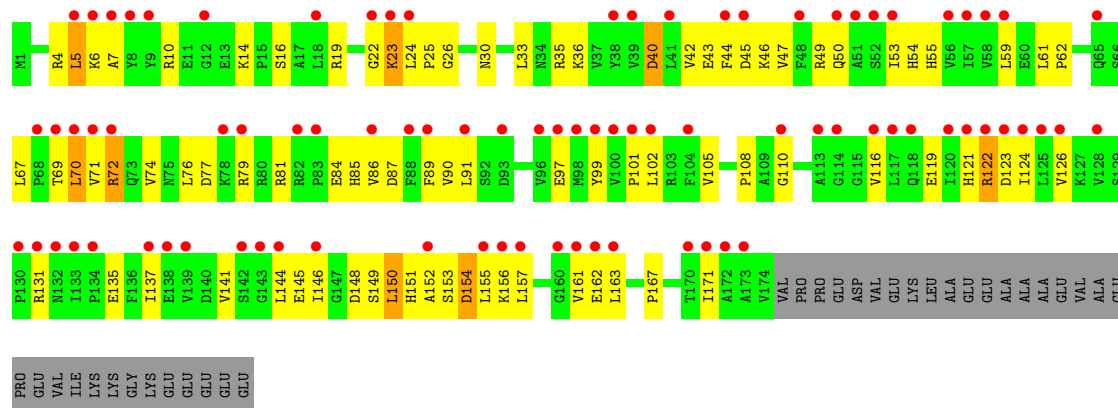
- Molecule 45: 50S ribosomal protein L25

Chain BZ: 



- Molecule 45: 50S ribosomal protein L25

Chain DZ: 



- Molecule 46: 50S ribosomal protein L27

Chain B0: 



- Molecule 46: 50S ribosomal protein L27

Chain D0: 





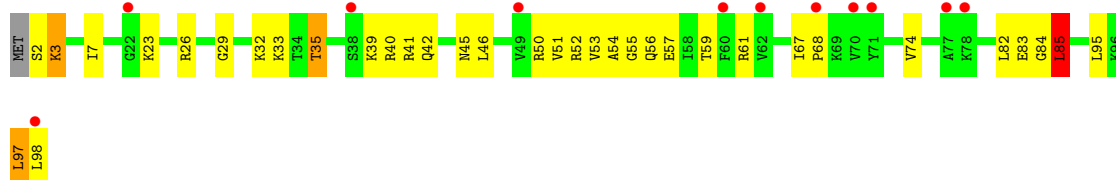
- Molecule 47: 50S ribosomal protein L28

Chain B1:



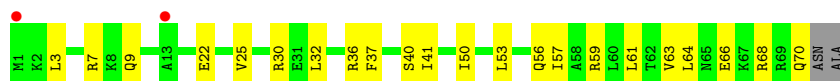
- Molecule 47: 50S ribosomal protein L28

Chain D1:



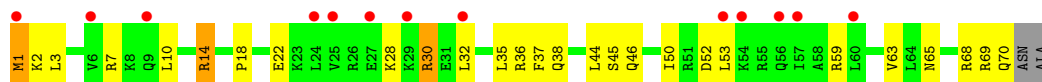
- Molecule 48: 50S ribosomal protein L29

Chain B2:



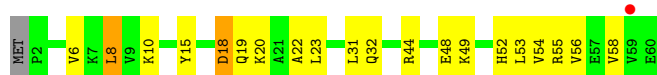
- Molecule 48: 50S ribosomal protein L29

Chain D2:



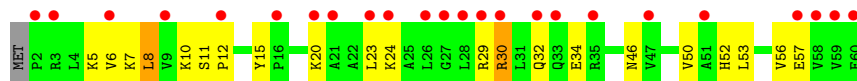
- Molecule 49: 50S ribosomal protein L30

Chain B3:



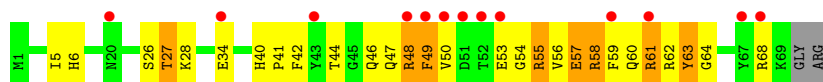
- Molecule 49: 50S ribosomal protein L30

Chain D3:



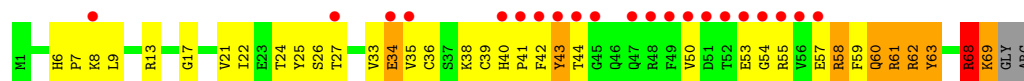
- Molecule 50: 50S ribosomal protein L31

Chain B4:



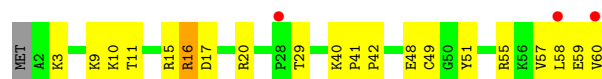
- Molecule 50: 50S ribosomal protein L31

Chain D4: 



- Molecule 51: 50S ribosomal protein L32

Chain B5: 



- Molecule 51: 50S ribosomal protein L32

Chain D5: 



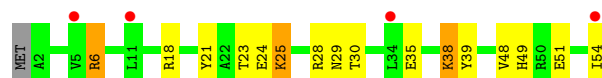
- Molecule 52: 50S ribosomal protein L33

Chain B6: 



- Molecule 52: 50S ribosomal protein L33

Chain D6: 



- Molecule 53: 50S ribosomal protein L34

Chain B7: 



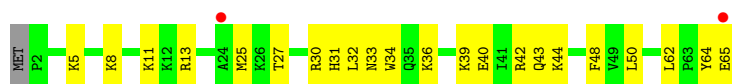
- Molecule 53: 50S ribosomal protein L34

Chain D7: 



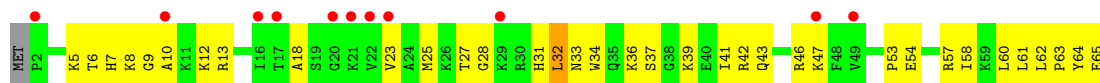
- Molecule 54: 50S ribosomal protein L35

Chain B8: 



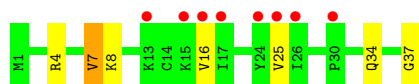
- Molecule 54: 50S ribosomal protein L35

Chain D8:



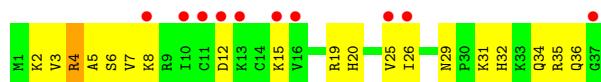
- Molecule 55: 50S ribosomal protein L36

Chain B9:



- Molecule 55: 50S ribosomal protein L36

Chain D9:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.25Å 448.46Å 618.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	362.98 – 2.90 362.98 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.9 (362.98-2.90) 96.9 (362.98-2.90)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.231 , 0.286 0.248 , 0.307	Depositor DCC
R_{free} test set	33963 reflections (2.76%)	DCC
Wilson B-factor (Å ²)	54.8	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 40.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.19$	Xtriage
Outliers	0 of 1229139 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	289646	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, MG, PPU, K, ZN, 31H, 5MC, 4SU, SF4, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AA	0.39	0/36049	0.94	50/56261 (0.1%)
1	CA	0.41	6/36170 (0.0%)	1.02	84/56452 (0.1%)
2	AB	0.31	0/1881	0.63	0/2542
2	CB	0.32	0/1860	0.65	3/2518 (0.1%)
3	AC	0.30	0/1576	0.51	0/2130
3	CC	0.31	0/1566	0.61	2/2119 (0.1%)
4	AD	0.31	0/1689	0.59	1/2267 (0.0%)
4	CD	0.30	0/1700	0.54	0/2280
5	AE	0.29	0/1145	0.56	0/1543
5	CE	0.32	0/1149	0.59	0/1548
6	AF	0.30	0/819	0.51	0/1111
6	CF	0.30	0/829	0.50	0/1123
7	AG	0.28	0/1250	0.51	0/1679
7	CG	0.30	0/1254	0.54	0/1683
8	AH	0.29	0/1108	0.51	0/1494
8	CH	0.28	0/1108	0.55	0/1494
9	AI	0.31	0/1002	0.59	0/1346
9	CI	0.32	0/997	0.56	0/1343
10	AJ	0.28	0/722	0.57	0/982
10	CJ	0.30	0/727	0.56	0/988
11	AK	0.28	0/844	0.51	0/1145
11	CK	0.29	0/848	0.51	0/1149
12	AL	0.31	0/946	0.51	0/1274
12	CL	0.31	0/946	0.57	0/1274
13	AM	0.28	0/969	0.63	0/1302
13	CM	0.32	0/961	0.61	0/1291
14	AN	0.32	0/501	0.54	0/664
14	CN	0.31	0/501	0.60	0/664
15	AO	0.29	0/739	0.50	0/985
15	CO	0.28	0/739	0.52	0/985
16	AP	0.30	0/697	0.54	0/939
16	CP	0.29	0/693	0.52	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.30	0/836	0.54	0/1117
17	CQ	0.29	0/836	0.52	0/1117
18	AR	0.29	0/560	0.54	0/746
18	CR	0.29	0/560	0.57	1/746 (0.1%)
19	AS	0.28	0/667	0.53	0/900
19	CS	0.32	0/661	0.67	0/893
20	AT	0.31	0/730	0.60	0/965
20	CT	0.29	0/729	0.63	1/965 (0.1%)
21	AU	0.28	0/203	0.49	0/266
21	CU	0.33	0/203	0.47	0/266
22	AV	0.42	0/310	0.95	0/480
22	CV	0.45	0/282	0.97	0/437
23	AW	0.35	0/18	0.66	0/26
23	CW	0.27	0/18	0.91	0/26
24	AX	0.52	0/1700	1.21	18/2650 (0.7%)
24	CX	0.55	3/1700 (0.2%)	1.24	16/2650 (0.6%)
25	BA	0.48	1/68013 (0.0%)	0.94	53/106165 (0.0%)
25	DA	0.42	0/67542	0.95	80/105428 (0.1%)
26	BB	0.42	0/2878	0.93	0/4490
26	DB	0.45	0/2878	1.00	3/4490 (0.1%)
27	BD	0.37	0/2186	0.57	0/2944
27	DD	0.33	0/2186	0.56	0/2944
28	BE	0.35	0/1592	0.55	0/2149
28	DE	0.33	0/1592	0.58	1/2149 (0.0%)
29	BF	0.34	0/1619	0.54	0/2193
29	DF	0.32	0/1615	0.57	0/2188
30	BG	0.30	0/1450	0.57	0/1959
30	DG	0.35	0/1449	0.61	0/1958
31	BH	0.32	0/1356	0.53	0/1834
31	DH	0.29	0/1356	0.55	0/1834
32	BI	0.29	0/1100	0.58	0/1501
32	DI	0.30	0/1076	0.60	1/1471 (0.1%)
33	BN	0.32	0/1144	0.52	0/1543
33	DN	0.31	0/1144	0.54	0/1543
34	BO	0.37	0/943	0.59	0/1269
34	DO	0.33	0/943	0.55	0/1269
35	BP	0.34	0/1152	0.58	1/1533 (0.1%)
35	DP	0.32	0/1152	0.60	0/1533
36	BQ	0.35	0/1143	0.53	0/1527
36	DQ	0.33	0/1143	0.55	0/1527
37	BR	0.34	0/982	0.55	0/1312
37	DR	0.30	0/982	0.53	0/1312
38	BS	0.33	0/887	0.56	0/1180

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DS	0.30	0/880	0.59	0/1172
39	BT	0.33	0/1105	0.56	0/1477
39	DT	0.30	0/1097	0.54	0/1468
40	BU	0.36	0/977	0.53	0/1301
40	DU	0.31	0/977	0.55	0/1301
41	BV	0.36	0/782	0.54	0/1049
41	DV	0.32	0/782	0.57	0/1049
42	BW	0.35	0/897	0.54	0/1205
42	DW	0.31	0/897	0.52	0/1205
43	BX	0.38	0/764	0.58	1/1025 (0.1%)
43	DX	0.32	0/764	0.56	1/1025 (0.1%)
44	BY	0.35	0/819	0.56	0/1095
44	DY	0.31	0/819	0.56	0/1095
45	BZ	0.33	0/1379	0.61	0/1873
45	DZ	0.30	0/1390	0.55	0/1890
46	B0	0.35	0/662	0.59	0/881
46	D0	0.31	0/662	0.50	0/881
47	B1	0.34	0/762	0.56	0/1014
47	D1	0.33	0/762	0.57	1/1014 (0.1%)
48	B2	0.32	0/590	0.57	0/781
48	D2	0.30	0/590	0.49	0/781
49	B3	0.35	0/474	0.55	0/635
49	D3	0.30	0/469	0.53	0/630
50	B4	0.36	0/565	0.71	0/761
50	D4	0.35	0/545	0.69	0/737
51	B5	0.33	0/469	0.55	0/635
51	D5	0.32	0/469	0.54	0/635
52	B6	0.39	0/460	0.53	0/613
52	D6	0.33	0/456	0.53	0/608
53	B7	0.37	0/426	0.56	0/561
53	D7	0.34	0/426	0.48	0/561
54	B8	0.37	0/519	0.55	0/684
54	D8	0.31	0/525	0.52	0/691
55	B9	0.35	0/310	0.50	0/407
55	D9	0.34	0/310	0.54	0/407
All	All	0.40	10/310281 (0.0%)	0.87	318/464152 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	2
7	AG	0	1
20	CT	0	1
27	BD	0	1
38	BS	0	1
All	All	0	6

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	1154	G	C6-N1	-12.01	1.31	1.39
1	CA	1154	G	N1-C2	-11.43	1.28	1.37
1	CA	1119	C	N3-C4	-10.12	1.26	1.33
1	CA	1154	G	N7-C5	-6.67	1.35	1.39
24	CX	14	A	N7-C5	-5.86	1.35	1.39
1	CA	1154	G	C5-C4	5.65	1.42	1.38
24	CX	14	A	N9-C4	5.31	1.41	1.37
1	CA	1119	C	C2-N3	-5.26	1.31	1.35
25	BA	1188	A	N9-C4	-5.24	1.34	1.37
24	CX	22	G	N7-C5	5.00	1.42	1.39

All (318) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1119	C	N1-C2-O2	29.84	136.81	118.90
1	CA	1154	G	C5-C6-O6	27.03	144.82	128.60
1	CA	1154	G	N3-C2-N2	25.60	137.82	119.90
1	CA	1154	G	N1-C2-N2	-23.27	95.25	116.20
1	CA	1119	C	C2-N3-C4	19.75	129.77	119.90
1	CA	1119	C	N3-C2-O2	-17.65	109.54	121.90
1	CA	1154	G	C5-C6-N1	-16.71	103.15	111.50
1	CA	1154	G	C6-N1-C2	15.60	134.46	125.10
1	CA	1119	C	C5-C4-N4	15.33	130.93	120.20
1	CA	1154	G	N1-C6-O6	-13.19	111.98	119.90
1	CA	1119	C	C2-N1-C1'	13.11	133.22	118.80
25	DA	2136	C	N1-C2-O2	12.82	126.59	118.90
1	CA	1119	C	N3-C4-N4	-12.64	109.15	118.00
25	DA	2187	G	C5-C6-O6	-11.87	121.48	128.60
25	DA	2155	G	N3-C2-N2	11.53	127.97	119.90
1	CA	1004	A	O4'-C1'-N9	11.16	117.13	108.20
1	CA	1154	G	C2-N3-C4	-10.97	106.41	111.90
24	CX	14	A	C4-C5-C6	10.85	122.43	117.00
24	CX	46	G	C6-N1-C2	-10.36	118.89	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1119	C	C6-N1-C1'	-10.09	108.70	120.80
1	CA	1154	G	C4-N9-C1'	9.82	139.26	126.50
24	AX	46	G	C6-N1-C2	-9.67	119.30	125.10
25	DA	2187	G	C6-C5-N7	-9.64	124.61	130.40
25	DA	2187	G	N1-C6-O6	9.61	125.67	119.90
1	CA	1150	U	C5-C4-O4	9.20	131.42	125.90
25	DA	2155	G	N3-C4-N9	9.01	131.41	126.00
25	DA	2152	G	C5-C6-O6	-8.96	123.22	128.60
1	CA	1119	C	N1-C2-N3	-8.91	112.96	119.20
1	CA	1119	C	C5-C6-N1	8.71	125.35	121.00
24	AX	14	A	C4-C5-C6	8.68	121.34	117.00
25	DA	2187	G	C4-C5-N7	8.67	114.27	110.80
25	DA	2187	G	N3-C4-N9	8.53	131.12	126.00
24	AX	14	A	C5-N7-C8	8.47	108.13	103.90
1	AA	1030(B)	C	N1-C2-O2	8.21	123.83	118.90
1	CA	1154	G	C8-N9-C1'	-8.15	116.40	127.00
1	CA	1119	C	C6-N1-C2	-8.07	117.07	120.30
25	BA	2162	C	C5-C4-N4	7.99	125.79	120.20
1	AA	1030(B)	C	C2-N1-C1'	7.99	127.59	118.80
1	AA	991	U	P-O3'-C3'	7.77	129.02	119.70
25	DA	2155	G	N1-C2-N2	-7.76	109.22	116.20
25	DA	2102	U	C2-N3-C4	7.66	131.60	127.00
1	CA	1001(A)	G	N3-C4-N9	7.61	130.56	126.00
25	DA	2167	U	C2-N1-C1'	7.60	126.81	117.70
25	DA	1313	U	C2-N1-C1'	7.56	126.77	117.70
1	CA	1123	A	C5-C6-N6	7.49	129.69	123.70
1	AA	1007	C	C2-N3-C4	7.48	123.64	119.90
24	CX	14	A	C5-N7-C8	7.43	107.62	103.90
25	DA	2167	U	N1-C2-O2	7.40	127.98	122.80
24	CX	46	G	C5-C6-N1	7.37	115.18	111.50
25	BA	354	A	C2-N3-C4	-7.36	106.92	110.60
1	CA	1225	A	C5-C6-N6	7.34	129.57	123.70
25	DA	2152	G	N1-C6-O6	7.32	124.29	119.90
25	BA	2804	C	C6-N1-C2	-7.32	117.37	120.30
1	CA	79	G	C5-C6-O6	7.28	132.97	128.60
25	BA	2162	C	N3-C4-N4	-7.27	112.91	118.00
24	AX	22	G	N3-C4-N9	-7.22	121.67	126.00
24	CX	46	G	C5-C6-O6	-7.22	124.27	128.60
25	DA	2155	G	N9-C4-C5	-7.22	102.51	105.40
1	AA	1036	G	C4-N9-C1'	7.21	135.87	126.50
1	CA	1154	G	C4-C5-C6	7.19	123.11	118.80
25	DA	2139	C	C2-N1-C1'	7.10	126.61	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1150	U	C2-N3-C4	7.06	131.24	127.00
25	DA	2136	C	N3-C2-O2	-7.05	116.97	121.90
1	CA	1023	G	N3-C4-N9	6.99	130.19	126.00
25	DA	2139	C	N1-C2-O2	6.96	123.08	118.90
25	DA	2121	G	N1-C6-O6	6.95	124.07	119.90
1	AA	1397	C	C2-N1-C1'	6.92	126.41	118.80
3	CC	43	LEU	CA-CB-CG	6.84	131.04	115.30
25	DA	790	C	O5'-P-OP2	-6.81	99.57	105.70
25	DA	2167	U	N3-C2-O2	-6.79	117.45	122.20
1	AA	346	G	C4-N9-C1'	6.76	135.29	126.50
1	CA	1225	A	N1-C6-N6	-6.75	114.55	118.60
4	AD	188	LEU	CA-CB-CG	6.75	130.82	115.30
24	AX	22	G	C4-C5-C6	-6.74	114.75	118.80
1	AA	405	U	O5'-P-OP2	-6.74	99.64	105.70
1	AA	1502	A	N1-C2-N3	6.73	132.67	129.30
1	CA	79	G	C6-N1-C2	6.73	129.14	125.10
25	DA	2187	G	N9-C4-C5	-6.70	102.72	105.40
25	DA	2121	G	C5-C6-O6	-6.70	124.58	128.60
2	CB	187	LEU	CA-CB-CG	6.69	130.70	115.30
1	CA	1119	C	C4-C5-C6	-6.69	114.06	117.40
24	CX	14	A	N1-C6-N6	6.67	122.60	118.60
25	BA	2172	U	N1-C2-N3	6.67	118.90	114.90
24	AX	22	G	N1-C6-O6	-6.66	115.91	119.90
24	AX	56	C	C2-N3-C4	6.63	123.22	119.90
25	BA	1931	C	C5-C6-N1	6.62	124.31	121.00
1	CA	1123	A	C6-N1-C2	6.62	122.57	118.60
25	DA	2629	A	O4'-C1'-N9	6.62	113.49	108.20
25	DA	2187	G	C4-N9-C1'	6.58	135.05	126.50
24	AX	14	A	C5-C6-N1	-6.55	114.42	117.70
25	DA	2137	C	C6-N1-C1'	6.53	128.64	120.80
25	BA	2147	G	N3-C4-N9	-6.52	122.09	126.00
25	BA	1660	A	O5'-P-OP1	-6.51	99.84	105.70
1	AA	73	G	O4'-C1'-N9	6.46	113.37	108.20
25	BA	1188	A	C2-N3-C4	-6.44	107.38	110.60
47	D1	85	LEU	CA-CB-CG	6.44	130.11	115.30
25	BA	2197	C	N1-C2-O2	6.42	122.75	118.90
24	CX	22	G	C5-N7-C8	-6.41	101.10	104.30
20	CT	23	ARG	NE-CZ-NH1	6.40	123.50	120.30
1	AA	97	G	N3-C4-N9	6.39	129.84	126.00
18	CR	31	LEU	CA-CB-CG	6.39	130.00	115.30
1	CA	997	U	C5-C4-O4	6.37	129.72	125.90
1	CA	1323	G	N3-C4-N9	6.34	129.81	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2383	G	C5-C6-O6	-6.32	124.81	128.60
1	AA	346	G	O4'-C1'-N9	6.32	113.25	108.20
1	AA	1276	G	C5-C6-O6	-6.30	124.82	128.60
24	AX	22	G	C5-N7-C8	-6.28	101.16	104.30
1	CA	754	C	C2-N1-C1'	6.27	125.69	118.80
1	CA	992	U	P-O3'-C3'	6.26	127.22	119.70
1	AA	1030(B)	C	N3-C2-O2	-6.25	117.53	121.90
25	BA	1931	C	C6-N1-C2	-6.24	117.80	120.30
25	DA	2152	G	N3-C4-N9	6.23	129.74	126.00
25	BA	2189	U	C2-N1-C1'	6.21	125.15	117.70
1	AA	1397	C	O4'-C1'-N1	6.20	113.16	108.20
1	CA	1064	G	P-O3'-C3'	6.20	127.14	119.70
43	DX	57	LEU	CA-CB-CG	6.19	129.54	115.30
1	AA	1285	A	P-O3'-C3'	6.18	127.12	119.70
1	CA	955	U	C2-N3-C4	6.17	130.71	127.00
25	BA	12	U	C2-N1-C1'	6.15	125.08	117.70
1	CA	1030(B)	C	C6-N1-C2	-6.13	117.85	120.30
25	DA	1531	C	C2-N1-C1'	6.12	125.53	118.80
25	DA	2159	G	N3-C4-N9	-6.07	122.36	126.00
1	CA	1003	G	C4-N9-C1'	6.05	134.37	126.50
24	AX	14	A	C8-N9-C1'	-6.04	116.83	127.70
1	CA	79	G	N3-C4-N9	-6.04	122.38	126.00
24	CX	14	A	C4-N9-C1'	6.04	137.16	126.30
1	AA	1036	G	C8-N9-C1'	-6.03	119.16	127.00
1	AA	1037	C	N1-C2-O2	6.03	122.52	118.90
25	BA	670	C	C2-N1-C1'	6.03	125.43	118.80
25	DA	2137	C	O4'-C1'-N1	6.03	113.02	108.20
25	BA	2486	C	N1-C2-O2	6.03	122.52	118.90
25	BA	1686	U	O5'-P-OP2	-6.02	100.28	105.70
24	CX	14	A	N3-C4-N9	6.00	132.20	127.40
1	AA	97	G	N3-C4-C5	-5.99	125.61	128.60
25	DA	2152	G	C4-C5-N7	5.99	113.19	110.80
24	AX	14	A	C4-N9-C1'	5.97	137.06	126.30
25	DA	2152	G	C6-C5-N7	-5.97	126.82	130.40
1	AA	347	G	O4'-C1'-N9	5.97	112.97	108.20
1	AA	1037	C	C6-N1-C2	-5.96	117.92	120.30
25	BA	1067	A	C2-N3-C4	-5.95	107.62	110.60
25	DA	2137	C	C2-N1-C1'	-5.93	112.28	118.80
25	BA	1068	G	N3-C4-N9	-5.90	122.46	126.00
1	CA	1126	U	C2-N1-C1'	5.89	124.77	117.70
25	DA	1531	C	C5-C6-N1	5.89	123.95	121.00
1	CA	1039	C	C5-C4-N4	-5.89	116.08	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	2152	G	N9-C4-C5	-5.87	103.05	105.40
24	CX	22	G	C4-C5-C6	-5.87	115.28	118.80
25	DA	2142	C	C5-C6-N1	5.86	123.93	121.00
1	AA	1131	G	C5-C6-O6	-5.85	125.09	128.60
1	CA	1183	A	P-O3'-C3'	5.82	126.68	119.70
1	AA	687	A	P-O3'-C3'	5.81	126.67	119.70
24	AX	46	G	C5-C6-N1	5.80	114.40	111.50
25	DA	2161	C	C5-C4-N4	5.80	124.26	120.20
26	DB	30	C	N3-C2-O2	-5.80	117.84	121.90
25	BA	537	G	O4'-C1'-N9	5.79	112.84	108.20
25	DA	2187	G	C8-N9-C1'	-5.78	119.49	127.00
24	CX	14	A	C8-N9-C1'	-5.78	117.30	127.70
25	BA	934	A	O4'-C1'-N9	5.77	112.82	108.20
25	BA	1221	G	OP1-P-O3'	5.76	117.88	105.20
1	AA	1037	C	C2-N1-C1'	5.74	125.11	118.80
1	CA	1067	A	P-O3'-C3'	5.74	126.58	119.70
25	DA	2139	C	C6-N1-C1'	-5.74	113.92	120.80
1	CA	1158	C	N1-C2-O2	5.73	122.34	118.90
1	CA	1256	A	O4'-C1'-N9	-5.73	103.62	108.20
25	BA	2173	G	C5-C6-N1	-5.72	108.64	111.50
24	CX	22	G	N1-C6-O6	-5.72	116.47	119.90
25	DA	2698	U	C5-C6-N1	-5.71	119.85	122.70
1	CA	1158	C	C2-N1-C1'	5.71	125.08	118.80
1	AA	1030(B)	C	C6-N1-C1'	-5.70	113.96	120.80
3	CC	101	LEU	CA-CB-CG	5.70	128.40	115.30
25	DA	2206	G	C4-N9-C1'	-5.68	119.12	126.50
24	AX	22	G	C6-C5-N7	5.67	133.81	130.40
25	DA	2866	U	C2-N1-C1'	5.67	124.50	117.70
25	BA	1824	C	C6-N1-C2	-5.66	118.04	120.30
24	CX	14	A	C6-C5-N7	-5.66	128.34	132.30
25	BA	2014	G	P-O3'-C3'	5.66	126.49	119.70
24	AX	22	G	C8-N9-C1'	5.65	134.35	127.00
1	AA	346	G	C8-N9-C1'	-5.64	119.67	127.00
1	CA	1123	A	N1-C6-N6	-5.64	115.22	118.60
1	CA	1397	C	N1-C2-O2	5.64	122.28	118.90
1	CA	1064	G	OP2-P-O3'	5.64	117.60	105.20
1	AA	991	U	OP2-P-O3'	5.63	117.59	105.20
25	BA	2147	G	C8-N9-C1'	5.62	134.31	127.00
25	DA	2187	G	N7-C8-N9	5.62	115.91	113.10
1	CA	927	G	C5-C6-O6	5.61	131.97	128.60
25	DA	1992	G	C8-N9-C4	-5.60	104.16	106.40
25	DA	1505	C	N1-C2-O2	5.59	122.25	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	2155	G	C8-N9-C1'	-5.58	119.74	127.00
1	AA	1131	G	N1-C6-O6	5.57	123.24	119.90
32	DI	123	LEU	CA-CB-CG	5.57	128.12	115.30
24	CX	14	A	N3-C4-C5	-5.57	122.91	126.80
43	BX	57	LEU	CA-CB-CG	5.56	128.09	115.30
25	DA	2155	G	C4-N9-C1'	5.56	133.73	126.50
1	CA	1154	G	N3-C4-C5	-5.55	125.82	128.60
1	CA	96	U	C2-N1-C1'	-5.55	111.05	117.70
1	CA	1154	G	N3-C4-N9	5.55	129.33	126.00
1	CA	60	A	P-O3'-C3'	5.54	126.34	119.70
1	CA	1001(A)	G	C4-N9-C1'	5.53	133.69	126.50
25	BA	2147	G	C4-N9-C1'	-5.52	119.32	126.50
24	CX	17	C	C6-N1-C2	-5.52	118.09	120.30
25	DA	2805	G	O4'-C1'-N9	5.52	112.61	108.20
1	CA	1001(A)	G	N3-C4-C5	-5.51	125.84	128.60
25	BA	2199	C	N1-C2-O2	5.51	122.20	118.90
24	CX	67	C	N1-C2-O2	5.50	122.20	118.90
25	DA	2159	G	N3-C2-N2	-5.50	116.05	119.90
1	CA	1125	U	O4'-C1'-N1	5.49	112.59	108.20
1	CA	1003	G	N3-C4-C5	-5.49	125.86	128.60
25	DA	2137	C	N1-C2-O2	-5.48	115.61	118.90
1	AA	1022	G	N3-C2-N2	5.47	123.73	119.90
25	DA	2150	U	N1-C2-O2	5.46	126.62	122.80
25	BA	2486	C	C2-N1-C1'	5.46	124.80	118.80
1	CA	754	C	N1-C2-O2	5.46	122.17	118.90
25	DA	2159	G	C8-N9-C1'	5.46	134.09	127.00
1	AA	1397	C	C6-N1-C1'	-5.44	114.27	120.80
25	DA	90	U	N3-C2-O2	-5.44	118.39	122.20
1	AA	1278	U	C5-C6-N1	5.44	125.42	122.70
1	CA	1493	A	P-O3'-C3'	5.43	126.22	119.70
25	DA	2155	G	C4-C5-N7	5.43	112.97	110.80
25	BA	2220	A	OP1-P-O3'	5.42	117.14	105.20
28	DE	72	VAL	C-N-CA	5.42	135.25	121.70
1	CA	1003	G	N7-C8-N9	5.41	115.81	113.10
25	DA	748	G	O4'-C1'-N9	5.41	112.53	108.20
25	DA	1644	C	C2-N1-C1'	5.41	124.75	118.80
1	CA	998	G	C5-C6-O6	5.40	131.84	128.60
1	CA	1154	G	C8-N9-C4	-5.40	104.24	106.40
1	AA	1276	G	N3-C4-N9	5.39	129.24	126.00
1	CA	78	G	N3-C4-N9	5.39	129.23	126.00
25	BA	2173	G	C6-N1-C2	5.38	128.33	125.10
25	DA	2150	U	C2-N3-C4	5.38	130.23	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2227	G	C4-N9-C1'	-5.38	119.51	126.50
1	CA	1125	U	C2-N1-C1'	5.37	124.14	117.70
1	AA	1131	G	C6-C5-N7	-5.36	127.18	130.40
26	DB	6	C	C2-N1-C1'	5.36	124.70	118.80
1	AA	1054	C	C2-N1-C1'	5.35	124.69	118.80
25	DA	2174	C	C2-N1-C1'	5.35	124.68	118.80
25	BA	2162	C	C6-N1-C1'	5.33	127.20	120.80
25	DA	2155	G	C6-C5-N7	-5.33	127.20	130.40
25	DA	2159	G	C4-N9-C1'	-5.33	119.57	126.50
1	AA	1037	C	N3-C2-O2	-5.33	118.17	121.90
25	BA	254	A	O4'-C1'-N9	5.33	112.46	108.20
25	BA	2161	C	N3-C4-C5	5.32	124.03	121.90
25	BA	2858	G	O4'-C1'-N9	5.32	112.45	108.20
1	CA	1026	G	N3-C4-C5	-5.31	125.94	128.60
1	CA	992	U	OP2-P-O3'	5.31	116.88	105.20
25	DA	528	A	C2-N3-C4	-5.31	107.95	110.60
25	DA	2187	G	C5-N7-C8	-5.31	101.65	104.30
2	CB	122	PHE	N-CA-C	-5.30	96.68	111.00
25	BA	354	A	N1-C2-N3	5.30	131.95	129.30
1	AA	1028	C	C5-C6-N1	5.30	123.65	121.00
25	BA	928	G	C4-N9-C1'	5.30	133.38	126.50
25	DA	1653	G	C4-N9-C1'	5.30	133.39	126.50
25	DA	2218	U	N1-C2-O2	5.30	126.51	122.80
24	AX	46	G	N1-C2-N3	5.29	127.07	123.90
1	CA	90	U	N1-C2-N3	5.27	118.06	114.90
25	BA	670	C	N1-C2-O2	5.27	122.06	118.90
24	AX	22	G	N3-C4-C5	5.27	131.23	128.60
25	DA	1313	U	N3-C2-O2	-5.27	118.51	122.20
1	CA	1001(A)	G	C8-N9-C1'	-5.26	120.16	127.00
26	DB	30	C	C6-N1-C2	-5.25	118.20	120.30
1	AA	1030(B)	C	C6-N1-C2	-5.24	118.20	120.30
25	BA	1985	U	C2-N1-C1'	5.23	123.97	117.70
1	CA	1012	U	O4'-C1'-N1	5.22	112.38	108.20
1	CA	1397	C	C2-N1-C1'	5.21	124.53	118.80
1	CA	1123	A	C5-C6-N1	-5.21	115.09	117.70
25	BA	410	U	C2-N1-C1'	-5.21	111.45	117.70
2	CB	154	LEU	CA-CB-CG	5.18	127.22	115.30
25	BA	303	C	C5-C6-N1	5.18	123.59	121.00
35	BP	148	LEU	CA-CB-CG	5.18	127.20	115.30
25	DA	2712	U	C2-N1-C1'	-5.18	111.49	117.70
1	AA	1276	G	N1-C6-O6	5.17	123.00	119.90
1	CA	1140	C	C6-N1-C1'	5.16	127.00	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1131	G	C4-C5-N7	5.16	112.86	110.80
1	CA	1397	C	N3-C2-O2	-5.14	118.30	121.90
1	AA	1276	G	C6-C5-N7	-5.14	127.32	130.40
25	BA	2143	G	N3-C4-N9	5.13	129.08	126.00
25	BA	1462	G	O4'-C1'-N9	5.13	112.30	108.20
1	AA	1259	C	C2-N1-C1'	5.13	124.44	118.80
1	CA	1355	G	N3-C4-N9	5.12	129.07	126.00
24	AX	56	C	C5-C6-N1	5.12	123.56	121.00
25	BA	2189	U	O4'-C1'-N1	5.12	112.30	108.20
25	DA	635	C	N3-C2-O2	-5.12	118.31	121.90
25	DA	2172	U	P-O3'-C3'	5.12	125.84	119.70
1	AA	1136	U	C5-C6-N1	5.11	125.26	122.70
25	BA	2902	G	P-O3'-C3'	5.11	125.83	119.70
1	AA	1001(A)	G	C4-N9-C1'	5.10	133.13	126.50
1	CA	1154	G	C5-N7-C8	5.10	106.85	104.30
25	DA	1204	A	O4'-C1'-N9	5.10	112.28	108.20
25	BA	1221	G	P-O3'-C3'	5.09	125.81	119.70
25	DA	2133	G	P-O3'-C3'	5.09	125.81	119.70
24	AX	14	A	C4-C5-N7	-5.09	108.16	110.70
25	DA	1614	A	O5'-P-OP1	-5.08	101.13	105.70
1	CA	1019	C	C6-N1-C2	-5.08	118.27	120.30
25	BA	2161	C	N1-C2-O2	5.06	121.94	118.90
25	DA	1313	U	N1-C2-O2	5.06	126.34	122.80
25	BA	1068	G	C6-C5-N7	5.06	133.44	130.40
1	CA	1158	C	C6-N1-C2	-5.06	118.28	120.30
1	AA	1531	A	O4'-C1'-N9	-5.06	104.15	108.20
25	DA	512	G	O4'-C1'-N9	5.06	112.25	108.20
25	DA	2154	G	C8-N9-C4	-5.05	104.38	106.40
1	AA	839	U	P-O3'-C3'	5.05	125.76	119.70
1	AA	1067	A	P-O3'-C3'	5.05	125.76	119.70
25	BA	139	A	N7-C8-N9	5.05	116.33	113.80
25	DA	1653	G	P-O3'-C3'	5.05	125.76	119.70
1	CA	1065	U	P-O3'-C3'	5.04	125.75	119.70
25	BA	1068	G	C4-N9-C1'	-5.04	119.94	126.50
1	AA	1065	U	P-O3'-C3'	5.04	125.75	119.70
25	DA	2150	U	N1-C2-N3	-5.04	111.88	114.90
25	DA	2155	G	N3-C4-C5	-5.04	126.08	128.60
1	CA	1154	G	N1-C2-N3	5.03	126.92	123.90
25	BA	2189	U	N1-C2-O2	5.03	126.32	122.80
1	AA	1040	U	C5-C4-O4	5.02	128.91	125.90
1	CA	1158	C	N3-C2-O2	-5.02	118.39	121.90
25	BA	1359	U	C2-N1-C1'	5.01	123.72	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1006	C	C5-C4-N4	-5.01	116.69	120.20
1	AA	1022	G	C6-N1-C2	5.01	128.11	125.10
1	AA	1054	C	N1-C2-O2	5.01	121.91	118.90
25	DA	2159	G	C6-C5-N7	5.00	133.40	130.40
25	DA	2136	C	C2-N1-C1'	5.00	124.30	118.80

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	231	GLU	Peptide
2	AB	9	GLU	Peptide
7	AG	79	ARG	Peptide
27	BD	274	ARG	Peptide
38	BS	58	LEU	Peptide
20	CT	9	ASN	Peptide

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32205	0	16254	640	0
1	CA	32312	0	16307	729	0
2	AB	1846	0	1867	85	0
2	CB	1825	0	1828	97	0
3	AC	1552	0	1546	67	0
3	CC	1542	0	1517	73	0
4	AD	1659	0	1676	65	0
4	CD	1670	0	1703	68	0
5	AE	1129	0	1185	30	0
5	CE	1133	0	1191	53	0
6	AF	806	0	793	28	0
6	CF	816	0	808	22	0
7	AG	1231	0	1238	28	0
7	CG	1235	0	1249	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	AH	1088	0	1126	25	0
8	CH	1088	0	1126	38	0
9	AI	983	0	986	52	0
9	CI	978	0	966	55	0
10	AJ	709	0	650	34	0
10	CJ	714	0	672	35	0
11	AK	829	0	825	18	0
11	CK	833	0	836	23	0
12	AL	930	0	979	31	0
12	CL	930	0	980	33	0
13	AM	958	0	1002	39	0
13	CM	950	0	988	56	0
14	AN	492	0	529	25	0
14	CN	492	0	529	36	0
15	AO	728	0	760	22	0
15	CO	728	0	760	30	0
16	AP	681	0	697	31	0
16	CP	677	0	686	26	0
17	AQ	823	0	891	24	0
17	CQ	823	0	891	21	0
18	AR	555	0	618	13	0
18	CR	555	0	618	21	0
19	AS	652	0	662	28	0
19	CS	646	0	644	52	0
20	AT	728	0	798	26	0
20	CT	727	0	796	28	0
21	AU	199	0	208	8	0
21	CU	199	0	208	12	0
22	AV	277	0	140	6	0
22	CV	252	0	130	8	0
23	AW	54	0	40	5	0
23	CW	54	0	40	7	0
24	AX	1635	0	816	34	0
24	CX	1635	0	816	39	0
25	BA	60729	0	30621	813	0
25	DA	60311	0	30408	1066	0
26	BB	2573	0	1306	29	0
26	DB	2573	0	1306	91	0
27	BD	2136	0	2218	58	0
27	DD	2136	0	2217	68	0
28	BE	1559	0	1618	52	0
28	DE	1559	0	1618	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	BF	1584	0	1625	36	0
29	DF	1580	0	1619	68	0
30	BG	1425	0	1443	45	0
30	DG	1424	0	1434	77	0
31	BH	1330	0	1407	29	0
31	DH	1330	0	1407	42	0
32	BI	1085	0	1114	39	0
32	DI	1061	0	1080	34	0
33	BN	1117	0	1184	24	0
33	DN	1117	0	1184	33	0
34	BO	933	0	996	26	0
34	DO	933	0	996	34	0
35	BP	1135	0	1212	34	0
35	DP	1135	0	1211	50	0
36	BQ	1122	0	1179	35	0
36	DQ	1122	0	1179	43	0
37	BR	968	0	1033	28	0
37	DR	968	0	1033	27	0
38	BS	877	0	938	22	0
38	DS	870	0	923	53	0
39	BT	1091	0	1151	30	0
39	DT	1083	0	1136	37	0
40	BU	959	0	1019	18	0
40	DU	959	0	1019	33	0
41	BV	771	0	830	14	0
41	DV	771	0	830	26	0
42	BW	886	0	940	9	0
42	DW	886	0	940	18	0
43	BX	750	0	814	13	0
43	DX	750	0	814	17	0
44	BY	806	0	881	31	0
44	DY	806	0	881	26	0
45	BZ	1349	0	1355	30	0
45	DZ	1360	0	1363	64	0
46	B0	653	0	674	26	0
46	D0	653	0	674	24	0
47	B1	755	0	826	12	0
47	D1	755	0	826	26	0
48	B2	588	0	643	12	0
48	D2	588	0	643	17	0
49	B3	469	0	518	9	0
49	D3	464	0	514	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	B4	552	0	533	25	0
50	D4	532	0	503	30	0
51	B5	455	0	465	12	0
51	D5	455	0	465	13	0
52	B6	453	0	473	9	0
52	D6	449	0	469	13	0
53	B7	418	0	467	13	0
53	D7	418	0	467	14	0
54	B8	511	0	571	18	0
54	D8	517	0	582	33	0
55	B9	307	0	335	4	0
55	D9	307	0	335	13	0
56	AA	187	0	0	0	0
56	AD	1	0	0	0	0
56	AE	2	0	0	0	0
56	AF	1	0	0	0	0
56	AK	1	0	0	0	0
56	AL	1	0	0	0	0
56	AM	1	0	0	0	0
56	AN	1	0	0	0	0
56	AX	7	0	0	0	0
56	B0	5	0	0	0	0
56	B3	2	0	0	0	0
56	B4	1	0	0	0	0
56	B5	2	0	0	0	0
56	B7	4	0	0	0	0
56	B8	1	0	0	0	0
56	B9	1	0	0	0	0
56	BA	675	0	0	0	0
56	BB	18	0	0	0	0
56	BD	8	0	0	0	0
56	BE	6	0	0	0	0
56	BF	5	0	0	0	0
56	BG	3	0	0	0	0
56	BH	1	0	0	0	0
56	BN	2	0	0	0	0
56	BO	1	0	0	0	0
56	BP	4	0	0	0	0
56	BQ	3	0	0	0	0
56	BR	3	0	0	0	0
56	BU	5	0	0	0	0
56	BV	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	BW	4	0	0	0	0
56	BX	3	0	0	0	0
56	BY	2	0	0	0	0
56	BZ	1	0	0	0	0
56	CA	154	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	CK	1	0	0	0	0
56	CT	1	0	0	0	0
56	CX	1	0	0	0	0
56	D0	1	0	0	0	0
56	D3	1	0	0	0	0
56	D5	1	0	0	0	0
56	D7	1	0	0	0	0
56	D8	2	0	0	0	0
56	DA	595	0	0	0	0
56	DB	12	0	0	0	0
56	DD	2	0	0	0	0
56	DE	5	0	0	0	0
56	DF	3	0	0	0	0
56	DG	1	0	0	0	0
56	DN	1	0	0	0	0
56	DP	1	0	0	0	0
56	DQ	3	0	0	0	0
56	DR	2	0	0	0	0
56	DT	1	0	0	0	0
56	DU	1	0	0	0	0
56	DV	2	0	0	0	0
56	DW	2	0	0	0	0
56	DY	1	0	0	0	0
57	AD	8	0	0	0	0
57	CD	8	0	0	0	0
58	AN	1	0	0	0	0
58	B4	1	0	0	0	0
58	B5	1	0	0	0	0
58	B6	1	0	0	0	0
58	B9	1	0	0	0	0
58	BY	1	0	0	0	0
58	CN	1	0	0	0	0
58	D4	1	0	0	0	0
58	D5	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	D6	1	0	0	0	0
58	D9	1	0	0	0	0
58	DY	1	0	0	0	0
59	AX	1	0	0	0	0
59	DA	1	0	0	0	0
60	AA	165	0	0	12	0
60	AJ	1	0	0	0	0
60	AL	3	0	0	2	0
60	AP	1	0	0	0	0
60	AU	1	0	0	0	0
60	AV	2	0	0	0	0
60	AW	3	0	0	0	0
60	B0	4	0	0	0	0
60	B1	2	0	0	0	0
60	B2	1	0	0	0	0
60	B3	1	0	0	0	0
60	B5	2	0	0	0	0
60	B7	2	0	0	1	0
60	B8	8	0	0	2	0
60	BA	924	0	0	61	0
60	BB	27	0	0	0	0
60	BD	6	0	0	2	0
60	BE	8	0	0	0	0
60	BF	6	0	0	1	0
60	BG	1	0	0	0	0
60	BH	1	0	0	1	0
60	BN	3	0	0	0	0
60	BO	1	0	0	0	0
60	BP	14	0	0	2	0
60	BQ	2	0	0	0	0
60	BS	1	0	0	0	0
60	BT	4	0	0	1	0
60	BU	2	0	0	0	0
60	BV	5	0	0	0	0
60	BW	1	0	0	0	0
60	BX	2	0	0	0	0
60	BZ	1	0	0	0	0
60	CA	113	0	0	5	0
60	CE	2	0	0	0	0
60	CJ	2	0	0	1	0
60	CL	1	0	0	1	0
60	CO	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	CW	1	0	0	1	0
60	CX	1	0	0	1	0
60	D0	5	0	0	0	0
60	D1	1	0	0	0	0
60	D3	1	0	0	3	0
60	D8	3	0	0	0	0
60	DA	689	0	0	58	0
60	DB	9	0	0	0	0
60	DD	11	0	0	2	0
60	DE	5	0	0	1	0
60	DF	6	0	0	0	0
60	DO	1	0	0	0	0
60	DP	6	0	0	0	0
60	DU	3	0	0	0	0
60	DV	1	0	0	0	0
60	DW	1	0	0	0	0
60	DX	3	0	0	0	0
All	All	289646	0	193040	5715	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 13.

All (5715) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2121:G:H1	25:DA:2177:C:N4	1.35	1.23
19:CS:42:PRO:HG3	50:D4:61:ARG:HG2	1.39	1.04
1:AA:1028:C:N4	1:AA:1033:G:H1	1.56	1.01
25:DA:2128:C:H42	25:DA:2160:G:H1	1.08	1.00
25:DA:2137:C:H42	25:DA:2154:G:H1	1.05	0.99
1:CA:1164:G:H1	1:CA:1172:C:N4	1.58	0.98
1:CA:76:C:H42	1:CA:93:G:H1	1.08	0.98
1:AA:1028:C:H42	1:AA:1033:G:H1	0.99	0.97
25:BA:2146:G:H1	25:BA:2196:C:N4	1.62	0.97
1:CA:1114:C:H42	1:CA:1186:G:H1	0.99	0.96
1:AA:1502:A:H2	1:AA:1505:G:H1	1.14	0.95
25:DA:1169:G:H1	25:DA:1180:C:H42	1.11	0.95
1:CA:70:G:H1	1:CA:99:U:H3	1.12	0.94
16:AP:57:ARG:NH2	16:AP:79:VAL:O	2.00	0.93
30:BG:138:GLN:H	30:BG:138:GLN:HE21	1.13	0.93
1:AA:1246:C:H42	1:AA:1291:G:H1	1.15	0.92
1:AA:997:U:H3	1:AA:1044:A:H61	1.12	0.92
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.35	0.92

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:AC:118:GLN:HE21	3:AC:118:GLN:H	1.14	0.91
45:DZ:126:VAL:HG11	45:DZ:161:VAL:HG22	1.53	0.90
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.51	0.89
1:CA:1114:C:N4	1:CA:1186:G:H1	1.68	0.89
25:DA:2121:G:N2	25:DA:2177:C:N3	2.19	0.89
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.06	0.89
25:BA:2146:G:H1	25:BA:2196:C:H42	1.01	0.89
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.06	0.89
1:AA:1008:C:H42	1:AA:1021:G:H1	1.12	0.88
28:DE:54:GLN:HG2	28:DE:76:ARG:HG2	1.53	0.87
2:AB:155:LEU:HD11	2:AB:159:PRO:HD3	1.55	0.87
25:BA:2695:C:O2	34:BO:70:LYS:NZ	2.07	0.87
43:BX:53:LYS:HB3	43:BX:82:GLN:HB3	1.57	0.87
4:AD:166:LYS:HA	4:AD:178:VAL:HG21	1.57	0.86
50:B4:57:GLU:HB3	50:B4:58:ARG:HA	1.57	0.86
25:DA:1607:C:N4	25:DA:1622:G:OP2	2.08	0.86
25:BA:239:G:OP2	54:B8:13:ARG:NH2	2.07	0.86
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.57	0.86
25:BA:894:U:O4	25:BA:978:A:N6	2.08	0.86
43:DX:53:LYS:HB3	43:DX:82:GLN:HB3	1.57	0.86
1:AA:991:U:O2'	1:AA:992:U:OP2	1.94	0.86
25:BA:2146:G:N2	25:BA:2196:C:N3	2.24	0.85
1:AA:1311:G:H1	1:AA:1326:C:H42	1.21	0.85
41:DV:60:GLU:OE2	41:DV:97:LYS:NZ	2.10	0.85
25:BA:2255:U:OP1	60:BA:3807:HOH:O	1.94	0.84
25:DA:740:U:OP2	60:DA:4407:HOH:O	1.95	0.84
25:DA:272(G):C:H42	25:DA:363(C):G:H1	1.22	0.84
1:AA:201:C:H42	1:AA:216:G:H22	1.25	0.84
25:BA:1039:G:OP1	40:BU:50:ARG:NH2	2.08	0.84
1:CA:400:C:H5''	4:CD:73:ARG:HH22	1.42	0.84
25:BA:1378:G:OP1	60:BA:4290:HOH:O	1.95	0.84
25:BA:1221:G:H1'	25:BA:1222:A:H5'	1.57	0.84
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.11	0.84
1:AA:1320:C:H5'	19:AS:70:LYS:HG3	1.58	0.84
45:DZ:121:HIS:HB2	45:DZ:171:ILE:HG22	1.60	0.84
25:DA:2807:G:N1	25:DA:2893:G:O6	2.11	0.83
25:DA:994:C:OP1	40:DU:53:ARG:NH2	2.11	0.83
1:AA:1028:C:N3	1:AA:1033:G:N2	2.27	0.83
25:BA:2162:C:O2	25:BA:2173:G:N1	2.10	0.83
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.60	0.83
39:DT:19:LEU:HD23	39:DT:20:PRO:HD2	1.60	0.83
3:AC:172:ARG:NH2	3:AC:206:GLU:OE1	2.12	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:303:C:H42	25:BA:385:G:H1	1.24	0.83
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.11	0.83
29:DF:53:THR:HG23	29:DF:55:GLY:H	1.44	0.83
25:BA:2162:C:N3	25:BA:2173:G:O6	2.12	0.83
25:BA:2161:C:N4	25:BA:2174:G:N1	2.27	0.83
25:BA:927:G:N2	25:BA:944:C:O2	2.12	0.83
25:DA:2683:C:O2	34:DO:70:LYS:NZ	2.10	0.82
50:B4:59:PHE:HD2	50:B4:62:ARG:HH22	1.26	0.82
25:DA:2867:G:OP2	39:DT:119:LYS:NZ	2.11	0.82
1:AA:975:A:H4'	1:AA:976:G:H5''	1.61	0.82
25:DA:299:A:H5''	44:DY:86:ARG:HH21	1.44	0.82
25:BA:2701:U:H4'	25:BA:2702:C:H5'	1.62	0.82
2:CB:80:ILE:HD13	2:CB:211:ILE:HB	1.61	0.82
3:AC:111:LEU:HD21	3:AC:144:SER:HB3	1.61	0.82
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.13	0.82
27:DD:85:ASP:OD2	27:DD:88:ARG:NH1	2.13	0.82
1:AA:1008:C:N4	1:AA:1021:G:H1	1.77	0.81
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.13	0.81
2:CB:84:GLU:HB3	2:CB:219:VAL:HG21	1.61	0.81
24:CX:21:A:H61	24:CX:46:G:H2'	1.44	0.81
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.62	0.81
46:D0:11:ARG:O	46:D0:14:ARG:NH2	2.14	0.81
25:DA:2166:G:H3'	25:DA:2167:U:H5''	1.60	0.81
35:DP:56:SER:HB2	35:DP:61:ARG:HD2	1.61	0.81
19:AS:65:ASN:HA	50:B4:58:ARG:HG3	1.63	0.81
25:BA:1736:A:H62	25:BA:1745:A:H2	1.24	0.81
1:AA:1008:C:N3	1:AA:1021:G:N2	2.29	0.81
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.43	0.81
1:AA:78:G:N2	1:AA:91:C:N3	2.28	0.81
1:CA:1262:C:N3	1:CA:1273:G:N2	2.29	0.81
25:BA:2164:C:N3	25:BA:2171:G:O6	2.14	0.81
1:CA:995:C:O2	14:CN:4:LYS:NZ	2.15	0.80
3:AC:82:GLU:HG2	3:AC:85:ARG:HH21	1.47	0.80
1:CA:1262:C:N4	1:CA:1273:G:N1	2.29	0.80
1:CA:1409:C:O2	1:CA:1491:G:N2	2.13	0.80
8:CH:41:ARG:NH2	8:CH:123:GLU:OE2	2.15	0.80
25:DA:1022:G:H22	25:DA:1142(A):A:H2	1.28	0.80
34:DO:35:VAL:HG11	34:DO:103:ALA:HB3	1.61	0.80
25:DA:245:G:O6	54:D8:8:LYS:NZ	2.15	0.80
25:DA:1693:U:O2'	27:DD:14:ARG:NH2	2.14	0.80
25:BA:656:A:OP1	35:BP:65:ARG:NH1	2.15	0.80
1:CA:76:C:N4	1:CA:93:G:H1	1.78	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2127:G:O6	25:DA:2161:C:N3	2.14	0.80
39:DT:16:ARG:NH2	39:DT:83:ILE:O	2.15	0.80
1:AA:664:G:H22	1:AA:741:G:H1	1.30	0.80
25:BA:2172:U:H2'	25:BA:2173:G:C8	2.17	0.80
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.64	0.80
25:DA:1039:G:O6	25:DA:1116:C:N4	2.15	0.80
32:DI:77:LEU:HB3	32:DI:142:VAL:HG12	1.62	0.80
3:CC:40:ARG:NH2	3:CC:55:VAL:O	2.15	0.80
1:AA:407:G:H5''	4:AD:115:ARG:HG2	1.64	0.80
23:CW:76:PPU:OP2	60:CW:101:HOH:O	1.99	0.80
32:BI:130:TYR:HB3	32:BI:138:ILE:HB	1.64	0.79
1:CA:1436:U:OP1	20:CT:23:ARG:NH2	2.14	0.79
25:DA:1019:U:H3	25:DA:1142(A):A:H62	1.28	0.79
15:CO:4:THR:OG1	15:CO:7:GLU:OE1	2.00	0.79
1:AA:1030:C:N3	1:AA:1031:G:N2	2.30	0.79
25:DA:2137:C:N4	25:DA:2154:G:H1	1.79	0.79
45:DZ:72:ARG:NH2	45:DZ:97:GLU:O	2.15	0.79
1:CA:950:U:H3	1:CA:1231:G:H1	1.29	0.79
1:CA:201:C:H42	1:CA:216:G:H1	1.29	0.79
1:AA:1025:U:O2	1:AA:1036:G:O6	2.01	0.79
25:BA:99:G:O2'	48:B2:7:ARG:NH2	2.15	0.79
54:B8:62:LEU:HB3	54:B8:65:GLU:HG3	1.64	0.79
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.64	0.79
1:AA:1228:C:OP1	13:AM:115:LYS:N	2.15	0.79
46:B0:11:ARG:O	46:B0:14:ARG:NH2	2.16	0.79
25:BA:1356:G:OP2	53:B7:9:ARG:NH1	2.15	0.79
25:BA:2299:A:H62	25:BA:2356:U:H3	1.29	0.79
29:BF:18:ARG:NH2	29:BF:127:GLU:OE1	2.15	0.79
28:DE:72:VAL:HG22	28:DE:73:GLU:HG3	1.64	0.79
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.15	0.79
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.15	0.78
25:BA:427:G:N7	60:BA:4516:HOH:O	2.16	0.78
35:BP:42:SER:O	60:BP:304:HOH:O	2.00	0.78
1:CA:613:C:N4	1:CA:627:G:O6	2.16	0.78
25:DA:2128:C:N4	25:DA:2160:G:H1	1.81	0.78
25:BA:2545:A:OP2	60:BA:3962:HOH:O	2.00	0.78
43:DX:8:ILE:O	48:D2:36:ARG:NH2	2.15	0.78
30:DG:114:ILE:HG23	30:DG:136:ARG:HH22	1.48	0.78
1:AA:78:G:N1	1:AA:91:C:N4	2.31	0.78
25:BA:2658:C:OP2	25:BA:2745:G:O2'	1.99	0.78
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.66	0.78
1:CA:1164:G:N2	1:CA:1172:C:N3	2.31	0.78

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2805:G:H2'	25:DA:2807:G:C8	2.18	0.78
1:AA:1246:C:N4	1:AA:1291:G:H1	1.82	0.78
35:BP:89:ALA:O	35:BP:121:LYS:NZ	2.15	0.78
1:AA:642:A:N3	8:AH:113:SER:OG	2.16	0.78
25:BA:1361:C:OP2	60:BA:4290:HOH:O	2.01	0.78
25:DA:1309:G:H4'	53:D7:7:PRO:HB2	1.65	0.78
1:CA:1075:C:OP1	2:CB:179:LYS:NZ	2.12	0.77
4:CD:103:ASN:OD1	4:CD:114:ARG:NH2	2.16	0.77
49:D3:5:LYS:NZ	49:D3:34:GLU:OE2	2.16	0.77
2:AB:15:VAL:O	2:AB:16:HIS:ND1	2.13	0.77
13:AM:58:GLU:O	13:AM:62:ASN:ND2	2.17	0.77
1:CA:1204:A:OP1	14:CN:3:ARG:NH1	2.17	0.77
27:BD:71:ASP:HB2	27:BD:103:ARG:HH22	1.48	0.77
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.66	0.77
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.02	0.77
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.17	0.77
25:DA:11:G:N7	60:DA:4445:HOH:O	2.17	0.77
27:DD:276:LYS:H	27:DD:276:LYS:HD3	1.49	0.77
1:CA:158:G:N2	1:CA:163:C:O2	2.16	0.77
25:DA:2357:U:OP1	46:D0:20:ARG:NH1	2.17	0.77
25:BA:2723:A:OP1	60:BA:4079:HOH:O	2.03	0.77
34:BO:35:VAL:HG11	34:BO:103:ALA:HB3	1.67	0.77
28:DE:1:MET:HE3	28:DE:199:ARG:HB3	1.67	0.77
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.18	0.77
1:CA:542:G:OP1	4:CD:10:ARG:NH1	2.16	0.77
3:CC:5:ILE:HD11	14:CN:58:LYS:HE3	1.66	0.77
4:CD:13:ARG:NH1	4:CD:38:TYR:O	2.18	0.77
22:CV:16:A:H61	24:CX:36:U:H3	1.33	0.77
25:BA:2297:C:OP2	52:B6:6:ARG:NH1	2.17	0.76
13:AM:39:ILE:HD12	13:AM:52:GLU:HG3	1.67	0.76
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.18	0.76
30:DG:176:LEU:HB2	30:DG:178:PHE:HE1	1.46	0.76
25:DA:2127:G:N1	25:DA:2161:C:O2	2.18	0.76
1:AA:997:U:H3	1:AA:1044:A:N6	1.83	0.76
1:CA:1310:G:OP1	13:CM:77:ASN:ND2	2.18	0.76
24:CX:19:G:H1	24:CX:56:C:H42	1.34	0.76
30:DG:176:LEU:HB2	30:DG:178:PHE:CE1	2.19	0.76
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.50	0.76
25:BA:1517:G:N7	60:BA:3868:HOH:O	2.17	0.76
1:CA:1392:G:H21	1:CA:1502:A:H8	1.31	0.76
25:DA:2657:A:O3'	31:DH:160:LYS:NZ	2.18	0.76
35:BP:26:GLY:O	60:BP:305:HOH:O	2.03	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.18	0.76
5:CE:50:GLU:HB2	5:CE:53:LEU:HD12	1.67	0.76
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.51	0.76
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.67	0.76
32:BI:77:LEU:HB3	32:BI:142:VAL:HG12	1.68	0.76
26:DB:22:U:H3	26:DB:61:G:H1	1.32	0.76
1:AA:1030:C:N4	1:AA:1031:G:N1	2.34	0.76
26:DB:5:C:OP1	26:DB:61:G:O2'	2.03	0.76
47:B1:23:LYS:HB3	47:B1:29:GLY:HA3	1.67	0.75
1:CA:575:G:N2	1:CA:880:C:O2	2.17	0.75
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.18	0.75
4:AD:173:TRP:HA	4:AD:187:ARG:CZ	2.16	0.75
25:DA:785:G:OP2	60:DA:4120:HOH:O	2.02	0.75
25:DA:1689:A:H62	25:DA:1698:A:H2	1.32	0.75
38:DS:41:ASP:O	38:DS:44:LYS:NZ	2.20	0.75
1:CA:975:A:H4'	1:CA:976:G:H5''	1.67	0.75
14:CN:37:PHE:HZ	14:CN:56:VAL:HG21	1.49	0.75
25:BA:2161:C:N4	25:BA:2174:G:C6	2.54	0.75
25:BA:2734:A:N7	60:BA:3890:HOH:O	2.19	0.75
27:BD:108:PRO:HB3	27:BD:143:HIS:CE1	2.21	0.75
30:BG:143:GLU:O	50:B4:28:LYS:NZ	2.19	0.75
27:DD:71:ASP:HB2	27:DD:103:ARG:HH22	1.50	0.75
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.04	0.75
34:BO:86:ILE:HG22	34:BO:94:ARG:HG3	1.69	0.75
25:BA:2726:A:OP1	37:BR:14:SER:OG	2.05	0.75
19:CS:36:ARG:NH2	19:CS:75:ALA:O	2.19	0.75
1:AA:1125:U:O2'	1:AA:1127:G:N7	2.16	0.75
45:BZ:69:THR:HG22	45:BZ:90:VAL:HA	1.68	0.75
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.68	0.75
25:DA:2121:G:H1	25:DA:2177:C:H42	0.76	0.75
25:BA:1742:G:N7	27:BD:14:ARG:NH2	2.34	0.75
41:DV:52:VAL:HG21	41:DV:55:ALA:HB3	1.68	0.75
25:BA:1001:G:O6	60:BA:3746:HOH:O	2.05	0.75
25:BA:2877:G:OP2	39:BT:119:LYS:NZ	2.19	0.75
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.20	0.75
13:AM:3:ARG:HG2	13:AM:8:GLU:HG3	1.69	0.74
49:B3:18:ASP:N	49:B3:18:ASP:OD1	2.20	0.74
6:CF:11:ASN:HB3	6:CF:14:LEU:HG	1.67	0.74
1:CA:1353:G:OP1	21:CU:10:ARG:NH1	2.19	0.74
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.69	0.74
1:CA:986:A:N3	19:CS:52:TYR:OH	2.20	0.74
38:DS:34:HIS:ND1	38:DS:53:SER:OG	2.19	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:AM:86:CYS:HB2	19:AS:73:GLU:HB3	1.68	0.74
26:BB:87:G:N2	26:BB:90:A:OP2	2.18	0.74
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.69	0.74
25:DA:2137:C:N3	25:DA:2154:G:N2	2.35	0.74
26:DB:87:G:N2	26:DB:90:A:OP2	2.21	0.74
25:DA:330:A:H2	25:DA:1210:A:H2'	1.52	0.74
25:DA:1828:G:OP1	60:DA:4417:HOH:O	2.06	0.74
25:DA:2114:A:N6	25:DA:2119:A:N7	2.36	0.74
25:BA:2136:A:N6	25:BA:2141:A:N7	2.35	0.74
25:BA:2164:C:O2	25:BA:2171:G:N1	2.15	0.74
25:DA:2122:U:O4	25:DA:2176:A:N1	2.21	0.74
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.69	0.74
25:BA:718:C:N4	60:BA:4439:HOH:O	2.20	0.74
1:CA:1029:C:N4	1:CA:1032:G:H1	1.84	0.74
2:CB:102:LEU:HD23	2:CB:182:ILE:HD13	1.70	0.74
13:CM:84:ILE:O	13:CM:86:CYS:N	2.16	0.74
25:DA:1143:A:OP1	33:DN:25:ARG:NH2	2.21	0.74
48:B2:22:GLU:OE2	48:B2:68:ARG:NH2	2.21	0.73
25:BA:2320:G:O6	25:BA:2323:A:N6	2.16	0.73
1:AA:153:C:H42	1:AA:168:G:H1	1.34	0.73
25:BA:234:G:O6	54:B8:8:LYS:NZ	2.21	0.73
25:BA:2163:G:O6	25:BA:2172:U:O2	2.06	0.73
4:CD:108:LEU:HD21	4:CD:183:GLY:HA3	1.70	0.73
25:DA:1890:A:OP2	60:DA:4558:HOH:O	2.06	0.73
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.52	0.73
25:DA:2518:A:OP2	60:DA:4240:HOH:O	2.06	0.73
16:AP:34:GLU:OE2	16:AP:55:ARG:NH2	2.20	0.73
1:CA:831:U:H3	1:CA:855:G:H1	1.35	0.73
25:DA:2629:A:O2'	25:DA:2630:G:OP2	2.04	0.73
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.52	0.73
4:AD:186:LEU:HB2	4:AD:187:ARG:HH21	1.54	0.73
1:CA:455:C:H42	1:CA:476:G:H1	1.37	0.73
1:CA:1120:G:C6	1:CA:1154:G:N2	2.57	0.73
1:CA:352:C:OP2	60:CA:4035:HOH:O	2.06	0.73
47:D1:52:ARG:HH21	47:D1:57:GLU:HB2	1.54	0.73
25:DA:782:A:OP2	60:DA:4013:HOH:O	2.07	0.73
25:BA:2118:U:H3	25:BA:2215:G:H1	1.35	0.73
25:DA:2119:A:H2	25:DA:2171:A:H5'	1.54	0.73
25:DA:2171:A:N3	25:DA:2172:U:N3	2.36	0.73
25:BA:2129:C:H42	25:BA:2204:G:H1	1.36	0.73
35:BP:126:VAL:HG12	35:BP:148:LEU:HD23	1.70	0.73
1:AA:662:G:H2'	1:AA:663:A:C8	2.24	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2753:A:N3	55:D9:15:LYS:NZ	2.36	0.72
10:AJ:31:GLY:HA3	10:AJ:81:THR:HG21	1.71	0.72
24:AX:49:G:H1	24:AX:65:C:H42	1.37	0.72
25:BA:2161:C:N3	25:BA:2174:G:N2	2.37	0.72
1:CA:875:C:H1'	8:CH:15:ASN:HD21	1.53	0.72
25:DA:2064:C:OP2	60:DA:4454:HOH:O	2.05	0.72
25:DA:918:A:O2'	26:DB:97:G:N2	2.20	0.72
25:BA:1740:U:O2'	27:BD:14:ARG:NH2	2.22	0.72
25:DA:2805:G:H2'	25:DA:2807:G:H8	1.51	0.72
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.72	0.72
25:BA:1065:U:H3	25:BA:1188:A:H62	1.35	0.72
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.22	0.72
25:DA:82:G:N1	25:DA:103:A:OP2	2.19	0.72
3:CC:111:LEU:HD22	3:CC:146:ALA:HB2	1.71	0.72
25:BA:542:C:OP1	51:B5:16:ARG:NH2	2.20	0.72
19:CS:15:LEU:HA	19:CS:18:LYS:HD2	1.70	0.72
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.56	0.72
29:BF:61:GLY:O	60:BF:406:HOH:O	2.06	0.72
30:BG:138:GLN:N	30:BG:138:GLN:HE21	1.87	0.72
37:BR:103:ARG:NH1	37:BR:108:GLY:O	2.22	0.72
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.70	0.72
46:D0:27:GLU:HG3	46:D0:68:GLU:HA	1.72	0.72
9:AI:17:VAL:HG11	9:AI:81:ILE:HA	1.70	0.72
15:AO:39:LEU:HD12	15:AO:56:LEU:HB2	1.71	0.72
25:BA:2027:A:OP1	60:BA:4104:HOH:O	2.06	0.72
26:DB:50:G:OP1	38:DS:63:THR:N	2.22	0.72
1:AA:1036:G:H3'	1:AA:1037:C:H6	1.53	0.72
1:AA:339:C:OP2	34:BO:97:ARG:NH1	2.21	0.72
1:AA:953:G:N7	13:AM:104:ARG:NH2	2.36	0.72
24:AX:76:31H:OP2	25:BA:2451:A:N6	2.23	0.72
25:BA:1717:C:OP1	60:BA:3797:HOH:O	2.07	0.72
1:CA:1035:A:H2'	1:CA:1036:G:H8	1.53	0.71
31:DH:3:ARG:HB3	31:DH:3:ARG:HH11	1.54	0.71
1:AA:574:A:OP2	60:AA:4009:HOH:O	2.08	0.71
1:AA:674:G:H2'	1:AA:675:A:H8	1.54	0.71
25:BA:1244:U:OP1	60:BA:4387:HOH:O	2.08	0.71
1:CA:1029:C:N3	1:CA:1032:G:N2	2.38	0.71
1:CA:1244:C:H42	1:CA:1293:G:H1	1.36	0.71
4:CD:98:GLU:HG2	4:CD:189:PRO:HG2	1.72	0.71
25:DA:2183:C:H2'	25:DA:2184:G:H8	1.55	0.71
37:DR:33:ARG:NH1	37:DR:115:GLU:OE2	2.23	0.71
7:CG:79:ARG:HE	7:CG:80:VAL:HG23	1.54	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:CP:57:ARG:NH2	16:CP:79:VAL:O	2.23	0.71
25:BA:1829:U:H5'	27:BD:259:THR:HG22	1.72	0.71
1:AA:936:C:O2	1:AA:1382:C:N4	2.21	0.71
3:AC:70:VAL:HG22	3:AC:72:LYS:H	1.55	0.71
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.70	0.71
45:BZ:45:ASP:OD2	45:BZ:49:ARG:NH1	2.23	0.71
1:CA:1006:C:OP1	1:CA:1037:C:O2'	2.08	0.71
25:DA:2302:G:N2	30:DG:126:ASP:OD1	2.21	0.71
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.71	0.71
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.24	0.71
25:DA:1449:A:HO2'	25:DA:1529:G:H21	1.36	0.71
25:BA:2512:U:O2'	25:BA:2516:U:OP1	2.09	0.71
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.24	0.71
25:DA:2238:G:N7	60:DA:4590:HOH:O	2.23	0.71
25:DA:997:G:OP1	40:DU:92:ARG:NE	2.24	0.71
35:DP:95:VAL:HA	35:DP:99:LEU:HD21	1.73	0.71
30:BG:5:VAL:HG22	30:BG:8:LYS:H	1.56	0.71
5:CE:43:LEU:HD22	5:CE:136:MET:HG3	1.72	0.71
12:CL:71:PRO:O	12:CL:102:ARG:NH1	2.22	0.71
49:D3:29:ARG:HB3	49:D3:30:ARG:HH11	1.56	0.71
36:DQ:43:THR:HA	36:DQ:94:VAL:HG12	1.73	0.71
42:DW:14:PRO:HG2	42:DW:78:GLU:HG2	1.71	0.71
6:AF:18:GLN:OE1	6:AF:18:GLN:N	2.23	0.71
25:BA:1388:A:O2'	25:BA:1390:G:OP2	2.07	0.71
25:DA:568:U:O4	60:DA:4115:HOH:O	2.06	0.71
4:AD:13:ARG:NH1	4:AD:38:TYR:O	2.24	0.70
25:DA:2830:G:OP1	28:DE:76:ARG:NH2	2.24	0.70
25:DA:2186:G:H2'	25:DA:2187:G:H5''	1.71	0.70
25:DA:500:G:N1	25:DA:503:A:OP2	2.22	0.70
20:AT:33:ILE:HD12	20:AT:62:LEU:HB3	1.73	0.70
25:DA:1939:U:OP1	25:DA:2604:U:O2'	2.08	0.70
25:BA:734:C:H5''	53:B7:2:LYS:HE2	1.73	0.70
25:BA:1234:A:OP2	60:BA:4298:HOH:O	2.10	0.70
25:BA:31:C:OP1	60:BA:4386:HOH:O	2.09	0.70
25:BA:863:C:OP2	60:BA:4006:HOH:O	2.09	0.70
2:CB:174:VAL:HG11	2:CB:196:LEU:HG	1.74	0.70
48:D2:38:GLN:HB3	48:D2:44:LEU:HB2	1.73	0.70
13:CM:65:LYS:HA	50:D4:50:VAL:HG11	1.73	0.70
45:DZ:119:GLU:HB2	45:DZ:122:ARG:HH11	1.56	0.70
1:AA:1069:C:OP2	60:AA:4012:HOH:O	2.09	0.70
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.07	0.70
1:AA:96:U:O2'	1:AA:97:G:H5'	1.92	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1859:G:OP1	60:BA:4340:HOH:O	2.09	0.70
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.72	0.70
3:CC:11:ARG:NH2	3:CC:177:THR:O	2.24	0.70
5:CE:144:THR:H	5:CE:147:ASP:HB2	1.57	0.70
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.09	0.70
13:AM:34:LEU:HD13	13:AM:41:PRO:HA	1.73	0.70
25:DA:1204:A:H2	25:DA:1241:A:H62	1.39	0.70
25:DA:2552:U:OP2	60:DA:4610:HOH:O	2.10	0.70
25:DA:601:C:OP1	29:DF:108:LYS:NZ	2.21	0.70
36:DQ:29:PHE:O	45:DZ:122:ARG:NH2	2.23	0.70
25:DA:993:G:OP1	40:DU:50:ARG:NH2	2.25	0.70
8:AH:73:ASP:OD1	8:AH:75:ARG:NH1	2.25	0.70
1:CA:1002:G:H1	1:CA:1038:C:N4	1.90	0.70
25:DA:2674:G:H5''	34:DO:26:LYS:HE3	1.72	0.70
42:DW:18:ARG:HG3	42:DW:76:VAL:HB	1.73	0.70
45:DZ:23:LYS:HG3	45:DZ:40:ASP:HA	1.74	0.70
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.26	0.70
1:CA:1228:C:OP1	13:CM:115:LYS:N	2.25	0.70
1:CA:986:A:O2'	19:CS:55:LYS:O	2.08	0.70
24:CX:23:C:H2'	24:CX:24:U:H6	1.57	0.70
6:AF:14:LEU:HB3	6:AF:18:GLN:NE2	2.06	0.70
24:AX:59:A:H2'	24:AX:60:U:H5'	1.74	0.70
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	1.92	0.70
32:DI:37:VAL:HG12	32:DI:38:LEU:HD12	1.73	0.70
29:BF:53:THR:HG23	29:BF:55:GLY:H	1.57	0.70
25:DA:2113:U:O2	25:DA:2169:A:N6	2.24	0.70
25:DA:643:A:N1	25:DA:2369:A:O2'	2.24	0.70
27:DD:242:ARG:O	60:DD:407:HOH:O	2.10	0.70
1:AA:1279:A:O2'	1:AA:1282:C:N4	2.25	0.69
1:AA:545:C:OP2	4:AD:65:ARG:NH2	2.25	0.69
1:CA:1164:G:N1	1:CA:1172:C:N4	2.38	0.69
2:CB:178:ARG:HH22	8:CH:68:ARG:HH22	1.38	0.69
2:CB:163:PHE:HD1	2:CB:185:ILE:HG13	1.57	0.69
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.73	0.69
1:AA:1311:G:H1	1:AA:1326:C:N4	1.90	0.69
1:CA:1262:C:N4	1:CA:1273:G:H1	1.90	0.69
25:BA:18:C:O2'	25:BA:577:U:OP1	2.10	0.69
34:BO:37:ASP:OD1	34:BO:109:LYS:NZ	2.25	0.69
37:BR:56:LYS:NZ	37:BR:87:TYR:O	2.25	0.69
25:DA:2646:C:OP2	25:DA:2732:G:O2'	2.08	0.69
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.09	0.69
1:AA:1259:C:H42	1:AA:1276:G:H1	1.36	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
53:B7:33:ARG:NH2	60:B7:3102:HOH:O	2.25	0.69
25:BA:1817:A:H1'	25:BA:1960:A:N6	2.06	0.69
27:BD:37:LEU:HD12	27:BD:62:TYR:HB2	1.73	0.69
25:DA:1783:A:H5'	25:DA:2608:G:H4'	1.75	0.69
30:DG:41:GLN:HE21	30:DG:155:MET:HB3	1.56	0.69
26:DB:75:G:N2	45:DZ:87:ASP:OD1	2.25	0.69
1:CA:991:U:O2'	1:CA:992:U:O5'	2.11	0.69
47:B1:86:SER:OG	47:B1:89:GLU:OE1	2.10	0.69
25:BA:1480:A:H61	25:BA:1605:A:H62	1.38	0.69
3:CC:82:GLU:HG2	3:CC:85:ARG:HH21	1.58	0.69
27:DD:221:VAL:O	60:DD:411:HOH:O	2.09	0.69
1:AA:13:U:OP1	60:AA:4118:HOH:O	2.10	0.69
28:DE:128:SER:OG	28:DE:129:HIS:N	2.21	0.69
1:AA:1007:C:N3	1:AA:1022:G:O6	2.25	0.69
27:BD:108:PRO:HB3	27:BD:143:HIS:HE1	1.58	0.69
30:DG:150:ASP:OD1	30:DG:153:ARG:NH1	2.22	0.69
34:DO:115:VAL:HG13	34:DO:121:VAL:HG21	1.75	0.69
25:BA:2166:U:H1'	25:BA:2170:G:H22	1.57	0.69
25:BA:786:G:OP1	60:BA:4315:HOH:O	2.10	0.69
25:BA:2821:G:H5'	28:BE:60:ASN:HD22	1.58	0.69
33:DN:20:GLY:HA2	33:DN:61:ARG:HE	1.58	0.69
1:AA:405:U:OP2	4:AD:3:ARG:NH2	2.25	0.69
1:AA:418:C:H42	1:AA:425:G:H1	1.41	0.69
10:AJ:13:HIS:HA	10:AJ:16:LEU:HB3	1.75	0.69
25:BA:1695:C:OP1	60:BA:4313:HOH:O	2.11	0.69
1:CA:446:G:H1	1:CA:488:C:H42	1.41	0.69
1:AA:328:C:H4'	1:AA:329:A:H5'	1.75	0.68
1:AA:509:A:N1	60:AA:4114:HOH:O	2.24	0.68
1:AA:78:G:C2	1:AA:91:C:N3	2.61	0.68
1:AA:903:G:OP1	60:AA:4036:HOH:O	2.10	0.68
2:AB:18:GLY:HA3	2:AB:41:ILE:HD13	1.73	0.68
44:BY:43:ASN:HB3	44:BY:65:ALA:HB3	1.76	0.68
25:DA:1269:A:N7	60:DA:4606:HOH:O	2.25	0.68
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.93	0.68
25:DA:2336:A:H61	46:D0:43:THR:HG22	1.57	0.68
29:DF:155:LEU:HD11	29:DF:176:LEU:HD12	1.74	0.68
1:AA:972:C:OP1	60:AA:4142:HOH:O	2.10	0.68
1:CA:985:C:H42	1:CA:1220:G:H1	1.40	0.68
25:DA:880:G:N2	25:DA:898:C:O2	2.26	0.68
24:AX:21:A:H61	24:AX:46:G:H2'	1.58	0.68
25:BA:848:G:O6	29:BF:53:THR:OG1	2.10	0.68
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	1.75	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:CI:116:LYS:HA	9:CI:123:PRO:HD3	1.73	0.68
25:DA:2130:U:H4'	25:DA:2133:G:H4'	1.74	0.68
30:DG:43:LEU:HD12	30:DG:45:GLU:HG3	1.75	0.68
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.75	0.68
25:BA:1992:A:OP2	60:BA:4046:HOH:O	2.12	0.68
1:CA:1464:G:OP1	39:DT:108:ARG:NH1	2.27	0.68
25:DA:2099:U:H3	25:DA:2190:G:H1	1.42	0.68
27:DD:76:PRO:HB2	27:DD:116:GLN:HE21	1.58	0.68
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.75	0.68
25:BA:2384:G:O6	60:BA:4144:HOH:O	2.10	0.68
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.75	0.68
10:CJ:30:SER:OG	10:CJ:84:GLN:OE1	2.12	0.68
25:DA:1902:C:OP1	60:DA:4018:HOH:O	2.11	0.68
1:AA:1502:A:H2	1:AA:1505:G:N1	1.91	0.68
2:CB:103:THR:HA	2:CB:180:LEU:HD11	1.76	0.68
25:DA:1800:C:OP2	27:DD:183:ARG:NH2	2.26	0.68
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.75	0.68
27:BD:85:ASP:OD2	27:BD:88:ARG:NH1	2.26	0.68
1:CA:403:C:OP1	4:CD:137:SER:OG	2.12	0.68
4:CD:122:ARG:NH1	4:CD:134:ASP:O	2.27	0.68
1:AA:1316:G:H22	1:AA:1319:A:H5''	1.58	0.68
2:AB:187:LEU:HD13	2:AB:205:ASP:HB3	1.75	0.68
25:BA:1384:G:N7	43:BX:62:LYS:NZ	2.41	0.68
1:CA:539:A:H2'	1:CA:540:G:C8	2.28	0.68
5:CE:18:ARG:HG2	5:CE:25:ARG:HB2	1.76	0.68
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	1.76	0.68
25:DA:31:C:OP1	60:DA:4439:HOH:O	2.10	0.68
41:DV:6:LYS:HB2	41:DV:38:LEU:HD21	1.76	0.68
29:BF:101:LEU:O	29:BF:106:ARG:NH1	2.26	0.68
1:CA:1029:C:N4	1:CA:1032:G:N1	2.42	0.68
26:DB:76:G:N2	26:DB:101:G:O6	2.26	0.68
30:DG:114:ILE:HG23	30:DG:136:ARG:NH2	2.09	0.68
25:BA:1346:U:H4'	25:BA:1347:A:H5''	1.75	0.67
25:DA:2128:C:N3	25:DA:2160:G:N2	2.43	0.67
25:DA:370:G:OP2	60:DA:4069:HOH:O	2.12	0.67
25:BA:1553:A:O2'	25:BA:1554:A:O4'	2.12	0.67
25:BA:2761:A:H5'	31:BH:4:ILE:HD12	1.75	0.67
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.41	0.67
25:DA:509:C:OP1	60:DA:4471:HOH:O	2.11	0.67
1:AA:103:C:O2'	1:AA:172:A:N1	2.26	0.67
1:AA:145:G:H1	1:AA:177:C:H42	1.42	0.67
3:AC:121:ALA:HB1	3:AC:189:ALA:HB2	1.75	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:AP:1:MET:N	16:AP:1:MET:SD	2.64	0.67
25:BA:560:C:O3'	40:BU:53:ARG:NH1	2.26	0.67
25:BA:1829:U:H5''	27:BD:260:ARG:HB3	1.76	0.67
36:BQ:135:ASP:OD2	45:BZ:49:ARG:NH2	2.25	0.67
39:BT:16:ARG:NH2	39:BT:83:ILE:O	2.27	0.67
44:BY:54:LYS:HA	44:BY:56:PRO:HD3	1.74	0.67
1:AA:976:G:H5'	1:AA:1358:U:O2'	1.94	0.67
25:BA:2457:G:OP1	29:BF:74:ARG:NH2	2.26	0.67
30:BG:138:GLN:HE22	30:BG:153:ARG:H	1.43	0.67
26:DB:48:A:OP2	38:DS:30:ARG:NH2	2.27	0.67
37:DR:79:LEU:HA	37:DR:83:ILE:HD12	1.77	0.67
1:AA:1005:A:HO2'	1:AA:1037:C:HO2'	1.40	0.67
35:BP:138:LEU:HD23	35:BP:145:PRO:HG3	1.76	0.67
19:CS:9:VAL:HG21	50:D4:61:ARG:HH22	1.59	0.67
25:DA:2136:C:H41	25:DA:2156:G:H21	1.42	0.67
25:DA:827:U:OP1	60:DA:4458:HOH:O	2.12	0.67
25:DA:631:A:OP1	35:DP:65:ARG:NH1	2.24	0.67
45:DZ:99:TYR:HB3	45:DZ:123:ASP:HB2	1.76	0.67
1:AA:911:U:OP2	12:AL:97:ARG:NH1	2.28	0.67
42:BW:18:ARG:HG3	42:BW:76:VAL:HB	1.76	0.67
1:CA:1162:C:H42	1:CA:1174:G:H1	1.43	0.67
25:DA:2404:C:O3'	35:DP:77:ARG:NH2	2.27	0.67
37:DR:33:ARG:NH2	51:D5:57:VAL:O	2.28	0.67
25:BA:1683:C:H2'	25:BA:1684:A:C8	2.30	0.67
25:DA:1986:A:OP1	60:DA:4251:HOH:O	2.12	0.67
25:DA:807:U:OP2	35:DP:41:ARG:NH2	2.27	0.67
39:DT:125:ARG:O	39:DT:129:ARG:NH1	2.27	0.67
39:DT:16:ARG:HD3	39:DT:19:LEU:HD12	1.77	0.67
44:DY:39:VAL:HB	44:DY:42:VAL:HB	1.75	0.67
25:BA:1221:G:H1'	25:BA:1222:A:C5'	2.25	0.67
6:CF:81:ILE:HD11	27:DD:125:ILE:HB	1.76	0.67
8:CH:10:LEU:HD22	8:CH:83:ILE:HD11	1.77	0.67
25:DA:458:G:O2'	25:DA:469:G:O6	2.11	0.67
1:AA:1279:A:O2'	1:AA:1281:U:OP2	2.13	0.67
25:BA:1345:G:OP1	60:BA:4327:HOH:O	2.11	0.67
25:BA:1760:U:H2'	25:BA:1761:G:H8	1.60	0.67
1:CA:402:G:H2'	1:CA:403:C:H5'	1.75	0.67
26:DB:29:A:O2'	26:DB:58:A:N1	2.27	0.67
34:DO:13:ASN:ND2	34:DO:96:THR:OG1	2.26	0.67
25:BA:2420:U:OP2	60:BA:3989:HOH:O	2.13	0.66
1:CA:1277:C:O2'	1:CA:1279:A:N7	2.28	0.66
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.24	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:630:G:H2'	1:AA:631:G:H8	1.60	0.66
20:AT:75:ASN:OD1	20:AT:75:ASN:N	2.28	0.66
25:BA:610:C:OP2	35:BP:21:ARG:NH2	2.29	0.66
1:CA:8:A:C6	4:CD:209:ARG:HB2	2.30	0.66
25:DA:1592:C:H2'	25:DA:1593:G:H8	1.60	0.66
29:DF:18:ARG:NH2	29:DF:127:GLU:OE1	2.27	0.66
30:DG:41:GLN:NE2	30:DG:154:GLY:O	2.28	0.66
48:D2:22:GLU:OE2	48:D2:68:ARG:NH2	2.28	0.66
36:DQ:135:ASP:OD2	45:DZ:49:ARG:NH2	2.26	0.66
45:DZ:119:GLU:O	45:DZ:122:ARG:NH1	2.29	0.66
1:AA:158:G:N2	1:AA:163:C:O2	2.28	0.66
3:AC:30:ARG:NH1	14:AN:35:ARG:O	2.29	0.66
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.26	0.66
25:BA:1002:A:N1	25:BA:2470:G:H4'	2.09	0.66
1:CA:1210:C:H2'	1:CA:1211:U:H5''	1.78	0.66
2:CB:81:VAL:O	2:CB:85:ALA:N	2.29	0.66
47:D1:3:LYS:HB2	47:D1:61:ARG:NH1	2.11	0.66
49:D3:11:SER:O	60:D3:4001:HOH:O	2.14	0.66
25:DA:83:G:O2'	25:DA:102:G:N2	2.29	0.66
36:DQ:141:GLN:HE22	45:DZ:74:VAL:HG13	1.60	0.66
25:BA:1171:G:H5'	55:B9:37:GLY:HA2	1.78	0.66
25:BA:2147:G:H22	25:BA:2194:U:P	2.18	0.66
25:BA:2125:C:H42	25:BA:2208:G:H1	1.42	0.66
27:BD:227:ASN:OD1	60:BD:405:HOH:O	2.13	0.66
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.77	0.66
2:AB:84:GLU:HB3	2:AB:219:VAL:HG21	1.76	0.66
25:BA:1068:G:H22	25:BA:1188:A:H2	1.41	0.66
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.28	0.66
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.59	0.66
25:BA:2173:G:H2'	25:BA:2174:G:C8	2.31	0.66
1:CA:1114:C:N3	1:CA:1186:G:N2	2.39	0.66
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.28	0.66
48:D2:14:ARG:HA	48:D2:63:VAL:HG11	1.77	0.66
1:AA:998:G:H1	1:AA:1043:C:H42	1.44	0.66
2:AB:231:GLU:HB2	2:AB:232:PRO:HD3	1.77	0.66
25:BA:1846:A:OP2	27:BD:54:ARG:NH2	2.29	0.66
25:BA:2339:A:H2'	25:BA:2340:A:C8	2.31	0.66
26:BB:7:G:H1	26:BB:114:C:H42	1.42	0.66
1:CA:953:G:H5'	1:CA:965:A:N6	2.10	0.66
25:DA:2079:U:O3'	47:D1:35:THR:OG1	2.14	0.66
25:DA:948:G:N2	25:DA:985:C:OP2	2.28	0.66
42:DW:4:LYS:HE2	42:DW:6:ILE:HD11	1.75	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:957:U:H5''	19:AS:81:ARG:HH12	1.61	0.66
25:BA:1825:U:H2'	25:BA:1826:C:H6	1.61	0.66
25:BA:2160:C:H42	25:BA:2175:G:H1	1.44	0.66
38:BS:28:VAL:HG11	38:BS:98:VAL:HG13	1.78	0.66
25:BA:2442:A:N3	25:BA:2442:A:H2'	2.10	0.66
25:BA:2699:U:OP2	60:BA:4420:HOH:O	2.14	0.66
24:CX:52:G:H1	24:CX:62:C:H42	1.44	0.66
25:DA:135:G:N2	25:DA:144:C:N3	2.34	0.66
7:AG:15:ASP:HB3	7:AG:24:THR:HG23	1.77	0.65
25:DA:2572:A:OP1	25:DA:2574:G:O2'	2.14	0.65
25:DA:543:C:N4	25:DA:549:G:O6	2.18	0.65
33:DN:29:LYS:NZ	33:DN:140:VAL:O	2.28	0.65
1:CA:1164:G:N2	1:CA:1172:C:C2	2.63	0.65
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.62	0.65
1:CA:560:U:OP2	60:CA:4097:HOH:O	2.12	0.65
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.29	0.65
25:DA:1645:G:H5''	25:DA:1646:C:H5'	1.79	0.65
31:DH:12:PRO:HD2	31:DH:76:VAL:HG21	1.77	0.65
1:AA:1273:G:H3'	1:AA:1274:G:H8	1.60	0.65
1:AA:596:C:OP2	60:AA:4064:HOH:O	2.13	0.65
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.78	0.65
25:DA:1269:A:OP2	60:DA:4607:HOH:O	2.13	0.65
25:DA:2689:U:OP2	25:DA:2719:G:N2	2.23	0.65
26:DB:55:U:H1'	30:DG:29:TRP:CD1	2.32	0.65
35:DP:96:THR:HG23	35:DP:99:LEU:HD23	1.78	0.65
25:DA:863:A:OP2	36:DQ:22:LYS:HD3	1.97	0.65
44:BY:92:ASN:N	44:BY:93:GLY:HA2	2.11	0.65
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.31	0.65
1:CA:1165:C:H42	1:CA:1171:G:H1	1.44	0.65
2:CB:204:ASN:O	2:CB:210:SER:OG	2.09	0.65
1:AA:1298:C:OP2	7:AG:114:ARG:NH2	2.30	0.65
26:BB:33:G:H5'	30:BG:2:PRO:HD3	1.79	0.65
25:BA:2495:C:N3	36:BQ:124:LYS:NZ	2.44	0.65
1:CA:1153:C:H42	1:CA:1154:G:H21	1.44	0.65
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.78	0.65
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.79	0.65
25:DA:1537:G:H2'	25:DA:1538:G:H8	1.62	0.65
25:DA:528:A:C2	25:DA:2042:A:H2'	2.32	0.65
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.25	0.65
8:AH:116:LYS:HD2	8:AH:129:VAL:HG11	1.77	0.65
9:AI:5:TYR:HE1	9:AI:16:ARG:HB2	1.62	0.65
31:BH:46:GLU:HB2	31:BH:49:VAL:HG12	1.79	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:40:ARG:HA	3:CC:43:LEU:HD22	1.79	0.65
24:CX:59:A:H2'	24:CX:60:U:H5'	1.79	0.65
25:DA:1025:G:C4	25:DA:1135:C:H1'	2.31	0.65
1:AA:1210:C:H2'	1:AA:1211:U:H5''	1.79	0.65
25:BA:2036:A:N1	60:BA:3705:HOH:O	2.29	0.65
1:CA:576:G:OP1	60:CA:4013:HOH:O	2.15	0.65
25:DA:1171:G:H1	25:DA:1178:C:H42	1.44	0.65
25:DA:559:G:H22	40:DU:49:HIS:CE1	2.14	0.65
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.78	0.65
25:BA:1094:A:OP2	25:BA:1155:C:N4	2.30	0.65
25:BA:1701:A:OP2	60:BA:3948:HOH:O	2.14	0.65
38:BS:27:SER:HA	38:BS:88:ASP:HB3	1.78	0.65
44:BY:92:ASN:HB2	44:BY:94:LYS:HG2	1.79	0.65
2:CB:111:ARG:HH21	2:CB:114:ARG:HB2	1.61	0.65
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.79	0.65
15:AO:8:LYS:HG2	15:AO:12:ILE:HD11	1.79	0.65
50:B4:26:SER:OG	50:B4:27:THR:N	2.29	0.65
30:BG:41:GLN:HB3	30:BG:43:LEU:HD13	1.79	0.65
1:CA:1035:A:H2'	1:CA:1036:G:C8	2.31	0.65
1:CA:297:G:O2'	1:CA:299:G:N7	2.26	0.65
46:D0:10:THR:HG22	46:D0:12:ASN:H	1.61	0.65
25:DA:2104:G:H1	25:DA:2185:C:H42	1.43	0.65
35:DP:48:PRO:O	54:D8:57:ARG:NH2	2.29	0.65
1:AA:1086:U:H3	1:AA:1099:G:H22	1.45	0.64
1:AA:21:G:OP1	60:AA:4101:HOH:O	2.15	0.64
3:AC:52:LEU:HD21	3:AC:55:VAL:HG23	1.79	0.64
23:AW:76:PPU:N	24:AX:76:31H:O2'	2.30	0.64
25:BA:1320:A:N3	25:BA:1343:C:H1'	2.12	0.64
1:CA:923:A:O2'	1:CA:1399:C:OP2	2.13	0.64
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.15	0.64
3:CC:42:LEU:O	3:CC:45:LYS:NZ	2.23	0.64
37:DR:67:LEU:HD13	37:DR:76:VAL:HG21	1.77	0.64
1:AA:1443:G:N2	1:AA:1459:C:O2	2.29	0.64
2:AB:76:GLN:HB2	2:AB:208:ILE:HG12	1.80	0.64
9:CI:23:ASN:ND2	9:CI:60:ASP:OD1	2.31	0.64
25:DA:182:A:N3	25:DA:433:C:O2'	2.24	0.64
37:DR:103:ARG:NH1	37:DR:108:GLY:O	2.29	0.64
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.30	0.64
25:BA:2515:A:OP1	60:BA:4285:HOH:O	2.15	0.64
25:BA:836:A:N1	60:BA:4021:HOH:O	2.30	0.64
16:CP:59:TRP:HA	16:CP:62:VAL:HG12	1.79	0.64
25:BA:1831:C:OP2	27:BD:183:ARG:NH2	2.31	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2593:G:O6	60:BA:4149:HOH:O	2.08	0.64
1:CA:1320:C:C2	19:CS:72:GLY:HA3	2.33	0.64
25:DA:2376:A:N3	38:DS:106:ARG:NH2	2.46	0.64
34:DO:48:PRO:HB2	34:DO:49:ARG:HD3	1.78	0.64
1:AA:139:G:N2	1:AA:224:C:O2	2.30	0.64
39:BT:107:ASP:HA	39:BT:110:ILE:HD12	1.79	0.64
1:CA:1318:A:H5''	19:CS:3:ARG:HH22	1.63	0.64
1:CA:405:U:OP2	4:CD:3:ARG:NH2	2.30	0.64
25:DA:2744:G:N2	31:DH:143:GLN:OE1	2.30	0.64
20:AT:33:ILE:O	20:AT:37:SER:OG	2.14	0.64
25:BA:788:G:OP2	60:BA:4321:HOH:O	2.15	0.64
1:CA:954:G:H21	1:CA:1227:A:H62	1.46	0.64
24:CX:21:A:N6	24:CX:46:G:H2'	2.10	0.64
24:CX:76:31H:OP2	25:DA:2439:A:N6	2.31	0.64
25:DA:1840:G:OP2	60:DA:4543:HOH:O	2.15	0.64
25:DA:648:G:O2'	25:DA:2351:G:OP1	2.09	0.64
25:DA:589:C:H2'	25:DA:590:A:C8	2.33	0.64
38:DS:27:SER:HA	38:DS:88:ASP:HB3	1.79	0.64
1:AA:363:A:OP2	12:AL:34:ARG:NH1	2.31	0.64
25:BA:1648:U:O4	60:BA:3971:HOH:O	2.09	0.64
45:BZ:77:ASP:OD2	45:BZ:80:ARG:NH1	2.30	0.64
1:CA:1086:U:H3	1:CA:1099:G:H22	1.46	0.64
25:DA:2815:C:H5'	51:D5:29:THR:HG21	1.79	0.64
25:DA:2291:U:H5''	25:DA:2380:C:H1'	1.79	0.64
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.31	0.64
38:BS:59:LYS:HE2	38:BS:60:GLY:H	1.61	0.64
25:DA:2356:C:OP1	46:D0:24:LYS:NZ	2.24	0.64
25:DA:1803:A:O2'	27:DD:259:THR:HG21	1.97	0.64
25:BA:907:U:OP2	60:BA:4251:HOH:O	2.15	0.64
1:CA:56:U:H2'	1:CA:57:G:C8	2.32	0.64
1:CA:955:U:H3	1:CA:1225:A:H2	1.46	0.64
2:CB:155:LEU:HD11	2:CB:159:PRO:HG3	1.80	0.64
24:CX:67:C:H2'	24:CX:68:C:H5'	1.79	0.64
25:DA:1220:A:OP2	40:DU:19:LYS:NZ	2.31	0.64
1:AA:1030:C:H42	1:AA:1031:G:H1	1.43	0.64
1:AA:1110:A:OP2	60:AA:4137:HOH:O	2.16	0.64
9:AI:50:LEU:HD13	9:AI:56:LEU:HA	1.78	0.64
1:AA:1125:U:H5'	10:AJ:5:ARG:HH22	1.62	0.64
25:BA:1430:A:N7	60:BA:3821:HOH:O	2.30	0.64
25:BA:1496:A:O2'	25:BA:1576:G:N2	2.22	0.64
25:BA:878:G:O2'	35:BP:38:GLN:NE2	2.31	0.64
25:DA:1192:G:N7	60:DA:4648:HOH:O	2.29	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:DF:24:LEU:HD21	29:DF:114:VAL:HG12	1.79	0.64
1:AA:1327:C:OP2	21:AU:12:LYS:NZ	2.31	0.63
1:AA:1187:G:N3	14:AN:60:SER:OG	2.31	0.63
25:BA:173:C:H2'	25:BA:174:U:C6	2.33	0.63
25:BA:441:C:H2'	25:BA:442:A:C8	2.33	0.63
38:BS:14:VAL:O	38:BS:18:ILE:HG12	1.98	0.63
1:CA:1120:G:O6	1:CA:1154:G:N2	2.28	0.63
25:DA:2345:G:OP2	52:D6:38:LYS:HD3	1.99	0.63
25:DA:2682:U:OP2	60:DA:4106:HOH:O	2.15	0.63
25:DA:729:G:C6	27:DD:208:LYS:HB2	2.33	0.63
1:AA:1416:G:N7	60:AA:4089:HOH:O	2.31	0.63
5:AE:144:THR:H	5:AE:147:ASP:HB2	1.62	0.63
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.79	0.63
25:DA:2000:G:N7	60:DA:4310:HOH:O	2.30	0.63
25:DA:2445:G:OP1	29:DF:74:ARG:NH2	2.31	0.63
25:DA:918:A:N3	26:DB:80:U:O2'	2.26	0.63
1:AA:11:G:O2'	1:AA:506:G:N2	2.30	0.63
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.31	0.63
25:BA:2127:C:H2'	25:BA:2128:G:C8	2.33	0.63
25:BA:956:A:OP2	60:BA:4252:HOH:O	2.15	0.63
38:BS:59:LYS:NZ	38:BS:68:GLN:OE1	2.30	0.63
12:CL:28:LYS:HD2	12:CL:62:SER:HB2	1.79	0.63
25:DA:1449:A:O2'	25:DA:1529:G:N2	2.23	0.63
26:DB:20:C:H2'	26:DB:21:G:H5'	1.78	0.63
28:DE:9:VAL:HG22	28:DE:25:VAL:HB	1.78	0.63
25:DA:442:G:H21	29:DF:48:THR:HB	1.63	0.63
38:DS:15:ARG:O	38:DS:19:LYS:NZ	2.31	0.63
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.80	0.63
25:BA:2786:C:OP1	28:BE:164:ARG:NE	2.22	0.63
25:DA:2169:A:O2'	25:DA:2170:A:O5'	2.16	0.63
26:DB:33:G:O6	26:DB:49:C:N4	2.29	0.63
29:DF:11:VAL:HB	29:DF:18:ARG:HB3	1.81	0.63
25:BA:1854:G:OP1	27:BD:54:ARG:NH1	2.29	0.63
1:CA:127:G:HO2'	17:CQ:2:PRO:N	1.96	0.63
25:DA:135:G:H1	25:DA:144:C:H42	1.43	0.63
25:DA:637:A:OP1	35:DP:133:SER:OG	2.14	0.63
45:DZ:5:LEU:HG	45:DZ:47:VAL:HG21	1.81	0.63
3:AC:5:ILE:HG12	3:AC:6:HIS:H	1.64	0.63
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.31	0.63
25:BA:303:C:N4	25:BA:385:G:H1	1.93	0.63
1:CA:78:G:H2'	1:CA:79:G:H5''	1.80	0.63
20:CT:10:LEU:HD23	20:CT:11:SER:H	1.63	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:DP:39:LYS:HB2	35:DP:45:LEU:HD23	1.79	0.63
1:AA:403:C:OP1	4:AD:137:SER:OG	2.16	0.63
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.11	0.63
15:CO:87:ILE:HG22	15:CO:88:ARG:H	1.63	0.63
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.14	0.63
24:CX:52:G:H2'	24:CX:53:G:H8	1.64	0.63
25:DA:2137:C:H2'	25:DA:2138:C:C6	2.34	0.63
25:DA:2630:G:H2'	25:DA:2631:G:H8	1.64	0.63
33:DN:58:ASP:OD1	33:DN:58:ASP:N	2.32	0.63
48:B2:22:GLU:HG3	48:B2:64:LEU:HD11	1.81	0.63
35:BP:63:PRO:HD3	54:B8:27:THR:HG22	1.81	0.63
29:BF:185:ASP:HA	29:BF:188:ARG:HD3	1.80	0.63
13:CM:29:ARG:HB3	13:CM:64:TRP:CZ3	2.34	0.63
50:D4:59:PHE:O	50:D4:62:ARG:NH2	2.26	0.63
25:DA:857:C:H4'	46:D0:23:VAL:HG21	1.80	0.63
30:DG:44:GLY:N	30:DG:88:ILE:O	2.31	0.63
1:AA:1097:C:O2'	1:AA:1169:A:N3	2.28	0.63
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.62	0.63
49:B3:6:VAL:HG13	49:B3:56:VAL:HG22	1.79	0.63
25:BA:1093:G:HO2'	25:BA:1094:A:H8	1.47	0.63
5:CE:8:GLU:HG3	5:CE:34:VAL:HG23	1.81	0.63
25:DA:2327:A:H2'	25:DA:2328:A:C8	2.34	0.63
25:DA:1012:U:H5	33:DN:28:THR:HG21	1.63	0.63
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.16	0.62
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.45	0.62
30:BG:138:GLN:H	30:BG:138:GLN:NE2	1.93	0.62
30:BG:15:VAL:HG21	30:BG:176:LEU:HD23	1.81	0.62
1:CA:110:C:O2'	16:CP:25:ARG:O	2.17	0.62
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.31	0.62
47:D1:3:LYS:HB2	47:D1:61:ARG:HH12	1.64	0.62
25:DA:2291:U:H2'	25:DA:2292:C:C6	2.34	0.62
25:DA:2747:G:N2	25:DA:2756:U:OP1	2.32	0.62
27:DD:171:ASP:N	27:DD:171:ASP:OD1	2.31	0.62
32:DI:1:MET:N	32:DI:20:ASP:OD1	2.26	0.62
1:AA:198:G:H2'	1:AA:199:G:H8	1.64	0.62
1:AA:97:G:O2'	1:AA:98:G:H5''	1.99	0.62
25:BA:1159:U:H2'	25:BA:1160:G:C8	2.33	0.62
25:BA:327:U:O4	60:BA:4299:HOH:O	2.13	0.62
15:CO:44:LYS:O	15:CO:47:LYS:NZ	2.32	0.62
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.31	0.62
31:DH:43:VAL:HG12	31:DH:52:VAL:HG22	1.81	0.62
1:AA:402:G:H2'	1:AA:403:C:H5'	1.79	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:624:C:H2'	1:AA:625:G:H8	1.64	0.62
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.31	0.62
25:BA:2152:U:H4'	25:BA:2155:G:H4'	1.80	0.62
28:BE:105:THR:OG1	28:BE:199:ARG:NH2	2.32	0.62
15:CO:2:PRO:O	15:CO:38:ARG:NH2	2.28	0.62
53:D7:5:TRP:NE1	53:D7:7:PRO:HG3	2.14	0.62
25:DA:1864:U:OP1	25:DA:2410:G:O2'	2.11	0.62
3:AC:118:GLN:NE2	3:AC:118:GLN:H	1.93	0.62
1:AA:1503:A:N3	22:AV:13:A:N6	2.47	0.62
1:CA:1516:G:N2	1:CA:1519:A:OP2	2.32	0.62
1:CA:642:A:N3	8:CH:113:SER:OG	2.32	0.62
2:CB:69:LEU:HB2	2:CB:159:PRO:HG2	1.82	0.62
45:DZ:102:LEU:HD23	45:DZ:137:ILE:HB	1.81	0.62
1:AA:674:G:H2'	1:AA:675:A:C8	2.33	0.62
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.81	0.62
25:BA:1087:C:H42	25:BA:1160:G:H1	1.46	0.62
25:BA:2328:C:O2'	30:BG:128:ARG:NH1	2.32	0.62
25:BA:1614:A:H2'	27:BD:86:PRO:HG3	1.81	0.62
30:BG:13:GLU:HG3	30:BG:14:GLU:HG3	1.80	0.62
1:CA:1055:A:H2'	3:CC:156:ARG:HD2	1.82	0.62
15:CO:64:ARG:NH2	25:DA:715:G:OP1	2.32	0.62
34:DO:88:ASN:ND2	34:DO:90:GLN:OE1	2.27	0.62
25:DA:831:G:O2'	35:DP:38:GLN:NE2	2.32	0.62
1:AA:262:A:H2'	1:AA:263:A:C8	2.34	0.62
25:BA:68:C:O2	25:BA:72:A:O2'	2.17	0.62
25:BA:693:G:H2'	25:BA:694:G:H5''	1.82	0.62
28:BE:9:VAL:HG22	28:BE:25:VAL:HB	1.82	0.62
25:DA:1530:C:O2'	25:DA:1531:C:O5'	2.12	0.62
25:DA:320:A:O2'	25:DA:322:A:OP2	2.12	0.62
1:AA:1469:G:H2'	1:AA:1470:G:C8	2.35	0.62
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.32	0.62
25:BA:1315:A:N7	60:BA:4105:HOH:O	2.31	0.62
38:BS:25:ARG:NH1	38:BS:42:ASP:OD1	2.32	0.62
1:CA:397:A:N7	1:CA:547:A:O2'	2.33	0.62
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.80	0.62
45:DZ:110:GLY:HA2	45:DZ:146:ILE:HG13	1.81	0.62
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.00	0.62
25:BA:2639:G:O2'	25:BA:2794:A:N1	2.30	0.62
25:BA:347:G:C8	29:BF:171:PRO:HG3	2.35	0.62
25:BA:776:G:C6	27:BD:208:LYS:HB2	2.34	0.62
32:BI:68:LEU:HD11	32:BI:109:ILE:HD11	1.82	0.62
25:DA:649:G:H4'	54:D8:46:ARG:HH22	1.65	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2001:A:H2'	25:DA:2002:G:C8	2.35	0.62
25:DA:2540:C:O2'	25:DA:2740:A:N3	2.32	0.62
28:DE:174:ASP:OD1	28:DE:175:VAL:N	2.32	0.62
32:DI:9:LEU:HD21	32:DI:35:LEU:HD22	1.80	0.62
25:BA:278:G:H2'	25:BA:279:G:H5''	1.81	0.62
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.14	0.62
25:DA:1692:U:H2'	25:DA:1694:C:C5	2.34	0.62
28:DE:9:VAL:HB	39:DT:3:ARG:HG2	1.81	0.62
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.34	0.62
1:AA:153:C:N4	1:AA:168:G:H1	1.98	0.62
25:BA:272:U:H5'	32:BI:50:ARG:HH12	1.63	0.62
25:BA:2804:C:H5'	25:BA:2902:G:N2	2.15	0.62
32:BI:106:GLY:HA2	32:BI:107:VAL:HB	1.82	0.62
1:CA:137:C:H2'	1:CA:138:G:H8	1.63	0.62
1:CA:392:G:H2'	1:CA:393:A:C8	2.34	0.62
2:CB:91:PRO:HG2	2:CB:155:LEU:HD13	1.82	0.62
25:DA:2784:C:O2'	28:DE:42:ASP:OD1	2.15	0.62
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.00	0.61
3:AC:118:GLN:N	3:AC:118:GLN:HE21	1.94	0.61
39:BT:29:ARG:HG3	39:BT:46:GLU:HB2	1.80	0.61
1:CA:948:C:H42	1:CA:1233:G:H1	1.48	0.61
1:CA:392:G:H2'	1:CA:393:A:H8	1.64	0.61
25:DA:1593:G:H2'	25:DA:1594:G:C8	2.35	0.61
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.33	0.61
1:AA:67:C:O2'	1:AA:171:A:N3	2.31	0.61
2:AB:115:LEU:O	2:AB:119:GLU:N	2.33	0.61
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.82	0.61
1:AA:584:G:H5'	17:AQ:91:ARG:HH22	1.65	0.61
25:BA:2155:G:O2'	25:BA:2179:G:N2	2.29	0.61
31:BH:24:VAL:HG22	31:BH:35:VAL:HB	1.81	0.61
1:CA:662:G:H2'	1:CA:663:A:H8	1.65	0.61
36:DQ:81:VAL:HG12	46:D0:5:LYS:HD3	1.80	0.61
25:DA:2029:G:N1	25:DA:2033:A:OP2	2.24	0.61
43:DX:32:PRO:O	43:DX:77:LYS:NZ	2.30	0.61
45:DZ:154:ASP:N	45:DZ:154:ASP:OD2	2.33	0.61
1:AA:26:A:N6	1:AA:558:G:O2'	2.32	0.61
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.29	0.61
25:BA:1065:U:HO2'	25:BA:1067:A:H2	1.48	0.61
1:CA:662:G:H2'	1:CA:663:A:C8	2.35	0.61
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.82	0.61
29:DF:40:GLN:HE22	29:DF:184:TYR:H	1.46	0.61
30:DG:179:PRO:HB2	50:D4:42:PHE:HE1	1.64	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:601:C:H2'	1:AA:602:A:H8	1.65	0.61
24:AX:64:G:O2'	36:BQ:10:ARG:NH2	2.30	0.61
25:BA:2132:G:O2'	25:BA:2142:G:OP2	2.19	0.61
2:CB:189:ASP:OD1	2:CB:189:ASP:N	2.31	0.61
3:CC:20:SER:HB2	3:CC:40:ARG:HH12	1.65	0.61
20:CT:57:ARG:HH12	20:CT:100:ILE:HD12	1.66	0.61
25:DA:526:A:OP1	60:DA:4386:HOH:O	2.15	0.61
30:DG:44:GLY:O	30:DG:47:LYS:HB2	2.00	0.61
38:DS:24:LEU:O	38:DS:86:ALA:N	2.29	0.61
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.83	0.61
25:BA:2340:A:H2'	25:BA:2341:G:C8	2.35	0.61
27:BD:253:GLN:HB2	27:BD:257:LEU:HD12	1.82	0.61
29:BF:155:LEU:HB3	29:BF:192:LEU:HD23	1.81	0.61
29:BF:157:VAL:HB	29:BF:194:MET:HG2	1.82	0.61
32:BI:92:VAL:HG13	32:BI:120:ILE:HB	1.82	0.61
1:CA:1297:C:OP1	13:CM:44:ARG:NH2	2.34	0.61
45:DZ:10:ARG:NH2	45:DZ:26:GLY:O	2.32	0.61
1:AA:1259:C:O2'	1:AA:1283:G:N2	2.29	0.61
25:BA:1495:G:O2'	25:BA:1575:A:N1	2.32	0.61
25:BA:2161:C:N3	25:BA:2174:G:C2	2.69	0.61
25:BA:2147:G:O2'	25:BA:2195:A:N6	2.34	0.61
1:CA:853:G:H2'	1:CA:854:G:H8	1.65	0.61
5:CE:144:THR:HB	5:CE:147:ASP:H	1.64	0.61
38:DS:19:LYS:HB2	38:DS:19:LYS:HZ3	1.64	0.61
32:BI:72:LEU:HD21	32:BI:107:VAL:HG11	1.82	0.61
10:CJ:27:ALA:HA	10:CJ:81:THR:HG21	1.82	0.61
25:DA:1300:U:H4'	25:DA:1301:A:H5''	1.81	0.61
25:DA:7:G:H1	25:DA:2896:C:H42	1.47	0.61
1:AA:953:G:H5'	1:AA:965:A:H61	1.66	0.61
37:BR:33:ARG:NH2	51:B5:57:VAL:O	2.28	0.61
25:BA:2163:G:C5	25:BA:2164:C:H1'	2.35	0.61
1:AA:1422:G:H5''	34:BO:48:PRO:HB3	1.83	0.61
26:DB:49:C:H2'	26:DB:50:G:C8	2.36	0.61
31:DH:24:VAL:HG13	31:DH:37:VAL:HG21	1.81	0.61
1:AA:1117:G:H5''	9:AI:104:ARG:NH2	2.14	0.61
1:CA:1062:U:O4	3:CC:2:GLY:N	2.33	0.61
1:CA:974:A:OP2	14:CN:29:ARG:NH2	2.33	0.61
25:DA:1630:G:N2	25:DA:1636:C:O2	2.34	0.61
29:DF:155:LEU:HB2	29:DF:189:THR:HG21	1.82	0.61
9:AI:16:ARG:HG3	9:AI:64:THR:HB	1.82	0.61
9:AI:7:THR:O	9:AI:83:ARG:NH1	2.31	0.61
25:BA:2769:U:O2'	60:BA:3904:HOH:O	2.16	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1048:G:H1	1:CA:1209:C:H42	1.49	0.61
1:CA:317:G:N2	1:CA:336:C:O2	2.34	0.61
1:CA:580:U:H5''	15:CO:58:MET:HG2	1.81	0.61
1:CA:977:A:N3	1:CA:977:A:H2'	2.15	0.61
3:CC:45:LYS:NZ	3:CC:46:GLU:HG2	2.15	0.61
4:CD:57:ARG:NH2	4:CD:205:GLU:OE2	2.34	0.61
9:CI:16:ARG:HB2	9:CI:64:THR:HB	1.82	0.61
20:CT:23:ARG:CG	20:CT:23:ARG:HH11	2.14	0.61
25:DA:1270:C:H5''	25:DA:1271:G:H5'	1.83	0.61
1:AA:167:G:H2'	1:AA:168:G:H8	1.66	0.60
1:AA:201:C:N4	1:AA:216:G:H22	1.96	0.60
1:AA:691:G:H2'	1:AA:692:U:C6	2.36	0.60
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.83	0.60
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.34	0.60
5:AE:77:PRO:HD2	5:AE:142:LEU:HD13	1.83	0.60
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.18	0.60
25:BA:2161:C:C4	25:BA:2174:G:N1	2.69	0.60
30:BG:16:ARG:HH21	30:BG:31:VAL:HG11	1.66	0.60
39:BT:26:ASP:OD1	39:BT:120:ARG:NH2	2.32	0.60
1:CA:97:G:O2'	1:CA:98:G:H5''	2.01	0.60
10:CJ:44:VAL:HG22	10:CJ:66:ARG:HG2	1.83	0.60
25:DA:2291:U:OP1	25:DA:2380:C:O2'	2.19	0.60
25:DA:89:G:H3'	25:DA:90:U:H5''	1.81	0.60
25:DA:1338:G:N7	43:DX:62:LYS:NZ	2.48	0.60
1:AA:673:G:H2'	1:AA:674:G:C8	2.36	0.60
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	1.83	0.60
25:BA:1338:U:H2'	25:BA:1339:C:C6	2.36	0.60
1:CA:1069:C:O2'	1:CA:1192:C:O2	2.18	0.60
1:CA:64:G:H4'	1:CA:65:U:H3'	1.83	0.60
49:D3:15:TYR:O	49:D3:20:LYS:NZ	2.34	0.60
25:DA:565:C:OP1	41:DV:82:ARG:NH2	2.33	0.60
30:DG:18:GLU:HG2	30:DG:175:LEU:HD21	1.83	0.60
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.83	0.60
8:AH:112:LEU:HA	8:AH:134:ILE:HG12	1.83	0.60
25:BA:185:A:H62	35:BP:38:GLN:HE22	1.49	0.60
34:BO:98:VAL:HG11	34:BO:114:ILE:HG23	1.83	0.60
1:CA:1058:G:H1	1:CA:1199:U:H3	1.49	0.60
25:DA:500:G:N2	25:DA:502:A:H3'	2.17	0.60
38:DS:67:ARG:O	38:DS:71:ARG:HG3	2.01	0.60
25:BA:1346:U:H4'	25:BA:1347:A:C5'	2.32	0.60
25:BA:1761:G:H1	25:BA:1775:C:H42	1.49	0.60
1:CA:1002:G:H1	1:CA:1038:C:H42	1.47	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:CH:34:GLU:OE1	8:CH:37:ARG:NH1	2.34	0.60
25:DA:1271:G:OP2	60:DA:4401:HOH:O	2.16	0.60
25:DA:2121:G:N1	25:DA:2177:C:N4	2.16	0.60
25:DA:956:G:H5''	36:DQ:77:LYS:HD2	1.82	0.60
30:DG:15:VAL:HG21	30:DG:176:LEU:HD23	1.82	0.60
25:DA:483:A:O2'	44:DY:49:VAL:O	2.13	0.60
1:AA:976:G:N2	1:AA:1363:C:OP2	2.35	0.60
1:AA:1469:G:H2'	1:AA:1470:G:H8	1.66	0.60
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.83	0.60
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.35	0.60
9:AI:31:GLN:HE21	9:AI:36:TYR:HD1	1.49	0.60
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.82	0.60
25:BA:664:U:H2'	25:BA:665:C:C6	2.36	0.60
6:CF:46:ARG:HH21	18:CR:37:VAL:HG11	1.66	0.60
25:DA:2118:U:C4	25:DA:2149:G:H1'	2.36	0.60
5:AE:100:VAL:HG22	5:AE:118:ILE:HG22	1.83	0.60
7:AG:78:ARG:HE	7:AG:156:TRP:HB3	1.67	0.60
15:AO:26:GLU:OE2	15:AO:77:ARG:NH2	2.23	0.60
25:BA:1154:U:O2'	25:BA:1155:C:O4'	2.20	0.60
25:BA:2187:G:H1	25:BA:2194:U:H5	1.50	0.60
25:BA:2389:A:H2'	25:BA:2390:A:C8	2.37	0.60
32:BI:100:ALA:HA	32:BI:103:ARG:HD2	1.82	0.60
38:BS:34:HIS:ND1	38:BS:53:SER:OG	2.32	0.60
5:CE:92:LYS:HB3	5:CE:119:LEU:HB2	1.83	0.60
7:CG:78:ARG:HG2	7:CG:79:ARG:HB2	1.83	0.60
25:DA:2492:U:OP1	60:DA:4358:HOH:O	2.16	0.60
32:DI:92:VAL:HG13	32:DI:120:ILE:HB	1.84	0.60
18:AR:31:LEU:H	18:AR:31:LEU:HD23	1.67	0.60
25:BA:553:A:N1	25:BA:2064:A:H2'	2.16	0.60
1:CA:222:U:H2'	1:CA:223:U:C6	2.37	0.60
1:CA:738:C:OP1	6:CF:2:ARG:NH1	2.35	0.60
9:CI:20:ARG:O	9:CI:60:ASP:N	2.34	0.60
1:CA:1047:G:H5''	14:CN:4:LYS:HE3	1.83	0.60
1:AA:67:C:H2'	1:AA:68:G:C8	2.36	0.60
2:AB:69:LEU:HB2	2:AB:159:PRO:HG2	1.83	0.60
25:BA:1219:A:H4'	25:BA:1220:U:OP1	2.01	0.60
25:BA:1615:G:H5''	27:BD:61:LEU:HD13	1.84	0.60
1:CA:975:A:N1	10:CJ:48:THR:HB	2.16	0.60
2:CB:84:GLU:OE1	2:CB:87:ARG:NH2	2.34	0.60
26:DB:55:U:O3'	30:DG:27:ASN:ND2	2.34	0.60
25:DA:1278:A:OP1	37:DR:36:THR:HG23	2.02	0.60
26:BB:45:A:OP2	30:BG:96:ARG:NH2	2.32	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1004:A:H5''	1:CA:1025:U:C5	2.36	0.60
1:CA:1327:C:OP2	21:CU:12:LYS:NZ	2.26	0.60
2:CB:76:GLN:HE21	2:CB:208:ILE:HG12	1.66	0.60
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.84	0.60
1:CA:35:G:O2'	12:CL:118:SER:O	2.15	0.60
49:D3:10:LYS:HB3	49:D3:53:LEU:HA	1.83	0.60
25:DA:1798:U:OP2	27:DD:274:ARG:NH2	2.35	0.60
31:DH:40:GLU:OE1	31:DH:61:HIS:NE2	2.34	0.60
37:BR:67:LEU:HD13	37:BR:76:VAL:HG21	1.84	0.60
1:CA:1189:C:H5''	3:CC:5:ILE:HD12	1.83	0.60
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.12	0.60
1:CA:1321:C:H5''	1:CA:1322:C:H2'	1.84	0.60
1:CA:58:C:O2'	1:CA:388:G:N7	2.32	0.60
1:CA:953:G:H5'	1:CA:965:A:H61	1.66	0.60
4:CD:158:ILE:HG23	4:CD:162:LEU:HD12	1.83	0.60
25:DA:2115:G:H4'	25:DA:2167:U:C4	2.37	0.60
25:DA:2135:A:H61	25:DA:2157:G:H21	1.49	0.60
25:DA:2537:U:H2'	25:DA:2538:C:C6	2.36	0.60
25:DA:833:U:H2'	25:DA:834:C:C6	2.37	0.60
1:AA:1278:U:H5'	1:AA:1279:A:H5'	1.84	0.59
2:AB:91:PRO:HG3	2:AB:154:LEU:HB3	1.83	0.59
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.24	0.59
49:B3:10:LYS:HB3	49:B3:53:LEU:HA	1.84	0.59
25:BA:2087:C:H2'	25:BA:2088:C:H6	1.66	0.59
25:BA:2190:G:C6	25:BA:2193:A:H8	2.20	0.59
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HG2	1.83	0.59
25:DA:2203:U:H2'	25:DA:2205:C:C6	2.37	0.59
29:DF:21:ALA:HB3	29:DF:22:ALA:HA	1.83	0.59
1:AA:193:C:H2'	1:AA:194:C:H6	1.67	0.59
10:AJ:81:THR:HA	10:AJ:84:GLN:HB3	1.82	0.59
25:BA:1071:G:C4	25:BA:1180:C:H1'	2.37	0.59
23:AW:76:PPU:H103	25:BA:2596:U:H5'	1.84	0.59
1:CA:437:U:H5'	4:CD:155:LEU:HD21	1.84	0.59
25:DA:987:G:O2'	25:DA:1000:A:N3	2.27	0.59
25:DA:106:C:O2	25:DA:294:A:O2'	2.20	0.59
35:DP:52:GLU:HB3	35:DP:55:ARG:HH11	1.67	0.59
42:DW:68:ARG:HB3	42:DW:109:GLU:HG2	1.84	0.59
45:DZ:45:ASP:OD2	45:DZ:49:ARG:NH1	2.35	0.59
45:DZ:19:ARG:NH1	45:DZ:84:GLU:O	2.35	0.59
1:CA:1028:C:N3	1:CA:1033:G:C6	2.71	0.59
1:CA:328:C:H4'	1:CA:329:A:H5'	1.85	0.59
25:DA:2693:A:H2'	25:DA:2694:G:H8	1.66	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DG:64:THR:HB	30:DG:94:LEU:HD21	1.83	0.59
1:AA:1226:C:OP1	13:AM:91:ARG:NH1	2.34	0.59
1:AA:429:U:O2'	4:AD:22:LYS:NZ	2.34	0.59
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.02	0.59
25:BA:694:G:H22	25:BA:696:C:H2'	1.68	0.59
27:BD:242:ARG:O	60:BD:403:HOH:O	2.17	0.59
27:BD:69:ARG:NH2	27:BD:128:GLY:O	2.35	0.59
1:CA:1318:A:OP1	19:CS:3:ARG:NH1	2.36	0.59
1:CA:309:G:O2'	1:CA:607:A:N1	2.36	0.59
20:CT:43:LEU:O	20:CT:47:GLY:N	2.35	0.59
25:DA:614(A):U:H4'	25:DA:614(B):G:H5'	1.84	0.59
25:DA:632:A:H2'	25:DA:633:A:C8	2.37	0.59
26:DB:95:C:H2'	26:DB:96:U:C6	2.36	0.59
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.37	0.59
1:AA:1273:G:H3'	1:AA:1274:G:C8	2.36	0.59
3:AC:179:ARG:NH1	3:AC:206:GLU:OE2	2.35	0.59
1:AA:376:G:H4'	16:AP:5:ARG:HE	1.67	0.59
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.65	0.59
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.84	0.59
3:CC:164:ARG:HD2	3:CC:165:THR:H	1.66	0.59
9:CI:50:LEU:HD21	9:CI:81:ILE:HD11	1.83	0.59
9:CI:7:THR:OG1	9:CI:83:ARG:NH1	2.36	0.59
28:DE:14:ILE:HD11	28:DE:173:VAL:HG11	1.84	0.59
36:DQ:79:LEU:HB3	36:DQ:80:GLU:HG3	1.84	0.59
1:AA:201:C:H42	1:AA:216:G:N2	2.00	0.59
25:BA:1825:U:H2'	25:BA:1826:C:C6	2.37	0.59
25:BA:2140:U:O4	25:BA:2171:G:H1'	2.03	0.59
25:DA:694:U:OP1	27:DD:59:LYS:NZ	2.34	0.59
1:AA:316:G:OP2	1:AA:351:G:O2'	2.20	0.59
1:AA:413:G:N2	1:AA:428:G:H1'	2.18	0.59
25:BA:186:A:N6	25:BA:2442:A:O2'	2.35	0.59
25:BA:599:U:OP1	60:BA:4285:HOH:O	2.17	0.59
25:BA:847:A:OP1	25:BA:847:A:H8	1.86	0.59
26:BB:91:C:OP2	36:BQ:16:ARG:NH1	2.35	0.59
25:DA:2879:C:OP2	60:DA:4350:HOH:O	2.17	0.59
25:BA:1897:C:H2'	25:BA:1898:A:O4'	2.03	0.59
25:DA:1590:U:H2'	25:DA:1591:G:H8	1.68	0.59
29:DF:33:LEU:HD13	29:DF:112:MET:HE2	1.83	0.59
42:DW:18:ARG:NH1	42:DW:76:VAL:O	2.36	0.59
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.34	0.59
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.85	0.59
25:BA:144:C:H5'	43:BX:2:LYS:HD2	1.84	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1189:C:OP1	10:CJ:51:ARG:NH2	2.35	0.59
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.85	0.59
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.85	0.59
11:CK:33:THR:HA	11:CK:39:PRO:HA	1.83	0.59
13:CM:6:GLY:O	30:DG:115:ARG:NH2	2.35	0.59
25:DA:2206:G:H3'	25:DA:2207:G:C8	2.38	0.59
25:DA:2515:C:H2'	25:DA:2516:G:H8	1.68	0.59
25:DA:2788:C:OP1	28:DE:61:ARG:NH2	2.36	0.59
25:DA:2276:G:H5'	36:DQ:86:GLY:HA2	1.83	0.59
8:AH:29:SER:HB2	8:AH:32:LYS:HG3	1.85	0.59
48:B2:25:VAL:HG13	48:B2:57:ILE:HG23	1.84	0.59
52:B6:11:LEU:HB2	52:B6:21:TYR:HB2	1.85	0.59
25:BA:1217:G:H3'	25:BA:1218:G:H5'	1.84	0.59
25:BA:591:U:H5'	25:BA:990:A:N1	2.18	0.59
34:BO:63:VAL:HG12	34:BO:106:LEU:HD11	1.85	0.59
25:DA:2398:U:H2'	25:DA:2399:G:C8	2.37	0.59
34:DO:60:ALA:HA	34:DO:87:ILE:HG12	1.85	0.59
1:AA:974:A:OP2	14:AN:29:ARG:NH2	2.35	0.58
1:AA:993:G:O6	1:AA:1045:C:N4	2.35	0.58
1:AA:1289:A:OP1	21:AU:9:ARG:NH2	2.36	0.58
25:BA:1449:C:H5''	25:BA:1518:A:H1'	1.84	0.58
27:BD:132:PRO:HG2	27:BD:135:PHE:CD2	2.38	0.58
32:BI:102:SER:O	32:BI:106:GLY:HA3	2.02	0.58
44:BY:92:ASN:HB2	44:BY:94:LYS:H	1.66	0.58
1:CA:1397:C:H4'	22:CV:23:A:C6	2.37	0.58
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.36	0.58
25:DA:1017:G:N7	60:DA:4475:HOH:O	2.31	0.58
25:DA:1265:A:OP2	60:DA:4244:HOH:O	2.16	0.58
25:DA:1721:G:H8	25:DA:1741:A:H62	1.49	0.58
25:DA:2126:A:N6	25:DA:2162:G:O2'	2.36	0.58
27:DD:206:LEU:HD22	27:DD:211:ARG:HG2	1.84	0.58
38:DS:26:LEU:HA	38:DS:39:ILE:HG12	1.85	0.58
1:AA:1286:A:C8	1:AA:1287:A:H4'	2.38	0.58
1:AA:78:G:C6	1:AA:91:C:N4	2.69	0.58
1:AA:376:G:H5''	16:AP:5:ARG:HB2	1.85	0.58
25:BA:2210:C:H2'	25:BA:2211:U:O4'	2.04	0.58
25:BA:776:G:OP1	27:BD:10:THR:OG1	2.15	0.58
1:CA:1153:C:H42	1:CA:1154:G:N2	2.01	0.58
1:CA:572:A:OP1	60:CA:4030:HOH:O	2.17	0.58
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.33	0.58
8:CH:37:ARG:NH2	8:CH:118:VAL:O	2.36	0.58
9:CI:53:VAL:O	9:CI:55:ALA:N	2.33	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.38	0.58
25:DA:131:G:OP1	60:DA:4073:HOH:O	2.17	0.58
25:DA:2125:G:H22	25:DA:2172:U:H5'	1.68	0.58
34:DO:19:ILE:HG22	34:DO:43:VAL:HA	1.86	0.58
25:DA:1665:A:H4'	34:DO:67:LYS:HB2	1.84	0.58
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.18	0.58
50:B4:63:TYR:N	50:B4:64:GLY:HA2	2.18	0.58
25:BA:905:U:O2	25:BA:2280:A:H2'	2.04	0.58
25:BA:2584:A:N7	28:BE:144:ARG:HD2	2.17	0.58
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.84	0.58
10:CJ:5:ARG:N	10:CJ:99:LYS:O	2.37	0.58
11:CK:22:HIS:HD2	11:CK:29:ILE:HD12	1.68	0.58
25:DA:958:U:OP2	36:DQ:14:ARG:NH1	2.37	0.58
1:AA:159:G:N2	1:AA:162:A:OP2	2.35	0.58
27:BD:145:VAL:HB	27:BD:155:LEU:HB2	1.84	0.58
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.38	0.58
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.38	0.58
1:CA:400:C:H5''	4:CD:73:ARG:NH2	2.15	0.58
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.84	0.58
25:DA:2611:U:C4	51:D5:3:LYS:HG2	2.38	0.58
25:DA:1592:C:H2'	25:DA:1593:G:C8	2.38	0.58
25:DA:2126:A:N3	25:DA:2127:G:H1'	2.19	0.58
28:DE:199:ARG:HH12	28:DE:202:LYS:HE2	1.68	0.58
30:DG:33:ARG:HE	30:DG:162:THR:HG21	1.66	0.58
41:DV:62:LEU:HD11	41:DV:95:LEU:HB2	1.86	0.58
44:DY:37:VAL:N	44:DY:67:LEU:O	2.32	0.58
1:AA:1241:G:H1	1:AA:1296:C:H42	1.49	0.58
1:CA:1032:G:H2'	1:CA:1033:G:C8	2.38	0.58
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.68	0.58
50:D4:40:HIS:HD2	50:D4:41:PRO:HD2	1.68	0.58
36:DQ:26:TYR:O	36:DQ:67:ARG:NH1	2.37	0.58
1:AA:401:C:H2'	1:AA:402:G:C8	2.37	0.58
1:AA:93:G:H2'	1:AA:96:U:O4'	2.03	0.58
10:AJ:47:PHE:N	10:AJ:63:PHE:O	2.37	0.58
1:CA:1123:A:H4'	10:CJ:36:GLY:HA3	1.86	0.58
1:CA:1164:G:H1	1:CA:1172:C:H42	1.49	0.58
18:CR:56:THR:HB	18:CR:58:LEU:HD23	1.85	0.58
25:DA:616:G:H5'	29:DF:205:ARG:HD2	1.85	0.58
27:DD:108:PRO:HG2	27:DD:111:LEU:HB2	1.85	0.58
8:AH:21:LYS:O	8:AH:65:TYR:OH	2.17	0.58
25:BA:715:G:H5'	25:BA:716:G:OP2	2.03	0.58
25:BA:1199:C:OP1	40:BU:92:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1378:C:H5''	7:CG:6:ARG:HH21	1.68	0.58
35:DP:63:PRO:HD3	54:D8:27:THR:HG22	1.86	0.58
25:DA:140:G:H22	25:DA:1596:A:H4'	1.69	0.58
25:DA:1674:G:N2	25:DA:1677:A:N1	2.51	0.58
25:DA:2273:A:H2'	25:DA:2274:A:C8	2.38	0.58
25:DA:644:A:H4'	25:DA:645:C:C5	2.39	0.58
25:DA:996:A:OP2	40:DU:93:LYS:NZ	2.26	0.58
28:DE:18:ASP:HB3	39:DT:82:LEU:HD21	1.85	0.58
35:DP:81:GLN:NE2	35:DP:105:LEU:O	2.37	0.58
47:B1:54:ALA:HB1	47:B1:83:GLU:HG3	1.86	0.58
25:BA:2443:U:OP1	60:BA:3998:HOH:O	2.16	0.58
28:BE:47:VAL:HG21	28:BE:86:PRO:HD2	1.84	0.58
33:BN:12:ARG:HH21	33:BN:138:LEU:HD11	1.67	0.58
1:CA:1002:G:N2	1:CA:1038:C:N3	2.51	0.58
1:CA:977:A:H1'	1:CA:982:U:O4	2.04	0.58
25:DA:1410:G:H2'	25:DA:1411:C:C6	2.38	0.58
25:DA:453:C:O2	25:DA:457:A:O2'	2.22	0.58
1:AA:1008:C:N4	1:AA:1021:G:N1	2.33	0.58
25:BA:1077:G:H5''	55:B9:8:LYS:HE3	1.86	0.58
25:BA:272:U:H5'	32:BI:50:ARG:NH1	2.18	0.58
25:BA:323:A:N1	25:BA:346:A:O2'	2.32	0.58
1:CA:1002:G:N3	1:CA:1003:G:H8	2.01	0.58
1:CA:664:G:OP1	18:CR:64:ARG:NH1	2.35	0.58
2:CB:122:PHE:HD1	2:CB:123:ALA:H	1.50	0.58
2:CB:33:TYR:HB2	2:CB:43:ASP:HA	1.84	0.58
13:CM:120:LYS:HA	13:CM:121:LYS:NZ	2.18	0.58
25:DA:1266:G:O2'	25:DA:2012:G:O6	2.19	0.58
1:CA:1423:G:H5'	34:DO:49:ARG:HH12	1.68	0.58
1:AA:988:G:H1	1:AA:1217:C:H42	1.51	0.58
4:AD:85:LYS:HG3	4:AD:86:LYS:H	1.67	0.58
5:AE:68:GLU:HG3	5:AE:70:PRO:HD3	1.86	0.58
25:BA:116:A:H5'	25:BA:117:A:H8	1.68	0.58
31:BH:40:GLU:OE1	31:BH:61:HIS:NE2	2.37	0.58
1:CA:427:U:O2'	1:CA:541:G:OP1	2.18	0.58
1:CA:985:C:H2'	1:CA:986:A:C8	2.39	0.58
3:CC:43:LEU:HD23	3:CC:44:GLU:N	2.19	0.58
22:CV:16:A:N6	24:CX:36:U:H3	2.01	0.58
25:DA:1688:U:O2	25:DA:1700:A:H5'	2.03	0.58
25:DA:375:C:H2'	25:DA:376:C:C6	2.39	0.58
39:DT:60:THR:HG22	39:DT:77:PRO:HA	1.86	0.58
25:DA:84:A:H5''	44:DY:8:LYS:HE3	1.86	0.58
25:BA:2087:C:H2'	25:BA:2088:C:C6	2.38	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
44:BY:99:CYS:HB2	44:BY:106:LEU:HD21	1.86	0.57
1:CA:401:C:OP2	4:CD:73:ARG:NH1	2.37	0.57
1:CA:1309:G:H5'	13:CM:78:ILE:HD11	1.86	0.57
25:DA:2143:C:H2'	25:DA:2144:U:O4'	2.04	0.57
25:DA:1827:C:OP2	27:DD:222:ARG:NH1	2.37	0.57
33:DN:15:LEU:HB2	33:DN:135:PRO:HB2	1.86	0.57
1:AA:353:A:H5'	1:AA:353:A:H8	1.69	0.57
28:BE:12:THR:HG22	28:BE:13:ARG:H	1.68	0.57
30:BG:64:THR:HB	30:BG:94:LEU:HD21	1.84	0.57
40:BU:66:ASN:O	40:BU:70:ARG:HG3	2.03	0.57
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.40	0.57
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.68	0.57
1:CA:59:A:H5''	1:CA:60:A:H5''	1.84	0.57
16:CP:19:ILE:HD11	16:CP:39:TYR:HB2	1.85	0.57
26:DB:20:C:H42	26:DB:63:G:H1	1.50	0.57
26:DB:7:G:N3	38:DS:38:GLN:NE2	2.43	0.57
38:DS:28:VAL:HG13	38:DS:35:ILE:HD11	1.86	0.57
38:DS:89:ARG:HG2	38:DS:92:TYR:O	2.04	0.57
1:AA:158:G:H21	1:AA:162:A:H62	1.50	0.57
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.86	0.57
3:AC:124:ILE:HD12	3:AC:196:LEU:HD12	1.86	0.57
1:AA:881:G:P	12:AL:12:ARG:HH22	2.26	0.57
41:BV:14:VAL:HB	41:BV:96:ILE:HG13	1.85	0.57
4:CD:153:ARG:O	4:CD:159:ARG:NH2	2.37	0.57
25:DA:2291:U:O2'	25:DA:2374:C:O2	2.19	0.57
39:DT:88:ILE:HG21	39:DT:91:ARG:HD3	1.86	0.57
1:AA:1259:C:N4	1:AA:1276:G:H1	2.02	0.57
1:AA:539:A:OP2	12:AL:115:LYS:HD2	2.05	0.57
25:BA:1223:C:H2'	25:BA:1224:C:C6	2.40	0.57
25:BA:2145:G:H1	25:BA:2197:C:H42	1.53	0.57
2:CB:87:ARG:NE	2:CB:233:SER:HB3	2.19	0.57
5:CE:19:MET:SD	5:CE:24:ARG:HG2	2.44	0.57
17:CQ:57:VAL:HG12	17:CQ:76:LEU:HA	1.86	0.57
20:CT:64:ASP:OD2	20:CT:81:LYS:NZ	2.36	0.57
25:DA:833:U:O2	35:DP:55:ARG:NH2	2.37	0.57
2:AB:163:PHE:HA	2:AB:185:ILE:HG12	1.84	0.57
25:BA:1001:G:OP2	36:BQ:14:ARG:NH2	2.38	0.57
25:BA:1890:A:N6	25:BA:1905:G:O2'	2.36	0.57
25:BA:2165:C:H2'	25:BA:2166:U:O4'	2.04	0.57
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.86	0.57
1:CA:1349:A:H5''	9:CI:121:ARG:HB2	1.85	0.57
1:CA:1326:C:H5''	21:CU:18:TYR:O	2.03	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:668:G:H5'	25:DA:669:G:OP2	2.04	0.57
25:DA:821:A:H2'	25:DA:946:G:H5''	1.84	0.57
26:DB:66:A:H61	26:DB:108:U:H3'	1.70	0.57
30:DG:178:PHE:N	30:DG:178:PHE:CD1	2.71	0.57
1:AA:559:A:H4'	1:AA:560:U:H3'	1.86	0.57
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.19	0.57
10:AJ:7:LYS:HB3	10:AJ:97:GLU:HB2	1.86	0.57
1:CA:1067:A:O2'	1:CA:1068:G:OP2	2.19	0.57
1:CA:190:U:H2'	1:CA:191:G:C8	2.40	0.57
2:CB:83:MET:HB3	2:CB:234:PRO:HB2	1.87	0.57
19:CS:9:VAL:HG21	50:D4:61:ARG:NH2	2.20	0.57
25:DA:1030:G:OP2	36:DQ:128:LYS:NZ	2.33	0.57
25:DA:2150:U:H2'	25:DA:2151:G:C8	2.40	0.57
27:DD:112:GLN:H	27:DD:115:GLN:NE2	2.02	0.57
1:AA:624:C:H2'	1:AA:625:G:C8	2.39	0.57
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.37	0.57
25:BA:1801:G:OP1	60:BA:4522:HOH:O	2.17	0.57
1:CA:1134:G:N3	1:CA:1134:G:H2'	2.19	0.57
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.45	0.57
25:DA:1565:C:H42	25:DA:1568:G:H1	1.52	0.57
25:DA:2454:G:O6	60:DA:4290:HOH:O	2.16	0.57
25:DA:656:G:H2'	25:DA:657:U:O4'	2.04	0.57
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.17	0.57
1:AA:21:G:H2'	1:AA:22:G:C8	2.40	0.57
3:AC:164:ARG:HG2	3:AC:165:THR:H	1.69	0.57
6:AF:97:PHE:HB2	18:AR:32:ARG:HE	1.68	0.57
25:BA:2589:A:H5'	51:B5:3:LYS:HD2	1.87	0.57
25:BA:1891:G:N2	25:BA:1905:G:H1'	2.20	0.57
25:BA:1985:U:H4'	25:BA:1986:G:OP1	2.03	0.57
25:BA:2820:A:N6	25:BA:2900:G:O2'	2.34	0.57
25:BA:625:G:O2'	25:BA:702:A:N6	2.37	0.57
25:BA:922:G:H1	25:BA:948:C:H42	1.51	0.57
2:CB:122:PHE:HA	2:CB:127:ILE:HD12	1.87	0.57
5:CE:10:MET:N	5:CE:10:MET:SD	2.77	0.57
17:CQ:12:SER:HB3	17:CQ:20:THR:HB	1.85	0.57
25:DA:2104:G:H1	25:DA:2185:C:N4	2.02	0.57
25:DA:2630:G:H2'	25:DA:2631:G:C8	2.40	0.57
29:DF:184:TYR:CE2	29:DF:188:ARG:HD2	2.40	0.57
1:AA:1194:U:H2'	1:AA:1195:C:C6	2.40	0.57
1:AA:1288:A:N1	1:AA:1371:G:H1'	2.20	0.57
1:AA:17:U:H2'	1:AA:18:C:C6	2.40	0.57
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.87	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:CG:116:ALA:O	7:CG:120:ILE:HG12	2.04	0.57
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.85	0.57
25:DA:1710:C:H2'	25:DA:1711:C:H6	1.70	0.57
25:DA:689:A:N3	25:DA:779:U:O2'	2.36	0.57
45:DZ:23:LYS:HE2	45:DZ:40:ASP:CG	2.25	0.57
27:BD:17:THR:O	27:BD:211:ARG:NH2	2.38	0.57
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.40	0.57
2:CB:187:LEU:HB2	2:CB:201:ILE:HB	1.87	0.57
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.87	0.57
25:DA:883:G:O6	25:DA:893:C:N4	2.29	0.57
25:DA:2679:A:H4'	28:DE:165:VAL:HG11	1.87	0.57
1:AA:346:G:H2'	1:AA:347:G:H4'	1.87	0.56
1:AA:56:U:H2'	1:AA:57:G:C8	2.40	0.56
20:AT:43:LEU:O	20:AT:47:GLY:N	2.38	0.56
25:BA:60:G:H5'	48:B2:50:ILE:HG21	1.86	0.56
25:BA:1042:A:OP2	40:BU:93:LYS:NZ	2.34	0.56
25:BA:2034:G:OP1	42:BW:11:ARG:NH2	2.36	0.56
25:BA:2576:A:C2	25:BA:2659:U:H4'	2.40	0.56
32:BI:96:ASP:OD1	32:BI:96:ASP:N	2.38	0.56
1:CA:1137:C:H5''	1:CA:1138:G:OP1	2.04	0.56
1:CA:36:C:OP1	12:CL:123:LYS:HE3	2.04	0.56
1:CA:486:U:H2'	1:CA:487:A:H8	1.70	0.56
10:CJ:30:SER:O	10:CJ:81:THR:OG1	2.23	0.56
11:CK:48:ILE:O	11:CK:50:TYR:N	2.38	0.56
25:DA:1916:A:H2'	25:DA:1917:U:O4'	2.05	0.56
26:DB:24:G:H21	26:DB:27:C:H42	1.53	0.56
25:DA:1971:A:OP2	27:DD:242:ARG:NH2	2.38	0.56
39:DT:53:ARG:HB3	39:DT:53:ARG:NH1	2.20	0.56
44:DY:61:ILE:HD11	44:DY:63:LYS:HE3	1.85	0.56
1:AA:1015:A:N3	1:AA:1218:C:O2'	2.35	0.56
1:AA:198:G:H2'	1:AA:199:G:C8	2.40	0.56
3:AC:26:LYS:HA	14:AN:36:PHE:HE1	1.70	0.56
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.37	0.56
48:B2:63:VAL:HA	48:B2:66:GLU:HB2	1.86	0.56
25:BA:2168:C:H4'	25:BA:2169:G:C4	2.40	0.56
30:BG:138:GLN:NE2	30:BG:153:ARG:H	2.02	0.56
1:CA:538:G:H5''	12:CL:114:LYS:HB2	1.87	0.56
1:CA:921:U:O2	5:CE:19:MET:HB2	2.06	0.56
50:D4:38:LYS:O	50:D4:40:HIS:N	2.27	0.56
51:D5:16:ARG:NH1	51:D5:17:ASP:OD1	2.38	0.56
25:DA:1165:U:H2'	25:DA:1166:C:C6	2.41	0.56
25:DA:2185:C:H2'	25:DA:2186:G:H8	1.71	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:300:A:H1'	25:DA:319:C:H1'	1.87	0.56
31:DH:70:THR:HA	31:DH:73:ALA:HB3	1.86	0.56
49:B3:44:ARG:O	49:B3:48:GLU:HG3	2.05	0.56
25:BA:2149:G:H21	25:BA:2195:A:H1'	1.70	0.56
25:BA:2255:U:H2'	25:BA:2256:U:C6	2.40	0.56
1:CA:1329:A:H5''	13:CM:26:GLY:N	2.20	0.56
25:DA:2507:C:H5''	25:DA:2573:C:N4	2.19	0.56
25:DA:751:A:H5'	42:DW:90:ARG:HA	1.87	0.56
28:DE:47:VAL:HG11	28:DE:86:PRO:HD2	1.87	0.56
29:DF:64:ILE:HD11	29:DF:75:HIS:HB2	1.87	0.56
25:DA:2562:U:H1'	34:DO:23:ARG:HH11	1.70	0.56
37:DR:55:ALA:HB2	37:DR:79:LEU:HD13	1.86	0.56
3:CC:45:LYS:HZ1	3:CC:46:GLU:HG2	1.70	0.56
25:DA:2249:U:N3	25:DA:2253:G:OP2	2.36	0.56
25:DA:989:G:H4'	25:DA:990:A:OP1	2.05	0.56
30:DG:173:LEU:HD22	30:DG:178:PHE:CZ	2.40	0.56
36:DQ:109:VAL:HG13	36:DQ:113:GLN:HB2	1.87	0.56
38:DS:10:ARG:HA	38:DS:13:ARG:HE	1.70	0.56
1:AA:1028:C:C4	1:AA:1029:C:H1'	2.40	0.56
1:AA:1330:U:O4	1:AA:1331:G:N1	2.39	0.56
47:B1:51:VAL:HG11	47:B1:74:VAL:HG21	1.86	0.56
34:BO:2:ILE:HD12	34:BO:6:THR:HG21	1.85	0.56
25:BA:1233:U:H4'	41:BV:79:VAL:HG22	1.86	0.56
1:CA:630:G:H2'	1:CA:631:G:H8	1.70	0.56
1:CA:693:G:H2'	1:CA:694:A:C8	2.40	0.56
7:CG:49:ILE:HA	7:CG:52:GLU:HG2	1.87	0.56
33:DN:4:TYR:CE2	40:DU:100:VAL:HG11	2.40	0.56
43:DX:50:LYS:HB3	43:DX:87:GLN:HE22	1.71	0.56
45:DZ:145:GLU:HG3	45:DZ:146:ILE:H	1.70	0.56
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.06	0.56
29:BF:183:VAL:O	29:BF:187:VAL:HG23	2.06	0.56
31:BH:11:VAL:HG21	31:BH:50:VAL:HG23	1.88	0.56
25:BA:957:A:H2'	36:BQ:9:TYR:OH	2.05	0.56
1:CA:1121:U:O4	1:CA:1152:A:N1	2.38	0.56
1:CA:958:A:N6	19:CS:77:THR:O	2.38	0.56
18:CR:47:THR:HG21	18:CR:49:LYS:HE2	1.88	0.56
20:CT:59:ALA:O	20:CT:63:ILE:HG13	2.05	0.56
25:DA:1794:U:H2'	25:DA:1795:C:C6	2.40	0.56
25:DA:1792:G:N2	25:DA:1827:C:O2	2.36	0.56
25:DA:511:U:H4'	25:DA:1235:G:H4'	1.86	0.56
25:DA:2788:C:H5''	28:DE:61:ARG:HH21	1.69	0.56
1:AA:711:G:OP1	6:AF:54:LYS:NZ	2.39	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:BH:33:LEU:HD21	31:BH:136:ILE:HG13	1.87	0.56
31:BH:56:SER:OG	31:BH:57:ASP:N	2.38	0.56
33:BN:108:PRO:O	33:BN:113:GLY:HA3	2.05	0.56
1:CA:1154:G:N7	1:CA:1155:G:C8	2.74	0.56
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.40	0.56
3:CC:5:ILE:HG12	3:CC:6:HIS:H	1.71	0.56
13:CM:120:LYS:HA	13:CM:121:LYS:HZ3	1.69	0.56
46:D0:40:GLN:HE21	46:D0:57:PHE:HB3	1.71	0.56
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.21	0.56
35:BP:95:VAL:HG13	35:BP:125:VAL:HG12	1.88	0.56
1:CA:1104:G:H4'	2:CB:111:ARG:HH11	1.71	0.56
3:CC:36:ASP:OD1	3:CC:57:ILE:HG21	2.06	0.56
1:CA:1074:G:OP1	5:CE:64:ARG:NH2	2.38	0.56
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.88	0.56
18:CR:25:THR:O	18:CR:25:THR:OG1	2.24	0.56
27:DD:127:VAL:HA	27:DD:193:VAL:HG23	1.87	0.56
27:DD:175:LEU:HD12	27:DD:185:VAL:HG21	1.87	0.56
42:DW:12:ILE:O	42:DW:101:SER:OG	2.23	0.56
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.06	0.56
4:AD:81:GLU:OE1	4:AD:139:ARG:NH2	2.38	0.56
1:AA:1309:G:OP2	13:AM:99:ARG:NH2	2.39	0.56
1:CA:977:A:O2'	1:CA:981:U:N3	2.32	0.56
8:CH:30:ARG:O	8:CH:34:GLU:HG2	2.06	0.56
13:CM:3:ARG:HA	50:D4:34:GLU:HG2	1.87	0.56
25:DA:1166:C:H2'	25:DA:1167:U:C6	2.40	0.56
25:DA:2059:A:O2'	29:DF:69:HIS:HD2	1.89	0.56
25:DA:2126:A:N6	25:DA:2162:G:HO2'	2.04	0.56
25:DA:2183:C:H2'	25:DA:2184:G:C8	2.39	0.56
25:DA:2331:G:O2'	25:DA:2336:A:N1	2.31	0.56
25:DA:271(U):G:H2'	25:DA:271(V):G:H8	1.70	0.56
25:DA:652(B):A:N1	25:DA:655:A:H1'	2.20	0.56
28:DE:116:VAL:HG13	28:DE:122:PHE:HB2	1.87	0.56
33:DN:43:THR:N	33:DN:48:MET:SD	2.77	0.56
1:AA:1399:C:C2	1:AA:1502:A:N6	2.73	0.56
1:AA:185:A:H2'	1:AA:186:C:C6	2.41	0.56
24:AX:67:C:H2'	24:AX:68:C:H5'	1.87	0.56
46:B0:27:GLU:HG3	46:B0:68:GLU:HA	1.88	0.56
25:BA:1681:A:OP2	60:BA:3951:HOH:O	2.18	0.56
25:BA:733:G:OP1	53:B7:11:LYS:NZ	2.38	0.56
1:CA:1014:A:H4'	19:CS:14:HIS:CE1	2.41	0.56
25:DA:1443:G:H1	25:DA:1548:C:H42	1.53	0.56
25:DA:2379:G:H4'	38:DS:21:THR:HG21	1.88	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2727:G:O2'	34:DO:70:LYS:NZ	2.39	0.56
32:DI:31:LEU:HD21	32:DI:38:LEU:HG	1.88	0.56
1:AA:1030:C:N4	1:AA:1031:G:H1	2.02	0.56
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.86	0.56
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.41	0.56
2:AB:114:ARG:NH2	2:AB:117:GLU:OE2	2.39	0.56
25:BA:210:A:N1	25:BA:254:A:O2'	2.37	0.56
1:CA:1438:G:H2'	1:CA:1439:C:C6	2.41	0.56
1:CA:890:G:O2'	1:CA:906:G:O6	2.18	0.56
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.71	0.56
9:CI:23:ASN:HD22	9:CI:24:GLY:N	2.03	0.56
50:D4:59:PHE:HA	50:D4:61:ARG:N	2.21	0.56
25:DA:1786:A:OP1	60:DA:4235:HOH:O	2.18	0.56
30:DG:41:GLN:HG3	30:DG:60:LEU:HD21	1.87	0.56
30:DG:5:VAL:HG22	30:DG:8:LYS:H	1.70	0.56
1:AA:448:A:P	1:AA:485:G:H22	2.29	0.55
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.88	0.55
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.39	0.55
1:AA:520:A:O2'	12:AL:73:GLU:OE1	2.24	0.55
1:AA:742:G:H5'	15:AO:58:MET:HE3	1.89	0.55
16:AP:50:LYS:HZ3	16:AP:50:LYS:HA	1.72	0.55
25:BA:1766:G:H8	25:BA:1770:A:H62	1.52	0.55
25:BA:1827:U:H2'	25:BA:1828:C:C6	2.41	0.55
25:BA:2802:C:H1'	25:BA:2903:G:H22	1.70	0.55
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.21	0.55
1:CA:1162:C:N4	1:CA:1174:G:H1	2.04	0.55
1:CA:447:G:O6	1:CA:485:G:O2'	2.18	0.55
7:CG:148:ASN:HD22	7:CG:151:TYR:HD2	1.55	0.55
20:CT:54:LYS:HB2	20:CT:100:ILE:HD11	1.87	0.55
24:CX:75:C:OP1	60:CX:201:HOH:O	2.18	0.55
25:DA:1270:C:O2'	25:DA:1648:C:OP2	2.14	0.55
25:DA:2364:C:H2'	25:DA:2365:G:O4'	2.07	0.55
25:DA:61:G:H1	25:DA:94:C:H42	1.54	0.55
26:DB:55:U:O2'	30:DG:27:ASN:OD1	2.24	0.55
27:DD:17:THR:O	27:DD:211:ARG:NH2	2.39	0.55
36:DQ:62:GLY:HA2	45:DZ:116:VAL:HG21	1.88	0.55
1:AA:1279:A:H4'	1:AA:1281:U:H5	1.71	0.55
7:AG:47:CYS:HA	7:AG:50:ILE:HG12	1.89	0.55
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.70	0.55
25:BA:2121:U:H3	25:BA:2212:G:H1	1.54	0.55
25:BA:849:A:OP1	60:BA:4135:HOH:O	2.18	0.55
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.41	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.06	0.55
25:DA:186:G:H2'	25:DA:187:G:H8	1.71	0.55
25:DA:492:A:H2'	25:DA:493:G:O4'	2.07	0.55
25:DA:657:U:H2'	25:DA:658:C:C6	2.41	0.55
25:DA:2019:A:H4'	40:DU:34:LYS:HD2	1.88	0.55
45:DZ:152:ALA:HA	45:DZ:155:LEU:HD13	1.86	0.55
2:AB:198:ASP:N	2:AB:198:ASP:OD2	2.39	0.55
1:AA:1189:C:H5''	3:AC:5:ILE:HD12	1.89	0.55
14:AN:3:ARG:O	14:AN:7:ILE:N	2.38	0.55
25:BA:2744:G:H5''	28:BE:203:LYS:HE3	1.87	0.55
5:CE:93:PRO:O	8:CH:105:ARG:NH2	2.40	0.55
52:D6:21:TYR:CE2	52:D6:38:LYS:HG3	2.41	0.55
25:DA:2117:A:H61	25:DA:2171:A:H61	1.54	0.55
25:DA:2163:C:H5''	25:DA:2172:U:H5'	1.87	0.55
25:DA:527:C:OP1	60:DA:4386:HOH:O	2.18	0.55
27:DD:12:SER:HB3	27:DD:208:LYS:HB3	1.88	0.55
30:DG:63:ILE:HA	30:DG:143:GLU:HG3	1.88	0.55
33:DN:33:LEU:HB3	33:DN:52:VAL:HG21	1.88	0.55
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.07	0.55
1:AA:300:A:O2'	1:AA:564:C:N3	2.33	0.55
25:BA:605:G:H2'	25:BA:606:G:C8	2.41	0.55
35:BP:86:LYS:HB3	35:BP:118:GLY:HA3	1.87	0.55
44:BY:13:VAL:HG12	44:BY:74:PRO:HA	1.88	0.55
7:CG:16:LEU:HD13	9:CI:41:VAL:HG12	1.88	0.55
49:D3:6:VAL:HG22	49:D3:56:VAL:HG13	1.88	0.55
25:DA:1149:G:H2'	25:DA:1150:C:C6	2.41	0.55
25:DA:918:A:C5	25:DA:919:G:H1'	2.42	0.55
28:DE:163:GLU:HG2	28:DE:164:ARG:N	2.20	0.55
1:AA:1003:G:C2	1:AA:1004:A:N3	2.74	0.55
13:AM:49:THR:HB	13:AM:52:GLU:H	1.72	0.55
50:B4:53:GLU:C	50:B4:55:ARG:H	2.10	0.55
25:BA:1069:U:OP2	60:BA:4468:HOH:O	2.18	0.55
25:BA:1153:G:H2'	25:BA:1153:G:N3	2.22	0.55
44:BY:92:ASN:CB	44:BY:94:LYS:HG2	2.37	0.55
45:BZ:99:TYR:HB3	45:BZ:123:ASP:HB2	1.87	0.55
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.06	0.55
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.75	0.55
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.40	0.55
22:CV:22:U:H2'	22:CV:23:A:C8	2.41	0.55
25:DA:2074:U:H2'	25:DA:2075:U:C6	2.41	0.55
25:DA:587:C:OP1	35:DP:21:ARG:NH2	2.40	0.55
25:DA:848:G:H2'	25:DA:849:A:C8	2.41	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:926:A:H2'	25:DA:927:G:H8	1.71	0.55
32:DI:62:LYS:O	32:DI:66:GLU:HG2	2.06	0.55
33:DN:38:HIS:CE1	33:DN:39:ARG:HG3	2.41	0.55
45:DZ:55:HIS:HE1	45:DZ:135:GLU:HG3	1.71	0.55
4:AD:111:ALA:HB2	4:AD:120:LEU:HD12	1.88	0.55
6:AF:14:LEU:HB3	6:AF:18:GLN:HE22	1.71	0.55
26:BB:75:G:H8	26:BB:75:G:H5''	1.71	0.55
41:BV:65:GLY:HA3	41:BV:91:TYR:CZ	2.42	0.55
43:BX:41:ASN:O	43:BX:45:THR:HG22	2.06	0.55
8:CH:112:LEU:HA	8:CH:134:ILE:HG12	1.88	0.55
16:CP:28:ARG:NH1	16:CP:29:ASP:OD2	2.40	0.55
25:DA:1532:C:N4	25:DA:1537:G:O6	2.38	0.55
25:DA:2755:C:H3'	55:D9:19:ARG:HH21	1.72	0.55
26:DB:8:U:H3	26:DB:113:G:H1	1.54	0.55
25:DA:83:G:OP2	44:DY:95:LYS:NZ	2.39	0.55
45:DZ:145:GLU:H	45:DZ:148:ASP:HB2	1.72	0.55
1:AA:1095:U:OP1	1:AA:1108:G:N2	2.31	0.55
1:AA:428:G:OP2	4:AD:10:ARG:NH1	2.36	0.55
37:BR:90:ARG:NH2	37:BR:118:GLU:OXT	2.40	0.55
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.89	0.55
17:CQ:18:THR:HG23	17:CQ:69:LYS:HD3	1.88	0.55
25:DA:1019:U:OP1	25:DA:1035:U:O2'	2.18	0.55
9:AI:23:ASN:HD22	9:AI:23:ASN:H	1.55	0.55
25:BA:1219:A:H1'	25:BA:1220:U:H5''	1.89	0.55
25:BA:2804:C:H2'	25:BA:2805:G:C8	2.42	0.55
1:CA:1127:G:N2	1:CA:1147:C:H41	2.05	0.55
1:CA:297:G:N2	1:CA:300:A:OP2	2.39	0.55
4:CD:96:LEU:HD12	4:CD:139:ARG:HH21	1.71	0.55
24:CX:19:G:H4'	24:CX:20:U:OP2	2.06	0.55
24:CX:53:G:C5	24:CX:54:5MU:H72	2.41	0.55
30:DG:112:PRO:HB3	50:D4:35:VAL:HG22	1.87	0.55
25:DA:2821:A:H2'	25:DA:2822:G:C8	2.42	0.55
26:DB:13:A:C2	26:DB:16:G:H1'	2.42	0.55
1:AA:186:C:H2'	1:AA:187:C:C6	2.41	0.55
1:AA:942:G:H21	9:AI:124:GLN:NE2	2.04	0.55
4:AD:98:GLU:OE1	4:AD:107:ARG:NH1	2.40	0.55
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.07	0.55
10:AJ:16:LEU:HD22	10:AJ:68:HIS:HB2	1.89	0.55
13:AM:3:ARG:HD2	13:AM:9:ILE:HG13	1.88	0.55
15:AO:74:ASP:HB3	15:AO:77:ARG:HB2	1.87	0.55
25:BA:1683:C:O2'	25:BA:1791:A:N3	2.37	0.55
25:BA:704:U:H2'	25:BA:705:C:C6	2.42	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:630:U:OP1	29:BF:102:PRO:HA	2.06	0.55
1:CA:1028:C:N3	1:CA:1033:G:O6	2.40	0.55
55:D9:25:VAL:HB	55:D9:34:GLN:HB2	1.88	0.55
25:DA:2135:A:H2'	25:DA:2136:C:C6	2.41	0.55
25:DA:2406:U:OP1	60:DA:4156:HOH:O	2.18	0.55
25:DA:2526:G:H5'	25:DA:2742:C:O2'	2.07	0.55
26:DB:66:A:N6	26:DB:108:U:H3'	2.22	0.55
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.36	0.55
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.42	0.55
16:AP:22:THR:HA	16:AP:33:ILE:HG12	1.89	0.55
52:B6:6:ARG:NH1	52:B6:26:ASN:HB2	2.22	0.55
25:BA:354:A:H2	25:BA:1255:A:HO2'	1.54	0.55
25:BA:2859:U:OP2	39:BT:95:ARG:NH1	2.40	0.55
27:BD:12:SER:HB3	27:BD:208:LYS:HB3	1.88	0.55
26:BB:105:A:P	45:BZ:72:ARG:HH12	2.29	0.55
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.22	0.55
1:CA:1025:U:N3	1:CA:1036:G:N1	2.55	0.55
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.07	0.55
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.89	0.55
3:CC:156:ARG:H	3:CC:196:LEU:HD22	1.72	0.55
3:CC:43:LEU:HD21	3:CC:55:VAL:HG21	1.87	0.55
25:DA:1227:G:H2'	25:DA:1228:G:O4'	2.07	0.55
25:DA:391:G:O2'	25:DA:410:G:OP1	2.16	0.55
25:DA:979:G:H5''	25:DA:980:A:H5''	1.88	0.55
30:DG:83:ARG:N	30:DG:86:MET:SD	2.70	0.55
32:DI:130:TYR:CE2	32:DI:132:PRO:HB3	2.42	0.55
34:DO:63:VAL:HG11	34:DO:85:VAL:HG23	1.87	0.55
25:DA:1250:G:OP2	35:DP:21:ARG:NH1	2.40	0.55
45:DZ:6:LYS:HE3	45:DZ:43:GLU:OE1	2.07	0.55
1:AA:1095:U:P	1:AA:1108:G:H1	2.30	0.54
1:AA:954:G:H21	1:AA:1227:A:H62	1.55	0.54
2:AB:21:ARG:HB3	2:AB:38:GLY:O	2.07	0.54
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.88	0.54
12:AL:34:ARG:NH2	60:AL:301:HOH:O	2.39	0.54
24:AX:7:G:O2'	24:AX:49:G:H5'	2.07	0.54
25:BA:1091:A:OP1	25:BA:1092:A:H3'	2.06	0.54
25:BA:1153:G:N2	25:BA:1154:U:O4	2.40	0.54
31:BH:159:GLU:HG2	31:BH:169:VAL:HG11	1.89	0.54
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.88	0.54
25:DA:1561:G:H2'	25:DA:1562:A:C8	2.41	0.54
25:DA:2115:G:H1'	25:DA:2117:A:H62	1.71	0.54
25:DA:286:C:H2'	25:DA:287:C:C6	2.41	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.22	0.54
1:AA:270:A:H2'	1:AA:271:C:C6	2.41	0.54
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.90	0.54
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.89	0.54
1:CA:1288:A:N3	1:CA:1352:C:O2'	2.39	0.54
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.27	0.54
25:DA:1019:U:H3	25:DA:1142(A):A:N6	2.03	0.54
25:DA:2150:U:H2'	25:DA:2151:G:H8	1.73	0.54
26:DB:42:C:O2	30:DG:93:THR:N	2.34	0.54
30:DG:68:PRO:HG2	30:DG:90:LEU:HD22	1.89	0.54
35:DP:121:LYS:HG2	35:DP:122:PRO:HD2	1.89	0.54
1:AA:1112:C:O2	3:AC:179:ARG:HG3	2.06	0.54
24:AX:59:A:C2'	24:AX:60:U:H5'	2.38	0.54
47:B1:85:LEU:HB3	47:B1:89:GLU:HG3	1.88	0.54
25:BA:10:G:N2	25:BA:2813:G:OP1	2.40	0.54
25:BA:1426:G:N2	25:BA:1617:A:N1	2.54	0.54
25:BA:831:A:H5'	25:BA:832:G:OP1	2.08	0.54
36:BQ:18:LYS:O	36:BQ:98:LYS:NZ	2.21	0.54
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.23	0.54
1:CA:1442(A):G:C8	39:DT:118:ARG:HG2	2.42	0.54
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.05	0.54
4:CD:162:LEU:HD22	4:CD:178:VAL:HG13	1.87	0.54
23:CW:76:PPU:H92	25:DA:2584:U:H4'	1.90	0.54
25:DA:861:A:N3	26:DB:79:C:O2'	2.35	0.54
1:AA:347:G:H2'	1:AA:348:G:C8	2.42	0.54
1:AA:677:U:H3	1:AA:713:G:H22	1.56	0.54
13:AM:9:ILE:HB	13:AM:18:ALA:HB1	1.89	0.54
1:AA:1296:C:OP1	13:AM:44:ARG:NH2	2.40	0.54
24:AX:19:G:H4'	24:AX:20:U:OP2	2.07	0.54
25:BA:2132:G:OP2	25:BA:2140:U:N3	2.41	0.54
25:BA:2260:C:OP2	60:BA:4101:HOH:O	2.18	0.54
25:BA:609:A:H5'	29:BF:89:VAL:HG21	1.87	0.54
25:BA:927:G:H2'	25:BA:928:G:C8	2.42	0.54
1:CA:982:U:H4'	1:CA:983:A:O5'	2.08	0.54
12:CL:60:LEU:HD21	12:CL:66:VAL:HG22	1.89	0.54
50:D4:33:VAL:HG12	50:D4:35:VAL:H	1.71	0.54
25:DA:2136:C:O2'	25:DA:2137:C:O5'	2.21	0.54
25:DA:2139:C:H42	25:DA:2152:G:H1	1.56	0.54
26:DB:32:C:H42	26:DB:50:G:H1	1.55	0.54
30:DG:111:LEU:HA	30:DG:114:ILE:HG13	1.88	0.54
32:DI:40:THR:HG23	32:DI:43:ASN:ND2	2.22	0.54
44:DY:37:VAL:O	44:DY:67:LEU:N	2.40	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1039:C:H2'	1:AA:1040:U:O4'	2.06	0.54
1:AA:518:C:O2'	1:AA:1492:A:N6	2.37	0.54
2:AB:95:GLN:HG3	2:AB:147:LYS:HG2	1.88	0.54
5:AE:92:LYS:HD3	5:AE:119:LEU:HD12	1.90	0.54
1:AA:877:C:H5''	8:AH:88:LYS:HD3	1.89	0.54
25:BA:215:G:H21	25:BA:217:A:H62	1.54	0.54
25:BA:2702:C:OP1	37:BR:17:ARG:NH1	2.27	0.54
25:BA:482:C:H4'	60:BA:3733:HOH:O	2.08	0.54
1:CA:1275:A:H2'	1:CA:1276:G:O4'	2.08	0.54
1:CA:1330:U:H4'	13:CM:23:TYR:CZ	2.42	0.54
1:CA:981:U:O5'	1:CA:981:U:H6	1.90	0.54
3:CC:181:ASN:HD21	3:CC:204:LEU:HD12	1.72	0.54
25:DA:1446:C:H42	25:DA:1465:G:H1	1.56	0.54
25:DA:2314:C:H2'	25:DA:2315:G:C8	2.43	0.54
25:DA:218:A:C2	25:DA:235:U:H4'	2.43	0.54
25:DA:463:G:N2	25:DA:466:A:OP2	2.29	0.54
36:DQ:32:TYR:CE1	36:DQ:133:ARG:HG3	2.42	0.54
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.72	0.54
8:AH:83:ILE:HG13	8:AH:137:VAL:HG22	1.88	0.54
29:BF:149:ASP:OD1	29:BF:149:ASP:N	2.38	0.54
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.42	0.54
25:DA:1031:G:H5''	55:D9:8:LYS:HE3	1.89	0.54
25:DA:134:C:H2'	25:DA:135:G:C8	2.42	0.54
25:DA:2391:G:O2'	25:DA:2422:A:N7	2.41	0.54
25:DA:352:G:N2	25:DA:429:A:H5''	2.23	0.54
27:DD:10:THR:OG1	27:DD:13:ARG:HG2	2.07	0.54
32:DI:38:LEU:HB2	32:DI:40:THR:HG22	1.90	0.54
1:AA:159:G:H2'	1:AA:161:A:OP2	2.08	0.54
25:BA:1283:A:OP1	60:BA:4542:HOH:O	2.19	0.54
25:BA:934:A:O2'	25:BA:935:C:OP2	2.24	0.54
25:BA:2324:U:H5'	30:BG:88:ILE:HD11	1.89	0.54
38:BS:83:LYS:HG2	38:BS:111:GLU:HG3	1.88	0.54
1:CA:1298:C:OP2	7:CG:114:ARG:NH2	2.41	0.54
1:CA:1318:A:H5''	19:CS:3:ARG:NH2	2.22	0.54
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.43	0.54
5:CE:57:LYS:HG2	5:CE:61:TYR:HE2	1.73	0.54
25:DA:1609:A:OP2	60:DA:4280:HOH:O	2.18	0.54
25:DA:885:C:H3'	25:DA:886:C:H5''	1.90	0.54
28:DE:36:ARG:NH1	28:DE:85:ASN:OD1	2.41	0.54
31:DH:28:GLY:N	31:DH:31:GLY:O	2.41	0.54
37:DR:38:VAL:HG12	37:DR:42:LYS:HE3	1.89	0.54
38:DS:67:ARG:HG3	38:DS:71:ARG:HD2	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
41:DV:21:ARG:HG2	41:DV:91:TYR:CD2	2.43	0.54
1:AA:1106:G:H5''	3:AC:172:ARG:HG2	1.90	0.54
1:AA:147:G:H2'	1:AA:148:G:H8	1.71	0.54
12:AL:54:LYS:HD2	12:AL:54:LYS:N	2.23	0.54
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.90	0.54
26:BB:12:C:H2'	46:B0:73:GLY:HA3	1.90	0.54
25:BA:1639:G:H2'	25:BA:1640:G:C8	2.43	0.54
1:CA:1392:G:N2	1:CA:1502:A:H8	2.04	0.54
2:CB:217:ARG:HA	2:CB:220:ASP:HB2	1.90	0.54
7:CG:51:GLN:HA	7:CG:55:GLY:HA2	1.90	0.54
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.89	0.54
25:DA:459:U:H5''	53:D7:40:TRP:CD2	2.43	0.54
28:DE:72:VAL:HG13	28:DE:73:GLU:O	2.08	0.54
31:DH:69:ARG:HG3	31:DH:70:THR:N	2.23	0.54
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.90	0.54
13:AM:65:LYS:O	13:AM:70:LEU:HD12	2.08	0.54
21:AU:12:LYS:HB3	21:AU:22:ARG:HD2	1.90	0.54
25:BA:2190:G:C6	25:BA:2193:A:C8	2.95	0.54
25:BA:895:G:H2'	25:BA:896:A:C8	2.42	0.54
27:BD:71:ASP:CB	27:BD:103:ARG:HH22	2.19	0.54
28:BE:174:ASP:OD1	28:BE:175:VAL:N	2.41	0.54
1:CA:156:G:N2	1:CA:165:C:O2	2.40	0.54
2:CB:91:PRO:HG3	2:CB:154:LEU:HB3	1.89	0.54
1:CA:1376:U:H3'	7:CG:94:ARG:HH21	1.72	0.54
25:DA:1023:U:OP2	60:DA:4482:HOH:O	2.18	0.54
25:DA:2042:A:OP1	60:DA:4137:HOH:O	2.19	0.54
25:DA:2173:A:OP2	25:DA:2173:A:H3'	2.08	0.54
27:DD:182:LEU:HB2	27:DD:272:ALA:HB3	1.89	0.54
25:BA:1467:G:O2'	25:BA:1540:A:N6	2.41	0.54
25:BA:2053:A:C6	25:BA:2510:C:H1'	2.43	0.54
25:BA:36:G:N3	25:BA:476:G:O2'	2.40	0.54
26:BB:50:G:OP1	38:BS:63:THR:OG1	2.26	0.54
34:BO:80:ASP:OD2	39:BT:64:ARG:NH2	2.41	0.54
1:CA:598:U:H2'	1:CA:599:C:C6	2.43	0.54
13:CM:65:LYS:NZ	50:D4:53:GLU:OE1	2.33	0.54
25:DA:1169:G:H1	25:DA:1180:C:N4	1.92	0.54
25:DA:1509(B):A:H2'	25:DA:1510:G:C8	2.42	0.54
25:DA:1894:C:H2'	25:DA:1895:C:H6	1.72	0.54
25:DA:2086:U:H2'	25:DA:2087:G:C8	2.42	0.54
1:AA:164:U:H2'	1:AA:165:C:C6	2.42	0.53
1:AA:299:G:H2'	1:AA:300:A:C8	2.43	0.53
1:AA:662:G:O2'	1:AA:836:G:OP1	2.26	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1099:G:OP2	2:AB:144:ARG:NH2	2.40	0.53
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.44	0.53
28:BE:2:LYS:NZ	28:BE:95:ILE:O	2.40	0.53
41:BV:98:GLU:OE1	41:BV:100:ARG:NH1	2.37	0.53
45:BZ:7:ALA:HB3	45:BZ:61:LEU:HD12	1.90	0.53
1:CA:1120:G:C6	1:CA:1121:U:C4	2.96	0.53
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.07	0.53
4:CD:88:VAL:HG22	5:CE:96:PRO:HB2	1.90	0.53
15:CO:87:ILE:HG22	15:CO:88:ARG:N	2.23	0.53
49:D3:6:VAL:HG13	49:D3:56:VAL:HG22	1.90	0.53
25:DA:1031:G:H21	55:D9:36:GLN:HE22	1.56	0.53
25:DA:1114:G:H2'	25:DA:1115:G:C8	2.42	0.53
25:DA:2588:G:OP1	60:DA:4367:HOH:O	2.18	0.53
27:DD:69:ARG:NH2	27:DD:128:GLY:O	2.42	0.53
30:DG:115:ARG:HG3	30:DG:136:ARG:HH21	1.73	0.53
25:DA:871:U:OP1	36:DQ:5:ARG:HG2	2.08	0.53
40:DU:83:LEU:HD12	40:DU:88:ILE:HB	1.90	0.53
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.33	0.53
25:BA:1417:G:H2'	25:BA:1418:U:H5	1.73	0.53
25:BA:2902:G:H4'	25:BA:2903:G:O5'	2.08	0.53
25:BA:553:A:C2	25:BA:2065:C:H4'	2.43	0.53
25:BA:572:A:O2'	25:BA:573:G:OP1	2.23	0.53
25:BA:672:G:H8	25:BA:672:G:O5'	1.91	0.53
33:BN:58:ASP:OD1	33:BN:58:ASP:N	2.41	0.53
1:CA:1244:C:N4	1:CA:1293:G:H1	2.04	0.53
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.42	0.53
1:CA:977:A:N1	1:CA:1224:G:N7	2.55	0.53
1:CA:1080:A:H5'	5:CE:14:ARG:HH21	1.73	0.53
10:CJ:43:ARG:HB2	10:CJ:67:THR:HG23	1.90	0.53
12:CL:113:ARG:NH2	60:CL:201:HOH:O	2.41	0.53
16:CP:21:VAL:HG22	16:CP:33:ILE:HB	1.89	0.53
24:CX:19:G:H1	24:CX:56:C:N4	2.03	0.53
25:DA:1427:A:H4'	25:DA:1428:C:O5'	2.08	0.53
25:DA:7:G:H2'	25:DA:8:A:H8	1.73	0.53
1:AA:184:G:H2'	1:AA:185:A:H8	1.72	0.53
9:AI:20:ARG:O	9:AI:60:ASP:N	2.42	0.53
25:BA:1451:U:H2'	25:BA:1452:U:C6	2.44	0.53
25:BA:302:A:O2'	25:BA:303:C:OP1	2.24	0.53
1:CA:412:A:O4'	4:CD:35:ARG:NH2	2.41	0.53
1:CA:920:U:H2'	1:CA:921:U:C6	2.43	0.53
1:CA:991:U:HO2'	1:CA:992:U:P	2.31	0.53
2:CB:178:ARG:NH1	2:CB:196:LEU:O	2.41	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:CD:175:SER:OG	4:CD:184:LYS:HB2	2.07	0.53
9:CI:99:LEU:HB3	9:CI:101:PHE:HE1	1.73	0.53
15:CO:54:ARG:HG2	15:CO:58:MET:HE2	1.89	0.53
48:D2:1:MET:HB2	48:D2:52:ASP:OD1	2.09	0.53
25:DA:1653:G:H3'	37:DR:2:ARG:HD3	1.89	0.53
25:DA:2156:G:H5''	25:DA:2157:G:OP2	2.08	0.53
25:DA:7:G:H1	25:DA:2896:C:N4	2.06	0.53
25:DA:797:C:H2'	25:DA:798:G:O4'	2.08	0.53
32:DI:56:LYS:O	32:DI:60:GLU:N	2.40	0.53
1:AA:1253:G:H1	1:AA:1284:C:H42	1.55	0.53
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.89	0.53
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.91	0.53
9:AI:86:VAL:HG13	9:AI:96:LEU:HD12	1.91	0.53
25:BA:956:A:H62	36:BQ:12:GLN:HA	1.73	0.53
28:BE:47:VAL:HG12	28:BE:49:LEU:HD12	1.89	0.53
1:CA:1013:G:N2	1:CA:1015:A:H3'	2.23	0.53
2:CB:216:SER:O	2:CB:220:ASP:N	2.42	0.53
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.90	0.53
13:CM:19:LEU:HD21	13:CM:56:LEU:HD21	1.90	0.53
24:CX:16:C:H3'	24:CX:17:C:O2	2.08	0.53
25:DA:212:G:H2'	25:DA:213:A:O4'	2.07	0.53
25:DA:2698:U:H2'	25:DA:2699:C:C6	2.44	0.53
25:DA:903:C:H2'	25:DA:904:C:C6	2.43	0.53
26:DB:90:A:C5	26:DB:91:C:H1'	2.43	0.53
41:DV:8:GLY:O	41:DV:10:LYS:NZ	2.41	0.53
1:AA:167:G:H2'	1:AA:168:G:C8	2.43	0.53
46:B0:40:GLN:HE21	46:B0:57:PHE:HB3	1.74	0.53
25:BA:2133:C:N3	25:BA:2167:C:O2'	2.38	0.53
31:BH:117:PRO:HG3	31:BH:123:PHE:CD2	2.44	0.53
43:BX:50:LYS:N	43:BX:87:GLN:OE1	2.41	0.53
1:CA:1023:G:H3'	1:CA:1024:G:H8	1.73	0.53
1:CA:1000:U:H3	1:CA:1041:A:H61	1.55	0.53
1:CA:337:C:H2'	1:CA:338:A:C8	2.44	0.53
1:CA:406:G:H2'	1:CA:407:G:H8	1.73	0.53
5:CE:33:VAL:HA	5:CE:43:LEU:HA	1.90	0.53
25:DA:1120:G:H2'	25:DA:1121:C:O4'	2.09	0.53
26:DB:24:G:H5'	26:DB:25:A:N7	2.24	0.53
27:DD:242:ARG:N	27:DD:242:ARG:HD3	2.23	0.53
25:DA:2312:U:H5'	30:DG:88:ILE:HD11	1.91	0.53
42:DW:88:ARG:NH1	42:DW:94:ASP:OD2	2.38	0.53
44:DY:23:ARG:HG2	44:DY:42:VAL:HG22	1.90	0.53
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.41	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:AX:66:C:H2'	24:AX:67:C:O4'	2.07	0.53
54:B8:39:LYS:O	54:B8:43:GLN:HG3	2.09	0.53
25:BA:2430:A:H2'	25:BA:2431:U:C6	2.43	0.53
25:BA:601:A:OP2	60:BA:3879:HOH:O	2.19	0.53
31:BH:102:ALA:HA	31:BH:117:PRO:HD3	1.91	0.53
32:BI:93:THR:H	32:BI:96:ASP:CG	2.12	0.53
34:BO:79:PHE:CD1	39:BT:72:VAL:HG22	2.44	0.53
44:BY:7:VAL:HG21	44:BY:72:VAL:HG12	1.89	0.53
1:CA:1023:G:C4	1:CA:1024:G:C8	2.97	0.53
1:CA:67:C:H2'	1:CA:68:G:C8	2.44	0.53
6:CF:14:LEU:HD22	6:CF:18:GLN:HB2	1.91	0.53
9:CI:99:LEU:HB3	9:CI:101:PHE:CE1	2.44	0.53
11:CK:58:PRO:O	11:CK:62:GLN:N	2.41	0.53
14:CN:48:ALA:HB2	14:CN:53:LEU:HD12	1.90	0.53
25:DA:10:G:H2'	25:DA:11:G:C8	2.44	0.53
25:DA:1449:A:HO2'	25:DA:1529:G:N2	2.01	0.53
25:DA:2218:U:N3	47:D1:55:GLY:O	2.42	0.53
25:DA:197:A:N6	25:DA:2430:A:O2'	2.41	0.53
29:DF:157:VAL:HB	29:DF:194:MET:HG2	1.90	0.53
30:DG:136:ARG:HD2	30:DG:137:GLU:N	2.23	0.53
1:AA:1027:C:N3	1:AA:1034:G:C6	2.76	0.53
1:AA:1168:A:H2'	1:AA:1169:A:C8	2.43	0.53
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.90	0.53
6:AF:20:ALA:O	6:AF:24:GLU:N	2.39	0.53
1:CA:975:A:N6	1:CA:1367:C:O4'	2.42	0.53
21:CU:12:LYS:HB3	21:CU:22:ARG:HD2	1.91	0.53
53:D7:12:ARG:HD3	53:D7:46:VAL:HB	1.91	0.53
25:DA:2136:C:O2'	25:DA:2137:C:H6	1.91	0.53
25:DA:2302:G:H2'	25:DA:2303:G:H5'	1.90	0.53
25:DA:806:C:O2	25:DA:2444:G:O2'	2.27	0.53
26:DB:70:C:H2'	26:DB:71:C:H6	1.73	0.53
26:DB:95:C:H2'	26:DB:96:U:H6	1.73	0.53
2:AB:119:GLU:OE2	2:AB:153:ARG:NH2	2.38	0.53
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	1.91	0.53
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.09	0.53
51:B5:16:ARG:HG3	51:B5:17:ASP:N	2.23	0.53
25:BA:1760:U:H2'	25:BA:1761:G:C8	2.42	0.53
40:BU:50:ARG:HG2	40:BU:53:ARG:NH2	2.23	0.53
1:CA:411:A:OP1	4:CD:30:LYS:NZ	2.26	0.53
4:CD:199:ASN:HB3	4:CD:202:LEU:HG	1.91	0.53
7:CG:138:LYS:HD3	7:CG:139:GLU:HG3	1.91	0.53
25:DA:2163:C:OP1	25:DA:2165:G:N2	2.42	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:220:G:O2'	25:DA:233:A:N3	2.37	0.53
25:DA:495:G:N3	42:DW:61:ASN:ND2	2.56	0.53
25:DA:642:G:H21	25:DA:646:A:H2	1.56	0.53
26:DB:2:C:H2'	26:DB:3:C:C6	2.44	0.53
28:DE:52:LEU:HD22	28:DE:77:ILE:HD11	1.90	0.53
25:DA:2547:U:O2	34:DO:23:ARG:NH2	2.41	0.53
45:DZ:102:LEU:HD11	45:DZ:124:ILE:HB	1.91	0.53
1:AA:826:C:H2'	1:AA:827:U:C6	2.44	0.53
11:AK:62:GLN:O	11:AK:66:LEU:HG	2.09	0.53
24:AX:4:G:H2'	24:AX:5:G:C8	2.44	0.53
25:BA:2283:G:C5'	46:B0:20:ARG:HE	2.22	0.53
25:BA:920:G:H1	25:BA:950:C:H42	1.57	0.53
28:BE:9:VAL:HB	39:BT:3:ARG:HG2	1.91	0.53
33:BN:34:LEU:HD21	33:BN:120:LEU:HB2	1.91	0.53
36:BQ:109:VAL:HG22	36:BQ:113:GLN:OE1	2.09	0.53
45:BZ:151:HIS:O	45:BZ:153:SER:N	2.42	0.53
1:CA:1004:A:H5'	1:CA:1024:G:H22	1.73	0.53
1:CA:1268:A:H2'	1:CA:1269:A:C8	2.44	0.53
2:CB:208:ILE:O	2:CB:212:GLN:HB2	2.09	0.53
5:CE:34:VAL:N	5:CE:42:GLY:O	2.27	0.53
1:CA:600:C:H5''	8:CH:129:VAL:HA	1.89	0.53
25:DA:2103:C:C2'	25:DA:2104:G:H5'	2.39	0.53
23:CW:76:PPU:O2'	25:DA:2585:U:O4	2.18	0.53
25:DA:2695:C:H2'	25:DA:2696:U:C6	2.44	0.53
25:DA:2886:G:H2'	25:DA:2887:U:H6	1.74	0.53
25:DA:963:U:OP1	60:DA:4035:HOH:O	2.19	0.53
26:DB:68:C:H2'	26:DB:69:G:H8	1.73	0.53
37:DR:29:LEU:HD23	37:DR:70:LEU:HD11	1.89	0.53
1:AA:1216:G:H5''	14:AN:5:ALA:HB2	1.90	0.53
1:AA:714:G:H2'	1:AA:715:A:C8	2.44	0.53
1:AA:661:G:H1	1:AA:744:C:H42	1.55	0.53
36:BQ:82:ARG:CZ	46:B0:4:LYS:HE3	2.39	0.53
25:BA:2124:U:H3	25:BA:2209:G:H1	1.56	0.53
25:BA:231:G:O2'	25:BA:243:G:O6	2.25	0.53
25:BA:2801:C:OP1	28:BE:61:ARG:NH2	2.42	0.53
30:BG:41:GLN:HG3	30:BG:60:LEU:HD21	1.91	0.53
32:BI:104:GLN:C	32:BI:106:GLY:H	2.11	0.53
45:BZ:29:TYR:HA	45:BZ:33:LEU:HD12	1.90	0.53
1:CA:589:C:C2'	1:CA:590:C:H5'	2.39	0.53
1:CA:985:C:H2'	1:CA:986:A:H8	1.73	0.53
10:CJ:51:ARG:HD3	14:CN:45:ARG:NH2	2.23	0.53
24:CX:10:G:O6	24:CX:25:C:N3	2.42	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:140:G:N2	25:DA:1596:A:H4'	2.24	0.53
25:DA:2116:G:N7	25:DA:2166:G:N2	2.44	0.53
25:DA:253:C:OP2	54:D8:5:LYS:NZ	2.33	0.53
25:DA:2725:A:H1'	25:DA:2726:U:H2'	1.90	0.53
25:DA:2032:G:H1'	28:DE:145:LYS:HD3	1.91	0.53
1:AA:765:G:N1	1:AA:812:C:O2'	2.40	0.52
12:AL:25:PRO:HG2	12:AL:97:ARG:HH21	1.74	0.52
13:AM:88:ARG:HG3	13:AM:98:VAL:HG11	1.91	0.52
54:B8:40:GLU:HG2	54:B8:44:LYS:HE2	1.90	0.52
25:BA:2660:C:H2'	25:BA:2661:U:C6	2.44	0.52
25:BA:596:G:O2'	25:BA:597:C:H3'	2.09	0.52
28:BE:28:ALA:HB3	28:BE:93:VAL:HG12	1.89	0.52
43:BX:27:THR:HG23	43:BX:80:ILE:HG13	1.90	0.52
13:CM:50:GLU:HG2	13:CM:54:VAL:HG13	1.91	0.52
13:CM:65:LYS:HB2	50:D4:50:VAL:HG21	1.91	0.52
19:CS:28:LYS:HB2	19:CS:29:ARG:CB	2.39	0.52
25:DA:2203:U:H2'	25:DA:2205:C:H6	1.73	0.52
25:DA:2378:A:H4'	38:DS:23:ARG:HD2	1.90	0.52
25:DA:538:G:H2'	25:DA:539:G:H8	1.73	0.52
36:DQ:37:LEU:HD21	36:DQ:130:LYS:HE2	1.91	0.52
41:DV:40:LEU:HB2	41:DV:46:VAL:HG13	1.90	0.52
45:DZ:7:ALA:HB3	45:DZ:61:LEU:HD12	1.91	0.52
1:AA:57:G:H2'	1:AA:58:C:C6	2.45	0.52
1:AA:673:G:H1	1:AA:717:C:H42	1.56	0.52
2:AB:7:VAL:HG11	2:AB:221:LEU:HD22	1.91	0.52
1:AA:619:U:N3	4:AD:134:ASP:OD1	2.37	0.52
10:AJ:65:LEU:HD13	14:AN:56:VAL:HG22	1.91	0.52
25:BA:2096:U:OP1	60:BA:4051:HOH:O	2.18	0.52
25:BA:908:A:OP2	60:BA:4253:HOH:O	2.19	0.52
34:BO:115:VAL:HG13	34:BO:121:VAL:HG21	1.90	0.52
1:CA:626:U:H2'	1:CA:627:G:H5''	1.92	0.52
16:CP:52:ASP:O	16:CP:54:GLU:N	2.37	0.52
25:DA:1359:A:H2'	25:DA:1360:A:H5'	1.91	0.52
25:DA:1913:A:H4'	25:DA:1914:C:C5'	2.39	0.52
26:DB:101:G:H2'	26:DB:102:A:O4'	2.09	0.52
1:AA:922:G:N3	1:AA:1398:A:H2	2.06	0.52
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.92	0.52
8:AH:84:ARG:NH1	8:AH:136:GLU:OE2	2.42	0.52
9:AI:85:LEU:HB3	9:AI:92:TYR:CD2	2.45	0.52
25:BA:868:A:O2'	25:BA:991:G:OP2	2.13	0.52
1:CA:1024:G:H2'	1:CA:1025:U:H5''	1.90	0.52
1:CA:1053:G:N7	1:CA:1200:C:H5''	2.24	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1342:C:H1'	9:CI:124:GLN:NE2	2.23	0.52
1:CA:955:U:O4	1:CA:1225:A:N1	2.42	0.52
4:CD:3:ARG:HD3	4:CD:118:ARG:HD3	1.91	0.52
1:CA:1328:C:O2'	13:CM:29:ARG:NH2	2.42	0.52
25:DA:1186:G:C2	25:DA:1187:G:H1'	2.44	0.52
25:DA:2376:A:H3'	25:DA:2377:A:H8	1.74	0.52
30:DG:122:PRO:HG3	30:DG:180:PHE:HB3	1.91	0.52
2:AB:212:GLN:O	2:AB:216:SER:OG	2.17	0.52
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.44	0.52
8:AH:45:ILE:HG21	8:AH:61:VAL:HG13	1.91	0.52
25:BA:2045:G:H5'	25:BA:2629:C:H4'	1.92	0.52
25:BA:2164:C:H2'	25:BA:2165:C:C6	2.44	0.52
1:CA:1002:G:C2	1:CA:1003:G:H8	2.27	0.52
1:CA:1004:A:H62	1:CA:1037:C:H3'	1.75	0.52
1:CA:258:G:H1	1:CA:268:C:H42	1.58	0.52
1:CA:76:C:N3	1:CA:93:G:N2	2.47	0.52
3:CC:8:ILE:HG23	3:CC:16:ARG:HG2	1.90	0.52
9:CI:47:LEU:HB3	9:CI:50:LEU:HD12	1.91	0.52
13:CM:23:TYR:HE1	13:CM:70:LEU:HD22	1.73	0.52
24:CX:52:G:H2'	24:CX:53:G:C8	2.42	0.52
25:DA:2172:U:O2'	25:DA:2173:A:O5'	2.26	0.52
25:DA:2345:G:H5'	25:DA:2347:C:O4'	2.09	0.52
25:DA:2261:C:H1'	25:DA:2388:A:N3	2.23	0.52
27:DD:264:LYS:O	27:DD:267:SER:OG	2.27	0.52
30:DG:32:PRO:HB2	30:DG:172:LEU:HD22	1.92	0.52
26:DB:92:C:H5''	45:DZ:79:ARG:HH22	1.73	0.52
1:AA:1260:C:O5'	1:AA:1284:C:H4'	2.10	0.52
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.91	0.52
25:BA:1511:C:H2'	25:BA:1512:G:C8	2.45	0.52
25:BA:2149:G:N2	25:BA:2195:A:H1'	2.25	0.52
1:CA:1118:C:N3	1:CA:1156:G:N2	2.57	0.52
1:CA:1286:A:H2	21:CU:18:TYR:HH	1.58	0.52
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.45	0.52
1:CA:187:C:O2'	20:CT:89:ARG:NH2	2.38	0.52
1:CA:835:U:H3	1:CA:851:G:H1	1.56	0.52
5:CE:93:PRO:HG2	8:CH:105:ARG:NE	2.25	0.52
13:CM:23:TYR:CE1	13:CM:70:LEU:HD22	2.43	0.52
24:CX:23:C:H2'	24:CX:24:U:C6	2.40	0.52
25:DA:2556:C:H2'	25:DA:2557:G:O4'	2.09	0.52
35:DP:97:PRO:HD3	35:DP:126:VAL:O	2.10	0.52
45:DZ:45:ASP:O	45:DZ:49:ARG:HG3	2.10	0.52
1:AA:269:C:H2'	1:AA:270:A:C8	2.44	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.44	0.52
25:BA:2108:U:H2'	25:BA:2109:G:C8	2.45	0.52
30:BG:108:ASN:N	30:BG:108:ASN:OD1	2.41	0.52
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.10	0.52
1:CA:922:G:N3	1:CA:1398:A:H2	2.08	0.52
1:CA:757:U:H2'	1:CA:758:G:O4'	2.09	0.52
1:CA:985:C:N4	1:CA:1220:G:H1	2.06	0.52
4:CD:31:CYS:O	4:CD:35:ARG:HG3	2.10	0.52
9:CI:23:ASN:ND2	9:CI:25:LYS:H	2.08	0.52
1:CA:1226:C:OP2	13:CM:91:ARG:NH2	2.43	0.52
14:CN:47:LEU:HD12	14:CN:53:LEU:HD21	1.92	0.52
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.22	0.52
24:CX:7:G:O2'	24:CX:49:G:H5'	2.09	0.52
25:DA:236:C:H2'	25:DA:237:C:C6	2.45	0.52
25:DA:224:G:N7	25:DA:420:C:H4'	2.24	0.52
25:DA:514:A:N3	25:DA:581:C:O2'	2.40	0.52
25:DA:857:C:OP2	46:D0:77:ARG:NH2	2.41	0.52
29:DF:110:LEU:HD21	29:DF:181:LEU:HG	1.92	0.52
31:DH:103:LEU:HD13	31:DH:125:VAL:HG21	1.92	0.52
35:DP:1:MET:HG2	35:DP:5:ASP:HB2	1.91	0.52
1:AA:630:G:H2'	1:AA:631:G:C8	2.43	0.52
2:AB:118:LEU:HD21	2:AB:138:LEU:HD22	1.92	0.52
4:AD:3:ARG:HD3	4:AD:118:ARG:HD2	1.92	0.52
5:AE:145:LYS:O	5:AE:149:GLU:HG2	2.09	0.52
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.45	0.52
24:AX:49:G:H1	24:AX:65:C:N4	2.04	0.52
46:B0:46:LYS:NZ	46:B0:75:LEU:O	2.42	0.52
26:BB:12:C:O2'	46:B0:74:ARG:HG2	2.09	0.52
25:BA:2504:U:H2'	25:BA:2505:U:H6	1.74	0.52
25:BA:929:G:H1	25:BA:940:C:H42	1.55	0.52
32:BI:60:GLU:HG3	32:BI:61:ARG:HH12	1.75	0.52
35:BP:97:PRO:HD3	35:BP:126:VAL:O	2.10	0.52
25:BA:997:G:OP1	36:BQ:16:ARG:NH2	2.43	0.52
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.25	0.52
1:CA:593:G:H1	1:CA:646:U:H3	1.58	0.52
2:CB:207:ALA:O	2:CB:210:SER:HB3	2.09	0.52
4:CD:63:LYS:O	4:CD:67:ILE:HG13	2.10	0.52
25:DA:1639:U:OP1	60:DA:4253:HOH:O	2.19	0.52
25:DA:2518:A:OP2	60:DA:4239:HOH:O	2.19	0.52
27:DD:148:GLU:HB2	27:DD:151:LYS:HD2	1.92	0.52
28:DE:67:PHE:HB3	28:DE:72:VAL:HG12	1.91	0.52
29:DF:130:ALA:H	29:DF:142:TRP:HD1	1.57	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
39:DT:53:ARG:HB3	39:DT:53:ARG:HH11	1.75	0.52
1:AA:1346:A:O2'	7:AG:10:ARG:NH2	2.43	0.52
1:AA:737:A:H5''	6:AF:92:LYS:HG3	1.91	0.52
50:B4:44:THR:OG1	50:B4:47:GLN:OE1	2.28	0.52
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.44	0.52
1:CA:1329:A:H5'	13:CM:29:ARG:HG3	1.91	0.52
1:CA:946:A:O2'	1:CA:1333:A:N3	2.31	0.52
25:DA:1264:G:H2'	25:DA:2014:A:N6	2.24	0.52
25:DA:2142:C:H2'	25:DA:2143:C:O4'	2.09	0.52
26:DB:37:C:N3	26:DB:48:A:O2'	2.42	0.52
34:DO:76:ALA:HB3	39:DT:75:ILE:HB	1.92	0.52
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.10	0.52
1:AA:158:G:H21	1:AA:162:A:N6	2.08	0.52
4:AD:188:LEU:H	4:AD:188:LEU:CD2	2.23	0.52
25:BA:1355:G:P	53:B7:9:ARG:HD3	2.50	0.52
25:BA:1957:G:H1'	25:BA:1986:G:N2	2.25	0.52
27:BD:132:PRO:HD3	27:BD:190:TYR:CZ	2.45	0.52
29:BF:155:LEU:HB2	29:BF:189:THR:HG21	1.92	0.52
1:CA:409:G:H1	1:CA:433:C:H42	1.58	0.52
1:CA:972:C:OP2	10:CJ:57:LYS:HE2	2.10	0.52
1:CA:975:A:N6	10:CJ:60:ARG:HH12	2.08	0.52
19:CS:27:GLU:HG2	19:CS:47:HIS:CE1	2.44	0.52
21:CU:3:LYS:HD3	21:CU:14:TRP:CD1	2.45	0.52
25:DA:2400:G:O3'	52:D6:18:ARG:NH1	2.43	0.52
25:DA:1742:G:H2'	25:DA:1743:C:C6	2.45	0.52
25:DA:2166:G:H2'	25:DA:2167:U:C2	2.44	0.52
25:DA:2752:C:H3'	25:DA:2753:A:H8	1.75	0.52
25:DA:479:A:H4'	25:DA:480:A:OP1	2.09	0.52
30:DG:167:GLU:N	30:DG:167:GLU:OE1	2.39	0.52
36:DQ:36:ALA:HB2	36:DQ:103:MET:SD	2.50	0.52
38:DS:44:LYS:H	38:DS:44:LYS:HZ2	1.58	0.52
39:DT:77:PRO:HB2	39:DT:80:SER:HB2	1.90	0.52
1:AA:1445:C:H42	1:AA:1457:G:H1	1.56	0.52
1:AA:693:G:H2'	1:AA:694:A:C8	2.45	0.52
3:AC:36:ASP:OD1	3:AC:59:ARG:NH2	2.34	0.52
17:AQ:59:ILE:HG22	17:AQ:73:VAL:HA	1.91	0.52
25:BA:1296:G:N7	35:BP:18:ARG:NH2	2.58	0.52
25:BA:2220:A:H4'	25:BA:2221:A:OP1	2.10	0.52
1:CA:998:G:H1	1:CA:1043:C:H42	1.58	0.52
3:CC:66:VAL:HG21	3:CC:91:LEU:HD21	1.92	0.52
13:CM:10:PRO:HG2	13:CM:21:TYR:CD2	2.44	0.52
25:DA:1753:G:OP1	39:DT:95:ARG:HD3	2.09	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:817:C:H2'	25:DA:818:G:O4'	2.10	0.52
1:AA:1277:C:HO2'	1:AA:1279:A:H8	1.57	0.51
1:AA:1457:G:H2'	1:AA:1458:G:C8	2.45	0.51
1:AA:1503:A:H1'	22:AV:13:A:H61	1.75	0.51
1:AA:631:G:H2'	1:AA:632:A:C8	2.45	0.51
1:AA:730:G:H5''	1:AA:731:G:OP2	2.09	0.51
25:BA:231:G:C8	54:B8:5:LYS:HG2	2.44	0.51
25:BA:2145:G:H1	25:BA:2197:C:N4	2.07	0.51
25:BA:2581:G:O6	60:BA:4451:HOH:O	2.19	0.51
25:BA:2840:G:OP1	28:BE:76:ARG:NH2	2.43	0.51
25:BA:736:A:N3	25:BA:826:U:O2'	2.39	0.51
25:BA:843:C:H2'	25:BA:844:C:C6	2.45	0.51
25:BA:987:G:OP2	35:BP:39:LYS:NZ	2.31	0.51
43:BX:49:VAL:HG11	43:BX:89:ILE:HG12	1.92	0.51
1:CA:1251:A:O2'	1:CA:1369:C:O2'	2.21	0.51
1:CA:1316:G:H4'	14:CN:18:VAL:HG13	1.92	0.51
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.26	0.51
1:CA:838:G:H1	1:CA:848:C:N4	2.08	0.51
1:CA:959:A:O2'	1:CA:984:C:O2'	2.20	0.51
25:DA:1024:G:C8	25:DA:1025:G:H2'	2.45	0.51
25:DA:1248:G:C5	40:DU:3:ARG:HB2	2.45	0.51
25:DA:1796:U:H2'	25:DA:1797:C:C6	2.45	0.51
25:DA:18:C:H2'	25:DA:19:C:C6	2.46	0.51
25:DA:455:C:N3	25:DA:472:A:H2'	2.25	0.51
25:DA:658:C:H2'	25:DA:659:C:C6	2.44	0.51
29:DF:150:GLY:HA2	29:DF:172:TRP:CD2	2.45	0.51
31:DH:159:GLU:HG2	31:DH:169:VAL:HG11	1.92	0.51
39:DT:59:THR:HG23	39:DT:78:LEU:HB3	1.92	0.51
1:AA:193:C:H2'	1:AA:194:C:C6	2.45	0.51
1:AA:689:C:OP1	11:AK:27:ASN:ND2	2.38	0.51
24:AX:6:G:H1	24:AX:67:C:H42	1.58	0.51
50:B4:48:ARG:NH1	50:B4:48:ARG:HA	2.24	0.51
25:BA:1735:U:O2	25:BA:1747:A:H5'	2.10	0.51
25:BA:2015:U:H4'	28:BE:128:SER:HB3	1.92	0.51
25:BA:2579:G:H2'	25:BA:2580:C:C6	2.45	0.51
25:BA:2748:G:H2'	25:BA:2749:G:C8	2.45	0.51
28:BE:143:ASN:HD22	28:BE:147:PRO:HD2	1.75	0.51
41:BV:76:LYS:HB2	41:BV:81:TYR:HB3	1.90	0.51
1:CA:344:A:H4'	1:CA:345:C:OP2	2.10	0.51
1:CA:540:G:H2'	1:CA:541:G:C8	2.45	0.51
3:CC:50:ALA:HB1	3:CC:72:LYS:O	2.10	0.51
14:CN:12:ARG:HG2	14:CN:13:THR:N	2.26	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2206:G:H5''	25:DA:2207:G:N7	2.25	0.51
27:DD:164:GLN:NE2	27:DD:166:GLN:OE1	2.41	0.51
1:AA:1130:A:H5'	9:AI:18:PHE:CE2	2.46	0.51
1:AA:324:G:OP1	20:AT:22:ARG:NE	2.38	0.51
2:AB:142:LEU:O	2:AB:146:GLN:N	2.31	0.51
8:AH:112:LEU:HB3	8:AH:133:LEU:HA	1.91	0.51
12:AL:53:ARG:HG2	12:AL:69:TYR:CE1	2.45	0.51
20:AT:47:GLY:HA2	20:AT:48:LYS:HB2	1.91	0.51
25:BA:1312:G:O5'	42:BW:15:ARG:NH2	2.43	0.51
25:BA:136:G:N3	43:BX:41:ASN:ND2	2.53	0.51
25:BA:2183:C:O2'	25:BA:2195:A:H4'	2.09	0.51
25:BA:2284:U:H5''	25:BA:2285:A:OP1	2.10	0.51
25:BA:240:A:C5	25:BA:241:G:H1'	2.45	0.51
25:BA:29:U:H2'	25:BA:30:G:C8	2.46	0.51
29:BF:31:HIS:NE2	29:BF:35:GLU:OE2	2.43	0.51
13:AM:6:GLY:O	30:BG:115:ARG:NH2	2.42	0.51
32:BI:91:SER:HB3	32:BI:119:PRO:HB2	1.93	0.51
1:CA:1010:G:H2'	1:CA:1011:G:H8	1.74	0.51
1:CA:103:C:O2'	1:CA:172:A:N1	2.37	0.51
1:CA:336:C:H2'	1:CA:337:C:C6	2.46	0.51
1:CA:601:C:H2'	1:CA:602:A:H8	1.76	0.51
1:CA:977:A:HO2'	1:CA:981:U:H3	1.57	0.51
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.08	0.51
12:CL:53:ARG:NH1	12:CL:92:ASP:OD2	2.37	0.51
43:DX:11:PRO:HG3	48:D2:37:PHE:CD2	2.46	0.51
51:D5:41:PRO:O	51:D5:44:THR:OG1	2.25	0.51
25:DA:1710:C:H2'	25:DA:1711:C:C6	2.45	0.51
25:DA:2430:A:H2'	25:DA:2430:A:N3	2.25	0.51
25:DA:262:A:H2'	25:DA:263:C:O4'	2.10	0.51
25:DA:2722:G:H2'	25:DA:2723:C:C6	2.45	0.51
25:DA:370:G:OP1	25:DA:403:U:N3	2.26	0.51
25:DA:839:U:H2'	25:DA:840:C:C6	2.46	0.51
30:DG:23:PHE:HB2	30:DG:25:TYR:CZ	2.45	0.51
25:DA:1226:A:H5''	40:DU:16:LYS:NZ	2.24	0.51
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.75	0.51
2:AB:121:LEU:HD13	2:AB:126:GLU:HG2	1.92	0.51
46:B0:40:GLN:HE22	46:B0:43:THR:HA	1.75	0.51
25:BA:1003:U:OP2	36:BQ:14:ARG:NH1	2.44	0.51
25:BA:1405:A:H2'	25:BA:1406:A:H5'	1.92	0.51
25:BA:927:G:H2'	25:BA:928:G:H8	1.75	0.51
44:BY:11:ASP:OD1	44:BY:97:ARG:NH2	2.41	0.51
1:CA:1122:U:O4	1:CA:1123:A:N6	2.43	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:686:U:HO2'	1:CA:687:A:H8	1.56	0.51
2:CB:212:GLN:O	2:CB:216:SER:OG	2.21	0.51
10:CJ:38:ILE:HG12	10:CJ:71:LEU:O	2.11	0.51
12:CL:102:ARG:HB3	12:CL:108:ALA:O	2.10	0.51
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.10	0.51
25:DA:651:G:H4'	54:D8:18:ALA:HB3	1.92	0.51
25:DA:2742:C:OP1	55:D9:35:ARG:HD3	2.10	0.51
29:DF:20:LEU:HD22	29:DF:21:ALA:H	1.76	0.51
1:AA:1427:U:H2'	1:AA:1428:A:C8	2.45	0.51
1:AA:166:G:H2'	1:AA:167:G:C8	2.45	0.51
1:AA:342:C:H2'	1:AA:343:U:H5''	1.93	0.51
4:AD:166:LYS:HB2	4:AD:168:ARG:NH1	2.25	0.51
7:AG:113:GLU:HG2	7:AG:119:ARG:HG2	1.91	0.51
1:AA:1525:G:OP2	11:AK:120:ARG:NH2	2.43	0.51
17:AQ:52:LYS:HG2	17:AQ:53:LEU:N	2.25	0.51
25:BA:1255:A:H5''	25:BA:1257:G:O4'	2.10	0.51
25:BA:1573:G:H5''	25:BA:1574:A:OP1	2.10	0.51
25:BA:2156:A:OP2	25:BA:2179:G:N2	2.43	0.51
44:BY:87:LYS:HD2	44:BY:95:LYS:HD3	1.92	0.51
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.46	0.51
1:CA:1249:C:H5'	9:CI:70:LYS:HE2	1.92	0.51
1:CA:460:G:N2	1:CA:471:G:OP2	2.37	0.51
1:CA:976:G:OP2	1:CA:1358:U:O2'	2.23	0.51
4:CD:150:GLU:HA	4:CD:153:ARG:HG3	1.93	0.51
19:CS:40:ILE:HB	19:CS:67:VAL:O	2.11	0.51
1:CA:986:A:H1'	19:CS:54:GLY:O	2.11	0.51
25:DA:2113:U:H3	25:DA:2170:A:H61	1.58	0.51
25:DA:2151:G:H2'	25:DA:2152:G:H8	1.76	0.51
25:DA:2347:C:H2'	25:DA:2348:U:C6	2.46	0.51
1:AA:1149:C:O2'	1:AA:1280:A:N1	2.43	0.51
14:AN:29:ARG:HH21	14:AN:31:ARG:HB2	1.75	0.51
23:AW:76:PPU:HM2	25:BA:2464:C:N3	2.26	0.51
25:BA:374:U:H2'	25:BA:375:G:O4'	2.10	0.51
2:CB:19:HIS:CD2	2:CB:20:GLU:H	2.29	0.51
1:CA:542:G:P	4:CD:10:ARG:HH12	2.33	0.51
13:CM:92:HIS:CE1	13:CM:98:VAL:HG21	2.46	0.51
23:CW:76:PPU:N	24:CX:76:31H:O2'	2.44	0.51
25:DA:1364:G:OP2	47:D1:3:LYS:HG3	2.10	0.51
25:DA:1593:G:H2'	25:DA:1594:G:H8	1.76	0.51
25:DA:172:C:H2'	25:DA:173:G:C8	2.46	0.51
25:DA:1791:A:H3'	25:DA:1792:G:C8	2.46	0.51
25:DA:323:G:H5'	29:DF:169:ASN:HD21	1.76	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:370:G:N7	60:DA:4068:HOH:O	2.34	0.51
25:DA:601:C:O2	25:DA:605:C:H4'	2.11	0.51
26:DB:80:U:H2'	26:DB:81:G:C8	2.45	0.51
25:DA:442:G:N2	29:DF:48:THR:HB	2.26	0.51
30:DG:165:THR:HB	30:DG:167:GLU:OE1	2.10	0.51
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.46	0.51
1:AA:240:C:H2'	1:AA:241:C:C6	2.45	0.51
3:AC:22:TRP:CH2	3:AC:32:LEU:HB3	2.46	0.51
6:AF:14:LEU:HD22	6:AF:18:GLN:HE21	1.76	0.51
12:AL:84:LEU:HB2	12:AL:105:TYR:CE2	2.46	0.51
25:BA:2348:A:H61	46:B0:43:THR:CG2	2.23	0.51
55:B9:16:VAL:HG22	55:B9:25:VAL:HG22	1.92	0.51
25:BA:1566:U:H2'	25:BA:1567:G:O4'	2.10	0.51
25:BA:2399:U:OP1	46:B0:55:ARG:NH2	2.43	0.51
25:BA:2699:U:H2'	25:BA:2700:U:O4'	2.09	0.51
25:BA:479:C:O2	25:BA:483:A:O2'	2.29	0.51
32:BI:92:VAL:HG11	32:BI:144:VAL:HG11	1.93	0.51
38:BS:39:ILE:HB	38:BS:49:VAL:HG12	1.93	0.51
1:CA:505:G:H2'	1:CA:506:G:C8	2.45	0.51
1:CA:959:A:HO2'	1:CA:984:C:HO2'	1.51	0.51
8:CH:4:ASP:O	8:CH:8:ASP:HB3	2.11	0.51
1:CA:1307:U:OP1	13:CM:101:GLN:NE2	2.43	0.51
25:DA:859:G:N2	25:DA:917:A:OP2	2.39	0.51
26:DB:27:C:C4	26:DB:28:C:C4	2.99	0.51
28:DE:36:ARG:HG2	28:DE:47:VAL:HG12	1.92	0.51
28:DE:54:GLN:HE22	28:DE:58:ARG:HG2	1.75	0.51
1:AA:1003:G:N2	1:AA:1038:C:N3	2.59	0.51
1:AA:1531:A:H2'	1:AA:1532:U:C4	2.46	0.51
3:AC:172:ARG:HB3	3:AC:174:PRO:HD3	1.92	0.51
4:AD:61:LYS:NZ	4:AD:72:GLU:OE2	2.28	0.51
8:AH:86:ILE:HG21	8:AH:133:LEU:HD13	1.91	0.51
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.11	0.51
14:AN:24:CYS:HB2	14:AN:40:CYS:HB3	1.92	0.51
19:AS:9:VAL:HG21	50:B4:61:ARG:HH12	1.74	0.51
25:BA:1067:A:O2'	25:BA:1169:C:OP1	2.22	0.51
25:BA:1903:C:H2'	25:BA:1904:C:C6	2.46	0.51
25:BA:2161:C:C2	25:BA:2174:G:N2	2.79	0.51
32:BI:68:LEU:HD22	32:BI:72:LEU:HG	1.92	0.51
40:BU:17:ILE:HG13	40:BU:32:PHE:HE1	1.76	0.51
2:CB:71:VAL:HB	2:CB:164:VAL:HA	1.92	0.51
14:CN:37:PHE:HE2	14:CN:53:LEU:HD13	1.74	0.51
25:DA:1379:A:H4'	25:DA:1380:G:OP2	2.11	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DG:64:THR:HG21	30:DG:92:VAL:HG11	1.91	0.51
31:DH:122:THR:O	31:DH:134:SER:OG	2.29	0.51
25:DA:2296:U:OP2	38:DS:9:ARG:NH2	2.43	0.51
44:DY:44:ILE:HD13	44:DY:64:GLU:HG3	1.93	0.51
1:AA:1179:A:H4'	9:AI:103:THR:HA	1.92	0.51
7:AG:138:LYS:NZ	7:AG:142:GLU:OE2	2.43	0.51
15:AO:82:ILE:O	15:AO:86:GLY:N	2.44	0.51
19:AS:19:VAL:HG11	19:AS:44:MET:HA	1.92	0.51
53:B7:34:ARG:NH1	53:B7:41:ARG:O	2.44	0.51
25:BA:1091:A:OP1	25:BA:1091:A:H4'	2.11	0.51
26:BB:66:A:H61	26:BB:108:U:H2'	1.76	0.51
26:BB:7:G:H1	26:BB:114:C:N4	2.08	0.51
30:BG:47:LYS:HG3	30:BG:48:GLU:H	1.76	0.51
25:BA:1002:A:H5'	36:BQ:76:LYS:HG3	1.92	0.51
1:CA:994:A:C5	1:CA:1216:G:H4'	2.46	0.51
1:CA:505:G:H2'	1:CA:506:G:H8	1.75	0.51
1:CA:522:C:H2'	1:CA:523:A:O4'	2.11	0.51
2:CB:177:ALA:HB1	2:CB:182:ILE:HB	1.92	0.51
2:CB:220:ASP:O	2:CB:223:ILE:HG13	2.11	0.51
3:CC:73:PRO:O	3:CC:77:ILE:HG12	2.11	0.51
16:CP:17:TYR:HE1	16:CP:41:PRO:HG3	1.76	0.51
25:DA:172:C:H2'	25:DA:173:G:H8	1.74	0.51
25:DA:2172:U:H1'	25:DA:2173:A:OP1	2.11	0.51
25:DA:30:G:H2'	25:DA:31:C:C6	2.45	0.51
28:DE:111:ARG:HG3	28:DE:160:TYR:CD2	2.46	0.51
35:DP:138:LEU:HD23	35:DP:145:PRO:HG3	1.93	0.51
1:AA:1047:G:H5''	14:AN:4:LYS:HD2	1.93	0.51
9:AI:9:ARG:HG2	9:AI:14:VAL:HG12	1.93	0.51
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.93	0.51
15:AO:62:GLN:HA	15:AO:65:ARG:NH1	2.25	0.51
25:BA:2612:A:N6	60:BA:4071:HOH:O	2.37	0.51
25:BA:561:A:H5'	40:BU:53:ARG:HD3	1.92	0.51
38:BS:3:ARG:HE	38:BS:4:LEU:H	1.59	0.51
25:BA:1272:A:OP1	41:BV:84:LYS:HE2	2.10	0.51
43:BX:65:ARG:NH1	43:BX:70:LEU:HD21	2.26	0.51
1:CA:1097:C:H2'	1:CA:1098:C:H6	1.74	0.51
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.46	0.51
3:CC:20:SER:HG	3:CC:22:TRP:HE1	1.56	0.51
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	1.93	0.51
46:D0:53:MET:HG3	46:D0:59:LEU:HD23	1.92	0.51
52:D6:25:LYS:HE2	52:D6:30:THR:O	2.11	0.51
25:DA:1021:A:H62	25:DA:1141:U:H3	1.58	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1239:G:H2'	25:DA:1240:U:O4'	2.09	0.51
25:DA:780:G:O2'	25:DA:783:A:N6	2.44	0.51
25:DA:797:C:OP1	29:DF:60:SER:OG	2.18	0.51
25:DA:2591:C:OP1	27:DD:239:ARG:HD2	2.11	0.51
2:AB:12:GLU:HA	2:AB:213:LEU:HD11	1.93	0.50
16:AP:50:LYS:HZ2	16:AP:51:VAL:H	1.59	0.50
24:AX:23:C:H2'	24:AX:24:U:H6	1.75	0.50
25:BA:2022:G:OP1	37:BR:5:LYS:NZ	2.44	0.50
25:BA:2122:G:H1	25:BA:2211:U:H3	1.58	0.50
25:BA:2451:A:H5'	25:BA:2451:A:H8	1.76	0.50
25:BA:924:U:H3	25:BA:945:A:H2	1.59	0.50
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.76	0.50
24:CX:52:G:H1	24:CX:62:C:N4	2.08	0.50
24:CX:55:PSU:N3	24:CX:58:A:OP2	2.31	0.50
25:DA:1819:A:H2	27:DD:274:ARG:HD3	1.77	0.50
25:DA:2180:U:H2'	25:DA:2181:G:O4'	2.11	0.50
25:DA:2483:C:N3	36:DQ:124:LYS:NZ	2.53	0.50
25:DA:362:U:O2'	25:DA:363:G:H5'	2.11	0.50
31:DH:104:GLU:HA	31:DH:113:VAL:O	2.11	0.50
45:DZ:22:GLY:O	45:DZ:23:LYS:HE3	2.10	0.50
1:AA:1038:C:H2'	1:AA:1039:C:C6	2.47	0.50
1:AA:1278:U:H5'	1:AA:1279:A:C5'	2.40	0.50
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.46	0.50
1:AA:376:G:H1	1:AA:387:U:H3	1.59	0.50
1:AA:982:U:H4'	1:AA:983:A:O5'	2.11	0.50
6:AF:2:ARG:HB2	6:AF:4:TYR:CZ	2.45	0.50
11:AK:32:ILE:O	11:AK:40:ILE:N	2.30	0.50
50:B4:41:PRO:HG3	50:B4:49:PHE:CE1	2.46	0.50
25:BA:2129:C:N4	25:BA:2204:G:H1	2.04	0.50
25:BA:2044:U:O2'	25:BA:2629:C:H5'	2.11	0.50
25:BA:615:G:HO2'	54:B8:64:TYR:HH	1.59	0.50
25:BA:438:G:C5	35:BP:72:PRO:HB3	2.47	0.50
1:CA:901:A:H5''	1:CA:902:G:OP2	2.10	0.50
43:DX:5:TYR:CE1	48:D2:30:ARG:HB2	2.46	0.50
30:DG:101:ILE:HD13	50:D4:25:TYR:HB2	1.92	0.50
25:DA:2687:U:H2'	25:DA:2688:U:O4'	2.11	0.50
25:DA:724:U:H2'	25:DA:725:G:O4'	2.10	0.50
33:DN:30:ILE:O	33:DN:34:LEU:HD22	2.11	0.50
41:DV:57:VAL:HG12	41:DV:99:ILE:HG23	1.93	0.50
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.11	0.50
1:AA:444:C:H2'	1:AA:445:G:C8	2.46	0.50
1:AA:900:A:H2'	1:AA:901:A:C8	2.46	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.74	0.50
25:BA:1189:A:OP1	33:BN:25:ARG:NH2	2.44	0.50
25:BA:7:G:H2'	25:BA:8:A:O4'	2.10	0.50
27:BD:132:PRO:HG2	27:BD:135:PHE:HD2	1.76	0.50
28:BE:101:ARG:CZ	28:BE:171:GLU:HB2	2.42	0.50
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.10	0.50
1:CA:1034:G:H5''	1:CA:1035:A:OP2	2.11	0.50
11:CK:62:GLN:HG3	11:CK:97:ALA:HB2	1.94	0.50
54:D8:6:THR:HG23	54:D8:64:TYR:HD2	1.77	0.50
25:DA:1450(A):C:N4	25:DA:1451:C:H41	2.09	0.50
1:CA:1517:G:H1'	25:DA:1919:A:O3'	2.10	0.50
25:DA:2747:G:H1	25:DA:2754:U:H2'	1.76	0.50
30:DG:106:LEU:O	30:DG:111:LEU:HD22	2.10	0.50
32:DI:14:ASP:N	32:DI:17:GLN:OE1	2.41	0.50
37:DR:36:THR:HG22	37:DR:37:THR:H	1.76	0.50
37:DR:83:ILE:O	37:DR:86:ARG:HG2	2.10	0.50
45:DZ:105:VAL:O	45:DZ:141:VAL:HG22	2.12	0.50
2:AB:78:GLN:NE2	2:AB:94:ASN:O	2.44	0.50
3:AC:157:ILE:HD12	3:AC:164:ARG:HB3	1.91	0.50
4:AD:107:ARG:NH2	4:AD:194:LEU:HD21	2.26	0.50
1:AA:1179:A:O3'	9:AI:103:THR:HB	2.12	0.50
10:AJ:44:VAL:HG22	10:AJ:66:ARG:HE	1.75	0.50
12:AL:8:ASN:O	12:AL:12:ARG:HG3	2.12	0.50
16:AP:48:TRP:HH2	16:AP:76:GLN:HE22	1.57	0.50
25:BA:2565:G:H1'	25:BA:2594:G:H21	1.77	0.50
27:BD:175:LEU:HD12	27:BD:185:VAL:HG21	1.93	0.50
1:CA:1010:G:H22	1:CA:1020:U:H1'	1.76	0.50
1:CA:768:A:H4'	1:CA:1523:G:N2	2.26	0.50
1:CA:448:A:P	1:CA:485:G:H22	2.34	0.50
1:CA:693:G:H2'	1:CA:694:A:H8	1.75	0.50
2:CB:71:VAL:HA	2:CB:93:VAL:HG23	1.93	0.50
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.11	0.50
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.93	0.50
25:DA:2286:A:P	52:D6:29:ASN:HD22	2.34	0.50
25:DA:450:G:OP1	25:DA:1248:G:N2	2.43	0.50
25:DA:1784:A:N7	60:DA:4017:HOH:O	2.35	0.50
25:DA:2370:G:C6	25:DA:2371:G:C6	3.00	0.50
26:DB:20:C:C2'	26:DB:21:G:H5'	2.42	0.50
1:AA:1089:G:H1	1:AA:1096:C:H42	1.60	0.50
2:AB:143:GLU:HA	2:AB:146:GLN:HB3	1.93	0.50
16:AP:38:TYR:OH	16:AP:47:ASP:OD2	2.20	0.50
25:BA:1472:G:O2'	25:BA:1619:A:N6	2.45	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:217:A:H8	25:BA:218:A:H5'	1.76	0.50
25:BA:2724:U:OP1	25:BA:2727:G:H4'	2.11	0.50
1:CA:343:U:H2'	1:CA:345:C:C5	2.46	0.50
2:CB:120:ALA:C	2:CB:122:PHE:H	2.13	0.50
24:CX:67:C:C2'	24:CX:68:C:H5'	2.41	0.50
25:DA:2119:A:C2	25:DA:2171:A:H5'	2.42	0.50
25:DA:536:A:H2'	25:DA:537:C:C6	2.47	0.50
25:DA:686:G:OP1	53:D7:11:LYS:NZ	2.43	0.50
25:DA:886:C:HO2'	25:DA:888:C:H5	1.58	0.50
26:DB:33:G:C6	26:DB:34:U:N3	2.80	0.50
26:DB:40:U:O2'	26:DB:42:C:H5'	2.11	0.50
31:DH:118:PRO:HD2	31:DH:121:ILE:HG21	1.94	0.50
39:DT:26:ASP:O	39:DT:49:VAL:HG12	2.11	0.50
1:AA:1264:C:H42	1:AA:1271:G:H1	1.59	0.50
1:AA:601:C:H2'	1:AA:602:A:C8	2.46	0.50
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.29	0.50
9:AI:4:TYR:CD1	9:AI:88:TYR:HA	2.47	0.50
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.45	0.50
25:BA:2682:A:H2'	25:BA:2683:A:O4'	2.11	0.50
1:CA:1015:A:H1'	1:CA:1219:U:H5'	1.94	0.50
1:CA:1065:U:H6	1:CA:1190:G:H21	1.57	0.50
1:CA:1224:G:N1	1:CA:1322:C:O4'	2.45	0.50
24:CX:59:A:C2'	24:CX:60:U:H5'	2.40	0.50
25:DA:2815:C:C5'	51:D5:29:THR:HG21	2.41	0.50
25:DA:1011:G:OP2	40:DU:66:ASN:ND2	2.42	0.50
26:DB:5:C:H42	26:DB:116:G:H1	1.59	0.50
31:DH:3:ARG:NH1	31:DH:3:ARG:HB3	2.24	0.50
38:DS:15:ARG:HD3	38:DS:25:ARG:HH21	1.76	0.50
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.47	0.50
30:BG:67:LYS:HE2	50:B4:5:ILE:HD12	1.94	0.50
25:BA:2227:G:H5'	25:BA:2228:G:N7	2.27	0.50
27:BD:142:VAL:HG22	27:BD:193:VAL:HA	1.94	0.50
26:BB:31:C:H4'	30:BG:29:TRP:CH2	2.47	0.50
2:CB:144:ARG:HH11	2:CB:144:ARG:HB3	1.76	0.50
2:CB:78:GLN:NE2	2:CB:95:GLN:HE22	2.09	0.50
4:CD:85:LYS:HG3	4:CD:86:LYS:H	1.75	0.50
15:CO:82:ILE:O	15:CO:86:GLY:N	2.45	0.50
25:DA:1289:C:H2'	25:DA:1290:C:H6	1.77	0.50
25:DA:1412:A:H2'	25:DA:1413:G:C8	2.46	0.50
25:DA:1639:U:H2'	25:DA:1640:C:H5''	1.92	0.50
25:DA:2646:C:H2'	25:DA:2647:U:O4'	2.11	0.50
25:DA:272(E):G:C2	25:DA:364:C:C2	3.00	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:459:U:H2'	25:DA:460:A:H8	1.77	0.50
26:DB:16:G:H1	26:DB:68:C:H42	1.59	0.50
28:DE:101:ARG:HB2	28:DE:201:THR:HG21	1.94	0.50
30:DG:61:ALA:HA	30:DG:66:GLN:O	2.12	0.50
31:DH:70:THR:O	31:DH:74:ASN:N	2.39	0.50
32:DI:72:LEU:HD21	32:DI:107:VAL:HG11	1.93	0.50
34:DO:68:GLU:HB3	34:DO:78:ARG:HB2	1.94	0.50
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.47	0.50
1:AA:532:A:N6	3:AC:156:ARG:HH12	2.10	0.50
1:AA:692:U:O2'	1:AA:694:A:N7	2.34	0.50
1:AA:69:G:H2'	1:AA:70:G:C8	2.47	0.50
1:AA:718:G:O6	18:AR:74:ARG:NH1	2.45	0.50
2:AB:71:VAL:HG12	2:AB:170:GLU:HG3	1.94	0.50
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.76	0.50
24:AX:21:A:N6	24:AX:46:G:H2'	2.26	0.50
24:AX:76:31H:O2'	25:BA:2463:A:O2'	2.27	0.50
36:BQ:85:LYS:HG2	46:B0:7:LEU:HB3	1.92	0.50
52:B6:33:LYS:HA	52:B6:33:LYS:HE3	1.92	0.50
25:BA:1218:G:N1	25:BA:1221:G:OP2	2.44	0.50
25:BA:2058:C:N4	60:BA:4309:HOH:O	2.45	0.50
25:BA:2060:G:H2'	25:BA:2061:C:O4'	2.12	0.50
25:BA:2376:C:H2'	25:BA:2377:G:O4'	2.12	0.50
30:BG:173:LEU:O	30:BG:178:PHE:HB2	2.11	0.50
25:BA:1232:G:H5''	41:BV:81:TYR:CE1	2.47	0.50
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.47	0.50
1:CA:1154:G:N7	1:CA:1155:G:C4	2.79	0.50
1:CA:1397:C:OP2	22:CV:23:A:O2'	2.14	0.50
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.26	0.50
1:CA:571:U:O2	1:CA:918:A:H5'	2.12	0.50
1:CA:973:G:OP1	10:CJ:57:LYS:HD3	2.12	0.50
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.94	0.50
11:CK:98:LEU:O	11:CK:101:SER:OG	2.20	0.50
25:DA:1557:C:OP2	25:DA:1558:A:O2'	2.24	0.50
25:DA:2136:C:N4	25:DA:2156:G:H21	2.10	0.50
25:DA:235:U:H2'	25:DA:236:C:C6	2.47	0.50
29:DF:102:PRO:HB2	29:DF:105:VAL:HG23	1.93	0.50
38:DS:8:GLU:CD	38:DS:8:GLU:H	2.15	0.50
42:DW:70:TYR:OH	42:DW:72:LYS:HG3	2.12	0.50
1:AA:1067:A:O2'	1:AA:1068:G:OP2	2.25	0.50
1:AA:45:U:H2'	1:AA:46:G:C8	2.47	0.50
1:AA:972:C:O3'	10:AJ:57:LYS:HD3	2.12	0.50
13:AM:96:LEU:HB3	13:AM:97:PRO:HD2	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.76	0.50
47:B1:60:PHE:HE2	47:B1:95:LEU:HD11	1.76	0.50
50:B4:61:ARG:HG3	50:B4:62:ARG:H	1.77	0.50
25:BA:1952:G:O2'	25:BA:1990:G:O6	2.22	0.50
25:BA:2014:G:N7	60:BA:4121:HOH:O	2.34	0.50
45:BZ:111:VAL:C	45:BZ:113:ALA:H	2.15	0.50
1:CA:36:C:H5''	12:CL:123:LYS:HD3	1.94	0.50
14:CN:47:LEU:HB2	14:CN:53:LEU:HG	1.93	0.50
3:CC:6:HIS:CE1	14:CN:50:LYS:HG3	2.46	0.50
24:CX:36:U:H2'	24:CX:37:A:C8	2.46	0.50
19:CS:68:GLY:H	50:D4:58:ARG:NH1	2.08	0.50
25:DA:1250:G:N7	35:DP:18:ARG:NH2	2.60	0.50
25:DA:195:A:H2'	25:DA:198:C:N4	2.27	0.50
25:DA:2299:G:N1	25:DA:2318:G:N7	2.59	0.50
25:DA:249:C:O2	54:D8:12:LYS:NZ	2.43	0.50
25:DA:2540:C:H2'	25:DA:2541:A:O4'	2.11	0.50
25:DA:459:U:H2'	25:DA:460:A:C8	2.47	0.50
27:DD:133:LEU:HB3	27:DD:173:VAL:HG11	1.94	0.50
31:DH:20:ALA:HB1	31:DH:21:PRO:HD2	1.94	0.50
35:DP:85:LEU:HA	35:DP:88:LEU:HD12	1.94	0.50
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.26	0.49
1:AA:1125:U:H1'	1:AA:1126:U:H2'	1.94	0.49
1:AA:166:G:H2'	1:AA:167:G:H8	1.76	0.49
1:AA:373:A:H2'	1:AA:374:A:H8	1.75	0.49
1:AA:503:C:C2'	1:AA:504:C:H5'	2.42	0.49
1:AA:584:G:H2'	1:AA:585:G:C8	2.47	0.49
2:AB:115:LEU:HD13	2:AB:145:LEU:HG	1.94	0.49
12:AL:53:ARG:HG2	12:AL:69:TYR:HE1	1.76	0.49
1:AA:584:G:H5'	17:AQ:91:ARG:NH2	2.27	0.49
25:BA:2394:G:H21	54:B8:42:ARG:NH2	2.10	0.49
25:BA:1258:A:H1'	25:BA:1284:G:N3	2.28	0.49
25:BA:1711:A:H1'	25:BA:2697:G:O2'	2.12	0.49
25:BA:294:C:H42	25:BA:390:G:H1	1.60	0.49
28:BE:7:VAL:HG23	28:BE:51:PHE:HE2	1.77	0.49
1:CA:1002:G:C2	1:CA:1003:G:C8	3.00	0.49
1:CA:1002:G:N2	1:CA:1039:C:C4	2.80	0.49
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.47	0.49
1:CA:1376:U:O5'	7:CG:94:ARG:NH2	2.45	0.49
1:CA:1458:G:C2'	1:CA:1459:C:H5'	2.42	0.49
1:CA:1412:C:H42	1:CA:1488:G:H1	1.59	0.49
1:CA:674:G:H2'	1:CA:675:A:H8	1.76	0.49
1:CA:701:C:OP1	1:CA:702:A:O2'	2.15	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:39:ILE:HG22	3:CC:43:LEU:HD13	1.93	0.49
9:CI:65:VAL:HG21	9:CI:73:GLN:HB3	1.92	0.49
12:CL:110:VAL:HG23	12:CL:120:TYR:HB3	1.93	0.49
29:DF:13:SER:OG	29:DF:16:GLY:O	2.22	0.49
29:DF:184:TYR:O	29:DF:188:ARG:HG3	2.12	0.49
25:DA:957:A:H5'	36:DQ:76:LYS:HG3	1.93	0.49
1:AA:1036:G:H5'	1:AA:1037:C:OP2	2.12	0.49
1:AA:757:U:O2'	1:AA:879:C:O2	2.29	0.49
3:AC:22:TRP:HA	10:AJ:93:GLY:HA2	1.94	0.49
25:BA:1159:U:H2'	25:BA:1160:G:H8	1.77	0.49
25:BA:2381:A:H2'	25:BA:2382:G:H8	1.76	0.49
29:BF:102:PRO:HB2	29:BF:105:VAL:HG23	1.94	0.49
34:BO:64:ARG:NH1	34:BO:81:ASP:OD1	2.45	0.49
39:BT:24:PRO:HD3	39:BT:52:ILE:HD12	1.94	0.49
1:CA:1318:A:H1'	19:CS:37:ARG:HD3	1.94	0.49
1:CA:826:C:H2'	1:CA:827:U:C6	2.46	0.49
2:CB:121:LEU:O	2:CB:127:ILE:HB	2.12	0.49
3:CC:54:ARG:HG3	3:CC:69:HIS:HB2	1.94	0.49
3:CC:83:ARG:O	3:CC:87:LEU:N	2.42	0.49
6:CF:37:VAL:HA	6:CF:65:VAL:HG12	1.92	0.49
1:CA:1279:A:OP1	10:CJ:7:LYS:NZ	2.45	0.49
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.39	0.49
15:CO:64:ARG:O	15:CO:68:ARG:N	2.45	0.49
18:CR:29:PHE:HE1	18:CR:31:LEU:HD13	1.77	0.49
25:DA:1016:G:H2'	25:DA:1017:G:O4'	2.12	0.49
25:DA:2123:G:H2'	25:DA:2124:G:C8	2.46	0.49
25:DA:479:A:N3	25:DA:481:G:H5''	2.27	0.49
25:DA:652(A):A:H2'	25:DA:652(A):A:N3	2.26	0.49
26:DB:6:C:C2	26:DB:116:G:N2	2.80	0.49
31:DH:27:LYS:HA	31:DH:32:GLU:HA	1.94	0.49
34:DO:119:PRO:HB2	39:DT:68:TYR:CE2	2.48	0.49
38:DS:44:LYS:H	38:DS:44:LYS:NZ	2.10	0.49
39:DT:51:ARG:HG3	39:DT:98:LYS:HD2	1.95	0.49
40:DU:109:LEU:HA	40:DU:112:ARG:HG3	1.93	0.49
1:AA:111:G:H5''	16:AP:27:LYS:HG2	1.94	0.49
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.27	0.49
1:AA:510:A:N3	1:AA:543:C:H1'	2.27	0.49
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.94	0.49
12:AL:28:LYS:HB2	12:AL:33:ARG:HH12	1.77	0.49
25:BA:1388:A:OP2	60:BA:3971:HOH:O	2.20	0.49
25:BA:2140:U:OP1	25:BA:2170:G:H4'	2.12	0.49
25:BA:2160:C:N4	25:BA:2175:G:H1	2.09	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2436:C:O2	25:BA:2441:G:O2'	2.18	0.49
27:BD:127:VAL:HA	27:BD:193:VAL:HG23	1.94	0.49
32:BI:104:GLN:O	32:BI:106:GLY:N	2.40	0.49
33:BN:47:ALA:HB2	33:BN:112:LEU:HD11	1.94	0.49
41:BV:55:ALA:HB2	41:BV:101:GLY:HA2	1.95	0.49
1:CA:1190:G:H5'	3:CC:176:HIS:CE1	2.48	0.49
1:CA:1227:A:C2	19:CS:83:HIS:HB3	2.48	0.49
1:CA:691:G:O6	11:CK:52:GLY:HA2	2.12	0.49
3:CC:181:ASN:ND2	3:CC:204:LEU:HD12	2.27	0.49
54:D8:33:ASN:HA	54:D8:36:LYS:HD2	1.93	0.49
25:DA:1023:U:O2'	25:DA:1122:G:H5'	2.11	0.49
25:DA:855:G:H2'	25:DA:856:C:C6	2.47	0.49
28:DE:34:VAL:HG22	28:DE:48:GLN:HB3	1.95	0.49
38:DS:50:SER:O	38:DS:76:LYS:NZ	2.34	0.49
45:DZ:157:LEU:HD11	45:DZ:163:LEU:HB2	1.94	0.49
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.47	0.49
1:AA:560:U:H5'	1:AA:566:G:N2	2.27	0.49
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.94	0.49
3:AC:17:ASP:HB3	3:AC:21:ARG:HH21	1.77	0.49
10:AJ:26:ALA:HB1	10:AJ:84:GLN:NE2	2.28	0.49
35:BP:62:LEU:O	54:B8:13:ARG:HD3	2.12	0.49
25:BA:1249:A:N6	25:BA:1286:U:H2'	2.27	0.49
25:BA:1735:U:H1'	25:BA:1748:A:C6	2.47	0.49
25:BA:1903:C:H2'	25:BA:1904:C:H6	1.77	0.49
25:BA:2119:C:H2'	25:BA:2120:U:O4'	2.13	0.49
25:BA:2505:U:OP1	60:BA:4231:HOH:O	2.20	0.49
25:BA:943:C:H2'	25:BA:944:C:C6	2.47	0.49
32:BI:93:THR:HG22	32:BI:119:PRO:HB3	1.94	0.49
39:BT:60:THR:HG22	39:BT:77:PRO:HA	1.92	0.49
44:BY:6:HIS:CD2	44:BY:6:HIS:H	2.31	0.49
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.46	0.49
1:CA:353:A:H8	1:CA:353:A:H5'	1.77	0.49
1:CA:418:C:H2'	1:CA:419:C:C6	2.46	0.49
1:CA:495:A:H4'	1:CA:496:A:OP1	2.13	0.49
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	1.94	0.49
4:CD:65:ARG:HG2	4:CD:75:PHE:CD1	2.46	0.49
46:D0:38:VAL:HG12	46:D0:40:GLN:HG2	1.95	0.49
48:D2:65:ASN:OD1	48:D2:69:ARG:NH1	2.46	0.49
25:DA:1022:G:N2	25:DA:1142(A):A:H2	2.05	0.49
25:DA:1316:U:H2'	25:DA:1317:A:H8	1.77	0.49
25:DA:2022:U:O2'	25:DA:2617:C:H5'	2.12	0.49
25:DA:2471:C:H2'	25:DA:2472:G:O4'	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:275:G:H2'	25:DA:276:A:O4'	2.12	0.49
25:DA:340:A:H2'	25:DA:341:G:O4'	2.12	0.49
25:DA:579:G:H2'	25:DA:580:C:C6	2.48	0.49
25:DA:62:C:H42	25:DA:93:G:H1	1.60	0.49
25:DA:896:A:N6	45:DZ:146:ILE:HD13	2.27	0.49
1:AA:1328:C:OP1	21:AU:21:TYR:OH	2.30	0.49
1:AA:524:G:H2'	1:AA:525:C:C6	2.48	0.49
2:AB:112:VAL:O	2:AB:116:GLU:N	2.31	0.49
25:BA:1081:U:H2'	25:BA:1082:G:C8	2.47	0.49
25:BA:1231:G:H2'	25:BA:1232:G:O4'	2.13	0.49
25:BA:1698:G:H5'	37:BR:39:PRO:HG2	1.94	0.49
25:BA:2228:G:O2'	25:BA:2229:A:OP1	2.27	0.49
25:BA:734:C:H2'	25:BA:735:U:O4'	2.12	0.49
31:BH:56:SER:HB3	31:BH:61:HIS:ND1	2.28	0.49
34:BO:97:ARG:NH2	34:BO:99:PHE:HE1	2.10	0.49
37:BR:51:LEU:HD22	37:BR:66:VAL:HG13	1.94	0.49
25:BA:333:G:H4'	44:BY:18:GLY:HA2	1.95	0.49
1:CA:364:A:H2'	1:CA:365:U:C6	2.48	0.49
1:CA:511:C:HO2'	1:CA:512:U:H6	1.59	0.49
1:CA:1106:G:H5''	3:CC:172:ARG:HG2	1.95	0.49
4:CD:17:VAL:HG13	4:CD:19:LEU:HD22	1.94	0.49
19:CS:40:ILE:HD11	19:CS:74:PHE:CE2	2.47	0.49
25:DA:1674:G:H21	25:DA:1677:A:H61	1.58	0.49
25:DA:2176:A:H2'	25:DA:2177:C:C5	2.48	0.49
25:DA:2351:G:H8	25:DA:2351:G:O5'	1.95	0.49
25:DA:1462:C:H4'	25:DA:2703:C:H5'	1.95	0.49
25:DA:192:C:O2'	25:DA:802:A:N3	2.40	0.49
25:DA:1813:G:H1'	27:DD:50:THR:OG1	2.12	0.49
28:DE:54:GLN:HE22	28:DE:58:ARG:HB3	1.77	0.49
30:DG:114:ILE:HA	30:DG:140:ILE:HD11	1.94	0.49
1:AA:1226:C:O2'	13:AM:111:LYS:NZ	2.45	0.49
1:AA:1366:C:H2'	1:AA:1367:C:H6	1.78	0.49
1:AA:558:G:OP1	60:AA:4061:HOH:O	2.20	0.49
1:AA:589:C:C2'	1:AA:590:C:H5'	2.43	0.49
1:AA:749:C:H2'	1:AA:750:G:H8	1.77	0.49
4:AD:188:LEU:H	4:AD:188:LEU:HD23	1.77	0.49
10:AJ:69:ASN:O	10:AJ:70:ARG:HD3	2.12	0.49
15:AO:16:ALA:HB1	15:AO:21:ASP:HB3	1.95	0.49
54:B8:42:ARG:NH1	60:B8:5105:HOH:O	2.25	0.49
25:BA:1312:G:O6	42:BW:13:SER:OG	2.23	0.49
25:BA:173:C:H2'	25:BA:174:U:H6	1.75	0.49
25:BA:2748:G:H2'	25:BA:2749:G:H8	1.78	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2804:C:O2	25:BA:2817:G:N1	2.45	0.49
25:BA:364:A:H2'	25:BA:365:G:O4'	2.13	0.49
25:BA:485:U:H2'	25:BA:486:A:H8	1.77	0.49
25:BA:892:G:HO2'	25:BA:893:C:H5	1.61	0.49
25:BA:2873:C:OP1	39:BT:93:ARG:NH2	2.45	0.49
1:CA:1151:A:N3	10:CJ:39:PRO:HG3	2.28	0.49
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.21	0.49
1:CA:1390:U:H2'	1:CA:1391:U:C6	2.47	0.49
1:CA:406:G:H2'	1:CA:407:G:C8	2.48	0.49
1:CA:690:G:H8	1:CA:690:G:O5'	1.96	0.49
1:CA:96:U:O2'	1:CA:97:G:H5'	2.12	0.49
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.94	0.49
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.93	0.49
9:CI:85:LEU:HB3	9:CI:92:TYR:CD2	2.48	0.49
25:DA:1005:C:H2'	25:DA:1006:C:H6	1.78	0.49
25:DA:1204:A:H2	25:DA:1241:A:N6	2.09	0.49
25:DA:1503:U:H2'	25:DA:1504:C:C6	2.48	0.49
25:DA:1623:G:H2'	25:DA:1624:G:H8	1.77	0.49
25:DA:2134:A:N3	25:DA:2159:G:O2'	2.40	0.49
25:DA:2683:C:OP1	39:DT:53:ARG:NH2	2.46	0.49
25:DA:565:C:H5	41:DV:78:LYS:HZ1	1.61	0.49
25:DA:614:U:H2'	25:DA:614(A):U:O4'	2.12	0.49
25:DA:895:U:H3	25:DA:897:C:N4	2.10	0.49
25:DA:935:C:H2'	25:DA:936:C:C6	2.48	0.49
38:DS:10:ARG:O	38:DS:14:VAL:HG12	2.12	0.49
1:AA:1131:G:O5'	1:AA:1131:G:H8	1.95	0.49
1:AA:1295:G:C2'	1:AA:1296:C:H5'	2.42	0.49
1:AA:69:G:H2'	1:AA:70:G:H8	1.78	0.49
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.28	0.49
3:AC:193:TYR:HE2	3:AC:196:LEU:HD11	1.78	0.49
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.94	0.49
3:AC:73:PRO:O	3:AC:77:ILE:HG12	2.12	0.49
1:AA:1239:A:O2'	7:AG:114:ARG:O	2.24	0.49
20:AT:43:LEU:HD13	20:AT:51:GLU:HB3	1.94	0.49
21:AU:3:LYS:HD3	21:AU:14:TRP:CD1	2.47	0.49
55:B9:7:VAL:HG12	55:B9:34:GLN:HB3	1.95	0.49
25:BA:1067:A:H62	25:BA:1186:U:H3	1.59	0.49
37:BR:36:THR:HG22	37:BR:37:THR:H	1.77	0.49
1:CA:1014:A:O5'	1:CA:1014:A:H8	1.95	0.49
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.47	0.49
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.12	0.49
1:CA:1366:C:H2'	1:CA:1367:C:H6	1.78	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:967:C:H3'	1:CA:968:A:H2'	1.93	0.49
2:CB:7:VAL:HG12	2:CB:8:LYS:H	1.77	0.49
11:CK:21:ILE:HB	11:CK:84:VAL:HG22	1.95	0.49
47:D1:54:ALA:HB1	47:D1:83:GLU:HG3	1.95	0.49
25:DA:1359:A:N6	25:DA:1372:U:H3	2.11	0.49
25:DA:2106:G:O6	25:DA:2183:C:N3	2.45	0.49
25:DA:2657:A:H3'	25:DA:2658:C:H6	1.78	0.49
29:DF:101:LEU:HD12	29:DF:102:PRO:HD2	1.95	0.49
30:DG:15:VAL:HG22	30:DG:175:LEU:HB3	1.95	0.49
34:DO:76:ALA:O	39:DT:74:ARG:HD2	2.13	0.49
1:AA:1492:A:N3	22:AV:20:U:O2'	2.39	0.49
1:AA:346:G:OP1	39:BT:41:ARG:NH1	2.46	0.49
5:AE:77:PRO:HG2	5:AE:142:LEU:HD22	1.95	0.49
12:AL:69:TYR:CD1	12:AL:90:VAL:HG21	2.48	0.49
25:BA:239:G:P	54:B8:13:ARG:HH22	2.34	0.49
25:BA:1314:A:H2'	25:BA:1315:A:O4'	2.11	0.49
25:BA:1921:G:H2'	25:BA:1921:G:N3	2.27	0.49
25:BA:325:G:OP2	44:BY:84:ARG:NH2	2.45	0.49
25:BA:636:G:O2'	25:BA:640:A:N1	2.36	0.49
29:BF:33:LEU:HB3	35:BP:6:LEU:HD21	1.94	0.49
4:CD:64:LEU:HB2	4:CD:198:VAL:HG21	1.95	0.49
4:CD:76:ARG:NE	4:CD:80:GLU:OE1	2.41	0.49
7:CG:153:HIS:CE1	11:CK:58:PRO:HD2	2.48	0.49
14:CN:45:ARG:O	14:CN:49:HIS:HD2	1.96	0.49
24:CX:29:G:C2'	24:CX:30:G:H5'	2.42	0.49
24:CX:36:U:H2'	24:CX:37:A:H8	1.78	0.49
25:DA:1028:A:N6	25:DA:1125:G:H2'	2.28	0.49
25:DA:1336:A:H2'	25:DA:1337:G:C8	2.47	0.49
25:DA:1514:U:H2'	25:DA:1515:G:C8	2.48	0.49
25:DA:1721:G:H5'	25:DA:1722:A:H5''	1.95	0.49
25:DA:1971:A:OP1	60:DA:4205:HOH:O	2.19	0.49
25:DA:35:G:H1'	25:DA:454:A:C4	2.47	0.49
25:DA:247:G:H4'	25:DA:386:G:C5	2.48	0.49
25:DA:888:C:H2'	25:DA:889:C:C4	2.48	0.49
26:DB:14:U:O3'	26:DB:108:U:O2'	2.30	0.49
31:DH:97:ARG:HE	31:DH:104:GLU:CD	2.16	0.49
35:DP:52:GLU:HB3	35:DP:55:ARG:NH1	2.27	0.49
36:DQ:52:VAL:O	36:DQ:56:ARG:HB2	2.12	0.49
45:DZ:30:ASN:ND2	45:DZ:90:VAL:O	2.38	0.49
25:BA:1864:U:O2'	25:BA:1991:A:N1	2.36	0.49
31:BH:113:VAL:HG11	31:BH:151:ILE:HD13	1.94	0.49
25:BA:878:G:N2	35:BP:53:GLY:O	2.46	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
39:BT:53:ARG:CZ	39:BT:53:ARG:HB3	2.42	0.49
40:BU:76:TYR:OH	40:BU:92:ARG:NH1	2.39	0.49
1:CA:1127:G:H21	1:CA:1147:C:H41	1.61	0.49
1:CA:20:U:H2'	1:CA:21:G:O4'	2.12	0.49
5:CE:80:ILE:HG22	5:CE:91:LEU:HB2	1.94	0.49
48:D2:10:LEU:O	48:D2:14:ARG:HB2	2.12	0.49
25:DA:7:G:H2'	25:DA:8:A:C8	2.47	0.49
37:DR:88:ARG:NH2	37:DR:89:ASP:OD2	2.46	0.49
43:DX:12:VAL:HG21	43:DX:27:THR:HG22	1.95	0.49
1:AA:425:G:C2'	1:AA:426:G:H5'	2.43	0.49
1:AA:998:G:H1	1:AA:1043:C:N4	2.10	0.49
4:AD:138:TYR:HD1	4:AD:139:ARG:N	2.11	0.49
20:AT:10:LEU:HD23	20:AT:11:SER:H	1.76	0.49
20:AT:53:LEU:HD13	20:AT:100:ILE:O	2.13	0.49
49:B3:8:LEU:O	49:B3:32:GLN:N	2.34	0.49
51:B5:16:ARG:O	51:B5:20:ARG:HG3	2.13	0.49
25:BA:496:A:OP1	29:BF:59:TYR:HE1	1.95	0.49
31:BH:5:GLY:HA2	31:BH:69:ARG:HB3	1.95	0.49
1:CA:1004:A:C8	1:CA:1005:A:H4'	2.45	0.49
1:CA:390:C:H2'	1:CA:391:G:C8	2.48	0.49
14:CN:24:CYS:O	14:CN:28:GLY:N	2.37	0.49
19:CS:53:ASN:HB2	19:CS:77:THR:HA	1.94	0.49
50:D4:26:SER:OG	50:D4:27:THR:N	2.46	0.49
25:DA:1495:A:H2'	25:DA:1496:A:C8	2.48	0.49
25:DA:1675:C:O5'	25:DA:1675:C:H6	1.96	0.49
25:DA:570:G:H2'	25:DA:2030:A:C5	2.48	0.49
25:DA:2123:G:H2'	25:DA:2124:G:H8	1.78	0.49
25:DA:586:A:N1	25:DA:809:G:O2'	2.39	0.49
25:DA:86:C:H4'	25:DA:104:U:H1'	1.95	0.49
25:DA:1798:U:H5'	27:DD:259:THR:HG22	1.95	0.49
28:DE:127:ASP:OD2	60:DE:3105:HOH:O	2.19	0.49
32:DI:123:LEU:H	32:DI:123:LEU:HD23	1.77	0.49
33:DN:47:ALA:HB2	33:DN:112:LEU:HD11	1.95	0.49
25:DA:566:U:P	41:DV:80:GLN:HE21	2.34	0.49
1:AA:1149:C:OP2	9:AI:9:ARG:NH2	2.38	0.48
1:AA:593:G:H2'	1:AA:594:G:O4'	2.13	0.48
2:AB:27:LYS:O	2:AB:30:ARG:NH1	2.46	0.48
3:AC:8:ILE:HG23	3:AC:16:ARG:HG2	1.95	0.48
9:AI:85:LEU:HB3	9:AI:92:TYR:HD2	1.76	0.48
1:AA:376:G:OP2	16:AP:67:THR:HG21	2.13	0.48
25:BA:1033:G:O2'	25:BA:1046:A:N3	2.43	0.48
25:BA:2368:C:H2'	25:BA:2369:U:O4'	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:354:A:H2	25:BA:1255:A:O2'	1.96	0.48
25:BA:860:U:H2'	25:BA:861:C:C6	2.48	0.48
25:BA:922:G:H1	25:BA:948:C:N4	2.11	0.48
25:BA:2518:U:OP1	28:BE:144:ARG:NH2	2.46	0.48
1:CA:1353:G:H2'	1:CA:1354:C:C6	2.48	0.48
1:CA:399:G:H2'	1:CA:400:C:C6	2.48	0.48
4:CD:129:ASN:HD21	4:CD:144:ASP:HA	1.77	0.48
1:CA:405:U:P	4:CD:3:ARG:HH21	2.35	0.48
10:CJ:5:ARG:N	60:CJ:5101:HOH:O	2.46	0.48
12:CL:27:LEU:O	12:CL:33:ARG:NE	2.32	0.48
13:CM:107:ALA:O	13:CM:111:LYS:HB2	2.13	0.48
1:CA:1114:C:H1'	14:CN:60:SER:HB3	1.94	0.48
25:DA:1365:A:O4'	47:D1:41:ARG:NH2	2.46	0.48
25:DA:2070:G:C2	25:DA:2442:C:C2	3.01	0.48
25:DA:2345:G:OP1	52:D6:38:LYS:NZ	2.45	0.48
23:CW:76:PPU:HD2	25:DA:2451:A:C4	2.48	0.48
30:DG:108:ASN:O	50:D4:36:CYS:HA	2.13	0.48
26:DB:55:U:H1'	30:DG:29:TRP:HD1	1.78	0.48
31:DH:28:GLY:HA3	31:DH:79:VAL:HB	1.94	0.48
45:DZ:150:LEU:HA	45:DZ:150:LEU:HD13	1.65	0.48
1:AA:1121:U:C2'	1:AA:1122:U:H5'	2.43	0.48
1:AA:946:A:H2'	1:AA:947:G:C8	2.49	0.48
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	1.94	0.48
6:AF:10:LEU:HB2	6:AF:59:TYR:HB3	1.95	0.48
25:BA:484:G:C8	53:B7:37:LYS:HG2	2.49	0.48
25:BA:1817:A:H1'	25:BA:1960:A:H61	1.78	0.48
25:BA:2285:A:H2'	25:BA:2286:A:C8	2.48	0.48
25:BA:610:C:C6	25:BA:718:C:H1'	2.49	0.48
27:BD:8:PRO:HB3	27:BD:14:ARG:HG3	1.95	0.48
31:BH:56:SER:OG	31:BH:58:GLU:HG2	2.13	0.48
38:BS:10:ARG:O	38:BS:14:VAL:HG13	2.12	0.48
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.13	0.48
1:CA:1258:G:H2'	1:CA:1259:C:C6	2.48	0.48
1:CA:1492:A:H2'	1:CA:1493:A:C8	2.48	0.48
1:CA:413:G:H21	1:CA:428:G:H1'	1.78	0.48
19:CS:38:SER:O	19:CS:71:LEU:HB2	2.13	0.48
25:DA:2756:U:H3'	55:D9:20:HIS:CD2	2.48	0.48
25:DA:1607:C:H4'	25:DA:1608:A:O5'	2.12	0.48
25:DA:1899:G:H2'	25:DA:1899:G:N3	2.27	0.48
25:DA:2128:C:N4	25:DA:2160:G:N1	2.43	0.48
25:DA:2562:U:H1'	34:DO:23:ARG:NH1	2.28	0.48
25:DA:2693:A:H2'	25:DA:2694:G:C8	2.46	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DE:72:VAL:HA	28:DE:73:GLU:CG	2.43	0.48
34:DO:34:THR:OG1	34:DO:35:VAL:N	2.46	0.48
35:DP:50:ARG:HG2	54:D8:61:LEU:HD11	1.96	0.48
1:AA:1014:A:H2'	1:AA:1015:A:C8	2.48	0.48
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.13	0.48
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.48	0.48
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.93	0.48
48:B2:9:GLN:HE22	48:B2:56:GLN:HG2	1.78	0.48
28:BE:128:SER:OG	28:BE:129:HIS:N	2.45	0.48
25:BA:1696:G:O2'	37:BR:107:ASP:OD2	2.25	0.48
1:CA:139:G:N2	1:CA:224:C:O2	2.43	0.48
1:CA:359:U:H2'	1:CA:360:A:C8	2.47	0.48
1:CA:375:U:H5''	16:CP:6:LEU:HD23	1.96	0.48
10:CJ:45:ARG:O	10:CJ:65:LEU:N	2.42	0.48
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.13	0.48
25:DA:2285:C:OP2	52:D6:6:ARG:NH1	2.45	0.48
25:DA:1225:G:OP1	41:DV:69:LYS:NZ	2.36	0.48
25:DA:2151:G:H2'	25:DA:2152:G:C8	2.48	0.48
25:DA:2287:A:O2'	25:DA:2288:A:H5''	2.13	0.48
25:DA:921:G:H2'	25:DA:922:U:C6	2.48	0.48
26:DB:24:G:H21	26:DB:27:C:N4	2.11	0.48
28:DE:34:VAL:HG21	28:DE:78:LEU:HD11	1.95	0.48
30:DG:3:LEU:HD11	30:DG:5:VAL:HG12	1.95	0.48
35:DP:64:LYS:HA	54:D8:13:ARG:HB3	1.94	0.48
37:DR:66:VAL:HG11	37:DR:79:LEU:HD12	1.96	0.48
1:AA:1151:A:O2'	1:AA:1152:A:O5'	2.26	0.48
1:AA:667:G:OP1	1:AA:732:C:O2'	2.20	0.48
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.93	0.48
4:AD:186:LEU:HB2	4:AD:187:ARG:NH2	2.25	0.48
8:AH:14:ARG:O	8:AH:18:ARG:HD3	2.12	0.48
26:BB:8:U:O3'	38:BS:25:ARG:NH2	2.45	0.48
25:BA:1057:G:OP2	40:BU:70:ARG:NH2	2.45	0.48
1:CA:559:A:H4'	1:CA:560:U:H3'	1.93	0.48
2:CB:82:ARG:HG3	2:CB:92:TYR:OH	2.14	0.48
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.13	0.48
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.14	0.48
1:CA:1227:A:N3	19:CS:83:HIS:HB3	2.27	0.48
25:DA:117:G:OP2	25:DA:119:A:O2'	2.26	0.48
25:DA:2849:U:H4'	25:DA:2868:A:C2	2.48	0.48
25:DA:583:G:OP2	40:DU:10:ARG:NH1	2.47	0.48
25:DA:615:G:OP1	29:DF:40:GLN:HG2	2.12	0.48
25:DA:686:G:P	53:D7:11:LYS:HZ3	2.37	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:80:G:H1	25:DA:106:C:H42	1.60	0.48
25:DA:729:G:C5	27:DD:208:LYS:HB2	2.49	0.48
1:CA:1422:G:H5'	34:DO:48:PRO:HB3	1.94	0.48
45:DZ:7:ALA:O	45:DZ:62:PRO:HD3	2.13	0.48
1:AA:165:C:H2'	1:AA:166:G:C8	2.49	0.48
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	1.96	0.48
3:AC:62:ASP:O	3:AC:97:LYS:HB3	2.14	0.48
11:AK:77:MET:HA	11:AK:77:MET:HE3	1.94	0.48
25:BA:1074:A:N6	25:BA:1171:G:H2'	2.29	0.48
25:BA:1570:G:H2'	25:BA:1571:G:O4'	2.14	0.48
25:BA:2819:A:H62	25:BA:2900:G:H2'	1.78	0.48
25:BA:1857:G:H4'	27:BD:242:ARG:CZ	2.43	0.48
32:BI:40:THR:O	32:BI:44:LEU:N	2.43	0.48
37:BR:55:ALA:HB2	37:BR:79:LEU:HD13	1.94	0.48
25:BA:922:G:O3'	45:BZ:151:HIS:HE1	1.96	0.48
1:CA:1023:G:H3'	1:CA:1024:G:C8	2.48	0.48
1:CA:1120:G:C6	1:CA:1154:G:C2	3.01	0.48
1:CA:674:G:H2'	1:CA:675:A:C8	2.49	0.48
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.49	0.48
10:CJ:45:ARG:HB3	10:CJ:65:LEU:HB3	1.94	0.48
12:CL:82:VAL:O	12:CL:106:ASP:HB2	2.13	0.48
13:CM:16:ASP:N	13:CM:16:ASP:OD1	2.46	0.48
14:CN:29:ARG:HG2	14:CN:31:ARG:H	1.79	0.48
25:DA:2392:A:O3'	54:D8:27:THR:HB	2.13	0.48
25:DA:639:U:H2'	25:DA:640:C:C6	2.49	0.48
26:DB:42:C:C4	26:DB:43:C:C4	3.02	0.48
28:DE:72:VAL:HG13	28:DE:73:GLU:C	2.34	0.48
29:DF:80:ALA:HB3	29:DF:83:PHE:HD1	1.78	0.48
34:DO:12:ASP:OD1	34:DO:14:THR:OG1	2.31	0.48
35:DP:21:ARG:HA	35:DP:21:ARG:HD3	1.51	0.48
36:DQ:30:GLY:O	36:DQ:134:ARG:HD3	2.14	0.48
45:DZ:69:THR:HG22	45:DZ:90:VAL:HG22	1.95	0.48
1:AA:352:C:O2'	1:AA:354:G:OP1	2.24	0.48
5:AE:137:GLU:HG2	5:AE:140:ARG:NH1	2.28	0.48
7:AG:89:MET:SD	7:AG:155:ARG:HB2	2.53	0.48
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.95	0.48
25:BA:54:G:O2'	25:BA:125:A:N1	2.38	0.48
25:BA:2102:G:OP1	47:B1:35:THR:HG21	2.13	0.48
25:BA:2262:G:O2'	25:BA:2508:C:OP1	2.24	0.48
25:BA:388:A:H2'	25:BA:389:G:C8	2.49	0.48
25:BA:1829:U:H5'	27:BD:259:THR:CG2	2.42	0.48
1:CA:1295:G:C2'	1:CA:1296:C:H5'	2.42	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1516:G:H2'	1:CA:1518:A:OP2	2.13	0.48
2:CB:142:LEU:HA	2:CB:145:LEU:HD22	1.96	0.48
2:CB:80:ILE:HD12	2:CB:208:ILE:HG23	1.95	0.48
1:CA:1328:C:O3'	13:CM:29:ARG:HG3	2.13	0.48
13:CM:65:LYS:O	13:CM:70:LEU:HD12	2.14	0.48
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.43	0.48
47:D1:50:ARG:HG2	47:D1:59:THR:HG22	1.95	0.48
25:DA:1328:G:O2'	25:DA:1329:U:H2'	2.13	0.48
25:DA:1467:C:C5	25:DA:1546:C:H2'	2.48	0.48
25:DA:1486:A:O2'	25:DA:1487:G:H5'	2.14	0.48
25:DA:1509(A):A:N3	25:DA:1509(A):A:H5''	2.29	0.48
25:DA:271(U):G:H2'	25:DA:271(V):G:C8	2.48	0.48
25:DA:272(B):G:H2'	25:DA:272(C):G:H8	1.79	0.48
25:DA:619:G:H3'	25:DA:620:G:H21	1.78	0.48
25:DA:820:A:H2'	25:DA:821:A:O4'	2.14	0.48
29:DF:111:ALA:HB2	29:DF:206:ILE:HG21	1.96	0.48
39:DT:92:GLY:O	39:DT:120:ARG:NH2	2.46	0.48
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.78	0.48
1:AA:448:A:O5'	1:AA:485:G:N2	2.42	0.48
2:AB:32:ILE:HD13	2:AB:40:HIS:CD2	2.48	0.48
22:AV:22:U:H2'	22:AV:23:A:C8	2.48	0.48
25:BA:671:A:H2'	25:BA:672:G:O4'	2.14	0.48
26:BB:14:U:OP2	26:BB:70:C:O2'	2.16	0.48
32:BI:72:LEU:C	32:BI:74:ASN:H	2.17	0.48
34:BO:34:THR:OG1	34:BO:35:VAL:N	2.45	0.48
35:BP:65:ARG:HG3	54:B8:25:MET:HG3	1.96	0.48
1:CA:407:G:H5''	4:CD:115:ARG:HB3	1.96	0.48
8:CH:73:ASP:OD1	8:CH:75:ARG:NH1	2.46	0.48
10:CJ:37:PRO:HA	10:CJ:72:VAL:HG12	1.96	0.48
17:CQ:43:LEU:HD12	17:CQ:68:ARG:HB3	1.95	0.48
19:CS:30:LEU:HD11	19:CS:32:LYS:HG3	1.95	0.48
46:D0:34:GLY:N	46:D0:61:ALA:O	2.37	0.48
50:D4:58:ARG:HG2	50:D4:59:PHE:HD1	1.79	0.48
53:D7:24:THR:O	53:D7:28:ARG:HG3	2.13	0.48
25:DA:1139:G:O3'	33:DN:24:GLY:HA3	2.14	0.48
25:DA:1155:A:H5''	40:DU:55:ARG:HD3	1.95	0.48
25:DA:475:U:H4'	25:DA:510:C:H5'	1.96	0.48
28:DE:2:LYS:HG3	28:DE:200:GLU:HB2	1.94	0.48
34:DO:120:GLU:HB2	39:DT:68:TYR:HE2	1.79	0.48
1:AA:625:G:H4'	16:AP:16:HIS:CG	2.49	0.48
1:AA:1229:A:O3'	24:AX:30:G:H5''	2.14	0.48
25:BA:2303:U:OP1	25:BA:2392:C:O2'	2.31	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2323:A:N1	30:BG:47:LYS:NZ	2.61	0.48
1:CA:1456:G:O6	20:CT:54:LYS:HE3	2.13	0.48
1:CA:442:C:H42	1:CA:492:G:H1	1.61	0.48
1:CA:66:G:OP1	1:CA:66:G:H8	1.95	0.48
1:CA:696:A:H8	1:CA:696:A:O5'	1.97	0.48
2:CB:158:LEU:HD12	2:CB:158:LEU:H	1.78	0.48
1:CA:8:A:N6	4:CD:209:ARG:HB2	2.28	0.48
25:DA:1416:G:O2'	25:DA:1417:C:OP2	2.21	0.48
25:DA:1665:A:OP2	60:DA:4604:HOH:O	2.20	0.48
25:DA:1927:A:H2'	25:DA:1928:A:C8	2.49	0.48
25:DA:2469:A:O2'	36:DQ:56:ARG:HD2	2.13	0.48
25:DA:2515:C:H2'	25:DA:2516:G:C8	2.48	0.48
26:DB:46:A:H2'	26:DB:47:C:C6	2.49	0.48
26:DB:3:C:H2'	26:DB:4:C:C6	2.48	0.48
31:DH:76:VAL:HA	31:DH:79:VAL:HG22	1.96	0.48
38:DS:23:ARG:NH2	38:DS:84:GLN:HG2	2.29	0.48
40:DU:20:LEU:HB3	40:DU:39:LEU:HD11	1.96	0.48
1:AA:405:U:OP2	4:AD:3:ARG:CZ	2.61	0.48
6:AF:18:GLN:N	6:AF:18:GLN:CD	2.66	0.48
12:AL:27:LEU:HD23	12:AL:30:ALA:O	2.14	0.48
16:AP:54:GLU:O	16:AP:57:ARG:HB3	2.13	0.48
17:AQ:6:LEU:HG	17:AQ:23:VAL:HG11	1.93	0.48
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.95	0.48
25:BA:236:G:H4'	25:BA:413:G:C5	2.49	0.48
25:BA:2644:A:O2'	25:BA:2821:G:O2'	2.20	0.48
25:BA:27:G:N2	25:BA:537:G:H1'	2.29	0.48
26:BB:75:G:N2	45:BZ:87:ASP:OD1	2.44	0.48
44:BY:92:ASN:HD22	44:BY:92:ASN:H	1.61	0.48
1:CA:1004:A:H5'	1:CA:1024:G:N2	2.29	0.48
1:CA:1246:C:H2'	1:CA:1247:U:H6	1.79	0.48
1:CA:1353:G:H2'	1:CA:1354:C:H6	1.79	0.48
10:CJ:47:PHE:HB2	10:CJ:63:PHE:HB2	1.94	0.48
35:DP:63:PRO:HG2	54:D8:25:MET:HB2	1.96	0.48
25:DA:1260:G:C6	25:DA:1261:C:C4	3.01	0.48
25:DA:1541:G:OP2	25:DA:1542:A:O2'	2.30	0.48
25:DA:2348:U:O4	25:DA:2382:G:N1	2.46	0.48
25:DA:2533:A:OP1	25:DA:2665:A:O2'	2.31	0.48
25:DA:271(K):U:H4'	25:DA:271(L):U:OP2	2.13	0.48
30:DG:171:ALA:O	30:DG:175:LEU:N	2.45	0.48
1:AA:1252:A:H61	1:AA:1285:A:H61	1.61	0.48
1:AA:551:U:H2'	1:AA:552:U:C6	2.49	0.48
2:AB:187:LEU:HD23	2:AB:201:ILE:O	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1320:C:N4	19:AS:36:ARG:HB2	2.29	0.48
25:BA:2138:G:N2	25:BA:2184:G:OP1	2.34	0.48
25:BA:2504:U:H2'	25:BA:2505:U:C6	2.48	0.48
25:BA:1686:U:H4'	25:BA:2711:C:H4'	1.95	0.48
25:BA:819:C:H2'	25:BA:820:U:H6	1.79	0.48
1:CA:105:G:H2'	1:CA:106:C:C6	2.49	0.48
1:CA:131:C:H2'	1:CA:132:C:C6	2.49	0.48
1:CA:382:A:H2'	1:CA:383:A:H8	1.79	0.48
1:CA:447:G:O6	60:CA:4099:HOH:O	2.17	0.48
1:CA:6:G:O2'	1:CA:7:G:H5'	2.14	0.48
2:CB:213:LEU:HD13	2:CB:214:ILE:HD13	1.95	0.48
8:CH:37:ARG:HH21	8:CH:38:ILE:HD11	1.78	0.48
12:CL:11:VAL:HG11	17:CQ:36:ILE:HG21	1.96	0.48
25:DA:1791:A:H3'	25:DA:1792:G:H8	1.79	0.48
25:DA:1803:A:H4'	27:DD:259:THR:HG23	1.96	0.48
25:DA:574:C:N3	28:DE:145:LYS:NZ	2.52	0.48
25:DA:595:C:H42	25:DA:662:G:H1	1.60	0.48
35:DP:44:GLY:CA	35:DP:45:LEU:HB2	2.43	0.48
1:AA:1200:C:OP1	60:AA:4099:HOH:O	2.20	0.47
1:AA:662:G:H2'	1:AA:663:A:H8	1.75	0.47
3:AC:81:GLY:O	3:AC:85:ARG:HG3	2.14	0.47
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.13	0.47
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.47	0.47
25:BA:101:A:H8	25:BA:101:A:O5'	1.97	0.47
25:BA:592:U:O2'	25:BA:1029:A:N1	2.33	0.47
25:BA:1091:A:H1'	25:BA:1093:G:N3	2.29	0.47
25:BA:1827:U:H2'	25:BA:1828:C:H6	1.77	0.47
25:BA:1848:G:OP1	27:BD:88:ARG:NH2	2.47	0.47
25:BA:2125:C:C2	25:BA:2209:G:C2	3.02	0.47
25:BA:1856:A:OP1	27:BD:249:PRO:HD3	2.14	0.47
34:BO:36:GLY:HA2	34:BO:106:LEU:HD23	1.96	0.47
36:BQ:32:TYR:OH	36:BQ:111:GLU:OE1	2.22	0.47
1:CA:1323:G:H4'	1:CA:1363:C:C2	2.49	0.47
1:CA:193:C:H2'	1:CA:194:C:H6	1.78	0.47
1:CA:397:A:H3'	1:CA:397:A:N3	2.29	0.47
5:CE:34:VAL:O	5:CE:42:GLY:N	2.45	0.47
13:CM:10:PRO:HG2	13:CM:21:TYR:HD2	1.79	0.47
15:CO:9:GLN:HA	15:CO:12:ILE:HD12	1.95	0.47
46:D0:19:LYS:HB2	46:D0:19:LYS:HE2	1.65	0.47
25:DA:1638:C:H5''	25:DA:2710:C:O2'	2.14	0.47
25:DA:289:A:H2'	25:DA:290:G:O4'	2.14	0.47
25:DA:317:G:H2'	25:DA:318:C:O4'	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:390:A:H4'	25:DA:391:G:H5'	1.96	0.47
25:DA:686:G:N2	25:DA:788:A:H61	2.12	0.47
30:DG:179:PRO:HB2	50:D4:42:PHE:CE1	2.48	0.47
25:DA:1012:U:C5	33:DN:28:THR:HG21	2.47	0.47
36:DQ:138:ASP:OD2	45:DZ:81:ARG:NH1	2.47	0.47
1:AA:1431:C:H2'	1:AA:1432:G:O4'	2.14	0.47
1:AA:1456:G:O6	20:AT:54:LYS:NZ	2.46	0.47
1:AA:339:C:H2'	1:AA:340:U:C6	2.50	0.47
1:AA:690:G:C6	1:AA:691:G:C6	3.02	0.47
1:AA:651:C:N4	1:AA:752:G:O2'	2.47	0.47
2:AB:207:ALA:O	2:AB:211:ILE:HG13	2.14	0.47
1:AA:429:U:H3'	4:AD:9:CYS:SG	2.54	0.47
11:AK:48:ILE:O	11:AK:50:TYR:N	2.47	0.47
1:AA:35:G:O2'	12:AL:118:SER:O	2.24	0.47
25:BA:1065:U:O2'	25:BA:1067:A:H2	1.96	0.47
26:BB:43:C:OP1	50:B4:6:HIS:NE2	2.40	0.47
1:CA:114:U:H2'	1:CA:115:G:C8	2.49	0.47
1:CA:1304:G:C6	1:CA:1305:G:N1	2.82	0.47
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.13	0.47
1:CA:926:G:H22	22:CV:16:A:P	2.36	0.47
14:CN:3:ARG:O	14:CN:7:ILE:HG23	2.14	0.47
20:CT:50:GLU:HG3	20:CT:100:ILE:HG23	1.96	0.47
46:D0:82:ARG:HA	46:D0:83:PRO:HD3	1.71	0.47
55:D9:4:ARG:HD3	55:D9:6:SER:O	2.14	0.47
25:DA:1481:U:H3	25:DA:1510:G:H1	1.61	0.47
25:DA:1670:C:O2	28:DE:129:HIS:NE2	2.40	0.47
25:DA:1959:G:OP2	60:DA:4575:HOH:O	2.20	0.47
25:DA:2296:U:OP2	38:DS:6:ALA:HB2	2.14	0.47
25:DA:2468:G:OP1	36:DQ:119:ARG:NH2	2.45	0.47
25:DA:2710:C:H2'	25:DA:2711:A:C8	2.50	0.47
26:DB:24:G:N2	26:DB:27:C:H42	2.11	0.47
25:DA:2572:A:N7	28:DE:144:ARG:HD2	2.28	0.47
29:DF:183:VAL:O	29:DF:187:VAL:HG23	2.14	0.47
25:DA:1188:U:C4'	41:DV:79:VAL:HG22	2.43	0.47
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.13	0.47
4:AD:173:TRP:HA	4:AD:187:ARG:NH2	2.28	0.47
4:AD:107:ARG:HH22	4:AD:194:LEU:HD21	1.80	0.47
7:AG:16:LEU:HD11	9:AI:45:ALA:HB2	1.96	0.47
25:BA:1093:G:H2'	25:BA:1156:G:H1	1.79	0.47
25:BA:1446:G:H2'	25:BA:1447:G:C8	2.49	0.47
34:BO:77:ILE:HD12	39:BT:74:ARG:HD3	1.97	0.47
45:BZ:137:ILE:HA	45:BZ:156:LYS:NZ	2.28	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1057:G:H2'	1:CA:1058:G:O4'	2.13	0.47
1:CA:1427:U:H2'	1:CA:1428:A:C8	2.48	0.47
1:CA:643:C:H2'	1:CA:644:G:H8	1.78	0.47
8:CH:28:ALA:HB3	8:CH:57:PRO:HB2	1.96	0.47
6:CF:97:PHE:HD2	18:CR:31:LEU:HD23	1.79	0.47
50:D4:57:GLU:HA	50:D4:58:ARG:HA	1.70	0.47
25:DA:1224:C:O2'	41:DV:86:GLY:N	2.42	0.47
25:DA:1292:U:H2'	25:DA:1293:C:C6	2.49	0.47
25:DA:2137:C:C2	25:DA:2155:G:C6	3.02	0.47
29:DF:24:LEU:HD23	29:DF:115:ALA:HA	1.95	0.47
30:DG:12:TYR:HA	30:DG:16:ARG:HG3	1.96	0.47
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.46	0.47
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.31	0.47
2:AB:184:VAL:HG12	2:AB:197:VAL:HG13	1.96	0.47
5:AE:113:ALA:HB3	5:AE:115:VAL:HG23	1.96	0.47
6:AF:2:ARG:NE	6:AF:69:GLU:HG2	2.29	0.47
7:AG:20:ASP:OD2	7:AG:63:LYS:NZ	2.37	0.47
1:AA:130:A:C8	17:AQ:63:ARG:HB2	2.49	0.47
6:AF:7:ASN:HD21	18:AR:34:TYR:HE1	1.62	0.47
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.47	0.47
25:BA:1016:C:H2'	25:BA:1017:G:O4'	2.14	0.47
25:BA:1223:C:H2'	25:BA:1224:C:H6	1.79	0.47
25:BA:1449:C:C5'	25:BA:1518:A:H1'	2.44	0.47
25:BA:2166:U:H2'	25:BA:2168:C:C5	2.49	0.47
25:BA:2299:A:N6	25:BA:2356:U:H3	2.04	0.47
25:BA:302:A:H2'	25:BA:303:C:C5	2.49	0.47
33:BN:15:LEU:HD12	33:BN:137:LYS:HG2	1.97	0.47
36:BQ:12:GLN:HG2	36:BQ:73:PRO:HD2	1.95	0.47
1:CA:1004:A:C6	1:CA:1037:C:C2	3.02	0.47
1:CA:1329:A:OP2	21:CU:7:ARG:NH2	2.47	0.47
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.29	0.47
1:CA:56:U:H2'	1:CA:57:G:H8	1.80	0.47
2:CB:172:ILE:HG22	2:CB:176:GLU:HG3	1.96	0.47
6:CF:14:LEU:HD13	6:CF:19:LEU:HA	1.96	0.47
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.49	0.47
25:DA:585:G:H2'	25:DA:1251:C:H42	1.79	0.47
25:DA:1300:U:H4'	25:DA:1301:A:C5'	2.43	0.47
25:DA:1613:G:C2	25:DA:1619:G:C5	3.02	0.47
25:DA:2171:A:H1'	25:DA:2172:U:C2	2.49	0.47
25:DA:235:U:H2'	25:DA:236:C:H6	1.79	0.47
25:DA:2371:G:C2	25:DA:2372:G:C8	3.03	0.47
29:DF:53:THR:HG22	29:DF:56:GLU:HG3	1.95	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:DN:36:GLY:HA2	33:DN:38:HIS:CE1	2.49	0.47
35:DP:121:LYS:HB3	35:DP:123:LEU:HG	1.96	0.47
36:DQ:29:PHE:HB2	36:DQ:105:GLU:OE2	2.14	0.47
38:DS:74:ALA:HB3	38:DS:108:GLY:HA3	1.95	0.47
4:AD:201:GLN:HE22	4:AD:204:ILE:HD12	1.79	0.47
15:AO:84:LYS:HD3	15:AO:84:LYS:O	2.14	0.47
25:BA:1096:A:H2'	25:BA:1097:G:C8	2.49	0.47
25:BA:1218:G:HO2'	25:BA:1219:A:C5'	2.27	0.47
25:BA:178:G:OP2	47:B1:39:LYS:NZ	2.42	0.47
25:BA:1935:A:H4'	25:BA:1936:C:C5'	2.45	0.47
25:BA:2336:C:H5''	25:BA:2337:G:H5'	1.96	0.47
25:BA:2672:A:H2'	25:BA:2673:G:O4'	2.14	0.47
25:BA:2825:C:H2'	25:BA:2826:C:C6	2.49	0.47
25:BA:741:U:OP1	27:BD:59:LYS:NZ	2.42	0.47
25:BA:794:U:O2	25:BA:2036:A:H1'	2.14	0.47
25:BA:946:A:H2'	25:BA:947:A:O4'	2.14	0.47
26:BB:24:G:N7	26:BB:56:G:H2'	2.29	0.47
30:BG:18:GLU:HG2	30:BG:175:LEU:HD21	1.96	0.47
31:BH:98:LEU:HD13	31:BH:125:VAL:HG23	1.97	0.47
36:BQ:31:ASP:N	36:BQ:106:VAL:O	2.40	0.47
1:CA:143:A:H5''	1:CA:144:G:H5'	1.95	0.47
2:CB:73:THR:OG1	2:CB:95:GLN:O	2.12	0.47
3:CC:20:SER:HB2	3:CC:40:ARG:NH1	2.28	0.47
6:CF:97:PHE:CZ	18:CR:61:LYS:HE3	2.49	0.47
1:CA:878:G:OP1	8:CH:88:LYS:HB3	2.14	0.47
13:CM:14:ARG:HG3	13:CM:44:ARG:NH1	2.29	0.47
13:CM:81:LEU:HD21	13:CM:88:ARG:NH2	2.29	0.47
14:CN:22:THR:HB	14:CN:33:VAL:HG21	1.96	0.47
19:CS:40:ILE:HA	19:CS:44:MET:SD	2.54	0.47
55:D9:3:VAL:HA	55:D9:35:ARG:O	2.15	0.47
25:DA:208:C:H2'	25:DA:209:C:C6	2.49	0.47
25:DA:2154:G:N3	25:DA:2154:G:H2'	2.29	0.47
25:DA:2156:G:N7	25:DA:2157:G:N1	2.62	0.47
25:DA:311:A:C6	25:DA:328:U:C4	3.02	0.47
25:DA:652(T):C:H2'	25:DA:652(U):G:C8	2.50	0.47
25:DA:58:G:O2'	25:DA:73:A:N1	2.45	0.47
26:DB:29:A:P	38:DS:31:SER:HB2	2.54	0.47
28:DE:170:LEU:HB3	28:DE:184:VAL:CG2	2.45	0.47
40:DU:82:GLY:O	40:DU:86:ALA:N	2.42	0.47
25:DA:1160:G:N2	41:DV:10:LYS:HZ2	2.13	0.47
45:DZ:24:LEU:HD12	45:DZ:25:PRO:HD2	1.96	0.47
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.35	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:189(D):C:O2	1:AA:189(H):G:N1	2.48	0.47
3:AC:123:GLN:HB3	3:AC:128:PHE:HD2	1.80	0.47
7:AG:15:ASP:OD1	7:AG:20:ASP:N	2.46	0.47
8:AH:87:SER:HA	8:AH:93:VAL:HG23	1.95	0.47
1:AA:376:G:O2'	16:AP:5:ARG:NH2	2.47	0.47
25:BA:2451:A:C8	25:BA:2451:A:H5'	2.49	0.47
25:BA:2892:A:OP1	37:BR:96:ARG:NE	2.40	0.47
25:BA:303:C:H2'	25:BA:304:C:H5'	1.97	0.47
25:BA:691:G:N2	25:BA:700:A:H1'	2.29	0.47
27:BD:13:ARG:HD2	27:BD:13:ARG:HA	1.67	0.47
27:BD:162:SER:HB3	27:BD:195:ALA:HB2	1.96	0.47
41:BV:72:VAL:HG13	41:BV:85:LYS:HB3	1.97	0.47
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.80	0.47
54:D8:54:GLU:O	54:D8:58:ILE:HG13	2.15	0.47
25:DA:2103:C:H2'	25:DA:2104:G:H5'	1.97	0.47
25:DA:2615:U:C2	51:D5:7:PRO:HA	2.49	0.47
25:DA:582:G:H2'	25:DA:583:G:C8	2.50	0.47
25:DA:971:C:OP1	25:DA:989:G:N1	2.33	0.47
29:DF:40:GLN:NE2	29:DF:184:TYR:H	2.12	0.47
1:AA:1103:C:H2'	1:AA:1104:G:O4'	2.14	0.47
1:AA:171:A:H2'	1:AA:172:A:C8	2.49	0.47
1:AA:975:A:N6	1:AA:1367:C:O4'	2.48	0.47
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.30	0.47
2:AB:211:ILE:O	2:AB:215:LEU:HB2	2.14	0.47
3:AC:47:LEU:HD13	3:AC:68:VAL:HG11	1.97	0.47
9:AI:49:PRO:HG2	9:AI:81:ILE:HG23	1.96	0.47
1:AA:134:A:H61	16:AP:25:ARG:NH1	2.13	0.47
25:BA:2088:C:C2'	25:BA:2089:G:H5'	2.45	0.47
25:BA:2543:A:N7	31:BH:175:LYS:HD2	2.30	0.47
28:BE:25:VAL:HG22	28:BE:183:LEU:HD11	1.96	0.47
30:BG:145:THR:HB	30:BG:148:MET:HG3	1.97	0.47
25:BA:7:G:H5''	33:BN:121:LYS:NZ	2.28	0.47
1:CA:1264:C:O2	1:CA:1272:G:N2	2.48	0.47
1:CA:176:C:H2'	1:CA:177:C:H6	1.79	0.47
3:CC:179:ARG:O	3:CC:206:GLU:HB3	2.15	0.47
3:CC:32:LEU:O	3:CC:36:ASP:HB2	2.13	0.47
4:CD:19:LEU:HA	4:CD:19:LEU:HD13	1.72	0.47
36:DQ:85:LYS:HG2	46:D0:7:LEU:HB3	1.96	0.47
54:D8:10:ALA:HB3	54:D8:62:LEU:HD21	1.97	0.47
25:DA:1446:C:O2	25:DA:1545:A:O2'	2.32	0.47
25:DA:442:G:H4'	29:DF:46:ARG:HG3	1.96	0.47
27:DD:111:LEU:HD22	27:DD:115:GLN:NE2	2.30	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DG:138:GLN:HB3	30:DG:153:ARG:O	2.15	0.47
33:DN:67:LEU:O	33:DN:88:GLU:HG3	2.15	0.47
25:DA:1188:U:H4'	41:DV:79:VAL:HG22	1.96	0.47
1:AA:266:G:H5''	1:AA:268:C:H41	1.79	0.47
1:AA:38:G:O2'	1:AA:39:G:H5''	2.15	0.47
1:AA:542:G:P	4:AD:10:ARG:HH22	2.38	0.47
1:AA:78:G:N2	1:AA:91:C:C2	2.83	0.47
4:AD:178:VAL:C	4:AD:180:GLY:H	2.18	0.47
9:AI:118:LYS:HG3	9:AI:121:ARG:HB3	1.97	0.47
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.50	0.47
25:BA:2184:G:H5''	25:BA:2194:U:H2'	1.96	0.47
25:BA:612:C:H2'	25:BA:613:A:C8	2.50	0.47
26:BB:1:U:O2'	26:BB:2:C:OP1	2.27	0.47
25:BA:470:C:H4'	29:BF:49:ALA:HB2	1.96	0.47
31:BH:3:ARG:HD3	31:BH:54:ARG:HH12	1.79	0.47
32:BI:123:LEU:HA	32:BI:144:VAL:HG23	1.97	0.47
36:BQ:21:THR:OG1	36:BQ:99:PRO:O	2.32	0.47
44:BY:92:ASN:HB2	44:BY:94:LYS:N	2.28	0.47
45:BZ:72:ARG:HG2	45:BZ:72:ARG:HH11	1.80	0.47
1:CA:438:G:N1	1:CA:495:A:OP2	2.36	0.47
1:CA:503:C:C2'	1:CA:504:C:H5'	2.44	0.47
5:CE:82:VAL:HG21	5:CE:138:ALA:HA	1.96	0.47
5:CE:139:LEU:HA	5:CE:142:LEU:HD12	1.97	0.47
1:CA:1367:C:HO2'	10:CJ:48:THR:HG1	1.58	0.47
17:CQ:59:ILE:HG22	17:CQ:73:VAL:HA	1.96	0.47
24:CX:10:G:N2	24:CX:26:G:H1'	2.30	0.47
25:DA:1226:A:OP1	41:DV:84:LYS:NZ	2.21	0.47
25:DA:450:G:P	25:DA:1248:G:H22	2.38	0.47
25:DA:1496:A:N3	25:DA:1577:C:O2'	2.41	0.47
26:DB:110:G:H2'	26:DB:111:G:H8	1.80	0.47
26:DB:2:C:O2'	26:DB:3:C:H5'	2.14	0.47
28:DE:143:ASN:HD22	28:DE:147:PRO:HD3	1.80	0.47
29:DF:116:ASP:O	29:DF:120:GLU:HG2	2.15	0.47
32:DI:66:GLU:OE2	32:DI:69:LYS:HD3	2.13	0.47
28:DE:181:LEU:HD11	39:DT:6:LEU:HG	1.97	0.47
1:AA:431:A:H2'	1:AA:432:A:O4'	2.15	0.47
1:AA:96:U:H2'	1:AA:97:G:C8	2.50	0.47
2:AB:210:SER:O	2:AB:214:ILE:HG12	2.15	0.47
4:AD:155:LEU:CD2	4:AD:157:LEU:H	2.28	0.47
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.15	0.47
14:AN:4:LYS:HA	14:AN:7:ILE:HG22	1.97	0.47
50:B4:40:HIS:CE1	50:B4:42:PHE:HB3	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
52:B6:40:CYS:HA	52:B6:41:PRO:HD3	1.72	0.47
25:BA:1078:A:H2	25:BA:1168:G:H22	1.63	0.47
25:BA:1522:G:H2'	25:BA:1523:C:C6	2.50	0.47
25:BA:2742:G:H2'	25:BA:2743:C:O4'	2.14	0.47
25:BA:551:A:N3	25:BA:2066:C:H1'	2.30	0.47
25:BA:704:U:H2'	25:BA:705:C:H6	1.80	0.47
36:BQ:23:GLY:O	36:BQ:101:ARG:NH1	2.48	0.47
1:CA:1028:C:O2	1:CA:1033:G:N1	2.48	0.47
1:CA:1187:G:H4'	9:CI:111:ARG:HH11	1.80	0.47
1:CA:1330:U:H2'	1:CA:1331:G:H5'	1.97	0.47
1:CA:444:C:H2'	1:CA:445:G:C8	2.50	0.47
1:CA:728:A:OP1	15:CO:54:ARG:NH1	2.48	0.47
15:CO:5:LYS:O	15:CO:9:GLN:HG2	2.15	0.47
47:D1:23:LYS:HB3	47:D1:29:GLY:HA3	1.97	0.47
47:D1:83:GLU:HA	47:D1:84:GLY:HA2	1.65	0.47
25:DA:1027:A:N6	25:DA:1126:A:C4	2.83	0.47
25:DA:1608:A:H1'	25:DA:1610:A:OP2	2.14	0.47
25:DA:1688:U:H2'	25:DA:1698:A:N6	2.30	0.47
25:DA:2820:A:O2'	25:DA:2821:A:OP1	2.30	0.47
32:DI:72:LEU:HA	32:DI:75:LEU:HD23	1.97	0.47
1:AA:1025:U:C2	1:AA:1036:G:O6	2.68	0.47
1:AA:539:A:H2'	1:AA:540:G:C8	2.50	0.47
1:AA:636:U:H2'	1:AA:637:G:C8	2.50	0.47
25:BA:593:G:H2'	25:BA:2052:A:C5	2.50	0.47
25:BA:599:U:O5'	25:BA:599:U:H6	1.98	0.47
25:BA:876:A:N7	25:BA:2260:C:H5'	2.30	0.47
25:BA:936:C:H2'	25:BA:936:C:OP2	2.15	0.47
28:BE:34:VAL:HG21	28:BE:78:LEU:HD11	1.96	0.47
44:BY:5:MET:HG2	44:BY:30:VAL:HG11	1.97	0.47
1:CA:1252:A:H61	1:CA:1285:A:H61	1.61	0.47
2:CB:19:HIS:CE1	2:CB:206:ASP:HB2	2.50	0.47
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.47	0.47
25:DA:1512:U:H2'	25:DA:1513:C:C6	2.50	0.47
25:DA:1537:G:H2'	25:DA:1538:G:C8	2.47	0.47
25:DA:2057:A:H2'	25:DA:2058:A:C8	2.50	0.47
25:DA:2156:G:O5'	25:DA:2156:G:H8	1.98	0.47
25:DA:385:C:O2	35:DP:71:VAL:HG21	2.14	0.47
32:DI:12:LEU:HD22	32:DI:19:VAL:HG21	1.97	0.47
1:AA:1005:A:N3	1:AA:1036:G:N2	2.62	0.47
1:AA:580:U:H5''	15:AO:58:MET:HG2	1.96	0.47
1:AA:868:C:H2'	1:AA:869:G:O4'	2.14	0.47
2:AB:231:GLU:HB2	2:AB:232:PRO:CD	2.38	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:AS:19:VAL:HG21	19:AS:44:MET:HG2	1.96	0.47
49:B3:19:GLN:OE1	49:B3:52:HIS:NE2	2.39	0.47
52:B6:39:TYR:HA	52:B6:46:HIS:HA	1.97	0.47
25:BA:1653:C:H5''	25:BA:1654:A:H5'	1.97	0.47
25:BA:1690:G:H2'	25:BA:1691:C:O4'	2.14	0.47
25:BA:207:A:C2	25:BA:224:U:H4'	2.50	0.47
25:BA:2303:U:H2'	25:BA:2304:C:C6	2.50	0.47
25:BA:2753:A:H2'	25:BA:2754:A:C8	2.50	0.47
34:BO:4:PRO:O	34:BO:5:GLN:HB2	2.15	0.47
3:CC:82:GLU:HG2	3:CC:85:ARG:NH2	2.28	0.47
5:CE:94:ALA:HB2	5:CE:119:LEU:HG	1.98	0.47
25:DA:1983:C:H2'	25:DA:1984:G:H5''	1.96	0.47
25:DA:2138:C:H42	25:DA:2153:G:H1	1.62	0.47
25:DA:571:A:N6	25:DA:2499:C:O3'	2.48	0.47
30:DG:82:LEU:HA	30:DG:86:MET:SD	2.55	0.47
33:DN:91:LEU:HG	33:DN:98:VAL:HG21	1.97	0.47
25:DA:335:C:H4'	44:DY:73:ARG:HD3	1.97	0.47
45:DZ:54:HIS:HB3	45:DZ:101:PRO:HD3	1.97	0.47
1:AA:438:G:N1	1:AA:495:A:OP2	2.27	0.46
1:AA:798:G:OP1	11:AK:122:LYS:NZ	2.46	0.46
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.50	0.46
48:B2:36:ARG:O	48:B2:40:SER:N	2.40	0.46
25:BA:1475:G:H2'	25:BA:1476:C:C6	2.51	0.46
25:BA:1688:A:H2'	25:BA:1689:G:O4'	2.16	0.46
25:BA:272:U:OP1	32:BI:50:ARG:NH1	2.42	0.46
25:BA:2860:A:OP2	25:BA:2876:U:H5	1.98	0.46
13:AM:83:ASP:HA	25:BA:935:C:O2	2.15	0.46
28:BE:144:ARG:HB3	28:BE:145:LYS:H	1.50	0.46
31:BH:149:ARG:NH1	31:BH:167:GLU:OE2	2.42	0.46
1:CA:1028:C:C2	1:CA:1033:G:N1	2.83	0.46
1:CA:1122:U:C4	1:CA:1123:A:N7	2.84	0.46
1:CA:1144:G:N2	1:CA:1146:A:H62	2.13	0.46
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.15	0.46
1:CA:472:A:H5''	16:CP:80:PHE:HB3	1.97	0.46
1:CA:952:U:H2'	1:CA:953:G:C8	2.50	0.46
2:CB:207:ALA:HB3	2:CB:210:SER:HB2	1.97	0.46
4:CD:150:GLU:OE2	4:CD:151:LYS:N	2.49	0.46
13:CM:16:ASP:HB3	13:CM:34:LEU:HD11	1.96	0.46
13:CM:90:LEU:HA	13:CM:93:ARG:HG3	1.98	0.46
21:CU:7:ARG:NH1	21:CU:21:TYR:OH	2.48	0.46
25:DA:1493:C:C5	25:DA:2206:G:H2'	2.50	0.46
25:DA:2206:G:H3'	25:DA:2207:G:H8	1.78	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2302:G:C2'	25:DA:2303:G:H5'	2.44	0.46
25:DA:2769:C:H2'	25:DA:2770:G:O4'	2.15	0.46
25:DA:2838:G:C6	25:DA:2839:G:C5	3.03	0.46
25:DA:479:A:H1'	25:DA:481:G:H5''	1.96	0.46
25:DA:706:A:OP1	27:DD:7:LYS:NZ	2.23	0.46
25:DA:839:U:H2'	25:DA:840:C:H6	1.80	0.46
29:DF:37:VAL:O	29:DF:41:LEU:HG	2.15	0.46
32:DI:40:THR:HG23	32:DI:43:ASN:HD21	1.79	0.46
26:DB:50:G:OP2	38:DS:62:LYS:HB2	2.14	0.46
45:DZ:121:HIS:HB3	45:DZ:123:ASP:O	2.15	0.46
1:AA:1097:C:O2	1:AA:1169:A:H2	1.98	0.46
1:AA:643:C:H2'	1:AA:644:G:H8	1.79	0.46
1:AA:737:A:OP2	6:AF:92:LYS:NZ	2.40	0.46
2:AB:101:MET:HA	2:AB:108:ILE:HD12	1.95	0.46
4:AD:102:ASP:OD1	4:AD:103:ASN:N	2.48	0.46
20:AT:64:ASP:OD2	20:AT:81:LYS:NZ	2.43	0.46
25:BA:2201:C:H2'	25:BA:2202:U:C6	2.49	0.46
25:BA:2347:A:O2'	25:BA:2348:A:OP2	2.26	0.46
25:BA:2479:C:H4'	36:BQ:123:HIS:CD2	2.51	0.46
31:BH:69:ARG:HG3	31:BH:70:THR:N	2.30	0.46
39:BT:112:ARG:HG3	39:BT:115:ARG:HH21	1.80	0.46
39:BT:33:LYS:HB3	39:BT:82:LEU:HD23	1.96	0.46
39:BT:53:ARG:NH1	39:BT:60:THR:OG1	2.48	0.46
45:BZ:145:GLU:O	45:BZ:148:ASP:N	2.48	0.46
1:CA:1344:C:H5'	9:CI:121:ARG:HA	1.98	0.46
1:CA:1431:C:H42	1:CA:1469:G:H1	1.63	0.46
1:CA:598:U:H4'	8:CH:94:TYR:CD2	2.50	0.46
1:CA:664:G:H22	1:CA:741:G:H1	1.62	0.46
1:CA:877:C:O2	8:CH:3:THR:OG1	2.32	0.46
5:CE:71:LEU:HD11	5:CE:115:VAL:HG22	1.96	0.46
9:CI:17:VAL:HG11	9:CI:80:GLY:C	2.35	0.46
11:CK:85:ARG:HG2	11:CK:112:THR:HA	1.97	0.46
25:DA:817:C:O2'	25:DA:839:U:H5''	2.14	0.46
25:DA:902:C:H2'	25:DA:903:C:C6	2.50	0.46
27:DD:2:ALA:HB3	27:DD:20:ASP:HB3	1.97	0.46
29:DF:192:LEU:HD13	29:DF:194:MET:HE2	1.97	0.46
38:DS:7:TYR:CE2	38:DS:11:LYS:HE2	2.51	0.46
44:DY:102:CYS:SG	44:DY:104:GLY:N	2.78	0.46
45:DZ:108:PRO:HB3	45:DZ:144:LEU:HD12	1.97	0.46
1:AA:1060:C:N4	3:AC:2:GLY:HA3	2.30	0.46
1:AA:107:G:H2'	1:AA:108:G:O4'	2.15	0.46
1:AA:278:G:C2	17:AQ:95:TYR:HD2	2.33	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:429:U:H1'	1:AA:430:A:H5''	1.97	0.46
3:AC:114:PRO:HD3	3:AC:183:ASP:OD1	2.16	0.46
1:AA:430:A:OP2	4:AD:8:VAL:HG12	2.15	0.46
25:BA:1014:U:H2'	25:BA:1015:C:C6	2.50	0.46
38:BS:15:ARG:O	38:BS:19:LYS:HG2	2.15	0.46
1:CA:1185:G:C2	1:CA:1186:G:H1'	2.50	0.46
1:CA:1530:G:OP1	1:CA:1530:G:H4'	2.14	0.46
1:CA:193:C:H2'	1:CA:194:C:C6	2.51	0.46
1:CA:601:C:H2'	1:CA:602:A:C8	2.50	0.46
1:CA:673:G:H2'	1:CA:674:G:C8	2.49	0.46
1:CA:689:C:H42	1:CA:698:G:H1	1.62	0.46
2:CB:8:LYS:HE2	2:CB:51:LEU:HD13	1.96	0.46
3:CC:45:LYS:HE3	3:CC:45:LYS:H	1.79	0.46
9:CI:23:ASN:HD22	9:CI:25:LYS:H	1.61	0.46
25:DA:415:A:H2'	25:DA:416:C:H6	1.80	0.46
25:DA:467:G:OP1	53:D7:33:ARG:NH1	2.48	0.46
25:DA:664:C:OP2	60:DA:4171:HOH:O	2.20	0.46
26:DB:90:A:N7	26:DB:91:C:H1'	2.30	0.46
38:DS:28:VAL:HG11	38:DS:98:VAL:HG13	1.98	0.46
1:AA:1414:U:H3	1:AA:1486:G:H1	1.64	0.46
1:AA:222:U:H2'	1:AA:223:U:C6	2.50	0.46
1:AA:384:G:H2'	1:AA:385:C:C6	2.50	0.46
1:AA:958:A:C6	19:AS:55:LYS:HB2	2.51	0.46
20:AT:45:GLN:HB3	20:AT:45:GLN:HE21	1.54	0.46
24:AX:53:G:H3'	24:AX:54:5MU:H71	1.96	0.46
25:BA:485:U:H5''	53:B7:40:TRP:CD2	2.50	0.46
25:BA:1722:C:N3	28:BE:128:SER:OG	2.49	0.46
38:BS:62:LYS:HB3	38:BS:97:ARG:NE	2.31	0.46
43:BX:65:ARG:HH11	43:BX:70:LEU:HD21	1.79	0.46
1:CA:1469:G:H2'	1:CA:1470:G:C8	2.50	0.46
1:CA:1502:A:H2	1:CA:1505:G:H1	1.63	0.46
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.51	0.46
1:CA:176:C:H2'	1:CA:177:C:C6	2.50	0.46
1:CA:922:G:H2'	1:CA:923:A:C8	2.50	0.46
9:CI:37:PHE:HB3	9:CI:43:ALA:CB	2.45	0.46
9:CI:70:LYS:O	9:CI:74:ILE:HG13	2.16	0.46
47:D1:53:VAL:HG22	47:D1:74:VAL:HG13	1.97	0.46
25:DA:1336:A:H2'	25:DA:1337:G:H8	1.81	0.46
25:DA:528:A:H2	25:DA:2042:A:H2'	1.79	0.46
25:DA:2392:A:N3	35:DP:61:ARG:HG2	2.31	0.46
25:DA:2630:G:H1	25:DA:2788:C:H42	1.63	0.46
33:DN:123:TYR:CE2	33:DN:129:PRO:HD2	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
34:DO:1:MET:HG3	34:DO:67:LYS:HG2	1.96	0.46
36:DQ:22:LYS:HE2	36:DQ:22:LYS:N	2.31	0.46
2:AB:24:TRP:CZ3	2:AB:26:PRO:HA	2.50	0.46
3:AC:64:VAL:HG22	3:AC:66:VAL:HG23	1.96	0.46
54:B8:33:ASN:HA	54:B8:36:LYS:HD2	1.97	0.46
25:BA:1249:A:H61	25:BA:1286:U:H2'	1.80	0.46
25:BA:1495:G:H1'	25:BA:1574:A:N1	2.31	0.46
25:BA:2450:U:O2'	25:BA:2452:C:OP1	2.29	0.46
26:BB:13:A:N1	26:BB:69:G:O2'	2.45	0.46
43:BX:54:VAL:HG22	43:BX:81:VAL:HG12	1.96	0.46
1:CA:1227:A:H8	1:CA:1227:A:H3'	1.80	0.46
1:CA:1247:U:H1'	1:CA:1291:G:N2	2.30	0.46
1:CA:1298:C:H4'	1:CA:1299:A:C4	2.50	0.46
1:CA:540:G:H2'	1:CA:541:G:H8	1.80	0.46
1:CA:659:U:H2'	1:CA:660:G:O4'	2.16	0.46
3:CC:116:VAL:HG22	3:CC:140:ARG:HH22	1.81	0.46
11:CK:20:TYR:CZ	11:CK:83:ILE:HD12	2.51	0.46
12:CL:109:GLY:HA3	12:CL:121:GLY:O	2.15	0.46
19:CS:50:ALA:HA	19:CS:58:VAL:O	2.15	0.46
52:D6:35:GLU:HA	52:D6:49:HIS:O	2.16	0.46
25:DA:1230:C:H2'	25:DA:1231:G:H8	1.80	0.46
25:DA:2809:A:H2'	25:DA:2810:A:C8	2.51	0.46
27:DD:164:GLN:NE2	27:DD:176:ARG:HH12	2.14	0.46
42:DW:86:LEU:HD22	42:DW:96:ILE:HD11	1.98	0.46
45:DZ:69:THR:HG22	45:DZ:90:VAL:HA	1.98	0.46
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.04	0.46
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.50	0.46
1:AA:1318:A:OP1	19:AS:7:LYS:NZ	2.29	0.46
1:AA:1452:C:O2'	1:AA:1456:G:H5''	2.16	0.46
1:AA:189(A):C:N4	1:AA:189(J):G:H1	2.14	0.46
1:AA:858:G:O6	1:AA:869:G:H3'	2.16	0.46
1:AA:98:G:H2'	1:AA:99:U:O4'	2.16	0.46
6:AF:11:ASN:HB3	6:AF:14:LEU:HG	1.98	0.46
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.16	0.46
25:BA:143:C:H2'	25:BA:144:C:H6	1.80	0.46
25:BA:2645:G:H2'	25:BA:2646:G:O4'	2.16	0.46
27:BD:275:LYS:HB3	27:BD:276:LYS:H	1.37	0.46
28:BE:105:THR:HG21	28:BE:164:ARG:CZ	2.45	0.46
44:BY:9:LYS:HA	44:BY:10:GLY:HA2	1.60	0.46
45:BZ:161:VAL:HG13	45:BZ:161:VAL:O	2.16	0.46
8:CH:29:SER:HB3	8:CH:32:LYS:HG3	1.96	0.46
14:CN:26:ARG:HB3	14:CN:43:CYS:SG	2.55	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
50:D4:53:GLU:HG2	50:D4:54:GLY:N	2.31	0.46
25:DA:1811:G:H2'	25:DA:1812:A:O4'	2.16	0.46
25:DA:2312:U:H4'	30:DG:71:THR:HB	1.96	0.46
25:DA:2382:G:H21	54:D8:42:ARG:NH2	2.13	0.46
25:DA:2682:U:H5'	28:DE:11:MET:O	2.16	0.46
25:DA:2712:U:H2'	25:DA:2714:G:H5''	1.97	0.46
25:DA:2850:A:H2'	25:DA:2851:A:C8	2.50	0.46
27:DD:133:LEU:HD12	27:DD:189:CYS:HB2	1.98	0.46
1:AA:255:G:C6	1:AA:256:U:C4	3.03	0.46
5:AE:51:VAL:O	5:AE:55:VAL:HG23	2.16	0.46
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.80	0.46
13:AM:19:LEU:HA	13:AM:22:ILE:HD12	1.98	0.46
25:BA:2388:A:N3	38:BS:106:ARG:NH2	2.61	0.46
25:BA:211:A:H5''	25:BA:448:U:OP1	2.16	0.46
25:BA:83:A:P	44:BY:8:LYS:HD2	2.55	0.46
25:BA:895:G:O6	25:BA:974:G:H2'	2.16	0.46
32:BI:1:MET:N	32:BI:21:VAL:O	2.33	0.46
1:CA:1003:G:H2'	1:CA:1004:A:H1'	1.97	0.46
1:CA:707:C:H2'	1:CA:708:C:C6	2.50	0.46
2:CB:16:HIS:O	2:CB:17:PHE:HD1	1.98	0.46
2:CB:54:THR:O	2:CB:57:PHE:HB3	2.15	0.46
4:CD:173:TRP:HB3	4:CD:187:ARG:HE	1.81	0.46
8:CH:46:LYS:HG2	8:CH:64:LYS:HE2	1.97	0.46
9:CI:78:LYS:HE2	9:CI:101:PHE:CD2	2.51	0.46
9:CI:89:ASN:O	9:CI:92:TYR:HB2	2.16	0.46
15:CO:69:TYR:CZ	15:CO:73:GLU:HG3	2.51	0.46
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.97	0.46
49:D3:10:LYS:HG2	60:D3:4001:HOH:O	2.15	0.46
25:DA:991:C:H42	25:DA:1163:G:H1	1.63	0.46
25:DA:1301:A:H2	25:DA:1626:G:N3	2.13	0.46
25:DA:1472:A:H2'	25:DA:1473:G:O4'	2.16	0.46
25:DA:1619:G:N7	60:DA:4281:HOH:O	2.36	0.46
25:DA:2126:A:H61	25:DA:2162:G:HO2'	1.62	0.46
25:DA:2126:A:H4'	25:DA:2127:G:OP1	2.15	0.46
25:DA:952:G:P	36:DQ:16:ARG:HH22	2.38	0.46
30:DG:96:ARG:O	30:DG:99:MET:HB3	2.15	0.46
1:AA:1296:C:H5''	13:AM:14:ARG:HD2	1.96	0.46
1:AA:518:C:HO2'	1:AA:1492:A:H61	1.63	0.46
1:AA:347:G:O2'	1:AA:348:G:OP1	2.33	0.46
25:BA:1216:G:C2	25:BA:1217:G:H1'	2.50	0.46
25:BA:1805:C:O5'	25:BA:1805:C:H6	1.99	0.46
25:BA:2125:C:N4	25:BA:2208:G:H1	2.10	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:673:G:O2'	25:BA:2363:G:OP1	2.27	0.46
1:CA:1126:U:H4'	1:CA:1281:U:H1'	1.97	0.46
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.51	0.46
1:CA:1496:C:H4'	25:DA:1920:C:O2'	2.16	0.46
1:CA:405:U:P	4:CD:3:ARG:NH2	2.89	0.46
1:CA:720:C:H2'	1:CA:721:G:C8	2.51	0.46
2:CB:125:PRO:HB2	2:CB:126:GLU:H	1.56	0.46
8:CH:78:GLN:HG2	8:CH:80:ILE:O	2.16	0.46
25:DA:1269:A:H2'	25:DA:1270:C:C6	2.51	0.46
25:DA:1344:G:O2'	25:DA:1385:G:H2'	2.16	0.46
25:DA:431:U:H6	25:DA:431:U:O5'	1.98	0.46
25:DA:78:A:H2'	25:DA:79:G:H8	1.80	0.46
26:DB:73:A:C4	26:DB:105:A:C2	3.04	0.46
30:DG:80:PHE:C	30:DG:82:LEU:H	2.18	0.46
31:DH:89:ILE:O	31:DH:129:THR:HG23	2.16	0.46
37:DR:95:THR:HG22	37:DR:116:LEU:HD23	1.98	0.46
45:DZ:119:GLU:HB2	45:DZ:122:ARG:NH1	2.29	0.46
25:DA:875:G:O2'	45:DZ:151:HIS:HE1	1.99	0.46
1:AA:1006:C:H42	1:AA:1023:G:H1	1.64	0.46
1:AA:1089:G:H1	1:AA:1096:C:N4	2.14	0.46
1:AA:946:A:O2'	1:AA:1333:A:N3	2.40	0.46
1:AA:358:U:H2'	1:AA:359:U:H6	1.81	0.46
1:AA:626:U:H2'	1:AA:627:G:C8	2.51	0.46
1:AA:924:C:H2'	1:AA:925:G:H8	1.81	0.46
3:AC:156:ARG:H	3:AC:196:LEU:HD22	1.81	0.46
13:AM:16:ASP:N	13:AM:16:ASP:OD1	2.49	0.46
50:B4:49:PHE:HB3	50:B4:50:VAL:H	1.53	0.46
54:B8:62:LEU:HB3	54:B8:65:GLU:CG	2.41	0.46
25:BA:1904:C:H2'	25:BA:1905:G:O4'	2.15	0.46
25:BA:2077:C:O2	60:BA:4028:HOH:O	2.21	0.46
25:BA:174:U:H4'	25:BA:207:A:H4'	1.97	0.46
37:BR:44:LEU:HD22	37:BR:48:VAL:HG23	1.98	0.46
44:BY:43:ASN:HD22	44:BY:43:ASN:HA	1.55	0.46
1:CA:1095:U:C4	1:CA:1096:C:C4	3.04	0.46
1:CA:1119:C:N3	1:CA:1154:G:O6	2.48	0.46
1:CA:1186:G:H4'	9:CI:110:GLU:CD	2.36	0.46
1:CA:1237:C:H5''	1:CA:1238:A:O4'	2.16	0.46
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.49	0.46
1:CA:581:G:N2	1:CA:759:A:OP2	2.41	0.46
7:CG:153:HIS:HE1	11:CK:57:THR:HG22	1.81	0.46
9:CI:15:ALA:HB2	9:CI:65:VAL:HG23	1.97	0.46
10:CJ:16:LEU:HD13	10:CJ:70:ARG:HG2	1.97	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:608:A:H4'	16:CP:32:TYR:OH	2.15	0.46
46:D0:24:LYS:HA	46:D0:24:LYS:HE2	1.97	0.46
25:DA:2037:G:O2'	25:DA:2038:G:H5'	2.16	0.46
25:DA:2165:G:H2'	25:DA:2166:G:C8	2.51	0.46
25:DA:2330:G:H2'	25:DA:2331:G:O4'	2.16	0.46
25:DA:2412:A:H2'	25:DA:2413:G:O4'	2.16	0.46
25:DA:2747:G:H1'	25:DA:2757:A:H61	1.81	0.46
25:DA:2773:C:H2'	25:DA:2774:C:H6	1.81	0.46
25:DA:2889:C:H3'	25:DA:2891:G:C8	2.51	0.46
25:DA:796:C:H2'	25:DA:797:C:C6	2.51	0.46
25:DA:924:C:H2'	25:DA:925:C:C6	2.51	0.46
32:DI:114:LEU:HD11	32:DI:128:LEU:HB3	1.98	0.46
33:DN:10:GLU:HA	33:DN:11:PRO:HD2	1.70	0.46
1:AA:999:C:H2'	1:AA:1000:U:O4'	2.15	0.46
1:AA:1445:C:N4	1:AA:1457:G:H1	2.14	0.46
1:AA:1515:C:H2'	1:AA:1516:G:C8	2.51	0.46
1:AA:126:G:H4'	1:AA:634:C:O2	2.16	0.46
1:AA:826:C:H2'	1:AA:827:U:H6	1.81	0.46
1:AA:266:G:O3'	17:AQ:67:LYS:HB2	2.16	0.46
51:B5:11:THR:HG23	51:B5:15:ARG:HB3	1.96	0.46
25:BA:1273:G:OP1	40:BU:13:LYS:HE3	2.16	0.46
25:BA:1405:A:N3	25:BA:1405:A:H5'	2.31	0.46
25:BA:1790:A:H1'	25:BA:2723:A:C2	2.51	0.46
25:BA:2250:G:H2'	25:BA:2250:G:N3	2.31	0.46
25:BA:895:G:C4	25:BA:978:A:H8	2.34	0.46
30:BG:179:PRO:HB2	50:B4:42:PHE:HE1	1.80	0.46
37:BR:26:LYS:HE2	37:BR:70:LEU:O	2.16	0.46
1:CA:1203:C:H2'	1:CA:1204:A:O4'	2.15	0.46
1:CA:145:G:H1	1:CA:177:C:H42	1.63	0.46
3:CC:38:ARG:O	3:CC:42:LEU:N	2.39	0.46
5:CE:68:GLU:HG3	5:CE:70:PRO:HD3	1.98	0.46
16:CP:4:ILE:HG13	16:CP:64:ALA:HB1	1.97	0.46
19:CS:32:LYS:HE2	19:CS:57:HIS:CD2	2.51	0.46
1:CA:926:G:N2	22:CV:16:A:OP1	2.48	0.46
25:DA:2615:U:N1	51:D5:7:PRO:HA	2.31	0.46
54:D8:32:LEU:O	54:D8:36:LYS:HE3	2.16	0.46
25:DA:1319:G:C6	25:DA:1320:C:N4	2.84	0.46
25:DA:1587:A:H2'	25:DA:1588:C:C6	2.51	0.46
25:DA:1630:G:H2'	25:DA:1631:C:C6	2.51	0.46
25:DA:2349:G:OP1	60:DA:4065:HOH:O	2.21	0.46
25:DA:251:A:C5	25:DA:252:G:H1'	2.51	0.46
25:DA:2723:C:H5"	37:DR:1:MET:HE2	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DE:6:GLY:HA2	28:DE:28:ALA:HA	1.98	0.46
31:DH:46:GLU:HB2	31:DH:49:VAL:HG12	1.97	0.46
36:DQ:75:THR:HG21	36:DQ:87:LYS:NZ	2.31	0.46
26:DB:27:C:O3'	38:DS:36:TYR:OH	2.33	0.46
1:AA:1030(B):C:O2	1:AA:1030(B):C:H2'	2.16	0.45
1:AA:283:C:H2'	1:AA:284:G:O4'	2.17	0.45
1:AA:757:U:H2'	1:AA:758:G:O4'	2.15	0.45
4:AD:164:ALA:O	4:AD:168:ARG:NH1	2.46	0.45
7:AG:26:PHE:CE2	7:AG:30:ILE:HD11	2.51	0.45
1:AA:1216:G:H5''	14:AN:5:ALA:CB	2.46	0.45
16:AP:38:TYR:CZ	16:AP:50:LYS:HB2	2.52	0.45
20:AT:16:HIS:O	20:AT:19:SER:OG	2.32	0.45
24:AX:33:U:O2'	24:AX:35:A:N7	2.37	0.45
50:B4:59:PHE:HB2	50:B4:62:ARG:HH12	1.82	0.45
25:BA:1248:G:O2'	25:BA:1288:A:N6	2.44	0.45
25:BA:1727:U:H2'	25:BA:1728:G:O4'	2.16	0.45
25:BA:261:A:H61	25:BA:284:G:H1'	1.81	0.45
28:BE:115:GLY:O	28:BE:119:ARG:HB2	2.17	0.45
30:BG:27:ASN:HB3	30:BG:30:GLU:HB2	1.98	0.45
25:BA:2287:C:O2	36:BQ:85:LYS:HG3	2.17	0.45
36:BQ:43:THR:HG22	36:BQ:94:VAL:HG12	1.99	0.45
39:BT:19:LEU:HD12	39:BT:78:LEU:HD13	1.97	0.45
1:CA:1024:G:C2'	1:CA:1025:U:H5''	2.45	0.45
1:CA:109:A:H2'	1:CA:326:G:N2	2.31	0.45
1:CA:1100:C:H2'	1:CA:1102:A:O5'	2.16	0.45
3:CC:47:LEU:CB	3:CC:52:LEU:HB2	2.46	0.45
1:CA:407:G:OP1	4:CD:115:ARG:NH2	2.49	0.45
4:CD:61:LYS:NZ	4:CD:72:GLU:OE1	2.39	0.45
54:D8:6:THR:HG22	54:D8:63:PRO:HD2	1.97	0.45
25:DA:2134:A:H3'	25:DA:2135:A:C8	2.51	0.45
25:DA:2206:G:H4'	25:DA:2206:G:OP2	2.16	0.45
25:DA:2774:C:H2'	25:DA:2775:A:O4'	2.16	0.45
25:DA:2776:A:H4'	25:DA:2777:G:H5''	1.97	0.45
25:DA:2886:G:H2'	25:DA:2887:U:C6	2.51	0.45
25:DA:506:G:O3'	25:DA:507:A:H8	1.99	0.45
25:DA:637:A:H2'	35:DP:117:GLU:OE2	2.16	0.45
34:DO:75:SER:OG	39:DT:74:ARG:NH1	2.49	0.45
35:DP:52:GLU:HG2	54:D8:57:ARG:HH12	1.81	0.45
25:DA:2849:U:P	39:DT:95:ARG:HH12	2.39	0.45
45:DZ:99:TYR:HA	45:DZ:124:ILE:O	2.16	0.45
1:AA:1241:G:H1	1:AA:1296:C:N4	2.14	0.45
1:AA:1295:G:H2'	1:AA:1296:C:H5'	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:147:G:C4	1:AA:148:G:C8	3.04	0.45
1:AA:576:G:O6	1:AA:880:C:O2'	2.28	0.45
1:AA:651:C:N4	1:AA:652:U:O4	2.49	0.45
1:AA:920:U:H2'	1:AA:921:U:C6	2.50	0.45
6:AF:100:ASN:HB2	18:AR:28:GLU:HA	1.98	0.45
1:AA:1151:A:N3	10:AJ:39:PRO:HG3	2.31	0.45
22:AV:19:U:H2'	22:AV:20:U:C6	2.51	0.45
46:B0:38:VAL:HG12	46:B0:40:GLN:HG2	1.99	0.45
51:B5:9:LYS:HD3	51:B5:9:LYS:HA	1.70	0.45
25:BA:2707:C:H2'	25:BA:2708:U:H6	1.81	0.45
25:BA:2724:U:H2'	25:BA:2727:G:H5''	1.99	0.45
25:BA:2784:C:H2'	25:BA:2785:C:C6	2.51	0.45
25:BA:302:A:H2'	25:BA:303:C:C6	2.51	0.45
25:BA:895:G:N3	25:BA:978:A:H1'	2.31	0.45
35:BP:100:LEU:HD12	35:BP:112:LEU:HD11	1.98	0.45
37:BR:38:VAL:HG12	37:BR:42:LYS:HE3	1.98	0.45
39:BT:37:GLY:HA2	39:BT:38:ASN:HA	1.72	0.45
1:CA:1154:G:N7	1:CA:1155:G:C5	2.84	0.45
1:CA:144:G:H1	1:CA:178:C:H42	1.64	0.45
3:CC:110:ASN:O	3:CC:141:VAL:HG22	2.16	0.45
14:CN:32:SER:OG	14:CN:32:SER:O	2.24	0.45
25:DA:2017:U:O2	51:D5:10:LYS:HB2	2.15	0.45
25:DA:1263:U:H1'	51:D5:10:LYS:HG3	1.99	0.45
53:D7:8:ASN:OD1	53:D7:11:LYS:N	2.26	0.45
55:D9:29:ASN:HB3	55:D9:32:HIS:ND1	2.30	0.45
25:DA:2023:G:H1	25:DA:2040:C:H42	1.64	0.45
25:DA:2137:C:N4	25:DA:2154:G:N1	2.47	0.45
25:DA:695:G:H2'	25:DA:696:G:O4'	2.17	0.45
29:DF:18:ARG:HG2	29:DF:19:GLU:H	1.81	0.45
30:DG:161:THR:HG22	30:DG:163:ALA:H	1.81	0.45
35:DP:38:GLN:O	35:DP:39:LYS:HB3	2.16	0.45
36:DQ:85:LYS:HD3	36:DQ:85:LYS:N	2.31	0.45
25:DA:1151:G:O2'	40:DU:77:SER:O	2.34	0.45
45:DZ:59:LEU:HD12	45:DZ:69:THR:HG21	1.97	0.45
1:AA:1024:G:H2'	1:AA:1025:U:H5'	1.98	0.45
4:AD:128:VAL:HG11	4:AD:138:TYR:CE2	2.51	0.45
13:AM:11:ARG:HA	13:AM:45:VAL:HB	1.98	0.45
25:BA:11:G:H2'	25:BA:12:U:H5'	1.97	0.45
25:BA:1387:U:OP2	25:BA:1440:U:O2'	2.27	0.45
25:BA:1604:C:OP2	25:BA:1605:A:O2'	2.24	0.45
25:BA:2638:C:H2'	25:BA:2639:G:O4'	2.16	0.45
25:BA:2787:C:H2'	25:BA:2788:A:O4'	2.15	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:360:C:H2'	25:BA:361:C:H6	1.81	0.45
25:BA:956:A:N3	25:BA:2276:C:O2'	2.41	0.45
25:BA:2075:G:OP1	28:BE:144:ARG:HG2	2.17	0.45
1:CA:1030(C):G:H2'	1:CA:1030(D):A:C8	2.51	0.45
1:CA:1095:U:P	1:CA:1108:G:H1	2.38	0.45
1:CA:1394:A:N6	1:CA:1501:C:H5'	2.31	0.45
4:CD:170:VAL:HG22	4:CD:171:GLY:H	1.82	0.45
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	1.97	0.45
25:DA:1925:C:H2'	25:DA:1926:U:H5''	1.98	0.45
25:DA:1978:A:H2'	25:DA:1979:C:H6	1.81	0.45
25:DA:2166:G:H3'	25:DA:2167:U:C5'	2.40	0.45
25:DA:589:C:H2'	25:DA:590:A:H8	1.79	0.45
25:DA:607:U:OP1	29:DF:102:PRO:HA	2.16	0.45
26:DB:30:C:H2'	26:DB:31:C:H5'	1.97	0.45
26:DB:43:C:C4	26:DB:45:A:N6	2.84	0.45
28:DE:144:ARG:HB3	28:DE:145:LYS:H	1.46	0.45
32:DI:48:GLU:HG3	32:DI:52:ARG:NH1	2.32	0.45
32:DI:77:LEU:HG	32:DI:101:LEU:HD12	1.99	0.45
43:DX:43:VAL:HG21	43:DX:81:VAL:HG11	1.97	0.45
45:DZ:77:ASP:HA	45:DZ:84:GLU:OE2	2.16	0.45
1:AA:988:G:H1	1:AA:1217:C:N4	2.13	0.45
4:AD:201:GLN:NE2	4:AD:204:ILE:HD12	2.31	0.45
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.52	0.45
1:AA:1321:C:O2'	19:AS:78:ARG:NH1	2.49	0.45
52:B6:35:GLU:HG2	52:B6:50:ARG:HD3	1.99	0.45
25:BA:2359:C:H2'	25:BA:2360:U:C6	2.52	0.45
25:BA:2760:G:O6	25:BA:2768:C:H5''	2.16	0.45
25:BA:603:C:H2'	25:BA:604:C:C6	2.51	0.45
27:BD:215:LEU:HB2	27:BD:217:ARG:HG3	1.98	0.45
43:BX:94:GLY:N	43:BX:95:LEU:HA	2.31	0.45
1:CA:1011:G:C6	1:CA:1012:U:C2	3.05	0.45
1:CA:189(C):C:H2'	1:CA:189(D):C:O4'	2.16	0.45
1:CA:827:U:H5''	1:CA:828:A:OP2	2.16	0.45
4:CD:61:LYS:HZ1	4:CD:72:GLU:CD	2.17	0.45
8:CH:119:LEU:HB3	8:CH:123:GLU:HB2	1.99	0.45
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.82	0.45
6:CF:100:ASN:ND2	18:CR:23:LYS:HE2	2.31	0.45
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.16	0.45
25:DA:1405:U:H2'	25:DA:1406:U:C6	2.51	0.45
25:DA:1877:A:H5'	25:DA:1878:G:OP2	2.17	0.45
25:DA:774:A:N3	25:DA:774:A:H2'	2.31	0.45
25:DA:855:G:C6	25:DA:856:C:N4	2.84	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DE:48:GLN:HG3	28:DE:80:GLU:HG2	1.98	0.45
29:DF:101:LEU:O	29:DF:106:ARG:NH1	2.45	0.45
30:DG:106:LEU:HA	30:DG:110:ALA:HB3	1.99	0.45
31:DH:124:GLU:OE1	31:DH:132:ARG:HB3	2.16	0.45
45:DZ:10:ARG:HG3	45:DZ:36:LYS:HB3	1.97	0.45
1:AA:1124:G:N7	1:AA:1145:C:O2'	2.47	0.45
1:AA:1246:C:N3	1:AA:1291:G:N2	2.51	0.45
1:AA:347:G:O2'	1:AA:348:G:P	2.74	0.45
1:AA:955:U:OP1	13:AM:120:LYS:HD2	2.17	0.45
4:AD:158:ILE:HG12	4:AD:159:ARG:N	2.31	0.45
4:AD:173:TRP:HA	4:AD:187:ARG:NE	2.31	0.45
5:AE:24:ARG:HE	5:AE:24:ARG:HB3	1.65	0.45
7:AG:45:ASP:O	7:AG:49:ILE:HG13	2.15	0.45
10:AJ:38:ILE:HG13	10:AJ:38:ILE:H	1.54	0.45
25:BA:1410:G:N7	47:B1:3:LYS:HE2	2.31	0.45
52:B6:25:LYS:NZ	52:B6:51:GLU:OE2	2.42	0.45
25:BA:11:G:H2'	25:BA:12:U:C5'	2.46	0.45
25:BA:2162:C:N3	25:BA:2173:G:C6	2.84	0.45
25:BA:2703:C:O3'	25:BA:2881:C:H4'	2.17	0.45
25:BA:2804:C:H2'	25:BA:2805:G:H8	1.81	0.45
30:BG:23:PHE:HB2	30:BG:25:TYR:CE1	2.51	0.45
31:BH:116:GLU:HG3	31:BH:117:PRO:HD2	1.97	0.45
44:BY:92:ASN:H	44:BY:92:ASN:ND2	2.14	0.45
1:CA:279:A:OP2	17:CQ:95:TYR:OH	2.32	0.45
1:CA:444:C:O2	1:CA:490:G:N1	2.49	0.45
3:CC:137:ALA:HA	3:CC:140:ARG:HH11	1.82	0.45
3:CC:140:ARG:CZ	3:CC:140:ARG:HB2	2.46	0.45
5:CE:43:LEU:HB3	5:CE:136:MET:SD	2.57	0.45
5:CE:76:ILE:O	5:CE:93:PRO:HB3	2.17	0.45
6:CF:61:LEU:HG	6:CF:63:TYR:CE1	2.51	0.45
9:CI:51:ARG:NH1	9:CI:56:LEU:HD21	2.32	0.45
15:CO:85:LEU:HB3	15:CO:87:ILE:HG13	1.97	0.45
25:DA:2051:A:H5'	25:DA:2578:G:O4'	2.16	0.45
25:DA:2130:U:H3	25:DA:2159:G:N2	2.15	0.45
25:DA:572:A:N7	60:DA:4291:HOH:O	2.36	0.45
27:DD:43:ARG:HA	27:DD:48:ARG:O	2.16	0.45
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.17	0.45
1:AA:189(A):C:H42	1:AA:189(J):G:H1	1.64	0.45
1:AA:193:C:H4'	20:AT:61:SER:HB2	1.99	0.45
1:AA:258:G:H2'	1:AA:259:G:H8	1.81	0.45
1:AA:461:A:O2'	1:AA:470:C:H5'	2.16	0.45
1:AA:952:U:H2'	1:AA:953:G:C8	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:215:LEU:O	2:AB:219:VAL:HG23	2.17	0.45
19:AS:63:THR:HG1	19:AS:66:MET:HG3	1.82	0.45
49:B3:22:ALA:HB2	49:B3:49:LYS:HD3	1.99	0.45
25:BA:2381:A:H2'	25:BA:2382:G:C8	2.51	0.45
25:BA:27:G:O2'	25:BA:28:A:OP2	2.31	0.45
25:BA:331:G:H21	25:BA:354:A:H62	1.65	0.45
25:BA:45:C:OP2	25:BA:204:G:H5'	2.17	0.45
25:BA:831:A:C8	25:BA:839:G:C5	3.05	0.45
33:BN:112:LEU:O	33:BN:116:LEU:HG	2.16	0.45
44:BY:47:LYS:NZ	44:BY:48:ALA:O	2.48	0.45
45:BZ:146:ILE:HA	45:BZ:147:GLY:HA2	1.75	0.45
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.50	0.45
7:CG:152:ALA:O	7:CG:155:ARG:HB3	2.16	0.45
9:CI:71:SER:HA	9:CI:74:ILE:HD12	1.99	0.45
11:CK:34:ASP:OD1	11:CK:38:ASN:N	2.46	0.45
17:CQ:62:SER:OG	17:CQ:72:ARG:HD3	2.16	0.45
17:CQ:92:ARG:NH1	17:CQ:95:TYR:OH	2.50	0.45
25:DA:2173:A:C2	25:DA:2174:C:H1'	2.52	0.45
25:DA:2443:C:OP1	29:DF:68:LYS:HD3	2.17	0.45
25:DA:29:U:H2'	25:DA:30:G:C8	2.51	0.45
25:DA:329:G:OP1	25:DA:329:G:H8	1.99	0.45
27:DD:108:PRO:HB3	27:DD:143:HIS:CE1	2.52	0.45
32:DI:48:GLU:HG3	32:DI:52:ARG:HH11	1.81	0.45
40:DU:112:ARG:H	40:DU:112:ARG:HG2	1.52	0.45
44:DY:43:ASN:OD1	44:DY:65:ALA:HB3	2.16	0.45
1:AA:1003:G:N2	1:AA:1038:C:C4	2.85	0.45
1:AA:1144:G:N2	1:AA:1146:A:H62	2.15	0.45
1:AA:300:A:H2'	1:AA:301:G:O4'	2.17	0.45
1:AA:840:C:H4'	1:AA:841:U:OP1	2.14	0.45
2:AB:19:HIS:HA	2:AB:39:ILE:HG23	1.98	0.45
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.16	0.45
8:AH:31:PHE:O	8:AH:35:ILE:HG12	2.17	0.45
1:AA:1149:C:OP1	9:AI:14:VAL:HG11	2.17	0.45
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.99	0.45
13:AM:108:ARG:O	13:AM:112:GLY:N	2.44	0.45
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.17	0.45
25:BA:1785:C:N3	25:BA:2729:U:O2'	2.45	0.45
25:BA:2146:G:N1	25:BA:2196:C:N4	2.30	0.45
28:BE:29:GLY:H	28:BE:93:VAL:HG13	1.80	0.45
29:BF:20:LEU:HD22	29:BF:21:ALA:H	1.82	0.45
32:BI:57:ARG:HD3	32:BI:58:LEU:N	2.31	0.45
25:BA:1068:G:N7	33:BN:66:LYS:HE2	2.32	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
37:BR:67:LEU:O	37:BR:71:GLN:N	2.48	0.45
1:CA:1154:G:O6	1:CA:1155:G:C6	2.70	0.45
1:CA:858:G:N1	1:CA:870:U:OP2	2.37	0.45
19:CS:37:ARG:O	19:CS:70:LYS:NZ	2.44	0.45
47:D1:67:ILE:N	47:D1:68:PRO:HD2	2.32	0.45
48:D2:18:PRO:HB3	48:D2:68:ARG:NH1	2.32	0.45
13:CM:57:ARG:NH1	50:D4:17:GLY:HA3	2.31	0.45
25:DA:1288:U:C2	25:DA:1327:C:O2	2.70	0.45
25:DA:1449:A:H8	25:DA:1449:A:OP2	1.99	0.45
25:DA:2262:U:H4'	25:DA:2328:A:C2	2.51	0.45
25:DA:2713:A:H4'	25:DA:2713:A:OP2	2.16	0.45
25:DA:531:C:H4'	25:DA:532:A:H5''	1.97	0.45
25:DA:977:G:N3	25:DA:1001:A:H2	2.15	0.45
31:DH:127:GLU:HB2	31:DH:130:ARG:HB2	1.98	0.45
35:DP:97:PRO:O	35:DP:101:VAL:HG23	2.16	0.45
38:DS:3:ARG:O	38:DS:4:LEU:HD23	2.17	0.45
1:AA:1028:C:C5	1:AA:1029:C:H1'	2.52	0.45
1:AA:1216:G:H2'	1:AA:1217:C:H5''	1.98	0.45
1:AA:1298:C:H4'	1:AA:1299:A:O4'	2.16	0.45
1:AA:227:G:H2'	1:AA:228:A:O4'	2.17	0.45
3:AC:120:VAL:O	3:AC:124:ILE:HG23	2.16	0.45
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.99	0.45
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.78	0.45
49:B3:31:LEU:HD23	49:B3:31:LEU:HA	1.77	0.45
25:BA:2403:G:O2'	25:BA:2436:C:N4	2.38	0.45
25:BA:2691:A:H4'	28:BE:165:VAL:HG11	1.99	0.45
1:CA:1277:C:O2'	1:CA:1279:A:C8	2.69	0.45
1:CA:628:G:C2'	1:CA:629:G:H5'	2.46	0.45
1:CA:69:G:H2'	1:CA:70:G:H8	1.82	0.45
1:CA:322:C:O2'	20:CT:23:ARG:HD2	2.16	0.45
24:CX:65:C:H2'	24:CX:66:C:O4'	2.17	0.45
25:DA:1013:C:H2'	25:DA:1014:U:C6	2.52	0.45
25:DA:1878:G:H2'	25:DA:1879:C:C6	2.51	0.45
25:DA:18:C:H2'	25:DA:19:C:H6	1.82	0.45
25:DA:375:C:H2'	25:DA:376:C:H6	1.79	0.45
25:DA:565:C:H2'	25:DA:566:U:O4'	2.17	0.45
25:DA:589:C:P	35:DP:16:ARG:HH12	2.40	0.45
32:DI:9:LEU:HA	32:DI:9:LEU:HD13	1.79	0.45
40:DU:49:HIS:HA	40:DU:52:ARG:HB3	1.98	0.45
1:AA:762:C:H2'	1:AA:763:G:C8	2.52	0.45
1:AA:953:G:H5'	1:AA:965:A:N6	2.32	0.45
2:AB:30:ARG:HH22	2:AB:194:PRO:HB2	1.81	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:266:G:O2'	17:AQ:67:LYS:HD3	2.17	0.45
24:AX:10:G:N2	24:AX:26:G:H1'	2.32	0.45
25:BA:1542:A:N3	25:BA:1624:C:O2'	2.35	0.45
25:BA:2524:C:H2'	25:BA:2525:G:O4'	2.17	0.45
25:BA:552:C:C5	25:BA:2792:U:H2'	2.52	0.45
25:BA:536:U:O4	25:BA:537:G:N1	2.50	0.45
29:BF:161:GLU:HG2	29:BF:164:ARG:NH2	2.32	0.45
1:CA:1097:C:H2'	1:CA:1098:C:C6	2.52	0.45
6:CF:68:PRO:HG2	6:CF:71:ARG:NH1	2.32	0.45
25:DA:186:G:H2'	25:DA:187:G:C8	2.52	0.45
25:DA:272(B):G:H2'	25:DA:272(C):G:C8	2.51	0.45
29:DF:157:VAL:HG12	29:DF:198:ALA:HB1	1.98	0.45
36:DQ:38:GLU:HB2	36:DQ:127:ILE:HG22	1.99	0.45
38:DS:84:GLN:HG3	38:DS:111:GLU:OE2	2.17	0.45
39:DT:64:ARG:NH1	39:DT:103:ARG:HA	2.31	0.45
1:AA:112:G:H4'	1:AA:389:A:H4'	1.98	0.45
6:AF:6:VAL:HG13	6:AF:90:VAL:HG22	1.99	0.45
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	1.99	0.45
1:AA:675:A:H1'	11:AK:116:HIS:CD2	2.52	0.45
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.47	0.45
25:BA:1342:G:OP1	25:BA:2721:G:O2'	2.30	0.45
25:BA:1884:A:H2'	25:BA:1885:A:C8	2.52	0.45
25:BA:289:G:H2'	25:BA:290:G:O4'	2.16	0.45
25:BA:354:A:HO2'	25:BA:355:A:H8	1.61	0.45
29:BF:155:LEU:HD11	29:BF:176:LEU:HD12	1.99	0.45
29:BF:53:THR:HG22	29:BF:56:GLU:HG3	1.98	0.45
37:BR:29:LEU:HA	37:BR:29:LEU:HD12	1.83	0.45
34:BO:104:ARG:HE	39:BT:36:GLU:HG2	1.82	0.45
1:CA:223:U:H2'	1:CA:224:C:H6	1.82	0.45
1:CA:543:C:C2'	1:CA:544:G:H5'	2.47	0.45
1:CA:838:G:N2	1:CA:848:C:N3	2.66	0.45
1:CA:984:C:O5'	1:CA:984:C:H6	2.00	0.45
2:CB:87:ARG:NH1	2:CB:230:VAL:HG11	2.33	0.45
5:CE:57:LYS:HG2	5:CE:61:TYR:CE2	2.52	0.45
13:CM:108:ARG:CZ	13:CM:114:ARG:HG2	2.47	0.45
16:CP:53:VAL:HG13	16:CP:79:VAL:HG22	1.98	0.45
25:DA:251:A:P	54:D8:7:HIS:HE2	2.39	0.45
25:DA:1359:A:N1	25:DA:1372:U:O4	2.50	0.45
25:DA:1474:C:H2'	25:DA:1475:G:H8	1.82	0.45
25:DA:1839:G:C8	25:DA:1927:A:H1'	2.52	0.45
25:DA:1637:A:H4'	25:DA:2711:A:O2'	2.17	0.45
25:DA:277:C:O2'	25:DA:278:A:OP1	2.30	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:670:A:H4'	25:DA:671:C:O5'	2.17	0.45
25:DA:863:A:H2'	25:DA:864:G:C8	2.52	0.45
25:DA:983:A:OP1	60:DA:4292:HOH:O	2.21	0.45
27:DD:62:TYR:HA	27:DD:87:ASN:OD1	2.17	0.45
29:DF:41:LEU:O	29:DF:44:ARG:HG2	2.16	0.45
30:DG:66:GLN:OE1	30:DG:98:ARG:NE	2.47	0.45
40:DU:17:ILE:HG13	40:DU:32:PHE:CE1	2.52	0.45
1:AA:1223:C:H5''	1:AA:1224:G:H5'	1.97	0.44
1:AA:881:G:OP2	12:AL:12:ARG:NH2	2.50	0.44
1:AA:92:C:H2'	1:AA:93:G:O4'	2.17	0.44
2:AB:130:ARG:HG3	2:AB:130:ARG:HH11	1.82	0.44
4:AD:128:VAL:HG12	4:AD:129:ASN:HD22	1.82	0.44
17:AQ:67:LYS:HA	17:AQ:70:ARG:HH12	1.81	0.44
18:AR:56:THR:HB	18:AR:58:LEU:HD23	1.99	0.44
25:BA:2702:C:H5''	25:BA:2882:G:H21	1.82	0.44
25:BA:925:A:C6	25:BA:946:A:C5	3.05	0.44
27:BD:70:TRP:HB3	27:BD:190:TYR:CE1	2.52	0.44
33:BN:75:TYR:CE2	33:BN:77:GLY:HA2	2.52	0.44
36:BQ:108:GLY:HA3	45:BZ:116:VAL:HG13	1.99	0.44
1:CA:1022:G:H2'	1:CA:1023:G:H8	1.82	0.44
1:CA:1063:C:H3'	1:CA:1064:G:H2'	1.99	0.44
1:CA:486:U:H2'	1:CA:487:A:C8	2.51	0.44
1:CA:868:C:H2'	1:CA:869:G:O4'	2.17	0.44
3:CC:186:PHE:HA	3:CC:198:VAL:O	2.17	0.44
3:CC:190:ARG:HG2	3:CC:190:ARG:O	2.18	0.44
5:CE:135:THR:O	5:CE:138:ALA:HB3	2.17	0.44
9:CI:37:PHE:HB3	9:CI:43:ALA:HB1	1.98	0.44
17:CQ:7:THR:O	17:CQ:23:VAL:HG13	2.17	0.44
25:DA:2365:G:H4'	46:D0:60:PHE:CZ	2.52	0.44
49:D3:7:LYS:HE3	49:D3:32:GLN:HG3	1.99	0.44
25:DA:2134:A:H1'	25:DA:2159:G:H21	1.82	0.44
25:DA:2292:C:OP1	38:DS:17:ARG:NH1	2.42	0.44
25:DA:272(D):G:H1	25:DA:364:C:H42	1.65	0.44
25:DA:887:A:H4'	25:DA:888:C:H5	1.82	0.44
40:DU:8:VAL:HG12	40:DU:11:ARG:NH2	2.32	0.44
45:DZ:70:LEU:O	45:DZ:89:PHE:N	2.42	0.44
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.52	0.44
4:AD:106:TYR:HD1	4:AD:107:ARG:HD2	1.83	0.44
1:AA:1147:C:O2'	9:AI:16:ARG:HD3	2.17	0.44
25:BA:76:C:OP1	48:B2:59:ARG:HD3	2.17	0.44
25:BA:1024:G:C2	25:BA:1032:C:C2	3.05	0.44
25:BA:150:C:H2'	25:BA:151:C:C6	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:209:G:O2'	25:BA:222:A:N3	2.41	0.44
27:BD:17:THR:OG1	27:BD:205:VAL:N	2.32	0.44
31:BH:164:TYR:HB2	31:BH:167:GLU:HB2	1.99	0.44
32:BI:81:VAL:O	32:BI:146:ALA:HA	2.18	0.44
45:BZ:56:VAL:HA	45:BZ:70:LEU:HD23	2.00	0.44
1:CA:10:A:OP2	5:CE:126:ARG:HD2	2.17	0.44
1:CA:256:U:OP1	17:CQ:17:LYS:NZ	2.37	0.44
1:CA:393:A:OP2	16:CP:12:LYS:HD2	2.17	0.44
1:CA:429:U:H1'	1:CA:430:A:H5''	1.98	0.44
1:CA:939:G:C6	1:CA:940:C:N4	2.85	0.44
2:CB:207:ALA:O	2:CB:211:ILE:HG13	2.17	0.44
3:CC:144:SER:OG	3:CC:144:SER:O	2.36	0.44
9:CI:23:ASN:HD22	9:CI:24:GLY:H	1.66	0.44
1:CA:1328:C:O2'	13:CM:29:ARG:NE	2.51	0.44
16:CP:69:THR:O	16:CP:73:LEU:HG	2.17	0.44
24:CX:12:G:H4'	25:DA:1908:C:O2	2.17	0.44
50:D4:40:HIS:HB3	50:D4:43:TYR:HB2	1.97	0.44
25:DA:1011:G:C2	25:DA:1151:G:C2	3.06	0.44
25:DA:1264:G:OP1	51:D5:19:ARG:NH2	2.40	0.44
25:DA:1359:A:N3	25:DA:1359:A:H5'	2.32	0.44
25:DA:1847:A:H4'	25:DA:1848:A:OP2	2.16	0.44
25:DA:1937:A:HO2'	25:DA:1939:U:H6	1.63	0.44
25:DA:2184:G:H2'	25:DA:2185:C:C6	2.52	0.44
25:DA:64:A:O3'	43:DX:71:GLY:HA3	2.17	0.44
25:DA:606:U:H4'	25:DA:658:C:H4'	1.98	0.44
25:DA:856:C:O2'	25:DA:857:C:OP1	2.31	0.44
31:DH:13:LYS:HA	31:DH:14:GLY:HA2	1.60	0.44
39:DT:16:ARG:HG2	39:DT:18:ASP:OD1	2.17	0.44
1:AA:1090:U:H2'	1:AA:1091:U:C6	2.52	0.44
1:AA:1133:G:C6	1:AA:1142:G:C6	3.06	0.44
1:AA:1241:G:H2'	1:AA:1242:C:H6	1.82	0.44
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.63	0.44
1:AA:346:G:C4	1:AA:347:G:H1'	2.52	0.44
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.53	0.44
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	2.00	0.44
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.66	0.44
1:AA:530:G:O6	22:AV:21:C:H1'	2.17	0.44
23:AW:76:PPU:H92	25:BA:2596:U:H4'	1.98	0.44
46:B0:10:THR:HB	46:B0:12:ASN:H	1.82	0.44
25:BA:1501:U:O2'	25:BA:1502:G:N7	2.47	0.44
25:BA:839:G:O2'	25:BA:2452:C:N3	2.39	0.44
25:BA:1814:A:H5'	25:BA:2620:G:H4'	1.99	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:694:G:N2	25:BA:696:C:H2'	2.31	0.44
25:BA:943:C:H2'	25:BA:944:C:H6	1.80	0.44
25:BA:2647:C:O2'	28:BE:80:GLU:OE1	2.23	0.44
29:BF:117:ARG:NH2	35:BP:1:MET:O	2.51	0.44
1:CA:1156:G:H5'	1:CA:1157:A:OP2	2.18	0.44
1:CA:1262:C:N4	1:CA:1273:G:C6	2.78	0.44
1:CA:255:G:OP1	17:CQ:69:LYS:NZ	2.38	0.44
1:CA:522:C:H41	12:CL:53:ARG:NH2	2.11	0.44
1:CA:826:C:H2'	1:CA:827:U:H6	1.83	0.44
1:CA:978:A:O2'	1:CA:1321:C:N4	2.49	0.44
3:CC:19:GLU:O	3:CC:56:ASP:HA	2.17	0.44
1:CA:229:U:O2'	16:CP:23:ASP:OD2	2.31	0.44
17:CQ:92:ARG:O	17:CQ:95:TYR:HB2	2.18	0.44
25:DA:95:G:H4'	48:D2:46:GLN:HA	1.98	0.44
52:D6:38:LYS:HE3	52:D6:39:TYR:H	1.83	0.44
25:DA:2419:U:OP1	54:D8:41:ILE:HD12	2.18	0.44
25:DA:2113:U:C2	25:DA:2169:A:N6	2.85	0.44
25:DA:2176:A:H2'	25:DA:2177:C:C6	2.53	0.44
25:DA:2419:U:O2'	52:D6:54:ILE:HD11	2.17	0.44
25:DA:953:A:OP2	36:DQ:16:ARG:NH2	2.41	0.44
43:DX:31:HIS:CD2	43:DX:33:LYS:H	2.35	0.44
25:DA:336:C:HO2'	44:DY:35:TYR:HH	1.61	0.44
1:AA:1007:C:N3	1:AA:1022:G:C6	2.85	0.44
1:AA:112:G:H5'	1:AA:389:A:O2'	2.18	0.44
1:AA:185:A:H2'	1:AA:186:C:H6	1.80	0.44
1:AA:1125:U:C5'	10:AJ:5:ARG:HH22	2.28	0.44
25:BA:1343:C:OP1	25:BA:2722:C:H4'	2.18	0.44
25:BA:2175:G:H2'	25:BA:2176:G:H8	1.83	0.44
25:BA:510:C:H2'	25:BA:511:C:C6	2.53	0.44
25:BA:876:A:N7	25:BA:2259:A:O2'	2.46	0.44
26:BB:114:C:O2'	38:BS:46:VAL:HG13	2.17	0.44
31:BH:85:LYS:NZ	60:BH:4001:HOH:O	2.51	0.44
45:BZ:155:LEU:HA	45:BZ:155:LEU:HD12	1.76	0.44
45:BZ:35:ARG:HD2	45:BZ:35:ARG:HA	1.69	0.44
1:CA:1042:G:C2	1:CA:1043:C:C2	3.05	0.44
1:CA:1118:C:H2'	1:CA:1119:C:H6	1.82	0.44
1:CA:1295:G:H2'	1:CA:1296:C:H5'	1.98	0.44
1:CA:413:G:N2	1:CA:428:G:H1'	2.33	0.44
1:CA:567:G:H2'	1:CA:568:G:O4'	2.18	0.44
1:CA:922:G:C6	1:CA:923:A:C6	3.04	0.44
5:CE:136:MET:O	5:CE:140:ARG:N	2.46	0.44
14:CN:37:PHE:CE2	14:CN:44:LEU:HD13	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:CO:87:ILE:CG2	15:CO:88:ARG:H	2.29	0.44
1:CA:375:U:H4'	16:CP:17:TYR:HE2	1.81	0.44
25:DA:1411:C:H2'	25:DA:1412:A:C8	2.53	0.44
25:DA:1657:C:H2'	25:DA:1658:C:C6	2.53	0.44
25:DA:793:A:OP2	25:DA:2072:G:H5'	2.16	0.44
25:DA:2270:G:H2'	25:DA:2271:G:O4'	2.16	0.44
25:DA:272(D):G:C2	25:DA:272(E):G:C8	3.05	0.44
25:DA:2788:C:O2'	25:DA:2809:A:N3	2.46	0.44
25:DA:320:A:H4'	25:DA:322:A:C8	2.53	0.44
25:DA:272(G):C:N4	25:DA:363(C):G:H1	2.02	0.44
25:DA:78:A:H2'	25:DA:79:G:C8	2.53	0.44
25:DA:889:C:O2'	25:DA:890:A:O5'	2.33	0.44
26:DB:16:G:H1	26:DB:68:C:N4	2.16	0.44
26:DB:42:C:O2'	30:DG:66:GLN:HG2	2.17	0.44
38:DS:75:GLU:OE2	38:DS:75:GLU:N	2.29	0.44
1:AA:452:A:O2'	1:AA:453:A:H5''	2.18	0.44
1:AA:599:C:C2'	1:AA:600:C:H5'	2.47	0.44
3:AC:41:GLY:O	3:AC:45:LYS:HG2	2.18	0.44
1:AA:405:U:OP2	4:AD:3:ARG:NH1	2.51	0.44
25:BA:2291:G:O6	46:B0:14:ARG:HD2	2.18	0.44
50:B4:53:GLU:HG3	50:B4:54:GLY:N	2.32	0.44
25:BA:1211:U:H2'	25:BA:1212:C:C6	2.53	0.44
25:BA:1452:U:H2'	25:BA:1453:C:C6	2.53	0.44
25:BA:1911:A:H2'	25:BA:1912:A:C8	2.53	0.44
25:BA:2735:G:H2'	25:BA:2736:C:C6	2.53	0.44
31:BH:88:LEU:HD23	31:BH:165:ALA:HA	1.98	0.44
32:BI:93:THR:O	32:BI:97:ILE:HG13	2.18	0.44
1:CA:1005:A:H1'	1:CA:1025:U:C2	2.53	0.44
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.53	0.44
1:CA:453:A:C6	1:CA:454:C:C4	3.06	0.44
1:CA:688:G:C6	1:CA:700:G:C2	3.06	0.44
1:CA:784:C:H4'	25:DA:1837:C:OP1	2.17	0.44
1:CA:90:U:C2'	1:CA:91:C:H5'	2.47	0.44
13:CM:14:ARG:HA	13:CM:43:THR:O	2.18	0.44
19:CS:19:VAL:O	19:CS:23:ASN:ND2	2.51	0.44
20:CT:56:MET:HG3	20:CT:57:ARG:N	2.33	0.44
47:D1:40:ARG:NH2	47:D1:42:GLN:HG2	2.33	0.44
25:DA:1028:A:OP2	25:DA:1126:A:N6	2.50	0.44
25:DA:1654:A:OP1	37:DR:1:MET:HA	2.18	0.44
25:DA:2318:G:H21	38:DS:3:ARG:CZ	2.30	0.44
25:DA:2472:G:H2'	25:DA:2475:C:H42	1.82	0.44
26:DB:41:U:C6	30:DG:69:ALA:HB1	2.53	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:430:A:P	4:AD:8:VAL:H	2.41	0.44
2:AB:114:ARG:O	2:AB:118:LEU:HB2	2.17	0.44
3:AC:32:LEU:HD22	3:AC:59:ARG:HD3	1.99	0.44
8:AH:75:ARG:HA	8:AH:76:PRO:HD2	1.91	0.44
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.32	0.44
50:B4:63:TYR:CD1	50:B4:63:TYR:N	2.85	0.44
53:B7:24:THR:HG22	53:B7:26:GLY:H	1.82	0.44
25:BA:1001:G:N2	25:BA:1004:A:H3'	2.33	0.44
25:BA:1224:C:H2'	25:BA:1225:C:H6	1.83	0.44
25:BA:1467:G:C2	25:BA:1468:G:C8	3.06	0.44
25:BA:2040:G:H21	40:BU:34:LYS:NZ	2.16	0.44
25:BA:403:C:H2'	25:BA:404:C:C6	2.53	0.44
33:BN:67:LEU:HD12	33:BN:67:LEU:HA	1.67	0.44
42:BW:14:PRO:HG2	42:BW:78:GLU:HG2	1.99	0.44
45:BZ:151:HIS:C	45:BZ:153:SER:H	2.21	0.44
1:CA:1014:A:C2	1:CA:1219:U:H1'	2.52	0.44
1:CA:1469:G:H2'	1:CA:1470:G:H8	1.82	0.44
1:CA:167:G:H2'	1:CA:168:G:H8	1.82	0.44
1:CA:377:G:H1	1:CA:386:C:H42	1.65	0.44
1:CA:59:A:H3'	1:CA:331:G:H22	1.82	0.44
1:CA:839:U:O2'	1:CA:840:C:OP1	2.33	0.44
1:CA:90:U:O2'	1:CA:91:C:H5'	2.18	0.44
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.99	0.44
1:CA:1014:A:H5'	19:CS:18:LYS:NZ	2.32	0.44
24:CX:19:G:N2	24:CX:56:C:N3	2.53	0.44
25:DA:1468:C:H42	25:DA:1524:G:H1	1.66	0.44
25:DA:1674:G:H21	25:DA:1677:A:N6	2.16	0.44
25:DA:1900:A:OP2	60:DA:4200:HOH:O	2.21	0.44
25:DA:2315:G:H2'	25:DA:2316:C:C6	2.53	0.44
25:DA:2552:U:H6	25:DA:2552:U:O5'	2.00	0.44
25:DA:2872:G:C2	25:DA:2873:A:N6	2.86	0.44
25:DA:379:G:O2'	25:DA:2232:U:OP1	2.35	0.44
25:DA:783:A:H2'	25:DA:783:A:N3	2.31	0.44
27:DD:123:ALA:O	27:DD:131:LEU:HD21	2.17	0.44
32:DI:57:ARG:HG3	32:DI:58:LEU:N	2.33	0.44
35:DP:94:GLU:HG3	35:DP:124:LYS:HD3	2.00	0.44
1:AA:1030:C:N4	1:AA:1031:G:C6	2.79	0.44
18:AR:65:ILE:O	18:AR:69:THR:HG23	2.18	0.44
24:AX:23:C:H2'	24:AX:24:U:C6	2.52	0.44
25:BA:139:A:H8	25:BA:1454:C:HO2'	1.54	0.44
25:BA:1480:A:N6	25:BA:1605:A:H62	2.10	0.44
25:BA:1316:C:O2'	25:BA:1695:C:OP2	2.30	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2316:G:H22	25:BA:2324:U:H3	1.64	0.44
25:BA:595:A:H2'	25:BA:596:G:O4'	2.18	0.44
25:BA:707:G:O3'	29:BF:38:ARG:NH2	2.50	0.44
32:BI:130:TYR:HD2	32:BI:138:ILE:HD12	1.83	0.44
1:CA:1079:G:H2'	1:CA:1080:A:C8	2.53	0.44
1:CA:260:G:C6	1:CA:261:U:C4	3.06	0.44
1:CA:730:G:H5''	1:CA:731:G:OP2	2.18	0.44
2:CB:35:GLU:HB2	2:CB:40:HIS:HD2	1.83	0.44
1:CA:410:G:H5''	4:CD:30:LYS:NZ	2.33	0.44
5:CE:41:VAL:O	5:CE:66:MET:HA	2.18	0.44
15:CO:32:LEU:HD23	15:CO:32:LEU:HA	1.87	0.44
25:DA:2230:G:H1'	47:D1:45:ASN:CG	2.38	0.44
48:D2:3:LEU:O	48:D2:7:ARG:HG3	2.18	0.44
49:D3:12:PRO:HB2	49:D3:20:LYS:HG2	1.99	0.44
25:DA:1447:G:O2'	25:DA:1544:A:N3	2.37	0.44
25:DA:614(C):A:C4	29:DF:180:GLY:HA2	2.52	0.44
25:DA:705:A:H1'	27:DD:9:TYR:CE2	2.52	0.44
28:DE:8:LYS:NZ	28:DE:188:VAL:O	2.48	0.44
31:DH:143:GLN:HE21	31:DH:147:ASN:HD21	1.65	0.44
44:DY:52:SER:HB2	44:DY:53:PRO:HD2	1.98	0.44
1:AA:1060:C:C4	3:AC:2:GLY:HA3	2.52	0.44
1:AA:1157:A:N7	1:AA:1180:A:N6	2.65	0.44
1:AA:1499:A:H1'	1:AA:1520:G:H5'	2.00	0.44
2:AB:20:GLU:HA	2:AB:21:ARG:NH2	2.32	0.44
3:AC:21:ARG:HG3	3:AC:58:GLU:HG2	2.00	0.44
17:AQ:38:ARG:HA	17:AQ:38:ARG:HD3	1.83	0.44
48:B2:61:LEU:HD23	48:B2:61:LEU:HA	1.74	0.44
25:BA:1273:G:OP2	40:BU:16:LYS:NZ	2.34	0.44
25:BA:1721:G:H1'	25:BA:1723:A:N6	2.32	0.44
25:BA:2013:U:H2'	25:BA:2014:G:H5''	2.00	0.44
25:BA:2702:C:H5''	25:BA:2882:G:N2	2.33	0.44
25:BA:2821:G:H5'	28:BE:60:ASN:ND2	2.29	0.44
25:BA:505:A:N3	25:BA:507:G:H5''	2.32	0.44
25:BA:731:G:OP1	53:B7:16:HIS:ND1	2.50	0.44
30:BG:43:LEU:C	30:BG:45:GLU:H	2.20	0.44
34:BO:16:ALA:HB2	34:BO:52:VAL:HG21	1.98	0.44
25:BA:1289:G:O2'	35:BP:4:SER:O	2.32	0.44
36:BQ:54:MET:SD	36:BQ:118:LEU:HD23	2.57	0.44
39:BT:50:ILE:HA	39:BT:99:LEU:HD12	2.00	0.44
1:CA:1064:G:H1'	1:CA:1065:U:OP2	2.18	0.44
1:CA:1429:C:H2'	1:CA:1430:C:H6	1.83	0.44
1:CA:358:U:H2'	1:CA:359:U:C6	2.53	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:CB:87:ARG:HH11	2:CB:230:VAL:HG11	1.83	0.44
4:CD:63:LYS:HD2	4:CD:197:PRO:O	2.17	0.44
51:D5:9:LYS:HD3	51:D5:9:LYS:HA	1.77	0.44
25:DA:1226:A:H5''	40:DU:16:LYS:HZ2	1.82	0.44
25:DA:1550:C:H2'	25:DA:1551:C:H6	1.82	0.44
25:DA:1777:U:H2'	25:DA:1778:U:C6	2.53	0.44
25:DA:2129:C:H2'	25:DA:2130:U:C4	2.52	0.44
25:DA:2138:C:N4	25:DA:2153:G:H1	2.16	0.44
25:DA:2474:C:H5''	25:DA:2475:C:OP2	2.17	0.44
25:DA:2657:A:H3'	25:DA:2658:C:C6	2.53	0.44
25:DA:271(N):U:O2'	25:DA:271(O):C:H5'	2.18	0.44
25:DA:698:C:O2'	25:DA:734:A:N6	2.51	0.44
26:DB:50:G:OP2	38:DS:62:LYS:HD2	2.17	0.44
29:DF:129:PHE:CE2	29:DF:163:VAL:HG11	2.53	0.44
29:DF:187:VAL:HG12	35:DP:3:LEU:HD12	1.99	0.44
30:DG:5:VAL:HG13	30:DG:8:LYS:HG3	2.00	0.44
34:DO:4:PRO:O	34:DO:5:GLN:HB2	2.17	0.44
40:DU:92:ARG:HA	40:DU:95:LEU:HB2	1.98	0.44
41:DV:89:GLN:HA	41:DV:90:PRO:HD3	1.84	0.44
41:DV:25:LEU:H	41:DV:92:THR:HG1	1.65	0.44
42:DW:16:LYS:O	42:DW:19:LEU:HB2	2.18	0.44
1:AA:288:A:H2'	1:AA:289:G:H4'	2.00	0.44
1:AA:77:G:C2'	1:AA:78:G:H5'	2.48	0.44
2:AB:166:ASP:HA	2:AB:167:PRO:HD3	1.85	0.44
2:AB:30:ARG:NH2	2:AB:194:PRO:HB2	2.33	0.44
4:AD:61:LYS:HA	4:AD:203:VAL:HG22	1.99	0.44
1:AA:502:G:OP1	12:AL:118:SER:HB3	2.18	0.44
25:BA:1067:A:H3'	25:BA:1067:A:H8	1.83	0.44
25:BA:139:A:C8	25:BA:1454:C:O2'	2.68	0.44
25:BA:2227:G:H3'	25:BA:2228:G:C8	2.53	0.44
25:BA:2568:C:H2'	25:BA:2569:G:O4'	2.18	0.44
28:BE:120:TRP:CE3	28:BE:155:LYS:HD3	2.53	0.44
29:BF:74:ARG:H	29:BF:74:ARG:HG3	1.44	0.44
32:BI:37:VAL:HG12	32:BI:38:LEU:HD12	1.99	0.44
25:BA:1177:G:H21	33:BN:73:THR:HG21	1.83	0.44
40:BU:28:ARG:HD3	40:BU:38:THR:OG1	2.18	0.44
1:CA:1202:G:C6	14:CN:42:ILE:HG21	2.52	0.44
1:CA:1429:C:H2'	1:CA:1430:C:C6	2.53	0.44
1:CA:401:C:H2'	1:CA:402:G:C8	2.53	0.44
1:CA:685:G:C2	1:CA:686:U:C4	3.06	0.44
1:CA:797:C:O2'	1:CA:798:G:H5'	2.18	0.44
1:CA:828:A:H4'	1:CA:828:A:OP1	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:CB:218:ALA:O	2:CB:222:ILE:HG23	2.18	0.44
1:CA:4:U:C4	8:CH:105:ARG:HD3	2.53	0.44
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.27	0.44
47:D1:51:VAL:HG12	47:D1:53:VAL:HG23	1.99	0.44
47:D1:52:ARG:HA	47:D1:56:GLN:O	2.17	0.44
52:D6:25:LYS:NZ	52:D6:51:GLU:OE2	2.39	0.44
1:CA:1493:A:C8	25:DA:1913:A:N1	2.86	0.44
25:DA:2135:A:H61	25:DA:2157:G:N2	2.15	0.44
25:DA:2193:G:C4	25:DA:2194:G:C8	3.06	0.44
25:DA:2651:C:O2'	25:DA:2652:C:H5'	2.17	0.44
25:DA:2695:C:H2'	25:DA:2696:U:H6	1.83	0.44
25:DA:380:U:H2'	25:DA:381:G:H8	1.83	0.44
25:DA:649:G:H2'	25:DA:650:C:O4'	2.18	0.44
25:DA:1826:G:H4'	27:DD:242:ARG:CZ	2.47	0.44
28:DE:101:ARG:CZ	28:DE:171:GLU:HB3	2.48	0.44
28:DE:14:ILE:HB	39:DT:14:TYR:CE2	2.52	0.44
28:DE:32:PRO:HD2	28:DE:50:GLY:O	2.18	0.44
28:DE:72:VAL:HA	28:DE:73:GLU:HG3	2.00	0.44
29:DF:107:LYS:HG2	29:DF:206:ILE:HA	2.00	0.44
26:DB:54:G:H21	30:DG:29:TRP:HZ2	1.64	0.44
30:DG:7:LEU:HD23	30:DG:100:TRP:HE3	1.81	0.44
33:DN:128:HIS:HA	33:DN:129:PRO:HD3	1.84	0.44
25:DA:910:A:H62	36:DQ:12:GLN:HA	1.83	0.44
39:DT:36:GLU:O	39:DT:39:ARG:HG3	2.18	0.44
44:DY:67:LEU:HA	44:DY:67:LEU:HD23	1.85	0.44
45:DZ:19:ARG:HG3	45:DZ:25:PRO:HD3	1.99	0.44
1:AA:1082:G:H2'	1:AA:1083:U:O4'	2.18	0.43
1:AA:1369:C:H2'	1:AA:1370:G:C8	2.53	0.43
1:AA:293:G:C6	1:AA:294:U:C4	3.05	0.43
1:AA:544:G:OP1	4:AD:59:ARG:NH2	2.33	0.43
1:AA:738:C:H2'	1:AA:739:C:C6	2.53	0.43
25:BA:1088:G:H2'	25:BA:1089:C:C6	2.53	0.43
25:BA:1289:G:O3'	35:BP:7:ARG:NH2	2.50	0.43
25:BA:2314:G:H1	25:BA:2326:C:H42	1.65	0.43
25:BA:880:U:O2	35:BP:55:ARG:NH2	2.51	0.43
25:BA:992:G:H2'	25:BA:993:G:C8	2.53	0.43
33:BN:73:THR:HG23	33:BN:82:LEU:HD11	2.00	0.43
25:BA:63:A:O3'	43:BX:71:GLY:HA3	2.18	0.43
1:CA:1042:G:C6	1:CA:1043:C:C4	3.06	0.43
1:CA:1066:C:H2'	1:CA:1067:A:C8	2.52	0.43
1:CA:991:U:H3'	1:CA:1212:U:N3	2.33	0.43
1:CA:589:C:H2'	1:CA:590:C:H5'	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:679:C:H2'	1:CA:680:C:C6	2.53	0.43
4:CD:12:CYS:SG	4:CD:19:LEU:N	2.87	0.43
1:CA:410:G:P	4:CD:30:LYS:HZ3	2.38	0.43
9:CI:127:LYS:O	9:CI:128:ARG:HB3	2.18	0.43
1:CA:36:C:O2'	12:CL:117:ARG:NH2	2.50	0.43
13:CM:65:LYS:O	13:CM:66:LEU:HD23	2.17	0.43
19:CS:69:HIS:HB3	19:CS:73:GLU:HG3	2.00	0.43
19:CS:77:THR:HG23	19:CS:78:ARG:HG2	2.00	0.43
20:CT:9:ASN:ND2	20:CT:10:LEU:HA	2.33	0.43
47:D1:82:LEU:O	47:D1:85:LEU:HD23	2.18	0.43
54:D8:39:LYS:HA	54:D8:42:ARG:NH1	2.33	0.43
25:DA:1410:G:H2'	25:DA:1411:C:H6	1.81	0.43
25:DA:1600:C:OP1	43:DX:58:HIS:NE2	2.29	0.43
25:DA:2137:C:O2'	25:DA:2138:C:H5'	2.18	0.43
25:DA:2781:A:H5''	25:DA:2782:G:H5'	2.00	0.43
25:DA:18:C:O2'	25:DA:554:U:OP1	2.36	0.43
25:DA:910:A:N3	25:DA:2264:C:O2'	2.39	0.43
29:DF:152:GLU:HA	29:DF:190:GLU:OE2	2.18	0.43
29:DF:40:GLN:NE2	29:DF:182:ASN:HB2	2.32	0.43
34:DO:77:ILE:HD12	39:DT:74:ARG:HD3	2.01	0.43
36:DQ:110:THR:HG23	36:DQ:113:GLN:OE1	2.18	0.43
1:AA:942:G:C2	1:AA:1342:C:C2	3.06	0.43
1:AA:457:C:N4	1:AA:475:G:O6	2.51	0.43
5:AE:116:THR:HG23	5:AE:117:ASP:OD2	2.19	0.43
8:AH:6:ILE:HB	8:AH:85:ARG:NH1	2.33	0.43
12:AL:33:ARG:HA	12:AL:33:ARG:HD2	1.80	0.43
12:AL:58:VAL:O	12:AL:65:GLU:HA	2.18	0.43
14:AN:50:LYS:HE2	14:AN:52:GLN:NE2	2.33	0.43
25:BA:1073:A:C6	25:BA:1172:A:C4	3.06	0.43
25:BA:1973:U:H2'	25:BA:1975:A:OP2	2.17	0.43
25:BA:2279:A:H5''	25:BA:2280:A:H5'	1.99	0.43
25:BA:2802:C:O2	25:BA:2903:G:N1	2.50	0.43
25:BA:485:U:H2'	25:BA:486:A:C8	2.52	0.43
25:BA:580:U:O2	33:BN:45:ASN:HB2	2.18	0.43
25:BA:746:A:H2'	25:BA:747:G:O4'	2.18	0.43
26:BB:29:A:H2'	26:BB:30:C:O4'	2.18	0.43
28:BE:54:GLN:OE1	28:BE:55:ASN:N	2.42	0.43
31:BH:154:PRO:HB3	31:BH:163:TYR:CZ	2.52	0.43
34:BO:17:ARG:HD3	34:BO:17:ARG:HA	1.87	0.43
1:CA:1058:G:H2'	1:CA:1059:C:O4'	2.18	0.43
1:CA:948:C:N4	1:CA:1233:G:H1	2.14	0.43
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.54	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:324:G:N1	1:CA:327:A:OP2	2.51	0.43
1:CA:958:A:H5''	1:CA:959:A:OP2	2.17	0.43
1:CA:995:C:N3	1:CA:1046:A:O2'	2.46	0.43
4:CD:98:GLU:O	4:CD:103:ASN:ND2	2.51	0.43
6:CF:23:LYS:HB3	6:CF:23:LYS:HE2	1.75	0.43
9:CI:72:GLY:O	9:CI:76:ALA:N	2.47	0.43
11:CK:33:THR:C	11:CK:40:ILE:HG12	2.38	0.43
12:CL:113:ARG:HB3	12:CL:122:THR:HG21	2.00	0.43
1:CA:377:G:OP1	16:CP:3:LYS:HD2	2.18	0.43
17:CQ:19:VAL:HG23	17:CQ:44:ALA:HB3	2.00	0.43
19:CS:30:LEU:HD12	19:CS:31:ILE:N	2.33	0.43
46:D0:68:GLU:HB2	46:D0:82:ARG:NH1	2.32	0.43
47:D1:51:VAL:HG11	47:D1:74:VAL:HG21	2.00	0.43
25:DA:78:A:N6	25:DA:109:G:O6	2.50	0.43
25:DA:1230:C:H2'	25:DA:1231:G:C8	2.52	0.43
25:DA:1443:G:H1	25:DA:1548:C:N4	2.15	0.43
25:DA:1660:C:H2'	25:DA:1661:G:H8	1.82	0.43
25:DA:2056:G:OP1	60:DA:4373:HOH:O	2.21	0.43
25:DA:2342:C:O2'	25:DA:2374:C:H5''	2.18	0.43
25:DA:833:U:H2'	25:DA:834:C:H6	1.79	0.43
25:DA:85:G:OP2	44:DY:9:LYS:HB3	2.18	0.43
26:DB:48:A:P	38:DS:30:ARG:HH12	2.40	0.43
29:DF:108:LYS:O	29:DF:112:MET:HG3	2.18	0.43
29:DF:33:LEU:HA	29:DF:33:LEU:HD12	1.80	0.43
34:DO:14:THR:HG21	34:DO:86:ILE:HB	2.00	0.43
35:DP:100:LEU:HD12	35:DP:112:LEU:HD11	1.99	0.43
29:DF:116:ASP:OD2	35:DP:1:MET:N	2.50	0.43
38:DS:91:PRO:HD2	38:DS:92:TYR:CE2	2.53	0.43
42:DW:28:SER:OG	42:DW:31:GLU:HG3	2.17	0.43
25:DA:144:C:H5'	43:DX:2:LYS:HG2	2.00	0.43
1:AA:109:A:C6	1:AA:326:G:C6	3.06	0.43
1:AA:1125:U:H4'	1:AA:1126:U:OP1	2.19	0.43
1:AA:262:A:C6	1:AA:263:A:C6	3.06	0.43
1:AA:452:A:H4'	16:AP:72:ARG:HH12	1.83	0.43
25:BA:779:C:H2'	25:BA:780:G:O4'	2.19	0.43
25:BA:911:G:OP2	36:BQ:22:LYS:HE2	2.19	0.43
36:BQ:48:GLU:O	36:BQ:52:VAL:HG23	2.19	0.43
37:BR:72:ASP:O	37:BR:76:VAL:HG23	2.18	0.43
1:CA:999:C:H42	1:CA:1042:G:H1	1.66	0.43
1:CA:1225:A:OP1	13:CM:103:THR:OG1	2.35	0.43
1:CA:461:A:O2'	1:CA:470:C:H5'	2.17	0.43
1:CA:721:G:H4'	1:CA:722:A:O4'	2.17	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:CB:184:VAL:HG12	2:CB:197:VAL:HG13	2.00	0.43
3:CC:61:ALA:C	3:CC:63:ASN:H	2.22	0.43
7:CG:103:TRP:HA	7:CG:106:GLN:HB2	2.00	0.43
13:CM:44:ARG:HB2	13:CM:47:ASP:OD1	2.19	0.43
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.18	0.43
25:DA:1788:C:H2'	25:DA:1789:A:H8	1.83	0.43
25:DA:1835:G:H5''	25:DA:1836:C:OP2	2.18	0.43
1:CA:1493:A:H8	25:DA:1913:A:N1	2.16	0.43
25:DA:182:A:H2	25:DA:433:C:O2	2.01	0.43
25:DA:2723:C:P	28:DE:109:LYS:HZ3	2.41	0.43
45:DZ:55:HIS:CE1	45:DZ:135:GLU:HG3	2.51	0.43
1:AA:1027:C:O2	1:AA:1034:G:N1	2.52	0.43
1:AA:608:A:H4'	16:AP:32:TYR:OH	2.19	0.43
2:AB:185:ILE:HA	2:AB:199:TYR:O	2.18	0.43
3:AC:23:TYR:CG	3:AC:24:ALA:N	2.86	0.43
6:AF:44:GLY:HA2	6:AF:59:TYR:CE2	2.53	0.43
8:AH:39:LEU:HD12	8:AH:44:PHE:HB2	2.01	0.43
9:AI:37:PHE:HB3	9:AI:43:ALA:CB	2.48	0.43
10:AJ:5:ARG:O	10:AJ:98:ILE:HA	2.19	0.43
14:AN:48:ALA:HB2	14:AN:53:LEU:HD12	2.01	0.43
16:AP:21:VAL:HG13	16:AP:33:ILE:HB	1.99	0.43
47:B1:78:LYS:HE3	47:B1:78:LYS:HB2	1.68	0.43
25:BA:1093:G:H2'	25:BA:1156:G:N1	2.33	0.43
25:BA:70:A:H3'	25:BA:70:A:OP2	2.19	0.43
28:BE:176:ILE:HB	28:BE:181:LEU:HB2	1.99	0.43
25:BA:83:A:H5''	44:BY:8:LYS:HG3	2.00	0.43
1:CA:1112:C:H42	3:CC:177:THR:HA	1.81	0.43
1:CA:1155:G:C6	1:CA:1156:G:C4	3.06	0.43
1:CA:335:C:O2'	1:CA:1433:A:N3	2.43	0.43
2:CB:100:GLY:O	2:CB:104:ASN:N	2.50	0.43
3:CC:124:ILE:HD12	3:CC:191:THR:HG23	2.01	0.43
3:CC:47:LEU:HB3	3:CC:52:LEU:HB2	2.00	0.43
5:CE:108:ALA:O	5:CE:112:LEU:HG	2.18	0.43
18:CR:58:LEU:HB3	18:CR:62:GLU:HG3	2.01	0.43
19:CS:14:HIS:CE1	19:CS:15:LEU:HD13	2.53	0.43
25:DA:1266:G:O5'	42:DW:15:ARG:NH2	2.51	0.43
25:DA:1581:G:H2'	25:DA:1582:C:O4'	2.17	0.43
25:DA:1637:A:OP2	60:DA:4628:HOH:O	2.21	0.43
25:DA:1788:C:H2'	25:DA:1789:A:C8	2.53	0.43
25:DA:1894:C:H2'	25:DA:1895:C:C6	2.52	0.43
25:DA:2037:G:H2'	25:DA:2038:G:C8	2.54	0.43
25:DA:2148:G:H2'	25:DA:2149:G:C8	2.53	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2466:C:H5'	55:D9:5:ALA:HB3	2.00	0.43
25:DA:590:A:OP1	29:DF:95:ARG:NH1	2.51	0.43
29:DF:162:LEU:HD22	29:DF:162:LEU:H	1.83	0.43
34:DO:120:GLU:HG2	34:DO:122:LEU:HG	2.00	0.43
25:DA:534:U:H5'	40:DU:42:ALA:HB1	2.00	0.43
42:DW:13:SER:HA	42:DW:14:PRO:HD3	1.88	0.43
1:AA:1077:G:H5''	1:AA:1078:U:OP2	2.18	0.43
1:AA:345:C:H4'	1:AA:346:G:C4	2.53	0.43
1:AA:540:G:H2'	1:AA:541:G:C8	2.54	0.43
1:AA:600:C:H2'	1:AA:601:C:C6	2.54	0.43
1:AA:90:U:C2'	1:AA:91:C:H5'	2.49	0.43
4:AD:31:CYS:O	4:AD:35:ARG:HG3	2.17	0.43
8:AH:17:THR:HB	8:AH:78:GLN:OE1	2.19	0.43
9:AI:4:TYR:CE1	9:AI:88:TYR:HA	2.53	0.43
14:AN:3:ARG:HB3	14:AN:3:ARG:HH21	1.83	0.43
17:AQ:12:SER:HB3	17:AQ:20:THR:HB	2.01	0.43
50:B4:55:ARG:N	50:B4:56:VAL:HA	2.32	0.43
25:BA:2675:G:C6	25:BA:2676:G:C4	3.06	0.43
25:BA:2822:G:H2'	25:BA:2823:A:C8	2.53	0.43
26:BB:7:G:H8	26:BB:7:G:H5''	1.84	0.43
27:BD:132:PRO:HG2	27:BD:135:PHE:CE2	2.53	0.43
32:BI:60:GLU:HG3	32:BI:61:ARG:NH1	2.33	0.43
25:BA:2388:A:N6	38:BS:89:ARG:HD3	2.33	0.43
42:BW:4:LYS:HG2	42:BW:5:ALA:N	2.33	0.43
1:CA:382:A:H2'	1:CA:383:A:C8	2.53	0.43
1:CA:452:A:O2'	1:CA:453:A:H5''	2.19	0.43
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.88	0.43
4:CD:158:ILE:HA	4:CD:158:ILE:HD13	1.91	0.43
5:CE:116:THR:HG23	5:CE:117:ASP:OD2	2.19	0.43
10:CJ:33:GLN:H	10:CJ:76:ASN:H	1.66	0.43
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.33	0.43
1:CA:750:G:N2	15:CO:23:GLY:O	2.43	0.43
16:CP:6:LEU:HB3	16:CP:17:TYR:HD2	1.82	0.43
25:DA:189:G:P	47:D1:39:LYS:HZ2	2.40	0.43
25:DA:1721:G:N1	25:DA:1739:U:OP2	2.51	0.43
25:DA:935:C:H2'	25:DA:936:C:H6	1.82	0.43
27:DD:108:PRO:HB3	27:DD:143:HIS:HE1	1.84	0.43
31:DH:149:ARG:NH1	31:DH:167:GLU:OE2	2.50	0.43
31:DH:9:ILE:HG12	31:DH:69:ARG:HD2	1.99	0.43
31:DH:97:ARG:O	31:DH:103:LEU:HD12	2.19	0.43
32:DI:73:GLU:HG3	32:DI:138:ILE:HG23	1.99	0.43
34:DO:106:LEU:HA	34:DO:106:LEU:HD23	1.87	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:DP:121:LYS:O	35:DP:123:LEU:N	2.49	0.43
41:DV:24:LYS:HA	41:DV:92:THR:OG1	2.19	0.43
41:DV:52:VAL:CG2	41:DV:55:ALA:HB3	2.44	0.43
45:DZ:156:LYS:HE2	45:DZ:156:LYS:HB3	1.79	0.43
1:AA:1118:C:O5'	1:AA:1118:C:H6	2.00	0.43
1:AA:589:C:H42	1:AA:650:G:H1	1.66	0.43
4:AD:36:ARG:HB2	4:AD:38:TYR:CZ	2.53	0.43
5:AE:69:VAL:HG22	5:AE:71:LEU:HD23	2.01	0.43
24:AX:16:C:O2'	24:AX:17:C:H5'	2.18	0.43
25:BA:1845:G:H2'	25:BA:1846:A:C8	2.54	0.43
25:BA:2724:U:O2'	25:BA:2726:A:H5'	2.18	0.43
25:BA:484:G:O2'	25:BA:495:G:O6	2.28	0.43
25:BA:1836:U:O2	27:BD:50:THR:HB	2.19	0.43
25:BA:2840:G:H5''	28:BE:58:ARG:CZ	2.49	0.43
30:BG:43:LEU:HB3	30:BG:44:GLY:H	1.59	0.43
25:BA:1700:G:H3'	37:BR:2:ARG:HB2	2.00	0.43
1:CA:1165:C:N4	1:CA:1171:G:H1	2.13	0.43
1:CA:1227:A:H3'	1:CA:1227:A:C8	2.53	0.43
1:CA:1328:C:H2'	1:CA:1329:A:O4'	2.19	0.43
3:CC:199:LYS:HB3	3:CC:201:TYR:HE1	1.83	0.43
3:CC:7:PRO:HG3	3:CC:175:LEU:HD23	2.00	0.43
10:CJ:42:THR:HG21	10:CJ:66:ARG:HB3	2.00	0.43
1:CA:191:G:N2	20:CT:103:GLY:HA2	2.33	0.43
25:DA:1785:A:H2'	25:DA:1787:A:N7	2.34	0.43
25:DA:2298:A:H2'	25:DA:2299:G:O4'	2.18	0.43
25:DA:898:C:H2'	25:DA:899:A:O4'	2.18	0.43
25:DA:910:A:C6	25:DA:911:A:C6	3.07	0.43
26:DB:110:G:H2'	26:DB:111:G:C8	2.54	0.43
26:DB:50:G:OP1	38:DS:63:THR:OG1	2.28	0.43
26:DB:83:G:H4'	49:D3:52:HIS:CG	2.53	0.43
42:DW:46:PHE:O	42:DW:50:VAL:HG23	2.19	0.43
1:AA:1164:G:H2'	1:AA:1165:C:C6	2.54	0.43
1:AA:1068:G:N2	1:AA:1191:A:N3	2.62	0.43
1:AA:1347:G:C8	9:AI:107:ARG:HB2	2.54	0.43
1:AA:1356:G:H2'	1:AA:1357:A:H8	1.78	0.43
1:AA:542:G:OP1	4:AD:10:ARG:NH2	2.47	0.43
3:AC:35:GLU:CD	3:AC:59:ARG:HH12	2.20	0.43
1:AA:404:U:H3'	4:AD:3:ARG:NH2	2.33	0.43
5:AE:72:GLN:O	5:AE:75:THR:HG22	2.19	0.43
8:AH:96:GLY:N	8:AH:99:GLU:OE2	2.24	0.43
16:AP:74:LEU:HG	16:AP:79:VAL:HG21	2.00	0.43
25:BA:1067:A:H61	25:BA:1188:A:H61	1.66	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:553:A:C2	25:BA:2064:A:H2'	2.53	0.43
25:BA:2163:G:C5	25:BA:2173:G:C2	3.07	0.43
25:BA:2175:G:H2'	25:BA:2176:G:C8	2.54	0.43
25:BA:2272:C:H2'	25:BA:2273:C:H6	1.84	0.43
28:BE:181:LEU:HD11	39:BT:6:LEU:HD12	2.01	0.43
33:BN:138:LEU:HD23	33:BN:138:LEU:HA	1.73	0.43
37:BR:36:THR:HG22	37:BR:37:THR:N	2.34	0.43
37:BR:2:ARG:NH1	37:BR:5:LYS:O	2.51	0.43
38:BS:15:ARG:NE	38:BS:88:ASP:OD2	2.29	0.43
39:BT:50:ILE:HB	39:BT:99:LEU:HB2	2.00	0.43
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.54	0.43
1:CA:1159:U:O4'	1:CA:1182:G:N2	2.52	0.43
1:CA:1328:C:OP2	21:CU:7:ARG:NH1	2.51	0.43
1:CA:1369:C:H2'	1:CA:1370:G:O4'	2.19	0.43
1:CA:153:C:H2'	1:CA:154:C:C6	2.53	0.43
1:CA:161:A:H2'	1:CA:162:A:C8	2.53	0.43
1:CA:375:U:H4'	16:CP:17:TYR:CE2	2.54	0.43
1:CA:599:C:C2'	1:CA:600:C:H5'	2.49	0.43
1:CA:933:G:C6	1:CA:1385:G:C6	3.06	0.43
1:CA:1057:G:H5'	3:CC:155:GLY:HA2	2.00	0.43
8:CH:50:ARG:HA	8:CH:59:LEU:HD23	2.00	0.43
1:CA:1347:G:H5''	9:CI:107:ARG:HB3	1.99	0.43
9:CI:9:ARG:HB2	9:CI:104:ARG:HD2	2.00	0.43
15:CO:58:MET:O	15:CO:62:GLN:N	2.49	0.43
52:D6:23:THR:OG1	52:D6:24:GLU:N	2.45	0.43
54:D8:39:LYS:O	54:D8:43:GLN:HG3	2.19	0.43
25:DA:1003:G:N2	25:DA:1153:C:C2	2.86	0.43
25:DA:1221:C:H2'	25:DA:1221(A):C:C6	2.53	0.43
25:DA:1907:G:C6	25:DA:1908:C:C4	3.06	0.43
25:DA:2397:G:N2	25:DA:2420:C:H1'	2.33	0.43
25:DA:458:G:C8	53:D7:37:LYS:HG2	2.54	0.43
25:DA:856:C:H2'	25:DA:857:C:C6	2.53	0.43
25:DA:903:C:H2'	25:DA:904:C:H6	1.80	0.43
26:DB:43:C:OP1	50:D4:6:HIS:NE2	2.50	0.43
26:DB:42:C:H2'	30:DG:66:GLN:HE21	1.83	0.43
26:DB:42:C:O2'	30:DG:67:LYS:O	2.19	0.43
37:DR:38:VAL:HB	37:DR:39:PRO:HD3	2.01	0.43
37:DR:26:LYS:HE2	37:DR:70:LEU:O	2.19	0.43
45:DZ:14:LYS:HE2	45:DZ:16:SER:OG	2.18	0.43
1:AA:543:C:C2'	1:AA:544:G:H5'	2.49	0.43
1:AA:575:G:O2'	1:AA:821:G:H5'	2.19	0.43
11:AK:104:GLN:HB3	11:AK:104:GLN:HE21	1.62	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.18	0.43
19:AS:36:ARG:NH1	19:AS:53:ASN:HA	2.34	0.43
24:AX:47:U:H5''	24:AX:48:C:OP1	2.19	0.43
25:BA:1067:A:H3'	25:BA:1067:A:C8	2.53	0.43
25:BA:1338:U:H2'	25:BA:1339:C:H6	1.84	0.43
25:BA:2290:A:OP2	46:B0:12:ASN:ND2	2.48	0.43
25:BA:2332:A:H2'	25:BA:2332:A:N3	2.34	0.43
25:BA:2519:C:H4'	25:BA:2585:C:N4	2.33	0.43
25:BA:2745:G:H3'	25:BA:2746:A:O4'	2.18	0.43
25:BA:2647:C:H4'	28:BE:48:GLN:HE21	1.84	0.43
29:BF:33:LEU:HA	29:BF:33:LEU:HD12	1.82	0.43
33:BN:28:THR:HG22	33:BN:29:LYS:N	2.33	0.43
35:BP:86:LYS:HE3	35:BP:117:GLU:HB3	2.01	0.43
44:BY:28:LYS:HD2	44:BY:40:GLU:HG3	2.01	0.43
1:CA:1312:G:H5'	19:CS:5:LEU:HD21	2.01	0.43
4:CD:91:SER:HA	4:CD:94:LEU:HD12	2.01	0.43
5:CE:93:PRO:HG2	8:CH:105:ARG:CZ	2.48	0.43
8:CH:17:THR:HB	8:CH:78:GLN:OE1	2.18	0.43
15:CO:54:ARG:O	15:CO:58:MET:HG3	2.18	0.43
25:DA:10:G:H2'	25:DA:11:G:H8	1.83	0.43
25:DA:1216:G:N2	25:DA:1234:U:H1'	2.33	0.43
25:DA:1516:C:H2'	25:DA:1517:G:C8	2.54	0.43
25:DA:2207:G:OP1	25:DA:2207:G:H8	2.01	0.43
25:DA:307:G:H2'	25:DA:309:G:OP2	2.19	0.43
25:DA:459:U:OP2	25:DA:469:G:N1	2.34	0.43
13:CM:93:ARG:NH1	25:DA:888:C:OP1	2.48	0.43
25:DA:1971:A:C4	27:DD:241:PRO:HD3	2.53	0.43
28:DE:181:LEU:HD12	28:DE:181:LEU:HA	1.82	0.43
32:DI:66:GLU:HA	32:DI:69:LYS:HB3	2.00	0.43
45:DZ:35:ARG:HD2	45:DZ:35:ARG:HA	1.74	0.43
1:AA:1128:C:H4'	1:AA:1148:U:O2	2.19	0.43
1:AA:1134:G:N3	1:AA:1134:G:H2'	2.32	0.43
1:AA:1285:A:H1'	1:AA:1286:A:OP2	2.19	0.43
1:AA:923:A:O2'	1:AA:1399:C:OP2	2.29	0.43
1:AA:56:U:H2'	1:AA:57:G:H8	1.83	0.43
1:AA:673:G:H1	1:AA:717:C:N4	2.17	0.43
1:AA:814:A:N7	1:AA:816:A:C4	2.87	0.43
4:AD:108:LEU:HD12	4:AD:108:LEU:HA	1.91	0.43
7:AG:76:ARG:N	7:AG:87:VAL:O	2.44	0.43
14:AN:3:ARG:HA	14:AN:3:ARG:HD2	1.61	0.43
15:AO:12:ILE:HG23	15:AO:27:VAL:HG11	2.01	0.43
15:AO:8:LYS:HE3	15:AO:31:LEU:HD22	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:AP:58:TYR:O	16:AP:62:VAL:HG23	2.18	0.43
18:AR:21:LYS:HE2	18:AR:54:ARG:O	2.19	0.43
25:BA:1331:G:C5	25:BA:1375:U:C4	3.07	0.43
25:BA:1491:A:H8	25:BA:1507:A:C5	2.37	0.43
25:BA:604:C:H2'	25:BA:605:G:H8	1.84	0.43
25:BA:611:U:H2'	25:BA:612:C:C6	2.54	0.43
27:BD:17:THR:HG1	27:BD:205:VAL:H	1.61	0.43
25:BA:1829:U:OP2	27:BD:274:ARG:NH2	2.52	0.43
30:BG:138:GLN:HE22	30:BG:153:ARG:N	2.11	0.43
30:BG:144:ILE:HA	30:BG:148:MET:HE1	2.00	0.43
35:BP:121:LYS:HB3	35:BP:123:LEU:HG	2.00	0.43
1:CA:1030(A):G:N3	1:CA:1030(C):G:C8	2.87	0.43
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.54	0.43
1:CA:1386:G:C2	1:CA:1387:G:C8	3.06	0.43
1:CA:129(A):G:O2'	1:CA:189(F):U:OP1	2.25	0.43
1:CA:241:C:H42	1:CA:285:G:H1	1.65	0.43
1:CA:944:G:C2	1:CA:1340:A:C6	3.06	0.43
2:CB:27:LYS:O	2:CB:30:ARG:NH1	2.51	0.43
2:CB:70:PHE:HB3	2:CB:81:VAL:HG11	2.00	0.43
5:CE:36:ASP:C	5:CE:38:GLN:H	2.22	0.43
8:CH:34:GLU:HB3	8:CH:118:VAL:HG21	1.99	0.43
9:CI:16:ARG:O	9:CI:64:THR:N	2.50	0.43
1:CA:675:A:O2'	11:CK:114:VAL:O	2.35	0.43
20:CT:40:ALA:HB2	20:CT:55:ILE:HG22	2.01	0.43
25:DA:1028:A:H2'	25:DA:1029:A:C8	2.54	0.43
25:DA:1366:A:H2'	25:DA:1367:A:O4'	2.19	0.43
25:DA:1880:C:C2'	25:DA:1881:C:H5'	2.49	0.43
25:DA:1938:A:N3	25:DA:2605:U:O2'	2.44	0.43
25:DA:195:A:H2'	25:DA:198:C:H41	1.83	0.43
25:DA:2369:A:H2'	25:DA:2370:G:H8	1.84	0.43
25:DA:2633:G:H5''	25:DA:2812:G:H5'	2.00	0.43
25:DA:330:A:H2	25:DA:1210:A:C2'	2.27	0.43
25:DA:602:G:H4'	25:DA:604:G:H4'	1.99	0.43
27:DD:218:ARG:HB3	27:DD:219:PRO:HD2	2.01	0.43
33:DN:115:ARG:HA	33:DN:118:LYS:HE3	2.01	0.43
38:DS:26:LEU:HD22	38:DS:87:PHE:CE1	2.53	0.43
40:DU:76:TYR:CE1	40:DU:80:ILE:HG13	2.54	0.43
1:AA:1030:C:N3	1:AA:1031:G:C2	2.87	0.43
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.18	0.43
1:AA:1237:C:H5''	1:AA:1238:A:O4'	2.18	0.43
1:AA:520:A:N1	1:AA:536:C:H1'	2.34	0.43
1:AA:616:G:C2	1:AA:617:G:C8	3.07	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:72:C:H2'	1:AA:73:G:O4'	2.19	0.43
2:AB:19:HIS:CD2	2:AB:206:ASP:HB2	2.54	0.43
2:AB:218:ALA:O	2:AB:222:ILE:HG13	2.19	0.43
4:AD:172:PRO:O	4:AD:187:ARG:NH2	2.51	0.43
12:AL:34:ARG:HH11	12:AL:61:THR:HG21	1.84	0.43
21:AU:3:LYS:HA	21:AU:11:GLY:HA2	2.01	0.43
24:AX:19:G:C4	24:AX:57:A:C2	3.06	0.43
24:AX:36:U:H2'	24:AX:37:A:C8	2.54	0.43
24:AX:55:PSU:O2'	24:AX:57:A:N7	2.34	0.43
47:B1:86:SER:O	47:B1:89:GLU:HG2	2.19	0.43
52:B6:35:GLU:CD	52:B6:50:ARG:HH11	2.22	0.43
25:BA:1377:A:H2'	25:BA:1379:C:C5	2.54	0.43
25:BA:1588:G:H3'	25:BA:1589:A:H2'	2.01	0.43
25:BA:1609:A:H2'	25:BA:1610:G:C8	2.53	0.43
34:BO:120:GLU:HG2	34:BO:122:LEU:HG	2.01	0.43
44:BY:39:VAL:HB	44:BY:42:VAL:HB	2.01	0.43
1:CA:1362:C:H2'	1:CA:1363:C:H5''	2.01	0.43
1:CA:375:U:C2	1:CA:376:G:C8	3.07	0.43
1:CA:691:G:H2'	1:CA:692:U:C6	2.54	0.43
1:CA:724:G:C2	1:CA:725:G:C8	3.06	0.43
1:CA:80:G:N2	1:CA:90:U:H1'	2.34	0.43
1:CA:857:C:H2'	1:CA:858:G:O4'	2.19	0.43
2:CB:160:ASP:OD1	2:CB:160:ASP:N	2.52	0.43
2:CB:28:PHE:CE1	2:CB:31:TYR:HB2	2.54	0.43
7:CG:115:ARG:O	7:CG:119:ARG:HG3	2.19	0.43
1:CA:827:U:O2'	8:CH:19:VAL:HG11	2.19	0.43
10:CJ:55:LYS:O	10:CJ:57:LYS:N	2.52	0.43
11:CK:120:ARG:HA	11:CK:121:PRO:HD3	1.85	0.43
11:CK:19:ALA:HB3	11:CK:82:VAL:HG22	1.99	0.43
20:CT:43:LEU:HD13	20:CT:51:GLU:HB3	2.01	0.43
25:DA:1221:C:H2'	25:DA:1221(A):C:H6	1.83	0.43
25:DA:1232:G:C6	25:DA:1233:C:C4	3.07	0.43
25:DA:1265:A:H61	25:DA:2013:A:H5''	1.84	0.43
25:DA:1652:A:OP1	37:DR:8:ARG:NH1	2.51	0.43
25:DA:2380:C:O5'	25:DA:2380:C:H6	2.02	0.43
25:DA:268:C:H2'	25:DA:269:U:O4'	2.18	0.43
25:DA:493:G:H2'	25:DA:494:G:O4'	2.18	0.43
25:DA:764:A:N1	25:DA:1789:A:O2'	2.43	0.43
27:DD:13:ARG:HD2	27:DD:13:ARG:HA	1.85	0.43
29:DF:64:ILE:HG13	29:DF:65:TRP:N	2.34	0.43
29:DF:64:ILE:HG21	29:DF:78:ILE:HG23	2.01	0.43
33:DN:42:TRP:HA	33:DN:48:MET:HE1	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
37:DR:10:LEU:HA	37:DR:10:LEU:HD23	1.85	0.43
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.53	0.42
1:AA:1157:A:H61	1:AA:1178:G:H21	1.67	0.42
1:AA:426:G:H2'	1:AA:427:U:C6	2.54	0.42
4:AD:166:LYS:HB2	4:AD:168:ARG:HH12	1.84	0.42
4:AD:60:GLU:OE2	4:AD:63:LYS:NZ	2.51	0.42
4:AD:94:LEU:O	4:AD:98:GLU:N	2.52	0.42
12:AL:116:SER:OG	60:AL:303:HOH:O	2.21	0.42
15:AO:3:ILE:H	15:AO:3:ILE:HD13	1.84	0.42
20:AT:48:LYS:HD3	20:AT:48:LYS:HA	1.90	0.42
25:BA:2376:C:H4'	46:B0:56:ASP:OD1	2.19	0.42
25:BA:1186:U:OP1	33:BN:25:ARG:NH1	2.52	0.42
25:BA:1822:A:H8	25:BA:1822:A:OP2	2.02	0.42
29:BF:24:LEU:HD21	29:BF:114:VAL:HG12	2.00	0.42
36:BQ:1:MET:N	36:BQ:1:MET:SD	2.83	0.42
42:BW:86:LEU:HD12	42:BW:87:PRO:HD2	2.01	0.42
45:BZ:110:GLY:CA	45:BZ:145:GLU:HA	2.49	0.42
45:BZ:110:GLY:N	45:BZ:144:LEU:O	2.48	0.42
1:CA:1008:C:C2	1:CA:1022:G:C2	3.07	0.42
2:CB:145:LEU:O	2:CB:149:LEU:HB2	2.20	0.42
3:CC:18:TRP:H	3:CC:18:TRP:HE3	1.67	0.42
5:CE:51:VAL:O	5:CE:55:VAL:HG23	2.19	0.42
6:CF:99:ALA:HB1	18:CR:23:LYS:HE3	2.01	0.42
13:CM:40:ASN:HA	13:CM:41:PRO:HD3	1.92	0.42
19:CS:56:GLN:HB3	19:CS:56:GLN:HE21	1.52	0.42
13:CM:80:ARG:HH21	19:CS:69:HIS:HE1	1.68	0.42
13:CM:94:ARG:NH1	19:CS:80:TYR:HD2	2.17	0.42
20:CT:23:ARG:HG3	20:CT:23:ARG:HH11	1.84	0.42
25:DA:271(R):G:H5''	47:D1:97:LEU:HD21	2.00	0.42
54:D8:62:LEU:HB3	54:D8:65:GLU:HG3	2.01	0.42
25:DA:1462:C:H2'	25:DA:1463:C:O4'	2.20	0.42
25:DA:1685:C:H2'	25:DA:1686:C:H6	1.83	0.42
25:DA:2305:A:H5''	30:DG:134:GLY:HA3	2.00	0.42
25:DA:2507:C:H2'	25:DA:2508:G:O4'	2.19	0.42
25:DA:1983:C:H4'	25:DA:2606:C:O3'	2.18	0.42
25:DA:539:G:H2'	25:DA:540:C:C6	2.54	0.42
25:DA:646:A:H2'	25:DA:647:G:O4'	2.19	0.42
25:DA:909:A:N6	25:DA:912:C:O2	2.52	0.42
26:DB:53:A:N3	26:DB:53:A:H2'	2.34	0.42
29:DF:168:ARG:HB2	29:DF:175:THR:HG21	2.01	0.42
39:DT:80:SER:HA	39:DT:81:PRO:HD2	1.90	0.42
44:DY:45:VAL:N	44:DY:63:LYS:O	2.37	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1038:C:H2'	1:AA:1039:C:H6	1.82	0.42
1:AA:1392:G:N2	1:AA:1502:A:H8	2.17	0.42
1:AA:1393:U:O2'	1:AA:1394:A:H2'	2.20	0.42
1:AA:1438:G:H2'	1:AA:1439:C:C6	2.54	0.42
1:AA:1503:A:H5'	1:AA:1532:U:OP2	2.19	0.42
1:AA:376:G:H2'	1:AA:377:G:H8	1.84	0.42
1:AA:518:C:O2'	1:AA:530:G:N2	2.52	0.42
1:AA:927:G:H1	1:AA:1390:U:H3	1.67	0.42
2:AB:180:LEU:C	2:AB:182:ILE:H	2.21	0.42
2:AB:32:ILE:HD13	2:AB:40:HIS:HD2	1.84	0.42
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.52	0.42
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.19	0.42
7:AG:38:LEU:O	7:AG:42:ILE:HG13	2.19	0.42
1:AA:1343:G:O2'	9:AI:121:ARG:HD3	2.19	0.42
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	2.01	0.42
1:AA:1220:G:N2	19:AS:54:GLY:O	2.48	0.42
51:B5:41:PRO:HA	51:B5:42:PRO:HD3	1.89	0.42
25:BA:1006:C:N4	60:BA:3765:HOH:O	2.36	0.42
25:BA:1499:C:H42	25:BA:1506:G:H1	1.68	0.42
25:BA:1541:A:H2'	25:BA:1542:A:C8	2.53	0.42
25:BA:1766:G:N1	25:BA:1768:U:OP2	2.52	0.42
25:BA:2096:U:H2'	25:BA:2097:U:C6	2.53	0.42
25:BA:2240:G:C5	25:BA:2241:C:C4	3.06	0.42
25:BA:2542:A:N7	31:BH:172:LYS:NZ	2.62	0.42
25:BA:556:C:H4'	25:BA:557:A:H5''	1.99	0.42
35:BP:2:LYS:HE3	35:BP:4:SER:OG	2.19	0.42
1:CA:1144:G:H21	1:CA:1146:A:H62	1.66	0.42
1:CA:1191:A:OP2	3:CC:3:ASN:ND2	2.52	0.42
1:CA:938:A:C2	1:CA:1376:U:H1'	2.54	0.42
1:CA:553:A:C6	1:CA:554:C:C4	3.07	0.42
2:CB:163:PHE:CD1	2:CB:185:ILE:HG13	2.46	0.42
2:CB:28:PHE:CD1	2:CB:190:THR:HA	2.54	0.42
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.67	0.42
5:CE:78:HIS:HB3	8:CH:107:LEU:HD12	2.00	0.42
6:CF:24:GLU:HG3	6:CF:28:ARG:HD2	2.01	0.42
9:CI:17:VAL:HG11	9:CI:81:ILE:N	2.34	0.42
12:CL:124:LYS:HB2	12:CL:124:LYS:NZ	2.35	0.42
49:D3:46:ASN:O	49:D3:50:VAL:HG22	2.20	0.42
55:D9:2:LYS:HE2	55:D9:31:LYS:O	2.20	0.42
25:DA:1653:G:H4'	25:DA:1654:A:O5'	2.19	0.42
25:DA:1816:G:O6	27:DD:35:LYS:NZ	2.49	0.42
25:DA:1817:G:C6	25:DA:1818:U:C4	3.06	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2400:G:H2'	25:DA:2401:U:H6	1.84	0.42
25:DA:2564:A:C2	25:DA:2647:U:H4'	2.53	0.42
25:DA:686:G:C4	53:D7:11:LYS:HG2	2.54	0.42
25:DA:873:G:N2	25:DA:905:U:O2	2.51	0.42
26:DB:64:C:H2'	26:DB:65:C:C6	2.55	0.42
26:DB:75:G:H21	45:DZ:85:HIS:CE1	2.37	0.42
29:DF:20:LEU:HA	29:DF:20:LEU:HD23	1.80	0.42
30:DG:14:GLU:C	30:DG:17:PRO:HD2	2.38	0.42
35:DP:27:HIS:O	35:DP:31:ALA:HA	2.18	0.42
37:DR:67:LEU:HD13	37:DR:67:LEU:HA	1.81	0.42
39:DT:27:THR:HB	39:DT:89:VAL:HG23	2.00	0.42
45:DZ:44:PHE:CZ	45:DZ:86:VAL:HG11	2.55	0.42
1:AA:99:U:H2'	1:AA:100:C:C6	2.54	0.42
1:AA:1346:A:OP1	9:AI:120:ARG:NH1	2.37	0.42
1:AA:142:G:H2'	1:AA:143:A:H8	1.85	0.42
1:AA:257:G:C6	1:AA:258:G:C5	3.07	0.42
1:AA:620:C:H2'	1:AA:621:A:O4'	2.19	0.42
2:AB:122:PHE:CE2	2:AB:139:LYS:HE2	2.54	0.42
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	2.01	0.42
5:AE:102:ALA:O	5:AE:107:ARG:NH1	2.52	0.42
25:BA:1218:G:O2'	25:BA:1219:A:O5'	2.33	0.42
25:BA:1466:U:O2'	25:BA:1467:G:OP1	2.31	0.42
25:BA:1473:A:H4'	25:BA:1474:C:O4'	2.19	0.42
25:BA:2213:G:H5'	25:BA:2214:G:OP2	2.19	0.42
25:BA:2645:G:H5'	25:BA:2821:G:O2'	2.19	0.42
25:BA:544:U:H2'	25:BA:545:G:C8	2.54	0.42
33:BN:39:ARG:NH2	33:BN:41:ASP:OD2	2.52	0.42
34:BO:78:ARG:HD2	60:BT:202:HOH:O	2.18	0.42
25:BA:854:U:OP2	35:BP:41:ARG:NH2	2.52	0.42
41:BV:40:LEU:HB2	41:BV:46:VAL:HG13	2.01	0.42
1:CA:1080:A:H5'	5:CE:14:ARG:NH2	2.34	0.42
1:CA:1118:C:C6	1:CA:1119:C:H5	2.37	0.42
1:CA:129(A):G:N3	1:CA:189(F):U:H5''	2.35	0.42
1:CA:187:C:H2'	1:CA:188:C:H6	1.83	0.42
1:CA:582:U:O4	1:CA:758:G:H2'	2.19	0.42
1:CA:93:G:C6	1:CA:96:U:C4	3.07	0.42
1:CA:939:G:H2'	1:CA:940:C:C6	2.54	0.42
13:CM:92:HIS:HA	13:CM:110:ARG:HH12	1.84	0.42
18:CR:59:SER:OG	18:CR:62:GLU:HG2	2.19	0.42
1:CA:191:G:C2	20:CT:103:GLY:HA2	2.54	0.42
54:D8:60:LEU:HA	54:D8:60:LEU:HD23	1.84	0.42
25:DA:1246:A:OP1	29:DF:38:ARG:NH1	2.52	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1385:G:H4'	25:DA:1386:C:OP1	2.19	0.42
25:DA:1970:A:OP2	60:DA:4202:HOH:O	2.22	0.42
25:DA:2400:G:H2'	25:DA:2401:U:C6	2.54	0.42
25:DA:2745:C:C4	25:DA:2746:U:C4	3.07	0.42
25:DA:350:U:H2'	25:DA:351:G:O4'	2.19	0.42
25:DA:577:G:H8	25:DA:577:G:O5'	2.03	0.42
25:DA:623:G:H2'	25:DA:624:C:C6	2.54	0.42
25:DA:660:G:H5'	29:DF:99:TYR:CE2	2.54	0.42
26:DB:62:C:H2'	26:DB:63:G:C8	2.54	0.42
27:DD:171:ASP:O	27:DD:187:GLY:N	2.46	0.42
31:DH:81:GLU:OE1	31:DH:81:GLU:N	2.46	0.42
32:DI:88:ILE:O	32:DI:121:LYS:NZ	2.44	0.42
33:DN:39:ARG:HA	33:DN:40:PRO:HD3	1.85	0.42
36:DQ:85:LYS:NZ	46:D0:7:LEU:HG	2.34	0.42
38:DS:38:GLN:HG3	38:DS:40:ILE:HD11	2.00	0.42
1:AA:1053:G:N7	1:AA:1200:C:H5''	2.34	0.42
7:AG:58:PRO:O	7:AG:61:VAL:HG12	2.19	0.42
9:AI:99:LEU:HB3	9:AI:101:PHE:HE1	1.84	0.42
1:AA:1316:G:O3'	14:AN:18:VAL:HG22	2.19	0.42
17:AQ:37:LYS:O	17:AQ:38:ARG:HD3	2.20	0.42
19:AS:15:LEU:HD13	19:AS:33:THR:HB	2.00	0.42
25:BA:2283:G:OP1	46:B0:18:ALA:HB1	2.20	0.42
25:BA:2283:G:H5''	46:B0:20:ARG:HE	1.85	0.42
25:BA:1298:G:OP1	40:BU:36:ARG:NH2	2.52	0.42
25:BA:2018:C:H4'	25:BA:2019:G:OP1	2.19	0.42
25:BA:2157:A:N6	25:BA:2178:G:O2'	2.47	0.42
25:BA:2188:G:N7	25:BA:2190:G:N2	2.61	0.42
25:BA:2348:A:H61	46:B0:43:THR:HG22	1.84	0.42
25:BA:2804:C:H6	25:BA:2804:C:OP2	2.02	0.42
25:BA:733:G:N2	25:BA:835:A:H61	2.17	0.42
25:BA:185:A:O2'	25:BA:852:G:O6	2.31	0.42
26:BB:39:A:O2'	26:BB:46:A:N1	2.45	0.42
27:BD:101:GLU:OE1	27:BD:103:ARG:HD3	2.19	0.42
27:BD:169:GLU:OE1	27:BD:184:LYS:NZ	2.35	0.42
25:BA:2523:U:O2'	28:BE:138:PRO:O	2.24	0.42
29:BF:7:TYR:O	29:BF:21:ALA:HA	2.18	0.42
29:BF:93:LYS:HD3	29:BF:93:LYS:HA	1.88	0.42
30:BG:121:ASN:HA	30:BG:122:PRO:HD2	1.88	0.42
41:BV:62:LEU:HD13	41:BV:95:LEU:HB2	2.01	0.42
1:CA:1014:A:H2'	1:CA:1015:A:C8	2.55	0.42
1:CA:1142:G:C2	1:CA:1143:G:H1'	2.54	0.42
1:CA:722:A:N6	1:CA:724:G:C2	2.88	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:784:C:H2'	1:CA:785:G:O4'	2.19	0.42
1:CA:975:A:H5'	1:CA:975:A:H8	1.83	0.42
1:CA:97:G:C4	1:CA:98:G:C8	3.07	0.42
6:CF:6:VAL:HG13	6:CF:90:VAL:HG22	2.02	0.42
8:CH:75:ARG:HA	8:CH:76:PRO:HD2	1.83	0.42
11:CK:48:ILE:H	11:CK:48:ILE:HG12	1.54	0.42
25:DA:1005:C:H4'	25:DA:1012:U:C6	2.54	0.42
25:DA:1337:G:H2'	25:DA:1338:G:O4'	2.19	0.42
25:DA:1514:U:H2'	25:DA:1515:G:H8	1.84	0.42
25:DA:1593:G:C2	25:DA:1594:G:C4	3.07	0.42
25:DA:1692:U:O2'	25:DA:1693:U:H2'	2.19	0.42
25:DA:2110:G:O6	25:DA:2179:C:N3	2.51	0.42
25:DA:2106:G:C6	25:DA:2184:G:C6	3.07	0.42
25:DA:2512:C:H2'	25:DA:2513:G:O4'	2.19	0.42
25:DA:2880:C:O3'	37:DR:90:ARG:NH1	2.52	0.42
25:DA:380:U:H2'	25:DA:381:G:C8	2.54	0.42
25:DA:588:U:H1'	29:DF:90:PHE:HB3	2.01	0.42
25:DA:690:G:H5'	60:DA:4052:HOH:O	2.19	0.42
25:DA:76:C:O3'	48:D2:59:ARG:HG3	2.20	0.42
27:DD:64:ILE:O	27:DD:104:TYR:HB2	2.19	0.42
27:DD:70:TRP:HB3	27:DD:190:TYR:CE1	2.54	0.42
32:DI:78:THR:HG23	32:DI:143:SER:OG	2.20	0.42
1:AA:1194:U:H2'	1:AA:1195:C:H6	1.84	0.42
1:AA:102:G:O2'	1:AA:151:A:N3	2.34	0.42
5:AE:35:GLY:HA3	5:AE:112:LEU:HB3	2.01	0.42
6:AF:8:ILE:HD13	6:AF:26:ILE:HD13	2.00	0.42
9:AI:49:PRO:HB3	9:AI:82:ALA:HB2	2.01	0.42
20:AT:38:LYS:O	20:AT:42:GLN:N	2.44	0.42
36:BQ:86:GLY:HA3	46:B0:10:THR:HG23	2.01	0.42
46:B0:40:GLN:NE2	46:B0:43:THR:HA	2.35	0.42
25:BA:1309:U:H1'	51:B5:10:LYS:HG3	2.01	0.42
25:BA:2406:C:OP1	54:B8:30:ARG:NH1	2.52	0.42
25:BA:1384:G:O2'	25:BA:1439:A:N1	2.37	0.42
25:BA:1722:C:O2	28:BE:128:SER:OG	2.37	0.42
25:BA:28:A:H1'	25:BA:538:A:C2	2.55	0.42
25:BA:410:U:H5''	25:BA:411:U:OP2	2.19	0.42
25:BA:484:G:C5	53:B7:37:LYS:HE2	2.53	0.42
25:BA:588:C:H4'	25:BA:1299:A:C6	2.55	0.42
25:BA:73:A:H5'	25:BA:74:G:O4'	2.20	0.42
25:BA:2745:G:OP1	28:BE:203:LYS:HE2	2.20	0.42
1:AA:345:C:H5	39:BT:39:ARG:HH22	1.68	0.42
40:BU:112:ARG:HG2	40:BU:112:ARG:H	1.42	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1048:G:OP2	14:CN:3:ARG:NH2	2.53	0.42
1:CA:1224:G:C6	1:CA:1322:C:O4'	2.72	0.42
1:CA:1306:A:C6	1:CA:1307:U:C4	3.06	0.42
1:CA:170:U:O2'	1:CA:171:A:H5'	2.20	0.42
12:CL:34:ARG:O	12:CL:61:THR:HG23	2.19	0.42
18:CR:73:ALA:HB3	18:CR:79:LEU:HD12	2.01	0.42
20:CT:65:LYS:HA	20:CT:68:LYS:HD3	2.01	0.42
25:DA:1426:G:O2'	25:DA:1572:A:N6	2.46	0.42
25:DA:2870:C:H2'	25:DA:2871:C:O4'	2.19	0.42
25:DA:995:C:O2	33:DN:3:THR:OG1	2.24	0.42
27:DD:232:PRO:HB3	27:DD:244:ARG:CZ	2.50	0.42
28:DE:119:ARG:HB3	28:DE:120:TRP:CD1	2.55	0.42
30:DG:16:ARG:HB2	30:DG:17:PRO:HD3	2.01	0.42
32:DI:116:LEU:HD21	32:DI:119:PRO:HA	2.01	0.42
36:DQ:22:LYS:HG2	36:DQ:22:LYS:H	1.60	0.42
25:DA:143(A):C:H4'	43:DX:38:GLU:OE1	2.19	0.42
44:DY:20:TYR:CE1	44:DY:43:ASN:HA	2.54	0.42
1:AA:924:C:H2'	1:AA:925:G:C8	2.54	0.42
3:AC:123:GLN:HB3	3:AC:128:PHE:CD2	2.55	0.42
3:AC:5:ILE:HG12	3:AC:6:HIS:N	2.32	0.42
13:AM:34:LEU:CD1	13:AM:41:PRO:HA	2.47	0.42
16:AP:48:TRP:HH2	16:AP:76:GLN:NE2	2.16	0.42
25:BA:1001:G:H5''	36:BQ:77:LYS:HD2	2.02	0.42
25:BA:1285:G:H2'	25:BA:1286:U:O4'	2.20	0.42
25:BA:1787:G:O2'	25:BA:1789:G:H5''	2.20	0.42
25:BA:1793:A:H2'	60:BA:4156:HOH:O	2.17	0.42
25:BA:2804:C:OP2	25:BA:2804:C:C6	2.73	0.42
25:BA:599:U:H2'	25:BA:600:G:C8	2.54	0.42
26:BB:11:C:H3'	26:BB:12:C:C6	2.55	0.42
29:BF:196:LEU:HA	29:BF:196:LEU:HD23	1.86	0.42
26:BB:41:U:O4	30:BG:70:VAL:HB	2.18	0.42
36:BQ:39:PRO:HA	36:BQ:97:VAL:O	2.19	0.42
44:BY:15:VAL:O	44:BY:22:GLY:N	2.47	0.42
25:BA:352:U:H4'	44:BY:68:HIS:CG	2.54	0.42
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.55	0.42
1:CA:1137:C:H6	1:CA:1137:C:O5'	2.02	0.42
1:CA:84:U:H4'	1:CA:89:C:N4	2.35	0.42
2:CB:171:ALA:O	2:CB:175:ARG:HG3	2.20	0.42
4:CD:156:GLU:O	4:CD:160:GLN:HG3	2.20	0.42
6:CF:10:LEU:HB2	6:CF:59:TYR:HB3	2.01	0.42
9:CI:128:ARG:OXT	9:CI:128:ARG:HG2	2.20	0.42
20:CT:39:LYS:HB2	20:CT:39:LYS:HE3	1.84	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:31:C:H5''	25:DA:1239:G:OP1	2.20	0.42
25:DA:1642:G:H2'	25:DA:1643:G:C8	2.55	0.42
25:DA:2018:G:H2'	25:DA:2019:A:O4'	2.18	0.42
25:DA:2130:U:H3	25:DA:2159:G:H22	1.66	0.42
25:DA:2332:U:O2'	25:DA:2335:A:N3	2.50	0.42
25:DA:2697:G:H2'	25:DA:2698:U:O4'	2.20	0.42
25:DA:2728:U:H2'	25:DA:2729:G:C8	2.54	0.42
25:DA:747:U:O2	25:DA:2014:A:H1'	2.20	0.42
35:DP:31:ALA:O	35:DP:32:THR:OG1	2.30	0.42
1:AA:1132:C:H2'	1:AA:1133:G:H8	1.82	0.42
1:AA:178:C:H2'	1:AA:179:A:H8	1.84	0.42
1:AA:901:A:H5''	1:AA:902:G:OP2	2.19	0.42
1:AA:985:C:H2'	1:AA:986:A:C8	2.54	0.42
2:AB:18:GLY:O	2:AB:19:HIS:HB3	2.19	0.42
3:AC:156:ARG:N	3:AC:196:LEU:HD22	2.35	0.42
3:AC:35:GLU:O	3:AC:39:ILE:HG13	2.19	0.42
1:AA:1280:A:H8	10:AJ:40:LEU:HD22	1.85	0.42
17:AQ:6:LEU:HA	17:AQ:6:LEU:HD12	1.83	0.42
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	2.01	0.42
48:B2:3:LEU:HD22	48:B2:7:ARG:HE	1.83	0.42
50:B4:62:ARG:HA	50:B4:62:ARG:HD3	1.86	0.42
25:BA:469:A:H1'	25:BA:1246:C:O4'	2.19	0.42
25:BA:2033:U:H2'	25:BA:2034:G:O4'	2.18	0.42
25:BA:2171:G:H3'	25:BA:2172:U:C6	2.54	0.42
25:BA:2147:G:N2	25:BA:2194:U:OP1	2.45	0.42
27:BD:94:LEU:HD22	27:BD:95:LEU:N	2.34	0.42
30:BG:41:GLN:NE2	30:BG:154:GLY:O	2.52	0.42
37:BR:72:ASP:OD2	37:BR:75:LEU:HB2	2.20	0.42
44:BY:67:LEU:HD23	44:BY:67:LEU:HA	1.92	0.42
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.85	0.42
1:CA:1140:C:H2'	1:CA:1141:C:C6	2.54	0.42
1:CA:1157:A:H5'	1:CA:1158:C:N1	2.34	0.42
1:CA:125:U:H2'	1:CA:126:G:C8	2.55	0.42
1:CA:652:U:O2'	1:CA:653:A:OP2	2.33	0.42
1:CA:789:U:H2'	1:CA:791:G:OP2	2.19	0.42
1:CA:827:U:H2'	1:CA:859:A:H61	1.85	0.42
1:CA:848:C:O2'	1:CA:849:C:H5'	2.20	0.42
2:CB:120:ALA:C	2:CB:122:PHE:N	2.73	0.42
2:CB:135:GLN:O	2:CB:139:LYS:HB2	2.20	0.42
6:CF:21:LEU:O	6:CF:25:ILE:HG13	2.20	0.42
15:CO:22:THR:OG1	15:CO:23:GLY:N	2.53	0.42
17:CQ:81:ARG:HA	17:CQ:81:ARG:HD2	1.83	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.20	0.42
1:CA:1327:C:H5''	21:CU:20:LYS:HB3	2.02	0.42
50:D4:68:ARG:HB3	50:D4:69:LYS:H	1.60	0.42
25:DA:191:A:H2'	25:DA:192:C:C6	2.54	0.42
25:DA:2127:G:C6	25:DA:2161:C:N3	2.86	0.42
25:DA:2282:G:H4'	25:DA:2389:G:O2'	2.18	0.42
25:DA:2061:G:H5''	25:DA:2503:A:C2	2.54	0.42
25:DA:2529:G:O6	55:D9:31:LYS:NZ	2.52	0.42
25:DA:464:U:H4'	53:D7:5:TRP:CZ3	2.54	0.42
25:DA:608:A:C6	25:DA:609:A:C6	3.07	0.42
25:DA:78:A:C6	25:DA:109:G:C6	3.07	0.42
27:DD:95:LEU:HD11	27:DD:105:ILE:HD13	2.00	0.42
35:DP:143:GLY:O	35:DP:145:PRO:HD3	2.19	0.42
36:DQ:112:GLU:HG2	36:DQ:113:GLN:N	2.32	0.42
36:DQ:133:ARG:HG2	36:DQ:134:ARG:N	2.35	0.42
38:DS:4:LEU:HD22	38:DS:8:GLU:OE1	2.20	0.42
44:DY:6:HIS:CD2	44:DY:6:HIS:H	2.38	0.42
45:DZ:67:LEU:HD23	45:DZ:67:LEU:HA	1.86	0.42
1:AA:1037:C:O2	1:AA:1037:C:H2'	2.18	0.42
1:AA:1063:C:H3'	1:AA:1064:G:H2'	2.01	0.42
1:AA:1311:G:N2	1:AA:1326:C:N3	2.56	0.42
4:AD:59:ARG:NH2	4:AD:62:GLN:HG3	2.34	0.42
9:AI:84:ALA:O	9:AI:88:TYR:N	2.47	0.42
11:AK:54:ARG:O	11:AK:57:THR:OG1	2.37	0.42
24:AX:17:C:OP2	24:AX:17(A):U:O2'	2.30	0.42
25:BA:1224:C:H2'	25:BA:1225:C:C6	2.54	0.42
25:BA:160:G:O2'	25:BA:161:C:H5'	2.19	0.42
25:BA:2294:G:OP1	25:BA:2295:C:H1'	2.20	0.42
25:BA:586:G:H22	25:BA:601:A:H2	1.66	0.42
25:BA:886:U:H2'	25:BA:887:C:C6	2.53	0.42
25:BA:989:G:H5''	25:BA:990:A:O5'	2.20	0.42
32:BI:50:ARG:HA	32:BI:50:ARG:HD2	1.90	0.42
36:BQ:79:LEU:HA	36:BQ:79:LEU:HD23	1.91	0.42
45:BZ:137:ILE:HA	45:BZ:156:LYS:HZ1	1.85	0.42
1:CA:1220:G:H5'	19:CS:35:SER:HA	2.01	0.42
1:CA:1303:C:C4	1:CA:1304:G:C5	3.08	0.42
1:CA:1442:G:HO2'	1:CA:1442(A):G:P	2.38	0.42
1:CA:190:U:H2'	1:CA:191:G:H8	1.80	0.42
1:CA:320:C:O2'	1:CA:1435:G:H1'	2.20	0.42
1:CA:995:C:H4'	14:CN:8:GLU:OE2	2.20	0.42
15:CO:21:ASP:OD2	15:CO:24:SER:HB3	2.19	0.42
49:D3:8:LEU:O	49:D3:32:GLN:N	2.43	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DG:61:ALA:HB1	50:D4:7:PRO:HG2	2.01	0.42
25:DA:1022:G:N7	33:DN:66:LYS:HE2	2.35	0.42
25:DA:79:G:H1	25:DA:107:C:H42	1.67	0.42
25:DA:1839:G:N7	25:DA:1927:A:H1'	2.35	0.42
25:DA:2155:G:H2'	25:DA:2156:G:H5'	2.01	0.42
25:DA:2186:G:C2'	25:DA:2187:G:H5''	2.44	0.42
25:DA:2224:G:H4'	25:DA:2226:C:C2	2.55	0.42
25:DA:704:G:O2'	25:DA:726:G:N2	2.41	0.42
29:DF:178:PRO:HB3	29:DF:198:ALA:CB	2.50	0.42
30:DG:21:ARG:HG3	30:DG:22:ARG:N	2.34	0.42
33:DN:120:LEU:HA	33:DN:120:LEU:HD23	1.92	0.42
1:AA:1458:G:C2'	1:AA:1459:C:H5'	2.50	0.42
1:AA:240:C:H2'	1:AA:241:C:H6	1.82	0.42
1:AA:337:C:H2'	1:AA:338:A:C8	2.54	0.42
1:AA:390:C:H2'	1:AA:391:G:C8	2.54	0.42
1:AA:44:G:C2	1:AA:45:U:H1'	2.55	0.42
1:AA:925:G:H1'	1:AA:1502:A:C4	2.55	0.42
6:AF:86:ARG:O	6:AF:87:ARG:HG2	2.20	0.42
7:AG:48:LYS:O	7:AG:52:GLU:HG2	2.20	0.42
10:AJ:50:ILE:HD11	10:AJ:57:LYS:HD2	2.01	0.42
18:AR:59:SER:OG	18:AR:60:ALA:N	2.53	0.42
46:B0:40:GLN:NE2	46:B0:42:GLY:O	2.53	0.42
25:BA:1617:A:H2'	25:BA:1618:A:C8	2.55	0.42
25:BA:2162:C:C2	25:BA:2173:G:N1	2.73	0.42
25:BA:234:G:O5'	35:BP:73:GLY:HA2	2.20	0.42
25:BA:2605:U:O4	60:BA:4071:HOH:O	2.18	0.42
25:BA:2797:C:H1'	28:BE:37:ARG:NH1	2.35	0.42
25:BA:30:G:H2'	25:BA:31:C:C6	2.55	0.42
25:BA:419:C:H2'	25:BA:420:C:C6	2.54	0.42
25:BA:1615:G:H1'	27:BD:58:HIS:HE1	1.85	0.42
30:BG:96:ARG:O	30:BG:99:MET:HB3	2.19	0.42
33:BN:14:VAL:HG13	33:BN:138:LEU:HB2	2.02	0.42
35:BP:82:GLY:HA2	35:BP:113:LYS:O	2.20	0.42
37:BR:81:ASP:O	37:BR:85:PRO:HG2	2.20	0.42
1:CA:1118:C:C2	1:CA:1119:C:C5	3.08	0.42
1:CA:373:A:H1'	1:CA:481:G:N3	2.35	0.42
1:CA:501:C:H2'	1:CA:502:G:H8	1.85	0.42
1:CA:576:G:O6	1:CA:880:C:O2'	2.23	0.42
1:CA:947:G:H2'	1:CA:948:C:O4'	2.20	0.42
7:CG:135:VAL:HA	7:CG:138:LYS:HB3	2.02	0.42
19:CS:49:ILE:O	19:CS:60:VAL:N	2.48	0.42
49:D3:5:LYS:HE3	49:D3:57:GLU:CD	2.39	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
54:D8:23:VAL:HG22	54:D8:47:LYS:HB3	2.02	0.42
35:DP:59:LEU:HD23	54:D8:58:ILE:HD13	2.01	0.42
25:DA:1902:C:H5'	27:DD:246:PRO:HD3	2.02	0.42
25:DA:1978:A:H2'	25:DA:1979:C:C6	2.55	0.42
25:DA:2035:G:P	25:DA:2036:C:H41	2.42	0.42
25:DA:19:C:H2'	25:DA:20:C:H6	1.83	0.42
25:DA:2169:A:H2'	25:DA:2170:A:C8	2.55	0.42
25:DA:2170:A:H8	25:DA:2170:A:OP2	2.02	0.42
25:DA:2378:A:H8	25:DA:2378:A:O5'	2.03	0.42
25:DA:2600:A:H2'	25:DA:2601:C:C6	2.55	0.42
25:DA:729:G:H5'	25:DA:730:C:H5''	2.02	0.42
27:DD:172:TYR:CD1	27:DD:186:HIS:HA	2.55	0.42
30:DG:5:VAL:O	30:DG:8:LYS:HB2	2.20	0.42
31:DH:3:ARG:HH12	31:DH:5:GLY:N	2.16	0.42
33:DN:134:ARG:N	33:DN:135:PRO:HD3	2.35	0.42
34:DO:98:VAL:HG13	34:DO:117:LEU:HB2	2.02	0.42
39:DT:7:ILE:O	39:DT:11:GLU:HG3	2.20	0.42
42:DW:37:ARG:HD2	42:DW:38:TYR:CE2	2.55	0.42
25:DA:1341:U:H5'	43:DX:57:LEU:HB3	2.01	0.42
1:AA:110:C:H2'	1:AA:111:G:O4'	2.20	0.42
1:AA:1136:U:H3'	1:AA:1136:U:H6	1.85	0.42
1:AA:418:C:N4	1:AA:425:G:H1	2.12	0.42
1:AA:585:G:OP1	17:AQ:37:LYS:HD2	2.19	0.42
4:AD:162:LEU:HD13	4:AD:181:MET:HG2	2.02	0.42
1:AA:1374:A:O2'	7:AG:28:ASN:HB3	2.20	0.42
11:AK:99:GLN:HG3	11:AK:105:VAL:HG11	2.01	0.42
13:AM:40:ASN:HA	13:AM:41:PRO:HD2	1.86	0.42
13:AM:40:ASN:HB3	13:AM:43:THR:OG1	2.20	0.42
1:AA:1320:C:C4	19:AS:36:ARG:HB2	2.55	0.42
19:AS:41:VAL:O	19:AS:44:MET:N	2.45	0.42
25:BA:1333:A:N7	37:BR:106:GLY:HA3	2.35	0.42
25:BA:1464:G:H8	25:BA:1464:G:O5'	2.02	0.42
25:BA:1888:G:C6	25:BA:1889:G:C6	3.07	0.42
25:BA:2156:A:OP2	25:BA:2156:A:H8	2.02	0.42
25:BA:2157:A:H61	25:BA:2178:G:C2'	2.33	0.42
25:BA:2481:A:C2	25:BA:2482:G:H1'	2.55	0.42
25:BA:2882:G:O2'	25:BA:2883:A:H5'	2.19	0.42
25:BA:819:C:H2'	25:BA:820:U:C6	2.54	0.42
25:BA:1855:G:OP1	27:BD:52:ARG:HD3	2.20	0.42
28:BE:51:PHE:HB3	28:BE:77:ILE:HD12	2.02	0.42
40:BU:83:LEU:HD12	40:BU:113:ALA:HB2	2.02	0.42
25:BA:1233:U:C4'	41:BV:79:VAL:HG22	2.50	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1154:G:N7	1:CA:1155:G:N9	2.68	0.42
1:CA:1223:C:H5''	1:CA:1224:G:H5'	2.01	0.42
1:CA:1258:G:H2'	1:CA:1259:C:H6	1.84	0.42
1:CA:675:A:H2'	1:CA:676:A:C8	2.55	0.42
1:CA:707:C:H2'	1:CA:708:C:H6	1.84	0.42
1:CA:664:G:H22	1:CA:741:G:H22	1.68	0.42
1:CA:834:C:H2'	1:CA:835:U:C6	2.55	0.42
1:CA:586:C:O2'	1:CA:878:G:H4'	2.19	0.42
1:CA:900:A:H2'	1:CA:901:A:C8	2.55	0.42
4:CD:155:LEU:HD22	4:CD:157:LEU:H	1.85	0.42
8:CH:68:ARG:NH1	8:CH:74:PRO:HB3	2.35	0.42
7:CG:149:ARG:HG2	11:CK:59:TYR:CE1	2.55	0.42
1:CA:33:A:N3	12:CL:32:PHE:HE2	2.18	0.42
15:CO:5:LYS:HB2	15:CO:5:LYS:NZ	2.35	0.42
18:CR:69:THR:HA	18:CR:72:ARG:HD2	2.02	0.42
25:DA:1536:C:O2'	25:DA:1537:G:OP2	2.33	0.42
25:DA:1580:A:H3'	25:DA:1581:G:C8	2.55	0.42
25:DA:196:A:N3	25:DA:196:A:H2'	2.35	0.42
25:DA:272:G:C2	25:DA:421:U:C4	3.07	0.42
25:DA:77:C:H2'	25:DA:78:A:H8	1.85	0.42
25:DA:947:G:N2	25:DA:971:C:C2	2.88	0.42
27:DD:67:PHE:CE1	27:DD:157:ARG:HD2	2.55	0.42
29:DF:196:LEU:O	29:DF:199:TRP:HB3	2.20	0.42
30:DG:3:LEU:CD1	30:DG:5:VAL:HG12	2.49	0.42
33:DN:48:MET:HB2	33:DN:48:MET:HE3	1.73	0.42
38:DS:39:ILE:HD13	38:DS:85:VAL:HG21	2.01	0.42
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.55	0.41
1:AA:1530:G:H4'	1:AA:1530:G:OP1	2.19	0.41
1:AA:375:U:O3'	16:AP:6:LEU:HB2	2.20	0.41
1:AA:405:U:H4'	1:AA:496:A:O2'	2.20	0.41
1:AA:922:G:H2'	1:AA:923:A:C8	2.55	0.41
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.53	0.41
9:AI:86:VAL:HA	9:AI:92:TYR:HB2	2.02	0.41
11:AK:21:ILE:HB	11:AK:84:VAL:HG22	2.02	0.41
13:AM:90:LEU:HA	13:AM:93:ARG:HG3	2.01	0.41
1:AA:1308:U:OP2	13:AM:99:ARG:HD2	2.20	0.41
25:BA:733:G:C4	53:B7:11:LYS:HG2	2.55	0.41
25:BA:1052:C:C2	25:BA:1183:G:N2	2.88	0.41
25:BA:107:G:H2'	25:BA:108:G:O4'	2.20	0.41
25:BA:1451:U:H2'	25:BA:1452:U:H6	1.85	0.41
25:BA:174:U:H2'	25:BA:175:G:H8	1.85	0.41
25:BA:1834:A:O2'	27:BD:259:THR:HG21	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1859:G:H4'	25:BA:1860:A:OP1	2.19	0.41
25:BA:1944:G:H2'	25:BA:1945:U:O4'	2.20	0.41
25:BA:201:G:H2'	25:BA:202:A:O4'	2.20	0.41
25:BA:2185:C:OP1	25:BA:2187:G:N1	2.53	0.41
25:BA:360:C:H2'	25:BA:361:C:C6	2.55	0.41
28:BE:183:LEU:HD12	28:BE:183:LEU:HA	1.87	0.41
35:BP:118:GLY:O	35:BP:137:LYS:NZ	2.50	0.41
25:BA:1235:G:H5''	35:BP:32:THR:HA	2.01	0.41
36:BQ:58:PHE:HB3	36:BQ:61:GLY:O	2.20	0.41
1:CA:1006:C:H2'	1:CA:1007:C:O4'	2.20	0.41
1:CA:1276:G:O2'	1:CA:1277:C:H5'	2.20	0.41
1:CA:1399:C:C2	1:CA:1502:A:N6	2.88	0.41
1:CA:657:G:N2	1:CA:749:C:O2	2.44	0.41
1:CA:918:A:H2'	1:CA:919:A:O4'	2.20	0.41
1:CA:922:G:N3	1:CA:1398:A:C2	2.88	0.41
2:CB:16:HIS:HB3	2:CB:210:SER:CB	2.50	0.41
2:CB:27:LYS:O	2:CB:194:PRO:HG2	2.20	0.41
1:CA:532:A:N6	3:CC:156:ARG:HH22	2.17	0.41
4:CD:100:ARG:NH1	4:CD:137:SER:HB3	2.35	0.41
1:CA:1292:U:H5'	9:CI:38:GLN:NE2	2.35	0.41
20:CT:54:LYS:HA	20:CT:57:ARG:NH1	2.35	0.41
46:D0:50:ASN:HA	46:D0:62:LEU:HD11	2.02	0.41
50:D4:9:LEU:HD23	50:D4:9:LEU:HA	1.90	0.41
25:DA:1145:C:H2'	25:DA:1146:C:C6	2.55	0.41
25:DA:1598:C:H2'	25:DA:1599:C:C6	2.55	0.41
25:DA:37:C:H4'	25:DA:451:C:OP1	2.20	0.41
25:DA:598:G:H2'	25:DA:599:G:O4'	2.20	0.41
32:DI:44:LEU:HA	32:DI:44:LEU:HD13	1.86	0.41
38:DS:84:GLN:H	38:DS:111:GLU:HB2	1.84	0.41
40:DU:28:ARG:HD3	40:DU:38:THR:OG1	2.20	0.41
1:AA:1319:A:OP2	19:AS:3:ARG:HG3	2.20	0.41
1:AA:971:G:N1	1:AA:1363(A):A:OP2	2.44	0.41
1:AA:540:G:H2'	1:AA:541:G:O4'	2.21	0.41
1:AA:59:A:N6	1:AA:331:G:H1'	2.35	0.41
1:AA:1117:G:H5''	9:AI:104:ARG:CZ	2.50	0.41
9:AI:26:VAL:HG22	9:AI:61:ALA:HB3	2.02	0.41
11:AK:85:ARG:HG2	11:AK:111:ASP:O	2.19	0.41
12:AL:97:ARG:HG3	12:AL:98:TYR:CE1	2.55	0.41
17:AQ:76:LEU:HD21	17:AQ:79:SER:OG	2.21	0.41
46:B0:82:ARG:HA	46:B0:83:PRO:HD3	1.87	0.41
25:BA:1176:U:O2	28:BE:149:ARG:NH2	2.45	0.41
25:BA:143:C:H2'	25:BA:144:C:C6	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:174:U:H2'	25:BA:175:G:C8	2.55	0.41
25:BA:2596:U:O2	25:BA:2597:U:C4	2.73	0.41
25:BA:419:C:H5''	25:BA:436:C:H5''	2.02	0.41
29:BF:110:LEU:HD21	29:BF:181:LEU:HG	2.02	0.41
32:BI:9:LEU:HD22	32:BI:9:LEU:HA	1.83	0.41
1:CA:1005:A:H5''	1:CA:1006:C:C5	2.55	0.41
1:CA:1092:A:H5''	7:CG:4:ARG:CZ	2.50	0.41
1:CA:1443:G:H2'	1:CA:1444:C:C6	2.55	0.41
1:CA:255:G:C6	1:CA:256:U:C4	3.08	0.41
1:CA:109:A:C6	1:CA:326:G:C6	3.08	0.41
1:CA:667:G:OP1	1:CA:732:C:O2'	2.22	0.41
5:CE:32:VAL:O	5:CE:44:GLY:N	2.36	0.41
8:CH:112:LEU:HB3	8:CH:133:LEU:HA	2.02	0.41
9:CI:102:LEU:H	9:CI:102:LEU:HG	1.57	0.41
25:DA:1124:C:H2'	25:DA:1125:G:O4'	2.20	0.41
25:DA:1316:U:H2'	25:DA:1317:A:C8	2.55	0.41
25:DA:1429:G:H2'	25:DA:1430:C:C6	2.55	0.41
25:DA:1436:G:C2	25:DA:1437:C:C2	3.08	0.41
25:DA:1497:U:H5''	25:DA:1498:C:C5	2.56	0.41
25:DA:1652:A:N7	25:DA:1653:G:C6	2.88	0.41
25:DA:1660:C:O2'	25:DA:1661:G:H5'	2.20	0.41
25:DA:729:G:H2'	25:DA:1775:U:H1'	2.03	0.41
25:DA:2432:A:C6	25:DA:2433:A:C6	3.09	0.41
25:DA:2454:G:N7	60:DA:4288:HOH:O	2.37	0.41
25:DA:2671:A:H2'	25:DA:2672:G:O4'	2.20	0.41
25:DA:538:G:H2'	25:DA:539:G:C8	2.53	0.41
30:DG:19:LEU:HD11	30:DG:172:LEU:HB2	2.02	0.41
31:DH:26:VAL:O	31:DH:33:LEU:N	2.36	0.41
31:DH:35:VAL:O	31:DH:37:VAL:HG23	2.19	0.41
35:DP:45:LEU:HA	35:DP:45:LEU:HD22	1.79	0.41
38:DS:15:ARG:HE	38:DS:88:ASP:CG	2.23	0.41
41:DV:22:VAL:O	41:DV:92:THR:N	2.24	0.41
25:DA:84:A:H5'	44:DY:8:LYS:HB3	2.03	0.41
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.55	0.41
1:AA:392:G:H2'	1:AA:393:A:H8	1.85	0.41
1:AA:432:A:H3'	1:AA:433:C:H6	1.85	0.41
1:AA:567:G:H2'	1:AA:568:G:O4'	2.20	0.41
9:AI:48:GLU:HA	9:AI:51:ARG:HG3	2.03	0.41
12:AL:39:VAL:HG12	12:AL:41:ARG:HG2	2.03	0.41
13:AM:17:VAL:O	13:AM:20:THR:OG1	2.28	0.41
16:AP:20:VAL:HG23	16:AP:35:LYS:HA	2.02	0.41
25:BA:2642:G:H2'	25:BA:2643:G:C8	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:292:G:C2	25:BA:394:C:C2	3.08	0.41
25:BA:2692:C:H5'	28:BE:189:PRO:HA	2.01	0.41
33:BN:67:LEU:O	33:BN:88:GLU:HG3	2.20	0.41
42:BW:86:LEU:HD22	42:BW:96:ILE:HD11	2.02	0.41
1:CA:1030(A):G:H4'	1:CA:1030(A):G:OP1	2.21	0.41
1:CA:1113:C:O2'	3:CC:14:ILE:HD11	2.20	0.41
1:CA:1145:C:H4'	1:CA:1146:A:C5'	2.51	0.41
1:CA:835:U:C2	1:CA:836:G:C8	3.08	0.41
5:CE:80:ILE:CG2	5:CE:91:LEU:HB2	2.50	0.41
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.56	0.41
11:CK:52:GLY:H	11:CK:55:LYS:HE2	1.84	0.41
25:DA:1580:A:H3'	25:DA:1581:G:H8	1.85	0.41
25:DA:554:U:O4	60:DA:4015:HOH:O	2.19	0.41
25:DA:581:C:H2'	25:DA:582:G:C8	2.54	0.41
25:DA:98:G:OP1	48:D2:2:LYS:HA	2.21	0.41
25:DA:2379:G:H4'	38:DS:21:THR:CG2	2.51	0.41
1:AA:1327:C:H2'	1:AA:1328:C:C6	2.55	0.41
1:AA:153:C:N3	1:AA:168:G:N2	2.48	0.41
1:AA:174:C:H2'	1:AA:175:C:C6	2.55	0.41
3:AC:32:LEU:HA	3:AC:32:LEU:HD23	1.81	0.41
7:AG:100:ALA:O	7:AG:104:LEU:HB2	2.20	0.41
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	2.02	0.41
16:AP:40:ASP:HB3	16:AP:48:TRP:HB2	2.02	0.41
50:B4:57:GLU:N	50:B4:60:GLN:HG3	2.36	0.41
54:B8:48:PHE:CE2	54:B8:50:LEU:HD23	2.56	0.41
25:BA:354:A:H2	25:BA:1255:A:C2'	2.32	0.41
25:BA:1702:A:H3'	25:BA:1703:C:C6	2.55	0.41
25:BA:2544:G:C6	25:BA:2545:A:C6	3.08	0.41
25:BA:2623:U:C4	51:B5:3:LYS:HG2	2.55	0.41
25:BA:2803:A:N3	25:BA:2803:A:H2'	2.35	0.41
25:BA:325:G:H1'	25:BA:326:C:C6	2.54	0.41
25:BA:83:A:H3'	44:BY:8:LYS:HG2	2.02	0.41
30:BG:136:ARG:HG3	30:BG:137:GLU:HG3	2.03	0.41
31:BH:71:LEU:HA	31:BH:71:LEU:HD12	1.86	0.41
25:BA:2697:G:H5'	34:BO:68:GLU:OE1	2.19	0.41
36:BQ:79:LEU:HB3	36:BQ:80:GLU:HG3	2.00	0.41
28:BE:14:ILE:HB	39:BT:14:TYR:CE2	2.55	0.41
42:BW:79:GLY:HA3	42:BW:100:THR:HG22	2.02	0.41
1:CA:1048:G:H1	1:CA:1209:C:N4	2.15	0.41
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.36	0.41
1:CA:1057:G:C5	1:CA:1204:A:C2	3.09	0.41
1:CA:1492:A:H2'	1:CA:1493:A:C4	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:664:G:OP1	18:CR:64:ARG:NH2	2.51	0.41
1:CA:942:G:C2	1:CA:1342:C:C2	3.08	0.41
3:CC:122:GLU:HA	3:CC:125:GLU:OE2	2.19	0.41
7:CG:20:ASP:OD2	7:CG:23:VAL:HG23	2.20	0.41
8:CH:4:ASP:OD1	8:CH:6:ILE:N	2.53	0.41
11:CK:116:HIS:O	11:CK:117:ASN:HB2	2.20	0.41
19:CS:36:ARG:NE	19:CS:72:GLY:HA2	2.34	0.41
20:CT:23:ARG:NH1	20:CT:23:ARG:CG	2.82	0.41
25:DA:76:C:O2'	48:D2:59:ARG:HA	2.20	0.41
25:DA:1184:G:OP1	49:D3:30:ARG:HD2	2.21	0.41
35:DP:60:MET:HA	54:D8:13:ARG:NH1	2.36	0.41
25:DA:1005:C:H2'	25:DA:1006:C:C6	2.55	0.41
25:DA:1651:G:OP1	37:DR:40:LYS:HE3	2.20	0.41
25:DA:1651:G:H2'	25:DA:1652:A:O4'	2.20	0.41
25:DA:118:A:N3	25:DA:178:G:H1'	2.36	0.41
25:DA:962:G:H4'	25:DA:2496:C:O2'	2.21	0.41
25:DA:2578:G:H2'	25:DA:2579:C:C6	2.55	0.41
25:DA:2655:G:HO2'	25:DA:2656:U:P	2.44	0.41
25:DA:800:A:OP1	25:DA:800:A:H8	2.04	0.41
25:DA:80:G:H5'	25:DA:346:A:H1'	2.01	0.41
25:DA:998:C:H2'	25:DA:999:U:O4'	2.20	0.41
26:DB:29:A:C2	26:DB:30:C:C2	3.09	0.41
32:DI:130:TYR:HD2	32:DI:138:ILE:HD12	1.85	0.41
33:DN:33:LEU:HA	33:DN:33:LEU:HD13	1.94	0.41
36:DQ:42:ILE:HD13	36:DQ:97:VAL:HB	2.02	0.41
41:DV:62:LEU:HD23	41:DV:93:GLU:HG2	2.01	0.41
45:DZ:42:VAL:HG13	45:DZ:43:GLU:HG3	2.02	0.41
1:AA:1147:C:O5'	1:AA:1147:C:H6	2.03	0.41
1:AA:1169:A:H8	1:AA:1169:A:O5'	2.03	0.41
1:AA:341:C:O2'	1:AA:342:C:H5'	2.21	0.41
9:AI:65:VAL:HG21	9:AI:73:GLN:HB3	2.02	0.41
11:AK:86:GLY:O	11:AK:91:ARG:HD3	2.21	0.41
14:AN:26:ARG:HD3	14:AN:43:CYS:HB3	2.02	0.41
19:AS:31:ILE:HB	19:AS:49:ILE:HG13	2.02	0.41
54:B8:42:ARG:HD2	60:B8:5105:HOH:O	2.21	0.41
25:BA:555:G:C5	25:BA:2044:U:H5''	2.55	0.41
25:BA:2108:U:H2'	25:BA:2109:G:H8	1.86	0.41
25:BA:2254:G:O6	60:BA:3937:HOH:O	2.21	0.41
25:BA:34:C:H5''	25:BA:35:G:OP2	2.21	0.41
32:BI:12:LEU:HA	32:BI:12:LEU:HD23	1.85	0.41
45:BZ:110:GLY:N	45:BZ:145:GLU:HA	2.36	0.41
1:CA:1121:U:C4	1:CA:1122:U:C4	3.08	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:15:G:C4	1:CA:16:A:C8	3.09	0.41
1:CA:514:C:H2'	1:CA:515:G:C8	2.55	0.41
1:CA:692:U:O2'	1:CA:694:A:N7	2.44	0.41
1:CA:781:A:C8	1:CA:782:A:C8	3.09	0.41
2:CB:72:GLY:O	2:CB:94:ASN:HA	2.21	0.41
4:CD:50:ARG:HA	4:CD:51:PRO:HD3	1.94	0.41
25:DA:2387:U:H1'	46:D0:41:ARG:HE	1.85	0.41
25:DA:1882:C:H5'	47:D1:26:ARG:HH22	1.86	0.41
25:DA:1889:A:H1'	25:DA:2087:G:O4'	2.20	0.41
25:DA:2125:G:H22	25:DA:2172:U:C5'	2.31	0.41
25:DA:2287:A:C5	25:DA:2289:G:C5	3.09	0.41
25:DA:2437:U:H2'	25:DA:2438:U:C6	2.56	0.41
25:DA:2525:G:H1	25:DA:2538:C:H42	1.69	0.41
25:DA:928:G:O5'	25:DA:928:G:H8	2.03	0.41
30:DG:144:ILE:HG23	30:DG:148:MET:HE1	2.03	0.41
30:DG:39:ILE:O	30:DG:91:ARG:HA	2.20	0.41
37:DR:36:THR:HG22	37:DR:37:THR:N	2.35	0.41
45:DZ:153:SER:HB3	45:DZ:167:PRO:HB3	2.03	0.41
1:AA:1493:A:H2'	25:BA:1935:A:N1	2.35	0.41
1:AA:57:G:H2'	1:AA:58:C:H6	1.85	0.41
1:AA:730:G:C5	1:AA:731:G:H1'	2.55	0.41
1:AA:762:C:H2'	1:AA:763:G:H8	1.86	0.41
1:AA:936:C:H2'	1:AA:937:A:O4'	2.21	0.41
17:AQ:52:LYS:HG2	17:AQ:53:LEU:H	1.83	0.41
19:AS:50:ALA:HA	19:AS:58:VAL:O	2.20	0.41
25:BA:1368:A:N1	25:BA:1379:C:O2'	2.38	0.41
25:BA:1727:U:O2	25:BA:1794:G:H3'	2.21	0.41
25:BA:2357:G:N3	25:BA:2393:C:H2'	2.36	0.41
25:BA:2837:C:H2'	25:BA:2838:C:C6	2.56	0.41
25:BA:376:G:O2'	25:BA:377:G:H5'	2.20	0.41
25:BA:887:C:H2'	25:BA:888:A:C8	2.55	0.41
27:BD:162:SER:HB3	27:BD:195:ALA:CB	2.51	0.41
29:BF:184:TYR:CE2	29:BF:188:ARG:HD2	2.55	0.41
25:BA:2456:G:P	29:BF:68:LYS:HD2	2.60	0.41
1:CA:1034:G:C6	1:CA:1035:A:C2	3.09	0.41
1:CA:1151:A:O2'	1:CA:1152:A:O5'	2.32	0.41
1:CA:1097:C:O2	1:CA:1169:A:H2	2.03	0.41
1:CA:250:A:H4'	1:CA:251:G:O5'	2.19	0.41
1:CA:264:U:O2	17:CQ:64:PRO:HG2	2.20	0.41
1:CA:853:G:H2'	1:CA:854:G:C8	2.51	0.41
2:CB:105:PHE:O	2:CB:109:SER:HB2	2.20	0.41
2:CB:180:LEU:HB2	2:CB:182:ILE:HD12	2.01	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:CF:20:ALA:O	6:CF:24:GLU:N	2.49	0.41
6:CF:99:ALA:HB2	18:CR:31:LEU:HD21	2.02	0.41
9:CI:5:TYR:H	9:CI:87:GLN:HE22	1.69	0.41
9:CI:8:GLY:HA3	9:CI:76:ALA:O	2.21	0.41
14:CN:47:LEU:HD12	14:CN:53:LEU:CD2	2.50	0.41
16:CP:55:ARG:HD2	16:CP:55:ARG:HA	1.80	0.41
18:CR:40:LEU:HD13	18:CR:79:LEU:HD11	2.03	0.41
49:D3:10:LYS:NZ	60:D3:4001:HOH:O	2.43	0.41
25:DA:1206:G:H2'	25:DA:1207:C:C6	2.54	0.41
25:DA:1474:C:H2'	25:DA:1475:G:C8	2.54	0.41
25:DA:1423:G:C4'	25:DA:1492:G:H21	2.33	0.41
25:DA:2078:C:H2'	25:DA:2079:U:C6	2.55	0.41
25:DA:2494:G:C6	25:DA:2495:G:C5	3.07	0.41
25:DA:272(F):C:H42	25:DA:363(D):G:H1	1.67	0.41
25:DA:608:A:H2'	25:DA:609:A:C8	2.56	0.41
25:DA:842:G:H2'	25:DA:843:G:O4'	2.20	0.41
26:DB:5:C:O2'	26:DB:27:C:O2	2.38	0.41
26:DB:2:C:H2'	26:DB:3:C:H6	1.86	0.41
26:DB:83:G:H4'	49:D3:52:HIS:ND1	2.35	0.41
27:DD:264:LYS:HA	27:DD:265:PRO:HD3	1.94	0.41
31:DH:101:ARG:NH2	31:DH:122:THR:HA	2.35	0.41
33:DN:76:SER:OG	33:DN:81:GLY:HA3	2.20	0.41
38:DS:87:PHE:CZ	38:DS:102:ALA:HB2	2.56	0.41
25:DA:994:C:H1'	41:DV:10:LYS:HE3	2.01	0.41
1:AA:1025:U:O2	1:AA:1036:G:C6	2.73	0.41
1:AA:1347:G:H5''	9:AI:107:ARG:HB3	2.01	0.41
1:AA:264:U:H2'	1:AA:265:G:O4'	2.21	0.41
1:AA:49:U:O4	1:AA:365:U:H5	2.04	0.41
1:AA:16:A:O2'	5:AE:16:THR:HB	2.21	0.41
7:AG:20:ASP:HB3	7:AG:23:VAL:HG23	2.01	0.41
10:AJ:7:LYS:N	10:AJ:97:GLU:O	2.38	0.41
11:AK:116:HIS:O	11:AK:117:ASN:HB2	2.20	0.41
13:AM:33:ALA:O	13:AM:37:THR:OG1	2.23	0.41
20:AT:33:ILE:CD1	20:AT:62:LEU:HB3	2.47	0.41
48:B2:37:PHE:O	48:B2:41:ILE:HG12	2.20	0.41
51:B5:48:GLU:O	51:B5:60:VAL:HG11	2.21	0.41
25:BA:1333:A:C5	25:BA:1334:U:C4	3.08	0.41
25:BA:1417:G:H2'	25:BA:1418:U:C5	2.54	0.41
25:BA:1520:G:H2'	25:BA:1521:C:O4'	2.21	0.41
25:BA:1954:A:H2'	25:BA:1955:G:O4'	2.19	0.41
25:BA:645:G:H5'	25:BA:645:G:N3	2.35	0.41
25:BA:85:C:H4'	25:BA:102:U:H1'	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BB:110:G:H2'	26:BB:111:G:C8	2.56	0.41
32:BI:72:LEU:O	32:BI:74:ASN:N	2.54	0.41
34:BO:79:PHE:HD1	39:BT:72:VAL:HG22	1.85	0.41
41:BV:51:VAL:HG23	41:BV:52:VAL:O	2.21	0.41
1:CA:976:G:N2	1:CA:1363:C:OP2	2.53	0.41
1:CA:1502:A:H2	1:CA:1505:G:N1	2.18	0.41
1:CA:405:U:H5''	1:CA:406:G:O5'	2.21	0.41
2:CB:221:LEU:HA	2:CB:221:LEU:HD23	1.87	0.41
5:CE:139:LEU:HA	5:CE:142:LEU:CD1	2.51	0.41
7:CG:73:MET:HG3	7:CG:90:GLU:HA	2.02	0.41
9:CI:23:ASN:ND2	9:CI:23:ASN:H	2.19	0.41
13:CM:91:ARG:HA	13:CM:91:ARG:HD2	1.81	0.41
14:CN:23:ARG:NH1	14:CN:28:GLY:O	2.53	0.41
24:CX:53:G:C4	24:CX:54:5MU:H72	2.56	0.41
23:CW:76:PPU:N	24:CX:76:31H:N3'	2.66	0.41
50:D4:60:GLN:O	50:D4:63:TYR:HE2	2.04	0.41
25:DA:565:C:H4'	25:DA:1253:A:C6	2.55	0.41
25:DA:1364:G:OP1	47:D1:2:SER:HA	2.20	0.41
25:DA:1777:U:H2'	25:DA:1778:U:H6	1.85	0.41
25:DA:2242:G:H2'	25:DA:2243:U:O4'	2.20	0.41
25:DA:2252:G:H2'	25:DA:2253:G:O4'	2.20	0.41
25:DA:2459:A:H5''	25:DA:2460:U:OP2	2.20	0.41
25:DA:2557:G:H2'	25:DA:2558:C:C6	2.55	0.41
25:DA:2683:C:H2'	25:DA:2684:U:H6	1.85	0.41
25:DA:2863:C:H2'	25:DA:2864:G:H8	1.86	0.41
25:DA:610:G:H2'	25:DA:611:C:C6	2.56	0.41
25:DA:740:U:H2'	25:DA:741:G:C8	2.56	0.41
26:DB:33:G:C2	26:DB:50:G:C2	3.09	0.41
31:DH:154:PRO:HB3	31:DH:163:TYR:CZ	2.56	0.41
31:DH:98:LEU:HD22	31:DH:125:VAL:HG23	2.02	0.41
33:DN:34:LEU:O	33:DN:49:GLY:HA3	2.20	0.41
1:AA:1435:G:N2	1:AA:1466:C:O2	2.44	0.41
1:AA:163:C:H2'	1:AA:164:U:C6	2.56	0.41
1:AA:623:C:H2'	1:AA:624:C:O4'	2.20	0.41
1:AA:79:G:C2	1:AA:90:U:O2	2.74	0.41
2:AB:114:ARG:HG2	2:AB:145:LEU:HD21	2.03	0.41
2:AB:166:ASP:HB3	2:AB:169:LYS:HB2	2.03	0.41
2:AB:162:ILE:HD11	2:AB:184:VAL:HG22	2.02	0.41
2:AB:215:LEU:HD23	2:AB:215:LEU:HA	1.85	0.41
3:AC:181:ASN:C	3:AC:181:ASN:HD22	2.24	0.41
4:AD:158:ILE:H	4:AD:158:ILE:HD13	1.86	0.41
6:AF:45:LEU:O	6:AF:46:ARG:HG3	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AG:28:ASN:HD22	7:AG:31:MET:CE	2.34	0.41
9:AI:16:ARG:CZ	9:AI:64:THR:HG21	2.51	0.41
1:AA:742:G:C5'	15:AO:58:MET:HE3	2.51	0.41
15:AO:62:GLN:O	15:AO:66:LEU:HD13	2.21	0.41
16:AP:52:ASP:CG	16:AP:55:ARG:HB2	2.40	0.41
25:BA:1276:C:H2'	25:BA:1277:G:C8	2.55	0.41
25:BA:1489:G:H2'	25:BA:1490:G:C8	2.56	0.41
25:BA:1539:C:C5	25:BA:2227:G:H1'	2.55	0.41
25:BA:1810:U:H2'	60:BA:4539:HOH:O	2.20	0.41
25:BA:1875:C:H2'	25:BA:1876:G:H8	1.86	0.41
25:BA:2152:U:O2'	25:BA:2153:G:N2	2.31	0.41
25:BA:2294:G:H4'	25:BA:2401:G:O2'	2.21	0.41
25:BA:379:G:H2'	25:BA:380:G:O4'	2.20	0.41
25:BA:236:G:H4'	25:BA:413:G:C6	2.56	0.41
26:BB:5:C:O2'	26:BB:27:C:O2	2.38	0.41
25:BA:1546:G:O2'	27:BD:100:GLY:O	2.38	0.41
29:BF:184:TYR:O	29:BF:188:ARG:HG3	2.21	0.41
26:BB:57:A:N3	30:BG:29:TRP:HB3	2.36	0.41
31:BH:94:TYR:CD1	31:BH:94:TYR:N	2.89	0.41
37:BR:24:GLN:HE21	37:BR:44:LEU:HG	1.85	0.41
44:BY:56:PRO:C	44:BY:58:GLY:H	2.24	0.41
45:BZ:54:HIS:ND1	45:BZ:101:PRO:HG3	2.36	0.41
1:CA:91:C:H2'	1:CA:92:C:C6	2.55	0.41
3:CC:186:PHE:HD1	3:CC:198:VAL:O	2.03	0.41
3:CC:66:VAL:O	3:CC:101:LEU:HA	2.20	0.41
4:CD:51:PRO:HB2	4:CD:56:VAL:HG23	2.03	0.41
9:CI:53:VAL:HG21	9:CI:92:TYR:CE1	2.55	0.41
12:CL:117:ARG:NH2	12:CL:124:LYS:HB3	2.35	0.41
17:CQ:43:LEU:HG	17:CQ:68:ARG:HG2	2.03	0.41
47:D1:7:ILE:HG23	47:D1:98:LEU:HD11	2.03	0.41
54:D8:9:GLY:O	54:D8:13:ARG:HG2	2.20	0.41
25:DA:1014:U:H2'	25:DA:1015:G:H8	1.85	0.41
25:DA:1142:U:H5''	25:DA:1142(A):A:H5'	2.03	0.41
25:DA:1429:G:H1'	25:DA:1568:G:H1'	2.03	0.41
25:DA:1655:A:H1'	28:DE:113:PHE:CE1	2.56	0.41
25:DA:1744:C:H2'	25:DA:1745:C:C6	2.55	0.41
25:DA:827:U:O2'	25:DA:2068:U:C2	2.60	0.41
25:DA:2113:U:H3	25:DA:2170:A:N6	2.19	0.41
25:DA:2456:C:C4	25:DA:2457:U:C4	3.09	0.41
25:DA:324:A:N6	25:DA:338:G:O2'	2.54	0.41
25:DA:598:G:C6	25:DA:599:G:C5	3.09	0.41
25:DA:663:G:C6	25:DA:664:C:C4	3.09	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:923:C:H2'	25:DA:924:C:C6	2.55	0.41
25:DA:953:A:H2'	25:DA:954:G:H8	1.85	0.41
26:DB:12:C:H2'	46:D0:73:GLY:HA3	2.03	0.41
31:DH:7:LEU:HD23	31:DH:69:ARG:CZ	2.50	0.41
40:DU:49:HIS:O	40:DU:53:ARG:N	2.53	0.41
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.61	0.41
1:AA:509:A:N3	1:AA:543:C:O2'	2.33	0.41
1:AA:621:A:H2'	1:AA:622:A:C8	2.55	0.41
1:AA:66:G:O4'	1:AA:173:U:C4	2.74	0.41
2:AB:130:ARG:HG3	2:AB:130:ARG:NH1	2.35	0.41
4:AD:120:LEU:HA	4:AD:120:LEU:HD23	1.84	0.41
4:AD:53:ASP:O	4:AD:57:ARG:HD2	2.21	0.41
12:AL:110:VAL:HG23	12:AL:120:TYR:HB3	2.02	0.41
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	2.02	0.41
17:AQ:52:LYS:NZ	17:AQ:52:LYS:HB3	2.35	0.41
20:AT:72:LEU:HD23	20:AT:72:LEU:HA	1.95	0.41
25:BA:399:G:H5'	47:B1:66:HIS:NE2	2.36	0.41
25:BA:1470:G:H2'	25:BA:1471:G:O4'	2.21	0.41
25:BA:1480:A:H61	25:BA:1605:A:N6	2.12	0.41
25:BA:2041:A:H5''	40:BU:27:LEU:HD12	2.03	0.41
25:BA:220:C:H2'	25:BA:221:G:O4'	2.20	0.41
25:BA:2517:G:O6	25:BA:2588:G:H2'	2.21	0.41
25:BA:330:U:H2'	25:BA:331:G:O4'	2.20	0.41
32:BI:6:LEU:HG	32:BI:36:ALA:HA	2.01	0.41
41:BV:35:LEU:HA	41:BV:36:PRO:HD3	1.92	0.41
1:CA:235:C:H2'	1:CA:236:G:H8	1.85	0.41
1:CA:848:C:H6	1:CA:848:C:O5'	2.04	0.41
1:CA:954:G:H5'	13:CM:120:LYS:HD3	2.03	0.41
2:CB:186:ALA:O	2:CB:200:ILE:HA	2.21	0.41
13:CM:86:CYS:HB2	19:CS:73:GLU:HB3	2.03	0.41
1:CA:187:C:H5''	20:CT:86:ARG:HG3	2.02	0.41
1:CA:1229:A:O3'	24:CX:30:G:H5''	2.20	0.41
25:DA:1479:G:C6	25:DA:1480:G:C5	3.09	0.41
25:DA:1633:G:N2	25:DA:1635:G:H1'	2.35	0.41
25:DA:910:A:N6	25:DA:2277:G:O2'	2.40	0.41
25:DA:2369:A:H2'	25:DA:2370:G:C8	2.56	0.41
25:DA:826:U:H5''	25:DA:2429:G:P	2.61	0.41
25:DA:2516:G:C6	25:DA:2517:C:C4	3.09	0.41
25:DA:2537:U:H2'	25:DA:2538:C:H6	1.81	0.41
25:DA:271(R):G:C2	25:DA:271(S):G:C5	3.08	0.41
25:DA:437:G:H2'	25:DA:438:G:O4'	2.21	0.41
25:DA:917:A:H2'	25:DA:917:A:N3	2.36	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:DH:98:LEU:HA	31:DH:98:LEU:HD13	1.93	0.41
36:DQ:75:THR:HG21	36:DQ:87:LYS:HZ3	1.86	0.41
38:DS:74:ALA:CB	38:DS:108:GLY:HA3	2.51	0.41
40:DU:97:ASP:OD2	40:DU:101:ARG:HD2	2.20	0.41
1:AA:1027:C:O2'	1:AA:1028:C:O5'	2.39	0.41
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.50	0.41
1:AA:115:G:H4'	1:AA:116:A:O5'	2.20	0.41
1:AA:1350:A:H2'	1:AA:1351:U:O4'	2.21	0.41
1:AA:250:A:H4'	1:AA:251:G:O5'	2.21	0.41
1:AA:448:A:H2'	1:AA:449:C:C6	2.56	0.41
1:AA:869:G:H8	1:AA:869:G:O5'	2.04	0.41
1:AA:811:C:O2'	1:AA:901:A:N1	2.46	0.41
1:AA:985:C:H2'	1:AA:986:A:H8	1.86	0.41
6:AF:15:ASP:O	6:AF:18:GLN:NE2	2.49	0.41
8:AH:98:LYS:HD2	8:AH:98:LYS:H	1.85	0.41
19:AS:28:LYS:HE3	19:AS:28:LYS:HB3	1.87	0.41
20:AT:29:LYS:O	20:AT:33:ILE:HG12	2.21	0.41
1:AA:1305:G:OP1	21:AU:2:GLY:HA3	2.21	0.41
24:AX:12:G:H4'	25:BA:1930:C:O2	2.21	0.41
24:AX:4:G:H2'	24:AX:5:G:H8	1.84	0.41
25:BA:1060:U:H2'	25:BA:1061:G:C8	2.55	0.41
25:BA:1736:A:N6	25:BA:1745:A:H2	2.05	0.41
25:BA:1766:G:H5'	25:BA:1767:A:OP2	2.20	0.41
25:BA:2125:C:H2'	25:BA:2126:G:C8	2.56	0.41
23:AW:76:PPU:HD1	25:BA:2518:U:H1'	2.02	0.41
25:BA:1613:A:OP1	27:BD:211:ARG:NH1	2.53	0.41
28:BE:9:VAL:CG2	28:BE:25:VAL:HB	2.50	0.41
30:BG:143:GLU:H	30:BG:143:GLU:HG2	1.46	0.41
30:BG:77:ILE:HG21	30:BG:80:PHE:CD2	2.56	0.41
30:BG:77:ILE:HD13	30:BG:82:LEU:HD12	2.02	0.41
33:BN:87:LEU:HA	33:BN:87:LEU:HD23	1.90	0.41
38:BS:36:TYR:CD1	38:BS:36:TYR:N	2.88	0.41
38:BS:87:PHE:HZ	38:BS:98:VAL:HG12	1.86	0.41
39:BT:53:ARG:NH1	39:BT:53:ARG:HB3	2.36	0.41
45:BZ:111:VAL:HG12	45:BZ:112:ARG:H	1.86	0.41
1:CA:1003:G:C6	1:CA:1004:A:C2	3.09	0.41
1:CA:1041:A:N6	1:CA:1042:G:C6	2.89	0.41
1:CA:1067:A:N3	1:CA:1068:G:H1'	2.36	0.41
1:CA:1273:G:H5'	1:CA:1274:G:OP2	2.21	0.41
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.33	0.41
1:CA:685:G:N1	1:CA:686:U:O4	2.54	0.41
1:CA:865:A:O5'	1:CA:865:A:H8	2.04	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:12:LEU:HD23	3:CC:12:LEU:HA	1.94	0.41
4:CD:15:GLU:HG2	4:CD:63:LYS:HG3	2.03	0.41
12:CL:66:VAL:HG21	12:CL:98:TYR:CE2	2.56	0.41
14:CN:13:THR:HA	14:CN:14:PRO:HD3	1.85	0.41
18:CR:74:ARG:HG3	18:CR:79:LEU:HB2	2.03	0.41
25:DA:1007:C:C4	25:DA:1008:C:C4	3.09	0.41
25:DA:1032:A:H2	25:DA:1122:G:H22	1.69	0.41
25:DA:330:A:C2	25:DA:1210:A:H2'	2.42	0.41
25:DA:1372:U:O5'	25:DA:1372:U:H6	2.04	0.41
25:DA:24:G:H2'	25:DA:25:U:O4'	2.21	0.41
25:DA:600:G:H5'	29:DF:32:LEU:HD12	2.02	0.41
26:DB:78:A:C2	26:DB:100:A:C4	3.09	0.41
27:DD:70:TRP:CE2	27:DD:150:LYS:HD3	2.56	0.41
32:DI:29:TYR:O	32:DI:33:ARG:HG3	2.21	0.41
33:DN:34:LEU:HD21	33:DN:120:LEU:HG	2.03	0.41
36:DQ:66:ILE:HG12	36:DQ:104:PHE:CE1	2.55	0.41
44:DY:83:THR:HA	44:DY:101:LYS:HZ3	1.85	0.41
1:AA:1057:G:C4	1:AA:1204:A:C2	3.09	0.41
1:AA:1353:G:O2'	1:AA:1354:C:H5'	2.21	0.41
1:AA:1233:G:O2'	1:AA:1365:G:OP1	2.38	0.41
1:AA:1371:G:O3'	9:AI:69:GLY:HA3	2.20	0.41
1:AA:271:C:H2'	1:AA:272:C:H6	1.85	0.41
1:AA:29:G:O2'	1:AA:295:C:H4'	2.21	0.41
1:AA:438:G:O2'	1:AA:494:U:O4	2.38	0.41
7:AG:52:GLU:H	7:AG:52:GLU:HG2	1.59	0.41
24:AX:56:C:H6	24:AX:56:C:O5'	2.04	0.41
46:B0:53:MET:HG3	46:B0:59:LEU:HD23	2.03	0.41
25:BA:1576:G:C6	25:BA:1577:C:N4	2.89	0.41
25:BA:1611:C:H2'	25:BA:1612:C:C6	2.56	0.41
25:BA:1874:C:H2'	25:BA:1875:C:C6	2.55	0.41
25:BA:2147:G:N1	25:BA:2194:U:OP1	2.52	0.41
25:BA:2559:U:H2'	25:BA:2560:G:C8	2.55	0.41
32:BI:9:LEU:HD13	32:BI:10:GLU:HG3	2.02	0.41
33:BN:102:ALA:O	33:BN:106:MET:HG3	2.21	0.41
36:BQ:104:PHE:HE2	36:BQ:125:LEU:HD11	1.86	0.41
37:BR:61:HIS:O	37:BR:65:LEU:HD22	2.21	0.41
45:BZ:6:LYS:HD3	45:BZ:8:TYR:OH	2.21	0.41
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.21	0.41
1:CA:1226:C:OP1	13:CM:91:ARG:NH1	2.53	0.41
1:CA:163:C:H2'	1:CA:164:U:O4'	2.21	0.41
1:CA:299:G:H2'	1:CA:300:A:C8	2.56	0.41
1:CA:989:C:HO2'	1:CA:1016:A:H2	1.66	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:137:ALA:HA	3:CC:140:ARG:HD3	2.02	0.41
4:CD:173:TRP:NE1	4:CD:189:PRO:HG3	2.35	0.41
5:CE:95:ALA:HB1	5:CE:96:PRO:HD2	2.03	0.41
12:CL:58:VAL:O	12:CL:65:GLU:HA	2.21	0.41
1:CA:750:G:N3	15:CO:23:GLY:HA3	2.35	0.41
1:CA:1014:A:H5'	19:CS:18:LYS:HZ2	1.86	0.41
24:CX:10:G:C2	24:CX:26:G:H1'	2.56	0.41
53:D7:9:ARG:NH2	53:D7:47:ARG:HD2	2.36	0.41
54:D8:28:GLY:O	54:D8:36:LYS:NZ	2.47	0.41
25:DA:2160:G:H2'	25:DA:2161:C:O4'	2.21	0.41
25:DA:2290:G:C6	25:DA:2291:U:C4	3.09	0.41
25:DA:710:G:H2'	25:DA:711:G:C8	2.55	0.41
25:DA:848:G:C2	25:DA:933:A:H1'	2.56	0.41
25:DA:84:A:N1	25:DA:98:G:O2'	2.44	0.41
26:DB:73:A:C6	26:DB:74:U:C2	3.09	0.41
32:DI:114:LEU:HD22	32:DI:130:TYR:HA	2.03	0.41
35:DP:138:LEU:HA	35:DP:138:LEU:HD12	1.93	0.41
37:DR:100:LEU:HD11	37:DR:113:LEU:HD23	2.02	0.41
43:DX:94:GLY:N	43:DX:95:LEU:HA	2.36	0.41
44:DY:7:VAL:HG11	44:DY:13:VAL:HG11	2.02	0.41
45:DZ:53:ILE:HG22	45:DZ:71:VAL:O	2.20	0.41
1:AA:1027:C:O2'	1:AA:1028:C:C6	2.69	0.40
1:AA:1209:C:O2'	1:AA:1214:C:N4	2.52	0.40
1:AA:1275:A:H2'	1:AA:1276:G:C8	2.55	0.40
1:AA:1375:A:H4'	7:AG:29:LYS:HE2	2.03	0.40
1:AA:20:U:H2'	1:AA:21:G:O4'	2.21	0.40
1:AA:136:C:H42	1:AA:227:G:H1	1.70	0.40
1:AA:716:A:N3	11:AK:118:GLY:HA2	2.36	0.40
1:AA:938:A:C6	1:AA:939:G:C5	3.09	0.40
2:AB:105:PHE:HB2	2:AB:158:LEU:HD11	2.02	0.40
3:AC:173:VAL:O	3:AC:175:LEU:HD12	2.21	0.40
5:AE:39:GLY:HA2	5:AE:71:LEU:HD21	2.02	0.40
1:AA:737:A:P	6:AF:92:LYS:HZ2	2.43	0.40
1:AA:689:C:P	11:AK:46:GLY:HA3	2.61	0.40
13:AM:3:ARG:HD2	13:AM:9:ILE:CG1	2.50	0.40
17:AQ:66:SER:OG	17:AQ:67:LYS:N	2.54	0.40
1:AA:719:C:H1'	18:AR:49:LYS:HB3	2.03	0.40
49:B3:15:TYR:O	49:B3:20:LYS:NZ	2.52	0.40
50:B4:61:ARG:HG3	50:B4:62:ARG:N	2.36	0.40
25:BA:1093:G:H2'	25:BA:1156:G:H22	1.86	0.40
25:BA:1702:A:H3'	25:BA:1703:C:H6	1.86	0.40
25:BA:208:G:H2'	25:BA:209:G:C8	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2163:G:C4	25:BA:2164:C:H1'	2.55	0.40
25:BA:2183:C:N4	25:BA:2184:G:O6	2.54	0.40
25:BA:395:C:H2'	25:BA:396:C:O4'	2.20	0.40
25:BA:40:C:H42	25:BA:465:G:H1	1.69	0.40
25:BA:649:C:O2'	25:BA:704:U:OP1	2.31	0.40
25:BA:785:G:C6	25:BA:786:G:C2	3.09	0.40
28:BE:72:VAL:HG12	28:BE:73:GLU:O	2.22	0.40
30:BG:16:ARG:HB2	30:BG:17:PRO:HD3	2.03	0.40
30:BG:44:GLY:N	30:BG:88:ILE:O	2.54	0.40
31:BH:13:LYS:HA	31:BH:14:GLY:HA2	1.61	0.40
31:BH:20:ALA:HB1	31:BH:21:PRO:HD2	2.03	0.40
35:BP:21:ARG:HD3	35:BP:21:ARG:HA	1.90	0.40
38:BS:3:ARG:HE	38:BS:4:LEU:N	2.18	0.40
1:CA:1120:G:N1	1:CA:1154:G:N3	2.69	0.40
1:CA:1216:G:H2'	1:CA:1217:C:H5''	2.01	0.40
1:CA:1493:A:C8	25:DA:1913:A:N6	2.86	0.40
1:CA:600:C:H2'	1:CA:601:C:C6	2.57	0.40
1:CA:717:C:H2'	1:CA:734:G:OP2	2.21	0.40
1:CA:889:A:OP1	1:CA:891:U:H1'	2.21	0.40
1:CA:967:C:H5''	1:CA:968:A:OP2	2.21	0.40
2:CB:87:ARG:HE	2:CB:233:SER:HB3	1.87	0.40
3:CC:108:ASN:OD1	3:CC:110:ASN:HB2	2.21	0.40
3:CC:199:LYS:HB3	3:CC:201:TYR:CE1	2.56	0.40
7:CG:45:ASP:O	7:CG:49:ILE:HG12	2.21	0.40
10:CJ:50:ILE:HB	14:CN:41:ARG:NE	2.35	0.40
14:CN:53:LEU:HA	14:CN:54:PRO:HD2	1.89	0.40
15:CO:67:LEU:HA	15:CO:67:LEU:HD23	1.88	0.40
19:CS:36:ARG:CZ	19:CS:72:GLY:HA2	2.51	0.40
54:D8:8:LYS:O	54:D8:12:LYS:HG3	2.21	0.40
25:DA:1321:A:H2'	25:DA:1322:A:O4'	2.21	0.40
25:DA:1407:C:H2'	25:DA:1408:C:C6	2.56	0.40
25:DA:1482:G:C6	25:DA:1507:A:C6	3.09	0.40
25:DA:1819:A:H2'	27:DD:178:PRO:HB2	2.03	0.40
25:DA:2351:G:O6	54:D8:39:LYS:HG3	2.21	0.40
25:DA:602:G:O2'	25:DA:655:A:N6	2.54	0.40
25:DA:856:C:HO2'	25:DA:857:C:P	2.44	0.40
26:DB:16:G:C6	26:DB:69:G:C2	3.09	0.40
26:DB:92:C:H2'	26:DB:93:G:H8	1.87	0.40
25:DA:2511:U:O2'	28:DE:138:PRO:O	2.29	0.40
25:DA:605:C:OP1	29:DF:104:LYS:NZ	2.54	0.40
31:DH:56:SER:HB2	31:DH:61:HIS:ND1	2.36	0.40
34:DO:47:ILE:HB	34:DO:48:PRO:HD2	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:DP:125:VAL:HG23	35:DP:130:PHE:HZ	1.86	0.40
36:DQ:17:LEU:HD21	36:DQ:96:VAL:HG13	2.03	0.40
40:DU:8:VAL:O	40:DU:12:ARG:HG3	2.21	0.40
45:DZ:161:VAL:O	45:DZ:161:VAL:HG13	2.20	0.40
1:AA:1079:G:C6	1:AA:1080:A:N6	2.89	0.40
1:AA:1157:A:H61	1:AA:1178:G:N2	2.19	0.40
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.50	0.40
1:AA:397:A:N3	1:AA:397:A:H3'	2.36	0.40
1:AA:633:G:H2'	1:AA:634:C:C6	2.56	0.40
1:AA:967:C:H5''	1:AA:968:A:OP2	2.21	0.40
20:AT:67:ALA:HB2	20:AT:77:ALA:HB2	2.02	0.40
24:AX:52:G:H2'	24:AX:53:G:H8	1.86	0.40
25:BA:177:G:H1	25:BA:197:C:H42	1.67	0.40
25:BA:2185:C:H2'	25:BA:2186:C:O4'	2.21	0.40
25:BA:822:G:O6	25:BA:834:U:H2'	2.21	0.40
25:BA:956:A:C5	36:BQ:13:GLN:HG3	2.56	0.40
32:BI:135:GLU:C	32:BI:137:PRO:HD3	2.40	0.40
34:BO:70:LYS:HE2	34:BO:70:LYS:HB3	1.82	0.40
1:CA:1003:G:C6	1:CA:1004:A:H2	2.39	0.40
1:CA:1155:G:C6	1:CA:1156:G:C5	3.09	0.40
1:CA:1353:G:O2'	1:CA:1354:C:H5'	2.21	0.40
1:CA:1358:U:H2'	1:CA:1359:C:O4'	2.21	0.40
1:CA:575:G:C6	1:CA:821:G:N7	2.89	0.40
5:CE:135:THR:O	5:CE:139:LEU:N	2.52	0.40
7:CG:126:ASP:O	7:CG:130:GLY:N	2.54	0.40
7:CG:74:GLU:OE1	7:CG:95:ARG:NE	2.44	0.40
8:CH:41:ARG:HB3	8:CH:41:ARG:CZ	2.52	0.40
15:CO:25:THR:HG21	15:CO:70:LEU:HB2	2.03	0.40
16:CP:20:VAL:HG22	16:CP:34:GLU:O	2.22	0.40
20:CT:29:LYS:O	20:CT:33:ILE:HG13	2.21	0.40
25:DA:2271:G:OP1	46:D0:18:ALA:HB1	2.20	0.40
48:D2:35:LEU:HA	48:D2:35:LEU:HD23	1.86	0.40
52:D6:38:LYS:CE	52:D6:39:TYR:H	2.34	0.40
54:D8:53:PRO:O	54:D8:57:ARG:HG3	2.22	0.40
25:DA:125:G:H1'	53:D7:48:LYS:HE2	2.03	0.40
25:DA:1412:A:N1	25:DA:1591:G:C6	2.89	0.40
25:DA:1759:A:H4'	25:DA:2715:C:O4'	2.20	0.40
25:DA:2153:G:H5''	25:DA:2154:G:OP2	2.21	0.40
25:DA:2291:U:O2'	25:DA:2374:C:H1'	2.20	0.40
25:DA:945:A:C4	25:DA:2448:A:C2	3.09	0.40
25:DA:2582:G:N2	25:DA:2583:G:H1'	2.36	0.40
25:DA:880:G:C2	25:DA:898:C:O2	2.74	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DG:114:ILE:HG22	30:DG:117:PHE:HB2	2.03	0.40
31:DH:54:ARG:HD3	31:DH:65:HIS:ND1	2.36	0.40
33:DN:67:LEU:HA	33:DN:67:LEU:HD12	1.81	0.40
1:CA:1423:G:OP1	34:DO:49:ARG:NH2	2.54	0.40
43:DX:57:LEU:HD13	43:DX:78:LYS:HB3	2.02	0.40
44:DY:98:VAL:HA	44:DY:105:ALA:HA	2.03	0.40
44:DY:5:MET:HE1	44:DY:32:PRO:HA	2.02	0.40
1:AA:1002:G:C2	1:AA:1003:G:H1'	2.56	0.40
1:AA:1259:C:O2	1:AA:1283:G:H1'	2.21	0.40
1:AA:1457:G:H2'	1:AA:1458:G:H8	1.82	0.40
1:AA:1531:A:H3'	1:AA:1532:U:C6	2.56	0.40
1:AA:34:C:H2'	1:AA:35:G:C8	2.57	0.40
1:AA:954:G:C6	1:AA:955:U:C4	3.09	0.40
1:AA:961:U:OP2	1:AA:1223:C:O2'	2.22	0.40
2:AB:30:ARG:HG3	2:AB:31:TYR:CD1	2.56	0.40
3:AC:134:ILE:HG22	3:AC:168:ALA:HB3	2.02	0.40
19:AS:71:LEU:HA	19:AS:71:LEU:HD23	1.89	0.40
9:AI:128:ARG:NH1	24:AX:35:A:OP2	2.54	0.40
51:B5:49:CYS:SG	51:B5:51:TYR:HB2	2.62	0.40
25:BA:1222:A:H2'	25:BA:1222:A:N3	2.35	0.40
25:BA:600:G:O2'	25:BA:1300:A:OP1	2.36	0.40
25:BA:1489:G:H2'	25:BA:1490:G:H8	1.86	0.40
25:BA:2490:A:H2'	25:BA:2491:G:O4'	2.22	0.40
25:BA:2596:U:O2	25:BA:2597:U:N3	2.54	0.40
25:BA:669:A:H4'	25:BA:670:C:C5	2.56	0.40
25:BA:799:A:H3'	53:B7:1:MET:HE1	2.04	0.40
25:BA:857:U:O5'	25:BA:857:U:H6	2.04	0.40
25:BA:933:C:H4'	25:BA:933:C:OP1	2.19	0.40
27:BD:108:PRO:HG2	27:BD:111:LEU:HB2	2.03	0.40
28:BE:47:VAL:HG23	28:BE:84:PHE:O	2.21	0.40
30:BG:114:ILE:HA	30:BG:140:ILE:HD11	2.04	0.40
45:BZ:33:LEU:H	45:BZ:33:LEU:HG	1.82	0.40
1:CA:1023:G:C5	1:CA:1024:G:C8	3.09	0.40
1:CA:1122:U:C4	1:CA:1123:A:C5	3.10	0.40
1:CA:1281:U:P	1:CA:1282:C:H41	2.44	0.40
1:CA:745:C:OP1	1:CA:851:G:O2'	2.19	0.40
2:CB:50:GLU:OE1	2:CB:200:ILE:HG12	2.21	0.40
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.56	0.40
10:CJ:19:SER:O	10:CJ:23:ILE:HG12	2.19	0.40
12:CL:34:ARG:HE	12:CL:34:ARG:HB3	1.45	0.40
25:DA:1034:G:C6	25:DA:1035:U:C4	3.09	0.40
25:DA:1162:G:H2'	25:DA:1163:G:H8	1.85	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1252:G:C2	25:DA:1253:A:C2	3.09	0.40
25:DA:1346:G:C6	25:DA:1601:G:C6	3.09	0.40
25:DA:1469:A:H2'	25:DA:1470:G:O4'	2.22	0.40
25:DA:239:U:H2'	25:DA:240:G:O4'	2.21	0.40
25:DA:2591:C:H2'	25:DA:2592:G:C8	2.56	0.40
25:DA:2647:U:H2'	25:DA:2648:C:C6	2.57	0.40
25:DA:619:G:H3'	25:DA:620:G:N2	2.35	0.40
25:DA:661:C:H2'	25:DA:662:G:C8	2.56	0.40
25:DA:862:G:H2'	25:DA:863:A:O4'	2.21	0.40
26:DB:40:U:HO2'	26:DB:42:C:H5'	1.85	0.40
27:DD:177:LEU:HB3	27:DD:178:PRO:HD2	2.04	0.40
25:DA:323:G:C8	29:DF:171:PRO:HG3	2.56	0.40
38:DS:35:ILE:HB	38:DS:97:ARG:HH21	1.85	0.40
26:DB:8:U:O2'	38:DS:40:ILE:HD13	2.21	0.40
40:DU:27:LEU:HA	40:DU:30:LYS:HB2	2.04	0.40
25:DA:1187:G:H5'	41:DV:81:TYR:CE1	2.57	0.40
45:DZ:53:ILE:HG22	45:DZ:71:VAL:HB	2.02	0.40
26:DB:104:U:O3'	45:DZ:72:ARG:HD2	2.21	0.40
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.86	0.40
1:AA:191:G:N3	20:AT:103:GLY:HA2	2.37	0.40
1:AA:657:G:H4'	15:AO:28:GLN:HG2	2.04	0.40
1:AA:684:A:H2'	1:AA:685:G:O4'	2.21	0.40
1:AA:664:G:N2	1:AA:741:G:H1	2.09	0.40
1:AA:939:G:N3	1:AA:1375:A:H2	2.19	0.40
3:AC:131:ARG:NH2	3:AC:166:GLU:OE2	2.52	0.40
13:AM:91:ARG:HA	13:AM:91:ARG:HD2	1.85	0.40
16:AP:40:ASP:N	16:AP:48:TRP:O	2.45	0.40
17:AQ:62:SER:OG	17:AQ:72:ARG:HG2	2.21	0.40
19:AS:42:PRO:HD3	50:B4:61:ARG:HD3	2.03	0.40
25:BA:1092:A:HO2'	25:BA:1093:G:P	2.44	0.40
25:BA:1530:G:H1	25:BA:1551:C:N4	2.20	0.40
25:BA:1952:G:N2	25:BA:1990:G:H2'	2.37	0.40
25:BA:2289:G:P	46:B0:10:THR:HG21	2.61	0.40
25:BA:2569:G:H2'	25:BA:2570:C:C6	2.56	0.40
25:BA:2694:U:H5'	28:BE:11:MET:O	2.21	0.40
25:BA:306:A:H2'	25:BA:306:A:N3	2.37	0.40
25:BA:57:G:O2'	25:BA:72:A:N1	2.48	0.40
27:BD:213:ARG:HD2	27:BD:217:ARG:O	2.22	0.40
39:BT:51:ARG:HG3	39:BT:98:LYS:HD2	2.03	0.40
1:CA:1168:A:H2'	1:CA:1169:A:C8	2.55	0.40
1:CA:1194:U:H2'	1:CA:1195:C:C6	2.56	0.40
1:CA:797:C:C2'	1:CA:798:G:H5'	2.51	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:949:A:C6	1:CA:950:U:C4	3.09	0.40
6:CF:84:ASN:O	6:CF:86:ARG:HG3	2.22	0.40
7:CG:87:VAL:HG11	7:CG:155:ARG:HA	2.03	0.40
9:CI:16:ARG:O	9:CI:63:ILE:HA	2.21	0.40
1:CA:1226:C:P	13:CM:91:ARG:HH12	2.45	0.40
24:CX:4:G:H2'	24:CX:5:G:C8	2.57	0.40
51:D5:19:ARG:HH11	51:D5:19:ARG:HD2	1.73	0.40
25:DA:1364:G:P	47:D1:3:LYS:HG3	2.62	0.40
25:DA:1411:C:H2'	25:DA:1412:A:H8	1.87	0.40
25:DA:1431:U:H2'	25:DA:1432:C:C6	2.56	0.40
25:DA:2027:G:H2'	25:DA:2028:U:O4'	2.22	0.40
25:DA:2126:A:N1	25:DA:2173:A:C8	2.90	0.40
25:DA:2187:G:H8	25:DA:2187:G:C5'	2.35	0.40
25:DA:2503:A:H4'	25:DA:2504:U:OP1	2.22	0.40
25:DA:2543:G:H2'	25:DA:2544:G:C8	2.56	0.40
25:DA:626:U:O2	35:DP:105:LEU:HD22	2.22	0.40
25:DA:882:G:N2	25:DA:894:C:N3	2.69	0.40
26:DB:24:G:H4'	26:DB:25:A:C8	2.56	0.40
25:DA:1814:G:H4'	27:DD:51:VAL:HG21	2.04	0.40
30:DG:173:LEU:O	30:DG:178:PHE:HB2	2.22	0.40
32:DI:40:THR:O	32:DI:44:LEU:HB2	2.21	0.40
28:DE:12:THR:HG22	39:DT:58:ASN:OD1	2.21	0.40
1:AA:1277:C:HO2'	1:AA:1279:A:H1'	1.85	0.40
1:AA:1396:A:O4'	1:AA:1398:A:H1'	2.22	0.40
1:AA:885:G:H1	1:AA:912:C:H42	1.70	0.40
9:AI:8:GLY:HA3	9:AI:76:ALA:O	2.22	0.40
18:AR:53:ARG:HG2	18:AR:58:LEU:O	2.21	0.40
25:BA:536:U:H4'	25:BA:1281:G:H4'	2.02	0.40
25:BA:2101:U:H2'	25:BA:2102:G:O4'	2.20	0.40
25:BA:2187:G:O6	25:BA:2193:A:O2'	2.36	0.40
25:BA:2257:U:H5''	25:BA:2258:G:H5'	2.04	0.40
25:BA:2648:U:H1'	25:BA:2796:G:N2	2.36	0.40
25:BA:284:G:C2	25:BA:285:U:O4	2.74	0.40
27:BD:232:PRO:HB3	27:BD:244:ARG:NH2	2.36	0.40
28:BE:164:ARG:HH11	28:BE:164:ARG:HD2	1.77	0.40
32:BI:52:ARG:HB2	32:BI:52:ARG:NH2	2.37	0.40
32:BI:57:ARG:HD3	32:BI:58:LEU:H	1.86	0.40
25:BA:6:A:H2	33:BN:133:GLN:HE22	1.68	0.40
39:BT:77:PRO:HB2	39:BT:80:SER:HB2	2.04	0.40
44:BY:90:LEU:HD13	44:BY:90:LEU:HA	1.93	0.40
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.51	0.40
1:CA:1017:G:H2'	1:CA:1018:C:O4'	2.22	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1089:G:C6	1:CA:1090:U:C4	3.10	0.40
5:CE:59:GLY:O	5:CE:62:ALA:HB3	2.21	0.40
13:CM:65:LYS:N	50:D4:50:VAL:HG21	2.36	0.40
17:CQ:91:ARG:HG2	17:CQ:95:TYR:HE1	1.85	0.40
5:CE:24:ARG:NH1	22:CV:24:A:OP2	2.54	0.40
23:CW:76:PPU:HM2	25:DA:2452:C:N3	2.37	0.40
25:DA:189:G:OP2	47:D1:39:LYS:NZ	2.54	0.40
25:DA:2080:G:H2'	25:DA:2081:C:H6	1.87	0.40
25:DA:2153:G:H3'	25:DA:2154:G:H8	1.86	0.40
25:DA:2431:U:O2'	25:DA:2433:A:N7	2.42	0.40
25:DA:2516:G:C6	25:DA:2517:C:N4	2.89	0.40
25:DA:2592:G:C6	25:DA:2593:U:C4	3.10	0.40
25:DA:2773:C:H2'	25:DA:2774:C:C6	2.57	0.40
25:DA:30:G:C5	25:DA:31:C:C4	3.10	0.40
25:DA:335:C:H4'	44:DY:73:ARG:CD	2.51	0.40
25:DA:534:U:O5'	25:DA:534:U:H6	2.04	0.40
25:DA:61:G:H5'	48:D2:50:ILE:HG21	2.03	0.40
25:DA:987:G:H2'	25:DA:988:A:O4'	2.22	0.40
26:DB:54:G:H8	26:DB:54:G:O5'	2.04	0.40
27:DD:71:ASP:CB	27:DD:103:ARG:HH22	2.27	0.40
27:DD:73:VAL:HG13	27:DD:120:GLY:HA3	2.02	0.40
28:DE:7:VAL:CG1	28:DE:27:LEU:HB3	2.51	0.40
37:DR:100:LEU:HD22	37:DR:112:ALA:HA	2.02	0.40
39:DT:59:THR:HG23	39:DT:78:LEU:CB	2.52	0.40
40:DU:108:GLU:O	40:DU:112:ARG:HG2	2.22	0.40
40:DU:90:VAL:HG13	41:DV:4:ILE:HG21	2.04	0.40
42:DW:36:LEU:HD12	42:DW:51:LEU:HD12	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	229/256 (90%)	208 (91%)	18 (8%)	3 (1%)	18	54
2	CB	229/256 (90%)	206 (90%)	17 (7%)	6 (3%)	8	32
3	AC	204/239 (85%)	193 (95%)	10 (5%)	1 (0%)	38	79
3	CC	204/239 (85%)	187 (92%)	15 (7%)	2 (1%)	22	63
4	AD	206/209 (99%)	195 (95%)	9 (4%)	2 (1%)	22	63
4	CD	206/209 (99%)	194 (94%)	11 (5%)	1 (0%)	38	79
5	AE	146/162 (90%)	140 (96%)	4 (3%)	2 (1%)	16	52
5	CE	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
6	AF	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
6	CF	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
7	AG	153/156 (98%)	148 (97%)	2 (1%)	3 (2%)	11	40
7	CG	153/156 (98%)	151 (99%)	1 (1%)	1 (1%)	30	72
8	AH	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
8	CH	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
9	AI	125/128 (98%)	118 (94%)	7 (6%)	0	100	100
9	CI	125/128 (98%)	120 (96%)	5 (4%)	0	100	100
10	AJ	95/105 (90%)	87 (92%)	7 (7%)	1 (1%)	21	60
10	CJ	94/105 (90%)	87 (93%)	5 (5%)	2 (2%)	11	39
11	AK	112/129 (87%)	104 (93%)	5 (4%)	3 (3%)	8	30
11	CK	112/129 (87%)	103 (92%)	7 (6%)	2 (2%)	13	44
12	AL	120/132 (91%)	115 (96%)	5 (4%)	0	100	100
12	CL	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
13	AM	121/126 (96%)	113 (93%)	8 (7%)	0	100	100
13	CM	120/126 (95%)	114 (95%)	5 (4%)	1 (1%)	27	68
14	AN	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
14	CN	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
15	AO	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
15	CO	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
16	AP	80/88 (91%)	77 (96%)	3 (4%)	0	100	100
16	CP	80/88 (91%)	77 (96%)	2 (2%)	1 (1%)	18	54
17	AQ	97/105 (92%)	92 (95%)	4 (4%)	1 (1%)	22	63
17	CQ	97/105 (92%)	94 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	AR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
18	CR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
19	AS	81/93 (87%)	76 (94%)	5 (6%)	0	100	100
19	CS	81/93 (87%)	75 (93%)	6 (7%)	0	100	100
20	AT	94/106 (89%)	87 (93%)	6 (6%)	1 (1%)	21	60
20	CT	94/106 (89%)	86 (92%)	5 (5%)	3 (3%)	6	25
21	AU	21/27 (78%)	21 (100%)	0	0	100	100
21	CU	21/27 (78%)	21 (100%)	0	0	100	100
27	BD	273/276 (99%)	263 (96%)	9 (3%)	1 (0%)	43	82
27	DD	273/276 (99%)	262 (96%)	9 (3%)	2 (1%)	30	72
28	BE	202/206 (98%)	195 (96%)	6 (3%)	1 (0%)	38	79
28	DE	202/206 (98%)	193 (96%)	7 (4%)	2 (1%)	22	63
29	BF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	38	79
29	DF	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	22	63
30	BG	179/182 (98%)	171 (96%)	7 (4%)	1 (1%)	33	76
30	DG	179/182 (98%)	167 (93%)	11 (6%)	1 (1%)	33	76
31	BH	172/180 (96%)	169 (98%)	3 (2%)	0	100	100
31	DH	172/180 (96%)	168 (98%)	4 (2%)	0	100	100
32	BI	144/148 (97%)	130 (90%)	10 (7%)	4 (3%)	8	29
32	DI	144/148 (97%)	137 (95%)	6 (4%)	1 (1%)	30	72
33	BN	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
33	DN	138/140 (99%)	135 (98%)	2 (1%)	1 (1%)	30	72
34	BO	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
34	DO	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
35	BP	147/150 (98%)	141 (96%)	6 (4%)	0	100	100
35	DP	147/150 (98%)	140 (95%)	5 (3%)	2 (1%)	16	52
36	BQ	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
36	DQ	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
37	BR	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
37	DR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
38	BS	108/112 (96%)	103 (95%)	4 (4%)	1 (1%)	25	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	DS	108/112 (96%)	105 (97%)	2 (2%)	1 (1%)	25	66
39	BT	129/146 (88%)	123 (95%)	4 (3%)	2 (2%)	14	47
39	DT	129/146 (88%)	125 (97%)	3 (2%)	1 (1%)	27	68
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%)	93 (94%)	6 (6%)	0	100	100
41	DV	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
42	BW	110/113 (97%)	110 (100%)	0	0	100	100
42	DW	110/113 (97%)	110 (100%)	0	0	100	100
43	BX	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
43	DX	93/96 (97%)	90 (97%)	3 (3%)	0	100	100
44	BY	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
44	DY	105/110 (96%)	102 (97%)	3 (3%)	0	100	100
45	BZ	169/206 (82%)	152 (90%)	16 (10%)	1 (1%)	33	76
45	DZ	172/206 (84%)	158 (92%)	14 (8%)	0	100	100
46	B0	81/85 (95%)	81 (100%)	0	0	100	100
46	D0	81/85 (95%)	79 (98%)	1 (1%)	1 (1%)	19	57
47	B1	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
47	D1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	21	60
48	B2	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
48	D2	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
49	B3	57/60 (95%)	57 (100%)	0	0	100	100
49	D3	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
50	B4	67/71 (94%)	56 (84%)	9 (13%)	2 (3%)	7	27
50	D4	67/71 (94%)	54 (81%)	8 (12%)	5 (8%)	2	4
51	B5	57/60 (95%)	57 (100%)	0	0	100	100
51	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
52	B6	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
52	D6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
53	B7	46/49 (94%)	46 (100%)	0	0	100	100
53	D7	46/49 (94%)	45 (98%)	0	1 (2%)	10	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	B8	62/65 (95%)	62 (100%)	0	0	100	100
54	D8	62/65 (95%)	62 (100%)	0	0	100	100
55	B9	35/37 (95%)	35 (100%)	0	0	100	100
55	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11409/12128 (94%)	10906 (96%)	432 (4%)	71 (1%)	33	76

All (71) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	19	HIS
2	AB	231	GLU
4	AD	166	LYS
7	AG	80	VAL
27	BD	275	LYS
29	BF	130	ALA
38	BS	60	GLY
39	BT	39	ARG
2	CB	20	GLU
2	CB	78	GLN
3	CC	4	LYS
10	CJ	56	HIS
20	CT	99	LEU
29	DF	130	ALA
30	DG	47	LYS
32	DI	10	GLU
47	D1	3	LYS
50	D4	39	CYS
50	D4	62	ARG
50	D4	68	ARG
53	D7	46	VAL
5	AE	85	GLY
7	AG	8	GLU
11	AK	49	GLY
17	AQ	68	ARG
20	AT	47	GLY
32	BI	106	GLY
45	BZ	152	ALA
50	B4	55	ARG
2	CB	21	ARG
2	CB	125	PRO
11	CK	49	GLY

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Mol	Chain	Res	Type
13	CM	85	GLY
20	CT	47	GLY
20	CT	96	GLY
27	DD	239	ARG
33	DN	2	LYS
35	DP	45	LEU
38	DS	84	GLN
10	AJ	56	HIS
11	AK	117	ASN
28	BE	52	LEU
30	BG	47	LYS
39	BT	127	ALA
50	B4	57	GLU
2	CB	10	LEU
10	CJ	55	LYS
7	AG	81	GLY
32	BI	73	GLU
32	BI	105	HIS
2	CB	8	LYS
3	CC	62	ASP
28	DE	52	LEU
29	DF	21	ALA
35	DP	36	LYS
46	D0	4	LYS
50	D4	55	ARG
4	AD	5	ILE
5	AE	86	ALA
7	CG	7	ALA
27	DD	3	VAL
2	AB	125	PRO
32	BI	107	VAL
28	DE	73	GLU
39	DT	127	ALA
50	D4	60	GLN
11	CK	105	VAL
16	CP	53	VAL
11	AK	105	VAL
4	CD	5	ILE
3	AC	66	VAL

5.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	192/220 (87%)	151 (79%)	41 (21%)	1	4
2	CB	187/220 (85%)	154 (82%)	33 (18%)	3	8
3	AC	143/188 (76%)	125 (87%)	18 (13%)	7	18
3	CC	140/188 (74%)	121 (86%)	19 (14%)	5	15
4	AD	170/181 (94%)	146 (86%)	24 (14%)	5	14
4	CD	172/181 (95%)	145 (84%)	27 (16%)	4	11
5	AE	113/123 (92%)	103 (91%)	10 (9%)	14	40
5	CE	114/123 (93%)	98 (86%)	16 (14%)	5	14
6	AF	83/90 (92%)	78 (94%)	5 (6%)	27	63
6	CF	85/90 (94%)	77 (91%)	8 (9%)	13	36
7	AG	119/127 (94%)	108 (91%)	11 (9%)	13	38
7	CG	120/127 (94%)	109 (91%)	11 (9%)	13	38
8	AH	114/119 (96%)	103 (90%)	11 (10%)	12	35
8	CH	114/119 (96%)	104 (91%)	10 (9%)	14	40
9	AI	90/99 (91%)	76 (84%)	14 (16%)	4	11
9	CI	89/99 (90%)	70 (79%)	19 (21%)	1	5
10	AJ	66/92 (72%)	63 (96%)	3 (4%)	38	77
10	CJ	69/92 (75%)	64 (93%)	5 (7%)	21	51
11	AK	82/99 (83%)	75 (92%)	7 (8%)	15	42
11	CK	83/99 (84%)	79 (95%)	4 (5%)	35	74
12	AL	97/109 (89%)	89 (92%)	8 (8%)	17	44
12	CL	97/109 (89%)	88 (91%)	9 (9%)	13	37
13	AM	93/101 (92%)	79 (85%)	14 (15%)	4	12
13	CM	92/101 (91%)	77 (84%)	15 (16%)	3	10
14	AN	49/50 (98%)	42 (86%)	7 (14%)	5	13
14	CN	49/50 (98%)	39 (80%)	10 (20%)	2	5
15	AO	78/80 (98%)	70 (90%)	8 (10%)	10	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	CO	78/80 (98%)	71 (91%)	7 (9%)	14	39
16	AP	69/74 (93%)	54 (78%)	15 (22%)	1	4
16	CP	68/74 (92%)	59 (87%)	9 (13%)	6	16
17	AQ	94/97 (97%)	87 (93%)	7 (7%)	20	50
17	CQ	94/97 (97%)	88 (94%)	6 (6%)	25	59
18	AR	59/77 (77%)	52 (88%)	7 (12%)	8	21
18	CR	59/77 (77%)	52 (88%)	7 (12%)	8	21
19	AS	69/80 (86%)	63 (91%)	6 (9%)	15	41
19	CS	67/80 (84%)	59 (88%)	8 (12%)	8	21
20	AT	70/82 (85%)	61 (87%)	9 (13%)	6	17
20	CT	70/82 (85%)	59 (84%)	11 (16%)	4	11
21	AU	18/22 (82%)	15 (83%)	3 (17%)	3	9
21	CU	18/22 (82%)	15 (83%)	3 (17%)	3	9
27	BD	215/218 (99%)	196 (91%)	19 (9%)	14	40
27	DD	215/218 (99%)	194 (90%)	21 (10%)	12	34
28	BE	164/166 (99%)	144 (88%)	20 (12%)	7	20
28	DE	164/166 (99%)	143 (87%)	21 (13%)	6	18
29	BF	160/166 (96%)	146 (91%)	14 (9%)	14	40
29	DF	159/166 (96%)	144 (91%)	15 (9%)	13	36
30	BG	143/156 (92%)	123 (86%)	20 (14%)	5	14
30	DG	142/156 (91%)	118 (83%)	24 (17%)	3	9
31	BH	144/148 (97%)	136 (94%)	8 (6%)	30	66
31	DH	144/148 (97%)	131 (91%)	13 (9%)	14	39
32	BI	110/124 (89%)	93 (84%)	17 (16%)	4	11
32	DI	104/124 (84%)	87 (84%)	17 (16%)	3	10
33	BN	118/119 (99%)	104 (88%)	14 (12%)	8	21
33	DN	118/119 (99%)	104 (88%)	14 (12%)	8	21
34	BO	100/100 (100%)	92 (92%)	8 (8%)	17	45
34	DO	100/100 (100%)	90 (90%)	10 (10%)	11	32
35	BP	115/116 (99%)	102 (89%)	13 (11%)	9	25
35	DP	115/116 (99%)	103 (90%)	12 (10%)	10	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	BQ	111/111 (100%)	100 (90%)	11 (10%)	11	34
36	DQ	111/111 (100%)	98 (88%)	13 (12%)	8	22
37	BR	101/101 (100%)	86 (85%)	15 (15%)	4	12
37	DR	101/101 (100%)	90 (89%)	11 (11%)	9	26
38	BS	87/88 (99%)	80 (92%)	7 (8%)	17	45
38	DS	85/88 (97%)	76 (89%)	9 (11%)	10	28
39	BT	115/127 (91%)	104 (90%)	11 (10%)	12	35
39	DT	113/127 (89%)	98 (87%)	15 (13%)	6	16
40	BU	93/94 (99%)	85 (91%)	8 (9%)	15	41
40	DU	93/94 (99%)	85 (91%)	8 (9%)	15	41
41	BV	80/82 (98%)	72 (90%)	8 (10%)	11	32
41	DV	80/82 (98%)	75 (94%)	5 (6%)	25	60
42	BW	90/92 (98%)	82 (91%)	8 (9%)	14	40
42	DW	90/92 (98%)	84 (93%)	6 (7%)	23	56
43	BX	77/78 (99%)	73 (95%)	4 (5%)	32	71
43	DX	77/78 (99%)	75 (97%)	2 (3%)	59	90
44	BY	85/91 (93%)	77 (91%)	8 (9%)	13	36
44	DY	85/91 (93%)	81 (95%)	4 (5%)	36	75
45	BZ	145/179 (81%)	126 (87%)	19 (13%)	6	17
45	DZ	145/179 (81%)	128 (88%)	17 (12%)	8	22
46	B0	65/67 (97%)	61 (94%)	4 (6%)	26	61
46	D0	65/67 (97%)	61 (94%)	4 (6%)	26	61
47	B1	80/83 (96%)	75 (94%)	5 (6%)	25	60
47	D1	80/83 (96%)	73 (91%)	7 (9%)	14	40
48	B2	65/67 (97%)	61 (94%)	4 (6%)	26	61
48	D2	65/67 (97%)	57 (88%)	8 (12%)	7	20
49	B3	51/52 (98%)	45 (88%)	6 (12%)	8	22
49	D3	50/52 (96%)	46 (92%)	4 (8%)	17	45
50	B4	59/63 (94%)	50 (85%)	9 (15%)	4	12
50	D4	53/63 (84%)	40 (76%)	13 (24%)	1	3
51	B5	50/52 (96%)	44 (88%)	6 (12%)	7	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	D5	50/52 (96%)	46 (92%)	4 (8%)	17	45
52	B6	51/52 (98%)	45 (88%)	6 (12%)	8	22
52	D6	50/52 (96%)	45 (90%)	5 (10%)	11	32
53	B7	41/42 (98%)	37 (90%)	4 (10%)	12	34
53	D7	41/42 (98%)	37 (90%)	4 (10%)	12	34
54	B8	53/55 (96%)	49 (92%)	4 (8%)	19	49
54	D8	54/55 (98%)	50 (93%)	4 (7%)	20	50
55	B9	34/34 (100%)	32 (94%)	2 (6%)	28	64
55	D9	34/34 (100%)	30 (88%)	4 (12%)	8	22
All	All	9318/10066 (93%)	8277 (89%)	1041 (11%)	9	25

All (1041) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	8	LYS
2	AB	15	VAL
2	AB	16	HIS
2	AB	17	PHE
2	AB	19	HIS
2	AB	20	GLU
2	AB	21	ARG
2	AB	24	TRP
2	AB	39	ILE
2	AB	48	MET
2	AB	81	VAL
2	AB	82	ARG
2	AB	96	ARG
2	AB	114	ARG
2	AB	127	ILE
2	AB	130	ARG
2	AB	133	LYS
2	AB	137	ARG
2	AB	139	LYS
2	AB	145	LEU
2	AB	154	LEU
2	AB	155	LEU
2	AB	157	ARG
2	AB	160	ASP
2	AB	185	ILE

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Mol	Chain	Res	Type
2	AB	187	LEU
2	AB	189	ASP
2	AB	190	THR
2	AB	192	SER
2	AB	198	ASP
2	AB	200	ILE
2	AB	205	ASP
2	AB	209	ARG
2	AB	213	LEU
2	AB	217	ARG
2	AB	221	LEU
2	AB	223	ILE
2	AB	226	ARG
2	AB	230	VAL
2	AB	231	GLU
2	AB	235	SER
3	AC	3	ASN
3	AC	17	ASP
3	AC	27	LYS
3	AC	28	GLN
3	AC	29	TYR
3	AC	72	LYS
3	AC	98	ASN
3	AC	101	LEU
3	AC	104	GLN
3	AC	112	SER
3	AC	118	GLN
3	AC	140	ARG
3	AC	144	SER
3	AC	154	SER
3	AC	181	ASN
3	AC	190	ARG
3	AC	192	THR
3	AC	196	LEU
4	AD	5	ILE
4	AD	19	LEU
4	AD	36	ARG
4	AD	46	LYS
4	AD	49	ARG
4	AD	58	LEU
4	AD	77	ASN
4	AD	122	ARG

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Mol	Chain	Res	Type
4	AD	127	THR
4	AD	135	LEU
4	AD	138	TYR
4	AD	141	ARG
4	AD	150	GLU
4	AD	152	SER
4	AD	157	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	182	LYS
4	AD	187	ARG
4	AD	188	LEU
4	AD	190	ASP
4	AD	194	LEU
4	AD	200	GLU
4	AD	208	SER
5	AE	10	MET
5	AE	12	LEU
5	AE	20	GLN
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	71	LEU
5	AE	120	THR
5	AE	137	GLU
5	AE	151	LEU
6	AF	18	GLN
6	AF	40	VAL
6	AF	55	ASP
6	AF	69	GLU
6	AF	82	ARG
7	AG	6	ARG
7	AG	8	GLU
7	AG	12	LEU
7	AG	13	GLN
7	AG	24	THR
7	AG	52	GLU
7	AG	61	VAL
7	AG	91	VAL
7	AG	104	LEU
7	AG	115	ARG
7	AG	155	ARG

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Mol	Chain	Res	Type
8	AH	19	VAL
8	AH	21	LYS
8	AH	39	LEU
8	AH	45	ILE
8	AH	51	VAL
8	AH	52	ASP
8	AH	78	GLN
8	AH	86	ILE
8	AH	98	LYS
8	AH	112	LEU
8	AH	122	ARG
9	AI	17	VAL
9	AI	23	ASN
9	AI	29	ASN
9	AI	42	ARG
9	AI	53	VAL
9	AI	66	ARG
9	AI	78	LYS
9	AI	87	GLN
9	AI	92	TYR
9	AI	103	THR
9	AI	108	VAL
9	AI	121	ARG
9	AI	124	GLN
9	AI	128	ARG
10	AJ	38	ILE
10	AJ	46	ARG
10	AJ	84	GLN
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	77	MET
11	AK	81	ASP
11	AK	96	ARG
11	AK	104	GLN
12	AL	33	ARG
12	AL	52	LEU
12	AL	53	ARG
12	AL	59	ARG
12	AL	83	VAL
12	AL	97	ARG
12	AL	115	LYS

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Mol	Chain	Res	Type
12	AL	118	SER
13	AM	3	ARG
13	AM	4	ILE
13	AM	8	GLU
13	AM	15	VAL
13	AM	19	LEU
13	AM	27	LYS
13	AM	43	THR
13	AM	55	ARG
13	AM	57	ARG
13	AM	84	ILE
13	AM	106	ASN
13	AM	109	THR
13	AM	110	ARG
13	AM	115	LYS
14	AN	3	ARG
14	AN	7	ILE
14	AN	18	VAL
14	AN	22	THR
14	AN	23	ARG
14	AN	33	VAL
14	AN	57	ARG
15	AO	3	ILE
15	AO	5	LYS
15	AO	7	GLU
15	AO	38	ARG
15	AO	41	GLU
15	AO	64	ARG
15	AO	76	GLU
15	AO	83	GLU
16	AP	1	MET
16	AP	2	VAL
16	AP	5	ARG
16	AP	8	ARG
16	AP	19	ILE
16	AP	20	VAL
16	AP	34	GLU
16	AP	45	THR
16	AP	50	LYS
16	AP	54	GLU
16	AP	55	ARG
16	AP	60	LEU

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Mol	Chain	Res	Type
16	AP	62	VAL
16	AP	67	THR
16	AP	72	ARG
17	AQ	6	LEU
17	AQ	24	GLU
17	AQ	62	SER
17	AQ	63	ARG
17	AQ	72	ARG
17	AQ	74	LEU
17	AQ	100	LYS
18	AR	26	LEU
18	AR	31	LEU
18	AR	32	ARG
18	AR	37	VAL
18	AR	41	LYS
18	AR	76	LEU
18	AR	82	THR
19	AS	28	LYS
19	AS	30	LEU
19	AS	47	HIS
19	AS	49	ILE
19	AS	65	ASN
19	AS	78	ARG
20	AT	9	ASN
20	AT	10	LEU
20	AT	13	LEU
20	AT	24	LEU
20	AT	37	SER
20	AT	45	GLN
20	AT	54	LYS
20	AT	75	ASN
20	AT	84	LEU
21	AU	7	ARG
21	AU	10	ARG
21	AU	15	ARG
27	BD	12	SER
27	BD	13	ARG
27	BD	37	LEU
27	BD	61	LEU
27	BD	94	LEU
27	BD	106	ILE
27	BD	113	VAL

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Mol	Chain	Res	Type
27	BD	126	GLN
27	BD	138	VAL
27	BD	142	VAL
27	BD	155	LEU
27	BD	183	ARG
27	BD	211	ARG
27	BD	212	SER
27	BD	221	VAL
27	BD	229	VAL
27	BD	242	ARG
27	BD	257	LEU
27	BD	260	ARG
28	BE	2	LYS
28	BE	9	VAL
28	BE	11	MET
28	BE	12	THR
28	BE	21	VAL
28	BE	24	THR
28	BE	33	VAL
28	BE	40	GLU
28	BE	73	GLU
28	BE	75	VAL
28	BE	94	GLU
28	BE	111	ARG
28	BE	116	VAL
28	BE	118	LYS
28	BE	119	ARG
28	BE	144	ARG
28	BE	154	LYS
28	BE	163	GLU
28	BE	181	LEU
28	BE	203	LYS
29	BF	20	LEU
29	BF	24	LEU
29	BF	43	LYS
29	BF	57	VAL
29	BF	70	THR
29	BF	72	ARG
29	BF	74	ARG
29	BF	95	ARG
29	BF	106	ARG
29	BF	110	LEU

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Mol	Chain	Res	Type
29	BF	125	LEU
29	BF	132	VAL
29	BF	192	LEU
29	BF	197	ASP
30	BG	7	LEU
30	BG	21	ARG
30	BG	28	VAL
30	BG	43	LEU
30	BG	45	GLU
30	BG	60	LEU
30	BG	70	VAL
30	BG	82	LEU
30	BG	90	LEU
30	BG	91	ARG
30	BG	108	ASN
30	BG	115	ARG
30	BG	128	ARG
30	BG	135	LEU
30	BG	138	GLN
30	BG	140	ILE
30	BG	143	GLU
30	BG	145	THR
30	BG	148	MET
30	BG	165	THR
31	BH	41	MET
31	BH	45	VAL
31	BH	57	ASP
31	BH	59	ARG
31	BH	69	ARG
31	BH	95	ARG
31	BH	105	LEU
31	BH	149	ARG
32	BI	5	LEU
32	BI	9	LEU
32	BI	10	GLU
32	BI	38	LEU
32	BI	42	SER
32	BI	57	ARG
32	BI	61	ARG
32	BI	68	LEU
32	BI	75	LEU
32	BI	77	LEU

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Mol	Chain	Res	Type
32	BI	92	VAL
32	BI	96	ASP
32	BI	103	ARG
32	BI	109	ILE
32	BI	116	LEU
32	BI	121	LYS
32	BI	140	LEU
33	BN	33	LEU
33	BN	34	LEU
33	BN	46	VAL
33	BN	48	MET
33	BN	61	ARG
33	BN	62	VAL
33	BN	67	LEU
33	BN	68	GLU
33	BN	73	THR
33	BN	83	LYS
33	BN	85	ILE
33	BN	87	LEU
33	BN	99	LEU
33	BN	120	LEU
34	BO	8	LEU
34	BO	9	GLU
34	BO	10	VAL
34	BO	24	VAL
34	BO	28	SER
34	BO	78	ARG
34	BO	89	ASN
34	BO	94	ARG
35	BP	1	MET
35	BP	21	ARG
35	BP	45	LEU
35	BP	55	ARG
35	BP	56	SER
35	BP	59	LEU
35	BP	65	ARG
35	BP	77	ARG
35	BP	106	LEU
35	BP	112	LEU
35	BP	119	GLU
35	BP	147	LEU
35	BP	148	LEU

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Mol	Chain	Res	Type
36	BQ	1	MET
36	BQ	6	ARG
36	BQ	7	MET
36	BQ	16	ARG
36	BQ	35	VAL
36	BQ	45	GLN
36	BQ	54	MET
36	BQ	55	VAL
36	BQ	85	LYS
36	BQ	109	VAL
36	BQ	110	THR
37	BR	1	MET
37	BR	14	SER
37	BR	18	LEU
37	BR	29	LEU
37	BR	33	ARG
37	BR	36	THR
37	BR	44	LEU
37	BR	60	LEU
37	BR	65	LEU
37	BR	67	LEU
37	BR	75	LEU
37	BR	79	LEU
37	BR	86	ARG
37	BR	100	LEU
37	BR	102	GLU
38	BS	3	ARG
38	BS	14	VAL
38	BS	25	ARG
38	BS	36	TYR
38	BS	52	SER
38	BS	57	LYS
38	BS	59	LYS
39	BT	1	MET
39	BT	28	VAL
39	BT	34	VAL
39	BT	53	ARG
39	BT	78	LEU
39	BT	85	LYS
39	BT	89	VAL
39	BT	93	ARG
39	BT	96	ARG

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Mol	Chain	Res	Type
39	BT	115	ARG
39	BT	118	ARG
40	BU	8	VAL
40	BU	20	LEU
40	BU	36	ARG
40	BU	74	LEU
40	BU	92	ARG
40	BU	104	GLN
40	BU	108	GLU
40	BU	112	ARG
41	BV	18	LEU
41	BV	43	GLU
41	BV	52	VAL
41	BV	72	VAL
41	BV	73	SER
41	BV	79	VAL
41	BV	95	LEU
41	BV	100	ARG
42	BW	4	LYS
42	BW	11	ARG
42	BW	15	ARG
42	BW	23	LEU
42	BW	51	LEU
42	BW	52	GLU
42	BW	67	ASP
42	BW	92	ARG
43	BX	35	THR
43	BX	52	VAL
43	BX	57	LEU
43	BX	65	ARG
44	BY	8	LYS
44	BY	21	LYS
44	BY	23	ARG
44	BY	43	ASN
44	BY	61	ILE
44	BY	72	VAL
44	BY	85	VAL
44	BY	91	GLU
45	BZ	5	LEU
45	BZ	11	GLU
45	BZ	19	ARG
45	BZ	31	ARG

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Mol	Chain	Res	Type
45	BZ	33	LEU
45	BZ	40	ASP
45	BZ	46	LYS
45	BZ	58	VAL
45	BZ	72	ARG
45	BZ	76	LEU
45	BZ	91	LEU
45	BZ	98	MET
45	BZ	112	ARG
45	BZ	135	GLU
45	BZ	136	PHE
45	BZ	144	LEU
45	BZ	145	GLU
45	BZ	154	ASP
45	BZ	171	ILE
46	B0	14	ARG
46	B0	20	ARG
46	B0	55	ARG
46	B0	82	ARG
47	B1	23	LYS
47	B1	30	VAL
47	B1	40	ARG
47	B1	78	LYS
47	B1	95	LEU
48	B2	30	ARG
48	B2	32	LEU
48	B2	53	LEU
48	B2	70	GLN
49	B3	8	LEU
49	B3	18	ASP
49	B3	23	LEU
49	B3	54	VAL
49	B3	55	ARG
49	B3	58	VAL
50	B4	27	THR
50	B4	34	GLU
50	B4	46	GLN
50	B4	48	ARG
50	B4	49	PHE
50	B4	58	ARG
50	B4	61	ARG
50	B4	63	TYR

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Mol	Chain	Res	Type
50	B4	68	ARG
51	B5	16	ARG
51	B5	29	THR
51	B5	40	LYS
51	B5	55	ARG
51	B5	58	LEU
51	B5	59	GLU
52	B6	4	GLU
52	B6	6	ARG
52	B6	18	ARG
52	B6	28	ARG
52	B6	33	LYS
52	B6	48	VAL
53	B7	1	MET
53	B7	10	ARG
53	B7	41	ARG
53	B7	43	THR
54	B8	11	LYS
54	B8	31	HIS
54	B8	32	LEU
54	B8	34	TRP
55	B9	4	ARG
55	B9	7	VAL
2	CB	8	LYS
2	CB	17	PHE
2	CB	23	ARG
2	CB	24	TRP
2	CB	48	MET
2	CB	56	ARG
2	CB	58	ILE
2	CB	60	ASP
2	CB	61	LEU
2	CB	67	THR
2	CB	98	LEU
2	CB	109	SER
2	CB	114	ARG
2	CB	115	LEU
2	CB	117	GLU
2	CB	126	GLU
2	CB	128	GLU
2	CB	138	LEU
2	CB	144	ARG

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Mol	Chain	Res	Type
2	CB	145	LEU
2	CB	154	LEU
2	CB	155	LEU
2	CB	160	ASP
2	CB	169	LYS
2	CB	187	LEU
2	CB	189	ASP
2	CB	192	SER
2	CB	200	ILE
2	CB	209	ARG
2	CB	213	LEU
2	CB	217	ARG
2	CB	230	VAL
2	CB	233	SER
3	CC	21	ARG
3	CC	29	TYR
3	CC	32	LEU
3	CC	43	LEU
3	CC	44	GLU
3	CC	45	LYS
3	CC	52	LEU
3	CC	54	ARG
3	CC	59	ARG
3	CC	72	LYS
3	CC	82	GLU
3	CC	105	GLU
3	CC	118	GLN
3	CC	126	ARG
3	CC	152	ILE
3	CC	164	ARG
3	CC	179	ARG
3	CC	190	ARG
3	CC	196	LEU
4	CD	5	ILE
4	CD	12	CYS
4	CD	19	LEU
4	CD	33	MET
4	CD	34	GLU
4	CD	45	GLN
4	CD	46	LYS
4	CD	47	ARG
4	CD	58	LEU

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Mol	Chain	Res	Type
4	CD	61	LYS
4	CD	77	ASN
4	CD	83	SER
4	CD	114	ARG
4	CD	122	ARG
4	CD	127	THR
4	CD	135	LEU
4	CD	137	SER
4	CD	150	GLU
4	CD	155	LEU
4	CD	158	ILE
4	CD	170	VAL
4	CD	181	MET
4	CD	187	ARG
4	CD	194	LEU
4	CD	200	GLU
4	CD	202	LEU
4	CD	203	VAL
5	CE	10	MET
5	CE	16	THR
5	CE	18	ARG
5	CE	20	GLN
5	CE	31	LEU
5	CE	38	GLN
5	CE	41	VAL
5	CE	43	LEU
5	CE	47	LYS
5	CE	60	TYR
5	CE	67	VAL
5	CE	71	LEU
5	CE	78	HIS
5	CE	137	GLU
5	CE	142	LEU
5	CE	150	ARG
6	CF	10	LEU
6	CF	40	VAL
6	CF	41	GLU
6	CF	45	LEU
6	CF	46	ARG
6	CF	61	LEU
6	CF	69	GLU
6	CF	92	LYS

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Mol	Chain	Res	Type
7	CG	9	VAL
7	CG	32	ARG
7	CG	51	GLN
7	CG	61	VAL
7	CG	72	ARG
7	CG	76	ARG
7	CG	79	ARG
7	CG	97	GLN
7	CG	104	LEU
7	CG	113	GLU
7	CG	155	ARG
8	CH	8	ASP
8	CH	51	VAL
8	CH	52	ASP
8	CH	78	GLN
8	CH	84	ARG
8	CH	85	ARG
8	CH	86	ILE
8	CH	98	LYS
8	CH	112	LEU
8	CH	127	LEU
9	CI	23	ASN
9	CI	29	ASN
9	CI	47	LEU
9	CI	48	GLU
9	CI	64	THR
9	CI	75	ASP
9	CI	81	ILE
9	CI	86	VAL
9	CI	87	GLN
9	CI	89	ASN
9	CI	92	TYR
9	CI	93	ARG
9	CI	102	LEU
9	CI	105	ASP
9	CI	108	VAL
9	CI	111	ARG
9	CI	117	HIS
9	CI	121	ARG
9	CI	124	GLN
10	CJ	29	ARG
10	CJ	33	GLN

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Mol	Chain	Res	Type
10	CJ	57	LYS
10	CJ	67	THR
10	CJ	74	ILE
11	CK	48	ILE
11	CK	77	MET
11	CK	96	ARG
11	CK	126	ARG
12	CL	6	THR
12	CL	34	ARG
12	CL	38	THR
12	CL	44	THR
12	CL	53	ARG
12	CL	59	ARG
12	CL	78	GLN
12	CL	83	VAL
12	CL	124	LYS
13	CM	15	VAL
13	CM	27	LYS
13	CM	34	LEU
13	CM	35	GLU
13	CM	44	ARG
13	CM	47	ASP
13	CM	49	THR
13	CM	60	VAL
13	CM	77	ASN
13	CM	102	ARG
13	CM	103	THR
13	CM	106	ASN
13	CM	115	LYS
13	CM	116	THR
13	CM	121	LYS
14	CN	3	ARG
14	CN	4	LYS
14	CN	8	GLU
14	CN	12	ARG
14	CN	18	VAL
14	CN	22	THR
14	CN	23	ARG
14	CN	32	SER
14	CN	33	VAL
14	CN	47	LEU
15	CO	3	ILE

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Mol	Chain	Res	Type
15	CO	5	LYS
15	CO	38	ARG
15	CO	39	LEU
15	CO	48	LYS
15	CO	68	ARG
15	CO	83	GLU
16	CP	5	ARG
16	CP	8	ARG
16	CP	20	VAL
16	CP	21	VAL
16	CP	28	ARG
16	CP	61	SER
16	CP	62	VAL
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	24	GLU
17	CQ	63	ARG
17	CQ	74	LEU
17	CQ	79	SER
17	CQ	99	SER
18	CR	25	THR
18	CR	26	LEU
18	CR	31	LEU
18	CR	32	ARG
18	CR	35	ARG
18	CR	41	LYS
18	CR	76	LEU
19	CS	16	LEU
19	CS	17	GLU
19	CS	28	LYS
19	CS	33	THR
19	CS	36	ARG
19	CS	56	GLN
19	CS	65	ASN
19	CS	78	ARG
20	CT	9	ASN
20	CT	10	LEU
20	CT	23	ARG
20	CT	41	ILE
20	CT	46	GLU
20	CT	54	LYS

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Mol	Chain	Res	Type
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	90	GLN
21	CU	7	ARG
21	CU	10	ARG
21	CU	15	ARG
27	DD	54	ARG
27	DD	69	ARG
27	DD	94	LEU
27	DD	106	ILE
27	DD	113	VAL
27	DD	115	GLN
27	DD	126	GLN
27	DD	134	ARG
27	DD	138	VAL
27	DD	155	LEU
27	DD	162	SER
27	DD	171	ASP
27	DD	211	ARG
27	DD	221	VAL
27	DD	229	VAL
27	DD	242	ARG
27	DD	257	LEU
27	DD	260	ARG
27	DD	267	SER
27	DD	274	ARG
27	DD	276	LYS
28	DE	9	VAL
28	DE	21	VAL
28	DE	24	THR
28	DE	40	GLU
28	DE	47	VAL
28	DE	48	GLN
28	DE	52	LEU
28	DE	54	GLN
28	DE	58	ARG
28	DE	72	VAL
28	DE	73	GLU
28	DE	75	VAL
28	DE	92	THR

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Mol	Chain	Res	Type
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	170	LEU
28	DE	181	LEU
29	DF	20	LEU
29	DF	24	LEU
29	DF	27	GLU
29	DF	33	LEU
29	DF	57	VAL
29	DF	70	THR
29	DF	74	ARG
29	DF	106	ARG
29	DF	110	LEU
29	DF	132	VAL
29	DF	135	LYS
29	DF	192	LEU
29	DF	195	ASP
29	DF	196	LEU
29	DF	200	GLU
30	DG	16	ARG
30	DG	21	ARG
30	DG	28	VAL
30	DG	31	VAL
30	DG	33	ARG
30	DG	40	ASN
30	DG	43	LEU
30	DG	45	GLU
30	DG	60	LEU
30	DG	91	ARG
30	DG	111	LEU
30	DG	115	ARG
30	DG	133	LEU
30	DG	136	ARG
30	DG	138	GLN
30	DG	140	ILE
30	DG	143	GLU
30	DG	145	THR
30	DG	148	MET

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Mol	Chain	Res	Type
30	DG	153	ARG
30	DG	165	THR
30	DG	167	GLU
30	DG	170	ARG
30	DG	178	PHE
31	DH	3	ARG
31	DH	27	LYS
31	DH	32	GLU
31	DH	63	SER
31	DH	69	ARG
31	DH	70	THR
31	DH	95	ARG
31	DH	98	LEU
31	DH	124	GLU
31	DH	130	ARG
31	DH	136	ILE
31	DH	149	ARG
31	DH	171	LEU
32	DI	5	LEU
32	DI	9	LEU
32	DI	38	LEU
32	DI	40	THR
32	DI	43	ASN
32	DI	44	LEU
32	DI	50	ARG
32	DI	51	ILE
32	DI	68	LEU
32	DI	75	LEU
32	DI	77	LEU
32	DI	78	THR
32	DI	86	THR
32	DI	93	THR
32	DI	114	LEU
32	DI	123	LEU
32	DI	143	SER
33	DN	9	VAL
33	DN	29	LYS
33	DN	33	LEU
33	DN	34	LEU
33	DN	38	HIS
33	DN	46	VAL
33	DN	48	MET

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Mol	Chain	Res	Type
33	DN	61	ARG
33	DN	62	VAL
33	DN	67	LEU
33	DN	87	LEU
33	DN	99	LEU
33	DN	120	LEU
33	DN	131	GLN
34	DO	8	LEU
34	DO	9	GLU
34	DO	24	VAL
34	DO	28	SER
34	DO	49	ARG
34	DO	53	LYS
34	DO	69	ILE
34	DO	88	ASN
34	DO	94	ARG
34	DO	98	VAL
35	DP	2	LYS
35	DP	4	SER
35	DP	21	ARG
35	DP	45	LEU
35	DP	55	ARG
35	DP	56	SER
35	DP	96	THR
35	DP	99	LEU
35	DP	106	LEU
35	DP	112	LEU
35	DP	119	GLU
35	DP	147	LEU
36	DQ	1	MET
36	DQ	16	ARG
36	DQ	22	LYS
36	DQ	31	ASP
36	DQ	45	GLN
36	DQ	54	MET
36	DQ	55	VAL
36	DQ	56	ARG
36	DQ	59	ARG
36	DQ	60	ARG
36	DQ	85	LYS
36	DQ	110	THR
36	DQ	112	GLU

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Mol	Chain	Res	Type
37	DR	1	MET
37	DR	18	LEU
37	DR	29	LEU
37	DR	33	ARG
37	DR	44	LEU
37	DR	65	LEU
37	DR	67	LEU
37	DR	75	LEU
37	DR	79	LEU
37	DR	86	ARG
37	DR	100	LEU
38	DS	3	ARG
38	DS	8	GLU
38	DS	12	PHE
38	DS	15	ARG
38	DS	19	LYS
38	DS	35	ILE
38	DS	44	LYS
38	DS	80	LEU
38	DS	83	LYS
39	DT	1	MET
39	DT	6	LEU
39	DT	8	LYS
39	DT	19	LEU
39	DT	34	VAL
39	DT	39	ARG
39	DT	53	ARG
39	DT	78	LEU
39	DT	89	VAL
39	DT	93	ARG
39	DT	96	ARG
39	DT	108	ARG
39	DT	113	LYS
39	DT	118	ARG
39	DT	125	ARG
40	DU	20	LEU
40	DU	36	ARG
40	DU	74	LEU
40	DU	92	ARG
40	DU	97	ASP
40	DU	104	GLN
40	DU	108	GLU

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Mol	Chain	Res	Type
40	DU	112	ARG
41	DV	5	VAL
41	DV	62	LEU
41	DV	71	LEU
41	DV	79	VAL
41	DV	95	LEU
42	DW	4	LYS
42	DW	11	ARG
42	DW	15	ARG
42	DW	51	LEU
42	DW	78	GLU
42	DW	92	ARG
43	DX	23	GLU
43	DX	57	LEU
44	DY	8	LYS
44	DY	43	ASN
44	DY	85	VAL
44	DY	90	LEU
45	DZ	4	ARG
45	DZ	5	LEU
45	DZ	23	LYS
45	DZ	33	LEU
45	DZ	40	ASP
45	DZ	46	LYS
45	DZ	50	GLN
45	DZ	70	LEU
45	DZ	72	ARG
45	DZ	76	LEU
45	DZ	91	LEU
45	DZ	122	ARG
45	DZ	131	ARG
45	DZ	149	SER
45	DZ	150	LEU
45	DZ	154	ASP
45	DZ	162	GLU
46	D0	10	THR
46	D0	20	ARG
46	D0	55	ARG
46	D0	62	LEU
47	D1	32	LYS
47	D1	33	LYS
47	D1	35	THR

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Mol	Chain	Res	Type
47	D1	46	LEU
47	D1	85	LEU
47	D1	95	LEU
47	D1	97	LEU
48	D2	1	MET
48	D2	14	ARG
48	D2	28	LYS
48	D2	30	ARG
48	D2	32	LEU
48	D2	45	SER
48	D2	53	LEU
48	D2	70	GLN
49	D3	8	LEU
49	D3	23	LEU
49	D3	24	LYS
49	D3	30	ARG
50	D4	8	LYS
50	D4	13	ARG
50	D4	21	VAL
50	D4	22	ILE
50	D4	24	THR
50	D4	34	GLU
50	D4	43	TYR
50	D4	44	THR
50	D4	58	ARG
50	D4	61	ARG
50	D4	63	TYR
50	D4	68	ARG
50	D4	69	LYS
51	D5	6	VAL
51	D5	40	LYS
51	D5	55	ARG
51	D5	59	GLU
52	D6	6	ARG
52	D6	25	LYS
52	D6	28	ARG
52	D6	38	LYS
52	D6	48	VAL
53	D7	10	ARG
53	D7	41	ARG
53	D7	43	THR
53	D7	48	LYS

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Mol	Chain	Res	Type
54	D8	31	HIS
54	D8	32	LEU
54	D8	34	TRP
54	D8	37	SER
55	D9	4	ARG
55	D9	7	VAL
55	D9	12	ASP
55	D9	26	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (128) such sidechains are listed below:

Mol	Chain	Res	Type
3	AC	6	HIS
3	AC	28	GLN
3	AC	37	GLN
3	AC	104	GLN
3	AC	118	GLN
3	AC	136	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	42	GLN
4	AD	45	GLN
4	AD	77	ASN
4	AD	123	HIS
4	AD	129	ASN
4	AD	201	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	148	ASN
9	AI	31	GLN
9	AI	73	GLN
9	AI	89	ASN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	93	GLN
11	AK	104	GLN
11	AK	116	HIS
12	AL	78	GLN
15	AO	28	GLN
16	AP	76	GLN
19	AS	65	ASN
19	AS	83	HIS

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Mol	Chain	Res	Type
20	AT	9	ASN
20	AT	45	GLN
20	AT	90	GLN
27	BD	115	GLN
27	BD	253	GLN
29	BF	69	HIS
29	BF	75	HIS
29	BF	169	ASN
29	BF	203	GLN
30	BG	27	ASN
30	BG	40	ASN
30	BG	138	GLN
32	BI	43	ASN
33	BN	133	GLN
35	BP	38	GLN
36	BQ	12	GLN
39	BT	43	GLN
39	BT	123	GLN
40	BU	94	ASN
43	BX	31	HIS
44	BY	6	HIS
44	BY	43	ASN
44	BY	92	ASN
45	BZ	73	GLN
45	BZ	151	HIS
48	B2	9	GLN
48	B2	70	GLN
49	B3	32	GLN
50	B4	46	GLN
52	B6	20	ASN
2	CB	19	HIS
2	CB	40	HIS
2	CB	76	GLN
2	CB	78	GLN
2	CB	212	GLN
2	CB	224	GLN
3	CC	28	GLN
3	CC	102	ASN
3	CC	136	GLN
3	CC	162	GLN
4	CD	45	GLN
4	CD	77	ASN

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Mol	Chain	Res	Type
4	CD	123	HIS
4	CD	125	HIS
4	CD	129	ASN
4	CD	161	ASN
5	CE	38	GLN
5	CE	141	GLN
6	CF	7	ASN
7	CG	28	ASN
7	CG	148	ASN
7	CG	153	HIS
8	CH	15	ASN
9	CI	23	ASN
9	CI	38	GLN
9	CI	58	HIS
9	CI	87	GLN
9	CI	89	ASN
10	CJ	62	HIS
10	CJ	69	ASN
11	CK	22	HIS
12	CL	78	GLN
15	CO	28	GLN
15	CO	62	GLN
16	CP	14	ASN
19	CS	23	ASN
19	CS	56	GLN
19	CS	57	HIS
19	CS	69	HIS
20	CT	9	ASN
27	DD	96	HIS
27	DD	115	GLN
27	DD	116	GLN
27	DD	164	GLN
27	DD	166	GLN
27	DD	253	GLN
29	DF	69	HIS
29	DF	75	HIS
29	DF	169	ASN
29	DF	203	GLN
30	DG	41	GLN
30	DG	132	ASN
30	DG	138	GLN
32	DI	43	ASN

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Mol	Chain	Res	Type
34	DO	89	ASN
35	DP	38	GLN
36	DQ	141	GLN
38	DS	68	GLN
39	DT	123	GLN
41	DV	64	HIS
43	DX	31	HIS
44	DY	43	ASN
45	DZ	50	GLN
45	DZ	55	HIS
45	DZ	151	HIS
47	D1	19	GLN
55	D9	20	HIS
55	D9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1521 (98%)	387 (25%)	22 (1%)
1	CA	1501/1521 (98%)	391 (26%)	24 (1%)
22	AV	12/24 (50%)	4 (33%)	0
22	CV	11/24 (45%)	4 (36%)	0
23	AW	0/2	-	-
23	CW	0/2	-	-
24	AX	74/77 (96%)	25 (33%)	1 (1%)
24	CX	74/77 (96%)	26 (35%)	1 (1%)
25	BA	2811/2915 (96%)	537 (19%)	24 (0%)
25	DA	2791/2915 (95%)	622 (22%)	29 (1%)
26	BB	120/121 (99%)	19 (15%)	3 (2%)
26	DB	119/121 (98%)	36 (30%)	0
All	All	9008/9320 (96%)	2051 (22%)	104 (1%)

All (2051) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	6	G
1	AA	7	G
1	AA	9	G
1	AA	22	G
1	AA	29	G

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Mol	Chain	Res	Type
1	AA	32	A
1	AA	39	G
1	AA	41	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	59	A
1	AA	61	G
1	AA	72	C
1	AA	73	G
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	92	C
1	AA	96	U
1	AA	97	G
1	AA	98	G
1	AA	116	A
1	AA	120	A
1	AA	121	C
1	AA	129	U
1	AA	129(A)	G
1	AA	131	C
1	AA	138	G
1	AA	143	A
1	AA	146	G
1	AA	152	A
1	AA	157	G
1	AA	163	C
1	AA	172	A
1	AA	173	U
1	AA	174	C
1	AA	180	U
1	AA	182	U
1	AA	189(A)	C
1	AA	189(D)	C
1	AA	189(F)	U
1	AA	189(G)	G
1	AA	189(H)	G
1	AA	189(I)	G
1	AA	189(K)	U
1	AA	189(L)	G

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Mol	Chain	Res	Type
1	AA	195	A
1	AA	197	A
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	243	A
1	AA	247	G
1	AA	251	G
1	AA	264	U
1	AA	266	G
1	AA	267	C
1	AA	276	G
1	AA	289	G
1	AA	306	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	342	C
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	374	A
1	AA	382	A
1	AA	383	A
1	AA	384	G
1	AA	397	A
1	AA	398	C
1	AA	403	C
1	AA	405	U
1	AA	406	G
1	AA	409	G
1	AA	411	A
1	AA	412	A
1	AA	413	G
1	AA	414	A

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Mol	Chain	Res	Type
1	AA	421	U
1	AA	424	G
1	AA	426	G
1	AA	429	U
1	AA	430	A
1	AA	434	U
1	AA	435	C
1	AA	436	C
1	AA	439	A
1	AA	441	A
1	AA	442	C
1	AA	443	C
1	AA	452	A
1	AA	453	A
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	483	C
1	AA	485	G
1	AA	491	G
1	AA	495	A
1	AA	496	A
1	AA	498	U
1	AA	504	C
1	AA	505	G
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	520	A
1	AA	521	G
1	AA	524	G
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	544	G
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	567	G

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Mol	Chain	Res	Type
1	AA	571	U
1	AA	572	A
1	AA	573	A
1	AA	575	G
1	AA	576	G
1	AA	577	G
1	AA	581	G
1	AA	582	U
1	AA	587	G
1	AA	590	C
1	AA	596	C
1	AA	600	C
1	AA	623	C
1	AA	625	G
1	AA	627	G
1	AA	629	G
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	653	A
1	AA	661	G
1	AA	665	A
1	AA	671	G
1	AA	680	C
1	AA	687	A
1	AA	688	G
1	AA	692	U
1	AA	693	G
1	AA	695	A
1	AA	712	A
1	AA	723	U
1	AA	724	G
1	AA	730	G
1	AA	731	G
1	AA	733	A
1	AA	748	C
1	AA	749	C
1	AA	751	U
1	AA	754	C
1	AA	755	G
1	AA	759	A
1	AA	760	G

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Mol	Chain	Res	Type
1	AA	764	C
1	AA	766	A
1	AA	774	G
1	AA	777	A
1	AA	787	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	798	G
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	821	G
1	AA	827	U
1	AA	828	A
1	AA	836	G
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	872	A
1	AA	884	U
1	AA	887	G
1	AA	902	G
1	AA	914	A
1	AA	919	A
1	AA	920	U
1	AA	925	G
1	AA	926	G
1	AA	927	G
1	AA	932	C
1	AA	934	C
1	AA	936	C
1	AA	942	G
1	AA	954	G
1	AA	958	A
1	AA	960	U
1	AA	961	U
1	AA	966	G
1	AA	968	A

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Mol	Chain	Res	Type
1	AA	969	A
1	AA	971	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	983	A
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	1001	A
1	AA	1002	G
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1009	G
1	AA	1010	G
1	AA	1016	A
1	AA	1020	U
1	AA	1021	G
1	AA	1022	G
1	AA	1024	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1032	G
1	AA	1033	G
1	AA	1037	C
1	AA	1044	A
1	AA	1045	C
1	AA	1053	G
1	AA	1054	C
1	AA	1061	G
1	AA	1065	U
1	AA	1066	C

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Mol	Chain	Res	Type
1	AA	1068	G
1	AA	1076	C
1	AA	1077	G
1	AA	1081	G
1	AA	1088	G
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1112	C
1	AA	1113	C
1	AA	1122	U
1	AA	1124	G
1	AA	1125	U
1	AA	1126	U
1	AA	1130	A
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	1146	A
1	AA	1152	A
1	AA	1157	A
1	AA	1159	U
1	AA	1163	C
1	AA	1166	G
1	AA	1168	A
1	AA	1169	A
1	AA	1179	A
1	AA	1180	A
1	AA	1181	G
1	AA	1183	A
1	AA	1184	G
1	AA	1191	A
1	AA	1194	U
1	AA	1196	U
1	AA	1197	G
1	AA	1199	U

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Mol	Chain	Res	Type
1	AA	1200	C
1	AA	1202	G
1	AA	1206	G
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1217	C
1	AA	1224	G
1	AA	1225	A
1	AA	1227	A
1	AA	1228	C
1	AA	1238	A
1	AA	1255	G
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1262	C
1	AA	1268	A
1	AA	1270	C
1	AA	1273	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1282	C
1	AA	1284	C
1	AA	1286	A
1	AA	1287	A
1	AA	1289	A
1	AA	1290	G
1	AA	1296	C
1	AA	1297	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1305	G
1	AA	1317	C
1	AA	1319	A
1	AA	1320	C
1	AA	1322	C
1	AA	1338	G
1	AA	1340	A

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Mol	Chain	Res	Type
1	AA	1346	A
1	AA	1347	G
1	AA	1353	G
1	AA	1354	C
1	AA	1355	G
1	AA	1358	U
1	AA	1360	A
1	AA	1363	C
1	AA	1368	G
1	AA	1370	G
1	AA	1372	U
1	AA	1377	A
1	AA	1379	G
1	AA	1383	C
1	AA	1397	C
1	AA	1398	A
1	AA	1400	C
1	AA	1402	C
1	AA	1406	U
1	AA	1409	C
1	AA	1419	G
1	AA	1425	U
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1447	A
1	AA	1452	C
1	AA	1457	G
1	AA	1459	C
1	AA	1487	G
1	AA	1489	G
1	AA	1490	C
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1520	G
1	AA	1529	G

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Mol	Chain	Res	Type
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	14	A
22	AV	15	A
22	AV	19	U
22	AV	24	A
24	AX	6	G
24	AX	7	G
24	AX	9	G
24	AX	16	C
24	AX	17	C
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	25	C
24	AX	30	G
24	AX	31	G
24	AX	34	C
24	AX	42	G
24	AX	47	U
24	AX	48	C
24	AX	52	G
24	AX	56	C
24	AX	58	A
24	AX	59	A
24	AX	60	U
24	AX	61	C
24	AX	64	G
24	AX	65	C
24	AX	67	C
24	AX	68	C
25	BA	10	G
25	BA	12	U
25	BA	27	G
25	BA	34	C
25	BA	37	C
25	BA	45	C
25	BA	49	U
25	BA	54	G
25	BA	60	G
25	BA	70	A

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Mol	Chain	Res	Type
25	BA	71	U
25	BA	73	A
25	BA	74	G
25	BA	95	G
25	BA	99	G
25	BA	100	G
25	BA	116	A
25	BA	117	A
25	BA	118	U
25	BA	119	G
25	BA	123	G
25	BA	138	G
25	BA	154	G
25	BA	155	C
25	BA	161	C
25	BA	164	G
25	BA	166	G
25	BA	171	A
25	BA	177	G
25	BA	185	A
25	BA	188	A
25	BA	194	G
25	BA	204	G
25	BA	205	A
25	BA	210	A
25	BA	211	A
25	BA	212	A
25	BA	214	A
25	BA	215	G
25	BA	218	A
25	BA	222	A
25	BA	237	G
25	BA	265	U
25	BA	269	G
25	BA	271	U
25	BA	272	U
25	BA	273	G
25	BA	274	U
25	BA	275	C
25	BA	279	G
25	BA	288	U
25	BA	289	G

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Mol	Chain	Res	Type
25	BA	294	C
25	BA	296	U
25	BA	303	C
25	BA	306	A
25	BA	335	A
25	BA	348	A
25	BA	353	G
25	BA	354	A
25	BA	357	G
25	BA	360	C
25	BA	376	G
25	BA	377	G
25	BA	381	A
25	BA	384	G
25	BA	387	G
25	BA	389	G
25	BA	393	A
25	BA	399	G
25	BA	410	U
25	BA	413	G
25	BA	418	G
25	BA	423	G
25	BA	426	G
25	BA	434	G
25	BA	438	G
25	BA	439	A
25	BA	442	A
25	BA	455	A
25	BA	469	A
25	BA	470	C
25	BA	474	U
25	BA	475	A
25	BA	477	C
25	BA	483	A
25	BA	496	A
25	BA	507	G
25	BA	519	G
25	BA	529	U
25	BA	530	A
25	BA	533	G
25	BA	534	C
25	BA	553	A

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Mol	Chain	Res	Type
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	578	U
25	BA	586	G
25	BA	596	G
25	BA	597	C
25	BA	598	A
25	BA	616	G
25	BA	625	G
25	BA	626	A
25	BA	627	G
25	BA	630	U
25	BA	633	G
25	BA	638	U
25	BA	639	G
25	BA	641	G
25	BA	642	G
25	BA	652	A
25	BA	662	A
25	BA	670	C
25	BA	671	A
25	BA	693	G
25	BA	694	G
25	BA	697	C
25	BA	698	G
25	BA	715	G
25	BA	716	G
25	BA	733	G
25	BA	764	G
25	BA	769	A
25	BA	777	C
25	BA	787	U
25	BA	811	A
25	BA	822	G
25	BA	823	G
25	BA	829	A
25	BA	830	A
25	BA	831	A

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Mol	Chain	Res	Type
25	BA	832	G
25	BA	836	A
25	BA	839	G
25	BA	840	A
25	BA	852	G
25	BA	859	C
25	BA	866	A
25	BA	874	U
25	BA	877	G
25	BA	913	A
25	BA	924	U
25	BA	926	G
25	BA	927	G
25	BA	928	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	942	A
25	BA	943	C
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	1003	U
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	1058	U
25	BA	1059	C
25	BA	1066	A
25	BA	1068	G

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Mol	Chain	Res	Type
25	BA	1071	G
25	BA	1072	U
25	BA	1079	U
25	BA	1084	C
25	BA	1085	G
25	BA	1087	C
25	BA	1090	G
25	BA	1091	A
25	BA	1092	A
25	BA	1093	G
25	BA	1094	A
25	BA	1097	G
25	BA	1153	G
25	BA	1154	U
25	BA	1155	C
25	BA	1156	G
25	BA	1158	G
25	BA	1165	C
25	BA	1175	A
25	BA	1176	U
25	BA	1178	A
25	BA	1180	C
25	BA	1181	G
25	BA	1183	G
25	BA	1184	G
25	BA	1216	G
25	BA	1217	G
25	BA	1218	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1222	A
25	BA	1255	A
25	BA	1256	U
25	BA	1263	C
25	BA	1282	G
25	BA	1290	G
25	BA	1294	G
25	BA	1296	G
25	BA	1299	A
25	BA	1302	G
25	BA	1317	G

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Mol	Chain	Res	Type
25	BA	1318	A
25	BA	1319	U
25	BA	1346	U
25	BA	1347	A
25	BA	1351	C
25	BA	1354	A
25	BA	1357	G
25	BA	1360	C
25	BA	1365	G
25	BA	1366	C
25	BA	1380	G
25	BA	1388	A
25	BA	1391	C
25	BA	1398	U
25	BA	1405	A
25	BA	1406	A
25	BA	1411	A
25	BA	1430	A
25	BA	1431	G
25	BA	1432	C
25	BA	1441	A
25	BA	1462	G
25	BA	1463	C
25	BA	1466	U
25	BA	1467	G
25	BA	1468	G
25	BA	1474	C
25	BA	1475	G
25	BA	1491	A
25	BA	1496	A
25	BA	1497	G
25	BA	1502	G
25	BA	1506	G
25	BA	1514	C
25	BA	1518	A
25	BA	1525	G
25	BA	1529	G
25	BA	1532	A
25	BA	1536	A
25	BA	1539	C
25	BA	1550	C
25	BA	1553	A

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Mol	Chain	Res	Type
25	BA	1554	A
25	BA	1555	C
25	BA	1556	A
25	BA	1571	G
25	BA	1573	G
25	BA	1578	C
25	BA	1579	C
25	BA	1589	A
25	BA	1590	C
25	BA	1593	C
25	BA	1605	A
25	BA	1613	A
25	BA	1616	A
25	BA	1625	U
25	BA	1627	A
25	BA	1628	G
25	BA	1631	C
25	BA	1632	A
25	BA	1638	C
25	BA	1653	C
25	BA	1654	A
25	BA	1655	A
25	BA	1681	A
25	BA	1682	G
25	BA	1693	C
25	BA	1694	G
25	BA	1695	C
25	BA	1698	G
25	BA	1701	A
25	BA	1711	A
25	BA	1714	G
25	BA	1721	G
25	BA	1730	C
25	BA	1735	U
25	BA	1743	G
25	BA	1747	A
25	BA	1748	A
25	BA	1750	G
25	BA	1766	G
25	BA	1767	A
25	BA	1768	U
25	BA	1769	G

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Mol	Chain	Res	Type
25	BA	1776	G
25	BA	1787	G
25	BA	1793	A
25	BA	1794	G
25	BA	1795	G
25	BA	1803	G
25	BA	1804	A
25	BA	1811	A
25	BA	1813	C
25	BA	1817	A
25	BA	1822	A
25	BA	1831	C
25	BA	1832	G
25	BA	1847	G
25	BA	1867	C
25	BA	1868	C
25	BA	1870	G
25	BA	1878	A
25	BA	1882	U
25	BA	1900	G
25	BA	1911	A
25	BA	1922	A
25	BA	1928	G
25	BA	1931	C
25	BA	1932	G
25	BA	1934	A
25	BA	1935	A
25	BA	1936	C
25	BA	1937	U
25	BA	1941	A
25	BA	1951	G
25	BA	1952	G
25	BA	1959	A
25	BA	1960	A
25	BA	1962	U
25	BA	1974	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

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Mol	Chain	Res	Type
25	BA	1994	A
25	BA	2014	G
25	BA	2015	U
25	BA	2019	G
25	BA	2023	A
25	BA	2043	C
25	BA	2045	G
25	BA	2053	A
25	BA	2054	G
25	BA	2055	A
25	BA	2057	G
25	BA	2058	C
25	BA	2061	C
25	BA	2065	C
25	BA	2071	G
25	BA	2077	C
25	BA	2078	G
25	BA	2082	A
25	BA	2083	G
25	BA	2084	A
25	BA	2085	C
25	BA	2089	G
25	BA	2091	G
25	BA	2115	G
25	BA	2119	C
25	BA	2121	U
25	BA	2122	G
25	BA	2131	U
25	BA	2133	C
25	BA	2135	U
25	BA	2140	U
25	BA	2141	A
25	BA	2142	G
25	BA	2143	G
25	BA	2149	G
25	BA	2152	U
25	BA	2154	U
25	BA	2155	G
25	BA	2156	A
25	BA	2157	A
25	BA	2158	C
25	BA	2159	C

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Mol	Chain	Res	Type
25	BA	2160	C
25	BA	2162	C
25	BA	2163	G
25	BA	2164	C
25	BA	2165	C
25	BA	2167	C
25	BA	2169	G
25	BA	2170	G
25	BA	2173	G
25	BA	2178	G
25	BA	2179	G
25	BA	2180	A
25	BA	2181	G
25	BA	2182	G
25	BA	2187	G
25	BA	2191	A
25	BA	2193	A
25	BA	2194	U
25	BA	2195	A
25	BA	2196	C
25	BA	2197	C
25	BA	2198	A
25	BA	2200	C
25	BA	2203	G
25	BA	2204	G
25	BA	2206	G
25	BA	2210	C
25	BA	2211	U
25	BA	2214	G
25	BA	2215	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	2238	C
25	BA	2250	G
25	BA	2251	G
25	BA	2280	A
25	BA	2281	A

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Mol	Chain	Res	Type
25	BA	2285	A
25	BA	2287	C
25	BA	2290	A
25	BA	2295	C
25	BA	2299	A
25	BA	2301	G
25	BA	2317	A
25	BA	2319	G
25	BA	2320	G
25	BA	2324	U
25	BA	2332	A
25	BA	2337	G
25	BA	2339	A
25	BA	2346	G
25	BA	2347	A
25	BA	2348	A
25	BA	2355	C
25	BA	2359	C
25	BA	2362	C
25	BA	2373	A
25	BA	2395	G
25	BA	2396	G
25	BA	2397	C
25	BA	2417	G
25	BA	2418	U
25	BA	2422	G
25	BA	2426	G
25	BA	2436	C
25	BA	2437	A
25	BA	2440	G
25	BA	2441	G
25	BA	2442	A
25	BA	2447	A
25	BA	2450	U
25	BA	2451	A
25	BA	2453	C
25	BA	2460	A
25	BA	2480	G
25	BA	2481	A
25	BA	2483	C
25	BA	2488	A
25	BA	2490	A

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Mol	Chain	Res	Type
25	BA	2495	C
25	BA	2499	G
25	BA	2502	G
25	BA	2514	G
25	BA	2516	U
25	BA	2517	G
25	BA	2530	A
25	BA	2537	G
25	BA	2541	G
25	BA	2566	U
25	BA	2567	U
25	BA	2576	A
25	BA	2578	A
25	BA	2579	G
25	BA	2585	C
25	BA	2594	G
25	BA	2597	U
25	BA	2614	A
25	BA	2621	U
25	BA	2623	U
25	BA	2624	C
25	BA	2635	G
25	BA	2640	C
25	BA	2641	A
25	BA	2642	G
25	BA	2666	A
25	BA	2685	G
25	BA	2701	U
25	BA	2702	C
25	BA	2703	C
25	BA	2714	U
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	2752	U
25	BA	2764	G
25	BA	2771	A
25	BA	2777	A
25	BA	2778	A

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Mol	Chain	Res	Type
25	BA	2779	G
25	BA	2782	C
25	BA	2791	A
25	BA	2803	A
25	BA	2804	C
25	BA	2805	G
25	BA	2806	G
25	BA	2807	C
25	BA	2813	G
25	BA	2818	U
25	BA	2828	G
25	BA	2830	A
25	BA	2831	A
25	BA	2845	A
25	BA	2856	G
25	BA	2882	G
25	BA	2883	A
25	BA	2890	C
25	BA	2896	G
25	BA	2899	C
25	BA	2901	A
25	BA	2902	G
25	BA	2903	G
26	BB	2	C
26	BB	7	G
26	BB	9	G
26	BB	24	G
26	BB	32	C
26	BB	47	C
26	BB	51	G
26	BB	52	A
26	BB	53	A
26	BB	56	G
26	BB	57	A
26	BB	72	G
26	BB	73	A
26	BB	75	G
26	BB	85	G
26	BB	86	G
26	BB	89	G
26	BB	106	G
26	BB	110	G

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Mol	Chain	Res	Type
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	59	A
1	CA	61	G
1	CA	66	G
1	CA	72	C
1	CA	73	G
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	91	C
1	CA	96	U
1	CA	97	G
1	CA	98	G
1	CA	116	A
1	CA	120	A
1	CA	121	C
1	CA	129	U
1	CA	129(A)	G
1	CA	131	C
1	CA	146	G
1	CA	157	G
1	CA	163	C
1	CA	172	A
1	CA	173	U
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(D)	C
1	CA	189(F)	U
1	CA	189(G)	G
1	CA	189(H)	G

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Mol	Chain	Res	Type
1	CA	189(I)	G
1	CA	189(J)	G
1	CA	189(K)	U
1	CA	189(L)	G
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	243	A
1	CA	247	G
1	CA	251	G
1	CA	264	U
1	CA	266	G
1	CA	267	C
1	CA	276	G
1	CA	289	G
1	CA	306	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	342	C
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	367	U
1	CA	372	C
1	CA	373	A
1	CA	374	A
1	CA	382	A
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	403	C
1	CA	405	U
1	CA	406	G
1	CA	409	G
1	CA	411	A

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Mol	Chain	Res	Type
1	CA	412	A
1	CA	413	G
1	CA	414	A
1	CA	421	U
1	CA	422	C
1	CA	424	G
1	CA	426	G
1	CA	429	U
1	CA	430	A
1	CA	434	U
1	CA	435	C
1	CA	436	C
1	CA	439	A
1	CA	441	A
1	CA	442	C
1	CA	443	C
1	CA	452	A
1	CA	453	A
1	CA	461	A
1	CA	470	C
1	CA	471	G
1	CA	483	C
1	CA	485	G
1	CA	491	G
1	CA	495	A
1	CA	496	A
1	CA	498	U
1	CA	504	C
1	CA	505	G
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	520	A
1	CA	521	G
1	CA	527	G
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	536	C
1	CA	544	G
1	CA	547	A

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Mol	Chain	Res	Type
1	CA	559	A
1	CA	560	U
1	CA	561	U
1	CA	567	G
1	CA	571	U
1	CA	572	A
1	CA	573	A
1	CA	575	G
1	CA	576	G
1	CA	577	G
1	CA	581	G
1	CA	582	U
1	CA	587	G
1	CA	590	C
1	CA	591	U
1	CA	596	C
1	CA	600	C
1	CA	623	C
1	CA	625	G
1	CA	627	G
1	CA	629	G
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	650	G
1	CA	653	A
1	CA	661	G
1	CA	665	A
1	CA	671	G
1	CA	680	C
1	CA	692	U
1	CA	693	G
1	CA	695	A
1	CA	712	A
1	CA	723	U
1	CA	724	G
1	CA	730	G
1	CA	731	G
1	CA	733	A
1	CA	748	C
1	CA	749	C
1	CA	751	U

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Mol	Chain	Res	Type
1	CA	754	C
1	CA	755	G
1	CA	759	A
1	CA	760	G
1	CA	764	C
1	CA	766	A
1	CA	774	G
1	CA	777	A
1	CA	787	A
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	798	G
1	CA	802	A
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	821	G
1	CA	827	U
1	CA	828	A
1	CA	836	G
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	868	C
1	CA	884	U
1	CA	902	G
1	CA	914	A
1	CA	919	A
1	CA	920	U
1	CA	925	G
1	CA	926	G
1	CA	927	G
1	CA	932	C
1	CA	934	C
1	CA	936	C
1	CA	942	G
1	CA	948	C
1	CA	954	G

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Mol	Chain	Res	Type
1	CA	958	A
1	CA	960	U
1	CA	961	U
1	CA	966	G
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	983	A
1	CA	991	U
1	CA	992	U
1	CA	993	G
1	CA	996	A
1	CA	1001	A
1	CA	1001(A)	G
1	CA	1002	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1010	G
1	CA	1016	A
1	CA	1020	U
1	CA	1022	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1029	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1030(D)	A
1	CA	1032	G
1	CA	1033	G
1	CA	1037	C
1	CA	1038	C
1	CA	1041	A
1	CA	1044	A
1	CA	1045	C

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Mol	Chain	Res	Type
1	CA	1053	G
1	CA	1054	C
1	CA	1061	G
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1077	G
1	CA	1081	G
1	CA	1088	G
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1112	C
1	CA	1113	C
1	CA	1117	G
1	CA	1122	U
1	CA	1124	G
1	CA	1125	U
1	CA	1126	U
1	CA	1129	C
1	CA	1130	A
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	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1156	G
1	CA	1157	A
1	CA	1159	U
1	CA	1163	C
1	CA	1168	A
1	CA	1169	A
1	CA	1179	A

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Mol	Chain	Res	Type
1	CA	1180	A
1	CA	1181	G
1	CA	1183	A
1	CA	1184	G
1	CA	1194	U
1	CA	1196	U
1	CA	1197	G
1	CA	1199	U
1	CA	1200	C
1	CA	1202	G
1	CA	1206	G
1	CA	1212	U
1	CA	1213	A
1	CA	1214	C
1	CA	1217	C
1	CA	1224	G
1	CA	1225	A
1	CA	1227	A
1	CA	1228	C
1	CA	1236	A
1	CA	1238	A
1	CA	1255	G
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1262	C
1	CA	1267	C
1	CA	1268	A
1	CA	1270	C
1	CA	1273	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1284	C
1	CA	1285	A
1	CA	1286	A
1	CA	1287	A
1	CA	1289	A
1	CA	1290	G

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Mol	Chain	Res	Type
1	CA	1296	C
1	CA	1297	C
1	CA	1300	G
1	CA	1305	G
1	CA	1310	G
1	CA	1317	C
1	CA	1319	A
1	CA	1322	C
1	CA	1338	G
1	CA	1340	A
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1354	C
1	CA	1355	G
1	CA	1358	U
1	CA	1360	A
1	CA	1363	C
1	CA	1363(A)	A
1	CA	1370	G
1	CA	1372	U
1	CA	1377	A
1	CA	1379	G
1	CA	1381	U
1	CA	1383	C
1	CA	1397	C
1	CA	1398	A
1	CA	1400	C
1	CA	1402	C
1	CA	1406	U
1	CA	1409	C
1	CA	1419	G
1	CA	1425	U
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1447	A
1	CA	1452	C
1	CA	1457	G
1	CA	1459	C
1	CA	1487	G
1	CA	1489	G

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Mol	Chain	Res	Type
1	CA	1490	C
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G
1	CA	1497	G
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	1532	U
22	CV	15	A
22	CV	19	U
22	CV	20	U
22	CV	24	A
24	CX	6	G
24	CX	7	G
24	CX	9	G
24	CX	16	C
24	CX	17	C
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	25	C
24	CX	30	G
24	CX	31	G
24	CX	34	C
24	CX	42	G
24	CX	47	U
24	CX	48	C
24	CX	52	G
24	CX	56	C
24	CX	58	A
24	CX	59	A
24	CX	60	U
24	CX	61	C
24	CX	64	G
24	CX	65	C
24	CX	67	C
24	CX	68	C

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Mol	Chain	Res	Type
24	CX	70	G
25	DA	7	G
25	DA	9	U
25	DA	10	G
25	DA	12	U
25	DA	13	A
25	DA	15	G
25	DA	34	C
25	DA	35	G
25	DA	45	C
25	DA	51	G
25	DA	63	U
25	DA	71	A
25	DA	74	A
25	DA	75	G
25	DA	78	A
25	DA	83	G
25	DA	84	A
25	DA	90	U
25	DA	94(A)	G
25	DA	96	G
25	DA	118	A
25	DA	120	U
25	DA	139	G
25	DA	139(A)	G
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	188	G
25	DA	196	A
25	DA	205	G
25	DA	206	U
25	DA	214	G
25	DA	216	A
25	DA	221	A
25	DA	222	A
25	DA	225	A
25	DA	228	A
25	DA	229	A

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Mol	Chain	Res	Type
25	DA	230	U
25	DA	233	A
25	DA	248	G
25	DA	271(D)	G
25	DA	271(I)	G
25	DA	271(K)	U
25	DA	271(L)	U
25	DA	271(M)	G
25	DA	271(N)	U
25	DA	271(O)	C
25	DA	272	G
25	DA	272(A)	U
25	DA	272(B)	G
25	DA	272(J)	C
25	DA	276	A
25	DA	277	C
25	DA	278	A
25	DA	282	A
25	DA	283	A
25	DA	290	G
25	DA	292	C
25	DA	295	G
25	DA	308	G
25	DA	311	A
25	DA	316	C
25	DA	317	G
25	DA	319	C
25	DA	322	A
25	DA	327	G
25	DA	329	G
25	DA	330	A
25	DA	333	G
25	DA	342	G
25	DA	345	A
25	DA	352	G
25	DA	354	G
25	DA	363	G
25	DA	363(B)	G
25	DA	385	C
25	DA	386	G
25	DA	396	G
25	DA	403	U

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Mol	Chain	Res	Type
25	DA	405	U
25	DA	406	G
25	DA	407	G
25	DA	411	G
25	DA	412	A
25	DA	415	A
25	DA	426	C
25	DA	428	A
25	DA	444	C
25	DA	454	A
25	DA	455	C
25	DA	456	C
25	DA	457	A
25	DA	470	A
25	DA	471	A
25	DA	479	A
25	DA	480	A
25	DA	481	G
25	DA	484	C
25	DA	487	C
25	DA	504	U
25	DA	505	A
25	DA	508	G
25	DA	509	C
25	DA	527	C
25	DA	529	A
25	DA	530	G
25	DA	531	C
25	DA	532	A
25	DA	533	G
25	DA	536	A
25	DA	545	G
25	DA	562	U
25	DA	563	G
25	DA	566	U
25	DA	568	U
25	DA	573	G
25	DA	574	C
25	DA	575	A
25	DA	587	C
25	DA	588	U
25	DA	595	C

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Mol	Chain	Res	Type
25	DA	603	A
25	DA	604	G
25	DA	607	U
25	DA	609	A
25	DA	610	G
25	DA	614(B)	G
25	DA	614(C)	A
25	DA	615	G
25	DA	616	G
25	DA	627	A
25	DA	637	A
25	DA	644	A
25	DA	645	C
25	DA	646	A
25	DA	647	G
25	DA	651	G
25	DA	652(B)	A
25	DA	652(C)	G
25	DA	652(U)	G
25	DA	652(V)	C
25	DA	669	G
25	DA	686	G
25	DA	701	G
25	DA	708	C
25	DA	715	G
25	DA	717	G
25	DA	726	G
25	DA	730	C
25	DA	751	A
25	DA	753	C
25	DA	758	C
25	DA	759	G
25	DA	765	G
25	DA	771	G
25	DA	775	G
25	DA	776	G
25	DA	781	A
25	DA	782	A
25	DA	784	A
25	DA	785	G
25	DA	792	G
25	DA	801	G

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Mol	Chain	Res	Type
25	DA	805	G
25	DA	812	C
25	DA	819	A
25	DA	827	U
25	DA	830	G
25	DA	843	G
25	DA	845	G
25	DA	847	U
25	DA	857	C
25	DA	859	G
25	DA	866	A
25	DA	869	G
25	DA	879	G
25	DA	880	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
25	DA	890	A
25	DA	893	C
25	DA	896	A
25	DA	898	C
25	DA	900	A
25	DA	901	A
25	DA	910	A
25	DA	912	C
25	DA	915	C
25	DA	917	A
25	DA	932	G
25	DA	933	A
25	DA	936	C
25	DA	938	G
25	DA	941	A
25	DA	945	A
25	DA	946	G
25	DA	959	A
25	DA	961	C
25	DA	974	G
25	DA	975	C
25	DA	979	G

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Mol	Chain	Res	Type
25	DA	980	A
25	DA	983	A
25	DA	989	G
25	DA	996	A
25	DA	1005	C
25	DA	1012	U
25	DA	1013	C
25	DA	1017	G
25	DA	1020	A
25	DA	1022	G
25	DA	1025	G
25	DA	1026	U
25	DA	1027	A
25	DA	1033	U
25	DA	1034	G
25	DA	1038	C
25	DA	1039	G
25	DA	1043	C
25	DA	1114	G
25	DA	1117	G
25	DA	1121	C
25	DA	1122	G
25	DA	1126	A
25	DA	1128	A
25	DA	1130	U
25	DA	1135	C
25	DA	1136	G
25	DA	1139	G
25	DA	1142(A)	A
25	DA	1166	C
25	DA	1170	G
25	DA	1171	G
25	DA	1180	C
25	DA	1194	A
25	DA	1195	G
25	DA	1206	G
25	DA	1210	A
25	DA	1211	U
25	DA	1219	G
25	DA	1220	A
25	DA	1227	G
25	DA	1229	G

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Mol	Chain	Res	Type
25	DA	1242	A
25	DA	1244	G
25	DA	1253	A
25	DA	1255	U
25	DA	1256	G
25	DA	1271	G
25	DA	1272	A
25	DA	1273	U
25	DA	1275	A
25	DA	1276	A
25	DA	1298	C
25	DA	1300	U
25	DA	1301	A
25	DA	1305	C
25	DA	1306	C
25	DA	1309	G
25	DA	1314	C
25	DA	1318	C
25	DA	1321	A
25	DA	1341	U
25	DA	1342	A
25	DA	1352	U
25	DA	1359	A
25	DA	1360	A
25	DA	1365	A
25	DA	1368	G
25	DA	1370	C
25	DA	1373	A
25	DA	1380	G
25	DA	1384	A
25	DA	1385	G
25	DA	1386	C
25	DA	1391	U
25	DA	1395	A
25	DA	1412	A
25	DA	1416	G
25	DA	1417	C
25	DA	1420	U
25	DA	1421	G
25	DA	1427	A
25	DA	1428	C
25	DA	1437	C

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Mol	Chain	Res	Type
25	DA	1445	A
25	DA	1446	C
25	DA	1449	A
25	DA	1450	G
25	DA	1459	G
25	DA	1467	C
25	DA	1471	A
25	DA	1472	A
25	DA	1473	G
25	DA	1482	G
25	DA	1490	A
25	DA	1493	C
25	DA	1497	U
25	DA	1508	A
25	DA	1509	C
25	DA	1509(A)	A
25	DA	1509(B)	A
25	DA	1531	C
25	DA	1533	G
25	DA	1537	G
25	DA	1539	G
25	DA	1543	C
25	DA	1544	A
25	DA	1547	C
25	DA	1554	A
25	DA	1558	A
25	DA	1559	G
25	DA	1566	A
25	DA	1569	A
25	DA	1578	U
25	DA	1580	A
25	DA	1582	C
25	DA	1583	A
25	DA	1584	C
25	DA	1586	A
25	DA	1598	C
25	DA	1607	C
25	DA	1608	A
25	DA	1609	A
25	DA	1610	A
25	DA	1612	C
25	DA	1616	A

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Mol	Chain	Res	Type
25	DA	1618	A
25	DA	1640	C
25	DA	1648	C
25	DA	1654	A
25	DA	1661	G
25	DA	1664	A
25	DA	1674	G
25	DA	1675	C
25	DA	1682	G
25	DA	1695	G
25	DA	1700	A
25	DA	1703	G
25	DA	1721	G
25	DA	1722	A
25	DA	1740	G
25	DA	1743	C
25	DA	1746	G
25	DA	1756	G
25	DA	1758	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	1800	C
25	DA	1801	G
25	DA	1806	C
25	DA	1812	A
25	DA	1816	G
25	DA	1823	G
25	DA	1833	U
25	DA	1835	G
25	DA	1847	A
25	DA	1848	A
25	DA	1866	C
25	DA	1877	A
25	DA	1878	G
25	DA	1881	C
25	DA	1889	A
25	DA	1900	A

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Mol	Chain	Res	Type
25	DA	1906	G
25	DA	1913	A
25	DA	1914	C
25	DA	1926	U
25	DA	1927	A
25	DA	1929	G
25	DA	1930	G
25	DA	1936	A
25	DA	1937	A
25	DA	1938	A
25	DA	1955	U
25	DA	1963	U
25	DA	1965	C
25	DA	1967	C
25	DA	1970	A
25	DA	1971	A
25	DA	1972	A
25	DA	1981	A
25	DA	1984	G
25	DA	1993	U
25	DA	1997	G
25	DA	2020	A
25	DA	2023	G
25	DA	2031	A
25	DA	2032	G
25	DA	2033	A
25	DA	2036	C
25	DA	2043	C
25	DA	2049	G
25	DA	2055	C
25	DA	2056	G
25	DA	2060	A
25	DA	2061	G
25	DA	2062	A
25	DA	2063	C
25	DA	2067	G
25	DA	2069	G
25	DA	2092	U
25	DA	2093	G
25	DA	2096	U
25	DA	2102	U
25	DA	2104	G

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Mol	Chain	Res	Type
25	DA	2106	G
25	DA	2108	C
25	DA	2109	U
25	DA	2111	C
25	DA	2112	G
25	DA	2113	U
25	DA	2116	G
25	DA	2119	A
25	DA	2121	G
25	DA	2122	U
25	DA	2126	A
25	DA	2127	G
25	DA	2128	C
25	DA	2130	U
25	DA	2131	G
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	2138	C
25	DA	2139	C
25	DA	2140	C
25	DA	2142	C
25	DA	2143	C
25	DA	2144	U
25	DA	2146	C
25	DA	2148	G
25	DA	2149	G
25	DA	2150	U
25	DA	2152	G
25	DA	2153	G
25	DA	2154	G
25	DA	2155	G
25	DA	2156	G
25	DA	2157	G
25	DA	2158	A
25	DA	2162	G
25	DA	2163	C
25	DA	2164	C
25	DA	2165	G

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Mol	Chain	Res	Type
25	DA	2166	G
25	DA	2167	U
25	DA	2168	G
25	DA	2169	A
25	DA	2170	A
25	DA	2172	U
25	DA	2173	A
25	DA	2177	C
25	DA	2178	C
25	DA	2181	G
25	DA	2185	C
25	DA	2187	G
25	DA	2188	C
25	DA	2189	U
25	DA	2192	G
25	DA	2193	G
25	DA	2196	C
25	DA	2198	A
25	DA	2199	A
25	DA	2205	C
25	DA	2206	G
25	DA	2207	G
25	DA	2208	A
25	DA	2218	U
25	DA	2225	A
25	DA	2235	G
25	DA	2238	G
25	DA	2239	G
25	DA	2254	C
25	DA	2273	A
25	DA	2275	C
25	DA	2278	A
25	DA	2280	G
25	DA	2283	C
25	DA	2287	A
25	DA	2288	A
25	DA	2294	C
25	DA	2299	G
25	DA	2302	G
25	DA	2303	G
25	DA	2305	A
25	DA	2308	G

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Mol	Chain	Res	Type
25	DA	2318	G
25	DA	2320	A
25	DA	2325	G
25	DA	2334	G
25	DA	2336	A
25	DA	2343	C
25	DA	2345	G
25	DA	2347	C
25	DA	2350	C
25	DA	2354	G
25	DA	2357	U
25	DA	2358	G
25	DA	2366	A
25	DA	2367	G
25	DA	2376	A
25	DA	2383	G
25	DA	2385	C
25	DA	2396	G
25	DA	2401	U
25	DA	2402	C
25	DA	2403	C
25	DA	2406	U
25	DA	2410	G
25	DA	2422	A
25	DA	2425	A
25	DA	2427	C
25	DA	2428	G
25	DA	2429	G
25	DA	2430	A
25	DA	2431	U
25	DA	2435	A
25	DA	2439	A
25	DA	2440	C
25	DA	2441	C
25	DA	2448	A
25	DA	2459	A
25	DA	2469	A
25	DA	2474	C
25	DA	2476	A
25	DA	2478	A
25	DA	2479	G
25	DA	2480	C

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Mol	Chain	Res	Type
25	DA	2487	G
25	DA	2492	U
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	2525	G
25	DA	2554	U
25	DA	2564	A
25	DA	2566	A
25	DA	2567	G
25	DA	2573	C
25	DA	2578	G
25	DA	2582	G
25	DA	2586	C
25	DA	2602	A
25	DA	2609	U
25	DA	2611	U
25	DA	2612	C
25	DA	2630	G
25	DA	2634	G
25	DA	2646	C
25	DA	2652	C
25	DA	2654	A
25	DA	2658	C
25	DA	2661	G
25	DA	2663	G
25	DA	2668	G
25	DA	2669	G
25	DA	2674	G
25	DA	2689	U
25	DA	2690	C
25	DA	2691	C
25	DA	2702	U
25	DA	2703	C
25	DA	2712(A)	A
25	DA	2713	A
25	DA	2714	G
25	DA	2720	U
25	DA	2721	A

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Mol	Chain	Res	Type
25	DA	2726	U
25	DA	2733	A
25	DA	2746	U
25	DA	2751	G
25	DA	2752	C
25	DA	2757	A
25	DA	2758	A
25	DA	2760	C
25	DA	2761	G
25	DA	2764	A
25	DA	2765	A
25	DA	2766	G
25	DA	2778	A
25	DA	2780	G
25	DA	2789	C
25	DA	2794	C
25	DA	2802	G
25	DA	2803	C
25	DA	2820	A
25	DA	2821	A
25	DA	2833	G
25	DA	2835	A
25	DA	2849	U
25	DA	2859	G
25	DA	2866	U
25	DA	2872	G
25	DA	2873	A
25	DA	2879	C
25	DA	2880	C
25	DA	2886	G
25	DA	2892	A
25	DA	2893	G
25	DA	2894	G
25	DA	2895	U
25	DA	2897	U
26	DB	2	C
26	DB	3	C
26	DB	4	C
26	DB	6	C
26	DB	7	G
26	DB	8	U
26	DB	13	A

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Mol	Chain	Res	Type
26	DB	21	G
26	DB	24	G
26	DB	30	C
26	DB	31	C
26	DB	33	G
26	DB	35	U
26	DB	39	A
26	DB	41	U
26	DB	42	C
26	DB	45	A
26	DB	55	U
26	DB	56	G
26	DB	58	A
26	DB	59	A
26	DB	63	G
26	DB	64	C
26	DB	65	C
26	DB	72	G
26	DB	73	A
26	DB	74	U
26	DB	75	G
26	DB	85	G
26	DB	86	G
26	DB	93	G
26	DB	101	G
26	DB	106	G
26	DB	108	U
26	DB	109	C
26	DB	110	G

All (104) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	839	U

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Mol	Chain	Res	Type
1	AA	913	A
1	AA	991	U
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1165	C
1	AA	1190	G
1	AA	1201	A
1	AA	1256	A
1	AA	1285	A
1	AA	1299	A
1	AA	1442	G
1	AA	1492	A
24	AX	16	C
25	BA	70	A
25	BA	184	A
25	BA	302	A
25	BA	793	A
25	BA	811	A
25	BA	874	U
25	BA	1092	A
25	BA	1093	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1255	A
25	BA	1346	U
25	BA	1466	U
25	BA	1577	C
25	BA	2014	G
25	BA	2148	A
25	BA	2203	G
25	BA	2205	C
25	BA	2220	A
25	BA	2250	G
25	BA	2418	U
25	BA	2701	U
25	BA	2902	G
26	BB	1	U
26	BB	52	A
26	BB	56	G
1	CA	5	U

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Mol	Chain	Res	Type
1	CA	60	A
1	CA	65	U
1	CA	115	G
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	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	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1279	A
1	CA	1442	G
1	CA	1492	A
24	CX	16	C
25	DA	34	C
25	DA	195	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	800	A
25	DA	856	C
25	DA	960	A
25	DA	1210	A
25	DA	1275	A
25	DA	1379	A
25	DA	1420	U
25	DA	1543	C
25	DA	1558	A
25	DA	1653	G
25	DA	1913	A

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Mol	Chain	Res	Type
25	DA	1992	G
25	DA	2110	G
25	DA	2133	G
25	DA	2169	A
25	DA	2172	U
25	DA	2282	G
25	DA	2406	U
25	DA	2422	A
25	DA	2430	A
25	DA	2689	U
25	DA	2756	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
23	PPU	AW	76	25,23	38,40,41	1.33	5 (13%)	54,57,60	2.28	14 (25%)
24	5MC	AX	32	24	20,22,23	1.73	4 (20%)	26,32,35	1.55	4 (15%)
24	5MU	AX	54	24,56	20,22,23	1.55	5 (25%)	25,32,35	2.58	5 (20%)
24	PSU	AX	55	24	19,21,22	1.88	5 (26%)	23,30,33	1.28	2 (8%)
24	31H	AX	76	24,56	32,34,35	1.18	3 (9%)	44,47,50	2.59	11 (25%)
24	4SU	AX	8	24	19,21,22	1.78	4 (21%)	23,30,33	28.80	2 (8%)
23	PPU	CW	76	23	38,40,41	1.29	4 (10%)	54,57,60	2.19	12 (22%)
24	5MC	CX	32	24	20,22,23	1.72	4 (20%)	26,32,35	1.48	4 (15%)
24	5MU	CX	54	24	20,22,23	1.57	4 (20%)	25,32,35	2.01	4 (16%)
24	PSU	CX	55	24	19,21,22	1.91	4 (21%)	23,30,33	1.09	2 (8%)
24	31H	CX	76	24	32,34,35	1.20	4 (12%)	44,47,50	2.57	11 (25%)
24	4SU	CX	8	24	19,21,22	1.94	4 (21%)	23,30,33	33.33	2 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	PPU	AW	76	25,23	-	0/26/43/44	0/4/4/4
24	5MC	AX	32	24	-	0/6/25/26	0/2/2/2
24	5MU	AX	54	24,56	-	0/6/25/26	0/2/2/2
24	PSU	AX	55	24	-	0/8/25/26	0/2/2/2
24	31H	AX	76	24,56	-	1/23/40/41	0/3/3/3
24	4SU	AX	8	24	-	0/6/25/26	0/2/2/2
23	PPU	CW	76	23	-	0/26/43/44	0/4/4/4
24	5MC	CX	32	24	-	0/6/25/26	0/2/2/2
24	5MU	CX	54	24	-	0/6/25/26	0/2/2/2
24	PSU	CX	55	24	-	0/8/25/26	0/2/2/2
24	31H	CX	76	24	-	1/23/40/41	0/3/3/3
24	4SU	CX	8	24	-	0/6/25/26	0/2/2/2

All (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CX	8	4SU	O2-C2	5.01	1.28	1.21
24	AX	32	5MC	C5-C4	4.72	1.48	1.41
24	CX	32	5MC	C5-C4	4.55	1.48	1.41
24	CX	55	PSU	C5-C1'	-4.50	1.48	1.52
24	AX	55	PSU	C5-C1'	-4.44	1.48	1.52
24	CX	55	PSU	P-OP1	4.40	1.51	1.46
24	CX	54	5MU	P-OP1	4.39	1.51	1.46
24	CX	32	5MC	P-OP1	4.25	1.51	1.46
23	CW	76	PPU	P-OP1	4.12	1.51	1.46
24	AX	55	PSU	P-OP1	4.08	1.51	1.46
24	CX	8	4SU	P-OP1	4.07	1.51	1.46
24	AX	8	4SU	P-OP1	4.03	1.51	1.46
24	AX	32	5MC	P-OP1	4.01	1.51	1.46
24	AX	54	5MU	P-OP1	3.98	1.51	1.46
23	AW	76	PPU	P-OP1	3.82	1.51	1.46
24	AX	8	4SU	O2-C2	3.81	1.26	1.21
24	AX	8	4SU	C4-S4	-3.79	1.60	1.67
24	CX	8	4SU	C4-S4	-3.60	1.60	1.67
24	CX	55	PSU	C4-C5	3.59	1.49	1.40
24	AX	76	31H	C5-C4	-3.55	1.32	1.40
24	CX	8	4SU	C2-N1	3.50	1.42	1.38
23	CW	76	PPU	C5-C4	3.35	1.48	1.40
23	AW	76	PPU	C5-C4	3.31	1.48	1.40
24	AX	54	5MU	C4-C5	3.28	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AX	32	5MC	C2-N1	3.19	1.41	1.38
24	CX	54	5MU	C4-C5	3.18	1.48	1.40
24	AX	55	PSU	C4-C5	3.11	1.48	1.40
24	CX	32	5MC	C2-N1	3.00	1.41	1.38
24	AX	55	PSU	O2-C2	2.93	1.25	1.21
24	CX	55	PSU	O2-C2	2.83	1.25	1.21
23	AW	76	PPU	C6-C5	2.73	1.49	1.44
24	AX	54	5MU	C2-N1	2.73	1.41	1.38
24	CX	32	5MC	O2-C2	2.67	1.25	1.21
24	CX	76	31H	CA-N	2.65	1.48	1.45
24	CX	54	5MU	O2-C2	2.61	1.25	1.21
23	CW	76	PPU	C4-N9	-2.55	1.34	1.37
24	AX	32	5MC	O2-C2	2.55	1.25	1.21
24	CX	76	31H	C5-C4	-2.37	1.35	1.40
24	CX	76	31H	C5-N7	-2.34	1.31	1.39
24	AX	8	4SU	C2-N1	2.33	1.40	1.38
24	CX	76	31H	C4-N9	-2.32	1.34	1.37
24	AX	54	5MU	C4-N3	-2.29	1.33	1.36
23	CW	76	PPU	C6-C5	2.27	1.48	1.44
24	CX	54	5MU	C2-N1	2.23	1.40	1.38
24	AX	54	5MU	O2-C2	2.19	1.24	1.21
23	AW	76	PPU	C4-N9	-2.18	1.34	1.37
24	AX	55	PSU	O4'-C1'	-2.10	1.41	1.44
24	AX	76	31H	C5-N7	-2.07	1.32	1.39
23	AW	76	PPU	O5'-C5'	-2.07	1.41	1.44
24	AX	76	31H	C4-N9	-2.07	1.34	1.37

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	CX	8	4SU	C4-N3-C2	159.52	128.42	121.60
24	AX	8	4SU	C4-N3-C2	138.03	127.50	121.60
24	AX	76	31H	N3-C2-N1	-10.57	119.59	128.89
24	CX	76	31H	N3-C2-N1	-10.03	120.06	128.89
24	CX	8	4SU	C2-N1-C1'	9.45	124.14	118.21
24	AX	54	5MU	C6-N1-C2	-8.97	119.86	122.41
23	AW	76	PPU	C5-C4-N3	-7.97	118.21	125.98
23	CW	76	PPU	C5-C4-N3	-7.65	118.52	125.98
24	AX	54	5MU	N3-C2-N1	7.36	122.12	115.97
24	CX	76	31H	C5-C4-N3	-6.67	119.47	125.98
24	CX	54	5MU	N3-C2-N1	6.63	121.51	115.97
24	AX	76	31H	C5-C4-N3	-6.29	119.84	125.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	CX	54	5MU	C6-N1-C2	-6.02	120.70	122.41
24	AX	76	31H	C4'-O4'-C1'	-5.79	103.35	109.72
23	CW	76	PPU	N3-C2-N1	-5.78	123.81	128.89
23	AW	76	PPU	N3-C2-N1	-5.72	123.86	128.89
23	AW	76	PPU	N3-C4-N9	5.67	135.12	125.39
23	CW	76	PPU	N3-C4-N9	5.44	134.73	125.39
23	CW	76	PPU	C2-N1-C6	5.15	122.68	111.52
24	CX	76	31H	O4'-C1'-N9	5.12	119.26	108.10
23	AW	76	PPU	C3'-N3'-C	-5.00	115.22	123.19
23	AW	76	PPU	C2-N1-C6	4.97	122.28	111.52
24	CX	76	31H	C4'-O4'-C1'	-4.86	104.38	109.72
24	CX	32	5MC	C2-N3-C4	4.72	120.02	115.50
24	AX	55	PSU	C5-C1'-C2'	-4.56	107.28	115.73
24	AX	76	31H	O4'-C1'-N9	-4.43	98.44	108.10
24	AX	8	4SU	C2-N1-C1'	4.34	120.93	118.21
23	CW	76	PPU	C3'-N3'-C	-4.08	116.69	123.19
24	CX	76	31H	N3-C4-N9	4.04	132.32	125.39
24	AX	32	5MC	C5-C6-N1	-4.02	118.41	122.02
24	CX	76	31H	C4'-C3'-N3'	-4.01	105.13	113.56
24	AX	32	5MC	C2-N3-C4	3.91	119.24	115.50
23	AW	76	PPU	N1-C6-N6	3.75	121.00	117.04
23	CW	76	PPU	N1-C6-N6	3.72	120.96	117.04
23	AW	76	PPU	C4-C5-N7	-3.59	105.94	109.41
24	AX	32	5MC	C6-N1-C2	3.48	121.35	118.86
24	AX	54	5MU	C2-N1-C1'	3.47	120.39	118.21
24	CX	76	31H	C5'-C4'-C3'	-3.47	109.70	115.85
24	AX	76	31H	N3-C4-N9	3.32	131.08	125.39
23	CW	76	PPU	C10-N6-C6	-3.30	109.69	119.88
24	AX	76	31H	C4'-C3'-N3'	-3.30	106.62	113.56
24	CX	55	PSU	C5-C1'-C2'	-3.26	109.69	115.73
23	AW	76	PPU	C5'-C4'-C3'	-3.24	110.11	115.85
23	CW	76	PPU	C5'-C4'-C3'	-3.22	110.14	115.85
24	AX	76	31H	O2'-C2'-C3'	3.19	118.54	110.69
23	CW	76	PPU	C4-C5-N7	-3.16	106.36	109.41
24	AX	76	31H	O4'-C1'-C2'	-3.09	102.20	106.69
24	AX	76	31H	C5'-C4'-C3'	-3.03	110.49	115.85
24	AX	76	31H	C6-C5-C4	2.96	120.87	117.55
23	AW	76	PPU	C10-N6-C6	-2.89	110.95	119.88
24	CX	32	5MC	C6-N1-C2	2.80	120.86	118.86
24	CX	32	5MC	C5-C6-N1	-2.77	119.53	122.02
24	CX	54	5MU	C5-C6-N1	-2.69	119.60	122.02
23	AW	76	PPU	C2-N3-C4	2.69	121.01	113.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	CX	32	5MC	N4-C4-N3	2.68	120.82	116.99
24	CX	76	31H	O2'-C2'-C3'	2.59	117.08	110.69
24	CX	76	31H	C2-N3-C4	2.55	120.60	113.27
23	CW	76	PPU	C2-N3-C4	2.54	120.59	113.27
24	AX	54	5MU	C5-C6-N1	-2.52	119.76	122.02
24	CX	76	31H	O4'-C1'-C2'	-2.48	103.08	106.69
23	AW	76	PPU	C4'-O4'-C1'	2.47	112.44	109.72
23	AW	76	PPU	C9-N6-C6	-2.39	112.48	119.88
24	CX	54	5MU	C4-N3-C2	-2.33	120.61	125.39
24	AX	76	31H	C2-N3-C4	2.32	119.94	113.27
24	CX	76	31H	CA-N-CN	-2.30	119.29	122.82
24	AX	54	5MU	C4-N3-C2	-2.26	120.75	125.39
23	CW	76	PPU	C4'-O4'-C1'	2.24	112.18	109.72
24	CX	55	PSU	C4-N3-C2	-2.21	120.87	125.36
24	AX	55	PSU	C4-N3-C2	-2.18	120.93	125.36
24	AX	32	5MC	N4-C4-N3	2.18	120.10	116.99
23	CW	76	PPU	C10-N6-C9	-2.16	108.49	115.87
23	AW	76	PPU	C10-N6-C9	-2.14	108.58	115.87
23	AW	76	PPU	C4'-C3'-N3'	-2.07	109.20	113.56

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 1780 ligands modelled in this entry, 1778 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length

(or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	SF4	AD	501	4	12,12,12	21.76	12 (100%)	0,24,24	0.00	-
57	SF4	CD	501	4	12,12,12	20.96	12 (100%)	0,24,24	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	SF4	AD	501	4	-	0/0/48/48	0/6/5/5
57	SF4	CD	501	4	-	0/0/48/48	0/6/5/5

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	AD	501	SF4	S1-FE3	-23.11	2.17	2.33
57	AD	501	SF4	S4-FE2	-22.99	2.17	2.33
57	AD	501	SF4	S4-FE3	-22.79	2.17	2.33
57	AD	501	SF4	S2-FE4	-22.65	2.18	2.33
57	AD	501	SF4	S2-FE1	-22.28	2.18	2.33
57	CD	501	SF4	S1-FE3	-22.05	2.18	2.33
57	AD	501	SF4	S2-FE3	-21.56	2.18	2.33
57	AD	501	SF4	S4-FE1	-21.55	2.18	2.33
57	CD	501	SF4	S2-FE4	-21.50	2.18	2.33
57	CD	501	SF4	S3-FE1	-21.46	2.18	2.33
57	CD	501	SF4	S3-FE4	-21.29	2.18	2.33
57	CD	501	SF4	S3-FE2	-21.20	2.19	2.33
57	AD	501	SF4	S3-FE1	-21.16	2.19	2.33
57	AD	501	SF4	S3-FE2	-21.10	2.19	2.33
57	CD	501	SF4	S1-FE4	-21.08	2.19	2.33
57	CD	501	SF4	S4-FE2	-20.98	2.19	2.33
57	CD	501	SF4	S4-FE1	-20.83	2.19	2.33
57	AD	501	SF4	S1-FE4	-20.68	2.19	2.33
57	AD	501	SF4	S1-FE2	-20.53	2.19	2.33
57	AD	501	SF4	S3-FE4	-20.50	2.19	2.33
57	CD	501	SF4	S4-FE3	-20.49	2.19	2.33
57	CD	501	SF4	S2-FE1	-20.40	2.19	2.33
57	CD	501	SF4	S2-FE3	-20.09	2.19	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	CD	501	SF4	S1-FE2	-20.03	2.19	2.33

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1498/1521 (98%)	0.21	14 (0%) 81 88	39, 74, 94, 105	0
1	CA	1503/1521 (98%)	0.12	23 (1%) 70 79	41, 75, 94, 105	0
2	AB	231/256 (90%)	1.18	62 (26%) 1 1	65, 82, 90, 96	0
2	CB	231/256 (90%)	1.83	83 (35%) 1 1	67, 83, 92, 96	0
3	AC	206/239 (86%)	1.19	55 (26%) 1 1	67, 78, 86, 94	0
3	CC	206/239 (86%)	1.33	66 (32%) 1 1	69, 80, 87, 92	0
4	AD	208/209 (99%)	1.17	54 (25%) 1 1	57, 72, 82, 86	0
4	CD	208/209 (99%)	1.06	39 (18%) 2 2	57, 73, 82, 87	0
5	AE	148/162 (91%)	0.63	11 (7%) 14 17	55, 71, 81, 86	0
5	CE	148/162 (91%)	0.83	16 (10%) 6 8	58, 73, 82, 89	0
6	AF	100/101 (99%)	0.27	2 (2%) 62 71	55, 71, 80, 82	0
6	CF	100/101 (99%)	0.41	10 (10%) 8 10	58, 73, 80, 82	0
7	AG	155/156 (99%)	0.91	27 (17%) 2 3	67, 76, 85, 94	0
7	CG	155/156 (99%)	1.45	50 (32%) 1 1	68, 78, 86, 96	0
8	AH	137/138 (99%)	0.24	2 (1%) 70 79	62, 72, 78, 86	0
8	CH	137/138 (99%)	0.90	22 (16%) 2 3	62, 73, 80, 88	0
9	AI	127/128 (99%)	1.13	29 (22%) 1 2	64, 82, 87, 90	0
9	CI	127/128 (99%)	2.96	80 (62%) 0 0	67, 83, 89, 91	0
10	AJ	97/105 (92%)	0.69	15 (15%) 3 4	63, 80, 89, 95	0
10	CJ	96/105 (91%)	3.01	65 (67%) 0 0	70, 86, 93, 100	0
11	AK	114/129 (88%)	0.75	16 (14%) 3 5	54, 72, 81, 83	0
11	CK	114/129 (88%)	0.98	22 (19%) 2 2	56, 72, 80, 83	0
12	AL	122/132 (92%)	0.66	11 (9%) 10 12	55, 65, 75, 78	0
12	CL	122/132 (92%)	0.72	15 (12%) 5 6	57, 67, 75, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	123/126 (97%)	1.21	29 (23%) 1 2	64, 78, 86, 91	0
13	CM	122/126 (96%)	1.84	47 (38%) 1 0	68, 80, 88, 93	0
14	AN	60/61 (98%)	1.10	13 (21%) 1 2	65, 76, 83, 86	0
14	CN	60/61 (98%)	3.33	43 (71%) 0 0	69, 79, 84, 88	0
15	AO	88/89 (98%)	0.58	5 (5%) 23 28	56, 69, 80, 90	0
15	CO	88/89 (98%)	0.67	10 (11%) 6 7	56, 70, 80, 90	0
16	AP	82/88 (93%)	1.12	19 (23%) 1 2	58, 73, 83, 85	0
16	CP	82/88 (93%)	1.04	12 (14%) 3 5	58, 72, 82, 85	0
17	AQ	99/105 (94%)	1.10	19 (19%) 2 2	60, 70, 81, 85	0
17	CQ	99/105 (94%)	0.66	7 (7%) 16 19	57, 70, 80, 84	0
18	AR	68/88 (77%)	1.08	14 (20%) 1 2	60, 70, 81, 85	0
18	CR	68/88 (77%)	0.54	3 (4%) 33 40	61, 72, 82, 86	0
19	AS	83/93 (89%)	1.16	21 (25%) 1 2	67, 81, 88, 96	0
19	CS	83/93 (89%)	1.85	35 (42%) 1 0	71, 83, 91, 97	0
20	AT	96/106 (90%)	1.39	31 (32%) 1 1	58, 72, 82, 89	0
20	CT	96/106 (90%)	0.99	18 (18%) 2 2	59, 72, 82, 88	0
21	AU	23/27 (85%)	0.58	0 100 100	65, 75, 80, 86	0
21	CU	23/27 (85%)	1.62	7 (30%) 1 1	66, 76, 83, 87	0
22	AV	13/24 (54%)	1.42	2 (15%) 3 4	60, 92, 100, 100	0
22	CV	12/24 (50%)	2.52	6 (50%) 0 0	63, 93, 99, 99	0
23	AW	2/2 (100%)	2.87	1 (50%) 0 0	35, 35, 35, 42	0
23	CW	2/2 (100%)	3.99	1 (50%) 0 0	52, 52, 52, 59	0
24	AX	75/77 (97%)	0.10	0 100 100	37, 71, 84, 92	0
24	CX	75/77 (97%)	-0.05	0 100 100	39, 73, 86, 92	0
25	BA	2819/2915 (96%)	0.45	47 (1%) 67 76	23, 46, 89, 107	0
25	DA	2800/2915 (96%)	0.10	33 (1%) 75 83	26, 50, 90, 107	0
26	BB	120/121 (99%)	0.41	0 100 100	40, 65, 76, 91	0
26	DB	120/121 (99%)	0.16	4 (3%) 44 53	44, 70, 81, 93	0
27	BD	275/276 (99%)	0.36	6 (2%) 59 67	24, 45, 61, 77	0
27	DD	275/276 (99%)	0.73	22 (8%) 12 15	27, 47, 63, 78	0
28	BE	204/206 (99%)	0.92	36 (17%) 2 3	18, 44, 66, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DE	204/206 (99%)	0.61	20 (9%) 8 10	32, 57, 72, 86	0
29	BF	203/210 (96%)	1.04	37 (18%) 2 3	26, 55, 74, 84	0
29	DF	203/210 (96%)	0.98	36 (17%) 2 3	26, 58, 75, 85	0
30	BG	181/182 (99%)	0.89	24 (13%) 4 6	56, 70, 82, 91	0
30	DG	181/182 (99%)	2.17	80 (44%) 1 0	61, 73, 85, 91	0
31	BH	174/180 (96%)	0.90	16 (9%) 9 11	51, 66, 76, 82	0
31	DH	174/180 (96%)	1.60	48 (27%) 1 1	55, 69, 80, 85	0
32	BI	146/148 (98%)	1.06	32 (21%) 1 2	46, 74, 85, 87	0
32	DI	146/148 (98%)	1.05	33 (22%) 1 2	50, 75, 84, 87	0
33	BN	140/140 (100%)	1.07	17 (12%) 5 7	33, 53, 72, 80	0
33	DN	140/140 (100%)	1.66	50 (35%) 1 1	36, 56, 72, 81	0
34	BO	122/122 (100%)	0.27	3 (2%) 54 64	25, 43, 60, 76	0
34	DO	122/122 (100%)	0.21	3 (2%) 54 64	42, 59, 73, 77	0
35	BP	149/150 (99%)	0.88	14 (9%) 9 11	27, 57, 73, 87	0
35	DP	149/150 (99%)	1.14	37 (24%) 1 2	29, 59, 76, 86	0
36	BQ	141/141 (100%)	1.08	24 (17%) 2 3	35, 53, 64, 71	0
36	DQ	141/141 (100%)	1.47	41 (29%) 1 1	38, 56, 68, 76	0
37	BR	118/118 (100%)	0.58	10 (8%) 11 13	25, 37, 56, 66	0
37	DR	118/118 (100%)	1.28	30 (25%) 1 2	40, 54, 66, 76	0
38	BS	110/112 (98%)	0.67	9 (8%) 12 15	40, 52, 63, 68	0
38	DS	110/112 (98%)	1.46	31 (28%) 1 1	57, 76, 86, 92	0
39	BT	131/146 (89%)	0.32	5 (3%) 38 45	32, 50, 74, 86	0
39	DT	131/146 (89%)	0.73	13 (9%) 8 10	44, 60, 75, 85	0
40	BU	116/118 (98%)	0.81	10 (8%) 11 13	23, 35, 55, 76	0
40	DU	116/118 (98%)	1.54	38 (32%) 1 1	41, 61, 77, 87	0
41	BV	101/101 (100%)	0.68	7 (6%) 17 20	19, 43, 64, 76	0
41	DV	101/101 (100%)	1.31	25 (24%) 1 2	44, 71, 80, 88	0
42	BW	112/113 (99%)	0.98	11 (9%) 8 10	21, 38, 53, 75	0
42	DW	112/113 (99%)	1.65	41 (36%) 1 0	31, 51, 69, 85	0
43	BX	95/96 (98%)	0.55	2 (2%) 60 69	25, 43, 64, 82	0
43	DX	95/96 (98%)	1.45	26 (27%) 1 1	43, 62, 78, 91	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BY	107/110 (97%)	0.97	15 (14%) 3 5	36, 51, 69, 80	0
44	DY	107/110 (97%)	1.25	30 (28%) 1 1	55, 72, 81, 89	0
45	BZ	171/206 (83%)	1.18	43 (25%) 1 2	42, 63, 77, 92	0
45	DZ	174/206 (84%)	2.24	85 (48%) 1 0	61, 80, 90, 100	0
46	B0	83/85 (97%)	0.53	7 (8%) 11 14	16, 43, 56, 67	0
46	D0	83/85 (97%)	1.01	12 (14%) 3 5	44, 65, 74, 80	0
47	B1	97/98 (98%)	0.26	3 (3%) 47 55	27, 49, 70, 77	0
47	D1	97/98 (98%)	0.73	11 (11%) 6 7	38, 59, 75, 78	0
48	B2	70/72 (97%)	0.52	2 (2%) 49 58	37, 50, 66, 72	0
48	D2	70/72 (97%)	1.21	13 (18%) 2 2	58, 70, 79, 85	0
49	B3	59/60 (98%)	0.63	1 (1%) 67 76	26, 41, 61, 72	0
49	D3	59/60 (98%)	1.97	24 (40%) 1 0	44, 64, 77, 80	0
50	B4	69/71 (97%)	0.80	13 (18%) 2 2	57, 76, 91, 94	0
50	D4	69/71 (97%)	1.51	21 (30%) 1 1	77, 87, 97, 104	0
51	B5	59/60 (98%)	0.37	3 (5%) 27 33	19, 38, 57, 78	0
51	D5	59/60 (98%)	0.88	8 (13%) 4 5	31, 52, 69, 76	0
52	B6	53/54 (98%)	0.41	1 (1%) 64 72	29, 43, 60, 71	0
52	D6	53/54 (98%)	0.50	4 (7%) 14 17	50, 63, 75, 83	0
53	B7	48/49 (97%)	0.71	6 (12%) 5 6	20, 30, 53, 72	0
53	D7	48/49 (97%)	0.88	6 (12%) 5 6	35, 46, 71, 76	0
54	B8	64/65 (98%)	0.75	2 (3%) 47 55	27, 36, 47, 55	0
54	D8	64/65 (98%)	1.10	11 (17%) 2 3	44, 58, 67, 75	0
55	B9	37/37 (100%)	1.30	8 (21%) 1 2	31, 52, 64, 69	0
55	D9	37/37 (100%)	1.39	10 (27%) 1 1	44, 58, 67, 73	0
All	All	20644/21448 (96%)	0.70	2392 (11%) 5 7	16, 65, 87, 107	0

All (2392) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	CM	124	PRO	14.4
10	CJ	71	LEU	11.6
10	CJ	6	ILE	10.8
2	CB	70	PHE	10.5
14	CN	25	VAL	10.4

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Mol	Chain	Res	Type	RSRZ
13	CM	123	ALA	9.8
9	CI	26	VAL	9.7
9	CI	46	ALA	9.4
45	DZ	125	LEU	9.1
31	DH	115	VAL	8.9
2	CB	187	LEU	8.9
30	DG	139	LEU	8.6
36	DQ	104	PHE	8.6
2	CB	214	ILE	8.5
13	CM	7	VAL	8.5
2	CB	165	VAL	8.4
33	DN	140	VAL	7.9
14	CN	55	GLY	7.9
45	DZ	124	ILE	7.9
2	CB	163	PHE	7.8
30	DG	173	LEU	7.5
13	AM	56	LEU	7.5
13	CM	122	LYS	7.4
5	CE	94	ALA	7.3
50	D4	52	THR	7.3
13	CM	6	GLY	7.2
31	DH	107	VAL	7.2
14	CN	56	VAL	7.2
30	DG	92	VAL	7.2
7	CG	80	VAL	7.1
2	CB	197	VAL	7.1
14	CN	34	TYR	7.1
9	CI	33	PHE	7.1
22	CV	21	C	7.0
3	CC	167	TRP	7.0
9	CI	63	ILE	7.0
2	CB	69	LEU	7.0
14	CN	37	PHE	6.9
2	CB	93	VAL	6.9
53	D7	48	LYS	6.9
9	CI	64	THR	6.8
40	BU	117	GLN	6.8
2	CB	101	MET	6.8
9	CI	42	ARG	6.8
30	DG	110	ALA	6.8
10	CJ	50	ILE	6.8
30	DG	140	ILE	6.7

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Mol	Chain	Res	Type	RSRZ
3	AC	87	LEU	6.7
13	AM	124	PRO	6.7
9	CI	19	LEU	6.7
2	CB	164	VAL	6.7
30	DG	160	VAL	6.7
4	CD	161	ASN	6.6
30	DG	159	VAL	6.6
50	D4	41	PRO	6.6
50	D4	51	ASP	6.6
45	DZ	5	LEU	6.6
30	DG	102	PHE	6.6
10	CJ	65	LEU	6.5
11	CK	32	ILE	6.5
14	CN	2	ALA	6.5
9	AI	47	LEU	6.5
10	CJ	27	ALA	6.5
3	CC	184	TYR	6.5
30	DG	39	ILE	6.5
10	CJ	49	VAL	6.5
2	CB	92	TYR	6.5
25	BA	2816	G	6.5
2	CB	215	LEU	6.4
9	CI	7	THR	6.4
45	DZ	171	ILE	6.4
2	CB	68	ILE	6.4
14	AN	15	LYS	6.4
9	CI	9	ARG	6.4
9	CI	65	VAL	6.3
10	CJ	62	HIS	6.3
2	AB	101	MET	6.3
2	CB	90	MET	6.3
30	DG	19	LEU	6.3
13	AM	2	ALA	6.3
45	DZ	96	VAL	6.3
30	DG	137	GLU	6.2
9	CI	61	ALA	6.2
7	AG	82	GLY	6.2
7	CG	39	ALA	6.1
3	AC	201	TYR	6.1
2	CB	97	TRP	6.1
14	CN	57	ARG	6.1
49	D3	26	LEU	6.1

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Mol	Chain	Res	Type	RSRZ
13	AM	123	ALA	6.1
44	DY	55	TYR	6.1
19	CS	32	LYS	6.1
10	CJ	61	GLU	6.1
21	CU	6	ARG	6.0
4	AD	110	PHE	6.0
23	CW	76	PPU	6.0
45	DZ	121	HIS	6.0
14	CN	36	PHE	6.0
7	CG	36	LYS	6.0
43	DX	92	LEU	6.0
30	DG	157	ILE	5.9
8	CH	2	LEU	5.9
30	DG	34	LEU	5.9
13	CM	66	LEU	5.9
7	AG	83	ALA	5.9
45	DZ	161	VAL	5.9
7	AG	85	TYR	5.9
30	DG	106	LEU	5.9
31	DH	94	TYR	5.9
51	B5	60	VAL	5.9
45	DZ	97	GLU	5.9
9	CI	5	TYR	5.9
22	AV	24	A	5.9
10	CJ	63	PHE	5.8
9	CI	123	PRO	5.8
50	D4	55	ARG	5.8
45	DZ	99	TYR	5.8
2	CB	218	ALA	5.8
30	DG	136	ARG	5.8
38	DS	54	LEU	5.8
13	CM	121	LYS	5.8
2	CB	81	VAL	5.8
38	DS	39	ILE	5.8
9	CI	18	PHE	5.8
31	DH	101	ARG	5.8
7	CG	16	LEU	5.8
49	D3	60	GLU	5.8
14	CN	59	ALA	5.8
9	CI	75	ASP	5.8
42	DW	112	GLY	5.8
10	CJ	8	LEU	5.7

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Mol	Chain	Res	Type	RSRZ
2	AB	163	PHE	5.7
50	D4	40	HIS	5.7
50	D4	50	VAL	5.7
5	CE	13	ILE	5.7
30	DG	115	ARG	5.7
14	CN	41	ARG	5.6
10	CJ	10	GLY	5.6
7	CG	154	TYR	5.6
30	DG	41	GLN	5.6
7	CG	81	GLY	5.6
40	DU	90	VAL	5.6
7	CG	37	ASN	5.6
25	BA	2815	C	5.6
3	CC	57	ILE	5.5
4	AD	2	GLY	5.5
3	CC	10	PHE	5.5
38	DS	32	LEU	5.5
32	DI	18	VAL	5.5
31	DH	105	LEU	5.5
9	CI	83	ARG	5.5
25	BA	2154	U	5.5
19	CS	14	HIS	5.5
38	DS	56	LEU	5.5
30	BG	146	TYR	5.5
45	DZ	122	ARG	5.5
29	DF	172	TRP	5.5
9	AI	106	ALA	5.4
30	BG	178	PHE	5.4
9	CI	79	LEU	5.4
9	CI	20	ARG	5.4
13	CM	69	GLU	5.4
10	CJ	5	ARG	5.4
19	CS	50	ALA	5.4
2	AB	165	VAL	5.4
10	CJ	72	VAL	5.4
50	D4	49	PHE	5.4
9	CI	17	VAL	5.4
30	BG	136	ARG	5.4
45	DZ	146	ILE	5.3
10	CJ	48	THR	5.3
45	DZ	155	LEU	5.3
49	D3	59	VAL	5.3

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Mol	Chain	Res	Type	RSRZ
4	AD	3	ARG	5.3
42	BW	111	HIS	5.2
10	CJ	85	LEU	5.2
45	DZ	138	GLU	5.2
38	DS	52	SER	5.2
33	DN	43	THR	5.2
7	AG	84	ASN	5.2
9	CI	4	TYR	5.2
38	DS	26	LEU	5.2
10	AJ	72	VAL	5.2
3	AC	39	ILE	5.2
16	AP	1	MET	5.2
22	CV	23	A	5.2
50	B4	49	PHE	5.2
9	AI	63	ILE	5.1
10	CJ	23	ILE	5.1
1	CA	1532	U	5.1
4	AD	120	LEU	5.1
30	BG	137	GLU	5.1
32	DI	3	VAL	5.1
2	CB	71	VAL	5.1
4	CD	164	ALA	5.1
31	DH	123	PHE	5.1
31	DH	116	GLU	5.1
2	AB	214	ILE	5.1
13	CM	65	LYS	5.1
9	CI	62	TYR	5.1
13	CM	4	ILE	5.1
25	BA	2151	C	5.1
50	B4	50	VAL	5.1
2	CB	188	ALA	5.1
13	AM	4	ILE	5.1
14	CN	44	LEU	5.0
3	CC	201	TYR	5.0
20	CT	72	LEU	5.0
10	CJ	47	PHE	5.0
3	CC	6	HIS	5.0
12	AL	89	ARG	5.0
45	DZ	114	GLY	5.0
10	AJ	71	LEU	5.0
33	BN	140	VAL	5.0
3	CC	8	ILE	5.0

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Mol	Chain	Res	Type	RSRZ
10	CJ	31	GLY	5.0
45	DZ	88	PHE	4.9
33	DN	23	LEU	4.9
30	DG	109	VAL	4.9
2	CB	232	PRO	4.9
33	DN	1	MET	4.9
20	AT	21	LYS	4.9
31	DH	148	ILE	4.9
50	D4	42	PHE	4.9
20	AT	18	GLN	4.9
2	AB	222	ILE	4.9
36	BQ	79	LEU	4.9
14	CN	10	ALA	4.9
3	CC	182	ILE	4.9
9	CI	27	THR	4.8
32	BI	79	ILE	4.8
33	DN	116	LEU	4.8
30	DG	161	THR	4.8
10	CJ	54	PHE	4.8
7	CG	83	ALA	4.8
9	CI	71	SER	4.8
41	DV	101	GLY	4.8
9	CI	21	PRO	4.8
25	DA	229	A	4.8
30	DG	28	VAL	4.8
39	DT	77	PRO	4.8
31	DH	43	VAL	4.8
2	CB	67	THR	4.8
10	CJ	12	ASP	4.8
41	DV	72	VAL	4.7
3	AC	169	ALA	4.7
45	BZ	164	ALA	4.7
3	CC	178	LEU	4.7
31	DH	103	LEU	4.7
13	CM	3	ARG	4.7
4	AD	170	VAL	4.7
13	AM	22	ILE	4.7
38	DS	35	ILE	4.7
2	CB	88	ALA	4.7
3	CC	13	GLY	4.7
9	CI	74	ILE	4.7
9	CI	114	TYR	4.7

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Mol	Chain	Res	Type	RSRZ
31	DH	95	ARG	4.7
19	CS	69	HIS	4.7
45	DZ	113	ALA	4.7
2	CB	228	GLY	4.7
7	CG	84	ASN	4.7
13	CM	119	GLY	4.7
30	DG	38	VAL	4.7
32	DI	12	LEU	4.6
45	DZ	156	LYS	4.6
50	D4	35	VAL	4.6
36	DQ	103	MET	4.6
9	CI	41	VAL	4.6
7	CG	78	ARG	4.6
9	CI	88	TYR	4.6
40	DU	48	ALA	4.6
17	AQ	10	VAL	4.6
31	BH	105	LEU	4.6
4	CD	4	TYR	4.6
9	CI	10	ARG	4.6
38	DS	57	LYS	4.6
45	DZ	163	LEU	4.6
33	DN	44	PRO	4.6
49	D3	2	PRO	4.6
22	CV	22	U	4.6
45	DZ	102	LEU	4.6
11	CK	25	TYR	4.6
2	CB	200	ILE	4.6
3	AC	151	VAL	4.6
28	BE	89	ASP	4.6
4	CD	110	PHE	4.6
7	CG	35	LYS	4.5
23	AW	76	PPU	4.5
28	BE	4	ILE	4.5
36	DQ	33	GLY	4.5
7	CG	38	LEU	4.5
10	CJ	55	LYS	4.5
12	CL	48	PRO	4.5
2	CB	162	ILE	4.5
42	DW	38	TYR	4.5
30	DG	85	GLY	4.5
25	BA	2141	A	4.5
29	BF	17	ARG	4.5

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Mol	Chain	Res	Type	RSRZ
20	CT	24	LEU	4.5
25	DA	1509	C	4.5
48	D2	60	LEU	4.5
5	CE	90	VAL	4.5
17	AQ	11	VAL	4.5
35	DP	79	ARG	4.5
19	CS	49	ILE	4.5
32	DI	35	LEU	4.4
29	DF	140	LEU	4.4
50	D4	44	THR	4.4
43	DX	33	LYS	4.4
14	CN	39	LEU	4.4
7	AG	42	ILE	4.4
3	CC	142	MET	4.4
3	CC	2	GLY	4.4
35	DP	15	ARG	4.4
45	BZ	5	LEU	4.4
10	CJ	98	ILE	4.4
2	CB	152	PHE	4.4
7	CG	40	ALA	4.4
45	DZ	133	ILE	4.4
25	BA	2139	A	4.4
50	D4	57	GLU	4.4
19	AS	19	VAL	4.4
45	BZ	165	VAL	4.4
7	AG	81	GLY	4.4
45	DZ	53	ILE	4.4
19	CS	12	ASP	4.4
36	DQ	28	ALA	4.4
4	AD	167	GLY	4.4
36	DQ	106	VAL	4.3
13	CM	5	ALA	4.3
31	DH	102	ALA	4.3
14	CN	53	LEU	4.3
14	CN	38	GLY	4.3
28	BE	75	VAL	4.3
45	DZ	52	SER	4.3
50	D4	56	VAL	4.3
2	AB	102	LEU	4.3
9	CI	57	GLY	4.3
14	CN	54	PRO	4.3
14	CN	7	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
40	DU	61	TRP	4.3
40	BU	90	VAL	4.3
10	CJ	70	ARG	4.3
22	CV	24	A	4.3
30	DG	73	ALA	4.3
45	DZ	82	ARG	4.3
8	CH	6	ILE	4.3
4	CD	69	GLY	4.3
3	AC	200	ALA	4.3
3	AC	91	LEU	4.3
45	DZ	38	TYR	4.3
41	DV	70	ILE	4.3
7	AG	26	PHE	4.3
45	DZ	24	LEU	4.2
10	CJ	100	THR	4.2
3	CC	180	ALA	4.2
50	D4	45	GLY	4.2
9	CI	49	PRO	4.2
20	AT	58	LYS	4.2
30	DG	141	PHE	4.2
43	DX	86	GLY	4.2
15	AO	81	LEU	4.2
19	AS	15	LEU	4.2
3	CC	14	ILE	4.2
21	CU	13	ILE	4.2
20	AT	30	LYS	4.2
35	BP	149	GLU	4.2
42	DW	36	LEU	4.2
2	CB	83	MET	4.2
8	CH	83	ILE	4.2
45	DZ	6	LYS	4.2
4	AD	148	VAL	4.2
8	AH	3	THR	4.2
30	DG	133	LEU	4.2
19	AS	41	VAL	4.2
43	DX	49	VAL	4.2
4	CD	167	GLY	4.2
12	CL	69	TYR	4.2
4	CD	120	LEU	4.2
10	CJ	64	GLU	4.2
32	DI	1	MET	4.1
7	AG	43	PHE	4.1

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Mol	Chain	Res	Type	RSRZ
45	DZ	70	LEU	4.1
45	DZ	91	LEU	4.1
45	BZ	124	ILE	4.1
7	CG	22	LEU	4.1
30	DG	158	ALA	4.1
32	BI	140	LEU	4.1
38	DS	85	VAL	4.1
7	CG	82	GLY	4.1
33	DN	30	ILE	4.1
14	CN	29	ARG	4.1
43	DX	83	VAL	4.1
4	AD	102	ASP	4.1
32	DI	14	ASP	4.1
7	CG	79	ARG	4.1
31	DH	17	VAL	4.1
35	DP	109	GLY	4.1
50	D4	43	TYR	4.1
13	CM	120	LYS	4.1
14	CN	17	LYS	4.1
45	BZ	121	HIS	4.1
55	D9	12	ASP	4.1
10	CJ	15	THR	4.1
9	AI	26	VAL	4.1
35	BP	13	ASN	4.1
1	CA	1030(B)	C	4.1
3	CC	4	LYS	4.1
9	CI	14	VAL	4.1
32	DI	37	VAL	4.1
53	B7	46	VAL	4.1
33	DN	12	ARG	4.0
4	AD	21	LEU	4.0
19	AS	40	ILE	4.0
32	BI	101	LEU	4.0
36	DQ	34	LEU	4.0
41	BV	38	LEU	4.0
31	DH	117	PRO	4.0
30	DG	25	TYR	4.0
11	AK	126	ARG	4.0
10	CJ	94	VAL	4.0
32	DI	92	VAL	4.0
44	DY	61	ILE	4.0
47	B1	98	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
7	AG	79	ARG	4.0
40	BU	116	ALA	4.0
5	CE	11	ILE	4.0
7	CG	18	TYR	4.0
10	CJ	67	THR	4.0
45	DZ	170	THR	4.0
9	CI	115	GLY	4.0
10	AJ	98	ILE	4.0
45	BZ	104	PHE	4.0
29	DF	193	VAL	4.0
30	DG	120	LEU	4.0
36	BQ	104	PHE	4.0
37	DR	29	LEU	4.0
14	CN	15	LYS	4.0
49	D3	29	ARG	4.0
36	DQ	32	TYR	4.0
35	DP	125	VAL	4.0
38	DS	51	ALA	4.0
40	DU	96	ALA	4.0
42	DW	46	PHE	4.0
42	DW	21	VAL	3.9
49	D3	6	VAL	3.9
4	AD	118	ARG	3.9
40	DU	20	LEU	3.9
2	CB	66	GLY	3.9
3	AC	55	VAL	3.9
32	DI	107	VAL	3.9
9	CI	54	ASP	3.9
53	D7	47	ARG	3.9
7	AG	78	ARG	3.9
17	AQ	12	SER	3.9
3	CC	147	LYS	3.9
21	CU	8	THR	3.9
14	CN	51	GLY	3.9
30	DG	138	GLN	3.9
35	DP	1	MET	3.9
4	AD	108	LEU	3.9
19	CS	71	LEU	3.9
20	AT	59	ALA	3.9
25	BA	2814	C	3.9
41	DV	74	LYS	3.9
8	CH	9	MET	3.9

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Mol	Chain	Res	Type	RSRZ
19	AS	44	MET	3.9
30	BG	106	LEU	3.9
32	DI	30	LEU	3.9
1	AA	1447	A	3.9
9	CI	15	ALA	3.9
19	CS	24	ALA	3.9
37	DR	41	ALA	3.9
13	AM	9	ILE	3.9
13	AM	105	THR	3.9
29	BF	206	ILE	3.9
33	DN	50	ASP	3.9
33	DN	52	VAL	3.9
3	AC	189	ALA	3.9
3	CC	153	VAL	3.9
49	D3	9	VAL	3.9
30	DG	32	PRO	3.9
25	DA	2897	U	3.9
2	AB	185	ILE	3.8
35	DP	78	PRO	3.8
3	CC	173	VAL	3.8
9	CI	28	VAL	3.8
45	BZ	157	LEU	3.8
31	DH	111	HIS	3.8
37	DR	21	TYR	3.8
30	DG	163	ALA	3.8
32	DI	4	ILE	3.8
32	DI	85	GLU	3.8
20	AT	20	LEU	3.8
10	AJ	63	PHE	3.8
30	DG	23	PHE	3.8
4	CD	144	ASP	3.8
14	CN	22	THR	3.8
3	CC	155	GLY	3.8
30	DG	49	ASP	3.8
2	AB	148	TYR	3.8
2	CB	201	ILE	3.8
3	CC	7	PRO	3.8
8	CH	93	VAL	3.8
41	DV	94	LEU	3.8
42	DW	29	LEU	3.8
14	CN	58	LYS	3.8
48	D2	9	GLN	3.8

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Mol	Chain	Res	Type	RSRZ
10	CJ	46	ARG	3.8
3	CC	152	ILE	3.8
2	CB	233	SER	3.8
4	AD	147	ALA	3.8
32	BI	107	VAL	3.8
42	DW	50	VAL	3.8
30	DG	93	THR	3.8
30	DG	165	THR	3.8
28	DE	176	ILE	3.8
53	B7	48	LYS	3.8
33	BN	54	VAL	3.8
35	DP	45	LEU	3.8
45	BZ	126	VAL	3.8
3	CC	172	ARG	3.8
44	DY	35	TYR	3.7
20	AT	24	LEU	3.7
48	D2	24	LEU	3.7
42	DW	45	TYR	3.7
50	B4	51	ASP	3.7
20	AT	23	ARG	3.7
33	DN	47	ALA	3.7
28	DE	116	VAL	3.7
10	CJ	69	ASN	3.7
25	BA	2196	C	3.7
4	AD	138	TYR	3.7
37	BR	69	ASP	3.7
3	CC	12	LEU	3.7
9	AI	56	LEU	3.7
19	AS	67	VAL	3.7
28	DE	196	VAL	3.7
49	D3	21	ALA	3.7
30	DG	155	MET	3.7
43	DX	89	ILE	3.7
4	AD	157	LEU	3.7
9	CI	80	GLY	3.7
10	CJ	43	ARG	3.7
36	DQ	63	LYS	3.7
4	CD	146	ILE	3.7
19	CS	16	LEU	3.7
46	D0	75	LEU	3.7
28	BE	90	THR	3.7
45	BZ	169	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
29	BF	154	VAL	3.7
38	DS	55	ALA	3.7
45	DZ	126	VAL	3.7
40	DU	16	LYS	3.7
9	CI	81	ILE	3.7
10	CJ	13	HIS	3.7
29	DF	78	ILE	3.7
30	BG	139	LEU	3.7
45	BZ	155	LEU	3.7
46	B0	7	LEU	3.7
9	CI	109	VAL	3.7
36	DQ	102	VAL	3.7
43	DX	79	ALA	3.7
4	AD	124	GLY	3.7
30	BG	114	ILE	3.7
25	BA	2137	G	3.7
25	DA	2894	G	3.7
3	AC	66	VAL	3.6
41	DV	73	SER	3.6
2	CB	77	ALA	3.6
2	CB	230	VAL	3.6
47	D1	68	PRO	3.6
2	AB	200	ILE	3.6
3	AC	199	LYS	3.6
32	DI	13	GLY	3.6
4	CD	188	LEU	3.6
16	AP	6	LEU	3.6
2	CB	91	PRO	3.6
36	DQ	47	ILE	3.6
43	DX	80	ILE	3.6
44	DY	44	ILE	3.6
45	DZ	93	ASP	3.6
6	CF	79	LEU	3.6
13	CM	40	ASN	3.6
30	DG	48	GLU	3.6
3	AC	168	ALA	3.6
9	CI	53	VAL	3.6
13	AM	60	VAL	3.6
13	CM	102	ARG	3.6
20	AT	80	ARG	3.6
29	DF	186	ILE	3.6
31	BH	148	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
42	DW	111	HIS	3.6
2	AB	181	PHE	3.6
9	AI	59	PHE	3.6
30	DG	35	GLU	3.6
19	CS	52	TYR	3.6
45	DZ	139	VAL	3.6
33	DN	8	GLN	3.6
3	AC	15	THR	3.6
32	DI	86	THR	3.6
2	CB	41	ILE	3.6
14	CN	8	GLU	3.6
46	B0	5	LYS	3.6
15	CO	15	PHE	3.6
33	DN	117	PHE	3.6
45	DZ	44	PHE	3.6
16	CP	51	VAL	3.6
31	BH	131	VAL	3.6
35	BP	15	ARG	3.6
41	BV	101	GLY	3.6
4	AD	158	ILE	3.6
40	DU	17	ILE	3.6
25	BA	2183	C	3.6
7	CG	62	PHE	3.6
3	AC	153	VAL	3.6
45	DZ	39	VAL	3.6
20	AT	72	LEU	3.6
4	CD	185	PHE	3.6
30	DG	86	MET	3.6
2	CB	72	GLY	3.6
3	CC	23	TYR	3.6
2	CB	85	ALA	3.6
9	CI	45	ALA	3.6
4	AD	101	LEU	3.6
16	AP	19	ILE	3.6
8	CH	92	ARG	3.5
1	CA	1202	G	3.5
3	CC	199	LYS	3.5
9	CI	125	TYR	3.5
35	DP	110	TYR	3.5
36	DQ	30	GLY	3.5
45	BZ	162	GLU	3.5
11	CK	72	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
32	DI	36	ALA	3.5
40	DU	60	LEU	3.5
43	DX	68	ARG	3.5
45	BZ	156	LYS	3.5
9	CI	59	PHE	3.5
38	DS	29	PHE	3.5
22	AV	23	A	3.5
3	CC	33	LEU	3.5
9	CI	76	ALA	3.5
14	CN	6	LEU	3.5
9	CI	66	ARG	3.5
20	AT	17	ARG	3.5
28	DE	15	PHE	3.5
3	AC	78	GLY	3.5
45	DZ	65	GLN	3.5
8	CH	95	VAL	3.5
9	CI	36	TYR	3.5
13	AM	122	LYS	3.5
28	BE	52	LEU	3.5
38	DS	58	LEU	3.5
33	BN	30	ILE	3.5
42	DW	103	ILE	3.5
4	AD	16	GLY	3.5
4	CD	183	GLY	3.5
7	AG	156	TRP	3.5
33	DN	42	TRP	3.5
45	DZ	98	MET	3.5
29	DF	154	VAL	3.5
37	DR	42	LYS	3.5
14	CN	47	LEU	3.5
19	CS	20	LEU	3.5
42	DW	23	LEU	3.5
15	AO	87	ILE	3.5
30	DG	112	PRO	3.5
35	BP	12	ALA	3.5
38	DS	37	ALA	3.5
40	DU	65	ILE	3.5
20	CT	26	ASN	3.5
2	CB	196	LEU	3.5
4	AD	174	LEU	3.5
19	CS	60	VAL	3.5
29	DF	37	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
32	DI	19	VAL	3.5
2	AB	201	ILE	3.5
31	DH	151	ILE	3.5
37	DR	110	PRO	3.5
45	DZ	120	ILE	3.5
37	DR	117	VAL	3.5
40	DU	9	VAL	3.5
42	DW	51	LEU	3.5
10	CJ	58	ASP	3.5
19	CS	13	ASP	3.5
10	CJ	74	ILE	3.5
45	DZ	134	PRO	3.5
29	BF	123	LEU	3.5
43	DX	9	LEU	3.5
9	CI	116	LYS	3.5
45	DZ	7	ALA	3.5
45	DZ	101	PRO	3.5
7	CG	26	PHE	3.5
7	CG	43	PHE	3.5
9	AI	33	PHE	3.5
36	DQ	65	PHE	3.5
5	CE	12	LEU	3.4
33	DN	26	LEU	3.4
31	DH	24	VAL	3.4
4	CD	158	ILE	3.4
31	BH	104	GLU	3.4
38	BS	44	LYS	3.4
2	AB	221	LEU	3.4
38	BS	24	LEU	3.4
35	DP	101	VAL	3.4
19	CS	35	SER	3.4
42	DW	37	ARG	3.4
40	DU	63	VAL	3.4
45	DZ	71	VAL	3.4
55	D9	16	VAL	3.4
2	CB	222	ILE	3.4
10	CJ	59	SER	3.4
16	AP	36	ILE	3.4
2	CB	100	GLY	3.4
11	CK	42	TRP	3.4
2	AB	70	PHE	3.4
3	CC	65	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
7	CG	25	ALA	3.4
11	AK	19	ALA	3.4
30	DG	84	LYS	3.4
13	AM	8	GLU	3.4
41	DV	71	LEU	3.4
14	CN	42	ILE	3.4
50	B4	52	THR	3.4
45	DZ	152	ALA	3.4
30	DG	94	LEU	3.4
14	CN	11	LYS	3.4
10	CJ	96	ILE	3.4
38	DS	40	ILE	3.4
40	DU	47	TYR	3.4
9	AI	61	ALA	3.4
21	CU	10	ARG	3.4
40	DU	70	ARG	3.4
19	AS	66	MET	3.4
42	DW	47	VAL	3.4
42	DW	24	ILE	3.4
45	BZ	99	TYR	3.4
5	AE	88	LYS	3.4
9	CI	3	GLN	3.4
12	CL	14	GLY	3.4
8	CH	134	ILE	3.4
11	CK	95	ILE	3.4
15	CO	27	VAL	3.4
44	DY	45	VAL	3.4
4	AD	169	LYS	3.4
43	DX	69	TYR	3.4
19	CS	57	HIS	3.4
25	BA	2134	G	3.4
37	DR	25	ALA	3.4
42	DW	44	ALA	3.4
3	AC	101	LEU	3.4
29	BF	148	LEU	3.4
54	D8	17	THR	3.4
35	DP	149	GLU	3.4
30	DG	37	VAL	3.4
10	CJ	51	ARG	3.4
30	DG	72	ARG	3.4
35	DP	124	LYS	3.4
37	DR	47	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
18	AR	73	ALA	3.3
30	BG	34	LEU	3.3
45	BZ	70	LEU	3.3
3	AC	64	VAL	3.3
3	CC	131	ARG	3.3
31	DH	97	ARG	3.3
44	DY	5	MET	3.3
10	CJ	97	GLU	3.3
36	DQ	17	LEU	3.3
33	DN	2	LYS	3.3
45	DZ	23	LYS	3.3
13	AM	6	GLY	3.3
13	CM	88	ARG	3.3
41	BV	1	MET	3.3
48	D2	1	MET	3.3
11	CK	108	ILE	3.3
28	BE	77	ILE	3.3
30	DG	117	PHE	3.3
31	BH	123	PHE	3.3
36	DQ	121	ALA	3.3
46	B0	3	HIS	3.3
2	AB	99	GLY	3.3
31	DH	106	THR	3.3
5	CE	10	MET	3.3
13	AM	23	TYR	3.3
28	BE	183	LEU	3.3
7	CG	32	ARG	3.3
30	DG	89	GLY	3.3
2	AB	152	PHE	3.3
14	CN	61	TRP	3.3
21	CU	14	TRP	3.3
3	AC	4	LYS	3.3
4	CD	184	LYS	3.3
20	CT	29	LYS	3.3
13	CM	70	LEU	3.3
20	CT	62	LEU	3.3
25	DA	2896	C	3.3
44	DY	63	LYS	3.3
9	CI	37	PHE	3.3
28	BE	104	VAL	3.3
53	D7	46	VAL	3.3
2	CB	98	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
4	CD	108	LEU	3.3
28	BE	182	LEU	3.3
40	DU	109	LEU	3.3
55	D9	11	CYS	3.3
32	BI	106	GLY	3.3
43	DX	4	ALA	3.3
54	D8	21	LYS	3.3
55	D9	15	LYS	3.3
33	DN	48	MET	3.3
45	BZ	53	ILE	3.3
45	DZ	57	ILE	3.3
1	CA	1030	C	3.3
5	CE	33	VAL	3.3
9	CI	16	ARG	3.3
1	CA	1257	U	3.3
4	AD	135	LEU	3.3
13	CM	34	LEU	3.3
46	D0	62	LEU	3.3
36	DQ	22	LYS	3.3
45	DZ	78	LYS	3.3
5	AE	95	ALA	3.3
31	DH	96	ALA	3.3
4	CD	168	ARG	3.3
14	CN	26	ARG	3.3
28	BE	51	PHE	3.3
28	BE	79	ARG	3.3
36	DQ	66	ILE	3.3
13	CM	60	VAL	3.3
19	CS	41	VAL	3.3
42	DW	39	THR	3.3
1	AA	103	C	3.3
2	AB	68	ILE	3.2
4	AD	116	GLN	3.2
7	CG	42	ILE	3.2
33	DN	51	PHE	3.2
16	CP	79	VAL	3.2
29	DF	175	THR	3.2
31	BH	113	VAL	3.2
4	AD	97	LEU	3.2
7	CG	156	TRP	3.2
42	BW	112	GLY	3.2
12	CL	51	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
2	AB	76	GLN	3.2
3	AC	150	LYS	3.2
13	CM	78	ILE	3.2
16	CP	4	ILE	3.2
52	D6	54	ILE	3.2
31	DH	133	VAL	3.2
38	BS	49	VAL	3.2
41	DV	43	GLU	3.2
17	AQ	22	LEU	3.2
18	CR	58	LEU	3.2
47	D1	62	VAL	3.2
19	AS	33	THR	3.2
45	DZ	69	THR	3.2
30	DG	142	PRO	3.2
9	CI	82	ALA	3.2
5	CE	109	ILE	3.2
10	AJ	38	ILE	3.2
10	CJ	38	ILE	3.2
13	CM	15	VAL	3.2
32	BI	38	LEU	3.2
4	CD	109	GLY	3.2
25	BA	2182	G	3.2
25	BA	2805	G	3.2
14	AN	49	HIS	3.2
16	CP	46	PRO	3.2
45	DZ	68	PRO	3.2
53	D7	18	PHE	3.2
13	CM	19	LEU	3.2
28	BE	198	VAL	3.2
29	DF	196	LEU	3.2
33	BN	1	MET	3.2
44	DY	42	VAL	3.2
49	D3	35	ARG	3.2
17	AQ	7	THR	3.2
19	AS	39	THR	3.2
2	CB	160	ASP	3.2
28	BE	30	PRO	3.2
30	BG	49	ASP	3.2
10	CJ	26	ALA	3.2
25	DA	2133	G	3.2
41	DV	15	GLU	3.2
30	DG	63	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
2	CB	102	LEU	3.2
28	BE	78	LEU	3.2
30	BG	135	LEU	3.2
35	BP	83	VAL	3.2
45	DZ	22	GLY	3.2
2	CB	167	PRO	3.2
2	CB	55	PHE	3.2
3	AC	10	PHE	3.2
30	DG	29	TRP	3.2
38	DS	11	LYS	3.2
1	CA	1492	A	3.2
3	CC	159	GLY	3.2
30	DG	90	LEU	3.2
36	DQ	2	LEU	3.2
25	BA	2138	G	3.2
46	D0	76	GLY	3.2
28	DE	21	VAL	3.2
45	BZ	96	VAL	3.2
3	AC	170	GLN	3.2
7	CG	14	PRO	3.2
38	DS	87	PHE	3.2
5	AE	89	ILE	3.2
30	DG	135	LEU	3.2
55	B9	17	ILE	3.2
35	DP	126	VAL	3.2
45	DZ	56	VAL	3.2
13	CM	13	LYS	3.2
49	D3	32	GLN	3.2
11	CK	43	SER	3.2
16	CP	19	ILE	3.2
20	AT	41	ILE	3.2
32	BI	75	LEU	3.2
33	BN	71	ILE	3.2
41	DV	42	GLY	3.2
55	D9	25	VAL	3.1
3	CC	37	GLN	3.1
53	B7	47	ARG	3.1
4	AD	176	LEU	3.1
7	AG	22	LEU	3.1
25	DA	2123	G	3.1
42	DW	82	LEU	3.1
45	BZ	125	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
49	D3	27	GLY	3.1
2	AB	97	TRP	3.1
10	AJ	7	LYS	3.1
25	BA	2807	C	3.1
22	CV	20	U	3.1
46	D0	69	PHE	3.1
10	CJ	41	PRO	3.1
28	BE	106	GLY	3.1
3	AC	8	ILE	3.1
13	AM	5	ALA	3.1
30	BG	103	LEU	3.1
48	D2	54	LYS	3.1
54	D8	16	ILE	3.1
55	D9	13	LYS	3.1
1	CA	1155	G	3.1
25	DA	2147	G	3.1
41	DV	47	VAL	3.1
9	CI	34	ASN	3.1
30	DG	178	PHE	3.1
2	CB	223	ILE	3.1
13	CM	10	PRO	3.1
16	AP	17	TYR	3.1
45	DZ	83	PRO	3.1
36	DQ	107	ALA	3.1
53	B7	45	ALA	3.1
31	DH	35	VAL	3.1
39	BT	115	ARG	3.1
47	D1	70	VAL	3.1
25	BA	2142	G	3.1
26	DB	118	G	3.1
2	AB	211	ILE	3.1
8	CH	35	ILE	3.1
9	AI	45	ALA	3.1
44	DY	48	ALA	3.1
14	CN	45	ARG	3.1
10	CJ	34	VAL	3.1
45	DZ	100	VAL	3.1
2	CB	193	ASP	3.1
19	CS	38	SER	3.1
28	BE	195	LEU	3.1
4	AD	5	ILE	3.1
31	DH	112	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
42	DW	68	ARG	3.1
45	DZ	137	ILE	3.1
3	CC	177	THR	3.1
29	BF	8	GLN	3.1
14	CN	46	GLU	3.1
30	DG	108	ASN	3.1
3	CC	80	GLY	3.1
19	AS	74	PHE	3.1
20	AT	101	GLY	3.1
10	CJ	68	HIS	3.1
29	BF	140	LEU	3.1
30	BG	140	ILE	3.1
31	BH	2	SER	3.1
18	AR	52	PRO	3.1
38	BS	37	ALA	3.1
3	CC	18	TRP	3.1
9	CI	102	LEU	3.1
11	CK	98	LEU	3.1
35	DP	123	LEU	3.1
37	BR	100	LEU	3.1
31	DH	77	LYS	3.1
13	AM	25	ILE	3.1
2	CB	202	PRO	3.1
12	CL	71	PRO	3.1
40	DU	8	VAL	3.1
40	DU	56	ASP	3.1
20	AT	14	LYS	3.0
25	BA	2806	G	3.0
15	CO	87	ILE	3.0
41	DV	12	TYR	3.0
47	D1	71	TYR	3.0
28	DE	25	VAL	3.0
32	BI	142	VAL	3.0
45	DZ	48	PHE	3.0
2	AB	98	LEU	3.0
4	AD	11	LEU	3.0
17	AQ	53	LEU	3.0
2	CB	216	SER	3.0
12	AL	7	ILE	3.0
9	CI	55	ALA	3.0
27	BD	276	LYS	3.0
2	AB	66	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
13	AM	24	GLY	3.0
31	DH	113	VAL	3.0
45	DZ	116	VAL	3.0
45	DZ	123	ASP	3.0
3	CC	204	LEU	3.0
19	AS	71	LEU	3.0
27	DD	53	PHE	3.0
43	DX	28	PHE	3.0
49	D3	57	GLU	3.0
4	AD	166	LYS	3.0
6	CF	82	ARG	3.0
13	CM	42	ALA	3.0
19	CS	66	MET	3.0
2	AB	158	LEU	3.0
18	AR	79	LEU	3.0
25	DA	896	A	3.0
45	BZ	41	LEU	3.0
30	DG	26	GLN	3.0
10	AJ	6	ILE	3.0
10	AJ	59	SER	3.0
13	CM	64	TRP	3.0
38	DS	53	SER	3.0
2	AB	174	VAL	3.0
41	DV	5	VAL	3.0
46	B0	54	GLY	3.0
18	AR	25	THR	3.0
27	BD	275	LYS	3.0
30	DG	75	LYS	3.0
42	DW	104	THR	3.0
3	AC	14	ILE	3.0
7	CG	41	ARG	3.0
30	DG	113	ARG	3.0
30	DG	179	PRO	3.0
2	AB	177	ALA	3.0
29	BF	118	ALA	3.0
38	BS	7	TYR	3.0
2	CB	30	ARG	3.0
3	AC	134	ILE	3.0
33	DN	85	ILE	3.0
45	DZ	162	GLU	3.0
50	D4	54	GLY	3.0
13	CM	107	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
29	BF	21	ALA	3.0
29	DF	115	ALA	3.0
33	BN	52	VAL	3.0
35	DP	127	ALA	3.0
34	DO	1	MET	3.0
7	CG	109	ASN	3.0
41	DV	92	THR	3.0
44	BY	22	GLY	3.0
44	DY	16	ALA	3.0
44	DY	27	VAL	3.0
47	D1	49	VAL	3.0
25	BA	2143	G	3.0
48	D2	57	ILE	3.0
25	DA	2143	C	2.9
40	DU	43	GLY	2.9
4	AD	111	ALA	2.9
30	DG	131	TYR	2.9
7	AG	105	VAL	2.9
32	DI	144	VAL	2.9
13	AM	121	LYS	2.9
45	BZ	119	GLU	2.9
32	BI	88	ILE	2.9
20	AT	25	ARG	2.9
11	CK	30	VAL	2.9
45	DZ	59	LEU	2.9
45	DZ	172	ALA	2.9
31	DH	93	GLY	2.9
4	AD	132	ARG	2.9
4	AD	209	ARG	2.9
10	CJ	60	ARG	2.9
4	CD	166	LYS	2.9
27	DD	155	LEU	2.9
30	BG	152	LEU	2.9
32	DI	17	GLN	2.9
41	DV	20	LEU	2.9
5	AE	100	VAL	2.9
47	D1	77	ALA	2.9
6	CF	8	ILE	2.9
14	CN	23	ARG	2.9
16	AP	4	ILE	2.9
33	BN	115	ARG	2.9
2	AB	95	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
3	AC	43	LEU	2.9
10	CJ	40	LEU	2.9
32	BI	6	LEU	2.9
40	BU	20	LEU	2.9
46	D0	45	PHE	2.9
38	DS	36	TYR	2.9
49	D3	12	PRO	2.9
2	CB	161	ALA	2.9
3	CC	120	VAL	2.9
1	AA	1456	G	2.9
9	CI	11	LYS	2.9
33	DN	38	HIS	2.9
36	BQ	76	LYS	2.9
44	BY	63	LYS	2.9
2	AB	187	LEU	2.9
28	BE	5	LEU	2.9
32	BI	86	THR	2.9
44	BY	70	SER	2.9
4	CD	189	PRO	2.9
31	DH	36	PRO	2.9
31	DH	118	PRO	2.9
3	AC	198	VAL	2.9
38	DS	46	VAL	2.9
49	B3	59	VAL	2.9
40	DU	73	GLY	2.9
4	CD	199	ASN	2.9
30	DG	144	ILE	2.9
32	DI	11	ASN	2.9
55	B9	26	ILE	2.9
3	CC	170	GLN	2.9
33	DN	69	GLN	2.9
20	CT	20	LEU	2.9
25	BA	2167	C	2.9
29	DF	148	LEU	2.9
29	DF	156	LEU	2.9
37	DR	69	ASP	2.9
19	AS	59	PRO	2.9
32	DI	26	ALA	2.9
33	DN	9	VAL	2.9
33	DN	84	LYS	2.9
37	DR	101	ALA	2.9
2	CB	89	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
17	CQ	8	GLY	2.9
36	BQ	61	GLY	2.9
7	CG	27	ILE	2.9
3	AC	178	LEU	2.9
9	CI	47	LEU	2.9
14	AN	37	PHE	2.9
38	BS	73	LEU	2.9
45	BZ	44	PHE	2.9
4	AD	104	VAL	2.9
4	CD	112	VAL	2.9
9	AI	7	THR	2.9
16	AP	39	TYR	2.9
17	AQ	88	TYR	2.9
31	DH	75	ALA	2.9
44	DY	69	ALA	2.9
29	DF	27	GLU	2.9
36	DQ	64	ILE	2.9
16	CP	48	TRP	2.9
13	AM	120	LYS	2.9
30	DG	36	LYS	2.9
32	BI	12	LEU	2.9
50	B4	59	PHE	2.9
9	CI	92	TYR	2.8
19	CS	51	VAL	2.8
54	D8	49	VAL	2.8
34	DO	74	GLY	2.8
12	CL	100	ILE	2.8
43	DX	31	HIS	2.8
2	AB	36	ARG	2.8
2	AB	53	ARG	2.8
53	D7	42	LEU	2.8
15	AO	15	PHE	2.8
22	CV	13	A	2.8
31	DH	109	PHE	2.8
25	BA	2906	U	2.8
2	CB	227	GLY	2.8
12	AL	90	VAL	2.8
11	CK	31	THR	2.8
2	CB	80	ILE	2.8
36	DQ	131	ILE	2.8
4	CD	11	LEU	2.8
4	CD	157	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
9	CI	40	LEU	2.8
32	DI	47	LEU	2.8
4	AD	112	VAL	2.8
9	CI	69	GLY	2.8
17	AQ	23	VAL	2.8
31	BH	140	LYS	2.8
3	AC	173	VAL	2.8
7	CG	23	VAL	2.8
31	DH	55	PRO	2.8
43	DX	43	VAL	2.8
33	BN	72	TYR	2.8
40	DU	12	ARG	2.8
4	AD	179	GLU	2.8
7	AG	16	LEU	2.8
9	CI	48	GLU	2.8
29	DF	192	LEU	2.8
33	DN	99	LEU	2.8
41	DV	18	LEU	2.8
2	CB	195	ASP	2.8
29	DF	116	ASP	2.8
10	AJ	35	SER	2.8
35	DP	68	GLN	2.8
36	DQ	5	ARG	2.8
9	AI	52	ALA	2.8
32	BI	4	ILE	2.8
7	AG	38	LEU	2.8
25	BA	2155	G	2.8
35	BP	106	LEU	2.8
35	DP	2	LYS	2.8
11	AK	81	ASP	2.8
4	CD	90	GLY	2.8
9	CI	126	SER	2.8
3	AC	138	VAL	2.8
13	AM	7	VAL	2.8
15	CO	29	VAL	2.8
37	DR	48	VAL	2.8
41	DV	76	LYS	2.8
42	DW	48	ALA	2.8
54	B8	65	GLU	2.8
5	CE	31	LEU	2.8
16	CP	60	LEU	2.8
19	CS	44	MET	2.8

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Mol	Chain	Res	Type	RSRZ
1	CA	1531	A	2.8
29	BF	193	VAL	2.8
7	AG	151	TYR	2.8
28	BE	26	ILE	2.8
32	BI	120	ILE	2.8
45	DZ	8	TYR	2.8
45	DZ	18	LEU	2.8
38	DS	5	THR	2.8
2	CB	220	ASP	2.8
3	AC	80	GLY	2.8
18	AR	42	ARG	2.8
20	CT	9	ASN	2.8
31	DH	132	ARG	2.8
6	CF	6	VAL	2.8
17	AQ	57	VAL	2.8
32	BI	19	VAL	2.8
2	CB	26	PRO	2.8
9	AI	81	ILE	2.8
7	CG	12	LEU	2.8
9	CI	13	ALA	2.8
16	AP	73	LEU	2.8
18	AR	78	LEU	2.8
33	DN	33	LEU	2.8
42	DW	74	ALA	2.8
46	D0	74	ARG	2.7
4	AD	183	GLY	2.7
40	DU	44	ASN	2.7
42	DW	34	ASN	2.7
33	BN	53	VAL	2.7
13	CM	97	PRO	2.7
2	AB	188	ALA	2.7
7	CG	152	ALA	2.7
20	AT	62	LEU	2.7
32	BI	97	ILE	2.7
36	BQ	50	ALA	2.7
36	DQ	118	LEU	2.7
45	BZ	38	TYR	2.7
11	AK	125	PHE	2.7
4	AD	69	GLY	2.7
13	CM	67	GLU	2.7
21	CU	5	ASP	2.7
16	AP	67	THR	2.7

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Mol	Chain	Res	Type	RSRZ
14	CN	32	SER	2.7
2	CB	217	ARG	2.7
9	CI	85	LEU	2.7
19	AS	16	LEU	2.7
32	DI	77	LEU	2.7
33	DN	70	LYS	2.7
45	BZ	91	LEU	2.7
45	DZ	131	ARG	2.7
50	B4	68	ARG	2.7
28	BE	28	ALA	2.7
4	AD	144	ASP	2.7
25	BA	218	A	2.7
36	BQ	33	GLY	2.7
36	BQ	80	GLU	2.7
36	BQ	91	GLU	2.7
48	B2	1	MET	2.7
2	CB	132	LYS	2.7
17	AQ	37	LYS	2.7
49	D3	24	LYS	2.7
10	CJ	11	PHE	2.7
47	D1	60	PHE	2.7
29	BF	172	TRP	2.7
14	CN	35	ARG	2.7
19	AS	18	LYS	2.7
10	AJ	49	VAL	2.7
49	D3	47	VAL	2.7
1	AA	1257	U	2.7
17	AQ	84	LEU	2.7
25	BA	2189	U	2.7
38	DS	24	LEU	2.7
45	DZ	41	LEU	2.7
45	DZ	157	LEU	2.7
9	CI	101	PHE	2.7
30	DG	169	ALA	2.7
25	DA	2803	C	2.7
32	BI	17	GLN	2.7
2	AB	133	LYS	2.7
4	AD	131	ARG	2.7
29	DF	160	ASN	2.7
45	DZ	132	ASN	2.7
12	AL	96	VAL	2.7
3	AC	152	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
12	CL	93	LEU	2.7
30	BG	31	VAL	2.7
37	DR	51	LEU	2.7
44	DY	7	VAL	2.7
45	BZ	61	LEU	2.7
9	CI	90	PRO	2.7
11	AK	23	ALA	2.7
11	AK	25	TYR	2.7
15	CO	30	ALA	2.7
37	DR	24	GLN	2.7
12	AL	99	HIS	2.7
35	DP	16	ARG	2.7
11	AK	82	VAL	2.7
45	BZ	144	LEU	2.7
3	CC	186	PHE	2.7
4	AD	182	LYS	2.7
10	CJ	52	GLY	2.7
25	BA	2135	U	2.7
33	DN	60	ILE	2.7
4	AD	4	TYR	2.7
8	CH	94	TYR	2.7
35	DP	80	TYR	2.7
36	DQ	105	GLU	2.7
1	CA	1131	G	2.7
27	DD	173	VAL	2.7
28	BE	175	VAL	2.7
28	DE	7	VAL	2.7
33	BN	43	THR	2.7
33	DN	83	LYS	2.7
13	CM	9	ILE	2.7
19	CS	40	ILE	2.7
44	DY	41	GLY	2.7
49	D3	58	VAL	2.7
3	AC	174	PRO	2.7
29	DF	139	PHE	2.7
45	DZ	45	ASP	2.7
36	DQ	139	GLU	2.7
19	CS	53	ASN	2.6
29	DF	155	LEU	2.6
37	DR	111	LEU	2.6
39	BT	99	LEU	2.6
39	DT	99	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
9	CI	6	GLY	2.6
12	CL	43	VAL	2.6
31	DH	92	ILE	2.6
33	DN	62	VAL	2.6
16	AP	28	ARG	2.6
45	BZ	52	SER	2.6
45	BZ	133	ILE	2.6
43	DX	47	PHE	2.6
12	AL	94	PRO	2.6
1	CA	1061	G	2.6
13	AM	21	TYR	2.6
16	AP	7	ALA	2.6
45	BZ	152	ALA	2.6
7	CG	28	ASN	2.6
18	AR	44	LEU	2.6
14	CN	12	ARG	2.6
3	AC	182	ILE	2.6
14	CN	33	VAL	2.6
19	AS	49	ILE	2.6
19	AS	64	GLU	2.6
19	CS	43	GLU	2.6
2	AB	77	ALA	2.6
10	CJ	7	LYS	2.6
32	BI	36	ALA	2.6
7	AG	153	HIS	2.6
14	CN	49	HIS	2.6
4	CD	176	LEU	2.6
32	BI	35	LEU	2.6
33	DN	138	LEU	2.6
37	DR	100	LEU	2.6
40	DU	66	ASN	2.6
7	AG	80	VAL	2.6
9	AI	17	VAL	2.6
11	CK	21	ILE	2.6
29	DF	174	VAL	2.6
42	DW	20	VAL	2.6
11	AK	43	SER	2.6
29	DF	129	PHE	2.6
2	AB	194	PRO	2.6
43	DX	85	PRO	2.6
11	CK	64	ALA	2.6
29	DF	113	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
31	DH	83	TYR	2.6
38	DS	102	ALA	2.6
7	AG	32	ARG	2.6
36	DQ	125	LEU	2.6
45	DZ	160	GLY	2.6
46	D0	73	GLY	2.6
10	CJ	44	VAL	2.6
29	DF	114	VAL	2.6
30	BG	102	PHE	2.6
33	DN	54	VAL	2.6
44	BY	72	VAL	2.6
25	BA	2136	A	2.6
33	DN	11	PRO	2.6
2	CB	186	ALA	2.6
11	CK	126	ARG	2.6
12	AL	98	TYR	2.6
3	CC	197	GLY	2.6
4	AD	80	GLU	2.6
8	CH	133	LEU	2.6
31	DH	124	GLU	2.6
35	BP	59	LEU	2.6
42	DW	30	GLU	2.6
51	D5	25	LEU	2.6
52	D6	11	LEU	2.6
2	AB	57	PHE	2.6
2	AB	229	VAL	2.6
5	CE	148	VAL	2.6
28	BE	91	VAL	2.6
39	DT	61	PHE	2.6
33	DN	39	ARG	2.6
10	CJ	32	ALA	2.6
16	AP	35	LYS	2.6
20	AT	29	LYS	2.6
6	CF	61	LEU	2.6
8	AH	2	LEU	2.6
30	DG	42	GLY	2.6
32	BI	5	LEU	2.6
40	DU	71	GLN	2.6
2	AB	37	ASN	2.6
2	AB	108	ILE	2.6
2	CB	105	PHE	2.6
3	CC	5	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
5	AE	118	ILE	2.6
8	CH	135	CYS	2.6
28	BE	188	VAL	2.6
29	BF	202	PHE	2.6
35	BP	125	VAL	2.6
5	AE	18	ARG	2.6
27	DD	217	ARG	2.6
40	DU	59	ARG	2.6
2	AB	167	PRO	2.6
33	DN	40	PRO	2.6
7	CG	85	TYR	2.6
9	AI	43	ALA	2.6
29	DF	194	MET	2.6
38	BS	92	TYR	2.6
44	DY	6	HIS	2.6
3	AC	12	LEU	2.6
8	CH	10	LEU	2.6
9	CI	50	LEU	2.6
28	DE	52	LEU	2.6
30	DG	107	LEU	2.6
35	DP	6	LEU	2.6
25	DA	2112	G	2.6
2	AB	164	VAL	2.6
3	AC	76	VAL	2.6
3	AC	124	ILE	2.6
19	AS	60	VAL	2.6
19	CS	10	PHE	2.6
30	DG	5	VAL	2.6
39	DT	76	PHE	2.6
48	D2	25	VAL	2.6
45	BZ	153	SER	2.6
2	CB	168	THR	2.6
2	CB	115	LEU	2.6
7	CG	132	GLY	2.6
15	AO	67	LEU	2.6
32	DI	38	LEU	2.6
40	DU	14	HIS	2.6
8	CH	44	PHE	2.6
18	AR	71	LYS	2.6
36	BQ	66	ILE	2.6
3	CC	143	GLU	2.5
9	AI	55	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
9	AI	114	TYR	2.5
30	BG	12	TYR	2.5
40	DU	18	LEU	2.5
52	B6	23	THR	2.5
1	AA	1028	C	2.5
31	DH	25	LYS	2.5
33	DN	29	LYS	2.5
4	AD	70	ILE	2.5
20	CT	100	ILE	2.5
32	DI	120	ILE	2.5
1	AA	151	A	2.5
27	DD	185	VAL	2.5
28	DE	184	VAL	2.5
31	DH	159	GLU	2.5
37	DR	102	GLU	2.5
11	CK	13	GLN	2.5
19	CS	68	GLY	2.5
2	AB	180	LEU	2.5
13	CM	90	LEU	2.5
33	DN	67	LEU	2.5
42	BW	74	ALA	2.5
20	AT	71	THR	2.5
3	CC	202	ILE	2.5
13	CM	73	GLU	2.5
40	DU	40	PHE	2.5
2	AB	197	VAL	2.5
6	AF	88	VAL	2.5
16	AP	68	ASP	2.5
42	DW	71	VAL	2.5
54	D8	23	VAL	2.5
18	CR	76	LEU	2.5
36	BQ	118	LEU	2.5
37	DR	44	LEU	2.5
39	DT	20	PRO	2.5
45	DZ	117	LEU	2.5
49	D3	3	ARG	2.5
29	BF	111	ALA	2.5
10	CJ	81	THR	2.5
28	BE	167	VAL	2.5
29	DF	163	VAL	2.5
44	DY	51	VAL	2.5
13	CM	56	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
50	B4	48	ARG	2.5
3	CC	206	GLU	2.5
13	AM	61	GLU	2.5
25	DA	6	A	2.5
3	CC	22	TRP	2.5
7	AG	154	TYR	2.5
14	AN	21	TYR	2.5
33	DN	57	ALA	2.5
36	DQ	54	MET	2.5
7	AG	62	PHE	2.5
44	DY	60	PHE	2.5
29	BF	29	ASN	2.5
55	B9	13	LYS	2.5
3	AC	68	VAL	2.5
4	CD	198	VAL	2.5
4	AD	100	ARG	2.5
42	BW	82	LEU	2.5
16	AP	41	PRO	2.5
6	AF	63	TYR	2.5
55	B9	24	TYR	2.5
1	CA	1447	A	2.5
7	AG	30	ILE	2.5
7	CG	30	ILE	2.5
18	CR	56	THR	2.5
6	CF	88	VAL	2.5
11	AK	80	VAL	2.5
30	BG	26	GLN	2.5
45	DZ	72	ARG	2.5
45	DZ	110	GLY	2.5
9	AI	50	LEU	2.5
13	CM	8	GLU	2.5
16	CP	6	LEU	2.5
17	AQ	39	SER	2.5
5	AE	92	LYS	2.5
32	BI	121	LYS	2.5
35	DP	145	PRO	2.5
36	DQ	130	LYS	2.5
38	DS	34	HIS	2.5
29	DF	167	ALA	2.5
36	BQ	103	MET	2.5
36	DQ	29	PHE	2.5
37	BR	19	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
40	DU	67	ALA	2.5
40	DU	62	ILE	2.5
7	CG	15	ASP	2.5
30	BG	115	ARG	2.5
35	DP	77	ARG	2.5
51	D5	11	THR	2.5
26	DB	58	A	2.5
42	BW	105	VAL	2.5
44	BY	37	VAL	2.5
52	D6	5	VAL	2.5
31	DH	104	GLU	2.5
40	DU	89	GLU	2.5
16	CP	74	LEU	2.5
41	BV	39	LEU	2.5
1	AA	1446	U	2.5
13	AM	87	TYR	2.5
54	D8	10	ALA	2.5
3	CC	39	ILE	2.5
12	CL	7	ILE	2.5
35	BP	79	ARG	2.5
25	BA	2164	C	2.5
40	DU	88	ILE	2.5
13	CM	106	ASN	2.5
14	AN	25	VAL	2.5
19	CS	8	GLY	2.5
29	BF	16	GLY	2.5
20	AT	74	LYS	2.5
38	DS	28	VAL	2.5
39	DT	10	VAL	2.5
2	CB	44	LEU	2.5
7	AG	99	LEU	2.5
29	BF	156	LEU	2.5
31	DH	88	LEU	2.5
32	BI	128	LEU	2.5
39	DT	78	LEU	2.5
46	D0	59	LEU	2.5
1	CA	204	U	2.4
3	AC	7	PRO	2.4
13	CM	92	HIS	2.4
3	AC	203	PHE	2.4
30	BG	169	ALA	2.4
30	DG	118	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
11	AK	32	ILE	2.4
27	DD	105	ILE	2.4
29	DF	28	ILE	2.4
31	BH	151	ILE	2.4
18	AR	57	GLY	2.4
3	CC	207	VAL	2.4
19	CS	58	VAL	2.4
27	DD	221	VAL	2.4
32	BI	93	THR	2.4
35	DP	95	VAL	2.4
30	BG	107	LEU	2.4
30	BG	120	LEU	2.4
37	DR	18	LEU	2.4
51	D5	26	THR	2.4
25	DA	2110	G	2.4
47	D1	38	SER	2.4
4	CD	49	ARG	2.4
25	BA	2192	A	2.4
36	BQ	29	PHE	2.4
9	CI	106	ALA	2.4
10	CJ	57	LYS	2.4
44	BY	65	ALA	2.4
4	AD	180	GLY	2.4
8	CH	111	ILE	2.4
4	AD	178	VAL	2.4
36	DQ	132	VAL	2.4
1	CA	1149	C	2.4
1	CA	1325	C	2.4
19	CS	36	ARG	2.4
12	AL	91	LYS	2.4
11	CK	125	PHE	2.4
27	DD	67	PHE	2.4
41	DV	75	PHE	2.4
1	CA	1036	G	2.4
1	CA	1220	G	2.4
9	AI	46	ALA	2.4
9	CI	43	ALA	2.4
25	BA	2843	G	2.4
32	DI	34	GLY	2.4
10	CJ	24	VAL	2.4
14	AN	56	VAL	2.4
17	AQ	9	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
32	DI	9	LEU	2.4
35	BP	3	LEU	2.4
36	DQ	109	VAL	2.4
40	BU	39	LEU	2.4
13	CM	110	ARG	2.4
33	DN	73	THR	2.4
3	CC	20	SER	2.4
29	BF	10	PRO	2.4
25	BA	2186	C	2.4
3	AC	148	GLY	2.4
2	CB	198	ASP	2.4
3	CC	146	ALA	2.4
4	CD	5	ILE	2.4
28	BE	6	GLY	2.4
29	DF	206	ILE	2.4
33	DN	41	ASP	2.4
1	CA	1001(A)	G	2.4
2	AB	196	LEU	2.4
4	CD	3	ARG	2.4
4	CD	148	VAL	2.4
9	CI	51	ARG	2.4
9	CI	107	ARG	2.4
18	AR	40	LEU	2.4
29	BF	157	VAL	2.4
29	DF	41	LEU	2.4
37	DR	113	LEU	2.4
42	BW	59	VAL	2.4
42	DW	19	LEU	2.4
45	DZ	58	VAL	2.4
3	AC	6	HIS	2.4
14	AN	14	PRO	2.4
54	D8	2	PRO	2.4
36	BQ	15	GLY	2.4
4	CD	67	ILE	2.4
13	CM	16	ASP	2.4
17	CQ	36	ILE	2.4
30	DG	114	ILE	2.4
36	DQ	138	ASP	2.4
43	BX	8	ILE	2.4
2	CB	8	LYS	2.4
3	CC	29	TYR	2.4
4	CD	20	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
9	AI	42	ARG	2.4
2	AB	81	VAL	2.4
14	AN	44	LEU	2.4
16	CP	20	VAL	2.4
19	CS	30	LEU	2.4
20	AT	84	LEU	2.4
29	BF	20	LEU	2.4
37	DR	76	VAL	2.4
38	BS	48	LEU	2.4
45	BZ	139	VAL	2.4
50	B4	53	GLU	2.4
25	BA	2191	A	2.4
1	CA	1156	G	2.4
17	AQ	79	SER	2.4
7	CG	133	GLY	2.4
5	AE	101	ILE	2.4
42	BW	103	ILE	2.4
43	DX	1	MET	2.4
44	DY	46	LYS	2.4
7	CG	119	ARG	2.4
2	AB	61	LEU	2.4
20	AT	53	LEU	2.4
44	BY	67	LEU	2.4
44	DY	31	LEU	2.4
29	DF	126	VAL	2.4
33	BN	9	VAL	2.4
55	B9	25	VAL	2.4
25	BA	1555	C	2.4
3	CC	145	GLY	2.4
4	AD	127	THR	2.4
5	CE	145	LYS	2.4
9	CI	127	LYS	2.4
28	BE	64	LYS	2.4
37	DR	35	THR	2.4
38	DS	31	SER	2.4
39	DT	59	THR	2.4
42	DW	13	SER	2.4
45	DZ	12	GLY	2.4
2	AB	160	ASP	2.4
9	CI	105	ASP	2.4
25	DA	1026	U	2.4
31	DH	121	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
3	CC	61	ALA	2.4
14	AN	2	ALA	2.4
17	AQ	24	GLU	2.4
31	DH	119	GLU	2.4
41	DV	1	MET	2.4
12	AL	93	LEU	2.4
29	BF	124	LEU	2.4
50	B4	43	TYR	2.4
9	CI	108	VAL	2.4
31	BH	115	VAL	2.4
39	BT	104	ASN	2.4
42	DW	85	VAL	2.4
42	DW	105	VAL	2.4
10	CJ	56	HIS	2.4
2	CB	231	GLU	2.4
25	BA	2152	U	2.4
38	DS	18	ILE	2.4
2	CB	237	ALA	2.4
13	AM	30	ALA	2.4
20	CT	59	ALA	2.4
2	AB	71	VAL	2.3
9	AI	41	VAL	2.3
32	BI	37	VAL	2.3
35	DP	108	LYS	2.3
36	BQ	81	VAL	2.3
43	DX	54	VAL	2.3
3	CC	108	ASN	2.3
34	BO	49	ARG	2.3
35	DP	111	ARG	2.3
45	BZ	122	ARG	2.3
5	CE	29	GLY	2.3
10	CJ	93	GLY	2.3
45	DZ	104	PHE	2.3
50	D4	53	GLU	2.3
1	CA	1240	U	2.3
4	CD	134	ASP	2.3
16	AP	15	PRO	2.3
50	D4	27	THR	2.3
19	AS	30	LEU	2.3
29	DF	181	LEU	2.3
31	BH	85	LYS	2.3
31	BH	103	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
32	BI	68	LEU	2.3
34	BO	46	ALA	2.3
35	DP	3	LEU	2.3
38	DS	73	LEU	2.3
44	BY	1	MET	2.3
44	BY	36	ALA	2.3
44	DY	106	LEU	2.3
47	B1	97	LEU	2.3
54	D8	29	LYS	2.3
1	CA	965	A	2.3
12	CL	101	VAL	2.3
30	BG	160	VAL	2.3
41	DV	22	VAL	2.3
29	BF	18	ARG	2.3
46	B0	6	GLY	2.3
1	CA	1026	G	2.3
2	CB	113	HIS	2.3
7	CG	112	PRO	2.3
13	AM	63	THR	2.3
33	BN	16	ILE	2.3
39	BT	52	ILE	2.3
49	D3	20	LYS	2.3
9	CI	119	ALA	2.3
11	CK	89	ALA	2.3
25	DA	277	C	2.3
25	DA	2794	C	2.3
7	CG	44	TYR	2.3
2	CB	7	VAL	2.3
3	CC	138	VAL	2.3
10	CJ	45	ARG	2.3
33	BN	14	VAL	2.3
44	DY	50	ARG	2.3
4	AD	109	GLY	2.3
13	CM	95	GLY	2.3
27	DD	128	GLY	2.3
35	DP	94	GLU	2.3
10	CJ	17	ASP	2.3
13	CM	103	THR	2.3
30	DG	152	LEU	2.3
42	DW	107	LEU	2.3
25	DA	2144	U	2.3
10	AJ	20	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
11	AK	68	ALA	2.3
13	AM	3	ARG	2.3
13	AM	71	ARG	2.3
16	AP	42	ARG	2.3
30	DG	128	ARG	2.3
33	DN	114	ARG	2.3
11	AK	117	ASN	2.3
25	DA	2164	C	2.3
36	DQ	27	VAL	2.3
43	DX	2	LYS	2.3
55	B9	15	LYS	2.3
25	BA	1935	A	2.3
7	CG	33	ASP	2.3
27	DD	215	LEU	2.3
28	DE	4	ILE	2.3
2	CB	144	ARG	2.3
3	AC	172	ARG	2.3
20	AT	86	ARG	2.3
30	DG	60	LEU	2.3
35	DP	134	ALA	2.3
37	BR	95	THR	2.3
45	DZ	51	ALA	2.3
51	D5	29	THR	2.3
2	CB	31	TYR	2.3
2	CB	229	VAL	2.3
5	CE	47	LYS	2.3
9	AI	44	VAL	2.3
36	DQ	137	TYR	2.3
43	DX	81	VAL	2.3
45	DZ	86	VAL	2.3
45	DZ	128	VAL	2.3
25	BA	2147	G	2.3
25	BA	2163	G	2.3
25	DA	100	G	2.3
2	AB	208	ILE	2.3
7	AG	120	ILE	2.3
14	AN	39	LEU	2.3
17	AQ	6	LEU	2.3
17	CQ	29	HIS	2.3
19	CS	15	LEU	2.3
20	AT	36	LEU	2.3
20	CT	80	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
27	BD	33	LEU	2.3
28	BE	176	ILE	2.3
30	DG	111	LEU	2.3
31	DH	162	ILE	2.3
32	DI	138	ILE	2.3
38	BS	32	LEU	2.3
40	BU	109	LEU	2.3
41	DV	4	ILE	2.3
45	BZ	120	ILE	2.3
45	BZ	123	ASP	2.3
2	CB	48	MET	2.3
20	CT	38	LYS	2.3
46	B0	2	ALA	2.3
11	AK	56	GLY	2.3
17	AQ	73	VAL	2.3
29	BF	37	VAL	2.3
29	DF	147	GLY	2.3
43	BX	43	VAL	2.3
9	AI	37	PHE	2.3
44	DY	43	ASN	2.3
7	CG	76	ARG	2.3
30	DG	181	ARG	2.3
53	B7	41	ARG	2.3
10	AJ	50	ILE	2.3
15	CO	70	LEU	2.3
25	BA	2153	G	2.3
25	BA	2197	C	2.3
30	DG	103	LEU	2.3
33	BN	26	LEU	2.3
37	DR	65	LEU	2.3
40	DU	39	LEU	2.3
51	D5	58	LEU	2.3
7	CG	86	GLN	2.3
55	D9	8	LYS	2.3
35	DP	97	PRO	2.3
4	AD	20	TYR	2.3
9	AI	4	TYR	2.3
11	CK	49	GLY	2.3
12	CL	64	TYR	2.3
28	BE	7	VAL	2.3
42	DW	17	VAL	2.3
50	B4	67	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
45	BZ	88	PHE	2.3
2	CB	94	ASN	2.3
3	AC	188	LEU	2.3
29	BF	192	LEU	2.3
33	DN	112	LEU	2.3
35	DP	74	GLU	2.3
42	DW	6	ILE	2.3
48	D2	53	LEU	2.3
55	D9	26	ILE	2.3
11	AK	17	GLY	2.3
25	BA	696	C	2.3
18	AR	67	ALA	2.3
25	DA	614(B)	G	2.3
25	DA	2804	C	2.3
36	DQ	108	GLY	2.3
39	BT	94	ALA	2.3
55	D9	37	GLY	2.3
3	AC	116	VAL	2.3
5	CE	69	VAL	2.3
19	AS	9	VAL	2.3
28	BE	173	VAL	2.3
31	BH	144	VAL	2.3
31	DH	114	VAL	2.3
39	DT	22	PHE	2.3
44	BY	3	VAL	2.3
44	BY	7	VAL	2.3
44	DY	72	VAL	2.3
2	CB	53	ARG	2.3
9	CI	78	LYS	2.2
20	AT	9	ASN	2.2
44	BY	71	LYS	2.2
29	BF	56	GLU	2.2
2	CB	205	ASP	2.2
5	AE	91	LEU	2.2
7	CG	13	GLN	2.2
45	BZ	45	ASP	2.2
48	D2	56	GLN	2.2
39	DT	80	SER	2.2
45	BZ	166	SER	2.2
4	AD	136	PRO	2.2
8	CH	5	PRO	2.2
3	CC	189	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
8	CH	124	ALA	2.2
8	CH	61	VAL	2.2
20	AT	83	ARG	2.2
33	DN	72	TYR	2.2
41	DV	79	VAL	2.2
48	D2	29	LYS	2.2
28	BE	73	GLU	2.2
25	DA	2802	G	2.2
2	CB	180	LEU	2.2
3	AC	36	ASP	2.2
12	CL	10	LEU	2.2
16	CP	49	LEU	2.2
45	DZ	50	GLN	2.2
45	DZ	144	LEU	2.2
51	B5	58	LEU	2.2
8	CH	38	ILE	2.2
27	DD	204	ILE	2.2
33	DN	16	ILE	2.2
42	DW	95	ILE	2.2
4	CD	152	SER	2.2
2	AB	232	PRO	2.2
6	CF	89	MET	2.2
14	AN	17	LYS	2.2
20	CT	25	ARG	2.2
29	DF	150	GLY	2.2
45	DZ	79	ARG	2.2
3	AC	186	PHE	2.2
12	AL	32	PHE	2.2
36	BQ	65	PHE	2.2
36	BQ	106	VAL	2.2
40	BU	96	ALA	2.2
42	DW	3	ALA	2.2
3	AC	175	LEU	2.2
3	CC	175	LEU	2.2
19	CS	5	LEU	2.2
25	BA	2150	C	2.2
37	BR	18	LEU	2.2
40	BU	98	LEU	2.2
20	AT	55	ILE	2.2
1	CA	973	G	2.2
2	AB	109	SER	2.2
9	AI	24	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
13	AM	102	ARG	2.2
29	BF	13	SER	2.2
46	D0	52	GLY	2.2
49	D3	16	PRO	2.2
2	AB	105	PHE	2.2
3	CC	151	VAL	2.2
13	CM	75	ALA	2.2
14	CN	16	PHE	2.2
17	CQ	35	VAL	2.2
20	AT	66	ALA	2.2
28	BE	102	VAL	2.2
32	DI	46	ALA	2.2
35	BP	105	LEU	2.2
45	DZ	118	GLN	2.2
19	CS	6	LYS	2.2
52	D6	34	LEU	2.2
7	CG	120	ILE	2.2
28	DE	77	ILE	2.2
44	DY	38	ILE	2.2
25	DA	2146	C	2.2
30	DG	87	PRO	2.2
25	DA	2801(A)	A	2.2
3	CC	60	ALA	2.2
3	CC	149	ALA	2.2
6	CF	9	VAL	2.2
11	CK	14	VAL	2.2
42	BW	32	ALA	2.2
3	AC	135	LYS	2.2
4	AD	68	TYR	2.2
16	CP	39	TYR	2.2
7	CG	59	LEU	2.2
33	BN	112	LEU	2.2
35	DP	112	LEU	2.2
3	AC	179	ARG	2.2
43	DX	3	THR	2.2
32	BI	138	ILE	2.2
42	DW	106	ILE	2.2
44	BY	2	ARG	2.2
2	AB	228	GLY	2.2
19	AS	57	HIS	2.2
46	B0	76	GLY	2.2
50	D4	34	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
2	CB	194	PRO	2.2
29	BF	194	MET	2.2
3	CC	66	VAL	2.2
11	CK	51	LYS	2.2
12	CL	68	ALA	2.2
4	AD	115	ARG	2.2
28	DE	181	LEU	2.2
29	DF	191	ARG	2.2
30	DG	62	LEU	2.2
35	DP	106	LEU	2.2
36	DQ	37	LEU	2.2
49	D3	30	ARG	2.2
46	D0	71	ASP	2.2
9	AI	6	GLY	2.2
20	AT	63	ILE	2.2
28	DE	26	ILE	2.2
34	DO	2	ILE	2.2
41	BV	41	GLY	2.2
41	BV	99	ILE	2.2
42	BW	106	ILE	2.2
45	BZ	97	GLU	2.2
44	DY	47	LYS	2.2
45	BZ	167	PRO	2.2
1	AA	1027	C	2.2
3	CC	30	ARG	2.2
5	CE	105	VAL	2.2
9	AI	94	ALA	2.2
14	CN	52	GLN	2.2
16	AP	18	ARG	2.2
17	AQ	85	VAL	2.2
29	BF	105	VAL	2.2
31	DH	42	ARG	2.2
37	DR	71	GLN	2.2
44	DY	3	VAL	2.2
29	BF	110	LEU	2.2
35	DP	100	LEU	2.2
37	DR	70	LEU	2.2
3	CC	58	GLU	2.2
45	DZ	9	TYR	2.2
4	AD	126	ILE	2.2
15	AO	3	ILE	2.2
19	AS	31	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
36	BQ	108	GLY	2.2
44	DY	75	ILE	2.2
7	CG	24	THR	2.2
13	CM	105	THR	2.2
14	CN	50	LYS	2.2
36	DQ	41	TRP	2.2
4	CD	165	MET	2.2
51	D5	27	PRO	2.2
34	BO	17	ARG	2.2
4	AD	128	VAL	2.2
13	CM	118	ALA	2.2
27	DD	98	VAL	2.2
33	DN	103	VAL	2.2
36	DQ	55	VAL	2.2
33	DN	15	LEU	2.2
36	BQ	34	LEU	2.2
49	D3	51	ALA	2.2
10	CJ	73	ASP	2.2
17	AQ	87	LYS	2.2
30	BG	63	ILE	2.2
37	DR	83	ILE	2.2
41	DV	67	GLY	2.2
46	D0	19	LYS	2.2
19	CS	48	THR	2.2
36	BQ	129	THR	2.2
1	CA	1236	A	2.1
3	AC	167	TRP	2.1
13	AM	64	TRP	2.1
19	CS	78	ARG	2.1
33	BN	48	MET	2.1
51	D5	28	PRO	2.1
2	AB	13	ALA	2.1
2	AB	184	VAL	2.1
3	AC	120	VAL	2.1
17	CQ	84	LEU	2.1
25	DA	2793	G	2.1
28	BE	63	LEU	2.1
37	DR	67	LEU	2.1
42	BW	69	LEU	2.1
17	CQ	42	TYR	2.1
36	BQ	32	TYR	2.1
42	DW	49	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
50	D4	8	LYS	2.1
42	DW	35	ILE	2.1
55	D9	10	ILE	2.1
25	BA	2201	C	2.1
3	CC	179	ARG	2.1
28	DE	24	THR	2.1
39	DT	79	HIS	2.1
20	CT	37	SER	2.1
40	DU	79	PHE	2.1
10	CJ	39	PRO	2.1
19	CS	34	TRP	2.1
48	D2	27	GLU	2.1
4	CD	18	LYS	2.1
13	AM	115	LYS	2.1
25	BA	2195	A	2.1
35	DP	76	LYS	2.1
6	CF	90	VAL	2.1
9	CI	44	VAL	2.1
47	D1	98	LEU	2.1
10	CJ	20	ALA	2.1
32	BI	84	GLY	2.1
45	BZ	106	GLY	2.1
1	AA	104	G	2.1
2	AB	162	ILE	2.1
9	CI	77	ILE	2.1
10	CJ	78	ASN	2.1
20	AT	33	ILE	2.1
25	BA	2190	G	2.1
26	DB	119	G	2.1
45	BZ	171	ILE	2.1
15	CO	77	ARG	2.1
15	CO	88	ARG	2.1
40	DU	64	ARG	2.1
50	D4	48	ARG	2.1
2	AB	55	PHE	2.1
29	BF	203	GLN	2.1
35	BP	98	GLU	2.1
51	D5	44	THR	2.1
25	DA	34	C	2.1
5	AE	119	LEU	2.1
10	CJ	88	LEU	2.1
36	BQ	83	MET	2.1

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Mol	Chain	Res	Type	RSRZ
27	DD	117	VAL	2.1
28	DE	175	VAL	2.1
29	BF	173	VAL	2.1
33	BN	5	VAL	2.1
40	DU	95	LEU	2.1
48	D2	6	VAL	2.1
20	AT	67	ALA	2.1
28	DE	20	ALA	2.1
38	DS	42	ASP	2.1
2	AB	31	TYR	2.1
11	CK	29	ILE	2.1
37	BR	21	TYR	2.1
41	DV	96	ILE	2.1
42	BW	95	ILE	2.1
14	CN	9	LYS	2.1
20	CT	30	LYS	2.1
9	CI	38	GLN	2.1
1	AA	1024	G	2.1
14	AN	16	PHE	2.1
8	CH	113	SER	2.1
3	AC	204	LEU	2.1
10	CJ	53	PRO	2.1
32	DI	72	LEU	2.1
3	CC	171	GLY	2.1
7	CG	75	VAL	2.1
12	AL	101	VAL	2.1
28	BE	47	VAL	2.1
32	DI	81	VAL	2.1
33	DN	46	VAL	2.1
35	BP	126	VAL	2.1
36	BQ	132	VAL	2.1
45	BZ	86	VAL	2.1
10	CJ	18	ALA	2.1
12	CL	89	ARG	2.1
30	DG	116	ASP	2.1
31	DH	152	ARG	2.1
38	DS	88	ASP	2.1
3	CC	134	ILE	2.1
4	CD	156	GLU	2.1
40	DU	80	ILE	2.1
38	DS	38	GLN	2.1
45	DZ	89	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
4	CD	64	LEU	2.1
9	AI	64	THR	2.1
9	AI	126	SER	2.1
45	DZ	142	SER	2.1
33	DN	107	LEU	2.1
49	D3	28	LEU	2.1
53	B7	24	THR	2.1
28	BE	184	VAL	2.1
30	DG	149	VAL	2.1
31	BH	41	MET	2.1
36	DQ	6	ARG	2.1
37	DR	38	VAL	2.1
45	BZ	141	VAL	2.1
53	D7	1	MET	2.1
46	D0	77	ARG	2.1
54	D8	20	GLY	2.1
4	AD	173	TRP	2.1
25	DA	2125	G	2.1
11	AK	92	GLU	2.1
29	DF	111	ALA	2.1
30	DG	74	LYS	2.1
44	BY	29	GLU	2.1
47	D1	78	LYS	2.1
48	B2	13	ALA	2.1
16	AP	32	TYR	2.1
32	BI	109	ILE	2.1
35	BP	68	GLN	2.1
35	DP	81	GLN	2.1
1	AA	152	A	2.1
40	DU	57	PHE	2.1
27	BD	95	LEU	2.1
27	DD	94	LEU	2.1
30	DG	82	LEU	2.1
2	AB	114	ARG	2.1
2	AB	190	THR	2.1
10	CJ	28	ARG	2.1
11	CK	57	THR	2.1
27	DD	35	LYS	2.1
31	DH	108	GLY	2.1
31	DH	129	THR	2.1
43	DX	50	LYS	2.1
7	AG	23	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
15	CO	60	VAL	2.1
27	BD	79	VAL	2.1
27	DD	142	VAL	2.1
43	DX	23	GLU	2.1
36	BQ	136	ALA	2.1
41	BV	3	ALA	2.1
41	DV	81	TYR	2.1
44	BY	38	ILE	2.1
45	BZ	146	ILE	2.1
1	AA	1026	G	2.1
1	AA	1034	G	2.1
25	DA	10	G	2.1
16	AP	80	PHE	2.1
18	AR	43	PHE	2.1
20	CT	16	HIS	2.1
25	BA	2210	C	2.1
25	DA	2145	C	2.1
20	AT	13	LEU	2.1
28	BE	3	GLY	2.1
29	DF	170	LEU	2.1
31	BH	42	ARG	2.1
36	DQ	133	ARG	2.1
37	BR	42	LYS	2.1
10	AJ	97	GLU	2.1
3	AC	67	THR	2.1
11	AK	57	THR	2.1
12	CL	55	VAL	2.1
36	DQ	96	VAL	2.1
3	CC	160	ALA	2.1
20	CT	32	ALA	2.1
5	CE	88	LYS	2.1
31	BH	13	LYS	2.1
33	DN	66	LYS	2.1
50	B4	20	ASN	2.1
54	D8	47	LYS	2.1
2	AB	96	ARG	2.1
2	AB	144	ARG	2.1
2	CB	87	ARG	2.1
15	CO	54	ARG	2.1
2	AB	227	GLY	2.1
8	CH	71	GLY	2.1
29	BF	12	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
30	DG	177	GLY	2.1
32	DI	116	LEU	2.1
25	DA	2166	G	2.1
2	CB	219	VAL	2.0
6	CF	91	VAL	2.0
9	AI	105	ASP	2.0
13	CM	41	PRO	2.0
27	BD	127	VAL	2.0
32	DI	145	VAL	2.0
35	DP	71	VAL	2.0
45	DZ	130	PRO	2.0
14	CN	13	THR	2.0
13	CM	76	ALA	2.0
25	DA	2132	U	2.0
27	DD	24	ILE	2.0
28	DE	48	GLN	2.0
28	DE	197	ILE	2.0
32	BI	115	ALA	2.0
40	DU	21	ALA	2.0
3	CC	150	LYS	2.0
43	DX	39	ILE	2.0
2	AB	111	ARG	2.0
7	AG	37	ASN	2.0
29	BF	106	ARG	2.0
35	DP	130	PHE	2.0
37	DR	105	ARG	2.0
8	CH	39	LEU	2.0
32	BI	77	LEU	2.0
37	BR	44	LEU	2.0
40	BU	83	LEU	2.0
49	D3	23	LEU	2.0
7	CG	77	SER	2.0
29	BF	15	SER	2.0
32	BI	91	SER	2.0
5	AE	82	VAL	2.0
7	CG	105	VAL	2.0
25	BA	935	C	2.0
28	BE	32	PRO	2.0
28	DE	11	MET	2.0
29	BF	183	VAL	2.0
31	DH	76	VAL	2.0
32	BI	145	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
37	BR	48	VAL	2.0
42	DW	10	VAL	2.0
43	DX	51	VAL	2.0
13	CM	63	THR	2.0
21	CU	17	THR	2.0
44	DY	95	LYS	2.0
50	D4	47	GLN	2.0
2	CB	185	ILE	2.0
14	AN	48	ALA	2.0
18	AR	70	ILE	2.0
25	BA	1072	U	2.0
32	DI	88	ILE	2.0
33	DN	18	ALA	2.0
45	DZ	173	ALA	2.0
54	B8	24	ALA	2.0
4	AD	141	ARG	2.0
26	DB	25	A	2.0
36	BQ	133	ARG	2.0
28	DE	96	PHE	2.0
29	BF	27	GLU	2.0
44	DY	29	GLU	2.0
2	CB	99	GLY	2.0
4	CD	186	LEU	2.0
10	AJ	40	LEU	2.0
39	DT	6	LEU	2.0
45	DZ	143	GLY	2.0
47	D1	22	GLY	2.0
2	AB	63	MET	2.0
7	AG	21	VAL	2.0
9	CI	86	VAL	2.0
37	BR	49	ASP	2.0
42	DW	76	VAL	2.0
47	B1	49	VAL	2.0
49	D3	33	GLN	2.0
51	B5	28	PRO	2.0
54	D8	22	VAL	2.0
55	B9	16	VAL	2.0
55	B9	30	PRO	2.0
2	CB	47	THR	2.0
20	CT	33	ILE	2.0
27	DD	52	ARG	2.0
29	DF	51	THR	2.0

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Mol	Chain	Res	Type	RSRZ
30	DG	170	ARG	2.0
3	AC	206	GLU	2.0
39	DT	94	ALA	2.0
50	B4	34	GLU	2.0
27	DD	104	TYR	2.0
37	DR	87	TYR	2.0
42	DW	75	TYR	2.0
18	AR	66	LEU	2.0
20	CT	36	LEU	2.0
25	DA	2135	A	2.0
29	BF	199	TRP	2.0
33	DN	13	TRP	2.0
11	CK	71	LYS	2.0
35	DP	47	ASP	2.0
3	CC	198	VAL	2.0
27	DD	79	VAL	2.0
28	BE	23	VAL	2.0
37	DR	39	PRO	2.0
40	DU	2	PRO	2.0
44	DY	24	VAL	2.0
50	B4	61	ARG	2.0
27	DD	271	ILE	2.0
29	BF	167	ALA	2.0
40	BU	68	ALA	2.0
1	AA	1452	C	2.0
3	AC	185	GLY	2.0
10	AJ	8	LEU	2.0
17	CQ	14	LYS	2.0
25	BA	2130	C	2.0
25	BA	2905	C	2.0
27	DD	220	HIS	2.0
30	BG	19	LEU	2.0
36	DQ	23	GLY	2.0
45	BZ	54	HIS	2.0
48	D2	32	LEU	2.0

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

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

of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
24	PSU	CX	55	20/21	0.12	-	59,68,84,85	0
24	5MC	CX	32	21/22	0.13	-	52,69,78,83	0
23	PPU	CW	76	37/38	0.26	-	31,50,63,70	0
24	5MU	CX	54	21/22	0.18	-	66,78,87,98	0
24	4SU	AX	8	20/21	0.16	-	50,63,78,79	0
24	5MU	AX	54	21/22	0.14	-	55,69,75,82	0
24	4SU	CX	8	20/21	0.14	-	65,84,90,94	0
24	5MC	AX	32	21/22	0.15	-	46,61,70,75	0
24	31H	AX	76	32/33	0.26	-	27,44,76,98	0
23	PPU	AW	76	37/38	0.22	-	25,33,43,45	0
24	PSU	AX	55	20/21	0.14	-	57,66,78,79	0
24	31H	CX	76	32/33	0.26	-	33,54,78,89	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
56	MG	DA	3590	1/1	0.31	-	38,38,38,38	0
56	MG	BA	3293	1/1	0.12	-	17,17,17,17	0
56	MG	CA	3057	1/1	0.13	-	41,41,41,41	0
56	MG	BA	3185	1/1	0.16	-	43,43,43,43	0
56	MG	DA	3528	1/1	0.05	-	37,37,37,37	0
56	MG	DA	3339	1/1	0.12	-	32,32,32,32	0
56	MG	BA	3436	1/1	0.10	-	35,35,35,35	0
56	MG	BG	3002	1/1	0.09	-	27,27,27,27	0
56	MG	DA	3455	1/1	0.17	-	45,45,45,45	0
56	MG	DA	3084	1/1	0.21	-	39,39,39,39	0
56	MG	DA	3351	1/1	0.11	-	46,46,46,46	0
56	MG	CA	3052	1/1	0.10	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3320	1/1	0.07	-	46,46,46,46	0
56	MG	BA	3551	1/1	0.09	-	48,48,48,48	0
56	MG	DA	3553	1/1	0.11	-	46,46,46,46	0
56	MG	AA	3186	1/1	0.11	-	55,55,55,55	0
56	MG	DA	3244	1/1	0.13	-	48,48,48,48	0
56	MG	BA	3188	1/1	0.14	-	39,39,39,39	0
56	MG	CA	3017	1/1	0.11	-	41,41,41,41	0
56	MG	BA	3553	1/1	0.67	-	48,48,48,48	0
56	MG	DA	3238	1/1	0.15	-	42,42,42,42	0
56	MG	DA	3293	1/1	0.15	-	34,34,34,34	0
56	MG	DA	3178	1/1	0.25	-	46,46,46,46	0
56	MG	BA	3113	1/1	0.14	-	41,41,41,41	0
56	MG	BA	3351	1/1	0.09	-	33,33,33,33	0
56	MG	B7	3003	1/1	0.23	-	28,28,28,28	0
56	MG	BA	3447	1/1	0.14	-	55,55,55,55	0
56	MG	CA	3092	1/1	0.12	-	54,54,54,54	0
56	MG	BA	3361	1/1	0.09	-	45,45,45,45	0
56	MG	DA	3379	1/1	0.08	-	26,26,26,26	0
56	MG	BA	3332	1/1	0.10	-	61,61,61,61	0
56	MG	BA	3423	1/1	0.12	-	47,47,47,47	0
56	MG	DA	3059	1/1	0.12	-	33,33,33,33	0
56	MG	BA	3217	1/1	0.23	-	29,29,29,29	0
56	MG	BA	3424	1/1	0.16	-	38,38,38,38	0
56	MG	CA	3154	1/1	0.14	-	62,62,62,62	0
56	MG	BB	3014	1/1	0.17	-	35,35,35,35	0
56	MG	CA	3005	1/1	0.10	-	42,42,42,42	0
56	MG	DA	3436	1/1	0.09	-	27,27,27,27	0
56	MG	BA	3474	1/1	0.16	-	53,53,53,53	0
56	MG	DA	3542	1/1	0.12	-	30,30,30,30	0
56	MG	CA	3125	1/1	0.23	-	71,71,71,71	0
56	MG	AF	3001	1/1	0.13	-	52,52,52,52	0
56	MG	CA	3114	1/1	0.06	-	80,80,80,80	0
56	MG	DA	3002	1/1	0.11	-	33,33,33,33	0
56	MG	DA	3425	1/1	0.13	-	37,37,37,37	0
56	MG	CA	3006	1/1	0.30	-	37,37,37,37	0
56	MG	DA	3415	1/1	0.18	-	40,40,40,40	0
56	MG	DA	3394	1/1	0.16	-	41,41,41,41	0
56	MG	BA	3240	1/1	0.26	-	43,43,43,43	0
56	MG	DA	3111	1/1	0.18	-	39,39,39,39	0
56	MG	DA	3120	1/1	0.20	-	33,33,33,33	0
56	MG	BA	3247	1/1	0.18	-	48,48,48,48	0
56	MG	DA	3108	1/1	0.09	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3058	1/1	0.25	-	45,45,45,45	0
56	MG	BA	3357	1/1	0.11	-	30,30,30,30	0
56	MG	BA	3629	1/1	0.17	-	60,60,60,60	0
56	MG	BA	3318	1/1	0.10	-	44,44,44,44	0
56	MG	BA	3655	1/1	0.12	-	18,18,18,18	0
56	MG	BA	3239	1/1	0.12	-	52,52,52,52	0
56	MG	BA	3146	1/1	0.16	-	31,31,31,31	0
56	MG	BA	3360	1/1	0.14	-	21,21,21,21	0
56	MG	CA	3103	1/1	0.12	-	52,52,52,52	0
56	MG	AA	3151	1/1	0.18	-	45,45,45,45	0
56	MG	DA	3540	1/1	0.11	-	46,46,46,46	0
56	MG	BB	3010	1/1	0.15	-	77,77,77,77	0
56	MG	DA	3044	1/1	0.11	-	47,47,47,47	0
56	MG	BA	3440	1/1	0.05	-	38,38,38,38	0
56	MG	DA	3081	1/1	0.11	-	44,44,44,44	0
56	MG	AA	3008	1/1	0.52	-	55,55,55,55	0
56	MG	AA	3034	1/1	0.18	-	54,54,54,54	0
56	MG	BA	3513	1/1	0.12	-	60,60,60,60	0
56	MG	BB	3015	1/1	0.15	-	48,48,48,48	0
56	MG	BA	3057	1/1	0.12	-	38,38,38,38	0
56	MG	CA	3112	1/1	0.11	-	55,55,55,55	0
56	MG	DA	3007	1/1	0.08	-	39,39,39,39	0
56	MG	DA	3290	1/1	0.09	-	36,36,36,36	0
56	MG	DA	3032	1/1	0.11	-	42,42,42,42	0
56	MG	DA	3441	1/1	0.12	-	45,45,45,45	0
56	MG	BA	3316	1/1	0.08	-	61,61,61,61	0
56	MG	BA	3523	1/1	0.08	-	50,50,50,50	0
56	MG	BA	3618	1/1	0.19	-	54,54,54,54	0
56	MG	DA	3532	1/1	0.06	-	51,51,51,51	0
56	MG	AA	3041	1/1	0.16	-	52,52,52,52	0
56	MG	DA	3266	1/1	0.11	-	46,46,46,46	0
56	MG	AA	3022	1/1	0.07	-	39,39,39,39	0
56	MG	CA	3123	1/1	0.15	-	66,66,66,66	0
56	MG	B0	105	1/1	0.10	-	43,43,43,43	0
56	MG	DA	3573	1/1	0.14	-	45,45,45,45	0
56	MG	AA	3125	1/1	0.19	-	41,41,41,41	0
56	MG	DA	3062	1/1	0.19	-	42,42,42,42	0
56	MG	BP	204	1/1	0.28	-	31,31,31,31	0
56	MG	BX	102	1/1	0.37	-	38,38,38,38	0
56	MG	AA	3137	1/1	0.09	-	79,79,79,79	0
56	MG	BE	302	1/1	0.71	-	36,36,36,36	0
56	MG	BA	3366	1/1	0.06	-	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AA	3039	1/1	0.09	-	45,45,45,45	0
56	MG	DA	3074	1/1	0.12	-	29,29,29,29	0
56	MG	DA	3153	1/1	0.13	-	42,42,42,42	0
56	MG	BA	3104	1/1	0.20	-	42,42,42,42	0
56	MG	BA	3174	1/1	0.09	-	29,29,29,29	0
56	MG	DA	3443	1/1	0.08	-	49,49,49,49	0
56	MG	BA	3646	1/1	0.10	-	23,23,23,23	0
56	MG	BA	3092	1/1	0.21	-	44,44,44,44	0
56	MG	DA	3110	1/1	0.14	-	42,42,42,42	0
56	MG	DA	3519	1/1	0.06	-	42,42,42,42	0
56	MG	BA	3624	1/1	0.28	-	49,49,49,49	0
56	MG	DA	3145	1/1	0.12	-	31,31,31,31	0
56	MG	DA	3413	1/1	0.15	-	24,24,24,24	0
56	MG	BR	3002	1/1	0.18	-	23,23,23,23	0
56	MG	CA	3108	1/1	0.14	-	59,59,59,59	0
56	MG	DA	3303	1/1	0.06	-	43,43,43,43	0
56	MG	BA	3526	1/1	0.22	-	25,25,25,25	0
56	MG	DA	3071	1/1	0.26	-	36,36,36,36	0
56	MG	DA	3240	1/1	0.13	-	54,54,54,54	0
56	MG	DA	3232	1/1	0.10	-	38,38,38,38	0
56	MG	AA	3178	1/1	0.27	-	62,62,62,62	0
56	MG	DA	3254	1/1	0.06	-	46,46,46,46	0
56	MG	AM	3001	1/1	0.13	-	54,54,54,54	0
56	MG	DA	3182	1/1	0.11	-	38,38,38,38	0
56	MG	BA	3065	1/1	0.16	-	29,29,29,29	0
56	MG	DA	3515	1/1	0.12	-	64,64,64,64	0
56	MG	DA	3336	1/1	0.17	-	22,22,22,22	0
56	MG	DA	3593	1/1	0.27	-	51,51,51,51	0
56	MG	DA	3435	1/1	0.18	-	33,33,33,33	0
56	MG	BA	3205	1/1	0.10	-	40,40,40,40	0
56	MG	BA	3005	1/1	0.15	-	29,29,29,29	0
56	MG	BA	3495	1/1	0.33	-	48,48,48,48	0
56	MG	DA	3410	1/1	0.13	-	64,64,64,64	0
56	MG	DA	3008	1/1	0.12	-	38,38,38,38	0
56	MG	DA	3547	1/1	0.16	-	41,41,41,41	0
56	MG	DA	3311	1/1	0.10	-	43,43,43,43	0
56	MG	DA	3304	1/1	0.14	-	32,32,32,32	0
56	MG	BA	3173	1/1	0.12	-	45,45,45,45	0
56	MG	DA	3205	1/1	0.14	-	32,32,32,32	0
56	MG	AX	3004	1/1	0.20	-	39,39,39,39	0
56	MG	AA	3176	1/1	0.14	-	60,60,60,60	0
56	MG	BA	3078	1/1	0.14	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AX	3006	1/1	0.12	-	54,54,54,54	0
56	MG	BG	3003	1/1	0.10	-	41,41,41,41	0
56	MG	DA	3557	1/1	0.11	-	62,62,62,62	0
56	MG	BA	3583	1/1	0.10	-	37,37,37,37	0
56	MG	BB	3002	1/1	0.25	-	41,41,41,41	0
56	MG	AA	3109	1/1	0.27	-	44,44,44,44	0
56	MG	BA	3614	1/1	0.05	-	55,55,55,55	0
56	MG	AA	3053	1/1	0.07	-	50,50,50,50	0
56	MG	BB	3016	1/1	0.09	-	24,24,24,24	0
56	MG	BA	3630	1/1	0.07	-	47,47,47,47	0
56	MG	DA	3377	1/1	0.14	-	37,37,37,37	0
56	MG	BA	3623	1/1	0.10	-	48,48,48,48	0
56	MG	BA	3410	1/1	0.10	-	43,43,43,43	0
56	MG	BA	3275	1/1	0.15	-	39,39,39,39	0
56	MG	BA	3602	1/1	0.20	-	31,31,31,31	0
56	MG	DA	3270	1/1	0.07	-	37,37,37,37	0
56	MG	BA	3154	1/1	0.22	-	40,40,40,40	0
56	MG	DA	3235	1/1	0.21	-	42,42,42,42	0
56	MG	AA	3032	1/1	0.14	-	42,42,42,42	0
56	MG	BA	3365	1/1	0.11	-	41,41,41,41	0
56	MG	DA	3287	1/1	0.10	-	38,38,38,38	0
56	MG	AA	3012	1/1	0.09	-	64,64,64,64	0
56	MG	DA	3196	1/1	0.13	-	33,33,33,33	0
56	MG	AA	3054	1/1	0.14	-	65,65,65,65	0
56	MG	BA	3027	1/1	0.17	-	28,28,28,28	0
56	MG	BA	3109	1/1	0.10	-	36,36,36,36	0
56	MG	DA	3215	1/1	0.13	-	31,31,31,31	0
56	MG	AA	3169	1/1	0.12	-	71,71,71,71	0
56	MG	CA	3070	1/1	0.06	-	39,39,39,39	0
56	MG	DA	3325	1/1	0.14	-	54,54,54,54	0
56	MG	DA	3299	1/1	0.10	-	50,50,50,50	0
56	MG	BA	3207	1/1	0.12	-	36,36,36,36	0
56	MG	BA	3196	1/1	0.17	-	17,17,17,17	0
56	MG	BA	3401	1/1	0.14	-	32,32,32,32	0
56	MG	CA	3023	1/1	0.10	-	38,38,38,38	0
56	MG	DA	3551	1/1	0.14	-	52,52,52,52	0
56	MG	BQ	202	1/1	0.12	-	14,14,14,14	0
56	MG	DA	3578	1/1	0.17	-	47,47,47,47	0
56	MG	AA	3027	1/1	0.19	-	71,71,71,71	0
56	MG	BA	3050	1/1	0.14	-	44,44,44,44	0
56	MG	DA	3020	1/1	0.36	-	50,50,50,50	0
56	MG	BA	3329	1/1	0.11	-	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DB	3009	1/1	0.12	-	60,60,60,60	0
56	MG	CA	3101	1/1	0.12	-	53,53,53,53	0
56	MG	AA	3115	1/1	0.06	-	35,35,35,35	0
56	MG	BA	3672	1/1	0.10	-	46,46,46,46	0
56	MG	CA	3036	1/1	0.10	-	56,56,56,56	0
56	MG	BA	3308	1/1	0.17	-	52,52,52,52	0
56	MG	BA	3449	1/1	0.06	-	47,47,47,47	0
56	MG	BA	3644	1/1	0.07	-	41,41,41,41	0
56	MG	DA	3364	1/1	0.05	-	37,37,37,37	0
56	MG	BA	3416	1/1	0.16	-	64,64,64,64	0
56	MG	DA	3506	1/1	0.12	-	65,65,65,65	0
56	MG	DA	3500	1/1	0.16	-	46,46,46,46	0
56	MG	BA	3274	1/1	0.20	-	47,47,47,47	0
56	MG	DA	3088	1/1	0.11	-	39,39,39,39	0
56	MG	BA	3179	1/1	0.11	-	27,27,27,27	0
56	MG	BU	204	1/1	0.20	-	29,29,29,29	0
56	MG	AA	3181	1/1	0.19	-	53,53,53,53	0
56	MG	DA	3370	1/1	0.12	-	44,44,44,44	0
56	MG	BA	3199	1/1	0.15	-	32,32,32,32	0
56	MG	DA	3512	1/1	0.11	-	36,36,36,36	0
56	MG	CA	3050	1/1	0.13	-	67,67,67,67	0
56	MG	BA	3162	1/1	0.16	-	39,39,39,39	0
56	MG	BA	3036	1/1	0.09	-	56,56,56,56	0
56	MG	BA	3411	1/1	0.15	-	25,25,25,25	0
56	MG	DE	3003	1/1	0.12	-	40,40,40,40	0
56	MG	AA	3102	1/1	0.15	-	60,60,60,60	0
56	MG	DA	3451	1/1	0.08	-	30,30,30,30	0
56	MG	BA	3397	1/1	0.10	-	30,30,30,30	0
56	MG	AA	3105	1/1	0.14	-	44,44,44,44	0
56	MG	DA	3345	1/1	0.15	-	33,33,33,33	0
56	MG	BA	3341	1/1	0.10	-	32,32,32,32	0
56	MG	DA	3439	1/1	0.11	-	28,28,28,28	0
56	MG	DA	3331	1/1	0.08	-	41,41,41,41	0
56	MG	CA	3093	1/1	0.12	-	72,72,72,72	0
56	MG	BA	3060	1/1	0.12	-	42,42,42,42	0
56	MG	BA	3586	1/1	0.18	-	45,45,45,45	0
56	MG	DN	5001	1/1	0.16	-	65,65,65,65	0
56	MG	CA	3081	1/1	0.23	-	56,56,56,56	0
56	MG	BA	3434	1/1	0.12	-	43,43,43,43	0
56	MG	DA	3317	1/1	0.11	-	53,53,53,53	0
56	MG	BA	3276	1/1	0.13	-	42,42,42,42	0
56	MG	DA	3038	1/1	0.10	-	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3510	1/1	0.10	-	53,53,53,53	0
56	MG	BA	3007	1/1	0.13	-	32,32,32,32	0
56	MG	DA	3305	1/1	0.15	-	30,30,30,30	0
56	MG	BA	3047	1/1	0.20	-	41,41,41,41	0
56	MG	CA	3094	1/1	0.13	-	67,67,67,67	0
56	MG	AA	3051	1/1	0.11	-	49,49,49,49	0
56	MG	BA	3389	1/1	0.19	-	35,35,35,35	0
58	ZN	CN	501	1/1	0.10	-	82,82,82,82	0
56	MG	BA	3379	1/1	0.16	-	31,31,31,31	0
56	MG	BA	3529	1/1	0.18	-	33,33,33,33	0
56	MG	BA	3230	1/1	0.15	-	40,40,40,40	0
56	MG	BU	202	1/1	0.11	-	40,40,40,40	0
56	MG	BA	3022	1/1	0.12	-	26,26,26,26	0
56	MG	BN	3001	1/1	0.16	-	57,57,57,57	0
56	MG	BA	3304	1/1	0.06	-	43,43,43,43	0
56	MG	DA	3558	1/1	0.08	-	39,39,39,39	0
56	MG	BA	3651	1/1	0.12	-	42,42,42,42	0
56	MG	BA	3202	1/1	0.12	-	30,30,30,30	0
56	MG	BA	3539	1/1	0.15	-	58,58,58,58	0
56	MG	DA	3286	1/1	0.07	-	35,35,35,35	0
56	MG	BA	3161	1/1	0.11	-	39,39,39,39	0
56	MG	BA	3534	1/1	0.14	-	20,20,20,20	0
56	MG	CA	3133	1/1	0.15	-	68,68,68,68	0
56	MG	BA	3609	1/1	0.12	-	44,44,44,44	0
56	MG	CA	3020	1/1	0.24	-	46,46,46,46	0
56	MG	DA	3480	1/1	0.10	-	32,32,32,32	0
56	MG	DA	3177	1/1	0.11	-	52,52,52,52	0
56	MG	AA	3078	1/1	0.15	-	34,34,34,34	0
56	MG	DA	3395	1/1	0.09	-	41,41,41,41	0
56	MG	AA	3146	1/1	0.13	-	41,41,41,41	0
56	MG	BA	3283	1/1	0.10	-	57,57,57,57	0
56	MG	BA	3466	1/1	0.23	-	49,49,49,49	0
56	MG	BA	3031	1/1	0.45	-	46,46,46,46	0
56	MG	DA	3060	1/1	0.10	-	45,45,45,45	0
56	MG	AA	3112	1/1	0.18	-	94,94,94,94	0
56	MG	DA	3033	1/1	0.17	-	37,37,37,37	0
56	MG	DA	3475	1/1	0.24	-	41,41,41,41	0
56	MG	DA	3169	1/1	0.09	-	38,38,38,38	0
56	MG	DA	3045	1/1	0.09	-	48,48,48,48	0
56	MG	AA	3067	1/1	0.12	-	42,42,42,42	0
56	MG	BA	3235	1/1	0.34	-	51,51,51,51	0
56	MG	DA	3456	1/1	0.13	-	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3045	1/1	0.13	-	34,34,34,34	0
56	MG	AA	3021	1/1	0.11	-	41,41,41,41	0
56	MG	CA	3056	1/1	0.20	-	40,40,40,40	0
56	MG	DA	3494	1/1	0.22	-	49,49,49,49	0
56	MG	BA	3485	1/1	0.11	-	64,64,64,64	0
56	MG	AA	3164	1/1	0.18	-	61,61,61,61	0
56	MG	DA	3384	1/1	0.14	-	52,52,52,52	0
56	MG	DA	3571	1/1	0.15	-	48,48,48,48	0
56	MG	AA	3046	1/1	0.10	-	42,42,42,42	0
56	MG	DA	3383	1/1	0.08	-	47,47,47,47	0
56	MG	AA	3101	1/1	0.10	-	53,53,53,53	0
56	MG	DA	3453	1/1	0.10	-	31,31,31,31	0
56	MG	BA	3395	1/1	0.14	-	54,54,54,54	0
56	MG	AA	3131	1/1	0.21	-	55,55,55,55	0
56	MG	AX	3002	1/1	0.16	-	56,56,56,56	0
56	MG	DA	3308	1/1	0.13	-	29,29,29,29	0
56	MG	BB	3004	1/1	0.09	-	49,49,49,49	0
56	MG	BA	3604	1/1	0.10	-	28,28,28,28	0
56	MG	BA	3037	1/1	0.11	-	24,24,24,24	0
56	MG	BA	3668	1/1	0.16	-	26,26,26,26	0
56	MG	BA	3058	1/1	0.13	-	43,43,43,43	0
56	MG	BW	3001	1/1	0.12	-	25,25,25,25	0
56	MG	BA	3671	1/1	0.27	-	48,48,48,48	0
56	MG	BA	3030	1/1	0.60	-	43,43,43,43	0
56	MG	BA	3600	1/1	0.11	-	68,68,68,68	0
56	MG	DA	3423	1/1	0.14	-	40,40,40,40	0
56	MG	BA	3556	1/1	0.05	-	41,41,41,41	0
56	MG	DA	3314	1/1	0.11	-	54,54,54,54	0
56	MG	BA	3435	1/1	0.18	-	36,36,36,36	0
56	MG	DA	3454	1/1	0.08	-	64,64,64,64	0
56	MG	BA	3422	1/1	0.08	-	46,46,46,46	0
56	MG	DA	3216	1/1	0.12	-	37,37,37,37	0
56	MG	DA	3517	1/1	0.21	-	47,47,47,47	0
56	MG	DA	3013	1/1	0.19	-	37,37,37,37	0
56	MG	DA	3525	1/1	0.05	-	44,44,44,44	0
56	MG	DA	3457	1/1	0.14	-	38,38,38,38	0
56	MG	BN	3002	1/1	0.14	-	27,27,27,27	0
56	MG	DA	3173	1/1	0.13	-	54,54,54,54	0
56	MG	AA	3065	1/1	0.08	-	48,48,48,48	0
56	MG	BA	3577	1/1	0.07	-	57,57,57,57	0
56	MG	AK	3001	1/1	0.15	-	43,43,43,43	0
56	MG	DA	3005	1/1	0.08	-	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3364	1/1	0.16	-	29,29,29,29	0
56	MG	CA	3153	1/1	0.13	-	37,37,37,37	0
56	MG	DA	3162	1/1	0.09	-	57,57,57,57	0
56	MG	BA	3356	1/1	0.09	-	46,46,46,46	0
56	MG	BA	3165	1/1	0.22	-	43,43,43,43	0
56	MG	DA	3426	1/1	0.20	-	35,35,35,35	0
56	MG	BA	3616	1/1	0.13	-	34,34,34,34	0
56	MG	DA	3407	1/1	0.04	-	40,40,40,40	0
56	MG	DA	3294	1/1	0.12	-	37,37,37,37	0
56	MG	DA	3042	1/1	0.09	-	32,32,32,32	0
56	MG	AA	3043	1/1	0.07	-	53,53,53,53	0
56	MG	DA	3230	1/1	0.11	-	41,41,41,41	0
56	MG	DA	3154	1/1	0.12	-	24,24,24,24	0
56	MG	CA	3116	1/1	0.14	-	59,59,59,59	0
56	MG	BP	203	1/1	0.12	-	47,47,47,47	0
56	MG	AA	3045	1/1	0.14	-	60,60,60,60	0
56	MG	DA	3388	1/1	0.05	-	35,35,35,35	0
56	MG	AA	3074	1/1	0.12	-	38,38,38,38	0
56	MG	BA	3100	1/1	0.14	-	29,29,29,29	0
56	MG	BG	3001	1/1	0.10	-	71,71,71,71	0
56	MG	DA	3581	1/1	0.17	-	53,53,53,53	0
56	MG	DA	3065	1/1	0.13	-	49,49,49,49	0
56	MG	B7	3004	1/1	0.09	-	34,34,34,34	0
56	MG	D8	5002	1/1	0.24	-	64,64,64,64	0
56	MG	DA	3431	1/1	0.10	-	61,61,61,61	0
56	MG	CA	3035	1/1	0.13	-	66,66,66,66	0
56	MG	CA	3030	1/1	0.10	-	41,41,41,41	0
56	MG	CA	3029	1/1	0.17	-	48,48,48,48	0
56	MG	CA	3145	1/1	0.12	-	59,59,59,59	0
56	MG	DA	3432	1/1	0.14	-	33,33,33,33	0
56	MG	DA	3501	1/1	0.08	-	55,55,55,55	0
56	MG	DA	3197	1/1	0.11	-	38,38,38,38	0
56	MG	BA	3455	1/1	0.12	-	21,21,21,21	0
56	MG	BA	3070	1/1	0.12	-	30,30,30,30	0
56	MG	BA	3482	1/1	0.07	-	23,23,23,23	0
56	MG	DA	3037	1/1	0.08	-	40,40,40,40	0
56	MG	DA	3118	1/1	0.19	-	49,49,49,49	0
56	MG	DA	3472	1/1	0.16	-	53,53,53,53	0
56	MG	BA	3580	1/1	0.10	-	62,62,62,62	0
56	MG	DF	303	1/1	0.09	-	57,57,57,57	0
56	MG	B7	3002	1/1	0.28	-	35,35,35,35	0
56	MG	DA	3126	1/1	0.19	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3116	1/1	0.16	-	29,29,29,29	0
56	MG	DA	3505	1/1	0.09	-	44,44,44,44	0
56	MG	BA	3370	1/1	0.12	-	29,29,29,29	0
56	MG	BA	3448	1/1	0.09	-	42,42,42,42	0
58	ZN	B5	501	1/1	0.14	-	42,42,42,42	0
56	MG	BA	3611	1/1	0.38	-	59,59,59,59	0
56	MG	CA	3022	1/1	0.13	-	34,34,34,34	0
56	MG	DA	3362	1/1	0.08	-	43,43,43,43	0
56	MG	BA	3396	1/1	0.18	-	38,38,38,38	0
56	MG	DA	3239	1/1	0.17	-	56,56,56,56	0
56	MG	DA	3445	1/1	0.11	-	48,48,48,48	0
56	MG	DA	3052	1/1	0.12	-	49,49,49,49	0
56	MG	DA	3567	1/1	0.14	-	41,41,41,41	0
56	MG	BA	3342	1/1	0.12	-	35,35,35,35	0
56	MG	DA	3504	1/1	0.13	-	49,49,49,49	0
56	MG	BA	3467	1/1	0.17	-	20,20,20,20	0
56	MG	BA	3427	1/1	0.19	-	49,49,49,49	0
56	MG	AA	3087	1/1	0.17	-	62,62,62,62	0
56	MG	AA	3145	1/1	0.13	-	35,35,35,35	0
56	MG	BA	3169	1/1	0.12	-	39,39,39,39	0
56	MG	DA	3210	1/1	0.09	-	37,37,37,37	0
56	MG	AA	3133	1/1	0.08	-	38,38,38,38	0
56	MG	DA	3138	1/1	0.08	-	33,33,33,33	0
56	MG	DB	3008	1/1	0.12	-	35,35,35,35	0
56	MG	DA	3412	1/1	0.20	-	53,53,53,53	0
56	MG	DA	3424	1/1	0.17	-	30,30,30,30	0
56	MG	D8	5001	1/1	0.07	-	50,50,50,50	0
56	MG	BA	3576	1/1	0.16	-	48,48,48,48	0
56	MG	BA	3143	1/1	0.47	-	36,36,36,36	0
56	MG	DA	3115	1/1	0.16	-	36,36,36,36	0
56	MG	DA	3277	1/1	0.06	-	48,48,48,48	0
56	MG	AA	3075	1/1	0.16	-	39,39,39,39	0
56	MG	DA	3589	1/1	0.15	-	33,33,33,33	0
56	MG	DA	3313	1/1	0.09	-	40,40,40,40	0
56	MG	DA	3533	1/1	0.07	-	60,60,60,60	0
56	MG	DA	3146	1/1	0.11	-	34,34,34,34	0
56	MG	DA	3171	1/1	0.17	-	51,51,51,51	0
56	MG	DA	3483	1/1	0.08	-	54,54,54,54	0
56	MG	DA	3082	1/1	0.16	-	58,58,58,58	0
56	MG	DA	3131	1/1	0.11	-	46,46,46,46	0
56	MG	DA	3167	1/1	0.08	-	51,51,51,51	0
56	MG	BA	3048	1/1	0.17	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3079	1/1	0.11	-	46,46,46,46	0
56	MG	AA	3015	1/1	0.13	-	56,56,56,56	0
56	MG	DA	3024	1/1	0.23	-	36,36,36,36	0
56	MG	DA	3458	1/1	0.12	-	34,34,34,34	0
56	MG	BA	3333	1/1	0.16	-	35,35,35,35	0
56	MG	DA	3550	1/1	0.11	-	46,46,46,46	0
56	MG	BA	3101	1/1	0.14	-	30,30,30,30	0
56	MG	DA	3261	1/1	0.13	-	49,49,49,49	0
56	MG	CA	3119	1/1	0.08	-	48,48,48,48	0
56	MG	BA	3452	1/1	0.14	-	38,38,38,38	0
56	MG	BA	3083	1/1	0.14	-	34,34,34,34	0
56	MG	DA	3570	1/1	0.29	-	52,52,52,52	0
56	MG	BA	3481	1/1	0.10	-	31,31,31,31	0
56	MG	CA	3069	1/1	0.12	-	34,34,34,34	0
56	MG	CA	3091	1/1	0.13	-	66,66,66,66	0
56	MG	BA	3320	1/1	0.12	-	44,44,44,44	0
56	MG	DA	3003	1/1	0.17	-	47,47,47,47	0
56	MG	BA	3521	1/1	0.14	-	54,54,54,54	0
56	MG	CA	3062	1/1	0.09	-	57,57,57,57	0
56	MG	DA	3490	1/1	0.12	-	34,34,34,34	0
56	MG	DA	3056	1/1	0.08	-	36,36,36,36	0
56	MG	DA	3057	1/1	0.11	-	30,30,30,30	0
56	MG	DA	3536	1/1	0.10	-	56,56,56,56	0
56	MG	BA	3667	1/1	0.53	-	38,38,38,38	0
56	MG	BW	3003	1/1	0.16	-	27,27,27,27	0
56	MG	DA	3249	1/1	0.07	-	34,34,34,34	0
56	MG	AA	3144	1/1	0.16	-	42,42,42,42	0
56	MG	BA	3090	1/1	0.21	-	44,44,44,44	0
56	MG	DA	3419	1/1	0.23	-	59,59,59,59	0
56	MG	AA	3028	1/1	0.20	-	39,39,39,39	0
56	MG	BA	3450	1/1	0.15	-	45,45,45,45	0
56	MG	AA	3142	1/1	0.17	-	60,60,60,60	0
56	MG	DA	3143	1/1	0.17	-	27,27,27,27	0
56	MG	BA	3327	1/1	0.10	-	44,44,44,44	0
59	K	DA	3001	1/1	0.09	-	48,48,48,48	0
56	MG	AA	3096	1/1	0.20	-	53,53,53,53	0
56	MG	BA	3399	1/1	0.11	-	42,42,42,42	0
56	MG	DA	3539	1/1	0.13	-	52,52,52,52	0
56	MG	BA	3493	1/1	0.12	-	40,40,40,40	0
56	MG	CA	3124	1/1	0.09	-	52,52,52,52	0
56	MG	CA	3075	1/1	0.18	-	53,53,53,53	0
56	MG	BA	3232	1/1	0.19	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3397	1/1	0.16	-	18,18,18,18	0
56	MG	DA	3104	1/1	0.13	-	35,35,35,35	0
56	MG	DA	3367	1/1	0.13	-	47,47,47,47	0
56	MG	AA	3183	1/1	0.20	-	55,55,55,55	0
56	MG	BA	3059	1/1	0.08	-	27,27,27,27	0
56	MG	BA	3549	1/1	0.09	-	57,57,57,57	0
56	MG	DA	3338	1/1	0.15	-	36,36,36,36	0
56	MG	BA	3430	1/1	0.09	-	29,29,29,29	0
56	MG	AA	3006	1/1	0.14	-	67,67,67,67	0
56	MG	BA	3081	1/1	0.24	-	42,42,42,42	0
56	MG	BB	3003	1/1	0.13	-	61,61,61,61	0
56	MG	BA	3052	1/1	0.12	-	27,27,27,27	0
56	MG	DA	3469	1/1	0.17	-	33,33,33,33	0
56	MG	DA	3470	1/1	0.14	-	52,52,52,52	0
56	MG	BA	3215	1/1	0.14	-	32,32,32,32	0
56	MG	AA	3040	1/1	0.14	-	27,27,27,27	0
56	MG	BA	3398	1/1	0.15	-	41,41,41,41	0
56	MG	BA	3665	1/1	0.09	-	30,30,30,30	0
56	MG	DA	3265	1/1	0.28	-	51,51,51,51	0
56	MG	BA	3354	1/1	0.12	-	42,42,42,42	0
56	MG	BA	3594	1/1	0.14	-	37,37,37,37	0
56	MG	DA	3521	1/1	0.20	-	51,51,51,51	0
56	MG	BA	3201	1/1	0.10	-	41,41,41,41	0
56	MG	BQ	201	1/1	0.07	-	52,52,52,52	0
56	MG	CA	3015	1/1	0.13	-	43,43,43,43	0
56	MG	DA	3079	1/1	0.10	-	54,54,54,54	0
56	MG	BA	3066	1/1	0.15	-	48,48,48,48	0
56	MG	BA	3610	1/1	0.16	-	47,47,47,47	0
56	MG	AA	3158	1/1	0.09	-	54,54,54,54	0
56	MG	BA	3160	1/1	0.16	-	29,29,29,29	0
56	MG	CA	3027	1/1	0.19	-	64,64,64,64	0
56	MG	BA	3390	1/1	0.10	-	47,47,47,47	0
56	MG	BA	3238	1/1	0.22	-	47,47,47,47	0
56	MG	BA	3574	1/1	0.13	-	55,55,55,55	0
56	MG	BA	3533	1/1	0.13	-	45,45,45,45	0
56	MG	BA	3674	1/1	0.17	-	54,54,54,54	0
56	MG	DA	3312	1/1	0.03	-	47,47,47,47	0
56	MG	BA	3358	1/1	0.12	-	39,39,39,39	0
56	MG	BF	301	1/1	0.25	-	56,56,56,56	0
56	MG	CA	3060	1/1	0.16	-	50,50,50,50	0
56	MG	BE	303	1/1	0.14	-	41,41,41,41	0
56	MG	BA	3628	1/1	0.14	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3262	1/1	0.18	-	24,24,24,24	0
56	MG	BF	303	1/1	0.28	-	20,20,20,20	0
56	MG	BA	3498	1/1	0.18	-	37,37,37,37	0
56	MG	AA	3091	1/1	0.10	-	36,36,36,36	0
56	MG	BA	3233	1/1	0.12	-	41,41,41,41	0
56	MG	BA	3376	1/1	0.13	-	39,39,39,39	0
56	MG	BA	3528	1/1	0.19	-	38,38,38,38	0
56	MG	CA	3045	1/1	0.18	-	52,52,52,52	0
56	MG	BA	3296	1/1	0.11	-	25,25,25,25	0
56	MG	DA	3150	1/1	0.75	-	55,55,55,55	0
56	MG	AA	3009	1/1	0.13	-	54,54,54,54	0
56	MG	AA	3077	1/1	0.13	-	39,39,39,39	0
56	MG	DA	3072	1/1	0.09	-	33,33,33,33	0
56	MG	CA	3010	1/1	0.18	-	53,53,53,53	0
56	MG	DA	3283	1/1	0.14	-	38,38,38,38	0
56	MG	BA	3186	1/1	0.13	-	39,39,39,39	0
56	MG	DA	3264	1/1	0.23	-	47,47,47,47	0
56	MG	BA	3546	1/1	0.12	-	57,57,57,57	0
56	MG	BA	3626	1/1	0.15	-	50,50,50,50	0
56	MG	BA	3505	1/1	0.20	-	46,46,46,46	0
56	MG	AA	3180	1/1	0.11	-	56,56,56,56	0
56	MG	AA	3141	1/1	0.05	-	47,47,47,47	0
56	MG	DA	3284	1/1	0.07	-	23,23,23,23	0
56	MG	DA	3546	1/1	0.05	-	40,40,40,40	0
56	MG	BA	3642	1/1	0.16	-	47,47,47,47	0
56	MG	DA	3468	1/1	0.17	-	55,55,55,55	0
56	MG	CA	3066	1/1	0.21	-	43,43,43,43	0
56	MG	DA	3376	1/1	0.06	-	38,38,38,38	0
56	MG	DA	3296	1/1	0.06	-	28,28,28,28	0
56	MG	AA	3058	1/1	0.10	-	62,62,62,62	0
56	MG	DA	3374	1/1	0.12	-	35,35,35,35	0
56	MG	DA	3474	1/1	0.10	-	62,62,62,62	0
56	MG	DA	3396	1/1	0.10	-	45,45,45,45	0
56	MG	BB	3018	1/1	0.15	-	30,30,30,30	0
56	MG	AA	3134	1/1	0.24	-	52,52,52,52	0
56	MG	BA	3008	1/1	0.08	-	27,27,27,27	0
56	MG	AA	3099	1/1	0.26	-	33,33,33,33	0
56	MG	BA	3033	1/1	0.16	-	33,33,33,33	0
56	MG	BA	3567	1/1	0.16	-	53,53,53,53	0
56	MG	AA	3182	1/1	0.14	-	57,57,57,57	0
56	MG	BA	3006	1/1	0.38	-	36,36,36,36	0
56	MG	AA	3118	1/1	0.16	-	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3591	1/1	0.07	-	42,42,42,42	0
56	MG	AA	3055	1/1	0.15	-	72,72,72,72	0
56	MG	BA	3660	1/1	0.07	-	49,49,49,49	0
56	MG	DA	3464	1/1	0.09	-	46,46,46,46	0
56	MG	B4	502	1/1	0.35	-	61,61,61,61	0
56	MG	BA	3558	1/1	0.12	-	59,59,59,59	0
56	MG	BA	3581	1/1	0.11	-	34,34,34,34	0
56	MG	AA	3147	1/1	0.09	-	67,67,67,67	0
56	MG	AA	3106	1/1	0.16	-	50,50,50,50	0
56	MG	BA	3647	1/1	0.12	-	30,30,30,30	0
56	MG	BA	3544	1/1	0.17	-	25,25,25,25	0
56	MG	AA	3080	1/1	0.26	-	39,39,39,39	0
56	MG	BW	3002	1/1	0.23	-	57,57,57,57	0
56	MG	B3	102	1/1	0.24	-	22,22,22,22	0
56	MG	BA	3381	1/1	0.19	-	31,31,31,31	0
56	MG	DE	3002	1/1	0.26	-	35,35,35,35	0
56	MG	BA	3261	1/1	0.11	-	53,53,53,53	0
56	MG	BA	3158	1/1	0.12	-	33,33,33,33	0
56	MG	BA	3475	1/1	0.11	-	45,45,45,45	0
56	MG	AE	3001	1/1	0.08	-	71,71,71,71	0
56	MG	DA	3498	1/1	0.12	-	48,48,48,48	0
56	MG	BV	203	1/1	0.07	-	24,24,24,24	0
56	MG	BA	3307	1/1	0.07	-	63,63,63,63	0
56	MG	DA	3237	1/1	0.46	-	39,39,39,39	0
56	MG	BA	3107	1/1	0.14	-	21,21,21,21	0
56	MG	BA	3190	1/1	0.28	-	31,31,31,31	0
56	MG	BA	3294	1/1	0.10	-	32,32,32,32	0
56	MG	CA	3115	1/1	0.08	-	62,62,62,62	0
56	MG	BA	3168	1/1	0.19	-	47,47,47,47	0
56	MG	CA	3090	1/1	0.19	-	66,66,66,66	0
56	MG	AA	3172	1/1	0.08	-	69,69,69,69	0
56	MG	DA	3430	1/1	0.22	-	30,30,30,30	0
56	MG	BX	103	1/1	0.23	-	25,25,25,25	0
56	MG	DA	3473	1/1	0.05	-	50,50,50,50	0
56	MG	BA	3194	1/1	0.11	-	23,23,23,23	0
56	MG	AA	3170	1/1	0.15	-	54,54,54,54	0
56	MG	BA	3251	1/1	0.19	-	37,37,37,37	0
56	MG	BA	3152	1/1	0.24	-	39,39,39,39	0
56	MG	BA	3652	1/1	0.07	-	49,49,49,49	0
56	MG	AA	3062	1/1	0.18	-	58,58,58,58	0
56	MG	BA	3004	1/1	0.08	-	23,23,23,23	0
56	MG	BA	3313	1/1	0.11	-	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3019	1/1	0.25	-	49,49,49,49	0
56	MG	DA	3228	1/1	0.07	-	51,51,51,51	0
58	ZN	BY	501	1/1	0.13	-	51,51,51,51	0
56	MG	BA	3373	1/1	0.17	-	41,41,41,41	0
56	MG	DB	3003	1/1	0.10	-	29,29,29,29	0
56	MG	DA	3399	1/1	0.14	-	40,40,40,40	0
56	MG	BA	3615	1/1	0.11	-	42,42,42,42	0
56	MG	BA	3111	1/1	0.12	-	27,27,27,27	0
56	MG	DA	3267	1/1	0.04	-	47,47,47,47	0
56	MG	BA	3271	1/1	0.15	-	49,49,49,49	0
56	MG	CA	3134	1/1	0.17	-	53,53,53,53	0
56	MG	CA	3131	1/1	0.07	-	65,65,65,65	0
56	MG	CA	3151	1/1	0.14	-	50,50,50,50	0
56	MG	DA	3355	1/1	0.06	-	36,36,36,36	0
56	MG	DA	3484	1/1	0.13	-	34,34,34,34	0
56	MG	BD	308	1/1	0.15	-	35,35,35,35	0
56	MG	B9	502	1/1	0.34	-	41,41,41,41	0
56	MG	BA	3253	1/1	0.50	-	47,47,47,47	0
56	MG	CA	3063	1/1	0.16	-	53,53,53,53	0
56	MG	DW	3001	1/1	0.20	-	38,38,38,38	0
56	MG	AA	3103	1/1	0.12	-	51,51,51,51	0
56	MG	BA	3557	1/1	0.16	-	42,42,42,42	0
56	MG	DA	3417	1/1	0.14	-	40,40,40,40	0
56	MG	B0	103	1/1	0.10	-	33,33,33,33	0
56	MG	AE	3002	1/1	0.11	-	38,38,38,38	0
56	MG	BA	3432	1/1	0.12	-	37,37,37,37	0
56	MG	BA	3648	1/1	0.09	-	28,28,28,28	0
56	MG	AA	3044	1/1	0.20	-	50,50,50,50	0
56	MG	CA	3080	1/1	0.10	-	41,41,41,41	0
56	MG	BA	3363	1/1	0.20	-	29,29,29,29	0
56	MG	AA	3025	1/1	0.14	-	37,37,37,37	0
56	MG	AA	3153	1/1	0.16	-	50,50,50,50	0
56	MG	BA	3289	1/1	0.12	-	28,28,28,28	0
56	MG	BA	3391	1/1	0.09	-	37,37,37,37	0
56	MG	DA	3568	1/1	0.14	-	60,60,60,60	0
56	MG	DA	3029	1/1	0.09	-	40,40,40,40	0
56	MG	DA	3017	1/1	0.19	-	46,46,46,46	0
56	MG	DA	3051	1/1	0.08	-	50,50,50,50	0
56	MG	BA	3650	1/1	0.11	-	31,31,31,31	0
56	MG	AA	3081	1/1	0.09	-	44,44,44,44	0
56	MG	BA	3524	1/1	0.10	-	57,57,57,57	0
56	MG	DE	3004	1/1	0.18	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3181	1/1	0.12	-	37,37,37,37	0
56	MG	BA	3639	1/1	0.18	-	64,64,64,64	0
56	MG	BA	3451	1/1	0.07	-	48,48,48,48	0
56	MG	BA	3541	1/1	0.10	-	26,26,26,26	0
56	MG	BA	3041	1/1	0.11	-	42,42,42,42	0
56	MG	AA	3063	1/1	0.25	-	39,39,39,39	0
56	MG	BA	3659	1/1	0.13	-	28,28,28,28	0
56	MG	CA	3058	1/1	0.12	-	56,56,56,56	0
56	MG	CA	3043	1/1	0.17	-	60,60,60,60	0
56	MG	BA	3559	1/1	0.12	-	52,52,52,52	0
56	MG	BA	3198	1/1	0.09	-	34,34,34,34	0
56	MG	BD	304	1/1	0.17	-	28,28,28,28	0
56	MG	BA	3164	1/1	0.10	-	37,37,37,37	0
56	MG	BA	3472	1/1	0.11	-	34,34,34,34	0
56	MG	BA	3428	1/1	0.07	-	58,58,58,58	0
56	MG	DA	3580	1/1	0.14	-	58,58,58,58	0
56	MG	AA	3135	1/1	0.11	-	46,46,46,46	0
56	MG	BA	3139	1/1	0.14	-	31,31,31,31	0
56	MG	BA	3470	1/1	0.14	-	48,48,48,48	0
56	MG	B5	503	1/1	0.16	-	47,47,47,47	0
56	MG	DA	3085	1/1	0.10	-	40,40,40,40	0
58	ZN	D6	501	1/1	0.18	-	68,68,68,68	0
56	MG	B8	5001	1/1	0.12	-	36,36,36,36	0
56	MG	DA	3117	1/1	0.17	-	43,43,43,43	0
56	MG	BA	3506	1/1	0.08	-	39,39,39,39	0
56	MG	BA	3536	1/1	0.19	-	53,53,53,53	0
56	MG	BO	5001	1/1	0.12	-	62,62,62,62	0
56	MG	BA	3224	1/1	0.22	-	45,45,45,45	0
56	MG	BA	3669	1/1	0.20	-	29,29,29,29	0
56	MG	DA	3450	1/1	0.11	-	37,37,37,37	0
56	MG	CA	3098	1/1	0.17	-	42,42,42,42	0
56	MG	BA	3612	1/1	0.18	-	51,51,51,51	0
56	MG	CA	3026	1/1	0.16	-	44,44,44,44	0
56	MG	BA	3142	1/1	0.09	-	40,40,40,40	0
56	MG	CA	3140	1/1	0.21	-	61,61,61,61	0
56	MG	BA	3148	1/1	0.19	-	25,25,25,25	0
56	MG	DA	3408	1/1	0.13	-	28,28,28,28	0
56	MG	DA	3036	1/1	0.07	-	38,38,38,38	0
56	MG	BA	3218	1/1	0.17	-	38,38,38,38	0
56	MG	DA	3492	1/1	0.09	-	44,44,44,44	0
56	MG	BA	3021	1/1	0.08	-	37,37,37,37	0
56	MG	CA	3016	1/1	0.14	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3105	1/1	0.14	-	32,32,32,32	0
56	MG	AA	3173	1/1	0.12	-	32,32,32,32	0
56	MG	BE	304	1/1	0.14	-	13,13,13,13	0
56	MG	BA	3561	1/1	0.09	-	55,55,55,55	0
56	MG	DA	3307	1/1	0.17	-	53,53,53,53	0
56	MG	DA	3569	1/1	0.21	-	55,55,55,55	0
56	MG	DA	3046	1/1	0.23	-	34,34,34,34	0
56	MG	DA	3234	1/1	0.13	-	45,45,45,45	0
56	MG	AA	3016	1/1	0.21	-	49,49,49,49	0
56	MG	BA	3265	1/1	0.31	-	47,47,47,47	0
56	MG	DB	3006	1/1	0.12	-	55,55,55,55	0
56	MG	AA	3149	1/1	0.12	-	68,68,68,68	0
56	MG	BA	3331	1/1	0.18	-	59,59,59,59	0
56	MG	DA	3070	1/1	0.14	-	49,49,49,49	0
56	MG	BA	3279	1/1	0.09	-	38,38,38,38	0
56	MG	BA	3299	1/1	0.12	-	36,36,36,36	0
56	MG	DA	3096	1/1	0.10	-	29,29,29,29	0
56	MG	BA	3312	1/1	0.09	-	18,18,18,18	0
56	MG	BA	3565	1/1	0.12	-	51,51,51,51	0
56	MG	BA	3144	1/1	0.33	-	44,44,44,44	0
56	MG	AA	3047	1/1	0.12	-	45,45,45,45	0
56	MG	B0	101	1/1	0.13	-	71,71,71,71	0
56	MG	DA	3018	1/1	0.10	-	39,39,39,39	0
56	MG	CA	3002	1/1	0.09	-	43,43,43,43	0
56	MG	BA	3471	1/1	0.16	-	35,35,35,35	0
56	MG	BA	3183	1/1	0.26	-	35,35,35,35	0
56	MG	BA	3155	1/1	0.30	-	27,27,27,27	0
56	MG	BA	3562	1/1	0.09	-	46,46,46,46	0
56	MG	DA	3301	1/1	0.10	-	56,56,56,56	0
56	MG	AA	3030	1/1	0.08	-	47,47,47,47	0
56	MG	BA	3213	1/1	0.23	-	21,21,21,21	0
56	MG	DA	3582	1/1	0.16	-	38,38,38,38	0
56	MG	DA	3136	1/1	0.14	-	36,36,36,36	0
56	MG	DA	3552	1/1	0.18	-	49,49,49,49	0
56	MG	CA	3121	1/1	0.13	-	61,61,61,61	0
56	MG	D0	5001	1/1	0.05	-	39,39,39,39	0
56	MG	BA	3445	1/1	0.07	-	22,22,22,22	0
56	MG	DA	3206	1/1	0.13	-	50,50,50,50	0
56	MG	DA	3080	1/1	0.17	-	29,29,29,29	0
56	MG	BA	3254	1/1	0.17	-	45,45,45,45	0
56	MG	DA	3555	1/1	0.12	-	51,51,51,51	0
56	MG	CA	3095	1/1	0.09	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3243	1/1	0.09	-	50,50,50,50	0
56	MG	BA	3334	1/1	0.09	-	32,32,32,32	0
56	MG	AA	3014	1/1	0.10	-	49,49,49,49	0
56	MG	BA	3026	1/1	0.19	-	46,46,46,46	0
56	MG	BA	3061	1/1	0.24	-	44,44,44,44	0
56	MG	BA	3054	1/1	0.12	-	42,42,42,42	0
56	MG	DA	3123	1/1	0.11	-	51,51,51,51	0
56	MG	CA	3147	1/1	0.14	-	52,52,52,52	0
56	MG	BA	3490	1/1	0.10	-	38,38,38,38	0
56	MG	BA	3484	1/1	0.11	-	46,46,46,46	0
56	MG	DA	3273	1/1	0.18	-	31,31,31,31	0
56	MG	BA	3548	1/1	0.08	-	30,30,30,30	0
56	MG	BA	3496	1/1	0.17	-	31,31,31,31	0
56	MG	AA	3108	1/1	0.12	-	54,54,54,54	0
56	MG	AA	3166	1/1	0.13	-	53,53,53,53	0
56	MG	DA	3565	1/1	0.10	-	51,51,51,51	0
56	MG	DA	3328	1/1	0.17	-	48,48,48,48	0
56	MG	BA	3400	1/1	0.41	-	45,45,45,45	0
56	MG	DA	3135	1/1	0.16	-	47,47,47,47	0
56	MG	DA	3572	1/1	0.07	-	51,51,51,51	0
56	MG	BB	3008	1/1	0.17	-	21,21,21,21	0
56	MG	CA	3130	1/1	0.13	-	57,57,57,57	0
56	MG	DA	3156	1/1	0.08	-	38,38,38,38	0
56	MG	CA	3079	1/1	0.15	-	55,55,55,55	0
56	MG	BX	101	1/1	0.18	-	46,46,46,46	0
56	MG	BA	3056	1/1	0.13	-	46,46,46,46	0
56	MG	BA	3252	1/1	0.26	-	51,51,51,51	0
56	MG	BA	3017	1/1	0.14	-	40,40,40,40	0
56	MG	BA	3593	1/1	0.24	-	39,39,39,39	0
56	MG	CA	3061	1/1	0.10	-	45,45,45,45	0
56	MG	DA	3337	1/1	0.08	-	42,42,42,42	0
56	MG	DA	3140	1/1	0.08	-	37,37,37,37	0
56	MG	DA	3548	1/1	0.17	-	40,40,40,40	0
56	MG	DA	3462	1/1	0.11	-	35,35,35,35	0
56	MG	BA	3637	1/1	0.17	-	24,24,24,24	0
56	MG	DA	3348	1/1	0.12	-	25,25,25,25	0
56	MG	CA	3055	1/1	0.17	-	62,62,62,62	0
56	MG	DA	3142	1/1	0.14	-	37,37,37,37	0
56	MG	CA	3032	1/1	0.12	-	68,68,68,68	0
56	MG	DA	3252	1/1	0.22	-	53,53,53,53	0
56	MG	DA	3092	1/1	0.19	-	45,45,45,45	0
56	MG	DA	3163	1/1	0.25	-	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DD	301	1/1	0.13	-	43,43,43,43	0
56	MG	DA	3574	1/1	0.11	-	56,56,56,56	0
56	MG	AX	3007	1/1	0.14	-	60,60,60,60	0
56	MG	DA	3440	1/1	0.14	-	52,52,52,52	0
56	MG	DB	3011	1/1	0.07	-	29,29,29,29	0
56	MG	BA	3039	1/1	0.09	-	31,31,31,31	0
56	MG	DA	3587	1/1	0.09	-	53,53,53,53	0
56	MG	BA	3270	1/1	0.13	-	21,21,21,21	0
56	MG	BA	3214	1/1	0.23	-	28,28,28,28	0
58	ZN	AN	501	1/1	0.14	-	67,67,67,67	0
56	MG	BA	3517	1/1	0.12	-	40,40,40,40	0
56	MG	AA	3126	1/1	0.08	-	54,54,54,54	0
56	MG	AA	3156	1/1	0.09	-	61,61,61,61	0
56	MG	BR	3003	1/1	0.12	-	39,39,39,39	0
56	MG	AA	3011	1/1	0.07	-	24,24,24,24	0
56	MG	BA	3631	1/1	0.12	-	41,41,41,41	0
56	MG	BA	3343	1/1	0.16	-	27,27,27,27	0
56	MG	DA	3158	1/1	0.17	-	36,36,36,36	0
56	MG	DA	3164	1/1	0.19	-	36,36,36,36	0
56	MG	DA	3055	1/1	0.09	-	34,34,34,34	0
56	MG	BA	3645	1/1	0.12	-	66,66,66,66	0
56	MG	CA	3087	1/1	0.11	-	33,33,33,33	0
56	MG	DA	3247	1/1	0.13	-	49,49,49,49	0
56	MG	AA	3116	1/1	0.15	-	51,51,51,51	0
56	MG	D5	502	1/1	0.44	-	36,36,36,36	0
56	MG	BA	3125	1/1	0.18	-	51,51,51,51	0
56	MG	CA	3025	1/1	0.09	-	48,48,48,48	0
56	MG	DA	3245	1/1	0.12	-	46,46,46,46	0
56	MG	BA	3016	1/1	0.12	-	50,50,50,50	0
56	MG	BA	3080	1/1	0.14	-	29,29,29,29	0
56	MG	BA	3491	1/1	0.10	-	39,39,39,39	0
56	MG	BA	3622	1/1	0.12	-	45,45,45,45	0
56	MG	BA	3387	1/1	0.24	-	49,49,49,49	0
56	MG	DA	3174	1/1	0.11	-	44,44,44,44	0
56	MG	CA	3152	1/1	0.16	-	75,75,75,75	0
56	MG	BA	3554	1/1	0.06	-	47,47,47,47	0
56	MG	DA	3109	1/1	0.13	-	50,50,50,50	0
56	MG	DA	3137	1/1	0.10	-	37,37,37,37	0
56	MG	CA	3044	1/1	0.14	-	56,56,56,56	0
56	MG	BA	3067	1/1	0.12	-	34,34,34,34	0
56	MG	BA	3393	1/1	0.14	-	49,49,49,49	0
56	MG	AA	3056	1/1	0.14	-	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AA	3003	1/1	0.16	-	57,57,57,57	0
56	MG	BA	3458	1/1	0.06	-	60,60,60,60	0
56	MG	DA	3381	1/1	0.26	-	56,56,56,56	0
56	MG	AA	3037	1/1	0.12	-	51,51,51,51	0
56	MG	BA	3123	1/1	0.16	-	36,36,36,36	0
56	MG	DA	3409	1/1	0.19	-	53,53,53,53	0
56	MG	DA	3181	1/1	0.10	-	40,40,40,40	0
56	MG	AA	3117	1/1	0.08	-	47,47,47,47	0
56	MG	BA	3140	1/1	0.14	-	33,33,33,33	0
56	MG	BA	3282	1/1	0.22	-	31,31,31,31	0
56	MG	DA	3496	1/1	0.07	-	46,46,46,46	0
56	MG	CA	3014	1/1	0.12	-	39,39,39,39	0
56	MG	BA	3446	1/1	0.13	-	61,61,61,61	0
56	MG	BA	3330	1/1	0.24	-	44,44,44,44	0
56	MG	BA	3236	1/1	0.26	-	42,42,42,42	0
56	MG	DA	3358	1/1	0.21	-	45,45,45,45	0
56	MG	AL	201	1/1	0.08	-	63,63,63,63	0
56	MG	DA	3097	1/1	0.09	-	46,46,46,46	0
56	MG	AA	3138	1/1	0.10	-	50,50,50,50	0
59	K	AX	3001	1/1	0.06	-	48,48,48,48	0
56	MG	BA	3537	1/1	0.13	-	58,58,58,58	0
56	MG	BD	306	1/1	0.18	-	36,36,36,36	0
56	MG	DA	3404	1/1	0.10	-	46,46,46,46	0
56	MG	DA	3048	1/1	0.23	-	41,41,41,41	0
56	MG	CA	3128	1/1	0.08	-	39,39,39,39	0
56	MG	DA	3391	1/1	0.06	-	42,42,42,42	0
56	MG	DA	3291	1/1	0.07	-	38,38,38,38	0
56	MG	BA	3285	1/1	0.09	-	48,48,48,48	0
56	MG	BA	3204	1/1	0.18	-	35,35,35,35	0
56	MG	AA	3013	1/1	0.08	-	58,58,58,58	0
56	MG	BA	3211	1/1	0.27	-	29,29,29,29	0
56	MG	AA	3143	1/1	0.08	-	32,32,32,32	0
56	MG	BA	3114	1/1	0.19	-	34,34,34,34	0
56	MG	AA	3175	1/1	0.10	-	53,53,53,53	0
56	MG	BA	3599	1/1	0.13	-	46,46,46,46	0
56	MG	BA	3287	1/1	0.13	-	46,46,46,46	0
56	MG	CA	3106	1/1	0.19	-	40,40,40,40	0
56	MG	DA	3076	1/1	0.10	-	43,43,43,43	0
56	MG	CA	3089	1/1	0.13	-	40,40,40,40	0
56	MG	CK	3001	1/1	0.13	-	50,50,50,50	0
56	MG	BA	3195	1/1	0.13	-	47,47,47,47	0
56	MG	CA	3054	1/1	0.09	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3289	1/1	0.14	-	26,26,26,26	0
56	MG	DA	3011	1/1	0.13	-	38,38,38,38	0
56	MG	AA	3184	1/1	0.16	-	74,74,74,74	0
56	MG	CA	3137	1/1	0.13	-	66,66,66,66	0
56	MG	DA	3165	1/1	0.10	-	34,34,34,34	0
56	MG	DA	3401	1/1	0.06	-	55,55,55,55	0
56	MG	CA	3019	1/1	0.22	-	71,71,71,71	0
56	MG	DB	3007	1/1	0.17	-	38,38,38,38	0
56	MG	AA	3136	1/1	0.17	-	56,56,56,56	0
56	MG	AA	3036	1/1	0.07	-	41,41,41,41	0
56	MG	DA	3102	1/1	0.16	-	51,51,51,51	0
56	MG	DA	3280	1/1	0.12	-	50,50,50,50	0
56	MG	AA	3129	1/1	0.10	-	35,35,35,35	0
56	MG	BA	3571	1/1	0.15	-	50,50,50,50	0
56	MG	CA	3047	1/1	0.19	-	51,51,51,51	0
56	MG	CA	3046	1/1	0.07	-	41,41,41,41	0
56	MG	BA	3512	1/1	0.12	-	45,45,45,45	0
56	MG	BA	3267	1/1	0.15	-	40,40,40,40	0
56	MG	BA	3492	1/1	0.15	-	42,42,42,42	0
56	MG	BA	3029	1/1	0.13	-	12,12,12,12	0
56	MG	DA	3026	1/1	0.08	-	34,34,34,34	0
56	MG	AA	3035	1/1	0.17	-	65,65,65,65	0
56	MG	DA	3329	1/1	0.08	-	48,48,48,48	0
56	MG	BA	3382	1/1	0.13	-	27,27,27,27	0
56	MG	CA	3149	1/1	0.15	-	66,66,66,66	0
56	MG	BA	3305	1/1	0.16	-	28,28,28,28	0
56	MG	BA	3014	1/1	0.34	-	35,35,35,35	0
56	MG	AA	3121	1/1	0.09	-	40,40,40,40	0
56	MG	AA	3174	1/1	0.10	-	55,55,55,55	0
56	MG	DA	3272	1/1	0.09	-	57,57,57,57	0
56	MG	BA	3034	1/1	0.19	-	24,24,24,24	0
56	MG	DA	3334	1/1	0.11	-	24,24,24,24	0
56	MG	DA	3019	1/1	0.10	-	40,40,40,40	0
56	MG	BA	3510	1/1	0.20	-	25,25,25,25	0
56	MG	AA	3154	1/1	0.20	-	51,51,51,51	0
56	MG	AA	3020	1/1	0.16	-	49,49,49,49	0
56	MG	DA	3523	1/1	0.08	-	40,40,40,40	0
56	MG	BA	3560	1/1	0.18	-	55,55,55,55	0
56	MG	BA	3585	1/1	0.16	-	50,50,50,50	0
56	MG	BA	3643	1/1	0.09	-	42,42,42,42	0
56	MG	AA	3111	1/1	0.22	-	45,45,45,45	0
56	MG	DV	3002	1/1	0.14	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3141	1/1	0.10	-	45,45,45,45	0
56	MG	DA	3365	1/1	0.10	-	29,29,29,29	0
56	MG	DA	3579	1/1	0.07	-	54,54,54,54	0
56	MG	BA	3552	1/1	0.09	-	31,31,31,31	0
56	MG	AA	3060	1/1	0.16	-	55,55,55,55	0
56	MG	BA	3494	1/1	0.14	-	34,34,34,34	0
56	MG	BA	3335	1/1	0.10	-	40,40,40,40	0
56	MG	DF	302	1/1	0.34	-	41,41,41,41	0
56	MG	DA	3549	1/1	0.09	-	41,41,41,41	0
56	MG	BY	503	1/1	0.12	-	42,42,42,42	0
56	MG	BA	3157	1/1	0.16	-	34,34,34,34	0
56	MG	DA	3114	1/1	0.07	-	37,37,37,37	0
56	MG	BA	3241	1/1	0.29	-	26,26,26,26	0
56	MG	BA	3071	1/1	0.12	-	32,32,32,32	0
56	MG	BA	3461	1/1	0.38	-	52,52,52,52	0
56	MG	CA	3150	1/1	0.12	-	62,62,62,62	0
56	MG	DA	3356	1/1	0.07	-	31,31,31,31	0
56	MG	BA	3468	1/1	0.15	-	32,32,32,32	0
56	MG	CA	3059	1/1	0.13	-	58,58,58,58	0
56	MG	BA	3462	1/1	0.05	-	44,44,44,44	0
56	MG	DA	3466	1/1	0.10	-	38,38,38,38	0
56	MG	CA	3068	1/1	0.08	-	74,74,74,74	0
56	MG	AA	3132	1/1	0.21	-	50,50,50,50	0
56	MG	BA	3540	1/1	0.13	-	46,46,46,46	0
56	MG	DA	3350	1/1	0.12	-	36,36,36,36	0
56	MG	DA	3187	1/1	0.12	-	46,46,46,46	0
56	MG	BA	3606	1/1	0.12	-	32,32,32,32	0
56	MG	DA	3566	1/1	0.12	-	61,61,61,61	0
56	MG	BE	306	1/1	0.07	-	32,32,32,32	0
56	MG	CA	3031	1/1	0.13	-	52,52,52,52	0
56	MG	BA	3383	1/1	0.10	-	33,33,33,33	0
56	MG	CA	3135	1/1	0.09	-	62,62,62,62	0
56	MG	DA	3061	1/1	0.07	-	35,35,35,35	0
56	MG	AA	3179	1/1	0.15	-	63,63,63,63	0
56	MG	DA	3366	1/1	0.14	-	43,43,43,43	0
56	MG	BA	3638	1/1	0.08	-	32,32,32,32	0
56	MG	CA	3100	1/1	0.09	-	56,56,56,56	0
56	MG	BA	3502	1/1	0.15	-	33,33,33,33	0
56	MG	BA	3309	1/1	0.13	-	32,32,32,32	0
56	MG	BA	3479	1/1	0.17	-	45,45,45,45	0
56	MG	BA	3151	1/1	0.09	-	34,34,34,34	0
56	MG	BA	3088	1/1	0.07	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AA	3127	1/1	0.04	-	68,68,68,68	0
56	MG	DA	3128	1/1	0.35	-	42,42,42,42	0
56	MG	DA	3422	1/1	0.09	-	63,63,63,63	0
56	MG	DA	3330	1/1	0.11	-	42,42,42,42	0
56	MG	BA	3126	1/1	0.10	-	45,45,45,45	0
56	MG	DA	3101	1/1	0.07	-	46,46,46,46	0
56	MG	DA	3281	1/1	0.14	-	56,56,56,56	0
56	MG	DA	3122	1/1	0.17	-	45,45,45,45	0
56	MG	DA	3463	1/1	0.14	-	28,28,28,28	0
56	MG	BA	3246	1/1	0.16	-	56,56,56,56	0
56	MG	AA	3114	1/1	0.14	-	56,56,56,56	0
56	MG	BA	3192	1/1	0.12	-	58,58,58,58	0
56	MG	BA	3153	1/1	0.20	-	39,39,39,39	0
56	MG	DA	3170	1/1	0.10	-	38,38,38,38	0
56	MG	DA	3049	1/1	0.10	-	40,40,40,40	0
56	MG	BA	3268	1/1	0.25	-	39,39,39,39	0
56	MG	BA	3457	1/1	0.13	-	29,29,29,29	0
56	MG	DA	3489	1/1	0.15	-	49,49,49,49	0
56	MG	DA	3322	1/1	0.16	-	23,23,23,23	0
56	MG	BA	3051	1/1	0.26	-	41,41,41,41	0
56	MG	BB	3005	1/1	0.24	-	30,30,30,30	0
56	MG	DG	3001	1/1	0.36	-	81,81,81,81	0
56	MG	DA	3258	1/1	0.17	-	49,49,49,49	0
56	MG	DA	3476	1/1	0.06	-	32,32,32,32	0
56	MG	DA	3352	1/1	0.10	-	45,45,45,45	0
56	MG	DA	3471	1/1	0.16	-	50,50,50,50	0
56	MG	DA	3389	1/1	0.11	-	42,42,42,42	0
56	MG	DA	3545	1/1	0.08	-	58,58,58,58	0
56	MG	BA	3654	1/1	0.16	-	64,64,64,64	0
56	MG	BA	3463	1/1	0.13	-	43,43,43,43	0
56	MG	BV	201	1/1	0.51	-	36,36,36,36	0
56	MG	DA	3421	1/1	0.14	-	52,52,52,52	0
56	MG	DA	3255	1/1	0.21	-	32,32,32,32	0
56	MG	BA	3621	1/1	0.13	-	30,30,30,30	0
56	MG	DA	3253	1/1	0.12	-	26,26,26,26	0
56	MG	BA	3120	1/1	0.20	-	44,44,44,44	0
56	MG	BA	3191	1/1	0.14	-	33,33,33,33	0
56	MG	BE	305	1/1	0.44	-	51,51,51,51	0
56	MG	BA	3322	1/1	0.11	-	40,40,40,40	0
56	MG	BA	3138	1/1	0.12	-	35,35,35,35	0
56	MG	DA	3113	1/1	0.09	-	41,41,41,41	0
56	MG	BA	3345	1/1	0.15	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3197	1/1	0.13	-	19,19,19,19	0
56	MG	BH	3001	1/1	0.16	-	56,56,56,56	0
56	MG	BA	3569	1/1	0.18	-	55,55,55,55	0
56	MG	BA	3156	1/1	0.16	-	48,48,48,48	0
56	MG	DA	3444	1/1	0.16	-	53,53,53,53	0
56	MG	BP	202	1/1	0.47	-	31,31,31,31	0
56	MG	DA	3372	1/1	0.08	-	21,21,21,21	0
56	MG	BA	3405	1/1	0.14	-	26,26,26,26	0
56	MG	DA	3353	1/1	0.12	-	32,32,32,32	0
56	MG	DA	3148	1/1	0.26	-	47,47,47,47	0
56	MG	AA	3128	1/1	0.12	-	57,57,57,57	0
56	MG	DA	3319	1/1	0.18	-	38,38,38,38	0
56	MG	AA	3083	1/1	0.09	-	59,59,59,59	0
56	MG	DA	3428	1/1	0.18	-	33,33,33,33	0
56	MG	DA	3269	1/1	0.19	-	43,43,43,43	0
56	MG	DA	3359	1/1	0.13	-	43,43,43,43	0
56	MG	BA	3419	1/1	0.13	-	20,20,20,20	0
56	MG	BA	3131	1/1	0.24	-	36,36,36,36	0
56	MG	DA	3285	1/1	0.13	-	52,52,52,52	0
56	MG	DA	3229	1/1	0.16	-	38,38,38,38	0
56	MG	BA	3598	1/1	0.12	-	48,48,48,48	0
56	MG	CA	3037	1/1	0.07	-	45,45,45,45	0
56	MG	DR	202	1/1	0.15	-	32,32,32,32	0
56	MG	AA	3163	1/1	0.11	-	49,49,49,49	0
56	MG	BA	3097	1/1	0.10	-	53,53,53,53	0
56	MG	DA	3157	1/1	0.11	-	40,40,40,40	0
56	MG	DA	3560	1/1	0.16	-	51,51,51,51	0
56	MG	DA	3030	1/1	0.15	-	30,30,30,30	0
56	MG	DA	3208	1/1	0.08	-	43,43,43,43	0
56	MG	BA	3608	1/1	0.10	-	45,45,45,45	0
56	MG	AA	3139	1/1	0.09	-	36,36,36,36	0
56	MG	DA	3147	1/1	0.20	-	47,47,47,47	0
56	MG	BA	3368	1/1	0.08	-	42,42,42,42	0
56	MG	BA	3297	1/1	0.11	-	39,39,39,39	0
56	MG	D3	3001	1/1	0.75	-	70,70,70,70	0
56	MG	AA	3107	1/1	0.21	-	36,36,36,36	0
56	MG	CA	3072	1/1	0.21	-	57,57,57,57	0
56	MG	DA	3185	1/1	0.16	-	32,32,32,32	0
56	MG	AA	3124	1/1	0.21	-	30,30,30,30	0
56	MG	BA	3129	1/1	0.14	-	42,42,42,42	0
56	MG	CA	3039	1/1	0.23	-	50,50,50,50	0
56	MG	BA	3627	1/1	0.10	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DB	3002	1/1	0.14	-	50,50,50,50	0
56	MG	AA	3140	1/1	0.11	-	31,31,31,31	0
56	MG	BA	3438	1/1	0.10	-	33,33,33,33	0
56	MG	BA	3588	1/1	0.11	-	51,51,51,51	0
56	MG	DA	3144	1/1	0.12	-	38,38,38,38	0
56	MG	DA	3537	1/1	0.10	-	47,47,47,47	0
56	MG	DA	3342	1/1	0.20	-	37,37,37,37	0
56	MG	DA	3538	1/1	0.11	-	39,39,39,39	0
56	MG	B0	102	1/1	0.29	-	42,42,42,42	0
56	MG	AA	3159	1/1	0.07	-	56,56,56,56	0
56	MG	AA	3031	1/1	0.07	-	60,60,60,60	0
56	MG	BA	3374	1/1	0.10	-	29,29,29,29	0
56	MG	CA	3082	1/1	0.13	-	62,62,62,62	0
56	MG	CA	3120	1/1	0.14	-	51,51,51,51	0
56	MG	BA	3108	1/1	0.12	-	38,38,38,38	0
56	MG	DA	3562	1/1	0.10	-	42,42,42,42	0
56	MG	DA	3095	1/1	0.31	-	47,47,47,47	0
56	MG	DA	3418	1/1	0.12	-	29,29,29,29	0
56	MG	BV	202	1/1	0.26	-	36,36,36,36	0
56	MG	BA	3453	1/1	0.07	-	27,27,27,27	0
56	MG	DA	3195	1/1	0.10	-	38,38,38,38	0
56	MG	DA	3543	1/1	0.06	-	63,63,63,63	0
56	MG	DA	3535	1/1	0.14	-	22,22,22,22	0
56	MG	AA	3071	1/1	0.14	-	36,36,36,36	0
56	MG	BA	3670	1/1	0.32	-	34,34,34,34	0
56	MG	DA	3224	1/1	0.16	-	22,22,22,22	0
56	MG	BA	3167	1/1	0.10	-	46,46,46,46	0
56	MG	BA	3442	1/1	0.12	-	20,20,20,20	0
56	MG	AD	502	1/1	0.17	-	55,55,55,55	0
56	MG	BA	3566	1/1	0.15	-	46,46,46,46	0
56	MG	BA	3460	1/1	0.11	-	57,57,57,57	0
56	MG	BA	3590	1/1	0.11	-	55,55,55,55	0
56	MG	BD	301	1/1	0.14	-	30,30,30,30	0
56	MG	BA	3132	1/1	0.14	-	25,25,25,25	0
56	MG	BA	3633	1/1	0.14	-	57,57,57,57	0
56	MG	DA	3213	1/1	0.08	-	34,34,34,34	0
56	MG	CA	3148	1/1	0.10	-	57,57,57,57	0
56	MG	AA	3029	1/1	0.10	-	52,52,52,52	0
56	MG	DA	3586	1/1	0.09	-	47,47,47,47	0
56	MG	BA	3062	1/1	0.17	-	46,46,46,46	0
56	MG	DA	3559	1/1	0.12	-	55,55,55,55	0
56	MG	DA	3083	1/1	0.07	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3368	1/1	0.08	-	25,25,25,25	0
56	MG	AA	3064	1/1	0.15	-	45,45,45,45	0
56	MG	BA	3171	1/1	0.13	-	44,44,44,44	0
56	MG	BB	3001	1/1	0.12	-	36,36,36,36	0
56	MG	BA	3619	1/1	0.16	-	30,30,30,30	0
56	MG	BA	3404	1/1	0.16	-	38,38,38,38	0
56	MG	BA	3042	1/1	0.16	-	33,33,33,33	0
56	MG	AA	3113	1/1	0.18	-	53,53,53,53	0
56	MG	BA	3355	1/1	0.07	-	31,31,31,31	0
56	MG	BA	3219	1/1	0.10	-	20,20,20,20	0
56	MG	DA	3487	1/1	0.10	-	50,50,50,50	0
56	MG	AA	3152	1/1	0.13	-	57,57,57,57	0
56	MG	DA	3333	1/1	0.15	-	38,38,38,38	0
56	MG	BA	3303	1/1	0.11	-	31,31,31,31	0
56	MG	BA	3542	1/1	0.04	-	51,51,51,51	0
56	MG	BA	3110	1/1	0.21	-	31,31,31,31	0
56	MG	DA	3129	1/1	0.13	-	54,54,54,54	0
56	MG	DA	3556	1/1	0.15	-	36,36,36,36	0
56	MG	CA	3127	1/1	0.08	-	49,49,49,49	0
56	MG	DA	3227	1/1	0.15	-	49,49,49,49	0
56	MG	DA	3176	1/1	0.11	-	29,29,29,29	0
56	MG	BA	3023	1/1	0.13	-	40,40,40,40	0
56	MG	BA	3663	1/1	0.10	-	20,20,20,20	0
56	MG	DU	201	1/1	0.41	-	41,41,41,41	0
56	MG	DD	302	1/1	0.41	-	39,39,39,39	0
56	MG	CA	3048	1/1	0.28	-	52,52,52,52	0
56	MG	BA	3091	1/1	0.10	-	19,19,19,19	0
56	MG	BA	3292	1/1	0.10	-	43,43,43,43	0
56	MG	BA	3417	1/1	0.15	-	24,24,24,24	0
56	MG	BA	3286	1/1	0.11	-	32,32,32,32	0
56	MG	AA	3002	1/1	0.14	-	43,43,43,43	0
56	MG	DA	3023	1/1	0.12	-	37,37,37,37	0
56	MG	CA	3138	1/1	0.17	-	58,58,58,58	0
56	MG	DA	3160	1/1	0.18	-	44,44,44,44	0
56	MG	BA	3068	1/1	0.09	-	39,39,39,39	0
56	MG	BA	3115	1/1	0.12	-	34,34,34,34	0
56	MG	DA	3192	1/1	0.09	-	51,51,51,51	0
56	MG	BA	3260	1/1	0.23	-	49,49,49,49	0
56	MG	BA	3040	1/1	0.12	-	43,43,43,43	0
56	MG	CA	3132	1/1	0.22	-	73,73,73,73	0
56	MG	BA	3367	1/1	0.18	-	49,49,49,49	0
56	MG	DA	3256	1/1	0.14	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3075	1/1	0.17	-	41,41,41,41	0
56	MG	BA	3273	1/1	0.11	-	29,29,29,29	0
56	MG	CA	3076	1/1	0.25	-	48,48,48,48	0
56	MG	BA	3486	1/1	0.15	-	21,21,21,21	0
56	MG	BB	3006	1/1	0.15	-	49,49,49,49	0
56	MG	BA	3545	1/1	0.08	-	54,54,54,54	0
56	MG	CA	3007	1/1	0.09	-	50,50,50,50	0
56	MG	AA	3048	1/1	0.19	-	42,42,42,42	0
56	MG	BA	3212	1/1	0.17	-	28,28,28,28	0
56	MG	DA	3202	1/1	0.19	-	24,24,24,24	0
56	MG	BA	3664	1/1	0.14	-	30,30,30,30	0
56	MG	BA	3210	1/1	0.21	-	24,24,24,24	0
56	MG	DE	3001	1/1	0.18	-	43,43,43,43	0
56	MG	DA	3112	1/1	0.12	-	24,24,24,24	0
56	MG	AA	3066	1/1	0.17	-	46,46,46,46	0
56	MG	DA	3053	1/1	0.09	-	41,41,41,41	0
56	MG	BA	3209	1/1	0.14	-	26,26,26,26	0
56	MG	BA	3009	1/1	0.10	-	34,34,34,34	0
58	ZN	D5	501	1/1	0.14	-	67,67,67,67	0
56	MG	AA	3095	1/1	0.16	-	55,55,55,55	0
56	MG	BA	3127	1/1	0.15	-	45,45,45,45	0
56	MG	BA	3242	1/1	0.29	-	46,46,46,46	0
56	MG	AA	3122	1/1	0.13	-	58,58,58,58	0
56	MG	BA	3641	1/1	0.18	-	33,33,33,33	0
56	MG	BA	3099	1/1	0.24	-	32,32,32,32	0
56	MG	BA	3656	1/1	0.07	-	12,12,12,12	0
56	MG	BA	3500	1/1	0.12	-	35,35,35,35	0
56	MG	DA	3346	1/1	0.12	-	33,33,33,33	0
56	MG	AA	3161	1/1	0.10	-	66,66,66,66	0
56	MG	BA	3015	1/1	0.11	-	27,27,27,27	0
56	MG	BA	3394	1/1	0.18	-	35,35,35,35	0
56	MG	DA	3390	1/1	0.07	-	41,41,41,41	0
56	MG	DB	3010	1/1	0.15	-	60,60,60,60	0
56	MG	CA	3049	1/1	0.14	-	51,51,51,51	0
56	MG	DA	3461	1/1	0.17	-	33,33,33,33	0
56	MG	BA	3362	1/1	0.14	-	30,30,30,30	0
56	MG	BA	3563	1/1	0.17	-	47,47,47,47	0
56	MG	CA	3129	1/1	0.11	-	55,55,55,55	0
56	MG	DA	3159	1/1	0.17	-	31,31,31,31	0
56	MG	DA	3105	1/1	0.09	-	36,36,36,36	0
56	MG	BA	3020	1/1	0.12	-	33,33,33,33	0
56	MG	AA	3052	1/1	0.26	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3280	1/1	0.12	-	48,48,48,48	0
56	MG	DA	3089	1/1	0.30	-	33,33,33,33	0
56	MG	DT	5001	1/1	0.06	-	42,42,42,42	0
56	MG	BA	3189	1/1	0.22	-	26,26,26,26	0
56	MG	BA	3522	1/1	0.09	-	52,52,52,52	0
56	MG	BA	3010	1/1	0.12	-	33,33,33,33	0
56	MG	BA	3501	1/1	0.11	-	44,44,44,44	0
56	MG	BA	3385	1/1	0.11	-	20,20,20,20	0
56	MG	BA	3180	1/1	0.20	-	33,33,33,33	0
56	MG	BA	3592	1/1	0.13	-	52,52,52,52	0
56	MG	AA	3157	1/1	0.07	-	55,55,55,55	0
56	MG	BA	3284	1/1	0.13	-	41,41,41,41	0
56	MG	BA	3613	1/1	0.17	-	45,45,45,45	0
56	MG	AA	3171	1/1	0.10	-	62,62,62,62	0
56	MG	BA	3344	1/1	0.12	-	35,35,35,35	0
56	MG	BA	3509	1/1	0.17	-	23,23,23,23	0
56	MG	AA	3092	1/1	0.18	-	61,61,61,61	0
56	MG	DA	3349	1/1	0.21	-	46,46,46,46	0
56	MG	DA	3271	1/1	0.09	-	55,55,55,55	0
56	MG	DA	3373	1/1	0.12	-	42,42,42,42	0
56	MG	CT	3001	1/1	0.09	-	50,50,50,50	0
56	MG	BA	3369	1/1	0.18	-	33,33,33,33	0
56	MG	BA	3420	1/1	0.09	-	24,24,24,24	0
57	SF4	CD	501	8/8	0.14	-	58,71,82,82	0
56	MG	DA	3133	1/1	0.10	-	53,53,53,53	0
56	MG	DA	3371	1/1	0.13	-	46,46,46,46	0
56	MG	DA	3106	1/1	0.05	-	43,43,43,43	0
56	MG	BA	3130	1/1	0.21	-	40,40,40,40	0
56	MG	BA	3245	1/1	0.17	-	27,27,27,27	0
56	MG	BA	3375	1/1	0.25	-	51,51,51,51	0
56	MG	DA	3378	1/1	0.15	-	31,31,31,31	0
56	MG	BA	3444	1/1	0.11	-	34,34,34,34	0
56	MG	CA	3028	1/1	0.11	-	52,52,52,52	0
56	MG	DA	3507	1/1	0.11	-	54,54,54,54	0
56	MG	DA	3478	1/1	0.12	-	53,53,53,53	0
56	MG	BA	3538	1/1	0.14	-	55,55,55,55	0
56	MG	DA	3518	1/1	0.21	-	53,53,53,53	0
56	MG	DA	3524	1/1	0.12	-	51,51,51,51	0
56	MG	DA	3344	1/1	0.15	-	31,31,31,31	0
56	MG	BA	3386	1/1	0.21	-	32,32,32,32	0
56	MG	DA	3119	1/1	0.17	-	37,37,37,37	0
56	MG	BA	3098	1/1	0.14	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3378	1/1	0.16	-	16,16,16,16	0
56	MG	CA	3038	1/1	0.09	-	44,44,44,44	0
56	MG	BA	3531	1/1	0.10	-	41,41,41,41	0
56	MG	DA	3121	1/1	0.47	-	50,50,50,50	0
56	MG	BA	3584	1/1	0.24	-	44,44,44,44	0
56	MG	BD	307	1/1	0.26	-	27,27,27,27	0
56	MG	CA	3041	1/1	0.12	-	67,67,67,67	0
56	MG	DA	3493	1/1	0.07	-	45,45,45,45	0
56	MG	DA	3323	1/1	0.12	-	35,35,35,35	0
56	MG	AA	3094	1/1	0.15	-	49,49,49,49	0
56	MG	BA	3353	1/1	0.09	-	39,39,39,39	0
56	MG	BA	3525	1/1	0.11	-	46,46,46,46	0
56	MG	AA	3093	1/1	0.20	-	45,45,45,45	0
56	MG	DA	3497	1/1	0.07	-	45,45,45,45	0
56	MG	BA	3337	1/1	0.12	-	37,37,37,37	0
56	MG	BA	3476	1/1	0.07	-	51,51,51,51	0
56	MG	BA	3259	1/1	0.15	-	35,35,35,35	0
56	MG	DA	3460	1/1	0.11	-	50,50,50,50	0
56	MG	AN	502	1/1	0.20	-	53,53,53,53	0
56	MG	DA	3477	1/1	0.11	-	42,42,42,42	0
56	MG	BA	3291	1/1	0.13	-	14,14,14,14	0
56	MG	BA	3564	1/1	0.15	-	29,29,29,29	0
56	MG	DA	3398	1/1	0.12	-	51,51,51,51	0
56	MG	AA	3123	1/1	0.16	-	38,38,38,38	0
56	MG	BA	3244	1/1	0.47	-	46,46,46,46	0
56	MG	CA	3042	1/1	0.19	-	56,56,56,56	0
56	MG	BA	3306	1/1	0.11	-	54,54,54,54	0
56	MG	AA	3005	1/1	0.17	-	37,37,37,37	0
56	MG	BA	3046	1/1	0.19	-	29,29,29,29	0
56	MG	BA	3338	1/1	0.12	-	48,48,48,48	0
56	MG	BA	3543	1/1	0.11	-	47,47,47,47	0
56	MG	CA	3104	1/1	0.16	-	74,74,74,74	0
56	MG	BA	3372	1/1	0.17	-	29,29,29,29	0
56	MG	AA	3057	1/1	0.29	-	67,67,67,67	0
56	MG	DV	3001	1/1	0.57	-	45,45,45,45	0
56	MG	BA	3314	1/1	0.20	-	36,36,36,36	0
56	MG	CA	3143	1/1	0.17	-	42,42,42,42	0
56	MG	BA	3582	1/1	0.08	-	31,31,31,31	0
56	MG	CA	3013	1/1	0.13	-	53,53,53,53	0
56	MG	DA	3009	1/1	0.09	-	42,42,42,42	0
56	MG	DA	3149	1/1	0.29	-	41,41,41,41	0
56	MG	BA	3075	1/1	0.32	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	CA	3040	1/1	0.27	-	52,52,52,52	0
56	MG	BA	3473	1/1	0.10	-	37,37,37,37	0
56	MG	DA	3485	1/1	0.12	-	60,60,60,60	0
56	MG	DA	3361	1/1	0.16	-	38,38,38,38	0
56	MG	BA	3443	1/1	0.10	-	44,44,44,44	0
56	MG	CA	3099	1/1	0.12	-	57,57,57,57	0
58	ZN	B9	501	1/1	0.14	-	45,45,45,45	0
56	MG	DQ	3002	1/1	0.15	-	38,38,38,38	0
56	MG	DA	3217	1/1	0.09	-	39,39,39,39	0
56	MG	CA	3009	1/1	0.17	-	55,55,55,55	0
56	MG	BF	304	1/1	0.19	-	37,37,37,37	0
56	MG	BA	3089	1/1	0.12	-	37,37,37,37	0
56	MG	DA	3103	1/1	0.08	-	56,56,56,56	0
56	MG	DA	3021	1/1	0.19	-	55,55,55,55	0
56	MG	DA	3010	1/1	0.13	-	36,36,36,36	0
56	MG	DA	3219	1/1	0.09	-	33,33,33,33	0
56	MG	DF	301	1/1	0.28	-	44,44,44,44	0
56	MG	BA	3076	1/1	0.07	-	29,29,29,29	0
56	MG	CA	3142	1/1	0.12	-	42,42,42,42	0
56	MG	BA	3464	1/1	0.08	-	41,41,41,41	0
56	MG	DA	3495	1/1	0.33	-	45,45,45,45	0
56	MG	BA	3163	1/1	0.11	-	31,31,31,31	0
56	MG	DR	201	1/1	0.16	-	36,36,36,36	0
56	MG	DA	3360	1/1	0.09	-	39,39,39,39	0
56	MG	DA	3161	1/1	0.13	-	24,24,24,24	0
56	MG	DA	3459	1/1	0.26	-	38,38,38,38	0
56	MG	BA	3441	1/1	0.12	-	44,44,44,44	0
56	MG	CA	3003	1/1	0.11	-	65,65,65,65	0
56	MG	DA	3246	1/1	0.37	-	38,38,38,38	0
56	MG	DA	3047	1/1	0.11	-	41,41,41,41	0
56	MG	DA	3194	1/1	0.11	-	47,47,47,47	0
56	MG	AA	3082	1/1	0.09	-	57,57,57,57	0
56	MG	DA	3073	1/1	0.12	-	51,51,51,51	0
56	MG	BA	3223	1/1	0.15	-	51,51,51,51	0
56	MG	DB	3005	1/1	0.21	-	56,56,56,56	0
56	MG	BA	3182	1/1	0.27	-	30,30,30,30	0
56	MG	BA	3187	1/1	0.13	-	37,37,37,37	0
56	MG	DA	3369	1/1	0.11	-	45,45,45,45	0
56	MG	DA	3067	1/1	0.14	-	53,53,53,53	0
56	MG	AA	3119	1/1	0.12	-	57,57,57,57	0
56	MG	BA	3044	1/1	0.14	-	30,30,30,30	0
56	MG	CA	3077	1/1	0.11	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3257	1/1	0.18	-	55,55,55,55	0
56	MG	DA	3482	1/1	0.09	-	46,46,46,46	0
56	MG	BW	3004	1/1	0.30	-	30,30,30,30	0
56	MG	BA	3415	1/1	0.22	-	54,54,54,54	0
56	MG	BA	3038	1/1	0.12	-	30,30,30,30	0
56	MG	BA	3480	1/1	0.21	-	43,43,43,43	0
56	MG	DA	3099	1/1	0.17	-	37,37,37,37	0
56	MG	DA	3347	1/1	0.13	-	41,41,41,41	0
56	MG	DA	3326	1/1	0.12	-	41,41,41,41	0
56	MG	CA	3067	1/1	0.07	-	63,63,63,63	0
56	MG	BA	3587	1/1	0.07	-	42,42,42,42	0
56	MG	CA	3083	1/1	0.19	-	66,66,66,66	0
56	MG	BA	3514	1/1	0.09	-	32,32,32,32	0
56	MG	DA	3594	1/1	0.12	-	48,48,48,48	0
56	MG	BA	3508	1/1	0.12	-	25,25,25,25	0
56	MG	BA	3336	1/1	0.09	-	43,43,43,43	0
56	MG	DA	3180	1/1	0.18	-	30,30,30,30	0
56	MG	CF	3001	1/1	0.09	-	45,45,45,45	0
56	MG	DA	3300	1/1	0.20	-	58,58,58,58	0
56	MG	BA	3555	1/1	0.14	-	42,42,42,42	0
56	MG	BQ	203	1/1	0.46	-	33,33,33,33	0
56	MG	BA	3002	1/1	0.14	-	39,39,39,39	0
56	MG	BE	301	1/1	0.07	-	45,45,45,45	0
56	MG	CA	3107	1/1	0.17	-	56,56,56,56	0
56	MG	BA	3225	1/1	0.09	-	31,31,31,31	0
56	MG	BA	3119	1/1	0.08	-	29,29,29,29	0
56	MG	BA	3326	1/1	0.17	-	28,28,28,28	0
56	MG	AA	3072	1/1	0.10	-	39,39,39,39	0
56	MG	BA	3359	1/1	0.13	-	54,54,54,54	0
56	MG	BA	3206	1/1	0.17	-	41,41,41,41	0
56	MG	DA	3207	1/1	0.11	-	39,39,39,39	0
56	MG	DA	3078	1/1	0.08	-	46,46,46,46	0
56	MG	BA	3134	1/1	0.28	-	40,40,40,40	0
56	MG	BA	3321	1/1	0.06	-	53,53,53,53	0
56	MG	AX	3003	1/1	0.28	-	50,50,50,50	0
56	MG	BA	3170	1/1	0.09	-	34,34,34,34	0
56	MG	CA	3109	1/1	0.12	-	50,50,50,50	0
56	MG	DA	3583	1/1	0.08	-	43,43,43,43	0
56	MG	AA	3042	1/1	0.14	-	54,54,54,54	0
56	MG	DA	3225	1/1	0.16	-	33,33,33,33	0
56	MG	DA	3585	1/1	0.06	-	37,37,37,37	0
56	MG	AA	3167	1/1	0.16	-	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	CA	3078	1/1	0.08	-	66,66,66,66	0
56	MG	CE	202	1/1	0.10	-	68,68,68,68	0
56	MG	DA	3068	1/1	0.13	-	35,35,35,35	0
56	MG	BA	3231	1/1	0.25	-	41,41,41,41	0
56	MG	DA	3199	1/1	0.09	-	52,52,52,52	0
56	MG	BA	3431	1/1	0.09	-	44,44,44,44	0
56	MG	BU	203	1/1	0.42	-	32,32,32,32	0
56	MG	DA	3124	1/1	0.12	-	29,29,29,29	0
56	MG	CA	3021	1/1	0.16	-	52,52,52,52	0
56	MG	DA	3241	1/1	0.14	-	36,36,36,36	0
56	MG	BA	3145	1/1	0.23	-	30,30,30,30	0
56	MG	AA	3185	1/1	0.05	-	64,64,64,64	0
56	MG	DA	3479	1/1	0.13	-	63,63,63,63	0
56	MG	DA	3502	1/1	0.12	-	39,39,39,39	0
56	MG	BA	3049	1/1	0.12	-	43,43,43,43	0
56	MG	BA	3573	1/1	0.18	-	44,44,44,44	0
56	MG	DA	3168	1/1	0.11	-	39,39,39,39	0
56	MG	DA	3544	1/1	0.15	-	51,51,51,51	0
56	MG	BA	3288	1/1	0.26	-	48,48,48,48	0
56	MG	CA	3144	1/1	0.13	-	56,56,56,56	0
56	MG	BA	3607	1/1	0.14	-	51,51,51,51	0
56	MG	BP	201	1/1	0.40	-	36,36,36,36	0
56	MG	BA	3086	1/1	0.16	-	39,39,39,39	0
56	MG	BF	302	1/1	0.06	-	45,45,45,45	0
56	MG	AA	3033	1/1	0.31	-	48,48,48,48	0
56	MG	DA	3400	1/1	0.16	-	38,38,38,38	0
56	MG	AA	3177	1/1	0.11	-	32,32,32,32	0
56	MG	BA	3519	1/1	0.13	-	53,53,53,53	0
56	MG	DA	3448	1/1	0.20	-	29,29,29,29	0
56	MG	BA	3035	1/1	0.19	-	21,21,21,21	0
56	MG	BA	3403	1/1	0.10	-	18,18,18,18	0
56	MG	BA	3489	1/1	0.26	-	41,41,41,41	0
56	MG	DA	3298	1/1	0.12	-	32,32,32,32	0
56	MG	DA	3526	1/1	0.07	-	64,64,64,64	0
56	MG	BA	3012	1/1	0.15	-	39,39,39,39	0
56	MG	BA	3673	1/1	0.08	-	37,37,37,37	0
56	MG	BA	3620	1/1	0.14	-	41,41,41,41	0
56	MG	BA	3675	1/1	0.39	-	33,33,33,33	0
56	MG	BA	3346	1/1	0.08	-	43,43,43,43	0
56	MG	DA	3054	1/1	0.25	-	45,45,45,45	0
56	MG	CA	3086	1/1	0.11	-	68,68,68,68	0
56	MG	BB	3013	1/1	0.14	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3352	1/1	0.11	-	32,32,32,32	0
56	MG	DA	3186	1/1	0.14	-	41,41,41,41	0
56	MG	BA	3220	1/1	0.13	-	31,31,31,31	0
56	MG	DA	3465	1/1	0.12	-	38,38,38,38	0
58	ZN	DY	501	1/1	0.11	-	92,92,92,92	0
56	MG	DA	3295	1/1	0.17	-	61,61,61,61	0
56	MG	AA	3084	1/1	0.07	-	43,43,43,43	0
56	MG	BA	3176	1/1	0.10	-	47,47,47,47	0
56	MG	DW	3002	1/1	0.35	-	60,60,60,60	0
56	MG	DA	3503	1/1	0.08	-	38,38,38,38	0
56	MG	BA	3074	1/1	0.11	-	45,45,45,45	0
56	MG	BA	3425	1/1	0.25	-	53,53,53,53	0
56	MG	DA	3592	1/1	0.64	-	52,52,52,52	0
56	MG	BA	3013	1/1	0.12	-	35,35,35,35	0
56	MG	CA	3084	1/1	0.11	-	72,72,72,72	0
56	MG	DA	3288	1/1	0.14	-	64,64,64,64	0
56	MG	CA	3136	1/1	0.13	-	53,53,53,53	0
56	MG	BA	3208	1/1	0.22	-	25,25,25,25	0
56	MG	DA	3248	1/1	0.27	-	52,52,52,52	0
56	MG	AA	3010	1/1	0.15	-	60,60,60,60	0
56	MG	DA	3151	1/1	0.12	-	34,34,34,34	0
56	MG	DA	3315	1/1	0.15	-	43,43,43,43	0
56	MG	BA	3166	1/1	0.10	-	35,35,35,35	0
56	MG	CA	3102	1/1	0.18	-	30,30,30,30	0
56	MG	BA	3172	1/1	0.12	-	54,54,54,54	0
56	MG	DA	3263	1/1	0.11	-	39,39,39,39	0
56	MG	BA	3175	1/1	0.13	-	33,33,33,33	0
56	MG	DA	3341	1/1	0.14	-	25,25,25,25	0
56	MG	BA	3406	1/1	0.19	-	39,39,39,39	0
56	MG	CA	3141	1/1	0.17	-	54,54,54,54	0
56	MG	BA	3632	1/1	0.14	-	54,54,54,54	0
56	MG	BA	3662	1/1	0.19	-	36,36,36,36	0
56	MG	BA	3250	1/1	0.32	-	33,33,33,33	0
56	MG	BA	3053	1/1	0.18	-	31,31,31,31	0
56	MG	DA	3251	1/1	0.16	-	62,62,62,62	0
56	MG	DA	3429	1/1	0.13	-	35,35,35,35	0
56	MG	DA	3387	1/1	0.05	-	53,53,53,53	0
56	MG	DA	3130	1/1	0.25	-	47,47,47,47	0
56	MG	BA	3657	1/1	0.12	-	24,24,24,24	0
56	MG	BB	3012	1/1	0.12	-	44,44,44,44	0
56	MG	BA	3087	1/1	0.17	-	36,36,36,36	0
56	MG	AA	3061	1/1	0.13	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3032	1/1	0.21	-	40,40,40,40	0
56	MG	BA	3597	1/1	0.09	-	43,43,43,43	0
56	MG	BA	3281	1/1	0.21	-	51,51,51,51	0
56	MG	BB	3017	1/1	0.07	-	40,40,40,40	0
56	MG	AA	3026	1/1	0.12	-	40,40,40,40	0
56	MG	AA	3162	1/1	0.11	-	40,40,40,40	0
56	MG	DA	3166	1/1	0.14	-	35,35,35,35	0
56	MG	BA	3413	1/1	0.15	-	26,26,26,26	0
56	MG	DA	3193	1/1	0.15	-	49,49,49,49	0
56	MG	BY	502	1/1	0.17	-	35,35,35,35	0
56	MG	BA	3272	1/1	0.07	-	37,37,37,37	0
56	MG	CA	3122	1/1	0.24	-	54,54,54,54	0
56	MG	BA	3063	1/1	0.09	-	47,47,47,47	0
56	MG	AX	3005	1/1	0.22	-	42,42,42,42	0
56	MG	DA	3405	1/1	0.14	-	45,45,45,45	0
56	MG	DA	3276	1/1	0.15	-	50,50,50,50	0
56	MG	BA	3547	1/1	0.04	-	60,60,60,60	0
56	MG	DQ	3001	1/1	0.17	-	48,48,48,48	0
56	MG	AA	3085	1/1	0.13	-	63,63,63,63	0
56	MG	BA	3488	1/1	0.28	-	36,36,36,36	0
56	MG	BA	3634	1/1	0.34	-	41,41,41,41	0
56	MG	DA	3274	1/1	0.10	-	56,56,56,56	0
56	MG	BA	3073	1/1	0.16	-	14,14,14,14	0
56	MG	DA	3433	1/1	0.17	-	33,33,33,33	0
56	MG	BA	3384	1/1	0.12	-	28,28,28,28	0
56	MG	BA	3421	1/1	0.11	-	36,36,36,36	0
56	MG	DA	3090	1/1	0.08	-	54,54,54,54	0
56	MG	BA	3347	1/1	0.09	-	53,53,53,53	0
56	MG	CA	3074	1/1	0.17	-	48,48,48,48	0
56	MG	DA	3385	1/1	0.07	-	45,45,45,45	0
56	MG	BA	3499	1/1	0.13	-	35,35,35,35	0
56	MG	DA	3132	1/1	0.12	-	35,35,35,35	0
56	MG	BB	3007	1/1	0.14	-	35,35,35,35	0
56	MG	BA	3591	1/1	0.07	-	36,36,36,36	0
56	MG	AA	3090	1/1	0.18	-	28,28,28,28	0
56	MG	DA	3514	1/1	0.04	-	40,40,40,40	0
56	MG	BA	3483	1/1	0.13	-	47,47,47,47	0
56	MG	BA	3203	1/1	0.12	-	35,35,35,35	0
56	MG	BA	3118	1/1	0.23	-	45,45,45,45	0
56	MG	CX	101	1/1	0.23	-	48,48,48,48	0
56	MG	BA	3298	1/1	0.11	-	28,28,28,28	0
56	MG	BA	3025	1/1	0.11	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AA	3089	1/1	0.13	-	36,36,36,36	0
56	MG	DA	3139	1/1	0.19	-	39,39,39,39	0
56	MG	BA	3277	1/1	0.20	-	32,32,32,32	0
56	MG	BA	3257	1/1	0.08	-	29,29,29,29	0
56	MG	AA	3017	1/1	0.17	-	63,63,63,63	0
56	MG	CA	3085	1/1	0.10	-	52,52,52,52	0
56	MG	BA	3504	1/1	0.17	-	39,39,39,39	0
56	MG	BA	3028	1/1	0.15	-	41,41,41,41	0
56	MG	DB	3012	1/1	0.12	-	53,53,53,53	0
56	MG	BA	3371	1/1	0.16	-	25,25,25,25	0
56	MG	DA	3335	1/1	0.15	-	36,36,36,36	0
56	MG	DA	3420	1/1	0.14	-	46,46,46,46	0
56	MG	DA	3214	1/1	0.18	-	30,30,30,30	0
56	MG	DA	3282	1/1	0.11	-	30,30,30,30	0
56	MG	DA	3200	1/1	0.08	-	28,28,28,28	0
56	MG	BA	3137	1/1	0.27	-	30,30,30,30	0
56	MG	CA	3024	1/1	0.08	-	64,64,64,64	0
56	MG	DB	3001	1/1	0.18	-	40,40,40,40	0
56	MG	DA	3306	1/1	0.14	-	38,38,38,38	0
56	MG	BA	3003	1/1	0.08	-	49,49,49,49	0
56	MG	DA	3310	1/1	0.08	-	41,41,41,41	0
56	MG	BA	3301	1/1	0.13	-	46,46,46,46	0
56	MG	AA	3130	1/1	0.10	-	50,50,50,50	0
56	MG	BA	3535	1/1	0.08	-	47,47,47,47	0
56	MG	AA	3038	1/1	0.11	-	53,53,53,53	0
56	MG	BA	3465	1/1	0.09	-	37,37,37,37	0
56	MG	AA	3187	1/1	0.11	-	33,33,33,33	0
56	MG	BA	3426	1/1	0.11	-	43,43,43,43	0
56	MG	AA	3079	1/1	0.32	-	49,49,49,49	0
56	MG	DA	3093	1/1	0.17	-	46,46,46,46	0
56	MG	BA	3234	1/1	0.14	-	57,57,57,57	0
56	MG	BA	3392	1/1	0.15	-	41,41,41,41	0
56	MG	DA	3006	1/1	0.12	-	33,33,33,33	0
56	MG	DA	3541	1/1	0.11	-	57,57,57,57	0
56	MG	BA	3311	1/1	0.15	-	39,39,39,39	0
56	MG	BA	3402	1/1	0.23	-	28,28,28,28	0
56	MG	DA	3279	1/1	0.11	-	27,27,27,27	0
56	MG	DA	3260	1/1	0.20	-	36,36,36,36	0
56	MG	DA	3031	1/1	0.09	-	21,21,21,21	0
56	MG	BA	3636	1/1	0.08	-	32,32,32,32	0
56	MG	AA	3165	1/1	0.10	-	43,43,43,43	0
56	MG	BA	3348	1/1	0.13	-	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3486	1/1	0.19	-	37,37,37,37	0
56	MG	CA	3088	1/1	0.10	-	41,41,41,41	0
56	MG	BA	3184	1/1	0.08	-	37,37,37,37	0
56	MG	AX	3008	1/1	0.15	-	23,23,23,23	0
56	MG	BA	3617	1/1	0.18	-	66,66,66,66	0
56	MG	DA	3125	1/1	0.12	-	47,47,47,47	0
56	MG	DA	3563	1/1	0.12	-	60,60,60,60	0
56	MG	BA	3323	1/1	0.06	-	61,61,61,61	0
56	MG	BA	3258	1/1	0.20	-	30,30,30,30	0
56	MG	DY	502	1/1	0.11	-	51,51,51,51	0
56	MG	BA	3412	1/1	0.17	-	48,48,48,48	0
56	MG	DA	3107	1/1	0.15	-	46,46,46,46	0
56	MG	DA	3467	1/1	0.10	-	47,47,47,47	0
56	MG	BA	3300	1/1	0.17	-	39,39,39,39	0
56	MG	AA	3004	1/1	0.15	-	67,67,67,67	0
58	ZN	D4	501	1/1	0.05	-	141,141,141,141	0
56	MG	DA	3039	1/1	0.25	-	51,51,51,51	0
56	MG	BA	3226	1/1	0.61	-	32,32,32,32	0
56	MG	BA	3520	1/1	0.12	-	24,24,24,24	0
56	MG	DA	3209	1/1	0.16	-	38,38,38,38	0
56	MG	DA	3340	1/1	0.09	-	47,47,47,47	0
56	MG	DA	3343	1/1	0.17	-	56,56,56,56	0
56	MG	CA	3146	1/1	0.07	-	42,42,42,42	0
56	MG	BA	3128	1/1	0.20	-	29,29,29,29	0
56	MG	AA	3024	1/1	0.16	-	60,60,60,60	0
56	MG	DA	3324	1/1	0.14	-	52,52,52,52	0
56	MG	DA	3297	1/1	0.14	-	38,38,38,38	0
56	MG	BA	3117	1/1	0.44	-	40,40,40,40	0
56	MG	CJ	5001	1/1	0.19	-	60,60,60,60	0
56	MG	BA	3518	1/1	0.15	-	41,41,41,41	0
56	MG	DA	3554	1/1	0.06	-	68,68,68,68	0
56	MG	BA	3228	1/1	0.12	-	40,40,40,40	0
56	MG	BA	3024	1/1	0.26	-	32,32,32,32	0
56	MG	BA	3328	1/1	0.13	-	39,39,39,39	0
56	MG	BD	303	1/1	0.41	-	37,37,37,37	0
56	MG	BA	3603	1/1	0.04	-	49,49,49,49	0
56	MG	DA	3141	1/1	0.08	-	42,42,42,42	0
56	MG	DA	3184	1/1	0.20	-	30,30,30,30	0
56	MG	BU	201	1/1	0.30	-	32,32,32,32	0
56	MG	BA	3429	1/1	0.18	-	41,41,41,41	0
56	MG	BA	3256	1/1	0.23	-	41,41,41,41	0
56	MG	DA	3513	1/1	0.11	-	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3427	1/1	0.14	-	25,25,25,25	0
56	MG	DA	3302	1/1	0.11	-	43,43,43,43	0
56	MG	BA	3579	1/1	0.15	-	46,46,46,46	0
56	MG	DA	3212	1/1	0.15	-	39,39,39,39	0
56	MG	DA	3190	1/1	0.17	-	34,34,34,34	0
56	MG	AA	3050	1/1	0.10	-	24,24,24,24	0
56	MG	DA	3262	1/1	0.10	-	39,39,39,39	0
56	MG	BA	3469	1/1	0.15	-	28,28,28,28	0
56	MG	BA	3302	1/1	0.11	-	55,55,55,55	0
56	MG	BA	3069	1/1	0.10	-	47,47,47,47	0
56	MG	BA	3243	1/1	0.15	-	45,45,45,45	0
56	MG	DA	3406	1/1	0.11	-	50,50,50,50	0
56	MG	CA	3073	1/1	0.10	-	57,57,57,57	0
56	MG	DA	3481	1/1	0.09	-	41,41,41,41	0
56	MG	CA	3033	1/1	0.09	-	52,52,52,52	0
56	MG	DA	3357	1/1	0.10	-	33,33,33,33	0
56	MG	CA	3096	1/1	0.14	-	61,61,61,61	0
56	MG	BA	3653	1/1	0.13	-	33,33,33,33	0
56	MG	DB	3004	1/1	0.16	-	36,36,36,36	0
56	MG	DA	3004	1/1	0.17	-	51,51,51,51	0
56	MG	DA	3022	1/1	0.12	-	39,39,39,39	0
56	MG	BA	3605	1/1	0.18	-	46,46,46,46	0
56	MG	BD	305	1/1	0.12	-	38,38,38,38	0
56	MG	BA	3388	1/1	0.06	-	54,54,54,54	0
56	MG	DA	3488	1/1	0.18	-	41,41,41,41	0
56	MG	DA	3012	1/1	0.10	-	30,30,30,30	0
56	MG	BA	3077	1/1	0.14	-	37,37,37,37	0
56	MG	CA	3018	1/1	0.12	-	43,43,43,43	0
56	MG	DA	3064	1/1	0.10	-	48,48,48,48	0
56	MG	BA	3248	1/1	0.20	-	21,21,21,21	0
56	MG	CA	3064	1/1	0.11	-	60,60,60,60	0
56	MG	BA	3503	1/1	0.14	-	30,30,30,30	0
56	MG	D7	101	1/1	0.66	-	51,51,51,51	0
56	MG	BA	3407	1/1	0.13	-	43,43,43,43	0
56	MG	DA	3534	1/1	0.12	-	54,54,54,54	0
56	MG	DA	3577	1/1	0.14	-	35,35,35,35	0
56	MG	DA	3332	1/1	0.08	-	43,43,43,43	0
56	MG	BA	3595	1/1	0.10	-	47,47,47,47	0
56	MG	DA	3034	1/1	0.12	-	46,46,46,46	0
56	MG	AA	3076	1/1	0.17	-	52,52,52,52	0
56	MG	DA	3226	1/1	0.10	-	27,27,27,27	0
56	MG	BD	302	1/1	0.41	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3082	1/1	0.28	-	47,47,47,47	0
56	MG	BA	3527	1/1	0.12	-	40,40,40,40	0
56	MG	DA	3179	1/1	0.13	-	20,20,20,20	0
56	MG	DA	3442	1/1	0.21	-	42,42,42,42	0
56	MG	DA	3127	1/1	0.19	-	41,41,41,41	0
56	MG	DA	3588	1/1	0.14	-	21,21,21,21	0
56	MG	AA	3100	1/1	0.10	-	35,35,35,35	0
56	MG	DA	3516	1/1	0.09	-	61,61,61,61	0
56	MG	DA	3183	1/1	0.07	-	37,37,37,37	0
56	MG	BA	3635	1/1	0.14	-	63,63,63,63	0
56	MG	BA	3112	1/1	0.19	-	40,40,40,40	0
56	MG	DA	3188	1/1	0.12	-	25,25,25,25	0
56	MG	DA	3204	1/1	0.06	-	37,37,37,37	0
56	MG	CA	3118	1/1	0.09	-	78,78,78,78	0
56	MG	DA	3531	1/1	0.11	-	69,69,69,69	0
56	MG	DA	3393	1/1	0.09	-	48,48,48,48	0
56	MG	DA	3411	1/1	0.07	-	36,36,36,36	0
56	MG	AA	3086	1/1	0.23	-	61,61,61,61	0
56	MG	BA	3578	1/1	0.15	-	59,59,59,59	0
56	MG	BA	3269	1/1	0.08	-	34,34,34,34	0
56	MG	BA	3136	1/1	0.18	-	44,44,44,44	0
56	MG	DA	3014	1/1	0.08	-	33,33,33,33	0
56	MG	DA	3511	1/1	0.06	-	53,53,53,53	0
56	MG	BB	3011	1/1	0.07	-	45,45,45,45	0
56	MG	DA	3318	1/1	0.10	-	43,43,43,43	0
56	MG	BA	3093	1/1	0.18	-	40,40,40,40	0
56	MG	BZ	3001	1/1	0.31	-	58,58,58,58	0
56	MG	DA	3043	1/1	0.11	-	30,30,30,30	0
56	MG	DA	3382	1/1	0.13	-	50,50,50,50	0
56	MG	AA	3155	1/1	0.07	-	61,61,61,61	0
56	MG	BA	3263	1/1	0.22	-	64,64,64,64	0
56	MG	BA	3625	1/1	0.14	-	25,25,25,25	0
56	MG	AA	3069	1/1	0.11	-	50,50,50,50	0
56	MG	DA	3077	1/1	0.09	-	34,34,34,34	0
56	MG	DP	3001	1/1	0.23	-	44,44,44,44	0
56	MG	DA	3402	1/1	0.09	-	63,63,63,63	0
56	MG	AA	3150	1/1	0.18	-	51,51,51,51	0
56	MG	AA	3059	1/1	0.08	-	54,54,54,54	0
58	ZN	D9	501	1/1	0.07	-	54,54,54,54	0
56	MG	BA	3658	1/1	0.09	-	27,27,27,27	0
56	MG	DA	3250	1/1	0.10	-	37,37,37,37	0
56	MG	CA	3113	1/1	0.14	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3106	1/1	0.11	-	40,40,40,40	0
56	MG	BA	3278	1/1	0.11	-	50,50,50,50	0
56	MG	DA	3416	1/1	0.14	-	44,44,44,44	0
56	MG	BA	3122	1/1	0.39	-	39,39,39,39	0
56	MG	DQ	3003	1/1	0.17	-	50,50,50,50	0
56	MG	DA	3414	1/1	0.04	-	42,42,42,42	0
56	MG	BA	3290	1/1	0.13	-	36,36,36,36	0
56	MG	BA	3150	1/1	0.12	-	32,32,32,32	0
58	ZN	B6	501	1/1	0.14	-	45,45,45,45	0
56	MG	DA	3447	1/1	0.07	-	33,33,33,33	0
56	MG	DA	3527	1/1	0.12	-	43,43,43,43	0
56	MG	BA	3221	1/1	0.25	-	41,41,41,41	0
56	MG	DA	3452	1/1	0.13	-	56,56,56,56	0
56	MG	BA	3666	1/1	0.36	-	35,35,35,35	0
56	MG	DA	3278	1/1	0.14	-	50,50,50,50	0
56	MG	BA	3085	1/1	0.17	-	27,27,27,27	0
56	MG	BA	3516	1/1	0.13	-	43,43,43,43	0
56	MG	DA	3041	1/1	0.08	-	35,35,35,35	0
56	MG	BA	3177	1/1	0.13	-	44,44,44,44	0
56	MG	DA	3189	1/1	0.26	-	31,31,31,31	0
56	MG	DA	3175	1/1	0.14	-	47,47,47,47	0
56	MG	BA	3589	1/1	0.13	-	27,27,27,27	0
56	MG	BA	3325	1/1	0.14	-	42,42,42,42	0
56	MG	AA	3023	1/1	0.20	-	71,71,71,71	0
56	MG	DA	3050	1/1	0.09	-	41,41,41,41	0
56	MG	DA	3203	1/1	0.15	-	21,21,21,21	0
56	MG	CA	3001	1/1	0.06	-	72,72,72,72	0
56	MG	BA	3414	1/1	0.15	-	31,31,31,31	0
56	MG	DA	3172	1/1	0.10	-	35,35,35,35	0
56	MG	DA	3221	1/1	0.10	-	33,33,33,33	0
56	MG	BA	3102	1/1	0.09	-	49,49,49,49	0
56	MG	BA	3437	1/1	0.13	-	58,58,58,58	0
56	MG	DA	3015	1/1	0.30	-	41,41,41,41	0
56	MG	AA	3120	1/1	0.14	-	47,47,47,47	0
56	MG	DA	3223	1/1	0.13	-	47,47,47,47	0
58	ZN	B4	501	1/1	0.06	-	106,106,106,106	0
56	MG	BA	3264	1/1	0.15	-	35,35,35,35	0
56	MG	DA	3354	1/1	0.17	-	51,51,51,51	0
56	MG	DA	3508	1/1	0.09	-	38,38,38,38	0
56	MG	BA	3550	1/1	0.19	-	44,44,44,44	0
56	MG	DA	3091	1/1	0.19	-	45,45,45,45	0
56	MG	CA	3034	1/1	0.12	-	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3135	1/1	0.12	-	36,36,36,36	0
56	MG	DA	3236	1/1	0.10	-	47,47,47,47	0
56	MG	DA	3386	1/1	0.08	-	48,48,48,48	0
56	MG	CA	3071	1/1	0.24	-	51,51,51,51	0
56	MG	DA	3363	1/1	0.07	-	36,36,36,36	0
56	MG	DA	3509	1/1	0.08	-	36,36,36,36	0
56	MG	DA	3564	1/1	0.07	-	36,36,36,36	0
56	MG	BA	3001	1/1	0.13	-	35,35,35,35	0
56	MG	DA	3596	1/1	0.31	-	54,54,54,54	0
56	MG	DA	3576	1/1	0.14	-	36,36,36,36	0
56	MG	DA	3392	1/1	0.12	-	54,54,54,54	0
56	MG	DA	3268	1/1	0.17	-	38,38,38,38	0
56	MG	BA	3454	1/1	0.15	-	21,21,21,21	0
56	MG	DA	3275	1/1	0.12	-	45,45,45,45	0
56	MG	DA	3087	1/1	0.17	-	35,35,35,35	0
56	MG	DA	3233	1/1	0.27	-	36,36,36,36	0
56	MG	DA	3499	1/1	0.10	-	45,45,45,45	0
56	MG	BA	3649	1/1	0.13	-	50,50,50,50	0
56	MG	BA	3456	1/1	0.13	-	33,33,33,33	0
56	MG	BA	3497	1/1	0.13	-	34,34,34,34	0
56	MG	DA	3446	1/1	0.09	-	46,46,46,46	0
56	MG	CA	3065	1/1	0.07	-	55,55,55,55	0
56	MG	CA	3053	1/1	0.15	-	44,44,44,44	0
56	MG	BA	3216	1/1	0.27	-	33,33,33,33	0
56	MG	DA	3069	1/1	0.11	-	35,35,35,35	0
56	MG	CA	3126	1/1	0.20	-	73,73,73,73	0
56	MG	BB	3009	1/1	0.11	-	67,67,67,67	0
56	MG	CA	3051	1/1	0.14	-	66,66,66,66	0
56	MG	DA	3198	1/1	0.15	-	54,54,54,54	0
56	MG	BA	3043	1/1	0.15	-	36,36,36,36	0
56	MG	DA	3100	1/1	0.13	-	34,34,34,34	0
56	MG	AA	3088	1/1	0.22	-	62,62,62,62	0
56	MG	DA	3530	1/1	0.09	-	60,60,60,60	0
56	MG	BA	3018	1/1	0.23	-	47,47,47,47	0
56	MG	BU	205	1/1	0.40	-	53,53,53,53	0
56	MG	AA	3168	1/1	0.08	-	56,56,56,56	0
56	MG	BA	3511	1/1	0.13	-	38,38,38,38	0
56	MG	DA	3028	1/1	0.36	-	47,47,47,47	0
56	MG	BA	3094	1/1	0.24	-	45,45,45,45	0
56	MG	CA	3097	1/1	0.18	-	67,67,67,67	0
56	MG	DA	3522	1/1	0.11	-	44,44,44,44	0
56	MG	BA	3193	1/1	0.21	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3601	1/1	0.13	-	50,50,50,50	0
56	MG	DA	3222	1/1	0.12	-	36,36,36,36	0
56	MG	DA	3259	1/1	0.18	-	42,42,42,42	0
56	MG	AA	3110	1/1	0.12	-	60,60,60,60	0
56	MG	BA	3350	1/1	0.21	-	59,59,59,59	0
56	MG	DA	3152	1/1	0.16	-	34,34,34,34	0
56	MG	BA	3349	1/1	0.11	-	46,46,46,46	0
56	MG	DA	3155	1/1	0.24	-	45,45,45,45	0
56	MG	BA	3147	1/1	0.24	-	35,35,35,35	0
56	MG	DA	3380	1/1	0.09	-	33,33,33,33	0
56	MG	DA	3231	1/1	0.12	-	37,37,37,37	0
56	MG	AA	3104	1/1	0.07	-	56,56,56,56	0
56	MG	DA	3098	1/1	0.11	-	46,46,46,46	0
56	MG	BA	3295	1/1	0.22	-	61,61,61,61	0
56	MG	BR	3001	1/1	0.18	-	31,31,31,31	0
56	MG	BA	3487	1/1	0.14	-	17,17,17,17	0
56	MG	BA	3121	1/1	0.53	-	43,43,43,43	0
56	MG	AA	3049	1/1	0.23	-	47,47,47,47	0
56	MG	DA	3375	1/1	0.18	-	49,49,49,49	0
56	MG	DA	3316	1/1	0.13	-	57,57,57,57	0
56	MG	DE	3005	1/1	0.11	-	20,20,20,20	0
56	MG	DA	3321	1/1	0.10	-	45,45,45,45	0
56	MG	DA	3201	1/1	0.09	-	51,51,51,51	0
56	MG	BA	3324	1/1	0.10	-	53,53,53,53	0
56	MG	BA	3340	1/1	0.13	-	42,42,42,42	0
56	MG	BA	3530	1/1	0.12	-	36,36,36,36	0
56	MG	BA	3159	1/1	0.16	-	27,27,27,27	0
56	MG	DA	3309	1/1	0.12	-	60,60,60,60	0
56	MG	BA	3310	1/1	0.17	-	35,35,35,35	0
56	MG	DA	3094	1/1	0.24	-	35,35,35,35	0
56	MG	BA	3439	1/1	0.19	-	30,30,30,30	0
56	MG	CA	3110	1/1	0.14	-	64,64,64,64	0
56	MG	BA	3084	1/1	0.17	-	34,34,34,34	0
56	MG	BF	305	1/1	0.33	-	61,61,61,61	0
56	MG	CA	3012	1/1	0.12	-	52,52,52,52	0
56	MG	DA	3520	1/1	0.10	-	34,34,34,34	0
56	MG	B0	104	1/1	0.51	-	48,48,48,48	0
56	MG	BA	3072	1/1	0.15	-	24,24,24,24	0
56	MG	DA	3595	1/1	0.08	-	43,43,43,43	0
56	MG	DA	3035	1/1	0.14	-	46,46,46,46	0
56	MG	DA	3584	1/1	0.10	-	61,61,61,61	0
56	MG	BA	3222	1/1	0.18	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3095	1/1	0.08	-	33,33,33,33	0
56	MG	DA	3529	1/1	0.19	-	41,41,41,41	0
56	MG	BA	3478	1/1	0.12	-	47,47,47,47	0
56	MG	CA	3008	1/1	0.28	-	31,31,31,31	0
56	MG	BA	3200	1/1	0.21	-	25,25,25,25	0
56	MG	AA	3160	1/1	0.12	-	71,71,71,71	0
56	MG	DA	3027	1/1	0.10	-	30,30,30,30	0
56	MG	BA	3124	1/1	0.19	-	58,58,58,58	0
56	MG	BA	3266	1/1	0.19	-	29,29,29,29	0
56	MG	BA	3661	1/1	0.20	-	38,38,38,38	0
56	MG	DA	3561	1/1	0.16	-	63,63,63,63	0
56	MG	BA	3575	1/1	0.09	-	55,55,55,55	0
56	MG	BA	3380	1/1	0.13	-	17,17,17,17	0
56	MG	BA	3096	1/1	0.09	-	44,44,44,44	0
56	MG	BA	3103	1/1	0.20	-	42,42,42,42	0
56	MG	BA	3237	1/1	0.15	-	57,57,57,57	0
56	MG	DA	3040	1/1	0.19	-	34,34,34,34	0
56	MG	AA	3001	1/1	0.15	-	57,57,57,57	0
56	MG	BA	3640	1/1	0.19	-	33,33,33,33	0
56	MG	DA	3242	1/1	0.16	-	60,60,60,60	0
56	MG	DA	3292	1/1	0.18	-	45,45,45,45	0
56	MG	AA	3007	1/1	0.09	-	30,30,30,30	0
56	MG	AA	3148	1/1	0.07	-	56,56,56,56	0
56	MG	BA	3227	1/1	0.15	-	32,32,32,32	0
56	MG	BA	3064	1/1	0.17	-	30,30,30,30	0
56	MG	BA	3116	1/1	0.23	-	50,50,50,50	0
56	MG	B7	3001	1/1	0.20	-	45,45,45,45	0
56	MG	AA	3097	1/1	0.15	-	49,49,49,49	0
56	MG	DA	3218	1/1	0.12	-	33,33,33,33	0
56	MG	DA	3211	1/1	0.17	-	35,35,35,35	0
56	MG	BA	3459	1/1	0.10	-	42,42,42,42	0
56	MG	BA	3249	1/1	0.11	-	48,48,48,48	0
56	MG	AA	3018	1/1	0.10	-	50,50,50,50	0
56	MG	BA	3339	1/1	0.13	-	34,34,34,34	0
56	MG	BA	3011	1/1	0.09	-	30,30,30,30	0
56	MG	DA	3191	1/1	0.09	-	53,53,53,53	0
56	MG	BA	3409	1/1	0.15	-	28,28,28,28	0
56	MG	CA	3111	1/1	0.17	-	43,43,43,43	0
56	MG	DA	3066	1/1	0.17	-	49,49,49,49	0
56	MG	DA	3025	1/1	0.08	-	41,41,41,41	0
56	MG	DA	3086	1/1	0.06	-	41,41,41,41	0
56	MG	DA	3438	1/1	0.10	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3220	1/1	0.13	-	43,43,43,43	0
56	MG	AA	3068	1/1	0.17	-	31,31,31,31	0
56	MG	CE	201	1/1	0.11	-	52,52,52,52	0
57	SF4	AD	501	8/8	0.17	-	50,63,78,83	0
56	MG	B3	101	1/1	0.35	-	35,35,35,35	0
56	MG	CA	3117	1/1	0.23	-	42,42,42,42	0
56	MG	BA	3319	1/1	0.24	-	39,39,39,39	0
56	MG	BA	3055	1/1	0.14	-	13,13,13,13	0
56	MG	BA	3568	1/1	0.11	-	42,42,42,42	0
56	MG	BA	3255	1/1	0.18	-	32,32,32,32	0
56	MG	BA	3178	1/1	0.24	-	26,26,26,26	0
56	MG	DA	3434	1/1	0.12	-	41,41,41,41	0
56	MG	BA	3149	1/1	0.09	-	50,50,50,50	0
56	MG	BA	3507	1/1	0.12	-	53,53,53,53	0
56	MG	DA	3437	1/1	0.29	-	48,48,48,48	0
56	MG	AA	3073	1/1	0.18	-	50,50,50,50	0
56	MG	BA	3433	1/1	0.09	-	33,33,33,33	0
56	MG	DA	3403	1/1	0.07	-	39,39,39,39	0
56	MG	BA	3532	1/1	0.04	-	53,53,53,53	0
56	MG	BA	3229	1/1	0.20	-	54,54,54,54	0
56	MG	AA	3098	1/1	0.18	-	48,48,48,48	0
56	MG	DA	3491	1/1	0.12	-	40,40,40,40	0
56	MG	BA	3515	1/1	0.16	-	25,25,25,25	0
56	MG	BA	3315	1/1	0.20	-	31,31,31,31	0
56	MG	DA	3575	1/1	0.09	-	49,49,49,49	0
56	MG	CA	3004	1/1	0.15	-	51,51,51,51	0
56	MG	BA	3133	1/1	0.10	-	33,33,33,33	0
56	MG	BA	3418	1/1	0.12	-	46,46,46,46	0
56	MG	CA	3139	1/1	0.08	-	67,67,67,67	0
56	MG	CA	3011	1/1	0.17	-	66,66,66,66	0
56	MG	DA	3063	1/1	0.11	-	31,31,31,31	0
56	MG	DA	3327	1/1	0.19	-	34,34,34,34	0
56	MG	DA	3016	1/1	0.18	-	31,31,31,31	0
56	MG	BA	3408	1/1	0.10	-	56,56,56,56	0
56	MG	DA	3449	1/1	0.14	-	29,29,29,29	0
56	MG	BA	3572	1/1	0.11	-	59,59,59,59	0
56	MG	BA	3377	1/1	0.16	-	31,31,31,31	0
56	MG	AA	3070	1/1	0.16	-	33,33,33,33	0
56	MG	AA	3019	1/1	0.20	-	62,62,62,62	0
56	MG	B5	502	1/1	0.33	-	34,34,34,34	0
56	MG	BA	3596	1/1	0.14	-	56,56,56,56	0
56	MG	DA	3134	1/1	0.24	-	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3570	1/1	0.05	-	36,36,36,36	0
56	MG	BA	3317	1/1	0.14	-	35,35,35,35	0
56	MG	BA	3477	1/1	0.10	-	50,50,50,50	0
56	MG	CA	3105	1/1	0.06	-	84,84,84,84	0

6.5 Other polymers

There are no such residues in this entry.