



Full wwPDB X-ray Structure Validation Report

Sep 10, 2014 – 11:09 PM EDT

PDB ID : 1VY5
Title : Crystal structure of the Thermus thermophilus 70S ribosome in the post-catalysis state of peptide bond formation containing dipeptidyl-tRNA in the A site and deacylated tRNA in the P site.
Authors : Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on : 2014-05-13
Resolution : 2.55 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>

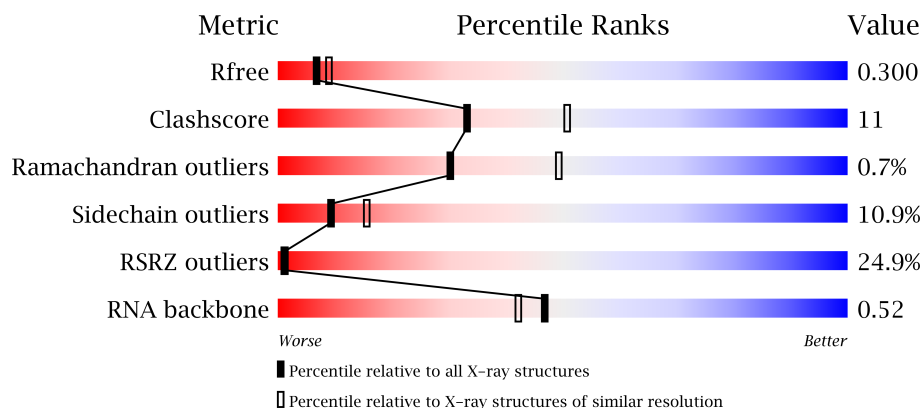
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.55 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	3413 (2.58-2.50)
Clashscore	79885	4284 (2.58-2.50)
Ramachandran outliers	78287	4193 (2.58-2.50)
Sidechain outliers	78261	4195 (2.58-2.50)
RSRZ outliers	66119	3414 (2.58-2.50)
RNA backbone	1838	1058 (3.10-1.98)

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	76	
23	CW	76	
24	AX	77	
24	CX	77	
25	AY	76	
25	CY	76	
26	BA	2915	
26	DA	2915	
27	BB	121	

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Mol	Chain	Length	Quality of chain
27	DB	121	
28	BD	276	
28	DD	276	
29	BE	206	
29	DE	206	
30	BF	210	
30	DF	210	
31	BG	182	
31	DG	182	
32	BH	180	
32	DH	180	
33	BI	148	
33	DI	148	
34	BN	140	
34	DN	140	
35	BO	122	
35	DO	122	
36	BP	150	
36	DP	150	
37	BQ	141	
37	DQ	141	
38	BR	118	
38	DR	118	
39	BS	112	
39	DS	112	
40	BT	146	
40	DT	146	
41	BU	118	
41	DU	118	
42	BV	101	
42	DV	101	
43	BW	113	
43	DW	113	
44	BX	96	
44	DX	96	
45	BY	110	
45	DY	110	
46	BZ	206	
46	DZ	206	
47	B0	85	
47	D0	85	
48	B1	98	

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Mol	Chain	Length	Quality of chain
48	D1	98	
49	B2	72	
49	D2	72	
50	B3	60	
50	D3	60	
51	B4	71	
51	D4	71	
52	B5	60	
52	D5	60	
53	B6	54	
53	D6	54	
54	B7	49	
54	D7	49	
55	B8	65	
55	D8	65	
56	B9	37	
56	D9	37	

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 297141 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
			1674	1050	333	284	7			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 22 is a RNA chain called mRNA.

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

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AW	74	Total	C	N	O	P	S	0	0	0
			1607	727	288	516	73	3			
23	CW	72	Total	C	N	O	P	S	0	0	0
			1560	702	281	503	72	2			

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

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

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
25	AY	74	Total	C	N	O	P	S	0	0	0
			1581	707	285	515	73	1			
25	CY	73	Total	C	N	O	P	S	0	0	0
			1561	698	283	507	72	1			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	B4	1	Total	Mg	0	0
			1	1		
57	BA	812	Total	Mg	0	0
			812	812		
57	AK	1	Total	Mg	0	0
			1	1		
57	DQ	4	Total	Mg	0	0
			4	4		
57	D3	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	DF	4	Total 4	Mg 4	0	0
57	CV	1	Total 1	Mg 1	0	0
57	B8	1	Total 1	Mg 1	0	0
57	BE	8	Total 8	Mg 8	0	0
57	AW	4	Total 4	Mg 4	0	0
57	DU	2	Total 2	Mg 2	0	0
57	B1	1	Total 1	Mg 1	0	0
57	AN	2	Total 2	Mg 2	0	0
57	BP	5	Total 5	Mg 5	0	0
57	AX	15	Total 15	Mg 15	0	0
57	DN	1	Total 1	Mg 1	0	0
57	CA	170	Total 170	Mg 170	0	0
57	B5	1	Total 1	Mg 1	0	0
57	BB	20	Total 20	Mg 20	0	0
57	D8	1	Total 1	Mg 1	0	0
57	AE	3	Total 3	Mg 3	0	0
57	DG	1	Total 1	Mg 1	0	0
57	B9	1	Total 1	Mg 1	0	0
57	BF	9	Total 9	Mg 9	0	0
57	BX	3	Total 3	Mg 3	0	0
57	B2	1	Total 1	Mg 1	0	0

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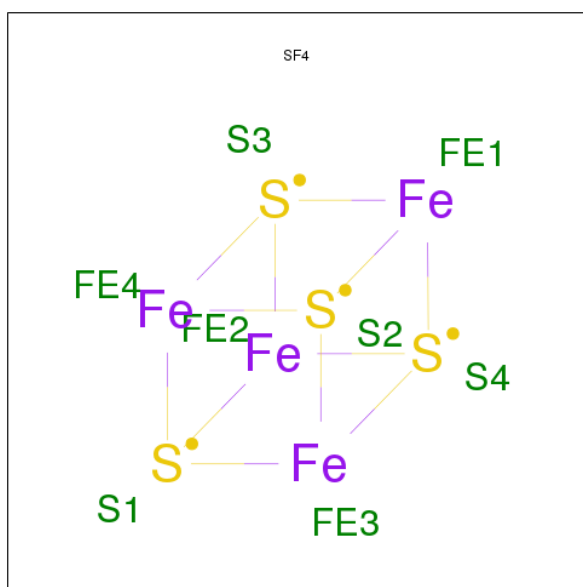
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AA	214	Total 214	Mg 214	0	0
57	BQ	5	Total 5	Mg 5	0	0
57	CX	3	Total 3	Mg 3	0	0
57	DV	3	Total 3	Mg 3	0	0
57	B6	2	Total 2	Mg 2	0	0
57	AM	1	Total 1	Mg 1	0	0
57	BU	8	Total 8	Mg 8	0	0
57	DR	1	Total 1	Mg 1	0	0
57	BN	6	Total 6	Mg 6	0	0
57	CT	1	Total 1	Mg 1	0	0
57	D0	1	Total 1	Mg 1	0	0
57	BG	3	Total 3	Mg 3	0	0
57	BY	1	Total 1	Mg 1	0	0
57	DE	4	Total 4	Mg 4	0	0
57	B3	2	Total 2	Mg 2	0	0
57	CJ	1	Total 1	Mg 1	0	0
57	BR	2	Total 2	Mg 2	0	0
57	DA	677	Total 677	Mg 677	0	0
57	DP	2	Total 2	Mg 2	0	0
57	DW	4	Total 4	Mg 4	0	0
57	B7	5	Total 5	Mg 5	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	CF	1	Total 1	Mg 1	0	0
57	BV	5	Total 5	Mg 5	0	0
57	DO	1	Total 1	Mg 1	0	0
57	BO	2	Total 2	Mg 2	0	0
57	DX	1	Total 1	Mg 1	0	0
57	BZ	1	Total 1	Mg 1	0	0
57	DY	1	Total 1	Mg 1	0	0
57	CW	1	Total 1	Mg 1	0	0
57	CD	1	Total 1	Mg 1	0	0
57	BD	9	Total 9	Mg 9	0	0
57	B0	3	Total 3	Mg 3	0	0
57	CE	1	Total 1	Mg 1	0	0
57	BW	4	Total 4	Mg 4	0	0
57	AY	3	Total 3	Mg 3	0	0
57	DD	9	Total 9	Mg 9	0	0
57	CK	1	Total 1	Mg 1	0	0
57	AF	1	Total 1	Mg 1	0	0
57	DB	13	Total 13	Mg 13	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



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

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

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

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

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

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

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AA	227	Total 227	O 227	0	0
61	AE	2	Total 2	O 2	0	0
61	AJ	1	Total 1	O 1	0	0
61	AL	1	Total 1	O 1	0	0
61	AM	1	Total 1	O 1	0	0
61	AU	1	Total 1	O 1	0	0
61	AV	3	Total 3	O 3	0	0
61	AW	3	Total 3	O 3	0	0
61	AX	6	Total 6	O 6	0	0
61	AY	1	Total 1	O 1	0	0
61	BA	1383	Total 1383	O 1383	0	0
61	BB	36	Total 36	O 36	0	0
61	BD	12	Total 12	O 12	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BE	14	Total 14	O 14	0	0
61	BF	8	Total 8	O 8	0	0
61	BG	3	Total 3	O 3	0	0
61	BI	1	Total 1	O 1	0	0
61	BO	4	Total 4	O 4	0	0
61	BP	16	Total 16	O 16	0	0
61	BQ	4	Total 4	O 4	0	0
61	BR	2	Total 2	O 2	0	0
61	BT	2	Total 2	O 2	0	0
61	BU	3	Total 3	O 3	0	0
61	BV	2	Total 2	O 2	0	0
61	BW	1	Total 1	O 1	0	0
61	BX	4	Total 4	O 4	0	0
61	BZ	1	Total 1	O 1	0	0
61	B0	3	Total 3	O 3	0	0
61	B1	1	Total 1	O 1	0	0
61	B3	2	Total 2	O 2	0	0
61	B5	2	Total 2	O 2	0	0
61	B6	1	Total 1	O 1	0	0
61	B7	2	Total 2	O 2	0	0
61	B8	8	Total 8	O 8	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	CA	185	Total 185	O 185	0	0
61	CJ	2	Total 2	O 2	0	0
61	CL	1	Total 1	O 1	0	0
61	CT	1	Total 1	O 1	0	0
61	CV	1	Total 1	O 1	0	0
61	CW	2	Total 2	O 2	0	0
61	DA	1025	Total 1025	O 1025	0	0
61	DB	9	Total 9	O 9	0	0
61	DD	19	Total 19	O 19	0	0
61	DE	11	Total 11	O 11	0	0
61	DF	3	Total 3	O 3	0	0
61	DN	2	Total 2	O 2	0	0
61	DO	1	Total 1	O 1	0	0
61	DP	16	Total 16	O 16	0	0
61	DR	1	Total 1	O 1	0	0
61	DT	3	Total 3	O 3	0	0
61	DU	2	Total 2	O 2	0	0
61	DX	3	Total 3	O 3	0	0
61	DY	2	Total 2	O 2	0	0
61	D0	3	Total 3	O 3	0	0
61	D1	1	Total 1	O 1	0	0

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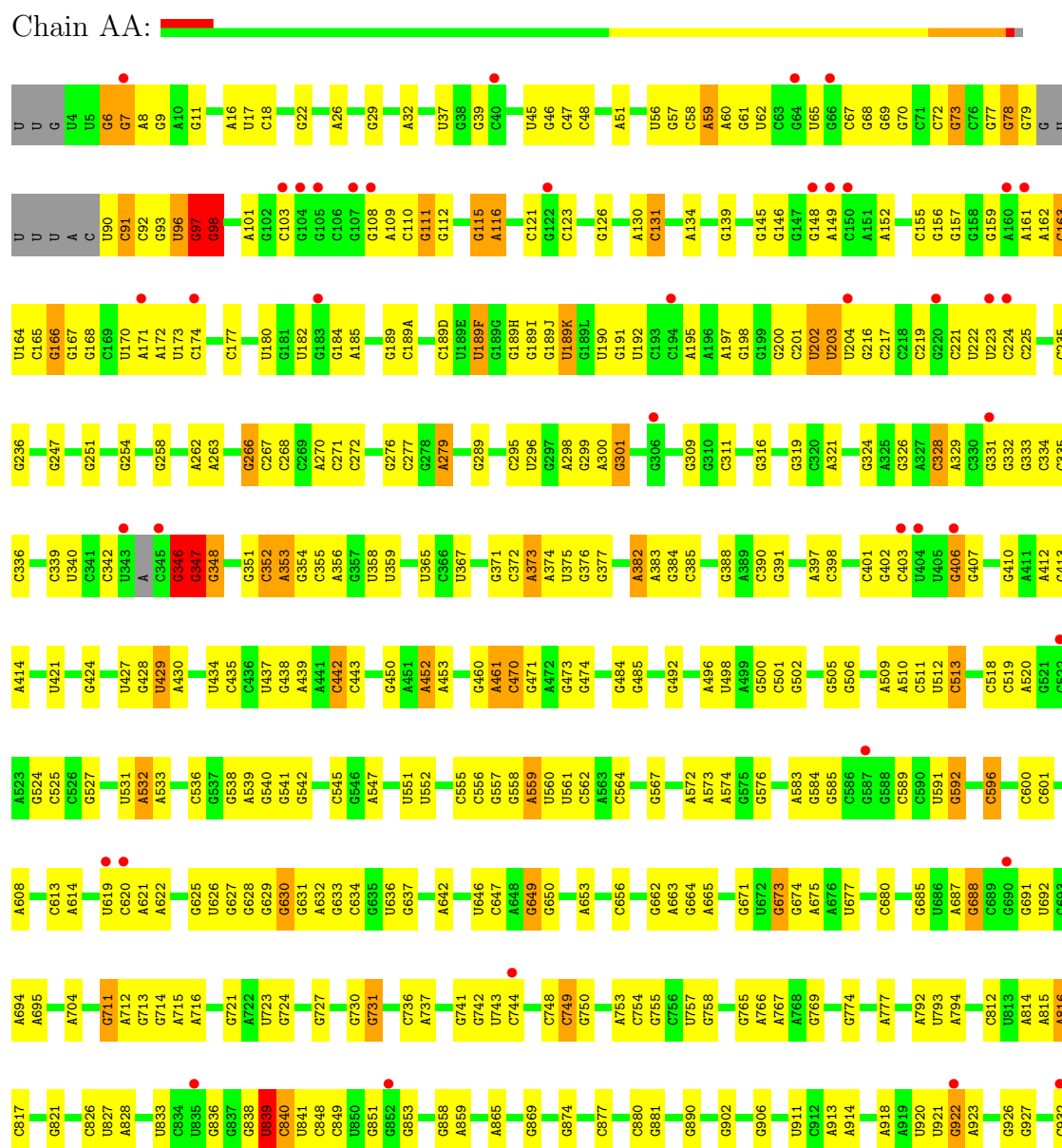
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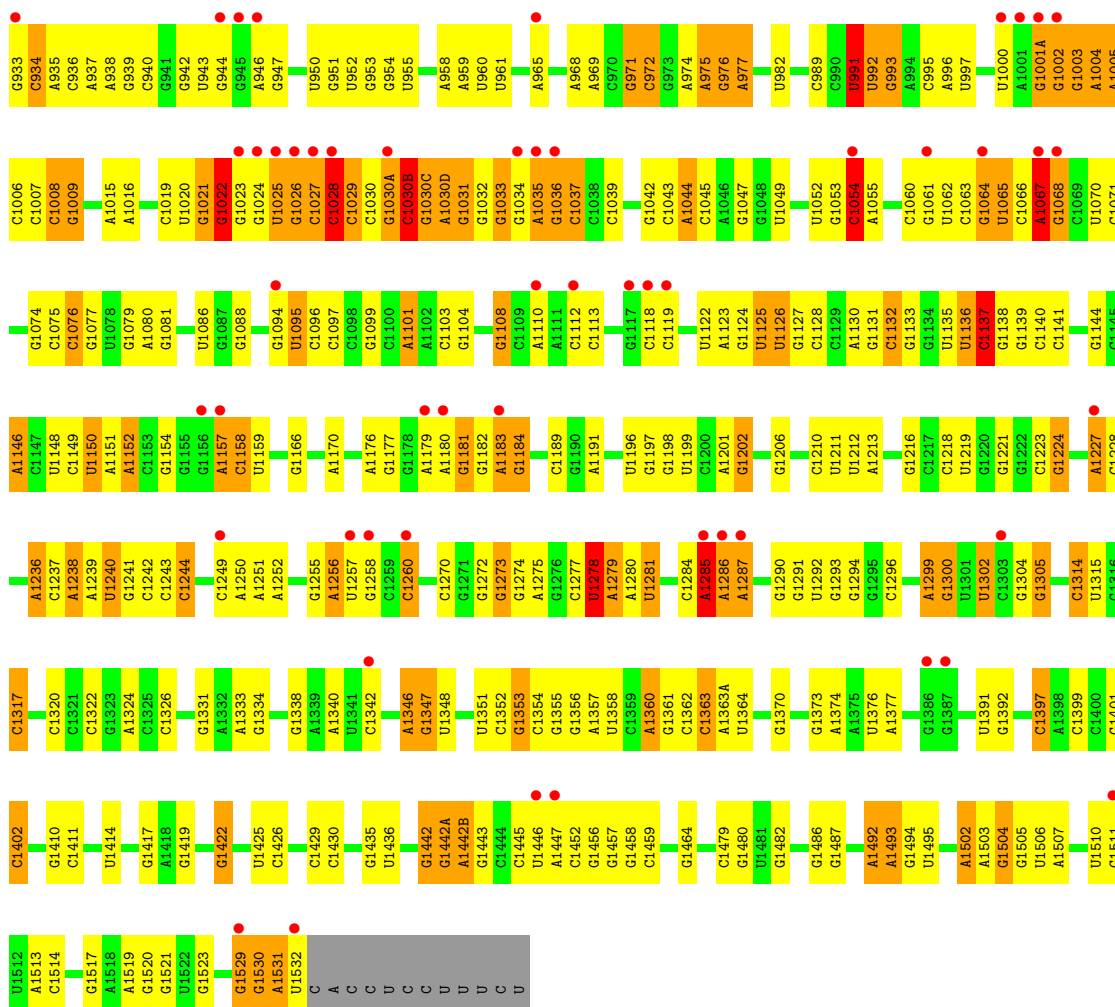
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	D3	1	Total	O	0	0
			1	1		
61	D7	3	Total	O	0	0
			3	3		
61	D8	4	Total	O	0	0
			4	4		

3 Residue-property plots

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

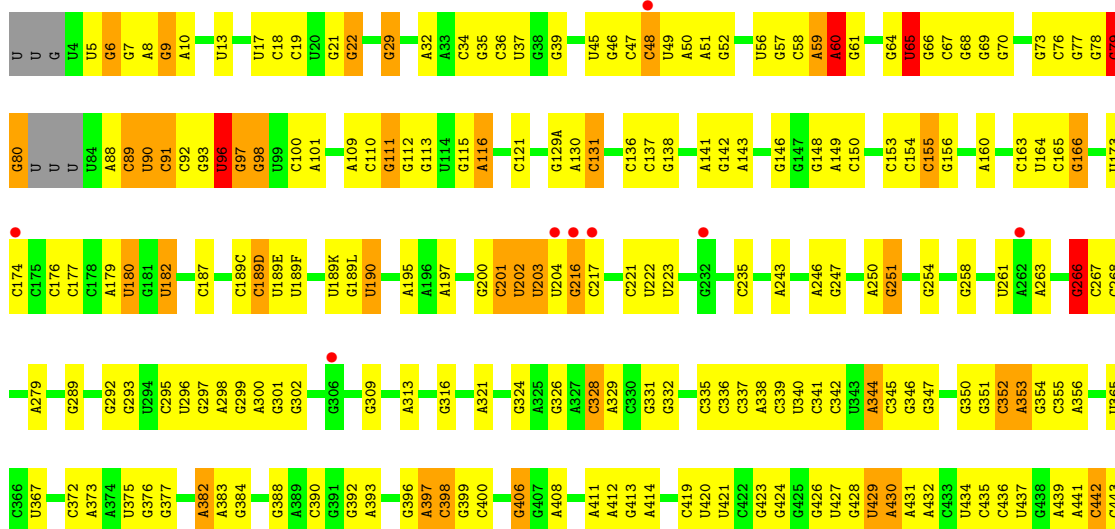
• Molecule 1: 16S Ribosomal RNA





- Molecule 1: 16S Ribosomal RNA

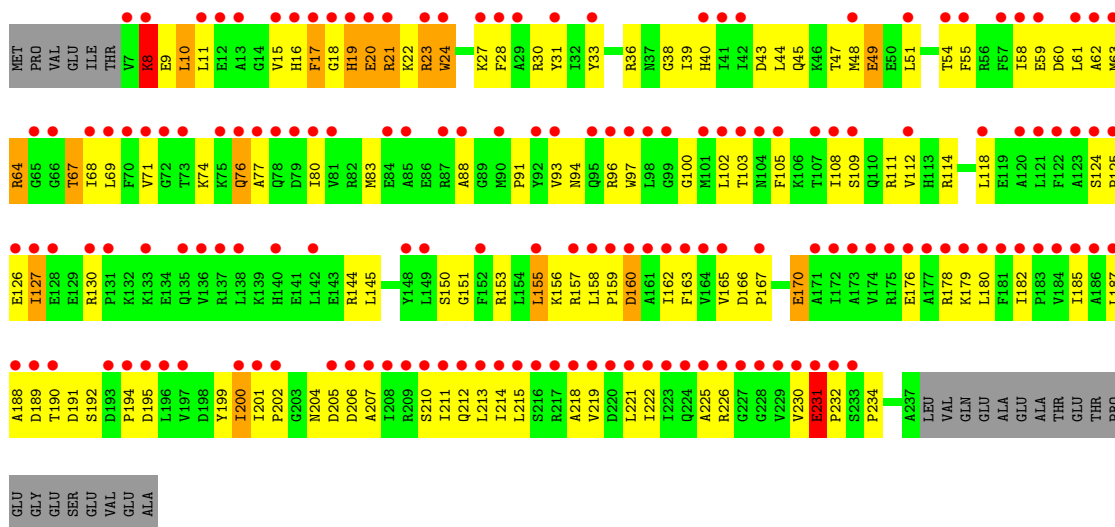
Chain CA:



C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1383	C1386	C1387	C1388	U1391	C1392	C1397	A1398	C1399	C1402	G1410	G1411	C1412	A1413	U1414	G1419	G1422	G1423	C1424	C1429	C1430	G1435	U1436	C1441	G1442	A1442B	U1446	A1447	C1452	G1456	G1457	C1469															
U1301	U1302	C1303	C1304	G1305	G1310	G1311	G1312	G1313	C1314	U1315	G1316	C1317	A1318	A1319	C1320	C1321	C1322	C1323	A1324	C1325	C1326	C1327	C1328	G1331	A1332	A1333	G1334	G1338	A1339	A1340	U1341	C1342	G1343	C1344	U1345	A1346	G1347	U1348	U1349	A1350	G1351	C1352	G1353	C1354	G1355	G1356	C1357	U1358	C1359	A1360	G1361	C1362	C1363	A1363A	C1368	U1364	C1365			
U1232	G1233	C1234	U1235	C1236	G1237	A1238	A1239	U1240	C1243	A1244	A1245	C1246	C1249	A1250	A1251	A1252	G1255	A1256	U1257	G1258	C1259	G1260	A1261	C1262	C1263	A1269	C1270	G1271	G1272	U1273	G1274	C1277	U1278	A1279	U1280	U1281	C1282	A1283	C1284	A1285	A1286	A1287	A1288	A1289	G1290	U1291	U1292	G1293	G1294	C1297	C1298	A1299	U1300							
C1162	C1163	C1164	C1165	A1169	A1170	A1171	G1172	G1173	G1174	G1175	A1176	G1177	G1178	A1179	U1180	G1181	A1182	A1183	G1184	G1185	G1186	G1190	A1191	C1192	U1196	U1197	U1198	U1199	C1200	G1201	G1202	U1203	A1204	U1205	G1206	U1211	U1212	U1213	C1214	G1215	C1216	C1217	C1218	U1219	G1220	G1221	G1222	C1223	G1224	A1225	C1226	A1227	C1228	G1231						
G1099	G1100	A1101	A1102	C1103	G1104	G1108	C1109	A1110	A1111	C1112	C1113	G1114	C1115	G1116	G1117	C1118	C1119	G1120	U1121	A1122	A1123	G1124	U1125	U1126	C1127	G1128	C1129	A1130	U1131	C1132	G1133	U1134	U1135	U1136	C1137	G1138	G1139	C1140	G1141	G1142	U1143	C1144	C1145	A1146	C1147	U1148	C1149	U1150	A1151	A1152	C1153	G1154	G1155	G1156	A1157	C1158	U1159			
C1037	C1038	C1039	U1040	A1041	C1042	C1043	A1044	G1047	U1048	U1049	G1050	C1051	U1052	G1053	C1054	U1055	U1056	G1057	G1058	C1059	C1060	G1061	U1062	C1063	U1064	C1065	C1066	A1067	G1068	C1069	U1070	G1071	G1072	U1073	G1074	C1075	C1076	G1079	A1080	G1081	G1082	U1083	U1084	U1085	U1086	G1087	G1088	U1089	U1090	U1091	A1092	A1093	U1094	U1095	C1096	C1097	C1098			
A914	U920	U921	G922	A923	C924	G925	G926	G927	C931	C932	G933	C934	A935	C936	A937	A938	G939	U1000	A1001	G1002	G1003	A1004	A1005	C1006	C1007	G947	U950	G951	U952	G953	G954	U955	U956	U957	A958	A959	U960	U961	C962	G963	A964	A965	G966	C967	A968	A969	C970	G971	C972	G973	A974	A975	A1030D	G1031	A901	G976	A977	A978	C979	U981
C811	A814	A815	A816	C817	G821	C825	U827	A828	U833	G838	U839	C840	U841	C848	G851	U852	G853	C857	G858	A859	G861	C866	C867	C868	C869	G874	C875	C876	C879	C880	C883	U884	C885	C890	G895	A896	A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913							
C720	G721	A722	U723	G724	G727	A728	A729	G730	G731	C736	A737	G741	G742	C748	G749	A753	C754	G755	C756	U757	G758	G765	A766	A767	A768	G769	C770	A771	U772	G773	G774	G775	G776	A777	G778	C779	A780	U781	A782	C783	C784	G791	G792	G793	A794	G795	A796	A797	A798	A799	A800	A801	A802	A803	A804	C805	C7913			
C444	G445	G446	G447	C448	C449	G450	A451	A452	A453	G460	A461	C470	G471	A472	G473	G474	G484	G485	C488	G492	A496	U498	A499	G500	C501	G502	C503	C504	G505	A509	A510	C511	U512	C513	C514	C518	G521	A522	A523	C525	G527	G528	G529	G530	U531	A532	G533	U534	A535	C536										
G537	G538	A539	G540	G541	G542	G543	G544	G545	G546	A547	U551	U552	A553	C556	A559	U560	U561	C562	G568	G576	G577	U580	G581	U582	A583	G584	G587	G592	U5912	C5913	C5914	C5918	A607	A608	A609	G610	C620	G625	U626	G627	G628	G629	A630	G631	A632	A633	U634	A635	C636											

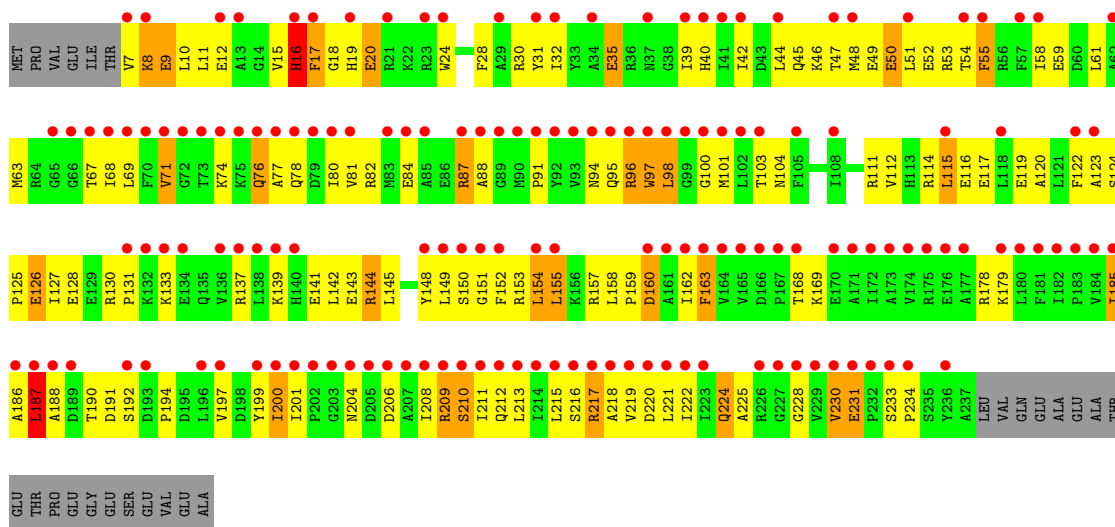
• Molecule 2: 30S ribosomal protein S2

Chain AB:



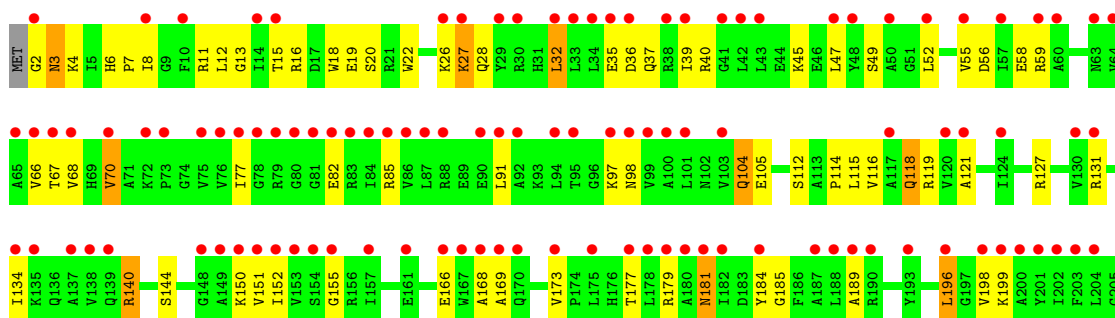
- Molecule 2: 30S ribosomal protein S2

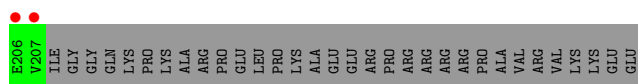
Chain CB:



- Molecule 3: 30S ribosomal protein S3

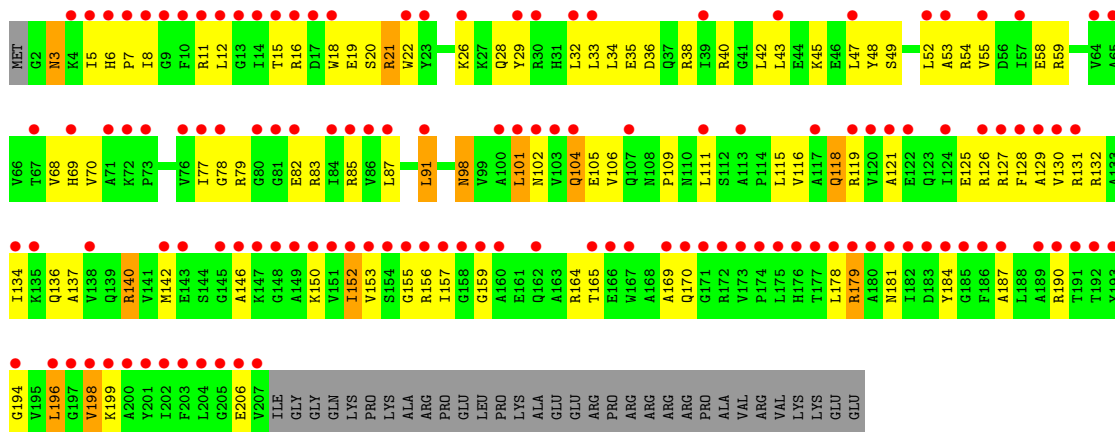
Chain AC:





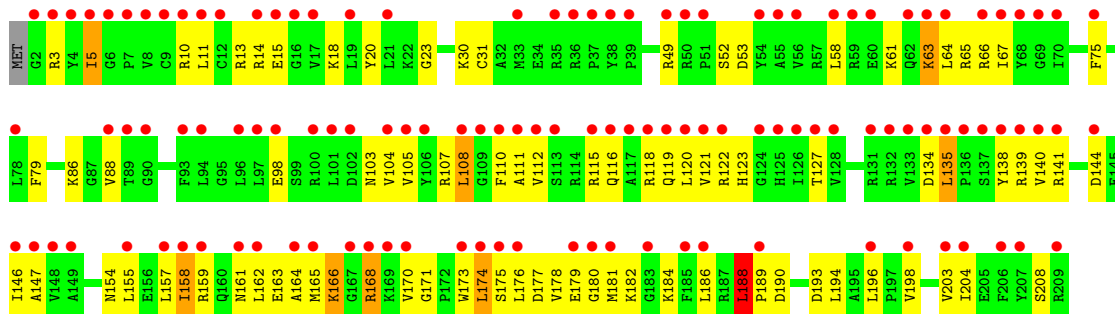
• Molecule 3: 30S ribosomal protein S3

Chain CC:



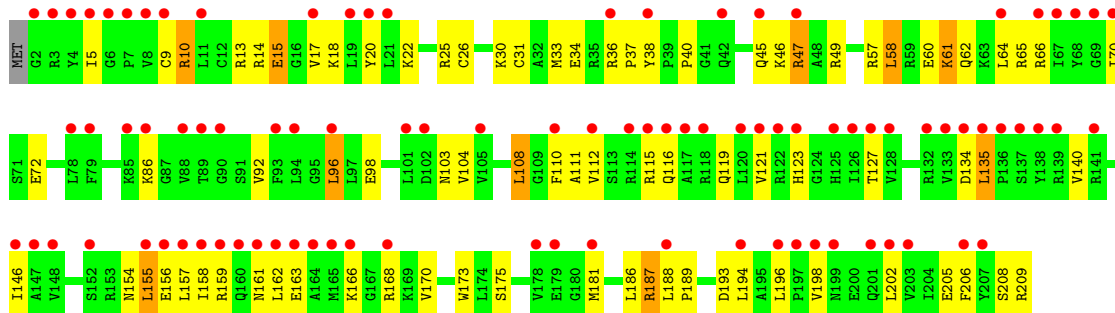
• Molecule 4: 30S ribosomal protein S4

Chain AD:



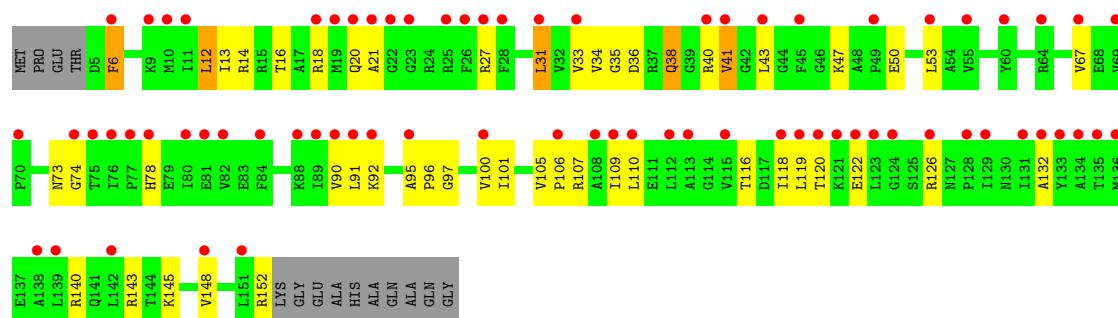
• Molecule 4: 30S ribosomal protein S4

Chain CD:



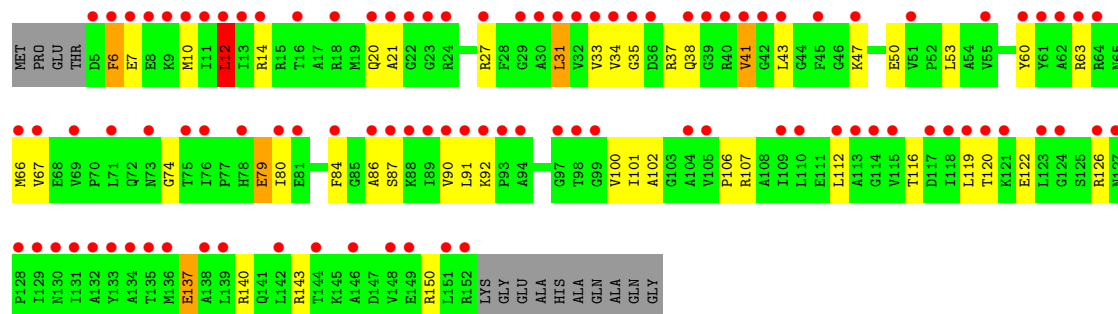
• Molecule 5: 30S ribosomal protein S5

Chain AE:



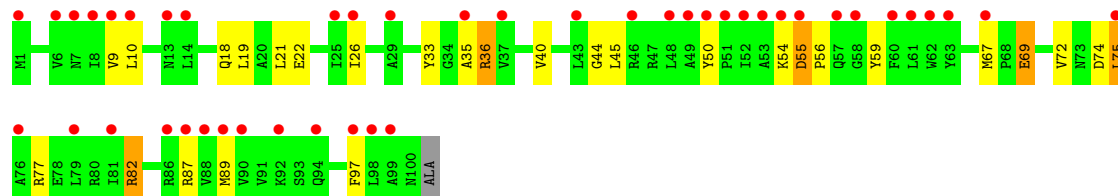
- Molecule 5: 30S ribosomal protein S5

Chain CE:



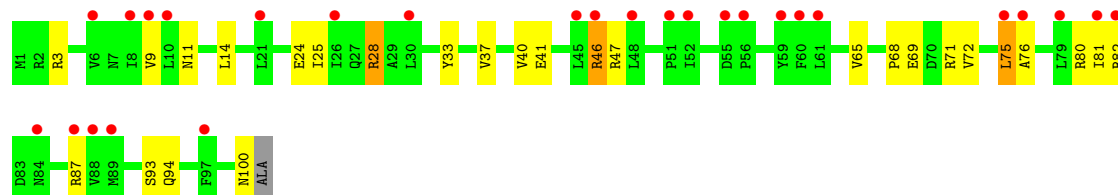
- Molecule 6: 30S ribosomal protein S6

Chain AF:



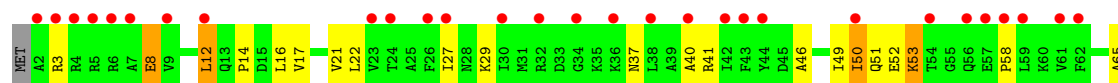
- Molecule 6: 30S ribosomal protein S6

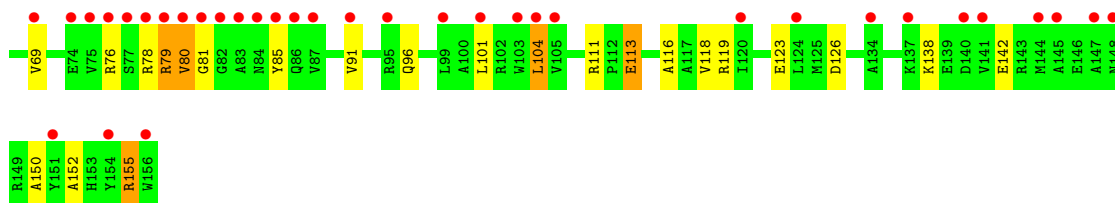
Chain CF:



- Molecule 7: 30S ribosomal protein S7

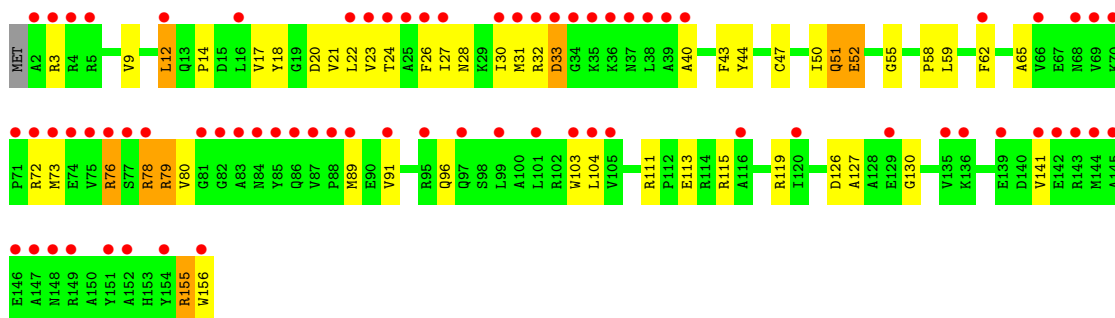
Chain AG:





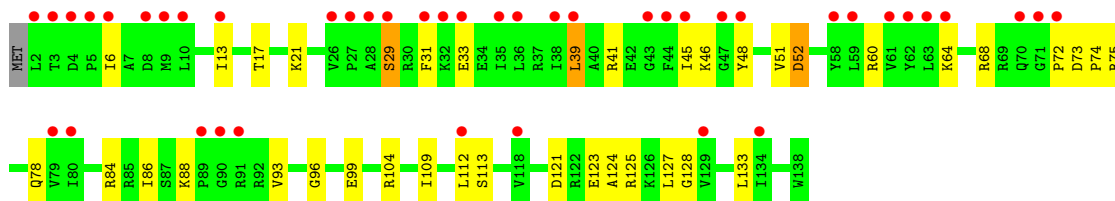
• Molecule 7: 30S ribosomal protein S7

Chain CG:



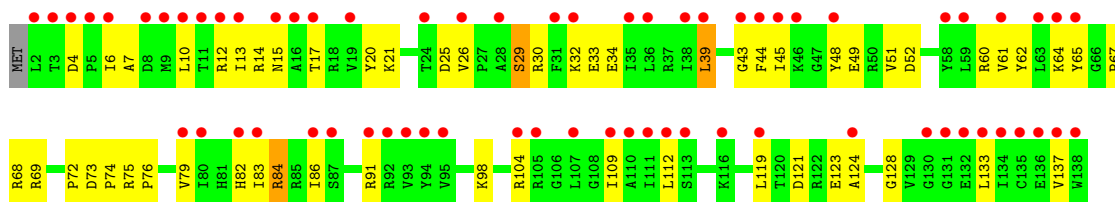
• Molecule 8: 30S ribosomal protein S8

Chain AH:



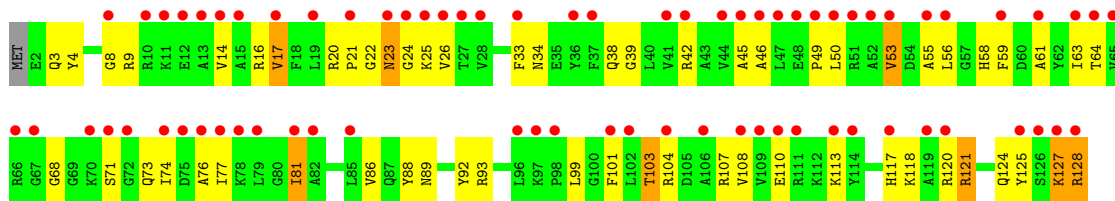
• Molecule 8: 30S ribosomal protein S8

Chain CH:

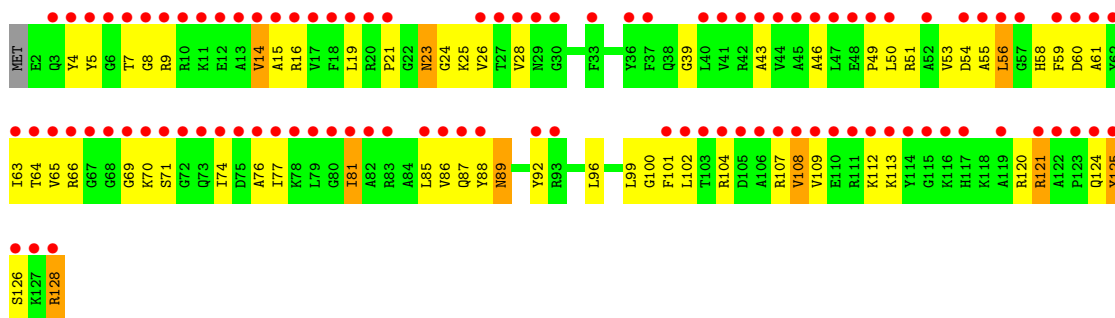


• Molecule 9: 30S ribosomal protein S9

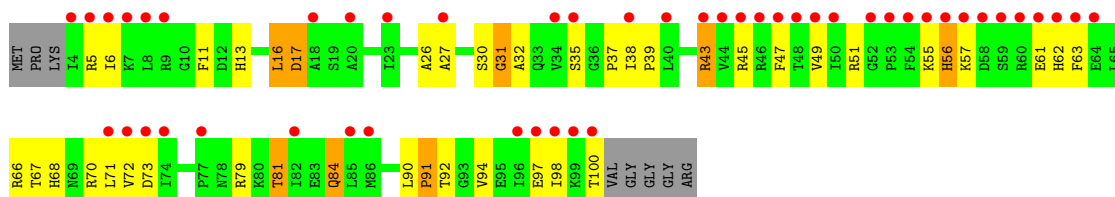
Chain AI:



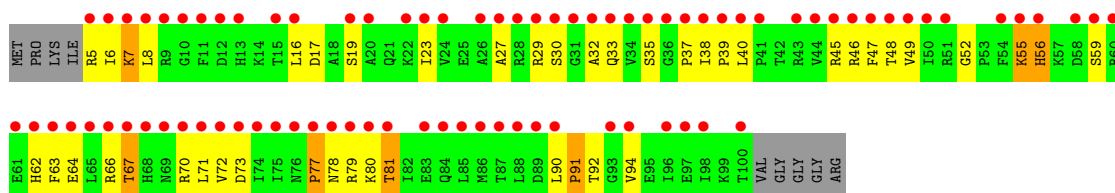
• Molecule 9: 30S ribosomal protein S9

Chain CI: 

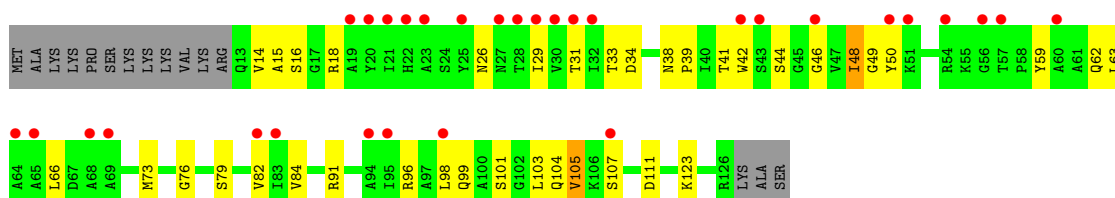
- Molecule 10: 30S ribosomal protein S10

Chain AJ: 

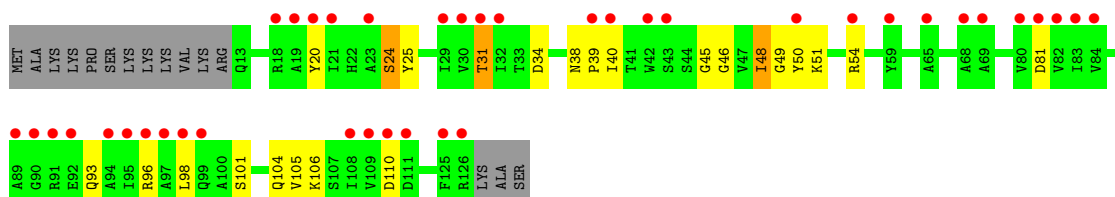
- Molecule 10: 30S ribosomal protein S10

Chain CJ: 

- Molecule 11: 30S ribosomal protein S11

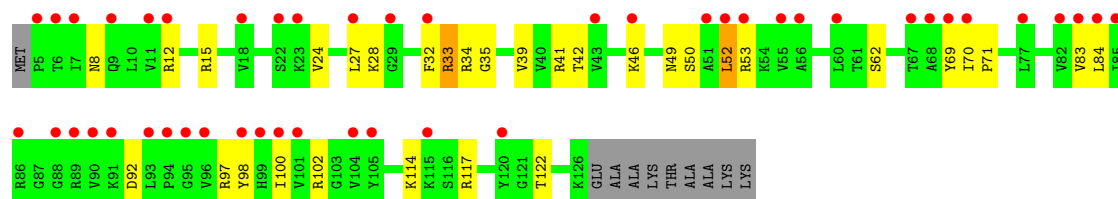
Chain AK: 

- Molecule 11: 30S ribosomal protein S11

Chain CK: 

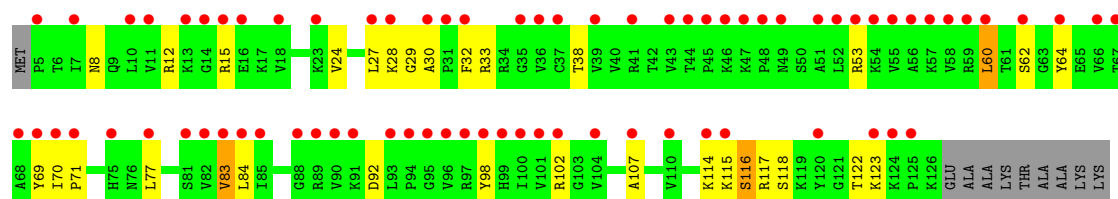
- Molecule 12: 30S ribosomal protein S12

Chain AL:



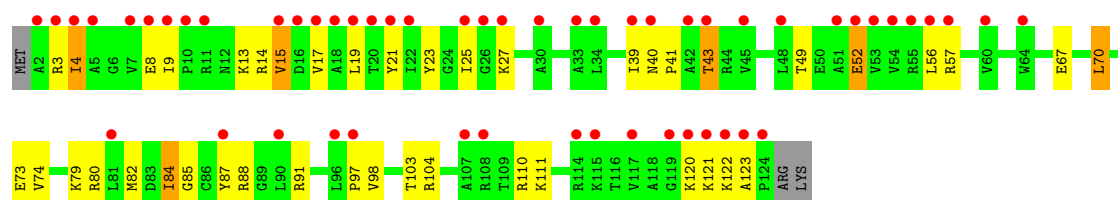
- Molecule 12: 30S ribosomal protein S12

Chain CL:



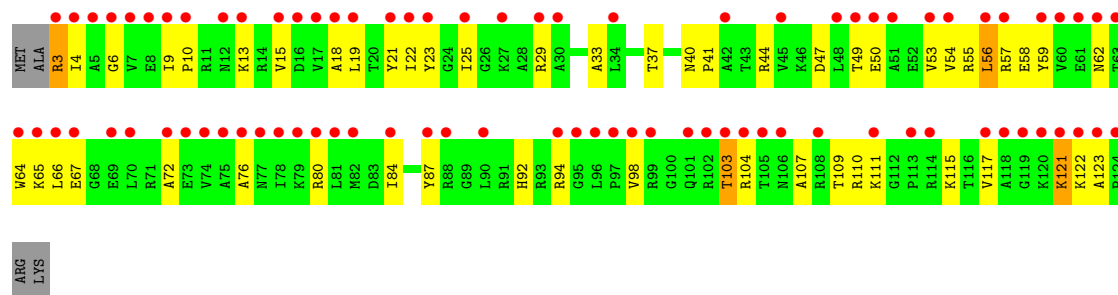
- Molecule 13: 30S ribosomal protein S13

Chain AM:



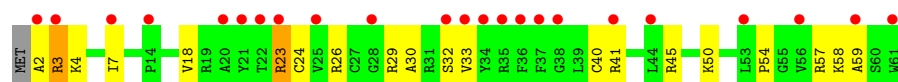
- Molecule 13: 30S ribosomal protein S13

Chain CM:



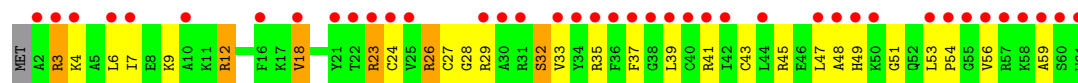
- Molecule 14: 30S ribosomal protein S14 type Z

Chain AN:



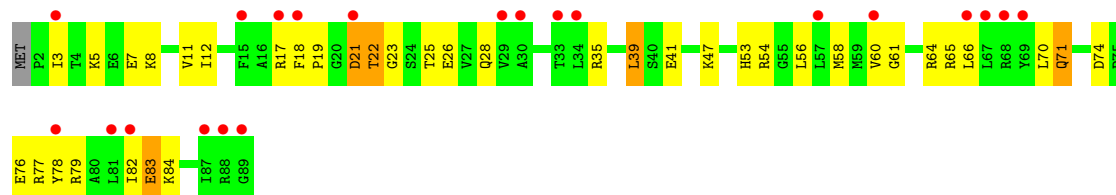
- Molecule 14: 30S ribosomal protein S14 type Z

Chain CN:



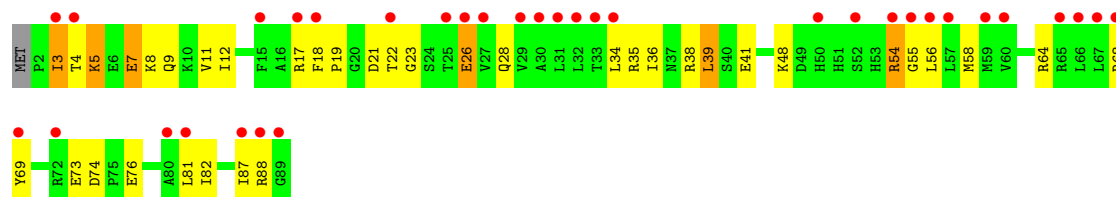
- Molecule 15: 30S ribosomal protein S15

Chain AO:



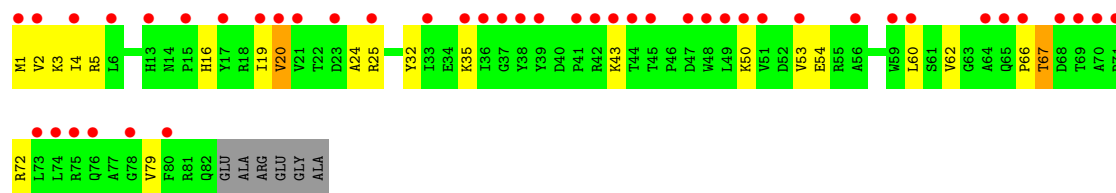
- Molecule 15: 30S ribosomal protein S15

Chain CO:



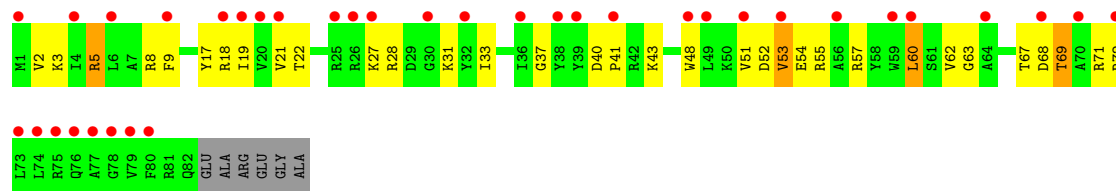
- Molecule 16: 30S ribosomal protein S16

Chain AP:



- Molecule 16: 30S ribosomal protein S16

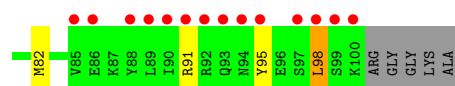
Chain CP:



- Molecule 17: 30S ribosomal protein S17

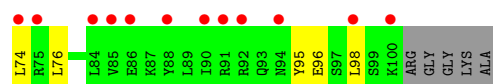
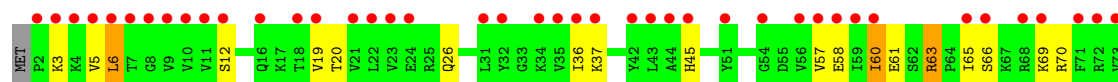
Chain AQ:





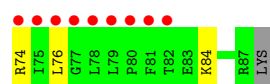
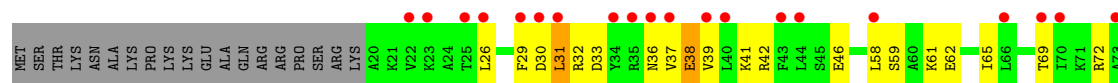
- Molecule 17: 30S ribosomal protein S17

Chain CQ:



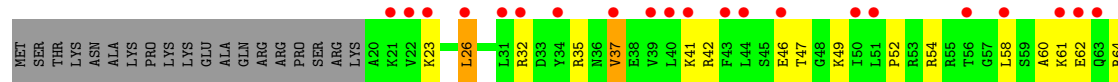
- Molecule 18: 30S ribosomal protein S18

Chain AR:



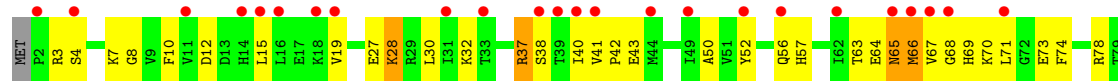
- Molecule 18: 30S ribosomal protein S18

Chain CR:



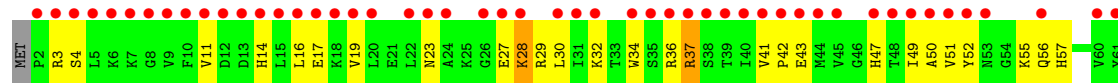
- Molecule 19: 30S ribosomal protein S19

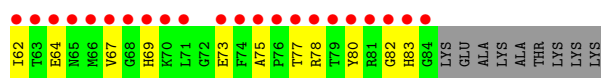
Chain AS:



- Molecule 19: 30S ribosomal protein S19

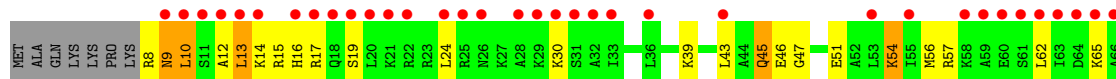
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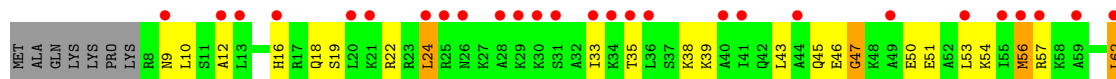
- Molecule 20: 30S ribosomal protein S20

Chain AT:



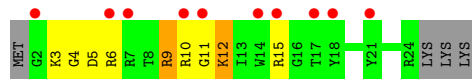
- Molecule 20: 30S ribosomal protein S20

Chain CT:



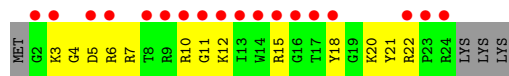
- Molecule 21: 30S ribosomal protein Thx

Chain AU:



- Molecule 21: 30S ribosomal protein Thx

Chain CU:



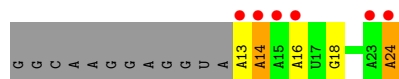
- Molecule 22: mRNA

Chain AV:



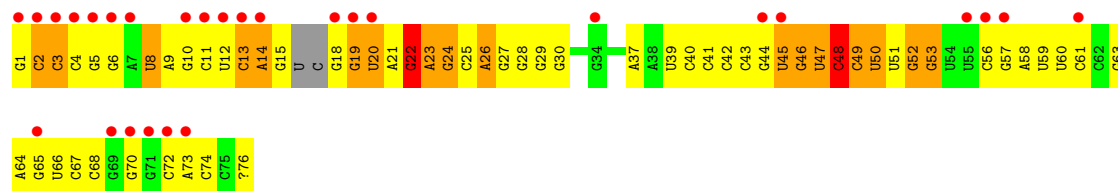
- Molecule 22: mRNA

Chain CV:



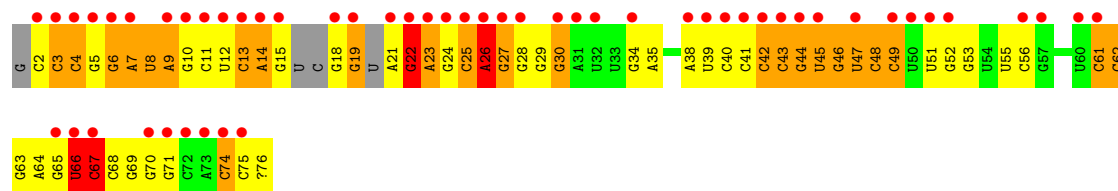
- Molecule 23: A-site tRNA

Chain AW: 



- Molecule 23: A-site tRNA

Chain CW: 



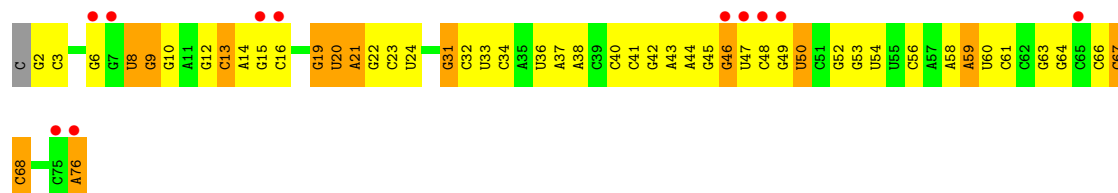
- Molecule 24: P-site tRNA

Chain AX: 



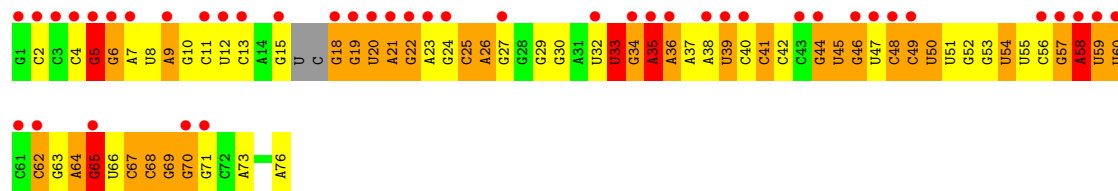
- Molecule 24: P-site tRNA

Chain CX: 



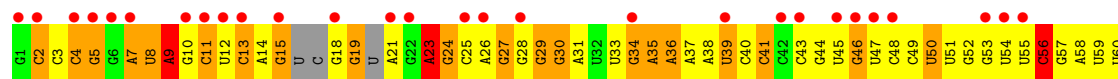
- Molecule 25: E-site tRNA

Chain AY: 



- Molecule 25: E-site tRNA

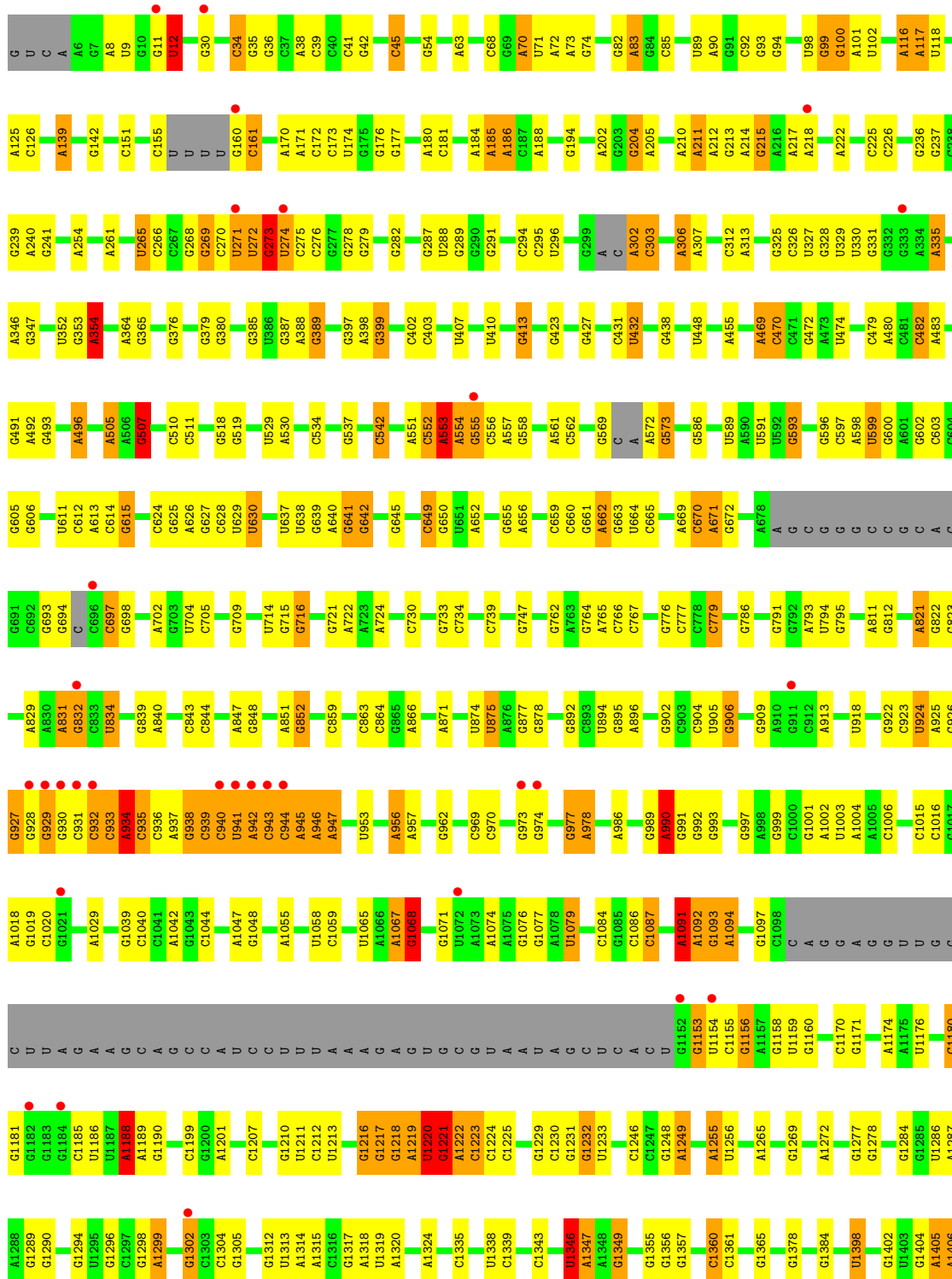
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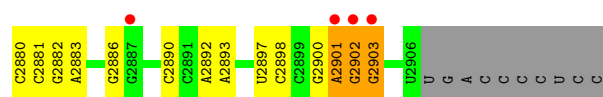


- Molecule 26: 23S Ribosomal RNA

Chain BA:

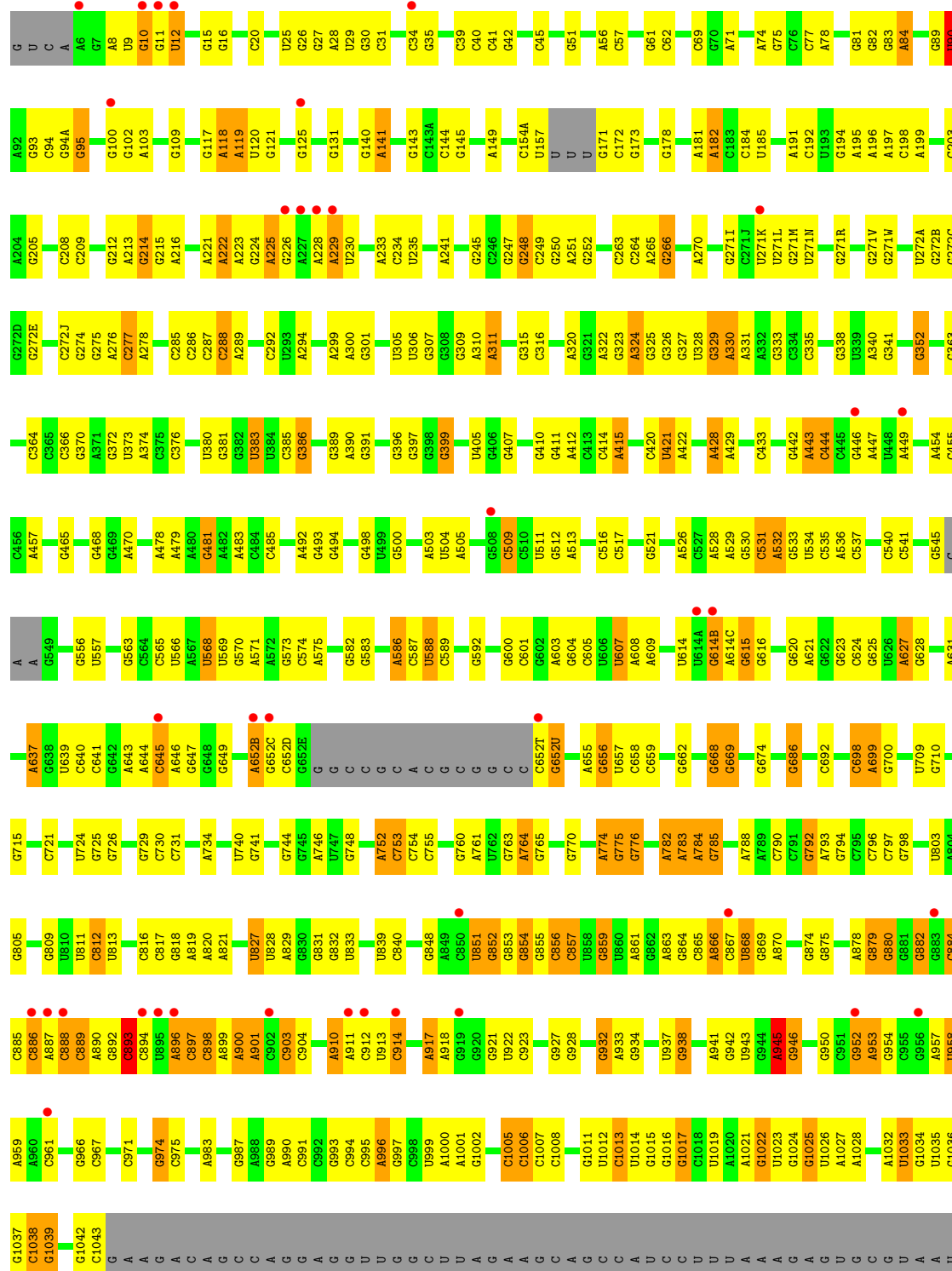


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A2882	U2783	U2686	G2585	C2585	G2394	G2267	C2204	A2141	A2027	U1897	C1683	C1683	C1683
C2883	G2784	C2687	G2586	C2586	G2395	G2268	U2205	A2142	A2028	U1898	C1684	C1684	C1684
A2884	U2785	U2688	G2587	C2587	G2396	G2269							

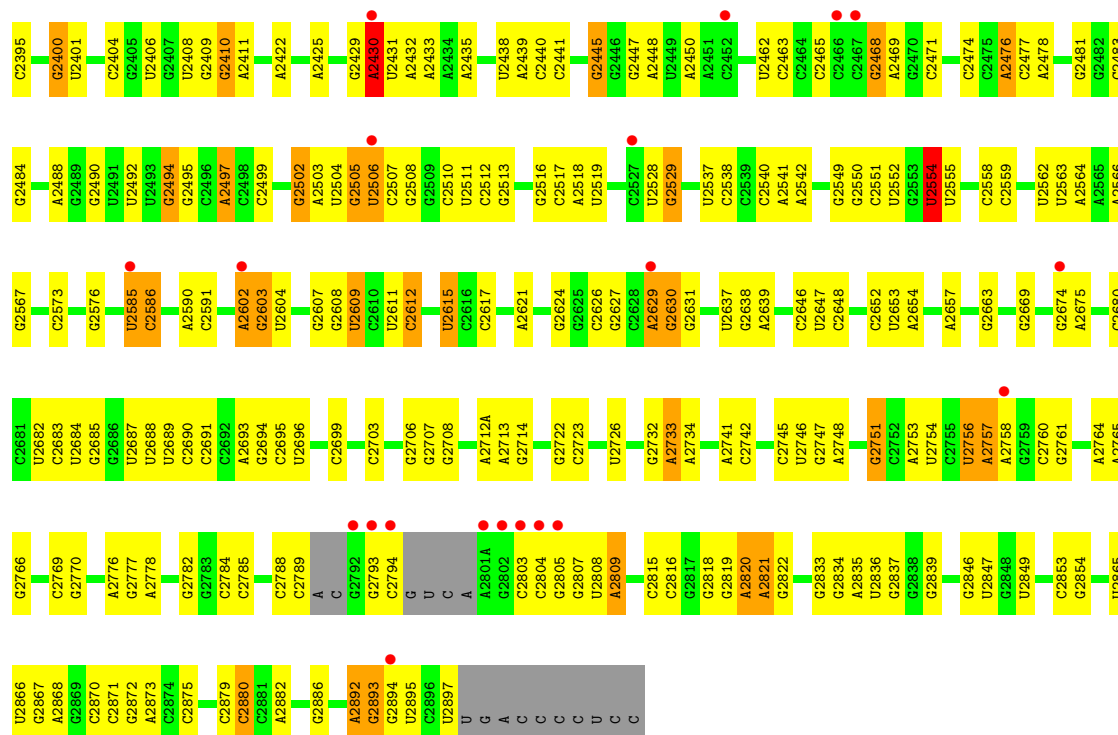


- Molecule 26: 23S Ribosomal RNA

Chain DA:

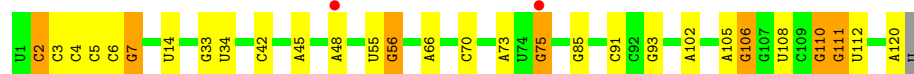


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G2315	G2239	G1889	G2087	C1996	A1889	C1648	U1540	C1467	G1368	C1261	G	G
G2318	G2242	G2152	G2093	G1997	A1890	G1653	A1542	G1470	G1369	C1178	A	C
G2319	G2243	G2153	G2094	G1998	A1891	A1654	C1543	A1471	C1370	C1179	C	U
A2320	G2244	G2154	C2095	G2002	C1894	A1655	A1544	A1472	G1371	C1180	C	A
G2321	G2245	G2155	C2096	C2006	C1895	C1656	A1545	G1473	A1265	A1265	C	C
A2322	G2246	G2156	U2099	C2007	G1899	C1657	C1546	A1477	G1267	G1183	U	U
G2323	G2251	A2158	G2100	A2013	A1900	C1658	C1547	G1478	U1272	G1184	G	G
G2324	G2252	G2159	G2101	A2014	C1905	A1668	A1554	G1482	A1378	G1197	U	U
G2325	G2253	G2160	G2102	G2019	G1906	A1669	A1555	G1484	G1379	G1198	G	G
G2326	G2254	C2161	U2103	A2020	G1907	C1670	A1556	G1486	G1380	G1199	U	U
G2327	G2255	C2162	C2103	A2021	C1908	U1671	A1557	G1488	G1271	G1187	C	C
A2328	G2256	C2163	G2104	G2022	C1909	A1672	A1558	G1491	A1272	A1189	G	A
U2332	G2259	G2164	C2105	C2023	G1910	G1673	A1559	G1492	U1273	G1112	A	A
A2333	G2260	U2165	C2106	G2024	U1911	A1674	A1560	G1493	G1278	U1113	U	U
G2334	C2261	G2166	C2107	G2025	U1912	U1688	C1575	G1494	A1285	G1114	U	U
A2335	U2262	G2167	U2108	C2026	A1913	A1689	U1576	C1495	G1286	G1115	U	U
A2336	C2263	A2169	G2110	G2027	C1914	U1693	C1577	A1496	A1287	G1116	U	U
G2339	G2271	A2171	G2111	U2028	U1915	A1696	U1578	G1497	U1288	G1117	U	U
C2343	U2272	U2172	G2112	G2029	U1916	G1697	U1579	A1498	U1289	G1118	U	U
U2344	A2273	A2173	U2113	A2030	U1917	C1698	A1580	G1499	U1290	G1122	U	U
G2345	A2274	C2174	A2114	A2031	A1918	U1700	A1581	U1503	U1291	G1125	U	U
G2346	C2275	G2175	G2115	G2032	A1919	G1703	A1582	U1504	U1292	A1126	U	U
A2347	G2276	A2176	G2116	G2033	U1920	G1704	A1583	U1505	U1293	A1127	U	U
U2348	G2277	C2177	U2117	A2034	G1922	G1756	C1584	U1506	G1301	A1128	U	U
G2349	A2278	C2178	A2118	G2037	U1923	U1757	A1585	U1507	A1302	A1129	U	U
C2350	G2279	U2180	G2120	G2038	C1924	G1758	A1586	U1508	A1303	U1130	U	U
U2351	G2280	G2181	G2121	U2041	A1927	G1763	A1587	U1509	G1304	G1131	U	U
G2354	C2283	G2182	U2122	A2042	U1928	U1764	A1588	U1510	U1305	C1135	U	U
C2355	G2284	C2183	G2123	G2043	G1929	G1765	A1589	U1511	G1306	G1136	U	U
G2356	C2285	G2184	G2124	C2044	U1930	U1766	A1590	U1512	G1307	C1137	U	U
U2357	C2286	C2185	G2125	G2045	U1931	C1767	A1591	U1513	G1308	C1138	U	U
C2364	G2287	G2186	A2126	G2046	A1932	U1768	A1592	U1514	U1309	C1139	U	U
G2365	A2288	G2187	G2127	G2047	G1933	A1741	A1593	U1515	G1310	U1141	U	U
A2366	U2291	C2188	C2128	G2048	U1934	G1759	C1594	U1516	U1311	U1142	U	U
G2369	C2292	U2189	U2129	G2049	A1935	U1760	A1595	U1517	U1312	A1142A	U	U
U2370	C2293	G2192	G2130	G2050	U1936	U1761	A1596	U1518	U1313	G1143	U	U
G2371	C2294	G2193	G2131	G2051	A1937	U1762	A1597	U1519	U1314	G1144	U	U
C2374	A2298	G2194	G2132	C2052	U1938	G1763	A1598	U1520	G1324	G1151	U	U
G2375	G2299	A2198	G2133	C2053	A1939	U1764	A1599	U1521	U1325	C1152	U	U
A2376	G2300	G2199	A2134	G2054	U1940	U1765	A1600	U1522	G1326	C1153	U	U
A2377	C2301	U2203	A2135	A2055	U1941	C1766	A1601	U1523	G1327	G1154	U	U
A2378	G2302	C2205	A2136	A2056	U1942	U1767	A1602	U1524	A1336	A1155	U	U
G2379	C2303	G2206	C2137	G2057	U1943	U1768	A1603	U1525	G1337	G1160	U	U
U2382	G2304	G2207	C2138	G2058	U1944	U1769	A1604	U1526	U1352	C1161	U	U
G2383	A2305	U2218	C2139	A2059	U1945	U1770	A1605	U1527	G1353	G1162	U	U
G2384	C2306	G2219	C2140	G2060	U1946	U1771	A1606	U1528	U1354	U1167	U	U
C2385	G2307	A2225	U2144	G2061	A1947	U1772	A1607	U1529	A1242	G1168	U	U
A2388	C2308	G2228	C2145	A2062	U1948	U1773	A1608	C1530	A1246	G1170	U	U
C2394	U2310	C2229	G2146	U2074	A1949	U1774	A1609	C1531	A1247	G1171	G	A
	U2311	U2148	U2147	U2075	U1950	U1775	A1610	C1532	A1248	G1172	U	U
	U2312	G2149	U2148	U2076	U1951	U1776	A1611	C1533	A1253	G1173	U	U
	C2313	U2150	U2149	A2082	G1992	U1777	A1612	U1534				
						U1778	A1613	U1535				
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						U1780	A1615	U1537				
						U1781	A1616	U1538				
						U1782	A1617	U1539				
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						U1789	A1624	U1546				
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						U1793	A1628	U1550				
						U1794	A1629	U1551				
						U1795	A1630	U1552				
						U1796	A1631	U1553				
						U1797	A1632	U1554				
						U1798	A1633	U1555				
						U1799	A1634	U1556				
						U1800	A1635	U1557				
						U1801	A1636	U1558				
						U1802	A1637	U1559				
						U1803	A1638	U1560				
						U1804	A1639	U1561				
						U1805	A1640	U1562				
						U1806	A1641	U1563				
						U1807	A1642	U1564				
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						U1809	A1644	U1566				
						U1810	A1645	U1567				
						U1811	A1646	U1568				
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						U1841	A1676	U1598				
						U1842	A1677	U1599				
						U1843	A1678	U1600				
						U1844	A1679	U1601				
						U1845	A1680	U1602				
						U1846	A1681	U1603				
						U1847	A1682	U1604				
						U1848	A1683	U1605				
						U1849	A1684	U1606				
						U1850	A1685	U1607				
						U1851	A1686	U1608				
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						U1855	A1690	U1612				
						U1856	A1691	U1613				
						U1857	A1692	U1614				
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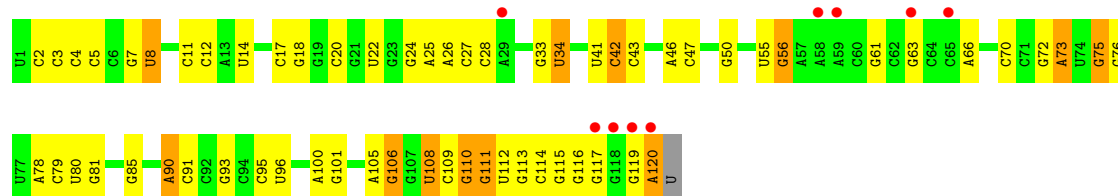
• Molecule 27: 5S Ribosomal RNA

Chain BB:



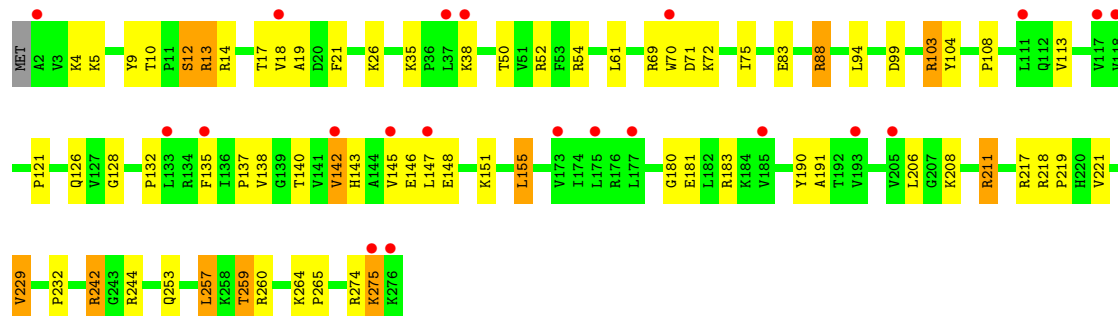
• Molecule 27: 5S Ribosomal RNA

Chain DB:



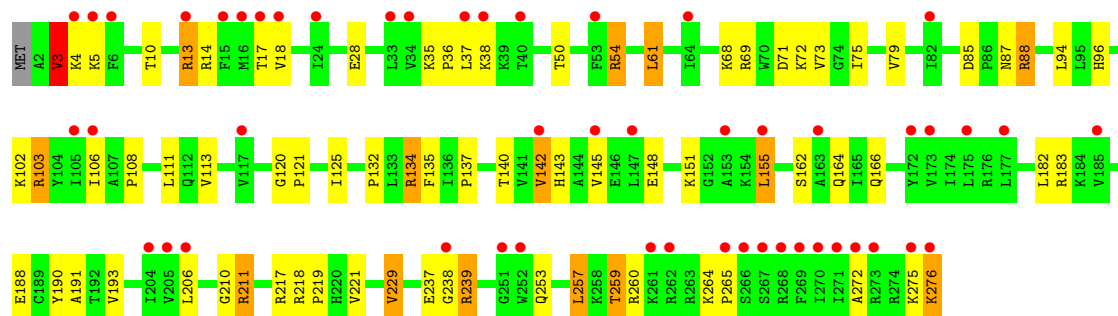
• Molecule 28: 50S ribosomal protein L2

Chain BD:



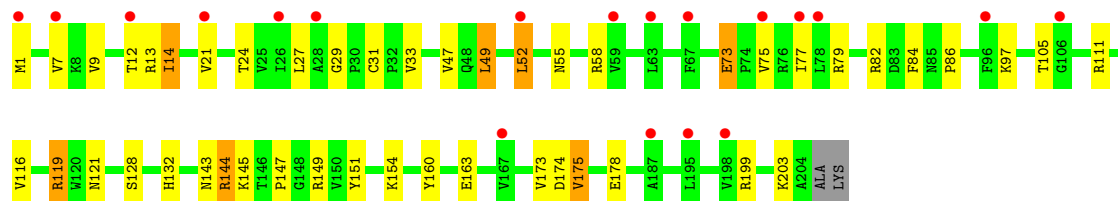
- Molecule 28: 50S ribosomal protein L2

Chain DD:



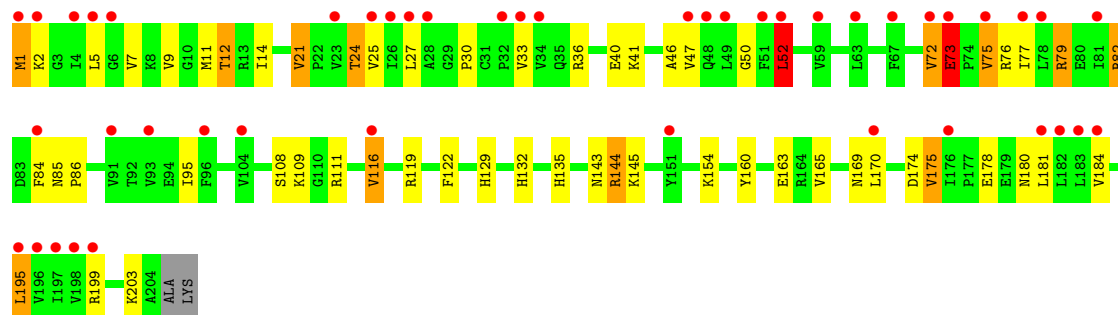
- Molecule 29: 50S ribosomal protein L3

Chain BE:



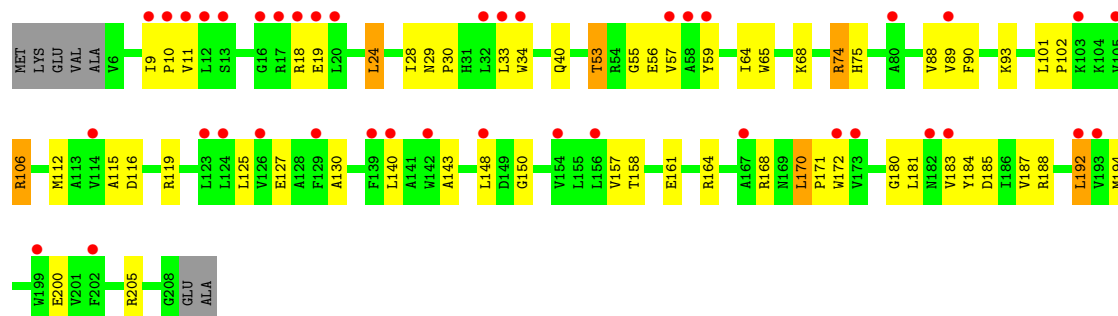
- Molecule 29: 50S ribosomal protein L3

Chain DE:

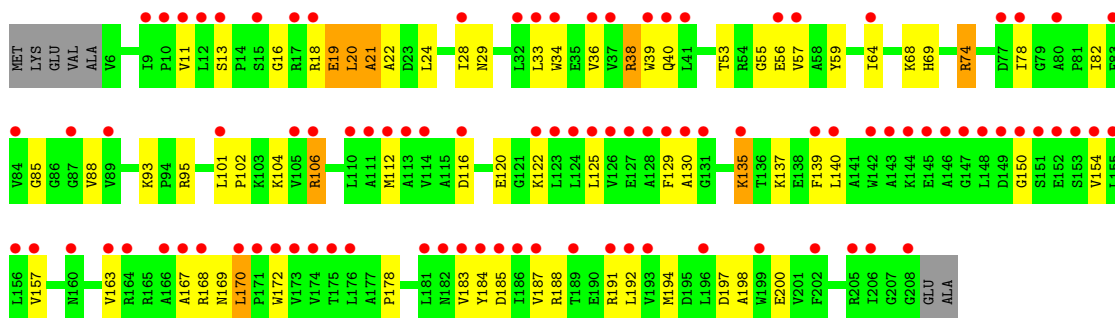


- Molecule 30: 50S ribosomal protein L4

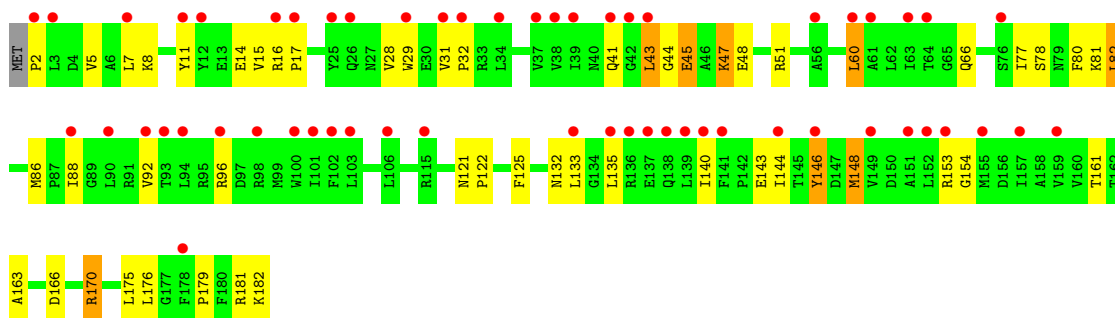
Chain BF:



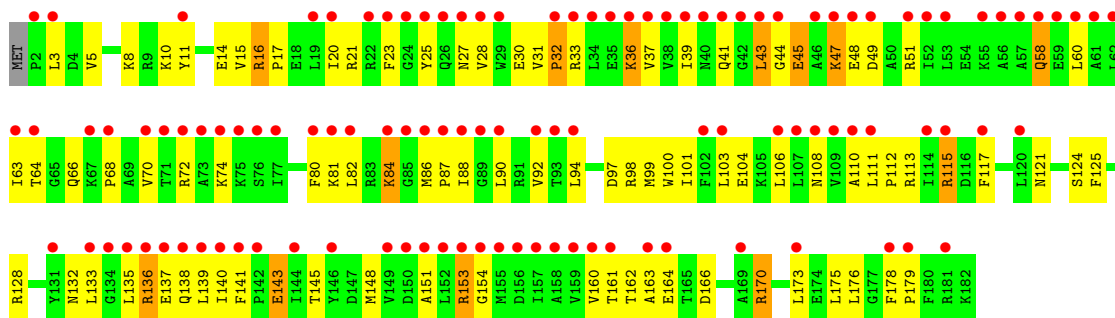
- Molecule 30: 50S ribosomal protein L4

Chain DF: 

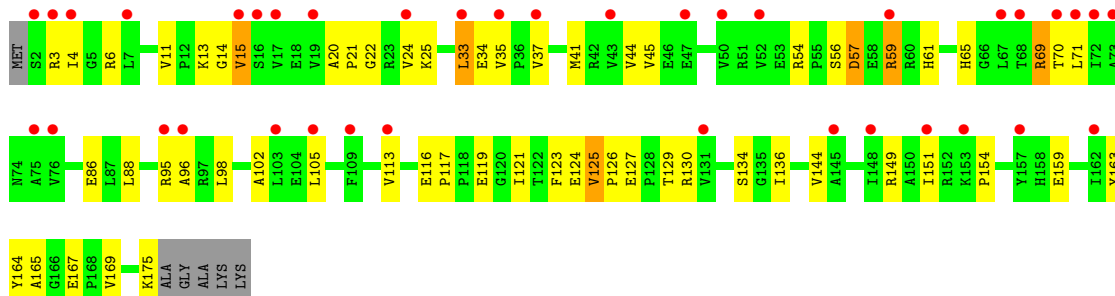
- Molecule 31: 50S ribosomal protein L5

Chain BG: 

- Molecule 31: 50S ribosomal protein L5

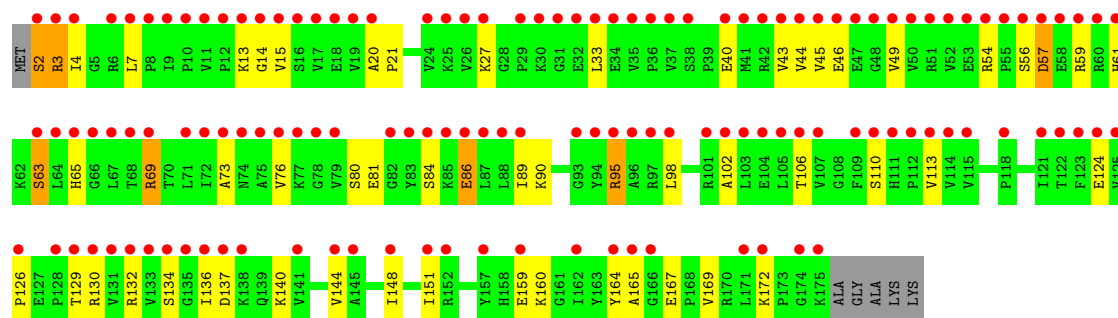
Chain DG: 

- Molecule 32: 50S ribosomal protein L6

Chain BH: 

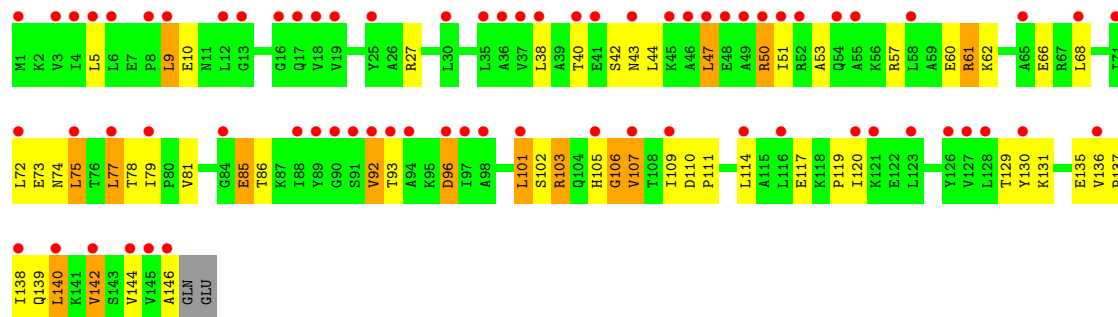
- Molecule 32: 50S ribosomal protein L6

Chain DH:



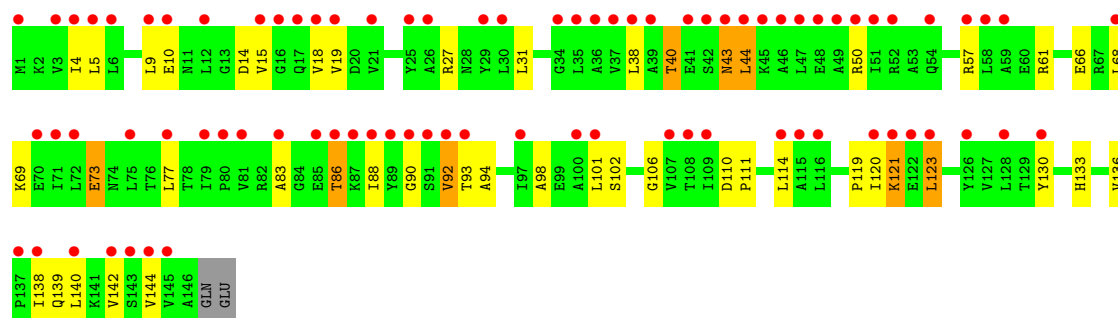
- Molecule 33: 50S ribosomal protein L9

Chain BI:



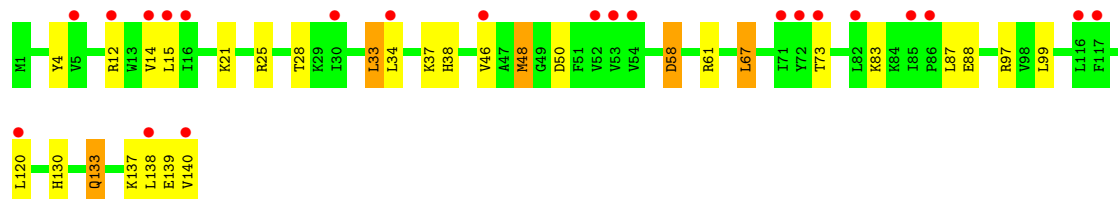
- Molecule 33: 50S ribosomal protein L9

Chain DI:



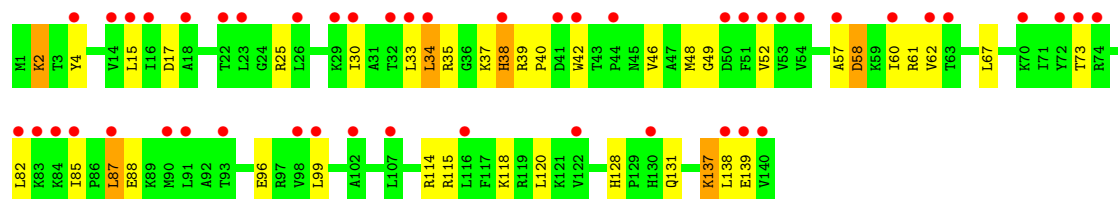
- Molecule 34: 50S ribosomal protein L13

Chain BN:



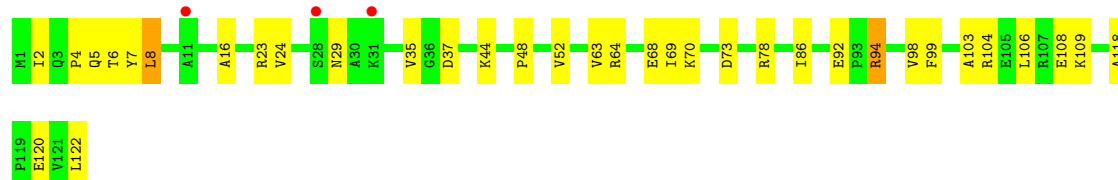
- Molecule 34: 50S ribosomal protein L13

Chain DN: 



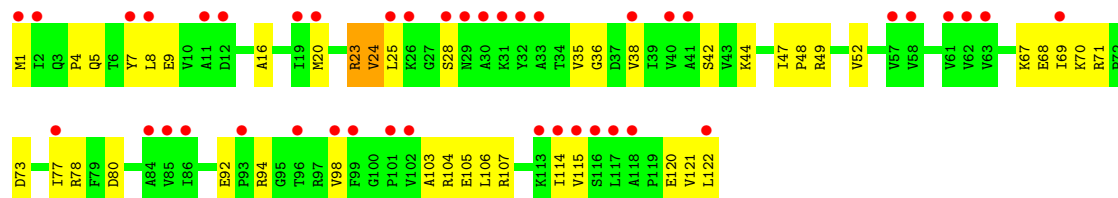
- Molecule 35: 50S ribosomal protein L14

Chain BO: 



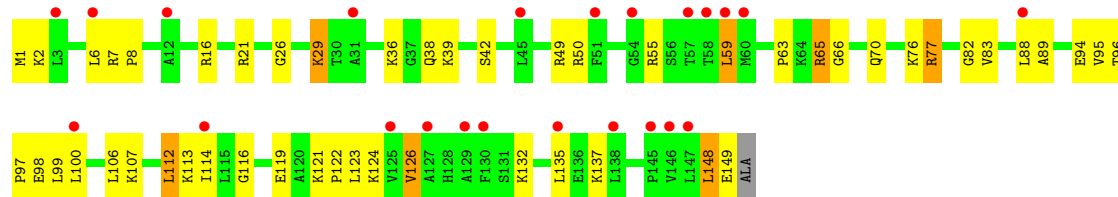
- Molecule 35: 50S ribosomal protein L14

Chain DO: 



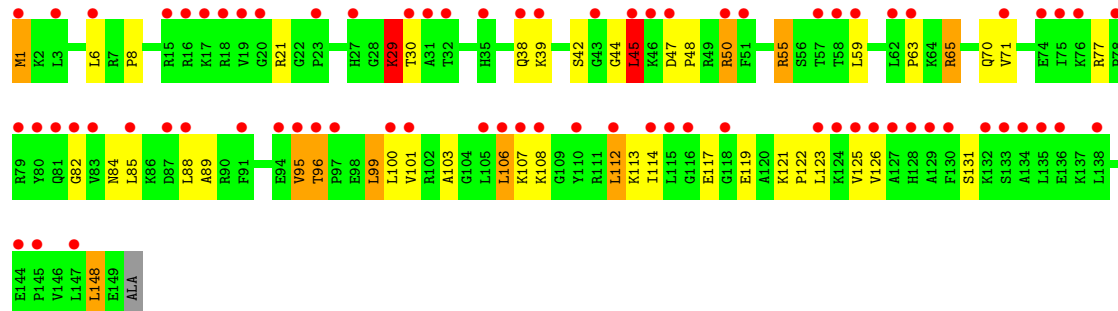
- Molecule 36: 50S ribosomal protein L15

Chain BP: 

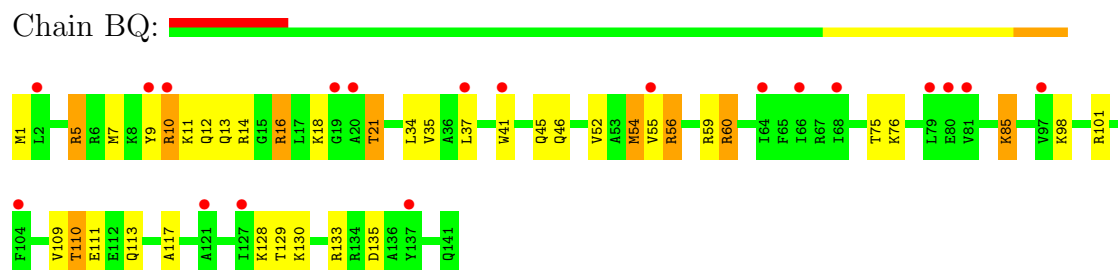


- Molecule 36: 50S ribosomal protein L15

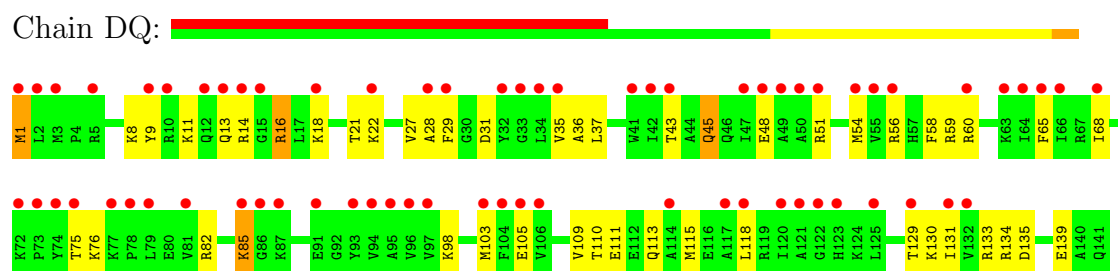
Chain DP: 



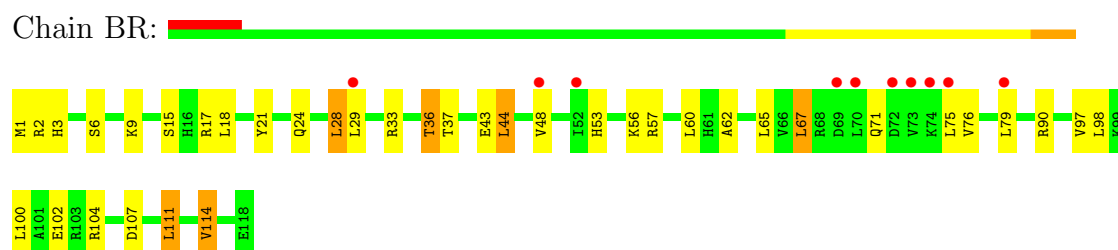
- Molecule 37: 50S ribosomal protein L16



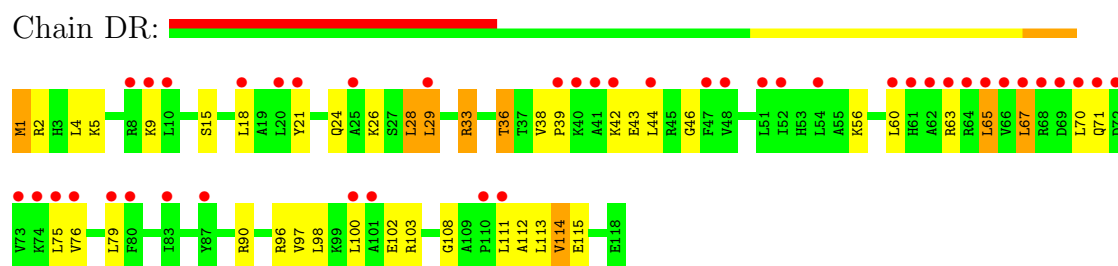
- Molecule 37: 50S ribosomal protein L16



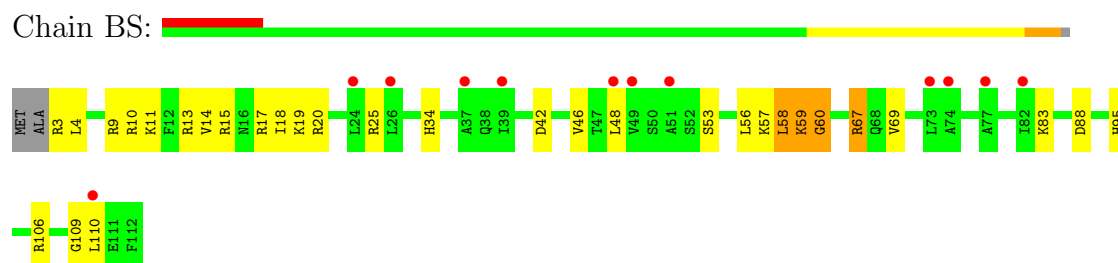
- Molecule 38: 50S ribosomal protein L17



- Molecule 38: 50S ribosomal protein L17

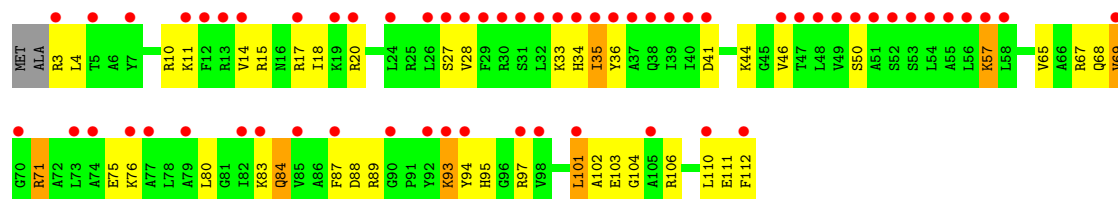


- Molecule 39: 50S ribosomal protein L18



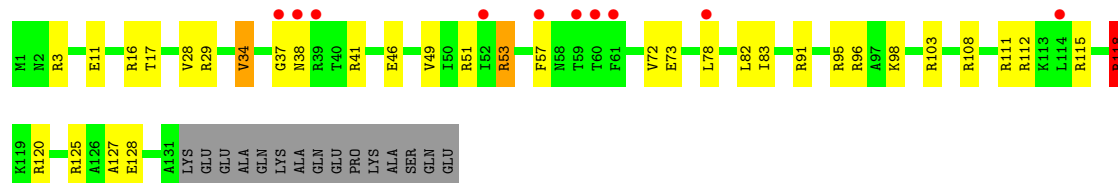
- Molecule 39: 50S ribosomal protein L18

Chain DS: 



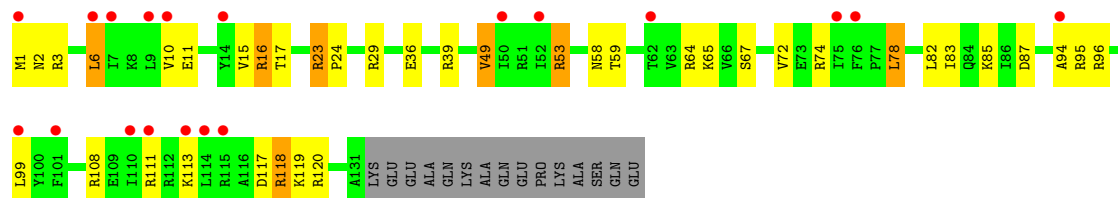
- Molecule 40: 50S ribosomal protein L19

Chain BT: 



- Molecule 40: 50S ribosomal protein L19

Chain DT: 



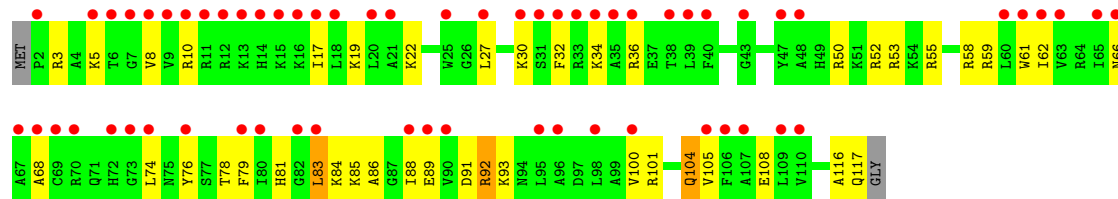
- Molecule 41: 50S ribosomal protein L20

Chain BU: 



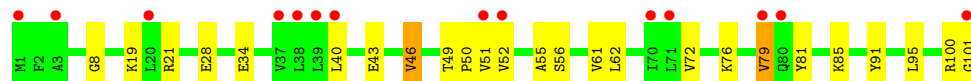
- Molecule 41: 50S ribosomal protein L20

Chain DU: 



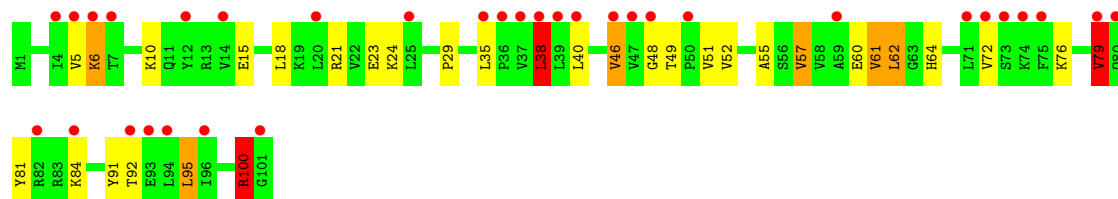
- Molecule 42: 50S ribosomal protein L21

Chain BV: 



- Molecule 42: 50S ribosomal protein L21

Chain DV:



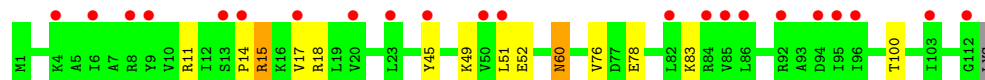
- Molecule 43: 50S ribosomal protein L22

Chain BW:



- Molecule 43: 50S ribosomal protein L22

Chain DW:



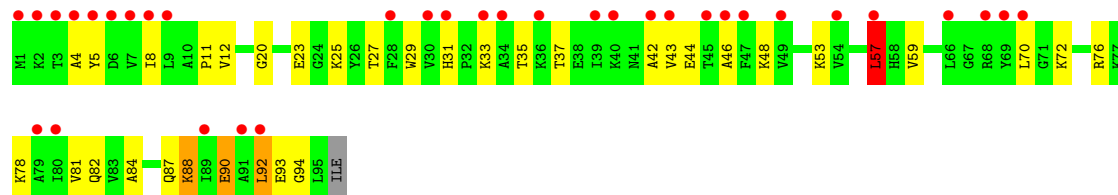
- Molecule 44: 50S ribosomal protein L23

Chain BX:



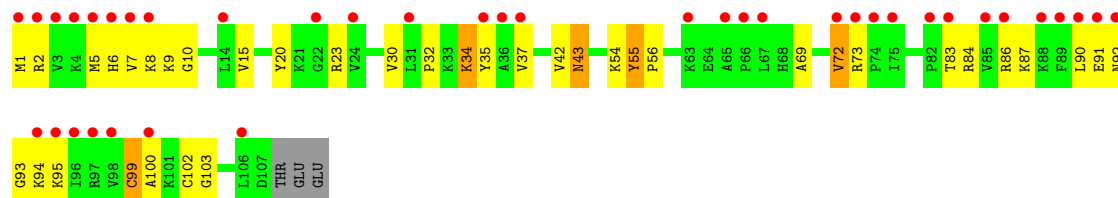
- Molecule 44: 50S ribosomal protein L23

Chain DX:



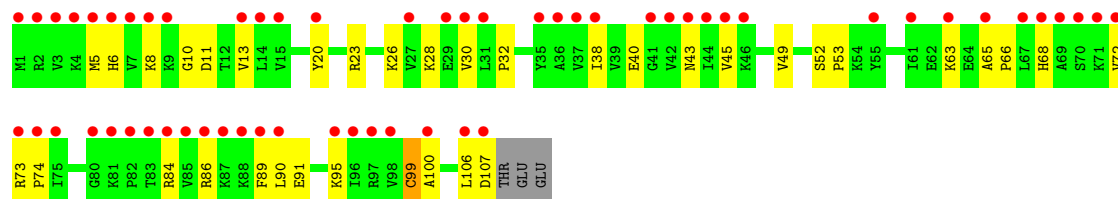
- Molecule 45: 50S ribosomal protein L24

Chain BY:



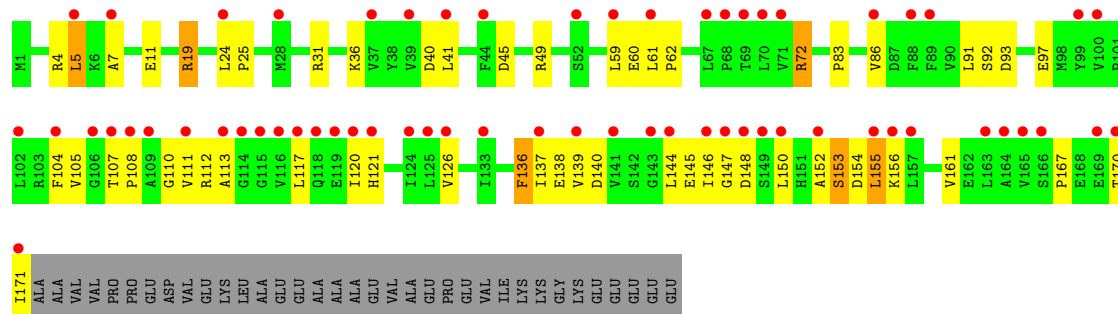
- Molecule 45: 50S ribosomal protein L24

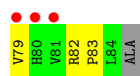
Chain DY:



- Molecule 46: 50S ribosomal protein L25

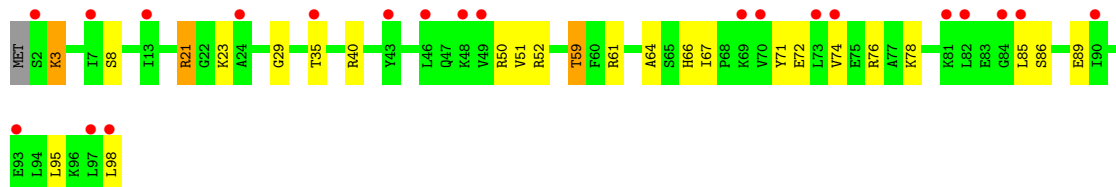
Chain BZ:





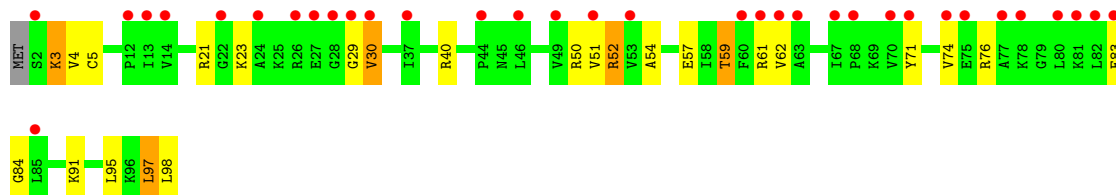
- Molecule 48: 50S ribosomal protein L28

Chain B1:



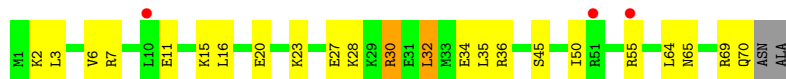
- Molecule 48: 50S ribosomal protein L28

Chain D1:



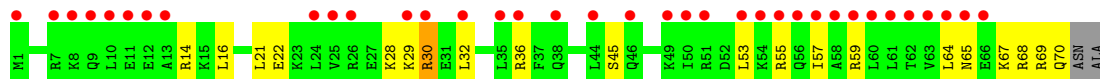
- Molecule 49: 50S ribosomal protein L29

Chain B2:



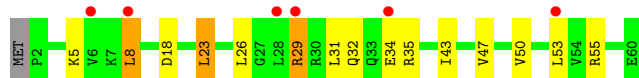
- Molecule 49: 50S ribosomal protein L29

Chain D2:



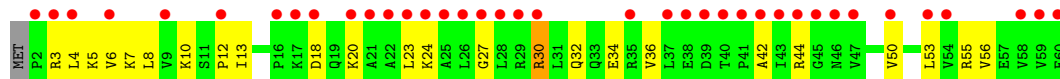
- Molecule 50: 50S ribosomal protein L30

Chain B3:



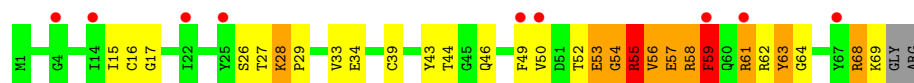
- Molecule 50: 50S ribosomal protein L30

Chain D3:



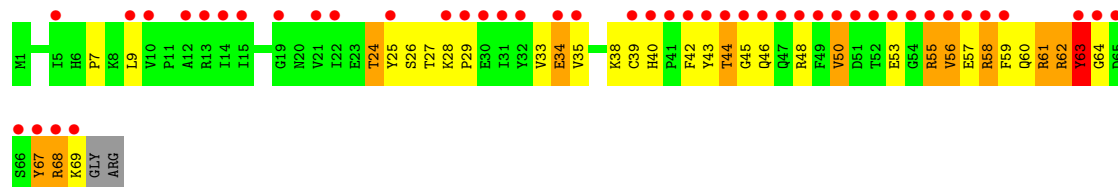
- Molecule 51: 50S ribosomal protein L31

Chain B4:



- Molecule 51: 50S ribosomal protein L31

Chain D4:



- Molecule 52: 50S ribosomal protein L32

Chain B5:



- Molecule 52: 50S ribosomal protein L32

Chain D5:



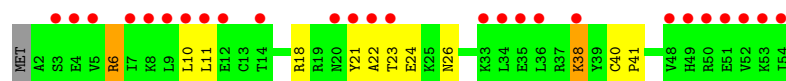
- Molecule 53: 50S ribosomal protein L33

Chain B6:



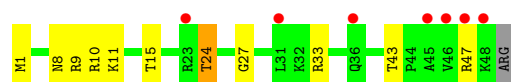
- Molecule 53: 50S ribosomal protein L33

Chain D6:



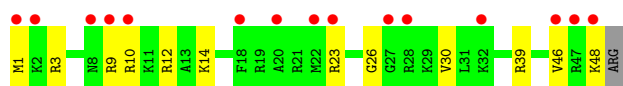
- Molecule 54: 50S ribosomal protein L34

Chain B7:



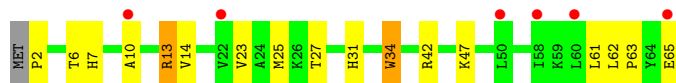
- Molecule 54: 50S ribosomal protein L34

Chain D7:



- Molecule 55: 50S ribosomal protein L35

Chain B8:



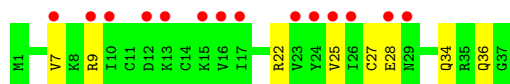
- Molecule 55: 50S ribosomal protein L35

Chain D8:



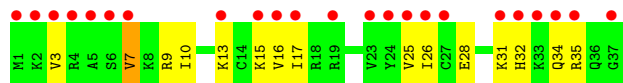
- Molecule 56: 50S ribosomal protein L36

Chain B9:



- Molecule 56: 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	209.32Å 450.06Å 622.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	152.51 – 2.55 255.92 – 2.55	Depositor EDS
% Data completeness (in resolution range)	95.8 (152.51-2.55) 95.8 (255.92-2.55)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.55Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.233 , 0.280 0.253 , 0.300	Depositor DCC
R_{free} test set	43781 reflections (2.43%)	DCC
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 1802139 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	297141	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 1.64% 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, ZN, 31M, MIA, SF4, MG, 5MC, 4SU, 7MG, K, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AA	0.37	0/36049	0.91	42/56261 (0.1%)
1	CA	0.40	6/36170 (0.0%)	1.00	88/56452 (0.2%)
2	AB	0.31	0/1881	0.60	0/2542
2	CB	0.33	0/1860	0.65	1/2518 (0.0%)
3	AC	0.28	0/1576	0.52	0/2130
3	CC	0.32	0/1566	0.61	0/2119
4	AD	0.29	0/1689	0.58	2/2267 (0.1%)
4	CD	0.30	0/1704	0.54	0/2284
5	AE	0.30	0/1145	0.55	0/1543
5	CE	0.31	0/1149	0.62	1/1548 (0.1%)
6	AF	0.28	0/819	0.49	0/1111
6	CF	0.31	0/829	0.52	0/1123
7	AG	0.27	0/1250	0.51	0/1679
7	CG	0.28	0/1254	0.53	0/1683
8	AH	0.27	0/1108	0.50	0/1494
8	CH	0.27	0/1108	0.52	0/1494
9	AI	0.30	0/1002	0.59	0/1346
9	CI	0.30	0/997	0.57	0/1343
10	AJ	0.28	0/722	0.59	0/982
10	CJ	0.31	0/727	0.59	0/988
11	AK	0.28	0/844	0.60	1/1145 (0.1%)
11	CK	0.28	0/848	0.53	0/1149
12	AL	0.30	0/946	0.52	0/1274
12	CL	0.30	0/946	0.55	0/1274
13	AM	0.28	0/969	0.61	0/1302
13	CM	0.29	0/961	0.57	0/1291
14	AN	0.30	0/501	0.50	0/664
14	CN	0.33	0/501	0.57	0/664
15	AO	0.28	0/739	0.55	0/985
15	CO	0.30	0/739	0.54	0/985
16	AP	0.28	0/697	0.52	0/939
16	CP	0.31	0/693	0.51	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.28	0/836	0.53	0/1117
17	CQ	0.29	0/836	0.50	0/1117
18	AR	0.27	0/560	0.56	0/746
18	CR	0.28	0/560	0.56	0/746
19	AS	0.29	0/667	0.58	0/900
19	CS	0.32	0/661	0.67	0/893
20	AT	0.28	0/730	0.58	0/965
20	CT	0.28	0/729	0.52	0/965
21	AU	0.26	0/203	0.52	0/266
21	CU	0.35	0/203	0.52	0/266
22	AV	0.41	0/310	0.94	0/480
22	CV	0.45	0/282	1.06	1/437 (0.2%)
23	AW	0.47	0/1577	1.18	6/2454 (0.2%)
23	CW	0.59	0/1531	1.46	25/2379 (1.1%)
24	AX	0.51	0/1725	1.17	14/2689 (0.5%)
24	CX	0.44	0/1725	1.12	10/2689 (0.4%)
25	AY	0.62	0/1602	1.43	22/2493 (0.9%)
25	CY	0.64	0/1579	1.46	32/2455 (1.3%)
26	BA	0.48	2/68013 (0.0%)	0.95	84/106165 (0.1%)
26	DA	0.42	1/67542 (0.0%)	0.94	72/105428 (0.1%)
27	BB	0.41	0/2878	0.88	0/4490
27	DB	0.44	0/2878	0.94	0/4490
28	BD	0.37	0/2186	0.59	0/2944
28	DD	0.33	0/2186	0.55	0/2944
29	BE	0.36	0/1592	0.57	0/2149
29	DE	0.34	0/1592	0.60	1/2149 (0.0%)
30	BF	0.35	0/1619	0.55	0/2193
30	DF	0.32	0/1615	0.58	0/2188
31	BG	0.31	0/1450	0.54	0/1959
31	DG	0.33	0/1449	0.57	0/1958
32	BH	0.33	0/1356	0.54	0/1834
32	DH	0.30	0/1356	0.52	0/1834
33	BI	0.29	0/1100	0.60	0/1501
33	DI	0.28	0/1076	0.57	0/1471
34	BN	0.32	0/1144	0.53	0/1543
34	DN	0.31	0/1144	0.54	0/1543
35	BO	0.34	0/943	0.58	1/1269 (0.1%)
35	DO	0.31	0/943	0.51	0/1269
36	BP	0.34	0/1152	0.58	0/1533
36	DP	0.31	0/1152	0.59	0/1533
37	BQ	0.34	0/1143	0.53	0/1527
37	DQ	0.31	0/1143	0.52	0/1527
38	BR	0.35	0/982	0.58	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DR	0.29	0/982	0.52	0/1312
39	BS	0.31	0/887	0.63	2/1180 (0.2%)
39	DS	0.29	0/880	0.61	0/1172
40	BT	0.33	0/1105	0.59	1/1477 (0.1%)
40	DT	0.29	0/1097	0.56	0/1468
41	BU	0.37	0/977	0.56	0/1301
41	DU	0.31	0/977	0.50	0/1301
42	BV	0.39	0/782	0.58	0/1049
42	DV	0.32	0/782	0.64	2/1049 (0.2%)
43	BW	0.38	0/897	0.57	0/1205
43	DW	0.31	0/897	0.52	0/1205
44	BX	0.39	0/764	0.59	1/1025 (0.1%)
44	DX	0.32	0/764	0.56	1/1025 (0.1%)
45	BY	0.34	0/819	0.57	0/1095
45	DY	0.31	0/819	0.55	0/1095
46	BZ	0.31	0/1379	0.61	0/1873
46	DZ	0.29	0/1390	0.57	0/1890
47	B0	0.35	0/662	0.57	0/881
47	D0	0.29	0/662	0.49	0/881
48	B1	0.34	0/762	0.56	0/1014
48	D1	0.32	0/762	0.54	0/1014
49	B2	0.32	0/590	0.56	0/781
49	D2	0.27	0/590	0.46	0/781
50	B3	0.36	0/474	0.58	0/635
50	D3	0.27	0/469	0.50	0/630
51	B4	0.35	0/571	0.71	0/768
51	D4	0.34	0/545	0.70	0/737
52	B5	0.38	0/469	0.60	0/635
52	D5	0.33	0/469	0.52	0/635
53	B6	0.36	0/460	0.51	0/613
53	D6	0.30	0/456	0.48	0/608
54	B7	0.39	0/426	0.55	0/561
54	D7	0.33	0/426	0.59	0/561
55	B8	0.36	0/519	0.58	0/684
55	D8	0.32	0/525	0.52	0/691
56	B9	0.35	0/310	0.51	0/407
56	D9	0.31	0/310	0.56	0/407
All	All	0.40	9/316594 (0.0%)	0.88	410/473970 (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	4
7	AG	0	2
7	CG	0	1
20	CT	0	1
28	BD	0	1
39	BS	0	1
51	B4	0	2
51	D4	0	1
All	All	0	13

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	1154	G	N1-C2	-11.01	1.28	1.37
1	CA	1154	G	C6-N1	-10.68	1.32	1.39
1	CA	1119	C	N3-C4	-9.86	1.27	1.33
1	CA	1154	G	N7-C5	-7.17	1.34	1.39
26	BA	354	A	N9-C4	-6.79	1.33	1.37
26	BA	1067	A	N9-C4	-5.85	1.34	1.37
26	DA	2287	A	N9-C4	-5.40	1.34	1.37
1	CA	1154	G	C5-C4	5.28	1.42	1.38
1	CA	1119	C	C2-N3	-5.06	1.31	1.35

All (410) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1119	C	N1-C2-O2	32.18	138.21	118.90
1	CA	1154	G	N3-C2-N2	24.48	137.03	119.90
1	CA	1154	G	C5-C6-O6	24.01	143.00	128.60
1	CA	1154	G	N1-C2-N2	-21.95	96.45	116.20
1	CA	1119	C	N3-C2-O2	-20.26	107.72	121.90
1	CA	1119	C	C2-N3-C4	18.04	128.92	119.90
1	CA	1119	C	C2-N1-C1'	16.83	137.32	118.80
1	CA	1154	G	C5-C6-N1	-16.70	103.15	111.50
1	CA	1154	G	C6-N1-C2	15.37	134.32	125.10
1	CA	1119	C	C5-C4-N4	13.49	129.64	120.20
1	CA	1119	C	C6-N1-C1'	-13.30	104.84	120.80
26	DA	2139	C	N1-C2-O2	11.63	125.88	118.90
1	CA	1119	C	N3-C4-N4	-11.16	110.19	118.00
1	CA	1001(A)	G	N3-C4-N9	10.62	132.37	126.00
23	CW	67	C	C5-C6-N1	10.56	126.28	121.00
1	CA	1154	G	C4-N9-C1'	10.47	140.11	126.50
25	AY	64	A	N1-C6-N6	-10.40	112.36	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	CY	23	A	N1-C6-N6	10.31	124.79	118.60
1	CA	1154	G	N1-C6-O6	-10.16	113.81	119.90
25	CY	66	U	C5-C4-O4	-10.02	119.89	125.90
25	AY	64	A	C5-C6-N6	9.87	131.59	123.70
26	BA	354	A	C2-N3-C4	-9.84	105.68	110.60
1	CA	1154	G	C2-N3-C4	-9.82	106.99	111.90
26	DA	2585	U	C5-C4-O4	-9.67	120.10	125.90
26	BA	2162	C	N1-C2-O2	9.55	124.63	118.90
1	CA	1119	C	C6-N1-C2	-9.51	116.49	120.30
26	DA	2174	C	C2-N1-C1'	9.37	129.11	118.80
1	CA	1119	C	C5-C6-N1	9.24	125.62	121.00
26	DA	2139	C	C2-N1-C1'	9.23	128.95	118.80
26	BA	1686	U	O5'-P-OP2	-9.22	97.40	105.70
1	CA	1054	C	P-O3'-C3'	9.21	130.75	119.70
26	DA	2152	G	C5-C6-O6	-9.21	123.08	128.60
1	CA	79	G	C5-C6-O6	9.02	134.01	128.60
24	AX	14	A	C4-C5-C6	8.97	121.48	117.00
1	CA	1154	G	C8-N9-C1'	-8.97	115.34	127.00
25	CY	4	C	N1-C2-O2	8.94	124.27	118.90
24	AX	46	G	C6-N1-C2	-8.94	119.74	125.10
24	CX	46	G	C6-N1-C2	-8.92	119.75	125.10
26	DA	2152	G	N1-C6-O6	8.87	125.22	119.90
26	BA	2162	C	N3-C2-O2	-8.83	115.72	121.90
1	CA	1004	A	O4'-C1'-N9	8.50	115.00	108.20
1	CA	1119	C	N1-C2-N3	-8.44	113.29	119.20
23	CW	7	A	N1-C6-N6	8.42	123.65	118.60
24	AX	14	A	C5-N7-C8	8.39	108.10	103.90
26	BA	1067	A	C2-N3-C4	-8.31	106.45	110.60
1	AA	1030(B)	C	C2-N1-C1'	8.24	127.86	118.80
26	DA	2136	C	N1-C2-O2	8.23	123.84	118.90
1	CA	1001(A)	G	N3-C4-C5	-8.21	124.49	128.60
23	CW	67	C	C2-N3-C4	8.09	123.95	119.90
1	AA	1137	C	C6-N1-C2	-8.06	117.07	120.30
26	BA	2162	C	C2-N1-C1'	8.06	127.67	118.80
25	CY	68	C	C2-N1-C1'	7.99	127.59	118.80
26	DA	2152	G	N9-C4-C5	-7.99	102.20	105.40
26	DA	2152	G	N3-C4-N9	7.99	130.79	126.00
24	CX	14	A	C4-C5-C6	7.97	120.98	117.00
39	BS	67	ARG	NE-CZ-NH1	-7.95	116.32	120.30
1	AA	1036	G	C4-N9-C1'	7.92	136.79	126.50
11	AK	18	ARG	NE-CZ-NH1	-7.89	116.36	120.30
1	CA	1001(A)	G	C4-N9-C1'	7.85	136.70	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1154	G	C4-C5-C6	7.84	123.51	118.80
26	BA	2162	C	C6-N1-C2	-7.82	117.17	120.30
23	CW	22	G	N3-C2-N2	-7.75	114.47	119.90
1	AA	1030(B)	C	N1-C2-O2	7.75	123.55	118.90
26	DA	2139	C	N3-C2-O2	-7.71	116.50	121.90
26	DA	2152	G	C6-C5-N7	-7.69	125.79	130.40
1	CA	1126	U	C2-N1-C1'	7.68	126.92	117.70
26	BA	215	G	O4'-C1'-N9	7.68	114.34	108.20
26	DA	2167	U	N1-C2-O2	7.67	128.17	122.80
25	CY	66	U	N3-C4-O4	7.66	124.76	119.40
1	AA	1054	C	P-O3'-C3'	7.60	128.81	119.70
1	AA	346	G	C4-N9-C1'	7.56	136.32	126.50
25	CY	68	C	N3-C2-O2	-7.46	116.67	121.90
25	CY	56	C	C2-N1-C1'	7.45	126.99	118.80
1	CA	1001(A)	G	C8-N9-C1'	-7.43	117.34	127.00
25	CY	7	A	C6-N1-C2	-7.43	114.14	118.60
25	CY	68	C	N1-C2-O2	7.39	123.34	118.90
1	CA	1054	C	O4'-C1'-N1	7.39	114.11	108.20
26	BA	934	A	O4'-C1'-N9	7.35	114.08	108.20
26	BA	12	U	C2-N1-C1'	7.29	126.45	117.70
26	BA	1068	G	N3-C2-N2	-7.29	114.80	119.90
26	BA	1985	U	C2-N1-C1'	7.25	126.40	117.70
26	DA	2167	U	C2-N1-C1'	7.25	126.40	117.70
26	DA	2139	C	C6-N1-C1'	-7.22	112.13	120.80
26	DA	2152	G	C4-C5-N7	7.19	113.68	110.80
35	BO	8	LEU	CA-CB-CG	7.19	131.83	115.30
23	CW	45	U	C2-N1-C1'	7.17	126.31	117.70
26	DA	2174	C	C6-N1-C1'	-7.16	112.20	120.80
26	DA	2206	G	C4-N9-C1'	-7.14	117.22	126.50
24	AX	14	A	C5-C6-N1	-7.14	114.13	117.70
23	CW	44	G	C5-C6-O6	-7.13	124.32	128.60
1	AA	254	G	O5'-P-OP1	-7.09	99.32	105.70
1	AA	1036	G	C8-N9-C1'	-7.08	117.79	127.00
26	DA	2155	G	N3-C2-N2	7.07	124.85	119.90
26	BA	537	G	O4'-C1'-N9	7.04	113.83	108.20
26	DA	2167	U	N3-C2-O2	-7.03	117.28	122.20
24	AX	22	G	C5-N7-C8	-7.00	100.80	104.30
26	DA	2152	G	C8-N9-C1'	-6.95	117.96	127.00
26	DA	1372	U	C5-C4-O4	-6.92	121.75	125.90
26	DA	2137	C	C6-N1-C2	-6.90	117.54	120.30
1	AA	1137	C	C5-C6-N1	6.88	124.44	121.00
25	CY	23	A	C6-C5-N7	-6.85	127.51	132.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CW	67	C	C2-N1-C1'	6.84	126.32	118.80
26	DA	2155	G	C6-N1-C2	6.83	129.20	125.10
23	CW	22	G	N3-C4-N9	-6.82	121.91	126.00
26	DA	893	C	C2-N1-C1'	6.82	126.30	118.80
26	DA	2585	U	C6-N1-C1'	-6.80	111.67	121.20
25	AY	5	G	N3-C4-N9	6.80	130.08	126.00
44	DX	57	LEU	CA-CB-CG	6.80	130.94	115.30
26	DA	2585	U	C2-N1-C1'	6.79	125.85	117.70
1	AA	346	G	O4'-C1'-N9	6.76	113.61	108.20
26	BA	273	G	OP1-P-O3'	6.75	120.05	105.20
44	BX	57	LEU	CA-CB-CG	6.75	130.82	115.30
26	BA	649	C	O5'-P-OP1	-6.73	99.64	105.70
1	CA	1003	G	C4-N9-C1'	6.73	135.25	126.50
24	AX	22	G	C4-C5-C6	-6.69	114.79	118.80
23	CW	45	U	N1-C2-O2	6.69	127.48	122.80
1	CA	1154	G	N3-C4-N9	6.66	130.00	126.00
25	AY	4	C	N3-C2-O2	-6.61	117.27	121.90
26	BA	795	G	O4'-C1'-N9	6.61	113.49	108.20
1	CA	754	C	C2-N1-C1'	6.59	126.05	118.80
23	CW	7	A	C5-C6-N6	-6.57	118.45	123.70
26	DA	2152	G	C4-N9-C1'	6.55	135.02	126.50
25	CY	7	A	C5-C6-N1	6.53	120.96	117.70
1	CA	1001(A)	G	C6-C5-N7	-6.51	126.49	130.40
26	BA	2083	G	O5'-P-OP2	-6.50	99.84	105.70
23	CW	67	C	N1-C2-O2	6.49	122.79	118.90
25	AY	4	C	N1-C2-O2	6.48	122.79	118.90
26	BA	1188	A	C2-N3-C4	-6.48	107.36	110.60
25	CY	56	C	C6-N1-C1'	-6.48	113.03	120.80
24	CX	22	G	N1-C6-O6	-6.45	116.03	119.90
25	CY	7	A	N3-C4-N9	6.45	132.56	127.40
23	CW	67	C	C6-N1-C2	-6.44	117.72	120.30
25	AY	33	U	N3-C2-O2	-6.42	117.71	122.20
26	DA	1372	U	N3-C4-O4	6.41	123.89	119.40
26	BA	354	A	N1-C2-N3	6.39	132.50	129.30
1	CA	998	G	N3-C4-N9	-6.39	122.17	126.00
26	BA	139	A	N7-C8-N9	6.38	116.99	113.80
25	AY	58	A	C4-N9-C1'	6.37	137.76	126.30
23	CW	66	U	C2-N1-C1'	6.36	125.33	117.70
26	BA	2014	G	P-O3'-C3'	6.36	127.33	119.70
24	AX	22	G	N3-C4-N9	-6.32	122.21	126.00
26	DA	2206	G	C8-N9-C1'	6.31	135.21	127.00
1	AA	1054	C	N3-C2-O2	-6.31	117.48	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	399	G	O4'-C1'-N9	6.30	113.24	108.20
23	CW	3	C	N1-C2-O2	6.29	122.67	118.90
26	BA	1302	G	N9-C4-C5	-6.28	102.89	105.40
1	AA	1397	C	C2-N1-C1'	6.28	125.70	118.80
1	AA	346	G	C8-N9-C4	-6.27	103.89	106.40
26	BA	354	A	N3-C4-C5	6.27	131.19	126.80
26	DA	1531	C	C2-N1-C1'	6.25	125.68	118.80
26	BA	1346	U	P-O3'-C3'	6.25	127.19	119.70
24	CX	46	G	C5-C6-N1	6.24	114.62	111.50
23	AW	15	G	N3-C2-N2	6.24	124.27	119.90
25	AY	69	G	N3-C4-N9	6.24	129.74	126.00
1	CA	1003	G	N7-C8-N9	6.20	116.20	113.10
23	AW	48	C	N1-C2-O2	-6.20	115.18	118.90
1	CA	1154	G	N3-C4-C5	-6.19	125.50	128.60
1	CA	96	U	O4'-C1'-N1	6.19	113.15	108.20
25	CY	23	A	C4-C5-C6	6.18	120.09	117.00
25	CY	23	A	C5-C6-N6	-6.17	118.77	123.70
25	AY	33	U	C2-N1-C1'	6.16	125.09	117.70
1	CA	1030(B)	C	C5-C6-N1	6.15	124.08	121.00
25	AY	68	C	N1-C2-O2	6.13	122.58	118.90
24	AX	14	A	C8-N9-C1'	-6.13	116.67	127.70
26	BA	1221	G	OP1-P-O3'	6.13	118.69	105.20
25	CY	4	C	N3-C2-O2	-6.13	117.61	121.90
1	AA	1054	C	C6-N1-C2	-6.12	117.85	120.30
1	CA	1052	U	N1-C2-O2	6.11	127.08	122.80
1	AA	1030(B)	C	N3-C2-O2	-6.11	117.62	121.90
1	CA	1256	A	O4'-C1'-N9	-6.11	103.31	108.20
1	CA	1119	C	C4-C5-C6	-6.11	114.35	117.40
26	BA	553	A	C2-N3-C4	-6.10	107.55	110.60
24	CX	46	G	N3-C2-N2	-6.07	115.65	119.90
1	CA	1064	G	P-O3'-C3'	6.07	126.98	119.70
25	AY	50	U	C2-N3-C4	6.05	130.63	127.00
26	BA	2058	C	O5'-P-OP1	-6.04	100.26	105.70
26	BA	354	A	N3-C4-N9	-6.04	122.57	127.40
1	CA	754	C	N1-C2-O2	6.00	122.50	118.90
26	BA	139	A	C5-N7-C8	-6.00	100.90	103.90
26	BA	834	U	O5'-P-OP1	-5.99	100.31	105.70
26	BA	273	G	P-O3'-C3'	5.99	126.89	119.70
26	DA	1531	C	N1-C2-O2	5.98	122.49	118.90
26	DA	2140	C	C2-N1-C1'	5.98	125.38	118.80
25	AY	33	U	N1-C2-O2	5.97	126.98	122.80
1	CA	1030	C	C2-N1-C1'	5.96	125.36	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	2260	C	O5'-P-OP2	-5.95	100.34	105.70
1	CA	65	U	P-O3'-C3'	5.95	126.84	119.70
1	AA	1030(B)	C	C6-N1-C1'	-5.94	113.67	120.80
26	BA	2014	G	C8-N9-C4	-5.94	104.02	106.40
26	BA	1807	G	O5'-P-OP2	-5.94	100.35	105.70
23	CW	22	G	N9-C4-C5	5.94	107.78	105.40
26	BA	2627	U	O5'-P-OP1	-5.92	100.37	105.70
39	BS	67	ARG	NE-CZ-NH2	5.92	123.26	120.30
1	CA	1030(B)	C	C6-N1-C2	-5.92	117.93	120.30
26	BA	978	A	O4'-C1'-N9	5.92	112.93	108.20
25	AY	69	G	N3-C4-C5	-5.91	125.64	128.60
1	AA	347	G	P-O3'-C3'	5.91	126.79	119.70
23	AW	3	C	C2-N1-C1'	5.91	125.30	118.80
26	BA	1067	A	N1-C2-N3	5.91	132.25	129.30
25	CY	56	C	N1-C2-O2	5.89	122.43	118.90
24	AX	46	G	C5-C6-N1	5.88	114.44	111.50
26	DA	614	U	N3-C2-O2	-5.88	118.08	122.20
24	AX	22	G	C8-N9-C1'	5.86	134.62	127.00
24	AX	14	A	C4-N9-C1'	5.86	136.84	126.30
1	CA	687	A	P-O3'-C3'	5.85	126.72	119.70
23	CW	3	C	C2-N3-C4	5.84	122.82	119.90
1	CA	1023	G	N3-C4-N9	5.83	129.50	126.00
24	CX	14	A	C5-N7-C8	5.82	106.81	103.90
1	CA	1067	A	P-O3'-C3'	5.81	126.67	119.70
26	DA	2139	C	C5-C6-N1	5.81	123.91	121.00
1	CA	997	U	C5-C4-O4	5.79	129.38	125.90
26	BA	1068	G	N3-C4-N9	-5.76	122.54	126.00
1	AA	839	U	P-O3'-C3'	5.75	126.60	119.70
23	CW	66	U	P-O3'-C3'	5.74	126.59	119.70
26	BA	1859	G	C5-C6-O6	-5.73	125.16	128.60
26	BA	553	A	C5-N7-C8	-5.73	101.04	103.90
25	AY	35	A	O5'-P-OP2	-5.72	100.55	105.70
26	BA	892	G	O4'-C1'-N9	5.71	112.77	108.20
26	DA	1204	A	O4'-C1'-N9	5.70	112.76	108.20
1	CA	1039	C	N1-C2-O2	5.69	122.32	118.90
26	BA	1539	C	N1-C2-O2	5.69	122.31	118.90
1	CA	1125	U	O3'-P-O5'	5.69	114.81	104.00
26	BA	1985	U	N1-C2-O2	5.68	126.78	122.80
23	CW	45	U	C6-N1-C1'	-5.68	113.25	121.20
1	AA	1067	A	P-O3'-C3'	5.68	126.51	119.70
1	CA	1039	C	C5-C4-N4	-5.68	116.23	120.20
1	CA	1001(A)	G	N9-C4-C5	-5.67	103.13	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	DE	72	VAL	C-N-CA	5.66	135.86	121.70
1	CA	79	G	N1-C6-O6	-5.66	116.50	119.90
1	AA	1054	C	C2-N1-C1'	5.66	125.02	118.80
25	CY	5	G	N3-C4-C5	-5.64	125.78	128.60
1	AA	1125	U	P-O3'-C3'	5.64	126.47	119.70
25	CY	50	U	C5-C4-O4	5.64	129.28	125.90
1	AA	346	G	N3-C4-C5	-5.63	125.79	128.60
42	DV	100	ARG	NE-CZ-NH1	5.63	123.11	120.30
26	DA	214	G	O4'-C1'-N9	5.62	112.70	108.20
26	DA	2137	C	O4'-C1'-N1	5.61	112.69	108.20
26	DA	893	C	N1-C2-O2	5.60	122.26	118.90
23	AW	22	G	N1-C6-O6	5.60	123.26	119.90
26	BA	1418	U	N3-C4-O4	5.59	123.32	119.40
1	CA	1154	G	C5-N7-C8	5.59	107.09	104.30
26	DA	748	G	C4-N9-C1'	-5.59	119.24	126.50
1	CA	1021	G	O4'-C1'-N9	5.58	112.66	108.20
1	AA	346	G	C8-N9-C1'	-5.57	119.76	127.00
26	BA	1221	G	P-O3'-C3'	5.57	126.38	119.70
26	DA	1937	A	O4'-C1'-N9	5.56	112.65	108.20
42	DV	38	LEU	CA-CB-CG	5.56	128.09	115.30
25	AY	58	A	C8-N9-C1'	-5.56	117.69	127.70
1	AA	1022	G	N3-C2-N2	5.55	123.78	119.90
1	CA	1126	U	N1-C2-O2	5.55	126.68	122.80
1	CA	1493	A	P-O3'-C3'	5.55	126.36	119.70
26	DA	2174	C	C5-C6-N1	5.54	123.77	121.00
1	CA	1225	A	C5-C6-N6	5.53	128.13	123.70
23	CW	6	G	C4-C5-N7	5.53	113.01	110.80
23	CW	6	G	N9-C4-C5	-5.53	103.19	105.40
24	AX	22	G	N3-C4-C5	5.53	131.36	128.60
1	AA	991	U	P-O3'-C3'	5.52	126.33	119.70
25	AY	58	A	P-O3'-C3'	5.52	126.33	119.70
25	CY	69	G	N3-C4-N9	5.52	129.31	126.00
26	DA	2140	C	N1-C2-O2	5.52	122.21	118.90
26	BA	593	G	C5-C6-O6	-5.52	125.29	128.60
26	BA	1302	G	C4-C5-N7	5.52	113.01	110.80
24	CX	34	C	C2-N1-C1'	5.52	124.87	118.80
25	CY	68	C	C6-N1-C1'	-5.51	114.19	120.80
24	AX	67	C	N1-C2-O2	5.50	122.20	118.90
26	DA	2139	C	N3-C4-C5	5.49	124.10	121.90
1	AA	1028	C	O4'-C1'-N1	5.48	112.59	108.20
1	CA	1154	G	C6-C5-N7	-5.48	127.11	130.40
26	DA	383	U	O4'-C1'-N1	5.48	112.58	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	1958	A	O4'-C1'-N9	5.46	112.57	108.20
1	CA	90	U	N1-C2-N3	5.46	118.18	114.90
26	BA	1232	G	N1-C6-O6	-5.46	116.62	119.90
26	BA	410	U	C2-N1-C1'	-5.46	111.15	117.70
26	BA	2802	C	N1-C2-O2	-5.46	115.62	118.90
1	AA	1054	C	N1-C2-O2	5.46	122.17	118.90
1	CA	1286	A	C8-N9-C4	-5.45	103.62	105.80
26	BA	2701	U	N3-C2-O2	-5.45	118.39	122.20
1	AA	1285	A	P-O3'-C3'	5.44	126.23	119.70
26	BA	894	U	C2-N1-C1'	-5.44	111.17	117.70
26	BA	12	U	N1-C2-O2	5.43	126.60	122.80
26	DA	1300	U	P-O3'-C3'	5.43	126.22	119.70
24	CX	22	G	C5-N7-C8	-5.43	101.59	104.30
26	DA	2685	G	N1-C6-O6	-5.42	116.65	119.90
1	AA	347	G	OP1-P-O3'	5.41	117.09	105.20
26	DA	2585	U	O4'-C1'-N1	-5.40	103.88	108.20
26	DA	2321	G	C4-N9-C1'	5.40	133.52	126.50
1	AA	1502	A	N1-C2-N3	5.39	132.00	129.30
1	AA	97	G	N3-C4-N9	5.39	129.24	126.00
26	BA	1577	C	P-O3'-C3'	5.38	126.16	119.70
23	CW	26	A	C5-C6-N6	-5.38	119.39	123.70
26	DA	1313	U	C2-N1-C1'	5.38	124.16	117.70
23	AW	50	U	C5-C4-O4	-5.38	122.67	125.90
26	BA	1249	A	O4'-C1'-N9	5.38	112.50	108.20
25	CY	7	A	C6-C5-N7	-5.38	128.54	132.30
26	BA	990	A	C2-N3-C4	-5.38	107.91	110.60
26	BA	599	U	O5'-P-OP1	-5.37	100.86	105.70
26	BA	1745	A	O4'-C1'-N9	5.37	112.50	108.20
1	CA	1286	A	N7-C8-N9	5.37	116.48	113.80
26	BA	989	G	C4-N9-C1'	5.36	133.47	126.50
25	CY	5	G	O4'-C1'-N9	5.36	112.49	108.20
1	CA	1529	G	C4-N9-C1'	5.36	133.47	126.50
1	AA	1278	U	C5-C6-N1	5.36	125.38	122.70
26	DA	1530	C	P-O3'-C3'	5.36	126.13	119.70
25	CY	68	C	C6-N1-C2	-5.35	118.16	120.30
25	CY	5	G	C2-N3-C4	5.35	114.58	111.90
24	CX	46	G	C5-C6-O6	-5.35	125.39	128.60
26	DA	1698	A	O4'-C1'-N9	5.35	112.48	108.20
23	CW	67	C	C4-C5-C6	-5.34	114.73	117.40
1	AA	1042	G	O4'-C1'-N9	5.34	112.47	108.20
2	CB	187	LEU	CA-CB-CG	5.34	127.58	115.30
26	BA	12	U	N3-C2-O2	-5.33	118.47	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	2605	U	N3-C4-O4	-5.33	115.67	119.40
1	AA	1030(B)	C	C6-N1-C2	-5.32	118.17	120.30
25	CY	5	G	N3-C4-N9	5.32	129.19	126.00
1	CA	1126	U	C6-N1-C1'	-5.31	113.76	121.20
25	CY	24	G	N3-C4-N9	5.31	129.19	126.00
25	AY	50	U	N3-C4-C5	-5.31	111.42	114.60
1	CA	992	U	P-O3'-C3'	5.30	126.06	119.70
1	CA	1206	G	C5-C6-O6	-5.30	125.42	128.60
26	BA	1660	A	O5'-P-OP1	-5.30	100.93	105.70
26	BA	1091	A	O5'-P-OP1	5.29	117.04	110.70
1	CA	1502	A	N1-C2-N3	5.29	131.94	129.30
26	BA	1220	U	P-O3'-C3'	5.28	126.04	119.70
23	CW	66	U	C5-C6-N1	5.28	125.34	122.70
4	AD	174	LEU	CA-CB-CG	5.26	127.41	115.30
23	AW	3	C	N1-C2-O2	5.26	122.06	118.90
1	CA	79	G	C6-N1-C2	5.26	128.25	125.10
26	DA	2629	A	O4'-C1'-N9	5.25	112.40	108.20
4	AD	188	LEU	CA-CB-CG	5.24	127.36	115.30
1	CA	1323	G	N3-C4-N9	5.24	129.15	126.00
5	CE	12	LEU	CA-CB-CG	5.24	127.35	115.30
25	CY	60	U	N3-C2-O2	-5.24	118.53	122.20
24	AX	22	G	C4-N9-C1'	-5.24	119.69	126.50
26	BA	1361	C	O5'-P-OP2	-5.24	100.99	105.70
1	CA	1126	U	P-O5'-C5'	5.23	129.27	120.90
1	CA	1126	U	C5-C6-N1	5.22	125.31	122.70
1	CA	1158	C	C2-N1-C1'	5.22	124.55	118.80
25	CY	7	A	N9-C4-C5	-5.22	103.71	105.80
26	BA	2802	C	C2-N1-C1'	-5.21	113.07	118.80
26	BA	1985	U	C6-N1-C1'	-5.21	113.91	121.20
1	CA	1003	G	C8-N9-C4	-5.21	104.32	106.40
1	CA	1183	A	P-O3'-C3'	5.21	125.95	119.70
1	CA	1158	C	N1-C2-O2	5.20	122.02	118.90
26	DA	2554	U	O5'-P-OP2	-5.20	101.02	105.70
26	DA	2154	G	N9-C1'-C2'	-5.20	106.28	112.00
1	CA	1220	G	N3-C4-N9	-5.20	122.88	126.00
1	CA	998	G	N9-C4-C5	5.19	107.48	105.40
26	BA	507	G	O4'-C1'-N9	5.19	112.35	108.20
26	BA	184	A	P-O3'-C3'	5.19	125.92	119.70
26	BA	139	A	O4'-C1'-N9	5.18	112.35	108.20
26	BA	552	C	N3-C2-O2	-5.18	118.27	121.90
26	DA	945	A	O4'-C1'-N9	5.18	112.35	108.20
25	CY	7	A	C5-C6-N6	-5.18	119.56	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1150	U	C2-N3-C4	5.17	130.10	127.00
1	AA	1502	A	N7-C8-N9	5.17	116.39	113.80
1	CA	1030	C	C6-N1-C1'	-5.17	114.59	120.80
1	AA	754	C	C2-N1-C1'	5.17	124.49	118.80
26	BA	2804	C	C6-N1-C2	-5.17	118.23	120.30
25	AY	5	G	N3-C4-C5	-5.17	126.02	128.60
1	AA	97	G	N3-C4-C5	-5.16	126.02	128.60
1	CA	848	C	C5-C6-N1	5.16	123.58	121.00
26	DA	2137	C	C6-N1-C1'	5.16	126.99	120.80
26	DA	914	C	N1-C2-O2	5.15	121.99	118.90
26	DA	748	G	C8-N9-C1'	5.15	133.69	127.00
1	CA	266	G	C4-N9-C1'	5.14	133.19	126.50
26	BA	254	A	O4'-C1'-N9	5.14	112.31	108.20
26	BA	1067	A	C5-N7-C8	-5.13	101.33	103.90
26	BA	2483	C	N1-C2-O2	5.13	121.98	118.90
25	AY	6	G	N9-C4-C5	-5.12	103.35	105.40
25	AY	18	G	C4-N9-C1'	-5.12	119.84	126.50
25	AY	45	U	C5-C6-N1	5.12	125.26	122.70
1	CA	60	A	P-O3'-C3'	5.12	125.84	119.70
1	CA	1158	C	C6-N1-C2	-5.11	118.26	120.30
25	CY	69	G	N3-C4-C5	-5.11	126.05	128.60
24	CX	22	G	C4-C5-C6	-5.10	115.74	118.80
26	BA	542	C	C6-N1-C2	-5.10	118.26	120.30
26	BA	2209	G	C5-C6-O6	5.10	131.66	128.60
23	CW	66	U	C5-C4-O4	-5.10	122.84	125.90
22	CV	24	A	O4'-C1'-N9	5.09	112.28	108.20
25	CY	9	A	C4-C5-C6	-5.09	114.45	117.00
1	AA	1397	C	O4'-C1'-N1	5.09	112.27	108.20
26	DA	893	C	C6-N1-C2	-5.08	118.27	120.30
26	DA	2430	A	O4'-C1'-N9	5.08	112.26	108.20
26	DA	893	C	C5-C6-N1	5.08	123.54	121.00
26	DA	2621	A	C8-N9-C4	5.07	107.83	105.80
26	DA	214	G	C4-N9-C1'	-5.07	119.91	126.50
26	DA	1992	G	P-O3'-C3'	5.06	125.78	119.70
1	CA	1003	G	C8-N9-C1'	-5.06	120.42	127.00
1	CA	955	U	C2-N3-C4	5.06	130.04	127.00
1	AA	346	G	N7-C8-N9	5.06	115.63	113.10
1	CA	79	G	N3-C4-N9	-5.06	122.97	126.00
1	CA	90	U	O4'-C1'-N1	5.06	112.25	108.20
26	BA	2858	G	O4'-C1'-N9	5.05	112.24	108.20
26	DA	1558	A	P-O3'-C3'	5.05	125.77	119.70
23	CW	22	G	N1-C2-N2	5.05	120.75	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	DA	1791	A	O5'-P-OP1	-5.05	101.16	105.70
26	DA	2136	C	N3-C2-O2	-5.04	118.37	121.90
26	BA	2565	G	N3-C4-C5	-5.04	126.08	128.60
25	AY	65	G	N9-C4-C5	5.04	107.42	105.40
1	AA	98	G	N3-C4-N9	5.04	129.02	126.00
26	BA	410	U	O4'-C1'-N1	5.04	112.23	108.20
1	AA	1035	A	N1-C2-N3	5.03	131.82	129.30
40	BT	118	ARG	NE-CZ-NH1	5.02	122.81	120.30
26	DA	512	G	O4'-C1'-N9	5.02	112.22	108.20
26	DA	1131	G	O4'-C1'-N9	5.01	112.21	108.20
26	DA	1899	G	N3-C4-N9	5.01	129.01	126.00
26	BA	821	A	C8-N9-C4	-5.01	103.80	105.80
26	BA	978	A	N7-C8-N9	5.01	116.30	113.80
26	DA	90	U	C2-N1-C1'	5.00	123.70	117.70
26	DA	2140	C	C6-N1-C2	-5.00	118.30	120.30

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	18	GLY	Peptide
2	AB	231	GLU	Peptide
2	AB	8	LYS	Peptide
2	AB	9	GLU	Peptide
7	AG	78	ARG	Peptide
7	AG	79	ARG	Peptide
51	B4	52	THR	Peptide
51	B4	59	PHE	Peptide
28	BD	274	ARG	Peptide
39	BS	58	LEU	Peptide
7	CG	78	ARG	Peptide
20	CT	9	ASN	Peptide
51	D4	67	TYR	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	495	0
1	CA	32312	0	16307	663	0
2	AB	1846	0	1867	92	0
2	CB	1825	0	1828	102	0
3	AC	1552	0	1546	53	0
3	CC	1542	0	1517	81	0
4	AD	1659	0	1676	73	0
4	CD	1674	0	1714	61	0
5	AE	1129	0	1185	34	0
5	CE	1133	0	1191	33	0
6	AF	806	0	793	24	0
6	CF	816	0	808	18	0
7	AG	1231	0	1238	28	0
7	CG	1235	0	1249	37	0
8	AH	1088	0	1126	26	0
8	CH	1088	0	1126	42	0
9	AI	983	0	986	47	0
9	CI	978	0	966	47	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	36	0
11	AK	829	0	825	20	0
11	CK	833	0	836	14	0
12	AL	930	0	980	24	0
12	CL	930	0	980	27	0
13	AM	958	0	1002	31	0
13	CM	950	0	988	39	0
14	AN	492	0	529	16	0
14	CN	492	0	529	33	0
15	AO	728	0	760	20	0
15	CO	728	0	760	31	0
16	AP	681	0	697	12	0
16	CP	677	0	686	23	0
17	AQ	823	0	891	22	0
17	CQ	823	0	891	15	0
18	AR	555	0	618	17	0
18	CR	555	0	618	16	0
19	AS	652	0	662	31	0
19	CS	646	0	644	42	0
20	AT	728	0	798	32	0
20	CT	727	0	796	25	0
21	AU	199	0	208	8	0
21	CU	199	0	208	10	0
22	AV	277	0	140	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	CV	252	0	130	7	0
23	AW	1607	0	808	52	0
23	CW	1560	0	772	52	0
24	AX	1625	0	828	34	0
24	CX	1625	0	828	32	0
25	AY	1581	0	805	96	0
25	CY	1561	0	796	79	0
26	BA	60729	0	30621	667	0
26	DA	60311	0	30409	875	0
27	BB	2573	0	1306	19	0
27	DB	2573	0	1306	50	0
28	BD	2136	0	2218	51	0
28	DD	2136	0	2218	61	0
29	BE	1559	0	1618	30	0
29	DE	1559	0	1618	45	0
30	BF	1584	0	1625	47	0
30	DF	1580	0	1619	50	0
31	BG	1425	0	1443	38	0
31	DG	1424	0	1434	66	0
32	BH	1330	0	1407	28	0
32	DH	1330	0	1407	30	0
33	BI	1085	0	1114	41	0
33	DI	1061	0	1080	25	0
34	BN	1117	0	1183	17	0
34	DN	1117	0	1184	27	0
35	BO	933	0	996	20	0
35	DO	933	0	996	29	0
36	BP	1135	0	1212	38	0
36	DP	1135	0	1212	43	0
37	BQ	1122	0	1179	31	0
37	DQ	1122	0	1179	35	0
38	BR	968	0	1033	18	0
38	DR	968	0	1033	28	0
39	BS	877	0	938	23	0
39	DS	870	0	923	34	0
40	BT	1091	0	1151	27	0
40	DT	1083	0	1136	31	0
41	BU	959	0	1019	17	0
41	DU	959	0	1019	38	0
42	BV	771	0	830	13	0
42	DV	771	0	830	25	0
43	BW	886	0	939	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	DW	886	0	940	9	0
44	BX	750	0	814	16	0
44	DX	750	0	814	23	0
45	BY	806	0	881	23	0
45	DY	806	0	881	26	0
46	BZ	1349	0	1355	44	0
46	DZ	1360	0	1363	61	0
47	B0	653	0	674	14	0
47	D0	653	0	674	20	0
48	B1	755	0	826	18	0
48	D1	755	0	826	18	0
49	B2	588	0	643	11	0
49	D2	588	0	643	12	0
50	B3	469	0	518	9	0
50	D3	464	0	514	12	0
51	B4	558	0	544	22	0
51	D4	532	0	503	31	0
52	B5	455	0	465	11	0
52	D5	455	0	465	12	0
53	B6	453	0	473	13	0
53	D6	449	0	469	9	0
54	B7	418	0	467	9	0
54	D7	418	0	467	10	0
55	B8	511	0	571	21	0
55	D8	517	0	582	10	0
56	B9	307	0	335	7	0
56	D9	307	0	335	13	0
57	AA	214	0	0	0	0
57	AE	3	0	0	0	0
57	AF	1	0	0	0	0
57	AK	1	0	0	0	0
57	AM	1	0	0	0	0
57	AN	2	0	0	0	0
57	AW	4	0	0	0	0
57	AX	15	0	0	0	0
57	AY	3	0	0	0	0
57	B0	3	0	0	0	0
57	B1	1	0	0	0	0
57	B2	1	0	0	0	0
57	B3	2	0	0	0	0
57	B4	1	0	0	0	0
57	B5	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	B6	2	0	0	0	0
57	B7	5	0	0	0	0
57	B8	1	0	0	0	0
57	B9	1	0	0	0	0
57	BA	812	0	0	0	0
57	BB	20	0	0	0	0
57	BD	9	0	0	0	0
57	BE	8	0	0	0	0
57	BF	9	0	0	0	0
57	BG	3	0	0	0	0
57	BN	6	0	0	0	0
57	BO	2	0	0	0	0
57	BP	5	0	0	0	0
57	BQ	5	0	0	0	0
57	BR	2	0	0	0	0
57	BU	8	0	0	0	0
57	BV	5	0	0	0	0
57	BW	4	0	0	0	0
57	BX	3	0	0	0	0
57	BY	1	0	0	0	0
57	BZ	1	0	0	0	0
57	CA	170	0	0	0	0
57	CD	1	0	0	0	0
57	CE	1	0	0	0	0
57	CF	1	0	0	0	0
57	CJ	1	0	0	0	0
57	CK	1	0	0	0	0
57	CT	1	0	0	0	0
57	CV	1	0	0	0	0
57	CW	1	0	0	0	0
57	CX	3	0	0	1	0
57	D0	1	0	0	0	0
57	D3	1	0	0	0	0
57	D8	1	0	0	0	0
57	DA	677	0	0	0	0
57	DB	13	0	0	0	0
57	DD	9	0	0	0	0
57	DE	4	0	0	0	0
57	DF	4	0	0	0	0
57	DG	1	0	0	0	0
57	DN	1	0	0	0	0
57	DO	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	DP	2	0	0	0	0
57	DQ	4	0	0	0	0
57	DR	1	0	0	0	0
57	DU	2	0	0	0	0
57	DV	3	0	0	0	0
57	DW	4	0	0	0	0
57	DX	1	0	0	0	0
57	DY	1	0	0	0	0
58	AD	8	0	0	0	0
58	CD	8	0	0	0	0
59	AN	1	0	0	0	0
59	B4	1	0	0	0	0
59	B5	1	0	0	0	0
59	B6	1	0	0	0	0
59	B9	1	0	0	0	0
59	BY	1	0	0	0	0
59	CN	1	0	0	0	0
59	D4	1	0	0	0	0
59	D5	1	0	0	0	0
59	D6	1	0	0	0	0
59	D9	1	0	0	0	0
59	DY	1	0	0	0	0
60	AX	1	0	0	0	0
60	CX	1	0	0	0	0
61	AA	227	0	0	17	0
61	AE	2	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	1	0	0	1	0
61	AM	1	0	0	0	0
61	AU	1	0	0	1	0
61	AV	3	0	0	0	0
61	AW	3	0	0	0	0
61	AX	6	0	0	2	0
61	AY	1	0	0	0	0
61	B0	3	0	0	0	0
61	B1	1	0	0	0	0
61	B3	2	0	0	0	0
61	B5	2	0	0	0	0
61	B6	1	0	0	0	0
61	B7	2	0	0	0	0
61	B8	8	0	0	1	0
61	BA	1383	0	0	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	BB	36	0	0	1	0
61	BD	12	0	0	1	0
61	BE	14	0	0	4	0
61	BF	8	0	0	0	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BO	4	0	0	0	0
61	BP	16	0	0	3	0
61	BQ	4	0	0	0	0
61	BR	2	0	0	0	0
61	BT	2	0	0	0	0
61	BU	3	0	0	0	0
61	BV	2	0	0	0	0
61	BW	1	0	0	0	0
61	BX	4	0	0	0	0
61	BZ	1	0	0	0	0
61	CA	185	0	0	17	0
61	CJ	2	0	0	1	0
61	CL	1	0	0	0	0
61	CT	1	0	0	0	0
61	CV	1	0	0	0	0
61	CW	2	0	0	0	0
61	D0	3	0	0	0	0
61	D1	1	0	0	0	0
61	D3	1	0	0	1	0
61	D7	3	0	0	0	0
61	D8	4	0	0	0	0
61	DA	1025	0	0	79	0
61	DB	9	0	0	0	0
61	DD	19	0	0	4	0
61	DE	11	0	0	0	0
61	DF	3	0	0	0	0
61	DN	2	0	0	1	0
61	DO	1	0	0	0	0
61	DP	16	0	0	2	0
61	DR	1	0	0	0	0
61	DT	3	0	0	0	0
61	DU	2	0	0	0	0
61	DX	3	0	0	0	0
61	DY	2	0	0	0	0
All	All	297141	0	196189	5222	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 11.

All (5222) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:CY:7:A:N6	25:CY:66:U:H3	1.37	1.21
25:AY:49:C:N4	25:AY:65:G:H1	1.44	1.16
26:DA:2139:C:N4	26:DA:2152:G:H1	1.42	1.16
1:CA:1000:U:H3	1:CA:1041:A:N6	1.44	1.15
1:CA:1002:G:H1	1:CA:1038:C:N4	1.48	1.12
26:BA:2158:C:N4	26:BA:2177:G:H1	1.51	1.08
26:DA:2138:C:N4	26:DA:2153:G:H1	1.54	1.03
26:DA:2121:G:H1	26:DA:2177:C:N4	1.54	1.02
23:AW:26:A:H61	23:AW:44:G:H1	1.04	1.02
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.36	1.01
25:CY:19:G:N2	25:CY:56:C:N3	2.08	1.01
25:CY:19:G:H1	25:CY:56:C:N4	1.58	1.01
1:CA:999:C:H42	1:CA:1042:G:H1	1.07	1.01
25:CY:50:U:H3	25:CY:64:A:N6	1.58	1.00
26:BA:1065:U:HO2'	26:BA:1067:A:H2	1.07	1.00
2:CB:16:HIS:HB3	2:CB:210:SER:HB2	1.44	1.00
1:CA:1162:C:H42	1:CA:1174:G:H1	1.01	0.99
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.41	0.98
25:CY:8:4SU:HN3	25:CY:14:A:H62	1.10	0.98
26:DA:2124:G:H1	26:DA:2174:C:N4	1.62	0.97
26:BA:1829:U:H5'	28:BD:259:THR:HG22	1.47	0.97
26:BA:1039:G:OP1	41:BU:50:ARG:NH2	1.98	0.97
25:AY:7:A:H61	25:AY:66:U:H3	1.11	0.97
1:CA:1162:C:N4	1:CA:1174:G:H1	1.63	0.96
1:AA:1502:A:H2	1:AA:1505:G:H1	1.10	0.96
7:AG:50:ILE:HD11	7:AG:58:PRO:HA	1.48	0.95
26:BA:2145:G:H1	26:BA:2197:C:H42	1.12	0.95
23:CW:66:U:H3'	23:CW:67:C:H5''	1.49	0.95
25:CY:51:U:H3	25:CY:63:G:H1	1.13	0.95
27:DB:22:U:H3	27:DB:61:G:H1	1.11	0.94
25:AY:49:C:N3	25:AY:65:G:N2	2.14	0.94
24:AX:5:G:H1	24:AX:68:C:N4	1.65	0.94
1:CA:76:C:N4	1:CA:93:G:H1	1.66	0.93
42:DV:100:ARG:HH11	42:DV:100:ARG:HG3	1.33	0.93
23:AW:29:G:H1	23:AW:41:C:H42	1.16	0.93
25:CY:50:U:H3	25:CY:64:A:H61	0.96	0.92
1:CA:76:C:H42	1:CA:93:G:H1	0.97	0.92
46:BZ:153:SER:HB3	46:BZ:167:PRO:HB3	1.49	0.92
26:BA:2158:C:H42	26:BA:2177:G:H1	0.96	0.92
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.02	0.92

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.51	0.91
23:AW:50:U:H3	23:AW:64:A:H61	1.02	0.91
26:BA:542:C:OP1	52:B5:16:ARG:NH2	2.04	0.91
26:DA:2124:G:H1	26:DA:2174:C:H42	1.17	0.91
26:DA:1204:A:H2	26:DA:1241:A:H62	1.19	0.90
24:AX:5:G:H1	24:AX:68:C:H42	0.92	0.90
26:DA:2206:G:H3'	26:DA:2207:G:C8	2.07	0.89
25:CY:15:G:N1	25:CY:48:C:N3	2.19	0.89
25:AY:26:A:H61	25:AY:44:G:H1	1.14	0.88
25:CY:9:A:N6	25:CY:23:A:OP2	2.06	0.88
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.56	0.88
1:CA:1000:U:H3	1:CA:1041:A:H61	0.88	0.88
1:CA:1502:A:H2	1:CA:1505:G:H1	1.22	0.87
1:AA:664:G:H22	1:AA:741:G:H1	1.19	0.87
1:CA:1002:G:N2	1:CA:1038:C:N3	2.23	0.87
47:B0:11:ARG:O	47:B0:14:ARG:NH2	2.07	0.87
23:AW:50:U:H3	23:AW:64:A:N6	1.71	0.87
26:DA:994:C:OP1	41:DU:53:ARG:NH2	2.08	0.87
26:DA:1689:A:H62	26:DA:1698:A:H2	1.20	0.86
26:DA:1798:U:H5'	28:DD:259:THR:HG22	1.55	0.86
1:AA:1025:U:O2	1:AA:1036:G:O6	1.93	0.86
29:BE:47:VAL:HG21	29:BE:86:PRO:HD2	1.57	0.86
26:DA:397:G:N7	61:DA:4625:HOH:O	2.08	0.86
1:CA:664:G:H22	1:CA:741:G:H1	1.24	0.86
26:DA:827:U:OP1	61:DA:4303:HOH:O	1.91	0.85
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.10	0.85
26:DA:1169:G:H1	26:DA:1180:C:H42	1.23	0.85
26:DA:2130:U:H4'	26:DA:2133:G:H4'	1.58	0.85
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.59	0.85
30:DF:53:THR:HG22	30:DF:56:GLU:HG3	1.58	0.84
26:BA:1736:A:H62	26:BA:1745:A:H2	1.25	0.84
26:DA:2430:A:OP2	61:DA:4303:HOH:O	1.94	0.84
26:BA:656:A:OP1	36:BP:65:ARG:NH1	2.10	0.84
7:CG:79:ARG:HE	7:CG:80:VAL:HG23	1.42	0.84
26:DA:2138:C:N3	26:DA:2153:G:N2	2.24	0.84
26:BA:99:G:O2'	49:B2:7:ARG:NH2	2.10	0.84
26:BA:2299:A:H62	26:BA:2356:U:H3	1.23	0.84
9:CI:51:ARG:HG2	9:CI:56:LEU:HD21	1.60	0.84
1:CA:36:C:OP1	12:CL:123:LYS:NZ	2.11	0.84
33:BI:92:VAL:HG13	33:BI:120:ILE:HB	1.60	0.83
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.11	0.83
23:AW:26:A:N6	23:AW:44:G:H1	1.75	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:53:THR:HG23	30:DF:55:GLY:H	1.44	0.83
23:AW:6:G:H1	23:AW:67:C:N4	1.77	0.82
10:CJ:7:LYS:HG3	10:CJ:71:LEU:HD12	1.60	0.82
29:DE:11:MET:HG2	29:DE:24:THR:HB	1.61	0.82
25:AY:50:U:O4	25:AY:64:A:N1	2.13	0.82
26:BA:1221:G:H1'	26:BA:1222:A:H5'	1.59	0.82
35:DO:35:VAL:HG11	35:DO:103:ALA:HB3	1.62	0.82
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.12	0.82
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.59	0.82
26:BA:932:C:H3'	26:BA:933:C:H5''	1.61	0.82
25:CY:31:A:N1	25:CY:39:PSU:O2	2.13	0.82
36:DP:100:LEU:HD12	36:DP:112:LEU:HD11	1.60	0.82
26:BA:2122:G:H1	26:BA:2211:U:H3	1.27	0.82
23:CW:4:C:N4	23:CW:69:G:H1	1.77	0.82
25:CY:19:G:H1	25:CY:56:C:H42	0.85	0.82
4:AD:158:ILE:H	4:AD:158:ILE:HD13	1.45	0.81
1:CA:1029:C:N3	1:CA:1032:G:N2	2.28	0.81
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.62	0.81
46:BZ:117:LEU:HD11	46:BZ:144:LEU:HD22	1.61	0.81
1:CA:1029:C:N4	1:CA:1032:G:N1	2.29	0.81
26:DA:2136:C:HO2'	26:DA:2137:C:H6	1.29	0.81
26:DA:2139:C:H42	26:DA:2152:G:H1	0.83	0.81
1:CA:1153:C:H42	1:CA:1154:G:H21	1.28	0.81
26:BA:303:C:H42	26:BA:385:G:H1	1.26	0.81
26:DA:2124:G:N2	26:DA:2174:C:N3	2.28	0.81
46:DZ:126:VAL:HG11	46:DZ:161:VAL:HG23	1.61	0.81
26:BA:1577:C:O2'	26:BA:1578:C:O5'	1.99	0.81
26:DA:2114:A:N6	26:DA:2119:A:N7	2.28	0.81
26:BA:2736:C:OP1	38:BR:3:HIS:ND1	2.12	0.81
1:CA:999:C:N4	1:CA:1042:G:H1	1.77	0.81
26:DA:2121:G:N2	26:DA:2177:C:N3	2.27	0.81
1:CA:201:C:H42	1:CA:216:G:H1	1.28	0.80
32:BH:59:ARG:HB2	32:BH:59:ARG:HH11	1.43	0.80
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.62	0.80
26:DA:2114:A:N1	26:DA:2171:A:N6	2.29	0.80
1:AA:407:G:H5''	4:AD:115:ARG:HG2	1.62	0.80
39:BS:25:ARG:NH1	39:BS:42:ASP:OD1	2.14	0.80
26:DA:1315:C:OP2	61:DA:4172:HOH:O	1.99	0.80
26:DA:529:A:N6	26:DA:2041:U:O2	2.14	0.80
1:CA:985:C:H42	1:CA:1220:G:H1	1.24	0.80
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.12	0.80
1:CA:1317:C:N3	19:CS:37:ARG:NH2	2.30	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2819:G:N7	61:DA:4078:HOH:O	2.15	0.80
26:BA:1513:G:HO2'	26:BA:1593:C:HO2'	1.22	0.79
25:CY:53:G:O6	25:CY:61:C:N4	2.16	0.79
26:DA:2139:C:N3	26:DA:2152:G:N2	2.26	0.79
25:AY:19:G:N2	25:AY:56:C:N3	2.30	0.79
25:CY:19:G:N1	25:CY:56:C:N4	2.23	0.79
1:CA:1133:G:H1	1:CA:1141:C:H42	1.26	0.79
25:CY:8:4SU:S4	25:CY:14:A:N7	2.56	0.79
26:DA:2682:U:OP2	61:DA:3832:HOH:O	2.00	0.79
1:CA:1000:U:O2	1:CA:1041:A:N1	2.15	0.79
26:DA:1530:C:O2'	26:DA:1531:C:O5'	2.01	0.79
26:BA:1552:C:H2'	26:BA:1553:A:H8	1.47	0.79
26:BA:2695:C:O2	35:BO:70:LYS:NZ	2.15	0.79
35:BO:35:VAL:HG11	35:BO:103:ALA:HB3	1.64	0.79
1:CA:1024:G:H2'	1:CA:1025:U:H5''	1.62	0.79
26:DA:2138:C:H42	26:DA:2153:G:H1	0.80	0.79
9:CI:71:SER:HA	9:CI:74:ILE:HD12	1.65	0.78
23:CW:29:G:H1	23:CW:41:C:H42	1.29	0.78
26:BA:2818:U:O2	26:BA:2901:A:N6	2.15	0.78
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.15	0.78
26:DA:1324:G:N7	61:DA:3887:HOH:O	2.15	0.78
1:CA:582:U:OP1	15:CO:68:ARG:NH2	2.16	0.78
26:BA:2163:G:H1	26:BA:2171:G:H22	1.31	0.78
1:CA:975:A:H4'	1:CA:976:G:H5''	1.64	0.78
1:AA:1158:C:H5	1:AA:1181:G:H1	1.32	0.78
1:AA:156:G:N2	1:AA:165:C:O2	2.17	0.78
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.16	0.78
47:D0:11:ARG:O	47:D0:14:ARG:NH2	2.17	0.78
26:BA:2145:G:H1	26:BA:2197:C:N4	1.81	0.78
25:CY:15:G:N2	25:CY:48:C:H42	1.82	0.78
26:DA:2608:G:N7	61:DA:4023:HOH:O	2.17	0.78
46:DZ:19:ARG:NH1	46:DZ:84:GLU:O	2.17	0.78
26:DA:1648:C:OP1	61:DA:4215:HOH:O	2.01	0.78
9:AI:50:LEU:HD23	9:AI:81:ILE:HD11	1.67	0.77
25:CY:62:C:H2'	25:CY:63:G:H8	1.49	0.77
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.18	0.77
26:DA:2287:A:H62	26:DA:2344:U:H3	1.30	0.77
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.32	0.77
1:CA:985:C:N4	1:CA:1220:G:H1	1.81	0.77
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.65	0.77
26:BA:2158:C:N3	26:BA:2177:G:N2	2.27	0.77
1:CA:1255:G:OP1	10:CJ:45:ARG:NH2	2.17	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1044:C:OP1	61:BA:4663:HOH:O	2.02	0.77
46:BZ:72:ARG:NH2	46:BZ:97:GLU:O	2.18	0.77
3:CC:129:ALA:HB3	3:CC:132:ARG:HB2	1.67	0.77
25:CY:25:C:H2'	25:CY:26:A:H8	1.47	0.77
1:AA:1260:C:O2	1:AA:1275:A:N6	2.17	0.77
33:BI:129:THR:HG22	33:BI:139:GLN:HE22	1.48	0.77
23:CW:19:G:H1	23:CW:56:C:H42	1.33	0.77
23:AW:53:G:OP1	37:BQ:60:ARG:NH2	2.17	0.77
25:AY:7:A:N6	25:AY:66:U:H3	1.82	0.77
26:BA:973:G:N7	61:BA:4413:HOH:O	2.17	0.76
1:AA:1422:G:H5''	35:BO:48:PRO:HB3	1.67	0.76
1:CA:1025:U:H3	1:CA:1036:G:H1	1.32	0.76
37:DQ:135:ASP:OD2	46:DZ:49:ARG:NH2	2.18	0.76
26:BA:427:G:N7	61:BA:5004:HOH:O	2.17	0.76
1:CA:838:G:H1	1:CA:848:C:N4	1.84	0.76
26:BA:1500:A:OP2	61:BA:4011:HOH:O	2.02	0.76
42:BV:40:LEU:HB2	42:BV:46:VAL:HG13	1.67	0.76
30:BF:18:ARG:NH2	30:BF:127:GLU:OE1	2.18	0.76
23:CW:4:C:N3	23:CW:69:G:N2	2.34	0.76
26:DA:2723:C:H5''	38:DR:1:MET:HE2	1.66	0.76
1:CA:1422:G:H5''	35:DO:48:PRO:HB3	1.67	0.76
26:DA:143:G:H4'	44:DX:35:THR:HG21	1.68	0.76
1:AA:975:A:H4'	1:AA:976:G:H5''	1.67	0.76
26:BA:2125:C:H42	26:BA:2208:G:H1	1.30	0.76
28:DD:238:GLY:O	61:DD:408:HOH:O	2.03	0.76
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.18	0.76
1:CA:1054:C:O2'	1:CA:1055:A:O5'	2.02	0.76
56:D9:25:VAL:HB	56:D9:34:GLN:HB2	1.66	0.76
3:CC:98:ASN:N	3:CC:98:ASN:OD1	2.19	0.76
26:BA:11:G:H2'	26:BA:12:U:H5''	1.68	0.76
26:DA:880:G:N1	26:DA:898:C:O2	2.18	0.76
51:D4:38:LYS:O	51:D4:40:HIS:N	2.17	0.76
13:CM:25:ILE:HD11	13:CM:66:LEU:HD13	1.68	0.75
36:BP:126:VAL:HG12	36:BP:148:LEU:HD22	1.66	0.75
2:CB:17:PHE:HB2	2:CB:44:LEU:HD11	1.66	0.75
26:DA:792:G:O6	61:DA:4162:HOH:O	2.03	0.75
29:DE:14:ILE:HG13	29:DE:21:VAL:HG13	1.68	0.75
36:DP:29:LYS:HG3	36:DP:30:THR:N	2.01	0.75
1:AA:532:A:H2	1:AA:1206:G:H21	1.35	0.75
24:AX:6:G:H1	24:AX:67:C:H42	1.34	0.75
26:BA:1378:G:OP1	61:BA:4653:HOH:O	2.03	0.75
42:BV:76:LYS:HB2	42:BV:81:TYR:HB3	1.68	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:CW:49:C:N4	23:CW:65:G:O6	2.20	0.75
23:CW:4:C:H42	23:CW:69:G:H1	1.33	0.75
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.68	0.75
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.20	0.75
1:CA:1013:G:N2	1:CA:1016:A:OP2	2.19	0.75
26:DA:631:A:OP1	36:DP:65:ARG:NH1	2.20	0.75
1:CA:1456:G:O6	20:CT:54:LYS:NZ	2.16	0.75
26:DA:2638:G:OP2	29:DE:82:ARG:NH2	2.19	0.75
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.69	0.75
26:BA:278:G:OP1	48:B1:76:ARG:NH1	2.19	0.75
26:BA:331:G:H21	26:BA:354:A:H62	1.35	0.75
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.18	0.75
1:AA:574:A:OP2	61:AA:4005:HOH:O	2.05	0.75
1:AA:78:G:N2	1:AA:91:C:N3	2.35	0.75
23:AW:29:G:H1	23:AW:41:C:N4	1.84	0.75
23:AW:6:G:N2	23:AW:67:C:N3	2.34	0.75
35:BO:64:ARG:NH2	35:BO:99:PHE:O	2.20	0.75
3:CC:179:ARG:HD2	3:CC:206:GLU:HB2	1.68	0.75
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.59	0.75
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.05	0.74
1:AA:642:A:N3	8:AH:113:SER:OG	2.20	0.74
26:BA:325:G:OP2	45:BY:84:ARG:NH2	2.19	0.74
1:AA:1036:G:H21	1:AA:1037:C:H1'	1.51	0.74
26:BA:2754:A:OP1	56:B9:22:ARG:NH2	2.17	0.74
19:CS:42:PRO:HG3	51:D4:61:ARG:HG2	1.69	0.74
26:DA:1189:A:OP2	61:DA:4184:HOH:O	2.04	0.74
4:CD:104:VAL:HG11	4:CD:146:ILE:HD13	1.68	0.74
27:DB:76:G:N2	27:DB:101:G:O6	2.19	0.74
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.52	0.74
28:DD:148:GLU:HB2	28:DD:151:LYS:HD2	1.68	0.74
46:DZ:72:ARG:NH2	46:DZ:97:GLU:O	2.21	0.74
26:BA:2479:C:OP2	61:BA:5096:HOH:O	2.05	0.74
1:CA:958:A:N6	19:CS:77:THR:O	2.20	0.74
4:CD:154:ASN:HA	4:CD:159:ARG:HH21	1.53	0.74
26:DA:449:A:OP2	61:DA:4657:HOH:O	2.05	0.74
26:DA:1815:A:OP2	28:DD:54:ARG:NH2	2.19	0.74
1:CA:811:C:N4	61:CA:4023:HOH:O	2.20	0.74
25:AY:50:U:H3	25:AY:64:A:H2	1.35	0.74
23:CW:7:A:N1	23:CW:66:U:O4	2.19	0.74
23:CW:2:C:N3	23:CW:71:G:O6	2.21	0.74
26:DA:2169:A:O2'	26:DA:2170:A:O5'	2.06	0.74
27:DB:75:G:N2	46:DZ:87:ASP:OD1	2.21	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1871:G:N7	61:BA:4332:HOH:O	2.20	0.74
26:DA:2049:G:N7	61:DA:3798:HOH:O	2.19	0.74
26:DA:884:C:N4	26:DA:892:G:O6	2.20	0.74
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.21	0.74
28:BD:17:THR:O	28:BD:211:ARG:NH2	2.21	0.74
3:CC:150:LYS:HG3	3:CC:169:ALA:HB2	1.70	0.74
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.20	0.74
26:DA:1314:C:OP1	61:DA:4172:HOH:O	2.04	0.74
4:AD:104:VAL:HG11	4:AD:146:ILE:HD13	1.69	0.74
26:BA:591:U:O4	61:BA:4141:HOH:O	2.05	0.74
36:DP:96:THR:H	36:DP:99:LEU:HD21	1.53	0.74
1:AA:911:U:OP2	12:AL:97:ARG:NH1	2.21	0.73
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.69	0.73
25:CY:62:C:H2'	25:CY:63:G:C8	2.23	0.73
49:D2:22:GLU:OE2	49:D2:68:ARG:NH2	2.21	0.73
1:AA:1505:G:O2'	22:AV:13:A:O2'	2.05	0.73
26:BA:1648:U:O4	61:BA:4228:HOH:O	2.06	0.73
26:BA:2209:G:O2'	26:BA:2210:C:OP1	2.07	0.73
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	1.68	0.73
25:CY:31:A:C6	25:CY:39:PSU:O2	2.41	0.73
26:DA:2121:G:H1	26:DA:2177:C:H42	0.80	0.73
29:DE:77:ILE:HD13	29:DE:195:LEU:HD13	1.70	0.73
51:D4:40:HIS:HB3	51:D4:43:TYR:HB2	1.71	0.73
51:D4:40:HIS:O	51:D4:44:THR:N	2.17	0.73
51:B4:53:GLU:C	51:B4:55:ARG:H	1.92	0.73
5:CE:80:ILE:HG22	5:CE:91:LEU:HB2	1.71	0.73
27:DB:20:C:N4	27:DB:63:G:O6	2.19	0.73
26:DA:2815:C:H5'	52:D5:29:THR:HG21	1.71	0.73
26:DA:1959:G:N7	61:DA:4503:HOH:O	2.21	0.73
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.21	0.73
26:DA:1352:U:OP2	61:DA:3767:HOH:O	2.06	0.73
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.22	0.73
25:CY:18:G:N2	25:CY:55:PSU:N3	2.37	0.73
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.05	0.73
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.71	0.73
11:CK:20:TYR:HB2	11:CK:31:THR:HG22	1.69	0.73
26:DA:11:G:N7	61:DA:4280:HOH:O	2.20	0.73
27:DB:24:G:N2	27:DB:27:C:N3	2.32	0.73
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	1.71	0.73
51:B4:59:PHE:H	51:B4:59:PHE:HD1	1.35	0.73
3:CC:43:LEU:HD21	3:CC:91:LEU:HD13	1.69	0.73
25:AY:26:A:N6	25:AY:44:G:H1	1.85	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AW:52:G:H4'	37:BQ:56:ARG:HH22	1.54	0.72
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.53	0.72
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.22	0.72
25:CY:36:A:H2'	25:CY:37:MIA:O4'	1.89	0.72
31:DG:136:ARG:HD2	31:DG:137:GLU:HG3	1.70	0.72
26:DA:2562:U:H1'	35:DO:23:ARG:HH11	1.53	0.72
36:BP:94:GLU:OE2	36:BP:124:LYS:NZ	2.22	0.72
26:DA:741:G:OP2	61:DA:4224:HOH:O	2.05	0.72
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.72	0.72
45:BY:92:ASN:HB3	45:BY:94:LYS:H	1.52	0.72
25:CY:31:A:N1	25:CY:39:PSU:C2	2.57	0.72
26:BA:1553:A:O2'	26:BA:1554:A:O4'	2.06	0.72
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.89	0.72
26:DA:1449:A:O2'	26:DA:1529:G:N2	2.22	0.72
36:DP:126:VAL:HG12	36:DP:148:LEU:HD22	1.71	0.72
42:DV:6:LYS:HB2	42:DV:38:LEU:HD21	1.69	0.72
1:AA:266:G:H5''	1:AA:268:C:H41	1.53	0.72
25:AY:56:C:H2'	25:AY:57:G:O4'	1.88	0.72
26:BA:1065:U:H3	26:BA:1188:A:H62	1.35	0.72
25:AY:76:A:N6	26:BA:2434:A:O4'	2.22	0.72
26:BA:2820:A:N6	26:BA:2900:G:O2'	2.21	0.72
1:CA:1055:A:N7	1:CA:1200:C:N4	2.37	0.72
25:CY:26:A:N1	25:CY:44:G:O6	2.23	0.72
26:DA:2683:C:O2	35:DO:70:LYS:NZ	2.23	0.72
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.06	0.72
1:AA:347:G:O2'	1:AA:348:G:OP1	2.08	0.72
26:BA:786:G:OP1	61:BA:5196:HOH:O	2.06	0.72
1:CA:324:G:N7	61:CA:4089:HOH:O	2.23	0.72
25:CY:5:G:H1	25:CY:68:C:H42	1.36	0.72
25:AY:62:C:H2'	25:AY:63:G:H8	1.55	0.72
47:B0:10:THR:HG22	47:B0:12:ASN:H	1.54	0.72
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.22	0.72
26:DA:2166:G:H3'	26:DA:2167:U:H5''	1.70	0.72
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.04	0.72
1:CA:977:A:N6	1:CA:1224:G:OP1	2.21	0.72
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.07	0.72
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.23	0.72
26:BA:1761:G:H1	26:BA:1775:C:H42	1.38	0.72
9:CI:53:VAL:O	9:CI:55:ALA:N	2.22	0.72
25:CY:71:G:H4'	26:DA:1851:U:H4'	1.71	0.72
26:DA:1670:C:OP1	61:DA:3752:HOH:O	2.06	0.72
28:DD:28:GLU:OE1	61:DD:416:HOH:O	2.06	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1445:C:O2	1:AA:1457:G:N2	2.20	0.72
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.14	0.72
26:DA:1604:C:OP2	61:DA:4546:HOH:O	2.08	0.72
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.07	0.71
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.70	0.71
1:CA:1162:C:N3	1:CA:1174:G:N2	2.34	0.71
48:B1:86:SER:OG	48:B1:89:GLU:OE1	2.07	0.71
26:DA:2134:A:N3	26:DA:2159:G:O2'	2.21	0.71
1:AA:1086:U:H3	1:AA:1099:G:H22	1.37	0.71
26:BA:1002:A:H5'	37:BQ:76:LYS:HG3	1.72	0.71
26:DA:1890:A:OP2	61:DA:4472:HOH:O	2.08	0.71
25:CY:15:G:N2	25:CY:48:C:N4	2.38	0.71
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.37	0.71
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.73	0.71
17:AQ:3:LYS:HD2	17:AQ:60:ILE:HD11	1.71	0.71
25:AY:25:C:O2'	25:AY:26:A:O5'	2.09	0.71
1:CA:1054:C:C4	23:CW:34:G:H1'	2.25	0.71
10:CJ:5:ARG:N	61:CJ:5101:HOH:O	2.22	0.71
23:CW:29:G:H1	23:CW:41:C:N4	1.87	0.71
26:DA:370:G:N7	61:DA:3786:HOH:O	2.23	0.71
46:DZ:144:LEU:HD11	46:DZ:172:ALA:HB1	1.72	0.71
26:BA:553:A:H2'	26:BA:554:A:H5''	1.72	0.71
36:BP:116:GLY:O	36:BP:137:LYS:NZ	2.22	0.71
44:BX:53:LYS:HB3	44:BX:82:GLN:HB3	1.73	0.71
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.72	0.71
26:BA:2146:G:H1	26:BA:2196:C:H42	1.37	0.71
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.73	0.71
26:BA:2152:U:H4'	26:BA:2155:G:H4'	1.72	0.71
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.24	0.71
23:CW:27:G:H1	23:CW:43:C:H42	1.37	0.71
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.73	0.71
2:CB:155:LEU:HD21	2:CB:159:PRO:HG3	1.71	0.71
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.24	0.71
61:DA:4209:HOH:O	29:DE:135:HIS:NE2	2.24	0.71
30:DF:33:LEU:HD13	30:DF:112:MET:HE2	1.72	0.71
46:DZ:92:SER:O	46:DZ:130:PRO:HG2	1.91	0.71
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.72	0.70
26:BA:1068:G:H22	26:BA:1188:A:H2	1.39	0.70
26:BA:1846:A:OP2	28:BD:54:ARG:NH2	2.22	0.70
40:BT:95:ARG:HG2	40:BT:95:ARG:HH11	1.54	0.70
26:DA:643:A:N1	26:DA:2369:A:O2'	2.22	0.70
26:DA:731:C:OP1	61:DA:4348:HOH:O	2.08	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:DG:63:ILE:HA	31:DG:143:GLU:HG3	1.72	0.70
46:DZ:145:GLU:H	46:DZ:148:ASP:HB2	1.57	0.70
1:AA:972:C:OP1	61:AA:4173:HOH:O	2.09	0.70
26:BA:2251:G:OP2	61:BA:4335:HOH:O	2.08	0.70
30:BF:185:ASP:HA	30:BF:188:ARG:HD3	1.70	0.70
40:BT:16:ARG:NH2	40:BT:83:ILE:O	2.24	0.70
1:CA:986:A:O2'	19:CS:55:LYS:O	2.08	0.70
38:BR:67:LEU:HD13	38:BR:76:VAL:HG21	1.72	0.70
26:DA:1637:A:OP2	61:DA:4569:HOH:O	2.09	0.70
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.08	0.70
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.73	0.70
26:BA:1356:G:OP2	54:B7:9:ARG:NH1	2.25	0.70
1:CA:771:G:N7	61:CA:4042:HOH:O	2.24	0.70
46:DZ:119:GLU:O	46:DZ:122:ARG:NH1	2.24	0.70
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.74	0.70
23:AW:6:G:H1	23:AW:67:C:H42	1.32	0.70
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.56	0.70
10:CJ:52:GLY:O	14:CN:41:ARG:NH2	2.21	0.70
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.56	0.70
2:CB:87:ARG:NH2	2:CB:220:ASP:OD1	2.24	0.70
25:CY:51:U:O2	25:CY:63:G:N2	2.23	0.70
26:BA:2130:C:H2'	26:BA:2131:U:H6	1.57	0.70
26:BA:2124:U:O2	26:BA:2209:G:N2	2.25	0.70
31:BG:41:GLN:NE2	31:BG:154:GLY:O	2.24	0.70
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.39	0.70
26:BA:2124:U:H3	26:BA:2209:G:H1	1.40	0.70
26:DA:2820:A:OP2	38:DR:2:ARG:NH2	2.24	0.70
1:AA:1027:C:O2	1:AA:1034:G:C2	2.45	0.70
1:AA:1076:C:H5'	1:AA:1076:C:H6	1.57	0.70
23:AW:47:U:H5'	23:AW:47:U:H6	1.57	0.70
26:BA:776:G:OP2	28:BD:13:ARG:NH1	2.24	0.70
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	1.73	0.70
26:DA:2138:C:N4	26:DA:2153:G:N1	2.27	0.70
18:AR:26:LEU:HD21	18:AR:39:VAL:HG13	1.74	0.69
26:DA:987:G:O2'	26:DA:1000:A:N3	2.23	0.69
1:AA:96:U:HO2'	1:AA:97:G:H8	1.40	0.69
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.25	0.69
26:BA:1296:G:OP2	36:BP:21:ARG:NH1	2.26	0.69
6:CF:81:ILE:HD11	28:DD:125:ILE:HB	1.73	0.69
48:D1:59:THR:O	48:D1:91:LYS:NZ	2.24	0.69
36:BP:59:LEU:HD21	55:B8:10:ALA:HA	1.75	0.69
26:BA:2297:C:OP2	53:B6:6:ARG:NH1	2.25	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
44:DX:8:ILE:O	49:D2:36:ARG:NH2	2.25	0.69
26:DA:2504:U:OP2	61:DA:4169:HOH:O	2.11	0.69
44:DX:53:LYS:HB3	44:DX:82:GLN:HB3	1.74	0.69
1:AA:1414:U:H3	1:AA:1486:G:H1	1.40	0.69
28:BD:147:LEU:HD13	28:BD:155:LEU:HD21	1.73	0.69
1:CA:76:C:N3	1:CA:93:G:N2	2.34	0.69
26:DA:1011:G:OP2	41:DU:66:ASN:ND2	2.24	0.69
54:B7:24:THR:HG22	54:B7:27:GLY:H	1.57	0.69
1:CA:664:G:OP1	18:CR:64:ARG:NH2	2.26	0.69
35:DO:80:ASP:OD1	40:DT:64:ARG:NH2	2.25	0.69
26:DA:993:G:OP1	41:DU:50:ARG:NH2	2.25	0.69
28:BD:148:GLU:HB2	28:BD:151:LYS:HD2	1.75	0.69
4:AD:23:GLY:HA3	4:AD:112:VAL:HG12	1.74	0.69
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.23	0.69
30:DF:184:TYR:CE2	30:DF:188:ARG:HD2	2.28	0.69
1:CA:200:G:H1	1:CA:217:C:H42	1.40	0.69
26:DA:2323:G:O6	26:DA:2332:U:N3	2.18	0.69
1:AA:78:G:N1	1:AA:91:C:N4	2.40	0.69
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.73	0.69
27:BB:106:G:H5'	46:BZ:31:ARG:HG2	1.75	0.69
10:CJ:49:VAL:HG23	14:CN:41:ARG:HD2	1.75	0.69
26:DA:2060:A:N3	61:DA:4112:HOH:O	2.25	0.69
26:DA:2206:G:H3'	26:DA:2207:G:H8	1.57	0.69
39:DS:93:LYS:HD2	39:DS:95:HIS:HB2	1.74	0.69
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.26	0.69
26:BA:552:C:OP1	61:BA:4682:HOH:O	2.11	0.69
37:BQ:21:THR:HG21	37:BQ:101:ARG:HD3	1.75	0.69
46:BZ:145:GLU:O	46:BZ:148:ASP:N	2.26	0.69
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.28	0.68
2:AB:20:GLU:HG2	2:AB:191:ASP:HB3	1.74	0.68
26:BA:1398:U:OP1	61:BA:4087:HOH:O	2.11	0.68
1:CA:560:U:OP2	61:CA:4161:HOH:O	2.11	0.68
26:DA:882:G:N2	26:DA:894:C:O2	2.18	0.68
26:BA:1185:C:O3'	34:BN:25:ARG:NH1	2.27	0.68
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.08	0.68
31:DG:161:THR:HG22	31:DG:163:ALA:H	1.59	0.68
5:CE:20:GLN:NE2	5:CE:21:ALA:O	2.26	0.68
31:DG:41:GLN:HB3	31:DG:43:LEU:HD22	1.76	0.68
1:CA:1129:C:OP1	9:CI:16:ARG:NH1	2.26	0.68
26:DA:1223:G:N2	26:DA:1226:A:OP2	2.23	0.68
29:DE:72:VAL:HG13	29:DE:73:GLU:O	1.93	0.68
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.74	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2624:C:OP2	52:B5:2:ALA:N	2.27	0.68
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.58	0.68
5:CE:7:GLU:OE1	5:CE:37:ARG:NH2	2.26	0.68
26:DA:880:G:H22	26:DA:898:C:H1'	1.59	0.68
26:DA:89:G:H3'	26:DA:90:U:H5''	1.76	0.68
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.73	0.68
26:BA:1874:C:H5'	28:BD:253:GLN:NE2	2.09	0.68
26:DA:2139:C:N4	26:DA:2152:G:N1	2.16	0.68
26:DA:2127:G:O6	26:DA:2161:C:N3	2.26	0.68
26:BA:1091:A:OP1	26:BA:1091:A:H4'	1.92	0.68
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.26	0.68
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.76	0.68
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	1.93	0.68
26:DA:194:G:N7	61:DA:4296:HOH:O	2.26	0.68
33:DI:4:ILE:HG12	33:DI:18:VAL:HG22	1.76	0.68
43:DW:18:ARG:NH1	43:DW:76:VAL:O	2.27	0.68
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.26	0.68
26:BA:2132:G:O2'	26:BA:2142:G:OP2	2.12	0.68
26:DA:2165:G:H22	26:DA:2172:U:H5	1.40	0.68
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.76	0.68
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.11	0.68
1:CA:952:U:O2'	1:CA:965:A:N6	2.27	0.68
15:CO:4:THR:OG1	15:CO:7:GLU:OE1	2.10	0.68
26:DA:1647:G:OP1	61:DA:4215:HOH:O	2.12	0.68
30:DF:157:VAL:HB	30:DF:194:MET:HG2	1.76	0.68
1:AA:1027:C:N3	1:AA:1034:G:C6	2.63	0.67
23:AW:66:U:H2'	23:AW:67:C:C6	2.29	0.67
26:BA:272:U:OP1	33:BI:50:ARG:NH1	2.26	0.67
1:CA:446:G:H1	1:CA:488:C:H42	1.39	0.67
26:DA:857:C:OP2	47:D0:77:ARG:NH2	2.26	0.67
51:B4:55:ARG:HB2	51:B4:56:VAL:O	1.94	0.67
26:BA:2324:U:H5'	31:BG:88:ILE:HD11	1.75	0.67
1:CA:1277:C:HO2'	1:CA:1279:A:H8	1.42	0.67
15:CO:22:THR:OG1	15:CO:23:GLY:N	2.24	0.67
25:CY:25:C:H2'	25:CY:26:A:C8	2.30	0.67
1:CA:1026:G:H5'	1:CA:1027:C:O5'	1.94	0.67
1:CA:1133:G:H1	1:CA:1141:C:N4	1.92	0.67
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	1.75	0.67
30:BF:53:THR:HG23	30:BF:55:GLY:H	1.58	0.67
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.76	0.67
49:D2:29:LYS:HE2	49:D2:57:ILE:HG21	1.74	0.67
26:DA:1449:A:HO2'	26:DA:1529:G:N2	1.92	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:324:G:N7	61:AA:4166:HOH:O	2.27	0.67
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.77	0.67
25:AY:66:U:H2'	25:AY:67:C:C6	2.29	0.67
26:BA:739:C:O2'	28:BD:38:LYS:NZ	2.26	0.67
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.24	0.67
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.27	0.67
26:BA:1814:A:N7	61:BA:5061:HOH:O	2.26	0.67
46:BZ:11:GLU:O	46:BZ:36:LYS:NZ	2.23	0.67
23:CW:43:C:H2'	23:CW:44:G:C8	2.29	0.67
51:D4:24:THR:OG1	51:D4:25:TYR:N	2.24	0.67
26:BA:709:G:H5''	36:BP:16:ARG:HG2	1.75	0.67
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.28	0.67
24:AX:5:G:N2	24:AX:68:C:N3	2.40	0.67
25:AY:22:G:H2'	25:AY:23:A:C8	2.29	0.67
26:BA:1040:C:OP1	41:BU:53:ARG:NH2	2.28	0.67
1:CA:999:C:N3	1:CA:1042:G:N2	2.38	0.67
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.77	0.67
26:DA:2886:G:N7	61:DA:4141:HOH:O	2.26	0.67
26:DA:307:G:N1	26:DA:310:A:OP2	2.26	0.67
28:DD:28:GLU:OE2	61:DD:417:HOH:O	2.13	0.67
31:DG:41:GLN:NE2	31:DG:154:GLY:O	2.27	0.67
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.13	0.67
13:CM:80:ARG:HH22	19:CS:69:HIS:CE1	2.12	0.67
26:BA:2772:G:N7	61:BA:4124:HOH:O	2.28	0.67
29:BE:149:ARG:O	61:BE:406:HOH:O	2.12	0.67
1:CA:316:G:OP2	1:CA:351:G:O2'	2.12	0.67
26:DA:2639:A:OP2	61:DA:3839:HOH:O	2.12	0.67
26:DA:600:G:O6	61:DA:4398:HOH:O	2.11	0.67
30:DF:178:PRO:HB3	30:DF:198:ALA:HA	1.77	0.67
1:AA:1238:A:OP2	61:AA:4160:HOH:O	2.12	0.66
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.95	0.66
3:CC:34:LEU:HG	3:CC:38:ARG:HH12	1.59	0.66
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.77	0.66
1:CA:664:G:P	18:CR:64:ARG:HH22	2.18	0.66
23:CW:51:U:H3	23:CW:63:G:H1	1.41	0.66
26:DA:1993:U:OP2	61:DA:4714:HOH:O	2.13	0.66
26:DA:692:C:O2'	28:DD:38:LYS:NZ	2.28	0.66
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.75	0.66
26:BA:1284:G:OP2	61:BA:5012:HOH:O	2.14	0.66
26:BA:591:U:O2'	61:BA:5168:HOH:O	2.13	0.66
26:DA:2499:C:OP2	61:DA:4653:HOH:O	2.12	0.66
26:DA:2805:G:H2'	26:DA:2807:G:C8	2.30	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:CM:3:ARG:NH2	13:CM:9:ILE:O	2.28	0.66
26:DA:1019:U:H3	26:DA:1142(A):A:H62	1.41	0.66
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.23	0.66
25:AY:9:A:H5'	25:AY:46:7MG:HN22	1.60	0.66
26:BA:83:A:H5'	45:BY:8:LYS:HG2	1.76	0.66
37:BQ:111:GLU:OE1	37:BQ:133:ARG:NH2	2.26	0.66
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.42	0.66
26:DA:2148:G:H2'	26:DA:2149:G:H8	1.60	0.66
26:DA:20:C:OP1	41:DU:22:LYS:NZ	2.25	0.66
24:AX:8:4SU:O2	24:AX:21:A:H2	1.79	0.66
25:AY:35:A:H2'	25:AY:36:A:C8	2.30	0.66
26:BA:302:A:H2'	26:BA:303:C:C6	2.30	0.66
25:CY:2:C:H2'	25:CY:3:C:H6	1.61	0.66
26:DA:2552:U:H2'	26:DA:2554:U:OP2	1.95	0.66
26:DA:307:G:H21	26:DA:330:A:H62	1.44	0.66
26:DA:770:G:OP2	61:DA:4267:HOH:O	2.12	0.66
36:DP:39:LYS:HB2	36:DP:45:LEU:HG	1.77	0.66
26:BA:239:G:OP2	55:B8:13:ARG:NH2	2.28	0.66
30:BF:53:THR:HG22	30:BF:56:GLU:HG3	1.78	0.66
1:CA:972:C:OP1	61:CA:4167:HOH:O	2.13	0.66
13:CM:6:GLY:H	13:CM:67:GLU:HG3	1.61	0.66
32:DH:46:GLU:HB2	32:DH:49:VAL:HG12	1.76	0.66
41:DU:83:LEU:HD12	41:DU:88:ILE:HD12	1.78	0.66
1:AA:1278:U:H5'	1:AA:1279:A:O4'	1.96	0.66
9:AI:71:SER:HA	9:AI:74:ILE:HD12	1.78	0.66
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.29	0.66
2:CB:125:PRO:O	2:CB:127:ILE:N	2.27	0.66
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.77	0.66
1:AA:165:C:H2'	1:AA:166:G:C8	2.31	0.66
1:AA:567:G:N3	61:AA:4131:HOH:O	2.28	0.66
25:AY:9:A:O2'	25:AY:10:G:N7	2.28	0.66
26:BA:649:C:O2'	26:BA:704:U:OP1	2.12	0.66
1:CA:1352:C:OP1	21:CU:3:LYS:NZ	2.19	0.66
2:CB:122:PHE:HD1	2:CB:123:ALA:H	1.43	0.66
52:D5:16:ARG:NH1	52:D5:17:ASP:OD1	2.29	0.66
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.77	0.66
20:AT:43:LEU:HD13	20:AT:51:GLU:HB3	1.78	0.66
40:DT:108:ARG:HG2	40:DT:111:ARG:HH12	1.60	0.66
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.29	0.66
26:DA:2171:A:N3	26:DA:2172:U:N3	2.44	0.66
27:DB:4:C:H42	27:DB:117:G:H1	1.45	0.66
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.64	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.27	0.65
3:CC:137:ALA:HA	3:CC:140:ARG:HH12	1.61	0.65
10:CJ:78:ASN:O	10:CJ:80:LYS:N	2.28	0.65
25:CY:28:G:N2	25:CY:43:C:H1'	2.10	0.65
26:DA:740:U:OP2	61:DA:4223:HOH:O	2.13	0.65
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.78	0.65
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.29	0.65
26:BA:83:A:H5''	45:BY:8:LYS:HE3	1.77	0.65
1:CA:673:G:H2'	1:CA:674:G:C8	2.31	0.65
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.78	0.65
51:D4:62:ARG:O	51:D4:64:GLY:N	2.29	0.65
26:DA:2336:A:H61	47:D0:43:THR:HG22	1.60	0.65
31:DG:15:VAL:HG22	31:DG:175:LEU:HB3	1.78	0.65
9:AI:53:VAL:HG11	9:AI:92:TYR:CZ	2.31	0.65
20:AT:9:ASN:O	20:AT:10:LEU:HB2	1.95	0.65
46:BZ:108:PRO:HB3	46:BZ:117:LEU:HD13	1.79	0.65
1:CA:460:G:O6	1:CA:470:C:H5''	1.96	0.65
2:CB:178:ARG:HH22	8:CH:68:ARG:HH22	1.43	0.65
26:DA:1140:C:O3'	34:DN:25:ARG:NH1	2.29	0.65
26:DA:2492:U:OP1	61:DA:4150:HOH:O	2.15	0.65
26:BA:791:G:OP1	61:BA:4704:HOH:O	2.14	0.65
37:BQ:110:THR:HG23	37:BQ:113:GLN:HB2	1.78	0.65
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.24	0.65
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.29	0.65
26:DA:1246:A:OP1	30:DF:38:ARG:NH1	2.30	0.65
26:DA:2260:C:OP1	61:DA:4688:HOH:O	2.14	0.65
26:DA:422:A:OP2	61:DA:3787:HOH:O	2.15	0.65
26:BA:1313:U:OP1	61:BA:5106:HOH:O	2.14	0.65
40:BT:118:ARG:HH11	40:BT:118:ARG:HG3	1.60	0.65
1:CA:396:G:O2'	1:CA:398:C:OP1	2.05	0.65
29:DE:72:VAL:HG22	29:DE:73:GLU:HG3	1.78	0.65
10:AJ:5:ARG:NE	10:AJ:73:ASP:OD1	2.30	0.65
27:BB:66:A:H61	27:BB:108:U:H2'	1.62	0.65
26:DA:2404:C:O3'	36:DP:77:ARG:NH2	2.26	0.65
31:DG:36:LYS:HG2	31:DG:160:VAL:HB	1.78	0.65
51:B4:63:TYR:N	51:B4:64:GLY:HA2	2.12	0.65
1:CA:1402:C:N4	22:CV:18:G:OP2	2.28	0.65
27:DB:5:C:H42	27:DB:116:G:H1	1.43	0.65
1:AA:1028:C:H42	1:AA:1033:G:H1	1.45	0.65
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.77	0.65
8:CH:29:SER:HB2	8:CH:32:LYS:HG3	1.78	0.65
30:DF:101:LEU:O	30:DF:106:ARG:NH1	2.29	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:140:LEU:HD21	30:DF:170:LEU:HD11	1.79	0.65
36:DP:42:SER:O	61:DP:304:HOH:O	2.14	0.65
26:BA:2101:U:OP1	48:B1:21:ARG:NH2	2.29	0.65
26:BA:1360:C:OP1	61:BA:4653:HOH:O	2.14	0.65
29:BE:105:THR:OG1	29:BE:199:ARG:NH2	2.29	0.65
1:CA:1011:G:N2	1:CA:1019:C:H1'	2.12	0.65
1:CA:1132:C:H2'	1:CA:1133:G:H8	1.61	0.65
8:CH:45:ILE:HD13	8:CH:61:VAL:HG13	1.79	0.65
26:DA:1642:G:N7	61:DA:4099:HOH:O	2.28	0.65
26:DA:2355:C:H4'	47:D0:24:LYS:HD3	1.79	0.65
1:AA:1502:A:H2	1:AA:1505:G:N1	1.91	0.64
4:AD:64:LEU:HA	4:AD:67:ILE:HD12	1.77	0.64
1:AA:166:G:H2'	1:AA:167:G:C8	2.32	0.64
26:BA:2299:A:N6	26:BA:2356:U:H3	1.93	0.64
26:BA:591:U:H5'	26:BA:990:A:N1	2.12	0.64
2:AB:16:HIS:HE1	2:AB:214:ILE:HD11	1.63	0.64
26:BA:1159:U:H2'	26:BA:1160:G:H8	1.62	0.64
26:BA:1346:U:H4'	26:BA:1347:A:C5'	2.27	0.64
26:BA:2620:G:N7	61:BA:4411:HOH:O	2.29	0.64
33:BI:130:TYR:HB3	33:BI:138:ILE:HB	1.78	0.64
1:CA:35:G:O2'	12:CL:118:SER:O	2.15	0.64
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.29	0.64
26:DA:299:A:N1	26:DA:322:A:O2'	2.25	0.64
31:DG:80:PHE:O	31:DG:82:LEU:N	2.30	0.64
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.27	0.64
47:B0:27:GLU:HG3	47:B0:68:GLU:HA	1.80	0.64
26:BA:1001:G:OP2	37:BQ:14:ARG:NH2	2.25	0.64
26:BA:1480:A:H61	26:BA:1605:A:H62	1.44	0.64
26:BA:2153:G:H5''	26:BA:2154:U:H3'	1.80	0.64
1:CA:1024:G:C2'	1:CA:1025:U:H5''	2.27	0.64
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.79	0.64
1:CA:187:C:O2'	20:CT:89:ARG:NH2	2.28	0.64
25:AY:19:G:N1	25:AY:56:C:N4	2.45	0.64
26:BA:1604:C:OP2	26:BA:1605:A:O2'	2.10	0.64
26:BA:630:U:OP1	30:BF:102:PRO:HA	1.98	0.64
30:BF:157:VAL:HB	30:BF:194:MET:HG2	1.79	0.64
1:CA:96:U:O2'	1:CA:97:G:H5'	1.97	0.64
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.80	0.64
1:CA:377:G:OP1	16:CP:3:LYS:HD2	1.98	0.64
20:CT:16:HIS:O	20:CT:19:SER:OG	2.13	0.64
26:DA:2624:G:N7	61:DA:4478:HOH:O	2.29	0.64
41:DU:76:TYR:OH	41:DU:92:ARG:NH1	2.30	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:AD:154:ASN:HA	4:AD:159:ARG:HH21	1.63	0.64
26:BA:934:A:O2'	26:BA:935:C:OP2	2.13	0.64
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.79	0.64
25:CY:12:U:O4	25:CY:23:A:N1	2.31	0.64
1:CA:1118:C:C2	1:CA:1119:C:H5	2.16	0.64
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.63	0.64
37:DQ:18:LYS:O	37:DQ:98:LYS:NZ	2.26	0.64
39:DS:84:GLN:H	39:DS:111:GLU:HB2	1.62	0.64
1:CA:1032:G:H2'	1:CA:1033:G:C8	2.33	0.64
22:CV:16:A:H61	24:CX:36:U:H3	1.46	0.64
31:DG:5:VAL:HG22	31:DG:8:LYS:H	1.62	0.64
2:AB:83:MET:HB3	2:AB:234:PRO:HG2	1.80	0.64
26:BA:1093:G:H2'	26:BA:1156:G:H1	1.62	0.64
26:BA:176:G:OP2	61:BA:4468:HOH:O	2.14	0.64
37:DQ:85:LYS:HG2	47:D0:7:LEU:HB3	1.80	0.64
26:DA:2161:C:H2'	26:DA:2162:G:C8	2.33	0.64
28:BD:69:ARG:NH2	28:BD:128:GLY:O	2.30	0.64
35:BO:37:ASP:OD1	35:BO:109:LYS:NZ	2.30	0.64
26:DA:568:U:H5'	26:DA:945:A:N1	2.13	0.64
40:DT:95:ARG:HG2	40:DT:95:ARG:HH11	1.62	0.64
1:AA:11:G:O2'	1:AA:506:G:N2	2.31	0.63
25:AY:26:A:N6	25:AY:44:G:N1	2.43	0.63
53:B6:6:ARG:NH1	53:B6:26:ASN:HB2	2.12	0.63
32:BH:149:ARG:NH1	32:BH:167:GLU:OE2	2.32	0.63
1:CA:1318:A:OP1	19:CS:3:ARG:NH2	2.31	0.63
26:DA:918:A:N3	27:DB:80:U:O2'	2.28	0.63
31:DG:33:ARG:NH2	31:DG:162:THR:HG21	2.13	0.63
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.79	0.63
11:AK:98:LEU:O	11:AK:101:SER:OG	2.16	0.63
26:BA:747:G:O2'	26:BA:1679:A:N3	2.29	0.63
26:BA:2340:A:H2'	26:BA:2341:G:C8	2.33	0.63
26:BA:551:A:OP1	61:BA:4682:HOH:O	2.15	0.63
1:CA:1157:A:H4'	1:CA:1158:C:O5'	1.98	0.63
1:CA:148:G:H2'	1:CA:149:A:H8	1.63	0.63
48:D1:51:VAL:HG11	48:D1:74:VAL:HG21	1.80	0.63
26:DA:2893:G:H5'	26:DA:2893:G:H8	1.63	0.63
2:AB:178:ARG:HG2	8:AH:72:PRO:HA	1.78	0.63
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.62	0.63
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.80	0.63
26:BA:2644:A:HO2'	26:BA:2821:G:HO2'	1.43	0.63
27:BB:105:A:OP1	46:BZ:72:ARG:NH1	2.30	0.63
1:CA:683:G:O6	61:CA:4143:HOH:O	2.14	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.80	0.63
26:DA:1022:G:H22	26:DA:1142(A):A:H2	1.42	0.63
26:DA:248:G:OP1	61:DA:4415:HOH:O	2.16	0.63
1:AA:1157:A:H4'	1:AA:1158:C:O5'	1.98	0.63
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.25	0.63
55:B8:23:VAL:HG11	55:B8:47:LYS:HD3	1.80	0.63
26:BA:2044:U:OP1	61:BA:4666:HOH:O	2.15	0.63
1:CA:991:U:O2'	1:CA:992:U:O5'	2.14	0.63
26:DA:2143:C:H2'	26:DA:2144:U:O4'	1.98	0.63
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	1.99	0.63
25:AY:55:PSU:C2	25:AY:57:G:H5'	2.34	0.63
26:BA:650:G:O6	36:BP:107:LYS:NZ	2.31	0.63
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.80	0.63
1:CA:406:G:H21	4:CD:119:GLN:HE22	1.46	0.63
21:CU:5:ASP:O	21:CU:11:GLY:HA3	1.98	0.63
29:DE:111:ARG:HG3	29:DE:160:TYR:CD2	2.33	0.63
1:CA:266:G:H5''	1:CA:268:C:H41	1.64	0.63
12:CL:32:PHE:HB3	12:CL:84:LEU:HD11	1.81	0.63
26:DA:662:G:OP1	61:DA:4188:HOH:O	2.15	0.63
31:DG:113:ARG:NH1	31:DG:141:PHE:O	2.32	0.63
1:AA:557:G:OP1	61:AA:4076:HOH:O	2.16	0.63
55:B8:62:LEU:HB3	55:B8:65:GLU:HG3	1.80	0.63
3:CC:125:GLU:HG3	3:CC:190:ARG:O	1.99	0.63
1:CA:1347:G:H5''	9:CI:107:ARG:HB3	1.81	0.63
26:DA:2148:G:H2'	26:DA:2149:G:C8	2.34	0.63
26:DA:2537:U:H2'	26:DA:2538:C:C6	2.33	0.63
26:DA:2839:G:H5'	38:DR:46:GLY:HA2	1.79	0.63
26:DA:852:G:H2'	26:DA:853:G:H8	1.63	0.63
1:AA:1003:G:C2	1:AA:1004:A:H1'	2.34	0.63
1:AA:352:C:OP2	61:AA:4116:HOH:O	2.15	0.63
2:AB:127:ILE:HD12	2:AB:130:ARG:HD3	1.80	0.63
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.80	0.63
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.81	0.63
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.79	0.63
26:BA:1417:G:O6	61:BA:4345:HOH:O	2.12	0.63
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.13	0.63
25:CY:27:G:O6	25:CY:43:C:N3	2.32	0.63
32:DH:159:GLU:HG3	32:DH:169:VAL:HG11	1.80	0.63
1:AA:1047:G:H5''	14:AN:4:LYS:HD2	1.81	0.62
1:AA:346:G:C4	1:AA:347:G:H1'	2.33	0.62
26:BA:1219:A:H4'	26:BA:1220:U:OP1	1.98	0.62
26:BA:1410:G:OP2	48:B1:3:LYS:HG3	1.99	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:BD:12:SER:HB3	28:BD:208:LYS:HB3	1.80	0.62
29:BE:121:ASN:ND2	61:BE:411:HOH:O	2.22	0.62
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.81	0.62
3:CC:22:TRP:CG	3:CC:59:ARG:HD2	2.34	0.62
25:CY:50:U:O2	25:CY:64:A:N1	2.32	0.62
49:D2:65:ASN:OD1	49:D2:69:ARG:NH1	2.32	0.62
26:DA:2183:C:H2'	26:DA:2184:G:H8	1.63	0.62
26:DA:1803:A:O2'	28:DD:259:THR:HG21	1.98	0.62
31:DG:113:ARG:NH1	31:DG:139:LEU:O	2.32	0.62
1:AA:1030(A):G:O2'	1:AA:1030(C):G:N7	2.27	0.62
1:AA:157:G:H1	1:AA:164:U:H3	1.47	0.62
33:BI:92:VAL:HG11	33:BI:144:VAL:HG11	1.82	0.62
46:BZ:117:LEU:HD21	46:BZ:144:LEU:HD13	1.80	0.62
1:CA:1029:C:N4	1:CA:1032:G:H1	1.96	0.62
1:CA:1076:C:H6	1:CA:1076:C:H5'	1.62	0.62
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.13	0.62
13:CM:122:LYS:HD3	13:CM:123:ALA:H	1.64	0.62
26:DA:2273:A:H2'	26:DA:2274:A:C8	2.33	0.62
1:AA:1347:G:H5''	9:AI:107:ARG:HB3	1.81	0.62
26:BA:2701:U:H4'	26:BA:2702:C:H5'	1.82	0.62
38:BR:97:VAL:HG22	38:BR:114:VAL:HG13	1.82	0.62
1:CA:473:G:H2'	1:CA:474:G:H8	1.62	0.62
2:CB:19:HIS:HB2	2:CB:204:ASN:HB2	1.80	0.62
15:CO:11:VAL:HG21	15:CO:34:LEU:HD22	1.81	0.62
23:CW:47:U:O2'	23:CW:48:C:OP1	2.16	0.62
1:AA:56:U:H2'	1:AA:57:G:C8	2.34	0.62
7:AG:37:ASN:ND2	9:AI:39:GLY:O	2.32	0.62
15:AO:22:THR:OG1	15:AO:23:GLY:N	2.31	0.62
26:BA:1189:A:OP1	34:BN:25:ARG:NH2	2.32	0.62
26:BA:2840:G:O6	61:BA:5189:HOH:O	2.13	0.62
26:DA:1842:G:O2'	28:DD:253:GLN:NE2	2.32	0.62
38:DR:97:VAL:HG22	38:DR:114:VAL:HG13	1.80	0.62
1:CA:1054:C:N4	23:CW:34:G:H1'	2.14	0.62
1:CA:983:A:N1	1:CA:1222:G:N2	2.47	0.62
1:CA:1244:C:H42	1:CA:1293:G:H1	1.47	0.62
26:DA:880:G:N2	26:DA:898:C:H1'	2.14	0.62
1:AA:202:U:O2'	1:AA:203:U:O5'	2.16	0.62
1:AA:277:C:H5''	17:AQ:68:ARG:NH2	2.15	0.62
25:AY:22:G:N7	25:AY:46:7MG:O6	2.32	0.62
3:CC:20:SER:HB2	3:CC:40:ARG:HH12	1.65	0.62
12:CL:60:LEU:N	12:CL:64:TYR:O	2.25	0.62
23:CW:19:G:N2	23:CW:56:C:N3	2.45	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:406:G:OP2	61:AA:4123:HOH:O	2.15	0.62
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.81	0.62
26:BA:2902:G:O2'	26:BA:2903:G:OP2	2.14	0.62
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.81	0.62
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.64	0.62
25:CY:9:A:O2'	25:CY:10:G:N7	2.32	0.62
27:DB:106:G:H5'	46:DZ:31:ARG:HG2	1.82	0.62
8:AH:121:ASP:OD1	8:AH:125:ARG:NH2	2.32	0.62
23:AW:56:C:H5	26:BA:943:C:O4'	1.83	0.62
26:BA:2584:A:N7	29:BE:144:ARG:HD2	2.15	0.62
34:BN:15:LEU:HD12	34:BN:137:LYS:HG2	1.82	0.62
1:CA:1067:A:N3	1:CA:1068:G:H1'	2.15	0.62
1:CA:959:A:O2'	1:CA:984:C:O2'	2.17	0.62
2:CB:50:GLU:HG3	2:CB:200:ILE:O	1.98	0.62
13:CM:4:ILE:HG23	13:CM:22:ILE:HD11	1.82	0.62
1:AA:92:C:H2'	1:AA:93:G:C8	2.35	0.62
1:CA:1151:A:O2'	1:CA:1152:A:H8	1.82	0.62
13:CM:121:LYS:H	13:CM:121:LYS:NZ	1.97	0.62
1:AA:1007:C:H2'	1:AA:1008:C:H5''	1.81	0.62
2:AB:231:GLU:HB3	2:AB:232:PRO:CD	2.30	0.62
18:AR:38:GLU:HA	18:AR:41:LYS:HD3	1.82	0.62
30:BF:101:LEU:O	30:BF:106:ARG:NH1	2.32	0.62
1:CA:1126:U:H3	10:CJ:40:LEU:HD11	1.65	0.62
26:DA:882:G:N1	26:DA:894:C:N3	2.46	0.62
26:DA:900:A:H2'	26:DA:901:A:H8	1.65	0.62
31:DG:179:PRO:HB2	51:D4:42:PHE:HE1	1.64	0.62
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.35	0.61
26:BA:779:C:OP2	61:BA:4004:HOH:O	2.16	0.61
1:CA:977:A:O2'	1:CA:981:U:N3	2.33	0.61
26:DA:509:C:OP1	61:DA:4324:HOH:O	2.16	0.61
28:DD:132:PRO:HD3	28:DD:190:TYR:CZ	2.35	0.61
1:AA:1027:C:C2	1:AA:1034:G:N1	2.67	0.61
1:AA:953:G:H5'	1:AA:965:A:H61	1.65	0.61
2:AB:17:PHE:HD2	2:AB:44:LEU:HD21	1.65	0.61
24:AX:6:G:H1	24:AX:67:C:N4	1.97	0.61
26:BA:2190:G:C6	26:BA:2193:A:H8	2.18	0.61
27:BB:45:A:OP2	31:BG:96:ARG:NH2	2.28	0.61
1:CA:345:C:OP2	40:DT:39:ARG:NH2	2.30	0.61
25:CY:8:4SU:HN3	25:CY:14:A:N6	1.91	0.61
26:DA:373:U:H2'	26:DA:374:A:H8	1.65	0.61
27:DB:24:G:N3	27:DB:26:A:N6	2.48	0.61
27:DB:24:G:N7	27:DB:56:G:H2'	2.15	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DD:206:LEU:HD22	28:DD:211:ARG:HG2	1.81	0.61
1:AA:976:G:H5'	1:AA:1358:U:O2'	1.99	0.61
26:BA:2071:G:N7	61:BA:5165:HOH:O	2.31	0.61
26:DA:1261:C:OP2	43:DW:83:LYS:NZ	2.33	0.61
26:DA:2022:U:O2'	26:DA:2617:C:H5'	2.00	0.61
29:DE:52:LEU:O	29:DE:76:ARG:N	2.25	0.61
1:AA:677:U:H3	1:AA:713:G:H22	1.47	0.61
2:AB:74:LYS:NZ	2:AB:205:ASP:OD2	2.33	0.61
15:AO:79:ARG:O	15:AO:83:GLU:HB2	1.99	0.61
26:BA:1831:C:OP2	28:BD:183:ARG:NH2	2.32	0.61
1:CA:757:U:H2'	1:CA:758:G:O4'	1.99	0.61
25:CY:26:A:N1	25:CY:44:G:C6	2.69	0.61
36:DP:99:LEU:O	36:DP:103:ALA:N	2.32	0.61
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.65	0.61
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.36	0.61
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.61
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.66	0.61
26:BA:1847:G:O6	28:BD:35:LYS:NZ	2.28	0.61
26:BA:2227:G:H5'	26:BA:2228:G:N7	2.14	0.61
29:BE:111:ARG:HG3	29:BE:160:TYR:CD2	2.34	0.61
1:CA:1120:G:O6	1:CA:1154:G:N2	2.33	0.61
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.83	0.61
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.82	0.61
3:CC:52:LEU:HD21	3:CC:55:VAL:HG23	1.80	0.61
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.81	0.61
50:D3:12:PRO:HB2	50:D3:20:LYS:HG2	1.81	0.61
26:DA:2074:U:H2'	26:DA:2075:U:C6	2.36	0.61
26:DA:2431:U:OP1	61:DA:3906:HOH:O	2.16	0.61
1:AA:1027:C:H2'	1:AA:1028:C:C5	2.35	0.61
1:AA:189:G:H1	1:AA:189(K):U:H3	1.48	0.61
26:BA:1431:G:O2'	26:BA:1442:U:O2	2.14	0.61
1:CA:1148:U:H1'	9:CI:66:ARG:HH12	1.66	0.61
1:CA:985:C:N3	1:CA:1220:G:N2	2.46	0.61
3:CC:18:TRP:H	3:CC:18:TRP:HE3	1.47	0.61
3:CC:179:ARG:NH1	3:CC:206:GLU:OE1	2.33	0.61
50:D3:6:VAL:HG13	50:D3:56:VAL:HG22	1.81	0.61
44:DX:46:ALA:O	49:D2:30:ARG:NH2	2.33	0.61
46:DZ:117:LEU:HD12	46:DZ:174:VAL:HG22	1.80	0.61
26:BA:2362:C:OP2	61:BA:4049:HOH:O	2.16	0.61
41:BU:76:TYR:OH	41:BU:92:ARG:NH1	2.33	0.61
50:D3:5:LYS:NZ	50:D3:34:GLU:OE2	2.18	0.61
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.35	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:AC:39:ILE:HG23	3:AC:91:LEU:HD11	1.83	0.61
26:BA:2727:G:OP1	61:BA:4546:HOH:O	2.16	0.61
1:CA:952:U:H2'	1:CA:953:G:C8	2.36	0.61
10:CJ:27:ALA:HA	10:CJ:81:THR:HG22	1.83	0.61
25:CY:5:G:H1	25:CY:68:C:N4	1.99	0.61
26:DA:1220:A:OP2	41:DU:19:LYS:NZ	2.29	0.61
26:DA:958:U:OP2	37:DQ:14:ARG:NH1	2.33	0.61
26:DA:952:G:OP1	37:DQ:16:ARG:NH2	2.33	0.61
38:DR:33:ARG:NH1	38:DR:115:GLU:OE2	2.29	0.61
26:DA:301:G:OP2	45:DY:84:ARG:NH2	2.33	0.61
1:AA:166:G:H2'	1:AA:167:G:H8	1.65	0.61
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.82	0.61
37:BQ:85:LYS:HG2	47:B0:7:LEU:HB3	1.83	0.61
1:CA:692:U:O2'	1:CA:694:A:N7	2.31	0.61
1:CA:920:U:H2'	1:CA:921:U:C6	2.35	0.61
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.83	0.61
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.64	0.61
1:CA:1317:C:O2	19:CS:37:ARG:NH1	2.33	0.61
26:DA:1939:U:OP1	26:DA:2604:U:O2'	2.19	0.61
26:DA:526:A:OP1	61:DA:4194:HOH:O	2.16	0.61
27:DB:110:G:H2'	27:DB:111:G:C8	2.36	0.61
1:AA:1025:U:O2'	1:AA:1026:G:O4'	2.19	0.61
26:BA:553:A:C2'	26:BA:554:A:H5''	2.31	0.61
43:BW:14:PRO:HG2	43:BW:78:GLU:HG2	1.82	0.61
1:CA:1067:A:O2'	1:CA:1068:G:OP2	2.17	0.61
1:CA:957:U:H2'	1:CA:959:A:OP2	2.01	0.61
26:DA:2126:A:N3	26:DA:2127:G:H1'	2.16	0.61
40:DT:85:LYS:NZ	40:DT:87:ASP:OD2	2.28	0.61
2:AB:55:PHE:HA	2:AB:58:ILE:HB	1.83	0.60
26:BA:2804:C:H2'	26:BA:2805:G:C8	2.36	0.60
1:CA:646:U:H2'	1:CA:647:C:C6	2.36	0.60
2:CB:47:THR:O	2:CB:51:LEU:N	2.32	0.60
9:CI:16:ARG:HB2	9:CI:64:THR:HB	1.82	0.60
26:DA:2046:G:H5'	52:D5:19:ARG:HA	1.83	0.60
26:DA:1005:C:H2'	26:DA:1006:C:C6	2.36	0.60
26:DA:2708:G:H1'	38:DR:71:GLN:HE22	1.65	0.60
13:AM:80:ARG:HH22	19:AS:69:HIS:HE1	1.48	0.60
26:BA:1249:A:H2	26:BA:1287:A:H62	1.49	0.60
29:BE:9:VAL:HB	40:BT:3:ARG:HG2	1.82	0.60
30:BF:143:ALA:HB1	30:BF:148:LEU:HB2	1.82	0.60
39:BS:56:LEU:HD12	39:BS:69:VAL:HG12	1.82	0.60
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.36	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1816:G:O6	28:DD:35:LYS:NZ	2.25	0.60
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.82	0.60
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.35	0.60
48:B1:51:VAL:HG11	48:B1:74:VAL:HG21	1.84	0.60
27:BB:33:G:H5'	31:BG:2:PRO:HD3	1.83	0.60
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.36	0.60
1:CA:148:G:H2'	1:CA:149:A:C8	2.37	0.60
38:DR:56:LYS:NZ	38:DR:90:ARG:O	2.33	0.60
46:DZ:7:ALA:HB3	46:DZ:61:LEU:HD12	1.81	0.60
1:AA:413:G:N2	1:AA:428:G:H1'	2.16	0.60
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	1.83	0.60
17:AQ:67:LYS:HA	17:AQ:70:ARG:HH12	1.66	0.60
51:B4:57:GLU:HB3	51:B4:58:ARG:HA	1.83	0.60
29:BE:29:GLY:HA3	61:BE:408:HOH:O	2.01	0.60
31:BG:47:LYS:HG3	31:BG:48:GLU:H	1.66	0.60
45:BY:92:ASN:N	45:BY:93:GLY:HA2	2.16	0.60
9:CI:23:ASN:ND2	9:CI:60:ASP:OD2	2.33	0.60
26:DA:1449:A:HO2'	26:DA:1529:G:H21	1.45	0.60
26:DA:1739:U:HO2'	26:DA:1740:G:H8	1.49	0.60
26:DA:954:G:H5''	37:DQ:13:GLN:HB3	1.83	0.60
1:AA:865:A:H2	1:AA:918:A:H4'	1.67	0.60
3:AC:150:LYS:HG3	3:AC:169:ALA:HB2	1.84	0.60
25:AY:59:U:H3'	25:AY:60:U:C6	2.35	0.60
28:BD:71:ASP:HB3	28:BD:103:ARG:NH2	2.16	0.60
36:BP:26:GLY:O	61:BP:311:HOH:O	2.16	0.60
1:CA:1120:G:C6	1:CA:1154:G:N2	2.69	0.60
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.35	0.60
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.02	0.60
11:CK:98:LEU:O	11:CK:101:SER:OG	2.19	0.60
46:DZ:159:PRO:HA	46:DZ:161:VAL:HG12	1.84	0.60
2:AB:201:ILE:HG21	2:AB:214:ILE:HG21	1.82	0.60
1:CA:9:G:H2'	1:CA:10:A:H8	1.66	0.60
48:D1:23:LYS:HB3	48:D1:29:GLY:HA3	1.84	0.60
26:DA:2400:G:O3'	53:D6:18:ARG:NH1	2.34	0.60
46:DZ:53:ILE:HG22	46:DZ:71:VAL:O	2.02	0.60
1:AA:1026:G:O6	1:AA:1034:G:N2	2.32	0.60
4:AD:108:LEU:HD13	4:AD:174:LEU:HD13	1.83	0.60
25:AY:19:G:H1	25:AY:56:C:N4	2.00	0.60
51:B4:53:GLU:O	51:B4:55:ARG:N	2.34	0.60
26:BA:2880:C:H2'	26:BA:2881:C:O4'	2.02	0.60
1:CA:1075:C:H2'	1:CA:1076:C:H5''	1.84	0.60
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.67	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1226:A:OP1	42:DV:84:LYS:HE2	2.01	0.60
26:DA:1007:C:OP1	34:DN:35:ARG:NH1	2.34	0.60
1:AA:662:G:H2'	1:AA:663:A:C8	2.37	0.60
19:AS:28:LYS:HZ2	19:AS:28:LYS:HB3	1.66	0.60
26:BA:2055:A:OP1	61:BA:4308:HOH:O	2.17	0.60
26:BA:2459:G:OP2	61:BA:4563:HOH:O	2.16	0.60
1:CA:662:G:H2'	1:CA:663:A:H8	1.67	0.60
26:DA:1693:U:O2'	28:DD:14:ARG:NH2	2.35	0.60
26:DA:2291:U:H2'	26:DA:2292:C:C6	2.37	0.60
26:DA:2747:G:H1	26:DA:2754:U:H2'	1.66	0.60
26:DA:774:A:N6	61:DA:3733:HOH:O	2.35	0.60
26:BA:927:G:N2	26:BA:944:C:O2	2.35	0.60
23:AW:56:C:P	26:BA:943:C:H5'	2.42	0.60
32:BH:25:LYS:HG2	32:BH:34:GLU:HG2	1.84	0.60
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.34	0.60
18:CR:60:ALA:O	18:CR:64:ARG:HG3	2.02	0.60
26:DA:2808:U:C2'	26:DA:2809:A:H5'	2.32	0.60
32:DH:20:ALA:HB1	32:DH:21:PRO:HD2	1.84	0.60
36:DP:38:GLN:O	36:DP:39:LYS:HB3	2.02	0.60
26:BA:1094:A:OP2	26:BA:1155:C:N4	2.30	0.60
1:CA:1505:G:HO2'	22:CV:13:A:H2	1.49	0.60
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.27	0.60
36:DP:59:LEU:HD21	55:D8:10:ALA:HA	1.82	0.60
26:DA:1247:A:OP1	30:DF:95:ARG:NH2	2.32	0.60
26:DA:2136:C:O2'	26:DA:2137:C:H6	1.85	0.60
26:DA:2499:C:N3	61:DA:3930:HOH:O	2.31	0.60
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.35	0.59
26:BA:1464:G:OP2	61:BA:4580:HOH:O	2.16	0.59
26:BA:2177:G:H2'	26:BA:2178:G:O4'	2.01	0.59
26:BA:2227:G:H3'	26:BA:2228:G:C8	2.37	0.59
26:BA:2881:C:N3	61:BA:4781:HOH:O	2.31	0.59
28:BD:132:PRO:HG2	28:BD:135:PHE:CD2	2.37	0.59
40:BT:118:ARG:HH22	40:BT:125:ARG:HH12	1.50	0.59
46:BZ:139:VAL:HG22	46:BZ:155:LEU:HD11	1.84	0.59
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.84	0.59
14:CN:6:LEU:HB3	14:CN:23:ARG:HH21	1.67	0.59
26:DA:2638:G:P	29:DE:82:ARG:HH22	2.25	0.59
26:DA:247:G:H4'	26:DA:386:G:C5	2.36	0.59
30:DF:116:ASP:OD2	36:DP:1:MET:N	2.24	0.59
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.67	0.59
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	1.84	0.59
26:BA:1218:G:O2'	26:BA:1219:A:O5'	2.20	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:944:C:H2'	26:BA:945:A:C8	2.37	0.59
31:BG:5:VAL:HG22	31:BG:8:LYS:H	1.67	0.59
32:BH:56:SER:HB3	32:BH:61:HIS:ND1	2.17	0.59
22:CV:14:A:C4	25:CY:34:G:C6	2.90	0.59
26:DA:1434:A:H61	26:DA:1558:A:H62	1.49	0.59
26:DA:2846:G:N7	61:DA:4073:HOH:O	2.32	0.59
31:DG:151:ALA:HB3	31:DG:153:ARG:HH11	1.66	0.59
42:DV:76:LYS:HB2	42:DV:81:TYR:HB3	1.83	0.59
1:AA:200:G:H1	1:AA:217:C:H42	1.51	0.59
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.25	0.59
31:BG:15:VAL:HG21	31:BG:176:LEU:HD23	1.82	0.59
46:BZ:150:LEU:O	46:BZ:171:ILE:HG13	2.03	0.59
1:CA:113:G:OP1	61:CA:4148:HOH:O	2.17	0.59
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.17	0.59
1:CA:539:A:H2'	1:CA:540:G:C8	2.37	0.59
1:CA:596:C:O2	1:CA:644:G:N2	2.17	0.59
3:CC:134:ILE:HD11	3:CC:153:VAL:HG21	1.83	0.59
13:CM:65:LYS:N	51:D4:50:VAL:HG21	2.18	0.59
14:CN:32:SER:OG	14:CN:32:SER:O	2.19	0.59
23:CW:14:A:H61	23:CW:21:A:H2	1.49	0.59
23:CW:61:C:O2'	23:CW:62:C:O5'	2.14	0.59
37:DQ:85:LYS:HB2	47:D0:7:LEU:HD12	1.83	0.59
1:CA:1495:U:O2'	26:DA:1919:A:N1	2.31	0.59
26:DA:1800:C:OP2	28:DD:183:ARG:NH2	2.35	0.59
36:DP:85:LEU:HA	36:DP:88:LEU:HD12	1.85	0.59
46:DZ:105:VAL:N	46:DZ:139:VAL:O	2.35	0.59
3:AC:19:GLU:HB3	3:AC:40:ARG:HH22	1.67	0.59
1:AA:428:G:OP2	4:AD:10:ARG:NH1	2.35	0.59
25:AY:59:U:H3'	25:AY:60:U:H6	1.68	0.59
26:BA:2125:C:N4	26:BA:2208:G:H1	1.98	0.59
1:CA:254:G:OP1	17:CQ:66:SER:OG	2.17	0.59
1:CA:538:G:H5''	12:CL:114:LYS:HB2	1.82	0.59
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.85	0.59
51:D4:33:VAL:HG12	51:D4:35:VAL:H	1.66	0.59
26:DA:1446:C:H42	26:DA:1465:G:H1	1.50	0.59
30:DF:185:ASP:HA	30:DF:188:ARG:HD3	1.84	0.59
34:DN:58:ASP:OD1	34:DN:58:ASP:N	2.34	0.59
46:DZ:108:PRO:HG3	46:DZ:141:VAL:HB	1.84	0.59
1:AA:189(A):C:H42	1:AA:189(J):G:H1	1.51	0.59
1:AA:736:C:H2'	1:AA:737:A:C8	2.37	0.59
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.20	0.59
3:AC:82:GLU:HG2	3:AC:85:ARG:NH2	2.17	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:AC:8:ILE:HD13	3:AC:184:TYR:HB3	1.84	0.59
26:BA:273:G:H4'	26:BA:274:U:OP1	2.01	0.59
26:DA:2023:G:H5'	26:DA:2617:C:H4'	1.83	0.59
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.35	0.59
9:AI:21:PRO:HA	9:AI:59:PHE:HA	1.85	0.59
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.85	0.59
23:AW:22:G:O2'	23:AW:23:A:OP1	2.18	0.59
50:B3:23:LEU:HD13	50:B3:50:VAL:HG11	1.85	0.59
26:BA:1086:C:H2'	26:BA:1087:C:O4'	2.01	0.59
26:BA:1071:G:C4	26:BA:1180:C:H1'	2.37	0.59
26:BA:1696:G:O2'	38:BR:107:ASP:OD2	2.17	0.59
26:DA:2140:C:H1'	26:DA:2152:G:N2	2.18	0.59
26:DA:2002:G:OP2	38:DR:9:LYS:NZ	2.35	0.59
1:AA:1002:G:H3'	1:AA:1003:G:C8	2.38	0.59
19:AS:32:LYS:HA	19:AS:50:ALA:HB3	1.84	0.59
26:BA:693:G:O6	26:BA:697:C:N4	2.30	0.59
39:BS:15:ARG:O	39:BS:19:LYS:HG2	2.03	0.59
23:CW:11:C:H42	23:CW:24:G:H1	1.50	0.59
25:CY:18:G:N2	25:CY:55:PSU:C4	2.71	0.59
50:D3:7:LYS:NZ	50:D3:32:GLN:O	2.29	0.59
26:DA:2176:A:H2'	26:DA:2177:C:C6	2.37	0.59
37:DQ:31:ASP:OD1	37:DQ:134:ARG:NH1	2.32	0.59
25:AY:58:A:H3'	25:AY:58:A:P	2.43	0.59
26:BA:1451:U:H2'	26:BA:1452:U:C6	2.38	0.59
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.36	0.59
26:DA:271(R):G:H5''	48:D1:97:LEU:HD21	1.84	0.59
31:DG:101:ILE:HD13	51:D4:25:TYR:HB2	1.84	0.59
26:DA:2062:A:OP1	61:DA:3829:HOH:O	2.17	0.59
1:AA:1239:A:H62	1:AA:1299:A:N6	2.01	0.59
23:AW:5:G:H2'	23:AW:6:G:H8	1.67	0.59
1:CA:1010:G:C2	1:CA:1011:G:C8	2.91	0.59
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.84	0.59
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.02	0.59
26:DA:2173:A:H2'	26:DA:2174:C:O4'	2.03	0.59
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.49	0.59
19:AS:30:LEU:HD11	19:AS:50:ALA:HB2	1.85	0.59
26:BA:1935:A:H4'	26:BA:1936:C:H5''	1.83	0.59
26:BA:346:A:OP1	30:BF:168:ARG:HD2	2.03	0.59
15:CO:18:PHE:HB2	15:CO:19:PRO:HD2	1.85	0.59
26:DA:2112:G:C5	26:DA:2113:U:H1'	2.37	0.59
26:DA:249:C:O2	55:D8:12:LYS:NZ	2.29	0.59
31:DG:64:THR:HB	31:DG:94:LEU:HD21	1.85	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:DZ:55:HIS:HE1	46:DZ:135:GLU:HG3	1.68	0.59
21:AU:5:ASP:OD2	61:AU:101:HOH:O	2.17	0.58
26:BA:2802:C:O2	26:BA:2903:G:N2	2.35	0.58
1:CA:1220:G:O3'	19:CS:36:ARG:HD3	2.03	0.58
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.37	0.58
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.36	0.58
8:CH:4:ASP:OD1	8:CH:7:ALA:N	2.23	0.58
26:DA:2151:G:H2'	26:DA:2152:G:H8	1.67	0.58
26:DA:848:G:N3	26:DA:933:A:H1'	2.18	0.58
45:DY:5:MET:HE1	45:DY:32:PRO:HA	1.84	0.58
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.35	0.58
1:AA:17:U:H2'	1:AA:18:C:C6	2.38	0.58
2:AB:162:ILE:O	2:AB:185:ILE:HG12	2.03	0.58
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	1.85	0.58
26:BA:551:A:O2'	26:BA:2065:C:O2	2.20	0.58
26:BA:661:G:OP1	36:BP:132:LYS:HE2	2.02	0.58
1:CA:1338:G:H21	24:CX:41:C:H1'	1.68	0.58
4:CD:64:LEU:HB2	4:CD:198:VAL:HG11	1.84	0.58
26:DA:2849:U:OP2	40:DT:95:ARG:NH1	2.37	0.58
37:DQ:111:GLU:O	37:DQ:115:MET:HG2	2.02	0.58
25:AY:53:G:C5	25:AY:54:5MU:H72	2.38	0.58
53:B6:6:ARG:NE	53:B6:24:GLU:OE1	2.22	0.58
1:CA:1204:A:OP1	14:CN:3:ARG:NH1	2.36	0.58
17:CQ:57:VAL:HG12	17:CQ:76:LEU:HA	1.84	0.58
37:DQ:48:GLU:OE1	37:DQ:51:ARG:NH2	2.33	0.58
39:DS:14:VAL:O	39:DS:18:ILE:HG12	2.03	0.58
1:AA:46:G:O6	61:AA:4200:HOH:O	2.15	0.58
23:AW:66:U:H2'	23:AW:67:C:H6	1.66	0.58
26:BA:1067:A:H62	26:BA:1186:U:H3	1.51	0.58
1:CA:504:C:OP1	61:CA:4008:HOH:O	2.17	0.58
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	1.85	0.58
35:DO:115:VAL:HG13	35:DO:121:VAL:HG21	1.86	0.58
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.38	0.58
23:AW:47:U:O2'	23:AW:48:C:OP1	2.20	0.58
26:BA:2348:A:H61	47:B0:43:THR:CG2	2.16	0.58
26:BA:2497:G:OP1	37:BQ:46:GLN:NE2	2.35	0.58
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	1.84	0.58
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.85	0.58
24:CX:50:U:H3	24:CX:64:G:H1	1.51	0.58
26:DA:2365:G:O6	55:D8:43:GLN:NE2	2.36	0.58
30:DF:21:ALA:HB3	30:DF:22:ALA:HA	1.84	0.58
1:AA:1302:U:C5	13:AM:17:VAL:HG21	2.38	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:173:C:H2'	26:BA:174:U:C6	2.38	0.58
1:CA:420:U:O2'	1:CA:423:G:O6	2.18	0.58
1:CA:48:C:OP2	61:CA:4100:HOH:O	2.16	0.58
26:DA:900:A:H2'	26:DA:901:A:C8	2.39	0.58
32:DH:3:ARG:NH1	32:DH:3:ARG:HB3	2.18	0.58
32:DH:73:ALA:O	32:DH:76:VAL:HG12	2.03	0.58
1:AA:1125:U:H1'	1:AA:1126:U:H2'	1.86	0.58
1:AA:473:G:H2'	1:AA:474:G:C8	2.39	0.58
46:BZ:24:LEU:HB2	46:BZ:41:LEU:HD23	1.85	0.58
2:CB:178:ARG:HE	8:CH:74:PRO:HG3	1.68	0.58
6:CF:24:GLU:HG3	6:CF:28:ARG:NH1	2.19	0.58
26:DA:1952:A:OP1	35:DO:42:SER:OG	2.21	0.58
26:DA:2137:C:H2'	26:DA:2138:C:C6	2.38	0.58
26:BA:2166:U:O2'	26:BA:2167:C:H2'	2.04	0.58
26:BA:2671:G:O2'	32:BH:175:LYS:NZ	2.37	0.58
26:BA:918:U:OP1	37:BQ:5:ARG:HD3	2.04	0.58
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.19	0.58
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.14	0.58
1:CA:473:G:H2'	1:CA:474:G:C8	2.39	0.58
15:CO:3:ILE:H	15:CO:3:ILE:HD13	1.67	0.58
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.04	0.58
26:DA:1300:U:H4'	26:DA:1301:A:H5''	1.86	0.58
26:DA:2318:G:H21	39:DS:3:ARG:HD2	1.69	0.58
26:DA:2438:U:O2'	26:DA:2440:C:OP1	2.20	0.58
46:DZ:117:LEU:HA	46:DZ:174:VAL:HA	1.86	0.58
1:AA:473:G:H2'	1:AA:474:G:H8	1.69	0.58
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.33	0.58
4:AD:111:ALA:HB2	4:AD:120:LEU:HD12	1.86	0.58
23:AW:28:G:H2'	23:AW:29:G:H8	1.67	0.58
26:BA:848:G:O6	30:BF:53:THR:OG1	2.20	0.58
38:BR:56:LYS:NZ	38:BR:90:ARG:O	2.36	0.58
26:DA:1253:A:N6	61:DA:3721:HOH:O	2.33	0.58
26:DA:2646:C:OP2	26:DA:2732:G:O2'	2.15	0.58
26:DA:997:G:OP1	41:DU:92:ARG:HG2	2.04	0.58
1:AA:347:G:H2'	1:AA:348:G:O4'	2.03	0.58
1:AA:727:G:N2	1:AA:730:G:OP2	2.36	0.58
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.86	0.58
13:AM:40:ASN:O	13:AM:43:THR:OG1	2.21	0.58
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.03	0.58
26:BA:327:U:O4	61:BA:4677:HOH:O	2.13	0.58
1:CA:1277:C:O2'	1:CA:1279:A:H8	1.86	0.58
1:CA:1422:G:O3'	35:DO:49:ARG:NH1	2.33	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:971:G:OP2	1:CA:1231:G:N2	2.26	0.58
9:CI:5:TYR:O	9:CI:87:GLN:NE2	2.37	0.58
25:CY:40:C:C2'	25:CY:41:C:H5'	2.34	0.58
48:D1:76:ARG:HH11	48:D1:97:LEU:HD22	1.67	0.58
50:B3:18:ASP:N	50:B3:18:ASP:OD1	2.37	0.57
26:BA:589:U:H5''	36:BP:29:LYS:HE3	1.86	0.57
33:BI:129:THR:HG22	33:BI:139:GLN:NE2	2.17	0.57
46:BZ:138:GLU:H	46:BZ:156:LYS:HD3	1.69	0.57
1:CA:1153:C:H42	1:CA:1154:G:N2	2.01	0.57
1:CA:995:C:O2	14:CN:4:LYS:NZ	2.28	0.57
26:DA:465:G:OP1	54:D7:12:ARG:NH2	2.37	0.57
7:AG:113:GLU:HG2	7:AG:119:ARG:HG2	1.86	0.57
9:AI:117:HIS:HB2	9:AI:121:ARG:HG3	1.85	0.57
25:AY:38:A:H2'	25:AY:39:PSU:O4'	2.04	0.57
26:BA:1212:C:H2'	26:BA:1213:U:C6	2.39	0.57
26:BA:2442:A:N3	26:BA:2442:A:H2'	2.18	0.57
27:BB:75:G:H8	27:BB:75:G:H5''	1.69	0.57
1:CA:34:C:H2'	1:CA:35:G:H8	1.69	0.57
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.85	0.57
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.86	0.57
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.04	0.57
23:AW:5:G:H2'	23:AW:6:G:C8	2.39	0.57
33:BI:140:LEU:HD22	33:BI:142:VAL:HG13	1.86	0.57
38:DR:33:ARG:NH2	52:D5:57:VAL:O	2.29	0.57
26:DA:2110:G:OP1	26:DA:2118:U:N3	2.33	0.57
26:DA:399:G:OP2	61:DA:4406:HOH:O	2.17	0.57
26:DA:322:A:OP2	30:DF:169:ASN:HB2	2.04	0.57
1:AA:224:C:H2'	1:AA:225:C:C6	2.38	0.57
1:AA:757:U:H2'	1:AA:758:G:O4'	2.04	0.57
2:AB:16:HIS:HD2	2:AB:17:PHE:N	2.00	0.57
5:AE:78:HIS:HD1	8:AH:104:ARG:HD2	1.68	0.57
10:AJ:5:ARG:O	10:AJ:98:ILE:HA	2.05	0.57
25:AY:63:G:H2'	25:AY:64:A:O4'	2.04	0.57
26:BA:939:C:H2'	26:BA:940:C:C6	2.39	0.57
41:BU:89:GLU:HG3	42:BV:50:PRO:HB3	1.86	0.57
1:CA:1026:G:O6	1:CA:1036:G:N2	2.37	0.57
1:CA:975:A:N1	10:CJ:48:THR:HB	2.19	0.57
5:CE:137:GLU:HG2	5:CE:140:ARG:HH11	1.68	0.57
15:CO:82:ILE:HB	15:CO:87:ILE:HB	1.87	0.57
26:DA:1359:A:H61	26:DA:1372:U:H3	1.52	0.57
26:DA:1448:G:H4'	26:DA:1542:A:OP1	2.05	0.57
26:DA:2630:G:H2'	26:DA:2631:G:C8	2.39	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DD:132:PRO:HG2	28:DD:135:PHE:CD2	2.40	0.57
1:AA:1392:G:N2	1:AA:1502:A:H8	2.01	0.57
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.69	0.57
31:BG:170:ARG:NH2	31:BG:182:LYS:O	2.37	0.57
26:BA:2346:G:H5'	39:BS:9:ARG:HG2	1.85	0.57
1:CA:942:G:H21	9:CI:124:GLN:NE2	2.01	0.57
47:D0:10:THR:HG22	47:D0:12:ASN:H	1.70	0.57
26:DA:1264:G:OP1	52:D5:19:ARG:NH2	2.35	0.57
26:DA:1593:G:H2'	26:DA:1594:G:C8	2.40	0.57
26:DA:1853:A:H2'	26:DA:1854:A:C8	2.40	0.57
26:DA:531:C:H4'	26:DA:532:A:H5''	1.86	0.57
26:DA:903:C:H2'	26:DA:904:C:C6	2.40	0.57
27:DB:3:C:H2'	27:DB:4:C:C6	2.40	0.57
48:B1:3:LYS:HB2	48:B1:61:ARG:HH12	1.69	0.57
49:B2:65:ASN:OD1	49:B2:69:ARG:NH1	2.35	0.57
27:BB:14:U:OP2	27:BB:70:C:O2'	2.20	0.57
1:CA:1099:G:OP2	2:CB:144:ARG:NH2	2.34	0.57
2:CB:63:MET:HG3	2:CB:225:ALA:HB1	1.86	0.57
10:CJ:64:GLU:OE2	10:CJ:66:ARG:NH1	2.37	0.57
26:DA:1209:G:O2'	26:DA:1237:A:N1	2.32	0.57
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.70	0.57
26:BA:2023:A:OP1	38:BR:9:LYS:NZ	2.36	0.57
26:BA:30:G:OP2	41:BU:5:LYS:NZ	2.29	0.57
26:BA:925:A:H61	26:BA:945:A:H1'	1.70	0.57
31:BG:144:ILE:HA	31:BG:148:MET:HE1	1.87	0.57
32:BH:113:VAL:HG11	32:BH:151:ILE:HD13	1.86	0.57
4:CD:173:TRP:HB3	4:CD:187:ARG:HE	1.70	0.57
15:CO:55:GLY:HA2	15:CO:58:MET:HE2	1.86	0.57
25:CY:2:C:H2'	25:CY:3:C:C6	2.39	0.57
27:DB:41:U:H5	31:DG:70:VAL:H	1.51	0.57
46:DZ:7:ALA:O	46:DZ:62:PRO:HD3	2.05	0.57
26:BA:2228:G:O2'	26:BA:2229:A:OP1	2.21	0.57
26:BA:602:G:H2'	26:BA:603:C:C6	2.40	0.57
1:CA:992:U:H3	1:CA:1044:A:H62	1.53	0.57
26:DA:1013:C:H2'	26:DA:1014:U:H6	1.69	0.57
26:DA:1857:G:O2'	26:DA:1885:A:N6	2.35	0.57
26:DA:658:C:H2'	26:DA:659:C:C6	2.40	0.57
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.40	0.57
1:AA:69:G:H2'	1:AA:70:G:C8	2.39	0.57
1:AA:993:G:H2'	1:AA:995:C:H41	1.69	0.57
26:BA:599:U:H2'	26:BA:600:G:C8	2.39	0.57
30:BF:24:LEU:HD23	30:BF:115:ALA:HA	1.87	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:BG:161:THR:HG22	31:BG:163:ALA:H	1.70	0.57
45:BY:54:LYS:H	45:BY:56:PRO:HD3	1.70	0.57
1:CA:1000:U:N3	1:CA:1041:A:N6	2.22	0.57
6:CF:25:ILE:HD13	6:CF:82:ARG:HE	1.70	0.57
11:CK:48:ILE:O	11:CK:50:TYR:N	2.37	0.57
14:CN:24:CYS:O	14:CN:28:GLY:N	2.30	0.57
24:CX:67:C:H2'	24:CX:68:C:H5'	1.86	0.57
25:CY:27:G:N1	25:CY:43:C:O2	2.38	0.57
26:DA:197:A:O2'	61:DA:3732:HOH:O	2.16	0.57
36:DP:44:GLY:CA	36:DP:45:LEU:HB2	2.33	0.57
38:DR:67:LEU:HD13	38:DR:76:VAL:HG21	1.86	0.57
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.37	0.57
14:AN:3:ARG:HH21	14:AN:3:ARG:HB3	1.70	0.57
25:AY:59:U:H5'	25:AY:60:U:H5	1.70	0.57
37:BQ:135:ASP:OD2	46:BZ:49:ARG:NH2	2.38	0.57
1:CA:1086:U:H3	1:CA:1099:G:H22	1.53	0.57
2:CB:178:ARG:NE	8:CH:74:PRO:HG3	2.20	0.57
26:DA:2875:C:O2'	40:DT:2:ASN:OD1	2.21	0.57
32:DH:80:SER:OG	32:DH:81:GLU:OE1	2.17	0.57
46:DZ:45:ASP:OD1	46:DZ:49:ARG:NH1	2.31	0.57
1:AA:1166:G:N2	1:AA:1170:A:OP2	2.38	0.56
26:BA:927:G:H2'	26:BA:928:G:H8	1.69	0.56
26:BA:1830:G:O2'	28:BD:181:GLU:OE2	2.22	0.56
40:BT:112:ARG:HG3	40:BT:115:ARG:HH21	1.70	0.56
44:BX:43:VAL:HG21	44:BX:81:VAL:HG11	1.86	0.56
1:CA:1321:C:H4'	13:CM:87:TYR:CE2	2.40	0.56
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.87	0.56
26:DA:2808:U:H2'	26:DA:2809:A:H5'	1.87	0.56
44:DX:31:HIS:CD2	44:DX:33:LYS:H	2.22	0.56
1:AA:977:A:N6	1:AA:1224:G:OP1	2.29	0.56
7:AG:22:LEU:HD11	7:AG:101:LEU:HD21	1.85	0.56
46:BZ:45:ASP:OD2	46:BZ:49:ARG:NH1	2.38	0.56
1:CA:953:G:H5'	1:CA:965:A:N6	2.20	0.56
3:CC:11:ARG:HB3	3:CC:15:THR:HB	1.87	0.56
25:CY:9:A:OP2	25:CY:13:C:N4	2.38	0.56
26:DA:1864:U:OP1	26:DA:2410:G:O2'	2.17	0.56
40:DT:53:ARG:HH11	40:DT:53:ARG:HB3	1.70	0.56
46:DZ:69:THR:HG22	46:DZ:90:VAL:HA	1.88	0.56
1:CA:1154:G:N7	1:CA:1155:G:C8	2.73	0.56
3:CC:126:ARG:HB3	3:CC:128:PHE:CE1	2.40	0.56
13:AM:23:TYR:HB3	13:AM:67:GLU:HA	1.87	0.56
1:AA:333:G:H4'	20:AT:16:HIS:CE1	2.41	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:BZ:137:ILE:HA	46:BZ:156:LYS:NZ	2.20	0.56
1:CA:1502:A:H2	1:CA:1505:G:N1	1.99	0.56
1:CA:426:G:OP1	4:CD:36:ARG:HD2	2.05	0.56
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	1.87	0.56
23:CW:30:G:H1	23:CW:40:C:H42	1.51	0.56
26:DA:2167:U:H2'	26:DA:2168:G:H21	1.68	0.56
26:DA:866:A:H2	26:DA:867:C:C4	2.23	0.56
33:DI:110:ASP:N	33:DI:130:TYR:OH	2.34	0.56
1:AA:952:U:H2'	1:AA:953:G:C8	2.41	0.56
2:AB:17:PHE:HB2	2:AB:44:LEU:HD21	1.88	0.56
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.70	0.56
24:AX:8:4SU:H6	24:AX:8:4SU:O5'	2.05	0.56
44:BX:5:TYR:CZ	49:B2:30:ARG:HB2	2.40	0.56
26:BA:1298:G:OP1	41:BU:36:ARG:NH2	2.39	0.56
26:BA:479:C:O2	26:BA:483:A:O2'	2.22	0.56
1:CA:222:U:H2'	1:CA:223:U:C6	2.39	0.56
20:CT:63:ILE:HD13	20:CT:80:ARG:HB3	1.88	0.56
26:DA:1405:U:H2'	26:DA:1406:U:C6	2.40	0.56
27:DB:110:G:H2'	27:DB:111:G:H8	1.70	0.56
46:DZ:141:VAL:HG12	46:DZ:144:LEU:HD12	1.87	0.56
1:AA:96:U:O2'	1:AA:97:G:H8	1.88	0.56
13:AM:84:ILE:HD12	19:AS:74:PHE:HE2	1.70	0.56
46:BZ:111:VAL:HG21	46:BZ:117:LEU:HB2	1.88	0.56
9:CI:49:PRO:HG2	9:CI:81:ILE:HG23	1.87	0.56
26:DA:1579:A:H2'	26:DA:1580:A:C8	2.41	0.56
26:DA:1805:U:O2	28:DD:50:THR:HB	2.05	0.56
26:DA:534:U:H2'	26:DA:535:C:C6	2.41	0.56
1:AA:58:C:O2'	1:AA:388:G:N7	2.33	0.56
5:AE:6:PHE:HB2	5:AE:34:VAL:HG22	1.88	0.56
26:BA:2720:G:H1'	38:BR:71:GLN:HE22	1.70	0.56
31:BG:16:ARG:HB2	31:BG:17:PRO:HD3	1.88	0.56
46:BZ:121:HIS:HB2	46:BZ:171:ILE:HG22	1.88	0.56
1:CA:9:G:H2'	1:CA:10:A:C8	2.41	0.56
1:CA:1392:G:N2	1:CA:1502:A:H8	2.03	0.56
8:CH:12:ARG:HD2	8:CH:26:VAL:HG12	1.88	0.56
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.88	0.56
26:DA:1507:A:O2'	26:DA:1508:A:O5'	2.20	0.56
26:DA:1639:U:H2'	26:DA:1640:C:H5''	1.88	0.56
26:DA:323:G:O2'	26:DA:1205:U:N3	2.35	0.56
31:DG:16:ARG:O	31:DG:20:ILE:HG13	2.05	0.56
1:AA:976:G:N2	1:AA:1363:C:OP2	2.38	0.56
1:AA:671:G:H5'	6:AF:77:ARG:HH22	1.70	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:160:G:O2'	26:BA:161:C:H5'	2.06	0.56
26:BA:2044:U:O2'	26:BA:2629:C:H5'	2.06	0.56
26:BA:2879:G:H2'	26:BA:2880:C:O4'	2.04	0.56
26:BA:611:U:H2'	26:BA:612:C:C6	2.41	0.56
26:BA:715:G:H5'	26:BA:716:G:OP2	2.06	0.56
30:BF:161:GLU:HG2	30:BF:164:ARG:NH2	2.20	0.56
31:BG:41:GLN:HG3	31:BG:60:LEU:HD21	1.88	0.56
26:DA:125:G:O2'	54:D7:48:LYS:NZ	2.36	0.56
26:DA:1787:A:N3	61:DA:3727:HOH:O	2.33	0.56
26:DA:2167:U:O2'	26:DA:2168:G:O4'	2.23	0.56
26:DA:2327:A:H2'	26:DA:2328:A:C8	2.41	0.56
26:DA:245:G:O6	55:D8:8:LYS:NZ	2.31	0.56
26:DA:912:C:OP1	37:DQ:8:LYS:NZ	2.25	0.56
45:DY:99:CYS:HB2	45:DY:106:LEU:HD21	1.88	0.56
1:AA:103:C:O2'	1:AA:172:A:N1	2.34	0.56
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.41	0.56
20:AT:9:ASN:HD22	20:AT:10:LEU:H	1.53	0.56
26:BA:2045:G:H5'	26:BA:2629:C:H4'	1.88	0.56
26:BA:70:A:H3'	26:BA:70:A:OP2	2.06	0.56
44:BX:35:THR:HG22	44:BX:38:GLU:HB2	1.87	0.56
16:CP:53:VAL:O	16:CP:57:ARG:HB2	2.06	0.56
21:CU:7:ARG:HD2	21:CU:21:TYR:HE2	1.69	0.56
28:DD:4:LYS:HB3	28:DD:18:VAL:HG23	1.88	0.56
37:DQ:1:MET:N	37:DQ:1:MET:SD	2.66	0.56
45:DY:20:TYR:CE1	45:DY:43:ASN:HA	2.41	0.56
26:BA:2173:G:H2'	26:BA:2174:G:C8	2.41	0.56
26:BA:2146:G:H1	26:BA:2196:C:N4	2.04	0.56
31:BG:77:ILE:HG22	31:BG:80:PHE:H	1.69	0.56
36:BP:89:ALA:O	36:BP:121:LYS:NZ	2.27	0.56
44:BX:31:HIS:CD2	44:BX:33:LYS:H	2.24	0.56
1:CA:1047:G:H5''	14:CN:4:LYS:HD2	1.87	0.56
2:CB:219:VAL:HA	2:CB:222:ILE:HG12	1.88	0.56
8:CH:39:LEU:HD12	8:CH:44:PHE:HB2	1.88	0.56
10:CJ:47:PHE:N	10:CJ:63:PHE:O	2.33	0.56
26:DA:2138:C:H2'	26:DA:2139:C:H5''	1.87	0.56
1:AA:139:G:N2	1:AA:224:C:O2	2.35	0.56
4:AD:173:TRP:CZ3	4:AD:174:LEU:HG	2.41	0.56
26:BA:2658:C:OP2	26:BA:2745:G:O2'	2.19	0.56
26:BA:831:A:H5'	26:BA:832:G:OP1	2.06	0.56
26:DA:1265:A:OP2	61:DA:4004:HOH:O	2.18	0.56
32:DH:113:VAL:HG11	32:DH:151:ILE:HD13	1.87	0.56
34:DN:4:TYR:HB2	41:DU:101:ARG:NH1	2.21	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:736:C:H2'	1:AA:737:A:H8	1.71	0.55
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.71	0.55
1:CA:1120:G:C6	1:CA:1121:U:C4	2.94	0.55
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.88	0.55
51:D4:59:PHE:HA	51:D4:60:GLN:C	2.27	0.55
30:DF:21:ALA:CB	30:DF:22:ALA:HA	2.37	0.55
1:AA:1392:G:H21	1:AA:1502:A:H8	1.54	0.55
4:AD:175:SER:HB3	4:AD:186:LEU:HD11	1.88	0.55
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.53	0.55
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.06	0.55
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.87	0.55
33:BI:27:ARG:HD2	48:B1:71:TYR:CE1	2.41	0.55
26:BA:1355:G:O6	61:BA:4912:HOH:O	2.17	0.55
26:BA:615:G:O6	61:BA:4937:HOH:O	2.16	0.55
1:CA:442:C:H42	1:CA:492:G:H1	1.53	0.55
2:CB:8:LYS:HG3	2:CB:9:GLU:HG3	1.87	0.55
1:CA:450:G:OP1	16:CP:43:LYS:NZ	2.38	0.55
24:CX:40:C:H2'	24:CX:41:C:H6	1.71	0.55
26:DA:1039:G:O6	26:DA:1116:C:N4	2.37	0.55
26:DA:1527:G:HO2'	26:DA:1544:A:H62	1.53	0.55
2:AB:231:GLU:HB3	2:AB:232:PRO:HD3	1.88	0.55
7:AG:16:LEU:HD11	9:AI:45:ALA:HB2	1.87	0.55
12:AL:24:VAL:HG13	12:AL:98:TYR:CE1	2.41	0.55
25:AY:19:G:H3'	25:AY:20:U:C6	2.41	0.55
26:BA:2250:G:H2'	26:BA:2250:G:N3	2.20	0.55
26:BA:2674:A:H2'	26:BA:2675:G:O4'	2.07	0.55
5:CE:50:GLU:HB2	5:CE:53:LEU:HD12	1.88	0.55
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.36	0.55
24:CX:31:G:H3'	24:CX:32:5MC:HM51	1.88	0.55
26:DA:140:G:N2	26:DA:1596:A:H4'	2.21	0.55
26:DA:2135:A:H2'	26:DA:2136:C:C6	2.41	0.55
34:DN:17:ASP:HB2	34:DN:137:LYS:HZ1	1.71	0.55
1:AA:442:C:H42	1:AA:492:G:H1	1.53	0.55
11:AK:34:ASP:OD1	11:AK:38:ASN:N	2.40	0.55
20:AT:9:ASN:ND2	20:AT:10:LEU:H	2.05	0.55
26:BA:2804:C:H2'	26:BA:2805:G:H8	1.71	0.55
30:BF:158:THR:O	30:BF:164:ARG:NH1	2.38	0.55
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.39	0.55
3:CC:6:HIS:CD2	3:CC:8:ILE:H	2.23	0.55
9:CI:125:TYR:HD1	9:CI:126:SER:N	2.03	0.55
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.40	0.55
23:CW:39:PSU:H2'	23:CW:40:C:C6	2.41	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:CM:65:LYS:HA	51:D4:50:VAL:HG11	1.87	0.55
26:DA:1378:A:OP1	54:D7:10:ARG:NH2	2.39	0.55
26:DA:2169:A:H2'	26:DA:2170:A:C8	2.41	0.55
33:DI:38:LEU:HB2	33:DI:40:THR:HG22	1.89	0.55
1:AA:1445:C:N3	1:AA:1457:G:N1	2.37	0.55
6:AF:50:TYR:OH	18:AR:74:ARG:O	2.18	0.55
26:BA:211:A:H5''	26:BA:448:U:OP1	2.07	0.55
1:CA:1154:G:N7	1:CA:1155:G:N9	2.55	0.55
3:CC:33:LEU:HD21	14:CN:53:LEU:HD23	1.88	0.55
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.88	0.55
26:DA:1239:G:H2'	26:DA:1240:U:O4'	2.06	0.55
26:DA:2400:G:H2'	26:DA:2401:U:H6	1.70	0.55
26:DA:2882:A:H5'	38:DR:96:ARG:HG3	1.87	0.55
26:DA:320:A:OP2	30:DF:137:LYS:NZ	2.33	0.55
26:DA:859:G:N2	26:DA:917:A:OP2	2.39	0.55
46:DZ:111:VAL:HG21	46:DZ:117:LEU:HB2	1.88	0.55
1:AA:123:C:OP1	1:AA:311:C:O2'	2.20	0.55
55:B8:62:LEU:HB3	55:B8:65:GLU:CG	2.36	0.55
26:BA:2132:G:C2	26:BA:2142:G:H1'	2.42	0.55
26:BA:2193:A:H1'	26:BA:2194:U:O4'	2.07	0.55
27:BB:91:C:H5'	37:BQ:18:LYS:HA	1.87	0.55
44:BX:2:LYS:NZ	44:BX:38:GLU:OE2	2.30	0.55
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.41	0.55
2:CB:48:MET:HA	2:CB:51:LEU:HB2	1.89	0.55
3:CC:22:TRP:CD2	3:CC:59:ARG:HD2	2.41	0.55
11:CK:24:SER:OG	11:CK:25:TYR:N	2.38	0.55
26:DA:848:G:C2	26:DA:933:A:H1'	2.42	0.55
36:DP:121:LYS:HG2	36:DP:122:PRO:HD2	1.89	0.55
26:DA:833:U:O2	36:DP:55:ARG:NH2	2.37	0.55
26:DA:84:A:H5''	45:DY:8:LYS:HE3	1.88	0.55
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.21	0.55
1:AA:353:A:H5'	1:AA:353:A:H8	1.72	0.55
18:AR:31:LEU:HD23	18:AR:31:LEU:H	1.72	0.55
20:AT:65:LYS:HA	20:AT:68:LYS:HD3	1.88	0.55
26:BA:354:A:H2	26:BA:1255:A:HO2'	1.54	0.55
26:BA:1613:A:OP1	28:BD:211:ARG:NH1	2.40	0.55
33:BI:106:GLY:HA2	33:BI:107:VAL:O	2.06	0.55
33:BI:72:LEU:C	33:BI:74:ASN:H	2.10	0.55
1:CA:1002:G:H1	1:CA:1038:C:H42	0.70	0.55
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.07	0.55
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.88	0.55
10:CJ:55:LYS:HG3	10:CJ:56:HIS:CD2	2.42	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
51:D4:46:GLN:C	51:D4:48:ARG:H	2.10	0.55
26:DA:1530:C:HO2'	26:DA:1531:C:P	2.29	0.55
26:DA:1803:A:H4'	28:DD:259:THR:HG23	1.89	0.55
26:DA:330:A:H2	26:DA:1210:A:HO2'	1.54	0.55
27:DB:24:G:H4'	27:DB:25:A:C8	2.41	0.55
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.72	0.55
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.20	0.55
26:BA:944:C:H2'	26:BA:945:A:H8	1.70	0.55
24:AX:64:G:H4'	37:BQ:10:ARG:HH21	1.71	0.55
1:CA:1376:U:H2'	1:CA:1377:A:H8	1.70	0.55
1:CA:328:C:H4'	1:CA:329:A:H5'	1.89	0.55
2:CB:45:GLN:O	2:CB:49:GLU:HB2	2.06	0.55
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.25	0.55
31:DG:179:PRO:HB2	51:D4:42:PHE:CE1	2.41	0.55
26:DA:1796:U:H2'	26:DA:1797:C:C6	2.42	0.55
1:AA:1255:G:N7	10:AJ:43:ARG:NH2	2.55	0.55
1:AA:1290:G:H2'	1:AA:1291:G:H8	1.71	0.55
2:AB:16:HIS:O	2:AB:17:PHE:HD1	1.89	0.55
25:AY:50:U:N3	25:AY:64:A:C2	2.69	0.55
26:BA:2163:G:H1	26:BA:2171:G:N2	2.02	0.55
26:BA:2348:A:H61	47:B0:43:THR:HG22	1.71	0.55
36:BP:36:LYS:O	61:BP:306:HOH:O	2.18	0.55
1:CA:1023:G:C4	1:CA:1024:G:C8	2.94	0.55
1:CA:1035:A:H2'	1:CA:1036:G:H8	1.71	0.55
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.22	0.55
4:CD:196:LEU:O	4:CD:198:VAL:N	2.36	0.55
26:DA:900:A:O2'	26:DA:901:A:OP1	2.24	0.55
30:DF:150:GLY:HA2	30:DF:172:TRP:CD2	2.41	0.55
34:DN:128:HIS:O	34:DN:131:GLN:NE2	2.40	0.55
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.88	0.55
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.06	0.55
35:BO:63:VAL:HG12	35:BO:106:LEU:HD11	1.88	0.55
7:CG:78:ARG:HB2	7:CG:156:TRP:HZ3	1.72	0.55
7:CG:91:VAL:HB	7:CG:96:GLN:HG2	1.88	0.55
26:DA:2349:G:OP1	61:DA:3781:HOH:O	2.18	0.55
36:DP:84:ASN:CG	36:DP:117:GLU:HB2	2.27	0.55
41:DU:85:LYS:HB2	41:DU:116:ALA:HB1	1.89	0.55
1:AA:109:A:OP1	61:AA:4215:HOH:O	2.18	0.54
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.07	0.54
13:AM:3:ARG:HG2	13:AM:8:GLU:HA	1.89	0.54
25:AY:33:U:H2'	25:AY:35:A:OP2	2.07	0.54
26:BA:1417:G:H2'	26:BA:1418:U:H5	1.70	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:CD:58:LEU:HD22	4:CD:62:GLN:HG2	1.89	0.54
25:CY:29:G:H1	25:CY:41:C:N4	2.05	0.54
26:DA:1467:C:C5	26:DA:1546:C:H2'	2.42	0.54
26:DA:223:A:O2'	26:DA:420:C:O2	2.25	0.54
46:DZ:163:LEU:HG	46:DZ:165:VAL:HG22	1.88	0.54
2:AB:109:SER:HA	2:AB:112:VAL:HG13	1.87	0.54
1:AA:1179:A:O3'	9:AI:103:THR:HB	2.06	0.54
26:BA:1299:A:OP1	61:BA:4931:HOH:O	2.18	0.54
26:BA:1740:U:O2'	28:BD:14:ARG:NH2	2.40	0.54
26:BA:2544:G:O2'	26:BA:2669:A:N1	2.39	0.54
1:CA:419:C:OP1	1:CA:513:C:O2'	2.23	0.54
4:CD:98:GLU:HG2	4:CD:189:PRO:HG2	1.89	0.54
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.90	0.54
15:CO:5:LYS:N	15:CO:5:LYS:HD3	2.23	0.54
16:CP:8:ARG:HG3	16:CP:17:TYR:CE1	2.42	0.54
25:CY:39:PSU:C2	25:CY:40:C:C2	2.95	0.54
48:D1:54:ALA:HB1	48:D1:83:GLU:HG3	1.88	0.54
26:DA:1014:U:H2'	26:DA:1015:G:H8	1.72	0.54
26:DA:1300:U:H4'	26:DA:1301:A:C5'	2.37	0.54
26:DA:191:A:N1	61:DA:4228:HOH:O	2.34	0.54
26:DA:2150:U:H2'	26:DA:2151:G:C8	2.41	0.54
26:DA:2155:G:H2'	26:DA:2156:G:H5'	1.89	0.54
26:DA:637:A:H2'	36:DP:117:GLU:OE2	2.08	0.54
30:DF:150:GLY:HA2	30:DF:172:TRP:CE3	2.42	0.54
39:DS:93:LYS:HD3	39:DS:94:TYR:N	2.22	0.54
1:AA:1007:C:N3	1:AA:1022:G:O6	2.41	0.54
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.31	0.54
1:AA:1149:C:H2'	1:AA:1150:U:C6	2.42	0.54
1:AA:501:C:H2'	1:AA:502:G:C8	2.43	0.54
2:AB:20:GLU:HA	2:AB:21:ARG:NH2	2.22	0.54
5:AE:33:VAL:HG21	5:AE:109:ILE:HA	1.89	0.54
7:AG:152:ALA:HB1	7:AG:155:ARG:HH21	1.72	0.54
26:BA:1093:G:HO2'	26:BA:1094:A:H8	1.55	0.54
26:BA:215:G:H21	26:BA:217:A:H62	1.54	0.54
26:BA:2202:U:H2'	26:BA:2203:G:O4'	2.08	0.54
26:BA:431:C:H4'	26:BA:432:U:H5'	1.89	0.54
26:BA:68:C:O2	26:BA:72:A:O2'	2.23	0.54
39:BS:34:HIS:ND1	39:BS:53:SER:OG	2.36	0.54
43:BW:25:ARG:NH2	43:BW:74:ALA:O	2.35	0.54
46:BZ:4:ARG:NE	46:BZ:60:GLU:OE1	2.28	0.54
26:DA:2136:C:O2'	26:DA:2137:C:O5'	2.25	0.54
26:DA:2612:C:OP2	52:D5:2:ALA:N	2.41	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:276:A:H5''	26:DA:277:C:H5'	1.88	0.54
31:DG:23:PHE:HB2	31:DG:25:TYR:CZ	2.42	0.54
25:AY:51:U:H3	25:AY:63:G:H1	1.55	0.54
26:BA:1159:U:H2'	26:BA:1160:G:C8	2.41	0.54
26:BA:2151:C:H2'	26:BA:2152:U:C6	2.42	0.54
26:BA:2457:G:OP1	30:BF:74:ARG:NH2	2.38	0.54
29:BE:55:ASN:HB3	29:BE:58:ARG:HG3	1.88	0.54
1:CA:1378:C:H5	1:CA:1379:G:C4	2.25	0.54
1:CA:859:A:OP2	1:CA:869:G:N1	2.34	0.54
3:CC:20:SER:OG	3:CC:22:TRP:NE1	2.40	0.54
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.90	0.54
26:DA:2733:A:N1	29:DE:203:LYS:HA	2.23	0.54
26:DA:796:C:H2'	26:DA:797:C:C6	2.42	0.54
40:DT:24:PRO:HA	40:DT:49:VAL:HG22	1.89	0.54
26:DA:300:A:P	45:DY:86:ARG:HH22	2.30	0.54
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.72	0.54
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.24	0.54
1:AA:848:C:H2'	1:AA:849:C:C6	2.43	0.54
2:AB:105:PHE:CE1	2:AB:155:LEU:HD12	2.43	0.54
3:AC:104:GLN:HE21	3:AC:105:GLU:N	2.05	0.54
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.41	0.54
5:AE:91:LEU:HB3	5:AE:118:ILE:HD11	1.89	0.54
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.06	0.54
26:BA:1766:G:H3'	26:BA:1767:A:H5''	1.88	0.54
26:BA:2138:G:N1	26:BA:2184:G:OP1	2.41	0.54
26:DA:641:C:H42	26:DA:647:G:H1	1.56	0.54
32:DH:56:SER:OG	32:DH:57:ASP:N	2.41	0.54
1:AA:1292:U:H5'	9:AI:38:GLN:NE2	2.22	0.54
1:AA:923:A:O2'	1:AA:1399:C:OP2	2.23	0.54
3:AC:150:LYS:HB2	3:AC:173:VAL:HG21	1.88	0.54
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	1.90	0.54
25:AY:67:C:H2'	25:AY:68:C:O4'	2.08	0.54
26:BA:1993:A:N1	61:BA:4352:HOH:O	2.33	0.54
29:BE:174:ASP:OD1	29:BE:175:VAL:N	2.40	0.54
36:BP:100:LEU:HD12	36:BP:112:LEU:HD11	1.90	0.54
23:AW:52:G:H4'	37:BQ:56:ARG:NH2	2.22	0.54
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.08	0.54
1:CA:701:C:OP1	1:CA:702:A:O2'	2.14	0.54
2:CB:61:LEU:HD23	2:CB:68:ILE:HD11	1.89	0.54
4:CD:57:ARG:HH22	5:CE:107:ARG:HD3	1.72	0.54
6:CF:46:ARG:HG3	6:CF:47:ARG:N	2.21	0.54
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.88	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:CR:61:LYS:O	18:CR:65:ILE:HG12	2.07	0.54
26:DA:1183:G:H5''	50:D3:30:ARG:HH12	1.73	0.54
33:DI:14:ASP:OD1	33:DI:15:VAL:N	2.38	0.54
1:AA:171:A:H2'	1:AA:172:A:C8	2.42	0.54
1:AA:45:U:H2'	1:AA:46:G:C8	2.42	0.54
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.88	0.54
19:AS:67:VAL:HG21	51:B4:59:PHE:HB3	1.88	0.54
24:AX:19:G:H4'	24:AX:20:U:OP2	2.06	0.54
26:BA:469:A:H1'	26:BA:1246:C:O4'	2.07	0.54
26:BA:2339:A:H2'	26:BA:2340:A:C8	2.42	0.54
1:CA:1003:G:N2	1:CA:1025:U:O4	2.40	0.54
3:CC:6:HIS:CG	14:CN:49:HIS:HB3	2.43	0.54
24:CX:58:A:H4'	24:CX:59:A:OP1	2.08	0.54
26:DA:2206:G:H3'	26:DA:2207:G:N7	2.23	0.54
26:DA:252:G:P	36:DP:50:ARG:HH12	2.31	0.54
26:DA:855:G:H2'	26:DA:856:C:C6	2.43	0.54
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.23	0.54
1:AA:159:G:O2'	1:AA:161:A:N7	2.30	0.54
1:AA:524:G:H2'	1:AA:525:C:C6	2.43	0.54
1:AA:539:A:H2'	1:AA:540:G:C8	2.43	0.54
1:AA:934:C:OP1	61:AA:4110:HOH:O	2.18	0.54
4:AD:188:LEU:H	4:AD:188:LEU:HD23	1.73	0.54
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.40	0.54
51:B4:54:GLY:C	51:B4:56:VAL:HA	2.28	0.54
26:BA:2255:U:OP1	61:BA:4017:HOH:O	2.17	0.54
26:BA:265:U:H2'	26:BA:266:C:C6	2.43	0.54
26:BA:831:A:C6	28:BD:229:VAL:HG11	2.43	0.54
1:CA:399:G:H2'	1:CA:400:C:C6	2.43	0.54
1:CA:441:A:H3'	1:CA:442:C:C6	2.43	0.54
1:CA:723:U:HO2'	1:CA:724:G:C5'	2.21	0.54
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.20	0.54
26:DA:1153:C:H2'	26:DA:1154:G:O4'	2.07	0.54
26:DA:879:G:H3'	26:DA:880:G:H8	1.72	0.54
26:DA:971:C:OP2	61:DA:4647:HOH:O	2.18	0.54
28:DD:3:VAL:HG13	28:DD:17:THR:HB	1.89	0.54
26:DA:2591:C:OP1	28:DD:239:ARG:HD2	2.08	0.54
31:DG:48:GLU:O	31:DG:51:ARG:HG3	2.07	0.54
42:DV:35:LEU:HB2	42:DV:57:VAL:HG23	1.90	0.54
1:AA:222:U:H2'	1:AA:223:U:C6	2.43	0.54
1:AA:316:G:OP2	1:AA:351:G:O2'	2.25	0.54
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.41	0.54
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.89	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AW:9:A:O2'	23:AW:10:G:N7	2.40	0.54
26:BA:1219:A:H1'	26:BA:1220:U:H5''	1.89	0.54
26:BA:1827:U:H2'	26:BA:1828:C:C6	2.43	0.54
26:BA:287:G:O2'	26:BA:448:U:OP2	2.22	0.54
26:BA:934:A:H4'	26:BA:935:C:C5	2.43	0.54
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.08	0.54
1:CA:1490:C:H2'	1:CA:1491:G:H8	1.72	0.54
3:CC:157:ILE:HD12	3:CC:164:ARG:HB3	1.90	0.54
3:CC:55:VAL:HG22	3:CC:68:VAL:HG22	1.88	0.54
1:CA:428:G:OP2	4:CD:10:ARG:NH1	2.41	0.54
26:DA:1013:C:H2'	26:DA:1014:U:C6	2.43	0.54
26:DA:391:G:O2'	26:DA:410:G:OP1	2.19	0.54
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.41	0.54
1:AA:26:A:N6	1:AA:558:G:O2'	2.39	0.54
1:AA:880:C:OP1	12:AL:8:ASN:ND2	2.39	0.54
25:AY:6:G:O6	25:AY:7:A:N6	2.40	0.54
26:BA:1517:G:N2	26:BA:1568:G:OP2	2.34	0.54
26:BA:2642:G:H2'	26:BA:2643:G:C8	2.43	0.54
26:BA:268:G:O2'	26:BA:269:G:H8	1.90	0.54
36:BP:97:PRO:HD3	36:BP:126:VAL:O	2.08	0.54
1:CA:411:A:OP1	4:CD:30:LYS:NZ	2.40	0.54
1:CA:59:A:H5''	1:CA:60:A:H5''	1.89	0.54
2:CB:16:HIS:CB	2:CB:210:SER:HB2	2.28	0.54
13:CM:64:TRP:HB2	13:CM:66:LEU:HD21	1.89	0.54
26:DA:2182:G:H2'	26:DA:2183:C:C6	2.42	0.54
26:DA:2102:U:H3	26:DA:2187:G:H1	1.56	0.54
26:DA:2723:C:OP2	29:DE:109:LYS:NZ	2.41	0.54
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.23	0.53
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.41	0.53
9:AI:17:VAL:HG11	9:AI:81:ILE:HA	1.90	0.53
25:AY:9:A:H5''	25:AY:46:7MG:N2	2.23	0.53
54:B7:24:THR:CG2	54:B7:27:GLY:H	2.20	0.53
26:BA:2705:A:H2'	26:BA:2706:G:H8	1.72	0.53
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.43	0.53
1:CA:299:G:H2'	1:CA:300:A:C8	2.43	0.53
1:CA:93:G:O2'	1:CA:96:U:H5'	2.08	0.53
2:CB:15:VAL:HG12	2:CB:16:HIS:H	1.73	0.53
1:CA:1206:G:O4'	3:CC:194:GLY:HA2	2.08	0.53
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.31	0.53
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.89	0.53
18:CR:58:LEU:HB3	18:CR:62:GLU:HG3	1.89	0.53
19:CS:49:ILE:HD13	19:CS:62:ILE:HD13	1.90	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:CW:66:U:C3'	23:CW:67:C:H5''	2.32	0.53
26:DA:203:C:OP2	61:DA:4309:HOH:O	2.19	0.53
26:DA:625:G:O6	36:DP:107:LYS:NZ	2.36	0.53
45:DY:28:LYS:HD2	45:DY:40:GLU:HG3	1.89	0.53
1:AA:159:G:N2	1:AA:162:A:OP2	2.37	0.53
37:BQ:85:LYS:HB2	47:B0:7:LEU:HD12	1.91	0.53
26:BA:1452:U:H2'	26:BA:1453:C:C6	2.44	0.53
26:BA:2164:C:H2'	26:BA:2165:C:C6	2.43	0.53
1:CA:1011:G:C6	1:CA:1012:U:C2	2.97	0.53
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.43	0.53
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.23	0.53
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.90	0.53
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.72	0.53
26:DA:500:G:N1	26:DA:503:A:OP2	2.40	0.53
29:DE:174:ASP:OD1	29:DE:175:VAL:N	2.40	0.53
33:DI:27:ARG:HD2	48:D1:71:TYR:CE1	2.43	0.53
2:AB:204:ASN:OD1	2:AB:206:ASP:N	2.29	0.53
1:AA:1191:A:H5''	3:AC:4:LYS:NZ	2.23	0.53
10:AJ:13:HIS:O	10:AJ:17:ASP:HB2	2.09	0.53
12:AL:32:PHE:HB3	12:AL:84:LEU:HD11	1.89	0.53
19:AS:65:ASN:ND2	19:AS:66:MET:HG2	2.23	0.53
38:BR:44:LEU:HD22	38:BR:48:VAL:HG23	1.90	0.53
1:CA:890:G:O2'	1:CA:906:G:O6	2.20	0.53
2:CB:95:GLN:HG3	2:CB:148:TYR:HA	1.90	0.53
4:CD:61:LYS:HD2	4:CD:206:PHE:CE2	2.43	0.53
5:CE:92:LYS:HB3	5:CE:119:LEU:HB2	1.90	0.53
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.74	0.53
26:DA:1021:A:H3'	26:DA:1021:A:H8	1.72	0.53
27:DB:90:A:C5	27:DB:91:C:H1'	2.44	0.53
36:DP:121:LYS:O	36:DP:123:LEU:N	2.40	0.53
26:DA:957:A:H5'	37:DQ:76:LYS:HG3	1.90	0.53
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.24	0.53
17:AQ:95:TYR:HA	17:AQ:98:LEU:HD22	1.89	0.53
13:AM:80:ARG:HH22	19:AS:69:HIS:CE1	2.25	0.53
51:B4:15:ILE:O	51:B4:33:VAL:N	2.39	0.53
26:BA:2137:G:H21	26:BA:2193:A:H61	1.57	0.53
26:BA:956:A:H62	37:BQ:12:GLN:HA	1.73	0.53
28:BD:132:PRO:HD3	28:BD:190:TYR:CZ	2.44	0.53
1:CA:1272:G:C2	1:CA:1273:G:H1'	2.43	0.53
1:CA:382:A:H2'	1:CA:383:A:C8	2.43	0.53
2:CB:186:ALA:O	2:CB:201:ILE:N	2.40	0.53
3:CC:125:GLU:OE2	3:CC:125:GLU:N	2.36	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.44	0.53
8:CH:86:ILE:HG13	8:CH:133:LEU:HD22	1.91	0.53
23:CW:27:G:H1	23:CW:43:C:N4	2.03	0.53
23:CW:8:4SU:H1'	23:CW:48:C:H1'	1.89	0.53
51:D4:59:PHE:HA	51:D4:61:ARG:N	2.23	0.53
26:DA:1203:G:O2'	26:DA:1242:A:N6	2.39	0.53
29:DE:36:ARG:HD3	29:DE:85:ASN:HD21	1.73	0.53
26:DA:1007:C:P	34:DN:37:LYS:HZ1	2.31	0.53
1:AA:198:G:O6	1:AA:219:C:N4	2.42	0.53
1:AA:346:G:OP1	40:BT:41:ARG:NH2	2.41	0.53
1:AA:715:A:H2'	1:AA:716:A:C8	2.44	0.53
26:BA:2549:U:H2'	26:BA:2550:C:C6	2.44	0.53
26:BA:2569:G:H2'	26:BA:2570:C:C6	2.44	0.53
33:BI:61:ARG:HA	33:BI:61:ARG:HH11	1.73	0.53
36:BP:42:SER:O	61:BP:305:HOH:O	2.18	0.53
1:CA:543:C:OP1	4:CD:14:ARG:NE	2.36	0.53
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.74	0.53
3:CC:155:GLY:HA3	3:CC:196:LEU:HD13	1.90	0.53
13:CM:22:ILE:HG23	13:CM:67:GLU:HG2	1.91	0.53
47:D0:27:GLU:HG3	47:D0:68:GLU:HA	1.91	0.53
26:DA:1266:G:O5'	43:DW:15:ARG:NH2	2.41	0.53
26:DA:2070:G:OP2	61:DA:4495:HOH:O	2.18	0.53
27:DB:95:C:H2'	27:DB:96:U:C6	2.44	0.53
39:DS:67:ARG:HG3	39:DS:104:GLY:HA3	1.90	0.53
1:AA:69:G:H2'	1:AA:70:G:H8	1.74	0.53
1:AA:848:C:H2'	1:AA:849:C:H6	1.74	0.53
1:AA:1112:C:O2	3:AC:179:ARG:HG3	2.09	0.53
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.09	0.53
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.23	0.53
23:AW:18:G:H4'	23:AW:60:U:C5	2.43	0.53
25:AY:49:C:H42	25:AY:65:G:H1	0.68	0.53
26:BA:2705:A:H2'	26:BA:2706:G:C8	2.44	0.53
29:BE:31:CYS:HB3	29:BE:49:LEU:HG	1.90	0.53
26:BA:572:A:H61	42:BV:19:LYS:H	1.56	0.53
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.24	0.53
26:DA:922:U:H2'	26:DA:923:C:C6	2.43	0.53
31:DG:106:LEU:HA	31:DG:110:ALA:HB3	1.90	0.53
35:DO:16:ALA:HB2	35:DO:52:VAL:HG21	1.91	0.53
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.08	0.53
26:BA:1809:U:H2'	26:BA:1815:A:N6	2.23	0.53
26:BA:2138:G:H2'	26:BA:2139:A:C6	2.44	0.53
26:BA:2159:C:H2'	26:BA:2160:C:C6	2.43	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2702:C:OP1	38:BR:17:ARG:NH1	2.33	0.53
1:CA:1120:G:C6	1:CA:1154:G:C2	2.96	0.53
1:CA:895:G:N7	61:CA:4069:HOH:O	2.34	0.53
2:CB:46:LYS:O	2:CB:50:GLU:N	2.42	0.53
26:DA:1364:G:OP2	48:D1:3:LYS:HG3	2.09	0.53
26:DA:1423:G:OP1	26:DA:1492:G:O2'	2.26	0.53
26:DA:1658:C:OP1	61:DA:4209:HOH:O	2.18	0.53
26:DA:2177:C:H2'	26:DA:2178:C:O4'	2.08	0.53
26:DA:2630:G:H2'	26:DA:2631:G:H8	1.74	0.53
26:DA:644:A:H4'	26:DA:645:C:C5	2.43	0.53
42:DV:24:LYS:HG3	42:DV:64:HIS:HD2	1.73	0.53
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.44	0.53
1:AA:946:A:H2'	1:AA:947:G:C8	2.43	0.53
4:AD:15:GLU:CG	4:AD:63:LYS:HB3	2.39	0.53
12:AL:39:VAL:HG11	12:AL:41:ARG:NH1	2.24	0.53
23:AW:1:G:H2'	23:AW:2:C:C6	2.44	0.53
23:AW:9:A:H1'	23:AW:45:U:O2'	2.09	0.53
26:BA:2137:G:N2	26:BA:2193:A:H61	2.06	0.53
46:BZ:126:VAL:HG11	46:BZ:161:VAL:HG23	1.89	0.53
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.27	0.53
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.90	0.53
8:CH:30:ARG:O	8:CH:34:GLU:HG2	2.08	0.53
23:CW:75:C:H2'	23:CW:76:31M:C4	2.39	0.53
39:DS:11:LYS:O	39:DS:15:ARG:HG3	2.08	0.53
26:DA:875:G:O2'	46:DZ:151:HIS:HE1	1.92	0.53
1:AA:270:A:H2'	1:AA:271:C:C6	2.44	0.53
1:AA:520:A:N1	1:AA:536:C:H1'	2.23	0.53
6:AF:9:VAL:HB	6:AF:87:ARG:HB2	1.90	0.53
24:AX:7:G:H1	24:AX:66:C:H42	1.56	0.53
29:BE:12:THR:HG22	29:BE:13:ARG:H	1.73	0.53
26:DA:1379:A:H4'	26:DA:1380:G:OP2	2.07	0.53
26:DA:1420:U:O2'	26:DA:1421:G:OP1	2.25	0.53
26:DA:144:C:H2'	26:DA:145:G:H8	1.73	0.53
39:DS:87:PHE:CZ	39:DS:102:ALA:HB2	2.44	0.53
1:AA:262:A:H2'	1:AA:263:A:C8	2.44	0.53
1:AA:97:G:O2'	1:AA:98:G:H5''	2.09	0.53
26:BA:664:U:H2'	26:BA:665:C:C6	2.44	0.53
33:BI:40:THR:O	33:BI:44:LEU:HB2	2.09	0.53
46:BZ:111:VAL:HG12	46:BZ:112:ARG:H	1.73	0.53
1:CA:1122:U:C4	1:CA:1123:A:N7	2.76	0.53
1:CA:1125:U:C3'	1:CA:1126:U:H5''	2.38	0.53
17:CQ:12:SER:HB3	17:CQ:20:THR:HB	1.89	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1532:C:N4	26:DA:1537:G:O6	2.20	0.53
26:DA:2112:G:N7	26:DA:2169:A:N6	2.57	0.53
46:DZ:53:ILE:HD13	46:DZ:99:TYR:HB2	1.91	0.53
1:AA:942:G:H21	9:AI:124:GLN:NE2	2.08	0.52
49:B2:11:GLU:O	49:B2:15:LYS:HG3	2.09	0.52
26:BA:241:G:OP1	36:BP:50:ARG:NH1	2.42	0.52
28:BD:10:THR:OG1	28:BD:13:ARG:HB2	2.08	0.52
1:CA:1125:U:O2	10:CJ:38:ILE:HG21	2.09	0.52
1:CA:437:U:H5'	4:CD:155:LEU:HD21	1.91	0.52
1:CA:620:C:C2	4:CD:135:LEU:HG	2.43	0.52
2:CB:91:PRO:HD3	2:CB:154:LEU:HD12	1.91	0.52
3:CC:54:ARG:HH11	3:CC:54:ARG:HB3	1.74	0.52
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.45	0.52
16:CP:52:ASP:O	16:CP:54:GLU:N	2.33	0.52
26:DA:1415:U:O2'	26:DA:1417:C:OP1	2.25	0.52
26:DA:2646:C:H2'	26:DA:2647:U:O4'	2.09	0.52
26:DA:857:C:H4'	47:D0:23:VAL:HG21	1.91	0.52
26:DA:878:A:N6	26:DA:899:A:O2'	2.43	0.52
28:DD:85:ASP:OD2	28:DD:88:ARG:NH1	2.40	0.52
26:DA:2684:U:O2'	35:DO:68:GLU:OE1	2.28	0.52
29:DE:27:LEU:HD22	40:DT:1:MET:HE1	1.90	0.52
1:AA:167:G:H2'	1:AA:168:G:H8	1.75	0.52
24:AX:56:C:O5'	24:AX:56:C:H6	1.92	0.52
25:AY:67:C:H2'	25:AY:68:C:C6	2.44	0.52
26:BA:1405:A:H2'	26:BA:1406:A:H5'	1.91	0.52
26:BA:354:A:H2	26:BA:1255:A:O2'	1.92	0.52
32:BH:159:GLU:HG3	32:BH:169:VAL:HG11	1.91	0.52
1:CA:1119:C:N3	1:CA:1154:G:O6	2.42	0.52
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.44	0.52
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.09	0.52
1:CA:164:U:H2'	1:CA:165:C:C6	2.44	0.52
26:DA:1790:C:H5''	26:DA:1791:A:OP1	2.09	0.52
26:DA:2180:U:H2'	26:DA:2181:G:O4'	2.09	0.52
1:AA:1027:C:N3	1:AA:1028:C:N4	2.57	0.52
1:AA:67:C:H2'	1:AA:68:G:C8	2.44	0.52
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.91	0.52
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.44	0.52
4:AD:155:LEU:HB3	4:AD:158:ILE:CD1	2.39	0.52
17:AQ:56:VAL:HB	17:AQ:78:GLU:HB3	1.91	0.52
50:B3:50:VAL:HB	50:B3:53:LEU:HD12	1.90	0.52
34:BN:21:LYS:HE3	34:BN:140:VAL:OXT	2.09	0.52
1:CA:1278:U:H5'	1:CA:1279:A:O4'	2.08	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:625:G:H2'	1:CA:626:U:H6	1.74	0.52
3:CC:3:ASN:N	3:CC:3:ASN:OD1	2.42	0.52
30:DF:120:GLU:HB2	30:DF:122:LYS:HG2	1.90	0.52
34:DN:67:LEU:O	34:DN:88:GLU:HG3	2.10	0.52
40:DT:11:GLU:O	40:DT:15:VAL:HG23	2.10	0.52
26:DA:1188:U:H4'	42:DV:79:VAL:HG22	1.91	0.52
1:AA:1053:G:C3'	1:AA:1054:C:H5'	2.39	0.52
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	1.92	0.52
12:AL:24:VAL:HG13	12:AL:98:TYR:HE1	1.73	0.52
31:BG:179:PRO:HG3	51:B4:43:TYR:OH	2.10	0.52
26:BA:1475:G:H2'	26:BA:1476:C:C6	2.44	0.52
26:BA:1529:G:O6	26:BA:1553:A:N6	2.42	0.52
27:BB:7:G:H5''	27:BB:7:G:H8	1.75	0.52
28:BD:108:PRO:HB3	28:BD:143:HIS:CE1	2.45	0.52
26:BA:1874:C:H5'	28:BD:253:GLN:HE22	1.74	0.52
32:BH:56:SER:OG	32:BH:57:ASP:N	2.42	0.52
37:BQ:54:MET:HG3	37:BQ:117:ALA:HB1	1.92	0.52
1:CA:1158:C:O3'	2:CB:133:LYS:NZ	2.43	0.52
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.42	0.52
3:CC:111:LEU:HD22	3:CC:146:ALA:HB2	1.92	0.52
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.44	0.52
55:D8:6:THR:HG22	55:D8:63:PRO:HD2	1.92	0.52
26:DA:1021:A:C8	26:DA:1021:A:H3'	2.45	0.52
26:DA:2176:A:H2'	26:DA:2177:C:C5	2.44	0.52
26:DA:2803:C:H2'	26:DA:2804:C:H6	1.74	0.52
28:DD:276:LYS:H	28:DD:276:LYS:HD3	1.74	0.52
26:DA:2748:A:H5'	32:DH:4:ILE:HD12	1.92	0.52
33:DI:40:THR:O	33:DI:44:LEU:HB2	2.09	0.52
44:DX:44:GLU:O	44:DX:48:LYS:N	2.42	0.52
44:DX:11:PRO:HB3	44:DX:92:LEU:HD11	1.90	0.52
6:AF:19:LEU:HD11	6:AF:59:TYR:CE2	2.45	0.52
23:AW:1:G:O6	23:AW:72:C:N3	2.42	0.52
26:BA:2158:C:N4	26:BA:2177:G:N1	2.32	0.52
36:BP:49:ARG:NH1	55:B8:61:LEU:HD23	2.24	0.52
26:BA:1232:G:H5''	42:BV:81:TYR:CE1	2.43	0.52
1:CA:1243:C:H42	1:CA:1294:G:H1	1.58	0.52
1:CA:1490:C:H2'	1:CA:1491:G:C8	2.44	0.52
3:CC:125:GLU:O	3:CC:127:ARG:NH1	2.41	0.52
26:DA:77:C:O2'	49:D2:14:ARG:NH2	2.42	0.52
50:D3:13:ILE:O	61:D3:3101:HOH:O	2.19	0.52
26:DA:1839:G:C8	26:DA:1927:A:H1'	2.44	0.52
36:DP:95:VAL:HG13	36:DP:125:VAL:HA	1.91	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1131:G:H2'	1:AA:1132:C:H6	1.74	0.52
1:AA:1320:C:OP1	19:AS:70:LYS:HE3	2.09	0.52
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.43	0.52
1:AA:1464:G:OP2	40:BT:111:ARG:NH2	2.43	0.52
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.09	0.52
1:AA:685:G:N2	1:AA:704:A:OP2	2.33	0.52
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.75	0.52
7:AG:49:ILE:O	7:AG:53:LYS:HG3	2.10	0.52
24:AX:4:G:H2'	24:AX:5:G:C8	2.44	0.52
26:BA:1002:A:N1	26:BA:2470:G:H4'	2.25	0.52
26:BA:139:A:H8	26:BA:1454:C:HO2'	1.54	0.52
1:CA:1469:G:N7	61:CA:4124:HOH:O	2.34	0.52
1:CA:876:G:O5'	8:CH:14:ARG:NH1	2.43	0.52
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.09	0.52
8:CH:13:ILE:O	8:CH:17:THR:HG23	2.10	0.52
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.91	0.52
25:CY:61:C:H2'	25:CY:62:C:C6	2.45	0.52
26:DA:1899:G:O2'	26:DA:1900:A:OP2	2.24	0.52
26:DA:821:A:N1	61:DA:4093:HOH:O	2.34	0.52
41:DU:81:HIS:HB3	41:DU:117:GLN:HE22	1.74	0.52
1:AA:838:G:H2'	1:AA:839:U:H2'	1.92	0.52
4:AD:107:ARG:HH22	4:AD:194:LEU:HD21	1.74	0.52
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.10	0.52
26:BA:1834:A:O2'	28:BD:259:THR:HG21	2.09	0.52
26:BA:2255:U:H2'	26:BA:2256:U:C6	2.45	0.52
39:BS:106:ARG:O	39:BS:109:GLY:N	2.40	0.52
1:CA:1075:C:C2'	1:CA:1076:C:H5''	2.40	0.52
1:CA:1154:G:N7	1:CA:1155:G:C4	2.78	0.52
1:CA:189(L):G:H2'	1:CA:190:U:H6	1.74	0.52
1:CA:296:U:O2'	1:CA:556:C:O2	2.27	0.52
2:CB:53:ARG:NH1	2:CB:53:ARG:HB3	2.25	0.52
5:CE:6:PHE:HB2	5:CE:34:VAL:HG22	1.91	0.52
8:CH:49:GLU:HG2	8:CH:62:TYR:HE1	1.75	0.52
17:CQ:5:VAL:HG22	17:CQ:60:ILE:HG12	1.91	0.52
20:CT:43:LEU:O	20:CT:47:GLY:N	2.42	0.52
47:D0:17:GLN:O	47:D0:19:LYS:NZ	2.38	0.52
26:DA:2171:A:C4	26:DA:2172:U:C4	2.98	0.52
31:DG:17:PRO:HA	31:DG:20:ILE:HD12	1.92	0.52
1:AA:346:G:H3'	1:AA:347:G:H4'	1.92	0.52
1:AA:649:G:H2'	1:AA:650:G:H8	1.74	0.52
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.91	0.52
4:AD:155:LEU:HB3	4:AD:158:ILE:HD11	1.92	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:AK:15:ALA:HA	11:AK:76:GLY:O	2.09	0.52
26:BA:2073:A:H5'	26:BA:2590:G:O4'	2.10	0.52
26:BA:2760:G:O6	26:BA:2768:C:H5''	2.10	0.52
1:CA:1070:U:H2'	1:CA:1071:C:H6	1.75	0.52
3:CC:126:ARG:HB3	3:CC:128:PHE:HE1	1.75	0.52
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.43	0.52
9:CI:15:ALA:HB2	9:CI:65:VAL:HG23	1.91	0.52
26:DA:2203:U:H2'	26:DA:2205:C:C6	2.45	0.52
26:DA:2785:C:OP1	29:DE:41:LYS:NZ	2.34	0.52
26:DA:657:U:H2'	26:DA:658:C:C6	2.44	0.52
31:DG:68:PRO:HB3	31:DG:92:VAL:HB	1.92	0.52
36:DP:44:GLY:HA3	36:DP:45:LEU:HB2	1.92	0.52
1:AA:428:G:H4'	1:AA:429:U:O5'	2.10	0.52
20:AT:14:LYS:HG3	20:AT:17:ARG:NH2	2.25	0.52
25:AY:5:G:H1'	25:AY:69:G:N2	2.25	0.52
26:BA:1222:A:H3'	26:BA:1223:C:C6	2.44	0.52
26:BA:2416:C:O3'	36:BP:77:ARG:NH2	2.43	0.52
40:BT:118:ARG:HG3	40:BT:118:ARG:NH1	2.22	0.52
1:CA:768:A:OP2	61:CA:4019:HOH:O	2.19	0.52
7:CG:50:ILE:HD11	7:CG:58:PRO:HA	1.92	0.52
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.74	0.52
23:CW:19:G:H1	23:CW:56:C:N4	2.04	0.52
26:DA:1033:U:OP1	56:D9:9:ARG:NH2	2.43	0.52
26:DA:942:G:OP2	36:DP:39:LYS:NZ	2.42	0.52
40:DT:16:ARG:NH2	40:DT:83:ILE:O	2.42	0.52
1:AA:1131:G:H2'	1:AA:1132:C:C6	2.45	0.52
7:AG:12:LEU:H	7:AG:12:LEU:HD12	1.74	0.52
32:BH:88:LEU:HD13	32:BH:130:ARG:HG2	1.92	0.52
39:BS:11:LYS:O	39:BS:15:ARG:HG3	2.09	0.52
39:BS:46:VAL:HG12	39:BS:48:LEU:HD12	1.91	0.52
1:CA:1004:A:H3'	1:CA:1005:A:C5'	2.38	0.52
1:CA:1006:C:OP1	1:CA:1037:C:O2'	2.27	0.52
1:CA:551:U:H2'	1:CA:552:U:C6	2.44	0.52
2:CB:76:GLN:HB2	2:CB:208:ILE:HG12	1.92	0.52
1:CA:261:U:OP2	20:CT:79:ARG:NH2	2.43	0.52
26:DA:171:G:H2'	26:DA:172:C:H6	1.75	0.52
26:DA:2590:A:OP2	28:DD:238:GLY:HA2	2.10	0.52
26:DA:373:U:H2'	26:DA:374:A:C8	2.44	0.52
26:DA:81:G:N7	61:DA:4166:HOH:O	2.33	0.52
30:DF:20:LEU:HD12	30:DF:125:LEU:HD13	1.91	0.52
36:DP:29:LYS:HG3	36:DP:30:THR:H	1.75	0.52
43:DW:45:TYR:CZ	43:DW:49:LYS:HE3	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:664:G:N2	1:AA:741:G:H1	2.00	0.51
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.56	0.51
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.92	0.51
8:AH:73:ASP:OD1	8:AH:75:ARG:HD3	2.10	0.51
19:AS:65:ASN:HD22	19:AS:66:MET:N	2.09	0.51
26:BA:1889:G:N2	26:BA:1905:G:H2'	2.24	0.51
29:BE:143:ASN:HD22	29:BE:147:PRO:HD3	1.76	0.51
33:BI:93:THR:HG22	33:BI:119:PRO:HB3	1.91	0.51
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.45	0.51
1:CA:1304:G:C6	1:CA:1305:G:N1	2.78	0.51
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.45	0.51
15:CO:8:LYS:O	15:CO:12:ILE:HG13	2.10	0.51
26:DA:2299:G:H2'	26:DA:2300:G:H8	1.75	0.51
29:DE:12:THR:HG22	40:DT:58:ASN:OD1	2.10	0.51
41:DU:58:ARG:HA	41:DU:61:TRP:CE3	2.45	0.51
1:AA:1036:G:H5'	1:AA:1037:C:OP2	2.09	0.51
1:AA:78:G:C2	1:AA:91:C:N3	2.78	0.51
13:AM:122:LYS:HD3	13:AM:123:ALA:H	1.74	0.51
25:AY:7:A:N1	25:AY:66:U:O2	2.42	0.51
49:B2:2:LYS:O	49:B2:6:VAL:HG23	2.09	0.51
26:BA:1639:G:H2'	26:BA:1640:G:C8	2.45	0.51
26:BA:2373:A:OP1	55:B8:27:THR:OG1	2.13	0.51
26:BA:840:A:OP2	26:BA:2093:A:O2'	2.27	0.51
29:BE:47:VAL:HG23	29:BE:84:PHE:O	2.10	0.51
1:CA:1118:C:C2	1:CA:1119:C:C5	2.96	0.51
1:CA:17:U:H2'	1:CA:18:C:C6	2.44	0.51
8:CH:67:PRO:O	8:CH:69:ARG:HG3	2.10	0.51
1:CA:1129:C:P	9:CI:16:ARG:HH12	2.33	0.51
9:CI:53:VAL:C	9:CI:55:ALA:H	2.10	0.51
1:CA:1327:C:H5''	21:CU:20:LYS:HB3	1.93	0.51
26:DA:1006:C:OP2	61:DA:4190:HOH:O	2.19	0.51
26:DA:1803:A:HO2'	28:DD:259:THR:HG21	1.76	0.51
29:DE:50:GLY:HA3	29:DE:75:VAL:HG11	1.91	0.51
31:DG:39:ILE:HB	31:DG:92:VAL:HG13	1.92	0.51
32:DH:81:GLU:OE1	32:DH:81:GLU:N	2.44	0.51
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.44	0.51
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.30	0.51
26:BA:2289:G:OP2	47:B0:10:THR:HG21	2.10	0.51
26:BA:8:A:H2'	26:BA:9:U:H6	1.74	0.51
1:CA:1360:A:O5'	1:CA:1360:A:H8	1.93	0.51
1:CA:955:U:O2'	19:CS:83:HIS:HD2	1.93	0.51
2:CB:168:THR:OG1	2:CB:192:SER:HA	2.09	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:CB:15:VAL:HG13	2:CB:209:ARG:HB3	1.92	0.51
4:CD:38:TYR:CE1	4:CD:45:GLN:HG2	2.45	0.51
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.75	0.51
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.24	0.51
1:CA:1226:C:H2'	13:CM:103:THR:HB	1.93	0.51
18:CR:47:THR:HG23	18:CR:49:LYS:HG3	1.92	0.51
26:DA:62:C:H42	26:DA:93:G:H1	1.57	0.51
26:DA:867:C:H2'	26:DA:868:U:H5'	1.92	0.51
44:DX:88:LYS:HG2	44:DX:93:GLU:HG3	1.92	0.51
1:AA:1035:A:H2	1:AA:1036:G:N7	2.09	0.51
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.10	0.51
50:B3:8:LEU:HD13	50:B3:31:LEU:HD23	1.90	0.51
26:BA:1210:G:H2'	26:BA:1211:U:C6	2.46	0.51
26:BA:1466:U:O2'	26:BA:1467:G:OP1	2.22	0.51
26:BA:2699:U:H2'	26:BA:2700:U:O4'	2.10	0.51
26:BA:662:A:H4'	26:BA:663:G:O5'	2.11	0.51
26:BA:625:G:O2'	26:BA:702:A:N6	2.43	0.51
1:CA:1004:A:H62	1:CA:1037:C:H3'	1.76	0.51
1:CA:1362:C:H2'	1:CA:1363:C:H5''	1.92	0.51
1:CA:179:A:H2'	1:CA:180:U:C6	2.46	0.51
1:CA:352:C:N3	1:CA:356:A:N6	2.58	0.51
1:CA:34:C:H2'	1:CA:35:G:C8	2.45	0.51
1:CA:784:C:H4'	26:DA:1837:C:OP1	2.10	0.51
3:CC:118:GLN:HA	3:CC:121:ALA:HB3	1.92	0.51
3:CC:187:ALA:O	3:CC:198:VAL:HG23	2.11	0.51
9:CI:96:LEU:O	9:CI:100:GLY:N	2.43	0.51
13:CM:3:ARG:HA	51:D4:34:GLU:HG2	1.92	0.51
17:CQ:95:TYR:HA	17:CQ:98:LEU:HD13	1.91	0.51
26:DA:1155:A:H5''	41:DU:55:ARG:HD3	1.93	0.51
23:CW:74:C:N4	26:DA:2507:C:O2'	2.44	0.51
26:DA:607:U:OP1	30:DF:102:PRO:HA	2.10	0.51
26:DA:710:G:H1	26:DA:721:C:H42	1.56	0.51
26:DA:832:G:OP1	61:DA:4285:HOH:O	2.19	0.51
29:DE:52:LEU:HB2	29:DE:76:ARG:HB2	1.92	0.51
26:DA:2019:A:H4'	41:DU:34:LYS:HD2	1.92	0.51
42:DV:10:LYS:HZ1	42:DV:23:GLU:HG3	1.74	0.51
1:AA:997:U:H3	1:AA:1044:A:H61	1.59	0.51
26:BA:34:C:H5''	26:BA:35:G:OP2	2.09	0.51
26:BA:45:C:OP2	26:BA:204:G:H2'	2.10	0.51
30:BF:53:THR:CG2	30:BF:55:GLY:H	2.24	0.51
1:CA:1050:G:H1'	1:CA:1214:C:O2	2.10	0.51
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.11	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:448:A:P	1:CA:485:G:H22	2.33	0.51
19:CS:11:VAL:HB	19:CS:16:LEU:HD12	1.93	0.51
23:CW:47:U:H3'	23:CW:48:C:H5'	1.92	0.51
51:D4:7:PRO:HB2	51:D4:27:THR:HG21	1.93	0.51
26:DA:1593:G:H2'	26:DA:1594:G:H8	1.76	0.51
26:DA:621:A:OP2	36:DP:108:LYS:NZ	2.43	0.51
26:DA:652(T):C:H2'	26:DA:652(U):G:C8	2.46	0.51
30:DF:154:VAL:HG22	30:DF:191:ARG:HB2	1.92	0.51
45:DY:6:HIS:CD2	45:DY:6:HIS:H	2.28	0.51
1:AA:1002:G:N3	1:AA:1003:G:H1'	2.26	0.51
1:AA:1025:U:C2	1:AA:1036:G:O6	2.63	0.51
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.43	0.51
2:AB:67:THR:N	2:AB:160:ASP:OD1	2.44	0.51
4:AD:162:LEU:HD13	4:AD:181:MET:HG2	1.91	0.51
9:AI:77:ILE:O	9:AI:81:ILE:HG22	2.10	0.51
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.11	0.51
26:BA:2145:G:N2	26:BA:2197:C:N3	2.48	0.51
26:BA:906:G:O2'	26:BA:962:G:O6	2.21	0.51
33:BI:72:LEU:O	33:BI:74:ASN:N	2.44	0.51
1:CA:1057:G:H2'	1:CA:1058:G:O4'	2.11	0.51
1:CA:1227:A:OP2	13:CM:111:LYS:HE3	2.09	0.51
1:CA:1392:G:H21	1:CA:1502:A:H8	1.57	0.51
4:CD:65:ARG:HD3	4:CD:70:ILE:O	2.11	0.51
31:DG:37:VAL:HG23	31:DG:99:MET:HG3	1.92	0.51
36:DP:82:GLY:HA2	36:DP:113:LYS:O	2.10	0.51
37:DQ:36:ALA:HA	37:DQ:129:THR:HG22	1.92	0.51
1:AA:1352:C:OP1	21:AU:3:LYS:NZ	2.40	0.51
1:AA:164:U:H2'	1:AA:165:C:C6	2.46	0.51
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.91	0.51
23:AW:28:G:H2'	23:AW:29:G:C8	2.46	0.51
26:BA:1552:C:H2'	26:BA:1553:A:C8	2.36	0.51
26:BA:1821:C:H5''	26:BA:1822:A:OP1	2.11	0.51
26:BA:895:G:C4	26:BA:978:A:H8	2.29	0.51
33:BI:75:LEU:HD22	33:BI:105:HIS:ND1	2.25	0.51
34:BN:12:ARG:NH1	34:BN:50:ASP:OD2	2.43	0.51
1:CA:662:G:H2'	1:CA:663:A:C8	2.46	0.51
15:CO:64:ARG:HD3	15:CO:68:ARG:NH2	2.25	0.51
26:DA:1023:U:OP2	61:DA:4648:HOH:O	2.20	0.51
26:DA:10:G:H2'	26:DA:11:G:H8	1.76	0.51
26:DA:1670:C:O2	29:DE:129:HIS:NE2	2.42	0.51
26:DA:2218:U:O4'	48:D1:52:ARG:NH2	2.44	0.51
26:DA:1639:U:H4'	26:DA:2699:C:H4'	1.92	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:145:G:H1	1:AA:177:C:H42	1.59	0.51
1:AA:954:G:H21	1:AA:1227:A:H62	1.59	0.51
24:AX:61:C:H2'	24:AX:62:C:H6	1.75	0.51
24:AX:76:A:O3'	61:AX:3101:HOH:O	2.19	0.51
26:BA:2703:C:O3'	26:BA:2881:C:H4'	2.10	0.51
26:BA:271:U:C2	33:BI:50:ARG:HD3	2.46	0.51
26:BA:554:A:H62	26:BA:2063:U:H3	1.59	0.51
1:CA:1004:A:C6	1:CA:1037:C:C2	2.98	0.51
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.45	0.51
1:CA:1457:G:H5''	20:CT:35:THR:HG21	1.93	0.51
1:CA:375:U:O4	61:CA:4093:HOH:O	2.17	0.51
1:CA:950:U:H2'	1:CA:951:G:H8	1.76	0.51
7:CG:78:ARG:HG2	7:CG:79:ARG:HB2	1.93	0.51
26:DA:82:G:N1	26:DA:103:A:OP2	2.37	0.51
26:DA:2364:C:OP1	47:D0:55:ARG:NH1	2.41	0.51
26:DA:2769:C:H2'	26:DA:2770:G:O4'	2.11	0.51
28:DD:134:ARG:NH1	28:DD:188:GLU:OE2	2.44	0.51
28:DD:218:ARG:HB3	28:DD:219:PRO:HD2	1.93	0.51
32:DH:90:LYS:HD3	32:DH:159:GLU:HG2	1.92	0.51
1:AA:1004:A:N7	1:AA:1036:G:C2	2.79	0.51
1:AA:600:C:H2'	1:AA:601:C:C6	2.45	0.51
25:AY:19:G:H1	25:AY:56:C:H42	1.48	0.51
26:BA:493:G:OP1	54:B7:33:ARG:NH1	2.44	0.51
26:BA:997:G:OP1	37:BQ:16:ARG:NH2	2.44	0.51
1:CA:1120:G:N1	1:CA:1154:G:N3	2.59	0.51
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.46	0.51
1:CA:1391:U:H2'	1:CA:1392:G:C8	2.45	0.51
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.51	0.51
1:CA:69:G:H2'	1:CA:70:G:H8	1.76	0.51
1:CA:587:G:N1	1:CA:754:C:OP2	2.41	0.51
3:CC:53:ALA:HB3	3:CC:106:VAL:HG21	1.93	0.51
9:CI:8:GLY:HA3	9:CI:76:ALA:O	2.10	0.51
44:DX:5:TYR:CE1	49:D2:30:ARG:HB2	2.46	0.51
26:DA:1688:U:O2	26:DA:1700:A:H5'	2.11	0.51
26:DA:2121:G:O6	26:DA:2176:A:N6	2.44	0.51
26:DA:2357:U:OP1	47:D0:20:ARG:NH1	2.35	0.51
1:AA:460:G:O5'	1:AA:460:G:H8	1.93	0.51
8:AH:124:ALA:O	8:AH:128:GLY:N	2.43	0.51
9:AI:128:ARG:NH1	24:AX:35:A:OP2	2.44	0.51
20:AT:76:ALA:HA	20:AT:79:ARG:NH1	2.26	0.51
26:BA:1411:A:OP2	48:B1:3:LYS:HG2	2.10	0.51
26:BA:2190:G:C6	26:BA:2193:A:C8	2.99	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1358:U:H2'	1:CA:1359:C:O4'	2.11	0.51
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.46	0.51
1:CA:533:A:O2'	1:CA:535:A:OP2	2.25	0.51
3:CC:130:VAL:O	3:CC:134:ILE:HD13	2.11	0.51
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.74	0.51
26:DA:1028:A:N6	26:DA:1125:G:H2'	2.26	0.51
26:DA:2142:C:H2'	26:DA:2143:C:C6	2.46	0.51
26:DA:309:G:N3	26:DA:329:G:O2'	2.43	0.51
41:DU:104:GLN:OE1	41:DU:105:VAL:N	2.34	0.51
41:DU:52:ARG:HA	41:DU:55:ARG:HE	1.74	0.51
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.11	0.50
1:AA:749:C:H2'	1:AA:750:G:H8	1.76	0.50
4:AD:108:LEU:HD12	4:AD:176:LEU:HB2	1.93	0.50
17:AQ:12:SER:HB3	17:AQ:20:THR:HB	1.92	0.50
19:AS:3:ARG:HH21	19:AS:7:LYS:HE2	1.76	0.50
25:AY:40:C:H2'	25:AY:41:C:H6	1.76	0.50
25:AY:8:4SU:H4'	25:AY:48:C:H4'	1.93	0.50
26:BA:1848:G:OP1	28:BD:88:ARG:NH2	2.40	0.50
31:BG:43:LEU:HD11	31:BG:153:ARG:HG2	1.93	0.50
1:CA:1014:A:H4'	19:CS:14:HIS:CE1	2.46	0.50
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.26	0.50
20:CT:56:MET:HG3	20:CT:57:ARG:N	2.27	0.50
25:CY:7:A:H61	25:CY:66:U:H3	0.60	0.50
26:DA:1671:U:HO2'	26:DA:1673:U:H5	1.57	0.50
26:DA:1916:A:H2'	26:DA:1917:U:O4'	2.12	0.50
31:DG:97:ASP:HA	31:DG:100:TRP:HD1	1.75	0.50
1:AA:1144:G:N2	1:AA:1146:A:H62	2.10	0.50
1:AA:377:G:OP1	16:AP:3:LYS:HD2	2.11	0.50
3:AC:35:GLU:OE2	3:AC:59:ARG:NH2	2.43	0.50
24:AX:61:C:H2'	24:AX:62:C:C6	2.46	0.50
48:B1:3:LYS:HB2	48:B1:61:ARG:NH1	2.26	0.50
56:B9:25:VAL:HB	56:B9:34:GLN:HB2	1.92	0.50
36:BP:88:LEU:HD11	36:BP:114:ILE:HD12	1.93	0.50
45:BY:87:LYS:HB3	45:BY:95:LYS:HD3	1.93	0.50
1:CA:160:A:H61	1:CA:347:G:H1'	1.76	0.50
1:CA:431:A:H2'	1:CA:432:A:C8	2.46	0.50
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.44	0.50
7:CG:28:ASN:HA	7:CG:31:MET:HE2	1.93	0.50
25:CY:11:C:N3	25:CY:24:G:O6	2.44	0.50
51:D4:62:ARG:HD3	51:D4:62:ARG:H	1.77	0.50
26:DA:376:C:OP1	61:DA:4418:HOH:O	2.19	0.50
26:DA:479:A:N3	26:DA:481:G:H5''	2.26	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:DE:116:VAL:HG13	29:DE:122:PHE:HB2	1.92	0.50
44:DX:43:VAL:HG21	44:DX:81:VAL:HG11	1.93	0.50
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.10	0.50
5:AE:36:ASP:OD2	5:AE:40:ARG:HB2	2.12	0.50
25:AY:62:C:H2'	25:AY:63:G:C8	2.40	0.50
26:BA:1076:G:OP2	37:BQ:128:LYS:NZ	2.44	0.50
26:BA:1320:A:N3	26:BA:1343:C:H1'	2.26	0.50
26:BA:1469:G:OP1	26:BA:1538:G:O2'	2.23	0.50
37:BQ:18:LYS:O	37:BQ:98:LYS:NZ	2.25	0.50
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.47	0.50
4:CD:173:TRP:CZ3	4:CD:193:ASP:HB3	2.46	0.50
7:CG:26:PHE:HE2	7:CG:104:LEU:HD23	1.76	0.50
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.46	0.50
53:D6:23:THR:OG1	53:D6:24:GLU:N	2.43	0.50
27:DB:17:C:H2'	27:DB:18:G:O4'	2.11	0.50
29:DE:2:LYS:HB2	29:DE:95:ILE:HD12	1.93	0.50
29:DE:7:VAL:HG12	29:DE:27:LEU:HB3	1.92	0.50
31:DG:70:VAL:HA	31:DG:90:LEU:HD23	1.92	0.50
45:DY:38:ILE:HD11	45:DY:66:PRO:HG3	1.92	0.50
1:AA:1176:A:H2'	1:AA:1177:G:C8	2.46	0.50
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.45	0.50
26:BA:843:C:H2'	26:BA:844:C:C6	2.46	0.50
27:BB:2:C:H2'	27:BB:3:C:C6	2.46	0.50
33:BI:135:GLU:C	33:BI:137:PRO:HD3	2.31	0.50
45:BY:20:TYR:CE1	45:BY:43:ASN:HA	2.46	0.50
1:CA:1119:C:H2'	1:CA:1120:G:H8	1.75	0.50
1:CA:923:A:O2'	1:CA:1399:C:OP2	2.21	0.50
3:CC:8:ILE:HG23	3:CC:16:ARG:HG2	1.94	0.50
16:CP:68:ASP:O	16:CP:71:ARG:HG2	2.11	0.50
26:DA:2153:G:C2	26:DA:2154:G:C4	2.99	0.50
26:DA:2753:A:N3	56:D9:15:LYS:NZ	2.54	0.50
32:DH:56:SER:HB3	32:DH:61:HIS:ND1	2.26	0.50
38:DR:2:ARG:NH1	38:DR:5:LYS:O	2.44	0.50
1:AA:1067:A:O2'	1:AA:1068:G:OP2	2.21	0.50
1:AA:1521:G:N3	61:AA:4065:HOH:O	2.35	0.50
1:AA:78:G:H1	1:AA:91:C:N4	2.07	0.50
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.12	0.50
4:AD:147:ALA:HB2	4:AD:182:LYS:HA	1.94	0.50
9:AI:4:TYR:CD2	9:AI:88:TYR:HA	2.47	0.50
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.26	0.50
26:BA:2524:C:H2'	26:BA:2525:G:O4'	2.12	0.50
43:BW:79:GLY:HA3	43:BW:100:THR:HG22	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1001(A):G:H3'	1:CA:1002:G:O4'	2.11	0.50
1:CA:1030:C:N4	1:CA:1032:G:O6	2.44	0.50
1:CA:67:C:H2'	1:CA:68:G:C8	2.47	0.50
2:CB:233:SER:HB2	2:CB:234:PRO:HD2	1.93	0.50
8:CH:43:GLY:O	8:CH:64:LYS:NZ	2.42	0.50
10:CJ:55:LYS:HG3	10:CJ:56:HIS:H	1.75	0.50
26:DA:286:C:H2'	26:DA:287:C:H6	1.77	0.50
26:DA:443:A:H1'	26:DA:1201:C:O4'	2.10	0.50
27:DB:11:C:OP2	27:DB:12:C:N4	2.32	0.50
26:DA:2318:G:N2	39:DS:3:ARG:HH11	2.09	0.50
34:DN:4:TYR:HB2	41:DU:101:ARG:HH12	1.76	0.50
26:DA:483:A:O2'	45:DY:49:VAL:O	2.25	0.50
4:AD:15:GLU:HG2	4:AD:63:LYS:CB	2.41	0.50
11:AK:29:ILE:HG23	11:AK:44:SER:HB3	1.94	0.50
12:AL:28:LYS:HG3	12:AL:62:SER:HB2	1.94	0.50
18:AR:42:ARG:HH21	18:AR:42:ARG:HA	1.75	0.50
23:AW:58:A:O2'	23:AW:60:U:OP2	2.24	0.50
55:B8:6:THR:HG22	55:B8:63:PRO:HD2	1.93	0.50
26:BA:1091:A:H1'	26:BA:1093:G:N3	2.26	0.50
26:BA:1495:G:H4'	26:BA:1589:A:OP1	2.11	0.50
26:BA:1496:A:H5'	26:BA:1497:G:OP2	2.12	0.50
26:BA:482:C:H4'	61:BA:3946:HOH:O	2.11	0.50
39:BS:15:ARG:HE	39:BS:88:ASP:CG	2.14	0.50
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.93	0.50
17:CQ:45:HIS:HA	17:CQ:69:LYS:HE3	1.94	0.50
23:CW:14:A:H2'	23:CW:15:G:O4'	2.11	0.50
25:CY:23:A:H8	25:CY:23:A:O5'	1.94	0.50
26:DA:1266:G:O4'	43:DW:15:ARG:NH2	2.45	0.50
26:DA:885:C:H2'	26:DA:886:C:H4'	1.94	0.50
33:DI:130:TYR:HB3	33:DI:138:ILE:HB	1.94	0.50
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.11	0.50
1:AA:376:G:P	16:AP:67:THR:HG21	2.51	0.50
5:AE:78:HIS:HD1	8:AH:104:ARG:CD	2.24	0.50
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.92	0.50
14:AN:33:VAL:HA	14:AN:40:CYS:HA	1.94	0.50
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.11	0.50
25:AY:69:G:C2	25:AY:70:G:H1'	2.47	0.50
26:BA:1425:A:H4'	26:BA:1426:G:OP2	2.10	0.50
26:BA:1735:U:O2	26:BA:1747:A:H5'	2.12	0.50
23:AW:37:MIA:O2'	26:BA:1935:A:N1	2.44	0.50
1:CA:677:U:H3	1:CA:713:G:H22	1.58	0.50
20:CT:67:ALA:HB2	20:CT:77:ALA:HB2	1.92	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:CU:6:ARG:O	21:CU:12:LYS:NZ	2.37	0.50
23:CW:9:A:O2'	23:CW:10:G:N7	2.43	0.50
24:CX:6:G:H1	24:CX:67:C:H42	1.58	0.50
26:DA:2139:C:N4	26:DA:2153:G:C2	2.79	0.50
26:DA:854:G:H2'	26:DA:855:G:H8	1.76	0.50
27:DB:75:G:H1'	46:DZ:27:VAL:HG11	1.94	0.50
31:DG:11:TYR:HB2	31:DG:176:LEU:HD21	1.93	0.50
36:DP:89:ALA:O	36:DP:121:LYS:NZ	2.39	0.50
39:DS:50:SER:O	39:DS:76:LYS:NZ	2.45	0.50
1:AA:1132:C:H2'	1:AA:1133:G:H8	1.76	0.50
1:AA:1181:G:O2'	1:AA:1182:G:N7	2.45	0.50
1:AA:714:G:H2'	1:AA:715:A:C8	2.47	0.50
2:AB:93:VAL:HG21	2:AB:97:TRP:CD1	2.46	0.50
6:AF:36:ARG:HH11	6:AF:36:ARG:HB3	1.77	0.50
19:AS:68:GLY:H	51:B4:58:ARG:HH11	1.59	0.50
23:AW:49:C:H42	23:AW:65:G:H1	1.60	0.50
52:B5:11:THR:HG23	52:B5:15:ARG:HB3	1.93	0.50
26:BA:1897:C:H2'	26:BA:1898:A:O4'	2.11	0.50
26:BA:2331:G:H22	39:BS:3:ARG:NE	2.09	0.50
26:BA:295:C:H42	26:BA:389:G:H1	1.58	0.50
45:BY:6:HIS:CD2	45:BY:6:HIS:H	2.30	0.50
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.76	0.50
1:CA:952:U:H2'	1:CA:953:G:H8	1.77	0.50
3:CC:136:GLN:O	3:CC:140:ARG:NH1	2.45	0.50
6:CF:37:VAL:HA	6:CF:65:VAL:HG12	1.93	0.50
26:DA:1021:A:H62	26:DA:1141:U:H3	1.59	0.50
26:DA:11:G:H2'	26:DA:12:U:H5''	1.93	0.50
26:DA:1399:C:OP1	44:DX:25:LYS:NZ	2.40	0.50
26:DA:1894:C:H2'	26:DA:1895:C:H6	1.77	0.50
26:DA:586:A:N1	26:DA:809:G:O2'	2.35	0.50
39:DS:93:LYS:CD	39:DS:95:HIS:HB2	2.40	0.50
26:DA:1187:G:H5'	42:DV:81:TYR:CE1	2.47	0.50
46:DZ:93:ASP:OD1	46:DZ:94:GLU:HG3	2.12	0.50
1:AA:1131:G:O2'	1:AA:1132:C:H5'	2.12	0.50
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.45	0.50
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.47	0.50
1:AA:673:G:H2'	1:AA:674:G:C8	2.47	0.50
9:AI:110:GLU:OE2	9:AI:113:LYS:NZ	2.45	0.50
16:AP:4:ILE:HB	16:AP:66:PRO:HA	1.94	0.50
23:AW:11:C:H42	23:AW:24:G:H1	1.58	0.50
25:AY:33:U:C3'	25:AY:34:G:H5''	2.41	0.50
26:BA:2453:C:OP2	26:BA:2598:C:O2'	2.26	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2724:U:H2'	26:BA:2727:G:H5''	1.93	0.50
30:BF:64:ILE:HD11	30:BF:75:HIS:HB2	1.94	0.50
40:BT:29:ARG:HG3	40:BT:46:GLU:HB2	1.93	0.50
26:BA:572:A:N6	42:BV:19:LYS:H	2.09	0.50
44:BX:61:GLY:HA3	44:BX:73:ARG:O	2.11	0.50
1:CA:1244:C:N4	1:CA:1293:G:H1	2.10	0.50
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.46	0.50
1:CA:933:G:N2	1:CA:935:A:O4'	2.45	0.50
1:CA:936:C:H2'	1:CA:937:A:O4'	2.10	0.50
1:CA:950:U:H2'	1:CA:951:G:C8	2.47	0.50
2:CB:186:ALA:HB3	2:CB:197:VAL:HG11	1.93	0.50
1:CA:406:G:N2	4:CD:119:GLN:HE22	2.09	0.50
4:CD:61:LYS:NZ	4:CD:72:GLU:OE2	2.42	0.50
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.12	0.50
7:CG:76:ARG:HB3	7:CG:156:TRP:CH2	2.47	0.50
12:CL:117:ARG:CZ	12:CL:117:ARG:HB2	2.41	0.50
26:DA:1300:U:O2'	26:DA:1635:G:OP1	2.27	0.50
26:DA:1996:C:H4'	26:DA:1997:G:OP1	2.11	0.50
26:DA:2302:G:C2'	26:DA:2303:G:H5'	2.41	0.50
26:DA:2657:A:O3'	32:DH:160:LYS:NZ	2.45	0.50
34:DN:73:THR:OG1	34:DN:82:LEU:HD11	2.11	0.50
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.47	0.49
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.47	0.49
1:AA:991:U:O2'	1:AA:992:U:OP2	2.23	0.49
4:AD:196:LEU:O	4:AD:198:VAL:N	2.41	0.49
9:AI:49:PRO:HG2	9:AI:81:ILE:HG23	1.93	0.49
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.41	0.49
1:AA:376:G:H5''	16:AP:5:ARG:HB3	1.92	0.49
48:B1:85:LEU:HB3	48:B1:89:GLU:HG2	1.94	0.49
51:B4:61:ARG:HG3	51:B4:62:ARG:N	2.26	0.49
26:BA:1810:U:H2'	61:BA:5061:HOH:O	2.11	0.49
26:BA:2150:C:O2'	26:BA:2151:C:H5'	2.12	0.49
26:BA:2290:A:OP2	47:B0:12:ASN:ND2	2.45	0.49
26:BA:306:A:N3	26:BA:306:A:H2'	2.27	0.49
26:BA:671:A:H2'	26:BA:672:G:O4'	2.12	0.49
26:BA:794:U:O2	26:BA:2036:A:H1'	2.12	0.49
28:BD:9:TYR:CZ	28:BD:13:ARG:HG2	2.47	0.49
26:BA:1055:A:P	34:BN:37:LYS:HZ1	2.32	0.49
38:BR:28:LEU:HD12	38:BR:48:VAL:HG21	1.94	0.49
41:BU:74:LEU:H	41:BU:74:LEU:HD12	1.77	0.49
44:BX:35:THR:HG22	44:BX:38:GLU:H	1.77	0.49
1:CA:1039:C:H2'	1:CA:1040:U:O4'	2.11	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.47	0.49
10:CJ:67:THR:O	10:CJ:67:THR:OG1	2.30	0.49
20:CT:50:GLU:HG3	20:CT:100:ILE:HD13	1.94	0.49
47:D0:37:LEU:HD13	47:D0:79:VAL:HG11	1.94	0.49
26:DA:1037:G:H2'	26:DA:1038:C:O4'	2.12	0.49
26:DA:1359:A:N6	26:DA:1372:U:H3	2.08	0.49
26:DA:2128:C:H5'	26:DA:2173:A:C2	2.47	0.49
35:DO:1:MET:HG3	35:DO:67:LYS:HG2	1.93	0.49
36:DP:99:LEU:HD23	36:DP:99:LEU:H	1.77	0.49
26:DA:1278:A:OP1	38:DR:36:THR:HG23	2.12	0.49
46:DZ:117:LEU:HD11	46:DZ:144:LEU:HD13	1.93	0.49
1:AA:1053:G:O2'	61:AA:4100:HOH:O	2.19	0.49
1:AA:1095:U:P	1:AA:1108:G:H1	2.35	0.49
1:AA:1125:U:O2'	1:AA:1127:G:N7	2.24	0.49
1:AA:1399:C:C2	1:AA:1502:A:N6	2.80	0.49
2:AB:103:THR:HA	2:AB:180:LEU:HD11	1.93	0.49
26:BA:1805:C:O5'	26:BA:1805:C:H6	1.95	0.49
26:BA:2271:G:C8	26:BA:2439:C:C4	3.00	0.49
39:BS:14:VAL:O	39:BS:18:ILE:HG12	2.11	0.49
45:BY:92:ASN:HB3	45:BY:94:LYS:N	2.25	0.49
46:BZ:7:ALA:HB3	46:BZ:61:LEU:HD12	1.93	0.49
1:CA:137:C:H2'	1:CA:138:G:H8	1.76	0.49
1:CA:155:C:H2'	1:CA:156:G:O4'	2.11	0.49
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.95	0.49
14:CN:48:ALA:HB2	14:CN:53:LEU:HD12	1.94	0.49
26:DA:1359:A:H2'	26:DA:1360:A:H5'	1.94	0.49
26:DA:1721:G:H8	26:DA:1741:A:H62	1.60	0.49
26:DA:2294:C:H5''	39:DS:10:ARG:HD2	1.94	0.49
26:DA:2483:C:H2'	26:DA:2484:G:O4'	2.11	0.49
26:DA:996:A:C2	26:DA:997:G:C8	3.00	0.49
34:DN:30:ILE:HG23	34:DN:52:VAL:HG11	1.94	0.49
26:DA:2849:U:P	40:DT:95:ARG:HH12	2.35	0.49
1:AA:1008:C:H2'	1:AA:1009:G:O4'	2.12	0.49
2:AB:20:GLU:HA	2:AB:21:ARG:HH21	1.78	0.49
26:BA:2357:G:H4'	26:BA:2358:A:H5''	1.94	0.49
26:BA:271:U:H1'	33:BI:50:ARG:CZ	2.43	0.49
26:BA:185:A:O2'	26:BA:852:G:O6	2.26	0.49
28:BD:70:TRP:HB3	28:BD:190:TYR:CE1	2.46	0.49
38:BR:21:TYR:OH	38:BR:43:GLU:HG2	2.12	0.49
26:BA:1201:A:OP1	41:BU:55:ARG:HD3	2.12	0.49
46:BZ:117:LEU:CD1	46:BZ:144:LEU:HD22	2.39	0.49
1:CA:110:C:H2'	1:CA:111:G:O4'	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:984:C:O5'	1:CA:984:C:H6	1.94	0.49
4:CD:57:ARG:NE	4:CD:205:GLU:OE2	2.44	0.49
15:CO:3:ILE:O	15:CO:3:ILE:HG12	2.13	0.49
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.12	0.49
26:DA:2805:G:H2'	26:DA:2807:G:H8	1.75	0.49
26:DA:286:C:H2'	26:DA:287:C:C6	2.47	0.49
30:DF:129:PHE:CD2	30:DF:163:VAL:HG21	2.48	0.49
32:DH:89:ILE:O	32:DH:129:THR:HG23	2.13	0.49
34:DN:38:HIS:CE1	34:DN:39:ARG:HG3	2.46	0.49
39:DS:68:GLN:O	39:DS:71:ARG:HG3	2.13	0.49
42:DV:62:LEU:HD11	42:DV:95:LEU:HB2	1.93	0.49
44:DX:31:HIS:CD2	44:DX:33:LYS:HB2	2.47	0.49
26:DA:335:C:H4'	45:DY:73:ARG:CZ	2.42	0.49
46:DZ:104:PHE:HA	46:DZ:139:VAL:HB	1.95	0.49
1:AA:1003:G:H2'	1:AA:1004:A:H4'	1.92	0.49
1:AA:110:C:H2'	1:AA:111:G:O4'	2.12	0.49
1:AA:1346:A:OP1	9:AI:120:ARG:NH1	2.45	0.49
1:AA:920:U:H2'	1:AA:921:U:C6	2.48	0.49
23:AW:63:G:H2'	23:AW:64:A:O4'	2.13	0.49
26:BA:82:G:N2	26:BA:101:A:OP2	2.44	0.49
26:BA:2825:C:H5'	52:B5:29:THR:HG21	1.94	0.49
26:BA:878:G:O2'	36:BP:38:GLN:NE2	2.44	0.49
37:BQ:16:ARG:HG2	37:BQ:18:LYS:HE2	1.94	0.49
1:CA:875:C:H1'	8:CH:15:ASN:HD21	1.77	0.49
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.93	0.49
26:DA:10:G:H2'	26:DA:11:G:C8	2.47	0.49
26:DA:1264:G:H2'	26:DA:2014:A:N6	2.27	0.49
26:DA:528:A:C2	26:DA:2042:A:H2'	2.47	0.49
30:DF:11:VAL:HG22	30:DF:125:LEU:HB2	1.94	0.49
30:DF:13:SER:OG	30:DF:16:GLY:O	2.26	0.49
34:DN:67:LEU:HD13	34:DN:87:LEU:HD13	1.94	0.49
35:DO:73:ASP:HB2	40:DT:82:LEU:HD13	1.93	0.49
1:AA:1523:G:OP1	11:AK:123:LYS:NZ	2.30	0.49
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	1.94	0.49
4:AD:166:LYS:HB2	4:AD:168:ARG:NH1	2.26	0.49
12:AL:33:ARG:HH11	12:AL:62:SER:HB3	1.77	0.49
25:AY:50:U:N3	25:AY:64:A:H2	2.05	0.49
26:BA:2051:G:H2'	26:BA:2053:A:OP1	2.12	0.49
26:BA:8:A:H2'	26:BA:9:U:C6	2.47	0.49
36:BP:50:ARG:HG2	55:B8:61:LEU:HD11	1.95	0.49
26:BA:1001:G:P	37:BQ:14:ARG:HH22	2.36	0.49
1:CA:444:C:H2'	1:CA:445:G:H8	1.78	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:528:C:H5'	1:CA:529:G:OP2	2.13	0.49
1:CA:91:C:H2'	1:CA:92:C:C6	2.48	0.49
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.47	0.49
1:CA:923:A:OP1	5:CE:21:ALA:HB2	2.11	0.49
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.94	0.49
26:DA:1778:U:H2'	26:DA:1784:A:N6	2.28	0.49
26:DA:2408:U:H2'	26:DA:2409:G:C8	2.46	0.49
26:DA:2471:C:N4	26:DA:2476:A:O2'	2.43	0.49
26:DA:2558:C:H2'	26:DA:2559:C:O4'	2.13	0.49
31:DG:43:LEU:HD11	31:DG:153:ARG:HG2	1.93	0.49
27:DB:41:U:H5	31:DG:70:VAL:N	2.09	0.49
42:DV:100:ARG:NH1	42:DV:100:ARG:HG3	2.10	0.49
1:AA:1492:A:H2'	1:AA:1493:A:C8	2.48	0.49
1:AA:630:G:O2'	1:AA:631:G:H5'	2.13	0.49
1:AA:674:G:OP1	6:AF:87:ARG:NH2	2.43	0.49
4:AD:166:LYS:HB2	4:AD:168:ARG:CZ	2.42	0.49
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.93	0.49
1:AA:1244:C:OP1	21:AU:9:ARG:HB2	2.13	0.49
26:BA:54:G:O2'	26:BA:125:A:N1	2.39	0.49
26:BA:1338:U:H2'	26:BA:1339:C:C6	2.47	0.49
26:BA:1402:G:OP1	61:BA:5239:HOH:O	2.20	0.49
26:BA:1825:U:H2'	26:BA:1826:C:H6	1.78	0.49
26:BA:2331:G:N1	39:BS:3:ARG:HA	2.28	0.49
1:CA:1287:A:N3	1:CA:1353:G:O2'	2.42	0.49
1:CA:45:U:H2'	1:CA:46:G:C8	2.47	0.49
2:CB:77:ALA:HB2	2:CB:211:ILE:HD13	1.94	0.49
12:CL:33:ARG:HG2	12:CL:60:LEU:HD12	1.94	0.49
23:CW:76:31M:O	24:CX:76:A:O2'	2.19	0.49
26:DA:1153:C:OP1	41:DU:92:ARG:NH1	2.42	0.49
26:DA:2058:A:N7	61:DA:3876:HOH:O	2.34	0.49
26:DA:2123:G:H2'	26:DA:2124:G:C8	2.47	0.49
26:DA:300:A:H3'	45:DY:84:ARG:HH22	1.77	0.49
26:DA:639:U:H2'	26:DA:640:C:C6	2.48	0.49
28:DD:275:LYS:HG3	28:DD:276:LYS:HA	1.94	0.49
31:DG:16:ARG:HB2	31:DG:17:PRO:HD3	1.94	0.49
31:DG:103:LEU:HD22	31:DG:178:PHE:HZ	1.77	0.49
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.78	0.49
24:AX:66:C:H2'	24:AX:67:C:O4'	2.13	0.49
25:AY:51:U:H2'	25:AY:52:G:C8	2.48	0.49
26:BA:1324:A:OP1	38:BR:36:THR:HG23	2.12	0.49
26:BA:2303:U:H2'	26:BA:2304:C:C6	2.48	0.49
26:BA:572:A:O2'	26:BA:573:G:OP1	2.27	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1002:G:N3	1:CA:1003:G:H8	2.10	0.49
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.45	0.49
1:CA:838:G:N2	1:CA:848:C:N3	2.58	0.49
1:CA:8:A:H5'	5:CE:101:ILE:HG22	1.95	0.49
6:CF:11:ASN:HB3	6:CF:14:LEU:HG	1.95	0.49
49:D2:32:LEU:HD23	49:D2:53:LEU:HB3	1.94	0.49
26:DA:588:U:H2'	26:DA:589:C:C6	2.46	0.49
26:DA:989:G:H4'	26:DA:990:A:OP1	2.12	0.49
26:DA:764:A:H5'	28:DD:210:GLY:HA2	1.94	0.49
44:DX:12:VAL:HG22	44:DX:29:TRP:CE2	2.47	0.49
1:AA:1030(D):A:N6	1:AA:1031:G:H21	2.10	0.49
1:AA:625:G:H4'	16:AP:16:HIS:CD2	2.48	0.49
1:AA:865:A:C2	1:AA:918:A:H4'	2.45	0.49
3:AC:114:PRO:HA	3:AC:185:GLY:HA3	1.94	0.49
23:AW:58:A:H2	23:AW:60:U:HO2'	1.59	0.49
24:AX:21:A:N6	24:AX:46:G:H2'	2.27	0.49
25:AY:22:G:H2'	25:AY:23:A:H8	1.75	0.49
51:B4:26:SER:OG	51:B4:27:THR:N	2.45	0.49
31:BG:28:VAL:O	31:BG:31:VAL:HG12	2.13	0.49
61:BA:4985:HOH:O	36:BP:39:LYS:HE3	2.12	0.49
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.77	0.49
1:CA:539:A:H2'	1:CA:540:G:H8	1.76	0.49
1:CA:815:A:N7	1:CA:1509:C:O2'	2.41	0.49
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD22	1.94	0.49
26:DA:25:U:C4	26:DA:26:G:C6	3.00	0.49
41:DU:86:ALA:O	42:DV:49:THR:HG23	2.13	0.49
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.13	0.49
19:AS:41:VAL:O	19:AS:43:GLU:N	2.45	0.49
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.46	0.49
26:BA:1921:G:H2'	26:BA:1921:G:N3	2.28	0.49
26:BA:2162:C:H1'	26:BA:2174:G:H22	1.77	0.49
26:BA:932:C:H3'	26:BA:933:C:C5'	2.40	0.49
36:BP:50:ARG:HH21	55:B8:7:HIS:HD2	1.59	0.49
44:BX:31:HIS:HD2	44:BX:33:LYS:H	1.59	0.49
1:CA:1029:C:N4	1:CA:1033:G:O6	2.46	0.49
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.13	0.49
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.94	0.49
3:CC:48:TYR:HE1	3:CC:118:GLN:HG3	1.78	0.49
5:CE:34:VAL:HG11	5:CE:63:ARG:HG3	1.94	0.49
7:CG:126:ASP:O	7:CG:130:GLY:N	2.46	0.49
9:CI:23:ASN:ND2	9:CI:25:LYS:HG2	2.27	0.49
1:CA:1494:G:H4'	26:DA:1913:A:N7	2.28	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2154:G:C2	26:DA:2155:G:C8	3.01	0.49
26:DA:812:C:H2'	26:DA:813:U:H6	1.77	0.49
46:DZ:5:LEU:HD21	46:DZ:43:GLU:HB3	1.94	0.49
1:AA:1216:G:OP1	14:AN:2:ALA:HA	2.13	0.49
1:AA:72:C:H2'	1:AA:73:G:O4'	2.13	0.49
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.47	0.49
12:AL:117:ARG:HB3	12:AL:122:THR:HB	1.95	0.49
26:BA:2359:C:O2'	53:B6:21:TYR:OH	2.30	0.49
26:BA:1211:U:H2'	26:BA:1212:C:C6	2.48	0.49
26:BA:172:C:N4	26:BA:202:A:H61	2.10	0.49
26:BA:2064:A:OP1	61:BA:5120:HOH:O	2.20	0.49
26:BA:2331:G:C2	39:BS:3:ARG:HA	2.48	0.49
28:BD:26:LYS:HB3	28:BD:83:GLU:HG2	1.94	0.49
30:BF:116:ASP:OD1	30:BF:119:ARG:NH2	2.46	0.49
24:AX:57:A:O4'	31:BG:78:SER:OG	2.31	0.49
46:BZ:41:LEU:HD21	46:BZ:83:PRO:HG2	1.94	0.49
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.47	0.49
1:CA:78:G:H2'	1:CA:79:G:H5''	1.95	0.49
8:CH:83:ILE:HB	8:CH:137:VAL:HG13	1.94	0.49
24:CX:9:G:N2	24:CX:46:G:OP2	2.46	0.49
25:CY:18:G:C2	25:CY:55:PSU:C4	3.00	0.49
26:DA:1268:A:H2'	26:DA:1269:A:O4'	2.12	0.49
26:DA:1512:U:H2'	26:DA:1513:C:C6	2.48	0.49
28:DD:132:PRO:HG2	28:DD:135:PHE:HD2	1.78	0.49
35:DO:122:LEU:HD13	40:DT:72:VAL:HG11	1.94	0.49
1:AA:236:G:OP1	17:AQ:40:LYS:NZ	2.45	0.48
11:AK:48:ILE:HD12	11:AK:63:LEU:HB2	1.95	0.48
23:AW:25:C:C2'	23:AW:26:A:H5'	2.43	0.48
24:AX:47:U:H5''	24:AX:48:C:OP1	2.13	0.48
27:BB:102:A:N7	61:BB:318:HOH:O	2.35	0.48
1:CA:1118:C:H1'	1:CA:1179:A:C4	2.48	0.48
25:CY:29:G:N2	25:CY:41:C:N3	2.61	0.48
55:D8:33:ASN:HA	55:D8:36:LYS:HD2	1.94	0.48
26:DA:131:G:OP1	61:DA:3791:HOH:O	2.19	0.48
26:DA:2037:G:H2'	26:DA:2038:G:C8	2.48	0.48
26:DA:2376:A:N3	39:DS:106:ARG:NH2	2.52	0.48
26:DA:2278:A:OP1	37:DQ:11:LYS:HD2	2.12	0.48
1:AA:1049:U:OP1	14:AN:3:ARG:HB2	2.14	0.48
53:B6:8:LYS:HG2	55:B8:34:TRP:CG	2.49	0.48
26:BA:1410:G:P	48:B1:3:LYS:HG3	2.53	0.48
30:BF:164:ARG:O	30:BF:168:ARG:HB2	2.12	0.48
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:189(L):G:H2'	1:CA:190:U:C6	2.48	0.48
1:CA:392:G:H2'	1:CA:393:A:H8	1.77	0.48
1:CA:50:A:H1'	1:CA:52:G:C8	2.48	0.48
1:CA:976:G:OP1	14:CN:32:SER:N	2.34	0.48
2:CB:119:GLU:OE2	2:CB:153:ARG:NH2	2.41	0.48
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.76	0.48
9:CI:86:VAL:HA	9:CI:89:ASN:O	2.13	0.48
23:CW:21:A:O2'	23:CW:22:G:OP1	2.28	0.48
56:D9:10:ILE:HD12	56:D9:32:HIS:HA	1.94	0.48
26:DA:2137:C:H42	26:DA:2154:G:H1	1.59	0.48
26:DA:2206:G:H5'	26:DA:2207:G:N7	2.28	0.48
26:DA:222:A:H5''	26:DA:421:U:OP1	2.13	0.48
26:DA:652(B):A:N1	26:DA:655:A:H1'	2.29	0.48
33:DI:40:THR:HG23	33:DI:43:ASN:HD21	1.77	0.48
39:DS:41:ASP:OD2	39:DS:44:LYS:HE2	2.13	0.48
43:DW:60:ASN:HD22	43:DW:60:ASN:N	2.11	0.48
1:AA:1284:C:OP2	1:AA:1285:A:O2'	2.29	0.48
1:AA:621:A:H2'	1:AA:622:A:C8	2.48	0.48
2:AB:163:PHE:CD2	2:AB:185:ILE:HG13	2.48	0.48
2:AB:76:GLN:H	2:AB:76:GLN:CD	2.16	0.48
3:AC:6:HIS:CD2	3:AC:8:ILE:HB	2.48	0.48
7:AG:80:VAL:HB	7:AG:85:TYR:HE2	1.77	0.48
8:AH:13:ILE:O	8:AH:17:THR:HG23	2.13	0.48
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.13	0.48
25:AY:32:PSU:C2	25:AY:33:U:H5	2.32	0.48
51:B4:53:GLU:C	51:B4:55:ARG:N	2.65	0.48
26:BA:2160:C:C2	26:BA:2176:G:C2	3.02	0.48
26:BA:236:G:H4'	26:BA:413:G:C5	2.48	0.48
34:BN:4:TYR:CD2	41:BU:100:VAL:HG11	2.48	0.48
34:BN:58:ASP:OD1	34:BN:58:ASP:N	2.40	0.48
37:BQ:52:VAL:HA	37:BQ:55:VAL:HG12	1.94	0.48
1:CA:73:G:C6	1:CA:97:G:C6	3.01	0.48
7:CG:20:ASP:HB3	7:CG:23:VAL:HB	1.95	0.48
8:CH:20:TYR:CE1	8:CH:76:PRO:HG2	2.48	0.48
8:CH:64:LYS:HG2	8:CH:79:VAL:HG21	1.94	0.48
25:CY:7:A:N6	25:CY:66:U:N3	2.17	0.48
26:DA:1309:G:H3'	54:D7:9:ARG:HH12	1.78	0.48
26:DA:1478:G:HO2'	26:DA:1558:A:H2	1.62	0.48
26:DA:1922:G:H2'	26:DA:1923:U:O4'	2.13	0.48
32:DH:164:TYR:HB2	32:DH:167:GLU:HB2	1.95	0.48
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.42	0.48
1:AA:1279:A:O2'	1:AA:1281:U:OP2	2.20	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1425:U:H2'	1:AA:1426:C:C6	2.48	0.48
1:AA:627:G:H2'	1:AA:628:G:H8	1.78	0.48
23:AW:26:A:N1	23:AW:44:G:N2	2.61	0.48
36:BP:63:PRO:HD3	55:B8:27:THR:HG22	1.94	0.48
55:B8:23:VAL:CG1	55:B8:47:LYS:HD3	2.43	0.48
56:B9:7:VAL:HG12	56:B9:34:GLN:HB3	1.94	0.48
26:BA:1817:A:H1'	26:BA:1960:A:N6	2.28	0.48
26:BA:2141:A:C2	26:BA:2192:A:H2'	2.48	0.48
26:BA:2784:C:H2'	26:BA:2785:C:C6	2.48	0.48
26:BA:655:G:OP1	55:B8:47:LYS:NZ	2.41	0.48
26:BA:847:A:OP1	26:BA:847:A:H8	1.96	0.48
26:BA:2652:G:OP1	34:BN:97:ARG:NH2	2.46	0.48
35:BO:98:VAL:HG22	35:BO:118:ALA:HA	1.96	0.48
39:BS:3:ARG:HE	39:BS:4:LEU:N	2.11	0.48
1:CA:1030(A):G:N3	1:CA:1030(C):G:H8	2.11	0.48
1:CA:1035:A:H2'	1:CA:1036:G:C8	2.48	0.48
1:CA:339:C:H2'	1:CA:340:U:C6	2.49	0.48
6:CF:76:ALA:O	6:CF:80:ARG:HG3	2.13	0.48
15:CO:26:GLU:HB3	15:CO:81:LEU:HD13	1.96	0.48
25:CY:35:A:H2'	25:CY:36:A:O4'	2.13	0.48
26:DA:2126:A:H4'	26:DA:2127:G:OP1	2.13	0.48
26:DA:2602:A:H4'	26:DA:2603:G:O5'	2.14	0.48
26:DA:2853:C:H2'	26:DA:2854:G:H8	1.77	0.48
28:DD:137:PRO:O	28:DD:140:THR:HG23	2.14	0.48
7:AG:150:ALA:HB2	11:AK:50:TYR:OH	2.13	0.48
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.27	0.48
26:BA:1451:U:H2'	26:BA:1452:U:H6	1.78	0.48
26:BA:347:G:C8	30:BF:171:PRO:HG3	2.48	0.48
30:BF:192:LEU:HD13	30:BF:194:MET:HE2	1.96	0.48
33:BI:85:GLU:HB3	33:BI:86:THR:H	1.52	0.48
46:BZ:111:VAL:C	46:BZ:113:ALA:H	2.17	0.48
1:CA:1002:G:H2'	1:CA:1003:G:H8	1.78	0.48
1:CA:1006:C:H2'	1:CA:1007:C:C6	2.49	0.48
1:CA:141:A:H1'	1:CA:182:U:O2	2.13	0.48
2:CB:71:VAL:HG23	2:CB:163:PHE:O	2.14	0.48
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.95	0.48
19:CS:17:GLU:O	19:CS:17:GLU:HG2	2.14	0.48
25:CY:69:G:C2	25:CY:70:G:H1'	2.48	0.48
26:DA:2203:U:H4'	28:DD:151:LYS:HG2	1.95	0.48
31:DG:43:LEU:HD12	31:DG:45:GLU:HG3	1.96	0.48
34:DN:38:HIS:ND1	34:DN:39:ARG:HG3	2.28	0.48
38:DR:103:ARG:NH1	38:DR:108:GLY:O	2.42	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
41:DU:78:THR:O	41:DU:117:GLN:NE2	2.46	0.48
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.94	0.48
48:B1:72:GLU:O	48:B1:76:ARG:HG3	2.13	0.48
26:BA:1587:U:H2'	26:BA:1588:G:O4'	2.13	0.48
26:BA:1715:A:H4'	26:BA:1716:A:O5'	2.14	0.48
26:BA:173:C:H2'	26:BA:174:U:H6	1.78	0.48
26:BA:2163:G:N3	26:BA:2164:C:H1'	2.29	0.48
26:BA:939:C:H2'	26:BA:940:C:H6	1.79	0.48
29:BE:178:GLU:OE2	29:BE:178:GLU:N	2.46	0.48
33:BI:47:LEU:O	33:BI:51:ILE:HG13	2.13	0.48
33:BI:61:ARG:HD2	33:BI:61:ARG:N	2.28	0.48
1:CA:1029:C:N4	1:CA:1032:G:C6	2.77	0.48
1:CA:1190:G:OP1	3:CC:5:ILE:N	2.38	0.48
1:CA:1262:C:H2'	1:CA:1263:C:H6	1.79	0.48
1:CA:189(C):C:H2'	1:CA:189(D):C:O4'	2.14	0.48
1:CA:428:G:H4'	1:CA:429:U:O5'	2.12	0.48
2:CB:178:ARG:NH2	8:CH:68:ARG:HH12	2.10	0.48
9:CI:16:ARG:HH11	9:CI:66:ARG:HH11	1.62	0.48
26:DA:1364:G:P	48:D1:3:LYS:HG3	2.53	0.48
26:DA:184:C:H2'	26:DA:185:U:C6	2.48	0.48
26:DA:861:A:N3	27:DB:79:C:O2'	2.41	0.48
30:DF:183:VAL:O	30:DF:187:VAL:HG23	2.13	0.48
40:DT:59:THR:HG23	40:DT:78:LEU:HB3	1.96	0.48
1:AA:1429:C:H2'	1:AA:1430:C:C6	2.48	0.48
1:AA:62:U:OP1	1:AA:385:C:O2'	2.26	0.48
8:AH:51:VAL:HG12	8:AH:52:ASP:N	2.28	0.48
25:AY:63:G:C2	25:AY:64:A:H1'	2.48	0.48
26:BA:1277:G:H2'	26:BA:1278:G:C8	2.48	0.48
26:BA:2018:C:H4'	26:BA:2019:G:OP1	2.12	0.48
26:BA:2151:C:H2'	26:BA:2152:U:H6	1.77	0.48
26:BA:2162:C:C2	26:BA:2173:G:N2	2.82	0.48
26:BA:2398:C:H2'	26:BA:2399:U:C6	2.49	0.48
26:BA:312:C:H2'	26:BA:313:A:H8	1.79	0.48
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.77	0.48
1:CA:1119:C:C4	1:CA:1154:G:O6	2.66	0.48
1:CA:1135:U:H2'	1:CA:1137:C:O2	2.14	0.48
1:CA:742:G:P	15:CO:35:ARG:HH22	2.36	0.48
1:CA:408:A:H4'	4:CD:112:VAL:HG21	1.96	0.48
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.28	0.48
26:DA:952:G:H5"	26:DA:953:A:OP2	2.14	0.48
31:DG:125:PHE:HB3	31:DG:166:ASP:OD1	2.14	0.48
35:DO:4:PRO:O	35:DO:5:GLN:HB2	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
44:DX:20:GLY:HA2	44:DX:23:GLU:OE2	2.14	0.48
1:AA:1158:C:H5	1:AA:1181:G:N1	2.06	0.48
6:AF:69:GLU:CD	6:AF:69:GLU:H	2.16	0.48
7:AG:111:ARG:HD2	7:AG:123:GLU:HB2	1.95	0.48
10:AJ:11:PHE:CE1	10:AJ:67:THR:HG22	2.49	0.48
19:AS:64:GLU:O	19:AS:67:VAL:HG23	2.14	0.48
24:AX:55:PSU:O2'	24:AX:57:A:N7	2.33	0.48
26:BA:1712:A:H2'	26:BA:1713:G:O4'	2.14	0.48
26:BA:185:A:H2'	26:BA:185:A:N3	2.27	0.48
26:BA:2340:A:H2'	26:BA:2341:G:H8	1.75	0.48
28:BD:70:TRP:HB3	28:BD:190:TYR:CZ	2.49	0.48
31:BG:11:TYR:CZ	31:BG:16:ARG:HD3	2.48	0.48
31:BG:66:GLN:HB3	31:BG:92:VAL:HG21	1.94	0.48
39:BS:59:LYS:HE3	39:BS:60:GLY:H	1.79	0.48
1:CA:1125:U:H3'	1:CA:1126:U:H5''	1.96	0.48
1:CA:1228:C:OP1	13:CM:115:LYS:N	2.23	0.48
2:CB:81:VAL:HB	2:CB:94:ASN:HD21	1.78	0.48
7:CG:12:LEU:HD12	7:CG:12:LEU:H	1.78	0.48
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.53	0.48
53:D6:11:LEU:HB2	53:D6:21:TYR:HB2	1.95	0.48
26:DA:1472:A:H2'	26:DA:1473:G:O4'	2.13	0.48
26:DA:171:G:H2'	26:DA:172:C:C6	2.49	0.48
26:DA:2162:G:H4'	26:DA:2172:U:O2'	2.13	0.48
26:DA:2695:C:H2'	26:DA:2696:U:C6	2.49	0.48
26:DA:851:U:O2'	50:D3:42:ALA:O	2.30	0.48
29:DE:108:SER:HB3	29:DE:165:VAL:HG21	1.96	0.48
30:DF:120:GLU:CB	30:DF:122:LYS:HG2	2.44	0.48
46:DZ:110:GLY:HA3	46:DZ:145:GLU:HA	1.96	0.48
1:AA:1149:C:H2'	1:AA:1150:U:H6	1.77	0.48
1:AA:328:C:H4'	1:AA:329:A:H5'	1.96	0.48
4:AD:3:ARG:HD3	4:AD:118:ARG:CD	2.44	0.48
5:AE:36:ASP:OD1	5:AE:38:GLN:N	2.38	0.48
47:B0:53:MET:HG3	47:B0:59:LEU:HD23	1.96	0.48
26:BA:2138:G:N2	26:BA:2184:G:OP1	2.46	0.48
26:BA:2205:C:H2'	26:BA:2206:G:H8	1.78	0.48
26:BA:2804:C:H6	26:BA:2804:C:OP2	1.96	0.48
26:BA:605:G:H2'	26:BA:606:G:C8	2.49	0.48
26:BA:895:G:H2'	26:BA:896:A:C8	2.48	0.48
39:BS:15:ARG:NE	39:BS:88:ASP:OD2	2.45	0.48
1:CA:1009:G:H22	1:CA:1021:G:H1'	1.78	0.48
1:CA:10:A:OP2	5:CE:126:ARG:HD2	2.14	0.48
1:CA:1133:G:N2	1:CA:1141:C:N3	2.58	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:707:C:H2'	1:CA:708:C:C6	2.49	0.48
2:CB:46:LYS:O	2:CB:50:GLU:HB2	2.14	0.48
3:CC:32:LEU:HD12	3:CC:59:ARG:HH22	1.79	0.48
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.96	0.48
5:CE:84:PHE:N	5:CE:87:SER:O	2.45	0.48
20:CT:10:LEU:HD23	20:CT:12:ALA:HB2	1.95	0.48
26:DA:77:C:H42	26:DA:109:G:H1	1.61	0.48
26:DA:1434:A:H61	26:DA:1558:A:N6	2.12	0.48
26:DA:1363:C:O2'	26:DA:1809:A:N3	2.37	0.48
26:DA:2118:U:C4	26:DA:2149:G:H1'	2.48	0.48
26:DA:2293:C:H42	26:DA:2339:G:H1	1.61	0.48
26:DA:2540:C:H2'	26:DA:2541:A:O4'	2.14	0.48
26:DA:390:A:H4'	26:DA:391:G:H5'	1.94	0.48
26:DA:828:U:H2'	26:DA:829:A:C8	2.49	0.48
28:DD:108:PRO:HB3	28:DD:143:HIS:CE1	2.49	0.48
31:DG:15:VAL:HG13	31:DG:175:LEU:HD23	1.96	0.48
34:DN:34:LEU:O	34:DN:49:GLY:HA3	2.13	0.48
37:DQ:36:ALA:HB2	37:DQ:103:MET:SD	2.54	0.48
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.49	0.48
1:AA:501:C:H2'	1:AA:502:G:H8	1.78	0.48
9:AI:99:LEU:HB3	9:AI:101:PHE:CD1	2.49	0.48
10:AJ:49:VAL:HG23	14:AN:41:ARG:HD2	1.96	0.48
12:AL:34:ARG:NH2	61:AL:201:HOH:O	2.25	0.48
23:AW:47:U:H5'	23:AW:47:U:C6	2.45	0.48
26:BA:2121:U:H2'	26:BA:2122:G:C8	2.49	0.48
26:BA:2298:A:H4'	26:BA:2299:A:O4'	2.14	0.48
26:BA:518:G:O6	61:BA:4550:HOH:O	2.19	0.48
26:BA:2584:A:C8	29:BE:144:ARG:HD2	2.49	0.48
32:BH:154:PRO:HB3	32:BH:163:TYR:CE2	2.49	0.48
35:BO:16:ALA:HB2	35:BO:52:VAL:HG21	1.96	0.48
1:CA:1030(A):G:N3	1:CA:1030(C):G:C8	2.81	0.48
1:CA:1063:C:H3'	1:CA:1064:G:H2'	1.96	0.48
1:CA:1179:A:H2'	1:CA:1180:A:O4'	2.13	0.48
1:CA:1058:G:H1	1:CA:1199:U:H3	1.62	0.48
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.14	0.48
1:CA:93:G:C2'	1:CA:96:U:H5'	2.44	0.48
3:CC:87:LEU:O	3:CC:91:LEU:N	2.36	0.48
6:CF:33:TYR:CD2	6:CF:75:LEU:HD23	2.49	0.48
12:CL:53:ARG:HH12	12:CL:92:ASP:HB2	1.79	0.48
53:D6:6:ARG:NH1	53:D6:26:ASN:HB2	2.28	0.48
26:DA:1889:A:H2'	26:DA:1890:A:C8	2.49	0.48
26:DA:2586:C:OP2	26:DA:2608:G:N1	2.42	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:272(E):G:C2	26:DA:364:C:C2	3.02	0.48
26:DA:2820:A:OP1	38:DR:4:LEU:HD23	2.14	0.48
28:DD:73:VAL:HG13	28:DD:120:GLY:HA3	1.95	0.48
30:DF:29:ASN:O	30:DF:112:MET:HE1	2.13	0.48
46:DZ:138:GLU:H	46:DZ:156:LYS:HZ1	1.62	0.48
1:AA:1137:C:H6	1:AA:1137:C:H3'	1.77	0.47
25:AY:58:A:H4'	25:AY:59:U:OP1	2.14	0.47
25:AY:5:G:C2	25:AY:6:G:C4	3.02	0.47
26:BA:552:C:C5	26:BA:2792:U:H2'	2.49	0.47
30:BF:150:GLY:HA2	30:BF:172:TRP:CD2	2.49	0.47
31:BG:16:ARG:HE	31:BG:31:VAL:HG11	1.79	0.47
36:BP:50:ARG:HD3	55:B8:7:HIS:CD2	2.49	0.47
1:CA:1121:U:C4	1:CA:1122:U:C4	3.01	0.47
1:CA:130:A:O2'	1:CA:131:C:O5'	2.28	0.47
1:CA:1371:G:O3'	9:CI:69:GLY:HA3	2.14	0.47
1:CA:89:C:H2'	1:CA:90:U:O4'	2.14	0.47
2:CB:139:LYS:O	2:CB:143:GLU:HG3	2.14	0.47
2:CB:212:GLN:NE2	2:CB:234:PRO:O	2.46	0.47
3:CC:101:LEU:HD12	3:CC:102:ASN:N	2.29	0.47
5:CE:6:PHE:HB3	5:CE:35:GLY:C	2.34	0.47
1:CA:933:G:O6	7:CG:3:ARG:NH2	2.47	0.47
26:DA:1365:A:OP2	48:D1:3:LYS:HG2	2.14	0.47
26:DA:2564:A:C2	26:DA:2647:U:H4'	2.49	0.47
27:DB:14:U:H5'	27:DB:70:C:O2	2.13	0.47
1:AA:950:U:H2'	1:AA:951:G:H8	1.80	0.47
5:AE:90:VAL:O	5:AE:120:THR:HA	2.14	0.47
13:AM:79:LYS:HA	13:AM:82:MET:HE2	1.96	0.47
19:AS:40:ILE:HD11	19:AS:74:PHE:HE1	1.78	0.47
13:AM:123:ALA:HB2	23:AW:39:PSU:H1'	1.95	0.47
26:BA:714:U:O2	55:B8:2:PRO:HD2	2.14	0.47
32:BH:117:PRO:HG3	32:BH:123:PHE:CD2	2.49	0.47
33:BI:130:TYR:N	33:BI:138:ILE:O	2.42	0.47
35:BO:4:PRO:O	35:BO:5:GLN:HB2	2.14	0.47
36:BP:82:GLY:HA2	36:BP:113:LYS:O	2.13	0.47
1:CA:1125:U:C2'	1:CA:1126:U:H5''	2.44	0.47
1:CA:1298:C:H4'	1:CA:1299:A:H5'	1.96	0.47
1:CA:392:G:H2'	1:CA:393:A:C8	2.48	0.47
1:CA:646:U:H2'	1:CA:647:C:H6	1.75	0.47
1:CA:657:G:H4'	15:CO:28:GLN:HG2	1.96	0.47
20:CT:24:LEU:HA	20:CT:24:LEU:HD13	1.69	0.47
23:CW:8:4SU:S4	23:CW:14:A:N7	2.88	0.47
24:CX:67:C:C2'	24:CX:68:C:H5'	2.43	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1641:A:H2'	26:DA:1642:G:O4'	2.14	0.47
26:DA:2141:G:H2'	26:DA:2142:C:O4'	2.14	0.47
26:DA:2304:G:H22	26:DA:2312:U:H3	1.61	0.47
26:DA:2776:A:H4'	26:DA:2777:G:H5''	1.96	0.47
26:DA:817:C:H2'	26:DA:818:G:O4'	2.14	0.47
26:DA:93:G:H2'	26:DA:94:C:C6	2.49	0.47
1:AA:165:C:H2'	1:AA:166:G:H8	1.79	0.47
1:AA:371:G:O2'	1:AA:373:A:N7	2.47	0.47
1:AA:596:C:OP2	61:AA:4083:HOH:O	2.20	0.47
1:AA:950:U:H2'	1:AA:951:G:C8	2.49	0.47
3:AC:118:GLN:HG2	3:AC:118:GLN:H	1.45	0.47
55:B8:42:ARG:HD2	61:B8:205:HOH:O	2.15	0.47
26:BA:1756:U:H2'	26:BA:1757:C:C6	2.48	0.47
26:BA:472:G:OP1	41:BU:3:ARG:NH1	2.42	0.47
26:BA:946:A:H2'	26:BA:947:A:O4'	2.14	0.47
33:BI:114:LEU:HD13	33:BI:130:TYR:HD1	1.78	0.47
37:BQ:34:LEU:HD11	37:BQ:129:THR:HB	1.95	0.47
1:CA:1128:C:H1'	1:CA:1147:C:N4	2.25	0.47
1:CA:934:C:OP1	61:CA:4164:HOH:O	2.20	0.47
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.96	0.47
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	1.95	0.47
1:CA:1320:C:O4'	19:CS:73:GLU:HG3	2.13	0.47
21:CU:12:LYS:HD3	21:CU:22:ARG:HB3	1.96	0.47
26:DA:39:C:H2'	26:DA:40:C:C6	2.49	0.47
26:DA:615:G:OP1	30:DF:40:GLN:HG2	2.14	0.47
28:DD:71:ASP:HB3	28:DD:103:ARG:NH2	2.28	0.47
29:DE:144:ARG:HB3	29:DE:145:LYS:H	1.48	0.47
29:DE:178:GLU:N	29:DE:178:GLU:OE2	2.42	0.47
26:DA:322:A:OP1	30:DF:168:ARG:HD2	2.14	0.47
32:DH:7:LEU:O	32:DH:69:ARG:NH1	2.40	0.47
37:DQ:37:LEU:HD21	37:DQ:130:LYS:HE2	1.96	0.47
42:DV:5:VAL:HG11	42:DV:57:VAL:HG21	1.96	0.47
44:DX:4:ALA:HB1	44:DX:42:ALA:HA	1.95	0.47
1:AA:461:A:O2'	1:AA:470:C:H5'	2.13	0.47
3:AC:134:ILE:HG22	3:AC:168:ALA:HB3	1.96	0.47
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.14	0.47
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.96	0.47
26:BA:1748:A:OP2	61:BA:5017:HOH:O	2.20	0.47
1:AA:1495:U:O2'	26:BA:1941:A:N1	2.40	0.47
26:BA:2724:U:OP1	26:BA:2727:G:H4'	2.14	0.47
26:BA:945:A:HO2'	26:BA:946:A:H8	1.60	0.47
27:BB:66:A:N6	27:BB:108:U:H2'	2.28	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:642:G:H5'	30:BF:205:ARG:HD2	1.96	0.47
41:BU:86:ALA:O	42:BV:49:THR:HG23	2.14	0.47
1:CA:1030(A):G:N2	1:CA:1030(C):G:H3'	2.30	0.47
1:CA:1181:G:O2'	1:CA:1182:G:N7	2.47	0.47
1:CA:736:C:H2'	1:CA:737:A:C8	2.49	0.47
1:CA:1057:G:H5'	3:CC:155:GLY:HA2	1.95	0.47
19:CS:32:LYS:HE3	19:CS:57:HIS:CD2	2.49	0.47
26:DA:816:C:OP1	26:DA:1185:C:O2'	2.22	0.47
35:DO:7:TYR:CZ	35:DO:44:LYS:HG3	2.50	0.47
42:DV:21:ARG:HG2	42:DV:91:TYR:CD2	2.49	0.47
1:AA:1027:C:H2'	1:AA:1028:C:C6	2.49	0.47
12:AL:97:ARG:HB2	12:AL:98:TYR:CE2	2.49	0.47
25:AY:32:PSU:C2	25:AY:33:U:C5	3.02	0.47
25:AY:50:U:H2'	25:AY:51:U:C6	2.48	0.47
26:BA:1077:G:H21	56:B9:36:GLN:HE22	1.62	0.47
32:BH:20:ALA:HB1	32:BH:21:PRO:HD2	1.97	0.47
35:BO:120:GLU:HG2	35:BO:122:LEU:HG	1.97	0.47
26:BA:326:C:OP2	45:BY:73:ARG:NH2	2.46	0.47
1:CA:727:G:P	1:CA:742:G:H21	2.38	0.47
2:CB:120:ALA:O	2:CB:122:PHE:N	2.43	0.47
3:CC:69:HIS:CD2	3:CC:104:GLN:HB3	2.49	0.47
4:CD:173:TRP:NE1	4:CD:189:PRO:HG3	2.29	0.47
8:CH:33:GLU:HG2	8:CH:48:TYR:CE1	2.49	0.47
1:CA:1328:C:O2'	13:CM:29:ARG:NH2	2.45	0.47
21:CU:15:ARG:HB2	21:CU:15:ARG:HH11	1.79	0.47
26:DA:709:U:H2'	26:DA:710:G:C8	2.50	0.47
28:DD:4:LYS:HB3	28:DD:18:VAL:CG2	2.44	0.47
29:DE:1:MET:HE1	29:DE:199:ARG:HD2	1.95	0.47
33:DI:31:LEU:HD21	33:DI:38:LEU:HG	1.96	0.47
1:AA:1179:A:H4'	9:AI:103:THR:HA	1.97	0.47
1:AA:1191:A:H5''	3:AC:4:LYS:HZ2	1.79	0.47
1:AA:1210:C:N4	1:AA:1211:U:O4	2.47	0.47
2:AB:166:ASP:O	2:AB:170:GLU:N	2.39	0.47
4:AD:175:SER:OG	4:AD:184:LYS:HB2	2.14	0.47
25:AY:18:G:H1	25:AY:55:PSU:H1'	1.80	0.47
25:AY:36:A:N6	25:AY:37:MIA:C6	2.78	0.47
26:BA:1223:C:H6	26:BA:1223:C:O5'	1.96	0.47
26:BA:142:G:H1'	44:BX:37:THR:HG21	1.97	0.47
1:CA:952:U:H4'	1:CA:964:A:N1	2.30	0.47
3:CC:42:LEU:HA	3:CC:45:LYS:HZ2	1.80	0.47
4:CD:57:ARG:NH2	5:CE:107:ARG:HD3	2.28	0.47
7:CG:89:MET:SD	7:CG:155:ARG:HB2	2.55	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:CN:26:ARG:HB3	14:CN:43:CYS:SG	2.54	0.47
24:CX:23:C:H2'	24:CX:24:U:C6	2.49	0.47
26:DA:1410:G:H2'	26:DA:1411:C:C6	2.49	0.47
26:DA:1528(A):A:H2'	26:DA:1529:G:O4'	2.15	0.47
26:DA:2528:U:H5''	56:D9:31:LYS:HE2	1.97	0.47
26:DA:310:A:H1'	26:DA:311:A:H2'	1.95	0.47
61:DA:3829:HOH:O	30:DF:68:LYS:HE2	2.14	0.47
32:DH:86:GLU:OE2	32:DH:132:ARG:NH2	2.47	0.47
1:AA:46:G:O2'	1:AA:365:U:O2	2.31	0.47
2:AB:188:ALA:HB1	2:AB:192:SER:OG	2.15	0.47
53:B6:16:CYS:SG	53:B6:18:ARG:HD3	2.54	0.47
26:BA:1091:A:OP1	26:BA:1092:A:H3'	2.15	0.47
26:BA:2139:A:O2'	26:BA:2140:U:H5''	2.15	0.47
26:BA:2713:C:H2'	26:BA:2714:U:H2'	1.96	0.47
31:BG:28:VAL:HG23	31:BG:29:TRP:CD1	2.50	0.47
32:BH:69:ARG:HG3	32:BH:70:THR:N	2.30	0.47
33:BI:93:THR:OG1	33:BI:96:ASP:OD1	2.24	0.47
41:BU:85:LYS:HE2	41:BU:117:GLN:HA	1.97	0.47
45:BY:30:VAL:HG13	45:BY:37:VAL:HG12	1.97	0.47
1:CA:988:G:C4'	1:CA:1014:A:H61	2.28	0.47
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.49	0.47
1:CA:1186:G:O3'	9:CI:113:LYS:NZ	2.46	0.47
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.96	0.47
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.14	0.47
9:CI:88:TYR:CD1	9:CI:89:ASN:HB2	2.49	0.47
10:CJ:37:PRO:HA	10:CJ:72:VAL:HG12	1.97	0.47
22:CV:14:A:OP1	22:CV:14:A:H8	1.97	0.47
48:D1:3:LYS:HB2	48:D1:61:ARG:NH1	2.30	0.47
26:DA:1514:U:H2'	26:DA:1515:G:H8	1.80	0.47
26:DA:1877:A:H5'	26:DA:1878:G:OP2	2.15	0.47
26:DA:2751:G:C8	32:DH:2:SER:HA	2.49	0.47
26:DA:2788:C:H2'	26:DA:2789:C:C6	2.50	0.47
26:DA:897:C:H3'	26:DA:898:C:C6	2.50	0.47
28:DD:5:LYS:HE3	28:DD:5:LYS:HB3	1.52	0.47
29:DE:5:LEU:HD11	29:DE:79:ARG:HB2	1.96	0.47
31:DG:121:ASN:HB3	31:DG:124:SER:HB2	1.97	0.47
1:AA:1360:A:H2'	1:AA:1361:G:O4'	2.15	0.47
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.30	0.47
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	1.96	0.47
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.97	0.47
3:AC:32:LEU:HD13	3:AC:59:ARG:HD3	1.97	0.47
25:AY:27:G:N2	25:AY:44:G:N3	2.63	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1218:G:N2	26:BA:1222:A:OP2	2.31	0.47
26:BA:2132:G:H4'	26:BA:2133:C:OP2	2.15	0.47
40:BT:53:ARG:NH1	40:BT:53:ARG:HB3	2.30	0.47
1:CA:109:A:C6	1:CA:326:G:C6	3.03	0.47
1:CA:627:G:H2'	1:CA:628:G:H8	1.78	0.47
2:CB:115:LEU:HD11	2:CB:153:ARG:CZ	2.44	0.47
10:CJ:46:ARG:HG2	10:CJ:64:GLU:HB3	1.97	0.47
13:CM:10:PRO:HD2	13:CM:18:ALA:HB1	1.95	0.47
13:CM:92:HIS:CE1	13:CM:98:VAL:HG11	2.49	0.47
26:DA:855:G:O2'	47:D0:27:GLU:OE2	2.31	0.47
48:D1:3:LYS:HB2	48:D1:61:ARG:HH12	1.80	0.47
26:DA:1196:C:H2'	26:DA:1197:G:H8	1.79	0.47
26:DA:118:A:N3	26:DA:178:G:H1'	2.30	0.47
26:DA:2086:U:H2'	26:DA:2087:G:C8	2.49	0.47
26:DA:2364:C:H2'	26:DA:2365:G:O4'	2.14	0.47
32:DH:144:VAL:O	32:DH:148:ILE:HG12	2.15	0.47
46:DZ:108:PRO:HB2	46:DZ:111:VAL:HG23	1.96	0.47
1:AA:1293:G:H2'	1:AA:1294:G:C8	2.49	0.47
1:AA:407:G:OP1	4:AD:115:ARG:NH2	2.48	0.47
26:BA:1357:G:O2'	54:B7:47:ARG:NH2	2.47	0.47
26:BA:41:C:H2'	26:BA:42:G:O4'	2.15	0.47
46:BZ:107:THR:HA	46:BZ:108:PRO:HD3	1.77	0.47
1:CA:1027:C:OP1	1:CA:1027:C:H4'	2.14	0.47
1:CA:1179:A:C6	1:CA:1180:A:C4	3.03	0.47
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.50	0.47
1:CA:337:C:H2'	1:CA:338:A:H8	1.79	0.47
3:CC:6:HIS:HB3	14:CN:49:HIS:ND1	2.30	0.47
8:CH:73:ASP:OD1	8:CH:75:ARG:HD3	2.15	0.47
24:CX:44:A:C6	24:CX:45:G:C6	3.02	0.47
51:D4:53:GLU:HG2	51:D4:55:ARG:N	2.29	0.47
26:DA:1025:G:C4	26:DA:1135:C:H1'	2.49	0.47
26:DA:121:G:H4'	26:DA:149:A:H5'	1.97	0.47
26:DA:1270:C:H5''	26:DA:1271:G:O5'	2.15	0.47
26:DA:2306:C:H3'	26:DA:2307:G:H2'	1.97	0.47
26:DA:2722:G:H2'	26:DA:2723:C:C6	2.50	0.47
26:DA:797:C:H2'	26:DA:798:G:O4'	2.14	0.47
26:DA:2506:U:OP1	29:DE:144:ARG:NH2	2.48	0.47
43:DW:14:PRO:HG2	43:DW:78:GLU:HG2	1.97	0.47
1:AA:1028:C:H2'	1:AA:1029:C:H4'	1.96	0.47
1:AA:1132:C:H2'	1:AA:1133:G:C8	2.50	0.47
1:AA:1443:G:N2	1:AA:1459:C:O2	2.37	0.47
1:AA:299:G:O6	61:AA:4081:HOH:O	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.48	0.47
1:AA:1227:A:P	13:AM:111:LYS:HZ2	2.37	0.47
28:BD:72:LYS:HB3	28:BD:75:ILE:HD12	1.97	0.47
26:BA:1289:G:O2'	36:BP:7:ARG:NH2	2.47	0.47
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.50	0.47
1:CA:1139:G:H4'	1:CA:1140:C:OP1	2.14	0.47
1:CA:1305:G:H5'	21:CU:4:GLY:C	2.36	0.47
9:CI:16:ARG:HH11	9:CI:64:THR:HG21	1.80	0.47
19:CS:32:LYS:HA	19:CS:50:ALA:HB3	1.96	0.47
24:CX:19:G:H4'	24:CX:20:U:OP2	2.15	0.47
26:DA:2166:G:H3'	26:DA:2167:U:C5'	2.40	0.47
26:DA:2563:U:H4'	35:DO:28:SER:HA	1.97	0.47
26:DA:315:G:H2'	26:DA:316:C:C6	2.50	0.47
26:DA:77:C:OP1	49:D2:59:ARG:HD3	2.14	0.47
40:DT:29:ARG:HB3	40:DT:87:ASP:HB2	1.97	0.47
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.15	0.47
1:AA:156:G:N1	1:AA:165:C:N3	2.55	0.47
2:AB:19:HIS:O	2:AB:39:ILE:HG23	2.15	0.47
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.35	0.47
36:BP:59:LEU:HD11	55:B8:10:ALA:HB2	1.97	0.47
2:CB:185:ILE:HG22	2:CB:199:TYR:HD2	1.79	0.47
4:CD:140:VAL:HG11	4:CD:146:ILE:HD11	1.95	0.47
7:CG:44:TYR:O	7:CG:47:CYS:HB2	2.15	0.47
8:CH:124:ALA:O	8:CH:128:GLY:N	2.48	0.47
13:CM:54:VAL:HA	13:CM:57:ARG:HB3	1.97	0.47
1:CA:136:C:O2'	16:CP:63:GLY:O	2.24	0.47
23:CW:29:G:N2	23:CW:41:C:N3	2.56	0.47
26:DA:1514:U:H2'	26:DA:1515:G:C8	2.50	0.47
26:DA:2298:A:C8	26:DA:2299:G:C8	3.03	0.47
26:DA:2319:G:N2	39:DS:3:ARG:HA	2.30	0.47
26:DA:2477:C:N4	56:D9:10:ILE:HG23	2.30	0.47
26:DA:571:A:N6	26:DA:2499:C:O3'	2.47	0.47
26:DA:511:U:H4'	26:DA:1235:G:H4'	1.96	0.47
27:DB:115:G:H2'	27:DB:116:G:O4'	2.15	0.47
31:DG:143:GLU:H	31:DG:143:GLU:HG2	1.41	0.47
46:DZ:57:ILE:HD12	46:DZ:71:VAL:HG23	1.97	0.47
1:AA:1028:C:N4	1:AA:1033:G:H1	2.10	0.46
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.35	0.46
1:AA:1530:G:H4'	1:AA:1530:G:OP1	2.14	0.46
1:AA:161:A:H2'	1:AA:162:A:C8	2.50	0.46
1:AA:163:C:H2'	1:AA:164:U:C6	2.49	0.46
1:AA:346:G:C3'	1:AA:347:G:H4'	2.45	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:625:G:H2'	1:AA:626:U:H6	1.79	0.46
1:AA:953:G:N7	13:AM:104:ARG:NH2	2.63	0.46
2:AB:30:ARG:HG3	2:AB:31:TYR:CD1	2.50	0.46
23:AW:52:G:H4'	37:BQ:56:ARG:HH12	1.80	0.46
26:BA:1633:A:H2'	26:BA:1634:C:C6	2.50	0.46
26:BA:1688:A:H2'	26:BA:1689:G:O4'	2.14	0.46
26:BA:327:U:H2'	26:BA:328:G:H8	1.80	0.46
26:BA:645:G:H5'	26:BA:645:G:N3	2.30	0.46
38:BR:104:ARG:HG3	38:BR:111:LEU:HD21	1.97	0.46
1:CA:309:G:O2'	1:CA:607:A:N1	2.48	0.46
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.48	0.46
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	1.96	0.46
1:CA:1456:G:N1	20:CT:51:GLU:OE1	2.45	0.46
26:DA:1116:C:H2'	26:DA:1117:G:H8	1.79	0.46
26:DA:1169:G:O5'	26:DA:1169:G:H8	1.98	0.46
26:DA:1430:C:H2'	26:DA:1431:U:C6	2.49	0.46
26:DA:2059:A:O2'	30:DF:69:HIS:HD2	1.98	0.46
26:DA:2516:G:O6	26:DA:2517:C:N4	2.48	0.46
26:DA:2846:G:H2'	26:DA:2847:U:O4'	2.14	0.46
26:DA:854:G:H2'	26:DA:855:G:C8	2.50	0.46
26:DA:1797:C:H4'	28:DD:257:LEU:O	2.15	0.46
42:DV:40:LEU:HB2	42:DV:46:VAL:HG13	1.96	0.46
1:AA:1002:G:H3'	1:AA:1003:G:H8	1.81	0.46
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.44	0.46
1:AA:382:A:H2'	1:AA:383:A:C8	2.49	0.46
2:AB:102:LEU:HD23	2:AB:182:ILE:HD12	1.98	0.46
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.96	0.46
2:AB:21:ARG:H	2:AB:21:ARG:HD2	1.80	0.46
5:AE:43:LEU:HD21	5:AE:132:ALA:HB1	1.97	0.46
23:AW:6:G:N1	23:AW:67:C:N4	2.39	0.46
26:BA:1074:A:N6	26:BA:1171:G:H2'	2.30	0.46
26:BA:1224:C:H2'	26:BA:1225:C:H6	1.80	0.46
26:BA:2897:U:H2'	26:BA:2898:C:C6	2.49	0.46
26:BA:791:G:OP1	29:BE:132:HIS:ND1	2.43	0.46
30:BF:93:LYS:HD3	30:BF:93:LYS:HA	1.68	0.46
31:BG:146:TYR:O	31:BG:146:TYR:HD1	1.98	0.46
26:BA:2032:G:H5''	43:BW:42:ARG:HB2	1.98	0.46
1:CA:772:U:H2'	1:CA:773:G:O4'	2.15	0.46
2:CB:76:GLN:HG3	2:CB:206:ASP:O	2.15	0.46
7:CG:76:ARG:HB3	7:CG:156:TRP:HH2	1.80	0.46
8:CH:82:HIS:NE2	8:CH:84:ARG:HG2	2.30	0.46
10:CJ:23:ILE:HA	10:CJ:23:ILE:HD13	1.77	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:CP:40:ASP:O	16:CP:48:TRP:HB2	2.16	0.46
23:CW:76:31M:N	24:CX:76:A:O3'	2.49	0.46
25:CY:74:C:H4'	48:D1:23:LYS:HE3	1.97	0.46
26:DA:1630:G:H2'	26:DA:1631:C:C6	2.51	0.46
26:DA:1932:A:H2'	26:DA:1933:G:O4'	2.15	0.46
26:DA:1786:A:H1'	26:DA:1938:A:N6	2.31	0.46
26:DA:2141:G:C8	26:DA:2151:G:N2	2.83	0.46
26:DA:229:A:H5''	26:DA:230:U:H5'	1.96	0.46
26:DA:2318:G:H4'	26:DA:2319:G:OP1	2.14	0.46
26:DA:2516:G:C6	26:DA:2517:C:C4	3.03	0.46
26:DA:2647:U:H2'	26:DA:2648:C:C6	2.51	0.46
26:DA:2836:U:H2'	26:DA:2837:G:C8	2.50	0.46
26:DA:528:A:OP2	34:DN:114:ARG:NH1	2.48	0.46
37:DQ:133:ARG:HG2	37:DQ:134:ARG:N	2.30	0.46
40:DT:16:ARG:HH11	40:DT:16:ARG:HB3	1.80	0.46
42:DV:60:GLU:HB3	42:DV:95:LEU:HB3	1.97	0.46
1:AA:406:G:H4'	4:AD:3:ARG:HH22	1.80	0.46
1:AA:743:U:H2'	1:AA:744:C:C6	2.51	0.46
2:AB:59:GLU:HG3	2:AB:225:ALA:HB2	1.96	0.46
4:AD:163:GLU:O	4:AD:165:MET:N	2.48	0.46
15:AO:18:PHE:CZ	15:AO:21:ASP:HB3	2.50	0.46
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.98	0.46
25:AY:12:U:C2	25:AY:24:G:C2	3.03	0.46
25:AY:69:G:C5	25:AY:70:G:C8	3.03	0.46
26:BA:1153:G:H2'	26:BA:1153:G:N3	2.29	0.46
26:BA:1700:G:H3'	38:BR:2:ARG:HD3	1.96	0.46
26:BA:552:C:C4	26:BA:2792:U:H2'	2.50	0.46
26:BA:302:A:O2'	26:BA:303:C:OP1	2.23	0.46
26:BA:641:G:OP1	30:BF:40:GLN:HG2	2.15	0.46
45:BY:55:TYR:CD2	45:BY:55:TYR:N	2.84	0.46
46:BZ:137:ILE:HA	46:BZ:156:LYS:HZ1	1.80	0.46
46:BZ:5:LEU:O	46:BZ:59:LEU:HA	2.15	0.46
1:CA:1492:A:H2'	1:CA:1493:A:C8	2.51	0.46
8:CH:44:PHE:CE2	8:CH:109:ILE:HG12	2.51	0.46
22:CV:16:A:N6	24:CX:36:U:H3	2.12	0.46
25:CY:69:G:C6	25:CY:70:G:C8	3.04	0.46
56:D9:13:LYS:HD3	56:D9:28:GLU:OE2	2.15	0.46
24:CX:13:C:O2'	26:DA:1924:C:H4'	2.15	0.46
26:DA:2263:C:N4	47:D0:15:ASP:OD1	2.47	0.46
26:DA:2510:C:C4	26:DA:2511:U:C4	3.03	0.46
26:DA:724:U:H2'	26:DA:725:G:O4'	2.15	0.46
26:DA:8:A:H2'	26:DA:9:U:H6	1.81	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:DE:50:GLY:HA2	29:DE:77:ILE:O	2.14	0.46
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.15	0.46
2:AB:210:SER:O	2:AB:214:ILE:HG12	2.16	0.46
7:AG:113:GLU:HG3	7:AG:118:VAL:HG12	1.96	0.46
7:AG:138:LYS:NZ	7:AG:142:GLU:OE2	2.49	0.46
23:AW:19:G:H4'	23:AW:20:U:OP1	2.16	0.46
23:AW:8:4SU:O2'	23:AW:46:7MG:N2	2.49	0.46
24:AX:17:C:H5'	24:AX:61:C:OP1	2.16	0.46
26:BA:2805:G:N2	26:BA:2816:G:H1'	2.31	0.46
29:BE:149:ARG:N	61:BE:406:HOH:O	2.38	0.46
37:BQ:37:LEU:HD21	37:BQ:130:LYS:HB2	1.98	0.46
43:BW:9:TYR:HA	43:BW:100:THR:HG23	1.98	0.46
1:CA:1318:A:H5''	19:CS:3:ARG:HH22	1.80	0.46
1:CA:1499:A:H1'	1:CA:1520:G:H5'	1.96	0.46
24:CX:37:A:H2'	24:CX:38:A:O4'	2.16	0.46
25:CY:15:G:C2	25:CY:48:C:N3	2.82	0.46
26:DA:1359:A:N1	26:DA:1372:U:O4	2.47	0.46
26:DA:2745:C:C4	26:DA:2746:U:C4	3.03	0.46
26:DA:2870:C:H5''	38:DR:65:LEU:HD21	1.97	0.46
26:DA:28:A:C2	26:DA:513:A:C8	3.03	0.46
26:DA:647:G:H8	26:DA:647:G:O5'	1.98	0.46
26:DA:995:C:N3	34:DN:2:LYS:HA	2.31	0.46
1:AA:1003:G:C2	1:AA:1004:A:N3	2.84	0.46
1:AA:224:C:H2'	1:AA:225:C:H6	1.81	0.46
9:AI:8:GLY:HA3	9:AI:76:ALA:O	2.15	0.46
10:AJ:70:ARG:HA	10:AJ:70:ARG:HD3	1.83	0.46
11:AK:82:VAL:N	11:AK:107:SER:O	2.45	0.46
25:AY:36:A:H2'	25:AY:37:MIA:O4'	2.15	0.46
49:B2:32:LEU:HD13	49:B2:36:ARG:NH1	2.30	0.46
26:BA:2152:U:H2'	26:BA:2153:G:N2	2.31	0.46
26:BA:225:C:H2'	26:BA:226:C:C6	2.50	0.46
30:BF:28:ILE:O	30:BF:30:PRO:HD3	2.15	0.46
26:BA:2761:A:H5'	32:BH:4:ILE:HD12	1.97	0.46
1:CA:69:G:H2'	1:CA:70:G:C8	2.51	0.46
1:CA:90:U:O2'	1:CA:91:C:H5'	2.15	0.46
1:CA:992:U:H6	1:CA:992:U:H5''	1.80	0.46
2:CB:149:LEU:HD22	2:CB:152:PHE:HD2	1.80	0.46
19:CS:27:GLU:HB2	19:CS:28:LYS:NZ	2.31	0.46
19:CS:27:GLU:HG2	19:CS:47:HIS:HE2	1.80	0.46
48:D1:83:GLU:HA	48:D1:84:GLY:HA2	1.62	0.46
26:DA:195:A:H2'	26:DA:198:C:N4	2.31	0.46
26:DA:2502:G:H5''	26:DA:2503:A:H5''	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:383:U:H2'	26:DA:385:C:H5	1.81	0.46
26:DA:783:A:O2'	26:DA:785:G:OP1	2.24	0.46
27:DB:55:U:O3'	31:DG:27:ASN:ND2	2.49	0.46
29:DE:1:MET:O	29:DE:84:PHE:HB2	2.15	0.46
32:DH:86:GLU:HB3	32:DH:165:ALA:HB2	1.97	0.46
26:DA:811:U:H2'	36:DP:21:ARG:HA	1.96	0.46
1:AA:1025:U:O2	1:AA:1036:G:C6	2.66	0.46
1:AA:1136:U:H5''	1:AA:1137:C:N3	2.30	0.46
2:AB:61:LEU:HD23	2:AB:68:ILE:HD11	1.96	0.46
4:AD:110:PHE:HE1	4:AD:176:LEU:HD13	1.80	0.46
1:AA:1351:U:O4	9:AI:118:LYS:NZ	2.49	0.46
18:AR:65:ILE:O	18:AR:69:THR:HG23	2.16	0.46
26:BA:1067:A:H3'	26:BA:1067:A:C8	2.50	0.46
26:BA:1221:G:H1'	26:BA:1222:A:C5'	2.38	0.46
26:BA:1541:A:H2'	26:BA:1542:A:C8	2.51	0.46
26:BA:1744:G:OP2	26:BA:1745:A:O2'	2.14	0.46
26:BA:180:A:H2'	26:BA:181:C:C6	2.51	0.46
26:BA:1890:A:N6	26:BA:1905:G:O2'	2.48	0.46
26:BA:2150:C:H2'	26:BA:2151:C:C6	2.50	0.46
26:BA:510:C:H2'	26:BA:511:C:C6	2.51	0.46
40:BT:51:ARG:HG3	40:BT:98:LYS:HD2	1.96	0.46
43:BW:13:SER:HA	43:BW:14:PRO:HD3	1.84	0.46
1:CA:1002:G:N3	1:CA:1003:G:C8	2.84	0.46
1:CA:1095:U:C4	1:CA:1096:C:C4	3.03	0.46
1:CA:1134:G:H2'	1:CA:1135:U:H5'	1.98	0.46
1:CA:1291:G:C6	1:CA:1292:U:C4	3.04	0.46
1:CA:630:G:H2'	1:CA:631:G:H8	1.81	0.46
14:CN:6:LEU:HB3	14:CN:23:ARG:NH2	2.30	0.46
18:CR:26:LEU:CD2	18:CR:42:ARG:HD2	2.46	0.46
25:CY:35:A:N6	25:CY:36:A:N1	2.63	0.46
52:D5:16:ARG:HD2	52:D5:20:ARG:NH1	2.31	0.46
26:DA:1310:G:OP2	54:D7:9:ARG:NH1	2.49	0.46
26:DA:1611:C:H2'	26:DA:1612:C:H5'	1.98	0.46
26:DA:191:A:H2'	26:DA:192:C:C6	2.50	0.46
26:DA:740:U:H2'	26:DA:741:G:C8	2.51	0.46
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.39	0.46
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.98	0.46
4:AD:3:ARG:HD3	4:AD:118:ARG:HD2	1.97	0.46
26:BA:1249:A:N6	26:BA:1286:U:H2'	2.30	0.46
26:BA:1346:U:H4'	26:BA:1347:A:H5'	1.97	0.46
26:BA:2108:U:H2'	26:BA:2109:G:C8	2.51	0.46
26:BA:2163:G:N7	26:BA:2173:G:C2	2.84	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2221:A:OP2	26:BA:2222:C:H5	1.99	0.46
26:BA:2642:G:H2'	26:BA:2643:G:H8	1.80	0.46
26:BA:929:G:H2'	26:BA:930:G:O4'	2.15	0.46
31:BG:47:LYS:O	31:BG:51:ARG:HG2	2.16	0.46
37:BQ:14:ARG:HG2	37:BQ:41:TRP:HH2	1.79	0.46
1:CA:937:A:H1'	1:CA:1379:G:N2	2.30	0.46
8:CH:6:ILE:O	8:CH:10:LEU:HG	2.16	0.46
10:CJ:30:SER:O	10:CJ:81:THR:HG23	2.16	0.46
25:CY:50:U:C2	25:CY:64:A:N1	2.84	0.46
26:DA:2347:C:O2'	53:D6:21:TYR:OH	2.34	0.46
26:DA:1913:A:H4'	26:DA:1914:C:O5'	2.15	0.46
26:DA:195:A:H2'	26:DA:198:C:H41	1.80	0.46
26:DA:2291:U:O2'	26:DA:2374:C:H1'	2.16	0.46
26:DA:2821:A:H2'	26:DA:2822:G:C8	2.51	0.46
26:DA:999:U:O2'	26:DA:1000:A:H5'	2.16	0.46
31:DG:10:LYS:HG3	31:DG:14:GLU:OE1	2.16	0.46
33:DI:77:LEU:HD11	33:DI:101:LEU:HB2	1.98	0.46
39:DS:27:SER:HA	39:DS:88:ASP:HB3	1.96	0.46
1:AA:1429:C:H2'	1:AA:1430:C:H6	1.80	0.46
1:AA:93:G:O2'	1:AA:96:U:H5'	2.16	0.46
3:AC:20:SER:OG	3:AC:40:ARG:NH1	2.48	0.46
11:AK:73:MET:HG2	11:AK:103:LEU:HD21	1.98	0.46
61:BA:5273:HOH:O	47:B0:41:ARG:HA	2.15	0.46
50:B3:26:LEU:O	50:B3:35:ARG:NE	2.49	0.46
51:B4:68:ARG:HD2	51:B4:69:LYS:H	1.81	0.46
26:BA:2545:A:H2'	26:BA:2546:A:O4'	2.16	0.46
26:BA:282:G:O6	61:BA:4948:HOH:O	2.20	0.46
26:BA:561:A:H2'	26:BA:562:C:C6	2.50	0.46
33:BI:85:GLU:OE1	33:BI:85:GLU:HA	2.16	0.46
1:CA:1220:G:H5'	19:CS:34:TRP:O	2.15	0.46
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.37	0.46
2:CB:28:PHE:HD1	2:CB:194:PRO:HG3	1.81	0.46
2:CB:30:ARG:HG3	2:CB:31:TYR:CD1	2.50	0.46
7:CG:79:ARG:HB3	7:CG:80:VAL:H	1.37	0.46
1:CA:450:G:H4'	16:CP:41:PRO:HB2	1.98	0.46
26:DA:774:A:N3	26:DA:774:A:H2'	2.30	0.46
31:DG:25:TYR:HB3	31:DG:30:GLU:HB3	1.98	0.46
1:AA:1237:C:O2'	1:AA:1300:G:N2	2.43	0.46
1:AA:1302:U:OP2	13:AM:21:TYR:OH	2.24	0.46
1:AA:262:A:C6	1:AA:263:A:C6	3.03	0.46
1:AA:6:G:O2'	1:AA:7:G:H5'	2.16	0.46
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.48	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
52:B5:42:PRO:HB2	52:B5:43:HIS:ND1	2.31	0.46
26:BA:2163:G:C4	26:BA:2164:C:H1'	2.51	0.46
26:BA:904:C:N4	26:BA:905:U:O4	2.49	0.46
30:BF:29:ASN:H	30:BF:112:MET:CE	2.28	0.46
38:BR:36:THR:HG22	38:BR:37:THR:H	1.81	0.46
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.31	0.46
1:CA:1006:C:H2'	1:CA:1007:C:O4'	2.16	0.46
1:CA:1516:G:N2	1:CA:1519:A:OP2	2.49	0.46
1:CA:202:U:O2'	1:CA:203:U:O5'	2.31	0.46
2:CB:100:GLY:HA2	2:CB:103:THR:OG1	2.15	0.46
2:CB:150:SER:OG	2:CB:151:GLY:N	2.48	0.46
2:CB:218:ALA:O	2:CB:222:ILE:HG23	2.15	0.46
4:CD:92:VAL:O	4:CD:96:LEU:HD22	2.16	0.46
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.49	0.46
1:CA:1317:C:H5	14:CN:18:VAL:HG21	1.80	0.46
26:DA:1032:A:H2	26:DA:1122:G:H22	1.61	0.46
26:DA:1484:G:C6	26:DA:1485:G:N7	2.84	0.46
25:CY:76:A:O2'	26:DA:2394:C:N3	2.44	0.46
26:DA:2687:U:H2'	26:DA:2688:U:O4'	2.16	0.46
26:DA:307:G:H22	26:DA:310:A:P	2.38	0.46
31:DG:44:GLY:O	31:DG:47:LYS:HB2	2.15	0.46
44:DX:92:LEU:HA	44:DX:92:LEU:HD12	1.83	0.46
46:DZ:150:LEU:HD12	46:DZ:150:LEU:HA	1.78	0.46
1:AA:1273:G:H3'	1:AA:1274:G:C8	2.51	0.46
1:AA:1457:G:H2'	1:AA:1458:G:C8	2.51	0.46
1:AA:93:G:C2'	1:AA:96:U:H5'	2.46	0.46
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.98	0.46
13:AM:4:ILE:HD12	13:AM:57:ARG:HA	1.97	0.46
26:BA:2371:C:H2'	26:BA:2372:A:O4'	2.16	0.46
26:BA:2687:A:H5'	35:BO:29:ASN:O	2.15	0.46
26:BA:2814:C:H2'	26:BA:2815:C:C6	2.51	0.46
26:BA:2033:U:OP1	43:BW:42:ARG:HD3	2.16	0.46
1:CA:994:A:C5	1:CA:1216:G:H4'	2.51	0.46
1:CA:664:G:H5''	18:CR:64:ARG:NH2	2.31	0.46
2:CB:96:ARG:HD2	2:CB:98:LEU:HD22	1.97	0.46
3:CC:121:ALA:HB2	3:CC:198:VAL:HG21	1.98	0.46
3:CC:36:ASP:O	3:CC:40:ARG:HG3	2.16	0.46
47:D0:82:ARG:HA	47:D0:83:PRO:HD3	1.78	0.46
26:DA:1477:A:H2'	26:DA:1478:G:O4'	2.14	0.46
26:DA:1539:G:H2'	26:DA:1540:U:O4'	2.16	0.46
26:DA:1857:G:C6	26:DA:1858:G:N1	2.84	0.46
26:DA:1913:A:H4'	26:DA:1914:C:C5'	2.46	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2119:A:H2	26:DA:2171:A:H5'	1.81	0.46
26:DA:330:A:HO2'	26:DA:331:A:H8	1.61	0.46
27:DB:5:C:N4	27:DB:116:G:H1	2.13	0.46
27:DB:80:U:H2'	27:DB:81:G:C8	2.51	0.46
33:DI:90:GLY:O	33:DI:121:LYS:HE3	2.16	0.46
38:DR:98:LEU:HB2	38:DR:113:LEU:HD11	1.98	0.46
26:DA:517:C:O2'	43:DW:18:ARG:NH2	2.49	0.46
1:AA:1075:C:H2'	1:AA:1076:C:H5''	1.98	0.45
1:AA:691:G:OP2	11:AK:26:ASN:ND2	2.38	0.45
2:AB:45:GLN:O	2:AB:49:GLU:HB2	2.16	0.45
50:B3:43:ILE:O	50:B3:47:VAL:HG23	2.16	0.45
26:BA:1223:C:H2'	26:BA:1224:C:C6	2.51	0.45
26:BA:275:C:H2'	26:BA:276:C:C6	2.51	0.45
33:BI:77:LEU:HB2	33:BI:142:VAL:HG12	1.97	0.45
42:BV:21:ARG:HG2	42:BV:91:TYR:CD1	2.51	0.45
1:CA:1084:G:C5	1:CA:1085:U:C4	3.04	0.45
1:CA:1423:G:H2'	1:CA:1424:C:H6	1.80	0.45
1:CA:59:A:H3'	1:CA:331:G:H22	1.81	0.45
1:CA:920:U:H2'	1:CA:921:U:H6	1.77	0.45
1:CA:976:G:C8	1:CA:1362:C:N4	2.84	0.45
7:CG:111:ARG:HB3	7:CG:113:GLU:OE2	2.16	0.45
1:CA:689:C:P	11:CK:46:GLY:HA3	2.56	0.45
12:CL:8:ASN:O	12:CL:12:ARG:HG3	2.16	0.45
15:CO:74:ASP:OD1	15:CO:76:GLU:HB2	2.16	0.45
19:CS:27:GLU:HB3	19:CS:28:LYS:HA	1.96	0.45
26:DA:1300:U:H4'	26:DA:1301:A:O5'	2.16	0.45
26:DA:385:C:O2	36:DP:71:VAL:HG21	2.16	0.45
26:DA:601:C:O2'	30:DF:104:LYS:NZ	2.44	0.45
26:DA:754:C:H2'	26:DA:755:C:C6	2.50	0.45
28:DD:72:LYS:HB3	28:DD:75:ILE:HD12	1.98	0.45
33:DI:102:SER:O	33:DI:106:GLY:N	2.37	0.45
1:AA:1034:G:H3'	1:AA:1035:A:C8	2.51	0.45
1:AA:59:A:H3'	1:AA:331:G:H22	1.81	0.45
2:AB:16:HIS:CB	2:AB:204:ASN:HB3	2.31	0.45
3:AC:155:GLY:HA3	3:AC:196:LEU:HD22	1.97	0.45
4:AD:162:LEU:CD1	4:AD:181:MET:HG2	2.46	0.45
5:AE:27:ARG:HB2	5:AE:27:ARG:HE	1.48	0.45
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.16	0.45
53:B6:11:LEU:HB3	53:B6:49:HIS:HB3	1.98	0.45
26:BA:1873:G:O2'	28:BD:253:GLN:NE2	2.49	0.45
26:BA:2579:G:H2'	26:BA:2580:C:C6	2.51	0.45
26:BA:2856:G:H2'	26:BA:2857:U:O4'	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1834:A:H4'	28:BD:259:THR:HG23	1.98	0.45
31:BG:16:ARG:NE	31:BG:31:VAL:HG11	2.30	0.45
26:BA:957:A:H2'	37:BQ:9:TYR:OH	2.16	0.45
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.51	0.45
1:CA:775:G:N2	1:CA:804:U:O4	2.48	0.45
3:CC:164:ARG:HG2	3:CC:165:THR:H	1.81	0.45
2:CB:178:ARG:NH2	8:CH:68:ARG:HH22	2.12	0.45
9:CI:99:LEU:HB3	9:CI:101:PHE:CE2	2.51	0.45
13:CM:37:THR:HG21	13:CM:56:LEU:HA	1.97	0.45
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.16	0.45
47:D0:53:MET:HG2	47:D0:57:PHE:HA	1.98	0.45
26:DA:752:A:P	54:D7:3:ARG:HH22	2.39	0.45
26:DA:1027:A:C6	26:DA:1126:A:C4	3.04	0.45
26:DA:1991:U:H2'	26:DA:1992:G:H5''	1.97	0.45
26:DA:2379:G:O2'	39:DS:17:ARG:NH2	2.36	0.45
26:DA:698:C:O2'	26:DA:734:A:N6	2.49	0.45
28:DD:96:HIS:CD2	28:DD:102:LYS:HG2	2.52	0.45
33:DI:93:THR:HG22	33:DI:119:PRO:HB3	1.97	0.45
38:DR:29:LEU:HA	38:DR:29:LEU:HD12	1.78	0.45
1:AA:1243:C:H2'	1:AA:1244:C:C6	2.50	0.45
2:AB:16:HIS:CE1	2:AB:214:ILE:HD11	2.46	0.45
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.44	0.45
26:BA:1347:A:C8	26:BA:1349:G:C8	3.04	0.45
26:BA:2163:G:C6	26:BA:2164:C:C2	3.04	0.45
26:BA:89:U:H4'	26:BA:90:A:H5'	1.99	0.45
28:BD:52:ARG:NH2	61:BD:411:HOH:O	2.22	0.45
31:BG:45:GLU:HG2	31:BG:45:GLU:H	1.36	0.45
34:BN:38:HIS:NE2	34:BN:50:ASP:OD2	2.50	0.45
1:CA:1053:G:C3'	1:CA:1054:C:H5'	2.45	0.45
1:CA:21:G:H2'	1:CA:22:G:C8	2.51	0.45
1:CA:580:U:H2'	1:CA:581:G:O4'	2.16	0.45
2:CB:97:TRP:CZ3	2:CB:101:MET:HB2	2.52	0.45
11:CK:81:ASP:OD1	11:CK:106:LYS:HB2	2.17	0.45
16:CP:19:ILE:N	16:CP:37:GLY:O	2.49	0.45
19:CS:41:VAL:HG12	19:CS:43:GLU:H	1.80	0.45
26:DA:2127:G:N1	26:DA:2161:C:O2	2.34	0.45
26:DA:2468:G:C2	26:DA:2481:G:N3	2.85	0.45
26:DA:2653:U:O2'	32:DH:110:SER:HB3	2.15	0.45
39:DS:3:ARG:HE	39:DS:4:LEU:N	2.15	0.45
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.52	0.45
1:AA:1273:G:H3'	1:AA:1274:G:H8	1.81	0.45
1:AA:356:A:N7	61:AA:4035:HOH:O	2.36	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:AD:138:TYR:HE1	4:AD:140:VAL:HA	1.81	0.45
5:AE:18:ARG:HE	5:AE:27:ARG:HH21	1.64	0.45
7:AG:91:VAL:HB	7:AG:96:GLN:HG2	1.99	0.45
13:AM:15:VAL:HG22	13:AM:43:THR:O	2.17	0.45
31:BG:31:VAL:HA	31:BG:32:PRO:HD2	1.79	0.45
36:BP:121:LYS:O	36:BP:123:LEU:N	2.45	0.45
1:CA:991:U:H3'	1:CA:1212:U:N3	2.32	0.45
1:CA:56:U:H2'	1:CA:57:G:C8	2.52	0.45
3:CC:79:ARG:H	3:CC:82:GLU:HB3	1.82	0.45
5:CE:90:VAL:O	5:CE:120:THR:HA	2.17	0.45
6:CF:28:ARG:HB2	6:CF:28:ARG:HH11	1.82	0.45
11:CK:45:GLY:O	11:CK:50:TYR:HB2	2.17	0.45
50:D3:4:LEU:O	50:D3:36:VAL:HA	2.17	0.45
26:DA:2019:A:C4'	41:DU:34:LYS:HD2	2.47	0.45
26:DA:241:A:H8	26:DA:241:A:OP1	2.00	0.45
26:DA:583:G:OP2	41:DU:10:ARG:NH1	2.49	0.45
26:DA:94(A):G:H2'	26:DA:95:G:O4'	2.16	0.45
29:DE:9:VAL:HG13	29:DE:25:VAL:O	2.16	0.45
45:DY:86:ARG:HD2	45:DY:100:ALA:HA	1.98	0.45
2:AB:150:SER:OG	2:AB:151:GLY:N	2.49	0.45
2:AB:22:LYS:H	2:AB:40:HIS:CE1	2.35	0.45
4:AD:170:VAL:HG12	4:AD:171:GLY:N	2.32	0.45
5:AE:12:LEU:HD22	5:AE:13:ILE:N	2.32	0.45
6:AF:44:GLY:HA2	6:AF:59:TYR:CE2	2.52	0.45
18:AR:31:LEU:HD11	18:AR:62:GLU:HB2	1.98	0.45
1:AA:1305:G:H5''	21:AU:4:GLY:HA3	1.98	0.45
32:BH:11:VAL:HG13	32:BH:15:VAL:HG22	1.98	0.45
35:BO:7:TYR:CZ	35:BO:44:LYS:HG3	2.52	0.45
46:BZ:105:VAL:N	46:BZ:139:VAL:O	2.41	0.45
1:CA:1097:C:O2'	1:CA:1169:A:N3	2.41	0.45
1:CA:189(F):U:O2	17:CQ:63:ARG:NH2	2.50	0.45
1:CA:22:G:H4'	1:CA:885:G:C8	2.52	0.45
12:CL:69:TYR:CE2	12:CL:71:PRO:HA	2.52	0.45
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.49	0.45
15:CO:17:ARG:HG3	15:CO:17:ARG:HH11	1.82	0.45
6:CF:46:ARG:HH21	18:CR:37:VAL:HG11	1.81	0.45
20:CT:43:LEU:HD13	20:CT:51:GLU:HB3	1.98	0.45
20:CT:53:LEU:O	20:CT:57:ARG:HG3	2.16	0.45
36:DP:63:PRO:HG2	55:D8:25:MET:HB2	1.99	0.45
26:DA:2287:A:N1	26:DA:2346:A:N7	2.65	0.45
26:DA:2447:G:N2	26:DA:2450:A:OP2	2.46	0.45
26:DA:468:G:N7	54:D7:39:ARG:NH2	2.63	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
42:DV:5:VAL:CG1	42:DV:57:VAL:HG21	2.47	0.45
26:DA:25:U:H5'	43:DW:78:GLU:O	2.16	0.45
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.81	0.45
1:AA:300:A:O2'	1:AA:564:C:N3	2.39	0.45
1:AA:836:G:OP1	18:AR:61:LYS:NZ	2.49	0.45
1:AA:8:A:N7	4:AD:208:SER:OG	2.48	0.45
3:AC:181:ASN:C	3:AC:181:ASN:HD22	2.20	0.45
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.50	0.45
11:AK:41:THR:OG1	11:AK:42:TRP:N	2.50	0.45
26:BA:1346:U:H4'	26:BA:1347:A:H5''	1.99	0.45
26:BA:553:A:N1	26:BA:2064:A:H2'	2.31	0.45
26:BA:2556:G:H1'	26:BA:2658:C:H4'	1.99	0.45
29:BE:7:VAL:HG12	29:BE:27:LEU:HB3	1.98	0.45
33:BI:102:SER:OG	33:BI:103:ARG:N	2.50	0.45
46:BZ:138:GLU:N	46:BZ:156:LYS:HD3	2.30	0.45
1:CA:1009:G:C2	1:CA:1010:G:C4	3.04	0.45
1:CA:1054:C:O2'	1:CA:1055:A:C5'	2.64	0.45
1:CA:93:G:C6	1:CA:96:U:C4	3.05	0.45
1:CA:97:G:O2'	1:CA:98:G:H5''	2.17	0.45
25:CY:21:A:N6	25:CY:46:7MG:H81	2.32	0.45
55:D8:62:LEU:HB3	55:D8:65:GLU:HG3	1.97	0.45
26:DA:1463:C:H2'	26:DA:1464:C:H6	1.81	0.45
26:DA:2450:A:OP1	26:DA:2497:A:O2'	2.35	0.45
26:DA:1782:C:H1'	26:DA:2609:U:H5''	1.98	0.45
26:DA:686:G:H21	26:DA:788:A:H61	1.65	0.45
26:DA:93:G:H2'	26:DA:94:C:H6	1.82	0.45
28:DD:17:THR:O	28:DD:211:ARG:NH2	2.45	0.45
26:DA:251:A:H5''	36:DP:50:ARG:HH11	1.81	0.45
41:DU:27:LEU:HD23	41:DU:30:LYS:HB2	1.98	0.45
42:DV:100:ARG:HH11	42:DV:100:ARG:CG	2.17	0.45
45:DY:13:VAL:HG12	45:DY:74:PRO:HA	1.99	0.45
46:DZ:113:ALA:HB3	46:DZ:146:ILE:HD11	1.97	0.45
1:AA:692:U:O2'	1:AA:694:A:N7	2.42	0.45
1:AA:78:G:C6	1:AA:91:C:N4	2.83	0.45
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.83	0.45
4:AD:61:LYS:HA	4:AD:203:VAL:HG22	1.98	0.45
16:AP:5:ARG:NH1	16:AP:24:ALA:HA	2.31	0.45
25:AY:50:U:C4	25:AY:64:A:N1	2.84	0.45
53:B6:13:CYS:SG	53:B6:47:THR:HG21	2.56	0.45
26:BA:139:A:H8	26:BA:1454:C:O2'	2.00	0.45
26:BA:1825:U:H2'	26:BA:1826:C:C6	2.50	0.45
28:BD:5:LYS:HE3	28:BD:5:LYS:HB3	1.56	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BI:136:VAL:N	33:BI:137:PRO:HD3	2.32	0.45
36:BP:135:LEU:HD23	36:BP:135:LEU:HA	1.77	0.45
37:BQ:18:LYS:HB2	37:BQ:18:LYS:HE3	1.72	0.45
1:CA:1000:U:C2	1:CA:1041:A:N1	2.83	0.45
1:CA:297:G:N2	1:CA:300:A:OP2	2.49	0.45
1:CA:335:C:H2'	1:CA:336:C:C6	2.51	0.45
2:CB:55:PHE:O	2:CB:59:GLU:N	2.33	0.45
3:CC:156:ARG:NH2	3:CC:159:GLY:O	2.27	0.45
15:CO:54:ARG:HD3	15:CO:58:MET:CE	2.47	0.45
23:CW:47:U:H3'	23:CW:48:C:C5'	2.47	0.45
25:CY:70:G:H2'	25:CY:71:G:H5'	1.99	0.45
26:DA:2348:U:O4	26:DA:2382:G:N1	2.50	0.45
26:DA:30:G:H2'	26:DA:31:C:C6	2.52	0.45
26:DA:864:G:C6	26:DA:865:C:N4	2.85	0.45
31:DG:74:LYS:O	31:DG:84:LYS:HD2	2.16	0.45
35:DO:107:ARG:CZ	40:DT:36:GLU:HG2	2.46	0.45
44:DX:92:LEU:C	44:DX:94:GLY:H	2.18	0.45
1:AA:1003:G:C2'	1:AA:1004:A:H4'	2.47	0.45
1:AA:279:A:C4	17:AQ:98:LEU:HD23	2.51	0.45
1:AA:300:A:H2'	1:AA:301:G:O4'	2.17	0.45
4:AD:121:VAL:O	4:AD:134:ASP:HA	2.15	0.45
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.33	0.45
26:BA:1814:A:H5'	26:BA:2620:G:H4'	1.98	0.45
1:CA:58:C:O2'	1:CA:388:G:N7	2.40	0.45
11:CK:34:ASP:OD2	11:CK:38:ASN:HB2	2.17	0.45
1:CA:1048:G:OP1	14:CN:3:ARG:HD2	2.17	0.45
24:CX:9:G:O2'	24:CX:10:G:N7	2.37	0.45
26:DA:1027:A:C2	26:DA:2488:A:H5'	2.52	0.45
26:DA:1740:G:H2'	26:DA:1741:A:C8	2.51	0.45
26:DA:2637:U:H1'	26:DA:2782:G:N2	2.32	0.45
26:DA:270:A:N1	26:DA:366:C:H4'	2.32	0.45
26:DA:443:A:OP2	26:DA:614(B):G:N2	2.38	0.45
26:DA:848:G:C4	26:DA:933:A:H8	2.35	0.45
26:DA:94(A):G:C6	26:DA:95:G:C5	3.05	0.45
30:DF:64:ILE:HG21	30:DF:78:ILE:HG23	1.99	0.45
37:DQ:118:LEU:HB3	37:DQ:131:ILE:HD12	1.97	0.45
40:DT:65:LYS:HE2	40:DT:67:SER:HB2	1.98	0.45
1:AA:189(A):C:N4	1:AA:189(J):G:H1	2.15	0.45
1:AA:662:G:H2'	1:AA:663:A:H8	1.79	0.45
8:AH:51:VAL:HG21	8:AH:60:ARG:HB2	1.98	0.45
11:AK:38:ASN:HA	11:AK:39:PRO:HD3	1.86	0.45
23:AW:18:G:O2'	23:AW:57:G:N2	2.39	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:AY:7:A:O2'	25:AY:49:C:OP2	2.21	0.45
26:BA:1979:C:H2'	26:BA:1980:C:C6	2.52	0.45
26:BA:2102:G:OP1	48:B1:35:THR:HG21	2.17	0.45
26:BA:776:G:C6	28:BD:208:LYS:HB2	2.52	0.45
26:BA:943:C:C4	26:BA:944:C:N4	2.85	0.45
31:BG:11:TYR:O	31:BG:16:ARG:HG2	2.17	0.45
34:BN:14:VAL:HG11	34:BN:138:LEU:HD12	1.99	0.45
45:BY:34:LYS:O	45:BY:34:LYS:HG3	2.15	0.45
1:CA:1010:G:H22	1:CA:1020:U:H1'	1.82	0.45
1:CA:1374:A:O2'	7:CG:28:ASN:HB3	2.16	0.45
2:CB:19:HIS:CG	2:CB:20:GLU:H	2.34	0.45
2:CB:15:VAL:HG21	2:CB:213:LEU:HD12	1.98	0.45
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	1.99	0.45
13:CM:33:ALA:HA	13:CM:59:TYR:CE2	2.51	0.45
23:CW:18:G:O6	23:CW:55:PSU:H1'	2.17	0.45
26:DA:1116:C:H2'	26:DA:1117:G:C8	2.52	0.45
26:DA:1395:A:OP1	61:DA:4546:HOH:O	2.21	0.45
26:DA:2052:G:H4'	29:DE:143:ASN:O	2.16	0.45
26:DA:2305:A:H2'	26:DA:2306:C:O4'	2.17	0.45
26:DA:263:C:H2'	26:DA:264:C:O4'	2.17	0.45
27:DB:66:A:N6	27:DB:108:U:H3'	2.32	0.45
27:DB:11:C:H3'	27:DB:12:C:C6	2.52	0.45
28:DD:96:HIS:HD2	28:DD:102:LYS:HG2	1.81	0.45
28:DD:10:THR:OG1	28:DD:13:ARG:HG2	2.16	0.45
40:DT:117:ASP:OD2	40:DT:120:ARG:NE	2.41	0.45
42:DV:40:LEU:HB2	42:DV:46:VAL:HG22	1.99	0.45
1:AA:1442(B):A:N3	40:BT:118:ARG:NH2	2.65	0.45
25:AY:54:5MU:H73	25:AY:55:PSU:O2	2.17	0.45
53:B6:40:CYS:HA	53:B6:41:PRO:HD3	1.78	0.45
26:BA:239:G:P	55:B8:13:ARG:HH22	2.39	0.45
26:BA:1018:A:OP2	61:BA:4141:HOH:O	2.20	0.45
26:BA:2190:G:O6	26:BA:2193:A:H8	1.99	0.45
26:BA:2588:G:H1'	61:BA:4454:HOH:O	2.17	0.45
26:BA:2902:G:HO2'	26:BA:2903:G:P	2.38	0.45
26:BA:945:A:O2'	26:BA:946:A:H8	2.00	0.45
30:BF:184:TYR:O	30:BF:188:ARG:HG3	2.17	0.45
61:BA:4103:HOH:O	30:BF:68:LYS:HE2	2.17	0.45
32:BH:98:LEU:HD12	32:BH:102:ALA:O	2.16	0.45
42:BV:55:ALA:HB2	42:BV:101:GLY:HA2	1.99	0.45
1:CA:1028:C:N3	1:CA:1033:G:C6	2.84	0.45
1:CA:1133:G:C4	1:CA:1134:G:C8	3.04	0.45
1:CA:1191:A:OP2	3:CC:3:ASN:ND2	2.49	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1338:G:C6	1:CA:1339:A:C6	3.05	0.45
1:CA:200:G:H1	1:CA:217:C:N4	2.09	0.45
1:CA:582:U:OP2	1:CA:758:G:N1	2.45	0.45
1:CA:986:A:H2'	1:CA:987:G:O4'	2.17	0.45
5:CE:79:GLU:OE1	8:CH:104:ARG:HA	2.17	0.45
26:DA:1427:A:H4'	26:DA:1428:C:O5'	2.15	0.45
26:DA:2303:G:O2'	31:DG:132:ASN:ND2	2.44	0.45
26:DA:2607:G:O6	61:DA:4661:HOH:O	2.20	0.45
26:DA:492:A:H2'	26:DA:493:G:O4'	2.17	0.45
30:DF:36:VAL:HG11	30:DF:183:VAL:HG11	1.99	0.45
34:DN:37:LYS:NZ	61:DN:5101:HOH:O	2.49	0.45
39:DS:106:ARG:HG3	39:DS:112:PHE:CZ	2.51	0.45
45:DY:5:MET:HG2	45:DY:30:VAL:HG11	1.99	0.45
1:AA:636:U:H2'	1:AA:637:G:C8	2.52	0.44
1:AA:6:G:H4'	1:AA:298:A:H4'	1.99	0.44
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	1.99	0.44
36:BP:50:ARG:NH2	55:B8:7:HIS:HD2	2.15	0.44
26:BA:1417:G:H2'	26:BA:1418:U:C5	2.50	0.44
26:BA:2627:U:H2'	26:BA:2628:C:H6	1.82	0.44
26:BA:276:C:O3'	33:BI:42:SER:OG	2.27	0.44
1:CA:1070:U:H2'	1:CA:1071:C:C6	2.52	0.44
1:CA:1249:C:O4'	9:CI:70:LYS:HE2	2.17	0.44
1:CA:1386:G:C2	1:CA:1387:G:C8	3.04	0.44
1:CA:353:A:H8	1:CA:353:A:H5'	1.82	0.44
1:CA:501:C:H2'	1:CA:502:G:C8	2.52	0.44
1:CA:866:C:C4	1:CA:867:G:H1'	2.52	0.44
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.98	0.44
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.16	0.44
20:CT:46:GLU:HG2	20:CT:46:GLU:O	2.16	0.44
1:CA:1326:C:H5''	21:CU:18:TYR:O	2.17	0.44
25:CY:66:U:H2'	25:CY:67:C:O4'	2.17	0.44
26:DA:1794:U:H2'	26:DA:1795:C:C6	2.53	0.44
26:DA:2203:U:H2'	26:DA:2205:C:H6	1.81	0.44
26:DA:2298:A:H2'	26:DA:2299:G:O4'	2.16	0.44
26:DA:307:G:H21	26:DA:330:A:N6	2.10	0.44
26:DA:182:A:H2	26:DA:433:C:O2	2.00	0.44
27:DB:66:A:H61	27:DB:109:C:H5'	1.82	0.44
37:DQ:58:PHE:CE2	37:DQ:109:VAL:HG21	2.52	0.44
46:DZ:157:LEU:C	46:DZ:161:VAL:HG11	2.37	0.44
1:AA:1149:C:P	9:AI:9:ARG:HH21	2.40	0.44
1:AA:767:A:N7	61:AA:4048:HOH:O	2.36	0.44
1:AA:923:A:OP1	5:AE:21:ALA:HB2	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.52	0.44
25:AY:41:C:H2'	25:AY:42:C:C6	2.53	0.44
26:BA:1065:U:H3	26:BA:1188:A:N6	2.10	0.44
26:BA:1676:G:H2'	26:BA:1677:C:C6	2.53	0.44
26:BA:2661:U:H2'	26:BA:2662:U:C6	2.51	0.44
26:BA:329:U:H2'	26:BA:330:U:C6	2.52	0.44
26:BA:496:A:OP1	30:BF:59:TYR:HE1	1.99	0.44
1:CA:153:C:H2'	1:CA:154:C:C6	2.52	0.44
2:CB:213:LEU:O	2:CB:217:ARG:HB2	2.17	0.44
8:CH:44:PHE:HE2	8:CH:109:ILE:HG12	1.82	0.44
9:CI:99:LEU:HB3	9:CI:101:PHE:CD2	2.52	0.44
15:CO:54:ARG:HD3	15:CO:58:MET:HE2	1.99	0.44
56:D9:3:VAL:HA	56:D9:35:ARG:O	2.18	0.44
26:DA:686:G:N2	26:DA:788:A:H61	2.14	0.44
27:DB:72:G:H1'	27:DB:105:A:H61	1.82	0.44
31:DG:138:GLN:OE1	31:DG:138:GLN:N	2.43	0.44
33:DI:133:HIS:HD2	33:DI:136:VAL:HG23	1.82	0.44
39:DS:34:HIS:O	39:DS:97:ARG:NH2	2.50	0.44
45:DY:52:SER:HB2	45:DY:53:PRO:HD2	1.99	0.44
1:AA:620:C:H2'	1:AA:621:A:O4'	2.16	0.44
3:AC:52:LEU:HA	3:AC:70:VAL:HG23	1.99	0.44
9:AI:99:LEU:HB3	9:AI:101:PHE:HE1	1.80	0.44
26:BA:1424:A:OP1	54:B7:10:ARG:NH2	2.51	0.44
26:BA:2673:G:H2'	26:BA:2674:A:C8	2.51	0.44
26:BA:2859:U:H4'	26:BA:2878:A:C2	2.52	0.44
26:BA:722:A:C8	26:BA:851:A:C6	3.05	0.44
29:BE:79:ARG:HA	29:BE:79:ARG:HD3	1.82	0.44
32:BH:54:ARG:HD3	32:BH:65:HIS:ND1	2.32	0.44
46:BZ:108:PRO:CG	46:BZ:117:LEU:HD22	2.47	0.44
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.51	0.44
1:CA:1318:A:H5''	19:CS:3:ARG:NH2	2.32	0.44
3:CC:131:ARG:NH1	5:CE:50:GLU:HG3	2.32	0.44
4:CD:173:TRP:CE2	4:CD:189:PRO:HG3	2.53	0.44
4:CD:47:ARG:HH11	4:CD:49:ARG:HH21	1.65	0.44
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.99	0.44
19:CS:30:LEU:CD1	19:CS:50:ALA:HB2	2.48	0.44
51:D4:57:GLU:HA	51:D4:58:ARG:HA	1.71	0.44
26:DA:2153:G:N2	26:DA:2154:G:N3	2.65	0.44
31:DG:173:LEU:HB3	31:DG:178:PHE:CG	2.53	0.44
31:DG:28:VAL:O	31:DG:31:VAL:HG12	2.18	0.44
36:DP:88:LEU:HD11	36:DP:114:ILE:HD12	1.99	0.44
46:DZ:128:VAL:HG23	46:DZ:160:GLY:O	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.99	0.44
3:AC:27:LYS:NZ	3:AC:27:LYS:HA	2.32	0.44
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HD23	1.98	0.44
23:AW:51:U:H2'	23:AW:52:G:H8	1.83	0.44
24:AX:31:G:N7	24:AX:32:5MC:HM52	2.32	0.44
25:AY:40:C:H2'	25:AY:41:C:C6	2.52	0.44
26:BA:1229:G:H5'	50:B3:29:ARG:NH1	2.32	0.44
26:BA:1314:A:C2	26:BA:2035:A:C4	3.05	0.44
26:BA:139:A:C8	26:BA:1454:C:O2'	2.69	0.44
26:BA:2396:G:OP2	47:B0:55:ARG:NH1	2.51	0.44
26:BA:335:A:C6	26:BA:352:U:C4	3.06	0.44
27:BB:4:C:H2'	27:BB:5:C:C6	2.52	0.44
33:BI:101:LEU:HD13	33:BI:107:VAL:O	2.16	0.44
40:BT:37:GLY:HA2	40:BT:38:ASN:HA	1.69	0.44
1:CA:1054:C:HO2'	1:CA:1055:A:P	2.36	0.44
1:CA:1084:G:OP1	1:CA:1086:U:C2	2.70	0.44
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.99	0.44
1:CA:1324:A:O4'	1:CA:1362:C:H4'	2.17	0.44
1:CA:142:G:H2'	1:CA:143:A:O4'	2.16	0.44
1:CA:551:U:H2'	1:CA:552:U:H6	1.81	0.44
2:CB:80:ILE:HD11	2:CB:212:GLN:CA	2.48	0.44
4:CD:163:GLU:O	4:CD:166:LYS:N	2.44	0.44
10:CJ:5:ARG:HA	10:CJ:73:ASP:HA	2.00	0.44
17:CQ:66:SER:H	17:CQ:69:LYS:HB3	1.82	0.44
25:CY:7:A:N1	25:CY:66:U:O2	2.50	0.44
49:D2:16:LEU:O	49:D2:67:LYS:NZ	2.47	0.44
26:DA:1035:U:H2'	26:DA:1036:G:C8	2.52	0.44
26:DA:1219:G:H1	26:DA:1230:C:H42	1.64	0.44
26:DA:2370:G:C6	26:DA:2371:G:C6	3.06	0.44
29:DE:181:LEU:HD12	29:DE:181:LEU:HA	1.84	0.44
35:DO:71:ARG:NE	35:DO:105:GLU:OE2	2.40	0.44
44:DX:59:VAL:HB	44:DX:76:ARG:HB2	1.99	0.44
1:AA:1028:C:H2'	1:AA:1029:C:C4'	2.47	0.44
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.53	0.44
1:AA:162:A:O5'	1:AA:162:A:H8	2.01	0.44
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	2.00	0.44
2:AB:21:ARG:CD	2:AB:21:ARG:H	2.30	0.44
4:AD:105:VAL:HG13	4:AD:110:PHE:HB2	1.99	0.44
4:AD:177:ASP:HB3	4:AD:182:LYS:HG2	2.00	0.44
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	2.00	0.44
8:AH:6:ILE:HD11	8:AH:31:PHE:HD2	1.82	0.44
3:AC:12:LEU:O	14:AN:57:ARG:NH2	2.50	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BI:27:ARG:HD2	48:B1:71:TYR:CZ	2.51	0.44
50:B3:31:LEU:HD23	50:B3:31:LEU:HA	1.69	0.44
26:BA:1047:A:H2'	26:BA:1048:G:O4'	2.18	0.44
26:BA:2074:G:H4'	29:BE:143:ASN:O	2.17	0.44
26:BA:2859:U:OP2	40:BT:95:ARG:NH1	2.50	0.44
26:BA:895:G:O6	26:BA:974:G:H2'	2.17	0.44
28:BD:232:PRO:HB3	28:BD:244:ARG:CZ	2.48	0.44
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.17	0.44
1:CA:1441:G:O5'	1:CA:1441:G:H8	2.00	0.44
1:CA:537:G:H2'	1:CA:538:G:C8	2.53	0.44
1:CA:938:A:C6	1:CA:939:G:C5	3.06	0.44
2:CB:74:LYS:HB3	2:CB:169:LYS:HE2	1.98	0.44
3:CC:33:LEU:HD12	3:CC:36:ASP:HB3	1.99	0.44
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.16	0.44
26:DA:1153:C:H5''	41:DU:62:ILE:HD13	2.00	0.44
26:DA:1463:C:H2'	26:DA:1464:C:C6	2.53	0.44
26:DA:1472:A:N6	26:DA:1519:G:H1'	2.32	0.44
26:DA:1894:C:H2'	26:DA:1895:C:C6	2.53	0.44
26:DA:2156:G:H8	26:DA:2156:G:O5'	1.99	0.44
26:DA:250:G:C6	26:DA:251:A:C6	3.05	0.44
26:DA:2892:A:N6	26:DA:2893:G:O6	2.51	0.44
26:DA:900:A:HO2'	26:DA:901:A:P	2.40	0.44
28:DD:79:VAL:HG21	28:DD:111:LEU:HD11	1.99	0.44
35:DO:103:ALA:HB1	35:DO:105:GLU:OE1	2.16	0.44
37:DQ:35:VAL:HG12	37:DQ:130:LYS:O	2.18	0.44
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.53	0.44
1:AA:636:U:H2'	1:AA:637:G:H8	1.83	0.44
1:AA:92:C:H2'	1:AA:93:G:H8	1.80	0.44
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.53	0.44
9:AI:4:TYR:CE1	9:AI:88:TYR:HD1	2.36	0.44
26:BA:1223:C:H2'	26:BA:1224:C:H6	1.82	0.44
26:BA:2115:G:C6	26:BA:2237:A:C8	3.06	0.44
26:BA:2137:G:C2	26:BA:2139:A:N7	2.86	0.44
26:BA:956:A:N1	26:BA:2289:G:H1'	2.32	0.44
26:BA:2315:G:O2'	31:BG:132:ASN:ND2	2.44	0.44
23:AW:56:C:OP1	26:BA:943:C:H5'	2.18	0.44
26:BA:1199:C:OP1	41:BU:92:ARG:NH1	2.50	0.44
45:BY:102:CYS:SG	45:BY:103:GLY:N	2.91	0.44
1:CA:1493:A:H5''	1:CA:1494:G:OP2	2.18	0.44
1:CA:1508:G:H2'	1:CA:1509:C:C6	2.52	0.44
1:CA:37:U:O2'	1:CA:500:G:H4'	2.17	0.44
1:CA:826:C:H2'	1:CA:827:U:C6	2.53	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:CD:161:ASN:HD22	4:CD:161:ASN:N	2.16	0.44
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.33	0.44
12:CL:24:VAL:HG12	12:CL:24:VAL:O	2.17	0.44
16:CP:9:PHE:CE1	16:CP:18:ARG:HD2	2.52	0.44
23:CW:39:PSU:H2'	23:CW:40:C:H6	1.83	0.44
26:DA:2336:A:H61	47:D0:43:THR:CG2	2.29	0.44
26:DA:2880:C:O3'	38:DR:90:ARG:NH1	2.51	0.44
26:DA:556:G:H2'	26:DA:557:U:C6	2.52	0.44
27:DB:3:C:H2'	27:DB:4:C:H6	1.83	0.44
27:DB:46:A:H2'	27:DB:47:C:C6	2.52	0.44
29:DE:77:ILE:CD1	29:DE:195:LEU:HD13	2.46	0.44
31:DG:128:ARG:HE	31:DG:128:ARG:HB2	1.67	0.44
35:DO:77:ILE:HB	40:DT:74:ARG:HD3	2.00	0.44
1:AA:1326:C:OP1	21:AU:12:LYS:NZ	2.50	0.44
1:AA:346:G:N3	1:AA:347:G:H1'	2.33	0.44
1:AA:434:U:H2'	1:AA:435:C:C6	2.52	0.44
1:AA:630:G:H2'	1:AA:631:G:H8	1.83	0.44
1:AA:674:G:H2'	1:AA:675:A:H8	1.83	0.44
1:AA:952:U:H2'	1:AA:953:G:H8	1.80	0.44
3:AC:140:ARG:HB2	3:AC:140:ARG:HE	1.51	0.44
7:AG:46:ALA:O	7:AG:50:ILE:HG23	2.18	0.44
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HB3	1.99	0.44
15:AO:53:HIS:O	15:AO:56:LEU:HB3	2.18	0.44
23:AW:22:G:H2'	23:AW:23:A:C8	2.53	0.44
49:B2:30:ARG:O	49:B2:34:GLU:HG3	2.17	0.44
54:B7:11:LYS:HE3	54:B7:15:THR:OG1	2.18	0.44
26:BA:2331:G:N2	39:BS:3:ARG:HA	2.33	0.44
26:BA:240:A:C5	26:BA:241:G:H1'	2.52	0.44
26:BA:555:G:O4'	26:BA:555:G:N3	2.50	0.44
32:BH:125:VAL:HG12	32:BH:127:GLU:O	2.18	0.44
32:BH:164:TYR:HB2	32:BH:167:GLU:HB2	1.99	0.44
32:BH:24:VAL:HG22	32:BH:35:VAL:HB	1.99	0.44
33:BI:79:ILE:HB	33:BI:144:VAL:HG12	2.00	0.44
39:BS:58:LEU:HD23	39:BS:58:LEU:HA	1.70	0.44
46:BZ:155:LEU:HD12	46:BZ:156:LYS:H	1.81	0.44
1:CA:1134:G:C2'	1:CA:1135:U:H5'	2.48	0.44
1:CA:1170:A:H2'	1:CA:1171:G:O4'	2.17	0.44
1:CA:576:G:O6	1:CA:880:C:O2'	2.30	0.44
1:CA:696:A:H8	1:CA:696:A:O5'	2.01	0.44
1:CA:79:G:N2	1:CA:80:G:C4	2.86	0.44
2:CB:224:GLN:HA	2:CB:228:GLY:O	2.18	0.44
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.99	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:CF:69:GLU:H	6:CF:69:GLU:CD	2.17	0.44
8:CH:68:ARG:NH1	8:CH:74:PRO:HB3	2.32	0.44
1:CA:684:A:O2'	11:CK:39:PRO:O	2.34	0.44
13:CM:40:ASN:ND2	13:CM:41:PRO:HD2	2.33	0.44
23:CW:14:A:N6	23:CW:21:A:H2	2.15	0.44
23:CW:38:A:H2'	23:CW:39:PSU:O4'	2.18	0.44
50:D3:18:ASP:N	50:D3:18:ASP:OD1	2.44	0.44
26:DA:1016:G:H2'	26:DA:1017:G:O4'	2.18	0.44
26:DA:2144:U:O3'	26:DA:2145:C:H2'	2.17	0.44
26:DA:2242:G:H2'	26:DA:2243:U:O4'	2.18	0.44
26:DA:582:G:H2'	26:DA:583:G:C8	2.53	0.44
26:DA:656:G:H2'	26:DA:657:U:O4'	2.18	0.44
26:DA:828:U:H4'	26:DA:831:G:N1	2.32	0.44
28:DD:108:PRO:HG2	28:DD:111:LEU:HB2	1.99	0.44
28:DD:164:GLN:NE2	28:DD:166:GLN:OE1	2.46	0.44
30:DF:39:TRP:HB3	30:DF:101:LEU:HD22	2.00	0.44
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.83	0.44
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.53	0.44
1:AA:184:G:H2'	1:AA:185:A:H8	1.81	0.44
1:AA:299:G:H2'	1:AA:300:A:C8	2.53	0.44
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.60	0.44
1:AA:68:G:C2	1:AA:69:G:H1'	2.53	0.44
1:AA:731:G:H5'	1:AA:766:A:H4'	2.00	0.44
1:AA:1250:A:H4'	9:AI:68:GLY:N	2.33	0.44
15:AO:54:ARG:O	15:AO:58:MET:HG3	2.18	0.44
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.99	0.44
20:AT:72:LEU:HD23	20:AT:72:LEU:HA	1.84	0.44
21:AU:15:ARG:HH11	21:AU:15:ARG:HB2	1.82	0.44
23:AW:51:U:H2'	23:AW:52:G:C8	2.53	0.44
26:BA:2052:A:H4'	26:BA:2053:A:C8	2.53	0.44
26:BA:2081:A:OP2	61:BA:4337:HOH:O	2.21	0.44
26:BA:922:G:H2'	26:BA:923:C:O4'	2.17	0.44
29:BE:73:GLU:H	29:BE:73:GLU:HG3	1.63	0.44
1:CA:1040:U:C4	1:CA:1041:A:C8	3.05	0.44
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.17	0.44
4:CD:47:ARG:NH1	4:CD:49:ARG:HH21	2.16	0.44
9:CI:4:TYR:CZ	9:CI:88:TYR:HD2	2.36	0.44
14:CN:26:ARG:HD2	14:CN:43:CYS:HB3	2.00	0.44
19:CS:19:VAL:O	19:CS:23:ASN:ND2	2.50	0.44
25:CY:65:G:H2'	25:CY:66:U:C6	2.53	0.44
50:D3:23:LEU:O	50:D3:27:GLY:N	2.50	0.44
51:D4:40:HIS:ND1	51:D4:43:TYR:HD2	2.15	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:330:A:H2	26:DA:1210:A:H2'	1.83	0.44
26:DA:1288:U:C2	26:DA:1327:C:O2	2.71	0.44
26:DA:2680:C:OP2	29:DE:111:ARG:NH2	2.50	0.44
26:DA:888:C:H5''	26:DA:889:C:OP2	2.18	0.44
28:DD:13:ARG:HA	28:DD:13:ARG:HD2	1.71	0.44
28:DD:237:GLU:OE2	61:DD:401:HOH:O	2.21	0.44
30:DF:11:VAL:HB	30:DF:18:ARG:HB3	1.99	0.44
34:DN:15:LEU:HD12	34:DN:137:LYS:HG2	1.99	0.44
1:AA:958:A:C6	1:AA:959:A:N1	2.86	0.44
8:AH:96:GLY:N	8:AH:99:GLU:OE2	2.28	0.44
11:AK:33:THR:HA	11:AK:39:PRO:HA	2.00	0.44
16:AP:20:VAL:HG23	16:AP:35:LYS:HA	2.00	0.44
26:BA:1683:C:H2'	26:BA:1684:A:C8	2.53	0.44
26:BA:2376:C:H2'	26:BA:2377:G:O4'	2.18	0.44
26:BA:597:C:N3	29:BE:145:LYS:NZ	2.63	0.44
26:BA:923:C:H2'	26:BA:924:U:O4'	2.18	0.44
28:BD:83:GLU:OE1	28:BD:104:TYR:OH	2.28	0.44
29:BE:143:ASN:HD22	29:BE:147:PRO:CD	2.31	0.44
32:BH:3:ARG:HH12	32:BH:65:HIS:HB3	1.83	0.44
34:BN:67:LEU:O	34:BN:88:GLU:HG3	2.17	0.44
35:BO:2:ILE:HD12	35:BO:6:THR:HG21	1.99	0.44
44:BX:88:LYS:NZ	44:BX:90:GLU:OE1	2.33	0.44
1:CA:292:G:N7	1:CA:293:G:H1'	2.33	0.44
1:CA:35:G:H2'	1:CA:36:C:C6	2.53	0.44
2:CB:192:SER:O	2:CB:194:PRO:HD3	2.17	0.44
6:CF:3:ARG:HB3	6:CF:93:SER:HB2	2.00	0.44
8:CH:39:LEU:HA	8:CH:39:LEU:HD13	1.74	0.44
12:CL:69:TYR:HE2	12:CL:71:PRO:HA	1.83	0.44
25:CY:30:G:C2	25:CY:31:A:C8	3.06	0.44
26:DA:1032:A:H4'	56:D9:16:VAL:HG11	2.00	0.44
26:DA:1301:A:H2	26:DA:1626:G:N3	2.14	0.44
26:DA:2070:G:H2'	26:DA:2071:A:H8	1.83	0.44
26:DA:2615:U:OP1	61:DA:4004:HOH:O	2.21	0.44
26:DA:265:A:C8	26:DA:266:G:H1'	2.53	0.44
26:DA:26:G:C6	26:DA:27:G:N1	2.86	0.44
26:DA:911:A:H2'	37:DQ:9:TYR:OH	2.18	0.44
26:DA:927:G:H2'	26:DA:928:G:O4'	2.17	0.44
31:DG:111:LEU:HB3	31:DG:117:PHE:CE2	2.53	0.44
39:DS:35:ILE:HD11	39:DS:101:LEU:HD12	1.99	0.44
26:DA:328:U:H4'	45:DY:68:HIS:CG	2.52	0.44
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.06	0.43
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.53	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:401:C:H2'	1:AA:402:G:C8	2.53	0.43
1:AA:858:G:O6	1:AA:869:G:H3'	2.18	0.43
2:AB:16:HIS:HD2	2:AB:17:PHE:H	1.56	0.43
4:AD:11:LEU:HD23	4:AD:66:ARG:HB3	1.99	0.43
9:AI:22:GLY:N	9:AI:58:HIS:O	2.39	0.43
1:AA:276:G:O3'	17:AQ:68:ARG:NH1	2.51	0.43
26:BA:1015:C:H2'	26:BA:1016:C:C6	2.53	0.43
26:BA:1486:G:H2'	26:BA:1487:G:O4'	2.18	0.43
26:BA:1857:G:H2'	26:BA:1858:C:O4'	2.17	0.43
30:BF:140:LEU:HD21	30:BF:170:LEU:HD11	2.00	0.43
26:BA:2697:G:H5'	35:BO:68:GLU:OE1	2.18	0.43
39:BS:3:ARG:HE	39:BS:4:LEU:H	1.66	0.43
46:BZ:111:VAL:CG2	46:BZ:117:LEU:HB2	2.48	0.43
46:BZ:7:ALA:O	46:BZ:62:PRO:HD3	2.18	0.43
1:CA:1095:U:H2'	1:CA:1096:C:O4'	2.18	0.43
1:CA:1118:C:N1	1:CA:1119:C:H5	2.16	0.43
1:CA:1136:U:H5''	1:CA:1137:C:C5	2.53	0.43
1:CA:1423:G:H2'	1:CA:1424:C:C6	2.53	0.43
2:CB:7:VAL:HG12	2:CB:8:LYS:HG2	2.00	0.43
3:CC:6:HIS:HA	3:CC:7:PRO:HD3	1.71	0.43
7:CG:18:TYR:HB3	7:CG:59:LEU:HD13	2.00	0.43
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.99	0.43
13:CM:72:ALA:O	13:CM:76:ALA:N	2.42	0.43
25:CY:37:MIA:H3'	25:CY:38:A:H8	1.82	0.43
26:DA:2164:C:H5	26:DA:2165:G:N3	2.16	0.43
26:DA:2347:C:H2'	26:DA:2348:U:C6	2.53	0.43
26:DA:2732:G:OP1	29:DE:203:LYS:NZ	2.43	0.43
26:DA:2742:C:OP1	56:D9:35:ARG:HD3	2.18	0.43
26:DA:668:G:H5'	26:DA:669:G:OP2	2.18	0.43
33:DI:88:ILE:HD11	33:DI:144:VAL:HG11	2.00	0.43
33:DI:57:ARG:O	33:DI:61:ARG:HG2	2.18	0.43
34:DN:4:TYR:CD2	41:DU:100:VAL:HG11	2.52	0.43
37:DQ:139:GLU:HG2	46:DZ:122:ARG:HG3	2.00	0.43
37:DQ:27:VAL:O	37:DQ:29:PHE:N	2.51	0.43
41:DU:76:TYR:HH	41:DU:92:ARG:HH11	1.63	0.43
45:DY:10:GLY:O	45:DY:26:LYS:HD3	2.18	0.43
37:DQ:29:PHE:O	46:DZ:122:ARG:NH2	2.51	0.43
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.82	0.43
1:AA:339:C:H2'	1:AA:340:U:C6	2.54	0.43
1:AA:646:U:H2'	1:AA:647:C:C6	2.53	0.43
4:AD:112:VAL:HG23	4:AD:116:GLN:OE1	2.18	0.43
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.80	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:AD:65:ARG:HG2	4:AD:75:PHE:CD2	2.53	0.43
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.33	0.43
23:AW:76:31M:N1	26:BA:2595:G:O2'	2.51	0.43
25:AY:57:G:C2	25:AY:58:A:H5'	2.53	0.43
26:BA:125:A:H5''	26:BA:126:C:C6	2.53	0.43
26:BA:1404:G:N2	26:BA:1418:U:C5	2.86	0.43
26:BA:2332:A:H2'	26:BA:2332:A:N3	2.34	0.43
26:BA:2459:G:N2	26:BA:2462:A:OP2	2.51	0.43
26:BA:388:A:H2'	26:BA:389:G:C8	2.53	0.43
26:BA:92:C:H2'	26:BA:93:G:O4'	2.19	0.43
35:BO:78:ARG:NH2	40:BT:73:GLU:OE2	2.49	0.43
41:BU:117:GLN:H	41:BU:117:GLN:HG2	1.42	0.43
46:BZ:150:LEU:HA	46:BZ:150:LEU:HD12	1.78	0.43
1:CA:1115:C:H2'	1:CA:1116:C:C6	2.53	0.43
1:CA:1152:A:C6	1:CA:1153:C:C4	3.06	0.43
1:CA:766:A:OP2	61:CA:4021:HOH:O	2.21	0.43
2:CB:20:GLU:HG3	2:CB:191:ASP:HB3	1.99	0.43
3:CC:18:TRP:CE3	3:CC:18:TRP:N	2.85	0.43
3:CC:47:LEU:HD12	3:CC:68:VAL:HG11	2.00	0.43
7:CG:26:PHE:CD2	7:CG:62:PHE:HE1	2.36	0.43
9:CI:108:VAL:HG12	9:CI:109:VAL:H	1.84	0.43
10:CJ:16:LEU:HD23	10:CJ:94:VAL:HG22	1.99	0.43
13:CM:50:GLU:O	13:CM:54:VAL:HG22	2.18	0.43
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.53	0.43
51:D4:26:SER:OG	51:D4:27:THR:N	2.51	0.43
26:DA:2006:C:O5'	26:DA:2006:C:H6	2.00	0.43
26:DA:2172:U:O2'	26:DA:2173:A:OP1	2.30	0.43
26:DA:910:A:N1	26:DA:2277:G:H1'	2.32	0.43
26:DA:2626:C:H2'	26:DA:2627:G:O4'	2.18	0.43
26:DA:288:C:H2'	26:DA:289:A:H8	1.82	0.43
26:DA:601:C:O2	26:DA:605:C:H4'	2.18	0.43
26:DA:817:C:OP2	61:DA:4676:HOH:O	2.21	0.43
26:DA:903:C:H2'	26:DA:904:C:H6	1.81	0.43
37:DQ:68:ILE:HD13	37:DQ:103:MET:HG2	2.00	0.43
38:DR:21:TYR:CZ	38:DR:43:GLU:HG2	2.52	0.43
46:DZ:154:ASP:N	46:DZ:154:ASP:OD1	2.39	0.43
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.44	0.43
1:AA:335:C:H2'	1:AA:336:C:C6	2.54	0.43
3:AC:52:LEU:HD11	3:AC:55:VAL:CG2	2.48	0.43
5:AE:41:VAL:HG23	5:AE:67:VAL:HG12	2.00	0.43
9:AI:61:ALA:HB1	9:AI:63:ILE:HD11	2.01	0.43
14:AN:24:CYS:HB2	14:AN:33:VAL:HG12	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:AT:92:LEU:HA	20:AT:92:LEU:HD23	1.84	0.43
26:BA:1640:G:H2'	26:BA:1641:G:O4'	2.18	0.43
26:BA:1992:A:H4'	26:BA:1993:A:OP1	2.18	0.43
26:BA:2418:U:H2'	26:BA:2418:U:OP2	2.19	0.43
30:BF:33:LEU:HD13	30:BF:112:MET:HE2	2.00	0.43
43:BW:14:PRO:HG2	43:BW:78:GLU:CG	2.45	0.43
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.18	0.43
1:CA:1002:G:N2	1:CA:1039:C:C4	2.86	0.43
1:CA:1080:A:H5''	1:CA:1081:G:OP2	2.19	0.43
1:CA:757:U:O2'	1:CA:879:C:O2	2.31	0.43
4:CD:111:ALA:HB1	4:CD:116:GLN:HB3	2.00	0.43
7:CG:27:ILE:HD12	7:CG:40:ALA:HA	2.00	0.43
16:CP:3:LYS:O	16:CP:21:VAL:HA	2.18	0.43
16:CP:60:LEU:HD13	16:CP:60:LEU:HA	1.84	0.43
6:CF:94:GLN:NE2	18:CR:72:ARG:HH12	2.16	0.43
20:CT:90:GLN:O	20:CT:93:GLU:HB3	2.18	0.43
51:D4:56:VAL:HG13	51:D4:57:GLU:H	1.83	0.43
26:DA:2674:G:H2'	26:DA:2675:A:C8	2.53	0.43
26:DA:324:A:H2'	26:DA:325:G:O4'	2.19	0.43
26:DA:623:G:H2'	26:DA:624:C:C6	2.54	0.43
35:DO:25:LEU:HD12	35:DO:38:VAL:HG12	1.99	0.43
1:AA:374:A:C6	1:AA:375:U:C4	3.05	0.43
1:AA:814:A:H2'	1:AA:816:A:H5''	1.99	0.43
2:AB:213:LEU:HD22	2:AB:214:ILE:HD13	2.00	0.43
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.83	0.43
7:AG:65:ALA:O	7:AG:69:VAL:HG23	2.17	0.43
1:AA:1302:U:H5	13:AM:17:VAL:HG21	1.83	0.43
13:AM:70:LEU:O	13:AM:74:VAL:HG23	2.19	0.43
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.18	0.43
26:BA:2190:G:H5'	26:BA:2191:A:H5''	2.00	0.43
26:BA:2389:A:H2'	26:BA:2390:A:C8	2.53	0.43
26:BA:2555:G:H2'	26:BA:2556:G:C8	2.53	0.43
26:BA:613:A:H2'	26:BA:614:C:O4'	2.18	0.43
26:BA:933:C:H4'	26:BA:933:C:OP1	2.17	0.43
30:BF:64:ILE:HD12	30:BF:65:TRP:CZ3	2.54	0.43
44:BX:50:LYS:N	44:BX:87:GLN:OE1	2.48	0.43
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.53	0.43
1:CA:1399:C:C2	1:CA:1502:A:N6	2.87	0.43
3:CC:34:LEU:HG	3:CC:38:ARG:NH1	2.31	0.43
14:CN:37:PHE:HZ	14:CN:56:VAL:HG21	1.83	0.43
51:D4:68:ARG:O	51:D4:69:LYS:HB3	2.18	0.43
26:DA:813:U:HO2'	26:DA:1225:G:HO2'	1.67	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1881:C:H2'	26:DA:1882:C:O4'	2.19	0.43
26:DA:2410:G:H2'	26:DA:2411:A:O4'	2.19	0.43
26:DA:2820:A:C5	38:DR:4:LEU:HD11	2.53	0.43
26:DA:540:C:H2'	26:DA:541:C:C6	2.53	0.43
26:DA:627:A:H4'	26:DA:628:G:H5'	2.00	0.43
30:DF:33:LEU:HB3	36:DP:6:LEU:HD21	2.01	0.43
34:DN:57:ALA:HB1	34:DN:96:GLU:HA	2.01	0.43
45:DY:89:PHE:CE2	45:DY:95:LYS:HB2	2.53	0.43
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.52	0.43
1:AA:262:A:H4'	20:AT:75:ASN:HB2	2.00	0.43
5:AE:105:VAL:O	5:AE:109:ILE:HD12	2.19	0.43
6:AF:10:LEU:HB2	6:AF:59:TYR:HB3	2.01	0.43
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.53	0.43
23:AW:56:C:H5'	26:BA:942:A:H1'	2.00	0.43
26:BA:1217:G:H3'	26:BA:1218:G:H5'	2.01	0.43
26:BA:1222:A:H2'	26:BA:1222:A:N3	2.33	0.43
26:BA:1477:U:H2'	26:BA:1478:C:C6	2.54	0.43
26:BA:1940:A:O2'	26:BA:1942:C:N4	2.51	0.43
31:BG:122:PRO:HD3	31:BG:181:ARG:HG2	2.00	0.43
32:BH:33:LEU:HD21	32:BH:136:ILE:HG13	2.00	0.43
33:BI:81:VAL:O	33:BI:146:ALA:HA	2.19	0.43
1:CA:1279:A:O2'	1:CA:1282:C:N4	2.51	0.43
1:CA:722:A:N6	1:CA:724:G:C2	2.87	0.43
2:CB:35:GLU:HB2	2:CB:40:HIS:HD2	1.82	0.43
12:CL:83:VAL:HG23	12:CL:107:ALA:HB2	2.01	0.43
16:CP:55:ARG:HD2	16:CP:55:ARG:HA	1.88	0.43
25:CY:4:C:H2'	25:CY:5:G:H5'	2.00	0.43
26:DA:1817:G:OP1	28:DD:88:ARG:NH2	2.48	0.43
26:DA:2134:A:C2	26:DA:2159:G:H4'	2.53	0.43
26:DA:2134:A:H3'	26:DA:2135:A:C8	2.53	0.43
26:DA:2516:G:C6	26:DA:2517:C:N4	2.86	0.43
27:DB:28:C:OP2	39:DS:33:LYS:NZ	2.32	0.43
28:DD:182:LEU:HB2	28:DD:272:ALA:HB3	2.01	0.43
31:DG:45:GLU:HG2	31:DG:45:GLU:H	1.43	0.43
32:DH:98:LEU:HD12	32:DH:102:ALA:O	2.18	0.43
41:DU:79:PHE:CZ	41:DU:83:LEU:HD21	2.54	0.43
45:DY:43:ASN:OD1	45:DY:65:ALA:HB3	2.19	0.43
1:AA:1061:G:H1'	10:AJ:56:HIS:CE1	2.53	0.43
13:AM:120:LYS:HE3	23:AW:40:C:O2'	2.19	0.43
19:AS:52:TYR:HA	19:AS:56:GLN:O	2.18	0.43
25:AY:33:U:H2'	25:AY:34:G:H5''	2.00	0.43
25:AY:71:G:H4'	26:BA:1882:U:H4'	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
51:B4:59:PHE:C	51:B4:61:ARG:H	2.21	0.43
26:BA:1304:C:H2'	26:BA:1305:G:O4'	2.19	0.43
26:BA:1765:U:H2'	26:BA:1766:G:O4'	2.18	0.43
26:BA:2205:C:O2'	26:BA:2206:G:OP1	2.35	0.43
26:BA:2603:C:H2'	26:BA:2604:G:C8	2.54	0.43
26:BA:2804:C:H5'	26:BA:2902:G:N2	2.34	0.43
28:BD:137:PRO:O	28:BD:140:THR:HG23	2.18	0.43
31:BG:43:LEU:HB3	31:BG:44:GLY:H	1.55	0.43
34:BN:67:LEU:HA	34:BN:67:LEU:HD12	1.80	0.43
40:BT:118:ARG:HD2	40:BT:118:ARG:HA	1.61	0.43
1:CA:1009:G:N2	1:CA:1010:G:H1'	2.33	0.43
1:CA:1030(A):G:C2	1:CA:1030(C):G:H8	2.36	0.43
1:CA:693:G:H2'	1:CA:694:A:C8	2.53	0.43
9:CI:43:ALA:HB2	9:CI:74:ILE:CD1	2.49	0.43
14:CN:47:LEU:O	14:CN:51:GLY:N	2.51	0.43
1:CA:750:G:N2	15:CO:23:GLY:O	2.48	0.43
24:CX:15:G:H2'	24:CX:59:A:N1	2.34	0.43
26:DA:2695:C:H2'	26:DA:2696:U:H6	1.84	0.43
26:DA:69:C:N4	61:DA:4335:HOH:O	2.52	0.43
26:DA:782:A:H5'	26:DA:783:A:N7	2.34	0.43
28:DD:142:VAL:HG13	28:DD:191:ALA:HB1	2.00	0.43
46:DZ:153:SER:HB3	46:DZ:167:PRO:HA	2.00	0.43
1:AA:1198:G:H2'	1:AA:1199:U:C6	2.54	0.43
1:AA:90:U:O2'	1:AA:91:C:H5'	2.19	0.43
2:AB:200:ILE:HD13	2:AB:200:ILE:H	1.84	0.43
2:AB:36:ARG:C	2:AB:38:GLY:H	2.21	0.43
7:AG:46:ALA:HA	7:AG:49:ILE:HD12	2.01	0.43
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.51	0.43
19:AS:27:GLU:HB3	19:AS:28:LYS:HB3	2.01	0.43
48:B1:50:ARG:HG2	48:B1:59:THR:HB	2.00	0.43
43:BW:19:LEU:HB3	52:B5:25:LEU:HD11	2.01	0.43
53:B6:10:LEU:HG	53:B6:54:ILE:HG13	2.00	0.43
26:BA:1091:A:H1'	26:BA:1093:G:C2	2.53	0.43
26:BA:2304:C:H2'	26:BA:2305:C:H6	1.83	0.43
26:BA:2718:G:N7	61:BA:4733:HOH:O	2.37	0.43
33:BI:50:ARG:HA	33:BI:53:ALA:HB3	2.01	0.43
42:BV:34:GLU:HB3	42:BV:56:SER:HB2	2.00	0.43
1:CA:1011:G:C2	1:CA:1012:U:H1'	2.54	0.43
1:CA:1014:A:H2'	1:CA:1015:A:C8	2.54	0.43
1:CA:1110:A:OP2	61:CA:4091:HOH:O	2.21	0.43
1:CA:1442(A):G:O2'	40:DT:118:ARG:HG2	2.18	0.43
1:CA:503:C:OP2	12:CL:116:SER:HB3	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:CM:50:GLU:HA	13:CM:53:VAL:HB	2.01	0.43
19:CS:28:LYS:HB2	19:CS:29:ARG:CB	2.48	0.43
25:CY:8:4SU:C2	25:CY:14:A:H62	2.30	0.43
26:DA:1503:U:H2'	26:DA:1504:C:C6	2.54	0.43
26:DA:2805:G:C6	26:DA:2807:G:C6	3.07	0.43
26:DA:2870:C:H2'	26:DA:2871:C:O4'	2.19	0.43
26:DA:991:C:OP2	26:DA:1186:G:H5'	2.18	0.43
30:DF:18:ARG:HG2	30:DF:19:GLU:H	1.84	0.43
32:DH:59:ARG:O	32:DH:63:SER:OG	2.36	0.43
33:DI:73:GLU:HG3	33:DI:139:GLN:O	2.18	0.43
1:AA:1151:A:O4'	10:AJ:39:PRO:HB2	2.19	0.43
1:AA:452:A:HO2'	1:AA:453:A:H8	1.65	0.43
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.99	0.43
4:AD:64:LEU:HB2	4:AD:198:VAL:HG21	2.00	0.43
5:AE:148:VAL:O	5:AE:152:ARG:HG3	2.18	0.43
12:AL:24:VAL:O	12:AL:24:VAL:HG12	2.18	0.43
17:AQ:53:LEU:HD23	17:AQ:82:MET:HE1	2.01	0.43
49:B2:16:LEU:HB3	49:B2:20:GLU:HB2	1.99	0.43
26:BA:11:G:C2'	26:BA:12:U:H5''	2.45	0.43
26:BA:2245:U:H2'	26:BA:2246:G:C8	2.54	0.43
26:BA:186:A:N6	26:BA:2442:A:O2'	2.51	0.43
26:BA:2803:A:N3	26:BA:2803:A:H2'	2.34	0.43
15:AO:56:LEU:HD21	26:BA:762:G:C2	2.54	0.43
26:BA:895:G:N9	26:BA:978:A:H8	2.17	0.43
27:BB:48:A:H4'	39:BS:95:HIS:HD2	1.83	0.43
38:BR:53:HIS:O	38:BR:56:LYS:HB2	2.18	0.43
1:CA:165:C:H2'	1:CA:166:G:C8	2.54	0.43
1:CA:302:G:N3	1:CA:556:C:H4'	2.33	0.43
1:CA:664:G:N2	1:CA:741:G:H1	2.04	0.43
2:CB:84:GLU:OE1	2:CB:216:SER:HA	2.18	0.43
4:CD:38:TYR:CZ	4:CD:45:GLN:HG2	2.54	0.43
7:CG:78:ARG:CZ	7:CG:79:ARG:HH12	2.32	0.43
1:CA:1320:C:C1'	19:CS:73:GLU:HG3	2.49	0.43
20:CT:86:ARG:O	20:CT:90:GLN:HB2	2.19	0.43
23:CW:61:C:O2'	23:CW:62:C:H6	2.02	0.43
49:D2:53:LEU:HA	49:D2:53:LEU:HD23	1.89	0.43
26:DA:1487:G:H2'	26:DA:1488:G:O4'	2.18	0.43
26:DA:1656:C:H2'	26:DA:1657:C:H6	1.84	0.43
26:DA:2494:G:C4	26:DA:2495:G:C8	3.07	0.43
26:DA:2602:A:H4'	26:DA:2603:G:C5'	2.48	0.43
26:DA:265:A:H1'	26:DA:266:G:O4'	2.19	0.43
26:DA:644:A:H5''	26:DA:645:C:OP1	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:974:G:C4	26:DA:989:G:C2	3.07	0.43
31:DG:164:GLU:OE2	31:DG:164:GLU:N	2.51	0.43
31:DG:37:VAL:O	31:DG:94:LEU:N	2.50	0.43
36:DP:101:VAL:HA	36:DP:106:LEU:O	2.18	0.43
45:DY:13:VAL:HB	45:DY:72:VAL:HG13	2.00	0.43
1:AA:1529:G:H4'	1:AA:1530:G:OP2	2.19	0.43
1:AA:402:G:C6	1:AA:403:C:C4	3.07	0.43
2:AB:88:ALA:O	2:AB:226:ARG:NH1	2.51	0.43
3:AC:6:HIS:HD2	3:AC:8:ILE:N	2.11	0.43
25:AY:49:C:N4	25:AY:65:G:N1	2.28	0.43
26:BA:1220:U:O3'	26:BA:1221:G:H4'	2.17	0.43
26:BA:1418:U:H2'	26:BA:1419:A:O4'	2.18	0.43
26:BA:2198:A:H2'	26:BA:2199:C:C6	2.54	0.43
26:BA:2203:G:O2'	26:BA:2204:G:OP1	2.34	0.43
26:BA:2308:U:OP2	39:BS:9:ARG:NH2	2.52	0.43
26:BA:2665:U:H2'	26:BA:2666:A:C8	2.53	0.43
26:BA:312:C:H2'	26:BA:313:A:C8	2.53	0.43
28:BD:71:ASP:HB3	28:BD:103:ARG:HH22	1.83	0.43
32:BH:121:ILE:HG13	32:BH:144:VAL:HG21	2.01	0.43
35:BO:104:ARG:NH1	40:BT:34:VAL:HG21	2.34	0.43
46:BZ:144:LEU:HD21	46:BZ:148:ASP:O	2.19	0.43
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.84	0.43
1:CA:1289:A:H2	1:CA:1372:U:O4'	2.01	0.43
1:CA:397:A:N3	1:CA:397:A:H3'	2.34	0.43
15:CO:87:ILE:HG22	15:CO:88:ARG:N	2.33	0.43
1:CA:607:A:C2	16:CP:31:LYS:HG3	2.54	0.43
24:CX:54:5MU:O5'	24:CX:54:5MU:H6	2.02	0.43
52:D5:48:GLU:O	52:D5:60:VAL:HG11	2.18	0.43
26:DA:1262:A:H2	52:D5:10:LYS:HD2	1.83	0.43
26:DA:208:C:H2'	26:DA:209:C:C6	2.54	0.43
26:DA:2228:G:C5	26:DA:2229:C:C4	3.07	0.43
26:DA:2400:G:H2'	26:DA:2401:U:C6	2.50	0.43
26:DA:380:U:H2'	26:DA:381:G:H8	1.83	0.43
26:DA:224:G:N7	26:DA:420:C:H4'	2.33	0.43
28:DD:68:LYS:O	28:DD:69:ARG:HB2	2.19	0.43
31:DG:43:LEU:C	31:DG:45:GLU:H	2.22	0.43
33:DI:14:ASP:OD1	33:DI:15:VAL:HG12	2.19	0.43
36:DP:39:LYS:CB	36:DP:45:LEU:HG	2.47	0.43
46:DZ:156:LYS:HE3	46:DZ:158:PRO:HD3	2.01	0.43
1:AA:1015:A:H2'	1:AA:1016:A:C8	2.54	0.43
1:AA:130:A:N3	1:AA:263:A:O2'	2.38	0.43
1:AA:1342:C:H4'	9:AI:125:TYR:HB3	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:584:G:H2'	1:AA:585:G:C8	2.54	0.43
1:AA:943:U:H2'	1:AA:944:G:H5'	2.00	0.43
4:AD:63:LYS:HG3	4:AD:64:LEU:N	2.33	0.43
9:AI:4:TYR:CE2	9:AI:88:TYR:HA	2.54	0.43
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	2.01	0.43
20:AT:90:GLN:O	20:AT:93:GLU:HB3	2.19	0.43
25:AY:6:G:H2'	25:AY:7:A:H5'	2.01	0.43
52:B5:59:GLU:HG2	52:B5:60:VAL:H	1.83	0.43
26:BA:1426:G:OP2	61:BA:5152:HOH:O	2.22	0.43
26:BA:1711:A:H1'	26:BA:2697:G:O2'	2.19	0.43
26:BA:213:G:H2'	26:BA:214:A:O4'	2.18	0.43
26:BA:2658:C:H2'	26:BA:2659:U:O4'	2.18	0.43
26:BA:364:A:H2'	26:BA:365:G:O4'	2.19	0.43
26:BA:704:U:H2'	26:BA:705:C:C6	2.53	0.43
26:BA:928:G:N3	26:BA:928:G:H2'	2.34	0.43
26:BA:938:G:C5	26:BA:939:C:C4	3.07	0.43
26:BA:929:G:N2	26:BA:941:U:O2	2.52	0.43
27:BB:110:G:H2'	27:BB:111:G:H8	1.84	0.43
28:BD:206:LEU:HD22	28:BD:211:ARG:HG2	2.00	0.43
26:BA:1857:G:H4'	28:BD:242:ARG:CZ	2.49	0.43
31:BG:77:ILE:HD12	31:BG:82:LEU:HD12	2.00	0.43
36:BP:96:THR:OG1	36:BP:99:LEU:HG	2.18	0.43
26:BA:2304:C:P	39:BS:17:ARG:HH12	2.41	0.43
41:BU:66:ASN:O	41:BU:70:ARG:HG3	2.19	0.43
44:BX:66:LEU:HD23	44:BX:66:LEU:HA	1.73	0.43
1:CA:1144:G:C6	1:CA:1145:C:N4	2.87	0.43
1:CA:337:C:H2'	1:CA:338:A:C8	2.53	0.43
1:CA:92:C:H2'	1:CA:93:G:O4'	2.19	0.43
7:CG:33:ASP:OD1	7:CG:33:ASP:N	2.51	0.43
10:CJ:90:LEU:HA	10:CJ:91:PRO:HD3	1.83	0.43
25:CY:34:G:C6	25:CY:35:A:C6	3.07	0.43
48:D1:50:ARG:HD2	48:D1:57:GLU:OE1	2.19	0.43
54:D7:26:GLY:O	54:D7:30:VAL:HG23	2.19	0.43
26:DA:140:G:H22	26:DA:1596:A:H4'	1.83	0.43
26:DA:1668:A:O2'	26:DA:1674:G:N7	2.43	0.43
26:DA:2028:U:H2'	26:DA:2029:G:O4'	2.19	0.43
26:DA:2529:G:O6	56:D9:31:LYS:NZ	2.52	0.43
26:DA:855:G:C6	26:DA:856:C:N4	2.86	0.43
26:DA:816:C:O2'	26:DA:932:G:O6	2.37	0.43
31:DG:44:GLY:N	31:DG:88:ILE:O	2.52	0.43
35:DO:104:ARG:NH2	35:DO:121:VAL:O	2.52	0.43
27:DB:114:C:H4'	39:DS:46:VAL:HG22	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
42:DV:55:ALA:HA	42:DV:100:ARG:O	2.19	0.43
1:AA:1353:G:H2'	1:AA:1354:C:H6	1.84	0.42
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.19	0.42
1:AA:839:U:H3'	1:AA:840:C:C5	2.53	0.42
1:AA:96:U:OP2	1:AA:96:U:H6	2.02	0.42
2:AB:28:PHE:CD1	2:AB:190:THR:HG22	2.54	0.42
2:AB:21:ARG:HB3	2:AB:39:ILE:HA	2.00	0.42
3:AC:104:GLN:HE21	3:AC:105:GLU:H	1.66	0.42
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.84	0.42
13:AM:19:LEU:HB3	13:AM:25:ILE:HG21	2.01	0.42
17:AQ:62:SER:OG	17:AQ:72:ARG:HD2	2.19	0.42
20:AT:13:LEU:HD12	20:AT:14:LYS:N	2.33	0.42
24:AX:19:G:H3'	24:AX:20:U:H6	1.84	0.42
26:BA:1827:U:H2'	26:BA:1828:C:H6	1.84	0.42
26:BA:2195:A:H2'	26:BA:2196:C:O4'	2.18	0.42
26:BA:2573:A:H2'	26:BA:2574:U:O4'	2.18	0.42
28:BD:145:VAL:HG12	28:BD:146:GLU:O	2.18	0.42
26:BA:640:A:C4	30:BF:180:GLY:HA2	2.54	0.42
40:BT:95:ARG:HH11	40:BT:95:ARG:CG	2.26	0.42
1:CA:1286:A:H3'	1:CA:1286:A:C8	2.54	0.42
1:CA:130:A:N3	1:CA:263:A:O2'	2.49	0.42
1:CA:580:U:H5''	15:CO:58:MET:HG2	2.00	0.42
1:CA:608:A:H2'	1:CA:609:A:O4'	2.18	0.42
1:CA:532:A:N6	3:CC:156:ARG:HH22	2.16	0.42
24:CX:21:A:N6	24:CX:46:G:H2'	2.34	0.42
24:CX:8:4SU:H5''	24:CX:49:G:H5'	2.01	0.42
26:DA:1161:C:H2'	26:DA:1162:G:C8	2.53	0.42
26:DA:140:G:H1'	26:DA:141:A:H2	1.84	0.42
26:DA:2137:C:O2'	26:DA:2138:C:H5'	2.19	0.42
26:DA:2865:U:C4	26:DA:2866:U:C4	3.07	0.42
26:DA:325:G:H2'	26:DA:326:G:O4'	2.20	0.42
26:DA:414:C:O2'	26:DA:415:A:H5'	2.19	0.42
26:DA:827:U:H4'	26:DA:828:U:C6	2.53	0.42
28:DD:121:PRO:HB3	28:DD:135:PHE:CE2	2.53	0.42
28:DD:36:PRO:HA	28:DD:61:LEU:HD13	2.01	0.42
30:DF:53:THR:HG23	30:DF:55:GLY:N	2.22	0.42
31:DG:125:PHE:CZ	31:DG:170:ARG:HA	2.54	0.42
33:DI:94:ALA:O	33:DI:98:ALA:N	2.44	0.42
37:DQ:31:ASP:HA	37:DQ:134:ARG:HH11	1.83	0.42
46:DZ:55:HIS:CE1	46:DZ:135:GLU:HG3	2.51	0.42
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.41	0.42
1:AA:346:G:H2'	1:AA:347:G:H4'	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:126:G:H4'	1:AA:634:C:O2	2.19	0.42
1:AA:711:G:OP1	6:AF:54:LYS:NZ	2.35	0.42
17:AQ:76:LEU:HD12	17:AQ:77:VAL:H	1.83	0.42
24:AX:7:G:O2'	24:AX:49:G:H5'	2.19	0.42
48:B1:8:SER:HB3	48:B1:66:HIS:CD2	2.55	0.42
51:B4:39:CYS:HA	51:B4:44:THR:HG21	2.01	0.42
26:BA:1760:U:H2'	26:BA:1761:G:H8	1.84	0.42
26:BA:2013:U:H2'	26:BA:2014:G:H5''	2.00	0.42
26:BA:38:A:H2'	26:BA:39:C:C6	2.54	0.42
26:BA:553:A:C2	26:BA:2065:C:H4'	2.53	0.42
29:BE:12:THR:HG22	29:BE:13:ARG:N	2.33	0.42
35:BO:122:LEU:HD13	40:BT:72:VAL:HG11	2.01	0.42
40:BT:118:ARG:HH11	40:BT:118:ARG:CG	2.30	0.42
45:BY:35:TYR:CE2	45:BY:69:ALA:HB3	2.53	0.42
1:CA:1051:C:N4	61:CA:4001:HOH:O	2.51	0.42
1:CA:1142:G:H2'	1:CA:1143:G:O4'	2.19	0.42
1:CA:49:U:O4	1:CA:365:U:H5	2.01	0.42
1:CA:684:A:H1'	11:CK:39:PRO:HD2	2.01	0.42
3:CC:6:HIS:HD2	3:CC:8:ILE:N	2.14	0.42
4:CD:155:LEU:HD23	4:CD:156:GLU:H	1.84	0.42
7:CG:103:TRP:CH2	7:CG:141:VAL:HG21	2.54	0.42
51:D4:62:ARG:HB2	51:D4:63:TYR:CD1	2.54	0.42
53:D6:40:CYS:HA	53:D6:41:PRO:HD3	1.90	0.42
26:DA:1235:G:C6	26:DA:1236:G:N1	2.87	0.42
26:DA:1292:U:H2'	26:DA:1293:C:C6	2.54	0.42
26:DA:1471:A:OP2	26:DA:1519:G:N1	2.42	0.42
26:DA:1587:A:H2'	26:DA:1588:C:C6	2.54	0.42
26:DA:212:G:H2'	26:DA:213:A:O4'	2.18	0.42
26:DA:2345:G:OP2	53:D6:38:LYS:NZ	2.42	0.42
26:DA:746:A:H2'	26:DA:2612:C:H5''	2.00	0.42
26:DA:760:G:H2'	26:DA:761:A:O4'	2.18	0.42
29:DE:170:LEU:HB3	29:DE:184:VAL:CG2	2.49	0.42
35:DO:23:ARG:HG3	35:DO:24:VAL:N	2.33	0.42
1:AA:1299:A:H5''	1:AA:1299:A:N3	2.35	0.42
1:AA:1236:A:O2'	1:AA:1304:G:H4'	2.19	0.42
1:AA:1317:C:N3	19:AS:37:ARG:NH2	2.63	0.42
1:AA:1410:G:H2'	1:AA:1411:C:C6	2.53	0.42
1:AA:540:G:H2'	1:AA:541:G:O4'	2.19	0.42
1:AA:8:A:H5'	5:AE:101:ILE:HG22	2.00	0.42
2:AB:166:ASP:HA	2:AB:167:PRO:HD3	1.81	0.42
4:AD:107:ARG:HD2	4:AD:107:ARG:HA	1.79	0.42
1:AA:16:A:O2'	5:AE:16:THR:HB	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:AF:89:MET:HE1	18:AR:72:ARG:HB3	2.00	0.42
8:AH:86:ILE:HG22	8:AH:93:VAL:HG21	2.01	0.42
13:AM:39:ILE:HD12	13:AM:52:GLU:HG2	2.00	0.42
20:AT:16:HIS:O	20:AT:19:SER:OG	2.25	0.42
24:AX:13:C:O2'	26:BA:1946:C:H4'	2.20	0.42
25:AY:55:PSU:N3	25:AY:57:G:H5'	2.33	0.42
51:B4:59:PHE:N	51:B4:59:PHE:CD1	2.77	0.42
26:BA:181:C:OP1	61:BA:4017:HOH:O	2.21	0.42
26:BA:215:G:N2	26:BA:217:A:H62	2.15	0.42
26:BA:669:A:H4'	26:BA:670:C:H5	1.83	0.42
26:BA:1828:C:H4'	28:BD:257:LEU:O	2.18	0.42
30:BF:9:ILE:HA	30:BF:10:PRO:HD2	1.82	0.42
30:BF:24:LEU:HB3	30:BF:115:ALA:HB2	2.02	0.42
30:BF:89:VAL:HG12	30:BF:90:PHE:CD2	2.55	0.42
31:BG:48:GLU:HA	31:BG:51:ARG:HG3	2.00	0.42
26:BA:1233:U:H4'	42:BV:79:VAL:HG22	2.01	0.42
46:BZ:136:PHE:O	46:BZ:137:ILE:HG13	2.20	0.42
1:CA:935:A:O2'	1:CA:1383:C:N3	2.44	0.42
1:CA:922:G:C6	1:CA:923:A:C6	3.07	0.42
4:CD:13:ARG:HB2	4:CD:40:PRO:HD3	2.01	0.42
12:CL:71:PRO:O	12:CL:102:ARG:HD2	2.18	0.42
19:CS:51:VAL:HB	19:CS:75:ALA:HB2	2.00	0.42
23:CW:74:C:C4	23:CW:75:C:C2	3.07	0.42
24:CX:53:G:H3'	24:CX:54:5MU:H71	2.01	0.42
25:CY:9:A:C8	25:CY:11:C:N4	2.87	0.42
53:D6:10:LEU:HD23	53:D6:22:ALA:HB2	2.01	0.42
26:DA:1545:A:H2'	26:DA:1546:C:O4'	2.20	0.42
26:DA:1575:C:H2'	26:DA:1576:U:O4'	2.19	0.42
26:DA:1656:C:H2'	26:DA:1657:C:C6	2.54	0.42
26:DA:1970:A:H4'	26:DA:1971:A:OP1	2.19	0.42
26:DA:2168:G:O3'	26:DA:2169:A:H8	2.02	0.42
26:DA:2272:U:H5''	26:DA:2273:A:OP1	2.18	0.42
26:DA:2745:C:H2'	26:DA:2746:U:O4'	2.19	0.42
26:DA:39:C:H2'	26:DA:40:C:H6	1.83	0.42
26:DA:699:A:H2'	26:DA:700:G:O4'	2.19	0.42
30:DF:33:LEU:HA	30:DF:33:LEU:HD12	1.75	0.42
32:DH:137:ASP:HB3	32:DH:140:LYS:HB3	1.99	0.42
35:DO:68:GLU:HB3	35:DO:78:ARG:HB2	2.01	0.42
37:DQ:43:THR:OG1	37:DQ:45:GLN:HG2	2.19	0.42
39:DS:67:ARG:HG3	39:DS:104:GLY:CA	2.49	0.42
41:DU:17:ILE:HG13	41:DU:32:PHE:HE1	1.83	0.42
46:DZ:138:GLU:H	46:DZ:156:LYS:NZ	2.16	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1479:C:H2'	1:AA:1480:G:H8	1.84	0.42
1:AA:741:G:H2'	1:AA:742:G:O4'	2.19	0.42
2:AB:207:ALA:O	2:AB:210:SER:HB3	2.19	0.42
20:AT:67:ALA:HA	20:AT:72:LEU:O	2.18	0.42
22:AV:15:A:O5'	22:AV:15:A:H8	2.02	0.42
24:AX:9:G:O2'	24:AX:10:G:N7	2.47	0.42
25:AY:50:U:H2'	25:AY:51:U:O4'	2.20	0.42
26:BA:1188:A:C4	26:BA:1190:G:C8	3.06	0.42
26:BA:1577:C:H1'	26:BA:1578:C:OP1	2.19	0.42
26:BA:2138:G:H2'	26:BA:2139:A:C5	2.54	0.42
26:BA:492:A:N3	26:BA:730:C:H1'	2.34	0.42
33:BI:93:THR:H	33:BI:96:ASP:HB2	1.84	0.42
34:BN:130:HIS:O	34:BN:133:GLN:HG2	2.19	0.42
38:BR:98:LEU:HD12	52:B5:57:VAL:HG11	2.01	0.42
46:BZ:19:ARG:HD3	46:BZ:25:PRO:CD	2.49	0.42
1:CA:1122:U:N3	1:CA:1123:A:N7	2.67	0.42
1:CA:1410:G:H2'	1:CA:1411:C:H6	1.84	0.42
1:CA:583:A:N6	1:CA:758:G:O2'	2.52	0.42
1:CA:898:G:N2	1:CA:901:A:OP2	2.50	0.42
1:CA:924:C:O2'	1:CA:1502:A:N6	2.49	0.42
2:CB:160:ASP:N	2:CB:160:ASP:OD1	2.52	0.42
4:CD:112:VAL:HG22	4:CD:116:GLN:OE1	2.20	0.42
4:CD:121:VAL:O	4:CD:134:ASP:HA	2.20	0.42
23:CW:11:C:N4	23:CW:24:G:H1	2.14	0.42
25:CY:50:U:H2'	25:CY:51:U:C6	2.53	0.42
51:D4:33:VAL:HG12	51:D4:34:GLU:N	2.34	0.42
26:DA:1847:A:H3'	26:DA:1848:A:H5'	2.00	0.42
26:DA:2110:G:C2	26:DA:2120:G:H1'	2.55	0.42
26:DA:2114:A:H2'	26:DA:2114:A:N3	2.34	0.42
26:DA:2251:G:OP1	37:DQ:82:ARG:NH1	2.52	0.42
26:DA:2376:A:H3'	26:DA:2377:A:H8	1.85	0.42
26:DA:729:G:O2'	26:DA:763:G:H4'	2.19	0.42
26:DA:910:A:C5	37:DQ:13:GLN:HG3	2.55	0.42
26:DA:996:A:C6	26:DA:1160:G:N1	2.87	0.42
27:DB:33:G:N3	27:DB:50:G:N2	2.67	0.42
36:DP:6:LEU:HA	36:DP:6:LEU:HD23	1.78	0.42
42:DV:48:GLY:HA2	42:DV:52:VAL:HG12	2.01	0.42
1:AA:1079:G:O3'	5:AE:14:ARG:NH2	2.52	0.42
1:AA:109:A:C6	1:AA:326:G:C6	3.07	0.42
1:AA:1125:U:H4'	1:AA:1126:U:OP1	2.19	0.42
1:AA:1401:G:C2	1:AA:1402:C:H1'	2.55	0.42
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.52	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:AH:46:LYS:HG3	8:AH:64:LYS:HB2	2.02	0.42
24:AX:2:G:H2'	24:AX:2:G:N3	2.34	0.42
53:B6:11:LEU:HD23	53:B6:11:LEU:HA	1.82	0.42
26:BA:1170:C:H1'	56:B9:36:GLN:NE2	2.34	0.42
26:BA:402:C:H2'	26:BA:403:C:C6	2.54	0.42
28:BD:218:ARG:HB3	28:BD:219:PRO:HD2	2.01	0.42
31:BG:121:ASN:HA	31:BG:122:PRO:HD3	1.87	0.42
32:BH:22:GLY:HA2	32:BH:37:VAL:O	2.20	0.42
1:CA:1173:G:H2'	1:CA:1174:G:H8	1.84	0.42
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.55	0.42
1:CA:1297:C:P	13:CM:44:ARG:HH22	2.42	0.42
4:CD:158:ILE:HG22	4:CD:162:LEU:HD12	2.02	0.42
6:CF:68:PRO:HB2	6:CF:71:ARG:HG3	2.01	0.42
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HA	2.00	0.42
26:DA:2171:A:OP1	26:DA:2171:A:H3'	2.19	0.42
26:DA:352:G:N2	61:DA:3734:HOH:O	2.32	0.42
26:DA:744:G:OP1	29:DE:132:HIS:ND1	2.47	0.42
26:DA:864:G:N2	26:DA:913:U:C2	2.87	0.42
30:DF:139:PHE:CD2	30:DF:167:ALA:HB2	2.55	0.42
30:DF:184:TYR:CZ	30:DF:188:ARG:HD2	2.54	0.42
39:DS:57:LYS:HE3	39:DS:57:LYS:HB2	1.80	0.42
46:DZ:144:LEU:CD1	46:DZ:172:ALA:HB1	2.47	0.42
1:AA:299:G:H8	1:AA:299:G:O5'	2.02	0.42
1:AA:60:A:OP1	1:AA:111:G:N2	2.51	0.42
2:AB:24:TRP:HD1	2:AB:24:TRP:H	1.68	0.42
1:AA:438:G:H4'	4:AD:123:HIS:CE1	2.55	0.42
4:AD:166:LYS:HD3	4:AD:166:LYS:HA	1.79	0.42
25:AY:52:G:H1	25:AY:62:C:H42	1.67	0.42
26:BA:1722:C:O2	29:BE:128:SER:OG	2.37	0.42
26:BA:2203:G:HO2'	26:BA:2204:G:P	2.42	0.42
26:BA:629:U:H4'	26:BA:705:C:H4'	2.00	0.42
27:BB:110:G:H2'	27:BB:111:G:C8	2.54	0.42
28:BD:242:ARG:HD3	28:BD:242:ARG:N	2.33	0.42
30:BF:34:TRP:CH2	36:BP:8:PRO:HB3	2.54	0.42
31:BG:77:ILE:N	31:BG:82:LEU:O	2.48	0.42
40:BT:127:ALA:O	40:BT:128:GLU:HB2	2.18	0.42
1:CA:1092:A:C6	1:CA:1093:A:C6	3.07	0.42
1:CA:1057:G:C5	1:CA:1204:A:C2	3.07	0.42
1:CA:444:C:H2'	1:CA:445:G:C8	2.55	0.42
1:CA:715:A:H5''	1:CA:805:C:H1'	2.02	0.42
1:CA:792:A:H4'	1:CA:793:U:H5''	2.01	0.42
1:CA:971:G:OP1	1:CA:971:G:H3'	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:979:C:H2'	1:CA:980:C:H5'	2.01	0.42
2:CB:133:LYS:O	2:CB:137:ARG:HG3	2.20	0.42
3:CC:43:LEU:HD11	3:CC:91:LEU:HD11	2.01	0.42
1:CA:1079:G:O3'	5:CE:14:ARG:NH2	2.53	0.42
23:CW:25:C:C2'	23:CW:26:A:H5'	2.49	0.42
25:CY:18:G:C2	25:CY:55:PSU:O4	2.72	0.42
26:DA:2271:G:OP1	47:D0:18:ALA:HB1	2.19	0.42
13:CM:65:LYS:CA	51:D4:50:VAL:HG11	2.49	0.42
26:DA:1151:G:C2	26:DA:1152:C:C2	3.07	0.42
26:DA:1354:A:H5''	28:DD:38:LYS:HD3	2.01	0.42
26:DA:1488:G:H5'	26:DA:1489:U:OP2	2.20	0.42
26:DA:2128:C:H2'	26:DA:2129:C:O4'	2.18	0.42
26:DA:2365:G:O6	55:D8:39:LYS:HE3	2.19	0.42
26:DA:251:A:C5	26:DA:252:G:H1'	2.55	0.42
26:DA:608:A:C6	26:DA:609:A:C6	3.08	0.42
26:DA:896:A:N6	46:DZ:146:ILE:HD13	2.34	0.42
27:DB:28:C:P	39:DS:36:TYR:HH	2.43	0.42
27:DB:33:G:C6	27:DB:34:U:C4	3.07	0.42
27:DB:73:A:C4	27:DB:105:A:C2	3.07	0.42
28:DD:264:LYS:HA	28:DD:265:PRO:HD3	1.88	0.42
29:DE:72:VAL:HA	29:DE:73:GLU:CB	2.50	0.42
31:DG:136:ARG:H	31:DG:136:ARG:HH11	1.68	0.42
33:DI:66:GLU:OE2	33:DI:69:LYS:HD3	2.18	0.42
35:DO:36:GLY:HA2	35:DO:106:LEU:HD23	2.01	0.42
26:DA:29:U:OP1	41:DU:5:LYS:NZ	2.52	0.42
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.54	0.42
1:AA:971:G:N1	1:AA:1363(A):A:OP2	2.45	0.42
1:AA:877:C:OP1	8:AH:88:LYS:NZ	2.33	0.42
11:AK:111:ASP:HB2	18:AR:84:LYS:HD3	2.01	0.42
47:B0:38:VAL:HG12	47:B0:40:GLN:HG2	2.01	0.42
26:BA:116:A:H3'	26:BA:117:A:H5''	2.02	0.42
26:BA:1314:A:H2'	26:BA:1315:A:O4'	2.18	0.42
26:BA:1779:G:H5''	26:BA:1779:G:H8	1.85	0.42
26:BA:518:G:H2'	26:BA:519:G:O4'	2.19	0.42
29:BE:14:ILE:HD11	29:BE:173:VAL:HG11	2.01	0.42
40:BT:91:ARG:HD2	40:BT:120:ARG:NH1	2.35	0.42
46:BZ:110:GLY:CA	46:BZ:145:GLU:HA	2.50	0.42
46:BZ:145:GLU:H	46:BZ:148:ASP:HB2	1.84	0.42
1:CA:1053:G:C4'	1:CA:1054:C:H5'	2.50	0.42
1:CA:116:A:H61	1:CA:313:A:H1'	1.84	0.42
1:CA:1325:C:O2'	1:CA:1326:C:H5'	2.18	0.42
1:CA:1446:U:H4'	1:CA:1447:A:C5	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:779:C:H2'	1:CA:780:A:O4'	2.19	0.42
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	2.01	0.42
19:CS:27:GLU:HB2	19:CS:28:LYS:HZ3	1.83	0.42
26:DA:1167:U:C2	26:DA:1168:G:C8	3.07	0.42
26:DA:2285:C:OP2	53:D6:6:ARG:NH1	2.52	0.42
26:DA:698:C:H5''	26:DA:699:A:OP1	2.20	0.42
26:DA:868:U:C4	26:DA:869:G:N7	2.88	0.42
26:DA:937:U:H2'	26:DA:938:G:O4'	2.20	0.42
28:DD:37:LEU:HD13	28:DD:87:ASN:ND2	2.34	0.42
30:DF:34:TRP:CE2	36:DP:8:PRO:HG3	2.55	0.42
44:DX:12:VAL:HG21	44:DX:27:THR:HG22	2.02	0.42
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.55	0.42
1:AA:1287:A:H2	1:AA:1353:G:N3	2.18	0.42
1:AA:938:A:C6	1:AA:939:G:C5	3.07	0.42
4:AD:107:ARG:HH22	4:AD:194:LEU:CD2	2.33	0.42
6:AF:35:ALA:HA	6:AF:67:MET:HB3	2.02	0.42
12:AL:53:ARG:HG2	12:AL:69:TYR:HE1	1.84	0.42
13:AM:84:ILE:HD12	19:AS:74:PHE:CE2	2.51	0.42
24:AX:32:5MC:HM53	24:AX:33:U:O4	2.20	0.42
25:AY:52:G:H1	25:AY:62:C:N4	2.17	0.42
49:B2:32:LEU:HD13	49:B2:36:ARG:HH11	1.85	0.42
56:B9:27:CYS:SG	56:B9:28:GLU:N	2.93	0.42
26:BA:1560:U:O2'	26:BA:1561:C:H5'	2.20	0.42
26:BA:1761:G:H1	26:BA:1775:C:N4	2.13	0.42
26:BA:593:G:H2'	26:BA:2052:A:C5	2.55	0.42
26:BA:764:G:H2'	26:BA:765:A:O4'	2.20	0.42
31:BG:77:ILE:HG21	31:BG:80:PHE:CD2	2.55	0.42
35:BO:73:ASP:HB2	40:BT:82:LEU:HD13	2.00	0.42
1:CA:1067:A:H1'	1:CA:1068:G:O4'	2.20	0.42
1:CA:1072:G:C6	1:CA:1073:U:C4	3.08	0.42
1:CA:1233:G:H2'	1:CA:1234:C:C6	2.55	0.42
1:CA:583:A:H2'	1:CA:584:G:O4'	2.20	0.42
1:CA:685:G:C2	1:CA:686:U:C4	3.08	0.42
2:CB:137:ARG:O	2:CB:141:GLU:N	2.36	0.42
15:CO:36:ILE:HG23	15:CO:56:LEU:HD11	2.01	0.42
15:CO:5:LYS:O	15:CO:9:GLN:HG2	2.19	0.42
51:D4:9:LEU:HD23	51:D4:9:LEU:HA	1.90	0.42
56:D9:7:VAL:HG12	56:D9:34:GLN:HB3	2.01	0.42
26:DA:1198:U:H2'	26:DA:1199:U:C6	2.55	0.42
26:DA:2107:C:H2'	26:DA:2108:C:O4'	2.20	0.42
26:DA:536:A:H2'	26:DA:537:C:C6	2.55	0.42
28:DD:145:VAL:HB	28:DD:155:LEU:HB2	2.02	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:DE:9:VAL:HB	40:DT:3:ARG:HG2	2.02	0.42
34:DN:40:PRO:HB3	41:DU:68:ALA:HB2	2.01	0.42
45:DY:45:VAL:N	45:DY:63:LYS:O	2.45	0.42
46:DZ:24:LEU:HA	46:DZ:25:PRO:HD3	1.90	0.42
1:AA:1006:C:H2'	1:AA:1007:C:C6	2.55	0.42
1:AA:1029:C:N3	1:AA:1032:G:O6	2.53	0.42
1:AA:1182:G:C3'	1:AA:1183:A:H5'	2.50	0.42
1:AA:130:A:O2'	1:AA:131:C:O5'	2.32	0.42
1:AA:152:A:N6	1:AA:170:U:C2	2.88	0.42
1:AA:583:A:N6	1:AA:758:G:O2'	2.53	0.42
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.84	0.42
15:AO:78:TYR:CZ	15:AO:82:ILE:HD13	2.55	0.42
17:AQ:66:SER:H	17:AQ:69:LYS:HB3	1.85	0.42
1:AA:108:G:O6	20:AT:15:ARG:HD2	2.19	0.42
25:AY:56:C:C2	25:AY:57:G:C8	3.08	0.42
26:BA:1889:G:H21	26:BA:1905:G:H2'	1.84	0.42
26:BA:2112:G:O6	61:BA:4756:HOH:O	2.19	0.42
26:BA:2133:C:OP2	26:BA:2167:C:N4	2.51	0.42
26:BA:2473:C:H2'	26:BA:2474:U:C6	2.55	0.42
26:BA:211:A:H3'	26:BA:448:U:H5'	2.00	0.42
29:BE:14:ILE:HG12	29:BE:21:VAL:HG13	2.00	0.42
33:BI:131:LYS:HA	33:BI:137:PRO:HA	2.02	0.42
40:BT:53:ARG:CZ	40:BT:53:ARG:HB3	2.50	0.42
45:BY:54:LYS:HA	45:BY:55:TYR:HA	1.85	0.42
1:CA:1269:A:H2	1:CA:1312:G:N3	2.17	0.42
1:CA:1357:A:N6	1:CA:1363(A):A:N1	2.67	0.42
1:CA:344:A:H5''	1:CA:345:C:H5	1.84	0.42
1:CA:6:G:H4'	1:CA:298:A:H4'	2.00	0.42
3:CC:19:GLU:HB3	3:CC:55:VAL:O	2.20	0.42
3:CC:77:ILE:HG13	3:CC:78:GLY:N	2.35	0.42
11:CK:38:ASN:HA	11:CK:39:PRO:HD3	1.80	0.42
23:CW:29:G:N2	23:CW:42:C:C2	2.88	0.42
26:DA:1231:G:H2'	26:DA:1232:G:C8	2.55	0.42
26:DA:1470:G:HO2'	26:DA:1471:A:H8	1.63	0.42
26:DA:1794:U:H2'	26:DA:1795:C:H6	1.85	0.42
24:CX:3:C:H5'	26:DA:2255:G:O2'	2.20	0.42
26:DA:234:C:H2'	26:DA:235:U:C6	2.54	0.42
26:DA:839:U:H2'	26:DA:840:C:C6	2.55	0.42
28:DD:73:VAL:O	28:DD:75:ILE:HG13	2.19	0.42
31:DG:72:ARG:NH1	31:DG:87:PRO:HG3	2.35	0.42
34:DN:138:LEU:HA	34:DN:138:LEU:HD23	1.73	0.42
26:DA:863:A:P	37:DQ:22:LYS:HG3	2.60	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
44:DX:84:ALA:HB3	44:DX:87:GLN:NE2	2.35	0.42
46:DZ:146:ILE:H	46:DZ:146:ILE:HG13	1.62	0.42
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.54	0.42
1:AA:922:G:C6	1:AA:923:A:C6	3.08	0.42
2:AB:62:ALA:HB3	2:AB:225:ALA:HB3	2.02	0.42
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.20	0.42
3:AC:131:ARG:NE	3:AC:166:GLU:OE2	2.53	0.42
3:AC:56:ASP:HB2	3:AC:67:THR:HB	2.02	0.42
4:AD:170:VAL:HG11	4:AD:174:LEU:HB2	2.02	0.42
9:AI:16:ARG:HB2	9:AI:64:THR:HB	2.01	0.42
1:AA:881:G:P	12:AL:12:ARG:HH22	2.42	0.42
13:AM:14:ARG:NH2	13:AM:41:PRO:O	2.53	0.42
18:AR:26:LEU:HD23	18:AR:29:PHE:CE2	2.55	0.42
25:AY:38:A:C5	25:AY:39:PSU:C6	3.08	0.42
25:AY:68:C:N3	25:AY:69:G:C8	2.88	0.42
50:B3:5:LYS:NZ	50:B3:34:GLU:OE2	2.40	0.42
51:B4:62:ARG:HB2	51:B4:63:TYR:CD1	2.54	0.42
26:BA:1793:A:H2'	61:BA:5184:HOH:O	2.19	0.42
26:BA:2123:G:H2'	26:BA:2124:U:C6	2.55	0.42
26:BA:2455:C:OP1	30:BF:68:LYS:HD3	2.20	0.42
26:BA:2631:C:H4'	29:BE:151:TYR:O	2.20	0.42
27:BB:55:U:H2'	27:BB:56:G:O4'	2.20	0.42
45:BY:9:LYS:HA	45:BY:10:GLY:HA2	1.71	0.42
1:CA:1154:G:C8	1:CA:1155:G:C8	3.07	0.42
1:CA:340:U:H2'	1:CA:341:C:C6	2.54	0.42
1:CA:375:U:OP1	16:CP:69:THR:HG21	2.20	0.42
1:CA:641:U:O3'	1:CA:642:A:H8	2.03	0.42
1:CA:989:C:HO2'	1:CA:1016:A:H2	1.67	0.42
3:CC:115:LEU:HD12	3:CC:115:LEU:HA	1.80	0.42
4:CD:57:ARG:HD3	4:CD:205:GLU:HB2	2.00	0.42
10:CJ:56:HIS:CD2	10:CJ:56:HIS:H	2.38	0.42
11:CK:110:ASP:HB3	18:CR:85:LEU:HB3	2.02	0.42
13:CM:94:ARG:CZ	19:CS:80:TYR:HD2	2.33	0.42
20:CT:33:ILE:HG13	20:CT:62:LEU:HD22	2.02	0.42
25:CY:15:G:H22	25:CY:48:C:N4	2.15	0.42
26:DA:1015:G:O2'	26:DA:1016:G:H5'	2.20	0.42
26:DA:1019:U:H3	26:DA:1142(A):A:N6	2.13	0.42
26:DA:2252:G:H2'	26:DA:2253:G:O4'	2.19	0.42
26:DA:2307:G:H8	26:DA:2307:G:OP1	2.03	0.42
26:DA:2262:U:H4'	26:DA:2328:A:H2	1.84	0.42
26:DA:2853:C:H2'	26:DA:2854:G:C8	2.54	0.42
26:DA:300:A:H3'	45:DY:84:ARG:NH2	2.35	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:526:A:N3	26:DA:2044:C:H1'	2.35	0.42
39:DS:80:LEU:HA	39:DS:80:LEU:HD12	1.84	0.42
46:DZ:5:LEU:HA	46:DZ:5:LEU:HD22	1.82	0.42
1:AA:1003:G:N3	1:AA:1004:A:H1'	2.34	0.41
1:AA:1035:A:H8	1:AA:1035:A:O5'	2.02	0.41
1:AA:555:C:H2'	1:AA:556:C:C6	2.55	0.41
1:AA:591:U:H2'	1:AA:592:G:C8	2.54	0.41
1:AA:688:G:H5'	11:AK:46:GLY:C	2.40	0.41
1:AA:78:G:N2	1:AA:91:C:C2	2.88	0.41
2:AB:71:VAL:HG13	2:AB:93:VAL:CG2	2.50	0.41
3:AC:47:LEU:CD1	3:AC:68:VAL:HG11	2.50	0.41
9:AI:93:ARG:HB2	9:AI:93:ARG:NH1	2.35	0.41
51:B4:63:TYR:CD1	51:B4:63:TYR:N	2.86	0.41
36:BP:63:PRO:HG2	55:B8:25:MET:HB2	2.02	0.41
33:BI:110:ASP:HA	33:BI:111:PRO:HD2	1.78	0.41
36:BP:121:LYS:HG2	36:BP:122:PRO:HD2	2.02	0.41
40:BT:11:GLU:OE1	40:BT:57:PHE:HB3	2.19	0.41
40:BT:73:GLU:OE1	40:BT:103:ARG:NE	2.41	0.41
45:BY:7:VAL:HG21	45:BY:72:VAL:HG12	2.02	0.41
45:BY:86:ARG:HH11	45:BY:100:ALA:HB1	1.85	0.41
1:CA:1039:C:C4	1:CA:1040:U:C4	3.07	0.41
1:CA:998:G:C6	1:CA:999:C:C4	3.08	0.41
4:CD:17:VAL:HG12	4:CD:18:LYS:N	2.35	0.41
23:CW:76:31M:N3'	26:DA:2585:U:O4	2.53	0.41
26:DA:1720:U:H2'	26:DA:1721:G:O4'	2.20	0.41
26:DA:2512:C:H2'	26:DA:2513:G:O4'	2.20	0.41
26:DA:2505:G:O6	26:DA:2576:G:H2'	2.20	0.41
26:DA:2788:C:C4	26:DA:2789:C:N4	2.88	0.41
26:DA:2815:C:H2'	26:DA:2816:C:H6	1.85	0.41
26:DA:569:U:H5''	61:DA:4096:HOH:O	2.20	0.41
26:DA:776:G:C8	26:DA:793:A:C2	3.08	0.41
26:DA:867:C:C2'	26:DA:868:U:H5'	2.50	0.41
26:DA:994:C:O2'	26:DA:996:A:OP1	2.16	0.41
26:DA:1843:C:H5'	28:DD:253:GLN:NE2	2.34	0.41
44:DX:88:LYS:NZ	44:DX:90:GLU:HG2	2.34	0.41
46:DZ:166:SER:O	46:DZ:169:GLU:HB2	2.20	0.41
46:DZ:67:LEU:HA	46:DZ:68:PRO:HD3	1.93	0.41
1:AA:1128:C:H4'	1:AA:1148:U:O2	2.19	0.41
1:AA:1296:C:H4'	1:AA:1302:U:C4	2.55	0.41
1:AA:1417:G:H22	1:AA:1482:G:H2'	1.84	0.41
1:AA:309:G:H1'	1:AA:608:A:C2	2.55	0.41
1:AA:765:G:N1	1:AA:812:C:O2'	2.43	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:890:G:O2'	1:AA:906:G:O6	2.24	0.41
2:AB:27:LYS:HB2	2:AB:194:PRO:HD2	2.01	0.41
4:AD:178:VAL:C	4:AD:180:GLY:H	2.23	0.41
5:AE:6:PHE:HB3	5:AE:35:GLY:C	2.40	0.41
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.21	0.41
11:AK:59:TYR:CZ	11:AK:63:LEU:HD11	2.55	0.41
12:AL:42:THR:OG1	12:AL:52:LEU:HD13	2.20	0.41
19:AS:27:GLU:HB3	19:AS:28:LYS:HA	2.01	0.41
19:AS:38:SER:HB2	19:AS:71:LEU:HD12	2.01	0.41
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.35	0.41
23:AW:25:C:H2'	23:AW:26:A:H5'	2.02	0.41
25:AY:22:G:C2	25:AY:23:A:C5	3.08	0.41
25:AY:39:PSU:H5'	25:AY:39:PSU:H6	1.86	0.41
26:BA:1577:C:HO2'	26:BA:1578:C:P	2.37	0.41
26:BA:2034:G:OP1	43:BW:11:ARG:NH2	2.45	0.41
26:BA:379:G:H2'	26:BA:380:G:O4'	2.20	0.41
26:BA:505:A:N3	26:BA:507:G:H5''	2.35	0.41
32:BH:96:ALA:HB2	32:BH:105:LEU:HD13	2.02	0.41
34:BN:33:LEU:HD12	34:BN:33:LEU:HA	1.84	0.41
26:BA:999:G:H5''	37:BQ:13:GLN:HB3	2.01	0.41
39:BS:10:ARG:HG3	39:BS:13:ARG:NH2	2.35	0.41
41:BU:17:ILE:HG13	41:BU:32:PHE:HE1	1.84	0.41
46:BZ:104:PHE:CD2	46:BZ:139:VAL:HB	2.55	0.41
1:CA:1135:U:HO2'	1:CA:1136:U:H5	1.66	0.41
1:CA:1178:G:N2	1:CA:1181:G:OP2	2.49	0.41
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.34	0.41
1:CA:791:G:N2	1:CA:1497:G:O3'	2.50	0.41
1:CA:434:U:H2'	1:CA:435:C:C6	2.55	0.41
1:CA:657:G:H1'	1:CA:750:G:N2	2.35	0.41
1:CA:814:A:N7	1:CA:816:A:C4	2.88	0.41
1:CA:971:G:H22	1:CA:1363(A):A:P	2.42	0.41
1:CA:986:A:N3	19:CS:52:TYR:OH	2.42	0.41
3:CC:116:VAL:HG13	3:CC:119:ARG:HD3	2.02	0.41
3:CC:82:GLU:O	3:CC:85:ARG:HB2	2.20	0.41
4:CD:112:VAL:HG13	4:CD:161:ASN:OD1	2.20	0.41
8:CH:72:PRO:O	8:CH:73:ASP:HB3	2.20	0.41
13:CM:56:LEU:HD23	13:CM:57:ARG:N	2.35	0.41
13:CM:92:HIS:CE1	13:CM:98:VAL:HG21	2.55	0.41
17:CQ:65:ILE:HB	17:CQ:69:LYS:HB3	2.03	0.41
25:CY:5:G:N2	25:CY:68:C:N3	2.63	0.41
26:DA:1885:A:H2'	26:DA:1886:C:O4'	2.20	0.41
26:DA:1905:C:H1'	26:DA:1928:A:H2	1.85	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2124:G:N1	26:DA:2174:C:N4	2.34	0.41
26:DA:2519:U:C4	26:DA:2542:A:C5	3.08	0.41
26:DA:27:G:O2'	26:DA:28:A:OP2	2.36	0.41
27:DB:108:U:H2'	27:DB:109:C:H5''	2.03	0.41
31:DG:86:MET:HA	31:DG:87:PRO:HD3	1.97	0.41
32:DH:40:GLU:OE1	32:DH:61:HIS:NE2	2.52	0.41
38:DR:26:LYS:HE2	38:DR:70:LEU:O	2.20	0.41
46:DZ:158:PRO:HA	46:DZ:159:PRO:HD3	1.69	0.41
1:AA:1027:C:C2	1:AA:1034:G:C6	3.07	0.41
1:AA:295:C:H2'	1:AA:296:U:O4'	2.21	0.41
1:AA:589:C:H5''	8:AH:29:SER:OG	2.20	0.41
1:AA:663:A:H5'	1:AA:836:G:OP1	2.19	0.41
1:AA:977:A:H1'	1:AA:982:U:O4	2.20	0.41
2:AB:48:MET:HA	2:AB:51:LEU:HD12	2.03	0.41
4:AD:190:ASP:H	4:AD:193:ASP:HB2	1.86	0.41
9:AI:127:LYS:O	9:AI:128:ARG:HG2	2.20	0.41
10:AJ:47:PHE:N	10:AJ:63:PHE:O	2.47	0.41
17:AQ:31:LEU:HD23	17:AQ:32:TYR:CZ	2.56	0.41
24:AX:15:G:H21	24:AX:21:A:H1'	1.84	0.41
25:AY:19:G:C4'	25:AY:57:G:H22	2.33	0.41
52:B5:35:GLU:HG3	52:B5:51:TYR:CG	2.55	0.41
26:BA:1985:U:H4'	26:BA:1986:G:OP1	2.20	0.41
26:BA:2710:U:H2'	26:BA:2711:C:C6	2.55	0.41
26:BA:327:U:H2'	26:BA:328:G:C8	2.55	0.41
26:BA:553:A:H3'	26:BA:553:A:C8	2.54	0.41
26:BA:641:G:OP1	30:BF:40:GLN:NE2	2.53	0.41
27:BB:110:G:O2'	27:BB:111:G:H5'	2.20	0.41
32:BH:88:LEU:HD23	32:BH:165:ALA:HA	2.01	0.41
38:BR:57:ARG:HH21	38:BR:62:ALA:HB2	1.85	0.41
46:BZ:105:VAL:O	46:BZ:140:ASP:HA	2.20	0.41
1:CA:1118:C:H2'	1:CA:1119:C:C6	2.56	0.41
1:CA:1240:U:OP2	7:CG:115:ARG:HA	2.19	0.41
1:CA:250:A:H4'	1:CA:251:G:O5'	2.18	0.41
1:CA:714:G:H2'	1:CA:715:A:C8	2.55	0.41
1:CA:741:G:H2'	1:CA:742:G:O4'	2.20	0.41
5:CE:41:VAL:O	5:CE:66:MET:HA	2.20	0.41
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.21	0.41
17:CQ:3:LYS:HD3	17:CQ:61:GLU:O	2.20	0.41
26:DA:1248:G:C5	41:DU:3:ARG:HB2	2.55	0.41
26:DA:1372:U:O5'	26:DA:1372:U:H6	2.03	0.41
26:DA:2172:U:O2'	26:DA:2173:A:P	2.78	0.41
26:DA:2541:A:N7	61:DA:3999:HOH:O	2.37	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:275:G:H2'	26:DA:276:A:O4'	2.20	0.41
26:DA:784:A:N6	28:DD:229:VAL:HG11	2.35	0.41
32:DH:86:GLU:CD	32:DH:130:ARG:HD3	2.40	0.41
32:DH:13:LYS:HA	32:DH:14:GLY:HA2	1.67	0.41
37:DQ:45:GLN:CD	37:DQ:45:GLN:H	2.23	0.41
39:DS:83:LYS:HE2	39:DS:83:LYS:HB3	1.90	0.41
26:DA:1008:C:H4'	41:DU:59:ARG:NH2	2.35	0.41
42:DV:46:VAL:HG23	42:DV:52:VAL:HG11	2.01	0.41
46:DZ:126:VAL:HG11	46:DZ:161:VAL:CG2	2.41	0.41
1:AA:103:C:OP2	20:AT:14:LYS:NZ	2.44	0.41
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.21	0.41
1:AA:382:A:H2'	1:AA:383:A:H8	1.85	0.41
1:AA:826:C:H2'	1:AA:827:U:C6	2.56	0.41
2:AB:218:ALA:O	2:AB:222:ILE:HG13	2.20	0.41
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.54	0.41
4:AD:64:LEU:HB2	4:AD:198:VAL:HG11	2.03	0.41
10:AJ:81:THR:HA	10:AJ:84:GLN:HB3	2.02	0.41
11:AK:62:GLN:O	11:AK:66:LEU:HG	2.21	0.41
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.34	0.41
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	2.03	0.41
19:AS:80:TYR:CZ	19:AS:82:GLY:HA2	2.56	0.41
25:AY:19:G:H4'	25:AY:20:U:OP2	2.19	0.41
25:AY:57:G:N3	25:AY:58:A:H5'	2.35	0.41
49:B2:35:LEU:HB3	49:B2:50:ILE:HG12	2.01	0.41
26:BA:1312:G:O4'	43:BW:15:ARG:NH2	2.50	0.41
26:BA:1449:C:H5''	26:BA:1518:A:H1'	2.01	0.41
26:BA:2141:A:C5	26:BA:2193:A:C6	3.08	0.41
26:BA:2576:A:C2	26:BA:2659:U:H4'	2.55	0.41
26:BA:2798:C:H2'	26:BA:2799:U:O4'	2.20	0.41
26:BA:1781:G:O2'	26:BA:2870:A:N1	2.38	0.41
26:BA:469:A:H5''	26:BA:470:C:OP1	2.21	0.41
26:BA:624:C:O2'	26:BA:628:C:H5''	2.20	0.41
26:BA:863:C:H2'	26:BA:864:C:C6	2.55	0.41
29:BE:119:ARG:HG2	29:BE:160:TYR:CG	2.56	0.41
33:BI:93:THR:H	33:BI:96:ASP:CG	2.23	0.41
45:BY:15:VAL:HG21	45:BY:42:VAL:HG11	2.02	0.41
1:CA:1041:A:H2'	1:CA:1042:G:O4'	2.20	0.41
1:CA:336:C:H2'	1:CA:337:C:C6	2.55	0.41
1:CA:501:C:H2'	1:CA:502:G:H8	1.84	0.41
1:CA:562:C:H1'	12:CL:15:ARG:HB3	2.02	0.41
2:CB:12:GLU:O	2:CB:15:VAL:N	2.50	0.41
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.76	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:28:GLN:HB2	3:CC:28:GLN:HE21	1.59	0.41
7:CG:23:VAL:HG13	7:CG:43:PHE:CE2	2.55	0.41
8:CH:51:VAL:HG12	8:CH:52:ASP:N	2.35	0.41
14:CN:45:ARG:O	14:CN:49:HIS:HD2	2.04	0.41
47:D0:50:ASN:HB3	47:D0:63:VAL:HG22	2.03	0.41
26:DA:1127:A:N7	26:DA:2488:A:O2'	2.47	0.41
26:DA:2867:G:OP2	40:DT:119:LYS:NZ	2.50	0.41
26:DA:752:A:OP1	54:D7:3:ARG:NH2	2.50	0.41
26:DA:8:A:H2'	26:DA:9:U:C6	2.55	0.41
32:DH:27:LYS:HB3	32:DH:27:LYS:HE3	1.82	0.41
33:DI:110:ASP:OD1	33:DI:111:PRO:HD2	2.21	0.41
34:DN:39:ARG:HA	34:DN:40:PRO:HD3	1.80	0.41
35:DO:120:GLU:HG2	35:DO:122:LEU:HG	2.02	0.41
38:DR:21:TYR:OH	38:DR:43:GLU:HG2	2.21	0.41
41:DU:81:HIS:O	41:DU:84:LYS:HB3	2.20	0.41
42:DV:29:PRO:HA	42:DV:61:VAL:HG22	2.02	0.41
1:AA:103:C:OP2	20:AT:17:ARG:NH2	2.53	0.41
51:B4:28:LYS:HA	51:B4:29:PRO:HD3	1.84	0.41
26:BA:1503:G:OP2	61:BA:4012:HOH:O	2.21	0.41
26:BA:2295:C:H2'	26:BA:2296:C:O4'	2.20	0.41
26:BA:491:G:H2'	26:BA:492:A:C8	2.55	0.41
26:BA:659:C:H2'	26:BA:660:C:C6	2.56	0.41
33:BI:109:ILE:HG23	33:BI:110:ASP:N	2.35	0.41
1:CA:1173:G:H2'	1:CA:1174:G:C8	2.55	0.41
1:CA:978:A:C6	1:CA:1319:A:C5	3.08	0.41
1:CA:971:G:N2	1:CA:1363(A):A:OP2	2.51	0.41
1:CA:29:G:O2'	1:CA:295:C:H4'	2.20	0.41
1:CA:723:U:HO2'	1:CA:724:G:H5'	1.85	0.41
1:CA:730:G:C5	1:CA:731:G:H1'	2.55	0.41
6:CF:94:GLN:HE22	18:CR:72:ARG:HH12	1.69	0.41
20:CT:72:LEU:HA	20:CT:72:LEU:HD23	1.84	0.41
26:DA:1024:G:C6	26:DA:1025:G:C6	3.08	0.41
26:DA:1127:A:C2'	26:DA:1128:A:H5''	2.50	0.41
26:DA:1580:A:OP2	26:DA:1580:A:H8	2.03	0.41
26:DA:1882:C:H3'	26:DA:1883:G:H8	1.85	0.41
26:DA:2169:A:C2	26:DA:2170:A:C2	3.08	0.41
26:DA:2550:G:C6	26:DA:2551:C:C4	3.08	0.41
26:DA:2683:C:OP1	40:DT:53:ARG:NH2	2.49	0.41
26:DA:2693:A:H2'	26:DA:2694:G:H8	1.85	0.41
26:DA:324:A:N6	26:DA:338:G:O2'	2.49	0.41
26:DA:932:G:H4'	26:DA:933:A:O5'	2.19	0.41
29:DE:169:ASN:HB2	29:DE:203:LYS:HG3	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:135:LYS:HE2	30:DF:135:LYS:HA	2.02	0.41
37:DQ:109:VAL:HG13	37:DQ:113:GLN:HB3	2.02	0.41
40:DT:6:LEU:O	40:DT:10:VAL:HG23	2.20	0.41
26:DA:996:A:H4'	41:DU:91:ASP:OD2	2.19	0.41
1:AA:600:C:H2'	1:AA:601:C:H6	1.85	0.41
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	2.02	0.41
2:AB:77:ALA:CB	2:AB:165:VAL:HG11	2.51	0.41
3:AC:27:LYS:HA	3:AC:27:LYS:HD2	1.76	0.41
4:AD:138:TYR:CE1	4:AD:140:VAL:HA	2.56	0.41
8:AH:33:GLU:HG2	8:AH:48:TYR:CZ	2.56	0.41
10:AJ:27:ALA:HA	10:AJ:81:THR:HG21	2.03	0.41
20:AT:57:ARG:HH22	20:AT:100:ILE:HD12	1.86	0.41
21:AU:6:ARG:O	21:AU:12:LYS:HD2	2.21	0.41
53:B6:9:LEU:HD11	53:B6:23:THR:HG23	2.03	0.41
26:BA:1787:G:H4'	26:BA:1789:G:O4'	2.21	0.41
26:BA:2651:A:OP2	61:BA:4129:HOH:O	2.22	0.41
26:BA:766:C:H2'	26:BA:767:C:H6	1.85	0.41
27:BB:6:C:H2'	27:BB:7:G:H5''	2.02	0.41
28:BD:142:VAL:HG13	28:BD:191:ALA:HB1	2.01	0.41
30:BF:183:VAL:O	30:BF:187:VAL:HG23	2.21	0.41
32:BH:13:LYS:HA	32:BH:14:GLY:HA2	1.68	0.41
33:BI:103:ARG:HE	33:BI:103:ARG:HB3	1.53	0.41
34:BN:48:MET:H	34:BN:48:MET:HG3	1.78	0.41
1:CA:983:A:O2'	1:CA:1050:G:OP2	2.33	0.41
1:CA:513:C:H2'	1:CA:514:C:O4'	2.19	0.41
1:CA:722:A:C8	1:CA:724:G:H1'	2.55	0.41
1:CA:857:C:H2'	1:CA:858:G:O4'	2.21	0.41
1:CA:942:G:C2	1:CA:1342:C:C2	3.09	0.41
1:CA:998:G:H2'	1:CA:999:C:O4'	2.20	0.41
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.88	0.41
4:CD:163:GLU:O	4:CD:166:LYS:HG2	2.21	0.41
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.20	0.41
14:CN:37:PHE:HB3	14:CN:39:LEU:HG	2.03	0.41
20:CT:86:ARG:CZ	20:CT:86:ARG:HB3	2.49	0.41
23:CW:23:A:H2'	23:CW:24:G:C8	2.56	0.41
26:DA:1021:A:C3'	26:DA:1021:A:C8	3.02	0.41
26:DA:1766:U:H2'	26:DA:1767:C:H6	1.85	0.41
26:DA:2114:A:N1	26:DA:2117:A:N6	2.69	0.41
26:DA:2154:G:N1	26:DA:2155:G:N7	2.69	0.41
26:DA:775:G:O3'	61:DA:4253:HOH:O	2.21	0.41
26:DA:869:G:C6	26:DA:870:A:C5	3.08	0.41
27:DB:8:U:H3	27:DB:113:G:H1	1.69	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:184:TYR:O	30:DF:188:ARG:HG3	2.21	0.41
32:DH:54:ARG:HD3	32:DH:65:HIS:ND1	2.34	0.41
33:DI:43:ASN:C	33:DI:43:ASN:HD22	2.24	0.41
35:DO:20:MET:HE3	35:DO:44:LYS:HE3	2.02	0.41
39:DS:65:VAL:O	39:DS:69:VAL:HG12	2.20	0.41
1:AA:1286:A:H2'	1:AA:1287:A:H4'	2.01	0.41
1:AA:161:A:O5'	1:AA:161:A:H8	2.02	0.41
1:AA:37:U:O2'	1:AA:500:G:H4'	2.20	0.41
1:AA:993:G:N3	1:AA:993:G:H2'	2.36	0.41
3:AC:15:THR:CG2	3:AC:181:ASN:HA	2.44	0.41
9:AI:26:VAL:HG22	9:AI:61:ALA:HB3	2.02	0.41
20:AT:46:GLU:HG2	20:AT:46:GLU:O	2.20	0.41
23:AW:13:C:O2'	23:AW:14:A:O5'	2.37	0.41
24:AX:31:G:C8	24:AX:32:5MC:HM52	2.56	0.41
25:AY:38:A:H3'	25:AY:39:PSU:H5'	2.02	0.41
52:B5:16:ARG:NH1	52:B5:17:ASP:OD1	2.50	0.41
26:BA:1384:G:N7	44:BX:62:LYS:NZ	2.65	0.41
26:BA:261:A:N1	26:BA:291:G:O2'	2.47	0.41
30:BF:101:LEU:HA	30:BF:101:LEU:HD12	1.84	0.41
30:BF:157:VAL:HG21	30:BF:181:LEU:HD13	2.02	0.41
33:BI:9:LEU:HD22	33:BI:9:LEU:HA	1.79	0.41
36:BP:6:LEU:HA	36:BP:6:LEU:HD23	1.80	0.41
45:BY:5:MET:HE1	45:BY:32:PRO:HA	2.03	0.41
1:CA:176:C:H2'	1:CA:177:C:C6	2.55	0.41
3:CC:26:LYS:HE3	3:CC:26:LYS:HB3	1.88	0.41
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.56	0.41
16:CP:17:TYR:HE2	16:CP:41:PRO:HG3	1.86	0.41
23:CW:34:G:H2'	23:CW:35:A:C8	2.56	0.41
26:DA:1498:C:O4'	26:DA:1577:C:H4'	2.21	0.41
26:DA:2025:C:H2'	26:DA:2026:C:C6	2.56	0.41
26:DA:2026:C:H2'	26:DA:2027:G:O4'	2.21	0.41
26:DA:2152:G:C2	26:DA:2153:G:H1'	2.54	0.41
26:DA:2228:G:C6	26:DA:2229:C:C4	3.09	0.41
26:DA:2314:C:H2'	26:DA:2315:G:C8	2.56	0.41
26:DA:2432:A:C6	26:DA:2433:A:C6	3.09	0.41
26:DA:2445:G:OP1	30:DF:74:ARG:NH2	2.45	0.41
26:DA:340:A:H2'	26:DA:341:G:O4'	2.20	0.41
26:DA:62:C:N4	26:DA:93:G:H1	2.19	0.41
27:DB:119:G:C6	27:DB:120:A:C6	3.09	0.41
27:DB:42:C:C4	27:DB:43:C:C4	3.09	0.41
27:DB:33:G:C2	27:DB:50:G:C2	3.08	0.41
31:DG:3:LEU:HD12	31:DG:5:VAL:HG12	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
34:DN:42:TRP:HD1	34:DN:48:MET:HE2	1.86	0.41
36:DP:55:ARG:HA	61:DP:309:HOH:O	2.21	0.41
39:DS:28:VAL:HG13	39:DS:35:ILE:HD11	2.03	0.41
39:DS:67:ARG:HG2	39:DS:71:ARG:HH11	1.85	0.41
45:DY:65:ALA:HA	45:DY:66:PRO:HD3	1.92	0.41
46:DZ:121:HIS:HB3	46:DZ:123:ASP:O	2.20	0.41
1:AA:109:A:H2'	1:AA:326:G:N2	2.35	0.41
1:AA:1256:A:N6	1:AA:1278:U:O4'	2.52	0.41
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.86	0.41
1:AA:358:U:H2'	1:AA:359:U:C6	2.56	0.41
1:AA:519:C:OP2	12:AL:50:SER:OG	2.26	0.41
2:AB:103:THR:HG23	2:AB:176:GLU:OE1	2.21	0.41
15:AO:71:GLN:HA	15:AO:71:GLN:HE21	1.85	0.41
15:AO:7:GLU:H	15:AO:7:GLU:HG3	1.65	0.41
6:AF:97:PHE:HB3	18:AR:32:ARG:HD3	2.01	0.41
20:AT:54:LYS:HB2	20:AT:100:ILE:HD11	2.03	0.41
25:AY:20:U:H4'	25:AY:21:A:OP1	2.20	0.41
25:AY:59:U:H3'	25:AY:60:U:C5	2.56	0.41
25:AY:70:G:C6	25:AY:71:G:C5	3.09	0.41
48:B1:23:LYS:HB3	48:B1:29:GLY:HA3	2.02	0.41
48:B1:64:ALA:HA	48:B1:67:ILE:HG13	2.02	0.41
54:B7:24:THR:HG22	54:B7:27:GLY:N	2.30	0.41
26:BA:1248:G:OP2	26:BA:1249:A:O2'	2.28	0.41
26:BA:2083:G:H5''	26:BA:2515:A:C2	2.56	0.41
26:BA:2430:A:H2'	26:BA:2431:U:C6	2.55	0.41
31:BG:14:GLU:O	31:BG:17:PRO:HD2	2.21	0.41
32:BH:3:ARG:HD3	32:BH:54:ARG:HH12	1.85	0.41
36:BP:65:ARG:HD3	36:BP:66:GLY:N	2.36	0.41
1:CA:1102:A:O3'	2:CB:96:ARG:NH1	2.47	0.41
1:CA:1315:U:H2'	1:CA:1316:G:O4'	2.21	0.41
1:CA:8:A:C6	4:CD:209:ARG:HG3	2.56	0.41
2:CB:145:LEU:O	2:CB:149:LEU:HB2	2.21	0.41
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.54	0.41
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.39	0.41
18:CR:76:LEU:HA	18:CR:76:LEU:HD12	1.81	0.41
23:CW:21:A:N6	23:CW:46:7MG:C4	2.89	0.41
25:CY:64:A:H2'	25:CY:65:G:C8	2.56	0.41
26:DA:2395:C:O2'	48:D1:30:VAL:HG22	2.21	0.41
51:D4:62:ARG:HB2	51:D4:63:TYR:CE1	2.55	0.41
52:D5:47:PRO:HG2	52:D5:48:GLU:OE1	2.21	0.41
26:DA:117:G:C6	26:DA:119:A:C6	3.09	0.41
26:DA:1449:A:C2	26:DA:1529:G:H1'	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2070:G:H2'	26:DA:2071:A:C8	2.56	0.41
26:DA:2185:C:H2'	26:DA:2186:G:O4'	2.20	0.41
26:DA:674:G:H1'	30:DF:74:ARG:HD3	2.03	0.41
31:DG:58:GLN:OE1	31:DG:58:GLN:HA	2.21	0.41
37:DQ:58:PHE:CZ	37:DQ:109:VAL:HG21	2.55	0.41
41:DU:85:LYS:HE2	41:DU:85:LYS:HB3	1.77	0.41
1:AA:1278:U:H6	1:AA:1278:U:H3'	1.85	0.41
1:AA:551:U:H2'	1:AA:552:U:C6	2.55	0.41
4:AD:157:LEU:HD23	4:AD:161:ASN:HD21	1.85	0.41
4:AD:88:VAL:HG22	5:AE:97:GLY:HA2	2.01	0.41
6:AF:97:PHE:CB	18:AR:32:ARG:HD3	2.51	0.41
20:AT:10:LEU:HD13	20:AT:12:ALA:HB2	2.01	0.41
24:AX:76:A:OP2	61:AX:3106:HOH:O	2.20	0.41
25:AY:21:A:H4'	25:AY:22:G:OP1	2.21	0.41
25:AY:58:A:H2'	25:AY:58:A:H8	1.72	0.41
26:BA:1216:G:C2	26:BA:1217:G:H1'	2.55	0.41
26:BA:1597:C:H4'	26:BA:1772:C:O2	2.21	0.41
26:BA:2087:C:H2'	26:BA:2088:C:C6	2.56	0.41
26:BA:2136:A:H2'	26:BA:2137:G:O4'	2.20	0.41
26:BA:2582:G:H2'	26:BA:2583:C:O4'	2.21	0.41
26:BA:2867:G:N2	26:BA:2870:A:OP2	2.43	0.41
26:BA:734:C:H42	26:BA:834:U:H4'	1.86	0.41
26:BA:85:C:H4'	26:BA:102:U:H1'	2.03	0.41
26:BA:992:G:H2'	26:BA:993:G:C8	2.56	0.41
26:BA:99:G:H3'	26:BA:100:G:C5'	2.50	0.41
28:BD:121:PRO:HB3	28:BD:135:PHE:CE2	2.56	0.41
28:BD:264:LYS:HA	28:BD:265:PRO:HD3	1.92	0.41
30:BF:11:VAL:HB	30:BF:18:ARG:HB3	2.03	0.41
1:CA:1002:G:C2	1:CA:1003:G:C8	3.09	0.41
1:CA:1133:G:H2'	1:CA:1134:G:O4'	2.20	0.41
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.56	0.41
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.55	0.41
1:CA:1511:G:H2'	1:CA:1512:U:O4'	2.21	0.41
1:CA:429:U:H1'	1:CA:430:A:H5''	2.03	0.41
1:CA:447:G:O6	1:CA:485:G:O2'	2.19	0.41
2:CB:112:VAL:O	2:CB:116:GLU:HB2	2.21	0.41
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.21	0.41
9:CI:56:LEU:HD23	9:CI:56:LEU:HA	1.86	0.41
26:DA:1283:G:O2'	26:DA:1285:G:N7	2.44	0.41
26:DA:2275:C:H5'	26:DA:2275:C:H6	1.86	0.41
26:DA:2803:C:H2'	26:DA:2804:C:C6	2.53	0.41
26:DA:821:A:H2'	26:DA:946:G:H5''	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:DB:24:G:H4'	27:DB:25:A:N7	2.36	0.41
32:DH:95:ARG:HB3	32:DH:95:ARG:HE	1.77	0.41
37:DQ:29:PHE:HB2	37:DQ:105:GLU:OE2	2.21	0.41
38:DR:28:LEU:HD23	38:DR:28:LEU:HA	1.93	0.41
39:DS:4:LEU:HD23	39:DS:4:LEU:HA	1.76	0.41
44:DX:57:LEU:HD22	44:DX:78:LYS:HG2	2.03	0.41
1:AA:115:G:H4'	1:AA:116:A:O5'	2.20	0.41
1:AA:1324:A:O4'	1:AA:1362:C:H4'	2.21	0.41
1:AA:277:C:H5''	17:AQ:68:ARG:HH22	1.86	0.41
6:AF:36:ARG:NH1	6:AF:36:ARG:HB3	2.36	0.41
7:AG:104:LEU:HD13	7:AG:104:LEU:HA	1.96	0.41
9:AI:49:PRO:HG3	9:AI:101:PHE:HD2	1.86	0.41
1:AA:192:U:O3'	20:AT:57:ARG:HD2	2.20	0.41
25:AY:69:G:H2'	25:AY:70:G:O4'	2.21	0.41
26:BA:1079:U:OP1	56:B9:9:ARG:NH2	2.54	0.41
26:BA:1093:G:O2'	26:BA:1094:A:H8	2.03	0.41
26:BA:2742:G:H2'	26:BA:2743:C:O4'	2.21	0.41
26:BA:553:A:C3'	26:BA:554:A:H5''	2.51	0.41
1:AA:1422:G:C5'	35:BO:48:PRO:HB3	2.44	0.41
35:BO:86:ILE:HG22	35:BO:94:ARG:HG3	2.03	0.41
41:BU:58:ARG:HA	41:BU:61:TRP:CE3	2.56	0.41
1:CA:1003:G:C6	1:CA:1004:A:C2	3.09	0.41
1:CA:1015:A:H2'	1:CA:1016:A:C8	2.56	0.41
1:CA:1029:C:N3	1:CA:1032:G:C2	2.89	0.41
1:CA:1243:C:H2'	1:CA:1244:C:H6	1.85	0.41
2:CB:100:GLY:O	2:CB:104:ASN:N	2.49	0.41
2:CB:48:MET:O	2:CB:52:GLU:N	2.37	0.41
24:CX:31:G:C8	24:CX:32:5MC:HM52	2.56	0.41
25:CY:8:4SU:S4	25:CY:14:A:C8	3.13	0.41
26:DA:1910:G:H2'	26:DA:1911:U:H6	1.85	0.41
26:DA:1268:A:C2	26:DA:2013:A:C4	3.09	0.41
26:DA:2113:U:N3	26:DA:2114:A:N7	2.69	0.41
26:DA:2133:G:O2'	26:DA:2134:A:P	2.79	0.41
26:DA:2761:G:N3	26:DA:2761:G:H2'	2.35	0.41
26:DA:446:G:OP1	41:DU:3:ARG:NH1	2.52	0.41
26:DA:516:C:H1'	26:DA:1261:C:O2'	2.21	0.41
26:DA:571:A:H5'	26:DA:2030:A:N7	2.36	0.41
26:DA:921:G:C6	26:DA:922:U:C4	3.09	0.41
29:DE:46:ALA:HB2	29:DE:82:ARG:HA	2.02	0.41
31:DG:101:ILE:O	31:DG:104:GLU:HB3	2.20	0.41
31:DG:108:ASN:O	31:DG:112:PRO:HG2	2.21	0.41
41:DU:61:TRP:CH2	41:DU:93:LYS:HB2	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:DZ:138:GLU:H	46:DZ:156:LYS:HE2	1.85	0.41
1:AA:1003:G:N2	1:AA:1004:A:N3	2.69	0.41
1:AA:1075:C:C2'	1:AA:1076:C:H5''	2.51	0.41
6:AF:19:LEU:HD11	6:AF:59:TYR:CZ	2.56	0.41
25:AY:21:A:H8	25:AY:21:A:OP2	2.04	0.41
26:BA:1405:A:C2	26:BA:1418:U:O4	2.74	0.41
26:BA:2902:G:H4'	26:BA:2903:G:O5'	2.21	0.41
26:BA:766:C:H2'	26:BA:767:C:C6	2.56	0.41
26:BA:934:A:H4'	26:BA:935:C:H5	1.82	0.41
31:BG:125:PHE:HB3	31:BG:166:ASP:OD1	2.20	0.41
34:BN:138:LEU:HA	34:BN:138:LEU:HD23	1.81	0.41
44:BX:88:LYS:HE3	44:BX:88:LYS:HB3	1.87	0.41
1:CA:1030(A):G:N2	1:CA:1030(C):G:H8	2.19	0.41
1:CA:1030(A):G:H2'	1:CA:1030(C):G:OP2	2.20	0.41
1:CA:1053:G:H4'	1:CA:1054:C:H5'	2.03	0.41
1:CA:344:A:H4'	1:CA:345:C:OP2	2.21	0.41
1:CA:436:C:H2'	1:CA:437:U:H6	1.86	0.41
1:CA:609:A:C5	1:CA:610:G:C8	3.09	0.41
1:CA:946:A:H2'	1:CA:947:G:C8	2.56	0.41
4:CD:18:LYS:HE3	4:CD:20:TYR:CE1	2.55	0.41
4:CD:33:MET:O	4:CD:37:PRO:HB3	2.20	0.41
7:CG:24:THR:O	7:CG:27:ILE:HB	2.21	0.41
10:CJ:6:ILE:N	10:CJ:72:VAL:O	2.36	0.41
14:CN:37:PHE:CE2	14:CN:53:LEU:HD22	2.56	0.41
6:CF:100:ASN:ND2	18:CR:23:LYS:HE3	2.36	0.41
26:DA:649:G:H4'	55:D8:46:ARG:HH22	1.86	0.41
56:D9:17:ILE:HD12	56:D9:17:ILE:HA	1.92	0.41
26:DA:1161:C:H2'	26:DA:1162:G:H8	1.86	0.41
26:DA:2193:G:H2'	26:DA:2194:G:C8	2.56	0.41
26:DA:2706:G:H2'	26:DA:2707:G:O4'	2.21	0.41
26:DA:41:C:H2'	26:DA:42:G:C8	2.56	0.41
26:DA:753:C:H6	26:DA:753:C:OP2	2.03	0.41
26:DA:966:G:H2'	26:DA:967:C:C6	2.55	0.41
33:DI:83:ALA:CB	33:DI:123:LEU:HD21	2.50	0.41
33:DI:86:THR:O	33:DI:123:LEU:HD23	2.21	0.41
35:DO:98:VAL:HG11	35:DO:114:ILE:HG23	2.02	0.41
36:DP:47:ASP:HA	36:DP:48:PRO:HD3	1.85	0.41
38:DR:38:VAL:HG12	38:DR:42:LYS:HE3	2.03	0.41
38:DR:38:VAL:HB	38:DR:39:PRO:HD3	2.03	0.41
44:DX:35:THR:HG22	44:DX:37:THR:N	2.36	0.41
46:DZ:120:ILE:HD11	46:DZ:173:ALA:CB	2.51	0.41
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1152:A:OP1	10:AJ:68:HIS:ND1	2.52	0.40
1:AA:319:G:H1	1:AA:334:C:H42	1.69	0.40
2:AB:21:ARG:NH2	2:AB:23:ARG:HE	2.19	0.40
3:AC:52:LEU:HD11	3:AC:55:VAL:HG23	2.02	0.40
4:AD:120:LEU:HA	4:AD:120:LEU:HD23	1.82	0.40
4:AD:178:VAL:HG12	4:AD:179:GLU:H	1.86	0.40
25:AY:6:G:C6	25:AY:7:A:C5	3.08	0.40
26:BA:1230:C:H5''	26:BA:1231:G:OP1	2.20	0.40
26:BA:1312:G:O5'	43:BW:15:ARG:NH2	2.54	0.40
26:BA:2135:U:C4	26:BA:2136:A:N7	2.89	0.40
26:BA:2294:G:OP1	26:BA:2295:C:H1'	2.21	0.40
26:BA:2815:C:H2'	26:BA:2816:G:O4'	2.21	0.40
26:BA:637:U:H5'	26:BA:640:A:N6	2.35	0.40
31:BG:14:GLU:C	31:BG:17:PRO:HD2	2.42	0.40
46:BZ:146:ILE:HA	46:BZ:147:GLY:HA2	1.77	0.40
46:BZ:92:SER:OG	46:BZ:93:ASP:N	2.55	0.40
1:CA:1134:G:N3	1:CA:1134:G:H2'	2.35	0.40
1:CA:1243:C:H2'	1:CA:1244:C:C6	2.56	0.40
1:CA:1497:G:HO2'	1:CA:1518:A:H2	1.62	0.40
1:CA:64:G:H4'	1:CA:65:U:H3'	2.02	0.40
1:CA:690:G:H8	1:CA:690:G:O5'	2.04	0.40
1:CA:861:G:OP1	8:CH:75:ARG:NH2	2.54	0.40
5:CE:31:LEU:HA	5:CE:31:LEU:HD23	1.86	0.40
1:CA:19:C:H5''	5:CE:86:ALA:HB3	2.03	0.40
7:CG:14:PRO:HG3	7:CG:21:VAL:HG13	2.03	0.40
11:CK:93:GLN:HA	11:CK:93:GLN:HE21	1.86	0.40
23:CW:27:G:H2'	23:CW:28:G:C8	2.56	0.40
26:DA:1309:G:H3'	54:D7:9:ARG:NH1	2.36	0.40
26:DA:1336:A:H2'	26:DA:1337:G:C8	2.56	0.40
26:DA:1853:A:N1	26:DA:2087:G:H1'	2.37	0.40
26:DA:225:A:N6	26:DA:226:G:C2	2.89	0.40
26:DA:2262:U:H4'	26:DA:2328:A:C2	2.57	0.40
26:DA:2849:U:O4	40:DT:23:ARG:NH2	2.43	0.40
26:DA:2849:U:H4'	26:DA:2868:A:C2	2.55	0.40
26:DA:478:A:N1	26:DA:500:G:H4'	2.35	0.40
27:DB:78:A:C2	27:DB:100:A:C4	3.09	0.40
40:DT:108:ARG:HG2	40:DT:111:ARG:NH1	2.32	0.40
42:DV:52:VAL:CG2	42:DV:55:ALA:HB3	2.51	0.40
26:DA:299:A:H5''	45:DY:86:ARG:NH2	2.36	0.40
46:DZ:161:VAL:O	46:DZ:161:VAL:HG13	2.20	0.40
1:AA:1223:C:P	19:AS:78:ARG:HH21	2.44	0.40
1:AA:613:C:H2'	1:AA:614:A:C8	2.55	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:118:LEU:HA	2:AB:118:LEU:HD23	1.84	0.40
8:AH:39:LEU:HD12	8:AH:39:LEU:HA	1.86	0.40
9:AI:50:LEU:HB2	9:AI:55:ALA:HB3	2.04	0.40
15:AO:7:GLU:O	15:AO:11:VAL:HG23	2.21	0.40
18:AR:59:SER:OG	18:AR:62:GLU:HG2	2.22	0.40
1:AA:955:U:O2'	19:AS:83:HIS:HD2	2.03	0.40
20:AT:92:LEU:O	20:AT:96:GLY:HA2	2.22	0.40
25:AY:36:A:C6	25:AY:37:MIA:C5	3.03	0.40
49:B2:23:LYS:O	49:B2:27:GLU:HG3	2.21	0.40
51:B4:16:CYS:SG	51:B4:17:GLY:N	2.94	0.40
53:B6:14:THR:HB	53:B6:48:VAL:O	2.22	0.40
54:B7:8:ASN:HB3	54:B7:11:LYS:HB3	2.02	0.40
26:BA:1269:G:N2	26:BA:1272:A:OP2	2.47	0.40
26:BA:875:U:C5	26:BA:2259:A:H4'	2.56	0.40
26:BA:864:C:H4'	26:BA:977:G:C5	2.56	0.40
28:BD:180:GLY:HA3	28:BD:275:LYS:HB2	2.03	0.40
26:BA:1836:U:O2	28:BD:50:THR:HB	2.21	0.40
30:BF:150:GLY:HA2	30:BF:172:TRP:CE3	2.56	0.40
26:BA:2290:A:OP1	37:BQ:11:LYS:HD2	2.22	0.40
26:BA:1207:C:O2'	42:BV:8:GLY:HA2	2.21	0.40
1:CA:1277:C:O2'	1:CA:1279:A:C8	2.66	0.40
1:CA:1414:U:H3	1:CA:1486:G:H1	1.68	0.40
1:CA:149:A:H2'	1:CA:150:C:C6	2.56	0.40
1:CA:993:G:O2'	1:CA:994:A:N7	2.51	0.40
2:CB:219:VAL:O	2:CB:222:ILE:HG12	2.21	0.40
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.60	0.40
7:CG:65:ALA:HB1	7:CG:127:ALA:HB3	2.02	0.40
8:CH:69:ARG:NH2	8:CH:75:ARG:O	2.53	0.40
14:CN:23:ARG:HG3	14:CN:28:GLY:O	2.21	0.40
19:CS:69:HIS:HD2	19:CS:73:GLU:OE1	2.05	0.40
22:CV:14:A:C2	25:CY:34:G:C2	3.10	0.40
23:CW:9:A:OP2	23:CW:13:C:N4	2.47	0.40
24:CX:2:G:H5'	57:CX:3002:MG:MG	1.46	0.40
24:CX:43:A:H2'	24:CX:44:A:C8	2.56	0.40
26:DA:1394:U:C4	26:DA:1395:A:C5	3.10	0.40
26:DA:565:C:H2'	26:DA:566:U:O4'	2.20	0.40
26:DA:820:A:N3	26:DA:943:U:H4'	2.36	0.40
27:DB:110:G:O2'	27:DB:111:G:H5'	2.21	0.40
27:DB:33:G:C6	27:DB:34:U:N3	2.89	0.40
27:DB:42:C:O2'	31:DG:66:GLN:HG2	2.21	0.40
29:DE:30:PRO:HD3	29:DE:180:ASN:ND2	2.35	0.40
30:DF:59:TYR:HE2	30:DF:85:GLY:O	2.04	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:93:LYS:HD3	30:DF:93:LYS:HA	1.86	0.40
31:DG:125:PHE:HB3	31:DG:166:ASP:CG	2.42	0.40
35:DO:47:ILE:HB	35:DO:48:PRO:HD2	2.04	0.40
38:DR:38:VAL:HG22	38:DR:112:ALA:HB2	2.03	0.40
38:DR:63:ARG:O	38:DR:67:LEU:HB2	2.22	0.40
1:AA:1272:G:H2'	1:AA:1273:G:O4'	2.22	0.40
1:AA:271:C:H2'	1:AA:272:C:H6	1.87	0.40
1:AA:542:G:O3'	4:AD:14:ARG:NH2	2.53	0.40
1:AA:936:C:H2'	1:AA:937:A:O4'	2.20	0.40
3:AC:121:ALA:HB1	3:AC:189:ALA:HB2	2.04	0.40
4:AD:11:LEU:HG	4:AD:66:ARG:HD3	2.03	0.40
9:AI:33:PHE:HD1	9:AI:34:ASN:ND2	2.20	0.40
10:AJ:90:LEU:HA	10:AJ:91:PRO:HD3	1.92	0.40
1:AA:189(F):U:C2	17:AQ:72:ARG:NH2	2.90	0.40
20:AT:56:MET:HE3	20:AT:88:VAL:HG21	2.03	0.40
25:AY:58:A:O2'	25:AY:60:U:OP2	2.29	0.40
47:B0:50:ASN:HB3	47:B0:63:VAL:HG22	2.02	0.40
26:BA:1219:A:H1'	26:BA:1220:U:C5'	2.50	0.40
26:BA:593:G:H2'	26:BA:2052:A:N7	2.37	0.40
26:BA:2286:A:C5	26:BA:2288:G:C8	3.10	0.40
26:BA:2627:U:H2'	26:BA:2628:C:C6	2.56	0.40
26:BA:969:C:H2'	26:BA:970:C:C6	2.56	0.40
28:BD:4:LYS:HB3	28:BD:18:VAL:HG23	2.04	0.40
1:CA:1084:G:H1'	1:CA:1102:A:N7	2.36	0.40
1:CA:1286:A:H3'	1:CA:1286:A:H8	1.85	0.40
1:CA:453:A:H4'	16:CP:72:ARG:HG3	2.02	0.40
1:CA:630:G:O2'	1:CA:631:G:H5'	2.21	0.40
1:CA:697:U:H2'	1:CA:698:G:H5'	2.04	0.40
1:CA:828:A:H4'	1:CA:828:A:OP1	2.21	0.40
2:CB:28:PHE:O	2:CB:32:ILE:HG13	2.21	0.40
4:CD:108:LEU:HB3	4:CD:110:PHE:CE1	2.56	0.40
7:CG:26:PHE:HE1	7:CG:30:ILE:HD11	1.87	0.40
12:CL:27:LEU:HD23	12:CL:30:ALA:O	2.22	0.40
3:CC:29:TYR:CZ	14:CN:54:PRO:HG2	2.57	0.40
51:D4:62:ARG:N	51:D4:62:ARG:HD3	2.35	0.40
26:DA:2022:U:OP2	52:D5:15:ARG:NH2	2.54	0.40
52:D5:49:CYS:SG	52:D5:51:TYR:HB2	2.61	0.40
26:DA:1014:U:H2'	26:DA:1015:G:C8	2.55	0.40
26:DA:1611:C:C2'	26:DA:1612:C:H5'	2.50	0.40
26:DA:2155:G:C2'	26:DA:2156:G:H5'	2.52	0.40
26:DA:234:C:H2'	26:DA:235:U:H6	1.87	0.40
26:DA:1669:A:H5''	26:DA:2550:G:OP1	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:856:C:H2'	26:DA:857:C:C6	2.56	0.40
26:DA:866:A:C6	26:DA:914:C:C5	3.10	0.40
29:DE:85:ASN:HA	29:DE:86:PRO:HD2	1.84	0.40
31:DG:115:ARG:HG2	31:DG:136:ARG:HH21	1.85	0.40
33:DI:92:VAL:HG22	33:DI:120:ILE:HB	2.03	0.40
34:DN:60:ILE:HG13	34:DN:61:ARG:N	2.36	0.40
42:DV:24:LYS:HA	42:DV:92:THR:OG1	2.21	0.40
46:DZ:79:ARG:HB2	46:DZ:80:ARG:NH1	2.36	0.40
1:AA:1024:G:H2'	1:AA:1025:U:H5'	2.04	0.40
1:AA:148:G:H2'	1:AA:149:A:C8	2.50	0.40
1:AA:390:C:H2'	1:AA:391:G:C8	2.56	0.40
1:AA:933:G:O6	7:AG:3:ARG:NH2	2.52	0.40
2:AB:19:HIS:CG	2:AB:20:GLU:H	2.39	0.40
2:AB:8:LYS:HG2	2:AB:8:LYS:H	1.51	0.40
7:AG:14:PRO:HG3	7:AG:21:VAL:HG13	2.03	0.40
10:AJ:26:ALA:O	10:AJ:30:SER:OG	2.39	0.40
13:AM:97:PRO:HG2	13:AM:103:THR:HG22	2.04	0.40
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.52	0.40
19:AS:15:LEU:O	19:AS:19:VAL:HG23	2.21	0.40
19:AS:69:HIS:HD2	19:AS:73:GLU:OE1	2.05	0.40
24:AX:19:G:H5''	24:AX:60:U:O4	2.21	0.40
52:B5:35:GLU:HG3	52:B5:51:TYR:CD2	2.57	0.40
26:BA:1452:U:H2'	26:BA:1453:C:H6	1.86	0.40
26:BA:2092:G:H2'	26:BA:2093:A:C8	2.57	0.40
26:BA:2367:C:H5'	61:BA:3944:HOH:O	2.22	0.40
26:BA:2410:U:H2'	26:BA:2411:G:C8	2.57	0.40
26:BA:612:C:H2'	26:BA:613:A:C8	2.56	0.40
28:BD:19:ALA:HB3	28:BD:21:PHE:CE1	2.56	0.40
30:BF:64:ILE:HG13	30:BF:65:TRP:N	2.37	0.40
42:BV:49:THR:HG22	42:BV:49:THR:O	2.21	0.40
44:BX:94:GLY:N	44:BX:95:LEU:HA	2.36	0.40
45:BY:83:THR:HG21	45:BY:99:CYS:HB2	2.02	0.40
1:CA:1075:C:H42	1:CA:1082:G:H1	1.68	0.40
1:CA:1164:G:O2'	1:CA:1165:C:H5'	2.22	0.40
1:CA:1360:A:H2'	1:CA:1361:G:O4'	2.21	0.40
1:CA:1429:C:H2'	1:CA:1430:C:C6	2.57	0.40
1:CA:1479:C:H2'	1:CA:1480:G:C8	2.56	0.40
1:CA:57:G:H2'	1:CA:58:C:C6	2.57	0.40
2:CB:16:HIS:ND1	2:CB:17:PHE:N	2.68	0.40
2:CB:53:ARG:CZ	2:CB:53:ARG:HB3	2.50	0.40
3:CC:109:PRO:HB3	3:CC:115:LEU:HD23	2.03	0.40
3:CC:178:LEU:HA	3:CC:178:LEU:HD13	1.93	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:CH:119:LEU:HB3	8:CH:123:GLU:CB	2.51	0.40
8:CH:25:ASP:N	8:CH:25:ASP:OD1	2.55	0.40
9:CI:23:ASN:HD22	9:CI:24:GLY:N	2.20	0.40
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.57	0.40
48:D1:5:CYS:SG	48:D1:62:VAL:HG23	2.62	0.40
49:D2:64:LEU:O	49:D2:68:ARG:HG3	2.22	0.40
50:D3:23:LEU:HD13	50:D3:50:VAL:HG11	2.02	0.40
26:DA:1486:A:O2'	26:DA:1487:G:H5'	2.21	0.40
24:CX:12:G:H4'	26:DA:1908:C:O2	2.21	0.40
26:DA:2174:C:H2'	26:DA:2174:C:O2	2.21	0.40
26:DA:2462:U:H2'	26:DA:2463:C:C6	2.56	0.40
26:DA:2741:A:H2'	26:DA:2742:C:O4'	2.21	0.40
26:DA:2756:U:H1'	26:DA:2757:A:H5''	2.02	0.40
26:DA:335:C:H4'	45:DY:73:ARG:NE	2.37	0.40
26:DA:428:A:H3'	26:DA:429:A:H8	1.87	0.40
26:DA:443:A:H5''	26:DA:444:C:OP1	2.21	0.40
26:DA:570:G:H2'	26:DA:2030:A:C5	2.56	0.40
26:DA:892:G:H2'	26:DA:893:C:C4'	2.52	0.40
31:DG:31:VAL:HA	31:DG:32:PRO:HD2	1.72	0.40
36:DP:84:ASN:OD1	36:DP:117:GLU:HB2	2.20	0.40
40:DT:94:ALA:HB1	40:DT:99:LEU:HD21	2.02	0.40
26:DA:996:A:O3'	41:DU:91:ASP:HB2	2.22	0.40
1:AA:1002:G:C6	1:AA:1003:G:C2	3.10	0.40
1:AA:1151:A:O2'	1:AA:1152:A:H8	2.05	0.40
1:AA:512:U:H2'	1:AA:513:C:C6	2.56	0.40
2:AB:215:LEU:HD23	2:AB:215:LEU:HA	1.79	0.40
3:AC:82:GLU:HA	3:AC:85:ARG:CZ	2.51	0.40
4:AD:18:LYS:HE3	4:AD:20:TYR:CZ	2.56	0.40
6:AF:22:GLU:O	6:AF:26:ILE:HG13	2.22	0.40
6:AF:55:ASP:HA	6:AF:56:PRO:HD2	1.98	0.40
13:AM:39:ILE:HG13	13:AM:56:LEU:HD12	2.03	0.40
25:AY:26:A:N1	25:AY:44:G:N2	2.54	0.40
26:BA:397:G:H4'	26:BA:398:A:OP2	2.21	0.40
30:BF:106:ARG:HG2	30:BF:106:ARG:H	1.70	0.40
26:BA:721:G:O2'	30:BF:74:ARG:HD3	2.22	0.40
1:CA:1154:G:O6	1:CA:1155:G:C6	2.75	0.40
1:CA:1367:C:O2'	10:CJ:62:HIS:HE1	2.04	0.40
1:CA:1496:C:H2'	1:CA:1497:G:O4'	2.20	0.40
1:CA:243:A:C2	1:CA:246:A:C8	3.10	0.40
2:CB:28:PHE:CD2	2:CB:190:THR:HA	2.56	0.40
7:CG:52:GLU:H	7:CG:52:GLU:HG2	1.62	0.40
1:CA:1350:A:OP1	9:CI:121:ARG:HD3	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:CN:9:LYS:HG3	14:CN:12:ARG:HH11	1.86	0.40
24:CX:66:C:H2'	24:CX:67:C:O4'	2.22	0.40
25:CY:29:G:N1	25:CY:41:C:N4	2.69	0.40
50:D3:10:LYS:HB3	50:D3:53:LEU:HA	2.02	0.40
51:D4:28:LYS:HA	51:D4:29:PRO:HD3	1.84	0.40
26:DA:1001:A:H2'	26:DA:1002:G:O4'	2.21	0.40
26:DA:1221(A):C:C2	26:DA:1229:G:C2	3.09	0.40
26:DA:1241:A:O2'	26:DA:1242:A:H5'	2.21	0.40
26:DA:2507:C:H2'	26:DA:2508:G:O4'	2.22	0.40
26:DA:305:U:H2'	26:DA:306:U:C6	2.56	0.40
26:DA:56:A:H2'	26:DA:57:C:O4'	2.22	0.40
26:DA:832:G:H5'	36:DP:45:LEU:HD21	2.04	0.40
26:DA:933:A:H2'	26:DA:934:G:O4'	2.22	0.40
34:DN:115:ARG:HA	34:DN:118:LYS:HE3	2.02	0.40
26:DA:2294:C:P	39:DS:89:ARG:HH22	2.44	0.40
46:DZ:171:ILE:HG13	46:DZ:171:ILE:H	1.65	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%)	14 (6%)	7 (3%)	7	8
2	CB	229/256 (90%)	206 (90%)	16 (7%)	7 (3%)	7	8
3	AC	204/239 (85%)	195 (96%)	8 (4%)	1 (0%)	38	60
3	CC	204/239 (85%)	189 (93%)	15 (7%)	0	100	100
4	AD	206/209 (99%)	197 (96%)	7 (3%)	2 (1%)	22	37
4	CD	206/209 (99%)	196 (95%)	9 (4%)	1 (0%)	38	60
5	AE	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
5	CE	146/162 (90%)	140 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AF	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
6	CF	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
7	AG	153/156 (98%)	144 (94%)	5 (3%)	4 (3%)	8	11
7	CG	153/156 (98%)	144 (94%)	8 (5%)	1 (1%)	30	49
8	AH	135/138 (98%)	134 (99%)	1 (1%)	0	100	100
8	CH	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
9	AI	125/128 (98%)	117 (94%)	8 (6%)	0	100	100
9	CI	125/128 (98%)	119 (95%)	5 (4%)	1 (1%)	27	45
10	AJ	95/105 (90%)	85 (90%)	6 (6%)	4 (4%)	4	4
10	CJ	94/105 (90%)	85 (90%)	4 (4%)	5 (5%)	3	2
11	AK	112/129 (87%)	104 (93%)	6 (5%)	2 (2%)	13	20
11	CK	112/129 (87%)	103 (92%)	7 (6%)	2 (2%)	13	20
12	AL	120/132 (91%)	117 (98%)	3 (2%)	0	100	100
12	CL	120/132 (91%)	118 (98%)	2 (2%)	0	100	100
13	AM	121/126 (96%)	116 (96%)	5 (4%)	0	100	100
13	CM	120/126 (95%)	113 (94%)	7 (6%)	0	100	100
14	AN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
14	CN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
15	AO	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
15	CO	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
16	AP	80/88 (91%)	79 (99%)	1 (1%)	0	100	100
16	CP	80/88 (91%)	78 (98%)	1 (1%)	1 (1%)	18	29
17	AQ	97/105 (92%)	93 (96%)	4 (4%)	0	100	100
17	CQ	97/105 (92%)	93 (96%)	4 (4%)	0	100	100
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%)	73 (90%)	7 (9%)	1 (1%)	19	31
19	CS	81/93 (87%)	72 (89%)	9 (11%)	0	100	100
20	AT	94/106 (89%)	87 (93%)	3 (3%)	4 (4%)	4	4
20	CT	94/106 (89%)	88 (94%)	3 (3%)	3 (3%)	6	7
21	AU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	CU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
28	BD	273/276 (99%)	264 (97%)	8 (3%)	1 (0%)	43	66
28	DD	273/276 (99%)	263 (96%)	8 (3%)	2 (1%)	30	49
29	BE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	38	60
29	DE	202/206 (98%)	196 (97%)	4 (2%)	2 (1%)	22	37
30	BF	201/210 (96%)	200 (100%)	0	1 (0%)	38	60
30	DF	201/210 (96%)	199 (99%)	0	2 (1%)	22	37
31	BG	179/182 (98%)	170 (95%)	8 (4%)	1 (1%)	33	54
31	DG	179/182 (98%)	171 (96%)	5 (3%)	3 (2%)	14	21
32	BH	172/180 (96%)	168 (98%)	3 (2%)	1 (1%)	33	54
32	DH	172/180 (96%)	166 (96%)	5 (3%)	1 (1%)	33	54
33	BI	144/148 (97%)	130 (90%)	11 (8%)	3 (2%)	11	16
33	DI	144/148 (97%)	133 (92%)	10 (7%)	1 (1%)	30	49
34	BN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
34	DN	138/140 (99%)	135 (98%)	2 (1%)	1 (1%)	30	49
35	BO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
35	DO	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
36	BP	147/150 (98%)	140 (95%)	6 (4%)	1 (1%)	30	49
36	DP	147/150 (98%)	138 (94%)	7 (5%)	2 (1%)	16	27
37	BQ	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
37	DQ	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	30	49
38	BR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
38	DR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
39	BS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	25	41
39	DS	108/112 (96%)	105 (97%)	2 (2%)	1 (1%)	25	41
40	BT	129/146 (88%)	122 (95%)	7 (5%)	0	100	100
40	DT	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
41	BU	114/118 (97%)	114 (100%)	0	0	100	100
41	DU	114/118 (97%)	114 (100%)	0	0	100	100
42	BV	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
42	DV	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	22	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	BW	110/113 (97%)	110 (100%)	0	0	100	100
43	DW	110/113 (97%)	110 (100%)	0	0	100	100
44	BX	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
44	DX	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
45	BY	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
45	DY	105/110 (96%)	101 (96%)	4 (4%)	0	100	100
46	BZ	169/206 (82%)	153 (90%)	15 (9%)	1 (1%)	33	54
46	DZ	172/206 (84%)	161 (94%)	11 (6%)	0	100	100
47	B0	81/85 (95%)	81 (100%)	0	0	100	100
47	D0	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
48	B1	95/98 (97%)	94 (99%)	0	1 (1%)	21	34
48	D1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	21	34
49	B2	68/72 (94%)	68 (100%)	0	0	100	100
49	D2	68/72 (94%)	68 (100%)	0	0	100	100
50	B3	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
50	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
51	B4	67/71 (94%)	53 (79%)	11 (16%)	3 (4%)	4	4
51	D4	67/71 (94%)	53 (79%)	9 (13%)	5 (8%)	2	1
52	B5	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
52	D5	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
53	B6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
53	D6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
54	B7	46/49 (94%)	46 (100%)	0	0	100	100
54	D7	46/49 (94%)	45 (98%)	0	1 (2%)	10	15
55	B8	62/65 (95%)	62 (100%)	0	0	100	100
55	D8	62/65 (95%)	62 (100%)	0	0	100	100
56	B9	35/37 (95%)	35 (100%)	0	0	100	100
56	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11409/12128 (94%)	10908 (96%)	416 (4%)	85 (1%)	30	49

All (85) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	126	GLU
7	AG	80	VAL
20	AT	10	LEU
20	AT	96	GLY
28	BD	275	LYS
29	BE	52	LEU
30	BF	130	ALA
33	BI	107	VAL
51	B4	55	ARG
2	CB	16	HIS
2	CB	20	GLU
2	CB	126	GLU
4	CD	46	LYS
9	CI	54	ASP
10	CJ	79	ARG
20	CT	99	LEU
30	DF	21	ALA
30	DF	130	ALA
33	DI	10	GLU
36	DP	29	LYS
51	D4	39	CYS
51	D4	63	TYR
54	D7	46	VAL
2	AB	10	LEU
2	AB	19	HIS
4	AD	166	LYS
7	AG	8	GLU
7	AG	81	GLY
10	AJ	31	GLY
10	AJ	56	HIS
11	AK	49	GLY
20	AT	47	GLY
33	BI	106	GLY
48	B1	3	LYS
51	B4	54	GLY
51	B4	57	GLU
2	CB	8	LYS
2	CB	9	GLU
10	CJ	56	HIS
10	CJ	77	PRO
11	CK	49	GLY
20	CT	47	GLY
20	CT	95	ALA

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Mol	Chain	Res	Type
29	DE	52	LEU
31	DG	81	LYS
32	DH	126	PRO
37	DQ	28	ALA
51	D4	45	GLY
2	AB	20	GLU
4	AD	164	ALA
10	AJ	79	ARG
19	AS	42	PRO
20	AT	95	ALA
31	BG	47	LYS
32	BH	126	PRO
39	BS	60	GLY
46	BZ	152	ALA
11	CK	105	VAL
28	DD	239	ARG
34	DN	2	LYS
39	DS	84	GLN
33	BI	73	GLU
36	BP	29	LYS
2	CB	10	LEU
10	CJ	55	LYS
28	DD	3	VAL
31	DG	32	PRO
31	DG	47	LYS
36	DP	45	LEU
48	D1	3	LYS
51	D4	55	ARG
10	AJ	91	PRO
29	DE	73	GLU
51	D4	62	ARG
2	AB	231	GLU
3	AC	66	VAL
2	CB	231	GLU
7	CG	17	VAL
16	CP	53	VAL
11	AK	105	VAL
2	AB	124	SER
10	CJ	91	PRO
42	DV	79	VAL
7	AG	17	VAL
2	AB	125	PRO

5.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	192/220 (87%)	163 (85%)	29 (15%)	4	7
2	CB	187/220 (85%)	149 (80%)	38 (20%)	2	3
3	AC	143/188 (76%)	121 (85%)	22 (15%)	4	6
3	CC	140/188 (74%)	124 (89%)	16 (11%)	8	14
4	AD	170/181 (94%)	152 (89%)	18 (11%)	10	17
4	CD	173/181 (96%)	152 (88%)	21 (12%)	7	12
5	AE	113/123 (92%)	105 (93%)	8 (7%)	21	36
5	CE	114/123 (93%)	101 (89%)	13 (11%)	8	14
6	AF	83/90 (92%)	76 (92%)	7 (8%)	16	27
6	CF	85/90 (94%)	80 (94%)	5 (6%)	28	46
7	AG	119/127 (94%)	108 (91%)	11 (9%)	13	23
7	CG	120/127 (94%)	109 (91%)	11 (9%)	13	23
8	AH	114/119 (96%)	105 (92%)	9 (8%)	18	30
8	CH	114/119 (96%)	107 (94%)	7 (6%)	26	44
9	AI	90/99 (91%)	76 (84%)	14 (16%)	4	6
9	CI	89/99 (90%)	76 (85%)	13 (15%)	5	7
10	AJ	66/92 (72%)	58 (88%)	8 (12%)	7	12
10	CJ	69/92 (75%)	63 (91%)	6 (9%)	15	26
11	AK	82/99 (83%)	77 (94%)	5 (6%)	26	44
11	CK	83/99 (84%)	76 (92%)	7 (8%)	16	27
12	AL	97/109 (89%)	93 (96%)	4 (4%)	41	66
12	CL	97/109 (89%)	93 (96%)	4 (4%)	41	66
13	AM	93/101 (92%)	82 (88%)	11 (12%)	8	13
13	CM	92/101 (91%)	80 (87%)	12 (13%)	6	10
14	AN	49/50 (98%)	42 (86%)	7 (14%)	5	8
14	CN	49/50 (98%)	41 (84%)	8 (16%)	3	5
15	AO	78/80 (98%)	64 (82%)	14 (18%)	2	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	CO	78/80 (98%)	69 (88%)	9 (12%)	8	14
16	AP	69/74 (93%)	60 (87%)	9 (13%)	6	10
16	CP	68/74 (92%)	61 (90%)	7 (10%)	10	18
17	AQ	94/97 (97%)	85 (90%)	9 (10%)	12	21
17	CQ	94/97 (97%)	87 (93%)	7 (7%)	20	34
18	AR	59/77 (77%)	54 (92%)	5 (8%)	15	27
18	CR	59/77 (77%)	52 (88%)	7 (12%)	8	13
19	AS	69/80 (86%)	64 (93%)	5 (7%)	21	35
19	CS	67/80 (84%)	63 (94%)	4 (6%)	27	45
20	AT	70/82 (85%)	62 (89%)	8 (11%)	8	14
20	CT	70/82 (85%)	62 (89%)	8 (11%)	8	14
21	AU	18/22 (82%)	15 (83%)	3 (17%)	3	5
21	CU	18/22 (82%)	17 (94%)	1 (6%)	30	49
28	BD	215/218 (99%)	195 (91%)	20 (9%)	13	22
28	DD	215/218 (99%)	193 (90%)	22 (10%)	11	18
29	BE	164/166 (99%)	146 (89%)	18 (11%)	9	15
29	DE	164/166 (99%)	145 (88%)	19 (12%)	8	13
30	BF	160/166 (96%)	149 (93%)	11 (7%)	22	37
30	DF	159/166 (96%)	144 (91%)	15 (9%)	13	22
31	BG	143/156 (92%)	128 (90%)	15 (10%)	10	17
31	DG	142/156 (91%)	122 (86%)	20 (14%)	5	8
32	BH	144/148 (97%)	126 (88%)	18 (12%)	7	11
32	DH	144/148 (97%)	126 (88%)	18 (12%)	7	11
33	BI	110/124 (89%)	86 (78%)	24 (22%)	1	2
33	DI	104/124 (84%)	88 (85%)	16 (15%)	4	6
34	BN	118/119 (99%)	103 (87%)	15 (13%)	6	11
34	DN	118/119 (99%)	106 (90%)	12 (10%)	11	18
35	BO	100/100 (100%)	93 (93%)	7 (7%)	21	37
35	DO	100/100 (100%)	93 (93%)	7 (7%)	21	37
36	BP	115/116 (99%)	98 (85%)	17 (15%)	4	7
36	DP	115/116 (99%)	100 (87%)	15 (13%)	6	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BQ	111/111 (100%)	95 (86%)	16 (14%)	5	8
37	DQ	111/111 (100%)	99 (89%)	12 (11%)	9	16
38	BR	101/101 (100%)	82 (81%)	19 (19%)	2	3
38	DR	101/101 (100%)	83 (82%)	18 (18%)	2	4
39	BS	87/88 (99%)	81 (93%)	6 (7%)	22	37
39	DS	85/88 (97%)	75 (88%)	10 (12%)	8	13
40	BT	115/127 (91%)	106 (92%)	9 (8%)	18	31
40	DT	113/127 (89%)	103 (91%)	10 (9%)	14	25
41	BU	93/94 (99%)	84 (90%)	9 (10%)	12	20
41	DU	93/94 (99%)	85 (91%)	8 (9%)	15	26
42	BV	80/82 (98%)	68 (85%)	12 (15%)	4	7
42	DV	80/82 (98%)	67 (84%)	13 (16%)	3	5
43	BW	90/92 (98%)	83 (92%)	7 (8%)	18	31
43	DW	90/92 (98%)	83 (92%)	7 (8%)	18	31
44	BX	77/78 (99%)	71 (92%)	6 (8%)	18	31
44	DX	77/78 (99%)	71 (92%)	6 (8%)	18	31
45	BY	85/91 (93%)	75 (88%)	10 (12%)	8	13
45	DY	85/91 (93%)	79 (93%)	6 (7%)	21	36
46	BZ	145/179 (81%)	133 (92%)	12 (8%)	16	28
46	DZ	145/179 (81%)	129 (89%)	16 (11%)	9	15
47	B0	65/67 (97%)	62 (95%)	3 (5%)	37	60
47	D0	65/67 (97%)	60 (92%)	5 (8%)	18	32
48	B1	80/83 (96%)	73 (91%)	7 (9%)	14	25
48	D1	80/83 (96%)	71 (89%)	9 (11%)	9	14
49	B2	65/67 (97%)	57 (88%)	8 (12%)	7	11
49	D2	65/67 (97%)	59 (91%)	6 (9%)	13	23
50	B3	51/52 (98%)	46 (90%)	5 (10%)	12	20
50	D3	50/52 (96%)	44 (88%)	6 (12%)	7	12
51	B4	60/63 (95%)	47 (78%)	13 (22%)	1	2
51	D4	53/63 (84%)	43 (81%)	10 (19%)	2	3
52	B5	50/52 (96%)	45 (90%)	5 (10%)	11	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	D5	50/52 (96%)	46 (92%)	4 (8%)	17	30
53	B6	51/52 (98%)	44 (86%)	7 (14%)	5	9
53	D6	50/52 (96%)	48 (96%)	2 (4%)	42	67
54	B7	41/42 (98%)	38 (93%)	3 (7%)	20	35
54	D7	41/42 (98%)	38 (93%)	3 (7%)	20	35
55	B8	53/55 (96%)	49 (92%)	4 (8%)	19	33
55	D8	54/55 (98%)	51 (94%)	3 (6%)	30	49
56	B9	34/34 (100%)	34 (100%)	0	100	100
56	D9	34/34 (100%)	32 (94%)	2 (6%)	28	46
All	All	9320/10066 (93%)	8304 (89%)	1016 (11%)	9	15

All (1016) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	8	LYS
2	AB	10	LEU
2	AB	11	LEU
2	AB	15	VAL
2	AB	17	PHE
2	AB	21	ARG
2	AB	23	ARG
2	AB	24	TRP
2	AB	49	GLU
2	AB	64	ARG
2	AB	67	THR
2	AB	76	GLN
2	AB	94	ASN
2	AB	108	ILE
2	AB	111	ARG
2	AB	114	ARG
2	AB	127	ILE
2	AB	144	ARG
2	AB	145	LEU
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	157	ARG
2	AB	160	ASP
2	AB	170	GLU

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Mol	Chain	Res	Type
2	AB	187	LEU
2	AB	200	ILE
2	AB	221	LEU
2	AB	230	VAL
3	AC	3	ASN
3	AC	26	LYS
3	AC	27	LYS
3	AC	28	GLN
3	AC	32	LEU
3	AC	37	GLN
3	AC	45	LYS
3	AC	49	SER
3	AC	70	VAL
3	AC	77	ILE
3	AC	97	LYS
3	AC	98	ASN
3	AC	104	GLN
3	AC	115	LEU
3	AC	118	GLN
3	AC	119	ARG
3	AC	127	ARG
3	AC	140	ARG
3	AC	144	SER
3	AC	181	ASN
3	AC	196	LEU
3	AC	198	VAL
4	AD	5	ILE
4	AD	31	CYS
4	AD	49	ARG
4	AD	52	SER
4	AD	53	ASP
4	AD	58	LEU
4	AD	63	LYS
4	AD	86	LYS
4	AD	108	LEU
4	AD	122	ARG
4	AD	127	THR
4	AD	135	LEU
4	AD	139	ARG
4	AD	141	ARG
4	AD	144	ASP
4	AD	158	ILE

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Mol	Chain	Res	Type
4	AD	168	ARG
4	AD	188	LEU
5	AE	6	PHE
5	AE	12	LEU
5	AE	31	LEU
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	73	ASN
5	AE	145	LYS
6	AF	36	ARG
6	AF	40	VAL
6	AF	55	ASP
6	AF	69	GLU
6	AF	74	ASP
6	AF	75	LEU
6	AF	82	ARG
7	AG	8	GLU
7	AG	12	LEU
7	AG	50	ILE
7	AG	51	GLN
7	AG	52	GLU
7	AG	53	LYS
7	AG	76	ARG
7	AG	79	ARG
7	AG	104	LEU
7	AG	113	GLU
7	AG	155	ARG
8	AH	21	LYS
8	AH	29	SER
8	AH	39	LEU
8	AH	52	ASP
8	AH	78	GLN
8	AH	84	ARG
8	AH	109	ILE
8	AH	112	LEU
8	AH	127	LEU
9	AI	14	VAL
9	AI	17	VAL
9	AI	23	ASN
9	AI	42	ARG
9	AI	53	VAL

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Mol	Chain	Res	Type
9	AI	56	LEU
9	AI	81	ILE
9	AI	86	VAL
9	AI	89	ASN
9	AI	103	THR
9	AI	108	VAL
9	AI	121	ARG
9	AI	127	LYS
9	AI	128	ARG
10	AJ	16	LEU
10	AJ	17	ASP
10	AJ	43	ARG
10	AJ	66	ARG
10	AJ	81	THR
10	AJ	84	GLN
10	AJ	94	VAL
10	AJ	100	THR
11	AK	14	VAL
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	96	ARG
12	AL	33	ARG
12	AL	46	LYS
12	AL	52	LEU
12	AL	83	VAL
13	AM	4	ILE
13	AM	15	VAL
13	AM	27	LYS
13	AM	43	THR
13	AM	49	THR
13	AM	52	GLU
13	AM	70	LEU
13	AM	73	GLU
13	AM	84	ILE
13	AM	110	ARG
13	AM	121	LYS
14	AN	3	ARG
14	AN	7	ILE
14	AN	18	VAL
14	AN	23	ARG
14	AN	26	ARG

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Mol	Chain	Res	Type
14	AN	32	SER
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	21	ASP
15	AO	22	THR
15	AO	26	GLU
15	AO	39	LEU
15	AO	41	GLU
15	AO	47	LYS
15	AO	64	ARG
15	AO	66	LEU
15	AO	71	GLN
15	AO	76	GLU
15	AO	83	GLU
15	AO	84	LYS
16	AP	1	MET
16	AP	2	VAL
16	AP	19	ILE
16	AP	20	VAL
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	62	VAL
16	AP	67	THR
17	AQ	14	LYS
17	AQ	19	VAL
17	AQ	24	GLU
17	AQ	60	ILE
17	AQ	63	ARG
17	AQ	72	ARG
17	AQ	74	LEU
17	AQ	91	ARG
17	AQ	98	LEU
18	AR	31	LEU
18	AR	37	VAL
18	AR	38	GLU
18	AR	46	GLU
18	AR	76	LEU
19	AS	12	ASP
19	AS	28	LYS
19	AS	37	ARG

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Mol	Chain	Res	Type
19	AS	65	ASN
19	AS	66	MET
20	AT	8	ARG
20	AT	9	ASN
20	AT	13	LEU
20	AT	24	LEU
20	AT	30	LYS
20	AT	45	GLN
20	AT	54	LYS
20	AT	62	LEU
21	AU	9	ARG
21	AU	10	ARG
21	AU	12	LYS
28	BD	12	SER
28	BD	13	ARG
28	BD	61	LEU
28	BD	88	ARG
28	BD	94	LEU
28	BD	99	ASP
28	BD	103	ARG
28	BD	113	VAL
28	BD	126	GLN
28	BD	138	VAL
28	BD	142	VAL
28	BD	155	LEU
28	BD	211	ARG
28	BD	217	ARG
28	BD	221	VAL
28	BD	229	VAL
28	BD	242	ARG
28	BD	257	LEU
28	BD	259	THR
28	BD	260	ARG
29	BE	1	MET
29	BE	14	ILE
29	BE	24	THR
29	BE	33	VAL
29	BE	49	LEU
29	BE	52	LEU
29	BE	73	GLU
29	BE	75	VAL
29	BE	77	ILE

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Mol	Chain	Res	Type
29	BE	82	ARG
29	BE	97	LYS
29	BE	116	VAL
29	BE	119	ARG
29	BE	144	ARG
29	BE	154	LYS
29	BE	163	GLU
29	BE	175	VAL
29	BE	203	LYS
30	BF	19	GLU
30	BF	24	LEU
30	BF	53	THR
30	BF	57	VAL
30	BF	74	ARG
30	BF	88	VAL
30	BF	106	ARG
30	BF	125	LEU
30	BF	170	LEU
30	BF	192	LEU
30	BF	200	GLU
31	BG	7	LEU
31	BG	43	LEU
31	BG	45	GLU
31	BG	60	LEU
31	BG	81	LYS
31	BG	82	LEU
31	BG	86	MET
31	BG	133	LEU
31	BG	135	LEU
31	BG	140	ILE
31	BG	143	GLU
31	BG	146	TYR
31	BG	148	MET
31	BG	170	ARG
31	BG	175	LEU
32	BH	6	ARG
32	BH	15	VAL
32	BH	33	LEU
32	BH	41	MET
32	BH	44	VAL
32	BH	45	VAL
32	BH	57	ASP

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Mol	Chain	Res	Type
32	BH	59	ARG
32	BH	69	ARG
32	BH	71	LEU
32	BH	86	GLU
32	BH	95	ARG
32	BH	116	GLU
32	BH	119	GLU
32	BH	124	GLU
32	BH	125	VAL
32	BH	129	THR
32	BH	134	SER
33	BI	5	LEU
33	BI	9	LEU
33	BI	10	GLU
33	BI	38	LEU
33	BI	43	ASN
33	BI	47	LEU
33	BI	50	ARG
33	BI	57	ARG
33	BI	60	GLU
33	BI	61	ARG
33	BI	62	LYS
33	BI	66	GLU
33	BI	68	LEU
33	BI	75	LEU
33	BI	77	LEU
33	BI	78	THR
33	BI	85	GLU
33	BI	92	VAL
33	BI	96	ASP
33	BI	101	LEU
33	BI	103	ARG
33	BI	117	GLU
33	BI	140	LEU
33	BI	142	VAL
34	BN	28	THR
34	BN	33	LEU
34	BN	34	LEU
34	BN	46	VAL
34	BN	48	MET
34	BN	58	ASP
34	BN	61	ARG

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Mol	Chain	Res	Type
34	BN	67	LEU
34	BN	73	THR
34	BN	83	LYS
34	BN	87	LEU
34	BN	99	LEU
34	BN	120	LEU
34	BN	133	GLN
34	BN	139	GLU
35	BO	8	LEU
35	BO	23	ARG
35	BO	24	VAL
35	BO	69	ILE
35	BO	92	GLU
35	BO	94	ARG
35	BO	108	GLU
36	BP	1	MET
36	BP	2	LYS
36	BP	55	ARG
36	BP	59	LEU
36	BP	65	ARG
36	BP	70	GLN
36	BP	76	LYS
36	BP	77	ARG
36	BP	83	VAL
36	BP	95	VAL
36	BP	98	GLU
36	BP	106	LEU
36	BP	112	LEU
36	BP	119	GLU
36	BP	126	VAL
36	BP	148	LEU
36	BP	149	GLU
37	BQ	1	MET
37	BQ	5	ARG
37	BQ	7	MET
37	BQ	10	ARG
37	BQ	16	ARG
37	BQ	21	THR
37	BQ	35	VAL
37	BQ	45	GLN
37	BQ	54	MET
37	BQ	56	ARG

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Mol	Chain	Res	Type
37	BQ	59	ARG
37	BQ	60	ARG
37	BQ	75	THR
37	BQ	85	LYS
37	BQ	109	VAL
37	BQ	110	THR
38	BR	1	MET
38	BR	6	SER
38	BR	15	SER
38	BR	18	LEU
38	BR	24	GLN
38	BR	28	LEU
38	BR	29	LEU
38	BR	33	ARG
38	BR	36	THR
38	BR	44	LEU
38	BR	60	LEU
38	BR	65	LEU
38	BR	67	LEU
38	BR	75	LEU
38	BR	79	LEU
38	BR	100	LEU
38	BR	102	GLU
38	BR	111	LEU
38	BR	114	VAL
39	BS	20	ARG
39	BS	57	LYS
39	BS	59	LYS
39	BS	67	ARG
39	BS	83	LYS
39	BS	110	LEU
40	BT	17	THR
40	BT	28	VAL
40	BT	34	VAL
40	BT	49	VAL
40	BT	53	ARG
40	BT	78	LEU
40	BT	96	ARG
40	BT	108	ARG
40	BT	118	ARG
41	BU	8	VAL
41	BU	31	SER

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Mol	Chain	Res	Type
41	BU	36	ARG
41	BU	74	LEU
41	BU	83	LEU
41	BU	92	ARG
41	BU	95	LEU
41	BU	104	GLN
41	BU	117	GLN
42	BV	28	GLU
42	BV	43	GLU
42	BV	46	VAL
42	BV	51	VAL
42	BV	52	VAL
42	BV	61	VAL
42	BV	62	LEU
42	BV	72	VAL
42	BV	79	VAL
42	BV	85	LYS
42	BV	95	LEU
42	BV	100	ARG
43	BW	4	LYS
43	BW	11	ARG
43	BW	15	ARG
43	BW	17	VAL
43	BW	51	LEU
43	BW	67	ASP
43	BW	100	THR
44	BX	35	THR
44	BX	45	THR
44	BX	57	LEU
44	BX	66	LEU
44	BX	72	LYS
44	BX	88	LYS
45	BY	1	MET
45	BY	2	ARG
45	BY	23	ARG
45	BY	34	LYS
45	BY	43	ASN
45	BY	55	TYR
45	BY	72	VAL
45	BY	90	LEU
45	BY	91	GLU
45	BY	99	CYS

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Mol	Chain	Res	Type
46	BZ	5	LEU
46	BZ	19	ARG
46	BZ	40	ASP
46	BZ	72	ARG
46	BZ	86	VAL
46	BZ	91	LEU
46	BZ	120	ILE
46	BZ	136	PHE
46	BZ	153	SER
46	BZ	154	ASP
46	BZ	155	LEU
46	BZ	170	THR
47	B0	20	ARG
47	B0	55	ARG
47	B0	82	ARG
48	B1	21	ARG
48	B1	40	ARG
48	B1	52	ARG
48	B1	59	THR
48	B1	78	LYS
48	B1	95	LEU
48	B1	98	LEU
49	B2	3	LEU
49	B2	28	LYS
49	B2	30	ARG
49	B2	32	LEU
49	B2	45	SER
49	B2	55	ARG
49	B2	64	LEU
49	B2	70	GLN
50	B3	8	LEU
50	B3	23	LEU
50	B3	29	ARG
50	B3	32	GLN
50	B3	55	ARG
51	B4	28	LYS
51	B4	34	GLU
51	B4	46	GLN
51	B4	49	PHE
51	B4	50	VAL
51	B4	53	GLU
51	B4	55	ARG

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Mol	Chain	Res	Type
51	B4	56	VAL
51	B4	58	ARG
51	B4	59	PHE
51	B4	61	ARG
51	B4	63	TYR
51	B4	68	ARG
52	B5	16	ARG
52	B5	29	THR
52	B5	40	LYS
52	B5	55	ARG
52	B5	60	VAL
53	B6	4	GLU
53	B6	6	ARG
53	B6	14	THR
53	B6	28	ARG
53	B6	38	LYS
53	B6	48	VAL
53	B6	52	VAL
54	B7	1	MET
54	B7	24	THR
54	B7	43	THR
55	B8	13	ARG
55	B8	14	VAL
55	B8	31	HIS
55	B8	34	TRP
2	CB	11	LEU
2	CB	16	HIS
2	CB	17	PHE
2	CB	24	TRP
2	CB	35	GLU
2	CB	39	ILE
2	CB	50	GLU
2	CB	55	PHE
2	CB	67	THR
2	CB	71	VAL
2	CB	76	GLN
2	CB	82	ARG
2	CB	87	ARG
2	CB	96	ARG
2	CB	97	TRP
2	CB	98	LEU
2	CB	114	ARG

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Mol	Chain	Res	Type
2	CB	115	LEU
2	CB	117	GLU
2	CB	124	SER
2	CB	126	GLU
2	CB	128	GLU
2	CB	142	LEU
2	CB	144	ARG
2	CB	154	LEU
2	CB	155	LEU
2	CB	157	ARG
2	CB	160	ASP
2	CB	163	PHE
2	CB	185	ILE
2	CB	187	LEU
2	CB	200	ILE
2	CB	209	ARG
2	CB	210	SER
2	CB	217	ARG
2	CB	221	LEU
2	CB	224	GLN
2	CB	230	VAL
3	CC	3	ASN
3	CC	21	ARG
3	CC	35	GLU
3	CC	49	SER
3	CC	70	VAL
3	CC	91	LEU
3	CC	98	ASN
3	CC	101	LEU
3	CC	104	GLN
3	CC	105	GLU
3	CC	118	GLN
3	CC	140	ARG
3	CC	152	ILE
3	CC	179	ARG
3	CC	196	LEU
3	CC	198	VAL
4	CD	10	ARG
4	CD	15	GLU
4	CD	31	CYS
4	CD	34	GLU
4	CD	47	ARG

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Mol	Chain	Res	Type
4	CD	58	LEU
4	CD	61	LYS
4	CD	86	LYS
4	CD	96	LEU
4	CD	108	LEU
4	CD	115	ARG
4	CD	127	THR
4	CD	135	LEU
4	CD	155	LEU
4	CD	157	LEU
4	CD	168	ARG
4	CD	170	VAL
4	CD	181	MET
4	CD	187	ARG
4	CD	188	LEU
4	CD	194	LEU
5	CE	6	PHE
5	CE	10	MET
5	CE	12	LEU
5	CE	27	ARG
5	CE	31	LEU
5	CE	38	GLN
5	CE	41	VAL
5	CE	47	LYS
5	CE	60	TYR
5	CE	67	VAL
5	CE	79	GLU
5	CE	137	GLU
5	CE	150	ARG
6	CF	28	ARG
6	CF	40	VAL
6	CF	41	GLU
6	CF	46	ARG
6	CF	75	LEU
7	CG	9	VAL
7	CG	12	LEU
7	CG	32	ARG
7	CG	33	ASP
7	CG	51	GLN
7	CG	52	GLU
7	CG	72	ARG
7	CG	73	MET

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Mol	Chain	Res	Type
7	CG	76	ARG
7	CG	79	ARG
7	CG	155	ARG
8	CH	21	LYS
8	CH	29	SER
8	CH	39	LEU
8	CH	84	ARG
8	CH	91	ARG
8	CH	98	LYS
8	CH	112	LEU
9	CI	7	THR
9	CI	14	VAL
9	CI	23	ASN
9	CI	50	LEU
9	CI	56	LEU
9	CI	81	ILE
9	CI	89	ASN
9	CI	102	LEU
9	CI	108	VAL
9	CI	112	LYS
9	CI	121	ARG
9	CI	125	TYR
9	CI	128	ARG
10	CJ	7	LYS
10	CJ	19	SER
10	CJ	29	ARG
10	CJ	59	SER
10	CJ	67	THR
10	CJ	81	THR
11	CK	24	SER
11	CK	31	THR
11	CK	48	ILE
11	CK	51	LYS
11	CK	54	ARG
11	CK	96	ARG
11	CK	104	GLN
12	CL	38	THR
12	CL	60	LEU
12	CL	83	VAL
12	CL	116	SER
13	CM	3	ARG
13	CM	15	VAL

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Mol	Chain	Res	Type
13	CM	19	LEU
13	CM	47	ASP
13	CM	49	THR
13	CM	56	LEU
13	CM	84	ILE
13	CM	103	THR
13	CM	104	ARG
13	CM	110	ARG
13	CM	117	VAL
13	CM	121	LYS
14	CN	3	ARG
14	CN	7	ILE
14	CN	12	ARG
14	CN	18	VAL
14	CN	23	ARG
14	CN	26	ARG
14	CN	32	SER
14	CN	33	VAL
15	CO	3	ILE
15	CO	5	LYS
15	CO	7	GLU
15	CO	26	GLU
15	CO	38	ARG
15	CO	39	LEU
15	CO	41	GLU
15	CO	48	LYS
15	CO	54	ARG
16	CP	2	VAL
16	CP	5	ARG
16	CP	27	LYS
16	CP	60	LEU
16	CP	62	VAL
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	19	VAL
17	CQ	36	ILE
17	CQ	60	ILE
17	CQ	63	ARG
17	CQ	74	LEU
17	CQ	96	GLU
18	CR	26	LEU

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Mol	Chain	Res	Type
18	CR	32	ARG
18	CR	35	ARG
18	CR	37	VAL
18	CR	41	LYS
18	CR	46	GLU
18	CR	76	LEU
19	CS	28	LYS
19	CS	37	ARG
19	CS	56	GLN
19	CS	78	ARG
20	CT	24	LEU
20	CT	38	LYS
20	CT	45	GLN
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	90	GLN
21	CU	10	ARG
28	DD	3	VAL
28	DD	13	ARG
28	DD	54	ARG
28	DD	61	LEU
28	DD	88	ARG
28	DD	94	LEU
28	DD	103	ARG
28	DD	106	ILE
28	DD	113	VAL
28	DD	134	ARG
28	DD	142	VAL
28	DD	155	LEU
28	DD	162	SER
28	DD	193	VAL
28	DD	211	ARG
28	DD	217	ARG
28	DD	221	VAL
28	DD	229	VAL
28	DD	257	LEU
28	DD	259	THR
28	DD	260	ARG
28	DD	276	LYS
29	DE	1	MET

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Mol	Chain	Res	Type
29	DE	12	THR
29	DE	21	VAL
29	DE	24	THR
29	DE	33	VAL
29	DE	40	GLU
29	DE	47	VAL
29	DE	52	LEU
29	DE	73	GLU
29	DE	75	VAL
29	DE	79	ARG
29	DE	82	ARG
29	DE	116	VAL
29	DE	119	ARG
29	DE	144	ARG
29	DE	154	LYS
29	DE	163	GLU
29	DE	175	VAL
29	DE	195	LEU
30	DF	19	GLU
30	DF	20	LEU
30	DF	24	LEU
30	DF	28	ILE
30	DF	38	ARG
30	DF	57	VAL
30	DF	74	ARG
30	DF	82	ILE
30	DF	88	VAL
30	DF	106	ARG
30	DF	135	LYS
30	DF	170	LEU
30	DF	192	LEU
30	DF	197	ASP
30	DF	200	GLU
31	DG	16	ARG
31	DG	21	ARG
31	DG	36	LYS
31	DG	43	LEU
31	DG	45	GLU
31	DG	49	ASP
31	DG	58	GLN
31	DG	60	LEU
31	DG	84	LYS

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Mol	Chain	Res	Type
31	DG	98	ARG
31	DG	115	ARG
31	DG	133	LEU
31	DG	135	LEU
31	DG	136	ARG
31	DG	140	ILE
31	DG	143	GLU
31	DG	145	THR
31	DG	148	MET
31	DG	153	ARG
31	DG	170	ARG
32	DH	2	SER
32	DH	3	ARG
32	DH	15	VAL
32	DH	33	LEU
32	DH	43	VAL
32	DH	44	VAL
32	DH	45	VAL
32	DH	57	ASP
32	DH	63	SER
32	DH	69	ARG
32	DH	84	SER
32	DH	86	GLU
32	DH	95	ARG
32	DH	106	THR
32	DH	124	GLU
32	DH	134	SER
32	DH	136	ILE
32	DH	172	LYS
33	DI	5	LEU
33	DI	9	LEU
33	DI	19	VAL
33	DI	40	THR
33	DI	43	ASN
33	DI	44	LEU
33	DI	50	ARG
33	DI	68	LEU
33	DI	73	GLU
33	DI	86	THR
33	DI	92	VAL
33	DI	114	LEU
33	DI	121	LYS

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Mol	Chain	Res	Type
33	DI	123	LEU
33	DI	140	LEU
33	DI	142	VAL
34	DN	33	LEU
34	DN	34	LEU
34	DN	38	HIS
34	DN	46	VAL
34	DN	58	ASP
34	DN	62	VAL
34	DN	85	ILE
34	DN	87	LEU
34	DN	99	LEU
34	DN	120	LEU
34	DN	137	LYS
34	DN	139	GLU
35	DO	8	LEU
35	DO	9	GLU
35	DO	23	ARG
35	DO	24	VAL
35	DO	69	ILE
35	DO	92	GLU
35	DO	94	ARG
36	DP	1	MET
36	DP	29	LYS
36	DP	45	LEU
36	DP	50	ARG
36	DP	55	ARG
36	DP	65	ARG
36	DP	70	GLN
36	DP	95	VAL
36	DP	96	THR
36	DP	99	LEU
36	DP	106	LEU
36	DP	112	LEU
36	DP	119	GLU
36	DP	131	SER
36	DP	148	LEU
37	DQ	1	MET
37	DQ	16	ARG
37	DQ	21	THR
37	DQ	45	GLN
37	DQ	54	MET

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Mol	Chain	Res	Type
37	DQ	56	ARG
37	DQ	59	ARG
37	DQ	60	ARG
37	DQ	65	PHE
37	DQ	75	THR
37	DQ	85	LYS
37	DQ	110	THR
38	DR	1	MET
38	DR	15	SER
38	DR	18	LEU
38	DR	24	GLN
38	DR	28	LEU
38	DR	29	LEU
38	DR	33	ARG
38	DR	36	THR
38	DR	44	LEU
38	DR	60	LEU
38	DR	65	LEU
38	DR	67	LEU
38	DR	75	LEU
38	DR	79	LEU
38	DR	100	LEU
38	DR	102	GLU
38	DR	111	LEU
38	DR	114	VAL
39	DS	20	ARG
39	DS	35	ILE
39	DS	57	LYS
39	DS	69	VAL
39	DS	71	ARG
39	DS	75	GLU
39	DS	93	LYS
39	DS	101	LEU
39	DS	103	GLU
39	DS	110	LEU
40	DT	6	LEU
40	DT	16	ARG
40	DT	17	THR
40	DT	23	ARG
40	DT	49	VAL
40	DT	53	ARG
40	DT	78	LEU

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Mol	Chain	Res	Type
40	DT	96	ARG
40	DT	113	LYS
40	DT	118	ARG
41	DU	8	VAL
41	DU	36	ARG
41	DU	74	LEU
41	DU	83	LEU
41	DU	89	GLU
41	DU	92	ARG
41	DU	104	GLN
41	DU	108	GLU
42	DV	6	LYS
42	DV	15	GLU
42	DV	18	LEU
42	DV	38	LEU
42	DV	46	VAL
42	DV	51	VAL
42	DV	57	VAL
42	DV	61	VAL
42	DV	62	LEU
42	DV	72	VAL
42	DV	79	VAL
42	DV	95	LEU
42	DV	100	ARG
43	DW	11	ARG
43	DW	15	ARG
43	DW	17	VAL
43	DW	51	LEU
43	DW	52	GLU
43	DW	60	ASN
43	DW	100	THR
44	DX	57	LEU
44	DX	70	LEU
44	DX	72	LYS
44	DX	88	LYS
44	DX	90	GLU
44	DX	92	LEU
45	DY	11	ASP
45	DY	23	ARG
45	DY	90	LEU
45	DY	91	GLU
45	DY	99	CYS

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Mol	Chain	Res	Type
45	DY	107	ASP
46	DZ	5	LEU
46	DZ	18	LEU
46	DZ	35	ARG
46	DZ	40	ASP
46	DZ	41	LEU
46	DZ	72	ARG
46	DZ	86	VAL
46	DZ	97	GLU
46	DZ	102	LEU
46	DZ	119	GLU
46	DZ	136	PHE
46	DZ	144	LEU
46	DZ	153	SER
46	DZ	154	ASP
46	DZ	155	LEU
46	DZ	159	PRO
47	D0	10	THR
47	D0	19	LYS
47	D0	20	ARG
47	D0	24	LYS
47	D0	55	ARG
48	D1	4	VAL
48	D1	21	ARG
48	D1	30	VAL
48	D1	40	ARG
48	D1	52	ARG
48	D1	59	THR
48	D1	95	LEU
48	D1	97	LEU
48	D1	98	LEU
49	D2	21	LEU
49	D2	28	LYS
49	D2	30	ARG
49	D2	45	SER
49	D2	55	ARG
49	D2	70	GLN
50	D3	3	ARG
50	D3	8	LEU
50	D3	24	LYS
50	D3	30	ARG
50	D3	44	ARG

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Mol	Chain	Res	Type
50	D3	55	ARG
51	D4	24	THR
51	D4	34	GLU
51	D4	44	THR
51	D4	50	VAL
51	D4	56	VAL
51	D4	58	ARG
51	D4	61	ARG
51	D4	63	TYR
51	D4	67	TYR
51	D4	68	ARG
52	D5	29	THR
52	D5	40	LYS
52	D5	55	ARG
52	D5	60	VAL
53	D6	6	ARG
53	D6	38	LYS
54	D7	1	MET
54	D7	14	LYS
54	D7	23	ARG
55	D8	13	ARG
55	D8	14	VAL
55	D8	34	TRP
56	D9	7	VAL
56	D9	26	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (130) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	16	HIS
2	AB	94	ASN
3	AC	6	HIS
3	AC	28	GLN
3	AC	104	GLN
3	AC	123	GLN
3	AC	136	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	45	GLN
4	AD	77	ASN
4	AD	123	HIS
4	AD	125	HIS

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Mol	Chain	Res	Type
4	AD	161	ASN
5	AE	20	GLN
5	AE	38	GLN
6	AF	94	GLN
6	AF	100	ASN
7	AG	13	GLN
7	AG	28	ASN
9	AI	23	ASN
9	AI	31	GLN
9	AI	34	ASN
9	AI	73	GLN
9	AI	89	ASN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	93	GLN
11	AK	104	GLN
12	AL	78	GLN
12	AL	99	HIS
13	AM	92	HIS
15	AO	9	GLN
15	AO	28	GLN
15	AO	46	HIS
15	AO	71	GLN
16	AP	76	GLN
19	AS	65	ASN
19	AS	69	HIS
19	AS	83	HIS
20	AT	9	ASN
20	AT	90	GLN
28	BD	87	ASN
28	BD	164	GLN
28	BD	166	GLN
28	BD	253	GLN
30	BF	69	HIS
30	BF	169	ASN
30	BF	203	GLN
31	BG	26	GLN
31	BG	40	ASN
33	BI	43	ASN
33	BI	54	GLN
35	BO	5	GLN
36	BP	38	GLN

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Mol	Chain	Res	Type
38	BR	71	GLN
40	BT	43	GLN
40	BT	58	ASN
40	BT	123	GLN
41	BU	94	ASN
44	BX	31	HIS
44	BX	82	GLN
45	BY	6	HIS
45	BY	43	ASN
49	B2	9	GLN
49	B2	70	GLN
51	B4	46	GLN
56	B9	36	GLN
2	CB	40	HIS
2	CB	94	ASN
2	CB	224	GLN
3	CC	6	HIS
3	CC	28	GLN
3	CC	69	HIS
3	CC	104	GLN
3	CC	118	GLN
3	CC	123	GLN
3	CC	136	GLN
4	CD	77	ASN
4	CD	119	GLN
4	CD	123	HIS
4	CD	125	HIS
4	CD	161	ASN
5	CE	20	GLN
5	CE	141	GLN
6	CF	94	GLN
7	CG	28	ASN
7	CG	51	GLN
9	CI	23	ASN
9	CI	31	GLN
9	CI	58	HIS
9	CI	89	ASN
9	CI	124	GLN
10	CJ	62	HIS
11	CK	93	GLN
12	CL	78	GLN
12	CL	99	HIS

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Mol	Chain	Res	Type
13	CM	77	ASN
13	CM	92	HIS
15	CO	28	GLN
15	CO	62	GLN
19	CS	56	GLN
19	CS	57	HIS
19	CS	65	ASN
19	CS	69	HIS
19	CS	83	HIS
28	DD	96	HIS
28	DD	164	GLN
28	DD	166	GLN
28	DD	253	GLN
29	DE	85	ASN
30	DF	69	HIS
30	DF	169	ASN
30	DF	203	GLN
31	DG	26	GLN
31	DG	40	ASN
33	DI	43	ASN
38	DR	71	GLN
39	DS	68	GLN
40	DT	58	ASN
40	DT	123	GLN
41	DU	117	GLN
42	DV	64	HIS
44	DX	31	HIS
44	DX	82	GLN
45	DY	43	ASN
46	DZ	55	HIS
46	DZ	151	HIS
56	D9	20	HIS
56	D9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1521 (98%)	304 (20%)	25 (1%)
1	CA	1501/1521 (98%)	316 (21%)	28 (1%)
22	AV	12/24 (50%)	3 (25%)	0
22	CV	11/24 (45%)	2 (18%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
23	AW	70/76 (92%)	30 (42%)	2 (2%)
23	CW	67/76 (88%)	32 (47%)	2 (2%)
24	AX	75/77 (97%)	16 (21%)	0
24	CX	75/77 (97%)	21 (28%)	0
25	AY	71/76 (93%)	35 (49%)	4 (5%)
25	CY	69/76 (90%)	32 (46%)	1 (1%)
26	BA	2811/2915 (96%)	450 (16%)	34 (1%)
26	DA	2791/2915 (95%)	552 (19%)	30 (1%)
27	BB	119/121 (98%)	14 (11%)	0
27	DB	119/121 (98%)	17 (14%)	0
All	All	9286/9620 (96%)	1824 (19%)	126 (1%)

All (1824) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	7	G
1	AA	9	G
1	AA	22	G
1	AA	29	G
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	59	A
1	AA	61	G
1	AA	65	U
1	AA	73	G
1	AA	77	G
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	96	U
1	AA	97	G
1	AA	98	G
1	AA	101	A
1	AA	111	G
1	AA	112	G
1	AA	116	A
1	AA	121	C
1	AA	131	C

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Mol	Chain	Res	Type
1	AA	146	G
1	AA	155	C
1	AA	163	C
1	AA	166	G
1	AA	173	U
1	AA	174	C
1	AA	180	U
1	AA	182	U
1	AA	189(D)	C
1	AA	189(F)	U
1	AA	189(H)	G
1	AA	189(I)	G
1	AA	189(K)	U
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	221	C
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C
1	AA	279	A
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	342	C
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U

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Mol	Chain	Res	Type
1	AA	372	C
1	AA	373	A
1	AA	382	A
1	AA	384	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	412	A
1	AA	414	A
1	AA	421	U
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	439	A
1	AA	442	C
1	AA	443	C
1	AA	452	A
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	484	G
1	AA	485	G
1	AA	496	A
1	AA	498	U
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	545	C
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	572	A
1	AA	573	A
1	AA	576	G

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Mol	Chain	Res	Type
1	AA	592	G
1	AA	596	C
1	AA	629	G
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	649	G
1	AA	653	A
1	AA	665	A
1	AA	673	G
1	AA	680	C
1	AA	687	A
1	AA	688	G
1	AA	695	A
1	AA	711	G
1	AA	712	A
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	753	A
1	AA	755	G
1	AA	774	G
1	AA	777	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	821	G
1	AA	828	A
1	AA	833	U
1	AA	840	C
1	AA	841	U
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	874	G
1	AA	902	G
1	AA	914	A

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Mol	Chain	Res	Type
1	AA	922	G
1	AA	926	G
1	AA	927	G
1	AA	932	C
1	AA	934	C
1	AA	935	A
1	AA	960	U
1	AA	961	U
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	972	C
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	989	C
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	1000	U
1	AA	1001(A)	G
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	1019	C
1	AA	1021	G
1	AA	1022	G
1	AA	1023	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(B)	C
1	AA	1030(C)	G
1	AA	1030(D)	A

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Mol	Chain	Res	Type
1	AA	1031	G
1	AA	1033	G
1	AA	1037	C
1	AA	1039	C
1	AA	1043	C
1	AA	1044	A
1	AA	1045	C
1	AA	1052	U
1	AA	1054	C
1	AA	1055	A
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1088	G
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1097	C
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1110	A
1	AA	1113	C
1	AA	1124	G
1	AA	1126	U
1	AA	1130	A
1	AA	1132	C
1	AA	1135	U
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1141	C
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1157	A
1	AA	1158	C
1	AA	1159	U

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Mol	Chain	Res	Type
1	AA	1183	A
1	AA	1184	G
1	AA	1196	U
1	AA	1197	G
1	AA	1202	G
1	AA	1212	U
1	AA	1213	A
1	AA	1224	G
1	AA	1227	A
1	AA	1228	C
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1244	C
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1270	C
1	AA	1273	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1281	U
1	AA	1286	A
1	AA	1287	A
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1305	G
1	AA	1314	C
1	AA	1317	C
1	AA	1322	C
1	AA	1338	G
1	AA	1340	A
1	AA	1346	A
1	AA	1347	G
1	AA	1353	G
1	AA	1355	G
1	AA	1360	A
1	AA	1363	C
1	AA	1364	U

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Mol	Chain	Res	Type
1	AA	1370	G
1	AA	1397	C
1	AA	1402	C
1	AA	1419	G
1	AA	1422	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1487	G
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1519	A
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	13	A
22	AV	14	A
22	AV	24	A
23	AW	2	C
23	AW	3	C
23	AW	4	C
23	AW	8	4SU
23	AW	12	U
23	AW	14	A
23	AW	19	G
23	AW	20	U
23	AW	21	A
23	AW	22	G
23	AW	23	A
23	AW	24	G
23	AW	26	A
23	AW	27	G

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Mol	Chain	Res	Type
23	AW	30	G
23	AW	42	C
23	AW	43	C
23	AW	45	U
23	AW	46	7MG
23	AW	47	U
23	AW	48	C
23	AW	49	C
23	AW	52	G
23	AW	53	G
23	AW	59	U
23	AW	61	C
23	AW	68	C
23	AW	70	G
23	AW	73	A
23	AW	74	C
24	AX	3	C
24	AX	9	G
24	AX	13	C
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	31	G
24	AX	42	G
24	AX	48	C
24	AX	56	C
24	AX	59	A
24	AX	63	G
24	AX	67	C
24	AX	68	C
24	AX	70	G
24	AX	76	A
25	AY	2	C
25	AY	5	G
25	AY	9	A
25	AY	11	C
25	AY	13	C
25	AY	15	G
25	AY	19	G
25	AY	20	U
25	AY	21	A
25	AY	22	G

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Mol	Chain	Res	Type
25	AY	26	A
25	AY	29	G
25	AY	30	G
25	AY	33	U
25	AY	34	G
25	AY	35	A
25	AY	36	A
25	AY	39	PSU
25	AY	41	C
25	AY	44	G
25	AY	45	U
25	AY	46	7MG
25	AY	47	U
25	AY	48	C
25	AY	49	C
25	AY	54	5MU
25	AY	57	G
25	AY	58	A
25	AY	59	U
25	AY	60	U
25	AY	62	C
25	AY	65	G
25	AY	67	C
25	AY	70	G
25	AY	73	A
26	BA	12	U
26	BA	34	C
26	BA	36	G
26	BA	45	C
26	BA	63	A
26	BA	70	A
26	BA	71	U
26	BA	73	A
26	BA	74	G
26	BA	83	A
26	BA	94	G
26	BA	98	U
26	BA	99	G
26	BA	100	G
26	BA	116	A
26	BA	117	A
26	BA	118	U

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Mol	Chain	Res	Type
26	BA	151	C
26	BA	155	C
26	BA	161	C
26	BA	170	A
26	BA	171	A
26	BA	177	G
26	BA	185	A
26	BA	186	A
26	BA	188	A
26	BA	194	G
26	BA	204	G
26	BA	205	A
26	BA	210	A
26	BA	211	A
26	BA	212	A
26	BA	218	A
26	BA	222	A
26	BA	237	G
26	BA	265	U
26	BA	269	G
26	BA	271	U
26	BA	272	U
26	BA	273	G
26	BA	274	U
26	BA	279	G
26	BA	288	U
26	BA	289	G
26	BA	294	C
26	BA	296	U
26	BA	303	C
26	BA	306	A
26	BA	307	A
26	BA	335	A
26	BA	353	G
26	BA	354	A
26	BA	376	G
26	BA	387	G
26	BA	389	G
26	BA	399	G
26	BA	407	U
26	BA	413	G
26	BA	423	G

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Mol	Chain	Res	Type
26	BA	432	U
26	BA	438	G
26	BA	455	A
26	BA	469	A
26	BA	470	C
26	BA	474	U
26	BA	480	A
26	BA	482	C
26	BA	496	A
26	BA	505	A
26	BA	507	G
26	BA	529	U
26	BA	530	A
26	BA	534	C
26	BA	553	A
26	BA	554	A
26	BA	555	G
26	BA	556	C
26	BA	557	A
26	BA	558	G
26	BA	569	G
26	BA	573	G
26	BA	586	G
26	BA	596	G
26	BA	598	A
26	BA	615	G
26	BA	626	A
26	BA	627	G
26	BA	630	U
26	BA	638	U
26	BA	639	G
26	BA	641	G
26	BA	642	G
26	BA	652	A
26	BA	662	A
26	BA	670	C
26	BA	671	A
26	BA	694	G
26	BA	697	C
26	BA	698	G
26	BA	716	G
26	BA	724	A

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Mol	Chain	Res	Type
26	BA	733	G
26	BA	777	C
26	BA	779	C
26	BA	811	A
26	BA	812	G
26	BA	822	G
26	BA	823	G
26	BA	829	A
26	BA	831	A
26	BA	832	G
26	BA	839	G
26	BA	852	G
26	BA	859	C
26	BA	866	A
26	BA	871	A
26	BA	874	U
26	BA	875	U
26	BA	877	G
26	BA	902	G
26	BA	906	G
26	BA	909	G
26	BA	913	A
26	BA	924	U
26	BA	926	G
26	BA	927	G
26	BA	929	G
26	BA	931	C
26	BA	932	C
26	BA	933	C
26	BA	934	A
26	BA	935	C
26	BA	936	C
26	BA	937	A
26	BA	938	G
26	BA	939	C
26	BA	940	C
26	BA	941	U
26	BA	942	A
26	BA	943	C
26	BA	944	C
26	BA	945	A
26	BA	946	A

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Mol	Chain	Res	Type
26	BA	947	A
26	BA	953	U
26	BA	956	A
26	BA	977	G
26	BA	986	A
26	BA	990	A
26	BA	991	G
26	BA	1003	U
26	BA	1004	A
26	BA	1006	C
26	BA	1019	G
26	BA	1020	C
26	BA	1029	A
26	BA	1042	A
26	BA	1058	U
26	BA	1059	C
26	BA	1068	G
26	BA	1079	U
26	BA	1084	C
26	BA	1087	C
26	BA	1091	A
26	BA	1092	A
26	BA	1093	G
26	BA	1094	A
26	BA	1097	G
26	BA	1153	G
26	BA	1154	U
26	BA	1156	G
26	BA	1158	G
26	BA	1174	A
26	BA	1176	U
26	BA	1180	C
26	BA	1181	G
26	BA	1216	G
26	BA	1217	G
26	BA	1218	G
26	BA	1219	A
26	BA	1220	U
26	BA	1221	G
26	BA	1222	A
26	BA	1223	C
26	BA	1255	A

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Mol	Chain	Res	Type
26	BA	1256	U
26	BA	1265	A
26	BA	1290	G
26	BA	1294	G
26	BA	1299	A
26	BA	1302	G
26	BA	1317	G
26	BA	1318	A
26	BA	1319	U
26	BA	1335	C
26	BA	1346	U
26	BA	1347	A
26	BA	1349	G
26	BA	1360	C
26	BA	1365	G
26	BA	1398	U
26	BA	1405	A
26	BA	1406	A
26	BA	1411	A
26	BA	1416	C
26	BA	1426	G
26	BA	1430	A
26	BA	1431	G
26	BA	1462	G
26	BA	1463	C
26	BA	1466	U
26	BA	1467	G
26	BA	1474	C
26	BA	1491	A
26	BA	1496	A
26	BA	1497	G
26	BA	1506	G
26	BA	1514	C
26	BA	1518	A
26	BA	1525	G
26	BA	1529	G
26	BA	1530	G
26	BA	1539	C
26	BA	1553	A
26	BA	1554	A
26	BA	1555	C
26	BA	1556	A

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Mol	Chain	Res	Type
26	BA	1578	C
26	BA	1585	G
26	BA	1590	C
26	BA	1605	A
26	BA	1613	A
26	BA	1616	A
26	BA	1625	U
26	BA	1627	A
26	BA	1628	G
26	BA	1631	C
26	BA	1632	A
26	BA	1654	A
26	BA	1656	A
26	BA	1695	C
26	BA	1701	A
26	BA	1711	A
26	BA	1721	G
26	BA	1741	C
26	BA	1747	A
26	BA	1748	A
26	BA	1750	G
26	BA	1767	A
26	BA	1768	U
26	BA	1776	G
26	BA	1779	G
26	BA	1787	G
26	BA	1790	A
26	BA	1793	A
26	BA	1794	G
26	BA	1795	G
26	BA	1804	A
26	BA	1811	A
26	BA	1813	C
26	BA	1817	A
26	BA	1822	A
26	BA	1831	C
26	BA	1847	G
26	BA	1870	G
26	BA	1878	A
26	BA	1879	A
26	BA	1892	G
26	BA	1899	A

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Mol	Chain	Res	Type
26	BA	1900	G
26	BA	1908	C
26	BA	1911	A
26	BA	1922	A
26	BA	1928	G
26	BA	1937	U
26	BA	1941	A
26	BA	1946	C
26	BA	1949	A
26	BA	1951	G
26	BA	1952	G
26	BA	1959	A
26	BA	1960	A
26	BA	1977	U
26	BA	1985	U
26	BA	1989	C
26	BA	1992	A
26	BA	1993	A
26	BA	1994	A
26	BA	2014	G
26	BA	2015	U
26	BA	2019	G
26	BA	2042	A
26	BA	2045	G
26	BA	2053	A
26	BA	2054	G
26	BA	2055	A
26	BA	2065	C
26	BA	2077	C
26	BA	2078	G
26	BA	2082	A
26	BA	2083	G
26	BA	2084	A
26	BA	2091	G
26	BA	2120	U
26	BA	2124	U
26	BA	2132	G
26	BA	2133	C
26	BA	2141	A
26	BA	2142	G
26	BA	2143	G
26	BA	2147	G

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Mol	Chain	Res	Type
26	BA	2148	A
26	BA	2149	G
26	BA	2150	C
26	BA	2151	C
26	BA	2154	U
26	BA	2155	G
26	BA	2156	A
26	BA	2157	A
26	BA	2158	C
26	BA	2160	C
26	BA	2162	C
26	BA	2163	G
26	BA	2164	C
26	BA	2165	C
26	BA	2167	C
26	BA	2168	C
26	BA	2169	G
26	BA	2171	G
26	BA	2179	G
26	BA	2180	A
26	BA	2181	G
26	BA	2182	G
26	BA	2187	G
26	BA	2189	U
26	BA	2190	G
26	BA	2191	A
26	BA	2193	A
26	BA	2194	U
26	BA	2195	A
26	BA	2196	C
26	BA	2200	C
26	BA	2203	G
26	BA	2204	G
26	BA	2206	G
26	BA	2210	C
26	BA	2211	U
26	BA	2214	G
26	BA	2220	A
26	BA	2221	A
26	BA	2227	G
26	BA	2228	G
26	BA	2229	A

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Mol	Chain	Res	Type
26	BA	2230	U
26	BA	2237	A
26	BA	2250	G
26	BA	2251	G
26	BA	2280	A
26	BA	2281	A
26	BA	2287	C
26	BA	2295	C
26	BA	2299	A
26	BA	2301	G
26	BA	2317	A
26	BA	2320	G
26	BA	2332	A
26	BA	2337	G
26	BA	2346	G
26	BA	2348	A
26	BA	2355	C
26	BA	2359	C
26	BA	2362	C
26	BA	2373	A
26	BA	2395	G
26	BA	2397	C
26	BA	2405	A
26	BA	2412	G
26	BA	2418	U
26	BA	2426	G
26	BA	2431	U
26	BA	2437	A
26	BA	2441	G
26	BA	2442	A
26	BA	2447	A
26	BA	2451	A
26	BA	2453	C
26	BA	2460	A
26	BA	2476	C
26	BA	2480	G
26	BA	2481	A
26	BA	2483	C
26	BA	2486	C
26	BA	2488	A
26	BA	2499	G
26	BA	2502	G

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Mol	Chain	Res	Type
26	BA	2514	G
26	BA	2517	G
26	BA	2530	A
26	BA	2541	G
26	BA	2547	G
26	BA	2561	G
26	BA	2566	U
26	BA	2578	A
26	BA	2579	G
26	BA	2585	C
26	BA	2586	G
26	BA	2614	A
26	BA	2621	U
26	BA	2623	U
26	BA	2624	C
26	BA	2641	A
26	BA	2642	G
26	BA	2666	A
26	BA	2681	G
26	BA	2701	U
26	BA	2702	C
26	BA	2703	C
26	BA	2714	U
26	BA	2725	A
26	BA	2726	A
26	BA	2739	U
26	BA	2746	A
26	BA	2770	A
26	BA	2771	A
26	BA	2774	G
26	BA	2777	A
26	BA	2778	A
26	BA	2779	G
26	BA	2791	A
26	BA	2803	A
26	BA	2804	C
26	BA	2805	G
26	BA	2806	G
26	BA	2813	G
26	BA	2816	G
26	BA	2818	U
26	BA	2828	G

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Mol	Chain	Res	Type
26	BA	2830	A
26	BA	2831	A
26	BA	2843	G
26	BA	2844	G
26	BA	2845	A
26	BA	2882	G
26	BA	2883	A
26	BA	2886	G
26	BA	2890	C
26	BA	2892	A
26	BA	2893	A
26	BA	2901	A
26	BA	2903	G
27	BB	2	C
27	BB	7	G
27	BB	34	U
27	BB	42	C
27	BB	56	G
27	BB	73	A
27	BB	75	G
27	BB	85	G
27	BB	93	G
27	BB	106	G
27	BB	110	G
27	BB	111	G
27	BB	112	U
27	BB	120	A
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	13	U
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	65	U

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Mol	Chain	Res	Type
1	CA	66	G
1	CA	77	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	100	C
1	CA	101	A
1	CA	111	G
1	CA	112	G
1	CA	116	A
1	CA	121	C
1	CA	131	C
1	CA	146	G
1	CA	155	C
1	CA	163	C
1	CA	166	G
1	CA	173	U
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(D)	C
1	CA	189(K)	U
1	CA	190	U
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	202	U
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	221	C
1	CA	247	G
1	CA	251	G
1	CA	258	G
1	CA	266	G
1	CA	267	C
1	CA	279	A

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Mol	Chain	Res	Type
1	CA	289	G
1	CA	301	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	342	C
1	CA	344	A
1	CA	346	G
1	CA	350	G
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	382	A
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	412	A
1	CA	413	G
1	CA	414	A
1	CA	421	U
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	439	A
1	CA	442	C
1	CA	443	C
1	CA	452	A
1	CA	461	A
1	CA	471	G
1	CA	484	G
1	CA	485	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A
1	CA	510	A
1	CA	511	C

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Mol	Chain	Res	Type
1	CA	513	C
1	CA	518	C
1	CA	521	G
1	CA	528	C
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	545	C
1	CA	547	A
1	CA	559	A
1	CA	561	U
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	592	G
1	CA	596	C
1	CA	629	G
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	649	G
1	CA	650	G
1	CA	653	A
1	CA	664	G
1	CA	665	A
1	CA	673	G
1	CA	680	C
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	695	A
1	CA	711	G
1	CA	712	A
1	CA	721	G
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	749	C
1	CA	753	A
1	CA	755	G
1	CA	774	G
1	CA	777	A

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Mol	Chain	Res	Type
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	815	A
1	CA	817	C
1	CA	821	G
1	CA	828	A
1	CA	833	U
1	CA	840	C
1	CA	841	U
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	874	G
1	CA	902	G
1	CA	914	A
1	CA	926	G
1	CA	927	G
1	CA	932	C
1	CA	934	C
1	CA	935	A
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	972	C
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	996	A
1	CA	997	U
1	CA	1000	U
1	CA	1001(A)	G
1	CA	1002	G
1	CA	1003	G
1	CA	1004	A
1	CA	1005	A

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Mol	Chain	Res	Type
1	CA	1006	C
1	CA	1009	G
1	CA	1019	C
1	CA	1021	G
1	CA	1022	G
1	CA	1023	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1030(D)	A
1	CA	1031	G
1	CA	1032	G
1	CA	1037	C
1	CA	1039	C
1	CA	1041	A
1	CA	1043	C
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1088	G
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1097	C
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1109	C
1	CA	1110	A
1	CA	1113	C
1	CA	1117	G
1	CA	1124	G

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Mol	Chain	Res	Type
1	CA	1125	U
1	CA	1126	U
1	CA	1129	C
1	CA	1130	A
1	CA	1131	G
1	CA	1132	C
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1141	C
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1157	A
1	CA	1158	C
1	CA	1159	U
1	CA	1183	A
1	CA	1184	G
1	CA	1196	U
1	CA	1197	G
1	CA	1202	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1224	G
1	CA	1227	A
1	CA	1228	C
1	CA	1236	A
1	CA	1238	A
1	CA	1240	U
1	CA	1244	C
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1262	C
1	CA	1270	C
1	CA	1273	G

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Mol	Chain	Res	Type
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1286	A
1	CA	1287	A
1	CA	1299	A
1	CA	1300	G
1	CA	1305	G
1	CA	1314	C
1	CA	1317	C
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	1355	G
1	CA	1363	C
1	CA	1364	U
1	CA	1370	G
1	CA	1397	C
1	CA	1402	C
1	CA	1419	G
1	CA	1422	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1446	U
1	CA	1447	A
1	CA	1452	C
1	CA	1456	G
1	CA	1487	G
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G
1	CA	1497	G
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U

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Mol	Chain	Res	Type
1	CA	1517	G
1	CA	1519	A
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	14	A
22	CV	24	A
23	CW	3	C
23	CW	4	C
23	CW	5	G
23	CW	6	G
23	CW	8	4SU
23	CW	9	A
23	CW	12	U
23	CW	14	A
23	CW	19	G
23	CW	22	G
23	CW	23	A
23	CW	25	C
23	CW	26	A
23	CW	27	G
23	CW	30	G
23	CW	42	C
23	CW	43	C
23	CW	45	U
23	CW	46	7MG
23	CW	47	U
23	CW	48	C
23	CW	49	C
23	CW	52	G
23	CW	53	G
23	CW	61	C
23	CW	62	C
23	CW	64	A
23	CW	66	U
23	CW	67	C
23	CW	68	C
23	CW	70	G
23	CW	74	C
24	CX	8	4SU

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Mol	Chain	Res	Type
24	CX	9	G
24	CX	13	C
24	CX	16	C
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	31	G
24	CX	42	G
24	CX	47	U
24	CX	48	C
24	CX	50	U
24	CX	52	G
24	CX	56	C
24	CX	59	A
24	CX	60	U
24	CX	61	C
24	CX	63	G
24	CX	67	C
24	CX	68	C
24	CX	76	A
25	CY	2	C
25	CY	8	4SU
25	CY	9	A
25	CY	11	C
25	CY	13	C
25	CY	15	G
25	CY	19	G
25	CY	23	A
25	CY	27	G
25	CY	29	G
25	CY	30	G
25	CY	33	U
25	CY	34	G
25	CY	35	A
25	CY	36	A
25	CY	39	PSU
25	CY	41	C
25	CY	45	U
25	CY	46	7MG
25	CY	47	U
25	CY	49	C
25	CY	52	G

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Mol	Chain	Res	Type
25	CY	54	5MU
25	CY	56	C
25	CY	57	G
25	CY	58	A
25	CY	59	U
25	CY	62	C
25	CY	65	G
25	CY	67	C
25	CY	70	G
25	CY	73	A
26	DA	10	G
26	DA	12	U
26	DA	15	G
26	DA	16	G
26	DA	34	C
26	DA	35	G
26	DA	45	C
26	DA	51	G
26	DA	61	G
26	DA	71	A
26	DA	74	A
26	DA	75	G
26	DA	78	A
26	DA	83	G
26	DA	84	A
26	DA	90	U
26	DA	95	G
26	DA	100	G
26	DA	102	G
26	DA	118	A
26	DA	119	A
26	DA	120	U
26	DA	141	A
26	DA	154(A)	C
26	DA	157	U
26	DA	173	G
26	DA	181	A
26	DA	182	A
26	DA	196	A
26	DA	199	A
26	DA	205	G
26	DA	214	G

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Mol	Chain	Res	Type
26	DA	215	G
26	DA	216	A
26	DA	221	A
26	DA	222	A
26	DA	225	A
26	DA	228	A
26	DA	229	A
26	DA	233	A
26	DA	248	G
26	DA	266	G
26	DA	271(I)	G
26	DA	271(K)	U
26	DA	271(L)	U
26	DA	271(M)	G
26	DA	271(N)	U
26	DA	271(V)	G
26	DA	271(W)	G
26	DA	272(A)	U
26	DA	272(B)	G
26	DA	272(C)	G
26	DA	272(J)	C
26	DA	274	G
26	DA	277	C
26	DA	278	A
26	DA	285	C
26	DA	288	C
26	DA	292	C
26	DA	294	A
26	DA	311	A
26	DA	324	A
26	DA	327	G
26	DA	329	G
26	DA	330	A
26	DA	333	G
26	DA	352	G
26	DA	363	G
26	DA	372	G
26	DA	386	G
26	DA	389	G
26	DA	396	G
26	DA	399	G
26	DA	405	U

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Mol	Chain	Res	Type
26	DA	407	G
26	DA	411	G
26	DA	412	A
26	DA	415	A
26	DA	421	U
26	DA	428	A
26	DA	442	G
26	DA	443	A
26	DA	444	C
26	DA	447	A
26	DA	454	A
26	DA	455	C
26	DA	457	A
26	DA	470	A
26	DA	481	G
26	DA	485	C
26	DA	494	G
26	DA	498	G
26	DA	504	U
26	DA	505	A
26	DA	509	C
26	DA	521	G
26	DA	530	G
26	DA	531	C
26	DA	532	A
26	DA	533	G
26	DA	545	G
26	DA	563	G
26	DA	568	U
26	DA	573	G
26	DA	574	C
26	DA	575	A
26	DA	586	A
26	DA	587	C
26	DA	588	U
26	DA	592	G
26	DA	603	A
26	DA	604	G
26	DA	607	U
26	DA	614(B)	G
26	DA	614(C)	A
26	DA	615	G

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Mol	Chain	Res	Type
26	DA	616	G
26	DA	620	G
26	DA	627	A
26	DA	637	A
26	DA	645	C
26	DA	646	A
26	DA	652(B)	A
26	DA	652(C)	G
26	DA	652(D)	C
26	DA	652(U)	G
26	DA	656	G
26	DA	668	G
26	DA	669	G
26	DA	686	G
26	DA	698	C
26	DA	699	A
26	DA	715	G
26	DA	726	G
26	DA	730	C
26	DA	752	A
26	DA	753	C
26	DA	765	G
26	DA	775	G
26	DA	776	G
26	DA	782	A
26	DA	783	A
26	DA	784	A
26	DA	785	G
26	DA	790	C
26	DA	792	G
26	DA	794	G
26	DA	803	U
26	DA	805	G
26	DA	812	C
26	DA	819	A
26	DA	827	U
26	DA	851	U
26	DA	852	G
26	DA	854	G
26	DA	857	C
26	DA	859	G
26	DA	866	A

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Mol	Chain	Res	Type
26	DA	868	U
26	DA	874	G
26	DA	879	G
26	DA	880	G
26	DA	882	G
26	DA	884	C
26	DA	886	C
26	DA	887	A
26	DA	888	C
26	DA	889	C
26	DA	890	A
26	DA	893	C
26	DA	896	A
26	DA	897	C
26	DA	898	C
26	DA	900	A
26	DA	901	A
26	DA	903	C
26	DA	910	A
26	DA	917	A
26	DA	932	G
26	DA	938	G
26	DA	941	A
26	DA	945	A
26	DA	946	G
26	DA	950	G
26	DA	952	G
26	DA	953	A
26	DA	958	U
26	DA	959	A
26	DA	961	C
26	DA	974	G
26	DA	975	C
26	DA	983	A
26	DA	996	A
26	DA	1005	C
26	DA	1006	C
26	DA	1012	U
26	DA	1013	C
26	DA	1017	G
26	DA	1022	G
26	DA	1025	G

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Mol	Chain	Res	Type
26	DA	1026	U
26	DA	1033	U
26	DA	1034	G
26	DA	1038	C
26	DA	1039	G
26	DA	1042	G
26	DA	1043	C
26	DA	1114	G
26	DA	1118	C
26	DA	1126	A
26	DA	1128	A
26	DA	1130	U
26	DA	1135	C
26	DA	1136	G
26	DA	1139	G
26	DA	1142(A)	A
26	DA	1144	G
26	DA	1171	G
26	DA	1180	C
26	DA	1196	C
26	DA	1205	U
26	DA	1210	A
26	DA	1211	U
26	DA	1220	A
26	DA	1221	C
26	DA	1229	G
26	DA	1242	A
26	DA	1247	A
26	DA	1253	A
26	DA	1256	G
26	DA	1271	G
26	DA	1272	A
26	DA	1273	U
26	DA	1287	A
26	DA	1300	U
26	DA	1301	A
26	DA	1303	G
26	DA	1305	C
26	DA	1314	C
26	DA	1332	G
26	DA	1352	U
26	DA	1359	A

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Mol	Chain	Res	Type
26	DA	1360	A
26	DA	1365	A
26	DA	1368	G
26	DA	1370	C
26	DA	1380	G
26	DA	1384	A
26	DA	1385	G
26	DA	1412	A
26	DA	1416	G
26	DA	1417	C
26	DA	1419	A
26	DA	1420	U
26	DA	1421	G
26	DA	1428	C
26	DA	1437	C
26	DA	1445	A
26	DA	1445(A)	C
26	DA	1449	A
26	DA	1450	G
26	DA	1459	G
26	DA	1467	C
26	DA	1471	A
26	DA	1482	G
26	DA	1490	A
26	DA	1493	C
26	DA	1494	A
26	DA	1495	A
26	DA	1496	A
26	DA	1497	U
26	DA	1508	A
26	DA	1509	C
26	DA	1509(A)	A
26	DA	1523	U
26	DA	1525	G
26	DA	1531	C
26	DA	1541	G
26	DA	1542	A
26	DA	1543	C
26	DA	1547	C
26	DA	1554	A
26	DA	1558	A
26	DA	1559	G

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Mol	Chain	Res	Type
26	DA	1566	A
26	DA	1569	A
26	DA	1578	U
26	DA	1580	A
26	DA	1583	A
26	DA	1584	C
26	DA	1586	A
26	DA	1595	G
26	DA	1598	C
26	DA	1608	A
26	DA	1609	A
26	DA	1610	A
26	DA	1612	C
26	DA	1639	U
26	DA	1640	C
26	DA	1647	G
26	DA	1648	C
26	DA	1654	A
26	DA	1674	G
26	DA	1696	G
26	DA	1700	A
26	DA	1703	G
26	DA	1721	G
26	DA	1722	A
26	DA	1740	G
26	DA	1756	G
26	DA	1758	G
26	DA	1763	G
26	DA	1764	G
26	DA	1773	A
26	DA	1780	A
26	DA	1782	C
26	DA	1791	A
26	DA	1800	C
26	DA	1801	G
26	DA	1812	A
26	DA	1816	G
26	DA	1835	G
26	DA	1836	C
26	DA	1847	A
26	DA	1848	A
26	DA	1866	C

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Mol	Chain	Res	Type
26	DA	1877	A
26	DA	1887	C
26	DA	1889	A
26	DA	1895	C
26	DA	1900	A
26	DA	1906	G
26	DA	1914	C
26	DA	1929	G
26	DA	1930	G
26	DA	1931	U
26	DA	1936	A
26	DA	1937	A
26	DA	1938	A
26	DA	1955	U
26	DA	1963	U
26	DA	1964	G
26	DA	1967	C
26	DA	1970	A
26	DA	1971	A
26	DA	1972	A
26	DA	1993	U
26	DA	1997	G
26	DA	2020	A
26	DA	2023	G
26	DA	2031	A
26	DA	2032	G
26	DA	2033	A
26	DA	2043	C
26	DA	2046	G
26	DA	2055	C
26	DA	2056	G
26	DA	2060	A
26	DA	2061	G
26	DA	2062	A
26	DA	2069	G
26	DA	2082	A
26	DA	2093	G
26	DA	2095	C
26	DA	2096	U
26	DA	2099	U
26	DA	2101	G
26	DA	2102	U

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Mol	Chain	Res	Type
26	DA	2103	C
26	DA	2104	G
26	DA	2105	C
26	DA	2108	C
26	DA	2111	C
26	DA	2112	G
26	DA	2113	U
26	DA	2115	G
26	DA	2116	G
26	DA	2117	A
26	DA	2119	A
26	DA	2122	U
26	DA	2124	G
26	DA	2125	G
26	DA	2126	A
26	DA	2127	G
26	DA	2129	C
26	DA	2130	U
26	DA	2131	G
26	DA	2132	U
26	DA	2133	G
26	DA	2134	A
26	DA	2135	A
26	DA	2136	C
26	DA	2137	C
26	DA	2138	C
26	DA	2139	C
26	DA	2143	C
26	DA	2145	C
26	DA	2146	C
26	DA	2148	G
26	DA	2150	U
26	DA	2151	G
26	DA	2153	G
26	DA	2154	G
26	DA	2155	G
26	DA	2157	G
26	DA	2158	A
26	DA	2159	G
26	DA	2160	G
26	DA	2163	C
26	DA	2164	C

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Mol	Chain	Res	Type
26	DA	2165	G
26	DA	2167	U
26	DA	2168	G
26	DA	2169	A
26	DA	2170	A
26	DA	2172	U
26	DA	2173	A
26	DA	2174	C
26	DA	2177	C
26	DA	2178	C
26	DA	2181	G
26	DA	2184	G
26	DA	2185	C
26	DA	2186	G
26	DA	2189	U
26	DA	2192	G
26	DA	2193	G
26	DA	2198	A
26	DA	2206	G
26	DA	2207	G
26	DA	2208	A
26	DA	2218	U
26	DA	2219	G
26	DA	2225	A
26	DA	2235	G
26	DA	2238	G
26	DA	2239	G
26	DA	2259	G
26	DA	2273	A
26	DA	2275	C
26	DA	2278	A
26	DA	2280	G
26	DA	2283	C
26	DA	2287	A
26	DA	2288	A
26	DA	2294	C
26	DA	2299	G
26	DA	2302	G
26	DA	2303	G
26	DA	2305	A
26	DA	2308	G
26	DA	2312	U

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Mol	Chain	Res	Type
26	DA	2318	G
26	DA	2319	G
26	DA	2320	A
26	DA	2321	G
26	DA	2325	G
26	DA	2327	A
26	DA	2328	A
26	DA	2334	G
26	DA	2336	A
26	DA	2339	G
26	DA	2343	C
26	DA	2347	C
26	DA	2350	C
26	DA	2354	G
26	DA	2366	A
26	DA	2376	A
26	DA	2383	G
26	DA	2385	C
26	DA	2388	A
26	DA	2400	G
26	DA	2406	U
26	DA	2410	G
26	DA	2422	A
26	DA	2425	A
26	DA	2429	G
26	DA	2430	A
26	DA	2435	A
26	DA	2439	A
26	DA	2441	C
26	DA	2445	G
26	DA	2448	A
26	DA	2465	C
26	DA	2468	G
26	DA	2469	A
26	DA	2474	C
26	DA	2476	A
26	DA	2478	A
26	DA	2490	G
26	DA	2494	G
26	DA	2497	A
26	DA	2502	G
26	DA	2505	G

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Mol	Chain	Res	Type
26	DA	2506	U
26	DA	2518	A
26	DA	2529	G
26	DA	2549	G
26	DA	2554	U
26	DA	2555	U
26	DA	2566	A
26	DA	2567	G
26	DA	2573	C
26	DA	2586	C
26	DA	2602	A
26	DA	2603	G
26	DA	2609	U
26	DA	2611	U
26	DA	2612	C
26	DA	2615	U
26	DA	2629	A
26	DA	2630	G
26	DA	2652	C
26	DA	2654	A
26	DA	2663	G
26	DA	2669	G
26	DA	2689	U
26	DA	2690	C
26	DA	2691	C
26	DA	2703	C
26	DA	2712(A)	A
26	DA	2713	A
26	DA	2714	G
26	DA	2726	U
26	DA	2733	A
26	DA	2734	A
26	DA	2751	G
26	DA	2757	A
26	DA	2758	A
26	DA	2760	C
26	DA	2764	A
26	DA	2765	A
26	DA	2766	G
26	DA	2778	A
26	DA	2784	C
26	DA	2793	G

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Mol	Chain	Res	Type
26	DA	2794	C
26	DA	2809	A
26	DA	2818	G
26	DA	2820	A
26	DA	2821	A
26	DA	2833	G
26	DA	2834	G
26	DA	2835	A
26	DA	2872	G
26	DA	2873	A
26	DA	2879	C
26	DA	2880	C
26	DA	2892	A
26	DA	2894	G
26	DA	2895	U
26	DA	2897	U
27	DB	2	C
27	DB	7	G
27	DB	8	U
27	DB	34	U
27	DB	42	C
27	DB	56	G
27	DB	73	A
27	DB	75	G
27	DB	85	G
27	DB	90	A
27	DB	93	G
27	DB	106	G
27	DB	108	U
27	DB	110	G
27	DB	111	G
27	DB	112	U
27	DB	120	A

All (126) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	96	U
1	AA	115	G
1	AA	266	G
1	AA	347	G
1	AA	429	U

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Mol	Chain	Res	Type
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	793	U
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1026	G
1	AA	1054	C
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1181	G
1	AA	1201	A
1	AA	1256	A
1	AA	1285	A
1	AA	1442	G
1	AA	1492	A
23	AW	13	C
23	AW	22	G
25	AY	19	G
25	AY	21	A
25	AY	25	C
25	AY	58	A
26	BA	70	A
26	BA	185	A
26	BA	270	C
26	BA	271	U
26	BA	273	G
26	BA	302	A
26	BA	793	A
26	BA	811	A
26	BA	821	A
26	BA	945	A
26	BA	1019	G
26	BA	1093	G
26	BA	1188	A
26	BA	1219	A
26	BA	1220	U
26	BA	1221	G

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Mol	Chain	Res	Type
26	BA	1255	A
26	BA	1346	U
26	BA	1347	A
26	BA	1425	A
26	BA	1466	U
26	BA	1577	C
26	BA	1700	G
26	BA	2014	G
26	BA	2132	G
26	BA	2148	A
26	BA	2203	G
26	BA	2205	C
26	BA	2209	G
26	BA	2418	U
26	BA	2442	A
26	BA	2701	U
26	BA	2769	U
26	BA	2902	G
1	CA	60	A
1	CA	65	U
1	CA	115	G
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	687	A
1	CA	748	C
1	CA	840	C
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1027	C
1	CA	1054	C
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1181	G
1	CA	1183	A
1	CA	1201	A
1	CA	1212	U

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Mol	Chain	Res	Type
1	CA	1256	A
1	CA	1299	A
1	CA	1442	G
1	CA	1492	A
23	CW	4	C
23	CW	13	C
25	CY	46	7MG
26	DA	271(K)	U
26	DA	271(M)	G
26	DA	277	C
26	DA	587	C
26	DA	752	A
26	DA	764	A
26	DA	774	A
26	DA	827	U
26	DA	856	C
26	DA	900	A
26	DA	1210	A
26	DA	1300	U
26	DA	1379	A
26	DA	1420	U
26	DA	1427	A
26	DA	1493	C
26	DA	1530	C
26	DA	1558	A
26	DA	1653	G
26	DA	1913	A
26	DA	1992	G
26	DA	2110	G
26	DA	2126	A
26	DA	2136	C
26	DA	2169	A
26	DA	2177	C
26	DA	2318	G
26	DA	2689	U
26	DA	2756	U
26	DA	2893	G

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
23	PSU	AW	32	23	19,21,22	1.79	4 (21%)	23,30,33	1.25	2 (8%)
23	MIA	AW	37	23	29,31,32	1.83	5 (17%)	41,44,47	1.87	9 (21%)
23	PSU	AW	39	23	19,21,22	1.96	5 (26%)	23,30,33	1.05	1 (4%)
23	7MG	AW	46	23	24,26,27	2.02	7 (29%)	34,39,42	2.55	10 (29%)
23	5MU	AW	54	23	20,22,23	1.64	4 (20%)	25,32,35	2.01	3 (12%)
23	PSU	AW	55	23	19,21,22	1.84	4 (21%)	23,30,33	1.35	2 (8%)
23	31M	AW	76	23	42,44,45	1.40	5 (11%)	58,61,64	1.99	11 (18%)
23	4SU	AW	8	23	19,21,22	1.78	4 (21%)	23,30,33	1.81	4 (17%)
24	5MC	AX	32	24	20,22,23	1.77	4 (20%)	26,32,35	1.58	4 (15%)
24	5MU	AX	54	24,57	20,22,23	1.69	5 (25%)	25,32,35	2.17	5 (20%)
24	PSU	AX	55	24,57	19,21,22	1.93	4 (21%)	23,30,33	1.11	3 (13%)
24	4SU	AX	8	24	19,21,22	1.75	4 (21%)	23,30,33	34.05	2 (8%)
25	PSU	AY	32	25	19,21,22	1.77	4 (21%)	23,30,33	1.26	3 (13%)
25	MIA	AY	37	25	20,24,32	1.77	5 (25%)	27,35,47	1.92	5 (18%)
25	PSU	AY	39	25	19,21,22	1.82	6 (31%)	23,30,33	1.55	1 (4%)
25	7MG	AY	46	25	24,26,27	2.00	7 (29%)	34,39,42	2.47	10 (29%)
25	5MU	AY	54	25	20,22,23	1.92	5 (25%)	25,32,35	2.00	5 (20%)
25	PSU	AY	55	25	19,21,22	2.03	5 (26%)	23,30,33	1.26	4 (17%)
25	4SU	AY	8	25	19,21,22	1.77	4 (21%)	23,30,33	2.51	4 (17%)
23	PSU	CW	32	23	19,21,22	1.87	4 (21%)	23,30,33	0.91	2 (8%)
23	MIA	CW	37	23	20,24,32	1.73	5 (25%)	27,35,47	1.99	4 (14%)
23	PSU	CW	39	23	19,21,22	1.97	4 (21%)	23,30,33	1.25	2 (8%)
23	7MG	CW	46	23	24,26,27	2.00	8 (33%)	34,39,42	2.24	9 (26%)
23	5MU	CW	54	23	20,22,23	1.68	4 (20%)	25,32,35	2.05	4 (16%)
23	PSU	CW	55	23	19,21,22	1.78	4 (21%)	23,30,33	1.29	2 (8%)
23	31M	CW	76	23	42,44,45	1.39	5 (11%)	58,61,64	1.93	9 (15%)
23	4SU	CW	8	23	19,21,22	1.69	4 (21%)	23,30,33	7.12	4 (17%)
24	5MC	CX	32	24	20,22,23	1.75	4 (20%)	26,32,35	1.53	4 (15%)
24	5MU	CX	54	24	20,22,23	1.57	5 (25%)	25,32,35	2.72	4 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	PSU	CX	55	24	19,21,22	1.83	4 (21%)	23,30,33	1.01	3 (13%)
24	4SU	CX	8	24	19,21,22	1.86	4 (21%)	23,30,33	23.29	2 (8%)
25	PSU	CY	32	25	19,21,22	1.79	4 (21%)	23,30,33	1.06	3 (13%)
25	MIA	CY	37	25	20,24,32	1.81	5 (25%)	27,35,47	2.02	5 (18%)
25	PSU	CY	39	25	19,21,22	1.86	4 (21%)	23,30,33	1.22	2 (8%)
25	7MG	CY	46	25	24,26,27	2.04	7 (29%)	34,39,42	2.48	10 (29%)
25	5MU	CY	54	25	20,22,23	1.67	5 (25%)	25,32,35	1.63	4 (16%)
25	PSU	CY	55	25	19,21,22	1.74	5 (26%)	23,30,33	2.17	3 (13%)
25	4SU	CY	8	25	19,21,22	1.80	4 (21%)	23,30,33	14.01	4 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	PSU	AW	32	23	-	0/8/25/26	0/2/2/2
23	MIA	AW	37	23	-	0/16/33/34	0/3/3/3
23	PSU	AW	39	23	-	0/8/25/26	0/2/2/2
23	7MG	AW	46	23	-	1/8/37/38	0/3/3/3
23	5MU	AW	54	23	-	0/6/25/26	0/2/2/2
23	PSU	AW	55	23	-	0/8/25/26	0/2/2/2
23	31M	AW	76	23	-	0/32/49/50	0/4/4/4
23	4SU	AW	8	23	-	0/6/25/26	0/2/2/2
24	5MC	AX	32	24	-	0/6/25/26	0/2/2/2
24	5MU	AX	54	24,57	-	0/6/25/26	0/2/2/2
24	PSU	AX	55	24,57	-	0/8/25/26	0/2/2/2
24	4SU	AX	8	24	-	0/6/25/26	0/2/2/2
25	PSU	AY	32	25	-	0/8/25/26	0/2/2/2
25	MIA	AY	37	25	-	0/8/25/34	0/3/3/3
25	PSU	AY	39	25	-	0/8/25/26	0/2/2/2
25	7MG	AY	46	25	-	1/8/37/38	0/3/3/3
25	5MU	AY	54	25	-	1/6/25/26	0/2/2/2
25	PSU	AY	55	25	-	0/8/25/26	0/2/2/2
25	4SU	AY	8	25	-	0/6/25/26	0/2/2/2
23	PSU	CW	32	23	-	0/8/25/26	0/2/2/2
23	MIA	CW	37	23	-	0/8/25/34	0/3/3/3
23	PSU	CW	39	23	-	0/8/25/26	0/2/2/2
23	7MG	CW	46	23	-	1/8/37/38	0/3/3/3
23	5MU	CW	54	23	-	0/6/25/26	0/2/2/2
23	PSU	CW	55	23	-	0/8/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	31M	CW	76	23	-	0/32/49/50	0/4/4/4
23	4SU	CW	8	23	-	0/6/25/26	0/2/2/2
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	4SU	CX	8	24	-	0/6/25/26	0/2/2/2
25	PSU	CY	32	25	-	0/8/25/26	0/2/2/2
25	MIA	CY	37	25	-	0/8/25/34	0/3/3/3
25	PSU	CY	39	25	-	0/8/25/26	0/2/2/2
25	7MG	CY	46	25	-	0/8/37/38	0/3/3/3
25	5MU	CY	54	25	-	0/6/25/26	0/2/2/2
25	PSU	CY	55	25	-	0/8/25/26	0/2/2/2
25	4SU	CY	8	25	-	1/6/25/26	0/2/2/2

All (180) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C2-S10	-6.34	1.70	1.75
25	CY	46	7MG	C6-C5	5.92	1.48	1.41
25	AY	55	PSU	C5-C1'	-5.64	1.47	1.52
23	CW	46	7MG	C6-C5	5.55	1.48	1.41
23	AW	46	7MG	C6-C5	5.10	1.47	1.41
25	AY	46	7MG	C6-C5	4.95	1.47	1.41
23	AW	76	31M	CB-CG	-4.86	1.39	1.51
23	CW	39	PSU	C5-C1'	-4.80	1.48	1.52
24	AX	32	5MC	C5-C4	4.73	1.48	1.41
25	AY	46	7MG	P-OP1	4.72	1.52	1.46
24	AX	55	PSU	C5-C1'	-4.71	1.48	1.52
25	CY	37	MIA	P-OP1	4.70	1.52	1.46
23	CW	76	31M	CB-CG	-4.69	1.39	1.51
25	CY	46	7MG	P-OP1	4.67	1.52	1.46
25	CY	54	5MU	P-OP1	4.66	1.52	1.46
23	AW	39	PSU	C5-C1'	-4.65	1.48	1.52
25	AY	54	5MU	P-OP1	4.64	1.52	1.46
24	CX	32	5MC	C5-C4	4.62	1.48	1.41
23	AW	39	PSU	P-OP1	4.55	1.51	1.46
23	CW	37	MIA	P-OP1	4.53	1.51	1.46
23	AW	46	7MG	P-OP1	4.49	1.51	1.46
23	CW	55	PSU	P-OP1	4.46	1.51	1.46
24	CX	8	4SU	O2-C2	4.43	1.27	1.21
23	CW	46	7MG	P-OP1	4.42	1.51	1.46
25	AY	54	5MU	C2-N1	4.42	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	CY	32	PSU	P-OP1	4.42	1.51	1.46
23	AW	8	4SU	P-OP1	4.39	1.51	1.46
23	CW	32	PSU	P-OP1	4.37	1.51	1.46
25	AY	55	PSU	P-OP1	4.36	1.51	1.46
25	AY	8	4SU	P-OP1	4.36	1.51	1.46
25	CY	55	PSU	P-OP1	4.33	1.51	1.46
25	AY	37	MIA	P-OP1	4.33	1.51	1.46
24	AX	55	PSU	P-OP1	4.33	1.51	1.46
25	CY	39	PSU	P-OP1	4.32	1.51	1.46
23	CW	39	PSU	P-OP1	4.30	1.51	1.46
23	CW	54	5MU	P-OP1	4.29	1.51	1.46
25	CY	8	4SU	P-OP1	4.23	1.51	1.46
23	CW	32	PSU	C5-C1'	-4.21	1.48	1.52
24	CX	54	5MU	P-OP1	4.21	1.51	1.46
23	AW	37	MIA	P-OP1	4.20	1.51	1.46
23	AW	55	PSU	P-OP1	4.19	1.51	1.46
24	CX	8	4SU	P-OP1	4.19	1.51	1.46
24	CX	32	5MC	P-OP1	4.18	1.51	1.46
24	CX	55	PSU	P-OP1	4.18	1.51	1.46
24	AX	54	5MU	P-OP1	4.13	1.51	1.46
25	AY	32	PSU	P-OP1	4.13	1.51	1.46
23	AW	55	PSU	C5-C1'	-4.10	1.48	1.52
24	AX	32	5MC	P-OP1	4.08	1.51	1.46
25	CY	55	PSU	C4-C5	4.08	1.50	1.40
23	AW	32	PSU	P-OP1	4.08	1.51	1.46
23	AW	54	5MU	P-OP1	4.07	1.51	1.46
25	CY	8	4SU	C4-S4	-4.06	1.59	1.67
24	AX	8	4SU	O2-C2	4.06	1.27	1.21
25	AY	39	PSU	P-OP1	4.03	1.51	1.46
23	CW	8	4SU	P-OP1	4.02	1.51	1.46
24	AX	8	4SU	P-OP1	4.01	1.51	1.46
25	CY	39	PSU	C5-C1'	-3.84	1.48	1.52
25	AY	8	4SU	C4-S4	-3.81	1.60	1.67
23	AW	8	4SU	C4-S4	-3.77	1.60	1.67
25	CY	39	PSU	C4-C5	3.76	1.49	1.40
24	AX	8	4SU	C4-S4	-3.74	1.60	1.67
24	CX	55	PSU	C5-C1'	-3.74	1.48	1.52
23	AW	32	PSU	C5-C1'	-3.74	1.48	1.52
23	CW	8	4SU	C4-S4	-3.67	1.60	1.67
24	CX	8	4SU	C4-S4	-3.66	1.60	1.67
24	CX	55	PSU	C4-C5	3.66	1.49	1.40
23	CW	76	31M	O4'-C1'	3.65	1.45	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	AY	32	PSU	C4-C5	3.65	1.49	1.40
25	AY	54	5MU	C4-C5	3.61	1.49	1.40
25	AY	39	PSU	C5-C1'	-3.60	1.49	1.52
25	CY	37	MIA	C5-C4	3.58	1.48	1.40
23	AW	8	4SU	C2-N1	3.57	1.42	1.38
25	CY	32	PSU	C4-C5	3.54	1.49	1.40
23	AW	76	31M	O4'-C1'	3.52	1.45	1.41
23	AW	32	PSU	C4-C5	3.52	1.49	1.40
25	AY	8	4SU	C2-N1	3.50	1.42	1.38
23	CW	54	5MU	C2-N1	3.48	1.42	1.38
23	CW	39	PSU	O2-C2	3.47	1.26	1.21
25	CY	37	MIA	C6-N6	3.46	1.36	1.28
23	CW	54	5MU	C4-C5	3.44	1.48	1.40
23	CW	55	PSU	C4-C5	3.44	1.48	1.40
24	CX	54	5MU	C4-C5	3.42	1.48	1.40
23	AW	76	31M	C5-C4	-3.41	1.32	1.40
25	AY	54	5MU	O2-C2	3.41	1.26	1.21
25	AY	37	MIA	C5-C4	3.40	1.48	1.40
23	CW	32	PSU	C4-C5	3.39	1.48	1.40
23	CW	76	31M	C5-C4	-3.37	1.32	1.40
24	AX	54	5MU	C2-N1	3.37	1.42	1.38
23	CW	8	4SU	C2-N1	3.35	1.42	1.38
23	CW	37	MIA	C5-C4	3.35	1.48	1.40
23	AW	55	PSU	C4-C5	3.32	1.48	1.40
24	AX	54	5MU	C4-C5	3.32	1.48	1.40
25	CY	8	4SU	C2-N1	3.31	1.42	1.38
25	AY	46	7MG	C2-N3	3.31	1.37	1.33
25	CY	32	PSU	C5-C1'	-3.28	1.49	1.52
25	AY	37	MIA	C6-N6	3.27	1.35	1.28
23	CW	55	PSU	C5-C1'	-3.26	1.49	1.52
23	AW	54	5MU	C2-N1	3.25	1.41	1.38
23	AW	54	5MU	C4-C5	3.25	1.48	1.40
23	CW	37	MIA	C6-N6	3.23	1.35	1.28
24	CX	32	5MC	C2-N1	3.22	1.41	1.38
23	AW	8	4SU	O2-C2	3.20	1.26	1.21
24	AX	32	5MC	C2-N1	3.19	1.41	1.38
25	CY	8	4SU	O2-C2	3.19	1.26	1.21
25	AY	39	PSU	C4-C5	3.15	1.48	1.40
24	CX	8	4SU	C2-N1	3.14	1.41	1.38
23	AW	37	MIA	C5-C4	3.13	1.47	1.40
23	CW	39	PSU	C4-C5	3.12	1.48	1.40
25	CY	54	5MU	C4-C5	3.12	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	39	PSU	C4-C5	3.11	1.48	1.40
23	AW	46	7MG	C2-N2	3.09	1.37	1.32
25	AY	32	PSU	C5-C1'	-3.08	1.49	1.52
25	AY	8	4SU	O2-C2	3.06	1.25	1.21
23	CW	54	5MU	O2-C2	3.05	1.25	1.21
24	AX	55	PSU	C4-C5	3.03	1.47	1.40
24	CX	55	PSU	O2-C2	3.02	1.25	1.21
25	CY	32	PSU	O2-C2	3.02	1.25	1.21
23	AW	37	MIA	C4-N9	-2.95	1.33	1.37
23	AW	39	PSU	O2-C2	2.95	1.25	1.21
23	AW	55	PSU	O2-C2	2.93	1.25	1.21
25	AY	32	PSU	O2-C2	2.92	1.25	1.21
23	AW	54	5MU	O2-C2	2.92	1.25	1.21
23	CW	32	PSU	O2-C2	2.92	1.25	1.21
25	AY	46	7MG	C5-N7	-2.91	1.33	1.39
23	CW	55	PSU	O2-C2	2.91	1.25	1.21
24	AX	55	PSU	O2-C2	2.90	1.25	1.21
24	AX	54	5MU	O2-C2	2.87	1.25	1.21
25	CY	54	5MU	C2-N1	2.86	1.41	1.38
25	AY	55	PSU	C4-C5	2.85	1.47	1.40
24	AX	32	5MC	O2-C2	2.84	1.25	1.21
23	AW	46	7MG	C2-N3	2.83	1.37	1.33
23	CW	46	7MG	C5-N7	-2.82	1.34	1.39
25	CY	54	5MU	O2-C2	2.80	1.25	1.21
23	AW	46	7MG	C5-N7	-2.79	1.34	1.39
25	AY	39	PSU	O2-C2	2.78	1.25	1.21
23	AW	32	PSU	O2-C2	2.77	1.25	1.21
24	CX	32	5MC	O2-C2	2.73	1.25	1.21
25	AY	37	MIA	C6-C5	2.69	1.49	1.44
23	CW	8	4SU	O2-C2	2.69	1.25	1.21
23	AW	46	7MG	C5-C4	2.69	1.48	1.39
23	CW	46	7MG	C5-C4	2.65	1.48	1.39
25	AY	46	7MG	C5-C4	2.63	1.47	1.39
23	AW	76	31M	C8-N9	-2.59	1.32	1.36
25	CY	46	7MG	C5-C4	2.58	1.47	1.39
25	AY	55	PSU	O2-C2	2.58	1.25	1.21
24	CX	54	5MU	C2-N1	2.51	1.41	1.38
25	CY	46	7MG	C5-N7	-2.45	1.34	1.39
23	CW	37	MIA	C6-C5	2.45	1.49	1.44
25	CY	46	7MG	C2-N2	2.42	1.36	1.32
25	CY	37	MIA	C4-N9	-2.42	1.34	1.37
25	CY	46	7MG	C4-N9	-2.42	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	AY	37	MIA	C4-N9	-2.42	1.34	1.37
25	AY	55	PSU	O4'-C1'	-2.41	1.40	1.44
25	AY	46	7MG	C2-N2	2.38	1.35	1.32
23	AW	37	MIA	C6-C5	2.35	1.48	1.44
25	AY	39	PSU	O4'-C1'	-2.34	1.40	1.44
25	CY	39	PSU	O2-C2	2.31	1.24	1.21
25	CY	55	PSU	C4-N3	-2.29	1.33	1.36
25	CY	55	PSU	O2-C2	2.27	1.24	1.21
23	CW	46	7MG	C2-N3	2.27	1.36	1.33
23	CW	46	7MG	C2-N2	2.26	1.35	1.32
25	CY	37	MIA	C6-C5	2.25	1.48	1.44
23	AW	39	PSU	C4-N3	-2.25	1.33	1.36
23	CW	46	7MG	C4-N9	-2.24	1.33	1.37
23	AW	76	31M	C2-N1	2.23	1.38	1.33
23	CW	76	31M	C5-N7	-2.20	1.32	1.39
25	CY	55	PSU	C5-C1'	-2.18	1.50	1.52
24	AX	54	5MU	C4-N3	-2.17	1.33	1.36
23	CW	37	MIA	C4-N9	-2.14	1.34	1.37
25	AY	54	5MU	O5'-C5'	-2.12	1.41	1.44
23	CW	76	31M	C4-N9	-2.12	1.34	1.37
25	AY	39	PSU	O5'-C5'	-2.11	1.41	1.44
25	AY	46	7MG	CM7-N7	2.10	1.49	1.46
24	CX	54	5MU	O2-C2	2.09	1.24	1.21
23	CW	46	7MG	CM7-N7	2.09	1.49	1.46
23	AW	46	7MG	CM7-N7	2.08	1.49	1.46
25	CY	54	5MU	C4-N3	-2.08	1.33	1.36
24	CX	54	5MU	C4-N3	-2.05	1.33	1.36
25	CY	46	7MG	C8-N9	2.03	1.47	1.46
24	AX	8	4SU	C2-N1	2.02	1.40	1.38

All (168) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	8	4SU	C4-N3-C2	163.15	128.58	121.60
24	CX	8	4SU	C4-N3-C2	111.39	126.36	121.60
25	CY	8	4SU	C4-N3-C2	-66.72	118.75	121.60
23	CW	8	4SU	C4-N3-C2	-33.23	120.18	121.60
23	AW	76	31M	N3-C2-N1	-10.00	120.09	128.89
23	CW	76	31M	N3-C2-N1	-9.67	120.38	128.89
24	CX	54	5MU	C6-N1-C2	-9.51	119.71	122.41
25	AY	46	7MG	N3-C4-N9	8.70	140.54	126.80
24	CX	54	5MU	N3-C2-N1	8.29	122.89	115.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	CX	8	4SU	C2-N1-C1'	7.76	123.08	118.21
25	AY	8	4SU	C4-N3-C2	7.74	121.93	121.60
23	AW	46	7MG	N3-C4-N9	7.60	138.81	126.80
23	AW	46	7MG	C6-N1-C2	7.51	124.44	120.20
24	AX	54	5MU	C6-N1-C2	-7.42	120.30	122.41
25	AY	8	4SU	C2-N1-C1'	7.31	122.79	118.21
23	CW	46	7MG	N3-C4-N9	6.82	137.58	126.80
25	CY	55	PSU	O4'-C1'-C5	6.77	121.15	109.80
23	CW	37	MIA	C5-C4-N3	-6.69	118.37	126.07
23	AW	54	5MU	C6-N1-C2	-6.66	120.51	122.41
25	CY	46	7MG	N3-C4-N9	6.66	137.32	126.80
23	CW	54	5MU	C6-N1-C2	-6.62	120.53	122.41
25	CY	55	PSU	C5-C1'-C2'	-6.35	103.95	115.73
25	AY	37	MIA	C5-C4-N3	-6.30	118.81	126.07
24	AX	54	5MU	N3-C2-N1	6.22	121.17	115.97
25	CY	46	7MG	N7-C8-N9	-6.13	94.99	103.13
25	CY	37	MIA	C5-C4-N3	-6.08	119.07	126.07
23	CW	76	31M	C5-C4-N3	-6.06	120.08	125.98
24	AX	8	4SU	C2-N1-C1'	6.05	122.00	118.21
23	CW	8	4SU	N3-C2-N1	6.01	120.99	115.97
23	AW	37	MIA	C5-C4-N3	-5.95	119.22	126.07
23	AW	54	5MU	N3-C2-N1	5.94	120.93	115.97
25	CY	37	MIA	N3-C4-N9	5.91	135.58	126.91
25	AY	39	PSU	O4'-C1'-C5	-5.88	99.94	109.80
23	CW	37	MIA	N3-C4-N9	5.87	135.52	126.91
25	CY	8	4SU	N3-C2-N1	5.86	120.86	115.97
25	AY	54	5MU	N3-C2-N1	5.83	120.84	115.97
25	AY	46	7MG	C5-C4-N3	-5.83	116.40	126.61
23	CW	54	5MU	N3-C2-N1	5.72	120.74	115.97
25	CY	46	7MG	C6-N1-C2	5.70	123.42	120.20
25	CY	54	5MU	N3-C2-N1	5.67	120.71	115.97
23	AW	46	7MG	N7-C8-N9	-5.65	95.63	103.13
25	AY	37	MIA	N3-C4-N9	5.59	135.10	126.91
23	AW	8	4SU	C2-N1-C1'	5.35	121.56	118.21
23	CW	46	7MG	N7-C8-N9	-5.28	96.12	103.13
24	CX	32	5MC	C2-N3-C4	5.14	120.42	115.50
25	AY	54	5MU	C6-N1-C2	-5.12	120.95	122.41
23	AW	55	PSU	C5-C1'-C2'	-5.07	106.33	115.73
25	AY	46	7MG	N7-C8-N9	-5.06	96.42	103.13
23	AW	76	31M	C5-C4-N3	-5.02	121.09	125.98
23	AW	37	MIA	N3-C4-N9	4.99	134.22	126.91
23	CW	46	7MG	C5-C4-N3	-4.76	118.28	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	8	4SU	N3-C2-N1	4.60	119.81	115.97
23	CW	46	7MG	C6-N1-C2	4.55	122.77	120.20
23	AW	46	7MG	C5-C4-N3	-4.53	118.68	126.61
24	AX	32	5MC	C2-N3-C4	4.51	119.81	115.50
23	CW	39	PSU	C5-C1'-C2'	-4.41	107.55	115.73
25	CY	46	7MG	C5-C4-N3	-4.37	118.96	126.61
23	AW	32	PSU	C5-C1'-C2'	-4.33	107.69	115.73
23	AW	37	MIA	C2-N3-C4	4.31	121.29	115.22
25	AY	54	5MU	C2-N1-C1'	4.29	120.90	118.21
23	AW	76	31M	C5'-C4'-C3'	-4.27	108.28	115.85
23	CW	55	PSU	C5-C1'-C2'	-4.24	107.87	115.73
25	AY	8	4SU	N3-C2-N1	4.22	119.50	115.97
23	AW	8	4SU	C4-N3-C2	-4.05	121.43	121.60
23	AW	76	31M	C4'-C3'-N3'	-3.93	105.29	113.56
25	CY	39	PSU	C5-C1'-C2'	-3.85	108.59	115.73
23	CW	54	5MU	C2-N1-C1'	3.83	120.61	118.21
25	CY	46	7MG	C8-N7-C5	3.81	116.43	108.83
23	CW	76	31M	C5'-C4'-C3'	-3.76	109.19	115.85
24	AX	32	5MC	C6-N1-C2	3.72	121.53	118.86
25	CY	37	MIA	C5-C6-N1	-3.70	116.88	120.10
23	CW	8	4SU	C2-N1-C1'	3.67	120.51	118.21
25	AY	32	PSU	O4'-C1'-C5	3.55	115.75	109.80
23	CW	46	7MG	C8-N7-C5	3.47	115.75	108.83
23	AW	46	7MG	C8-N7-C5	3.45	115.71	108.83
24	AX	32	5MC	C5-C6-N1	-3.43	118.94	122.02
25	AY	46	7MG	C8-N7-C5	3.37	115.56	108.83
23	AW	37	MIA	C12-N6-C6	-3.35	118.97	123.33
23	AW	39	PSU	C5-C1'-C2'	-3.34	109.53	115.73
23	CW	76	31M	CGM-CBM-CAM	-3.30	107.98	113.30
24	AX	55	PSU	C5-C1'-C2'	-3.21	109.77	115.73
25	AY	46	7MG	C8-N9-C1'	-3.20	112.23	121.06
25	AY	46	7MG	C6-N1-C2	3.20	122.00	120.20
25	CY	46	7MG	N2-C2-N3	-3.19	116.16	120.29
25	AY	46	7MG	C6-C5-C4	3.17	120.32	116.01
25	CY	54	5MU	C5-C6-N1	-3.14	119.20	122.02
23	CW	76	31M	N3-C4-N9	3.13	130.76	125.39
25	CY	55	PSU	C4-N3-C2	-3.07	119.14	125.36
23	AW	76	31M	N3-C4-N9	3.07	130.66	125.39
23	AW	37	MIA	C2-N1-C6	3.06	122.38	113.31
25	CY	54	5MU	C6-N1-C2	-3.01	121.55	122.41
25	CY	8	4SU	C5-C4-N3	3.00	121.24	116.04
23	AW	37	MIA	C4-C5-N7	-2.95	106.56	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AY	55	PSU	C5-C1'-C2'	-2.95	110.26	115.73
25	AY	37	MIA	C4-C5-N7	-2.95	106.56	109.41
23	AW	46	7MG	C8-N9-C1'	-2.93	112.97	121.06
24	CX	32	5MC	C6-N1-C2	2.91	120.95	118.86
23	CW	37	MIA	C4-C5-N7	-2.90	106.61	109.41
23	AW	76	31M	O4'-C4'-C3'	2.83	107.90	103.83
24	AX	32	5MC	N4-C4-N3	2.70	120.84	116.99
25	CY	39	PSU	C4-N3-C2	-2.70	119.89	125.36
24	AX	54	5MU	C2-N1-C1'	2.69	119.89	118.21
25	CY	46	7MG	N2-C2-N1	2.66	120.67	117.82
24	CX	54	5MU	C4-N3-C2	-2.63	120.00	125.39
25	AY	55	PSU	C4-N3-C2	-2.62	120.05	125.36
24	CX	32	5MC	C5-C6-N1	-2.61	119.68	122.02
23	CW	37	MIA	C5-C6-N1	-2.60	117.84	120.10
24	CX	55	PSU	C5-C1'-C2'	-2.60	110.90	115.73
24	CX	54	5MU	C5-C6-N1	-2.59	119.69	122.02
24	CX	32	5MC	N4-C4-N3	2.58	120.67	116.99
25	AY	37	MIA	C5-C6-N1	-2.58	117.86	120.10
25	CY	8	4SU	C2-N1-C1'	2.56	119.81	118.21
23	AW	37	MIA	N3-C2-N1	-2.56	122.26	126.87
25	CY	32	PSU	O4'-C1'-C5	-2.55	105.52	109.80
23	CW	46	7MG	C6-C5-C4	2.54	119.46	116.01
23	AW	46	7MG	C8-N9-C4	2.53	118.68	110.66
25	AY	55	PSU	O4'-C1'-C5	-2.52	105.58	109.80
23	CW	76	31M	C6-C5-C4	2.51	120.37	117.55
25	CY	46	7MG	C8-N9-C4	2.50	118.57	110.66
23	AW	37	MIA	C5-C6-N1	-2.50	117.80	120.46
23	AW	76	31M	OTM-CTM-CAM	-2.49	113.55	119.80
23	CW	46	7MG	N2-C2-N3	-2.47	117.08	120.29
25	AY	32	PSU	C4-N3-C2	-2.44	120.41	125.36
25	AY	32	PSU	C5-C1'-C2'	-2.44	111.21	115.73
25	AY	55	PSU	O4'-C1'-C2'	2.41	108.55	104.43
25	CY	37	MIA	C8-N9-C4	2.40	108.91	106.96
23	AW	37	MIA	C11-S10-C2	-2.40	100.49	102.23
23	CW	76	31M	OTM-CTM-CAM	-2.40	113.79	119.80
23	AW	46	7MG	C6-C5-C4	2.39	119.27	116.01
25	AY	54	5MU	C5-C6-N1	-2.38	119.88	122.02
23	AW	46	7MG	C5-C4-N9	-2.38	102.51	106.08
24	AX	55	PSU	C4-N3-C2	-2.37	120.55	125.36
25	CY	46	7MG	O4'-C1'-N9	-2.37	105.60	108.93
23	AW	8	4SU	C5-C4-N3	2.36	120.13	116.04
23	AW	54	5MU	C5-C6-N1	-2.35	119.91	122.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CW	55	PSU	C4-N3-C2	-2.34	120.61	125.36
25	CY	54	5MU	C4-N3-C2	-2.34	120.58	125.39
24	CX	55	PSU	C4-N3-C2	-2.34	120.62	125.36
25	AY	54	5MU	C4-N3-C2	-2.33	120.61	125.39
23	AW	32	PSU	C4-N3-C2	-2.29	120.71	125.36
24	AX	54	5MU	C5-C6-N1	-2.26	119.99	122.02
23	CW	8	4SU	C5-C4-N3	2.26	119.95	116.04
23	CW	32	PSU	C4-N3-C2	-2.24	120.81	125.36
23	CW	76	31M	C8-N9-C4	-2.24	105.14	106.96
23	AW	76	31M	CGM-CBM-CAM	-2.23	109.71	113.30
25	AY	8	4SU	C5-C4-N3	2.20	119.85	116.04
23	CW	76	31M	C2-N3-C4	2.20	119.61	113.27
25	CY	37	MIA	C4-C5-N7	-2.18	107.30	109.41
23	AW	46	7MG	CM7-N7-C5	2.18	131.40	123.46
25	AY	37	MIA	C8-N9-C4	2.14	108.70	106.96
25	AY	46	7MG	CM7-N7-C5	2.14	131.26	123.46
25	CY	32	PSU	O4'-C1'-C2'	2.14	108.09	104.43
23	CW	46	7MG	C8-N9-C4	2.12	117.36	110.66
25	AY	46	7MG	C8-N9-C4	2.12	117.36	110.66
23	AW	76	31M	C2'-C3'-C4'	2.07	104.83	102.27
25	CY	46	7MG	CM7-N7-C5	2.06	130.96	123.46
23	AW	76	31M	C2-N3-C4	2.04	119.14	113.27
24	AX	55	PSU	O4'-C1'-C2'	2.03	107.91	104.43
25	CY	32	PSU	C4-N3-C2	-2.03	121.23	125.36
23	CW	46	7MG	CM7-N7-C5	2.03	130.86	123.46
23	CW	39	PSU	C4-N3-C2	-2.03	121.24	125.36
23	AW	55	PSU	C4-N3-C2	-2.03	121.25	125.36
25	AY	46	7MG	C5-C4-N9	-2.03	103.05	106.08
24	AX	54	5MU	C4-N3-C2	-2.02	121.23	125.39
23	AW	76	31M	C4-C5-N7	-2.01	107.47	109.41
23	CW	54	5MU	C4-N3-C2	-2.01	121.27	125.39
23	CW	32	PSU	O4'-C1'-C2'	2.01	107.86	104.43
24	CX	55	PSU	O4'-C1'-C2'	2.01	107.86	104.43

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	CY	8	4SU	OP2-P-O5'-C5'
23	CW	46	7MG	OP2-P-O5'-C5'
25	AY	46	7MG	OP2-P-O5'-C5'
25	AY	54	5MU	OP2-P-O5'-C5'

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Mol	Chain	Res	Type	Atoms
23	AW	46	7MG	OP2-P-O5'-C5'

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2093 ligands modelled in this entry, 2091 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	SF4	AD	501	4	12,12,12	22.07	12 (100%)	0,24,24	0.00	-
58	SF4	CD	302	4	12,12,12	21.92	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
58	SF4	AD	501	4	-	0/0/48/48	0/6/5/5
58	SF4	CD	302	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)
58	CD	302	SF4	S4-FE2	-23.18	2.17	2.33
58	AD	501	SF4	S3-FE2	-22.89	2.17	2.33
58	CD	302	SF4	S1-FE2	-22.79	2.17	2.33
58	CD	302	SF4	S4-FE1	-22.67	2.18	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	AD	501	SF4	S2-FE1	-22.60	2.18	2.33
58	AD	501	SF4	S3-FE4	-22.43	2.18	2.33
58	AD	501	SF4	S3-FE1	-22.41	2.18	2.33
58	AD	501	SF4	S1-FE2	-22.29	2.18	2.33
58	CD	302	SF4	S3-FE4	-22.19	2.18	2.33
58	AD	501	SF4	S4-FE1	-22.05	2.18	2.33
58	AD	501	SF4	S4-FE3	-21.95	2.18	2.33
58	AD	501	SF4	S1-FE4	-21.94	2.18	2.33
58	AD	501	SF4	S4-FE2	-21.91	2.18	2.33
58	AD	501	SF4	S2-FE4	-21.81	2.18	2.33
58	CD	302	SF4	S4-FE3	-21.76	2.18	2.33
58	CD	302	SF4	S1-FE4	-21.74	2.18	2.33
58	CD	302	SF4	S3-FE1	-21.66	2.18	2.33
58	CD	302	SF4	S2-FE4	-21.57	2.18	2.33
58	AD	501	SF4	S2-FE3	-21.48	2.18	2.33
58	CD	302	SF4	S2-FE1	-21.47	2.18	2.33
58	CD	302	SF4	S1-FE3	-21.46	2.18	2.33
58	CD	302	SF4	S3-FE2	-21.39	2.18	2.33
58	CD	302	SF4	S2-FE3	-21.06	2.19	2.33
58	AD	501	SF4	S1-FE3	-20.96	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%)	0.84	92 (6%) 21 21	42, 72, 93, 108	0
1	CA	1503/1521 (98%)	0.86	178 (11%) 5 5	44, 74, 94, 109	0
2	AB	231/256 (90%)	3.78	158 (68%) 0 0	72, 82, 90, 94	0
2	CB	231/256 (90%)	4.30	154 (66%) 0 0	73, 84, 90, 95	0
3	AC	206/239 (86%)	2.65	111 (53%) 0 0	68, 79, 87, 94	0
3	CC	206/239 (86%)	3.23	129 (62%) 0 0	71, 81, 89, 94	0
4	AD	208/209 (99%)	2.74	121 (58%) 0 0	57, 72, 81, 90	0
4	CD	208/209 (99%)	2.17	92 (44%) 1 0	58, 71, 80, 91	0
5	AE	148/162 (91%)	2.21	72 (48%) 1 0	58, 71, 80, 85	0
5	CE	148/162 (91%)	3.17	99 (66%) 0 0	60, 73, 81, 86	0
6	AF	100/101 (99%)	2.02	44 (44%) 1 0	56, 69, 78, 82	0
6	CF	100/101 (99%)	1.58	27 (27%) 1 1	57, 70, 78, 82	0
7	AG	155/156 (99%)	2.07	64 (41%) 1 0	65, 75, 83, 91	0
7	CG	155/156 (99%)	2.09	72 (46%) 1 0	66, 76, 84, 92	0
8	AH	137/138 (99%)	1.80	43 (31%) 1 1	62, 72, 79, 87	0
8	CH	137/138 (99%)	2.82	66 (48%) 1 0	64, 74, 80, 87	0
9	AI	127/128 (99%)	2.82	72 (56%) 0 0	65, 80, 86, 89	0
9	CI	127/128 (99%)	4.52	100 (78%) 0 0	68, 82, 88, 91	0
10	AJ	97/105 (92%)	2.12	48 (49%) 1 0	64, 82, 90, 93	0
10	CJ	96/105 (91%)	4.62	82 (85%) 0 0	67, 84, 91, 93	0
11	AK	114/129 (88%)	1.57	31 (27%) 1 1	48, 70, 79, 84	0
11	CK	114/129 (88%)	1.94	40 (35%) 1 1	51, 71, 79, 84	0
12	AL	122/132 (92%)	1.84	46 (37%) 1 0	50, 65, 73, 78	0
12	CL	122/132 (92%)	2.81	75 (61%) 0 0	53, 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%)	2.40	54 (43%)	1	0	55, 70, 81, 89	0
13	CM	122/126 (96%)	3.96	83 (68%)	0	0	70, 84, 91, 99	0
14	AN	60/61 (98%)	1.83	23 (38%)	1	0	67, 74, 83, 84	0
14	CN	60/61 (98%)	4.29	40 (66%)	0	0	69, 77, 84, 88	0
15	AO	88/89 (98%)	1.46	21 (23%)	1	1	56, 67, 80, 81	0
15	CO	88/89 (98%)	1.92	34 (38%)	1	0	59, 69, 80, 83	0
16	AP	82/88 (93%)	2.78	45 (54%)	0	0	57, 71, 80, 84	0
16	CP	82/88 (93%)	2.32	36 (43%)	1	0	58, 70, 80, 84	0
17	AQ	99/105 (94%)	1.73	35 (35%)	1	1	59, 71, 80, 84	0
17	CQ	99/105 (94%)	2.71	54 (54%)	0	0	61, 71, 81, 85	0
18	AR	68/88 (77%)	2.27	29 (42%)	1	0	59, 68, 81, 83	0
18	CR	68/88 (77%)	2.67	39 (57%)	0	0	61, 70, 80, 84	0
19	AS	83/93 (89%)	1.54	25 (30%)	1	1	71, 80, 86, 95	0
19	CS	83/93 (89%)	5.55	72 (86%)	0	0	74, 82, 89, 96	0
20	AT	96/106 (90%)	2.82	52 (54%)	0	0	57, 71, 81, 85	0
20	CT	96/106 (90%)	2.06	45 (46%)	1	0	58, 70, 82, 85	0
21	AU	23/27 (85%)	2.65	10 (43%)	1	0	67, 74, 77, 81	0
21	CU	23/27 (85%)	4.10	18 (78%)	0	0	71, 75, 80, 84	0
22	AV	13/24 (54%)	1.45	4 (30%)	1	1	58, 81, 96, 99	0
22	CV	12/24 (50%)	2.45	6 (50%)	0	0	63, 84, 93, 94	0
23	AW	72/76 (94%)	2.08	28 (38%)	1	0	68, 96, 103, 105	0
23	CW	70/76 (92%)	3.82	53 (75%)	0	0	73, 97, 103, 106	0
24	AX	76/77 (98%)	0.82	7 (9%)	9	9	39, 68, 87, 91	0
24	CX	76/77 (98%)	0.78	11 (14%)	3	3	53, 82, 93, 97	0
25	AY	73/76 (96%)	2.94	43 (58%)	0	0	44, 97, 102, 105	0
25	CY	72/76 (94%)	2.15	36 (50%)	0	0	47, 98, 103, 105	0
26	BA	2819/2915 (96%)	1.10	88 (3%)	47	49	26, 45, 89, 104	0
26	DA	2800/2915 (96%)	0.55	104 (3%)	39	42	30, 49, 90, 108	0
27	BB	120/121 (99%)	1.07	2 (1%)	67	70	40, 64, 73, 86	0
27	DB	120/121 (99%)	0.48	9 (7%)	14	14	46, 69, 76, 90	0
28	BD	275/276 (99%)	0.94	21 (7%)	14	14	27, 43, 58, 82	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DD	275/276 (99%)	1.26	50 (18%) 2 2	29, 45, 61, 81	0
29	BE	204/206 (99%)	1.00	19 (9%) 9 8	25, 48, 66, 80	0
29	DE	204/206 (99%)	1.13	45 (22%) 1 1	29, 52, 67, 81	0
30	BF	203/210 (96%)	1.20	40 (19%) 2 1	26, 53, 76, 87	0
30	DF	203/210 (96%)	2.40	95 (46%) 1 0	30, 58, 77, 87	0
31	BG	181/182 (99%)	1.63	56 (30%) 1 1	51, 69, 81, 88	0
31	DG	181/182 (99%)	3.42	111 (61%) 0 0	56, 73, 82, 90	0
32	BH	174/180 (96%)	1.27	38 (21%) 1 1	51, 65, 75, 88	0
32	DH	174/180 (96%)	4.13	132 (75%) 0 0	55, 70, 78, 88	0
33	BI	146/148 (98%)	2.22	71 (48%) 1 0	50, 74, 82, 87	0
33	DI	146/148 (98%)	2.77	82 (56%) 0 0	52, 75, 82, 86	0
34	BN	140/140 (100%)	1.23	22 (15%) 3 2	32, 50, 67, 76	0
34	DN	140/140 (100%)	1.67	48 (34%) 1 1	36, 55, 70, 77	0
35	BO	122/122 (100%)	0.71	3 (2%) 54 58	30, 43, 59, 70	0
35	DO	122/122 (100%)	1.58	42 (34%) 1 1	45, 59, 73, 78	0
36	BP	149/150 (99%)	1.11	23 (15%) 3 2	26, 55, 75, 83	0
36	DP	149/150 (99%)	2.27	75 (50%) 0 0	30, 59, 77, 85	0
37	BQ	141/141 (100%)	1.17	19 (13%) 4 3	36, 52, 67, 80	0
37	DQ	141/141 (100%)	2.10	67 (47%) 1 0	41, 57, 70, 82	0
38	BR	118/118 (100%)	0.80	10 (8%) 11 10	25, 36, 54, 59	0
38	DR	118/118 (100%)	1.62	43 (36%) 1 0	41, 54, 65, 72	0
39	BS	110/112 (98%)	0.91	12 (10%) 6 6	38, 51, 65, 72	0
39	DS	110/112 (98%)	2.99	61 (55%) 0 0	63, 77, 84, 92	0
40	BT	131/146 (89%)	0.70	10 (7%) 14 14	32, 47, 69, 82	0
40	DT	131/146 (89%)	0.90	19 (14%) 3 3	48, 63, 79, 85	0
41	BU	116/118 (98%)	0.92	7 (6%) 21 22	18, 33, 49, 59	0
41	DU	116/118 (98%)	2.33	62 (53%) 0 0	42, 61, 78, 84	0
42	BV	101/101 (100%)	0.89	14 (13%) 4 3	21, 41, 58, 67	0
42	DV	101/101 (100%)	1.57	33 (32%) 1 1	41, 71, 83, 91	0
43	BW	112/113 (99%)	0.73	3 (2%) 52 55	23, 34, 54, 79	0
43	DW	112/113 (99%)	1.29	22 (19%) 2 1	39, 50, 67, 83	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BX	95/96 (98%)	0.65	3 (3%) 45 48	23, 38, 61, 84	0
44	DX	95/96 (98%)	1.80	34 (35%) 1 1	43, 60, 76, 79	0
45	BY	107/110 (97%)	1.62	39 (36%) 1 0	32, 50, 69, 83	0
45	DY	107/110 (97%)	2.78	58 (54%) 0 0	57, 71, 81, 88	0
46	BZ	171/206 (83%)	2.00	62 (36%) 1 0	39, 64, 91, 95	0
46	DZ	174/206 (84%)	4.56	129 (74%) 0 0	66, 84, 94, 101	0
47	B0	83/85 (97%)	1.25	14 (16%) 2 2	27, 39, 61, 73	0
47	D0	83/85 (97%)	2.41	42 (50%) 0 0	47, 66, 75, 82	0
48	B1	97/98 (98%)	1.33	21 (21%) 1 1	30, 48, 70, 76	0
48	D1	97/98 (98%)	1.64	34 (35%) 1 1	38, 58, 74, 83	0
49	B2	70/72 (97%)	0.74	3 (4%) 34 36	34, 50, 64, 79	0
49	D2	70/72 (97%)	2.57	36 (51%) 0 0	56, 70, 80, 86	0
50	B3	59/60 (98%)	0.85	6 (10%) 7 7	24, 37, 63, 71	0
50	D3	59/60 (98%)	3.29	38 (64%) 0 0	49, 64, 79, 85	0
51	B4	69/71 (97%)	0.91	9 (13%) 4 4	54, 73, 87, 92	0
51	D4	69/71 (97%)	3.53	46 (66%) 0 0	74, 88, 94, 99	0
52	B5	59/60 (98%)	0.70	5 (8%) 11 10	20, 33, 54, 67	0
52	D5	59/60 (98%)	0.97	7 (11%) 5 5	36, 51, 67, 73	0
53	B6	53/54 (98%)	1.24	9 (16%) 2 2	31, 44, 61, 68	0
53	D6	53/54 (98%)	2.39	26 (49%) 1 0	52, 63, 76, 79	0
54	B7	48/49 (97%)	1.18	7 (14%) 3 3	21, 30, 62, 76	0
54	D7	48/49 (97%)	1.81	15 (31%) 1 1	33, 42, 61, 70	0
55	B8	64/65 (98%)	0.97	6 (9%) 9 8	25, 36, 45, 60	0
55	D8	64/65 (98%)	2.39	39 (60%) 0 0	46, 58, 66, 72	0
56	B9	37/37 (100%)	2.15	14 (37%) 1 0	31, 49, 73, 74	0
56	D9	37/37 (100%)	3.19	23 (62%) 0 0	46, 57, 73, 76	0
All	All	20929/21748 (96%)	1.58	5202 (24%) 1 1	18, 64, 89, 109	0

All (5202) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	CB	165	VAL	29.5
51	D4	49	PHE	22.0

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Mol	Chain	Res	Type	RSRZ
2	CB	163	PHE	19.2
10	CJ	85	LEU	18.9
46	DZ	155	LEU	18.9
2	CB	164	VAL	18.8
2	CB	187	LEU	18.6
19	CS	41	VAL	18.0
13	CM	4	ILE	17.8
46	DZ	171	ILE	17.4
2	AB	214	ILE	16.8
2	CB	71	VAL	16.8
2	CB	70	PHE	16.3
2	CB	97	TRP	16.3
19	CS	40	ILE	16.0
14	CN	37	PHE	16.0
45	DY	5	MET	15.3
10	CJ	47	PHE	15.2
14	CN	36	PHE	15.2
2	AB	222	ILE	14.9
2	AB	221	LEU	14.7
13	CM	124	PRO	14.6
2	CB	211	ILE	14.6
2	CB	101	MET	14.4
46	DZ	172	ALA	14.4
32	DH	72	ILE	14.3
3	AC	87	LEU	14.1
2	CB	214	ILE	14.1
14	CN	34	TYR	14.1
3	AC	39	ILE	14.0
2	CB	207	ALA	13.9
26	DA	229	A	13.9
2	AB	215	LEU	13.8
2	AB	101	MET	13.6
13	CM	123	ALA	13.5
46	DZ	96	VAL	13.4
2	CB	69	LEU	13.3
46	DZ	139	VAL	13.3
2	CB	162	ILE	13.3
10	CJ	26	ALA	13.2
9	AI	47	LEU	13.2
3	CC	8	ILE	13.2
31	DG	41	GLN	13.1
2	CB	152	PHE	13.1

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Mol	Chain	Res	Type	RSRZ
3	CC	124	ILE	13.0
2	AB	213	LEU	13.0
14	CN	53	LEU	12.9
9	CI	19	LEU	12.9
13	CM	60	VAL	12.9
2	AB	228	GLY	12.8
31	DG	157	ILE	12.8
46	DZ	170	THR	12.6
46	DZ	125	LEU	12.6
9	CI	109	VAL	12.5
13	AM	2	ALA	12.5
10	CJ	6	ILE	12.5
37	DQ	104	PHE	12.4
14	CN	39	LEU	12.3
39	DS	32	LEU	12.3
10	CJ	71	LEU	12.3
32	DH	43	VAL	12.3
31	DG	39	ILE	12.2
3	CC	153	VAL	12.2
19	CS	5	LEU	12.1
2	AB	227	GLY	12.1
2	CB	222	ILE	12.0
46	DZ	120	ILE	12.0
30	DF	172	TRP	12.0
2	CB	215	LEU	11.9
3	CC	155	GLY	11.9
21	CU	14	TRP	11.8
2	CB	76	GLN	11.8
7	AG	83	ALA	11.8
51	D4	50	VAL	11.7
9	CI	76	ALA	11.6
46	DZ	137	ILE	11.5
3	CC	198	VAL	11.5
32	DH	17	VAL	11.5
9	CI	66	ARG	11.4
2	CB	77	ALA	11.4
46	DZ	102	LEU	11.3
7	AG	82	GLY	11.2
8	CH	45	ILE	11.2
4	AD	5	ILE	11.1
31	DG	28	VAL	11.1
10	CJ	72	VAL	11.1

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Mol	Chain	Res	Type	RSRZ
8	CH	2	LEU	11.1
9	CI	14	VAL	11.0
10	CJ	74	ILE	11.0
9	CI	9	ARG	11.0
19	CS	66	MET	11.0
10	CJ	27	ALA	11.0
2	CB	218	ALA	10.9
19	CS	4	SER	10.9
8	CH	9	MET	10.9
32	DH	105	LEU	10.9
13	CM	64	TRP	10.9
32	DH	45	VAL	10.9
30	DF	148	LEU	10.9
46	DZ	124	ILE	10.9
20	AT	72	LEU	10.9
2	CB	185	ILE	10.8
51	D4	67	TYR	10.8
19	CS	71	LEU	10.8
45	DY	106	LEU	10.7
46	DZ	156	LYS	10.7
8	CH	83	ILE	10.6
7	CG	83	ALA	10.5
53	D6	54	ILE	10.5
2	AB	211	ILE	10.5
50	D3	26	LEU	10.5
9	CI	18	PHE	10.4
2	AB	152	PHE	10.4
2	CB	68	ILE	10.3
5	CE	12	LEU	10.3
2	CB	81	VAL	10.3
5	CE	109	ILE	10.3
2	AB	163	PHE	10.3
32	DH	123	PHE	10.3
13	CM	122	LYS	10.3
2	CB	58	ILE	10.2
3	CC	189	ALA	10.2
7	AG	85	TYR	10.2
18	AR	78	LEU	10.2
39	DS	26	LEU	10.2
3	AC	91	LEU	10.2
46	DZ	59	LEU	10.1
31	DG	140	ILE	10.1

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Mol	Chain	Res	Type	RSRZ
31	DG	102	PHE	10.1
2	CB	177	ALA	10.0
19	CS	16	LEU	10.0
2	CB	201	ILE	10.0
10	CJ	63	PHE	10.0
39	DS	35	ILE	10.0
53	D6	11	LEU	9.9
18	AR	76	LEU	9.9
9	CI	61	ALA	9.9
13	CM	66	LEU	9.9
3	CC	157	ILE	9.8
20	AT	67	ALA	9.8
9	CI	10	ARG	9.8
16	AP	19	ILE	9.8
14	CN	25	VAL	9.8
2	AB	70	PHE	9.7
13	CM	6	GLY	9.7
3	CC	134	ILE	9.7
18	CR	66	LEU	9.6
32	DH	52	VAL	9.6
32	DH	35	VAL	9.6
19	CS	10	PHE	9.6
46	DZ	121	HIS	9.6
19	CS	68	GLY	9.6
31	DG	56	ALA	9.6
9	CI	15	ALA	9.5
46	DZ	5	LEU	9.5
20	AT	74	LYS	9.5
2	CB	92	TYR	9.5
19	CS	49	ILE	9.5
46	DZ	38	TYR	9.5
3	AC	81	GLY	9.5
8	AH	3	THR	9.5
8	CH	135	CYS	9.4
13	AM	124	PRO	9.4
31	DG	106	LEU	9.4
8	CH	35	ILE	9.4
13	AM	18	ALA	9.4
9	CI	7	THR	9.4
23	CW	24	G	9.3
10	CJ	49	VAL	9.3
13	CM	90	LEU	9.3

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Mol	Chain	Res	Type	RSRZ
39	DS	73	LEU	9.3
26	DA	896	A	9.3
2	AB	105	PHE	9.3
4	AD	135	LEU	9.3
47	B0	7	LEU	9.2
13	CM	65	LYS	9.2
4	AD	3	ARG	9.2
2	CB	133	LYS	9.2
46	DZ	152	ALA	9.2
46	DZ	99	TYR	9.2
25	AY	5	G	9.2
20	AT	62	LEU	9.1
31	DG	149	VAL	9.2
4	AD	11	LEU	9.1
9	CI	4	TYR	9.1
2	CB	88	ALA	9.1
2	AB	71	VAL	9.1
13	AM	19	LEU	9.1
19	CS	39	THR	9.1
23	CW	10	G	9.1
33	DI	88	ILE	9.1
10	CJ	34	VAL	9.1
21	CU	16	GLY	9.1
2	AB	185	ILE	9.0
49	D2	60	LEU	9.0
31	DG	63	ILE	9.0
51	D4	51	ASP	9.0
33	BI	97	ILE	9.0
2	AB	229	VAL	9.0
4	AD	138	TYR	9.0
2	CB	186	ALA	9.0
10	AJ	47	PHE	9.0
51	D4	52	THR	8.9
2	CB	80	ILE	8.9
13	CM	120	LYS	8.9
19	CS	80	TYR	8.8
2	CB	66	GLY	8.8
19	CS	6	LYS	8.8
1	CA	1034	G	8.8
2	AB	15	VAL	8.8
32	DH	113	VAL	8.8
14	CN	44	LEU	8.8

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Mol	Chain	Res	Type	RSRZ
6	AF	79	LEU	8.8
19	CS	15	LEU	8.7
13	AM	4	ILE	8.7
8	CH	137	VAL	8.7
8	AH	2	LEU	8.7
2	AB	223	ILE	8.7
31	DG	138	GLN	8.7
13	CM	78	ILE	8.7
46	DZ	7	ALA	8.7
12	CL	69	TYR	8.7
4	AD	174	LEU	8.7
11	AK	29	ILE	8.7
32	DH	36	PRO	8.7
23	CW	73	A	8.7
10	AJ	98	ILE	8.6
47	D0	37	LEU	8.6
50	D3	60	GLU	8.6
32	DH	107	VAL	8.6
5	CE	94	ALA	8.6
32	DH	50	VAL	8.6
4	CD	134	ASP	8.6
4	AD	134	ASP	8.6
2	AB	80	ILE	8.6
8	CH	13	ILE	8.6
9	CI	36	TYR	8.6
2	CB	228	GLY	8.5
3	CC	101	LEU	8.5
31	DG	60	LEU	8.5
31	DG	159	VAL	8.5
46	DZ	57	ILE	8.5
4	CD	157	LEU	8.5
22	CV	13	A	8.5
46	DZ	138	GLU	8.5
2	CB	93	VAL	8.5
3	AC	64	VAL	8.5
30	DF	140	LEU	8.5
9	AI	81	ILE	8.4
32	DH	103	LEU	8.4
46	BZ	144	LEU	8.4
16	AP	38	TYR	8.4
12	CL	55	VAL	8.4
46	DZ	149	SER	8.4

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Mol	Chain	Res	Type	RSRZ
19	CS	35	SER	8.4
19	CS	38	SER	8.4
39	DS	56	LEU	8.4
2	AB	97	TRP	8.3
30	DF	154	VAL	8.3
31	DG	151	ALA	8.3
8	CH	10	LEU	8.3
26	DA	2802	G	8.3
13	CM	7	VAL	8.3
4	CD	158	ILE	8.3
30	DF	146	ALA	8.3
2	AB	207	ALA	8.3
5	CE	90	VAL	8.3
9	CI	17	VAL	8.3
3	CC	120	VAL	8.2
34	DN	140	VAL	8.2
32	DH	7	LEU	8.2
31	DG	146	TYR	8.2
31	DG	152	LEU	8.2
46	DZ	163	LEU	8.2
2	CB	223	ILE	8.2
13	AM	56	LEU	8.2
19	AS	40	ILE	8.2
25	CY	6	G	8.2
46	BZ	141	VAL	8.2
18	CR	87	ARG	8.2
11	CK	19	ALA	8.1
32	DH	6	ARG	8.1
30	DF	12	LEU	8.1
45	DY	69	ALA	8.1
12	CL	70	ILE	8.1
5	CE	33	VAL	8.1
9	CI	110	GLU	8.1
19	CS	44	MET	8.1
32	DH	37	VAL	8.1
56	D9	16	VAL	8.1
30	DF	142	TRP	8.1
26	DA	1536	C	8.1
4	AD	2	GLY	8.1
45	DY	72	VAL	8.1
13	AM	123	ALA	8.1
44	DX	92	LEU	8.1

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Mol	Chain	Res	Type	RSRZ
46	BZ	114	GLY	8.1
16	AP	39	TYR	8.1
46	DZ	24	LEU	8.1
31	DG	155	MET	8.0
9	CI	49	PRO	8.0
19	CS	9	VAL	8.0
23	CW	31	A	8.0
10	CJ	84	GLN	8.0
9	CI	79	LEU	8.0
45	DY	1	MET	8.0
2	AB	61	LEU	8.0
13	CM	56	LEU	8.0
5	CE	6	PHE	8.0
18	AR	75	ILE	8.0
46	DZ	146	ILE	8.0
39	DS	39	ILE	8.0
2	AB	7	VAL	8.0
9	AI	109	VAL	8.0
19	CS	67	VAL	8.0
56	D9	37	GLY	8.0
39	DS	51	ALA	8.0
46	DZ	173	ALA	8.0
31	DG	139	LEU	8.0
32	DH	76	VAL	7.9
13	CM	48	LEU	7.9
4	CD	4	TYR	7.9
9	CI	42	ARG	7.9
4	AD	4	TYR	7.9
8	CH	111	ILE	7.9
19	CS	62	ILE	7.9
46	DZ	8	TYR	7.9
46	DZ	126	VAL	7.9
3	CC	152	ILE	7.9
3	CC	182	ILE	7.9
4	AD	158	ILE	7.9
32	DH	106	THR	7.9
2	AB	102	LEU	7.9
32	DH	71	LEU	7.9
25	AY	36	A	7.9
2	AB	173	ALA	7.9
13	CM	15	VAL	7.9
36	DP	125	VAL	7.9

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Mol	Chain	Res	Type	RSRZ
19	CS	43	GLU	7.8
10	CJ	50	ILE	7.8
46	BZ	120	ILE	7.8
46	DZ	147	GLY	7.8
8	CH	61	VAL	7.8
25	AY	48	C	7.8
46	DZ	144	LEU	7.8
14	CN	55	GLY	7.8
9	CI	65	VAL	7.8
9	CI	81	ILE	7.8
39	DS	82	ILE	7.8
2	AB	68	ILE	7.8
25	AY	38	A	7.8
21	CU	6	ARG	7.8
2	AB	208	ILE	7.7
9	AI	19	LEU	7.7
9	AI	106	ALA	7.7
32	DH	75	ALA	7.7
16	AP	36	ILE	7.7
18	AR	79	LEU	7.7
19	CS	3	ARG	7.7
18	CR	43	PHE	7.7
2	CB	132	LYS	7.7
7	CG	22	LEU	7.7
10	CJ	23	ILE	7.7
46	DZ	164	ALA	7.7
19	CS	20	LEU	7.7
8	CH	80	ILE	7.7
33	DI	72	LEU	7.7
39	DS	54	LEU	7.7
9	AI	65	VAL	7.7
16	CP	51	VAL	7.7
9	CI	75	ASP	7.7
33	DI	47	LEU	7.7
14	CN	56	VAL	7.6
44	DX	43	VAL	7.6
19	CS	63	THR	7.6
13	CM	94	ARG	7.6
45	DY	6	HIS	7.6
3	CC	81	GLY	7.6
4	AD	133	VAL	7.6
2	AB	98	LEU	7.6

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Mol	Chain	Res	Type	RSRZ
37	DQ	65	PHE	7.6
14	CN	2	ALA	7.6
19	CS	82	GLY	7.6
2	AB	55	PHE	7.6
2	AB	175	ARG	7.6
10	CJ	48	THR	7.6
33	DI	12	LEU	7.6
2	AB	216	SER	7.5
46	DZ	37	VAL	7.5
4	AD	122	ARG	7.5
54	D7	46	VAL	7.5
3	AC	169	ALA	7.5
14	CN	38	GLY	7.5
19	CS	8	GLY	7.5
3	AC	66	VAL	7.5
30	DF	186	ILE	7.5
2	CB	210	SER	7.5
12	CL	85	ILE	7.4
33	BI	101	LEU	7.4
44	DX	1	MET	7.4
45	DY	83	THR	7.4
46	DZ	104	PHE	7.4
23	CW	25	C	7.4
31	DG	88	ILE	7.4
9	CI	64	THR	7.4
8	CH	6	ILE	7.4
13	CM	9	ILE	7.4
31	DG	43	LEU	7.4
3	AC	153	VAL	7.4
3	CC	197	GLY	7.4
10	CJ	38	ILE	7.4
3	AC	101	LEU	7.4
37	DQ	33	GLY	7.4
16	CP	74	LEU	7.4
3	AC	168	ALA	7.4
41	DU	88	ILE	7.4
3	AC	204	LEU	7.4
2	CB	197	VAL	7.3
2	CB	122	PHE	7.3
46	DZ	150	LEU	7.3
32	DH	19	VAL	7.3
4	AD	110	PHE	7.3

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Mol	Chain	Res	Type	RSRZ
5	CE	31	LEU	7.3
36	DP	76	LYS	7.3
7	CG	82	GLY	7.3
46	DZ	88	PHE	7.3
3	CC	12	LEU	7.3
4	AD	8	VAL	7.3
8	CH	134	ILE	7.3
50	D3	2	PRO	7.3
10	CJ	8	LEU	7.3
1	CA	1035	A	7.3
13	CM	3	ARG	7.3
33	DI	85	GLU	7.3
33	DI	92	VAL	7.3
50	D3	43	ILE	7.3
56	D9	3	VAL	7.3
3	CC	160	ALA	7.3
13	AM	5	ALA	7.3
20	AT	66	ALA	7.3
33	BI	128	LEU	7.3
33	DI	77	LEU	7.3
2	CB	83	MET	7.2
4	AD	120	LEU	7.2
2	CB	184	VAL	7.2
32	DH	9	ILE	7.2
56	D9	26	ILE	7.2
32	DH	96	ALA	7.2
46	DZ	114	GLY	7.2
19	CS	69	HIS	7.2
9	CI	63	ILE	7.2
48	B1	98	LEU	7.2
13	AM	122	LYS	7.2
2	AB	182	ILE	7.2
33	DI	4	ILE	7.2
2	CB	102	LEU	7.2
32	DH	115	VAL	7.2
2	CB	161	ALA	7.2
20	AT	64	ASP	7.2
33	BI	120	ILE	7.2
20	CT	72	LEU	7.1
6	CF	9	VAL	7.1
19	CS	11	VAL	7.1
9	CI	106	ALA	7.1

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Mol	Chain	Res	Type	RSRZ
32	DH	25	LYS	7.1
54	D7	48	LYS	7.1
31	DG	25	TYR	7.1
2	CB	221	LEU	7.1
9	CI	85	LEU	7.1
11	CK	32	ILE	7.1
9	CI	102	LEU	7.1
14	AN	34	TYR	7.1
36	DP	1	MET	7.1
46	DZ	97	GLU	7.1
2	AB	187	LEU	7.1
31	BG	146	TYR	7.1
13	CM	19	LEU	7.1
51	D4	57	GLU	7.1
16	CP	80	PHE	7.1
46	DZ	141	VAL	7.1
9	CI	20	ARG	7.1
46	DZ	70	LEU	7.0
32	DH	95	ARG	7.0
3	AC	43	LEU	7.0
37	DQ	2	LEU	7.0
31	DG	136	ARG	7.0
10	CJ	88	LEU	7.0
11	CK	21	ILE	7.0
12	CL	68	ALA	7.0
30	DF	139	PHE	7.0
31	DG	29	TRP	7.0
46	BZ	104	PHE	7.0
13	CM	121	LYS	7.0
46	DZ	169	GLU	7.0
5	AE	89	ILE	7.0
9	CI	46	ALA	7.0
13	AM	9	ILE	7.0
33	DI	79	ILE	7.0
2	CB	216	SER	7.0
19	CS	42	PRO	7.0
2	AB	165	VAL	7.0
19	CS	79	THR	7.0
20	AT	63	ILE	7.0
23	AW	71	G	7.0
39	DS	49	VAL	7.0
34	DN	26	LEU	7.0

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Mol	Chain	Res	Type	RSRZ
47	D0	7	LEU	7.0
9	AI	126	SER	7.0
2	AB	122	PHE	6.9
19	CS	12	ASP	6.9
23	AW	70	G	6.9
9	CI	67	GLY	6.9
46	DZ	108	PRO	6.9
14	CN	61	TRP	6.9
33	DI	46	ALA	6.9
1	AA	1026	G	6.9
5	CE	67	VAL	6.9
21	CU	24	ARG	6.9
5	CE	11	ILE	6.9
31	DG	156	ASP	6.9
5	AE	90	VAL	6.9
20	AT	71	THR	6.9
31	DG	19	LEU	6.9
9	AI	59	PHE	6.9
5	AE	91	LEU	6.9
32	DH	24	VAL	6.9
3	AC	63	ASN	6.9
2	CB	219	VAL	6.8
4	AD	118	ARG	6.8
48	D1	26	ARG	6.8
5	CE	30	ALA	6.8
12	CL	56	ALA	6.8
23	CW	71	G	6.8
8	CH	93	VAL	6.8
47	D0	45	PHE	6.8
49	D2	25	VAL	6.8
3	AC	77	ILE	6.8
9	CI	112	LYS	6.8
4	AD	140	VAL	6.8
13	AM	22	ILE	6.8
23	CW	13	C	6.8
12	CL	64	TYR	6.8
45	DY	85	VAL	6.8
12	CL	100	ILE	6.8
2	AB	158	LEU	6.7
3	AC	94	LEU	6.7
19	CS	7	LYS	6.7
5	CE	22	GLY	6.7

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Mol	Chain	Res	Type	RSRZ
51	D4	64	GLY	6.7
15	CO	57	LEU	6.7
26	BA	942	A	6.7
8	AH	35	ILE	6.7
41	DU	17	ILE	6.7
2	AB	180	LEU	6.7
33	DI	145	VAL	6.7
23	CW	72	C	6.7
2	AB	58	ILE	6.7
5	AE	6	PHE	6.7
19	CS	14	HIS	6.7
17	CQ	36	ILE	6.7
33	BI	68	LEU	6.7
2	AB	210	SER	6.7
3	CC	194	GLY	6.7
25	AY	6	G	6.7
5	CE	123	LEU	6.7
8	AH	39	LEU	6.7
34	DN	23	LEU	6.7
36	DP	59	LEU	6.7
8	CH	64	LYS	6.7
30	DF	147	GLY	6.7
33	BI	140	LEU	6.7
17	CQ	73	VAL	6.7
3	AC	201	TYR	6.6
9	CI	62	TYR	6.6
23	CW	32	PSU	6.6
46	DZ	86	VAL	6.6
4	CD	122	ARG	6.6
2	AB	218	ALA	6.6
19	CS	70	LYS	6.6
9	CI	69	GLY	6.6
25	CY	5	G	6.6
10	CJ	65	LEU	6.6
17	CQ	84	LEU	6.6
30	DF	155	LEU	6.6
7	CG	33	ASP	6.6
33	BI	92	VAL	6.6
3	CC	167	TRP	6.6
48	B1	2	SER	6.6
30	DF	193	VAL	6.6
2	CB	55	PHE	6.6

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Mol	Chain	Res	Type	RSRZ
32	DH	16	SER	6.6
8	CH	39	LEU	6.6
12	CL	90	VAL	6.6
2	AB	232	PRO	6.6
16	CP	79	VAL	6.6
51	D4	44	THR	6.6
2	CB	75	LYS	6.6
32	DH	14	GLY	6.6
20	AT	73	HIS	6.6
32	DH	38	SER	6.6
4	AD	108	LEU	6.6
21	CU	17	THR	6.6
10	CJ	32	ALA	6.6
47	D0	21	LEU	6.6
32	DH	47	GLU	6.6
35	DO	114	ILE	6.6
46	BZ	146	ILE	6.6
46	DZ	72	ARG	6.5
47	B0	5	LYS	6.5
45	DY	73	ARG	6.5
8	CH	36	LEU	6.5
33	DI	123	LEU	6.5
39	DS	34	HIS	6.5
25	AY	47	U	6.5
3	AC	134	ILE	6.5
1	CA	1001	A	6.5
46	BZ	149	SER	6.5
26	DA	2160	G	6.5
30	DF	192	LEU	6.5
10	AJ	63	PHE	6.5
14	AN	37	PHE	6.5
12	AL	7	ILE	6.5
39	DS	50	SER	6.5
1	AA	1447	A	6.5
5	CE	110	LEU	6.5
6	AF	88	VAL	6.5
20	AT	75	ASN	6.5
46	BZ	139	VAL	6.5
2	CB	72	GLY	6.5
9	CI	59	PHE	6.5
2	AB	162	ILE	6.5
4	CD	5	ILE	6.5

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Mol	Chain	Res	Type	RSRZ
3	CC	184	TYR	6.5
7	AG	151	TYR	6.5
31	DG	57	ALA	6.5
50	D3	23	LEU	6.5
32	DH	124	GLU	6.5
3	AC	47	LEU	6.5
10	CJ	81	THR	6.5
13	CM	88	ARG	6.5
1	AA	1001	A	6.5
37	DQ	47	ILE	6.5
5	CE	133	TYR	6.4
3	AC	76	VAL	6.4
39	DS	52	SER	6.4
2	CB	57	PHE	6.4
20	AT	55	ILE	6.4
32	DH	51	ARG	6.4
33	DI	86	THR	6.4
3	CC	201	TYR	6.4
9	AI	37	PHE	6.4
30	DF	167	ALA	6.4
46	BZ	124	ILE	6.4
4	AD	115	ARG	6.4
26	DA	2164	C	6.4
31	DG	141	PHE	6.4
46	BZ	143	GLY	6.4
31	DG	135	LEU	6.4
14	AN	36	PHE	6.4
9	AI	77	ILE	6.4
31	BG	139	LEU	6.4
1	CA	1094	G	6.4
1	AA	1027	C	6.4
16	CP	73	LEU	6.4
50	D3	47	VAL	6.4
38	DR	70	LEU	6.3
53	D6	52	VAL	6.4
23	AW	44	G	6.3
25	CY	1	G	6.3
20	AT	12	ALA	6.3
2	CB	73	THR	6.3
4	CD	146	ILE	6.3
5	AE	118	ILE	6.3
10	AJ	72	VAL	6.3

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Mol	Chain	Res	Type	RSRZ
39	DS	40	ILE	6.3
3	CC	159	GLY	6.3
2	AB	133	LYS	6.3
9	AI	26	VAL	6.3
20	CT	9	ASN	6.3
32	DH	64	LEU	6.3
25	AY	39	PSU	6.3
39	DS	33	LYS	6.3
2	AB	77	ALA	6.3
11	AK	42	TRP	6.3
10	CJ	93	GLY	6.3
18	CR	85	LEU	6.3
28	DD	37	LEU	6.3
46	DZ	105	VAL	6.3
5	CE	76	ILE	6.3
9	AI	15	ALA	6.3
3	CC	181	ASN	6.3
8	CH	17	THR	6.3
8	CH	94	TYR	6.3
11	CK	82	VAL	6.3
50	D3	28	LEU	6.3
50	D3	25	ALA	6.3
3	AC	207	VAL	6.3
46	DZ	133	ILE	6.3
56	D9	1	MET	6.2
46	BZ	108	PRO	6.2
46	DZ	165	VAL	6.2
18	CR	76	LEU	6.2
30	DF	32	LEU	6.2
17	CQ	5	VAL	6.2
3	CC	178	LEU	6.2
19	CS	19	VAL	6.2
44	DX	2	LYS	6.2
46	DZ	157	LEU	6.2
4	CD	115	ARG	6.2
5	AE	119	LEU	6.2
9	AI	46	ALA	6.2
15	AO	87	ILE	6.2
30	DF	149	ASP	6.2
9	AI	24	GLY	6.2
46	DZ	161	VAL	6.2
3	AC	32	LEU	6.2

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Mol	Chain	Res	Type	RSRZ
8	CH	63	LEU	6.2
28	DD	38	LYS	6.2
2	AB	212	GLN	6.2
46	DZ	107	THR	6.2
45	DY	45	VAL	6.2
17	AQ	90	ILE	6.2
30	DF	208	GLY	6.2
33	DI	37	VAL	6.1
3	CC	154	SER	6.1
18	CR	63	GLN	6.1
2	CB	175	ARG	6.1
16	AP	48	TRP	6.1
41	DU	106	PHE	6.1
2	CB	203	GLY	6.1
19	CS	2	PRO	6.1
32	DH	148	ILE	6.1
3	CC	173	VAL	6.1
41	DU	9	VAL	6.1
9	CI	11	LYS	6.1
18	CR	58	LEU	6.1
4	CD	3	ARG	6.1
4	AD	185	PHE	6.1
8	CH	44	PHE	6.1
5	CE	13	ILE	6.1
38	DR	69	ASP	6.1
1	CA	1220	G	6.1
8	CH	92	ARG	6.1
3	AC	206	GLU	6.1
9	AI	61	ALA	6.1
19	CS	45	VAL	6.1
17	CQ	54	GLY	6.1
25	AY	21	A	6.1
31	DG	154	GLY	6.1
45	DY	35	TYR	6.1
4	CD	160	GLN	6.1
46	BZ	170	THR	6.1
4	CD	6	GLY	6.1
1	CA	1149	C	6.1
8	AH	79	VAL	6.1
53	D6	9	LEU	6.1
1	CA	1033	G	6.1
2	AB	66	GLY	6.1

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Mol	Chain	Res	Type	RSRZ
6	CF	8	ILE	6.1
13	CM	5	ALA	6.1
36	DP	75	ILE	6.1
32	DH	97	ARG	6.0
33	DI	30	LEU	6.0
32	DH	112	PRO	6.0
7	CG	2	ALA	6.0
11	CK	68	ALA	6.0
4	CD	126	ILE	6.0
5	CE	69	VAL	6.0
32	DH	44	VAL	6.0
16	CP	60	LEU	6.0
56	D9	2	LYS	6.0
1	CA	1028	C	6.0
9	CI	115	GLY	6.0
9	AI	10	ARG	6.0
2	AB	174	VAL	6.0
13	CM	45	VAL	6.0
17	CQ	21	VAL	6.0
32	DH	133	VAL	6.0
33	BI	142	VAL	6.0
44	DX	39	ILE	6.0
46	DZ	100	VAL	6.0
7	AG	86	GLN	6.0
31	DG	133	LEU	6.0
32	DH	55	PRO	6.0
19	CS	81	ARG	6.0
3	CC	87	LEU	6.0
10	CJ	62	HIS	6.0
14	CN	58	LYS	6.0
12	CL	18	VAL	6.0
2	CB	208	ILE	6.0
20	CT	63	ILE	6.0
9	CI	116	LYS	6.0
6	CF	75	LEU	6.0
8	AH	10	LEU	6.0
3	AC	68	VAL	6.0
5	CE	105	VAL	6.0
8	AH	61	VAL	6.0
16	AP	51	VAL	6.0
9	CI	74	ILE	6.0
3	CC	71	ALA	5.9

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Mol	Chain	Res	Type	RSRZ
17	CQ	44	ALA	5.9
10	CJ	55	LYS	5.9
3	AC	151	VAL	5.9
3	CC	29	TYR	5.9
50	D3	6	VAL	5.9
1	AA	1036	G	5.9
24	CX	7	G	5.9
8	AH	13	ILE	5.9
16	CP	19	ILE	5.9
32	DH	48	GLY	5.9
14	CN	35	ARG	5.9
46	DZ	98	MET	5.9
36	DP	114	ILE	5.9
2	CB	167	PRO	5.9
33	DI	81	VAL	5.9
47	D0	59	LEU	5.9
33	DI	122	GLU	5.9
2	AB	62	ALA	5.9
2	CB	173	ALA	5.9
45	DY	97	ARG	5.9
3	AC	26	LYS	5.9
10	AJ	73	ASP	5.9
17	CQ	6	LEU	5.9
15	AO	88	ARG	5.9
56	B9	17	ILE	5.9
32	DH	128	PRO	5.9
17	CQ	23	VAL	5.9
18	CR	62	GLU	5.9
46	DZ	25	PRO	5.9
11	CK	98	LEU	5.9
20	AT	20	LEU	5.9
7	CG	32	ARG	5.8
5	AE	92	LYS	5.8
3	CC	158	GLY	5.8
13	CM	34	LEU	5.8
33	DI	38	LEU	5.8
48	B1	97	LEU	5.8
16	AP	68	ASP	5.8
7	AG	84	ASN	5.8
13	CM	10	PRO	5.8
4	AD	97	LEU	5.8
33	DI	44	LEU	5.8

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Mol	Chain	Res	Type	RSRZ
13	CM	102	ARG	5.8
54	D7	47	ARG	5.8
11	CK	95	ILE	5.8
49	D2	50	ILE	5.8
9	CI	114	TYR	5.8
54	B7	46	VAL	5.8
4	AD	132	ARG	5.8
38	DR	68	ARG	5.8
13	AM	48	LEU	5.8
32	DH	2	SER	5.8
30	DF	173	VAL	5.8
4	AD	101	LEU	5.8
10	CJ	40	LEU	5.8
3	CC	174	PRO	5.8
2	AB	220	ASP	5.8
9	CI	105	ASP	5.8
33	DI	120	ILE	5.8
8	AH	9	MET	5.8
10	AJ	49	VAL	5.8
3	CC	175	LEU	5.8
5	AE	123	LEU	5.8
46	BZ	155	LEU	5.8
10	CJ	98	ILE	5.8
31	DG	70	VAL	5.8
2	AB	123	ALA	5.8
2	AB	177	ALA	5.8
2	CB	98	LEU	5.8
16	AP	73	LEU	5.8
19	AS	15	LEU	5.8
23	CW	26	A	5.8
33	BI	72	LEU	5.8
46	DZ	18	LEU	5.8
53	D6	34	LEU	5.8
30	DF	175	THR	5.8
5	CE	115	VAL	5.7
45	DY	87	LYS	5.7
2	CB	196	LEU	5.7
3	AC	100	ALA	5.7
6	CF	48	LEU	5.7
47	D0	69	PHE	5.7
33	DI	51	ILE	5.7
23	CW	15	G	5.7

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Mol	Chain	Res	Type	RSRZ
41	DU	63	VAL	5.7
4	AD	157	LEU	5.7
8	AH	63	LEU	5.7
31	DG	48	GLU	5.7
2	AB	172	ILE	5.7
11	CK	80	VAL	5.7
53	D6	10	LEU	5.7
32	DH	157	TYR	5.7
3	CC	177	THR	5.7
2	AB	226	ARG	5.7
3	AC	88	ARG	5.7
32	DH	26	VAL	5.7
46	DZ	39	VAL	5.7
4	CD	135	LEU	5.7
12	CL	83	VAL	5.7
11	CK	108	ILE	5.7
30	DF	33	LEU	5.7
33	DI	140	LEU	5.7
23	AW	3	C	5.7
55	D8	26	LYS	5.6
15	CO	29	VAL	5.6
2	CB	170	GLU	5.6
3	CC	204	LEU	5.6
46	DZ	174	VAL	5.6
16	AP	37	GLY	5.6
13	CM	105	THR	5.6
39	DS	37	ALA	5.6
47	D0	2	ALA	5.6
3	CC	80	GLY	5.6
3	CC	77	ILE	5.6
46	DZ	153	SER	5.6
4	AD	148	VAL	5.6
3	CC	10	PHE	5.6
23	CW	14	A	5.6
11	CK	94	ALA	5.6
2	CB	136	VAL	5.6
10	CJ	5	ARG	5.6
33	DI	3	VAL	5.6
19	AS	71	LEU	5.6
26	DA	2116	G	5.6
36	DP	110	TYR	5.6
46	BZ	102	LEU	5.6

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Mol	Chain	Res	Type	RSRZ
4	AD	70	ILE	5.6
23	CW	75	C	5.6
9	CI	28	VAL	5.6
17	AQ	11	VAL	5.6
51	D4	40	HIS	5.6
51	D4	69	LYS	5.6
32	DH	33	LEU	5.6
33	DI	35	LEU	5.6
13	CM	50	GLU	5.6
20	AT	69	GLY	5.5
2	CB	188	ALA	5.5
20	AT	29	LYS	5.5
51	D4	48	ARG	5.5
20	AT	18	GLN	5.5
12	CL	101	VAL	5.5
25	AY	22	G	5.5
2	CB	90	MET	5.5
31	DG	49	ASP	5.5
17	CQ	22	LEU	5.5
2	AB	201	ILE	5.5
3	AC	152	ILE	5.5
13	CM	87	TYR	5.5
2	CB	85	ALA	5.5
5	CE	34	VAL	5.5
8	CH	112	LEU	5.5
9	CI	77	ILE	5.5
10	CJ	20	ALA	5.5
26	BA	1555	C	5.5
2	AB	230	VAL	5.5
4	CD	148	VAL	5.5
9	CI	108	VAL	5.5
23	CW	23	A	5.5
30	DF	37	VAL	5.5
33	DI	16	GLY	5.5
9	CI	12	GLU	5.5
30	DF	170	LEU	5.5
2	AB	217	ARG	5.5
10	CJ	75	ILE	5.5
31	DG	46	ALA	5.5
26	BA	2139	A	5.5
5	AE	18	ARG	5.5
30	DF	191	ARG	5.5

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Mol	Chain	Res	Type	RSRZ
46	DZ	62	PRO	5.5
46	DZ	6	LYS	5.5
9	CI	43	ALA	5.5
32	DH	49	VAL	5.5
16	CP	48	TRP	5.5
23	CW	40	C	5.5
25	AY	3	C	5.5
50	D3	21	ALA	5.5
16	AP	80	PHE	5.4
9	CI	125	TYR	5.4
31	DG	110	ALA	5.4
23	CW	6	G	5.4
47	D0	3	HIS	5.4
4	CD	69	GLY	5.4
21	CU	15	ARG	5.4
5	CE	135	THR	5.4
4	AD	126	ILE	5.4
18	CR	83	GLU	5.4
19	AS	41	VAL	5.4
41	DU	79	PHE	5.4
46	BZ	111	VAL	5.4
12	CL	98	TYR	5.4
17	CQ	42	TYR	5.4
21	AU	6	ARG	5.4
39	DS	36	TYR	5.4
56	D9	24	TYR	5.4
31	BG	152	LEU	5.4
2	CB	205	ASP	5.4
32	DH	11	VAL	5.4
41	DU	90	VAL	5.4
2	AB	167	PRO	5.4
31	DG	142	PRO	5.4
2	AB	126	GLU	5.4
49	D2	53	LEU	5.4
14	CN	41	ARG	5.4
26	DA	2132	U	5.4
30	DF	174	VAL	5.4
3	CC	171	GLY	5.4
16	AP	49	LEU	5.4
46	DZ	9	TYR	5.4
5	CE	8	GLU	5.4
32	DH	114	VAL	5.4

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Mol	Chain	Res	Type	RSRZ
39	DS	31	SER	5.4
8	AH	45	ILE	5.4
14	CN	54	PRO	5.4
17	CQ	60	ILE	5.4
9	CI	5	TYR	5.4
13	AM	21	TYR	5.4
4	CD	179	GLU	5.4
26	DA	2136	C	5.4
32	DH	65	HIS	5.4
16	AP	2	VAL	5.4
31	DG	92	VAL	5.4
36	DP	95	VAL	5.4
46	DZ	71	VAL	5.4
2	CB	232	PRO	5.4
9	AI	33	PHE	5.4
37	DQ	64	ILE	5.4
16	AP	60	LEU	5.3
8	AH	4	ASP	5.3
12	AL	98	TYR	5.3
19	CS	52	TYR	5.3
3	CC	147	LYS	5.3
5	AE	88	LYS	5.3
12	AL	96	VAL	5.3
13	AM	53	VAL	5.3
2	CB	32	ILE	5.3
16	CP	76	GLN	5.3
18	CR	78	LEU	5.3
46	BZ	109	ALA	5.3
2	AB	233	SER	5.3
9	AI	125	TYR	5.3
32	DH	41	MET	5.3
3	CC	103	VAL	5.3
23	AW	56	C	5.3
25	CY	13	C	5.3
39	DS	87	PHE	5.3
2	AB	69	LEU	5.3
6	CF	79	LEU	5.3
20	AT	24	LEU	5.3
31	DG	111	LEU	5.3
49	D2	35	LEU	5.3
49	D2	61	LEU	5.3
9	CI	72	GLY	5.3

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Mol	Chain	Res	Type	RSRZ
39	DS	53	SER	5.3
54	D7	1	MET	5.3
2	AB	76	GLN	5.3
11	CK	99	GLN	5.3
45	DY	3	VAL	5.3
28	BD	276	LYS	5.3
8	CH	31	PHE	5.3
23	CW	44	G	5.3
2	AB	160	ASP	5.3
2	AB	184	VAL	5.3
2	CB	230	VAL	5.3
8	CH	32	LYS	5.3
16	AP	50	LYS	5.3
12	AL	100	ILE	5.3
33	BI	109	ILE	5.3
12	CL	27	LEU	5.3
12	CL	84	LEU	5.3
33	BI	75	LEU	5.3
39	BS	73	LEU	5.3
19	CS	36	ARG	5.3
23	AW	6	G	5.3
32	DH	104	GLU	5.3
32	DH	131	VAL	5.3
33	DI	144	VAL	5.3
36	DP	83	VAL	5.3
42	DV	72	VAL	5.3
21	CU	10	ARG	5.3
23	AW	13	C	5.3
6	AF	61	LEU	5.3
10	AJ	71	LEU	5.3
13	CM	25	ILE	5.3
20	CT	55	ILE	5.3
31	BG	39	ILE	5.3
4	CD	121	VAL	5.2
4	CD	166	LYS	5.2
46	DZ	118	GLN	5.2
2	AB	209	ARG	5.2
32	DH	54	ARG	5.2
3	AC	33	LEU	5.2
31	DG	120	LEU	5.2
32	DH	94	TYR	5.2
45	DY	55	TYR	5.2

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Mol	Chain	Res	Type	RSRZ
20	CT	100	ILE	5.2
51	D4	66	SER	5.2
20	AT	68	LYS	5.2
56	D9	15	LYS	5.2
1	AA	1001(A)	G	5.2
9	AI	108	VAL	5.2
2	CB	123	ALA	5.2
31	DG	137	GLU	5.2
36	DP	45	LEU	5.2
37	DQ	66	ILE	5.2
4	AD	136	PRO	5.2
5	AE	120	THR	5.2
46	DZ	143	GLY	5.2
19	CS	37	ARG	5.2
46	DZ	27	VAL	5.2
26	BA	2137	G	5.2
47	D0	5	LYS	5.2
49	D2	8	LYS	5.2
3	CC	193	TYR	5.2
8	CH	65	TYR	5.2
12	CL	32	PHE	5.2
31	DG	117	PHE	5.2
42	DV	101	GLY	5.2
42	DV	5	VAL	5.2
44	DX	33	LYS	5.2
3	CC	206	GLU	5.2
18	AR	31	LEU	5.2
32	DH	132	ARG	5.2
2	AB	28	PHE	5.2
10	AJ	4	ILE	5.2
13	CM	13	LYS	5.2
2	AB	164	VAL	5.2
30	DF	36	VAL	5.2
46	DZ	113	ALA	5.2
4	CD	161	ASN	5.2
2	AB	48	MET	5.2
5	CE	142	LEU	5.2
33	BI	77	LEU	5.2
37	DQ	34	LEU	5.2
3	CC	4	LYS	5.2
10	AJ	6	ILE	5.2
15	AO	82	ILE	5.2

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Mol	Chain	Res	Type	RSRZ
21	AU	17	THR	5.2
49	D2	57	ILE	5.2
7	AG	154	TYR	5.2
13	CM	61	GLU	5.2
19	CS	24	ALA	5.2
33	BI	107	VAL	5.2
39	DS	55	ALA	5.2
4	AD	21	LEU	5.2
42	DV	35	LEU	5.2
46	DZ	91	LEU	5.2
5	CE	118	ILE	5.2
1	CA	1111	A	5.1
16	CP	75	ARG	5.2
4	AD	121	VAL	5.1
4	CD	152	SER	5.1
2	AB	59	GLU	5.1
5	CE	91	LEU	5.1
6	CF	10	LEU	5.1
7	AG	74	GLU	5.1
12	CL	60	LEU	5.1
46	DZ	117	LEU	5.1
2	CB	200	ILE	5.1
13	CM	84	ILE	5.1
3	CC	53	ALA	5.1
2	AB	19	HIS	5.1
18	AR	34	TYR	5.1
32	DH	125	VAL	5.1
8	AH	5	PRO	5.1
15	AO	81	LEU	5.1
20	CT	99	LEU	5.1
30	DF	124	LEU	5.1
41	DU	95	LEU	5.1
9	CI	37	PHE	5.1
33	DI	54	GLN	5.1
3	CC	149	ALA	5.1
17	AQ	36	ILE	5.1
17	CQ	59	ILE	5.1
51	D4	14	ILE	5.1
9	AI	75	ASP	5.1
49	D2	1	MET	5.1
4	CD	120	LEU	5.1
8	CH	133	LEU	5.1

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Mol	Chain	Res	Type	RSRZ
14	CN	6	LEU	5.1
32	DH	87	LEU	5.1
41	DU	109	LEU	5.1
16	AP	76	GLN	5.1
4	AD	180	GLY	5.1
51	D4	42	PHE	5.1
9	CI	123	PRO	5.1
14	CN	4	LYS	5.1
5	AE	135	THR	5.1
11	AK	30	VAL	5.1
15	CO	3	ILE	5.1
33	DI	138	ILE	5.1
30	BF	156	LEU	5.1
10	CJ	46	ARG	5.1
2	CB	67	THR	5.1
4	AD	69	GLY	5.1
50	D3	3	ARG	5.1
19	CS	32	LYS	5.1
4	CD	67	ILE	5.1
26	BA	218	A	5.1
12	AL	5	PRO	5.1
3	CC	205	GLY	5.1
38	DR	21	TYR	5.1
43	DW	86	LEU	5.1
49	D2	24	LEU	5.1
2	CB	171	ALA	5.1
7	CG	26	PHE	5.1
13	AM	39	ILE	5.1
20	AT	80	ARG	5.1
37	DQ	103	MET	5.0
21	AU	21	TYR	5.0
25	AY	1	G	5.0
9	CI	71	SER	5.0
31	DG	178	PHE	5.0
21	CU	13	ILE	5.0
26	BA	943	C	5.0
31	DG	40	ASN	5.0
39	DS	48	LEU	5.0
8	CH	11	THR	5.0
32	DH	102	ALA	5.0
12	CL	71	PRO	5.0
30	DF	126	VAL	5.0

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Mol	Chain	Res	Type	RSRZ
41	DU	32	PHE	5.0
8	CH	109	ILE	5.0
31	DG	44	GLY	5.0
3	CC	196	LEU	5.0
33	BI	6	LEU	5.0
55	D8	61	LEU	5.0
46	BZ	164	ALA	5.0
45	DY	61	ILE	5.0
9	CI	127	LYS	5.0
31	DG	58	GLN	5.0
49	D2	9	GLN	5.0
3	CC	91	LEU	5.0
19	CS	75	ALA	5.0
26	DA	894	C	5.0
6	AF	6	VAL	5.0
15	CO	27	VAL	5.0
45	BY	7	VAL	5.0
9	AI	11	LYS	5.0
7	CG	37	ASN	5.0
39	DS	110	LEU	5.0
8	CH	16	ALA	5.0
33	DI	83	ALA	5.0
1	CA	1131	G	5.0
41	DU	12	ARG	5.0
25	AY	4	C	5.0
9	AI	14	VAL	5.0
43	DW	95	ILE	5.0
53	D6	7	ILE	5.0
3	CC	180	ALA	5.0
32	DH	67	LEU	5.0
6	CF	55	ASP	5.0
3	CC	151	VAL	5.0
1	CA	1325	C	5.0
33	DI	43	ASN	5.0
1	CA	1001(A)	G	5.0
32	DH	121	ILE	5.0
39	BS	37	ALA	4.9
39	DS	58	LEU	4.9
39	DS	79	ALA	4.9
55	D8	50	LEU	4.9
36	DP	32	THR	4.9
14	CN	49	HIS	4.9

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Mol	Chain	Res	Type	RSRZ
42	DV	14	VAL	4.9
7	CG	84	ASN	4.9
2	AB	148	TYR	4.9
46	DZ	148	ASP	4.9
3	CC	121	ALA	4.9
26	BA	2138	G	4.9
26	DA	2125	G	4.9
7	CG	148	ASN	4.9
56	D9	25	VAL	4.9
47	D0	65	GLY	4.9
13	AM	25	ILE	4.9
17	AQ	99	SER	4.9
45	DY	31	LEU	4.9
23	CW	11	C	4.9
46	BZ	116	VAL	4.9
26	DA	2793	G	4.9
7	AG	26	PHE	4.9
19	CS	30	LEU	4.9
31	DG	107	LEU	4.9
55	D8	16	ILE	4.9
19	CS	65	ASN	4.9
7	AG	87	VAL	4.9
7	CG	141	VAL	4.9
10	CJ	73	ASP	4.9
17	CQ	35	VAL	4.9
23	CW	56	C	4.9
46	DZ	111	VAL	4.9
45	DY	71	LYS	4.9
46	DZ	4	ARG	4.9
2	CB	213	LEU	4.9
4	AD	64	LEU	4.9
19	AS	16	LEU	4.9
32	BH	105	LEU	4.9
43	DW	82	LEU	4.9
4	AD	104	VAL	4.9
32	DH	82	GLY	4.9
50	D3	58	VAL	4.9
13	AM	3	ARG	4.9
31	DG	153	ARG	4.9
20	AT	77	ALA	4.9
13	CM	70	LEU	4.9
48	B1	82	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
6	AF	63	TYR	4.9
37	DQ	63	LYS	4.9
55	D8	58	ILE	4.9
31	DG	86	MET	4.9
17	AQ	35	VAL	4.9
46	DZ	58	VAL	4.9
3	CC	200	ALA	4.9
2	AB	8	LYS	4.9
42	DV	39	LEU	4.9
7	CG	75	VAL	4.8
17	CQ	10	VAL	4.8
23	CW	45	U	4.8
31	DG	67	LYS	4.8
4	AD	155	LEU	4.8
13	AM	114	ARG	4.8
15	CO	31	LEU	4.8
31	BG	103	LEU	4.8
31	BG	106	LEU	4.8
51	D4	68	ARG	4.8
8	CH	138	TRP	4.8
3	CC	130	VAL	4.8
12	CL	43	VAL	4.8
30	DF	105	VAL	4.8
9	AI	76	ALA	4.8
20	CT	28	ALA	4.8
26	DA	2173	A	4.8
16	CP	49	LEU	4.8
3	CC	199	LYS	4.8
11	CK	29	ILE	4.8
28	DD	271	ILE	4.8
32	DH	111	HIS	4.8
1	AA	104	G	4.8
44	DX	69	TYR	4.8
1	CA	1354	C	4.8
10	CJ	83	GLU	4.8
13	CM	80	ARG	4.8
3	CC	7	PRO	4.8
4	CD	2	GLY	4.8
7	CG	34	GLY	4.8
36	DP	57	THR	4.8
26	BA	2141	A	4.8
11	CK	96	ARG	4.8

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Mol	Chain	Res	Type	RSRZ
6	AF	9	VAL	4.8
21	CU	2	GLY	4.8
25	CY	18	G	4.8
26	DA	2803	C	4.8
2	AB	149	LEU	4.8
18	CR	79	LEU	4.8
31	DG	64	THR	4.8
42	DV	46	VAL	4.8
9	CI	21	PRO	4.8
10	CJ	31	GLY	4.8
16	CP	70	ALA	4.8
18	AR	73	ALA	4.8
33	DI	100	ALA	4.8
32	DH	53	GLU	4.8
2	AB	57	PHE	4.8
4	CD	196	LEU	4.8
29	DE	49	LEU	4.8
23	CW	2	C	4.8
47	B0	2	ALA	4.8
2	CB	206	ASP	4.8
6	AF	48	LEU	4.8
9	AI	50	LEU	4.8
41	DU	83	LEU	4.8
49	D2	54	LYS	4.8
17	CQ	19	VAL	4.8
31	BG	149	VAL	4.8
32	DH	12	PRO	4.8
34	BN	52	VAL	4.8
14	AN	2	ALA	4.8
2	AB	16	HIS	4.7
33	DI	121	LYS	4.7
12	CL	67	THR	4.7
31	BG	102	PHE	4.7
5	CE	114	GLY	4.7
5	CE	55	VAL	4.7
46	DZ	56	VAL	4.7
50	D3	59	VAL	4.7
2	CB	74	LYS	4.7
3	CC	5	ILE	4.7
4	AD	147	ALA	4.7
35	DO	31	LYS	4.7
1	AA	403	C	4.7

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Mol	Chain	Res	Type	RSRZ
46	BZ	118	GLN	4.7
9	CI	40	LEU	4.7
30	BF	17	ARG	4.7
36	DP	15	ARG	4.7
46	BZ	115	GLY	4.7
46	DZ	44	PHE	4.7
32	DH	13	LYS	4.7
32	DH	134	SER	4.7
39	DS	76	LYS	4.7
7	CG	86	GLN	4.7
7	CG	135	VAL	4.7
1	CA	1036	G	4.7
20	AT	33	ILE	4.7
7	CG	81	GLY	4.7
21	CU	11	GLY	4.7
43	DW	112	GLY	4.7
49	D2	29	LYS	4.7
45	BY	90	LEU	4.7
46	DZ	13	GLU	4.7
3	AC	189	ALA	4.7
9	CI	119	ALA	4.7
13	AM	45	VAL	4.7
14	CN	59	ALA	4.7
39	DS	57	LYS	4.7
5	CE	66	MET	4.7
19	CS	64	GLU	4.7
10	CJ	28	ARG	4.7
9	CI	33	PHE	4.7
17	AQ	27	PHE	4.7
9	AI	55	ALA	4.7
33	BI	36	ALA	4.7
37	DQ	121	ALA	4.7
45	DY	4	LYS	4.7
1	CA	1112	C	4.7
4	AD	105	VAL	4.7
46	DZ	116	VAL	4.7
55	D8	23	VAL	4.7
2	AB	72	GLY	4.7
47	B0	6	GLY	4.7
3	CC	30	ARG	4.7
44	DX	3	THR	4.7
2	CB	220	ASP	4.7

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Mol	Chain	Res	Type	RSRZ
32	DH	8	PRO	4.7
3	CC	23	TYR	4.7
13	AM	60	VAL	4.7
13	CM	21	TYR	4.7
33	DI	36	ALA	4.7
12	AL	85	ILE	4.7
33	BI	79	ILE	4.7
34	DN	30	ILE	4.7
10	CJ	41	PRO	4.6
3	AC	193	TYR	4.6
12	CL	66	VAL	4.6
21	AU	18	TYR	4.6
32	DH	79	VAL	4.6
5	CE	40	ARG	4.6
12	CL	89	ARG	4.6
8	AH	6	ILE	4.6
18	CR	70	ILE	4.6
45	DY	44	ILE	4.6
26	DA	2131	G	4.6
46	DZ	69	THR	4.6
8	AH	59	LEU	4.6
33	DI	68	LEU	4.6
33	DI	128	LEU	4.6
46	DZ	61	LEU	4.6
7	CG	76	ARG	4.6
51	D4	58	ARG	4.6
8	AH	48	TYR	4.6
1	AA	160	A	4.6
23	CW	7	A	4.6
17	CQ	90	ILE	4.6
4	CD	141	ARG	4.6
44	DX	68	ARG	4.6
49	D2	10	LEU	4.6
5	CE	148	VAL	4.6
9	AI	78	LYS	4.6
3	CC	145	GLY	4.6
21	AU	2	GLY	4.6
41	DU	18	LEU	4.6
48	D1	28	GLY	4.6
7	AG	40	ALA	4.6
41	DU	21	ALA	4.6
13	CM	74	VAL	4.6

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Mol	Chain	Res	Type	RSRZ
19	CS	13	ASP	4.6
46	BZ	165	VAL	4.6
3	CC	6	HIS	4.6
3	CC	190	ARG	4.6
9	CI	80	GLY	4.6
46	DZ	106	GLY	4.6
3	CC	14	ILE	4.6
31	DG	144	ILE	4.6
34	DN	63	THR	4.6
4	CD	21	LEU	4.6
5	CE	43	LEU	4.6
12	AL	93	LEU	4.6
31	DG	90	LEU	4.6
26	DA	2119	A	4.6
10	CJ	29	ARG	4.6
17	CQ	71	PHE	4.6
33	DI	142	VAL	4.6
36	DP	51	PHE	4.6
49	D2	55	ARG	4.6
2	CB	231	GLU	4.6
3	AC	35	GLU	4.6
16	AP	74	LEU	4.6
45	DY	96	ILE	4.6
1	CA	1023	G	4.6
9	CI	111	ARG	4.6
3	AC	103	VAL	4.6
47	B0	3	HIS	4.6
50	D3	54	VAL	4.6
45	DY	43	ASN	4.6
9	AI	113	LYS	4.6
26	BA	940	C	4.6
31	DG	158	ALA	4.6
33	BI	98	ALA	4.6
38	DR	67	LEU	4.6
2	CB	212	GLN	4.5
19	AS	19	VAL	4.5
7	CG	62	PHE	4.5
23	AW	69	G	4.5
12	AL	89	ARG	4.5
4	AD	176	LEU	4.5
6	CF	81	ILE	4.5
18	AR	40	LEU	4.5

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Mol	Chain	Res	Type	RSRZ
49	D2	32	LEU	4.5
7	CG	66	VAL	4.5
32	DH	31	GLY	4.5
45	DY	7	VAL	4.5
47	D0	52	GLY	4.5
12	AL	23	LYS	4.5
46	BZ	169	GLU	4.5
15	CO	25	THR	4.5
4	CD	164	ALA	4.5
4	CD	64	LEU	4.5
7	CG	101	LEU	4.5
20	AT	13	LEU	4.5
38	DR	65	LEU	4.5
50	D3	53	LEU	4.5
14	CN	42	ILE	4.5
44	DX	28	PHE	4.5
46	BZ	69	THR	4.5
3	AC	175	LEU	4.5
44	DX	9	LEU	4.5
3	AC	124	ILE	4.5
39	DS	20	ARG	4.5
46	DZ	115	GLY	4.5
5	CE	41	VAL	4.5
32	DH	73	ALA	4.5
51	D4	55	ARG	4.5
8	CH	130	GLY	4.5
30	DF	150	GLY	4.5
45	DY	14	LEU	4.5
32	DH	151	ILE	4.5
46	BZ	171	ILE	4.5
2	AB	81	VAL	4.5
6	AF	89	MET	4.5
20	AT	21	LYS	4.5
1	AA	1257	U	4.5
26	BA	2901	A	4.5
3	CC	9	GLY	4.5
9	CI	57	GLY	4.5
8	CH	119	LEU	4.5
25	AY	40	C	4.5
3	AC	55	VAL	4.5
11	AK	25	TYR	4.5
31	DG	87	PRO	4.5

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Mol	Chain	Res	Type	RSRZ
23	CW	50	U	4.5
8	AH	36	LEU	4.5
17	AQ	98	LEU	4.5
45	DY	63	LYS	4.5
9	CI	73	GLN	4.5
30	DF	205	ARG	4.5
30	DF	183	VAL	4.5
32	DH	4	ILE	4.5
33	DI	18	VAL	4.5
56	B9	7	VAL	4.5
2	CB	100	GLY	4.4
9	CI	8	GLY	4.4
7	AG	43	PHE	4.4
32	DH	137	ASP	4.4
38	DR	10	LEU	4.4
4	AD	181	MET	4.4
2	AB	200	ILE	4.4
52	B5	60	VAL	4.4
10	CJ	78	ASN	4.4
36	DP	130	PHE	4.4
38	DR	47	PHE	4.4
33	BI	93	THR	4.4
30	DF	181	LEU	4.4
37	DQ	1	MET	4.4
47	D0	4	LYS	4.4
9	CI	26	VAL	4.4
3	AC	182	ILE	4.4
1	CA	1318	A	4.4
25	CY	54	5MU	4.4
2	CB	23	ARG	4.4
4	AD	54	TYR	4.4
32	DH	83	TYR	4.4
48	D1	85	LEU	4.4
2	CB	99	GLY	4.4
12	CL	48	PRO	4.4
23	AW	5	G	4.4
29	DE	81	ILE	4.4
41	DU	65	ILE	4.4
53	D6	20	ASN	4.4
5	CE	45	PHE	4.4
2	AB	196	LEU	4.4
34	DN	116	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
36	BP	147	LEU	4.4
5	CE	81	GLU	4.4
13	CM	119	GLY	4.4
32	DH	69	ARG	4.4
32	DH	110	SER	4.4
55	D8	22	VAL	4.4
5	CE	80	ILE	4.4
10	CJ	33	GLN	4.4
46	DZ	151	HIS	4.4
4	AD	19	LEU	4.4
5	AE	139	LEU	4.4
15	CO	32	LEU	4.4
18	AR	66	LEU	4.4
18	CR	31	LEU	4.4
33	DI	5	LEU	4.4
42	DV	94	LEU	4.4
51	D4	32	TYR	4.4
51	D4	54	GLY	4.4
3	CC	183	ASP	4.4
13	AM	15	VAL	4.4
13	CM	101	GLN	4.4
17	CQ	57	VAL	4.4
42	DV	37	VAL	4.4
46	DZ	23	LYS	4.4
6	AF	52	ILE	4.4
9	CI	82	ALA	4.4
2	CB	137	ARG	4.4
10	AJ	45	ARG	4.4
4	CD	110	PHE	4.4
4	CD	188	LEU	4.4
32	DH	98	LEU	4.4
33	BI	130	TYR	4.4
48	D1	82	LEU	4.4
50	D3	37	LEU	4.4
56	D9	33	LYS	4.4
42	DV	80	GLN	4.4
11	CK	30	VAL	4.4
46	DZ	119	GLU	4.4
6	AF	8	ILE	4.4
14	CN	29	ARG	4.4
15	CO	87	ILE	4.4
35	DO	19	ILE	4.4

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Mol	Chain	Res	Type	RSRZ
41	DU	14	HIS	4.4
2	CB	166	ASP	4.3
51	D4	65	ASP	4.3
2	CB	131	PRO	4.3
10	CJ	19	SER	4.3
38	DR	51	LEU	4.3
12	CL	120	TYR	4.3
39	BS	74	ALA	4.3
16	AP	4	ILE	4.3
19	CS	84	GLY	4.3
23	CW	9	A	4.3
23	CW	19	G	4.3
25	AY	23	A	4.3
31	BG	63	ILE	4.3
41	DU	6	THR	4.3
19	CS	74	PHE	4.3
9	CI	50	LEU	4.3
18	CR	44	LEU	4.3
26	DA	2794	C	4.3
42	DV	73	SER	4.3
3	CC	150	LYS	4.3
8	CH	79	VAL	4.3
13	CM	53	VAL	4.3
31	DG	47	LYS	4.3
31	DG	131	TYR	4.3
32	DH	85	LYS	4.3
10	CJ	36	GLY	4.3
33	DI	97	ILE	4.3
33	BI	52	ARG	4.3
48	D1	2	SER	4.3
1	CA	1024	G	4.3
3	AC	150	LYS	4.3
3	AC	196	LEU	4.3
12	CL	77	LEU	4.3
26	DA	2894	G	4.3
40	DT	114	LEU	4.3
4	AD	170	VAL	4.3
6	AF	90	VAL	4.3
5	CE	29	GLY	4.3
37	DQ	32	TYR	4.3
2	AB	231	GLU	4.3
3	AC	179	ARG	4.3

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Mol	Chain	Res	Type	RSRZ
7	CG	4	ARG	4.3
5	AE	80	ILE	4.3
32	DH	68	THR	4.3
14	CN	50	LYS	4.3
30	DF	13	SER	4.3
51	D4	29	PRO	4.3
19	CS	53	ASN	4.3
2	CB	16	HIS	4.3
46	DZ	22	GLY	4.3
3	AC	170	GLN	4.3
25	CY	53	G	4.3
26	DA	2133	G	4.3
6	AF	26	ILE	4.3
32	DH	84	SER	4.3
33	BI	38	LEU	4.3
4	AD	16	GLY	4.3
7	CG	154	TYR	4.3
11	AK	50	TYR	4.3
3	CC	192	THR	4.3
9	AI	98	PRO	4.3
7	AG	120	ILE	4.3
23	CW	27	G	4.3
23	CW	30	G	4.3
26	DA	883	G	4.3
31	DG	115	ARG	4.3
32	DH	57	ASP	4.3
33	DI	101	LEU	4.3
36	DP	112	LEU	4.3
3	AC	27	LYS	4.3
31	DG	84	LYS	4.3
56	B9	25	VAL	4.3
31	BG	88	ILE	4.3
32	DH	89	ILE	4.3
36	DP	100	LEU	4.2
39	DS	29	PHE	4.2
4	CD	117	ALA	4.2
45	DY	30	VAL	4.2
50	D3	29	ARG	4.2
4	AD	165	MET	4.2
41	DU	13	LYS	4.2
2	AB	135	GLN	4.2
40	DT	75	ILE	4.2

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Mol	Chain	Res	Type	RSRZ
3	AC	42	LEU	4.2
7	AG	101	LEU	4.2
17	CQ	43	LEU	4.2
30	BF	19	GLU	4.2
40	DT	99	LEU	4.2
42	BV	38	LEU	4.2
5	AE	69	VAL	4.2
11	CK	84	VAL	4.2
16	AP	21	VAL	4.2
33	BI	144	VAL	4.2
46	BZ	152	ALA	4.2
2	AB	73	THR	4.2
3	AC	98	ASN	4.2
32	DH	135	GLY	4.2
23	AW	20	U	4.2
26	BA	2902	G	4.2
3	AC	188	LEU	4.2
29	BE	195	LEU	4.2
54	D7	23	ARG	4.2
13	CM	97	PRO	4.2
32	DH	40	GLU	4.2
23	AW	4	C	4.2
35	DO	96	THR	4.2
45	BY	2	ARG	4.2
47	B0	4	LYS	4.2
17	AQ	88	TYR	4.2
5	CE	32	VAL	4.2
8	AH	31	PHE	4.2
18	AR	29	PHE	4.2
35	DO	99	PHE	4.2
32	DH	18	GLU	4.2
13	AM	10	PRO	4.2
46	BZ	147	GLY	4.2
46	DZ	167	PRO	4.2
1	CA	1357	A	4.2
26	BA	944	C	4.2
17	AQ	60	ILE	4.2
33	DI	9	LEU	4.2
3	CC	187	ALA	4.2
4	AD	38	TYR	4.2
56	B9	26	ILE	4.2
11	CK	97	ALA	4.2

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Mol	Chain	Res	Type	RSRZ
3	AC	78	GLY	4.2
6	CF	6	VAL	4.2
29	DE	72	VAL	4.2
41	DU	40	PHE	4.2
48	D1	53	VAL	4.2
48	D1	62	VAL	4.2
9	AI	49	PRO	4.2
2	CB	204	ASN	4.2
32	DH	3	ARG	4.2
35	DO	29	ASN	4.2
40	BT	38	ASN	4.2
50	D3	17	LYS	4.2
55	D8	59	LYS	4.2
11	AK	57	THR	4.2
4	CD	94	LEU	4.2
5	CE	71	LEU	4.2
7	CG	85	TYR	4.2
4	AD	7	PRO	4.2
7	CG	139	GLU	4.2
25	AY	60	U	4.2
12	CL	13	LYS	4.2
3	CC	179	ARG	4.2
41	DU	10	ARG	4.2
1	CA	1088	G	4.2
11	AK	21	ILE	4.2
4	AD	68	TYR	4.1
46	DZ	166	SER	4.1
51	D4	53	GLU	4.1
1	AA	174	C	4.1
23	CW	41	C	4.1
25	AY	49	C	4.1
26	BA	2183	C	4.1
26	DA	652(T)	C	4.1
18	CR	84	LYS	4.1
7	AG	76	ARG	4.1
12	CL	93	LEU	4.1
13	CM	81	LEU	4.1
20	CT	59	ALA	4.1
36	DP	115	LEU	4.1
4	AD	15	GLU	4.1
3	CC	76	VAL	4.1
6	CF	52	ILE	4.1

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Mol	Chain	Res	Type	RSRZ
10	AJ	23	ILE	4.1
12	AL	18	VAL	4.1
33	BI	4	ILE	4.1
16	AP	17	TYR	4.1
1	CA	1002	G	4.1
23	CW	28	G	4.1
12	AL	67	THR	4.1
3	AC	34	LEU	4.1
36	DP	27	HIS	4.1
2	CB	174	VAL	4.1
7	AG	77	SER	4.1
7	CG	91	VAL	4.1
9	AI	63	ILE	4.1
12	CL	104	VAL	4.1
30	BF	9	ILE	4.1
38	DR	40	LYS	4.1
2	CB	87	ARG	4.1
5	AE	133	TYR	4.1
8	CH	4	ASP	4.1
8	CH	8	ASP	4.1
8	CH	43	GLY	4.1
26	DA	2801(A)	A	4.1
6	CF	21	LEU	4.1
30	DF	41	LEU	4.1
33	BI	47	LEU	4.1
36	DP	85	LEU	4.1
2	AB	109	SER	4.1
9	CI	83	ARG	4.1
10	CJ	45	ARG	4.1
17	CQ	9	VAL	4.1
16	CP	4	ILE	4.1
50	D3	38	GLU	4.1
51	D4	25	TYR	4.1
40	DT	113	LYS	4.1
1	CA	1150	U	4.1
31	BG	151	ALA	4.1
4	AD	66	ARG	4.1
15	CO	66	LEU	4.1
7	CG	73	MET	4.1
5	AE	23	GLY	4.1
6	AF	60	PHE	4.1
12	AL	69	TYR	4.1

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Mol	Chain	Res	Type	RSRZ
17	CQ	51	TYR	4.1
13	CM	76	ALA	4.1
13	CM	77	ASN	4.1
20	CT	49	ALA	4.1
2	AB	118	LEU	4.1
7	CG	16	LEU	4.1
18	CR	68	LYS	4.1
43	DW	85	VAL	4.1
45	DY	42	VAL	4.1
47	D0	6	GLY	4.1
4	AD	10	ARG	4.1
13	CM	114	ARG	4.1
26	BA	2807	C	4.1
1	CA	1373	G	4.1
14	AN	21	TYR	4.1
28	DD	155	LEU	4.1
18	AR	77	GLY	4.1
41	DU	8	VAL	4.1
47	D0	38	VAL	4.1
21	AU	7	ARG	4.1
2	CB	108	ILE	4.1
41	DU	62	ILE	4.1
1	CA	1110	A	4.0
1	CA	1219	U	4.0
5	AE	132	ALA	4.0
7	AG	4	ARG	4.0
7	CG	38	LEU	4.0
10	CJ	60	ARG	4.0
12	AL	84	LEU	4.0
17	CQ	72	ARG	4.0
50	D3	27	GLY	4.0
3	AC	99	VAL	4.0
12	AL	83	VAL	4.0
17	CQ	56	VAL	4.0
12	CL	99	HIS	4.0
51	D4	22	ILE	4.0
44	DX	6	ASP	4.0
4	CD	118	ARG	4.0
7	AG	78	ARG	4.0
22	CV	15	A	4.0
34	DN	33	LEU	4.0
36	DP	123	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
33	DI	21	VAL	4.0
44	DX	54	VAL	4.0
7	AG	156	TRP	4.0
30	DF	206	ILE	4.0
32	DH	109	PHE	4.0
6	AF	76	ALA	4.0
35	DO	33	ALA	4.0
36	DP	79	ARG	4.0
50	B3	29	ARG	4.0
30	DF	171	PRO	4.0
36	DP	118	GLY	4.0
5	AE	110	LEU	4.0
45	BY	67	LEU	4.0
24	CX	76	A	4.0
26	DA	2161	C	4.0
12	AL	6	THR	4.0
32	DH	136	ILE	4.0
16	AP	41	PRO	4.0
31	DG	2	PRO	4.0
46	BZ	163	LEU	4.0
1	CA	1371	G	4.0
25	AY	24	G	4.0
26	DA	614(B)	G	4.0
3	CC	15	THR	4.0
13	AM	119	GLY	4.0
13	CM	63	THR	4.0
17	CQ	7	THR	4.0
19	AS	33	THR	4.0
36	DP	31	ALA	4.0
15	CO	67	LEU	4.0
41	DU	36	ARG	4.0
37	DQ	81	VAL	4.0
9	AI	127	LYS	4.0
20	AT	65	LYS	4.0
3	CC	148	GLY	4.0
2	AB	186	ALA	4.0
9	CI	13	ALA	4.0
13	AM	30	ALA	4.0
26	DA	100	G	4.0
26	DA	2120	G	4.0
31	DG	179	PRO	4.0
36	DP	78	PRO	4.0

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Mol	Chain	Res	Type	RSRZ
16	CP	36	ILE	4.0
22	AV	12	A	4.0
31	DG	80	PHE	4.0
36	DP	91	PHE	4.0
3	CC	85	ARG	4.0
26	BA	941	U	4.0
4	CD	155	LEU	4.0
5	CE	139	LEU	4.0
12	CL	28	LYS	4.0
28	DD	177	LEU	4.0
30	DF	156	LEU	4.0
33	DI	45	LYS	4.0
52	D5	58	LEU	4.0
33	DI	19	VAL	4.0
2	AB	12	GLU	4.0
10	CJ	87	THR	4.0
11	CK	126	ARG	4.0
56	D9	5	ALA	4.0
14	CN	7	ILE	4.0
28	DD	270	ILE	4.0
23	CW	12	U	4.0
31	DG	74	LYS	4.0
1	CA	1021	G	3.9
4	CD	162	LEU	3.9
25	AY	19	G	3.9
26	DA	11	G	3.9
12	CL	36	VAL	3.9
34	DN	52	VAL	3.9
4	CD	159	ARG	3.9
8	CH	104	ARG	3.9
2	AB	13	ALA	3.9
7	CG	88	PRO	3.9
9	CI	45	ALA	3.9
10	CJ	39	PRO	3.9
11	AK	69	ALA	3.9
11	AK	43	SER	3.9
19	CS	77	THR	3.9
45	DY	65	ALA	3.9
13	CM	16	ASP	3.9
7	AG	42	ILE	3.9
28	DD	24	ILE	3.9
3	AC	178	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
3	CC	13	GLY	3.9
5	CE	119	LEU	3.9
11	CK	92	GLU	3.9
28	DD	268	ARG	3.9
36	DP	81	GLN	3.9
39	DS	3	ARG	3.9
44	DX	7	VAL	3.9
23	CW	49	C	3.9
32	DH	27	LYS	3.9
3	AC	36	ASP	3.9
5	CE	75	THR	3.9
18	AR	30	ASP	3.9
9	CI	88	TYR	3.9
29	DE	26	ILE	3.9
31	BG	141	PHE	3.9
31	DG	77	ILE	3.9
41	DU	80	ILE	3.9
10	AJ	46	ARG	3.9
8	CH	15	ASN	3.9
16	CP	30	GLY	3.9
14	CN	47	LEU	3.9
29	DE	5	LEU	3.9
31	DG	62	LEU	3.9
42	DV	20	LEU	3.9
2	CB	91	PRO	3.9
46	DZ	21	ALA	3.9
10	CJ	61	GLU	3.9
25	AY	35	A	3.9
56	B9	24	TYR	3.9
5	CE	42	GLY	3.9
10	AJ	50	ILE	3.9
25	CY	12	U	3.9
48	D1	37	ILE	3.9
1	AA	1024	G	3.9
26	DA	1537	G	3.9
39	DS	98	VAL	3.9
2	AB	130	ARG	3.9
1	AA	1000	U	3.9
8	AH	80	ILE	3.9
15	AO	69	TYR	3.9
25	AY	13	C	3.9
25	CY	61	C	3.9

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Mol	Chain	Res	Type	RSRZ
46	DZ	48	PHE	3.9
3	CC	43	LEU	3.9
2	AB	93	VAL	3.9
56	B9	16	VAL	3.9
2	CB	21	ARG	3.9
2	CB	226	ARG	3.9
13	AM	108	ARG	3.9
45	DY	74	PRO	3.9
4	AD	175	SER	3.9
19	AS	68	GLY	3.9
13	CM	82	MET	3.9
23	CW	39	PSU	3.9
39	DS	92	TYR	3.9
17	CQ	98	LEU	3.9
1	CA	1066	C	3.9
2	CB	183	PRO	3.9
23	AW	73	A	3.9
55	D8	21	LYS	3.9
13	CM	72	ALA	3.9
5	AE	74	GLY	3.9
14	CN	22	THR	3.9
1	CA	1068	G	3.9
7	CG	103	TRP	3.9
23	CW	47	U	3.9
26	DA	2110	G	3.9
32	DH	42	ARG	3.9
17	AQ	100	LYS	3.9
4	CD	101	LEU	3.9
5	CE	89	ILE	3.9
12	AL	105	TYR	3.9
33	BI	126	TYR	3.9
33	DI	25	TYR	3.9
33	DI	58	LEU	3.9
33	DI	116	LEU	3.9
7	CG	39	ALA	3.8
9	CI	122	ALA	3.8
39	BS	77	ALA	3.8
49	D2	58	ALA	3.8
6	AF	58	GLY	3.8
45	DY	29	GLU	3.8
4	AD	168	ARG	3.8
7	AG	79	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
13	CM	108	ARG	3.8
47	D0	49	LYS	3.8
53	D6	8	LYS	3.8
41	DU	69	CYS	3.8
5	AE	129	ILE	3.8
6	AF	10	LEU	3.8
15	CO	15	PHE	3.8
20	CT	33	ILE	3.8
34	BN	71	ILE	3.8
34	DN	60	ILE	3.8
15	CO	60	VAL	3.8
28	DD	117	VAL	3.8
31	BG	25	TYR	3.8
1	CA	1108	G	3.8
23	CW	65	G	3.8
26	BA	930	G	3.8
12	AL	91	LYS	3.8
45	BY	73	ARG	3.8
22	CV	23	A	3.8
25	CY	26	A	3.8
46	BZ	121	HIS	3.8
13	CM	8	GLU	3.8
4	AD	162	LEU	3.8
3	AC	120	VAL	3.8
12	CL	7	ILE	3.8
30	DF	176	LEU	3.8
12	CL	96	VAL	3.8
30	DF	114	VAL	3.8
40	BT	37	GLY	3.8
4	AD	209	ARG	3.8
44	DX	42	ALA	3.8
51	D4	63	TYR	3.8
2	CB	79	ASP	3.8
46	DZ	140	ASP	3.8
1	CA	993	G	3.8
23	CW	21	A	3.8
23	CW	61	C	3.8
46	BZ	156	LYS	3.8
3	AC	52	LEU	3.8
4	CD	93	PHE	3.8
18	AR	81	PHE	3.8
29	DE	4	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
30	DF	157	VAL	3.8
45	DY	89	PHE	3.8
55	D8	48	PHE	3.8
10	CJ	59	SER	3.8
34	BN	30	ILE	3.8
5	AE	75	THR	3.8
6	AF	86	ARG	3.8
1	CA	1372	U	3.8
5	CE	23	GLY	3.8
2	CB	172	ILE	3.8
5	CE	131	ILE	3.8
13	CM	69	GLU	3.8
17	CQ	11	VAL	3.8
48	B1	70	VAL	3.8
23	AW	7	A	3.8
26	DA	2062	A	3.8
17	AQ	29	HIS	3.8
35	DO	20	MET	3.8
30	DF	17	ARG	3.8
36	DP	50	ARG	3.8
14	CN	40	CYS	3.8
25	AY	46	7MG	3.8
7	AG	38	LEU	3.8
11	AK	68	ALA	3.8
31	DG	76	SER	3.8
16	CP	20	VAL	3.8
32	BH	17	VAL	3.8
36	DP	101	VAL	3.8
46	BZ	113	ALA	3.8
17	CQ	4	LYS	3.8
2	AB	90	MET	3.8
4	CD	181	MET	3.8
1	CA	1260	C	3.8
21	CU	18	TYR	3.8
22	AV	13	A	3.8
25	CY	2	C	3.8
26	BA	2803	A	3.8
3	AC	148	GLY	3.8
4	CD	102	ASP	3.8
17	AQ	28	PRO	3.8
2	AB	188	ALA	3.8
7	AG	2	ALA	3.8

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Mol	Chain	Res	Type	RSRZ
10	AJ	85	LEU	3.8
20	AT	59	ALA	3.8
30	DF	143	ALA	3.8
39	DS	83	LYS	3.8
49	D2	46	GLN	3.8
5	AE	25	ARG	3.8
14	AN	23	ARG	3.8
51	D4	35	VAL	3.8
3	CC	84	ILE	3.8
48	B1	13	ILE	3.8
16	AP	1	MET	3.8
8	CH	24	THR	3.8
15	CO	4	THR	3.8
32	DH	122	THR	3.8
1	CA	1280	A	3.7
4	AD	173	TRP	3.7
7	CG	5	ARG	3.7
9	CI	3	GLN	3.7
9	CI	16	ARG	3.7
8	CH	107	LEU	3.7
20	AT	76	ALA	3.7
26	BA	929	G	3.7
29	BE	59	VAL	3.7
31	DG	53	LEU	3.7
32	BH	67	LEU	3.7
33	BI	37	VAL	3.7
33	BI	43	ASN	3.7
34	BN	54	VAL	3.7
36	DP	147	LEU	3.7
41	DU	20	LEU	3.7
41	DU	74	LEU	3.7
42	DV	38	LEU	3.7
55	D8	14	VAL	3.7
8	CH	136	GLU	3.7
51	D4	30	GLU	3.7
3	CC	142	MET	3.7
13	AM	26	GLY	3.7
32	BH	4	ILE	3.7
3	CC	191	THR	3.7
12	CL	54	LYS	3.7
46	DZ	162	GLU	3.7
50	D3	42	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
33	BI	12	LEU	3.7
36	DP	62	LEU	3.7
49	D2	63	VAL	3.7
30	DF	129	PHE	3.7
30	DF	202	PHE	3.7
32	BH	72	ILE	3.7
46	DZ	87	ASP	3.7
56	D9	17	ILE	3.7
1	AA	1023	G	3.7
14	AN	35	ARG	3.7
26	BA	2806	G	3.7
20	CT	73	HIS	3.7
44	DX	4	ALA	3.7
5	AE	43	LEU	3.7
7	CG	104	LEU	3.7
8	AH	26	VAL	3.7
31	BG	133	LEU	3.7
8	AH	43	GLY	3.7
5	CE	10	MET	3.7
14	CN	57	ARG	3.7
1	AA	1028	C	3.7
31	BG	26	GLN	3.7
43	DW	96	ILE	3.7
2	AB	159	PRO	3.7
33	BI	105	HIS	3.7
2	AB	161	ALA	3.7
3	AC	200	ALA	3.7
13	CM	18	ALA	3.7
30	DF	113	ALA	3.7
8	AH	71	GLY	3.7
8	CH	95	VAL	3.7
15	CO	34	LEU	3.7
15	CO	54	ARG	3.7
18	CR	86	VAL	3.7
20	CT	36	LEU	3.7
36	DP	105	LEU	3.7
39	DS	101	LEU	3.7
36	DP	87	ASP	3.7
31	DG	26	GLN	3.7
10	CJ	54	PHE	3.7
3	CC	202	ILE	3.7
18	CR	56	THR	3.7

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Mol	Chain	Res	Type	RSRZ
28	DD	276	LYS	3.7
31	DG	68	PRO	3.7
26	DA	228	A	3.7
20	AT	22	ARG	3.7
20	CT	80	ARG	3.7
50	D3	45	GLY	3.7
2	AB	121	LEU	3.7
3	CC	47	LEU	3.7
7	CG	99	LEU	3.7
34	DN	98	VAL	3.7
42	DV	12	TYR	3.7
45	BY	85	VAL	3.7
51	B4	67	TYR	3.7
13	AM	43	THR	3.7
31	BG	140	ILE	3.7
40	BT	52	ILE	3.7
42	DV	82	ARG	3.7
3	CC	146	ALA	3.7
7	AG	7	ALA	3.7
23	AW	2	C	3.7
36	DP	47	ASP	3.7
23	CW	38	A	3.7
4	CD	11	LEU	3.7
4	CD	17	VAL	3.7
30	DF	110	LEU	3.7
45	DY	67	LEU	3.7
54	B7	31	LEU	3.7
56	B9	15	LYS	3.7
11	CK	20	TYR	3.7
17	AQ	32	TYR	3.7
17	CQ	2	PRO	3.7
29	DE	51	PHE	3.7
53	D6	50	ARG	3.7
29	DE	77	ILE	3.7
46	DZ	60	GLU	3.7
3	AC	80	GLY	3.7
30	DF	34	TRP	3.7
9	CI	55	ALA	3.6
14	CN	10	ALA	3.6
31	DG	163	ALA	3.6
32	BH	145	ALA	3.6
7	AG	141	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
10	CJ	90	LEU	3.6
11	CK	109	VAL	3.6
36	DP	3	LEU	3.6
37	DQ	106	VAL	3.6
45	DY	37	VAL	3.6
3	CC	11	ARG	3.6
9	AI	42	ARG	3.6
48	B1	93	GLU	3.6
11	CK	31	THR	3.6
46	BZ	106	GLY	3.6
44	DX	8	ILE	3.6
50	D3	39	ASP	3.6
9	AI	52	ALA	3.6
6	AF	62	TRP	3.6
16	AP	59	TRP	3.6
16	AP	42	ARG	3.6
31	BG	153	ARG	3.6
4	CD	105	VAL	3.6
7	CG	74	GLU	3.6
13	CM	73	GLU	3.6
35	DO	98	VAL	3.6
1	AA	1034	G	3.6
3	AC	97	LYS	3.6
10	CJ	77	PRO	3.6
41	DU	16	LYS	3.6
51	D4	41	PRO	3.6
1	CA	1096	C	3.6
2	AB	95	GLN	3.6
2	AB	181	PHE	3.6
7	CG	151	TYR	3.6
8	AH	62	TYR	3.6
10	CJ	100	THR	3.6
26	DA	1914	C	3.6
31	BG	144	ILE	3.6
18	CR	40	LEU	3.6
30	BF	192	LEU	3.6
34	DN	15	LEU	3.6
49	D2	44	LEU	3.6
5	CE	92	LYS	3.6
46	DZ	130	PRO	3.6
2	CB	94	ASN	3.6
31	DG	23	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
1	CA	1008	C	3.6
4	CD	70	ILE	3.6
5	CE	21	ALA	3.6
23	CW	22	G	3.6
20	AT	30	LYS	3.6
2	CB	155	LEU	3.6
5	CE	112	LEU	3.6
16	AP	6	LEU	3.6
30	DF	84	VAL	3.6
39	DS	28	VAL	3.6
53	D6	5	VAL	3.6
7	CG	71	PRO	3.6
11	CK	111	ASP	3.6
4	CD	156	GLU	3.6
30	DF	152	GLU	3.6
10	CJ	7	LYS	3.6
3	AC	57	ILE	3.6
25	CY	25	C	3.6
26	DA	645	C	3.6
26	DA	888	C	3.6
2	CB	118	LEU	3.6
9	AI	79	LEU	3.6
9	CI	47	LEU	3.6
23	CW	52	G	3.6
24	CX	49	G	3.6
50	D3	4	LEU	3.6
18	CR	80	PRO	3.6
11	AK	28	THR	3.6
16	AP	69	THR	3.6
5	CE	104	ALA	3.6
6	CF	97	PHE	3.6
9	AI	13	ALA	3.6
28	DD	6	PHE	3.6
3	CC	57	ILE	3.6
10	AJ	74	ILE	3.6
31	DG	52	ILE	3.6
2	CB	96	ARG	3.6
45	BY	1	MET	3.6
46	BZ	148	ASP	3.6
46	DZ	103	ARG	3.6
46	DZ	145	GLU	3.6
46	DZ	154	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
2	CB	202	PRO	3.6
13	AM	17	VAL	3.6
31	BG	60	LEU	3.6
34	DN	99	LEU	3.6
37	DQ	125	LEU	3.6
45	DY	90	LEU	3.6
46	BZ	59	LEU	3.6
5	AE	121	LYS	3.6
25	AY	56	C	3.6
1	CA	657	G	3.6
5	CE	113	ALA	3.6
7	AG	3	ARG	3.6
48	D1	83	GLU	3.6
21	CU	5	ASP	3.6
32	DH	175	LYS	3.6
45	DY	95	LYS	3.6
2	CB	7	VAL	3.6
20	CT	98	PRO	3.6
32	BH	103	LEU	3.5
33	BI	35	LEU	3.5
36	DP	19	VAL	3.6
39	DS	24	LEU	3.5
41	DU	27	LEU	3.5
41	DU	39	LEU	3.5
46	BZ	39	VAL	3.6
9	AI	71	SER	3.5
9	CI	27	THR	3.5
13	CM	104	ARG	3.5
20	AT	28	ALA	3.5
4	AD	169	LYS	3.5
17	AQ	45	HIS	3.5
31	BG	157	ILE	3.5
55	D8	25	MET	3.5
5	CE	128	PRO	3.5
13	CM	106	ASN	3.5
25	AY	27	G	3.5
19	CS	22	LEU	3.5
45	BY	3	VAL	3.5
45	DY	82	PRO	3.5
49	D2	36	ARG	3.5
56	D9	19	ARG	3.5
33	BI	54	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
4	AD	102	ASP	3.5
13	AM	107	ALA	3.5
28	DD	272	ALA	3.5
55	D8	29	LYS	3.5
26	BA	2167	C	3.5
32	DH	74	ASN	3.5
3	CC	16	ARG	3.5
9	AI	28	VAL	3.5
17	AQ	95	TYR	3.5
20	CT	13	LEU	3.5
30	DF	184	TYR	3.5
39	DS	7	TYR	3.5
1	AA	105	G	3.5
3	CC	185	GLY	3.5
4	AD	117	ALA	3.5
23	CW	18	G	3.5
23	CW	57	G	3.5
41	DU	7	GLY	3.5
6	AF	1	MET	3.5
7	AG	144	MET	3.5
45	BY	5	MET	3.5
25	CY	55	PSU	3.5
2	CB	41	ILE	3.5
2	CB	78	GLN	3.5
30	DF	39	TRP	3.5
23	AW	72	C	3.5
33	BI	19	VAL	3.5
38	DR	54	LEU	3.5
34	DN	72	TYR	3.5
35	DO	7	TYR	3.5
51	D4	43	TYR	3.5
9	CI	103	THR	3.5
9	CI	117	HIS	3.5
37	DQ	28	ALA	3.5
55	D8	46	ARG	3.5
5	AE	136	MET	3.5
12	CL	46	LYS	3.5
17	CQ	100	LYS	3.5
46	DZ	89	PHE	3.5
47	D0	53	MET	3.5
23	CW	70	G	3.5
2	CB	233	SER	3.5

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Mol	Chain	Res	Type	RSRZ
4	CD	8	VAL	3.5
10	CJ	94	VAL	3.5
13	CM	17	VAL	3.5
34	BN	53	VAL	3.5
41	DU	31	SER	3.5
45	BY	96	ILE	3.5
48	D1	30	VAL	3.5
48	D1	70	VAL	3.5
5	CE	99	GLY	3.5
17	CQ	32	TYR	3.5
31	DG	42	GLY	3.5
1	CA	1352	C	3.5
13	CM	30	ALA	3.5
53	D6	22	ALA	3.5
12	CL	91	LYS	3.5
28	BD	38	LYS	3.5
2	AB	78	GLN	3.5
3	AC	90	GLU	3.5
39	DS	41	ASP	3.5
2	CB	149	LEU	3.5
5	CE	35	GLY	3.5
8	CH	26	VAL	3.5
10	AJ	8	LEU	3.5
10	CJ	44	VAL	3.5
17	CQ	12	SER	3.5
31	BG	43	LEU	3.5
33	BI	5	LEU	3.5
47	D0	79	VAL	3.5
18	CR	65	ILE	3.5
45	BY	97	ARG	3.5
17	CQ	69	LYS	3.5
1	CA	1117	G	3.5
5	CE	60	TYR	3.5
19	CS	61	TYR	3.5
43	DW	9	TYR	3.5
13	CM	67	GLU	3.5
16	AP	66	PRO	3.5
1	CA	1250	A	3.5
2	CB	189	ASP	3.5
20	AT	98	PRO	3.5
9	AI	70	LYS	3.5
10	CJ	79	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
21	AU	15	ARG	3.5
38	DR	63	ARG	3.5
49	B2	55	ARG	3.5
47	D0	51	VAL	3.5
2	AB	108	ILE	3.5
33	BI	88	ILE	3.5
5	AE	134	ALA	3.5
16	CP	39	TYR	3.4
29	DE	1	MET	3.4
1	AA	1387	G	3.4
20	AT	14	LYS	3.4
26	BA	2147	G	3.4
26	BA	2184	G	3.4
1	CA	1109	C	3.4
10	CJ	30	SER	3.4
2	AB	155	LEU	3.4
3	CC	111	LEU	3.4
6	AF	75	LEU	3.4
6	CF	30	LEU	3.4
7	AG	99	LEU	3.4
46	DZ	53	ILE	3.4
13	CM	49	THR	3.4
2	CB	148	TYR	3.4
31	DG	51	ARG	3.4
32	DH	152	ARG	3.4
3	AC	167	TRP	3.4
12	CL	88	GLY	3.4
2	CB	40	HIS	3.4
9	CI	126	SER	3.4
17	AQ	71	PHE	3.4
1	AA	223	U	3.4
2	CB	180	LEU	3.4
26	DA	2804	C	3.4
36	DP	6	LEU	3.4
1	CA	976	G	3.4
3	AC	135	LYS	3.4
3	AC	149	ALA	3.4
7	AG	27	ILE	3.4
13	AM	51	ALA	3.4
23	AW	10	G	3.4
9	AI	64	THR	3.4
20	AT	58	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	CA	1213	A	3.4
11	AK	27	ASN	3.4
4	AD	6	GLY	3.4
7	CG	89	MET	3.4
15	CO	69	TYR	3.4
3	AC	72	LYS	3.4
3	AC	198	VAL	3.4
4	AD	63	LYS	3.4
7	AG	80	VAL	3.4
7	AG	124	LEU	3.4
12	CL	59	ARG	3.4
20	CT	53	LEU	3.4
21	AU	10	ARG	3.4
26	BA	271	U	3.4
45	DY	2	ARG	3.4
48	D1	46	LEU	3.4
12	CL	51	ALA	3.4
33	BI	94	ALA	3.4
37	BQ	20	ALA	3.4
2	AB	103	THR	3.4
3	CC	39	ILE	3.4
5	CE	129	ILE	3.4
9	AI	23	ASN	3.4
34	DN	22	THR	3.4
35	DO	2	ILE	3.4
31	DG	85	GLY	3.4
1	CA	1041	A	3.4
25	AY	70	G	3.4
4	CD	68	TYR	3.4
9	CI	128	ARG	3.4
3	CC	128	PHE	3.4
4	CD	203	VAL	3.4
4	AD	78	LEU	3.4
15	AO	34	LEU	3.4
20	CT	24	LEU	3.4
41	DU	66	ASN	3.4
19	CS	17	GLU	3.4
33	DI	109	ILE	3.4
34	DN	85	ILE	3.4
36	DP	58	THR	3.4
2	CB	95	GLN	3.4
9	CI	78	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
50	D3	24	LYS	3.4
4	CD	139	ARG	3.4
6	CF	82	ARG	3.4
15	CO	68	ARG	3.4
32	DH	56	SER	3.4
1	AA	1025	U	3.4
12	AL	43	VAL	3.4
31	DG	160	VAL	3.4
32	DH	144	VAL	3.4
1	CA	1370	G	3.4
11	CK	65	ALA	3.4
25	AY	15	G	3.4
26	DA	2159	G	3.4
27	DB	119	G	3.4
29	BE	63	LEU	3.4
31	DG	61	ALA	3.4
38	DR	44	LEU	3.4
47	D0	62	LEU	3.4
14	AN	22	THR	3.4
31	DG	134	GLY	3.4
45	BY	63	LYS	3.4
56	D9	31	LYS	3.4
2	AB	21	ARG	3.4
5	CE	20	GLN	3.4
9	AI	128	ARG	3.4
10	AJ	60	ARG	3.4
13	CM	22	ILE	3.4
32	DH	60	ARG	3.4
48	B1	7	ILE	3.4
3	AC	154	SER	3.4
32	DH	34	GLU	3.4
39	DS	14	VAL	3.4
3	CC	129	ALA	3.4
32	DH	93	GLY	3.4
36	DP	138	LEU	3.4
34	DN	73	THR	3.4
4	AD	12	CYS	3.4
46	BZ	137	ILE	3.4
1	AA	1156	G	3.4
19	CS	73	GLU	3.4
26	BA	2903	G	3.4
28	DD	275	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
37	DQ	85	LYS	3.3
48	B1	48	LYS	3.3
4	AD	100	ARG	3.3
4	CD	66	ARG	3.3
6	AF	46	ARG	3.3
9	AI	41	VAL	3.3
13	CM	54	VAL	3.3
14	CN	48	ALA	3.3
30	DF	57	VAL	3.3
31	DG	73	ALA	3.3
33	DI	107	VAL	3.3
46	DZ	136	PHE	3.3
48	D1	71	TYR	3.3
1	CA	1129	C	3.3
1	CA	1320	C	3.3
26	BA	696	C	3.3
2	AB	131	PRO	3.3
46	DZ	168	GLU	3.3
3	CC	22	TRP	3.3
19	CS	31	ILE	3.3
26	DA	2135	A	3.3
33	DI	71	ILE	3.3
46	DZ	92	SER	3.3
37	DQ	5	ARG	3.3
4	AD	17	VAL	3.3
10	CJ	24	VAL	3.3
26	DA	271(K)	U	3.3
37	DQ	114	ALA	3.3
47	D0	61	ALA	3.3
17	CQ	24	GLU	3.3
19	CS	47	HIS	3.3
29	DE	52	LEU	3.3
34	DN	107	LEU	3.3
45	BY	106	LEU	3.3
37	DQ	75	THR	3.3
17	CQ	37	LYS	3.3
32	BH	2	SER	3.3
2	AB	87	ARG	3.3
55	B8	58	ILE	3.3
55	D8	34	TRP	3.3
2	AB	224	GLN	3.3
48	D1	27	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
3	CC	117	ALA	3.3
18	AR	39	VAL	3.3
32	BH	131	VAL	3.3
33	BI	46	ALA	3.3
45	BY	6	HIS	3.3
1	CA	1126	U	3.3
2	AB	27	LYS	3.3
17	CQ	3	LYS	3.3
51	B4	59	PHE	3.3
2	CB	103	THR	3.3
19	AS	44	MET	3.3
31	BG	12	TYR	3.3
37	BQ	9	TYR	3.3
1	CA	998	G	3.3
51	D4	13	ARG	3.3
20	AT	61	SER	3.3
29	DE	176	ILE	3.3
1	CA	979	C	3.3
2	CB	19	HIS	3.3
17	CQ	45	HIS	3.3
5	AE	33	VAL	3.3
29	DE	198	VAL	3.3
31	BG	159	VAL	3.3
32	DH	20	ALA	3.3
46	DZ	17	ALA	3.3
1	CA	1313	U	3.3
13	CM	99	ARG	3.3
17	AQ	30	PRO	3.3
30	BF	123	LEU	3.3
31	DG	32	PRO	3.3
42	DV	40	LEU	3.3
55	B8	60	LEU	3.3
5	AE	19	MET	3.3
21	CU	8	THR	3.3
4	AD	116	GLN	3.3
5	CE	124	GLY	3.3
11	CK	90	GLY	3.3
6	AF	92	LYS	3.3
14	AN	7	ILE	3.3
19	AS	18	LYS	3.3
20	AT	100	ILE	3.3
20	AT	17	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
1	CA	1362	C	3.3
4	CD	112	VAL	3.3
6	AF	87	ARG	3.3
31	BG	29	TRP	3.3
36	DP	134	ALA	3.3
6	CF	61	LEU	3.3
13	AM	52	GLU	3.3
37	BQ	79	LEU	3.3
42	BV	39	LEU	3.3
4	AD	33	MET	3.3
5	CE	120	THR	3.3
10	AJ	100	THR	3.3
15	CO	59	MET	3.3
16	CP	1	MET	3.3
31	BG	178	PHE	3.3
32	BH	68	THR	3.3
1	CA	814	A	3.3
4	AD	137	SER	3.3
22	CV	14	A	3.3
25	CY	64	A	3.3
26	BA	2084	A	3.3
37	DQ	72	LYS	3.3
37	DQ	74	TYR	3.3
11	CK	83	ILE	3.3
18	CR	50	ILE	3.3
20	AT	16	HIS	3.3
31	BG	101	ILE	3.3
5	AE	82	VAL	3.3
5	CE	93	PRO	3.3
35	DO	38	VAL	3.3
42	DV	47	VAL	3.3
46	BZ	100	VAL	3.3
5	AE	151	LEU	3.3
31	BG	3	LEU	3.3
32	BH	71	LEU	3.3
8	CH	46	LYS	3.3
11	AK	51	LYS	3.3
1	AA	220	G	3.3
1	AA	1342	C	3.3
18	AR	43	PHE	3.3
26	DA	886	C	3.3
4	AD	36	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
1	CA	1289	A	3.3
24	AX	76	A	3.3
5	AE	76	ILE	3.3
49	D2	13	ALA	3.3
9	AI	53	VAL	3.2
12	AL	90	VAL	3.2
32	BH	19	VAL	3.2
36	DP	145	PRO	3.2
37	BQ	97	VAL	3.2
2	CB	51	LEU	3.2
8	AH	90	GLY	3.2
46	BZ	5	LEU	3.2
46	BZ	117	LEU	3.2
53	D6	36	LEU	3.2
30	BF	142	TRP	3.2
32	DH	46	GLU	3.2
34	DN	38	HIS	3.2
1	CA	1051	C	3.2
1	CA	1009	G	3.2
25	AY	57	G	3.2
31	DG	75	LYS	3.2
33	DI	130	TYR	3.2
8	CH	38	ILE	3.2
9	CI	52	ALA	3.2
11	CK	69	ALA	3.2
7	AG	61	VAL	3.2
7	CG	105	VAL	3.2
13	AM	54	VAL	3.2
45	DY	98	VAL	3.2
6	CF	46	ARG	3.2
26	BA	2518	U	3.2
33	BI	114	LEU	3.2
33	BI	116	LEU	3.2
3	AC	95	THR	3.2
10	AJ	59	SER	3.2
5	AE	84	PHE	3.2
9	CI	70	LYS	3.2
36	DP	108	LYS	3.2
30	DF	130	ALA	3.2
2	AB	125	PRO	3.2
30	DF	9	ILE	3.2
43	DW	6	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
8	CH	131	GLY	3.2
3	CC	207	VAL	3.2
7	AG	91	VAL	3.2
51	D4	56	VAL	3.2
11	AK	98	LEU	3.2
31	BG	155	MET	3.2
24	CX	6	G	3.2
36	BP	138	LEU	3.2
37	DQ	118	LEU	3.2
46	BZ	166	SER	3.2
49	D2	64	LEU	3.2
7	AG	36	LYS	3.2
12	CL	114	LYS	3.2
16	AP	44	THR	3.2
25	AY	9	A	3.2
32	BH	95	ARG	3.2
36	DP	18	ARG	3.2
2	AB	18	GLY	3.2
46	DZ	26	GLY	3.2
50	D3	12	PRO	3.2
7	CG	120	ILE	3.2
7	AG	69	VAL	3.2
28	DD	18	VAL	3.2
30	BF	11	VAL	3.2
31	DG	109	VAL	3.2
1	CA	204	U	3.2
3	CC	33	LEU	3.2
11	CK	110	ASP	3.2
25	CY	45	U	3.2
36	BP	59	LEU	3.2
50	D3	44	ARG	3.2
9	AI	8	GLY	3.2
23	AW	57	G	3.2
25	AY	34	G	3.2
2	CB	193	ASP	3.2
13	CM	117	VAL	3.2
30	BF	20	LEU	3.2
36	DP	106	LEU	3.2
4	CD	90	GLY	3.2
2	AB	88	ALA	3.2
11	AK	60	ALA	3.2
20	CT	76	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	AA	161	A	3.2
4	CD	9	CYS	3.2
26	BA	2136	A	3.2
27	DB	29	A	3.2
4	AD	144	ASP	3.2
16	AP	20	VAL	3.2
1	CA	1050	G	3.2
3	AC	190	ARG	3.2
20	CT	41	ILE	3.2
24	AX	7	G	3.2
28	DD	13	ARG	3.2
31	DG	20	ILE	3.2
39	BS	82	ILE	3.2
45	BY	24	VAL	3.2
45	DY	70	SER	3.2
12	AL	27	LEU	3.2
34	BN	72	TYR	3.2
38	DR	20	LEU	3.2
4	AD	93	PHE	3.2
1	CA	1214	C	3.2
13	AM	97	PRO	3.2
26	BA	932	C	3.2
26	BA	2186	C	3.2
31	DG	169	ALA	3.2
2	CB	176	GLU	3.2
46	DZ	20	ARG	3.2
3	CC	176	HIS	3.2
8	AH	70	GLN	3.2
1	CA	1130	A	3.2
5	CE	9	LYS	3.2
6	CF	88	VAL	3.2
10	AJ	96	ILE	3.2
13	AM	115	LYS	3.2
15	AO	60	VAL	3.2
30	BF	183	VAL	3.2
51	B4	50	VAL	3.2
36	BP	114	ILE	3.2
36	BP	88	LEU	3.2
11	CK	50	TYR	3.2
4	AD	167	GLY	3.1
1	AA	852	G	3.1
1	CA	1190	G	3.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1258	G	3.1
1	CA	1368	G	3.1
15	AO	15	PHE	3.1
2	CB	62	ALA	3.1
15	AO	30	ALA	3.1
34	DN	74	ARG	3.1
51	D4	34	GLU	3.1
50	D3	16	PRO	3.1
37	DQ	77	LYS	3.1
54	D7	32	LYS	3.1
1	CA	980	C	3.1
6	AF	67	MET	3.1
26	BA	2130	C	3.1
37	DQ	96	VAL	3.1
9	AI	74	ILE	3.1
17	AQ	31	LEU	3.1
24	CX	47	U	3.1
34	DN	138	LEU	3.1
36	DP	135	LEU	3.1
37	DQ	79	LEU	3.1
31	BG	93	THR	3.1
5	AE	81	GLU	3.1
37	DQ	41	TRP	3.1
6	CF	59	TYR	3.1
5	AE	106	PRO	3.1
10	CJ	37	PRO	3.1
33	BI	45	LYS	3.1
23	AW	1	G	3.1
32	BH	24	VAL	3.1
1	CA	1532	U	3.1
5	CE	152	ARG	3.1
7	AG	12	LEU	3.1
9	AI	56	LEU	3.1
17	CQ	8	GLY	3.1
37	DQ	86	GLY	3.1
28	DD	5	LYS	3.1
3	AC	184	TYR	3.1
36	DP	127	ALA	3.1
45	BY	74	PRO	3.1
1	AA	1286	A	3.1
22	CV	24	A	3.1
26	DA	2310	A	3.1

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Mol	Chain	Res	Type	RSRZ
14	AN	33	VAL	3.1
14	AN	56	VAL	3.1
45	DY	86	ARG	3.1
51	D4	45	GLY	3.1
13	AM	27	LYS	3.1
17	CQ	74	LEU	3.1
19	AS	39	THR	3.1
33	BI	40	THR	3.1
33	BI	58	LEU	3.1
37	DQ	131	ILE	3.1
25	CY	34	G	3.1
1	CA	999	C	3.1
9	AI	45	ALA	3.1
13	AM	42	ALA	3.1
23	CW	74	C	3.1
25	CY	43	C	3.1
40	DT	94	ALA	3.1
2	CB	105	PHE	3.1
7	CG	142	GLU	3.1
14	CN	16	PHE	3.1
10	CJ	10	GLY	3.1
26	DA	2602	A	3.1
29	BE	52	LEU	3.1
29	BE	78	LEU	3.1
42	BV	20	LEU	3.1
56	D9	34	GLN	3.1
4	AD	204	ILE	3.1
2	AB	120	ALA	3.1
35	DO	41	ALA	3.1
2	CB	8	LYS	3.1
52	D5	13	LYS	3.1
3	AC	2	GLY	3.1
29	DE	96	PHE	3.1
1	CA	1156	G	3.1
3	AC	173	VAL	3.1
9	AI	17	VAL	3.1
12	AL	82	VAL	3.1
15	AO	21	ASP	3.1
16	AP	65	GLN	3.1
32	DH	141	VAL	3.1
33	DI	15	VAL	3.1
28	DD	175	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
36	DP	94	GLU	3.1
1	CA	262	A	3.1
50	B3	28	LEU	3.1
7	CG	149	ARG	3.1
16	AP	75	ARG	3.1
2	CB	13	ALA	3.1
2	CB	179	LYS	3.1
3	AC	199	LYS	3.1
6	AF	81	ILE	3.1
10	CJ	80	LYS	3.1
18	CR	61	LYS	3.1
30	DF	78	ILE	3.1
33	DI	26	ALA	3.1
35	DO	30	ALA	3.1
42	DV	50	PRO	3.1
20	AT	9	ASN	3.1
20	CT	26	ASN	3.1
2	AB	31	TYR	3.1
6	CF	89	MET	3.1
29	BE	67	PHE	3.1
33	DI	89	TYR	3.1
34	DN	51	PHE	3.1
7	AG	56	GLN	3.1
4	AD	198	VAL	3.1
4	CD	178	VAL	3.1
19	AS	67	VAL	3.1
28	BD	118	VAL	3.1
45	DY	15	VAL	3.1
47	B0	30	VAL	3.1
3	AC	83	ARG	3.1
4	CD	114	ARG	3.1
23	CW	4	C	3.1
4	CD	127	THR	3.1
20	AT	53	LEU	3.1
20	CT	20	LEU	3.1
34	DN	70	LYS	3.1
38	DR	74	LYS	3.1
23	CW	66	U	3.1
26	DA	614(A)	U	3.1
1	CA	1061	G	3.1
26	DA	2149	G	3.1
26	DA	2165	G	3.1

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Mol	Chain	Res	Type	RSRZ
8	AH	38	ILE	3.1
13	CM	75	ALA	3.1
14	AN	20	ALA	3.1
20	AT	32	ALA	3.1
30	BF	58	ALA	3.1
39	DS	77	ALA	3.1
1	CA	983	A	3.1
26	DA	887	A	3.1
27	DB	58	A	3.1
31	BG	42	GLY	3.1
5	CE	136	MET	3.0
6	AF	55	ASP	3.0
31	BG	137	GLU	3.0
31	DG	35	GLU	3.0
33	DI	42	SER	3.0
5	AE	28	PHE	3.0
9	CI	101	PHE	3.0
12	AL	32	PHE	3.0
9	AI	104	ARG	3.0
9	CI	92	TYR	3.0
10	AJ	43	ARG	3.0
16	CP	25	ARG	3.0
32	DH	130	ARG	3.0
55	D8	3	LYS	3.0
31	DG	38	VAL	3.0
2	AB	190	THR	3.0
14	AN	44	LEU	3.0
15	AO	57	LEU	3.0
16	CP	59	TRP	3.0
31	DG	173	LEU	3.0
34	BN	73	THR	3.0
4	AD	51	PRO	3.0
3	AC	137	ALA	3.0
11	CK	23	ALA	3.0
26	DA	2137	C	3.0
33	DI	49	ALA	3.0
40	DT	110	ILE	3.0
41	DU	107	ALA	3.0
46	BZ	119	GLU	3.0
51	D4	15	ILE	3.0
4	AD	62	GLN	3.0
17	AQ	12	SER	3.0

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Mol	Chain	Res	Type	RSRZ
3	CC	156	ARG	3.0
7	CG	35	LYS	3.0
47	D0	44	ARG	3.0
53	D6	53	LYS	3.0
54	D7	2	LYS	3.0
26	BA	160	G	3.0
18	CR	22	VAL	3.0
30	BF	154	VAL	3.0
45	BY	98	VAL	3.0
37	DQ	73	PRO	3.0
4	AD	111	ALA	3.0
7	AG	134	ALA	3.0
7	CG	147	ALA	3.0
11	AK	19	ALA	3.0
35	DO	11	ALA	3.0
41	DU	48	ALA	3.0
3	AC	14	ILE	3.0
13	AM	120	LYS	3.0
32	DH	77	LYS	3.0
41	DU	47	TYR	3.0
2	CB	209	ARG	3.0
7	CG	12	LEU	3.0
15	CO	30	ALA	3.0
20	AT	25	ARG	3.0
25	AY	71	G	3.0
31	DG	55	LYS	3.0
37	DQ	50	ALA	3.0
56	D9	4	ARG	3.0
18	AR	70	ILE	3.0
33	BI	71	ILE	3.0
6	CF	60	PHE	3.0
15	AO	18	PHE	3.0
25	CY	42	C	3.0
51	B4	49	PHE	3.0
5	AE	148	VAL	3.0
10	CJ	9	ARG	3.0
39	BS	49	VAL	3.0
43	DW	92	ARG	3.0
48	D1	51	VAL	3.0
55	D8	35	GLN	3.0
6	AF	43	LEU	3.0
8	CH	3	THR	3.0

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Mol	Chain	Res	Type	RSRZ
8	CH	59	LEU	3.0
1	CA	1257	U	3.0
3	AC	50	ALA	3.0
12	AL	120	TYR	3.0
12	CL	44	THR	3.0
15	CO	81	LEU	3.0
28	DD	40	THR	3.0
44	BX	66	LEU	3.0
8	CH	124	ALA	3.0
15	CO	26	GLU	3.0
53	D6	51	GLU	3.0
1	AA	922	G	3.0
10	AJ	82	ILE	3.0
23	AW	65	G	3.0
30	DF	199	TRP	3.0
16	AP	35	LYS	3.0
53	B6	45	LYS	3.0
3	CC	172	ARG	3.0
11	AK	54	ARG	3.0
12	CL	41	ARG	3.0
31	BG	136	ARG	3.0
4	CD	198	VAL	3.0
32	DH	15	VAL	3.0
37	BQ	81	VAL	3.0
3	CC	102	ASN	3.0
55	D8	2	PRO	3.0
5	CE	86	ALA	3.0
7	AG	104	LEU	3.0
15	CO	22	THR	3.0
26	BA	2154	U	3.0
29	BE	187	ALA	3.0
31	DG	161	THR	3.0
48	D1	80	LEU	3.0
49	D2	66	GLU	3.0
9	AI	114	TYR	3.0
41	DU	76	TYR	3.0
4	CD	125	HIS	3.0
10	AJ	99	LYS	3.0
12	CL	47	LYS	3.0
46	DZ	55	HIS	3.0
7	CG	78	ARG	3.0
9	CI	93	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
32	BH	148	ILE	3.0
3	CC	18	TRP	3.0
39	DS	90	GLY	3.0
34	DN	50	ASP	3.0
2	CB	234	PRO	3.0
4	CD	133	VAL	3.0
10	AJ	44	VAL	3.0
12	AL	94	PRO	3.0
28	DD	15	PHE	3.0
30	DF	163	VAL	3.0
31	DG	59	GLU	3.0
33	BI	18	VAL	3.0
37	DQ	48	GLU	3.0
46	DZ	68	PRO	3.0
48	D1	74	VAL	3.0
1	CA	658	G	3.0
26	BA	2174	G	3.0
9	CI	56	LEU	3.0
11	AK	31	THR	3.0
16	AP	64	ALA	3.0
17	AQ	89	LEU	3.0
18	CR	26	LEU	3.0
34	BN	120	LEU	3.0
36	DP	88	LEU	3.0
50	D3	40	THR	3.0
53	B6	34	LEU	3.0
5	CE	27	ARG	3.0
10	CJ	51	ARG	3.0
17	CQ	88	TYR	3.0
47	D0	55	ARG	3.0
19	AS	66	MET	3.0
45	DY	38	ILE	3.0
33	DI	41	GLU	3.0
3	AC	138	VAL	2.9
4	CD	88	VAL	2.9
18	AR	22	VAL	2.9
18	AR	37	VAL	2.9
19	CS	34	TRP	2.9
32	BH	113	VAL	2.9
33	DI	80	PRO	2.9
38	DR	48	VAL	2.9
4	AD	49	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
7	CG	143	ARG	2.9
13	CM	57	ARG	2.9
20	AT	84	LEU	2.9
28	DD	206	LEU	2.9
36	BP	57	THR	2.9
39	BS	51	ALA	2.9
45	BY	86	ARG	2.9
51	D4	9	LEU	2.9
1	AA	343	U	2.9
32	DH	63	SER	2.9
33	BI	91	SER	2.9
3	CC	170	GLN	2.9
1	CA	1255	G	2.9
2	AB	99	GLY	2.9
4	CD	138	TYR	2.9
9	CI	30	GLY	2.9
15	AO	89	GLY	2.9
23	AW	19	G	2.9
25	AY	18	G	2.9
26	DA	2115	G	2.9
26	DA	2308	G	2.9
36	DP	43	GLY	2.9
39	DS	94	TYR	2.9
53	D6	12	GLU	2.9
1	AA	150	C	2.9
1	AA	932	C	2.9
6	AF	25	ILE	2.9
25	AY	2	C	2.9
46	DZ	46	LYS	2.9
55	D8	41	ILE	2.9
5	AE	115	VAL	2.9
8	AH	118	VAL	2.9
29	BE	75	VAL	2.9
34	BN	14	VAL	2.9
7	CG	25	ALA	2.9
20	CT	67	ALA	2.9
38	DR	62	ALA	2.9
44	DX	45	THR	2.9
46	DZ	109	ALA	2.9
6	CF	45	LEU	2.9
8	AH	112	LEU	2.9
1	AA	404	U	2.9

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Mol	Chain	Res	Type	RSRZ
1	CA	816	A	2.9
25	CY	47	U	2.9
26	DA	2134	A	2.9
30	DF	196	LEU	2.9
5	CE	38	GLN	2.9
7	AG	140	ASP	2.9
2	AB	75	LYS	2.9
9	CI	113	LYS	2.9
13	AM	121	LYS	2.9
20	CT	29	LYS	2.9
42	DV	6	LYS	2.9
12	CL	94	PRO	2.9
1	CA	755	G	2.9
1	CA	1089	G	2.9
4	CD	128	VAL	2.9
7	CG	69	VAL	2.9
23	CW	5	G	2.9
24	AX	67	C	2.9
35	DO	63	VAL	2.9
41	BU	8	VAL	2.9
9	CI	124	GLN	2.9
2	AB	138	LEU	2.9
10	AJ	48	THR	2.9
11	CK	89	ALA	2.9
36	DP	74	GLU	2.9
30	DF	101	LEU	2.9
7	AG	81	GLY	2.9
7	AG	103	TRP	2.9
27	DB	59	A	2.9
8	CH	58	TYR	2.9
2	AB	41	ILE	2.9
2	AB	176	GLU	2.9
38	DR	110	PRO	2.9
43	DW	103	ILE	2.9
44	DX	89	ILE	2.9
48	B1	90	ILE	2.9
2	AB	29	ALA	2.9
3	CC	26	LYS	2.9
5	AE	21	ALA	2.9
5	AE	138	ALA	2.9
11	AK	65	ALA	2.9
12	CL	115	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
12	CL	123	LYS	2.9
43	DW	4	LYS	2.9
56	B9	13	LYS	2.9
30	DF	15	SER	2.9
45	BY	83	THR	2.9
1	AA	620	C	2.9
4	CD	19	LEU	2.9
4	CD	96	LEU	2.9
12	AL	60	LEU	2.9
24	CX	65	C	2.9
37	BQ	37	LEU	2.9
40	DT	6	LEU	2.9
5	AE	27	ARG	2.9
12	AL	86	ARG	2.9
13	CM	29	ARG	2.9
30	BF	18	ARG	2.9
56	B9	9	ARG	2.9
25	CY	22	G	2.9
51	D4	39	CYS	2.9
26	DA	6	A	2.9
39	BS	39	ILE	2.9
3	CC	138	VAL	2.9
5	AE	113	ALA	2.9
31	DG	37	VAL	2.9
32	BH	35	VAL	2.9
34	DN	54	VAL	2.9
41	DU	110	VAL	2.9
3	CC	126	ARG	2.9
21	AU	11	GLY	2.9
49	D2	7	ARG	2.9
43	BW	86	LEU	2.9
46	BZ	24	LEU	2.9
1	AA	1260	C	2.9
13	CM	62	ASN	2.9
47	D0	12	ASN	2.9
4	AD	37	PRO	2.9
19	AS	2	PRO	2.9
29	DE	32	PRO	2.9
1	CA	966	G	2.9
4	CD	168	ARG	2.9
5	AE	108	ALA	2.9
7	CG	152	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
12	AL	70	ILE	2.9
13	CM	59	TYR	2.9
29	BE	21	VAL	2.9
29	BE	26	ILE	2.9
29	BE	28	ALA	2.9
31	BG	37	VAL	2.9
32	DH	165	ALA	2.9
48	D1	14	VAL	2.9
54	D7	20	ALA	2.9
1	CA	946	A	2.9
1	CA	1236	A	2.9
1	CA	1286	A	2.9
1	CA	1324	A	2.9
9	AI	110	GLU	2.9
2	CB	138	LEU	2.9
4	AD	58	LEU	2.9
5	AE	26	PHE	2.9
28	DD	269	PHE	2.9
31	BG	7	LEU	2.9
33	DI	6	LEU	2.9
25	AY	20	U	2.9
26	BA	1466	U	2.9
33	DI	87	LYS	2.9
36	DP	124	LYS	2.9
38	DR	9	LYS	2.9
5	AE	70	PRO	2.9
7	AG	58	PRO	2.9
21	CU	22	ARG	2.9
26	BA	931	C	2.9
26	DA	912	C	2.9
26	DA	2174	C	2.9
28	DD	252	TRP	2.9
31	DG	150	ASP	2.9
33	DI	90	GLY	2.9
3	CC	65	ALA	2.9
5	AE	95	ALA	2.9
28	BD	142	VAL	2.9
39	DS	85	VAL	2.9
5	CE	16	THR	2.9
7	AG	44	TYR	2.9
19	CS	28	LYS	2.9
32	DH	164	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
40	BT	59	THR	2.9
46	BZ	107	THR	2.9
53	B6	23	THR	2.9
53	D6	38	LYS	2.9
7	CG	144	MET	2.8
29	DE	181	LEU	2.8
38	DR	75	LEU	2.8
23	AW	18	G	2.8
24	AX	47	U	2.8
26	BA	2182	G	2.8
27	DB	120	A	2.8
31	DG	27	ASN	2.8
31	DG	181	ARG	2.8
41	DU	11	ARG	2.8
4	AD	179	GLU	2.8
5	CE	5	ASP	2.8
8	CH	5	PRO	2.8
12	AL	99	HIS	2.8
43	DW	94	ASP	2.8
12	CL	124	LYS	2.8
19	CS	18	LYS	2.8
2	AB	219	VAL	2.8
6	AF	99	ALA	2.8
20	CT	66	ALA	2.8
28	DD	267	SER	2.8
30	DF	153	SER	2.8
32	DH	145	ALA	2.8
37	DQ	117	ALA	2.8
50	D3	9	VAL	2.8
23	CW	3	C	2.8
29	DE	197	ILE	2.8
3	CC	52	LEU	2.8
4	AD	96	LEU	2.8
5	CE	14	ARG	2.8
12	CL	10	LEU	2.8
14	CN	21	TYR	2.8
39	DS	5	THR	2.8
53	D6	23	THR	2.8
41	DU	60	LEU	2.8
42	DV	75	PHE	2.8
51	D4	59	PHE	2.8
55	D8	62	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
3	CC	82	GLU	2.8
49	D2	11	GLU	2.8
32	DH	29	PRO	2.8
32	DH	126	PRO	2.8
44	DX	31	HIS	2.8
46	DZ	83	PRO	2.8
1	AA	149	A	2.8
22	AV	24	A	2.8
26	DA	652(B)	A	2.8
26	BA	2805	G	2.8
34	DN	57	ALA	2.8
3	AC	130	VAL	2.8
7	AG	75	VAL	2.8
28	BD	173	VAL	2.8
30	BF	89	VAL	2.8
30	DF	11	VAL	2.8
35	DO	62	VAL	2.8
39	DS	69	VAL	2.8
16	CP	18	ARG	2.8
7	CG	156	TRP	2.8
10	CJ	96	ILE	2.8
28	DD	262	ARG	2.8
10	CJ	16	LEU	2.8
1	CA	931	C	2.8
2	CB	160	ASP	2.8
4	CD	79	PHE	2.8
6	AF	7	ASN	2.8
30	BF	139	PHE	2.8
47	D0	50	ASN	2.8
49	D2	65	ASN	2.8
35	BO	31	LYS	2.8
47	D0	13	GLY	2.8
7	CG	77	SER	2.8
1	CA	1014	A	2.8
3	CC	86	VAL	2.8
5	CE	51	VAL	2.8
9	AI	48	GLU	2.8
32	BH	76	VAL	2.8
36	DP	126	VAL	2.8
1	AA	331	G	2.8
1	CA	1338	G	2.8
4	AD	146	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
10	AJ	57	LYS	2.8
16	AP	45	THR	2.8
37	DQ	42	ILE	2.8
38	DR	52	ILE	2.8
55	D8	17	THR	2.8
26	DA	2805	G	2.8
27	DB	118	G	2.8
31	DG	3	LEU	2.8
31	DG	94	LEU	2.8
1	AA	1446	U	2.8
1	CA	1090	U	2.8
30	BF	59	TYR	2.8
31	DG	24	GLY	2.8
33	DI	126	TYR	2.8
36	BP	51	PHE	2.8
36	BP	145	PRO	2.8
17	AQ	91	ARG	2.8
24	AX	48	C	2.8
26	BA	2185	C	2.8
56	B9	28	GLU	2.8
42	DV	79	VAL	2.8
45	BY	8	LYS	2.8
56	D9	27	CYS	2.8
3	AC	67	THR	2.8
5	CE	117	ASP	2.8
9	CI	29	ASN	2.8
34	DN	90	MET	2.8
56	B9	12	ASP	2.8
1	CA	1093	A	2.8
2	CB	89	GLY	2.8
2	CB	154	LEU	2.8
5	AE	109	ILE	2.8
26	DA	2117	A	2.8
33	DI	75	LEU	2.8
39	BS	48	LEU	2.8
41	DU	82	GLY	2.8
45	BY	14	LEU	2.8
55	D8	38	GLY	2.8
1	CA	1212	U	2.8
7	AG	62	PHE	2.8
9	CI	104	ARG	2.8
11	AK	20	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
36	DP	80	TYR	2.8
53	D6	35	GLU	2.8
20	AT	81	LYS	2.8
25	CY	10	G	2.8
36	DP	132	LYS	2.8
38	DR	41	ALA	2.8
1	CA	1388	C	2.8
5	AE	67	VAL	2.8
34	DN	41	ASP	2.8
36	DP	71	VAL	2.8
46	DZ	90	VAL	2.8
3	AC	15	THR	2.8
2	CB	182	ILE	2.8
31	BG	16	ARG	2.8
38	DR	8	ARG	2.8
46	DZ	19	ARG	2.8
54	B7	23	ARG	2.8
15	AO	66	LEU	2.8
30	BF	32	LEU	2.8
34	DN	91	LEU	2.8
42	DV	36	PRO	2.8
36	DP	46	LYS	2.8
41	DU	5	LYS	2.8
44	DX	47	PHE	2.8
26	DA	2126	A	2.8
28	DD	172	TYR	2.8
10	AJ	27	ALA	2.8
14	AN	32	SER	2.8
28	DD	266	SER	2.8
30	DF	185	ASP	2.8
2	CB	229	VAL	2.8
5	CE	78	HIS	2.8
14	AN	25	VAL	2.8
1	AA	64	G	2.8
1	AA	183	G	2.8
1	CA	1087	G	2.8
1	CA	1353	G	2.8
1	CA	1361	G	2.8
7	CG	31	MET	2.8
10	AJ	97	GLU	2.8
18	CR	46	GLU	2.8
28	BD	145	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
28	DD	273	ARG	2.8
30	DF	160	ASN	2.8
32	DH	61	HIS	2.8
34	DN	62	VAL	2.8
35	DO	85	VAL	2.8
36	BP	54	GLY	2.8
37	DQ	123	HIS	2.8
56	D9	32	HIS	2.8
36	DP	39	LYS	2.8
48	D1	81	LYS	2.8
12	CL	5	PRO	2.8
20	CT	62	LEU	2.8
29	DE	48	GLN	2.8
32	DH	88	LEU	2.8
38	DR	100	LEU	2.8
48	D1	13	ILE	2.8
2	AB	33	TYR	2.7
12	CL	30	ALA	2.7
28	BD	2	ALA	2.7
33	BI	96	ASP	2.7
17	CQ	58	GLU	2.7
25	AY	7	A	2.7
26	DA	2170	A	2.7
11	AK	56	GLY	2.7
2	AB	179	LYS	2.7
12	CL	49	ASN	2.7
2	CB	48	MET	2.7
11	AK	82	VAL	2.7
12	AL	11	VAL	2.7
38	DR	66	VAL	2.7
39	DS	93	LYS	2.7
2	CB	115	LEU	2.7
42	BV	71	LEU	2.7
5	AE	131	ILE	2.7
17	CQ	65	ILE	2.7
23	AW	45	U	2.7
1	CA	216	G	2.7
1	CA	1127	G	2.7
2	CB	134	GLU	2.7
10	AJ	54	PHE	2.7
26	DA	2162	G	2.7
26	DA	2318	G	2.7

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Mol	Chain	Res	Type	RSRZ
30	BF	202	PHE	2.7
36	BP	130	PHE	2.7
36	DP	144	GLU	2.7
8	CH	28	ALA	2.7
12	AL	68	ALA	2.7
15	CO	55	GLY	2.7
20	CT	21	LYS	2.7
20	CT	101	GLY	2.7
38	DR	42	LYS	2.7
3	AC	86	VAL	2.7
12	CL	58	VAL	2.7
14	CN	33	VAL	2.7
29	BE	1	MET	2.7
34	DN	14	VAL	2.7
42	BV	37	VAL	2.7
42	BV	51	VAL	2.7
48	D1	68	PRO	2.7
30	BF	148	LEU	2.7
32	DH	58	GLU	2.7
40	BT	78	LEU	2.7
46	BZ	61	LEU	2.7
11	CK	91	ARG	2.7
53	B6	35	GLU	2.7
55	B8	65	GLU	2.7
56	D9	35	ARG	2.7
32	DH	162	ILE	2.7
39	DS	11	LYS	2.7
16	CP	9	PHE	2.7
25	AY	32	PSU	2.7
33	DI	143	SER	2.7
35	DO	28	SER	2.7
37	DQ	29	PHE	2.7
6	AF	35	ALA	2.7
12	CL	14	GLY	2.7
28	DD	153	ALA	2.7
32	DH	166	GLY	2.7
33	DI	115	ALA	2.7
39	DS	74	ALA	2.7
41	DU	96	ALA	2.7
48	D1	29	GLY	2.7
31	BG	138	GLN	2.7
49	D2	56	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
5	AE	55	VAL	2.7
9	AI	36	TYR	2.7
19	CS	51	VAL	2.7
26	DA	10	G	2.7
29	BE	167	VAL	2.7
45	BY	72	VAL	2.7
3	CC	166	GLU	2.7
16	AP	71	ARG	2.7
9	CI	54	ASP	2.7
20	AT	36	LEU	2.7
41	BU	95	LEU	2.7
41	DU	98	LEU	2.7
45	BY	31	LEU	2.7
46	DZ	41	LEU	2.7
48	B1	46	LEU	2.7
1	AA	1183	A	2.7
1	CA	781	A	2.7
2	AB	171	ALA	2.7
5	AE	78	HIS	2.7
30	BF	16	GLY	2.7
6	AF	57	GLN	2.7
20	AT	26	ASN	2.7
44	DX	79	ALA	2.7
45	BY	65	ALA	2.7
40	DT	115	ARG	2.7
1	CA	1029	C	2.7
2	CB	139	LYS	2.7
36	DP	107	LYS	2.7
55	D8	15	LYS	2.7
2	CB	47	THR	2.7
10	AJ	58	ASP	2.7
36	DP	97	PRO	2.7
38	BR	72	ASP	2.7
2	AB	11	LEU	2.7
35	DO	8	LEU	2.7
12	CL	35	GLY	2.7
14	CN	24	CYS	2.7
37	DQ	12	GLN	2.7
48	D1	67	ILE	2.7
2	AB	20	GLU	2.7
10	CJ	64	GLU	2.7
11	AK	23	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
41	DU	68	ALA	2.7
55	D8	10	ALA	2.7
3	AC	38	ARG	2.7
5	AE	40	ARG	2.7
20	CT	25	ARG	2.7
46	DZ	122	ARG	2.7
47	D0	14	ARG	2.7
49	B2	51	ARG	2.7
50	D3	35	ARG	2.7
12	CL	11	VAL	2.7
16	AP	53	VAL	2.7
31	BG	38	VAL	2.7
32	BH	37	VAL	2.7
3	AC	73	PRO	2.7
6	CF	51	PRO	2.7
15	CO	33	THR	2.7
18	AR	82	THR	2.7
36	DP	30	THR	2.7
46	DZ	15	PRO	2.7
47	D0	78	TYR	2.7
48	B1	43	TYR	2.7
4	CD	202	LEU	2.7
6	AF	14	LEU	2.7
23	CW	43	C	2.7
26	DA	2527	C	2.7
27	DB	65	C	2.7
35	DO	122	LEU	2.7
37	BQ	80	GLU	2.7
42	DV	25	LEU	2.7
4	AD	125	HIS	2.7
3	AC	131	ARG	2.7
5	CE	63	ARG	2.7
14	CN	23	ARG	2.7
15	CO	17	ARG	2.7
15	CO	72	ARG	2.7
17	AQ	68	ARG	2.7
20	AT	79	ARG	2.7
26	BA	2172	U	2.7
33	DI	50	ARG	2.7
17	AQ	59	ILE	2.7
45	BY	95	LYS	2.7
50	D3	46	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
3	CC	203	PHE	2.7
38	DR	80	PHE	2.7
4	CD	165	MET	2.7
25	CY	69	G	2.7
26	DA	2112	G	2.7
46	DZ	28	MET	2.7
1	AA	1227	A	2.7
3	AC	70	VAL	2.7
22	AV	14	A	2.7
25	AY	58	A	2.7
28	BD	193	VAL	2.7
28	DD	34	VAL	2.7
40	DT	10	VAL	2.7
47	D0	31	VAL	2.7
4	CD	45	GLN	2.7
4	AD	207	TYR	2.7
9	AI	111	ARG	2.7
12	CL	15	ARG	2.7
16	CP	27	LYS	2.7
18	AR	44	LEU	2.7
30	BF	12	LEU	2.7
31	BG	96	ARG	2.7
36	DP	128	HIS	2.7
48	B1	73	LEU	2.7
49	D2	51	ARG	2.7
10	AJ	35	SER	2.7
13	CM	12	ASN	2.7
16	CP	56	ALA	2.7
25	AY	43	C	2.7
25	CY	62	C	2.7
2	CB	42	ILE	2.7
3	AC	203	PHE	2.7
11	CK	125	PHE	2.7
18	CR	39	VAL	2.6
30	BF	105	VAL	2.6
30	BF	193	VAL	2.6
3	CC	67	THR	2.6
3	CC	78	GLY	2.6
5	CE	39	GLY	2.6
6	CF	87	ARG	2.6
30	DF	144	LYS	2.6
34	DN	84	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
45	DY	88	LYS	2.6
12	CL	75	HIS	2.6
55	D8	7	HIS	2.6
1	CA	728	A	2.6
23	AW	55	PSU	2.6
31	BG	34	LEU	2.6
42	BV	40	LEU	2.6
46	BZ	150	LEU	2.6
4	CD	38	TYR	2.6
8	AH	58	TYR	2.6
43	DW	45	TYR	2.6
20	CT	40	ALA	2.6
44	DX	91	ALA	2.6
16	AP	47	ASP	2.6
11	CK	40	ILE	2.6
45	DY	75	ILE	2.6
48	D1	60	PHE	2.6
1	CA	1477	C	2.6
15	CO	88	ARG	2.6
49	D2	49	LYS	2.6
53	D6	33	LYS	2.6
19	CS	76	PRO	2.6
9	AI	44	VAL	2.6
28	DD	205	VAL	2.6
34	BN	5	VAL	2.6
37	DQ	15	GLY	2.6
47	D0	81	VAL	2.6
48	D1	49	VAL	2.6
18	CR	69	THR	2.6
45	DY	68	HIS	2.6
46	DZ	85	HIS	2.6
12	AL	77	LEU	2.6
28	BD	37	LEU	2.6
28	BD	111	LEU	2.6
16	AP	70	ALA	2.6
17	CQ	86	GLU	2.6
33	BI	65	ALA	2.6
33	BI	89	TYR	2.6
37	DQ	93	TYR	2.6
38	DR	87	TYR	2.6
28	BD	275	LYS	2.6
32	BH	59	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
54	B7	47	ARG	2.6
3	CC	162	GLN	2.6
20	CT	56	MET	2.6
25	CY	70	G	2.6
31	BG	41	GLN	2.6
2	AB	183	PRO	2.6
3	AC	155	GLY	2.6
4	CD	206	PHE	2.6
15	CO	89	GLY	2.6
16	AP	78	GLY	2.6
4	AD	88	VAL	2.6
12	CL	39	VAL	2.6
35	DO	58	VAL	2.6
36	DP	35	HIS	2.6
38	DR	61	HIS	2.6
1	CA	174	C	2.6
25	CY	4	C	2.6
32	BH	70	THR	2.6
17	AQ	94	ASN	2.6
32	BH	47	GLU	2.6
33	BI	48	GLU	2.6
5	CE	47	LYS	2.6
7	CG	36	LYS	2.6
18	AR	26	LEU	2.6
21	CU	3	LYS	2.6
33	DI	114	LEU	2.6
34	DN	34	LEU	2.6
3	AC	65	ALA	2.6
5	CE	126	ARG	2.6
5	CE	138	ALA	2.6
10	CJ	70	ARG	2.6
26	DA	895	U	2.6
37	BQ	10	ARG	2.6
5	AE	10	MET	2.6
30	DF	112	MET	2.6
11	AK	95	ILE	2.6
31	DG	89	GLY	2.6
26	BA	2463	A	2.6
34	DN	16	ILE	2.6
10	CJ	97	GLU	2.6
11	AK	22	HIS	2.6
47	D0	60	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
15	AO	29	VAL	2.6
46	BZ	71	VAL	2.6
16	AP	43	LYS	2.6
40	DT	62	THR	2.6
1	AA	148	G	2.6
1	AA	1386	G	2.6
10	CJ	35	SER	2.6
20	CT	31	SER	2.6
26	BA	2816	G	2.6
54	D7	8	ASN	2.6
15	CO	56	LEU	2.6
18	AR	58	LEU	2.6
24	CX	48	C	2.6
38	DR	111	LEU	2.6
3	AC	139	GLN	2.6
5	AE	20	GLN	2.6
5	CE	146	ALA	2.6
31	BG	61	ALA	2.6
42	DV	59	ALA	2.6
4	AD	124	GLY	2.6
2	CB	31	TYR	2.6
7	CG	146	GLU	2.6
10	AJ	64	GLU	2.6
37	BQ	137	TYR	2.6
45	BY	82	PRO	2.6
5	CE	84	PHE	2.6
18	CR	71	LYS	2.6
28	DD	53	PHE	2.6
32	BH	151	ILE	2.6
34	BN	16	ILE	2.6
10	AJ	34	VAL	2.6
5	CE	36	ASP	2.6
10	CJ	43	ARG	2.6
17	CQ	91	ARG	2.6
29	DE	59	VAL	2.6
20	AT	11	SER	2.6
3	AC	121	ALA	2.6
5	AE	142	LEU	2.6
7	AG	59	LEU	2.6
9	AI	102	LEU	2.6
20	CT	12	ALA	2.6
4	CD	163	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
42	DV	48	GLY	2.6
1	AA	1030(A)	G	2.6
26	DA	226	G	2.6
26	DA	652(C)	G	2.6
47	D0	80	HIS	2.6
2	CB	39	ILE	2.6
4	AD	206	PHE	2.6
31	DG	114	ILE	2.6
38	DR	83	ILE	2.6
6	CF	84	ASN	2.6
12	AL	104	VAL	2.6
28	BD	117	VAL	2.6
2	AB	124	SER	2.6
5	CE	144	THR	2.6
18	CR	82	THR	2.6
20	CT	71	THR	2.6
36	DP	133	SER	2.6
39	DS	47	THR	2.6
10	AJ	61	GLU	2.6
9	AI	119	ALA	2.6
12	CL	107	ALA	2.6
16	CP	64	ALA	2.6
31	DG	34	LEU	2.6
33	BI	9	LEU	2.6
34	BN	116	LEU	2.6
36	DP	116	GLY	2.6
37	DQ	49	ALA	2.6
38	BR	70	LEU	2.6
44	DX	66	LEU	2.6
50	D3	22	ALA	2.6
1	CA	1319	A	2.6
18	AR	23	LYS	2.6
26	DA	227	A	2.6
42	DV	84	LYS	2.6
55	D8	52	LYS	2.6
26	DA	2172	U	2.6
3	AC	85	ARG	2.6
30	DF	164	ARG	2.6
32	DH	118	PRO	2.6
45	DY	84	ARG	2.6
50	D3	18	ASP	2.6
1	CA	1141	C	2.6

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Mol	Chain	Res	Type	RSRZ
2	CB	236	TYR	2.6
5	AE	100	VAL	2.6
23	AW	11	C	2.6
26	DA	850	C	2.6
37	DQ	97	VAL	2.6
41	DU	105	VAL	2.6
46	BZ	88	PHE	2.6
25	AY	44	G	2.6
26	BA	2163	G	2.6
12	AL	46	LYS	2.6
32	DH	30	LYS	2.6
38	BR	74	LYS	2.6
42	DV	74	LYS	2.6
47	D0	19	LYS	2.6
2	CB	34	ALA	2.5
5	AE	22	GLY	2.5
19	CS	50	ALA	2.5
9	AI	66	ARG	2.5
19	CS	78	ARG	2.5
20	AT	10	LEU	2.5
35	DO	118	ALA	2.5
39	BS	24	LEU	2.5
41	DU	35	ALA	2.5
46	BZ	70	LEU	2.5
50	B3	8	LEU	2.5
52	D5	14	ALA	2.5
1	CA	1000	U	2.5
1	CA	1030(D)	A	2.5
2	CB	24	TRP	2.5
16	CP	68	ASP	2.5
25	CY	21	A	2.5
3	CC	104	GLN	2.5
30	DF	145	GLU	2.5
51	D4	47	GLN	2.5
30	BF	182	ASN	2.5
8	CH	116	LYS	2.5
12	AL	55	VAL	2.5
12	CL	57	LYS	2.5
29	DE	196	VAL	2.5
30	BF	57	VAL	2.5
35	DO	86	ILE	2.5
37	DQ	18	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
9	AI	27	THR	2.5
9	CI	68	GLY	2.5
16	CP	78	GLY	2.5
18	AR	69	THR	2.5
44	DX	5	TYR	2.5
1	CA	1116	C	2.5
26	DA	2108	C	2.5
26	DA	2452	C	2.5
31	DG	72	ARG	2.5
38	DR	64	ARG	2.5
5	CE	62	ALA	2.5
9	AI	82	ALA	2.5
2	AB	142	LEU	2.5
13	AM	34	LEU	2.5
31	DG	103	LEU	2.5
36	BP	6	LEU	2.5
1	CA	1456	G	2.5
13	AM	16	ASP	2.5
33	DI	137	PRO	2.5
39	DS	38	GLN	2.5
14	AN	61	TRP	2.5
17	CQ	92	ARG	2.5
35	DO	61	VAL	2.5
41	DU	43	GLY	2.5
45	DY	13	VAL	2.5
46	DZ	128	VAL	2.5
49	D2	26	ARG	2.5
55	D8	49	VAL	2.5
3	AC	8	ILE	2.5
34	BN	85	ILE	2.5
37	DQ	120	ILE	2.5
46	BZ	133	ILE	2.5
2	AB	225	ALA	2.5
10	AJ	20	ALA	2.5
42	BV	3	ALA	2.5
35	DO	25	LEU	2.5
16	CP	41	PRO	2.5
37	DQ	54	MET	2.5
48	D1	78	LYS	2.5
7	AG	6	ARG	2.5
9	CI	107	ARG	2.5
18	AR	74	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
20	CT	75	ASN	2.5
31	BG	115	ARG	2.5
48	D1	22	GLY	2.5
1	AA	933	G	2.5
9	CI	44	VAL	2.5
13	AM	117	VAL	2.5
18	CR	37	VAL	2.5
26	DA	2182	G	2.5
47	B0	51	VAL	2.5
2	AB	54	THR	2.5
4	CD	89	THR	2.5
13	AM	8	GLU	2.5
51	B4	14	ILE	2.5
56	B9	10	ILE	2.5
3	CC	169	ALA	2.5
7	AG	147	ALA	2.5
13	AM	33	ALA	2.5
1	CA	802	A	2.5
1	CA	1363(A)	A	2.5
5	CE	61	TYR	2.5
16	CP	38	TYR	2.5
18	CR	34	TYR	2.5
30	DF	166	ALA	2.5
31	BG	56	ALA	2.5
26	BA	2462	A	2.5
44	BX	69	TYR	2.5
56	D9	13	LYS	2.5
2	AB	51	LEU	2.5
4	AD	119	GLN	2.5
28	DD	33	LEU	2.5
30	DF	125	LEU	2.5
31	BG	94	LEU	2.5
34	BN	82	LEU	2.5
42	DV	71	LEU	2.5
30	BF	10	PRO	2.5
35	DO	1	MET	2.5
41	DU	2	PRO	2.5
55	D8	63	PRO	2.5
11	CK	18	ARG	2.5
30	DF	182	ASN	2.5
1	CA	962	C	2.5
4	AD	98	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
4	AD	109	GLY	2.5
12	AL	29	GLY	2.5
33	BI	16	GLY	2.5
33	DI	48	GLU	2.5
4	CD	85	LYS	2.5
10	CJ	15	THR	2.5
2	CB	29	ALA	2.5
3	AC	180	ALA	2.5
5	AE	45	PHE	2.5
7	AG	54	THR	2.5
37	BQ	127	ILE	2.5
43	BW	96	ILE	2.5
46	BZ	44	PHE	2.5
54	B7	45	ALA	2.5
4	AD	139	ARG	2.5
13	CM	96	LEU	2.5
14	AN	53	LEU	2.5
34	BN	12	ARG	2.5
1	AA	107	G	2.5
26	BA	2517	G	2.5
5	CE	130	ASN	2.5
23	AW	14	A	2.5
26	BA	1465	A	2.5
5	CE	88	LYS	2.5
33	BI	121	LYS	2.5
50	D3	20	LYS	2.5
1	CA	748	C	2.5
2	AB	206	ASP	2.5
10	AJ	62	HIS	2.5
13	AM	7	VAL	2.5
33	BI	136	VAL	2.5
34	BN	140	VAL	2.5
38	BR	73	VAL	2.5
4	CD	36	ARG	2.5
37	DQ	51	ARG	2.5
2	CB	17	PHE	2.5
2	CB	181	PHE	2.5
13	AM	90	LEU	2.5
20	AT	43	LEU	2.5
28	DD	16	MET	2.5
29	DE	195	LEU	2.5
31	BG	135	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
37	BQ	2	LEU	2.5
2	CB	37	ASN	2.5
3	AC	29	TYR	2.5
8	CH	48	TYR	2.5
9	AI	97	LYS	2.5
13	CM	23	TYR	2.5
12	CL	95	GLY	2.5
23	CW	51	U	2.5
32	BH	153	LYS	2.5
32	DH	138	LYS	2.5
37	DQ	87	LYS	2.5
44	DX	36	LYS	2.5
46	BZ	52	SER	2.5
1	AA	1068	G	2.5
9	AI	51	ARG	2.5
26	BA	1467	G	2.5
26	BA	1960	A	2.5
26	DA	2171	A	2.5
4	AD	128	VAL	2.5
8	CH	19	VAL	2.5
28	DD	142	VAL	2.5
35	DO	57	VAL	2.5
53	D6	48	VAL	2.5
5	CE	7	GLU	2.5
2	AB	202	PRO	2.5
4	AD	189	PRO	2.5
10	AJ	38	ILE	2.5
19	AS	62	ILE	2.5
30	DF	83	PHE	2.5
37	BQ	104	PHE	2.5
33	BI	8	PRO	2.5
45	BY	88	LYS	2.5
50	D3	41	PRO	2.5
10	AJ	40	LEU	2.5
12	AL	95	GLY	2.5
28	BD	133	LEU	2.5
29	DE	27	LEU	2.5
11	CK	42	TRP	2.5
30	BF	199	TRP	2.5
1	CA	1085	U	2.4
3	AC	48	TYR	2.4
32	BH	157	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
7	CG	72	ARG	2.4
40	DT	111	ARG	2.4
4	AD	113	SER	2.4
30	BF	173	VAL	2.4
33	BI	145	VAL	2.4
44	DX	30	VAL	2.4
4	CD	147	ALA	2.4
6	AF	29	ALA	2.4
7	CG	116	ALA	2.4
13	CM	118	ALA	2.4
14	AN	59	ALA	2.4
37	DQ	22	LYS	2.4
44	DX	46	ALA	2.4
5	AE	128	PRO	2.4
6	CF	56	PRO	2.4
40	DT	101	PHE	2.4
45	BY	89	PHE	2.4
1	CA	587	G	2.4
3	AC	181	ASN	2.4
7	AG	30	ILE	2.4
7	AG	50	ILE	2.4
26	DA	125	G	2.4
28	DD	105	ILE	2.4
28	DD	251	GLY	2.4
40	DT	52	ILE	2.4
42	DV	4	ILE	2.4
16	CP	6	LEU	2.4
33	BI	123	LEU	2.4
36	BP	135	LEU	2.4
4	AD	50	ARG	2.4
18	AR	35	ARG	2.4
30	DF	18	ARG	2.4
54	D7	9	ARG	2.4
1	AA	619	U	2.4
1	CA	990	C	2.4
1	CA	1218	C	2.4
26	BA	2464	C	2.4
26	DA	34	C	2.4
30	DF	77	ASP	2.4
13	AM	64	TRP	2.4
33	DI	29	TYR	2.4
41	DU	89	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
53	D6	49	HIS	2.4
13	CM	79	LYS	2.4
48	B1	81	LYS	2.4
13	CM	98	VAL	2.4
28	BD	18	VAL	2.4
28	DD	163	ALA	2.4
34	DN	122	VAL	2.4
2	AB	107	THR	2.4
13	AM	20	THR	2.4
32	DH	129	THR	2.4
37	BQ	121	ALA	2.4
45	BY	36	ALA	2.4
4	CD	7	PRO	2.4
5	CE	24	ARG	2.4
10	CJ	86	MET	2.4
11	CK	54	ARG	2.4
16	CP	72	ARG	2.4
29	BE	106	GLY	2.4
33	BI	13	GLY	2.4
51	B4	4	GLY	2.4
2	CB	44	LEU	2.4
3	AC	202	ILE	2.4
7	CG	97	GLN	2.4
32	BH	7	LEU	2.4
1	CA	1358	U	2.4
5	CE	121	LYS	2.4
8	CH	82	HIS	2.4
1	CA	654	G	2.4
1	CA	1392	G	2.4
5	AE	60	TYR	2.4
25	CY	15	G	2.4
31	BG	100	TRP	2.4
5	CE	98	THR	2.4
7	CG	3	ARG	2.4
7	CG	23	VAL	2.4
7	CG	145	ALA	2.4
19	AS	11	VAL	2.4
29	DE	23	VAL	2.4
32	BH	52	VAL	2.4
45	DY	80	GLY	2.4
46	DZ	10	ARG	2.4
48	D1	24	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
49	D2	62	THR	2.4
51	D4	12	ALA	2.4
52	D5	24	ALA	2.4
14	AN	38	GLY	2.4
7	CG	129	GLU	2.4
16	AP	15	PRO	2.4
45	BY	22	GLY	2.4
17	AQ	93	GLN	2.4
2	AB	42	ILE	2.4
5	AE	31	LEU	2.4
6	AF	98	LEU	2.4
18	CR	51	LEU	2.4
28	DD	147	LEU	2.4
41	BU	27	LEU	2.4
44	DX	57	LEU	2.4
1	CA	1095	U	2.4
4	CD	137	SER	2.4
53	D6	3	SER	2.4
39	DS	97	ARG	2.4
41	DU	70	ARG	2.4
2	AB	112	VAL	2.4
3	CC	55	VAL	2.4
5	AE	41	VAL	2.4
11	AK	94	ALA	2.4
20	CT	102	GLY	2.4
30	DF	111	ALA	2.4
32	BH	15	VAL	2.4
33	BI	41	GLU	2.4
33	BI	90	GLY	2.4
33	DI	59	ALA	2.4
34	DN	139	GLU	2.4
41	DU	61	TRP	2.4
41	DU	100	VAL	2.4
43	DW	17	VAL	2.4
7	CG	24	THR	2.4
1	AA	194	C	2.4
1	CA	1119	C	2.4
4	CD	86	LYS	2.4
8	AH	89	PRO	2.4
9	AI	21	PRO	2.4
18	AR	80	PRO	2.4
21	CU	23	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
45	BY	4	LYS	2.4
46	BZ	68	PRO	2.4
51	D4	28	LYS	2.4
53	D6	14	THR	2.4
24	CX	75	C	2.4
26	BA	2162	C	2.4
46	DZ	40	ASP	2.4
1	AA	1002	G	2.4
26	BA	974	G	2.4
26	BA	1182	G	2.4
26	BA	2173	G	2.4
2	AB	17	PHE	2.4
4	CD	78	LEU	2.4
29	DE	182	LEU	2.4
33	BI	51	ILE	2.4
37	DQ	68	ILE	2.4
44	DX	80	ILE	2.4
12	CL	81	SER	2.4
18	CR	32	ARG	2.4
3	CC	122	GLU	2.4
45	DY	41	GLY	2.4
7	AG	9	VAL	2.4
7	AG	145	ALA	2.4
26	DA	2758	A	2.4
29	DE	33	VAL	2.4
37	BQ	55	VAL	2.4
55	D8	24	ALA	2.4
6	AF	51	PRO	2.4
10	CJ	89	ASP	2.4
30	DF	189	THR	2.4
41	DU	38	THR	2.4
45	BY	35	TYR	2.4
37	BQ	41	TRP	2.4
46	BZ	28	MET	2.4
10	AJ	56	HIS	2.4
1	AA	1119	C	2.4
1	CA	1321	C	2.4
2	AB	23	ARG	2.4
3	AC	79	ARG	2.4
4	CD	132	ARG	2.4
6	AF	97	PHE	2.4
7	AG	5	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
26	BA	2158	C	2.4
29	DE	170	LEU	2.4
30	BF	33	LEU	2.4
30	BF	140	LEU	2.4
33	DI	52	ARG	2.4
3	AC	166	GLU	2.4
55	D8	60	LEU	2.4
19	AS	49	ILE	2.4
20	AT	19	SER	2.4
37	BQ	66	ILE	2.4
39	DS	27	SER	2.4
41	BU	17	ILE	2.4
8	AH	32	LYS	2.4
18	CR	23	LYS	2.4
26	BA	1152	G	2.4
26	BA	2134	G	2.4
26	BA	2153	G	2.4
31	DG	36	LYS	2.4
14	AN	28	GLY	2.4
7	CG	40	ALA	2.4
29	DE	28	ALA	2.4
35	BO	11	ALA	2.4
36	DP	129	ALA	2.4
45	BY	100	ALA	2.4
55	D8	55	ALA	2.4
4	AD	39	PRO	2.4
6	AF	13	ASN	2.4
10	CJ	76	ASN	2.4
12	CL	110	VAL	2.4
7	AG	24	THR	2.4
31	DG	93	THR	2.4
43	DW	14	PRO	2.4
4	CD	20	TYR	2.4
40	DT	14	TYR	2.4
9	CI	48	GLU	2.4
22	CV	16	A	2.4
26	BA	2041	A	2.4
4	AD	196	LEU	2.4
10	AJ	55	LYS	2.4
17	CQ	31	LEU	2.4
18	CR	21	LYS	2.4
34	BN	117	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
46	BZ	125	LEU	2.4
7	AG	34	GLY	2.4
33	DI	34	GLY	2.4
37	DQ	122	GLY	2.4
1	CA	526	C	2.4
1	CA	1069	C	2.4
1	CA	1259	C	2.4
25	AY	61	C	2.4
25	CY	48	C	2.4
26	DA	2467	C	2.4
46	DZ	73	GLN	2.4
54	B7	36	GLN	2.4
18	CR	73	ALA	2.3
19	CS	23	ASN	2.3
30	BF	167	ALA	2.3
32	BH	96	ALA	2.3
35	DO	84	ALA	2.3
7	AG	95	ARG	2.3
8	AH	129	VAL	2.3
9	CI	41	VAL	2.3
12	AL	101	VAL	2.3
20	CT	57	ARG	2.3
31	DG	33	ARG	2.3
33	BI	50	ARG	2.3
34	BN	46	VAL	2.3
34	DN	32	THR	2.3
37	DQ	94	VAL	2.3
38	DR	73	VAL	2.3
38	DR	76	VAL	2.3
45	BY	91	GLU	2.3
50	B3	34	GLU	2.3
53	D6	4	GLU	2.3
1	AA	1094	G	2.3
1	CA	577	G	2.3
26	DA	2792	G	2.3
31	DG	81	LYS	2.3
41	DU	30	LYS	2.3
52	D5	9	LYS	2.3
2	CB	199	TYR	2.3
45	DY	20	TYR	2.3
46	BZ	99	TYR	2.3
51	B4	25	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
4	AD	183	GLY	2.3
9	AI	67	GLY	2.3
12	AL	9	GLN	2.3
35	DO	117	LEU	2.3
36	BP	3	LEU	2.3
38	DR	18	LEU	2.3
30	BF	34	TRP	2.3
39	DS	112	PHE	2.3
3	AC	157	ILE	2.3
8	AH	134	ILE	2.3
10	CJ	58	ASP	2.3
29	BE	77	ILE	2.3
7	CG	95	ARG	2.3
9	AI	120	ARG	2.3
52	B5	59	GLU	2.3
4	AD	161	ASN	2.3
7	AG	148	ASN	2.3
45	DY	100	ALA	2.3
1	CA	932	C	2.3
3	CC	69	HIS	2.3
16	CP	21	VAL	2.3
20	CT	35	THR	2.3
28	DD	185	VAL	2.3
29	DE	116	VAL	2.3
35	DO	26	LYS	2.3
35	DO	115	VAL	2.3
36	DP	17	LYS	2.3
41	DU	34	LYS	2.3
33	DI	93	THR	2.3
2	AB	65	GLY	2.3
8	AH	29	SER	2.3
28	BD	147	LEU	2.3
29	DE	6	GLY	2.3
31	BG	11	TYR	2.3
53	B6	43	CYS	2.3
17	AQ	22	LEU	2.3
38	BR	79	LEU	2.3
1	AA	945	G	2.3
2	AB	84	GLU	2.3
4	AD	35	ARG	2.3
4	AD	75	PHE	2.3
5	AE	64	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
8	AH	33	GLU	2.3
13	AM	55	ARG	2.3
17	CQ	75	ARG	2.3
26	BA	911	G	2.3
26	BA	973	G	2.3
28	BD	135	PHE	2.3
32	DH	86	GLU	2.3
23	CW	60	U	2.3
30	DF	135	LYS	2.3
34	DN	42	TRP	2.3
3	AC	92	ALA	2.3
13	CM	51	ALA	2.3
18	AR	36	ASN	2.3
26	BA	2584	A	2.3
31	BG	2	PRO	2.3
35	DO	101	PRO	2.3
38	DR	101	ALA	2.3
1	AA	1035	A	2.3
1	CA	1531	A	2.3
2	AB	197	VAL	2.3
3	AC	75	VAL	2.3
4	AD	112	VAL	2.3
14	CN	18	VAL	2.3
30	BF	114	VAL	2.3
39	DS	46	VAL	2.3
56	D9	23	VAL	2.3
19	AS	56	GLN	2.3
1	AA	522	C	2.3
1	CA	217	C	2.3
23	CW	42	C	2.3
2	AB	79	ASP	2.3
2	AB	195	ASP	2.3
17	CQ	68	ARG	2.3
30	DF	106	ARG	2.3
31	DG	22	ARG	2.3
33	DI	70	GLU	2.3
35	DO	116	SER	2.3
42	DV	93	GLU	2.3
46	DZ	16	SER	2.3
51	B4	61	ARG	2.3
4	CD	207	TYR	2.3
6	AF	54	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
7	CG	70	LYS	2.3
9	AI	85	LEU	2.3
25	CY	46	7MG	2.3
29	DE	63	LEU	2.3
29	DE	183	LEU	2.3
37	DQ	9	TYR	2.3
47	D0	24	LYS	2.3
53	D6	21	TYR	2.3
40	BT	61	PHE	2.3
3	AC	84	ILE	2.3
17	CQ	94	ASN	2.3
28	DD	265	PRO	2.3
32	BH	73	ALA	2.3
33	BI	138	ILE	2.3
25	AY	65	G	2.3
29	DE	25	VAL	2.3
30	DF	187	VAL	2.3
37	DQ	105	GLU	2.3
40	BT	60	THR	2.3
49	D2	12	GLU	2.3
55	D8	56	GLU	2.3
1	CA	1447	A	2.3
3	AC	59	ARG	2.3
4	AD	59	ARG	2.3
12	CL	53	ARG	2.3
3	CC	135	LYS	2.3
5	AE	124	GLY	2.3
26	DA	1913	A	2.3
47	D0	11	ARG	2.3
10	CJ	12	ASP	2.3
14	CN	60	SER	2.3
31	BG	76	SER	2.3
32	BH	33	LEU	2.3
32	DH	171	LEU	2.3
1	AA	40	C	2.3
15	CO	18	PHE	2.3
16	CP	32	TYR	2.3
1	AA	1532	U	2.3
2	AB	140	HIS	2.3
4	AD	67	ILE	2.3
4	AD	164	ALA	2.3
13	CM	113	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
23	AW	12	U	2.3
19	AS	31	ILE	2.3
33	BI	49	ALA	2.3
35	DO	69	ILE	2.3
36	BP	129	ALA	2.3
38	DR	25	ALA	2.3
46	DZ	134	PRO	2.3
2	AB	157	ARG	2.3
5	CE	18	ARG	2.3
37	DQ	13	GLN	2.3
2	CB	151	GLY	2.3
10	CJ	22	LYS	2.3
12	AL	88	GLY	2.3
17	AQ	9	VAL	2.3
29	DE	184	VAL	2.3
32	DH	78	GLY	2.3
37	BQ	19	GLY	2.3
41	DU	73	GLY	2.3
42	DV	92	THR	2.3
43	DW	20	VAL	2.3
46	BZ	37	VAL	2.3
55	D8	47	LYS	2.3
2	CB	192	SER	2.3
8	CH	87	SER	2.3
8	CH	113	SER	2.3
1	AA	66	G	2.3
1	AA	406	G	2.3
1	AA	1061	G	2.3
1	AA	1067	A	2.3
1	AA	1117	G	2.3
1	AA	1157	A	2.3
1	CA	1003	G	2.3
1	CA	1042	G	2.3
26	DA	2246	G	2.3
27	DB	117	G	2.3
6	AF	94	GLN	2.3
8	AH	72	PRO	2.3
20	CT	30	LYS	2.3
41	DU	33	ARG	2.3
50	D3	30	ARG	2.3
1	CA	1097	C	2.3
13	CM	95	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
36	DP	82	GLY	2.3
40	DT	7	ILE	2.3
43	BW	95	ILE	2.3
51	D4	5	ILE	2.3
4	AD	127	THR	2.3
7	CG	87	VAL	2.3
29	BE	12	THR	2.3
29	BE	198	VAL	2.3
30	DF	89	VAL	2.3
36	BP	58	THR	2.3
36	BP	146	VAL	2.3
45	DY	27	VAL	2.3
11	CK	43	SER	2.3
21	AU	14	TRP	2.3
2	CB	12	GLU	2.3
3	AC	82	GLU	2.3
5	AE	122	GLU	2.3
7	AG	57	GLU	2.3
3	CC	127	ARG	2.3
33	DI	57	ARG	2.3
37	DQ	14	ARG	2.3
37	DQ	56	ARG	2.3
39	DS	30	ARG	2.3
44	DX	40	LYS	2.3
45	DY	9	LYS	2.3
46	BZ	67	LEU	2.3
5	CE	134	ALA	2.3
1	AA	171	A	2.3
1	AA	1179	A	2.3
1	CA	559	A	2.3
9	AI	101	PHE	2.3
53	B6	2	ALA	2.3
25	CY	7	A	2.3
26	DA	2430	A	2.3
54	D7	27	GLY	2.3
1	CA	825	G	2.3
1	CA	1197	G	2.3
1	CA	1224	G	2.3
26	BA	2212	G	2.3
26	DA	2100	G	2.3
26	DA	2319	G	2.3
27	BB	75	G	2.3

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Mol	Chain	Res	Type	RSRZ
2	AB	136	VAL	2.3
25	CY	72	C	2.3
28	DD	17	THR	2.3
31	BG	31	VAL	2.3
37	DQ	55	VAL	2.3
51	D4	10	VAL	2.3
1	CA	1030	C	2.3
4	AD	60	GLU	2.3
12	CL	16	GLU	2.3
37	DQ	91	GLU	2.3
29	DE	199	ARG	2.2
49	D2	30	ARG	2.2
3	CC	32	LEU	2.2
9	CI	87	GLN	2.2
41	DU	25	TRP	2.2
12	AL	52	LEU	2.2
12	CL	52	LEU	2.2
13	AM	96	LEU	2.2
29	DE	78	LEU	2.2
34	BN	15	LEU	2.2
34	BN	138	LEU	2.2
44	DX	70	LEU	2.2
46	DZ	65	GLN	2.2
4	CD	197	PRO	2.2
6	AF	49	ALA	2.2
13	CM	42	ALA	2.2
33	BI	146	ALA	2.2
37	DQ	78	PRO	2.2
40	BT	57	PHE	2.2
47	B0	57	PHE	2.2
2	AB	63	MET	2.2
19	AS	52	TYR	2.2
33	BI	25	TYR	2.2
40	DT	1	MET	2.2
48	D1	75	GLU	2.2
54	D7	22	MET	2.2
5	AE	11	ILE	2.2
28	DD	64	ILE	2.2
42	BV	70	ILE	2.2
1	CA	978	A	2.2
10	AJ	5	ARG	2.2
17	CQ	18	THR	2.2

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Mol	Chain	Res	Type	RSRZ
20	AT	70	SER	2.2
20	CT	34	LYS	2.2
20	CT	74	LYS	2.2
30	BF	103	LYS	2.2
30	DF	168	ARG	2.2
35	DO	113	LYS	2.2
48	B1	69	LYS	2.2
2	AB	40	HIS	2.2
10	CJ	56	HIS	2.2
17	CQ	16	GLN	2.2
1	AA	122	G	2.2
1	AA	1258	G	2.2
5	CE	73	ASN	2.2
23	CW	34	G	2.2
38	BR	75	LEU	2.2
46	DZ	93	ASP	2.2
30	BF	80	ALA	2.2
45	DY	36	ALA	2.2
46	BZ	7	ALA	2.2
13	CM	27	LYS	2.2
32	DH	172	LYS	2.2
46	BZ	89	PHE	2.2
4	AD	14	ARG	2.2
13	AM	11	ARG	2.2
16	CP	26	ARG	2.2
32	DH	59	ARG	2.2
40	BT	39	ARG	2.2
2	AB	92	TYR	2.2
2	AB	127	ILE	2.2
29	DE	47	VAL	2.2
36	DP	96	THR	2.2
42	BV	79	VAL	2.2
42	DV	7	THR	2.2
46	BZ	126	VAL	2.2
47	B0	10	THR	2.2
51	B4	22	ILE	2.2
53	B6	54	ILE	2.2
10	CJ	69	ASN	2.2
12	CL	45	PRO	2.2
28	BD	175	LEU	2.2
31	DG	82	LEU	2.2
34	DN	87	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
48	D1	44	PRO	2.2
51	D4	19	GLY	2.2
13	CM	111	LYS	2.2
18	CR	41	LYS	2.2
1	CA	1063	C	2.2
1	CA	1314	C	2.2
2	AB	85	ALA	2.2
20	CT	44	ALA	2.2
28	DD	261	LYS	2.2
25	AY	62	C	2.2
30	DF	80	ALA	2.2
2	AB	24	TRP	2.2
2	CB	217	ARG	2.2
3	CC	131	ARG	2.2
15	CO	65	ARG	2.2
1	CA	765	G	2.2
1	CA	1221	G	2.2
25	CY	28	G	2.2
26	BA	30	G	2.2
29	DE	67	PHE	2.2
32	BH	109	PHE	2.2
4	CD	116	GLN	2.2
4	CD	123	HIS	2.2
9	AI	117	HIS	2.2
12	CL	82	VAL	2.2
19	AS	4	SER	2.2
29	DE	91	VAL	2.2
31	BG	92	VAL	2.2
35	DO	102	VAL	2.2
38	BR	48	VAL	2.2
15	AO	3	ILE	2.2
28	DD	204	ILE	2.2
51	D4	31	ILE	2.2
20	AT	60	GLU	2.2
30	DF	127	GLU	2.2
12	CL	23	LYS	2.2
19	AS	84	GLY	2.2
4	AD	94	LEU	2.2
4	AD	186	LEU	2.2
5	AE	53	LEU	2.2
12	AL	53	ARG	2.2
14	AN	41	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
32	DH	10	PRO	2.2
34	BN	86	PRO	2.2
40	BT	114	LEU	2.2
43	DW	51	LEU	2.2
46	BZ	41	LEU	2.2
53	B6	36	LEU	2.2
3	AC	60	ALA	2.2
5	CE	132	ALA	2.2
8	AH	28	ALA	2.2
16	AP	56	ALA	2.2
1	AA	946	A	2.2
1	CA	965	A	2.2
25	AY	12	U	2.2
37	DQ	3	MET	2.2
42	BV	1	MET	2.2
46	DZ	50	GLN	2.2
51	D4	46	GLN	2.2
23	AW	61	C	2.2
26	BA	2165	C	2.2
30	BF	129	PHE	2.2
41	BU	79	PHE	2.2
47	D0	57	PHE	2.2
2	CB	150	SER	2.2
3	CC	143	GLU	2.2
17	AQ	86	GLU	2.2
28	DD	145	VAL	2.2
28	DD	173	VAL	2.2
32	BH	50	VAL	2.2
33	BI	3	VAL	2.2
46	DZ	52	SER	2.2
2	CB	54	THR	2.2
56	B9	23	VAL	2.2
11	AK	32	ILE	2.2
29	DE	2	LYS	2.2
24	CX	15	G	2.2
26	BA	928	G	2.2
26	BA	2155	G	2.2
26	DA	956	G	2.2
32	DH	66	GLY	2.2
36	DP	23	PRO	2.2
5	CE	151	LEU	2.2
6	AF	53	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
12	AL	56	ALA	2.2
18	CR	67	ALA	2.2
32	BH	75	ALA	2.2
49	D2	38	GLN	2.2
1	CA	560	U	2.2
26	BA	1072	U	2.2
7	AG	137	LYS	2.2
15	CO	50	HIS	2.2
17	CQ	34	LYS	2.2
41	DU	72	HIS	2.2
43	DW	13	SER	2.2
55	D8	39	LYS	2.2
4	AD	131	ARG	2.2
15	AO	33	THR	2.2
19	CS	60	VAL	2.2
29	DE	75	VAL	2.2
34	DN	53	VAL	2.2
48	B1	35	THR	2.2
51	D4	21	VAL	2.2
3	AC	41	GLY	2.2
9	CI	6	GLY	2.2
10	AJ	52	GLY	2.2
36	DP	20	GLY	2.2
1	AA	744	C	2.2
1	AA	1112	C	2.2
1	AA	1249	C	2.2
1	CA	1007	C	2.2
7	CG	30	ILE	2.2
26	DA	1881	C	2.2
30	DF	64	ILE	2.2
2	AB	194	PRO	2.2
6	AF	50	TYR	2.2
8	AH	27	PRO	2.2
11	CK	39	PRO	2.2
20	CT	77	ALA	2.2
34	DN	82	LEU	2.2
38	DR	71	GLN	2.2
38	DR	79	LEU	2.2
1	AA	7	G	2.2
1	AA	587	G	2.2
1	AA	1064	G	2.2
1	CA	944	G	2.2

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Mol	Chain	Res	Type	RSRZ
26	DA	1816	G	2.2
1	CA	1446	U	2.2
2	AB	178	ARG	2.2
8	CH	105	ARG	2.2
25	AY	59	U	2.2
8	AH	8	ASP	2.2
17	AQ	97	SER	2.2
2	CB	227	GLY	2.2
7	AG	105	VAL	2.2
8	AH	44	PHE	2.2
10	CJ	11	PHE	2.2
19	CS	48	THR	2.2
28	BD	205	VAL	2.2
30	BF	126	VAL	2.2
43	DW	50	VAL	2.2
45	BY	37	VAL	2.2
6	CF	26	ILE	2.2
16	AP	33	ILE	2.2
26	BA	2157	A	2.2
30	BF	172	TRP	2.2
36	DP	136	GLU	2.2
37	BQ	64	ILE	2.2
12	CL	31	PRO	2.2
31	DG	11	TYR	2.2
34	DN	4	TYR	2.2
34	DN	83	LYS	2.2
13	AM	81	LEU	2.1
25	CY	11	C	2.2
34	DN	102	ALA	2.2
36	BP	31	ALA	2.2
40	DT	9	LEU	2.1
44	DX	34	ALA	2.2
46	DZ	33	LEU	2.1
50	B3	53	LEU	2.1
55	B8	50	LEU	2.1
10	AJ	9	ARG	2.1
16	AP	13	HIS	2.1
32	BH	3	ARG	2.1
32	DH	101	ARG	2.1
20	CT	64	ASP	2.1
35	DO	12	ASP	2.1
9	AI	72	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
20	AT	31	SER	2.1
30	DF	151	SER	2.1
32	BH	16	SER	2.1
32	DH	174	GLY	2.1
4	AD	56	VAL	2.1
13	CM	103	THR	2.1
29	BE	7	VAL	2.1
32	DH	32	GLU	2.1
33	BI	127	VAL	2.1
33	DI	108	THR	2.1
36	BP	125	VAL	2.1
42	BV	52	VAL	2.1
50	D3	50	VAL	2.1
1	CA	232	G	2.1
1	CA	730	G	2.1
7	CG	136	LYS	2.1
23	AW	34	G	2.1
26	BA	832	G	2.1
26	BA	1021	G	2.1
33	DI	17	GLN	2.1
5	AE	49	PRO	2.1
8	CH	86	ILE	2.1
10	AJ	53	PRO	2.1
11	AK	83	ILE	2.1
28	DD	82	ILE	2.1
8	CH	110	ALA	2.1
12	AL	51	ALA	2.1
41	DU	67	ALA	2.1
1	AA	1110	A	2.1
1	AA	1285	A	2.1
9	AI	96	LEU	2.1
10	CJ	13	HIS	2.1
15	AO	78	TYR	2.1
26	BA	1711	A	2.1
28	BD	177	LEU	2.1
29	DE	151	TYR	2.1
10	AJ	86	MET	2.1
30	DF	116	ASP	2.1
1	CA	1228	C	2.1
5	CE	127	ASN	2.1
5	CE	149	GLU	2.1
9	AI	12	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
12	AL	22	SER	2.1
15	CO	52	SER	2.1
25	CY	39	PSU	2.1
26	DA	12	U	2.1
26	DA	2506	U	2.1
42	BV	101	GLY	2.1
55	D8	65	GLU	2.1
56	B9	29	ASN	2.1
2	CB	168	THR	2.1
4	CD	201	GLN	2.1
16	CP	53	VAL	2.1
29	DE	104	VAL	2.1
47	D0	63	VAL	2.1
48	B1	74	VAL	2.1
52	D5	57	VAL	2.1
2	AB	137	ARG	2.1
3	CC	73	PRO	2.1
12	AL	12	ARG	2.1
16	AP	25	ARG	2.1
31	BG	32	PRO	2.1
36	DP	63	PRO	2.1
11	AK	64	ALA	2.1
32	BH	162	ILE	2.1
20	CT	16	HIS	2.1
2	CB	84	GLU	2.1
24	AX	49	G	2.1
26	DA	2061	G	2.1
26	DA	2674	G	2.1
28	BD	70	TRP	2.1
39	BS	26	LEU	2.1
1	AA	1529	G	2.1
5	CE	97	GLY	2.1
9	AI	25	LYS	2.1
13	AM	87	TYR	2.1
17	AQ	37	LYS	2.1
35	DO	32	TYR	2.1
45	DY	8	LYS	2.1
45	DY	46	LYS	2.1
47	B0	8	GLY	2.1
47	D0	54	GLY	2.1
1	CA	768	A	2.1
4	CD	199	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1040	U	2.1
1	CA	1285	A	2.1
56	D9	6	SER	2.1
26	DA	2585	U	2.1
30	DF	40	GLN	2.1
1	AA	1303	C	2.1
1	CA	1118	C	2.1
1	CA	1226	C	2.1
9	CI	121	ARG	2.1
10	CJ	67	THR	2.1
14	AN	3	ARG	2.1
17	AQ	85	VAL	2.1
29	DE	93	VAL	2.1
31	BG	98	ARG	2.1
39	DS	13	ARG	2.1
39	DS	17	ARG	2.1
46	BZ	86	VAL	2.1
48	B1	49	VAL	2.1
52	D5	11	THR	2.1
5	AE	77	PRO	2.1
30	DF	10	PRO	2.1
31	BG	17	PRO	2.1
38	DR	39	PRO	2.1
3	CC	113	ALA	2.1
4	AD	149	ALA	2.1
8	CH	132	GLU	2.1
10	CJ	68	HIS	2.1
14	CN	30	ALA	2.1
28	DD	106	ILE	2.1
30	DF	28	ILE	2.1
35	DO	77	ILE	2.1
36	BP	127	ALA	2.1
10	AJ	7	LYS	2.1
34	DN	29	LYS	2.1
40	DT	50	ILE	2.1
41	BU	88	ILE	2.1
54	B7	48	LYS	2.1
5	AE	112	LEU	2.1
11	AK	46	GLY	2.1
30	DF	87	GLY	2.1
33	BI	30	LEU	2.1
46	BZ	157	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
49	B2	10	LEU	2.1
2	AB	104	ASN	2.1
4	AD	159	ARG	2.1
5	CE	64	ARG	2.1
7	AG	32	ARG	2.1
43	DW	8	ARG	2.1
1	CA	981	U	2.1
1	AA	108	G	2.1
1	AA	1511	G	2.1
1	CA	926	G	2.1
6	AF	37	VAL	2.1
1	CA	1055	A	2.1
1	CA	1251	A	2.1
1	CA	1287	A	2.1
1	CA	1310	G	2.1
1	CA	1316	G	2.1
1	CA	1356	G	2.1
26	BA	2528	G	2.1
28	BD	185	VAL	2.1
44	DX	49	VAL	2.1
2	AB	128	GLU	2.1
5	AE	9	LYS	2.1
45	BY	94	LYS	2.1
1	AA	1054	C	2.1
1	AA	1118	C	2.1
3	AC	187	ALA	2.1
26	DA	914	C	2.1
8	AH	47	GLY	2.1
12	CL	97	ARG	2.1
21	CU	9	ARG	2.1
30	DF	123	LEU	2.1
37	DQ	10	ARG	2.1
43	DW	23	LEU	2.1
46	DZ	67	LEU	2.1
12	CL	62	SER	2.1
19	AS	38	SER	2.1
33	DI	91	SER	2.1
52	B5	12	SER	2.1
4	AD	106	TYR	2.1
29	DE	73	GLU	2.1
3	CC	72	LYS	2.1
3	CC	165	THR	2.1

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Mol	Chain	Res	Type	RSRZ
4	CD	136	PRO	2.1
7	AG	23	VAL	2.1
32	BH	43	VAL	2.1
37	DQ	35	VAL	2.1
37	DQ	43	THR	2.1
39	DS	19	LYS	2.1
45	DY	81	LYS	2.1
14	AN	14	PRO	2.1
47	B0	79	VAL	2.1
55	B8	22	VAL	2.1
56	D9	7	VAL	2.1
3	AC	10	PHE	2.1
3	CC	186	PHE	2.1
34	DN	130	HIS	2.1
1	AA	965	A	2.1
1	CA	1288	A	2.1
3	AC	117	ALA	2.1
3	CC	100	ALA	2.1
13	AM	57	ARG	2.1
16	CP	77	ALA	2.1
27	BB	48	A	2.1
30	DF	128	ALA	2.1
39	DS	70	GLY	2.1
43	DW	84	ARG	2.1
48	B1	84	GLY	2.1
48	D1	63	ALA	2.1
49	D2	59	ARG	2.1
54	D7	28	ARG	2.1
1	AA	345	C	2.1
1	AA	944	G	2.1
13	AM	40	ASN	2.1
15	AO	67	LEU	2.1
25	CY	71	G	2.1
26	BA	555	G	2.1
26	BA	1184	G	2.1
26	BA	2083	G	2.1
26	BA	2188	G	2.1
26	BA	2887	G	2.1
26	DA	446	G	2.1
26	DA	867	C	2.1
26	DA	961	C	2.1
31	BG	90	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
38	BR	29	LEU	2.1
38	BR	52	ILE	2.1
31	DG	164	GLU	2.1
38	DR	60	LEU	2.1
47	D0	68	GLU	2.1
26	BA	274	U	2.1
26	BA	2194	U	2.1
4	AD	9	CYS	2.1
12	CL	37	CYS	2.1
17	CQ	85	VAL	2.1
31	DG	71	THR	2.1
34	DN	93	THR	2.1
38	DR	72	ASP	2.1
19	AS	14	HIS	2.1
46	DZ	95	PRO	2.1
2	AB	96	ARG	2.1
3	CC	119	ARG	2.1
8	CH	12	ARG	2.1
28	DD	238	GLY	2.1
47	D0	22	GLY	2.1
3	CC	107	GLN	2.1
36	BP	12	ALA	2.1
36	DP	38	GLN	2.1
54	D7	18	PHE	2.1
6	CF	76	ALA	2.1
33	BI	55	ALA	2.1
33	DI	39	ALA	2.1
39	DS	105	ALA	2.1
48	D1	77	ALA	2.1
55	B8	10	ALA	2.1
7	CG	68	ASN	2.1
4	CD	194	LEU	2.1
17	CQ	66	SER	2.1
20	CT	84	LEU	2.1
36	BP	45	LEU	2.1
41	DU	15	LYS	2.1
37	BQ	68	ILE	2.1
48	B1	85	LEU	2.1
1	CA	1067	A	2.1
24	AX	59	A	2.1
1	AA	224	C	2.0
1	CA	48	C	2.0

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Mol	Chain	Res	Type	RSRZ
1	CA	1326	C	2.0
3	CC	17	ASP	2.1
24	CX	16	C	2.0
25	AY	11	C	2.0
26	DA	902	C	2.0
45	DY	107	ASP	2.1
1	AA	306	G	2.0
1	AA	690	G	2.0
1	CA	306	G	2.0
1	CA	568	G	2.0
3	AC	30	ARG	2.0
4	CD	47	ARG	2.0
10	CJ	66	ARG	2.0
12	CL	102	ARG	2.0
15	AO	68	ARG	2.0
2	CB	65	GLY	2.0
3	AC	177	THR	2.0
18	AR	25	THR	2.0
19	CS	83	HIS	2.0
25	CY	63	G	2.0
26	DA	508	G	2.0
26	DA	952	G	2.0
26	DA	2155	G	2.0
35	DO	93	PRO	2.0
36	DP	16	ARG	2.0
48	D1	61	ARG	2.0
54	D7	10	ARG	2.0
29	DE	34	VAL	2.0
3	AC	161	GLU	2.0
17	AQ	42	TYR	2.0
19	CS	27	GLU	2.0
33	DI	10	GLU	2.0
55	D8	64	TYR	2.0
4	AD	55	ALA	2.0
10	AJ	18	ALA	2.0
12	AL	115	LYS	2.0
29	DE	84	PHE	2.0
30	DF	122	LYS	2.0
39	DS	12	PHE	2.0
48	B1	24	ALA	2.0
31	DG	108	ASN	2.0
45	BY	92	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
30	BF	13	SER	2.0
30	BF	124	LEU	2.0
39	BS	110	LEU	2.0
2	AB	193	ASP	2.0
4	AD	141	ARG	2.0
8	AH	91	ARG	2.0
8	CH	91	ARG	2.0
17	AQ	92	ARG	2.0
38	BR	69	ASP	2.0
55	D8	30	ARG	2.0
1	AA	835	U	2.0
2	CB	140	HIS	2.0
1	AA	1287	A	2.0
1	CA	553	A	2.0
1	CA	782	A	2.0
4	CD	42	GLN	2.0
19	CS	26	GLY	2.0
26	BA	2140	U	2.0
26	DA	449	A	2.0
30	DF	131	GLY	2.0
32	DH	159	GLU	2.0
33	BI	17	GLN	2.0
42	BV	80	GLN	2.0
45	BY	66	PRO	2.0
52	B5	5	PRO	2.0
53	B6	4	GLU	2.0
8	AH	64	LYS	2.0
21	CU	12	LYS	2.0
37	DQ	129	THR	2.0
46	DZ	42	VAL	2.0
1	CA	883	C	2.0
1	CA	1006	C	2.0
23	CW	67	C	2.0
26	BA	2510	C	2.0
34	DN	18	ALA	2.0
37	DQ	95	ALA	2.0
29	BE	96	PHE	2.0
40	DT	76	PHE	2.0
1	CA	1216	G	2.0
11	AK	107	SER	2.0
26	BA	11	G	2.0
26	BA	2555	G	2.0

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Mol	Chain	Res	Type	RSRZ
26	BA	2588	G	2.0
26	DA	1533	G	2.0
27	DB	63	G	2.0
35	BO	28	SER	2.0
36	BP	60	MET	2.0
11	CK	81	ASP	2.0
16	AP	23	ASP	2.0
37	DQ	60	ARG	2.0
34	BN	34	LEU	2.0
30	DF	56	GLU	2.0
42	DV	96	ILE	2.0
19	CS	56	GLN	2.0
28	DD	4	LYS	2.0
33	BI	84	GLY	2.0
1	AA	204	U	2.0
1	CA	1056	U	2.0
48	D1	12	PRO	2.0
3	CC	64	VAL	2.0
4	AD	203	VAL	2.0
9	CI	86	VAL	2.0
31	BG	64	THR	2.0
35	DO	40	VAL	2.0
37	DQ	132	VAL	2.0
47	B0	38	VAL	2.0
50	B3	6	VAL	2.0
1	AA	1180	A	2.0
1	CA	958	A	2.0
15	CO	80	ALA	2.0
5	AE	126	ARG	2.0
11	CK	59	TYR	2.0
14	CN	3	ARG	2.0
14	CN	31	ARG	2.0
15	AO	17	ARG	2.0
19	AS	65	ASN	2.0
26	BA	2465	A	2.0
26	DA	911	A	2.0
26	DA	2629	A	2.0
55	D8	18	ALA	2.0
47	D0	26	TYR	2.0
1	AA	103	C	2.0
1	CA	620	C	2.0
1	CA	1369	C	2.0

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Mol	Chain	Res	Type	RSRZ
2	AB	189	ASP	2.0
2	AB	205	ASP	2.0
5	CE	87	SER	2.0
9	CI	60	ASP	2.0
26	DA	2466	C	2.0
33	BI	1	MET	2.0
33	DI	1	MET	2.0
46	DZ	123	ASP	2.0
17	AQ	69	LYS	2.0
36	BP	100	LEU	2.0
38	DR	29	LEU	2.0
41	BU	83	LEU	2.0
44	BX	70	LEU	2.0
47	B0	37	LEU	2.0
55	D8	44	LYS	2.0
4	AD	90	GLY	2.0
7	CG	27	ILE	2.0
17	AQ	65	ILE	2.0
45	BY	75	ILE	2.0
47	D0	8	GLY	2.0
1	CA	630	G	2.0
10	AJ	77	PRO	2.0
12	CL	125	PRO	2.0
1	CA	1235	U	2.0
1	CA	1523	G	2.0
24	CX	46	G	2.0
26	BA	333	G	2.0
26	BA	1154	U	2.0
26	BA	1302	G	2.0
26	DA	919	G	2.0
34	DN	44	PRO	2.0
4	AD	89	THR	2.0
47	D0	10	THR	2.0
52	B5	11	THR	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(\AA^2)	Q<0.9
23	5MU	CW	54	21/22	0.21	-	74,88,99,101	0
24	5MC	AX	32	21/22	0.18	-	43,53,62,78	0
23	MIA	AW	37	29/30	0.20	-	59,71,81,86	0
25	PSU	CY	55	20/21	0.34	-	94,102,110,124	0
23	4SU	AW	8	20/21	0.22	-	86,95,112,128	0
23	PSU	CW	39	20/21	0.36	-	78,84,97,98	0
25	MIA	CY	37	22/30	0.24	-	72,95,113,138	0
24	5MC	CX	32	21/22	0.17	-	63,76,86,88	0
23	PSU	AW	32	20/21	0.23	-	77,83,92,98	0
23	PSU	CW	32	20/21	0.51	-	81,87,94,103	0
25	7MG	CY	46	24/25	0.38	-	86,105,111,137	0
23	31M	CW	76	41/42	0.65	-	50,63,73,88	20
25	4SU	AY	8	20/21	0.24	-	82,96,103,118	0
23	PSU	AW	55	20/21	0.29	-	77,90,98,104	0
24	PSU	AX	55	20/21	0.18	-	50,63,73,83	0
25	PSU	AY	55	20/21	0.24	-	93,101,108,122	0
25	PSU	CY	32	20/21	0.14	-	80,92,101,107	0
23	PSU	CW	55	20/21	0.21	-	79,89,99,104	0
24	5MU	CX	54	21/22	0.16	-	70,81,89,99	0
24	4SU	CX	8	20/21	0.38	-	77,87,95,97	0
25	PSU	AY	32	20/21	0.29	-	78,93,100,106	0
24	4SU	AX	8	20/21	0.20	-	54,66,82,89	0
23	MIA	CW	37	22/30	0.19	-	75,85,92,100	0
23	5MU	AW	54	21/22	0.21	-	65,82,91,93	0
23	7MG	AW	46	24/25	0.24	-	84,99,117,133	0
24	PSU	CX	55	20/21	0.12	-	70,80,91,96	0
23	7MG	CW	46	24/25	0.31	-	79,96,109,133	0
25	PSU	CY	39	20/21	0.26	-	79,90,116,130	0
23	PSU	AW	39	20/21	0.15	-	73,82,95,97	0
25	MIA	AY	37	22/30	0.35	-	77,90,111,119	0
23	31M	AW	76	41/42	0.43	-	37,54,66,83	9
25	5MU	AY	54	21/22	0.17	-	80,96,105,131	0
25	4SU	CY	8	20/21	0.27	-	93,103,113,128	0
25	5MU	CY	54	21/22	0.40	-	78,94,109,140	0
25	PSU	AY	39	20/21	0.49	-	78,90,117,123	0
25	7MG	AY	46	24/25	0.50	-	75,101,111,123	0
24	5MU	AX	54	21/22	0.17	-	49,68,79,84	0
23	4SU	CW	8	20/21	0.34	-	81,98,120,127	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
57	MG	DA	3266	1/1	0.06	-	57,57,57,57	0
57	MG	AA	3124	1/1	0.08	-	47,47,47,47	0
57	MG	B3	3002	1/1	0.09	-	66,66,66,66	0
57	MG	CA	3161	1/1	0.09	-	56,56,56,56	0
57	MG	DA	3335	1/1	0.12	-	47,47,47,47	0
57	MG	DA	3543	1/1	0.09	-	53,53,53,53	0
57	MG	BA	3674	1/1	0.12	-	63,63,63,63	0
57	MG	BA	3095	1/1	0.19	-	51,51,51,51	0
57	MG	BA	3480	1/1	0.19	-	35,35,35,35	0
57	MG	DA	3425	1/1	0.11	-	61,61,61,61	0
57	MG	CA	3061	1/1	0.19	-	66,66,66,66	0
57	MG	DA	3393	1/1	0.06	-	50,50,50,50	0
57	MG	BA	3569	1/1	0.18	-	49,49,49,49	0
57	MG	DA	3034	1/1	0.10	-	38,38,38,38	0
57	MG	BA	3340	1/1	0.10	-	39,39,39,39	0
57	MG	BA	3594	1/1	0.14	-	40,40,40,40	0
57	MG	CA	3130	1/1	0.09	-	57,57,57,57	0
57	MG	CA	3045	1/1	0.19	-	54,54,54,54	0
57	MG	BA	3316	1/1	0.12	-	66,66,66,66	0
57	MG	DA	3314	1/1	0.14	-	43,43,43,43	0
57	MG	AA	3198	1/1	0.09	-	61,61,61,61	0
57	MG	BA	3491	1/1	0.12	-	45,45,45,45	0
57	MG	AA	3100	1/1	0.10	-	65,65,65,65	0
57	MG	BA	3496	1/1	0.19	-	41,41,41,41	0
57	MG	BA	3671	1/1	0.20	-	63,63,63,63	0
57	MG	BA	3604	1/1	0.12	-	36,36,36,36	0
57	MG	AA	3096	1/1	0.20	-	63,63,63,63	0
57	MG	DA	3434	1/1	0.12	-	39,39,39,39	0
57	MG	BA	3656	1/1	0.23	-	53,53,53,53	0
57	MG	BA	3038	1/1	0.18	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3144	1/1	0.22	-	71,71,71,71	0
57	MG	BA	3250	1/1	0.61	-	42,42,42,42	0
57	MG	AA	3065	1/1	0.19	-	63,63,63,63	0
57	MG	DA	3609	1/1	0.10	-	46,46,46,46	0
57	MG	DA	3070	1/1	0.14	-	58,58,58,58	0
57	MG	BA	3217	1/1	0.12	-	37,37,37,37	0
57	MG	BA	3328	1/1	0.22	-	40,40,40,40	0
57	MG	DA	3313	1/1	0.18	-	47,47,47,47	0
57	MG	CA	3037	1/1	0.10	-	73,73,73,73	0
57	MG	DA	3327	1/1	0.20	-	57,57,57,57	0
57	MG	DA	3511	1/1	0.14	-	49,49,49,49	0
57	MG	BA	3366	1/1	0.11	-	57,57,57,57	0
57	MG	CW	3001	1/1	0.19	-	67,67,67,67	0
57	MG	DA	3595	1/1	0.17	-	59,59,59,59	0
57	MG	CA	3030	1/1	0.08	-	57,57,57,57	0
57	MG	DA	3247	1/1	0.15	-	45,45,45,45	0
57	MG	DA	3550	1/1	0.13	-	57,57,57,57	0
57	MG	DA	3317	1/1	0.12	-	44,44,44,44	0
57	MG	AA	3043	1/1	0.22	-	51,51,51,51	0
57	MG	DA	3494	1/1	0.20	-	47,47,47,47	0
57	MG	AA	3195	1/1	0.14	-	57,57,57,57	0
57	MG	BA	3522	1/1	0.10	-	52,52,52,52	0
57	MG	DA	3192	1/1	0.15	-	60,60,60,60	0
57	MG	BA	3764	1/1	0.16	-	51,51,51,51	0
57	MG	DA	3563	1/1	0.26	-	74,74,74,74	0
57	MG	DA	3265	1/1	0.12	-	30,30,30,30	0
57	MG	DA	3618	1/1	0.10	-	53,53,53,53	0
57	MG	DA	3517	1/1	0.12	-	51,51,51,51	0
57	MG	BB	209	1/1	0.21	-	65,65,65,65	0
57	MG	BA	3104	1/1	0.27	-	42,42,42,42	0
57	MG	BA	3450	1/1	0.15	-	48,48,48,48	0
57	MG	DA	3048	1/1	0.07	-	53,53,53,53	0
57	MG	DA	3506	1/1	0.08	-	42,42,42,42	0
57	MG	AY	3001	1/1	0.30	-	65,65,65,65	0
57	MG	CA	3141	1/1	0.05	-	92,92,92,92	0
57	MG	DA	3339	1/1	0.16	-	61,61,61,61	0
57	MG	DA	3603	1/1	0.07	-	41,41,41,41	0
57	MG	DA	3280	1/1	0.19	-	33,33,33,33	0
57	MG	DW	3001	1/1	0.58	-	54,54,54,54	0
57	MG	BA	3738	1/1	0.12	-	43,43,43,43	0
57	MG	BA	3549	1/1	0.14	-	39,39,39,39	0
57	MG	BA	3025	1/1	0.11	-	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3133	1/1	0.16	-	59,59,59,59	0
57	MG	B7	104	1/1	0.35	-	48,48,48,48	0
57	MG	CA	3075	1/1	0.14	-	59,59,59,59	0
57	MG	BA	3040	1/1	0.39	-	35,35,35,35	0
57	MG	CA	3016	1/1	0.12	-	57,57,57,57	0
57	MG	BA	3358	1/1	0.23	-	49,49,49,49	0
57	MG	BA	3468	1/1	0.07	-	62,62,62,62	0
57	MG	AA	3076	1/1	0.26	-	77,77,77,77	0
57	MG	BA	3051	1/1	0.16	-	43,43,43,43	0
57	MG	CX	3002	1/1	0.17	-	70,70,70,70	0
57	MG	DA	3193	1/1	0.06	-	57,57,57,57	0
57	MG	BA	3162	1/1	0.11	-	38,38,38,38	0
59	ZN	DY	501	1/1	0.14	-	96,96,96,96	0
57	MG	DA	3347	1/1	0.23	-	27,27,27,27	0
57	MG	DA	3363	1/1	0.16	-	29,29,29,29	0
57	MG	DA	3612	1/1	0.09	-	62,62,62,62	0
57	MG	BA	3767	1/1	0.11	-	73,73,73,73	0
57	MG	CA	3100	1/1	0.11	-	52,52,52,52	0
57	MG	DA	3644	1/1	0.05	-	55,55,55,55	0
57	MG	BA	3690	1/1	0.15	-	58,58,58,58	0
57	MG	DA	3269	1/1	0.05	-	49,49,49,49	0
57	MG	AA	3121	1/1	0.11	-	70,70,70,70	0
57	MG	BA	3658	1/1	0.29	-	61,61,61,61	0
57	MG	DA	3646	1/1	0.12	-	59,59,59,59	0
57	MG	BA	3627	1/1	0.16	-	56,56,56,56	0
57	MG	AA	3196	1/1	0.39	-	74,74,74,74	0
57	MG	DA	3372	1/1	0.04	-	56,56,56,56	0
57	MG	BA	3686	1/1	0.13	-	60,60,60,60	0
57	MG	DA	3401	1/1	0.07	-	38,38,38,38	0
57	MG	DB	3007	1/1	0.20	-	58,58,58,58	0
57	MG	DA	3001	1/1	0.21	-	60,60,60,60	0
57	MG	BA	3538	1/1	0.14	-	40,40,40,40	0
57	MG	BA	3003	1/1	0.19	-	60,60,60,60	0
57	MG	BA	3282	1/1	0.15	-	39,39,39,39	0
57	MG	DA	3325	1/1	0.12	-	35,35,35,35	0
57	MG	BA	3528	1/1	0.20	-	56,56,56,56	0
57	MG	DA	3007	1/1	0.11	-	50,50,50,50	0
57	MG	CA	3070	1/1	0.17	-	63,63,63,63	0
57	MG	DA	3306	1/1	0.13	-	55,55,55,55	0
59	ZN	AN	501	1/1	0.19	-	69,69,69,69	0
57	MG	BA	3176	1/1	0.11	-	45,45,45,45	0
57	MG	CV	101	1/1	0.09	-	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3555	1/1	0.23	-	53,53,53,53	0
57	MG	DA	3282	1/1	0.07	-	52,52,52,52	0
57	MG	BA	3796	1/1	0.19	-	45,45,45,45	0
57	MG	AA	3068	1/1	0.15	-	69,69,69,69	0
57	MG	BU	202	1/1	0.48	-	40,40,40,40	0
57	MG	BA	3343	1/1	0.14	-	53,53,53,53	0
57	MG	BA	3625	1/1	0.14	-	39,39,39,39	0
57	MG	BA	3375	1/1	0.25	-	68,68,68,68	0
57	MG	AX	3012	1/1	0.16	-	59,59,59,59	0
57	MG	CA	3038	1/1	0.13	-	58,58,58,58	0
57	MG	DA	3349	1/1	0.04	-	52,52,52,52	0
57	MG	AA	3004	1/1	0.12	-	67,67,67,67	0
57	MG	BA	3407	1/1	0.15	-	47,47,47,47	0
57	MG	BA	3732	1/1	0.37	-	51,51,51,51	0
57	MG	BA	3759	1/1	0.18	-	33,33,33,33	0
57	MG	DA	3156	1/1	0.07	-	51,51,51,51	0
57	MG	DA	3395	1/1	0.10	-	47,47,47,47	0
57	MG	DA	3263	1/1	0.16	-	41,41,41,41	0
57	MG	BA	3427	1/1	0.22	-	61,61,61,61	0
57	MG	AA	3024	1/1	0.09	-	54,54,54,54	0
57	MG	BV	203	1/1	0.19	-	38,38,38,38	0
57	MG	BA	3184	1/1	0.24	-	43,43,43,43	0
57	MG	DA	3049	1/1	0.11	-	52,52,52,52	0
57	MG	DA	3223	1/1	0.10	-	50,50,50,50	0
57	MG	BA	3349	1/1	0.10	-	56,56,56,56	0
57	MG	DA	3613	1/1	0.09	-	54,54,54,54	0
57	MG	DA	3285	1/1	0.10	-	32,32,32,32	0
57	MG	BA	3798	1/1	0.17	-	28,28,28,28	0
57	MG	DD	306	1/1	0.35	-	39,39,39,39	0
57	MG	DA	3259	1/1	0.26	-	43,43,43,43	0
57	MG	DQ	3004	1/1	0.41	-	54,54,54,54	0
57	MG	BA	3506	1/1	0.21	-	58,58,58,58	0
57	MG	BA	3295	1/1	0.19	-	38,38,38,38	0
57	MG	BA	3545	1/1	0.14	-	65,65,65,65	0
57	MG	BA	3317	1/1	0.20	-	53,53,53,53	0
57	MG	BA	3310	1/1	0.15	-	58,58,58,58	0
57	MG	BA	3012	1/1	0.19	-	39,39,39,39	0
57	MG	BA	3560	1/1	0.11	-	56,56,56,56	0
57	MG	CA	3085	1/1	0.10	-	54,54,54,54	0
57	MG	CA	3002	1/1	0.12	-	63,63,63,63	0
57	MG	BA	3464	1/1	0.13	-	45,45,45,45	0
57	MG	DA	3218	1/1	0.21	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3440	1/1	0.12	-	61,61,61,61	0
57	MG	DA	3354	1/1	0.16	-	44,44,44,44	0
57	MG	DA	3043	1/1	0.11	-	38,38,38,38	0
57	MG	BA	3661	1/1	0.10	-	44,44,44,44	0
57	MG	BA	3356	1/1	0.15	-	37,37,37,37	0
57	MG	DA	3406	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3257	1/1	0.19	-	50,50,50,50	0
57	MG	BA	3195	1/1	0.10	-	46,46,46,46	0
57	MG	DA	3518	1/1	0.21	-	54,54,54,54	0
57	MG	BA	3441	1/1	0.13	-	35,35,35,35	0
57	MG	BA	3599	1/1	0.19	-	43,43,43,43	0
57	MG	AA	3188	1/1	0.08	-	69,69,69,69	0
57	MG	BA	3654	1/1	0.14	-	57,57,57,57	0
57	MG	DA	3159	1/1	0.18	-	58,58,58,58	0
57	MG	CA	3029	1/1	0.14	-	63,63,63,63	0
57	MG	CA	3079	1/1	0.15	-	66,66,66,66	0
57	MG	BA	3109	1/1	0.15	-	51,51,51,51	0
57	MG	BA	3411	1/1	0.18	-	33,33,33,33	0
57	MG	DA	3439	1/1	0.15	-	42,42,42,42	0
57	MG	BA	3234	1/1	0.14	-	38,38,38,38	0
57	MG	DA	3482	1/1	0.06	-	50,50,50,50	0
57	MG	BA	3149	1/1	0.13	-	40,40,40,40	0
57	MG	BA	3208	1/1	0.13	-	44,44,44,44	0
57	MG	AA	3095	1/1	0.22	-	60,60,60,60	0
57	MG	BA	3187	1/1	0.20	-	29,29,29,29	0
57	MG	DA	3624	1/1	0.15	-	56,56,56,56	0
57	MG	DA	3539	1/1	0.10	-	53,53,53,53	0
57	MG	BA	3478	1/1	0.13	-	58,58,58,58	0
57	MG	DA	3611	1/1	0.13	-	48,48,48,48	0
57	MG	CA	3064	1/1	0.12	-	60,60,60,60	0
57	MG	CA	3101	1/1	0.06	-	49,49,49,49	0
57	MG	DA	3510	1/1	0.20	-	49,49,49,49	0
57	MG	DA	3362	1/1	0.17	-	44,44,44,44	0
57	MG	CA	3116	1/1	0.21	-	68,68,68,68	0
57	MG	BA	3171	1/1	0.36	-	31,31,31,31	0
57	MG	DA	3342	1/1	0.12	-	42,42,42,42	0
57	MG	BA	3459	1/1	0.21	-	48,48,48,48	0
57	MG	BU	208	1/1	0.19	-	40,40,40,40	0
57	MG	BA	3544	1/1	0.16	-	44,44,44,44	0
57	MG	BA	3525	1/1	0.16	-	34,34,34,34	0
57	MG	DA	3301	1/1	0.18	-	52,52,52,52	0
57	MG	DA	3413	1/1	0.24	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DD	309	1/1	0.34	-	59,59,59,59	0
57	MG	AA	3080	1/1	0.18	-	58,58,58,58	0
57	MG	DA	3385	1/1	0.10	-	52,52,52,52	0
57	MG	BA	3303	1/1	0.21	-	36,36,36,36	0
57	MG	AA	3101	1/1	0.12	-	43,43,43,43	0
57	MG	DA	3544	1/1	0.17	-	65,65,65,65	0
57	MG	BA	3786	1/1	0.12	-	35,35,35,35	0
57	MG	AA	3177	1/1	0.08	-	66,66,66,66	0
57	MG	DA	3540	1/1	0.15	-	42,42,42,42	0
57	MG	CA	3049	1/1	0.26	-	63,63,63,63	0
57	MG	DA	3308	1/1	0.19	-	61,61,61,61	0
57	MG	BA	3315	1/1	0.21	-	31,31,31,31	0
57	MG	DA	3226	1/1	0.35	-	45,45,45,45	0
57	MG	DA	3429	1/1	0.17	-	41,41,41,41	0
57	MG	DA	3029	1/1	0.51	-	49,49,49,49	0
57	MG	BA	3446	1/1	0.17	-	40,40,40,40	0
57	MG	DA	3645	1/1	0.11	-	45,45,45,45	0
57	MG	BA	3369	1/1	0.10	-	44,44,44,44	0
57	MG	DA	3186	1/1	0.16	-	54,54,54,54	0
57	MG	DA	3112	1/1	0.10	-	59,59,59,59	0
57	MG	CA	3011	1/1	0.23	-	61,61,61,61	0
57	MG	DA	3577	1/1	0.10	-	58,58,58,58	0
57	MG	DA	3153	1/1	0.16	-	47,47,47,47	0
57	MG	AA	3071	1/1	0.28	-	53,53,53,53	0
57	MG	BA	3159	1/1	0.33	-	50,50,50,50	0
57	MG	BA	3117	1/1	0.19	-	59,59,59,59	0
57	MG	DA	3649	1/1	0.12	-	58,58,58,58	0
57	MG	BW	201	1/1	0.24	-	44,44,44,44	0
57	MG	BA	3157	1/1	0.15	-	45,45,45,45	0
57	MG	BA	3547	1/1	0.23	-	39,39,39,39	0
57	MG	DA	3260	1/1	0.09	-	55,55,55,55	0
57	MG	BA	3150	1/1	0.21	-	55,55,55,55	0
57	MG	CA	3149	1/1	0.13	-	52,52,52,52	0
57	MG	BA	3059	1/1	0.15	-	26,26,26,26	0
57	MG	DA	3598	1/1	0.09	-	61,61,61,61	0
57	MG	BA	3219	1/1	0.13	-	36,36,36,36	0
57	MG	AA	3189	1/1	0.11	-	65,65,65,65	0
57	MG	AA	3119	1/1	0.09	-	51,51,51,51	0
57	MG	BO	202	1/1	0.10	-	65,65,65,65	0
57	MG	DF	3001	1/1	0.28	-	44,44,44,44	0
57	MG	AK	3001	1/1	0.13	-	44,44,44,44	0
57	MG	BA	3384	1/1	0.17	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3326	1/1	0.15	-	43,43,43,43	0
57	MG	BA	3412	1/1	0.21	-	40,40,40,40	0
57	MG	DA	3408	1/1	0.07	-	58,58,58,58	0
57	MG	DA	3012	1/1	0.09	-	33,33,33,33	0
57	MG	BA	3011	1/1	0.15	-	35,35,35,35	0
57	MG	CA	3159	1/1	0.21	-	70,70,70,70	0
57	MG	AA	3169	1/1	0.12	-	62,62,62,62	0
57	MG	DA	3442	1/1	0.13	-	39,39,39,39	0
57	MG	BA	3377	1/1	0.17	-	44,44,44,44	0
57	MG	AA	3058	1/1	0.22	-	59,59,59,59	0
57	MG	BA	3337	1/1	0.12	-	58,58,58,58	0
57	MG	CA	3151	1/1	0.26	-	59,59,59,59	0
57	MG	DA	3397	1/1	0.08	-	57,57,57,57	0
57	MG	BA	3136	1/1	0.11	-	30,30,30,30	0
57	MG	BA	3681	1/1	0.08	-	66,66,66,66	0
57	MG	DA	3249	1/1	0.11	-	45,45,45,45	0
57	MG	DA	3351	1/1	0.16	-	48,48,48,48	0
57	MG	BA	3057	1/1	0.17	-	34,34,34,34	0
57	MG	BA	3622	1/1	0.15	-	48,48,48,48	0
57	MG	BA	3233	1/1	0.11	-	56,56,56,56	0
57	MG	DA	3065	1/1	0.13	-	43,43,43,43	0
57	MG	BA	3616	1/1	0.19	-	65,65,65,65	0
57	MG	BN	3002	1/1	0.12	-	39,39,39,39	0
57	MG	BA	3200	1/1	0.17	-	67,67,67,67	0
57	MG	DA	3590	1/1	0.08	-	51,51,51,51	0
57	MG	BA	3359	1/1	0.28	-	62,62,62,62	0
57	MG	DA	3166	1/1	0.11	-	55,55,55,55	0
57	MG	DA	3224	1/1	0.17	-	49,49,49,49	0
57	MG	AA	3087	1/1	0.08	-	41,41,41,41	0
57	MG	BA	3719	1/1	0.13	-	53,53,53,53	0
57	MG	BA	3791	1/1	0.16	-	28,28,28,28	0
57	MG	BA	3017	1/1	0.23	-	48,48,48,48	0
57	MG	DA	3144	1/1	0.10	-	38,38,38,38	0
57	MG	CA	3051	1/1	0.25	-	81,81,81,81	0
57	MG	BA	3186	1/1	0.53	-	45,45,45,45	0
57	MG	DA	3028	1/1	0.27	-	52,52,52,52	0
57	MG	DA	3654	1/1	0.11	-	56,56,56,56	0
57	MG	DA	3107	1/1	0.09	-	51,51,51,51	0
57	MG	BG	203	1/1	0.14	-	42,42,42,42	0
57	MG	DA	3126	1/1	0.08	-	55,55,55,55	0
57	MG	BA	3403	1/1	0.13	-	54,54,54,54	0
57	MG	DA	3564	1/1	0.13	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3433	1/1	0.20	-	32,32,32,32	0
57	MG	DA	3593	1/1	0.14	-	40,40,40,40	0
57	MG	BA	3154	1/1	0.19	-	47,47,47,47	0
57	MG	BA	3696	1/1	0.16	-	33,33,33,33	0
57	MG	BX	3001	1/1	0.89	-	48,48,48,48	0
57	MG	AX	3014	1/1	0.20	-	72,72,72,72	0
57	MG	BA	3286	1/1	0.16	-	34,34,34,34	0
59	ZN	B6	103	1/1	0.20	-	49,49,49,49	0
57	MG	BA	3122	1/1	0.10	-	41,41,41,41	0
57	MG	BA	3624	1/1	0.07	-	68,68,68,68	0
57	MG	AA	3181	1/1	0.17	-	51,51,51,51	0
57	MG	BA	3720	1/1	0.14	-	65,65,65,65	0
57	MG	BA	3114	1/1	0.14	-	53,53,53,53	0
57	MG	BA	3474	1/1	0.18	-	55,55,55,55	0
57	MG	CT	3001	1/1	0.09	-	56,56,56,56	0
57	MG	DA	3233	1/1	0.28	-	53,53,53,53	0
57	MG	BW	204	1/1	0.34	-	42,42,42,42	0
57	MG	BA	3245	1/1	0.25	-	34,34,34,34	0
57	MG	DA	3222	1/1	0.12	-	57,57,57,57	0
57	MG	BA	3774	1/1	0.31	-	46,46,46,46	0
57	MG	CA	3156	1/1	0.06	-	73,73,73,73	0
57	MG	BA	3629	1/1	0.18	-	43,43,43,43	0
57	MG	DA	3452	1/1	0.13	-	51,51,51,51	0
57	MG	BA	3470	1/1	0.13	-	62,62,62,62	0
57	MG	AA	3194	1/1	0.12	-	56,56,56,56	0
57	MG	DA	3082	1/1	0.12	-	47,47,47,47	0
57	MG	DA	3322	1/1	0.18	-	51,51,51,51	0
57	MG	AA	3118	1/1	0.18	-	47,47,47,47	0
57	MG	BA	3527	1/1	0.15	-	54,54,54,54	0
57	MG	BA	3074	1/1	0.17	-	46,46,46,46	0
57	MG	BA	3248	1/1	0.18	-	42,42,42,42	0
57	MG	BA	3490	1/1	0.08	-	54,54,54,54	0
57	MG	DA	3450	1/1	0.10	-	40,40,40,40	0
57	MG	BF	305	1/1	0.11	-	49,49,49,49	0
57	MG	CA	3008	1/1	0.23	-	51,51,51,51	0
57	MG	DA	3675	1/1	0.10	-	52,52,52,52	0
57	MG	BA	3334	1/1	0.11	-	37,37,37,37	0
57	MG	AA	3182	1/1	0.09	-	49,49,49,49	0
57	MG	BA	3784	1/1	0.16	-	33,33,33,33	0
58	SF4	CD	302	8/8	0.18	-	60,68,83,86	0
57	MG	BA	3745	1/1	0.24	-	75,75,75,75	0
57	MG	DA	3036	1/1	0.13	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3731	1/1	0.27	-	37,37,37,37	0
57	MG	AA	3157	1/1	0.15	-	45,45,45,45	0
57	MG	DA	3146	1/1	0.12	-	55,55,55,55	0
57	MG	AA	3163	1/1	0.17	-	56,56,56,56	0
57	MG	BA	3189	1/1	0.09	-	39,39,39,39	0
57	MG	AA	3147	1/1	0.13	-	70,70,70,70	0
57	MG	BA	3275	1/1	0.22	-	58,58,58,58	0
57	MG	BA	3501	1/1	0.17	-	71,71,71,71	0
57	MG	BA	3212	1/1	0.24	-	54,54,54,54	0
57	MG	AA	3180	1/1	0.14	-	73,73,73,73	0
57	MG	DA	3113	1/1	0.11	-	60,60,60,60	0
57	MG	DA	3087	1/1	0.10	-	58,58,58,58	0
57	MG	BA	3015	1/1	0.15	-	32,32,32,32	0
57	MG	BA	3466	1/1	0.14	-	49,49,49,49	0
57	MG	BA	3254	1/1	0.18	-	25,25,25,25	0
57	MG	BB	211	1/1	0.09	-	51,51,51,51	0
57	MG	CA	3137	1/1	0.12	-	56,56,56,56	0
57	MG	BA	3269	1/1	0.24	-	53,53,53,53	0
57	MG	DA	3358	1/1	0.13	-	45,45,45,45	0
57	MG	DB	3012	1/1	0.23	-	61,61,61,61	0
57	MG	DA	3318	1/1	0.07	-	40,40,40,40	0
57	MG	DA	3639	1/1	0.75	-	59,59,59,59	0
57	MG	AA	3023	1/1	0.14	-	74,74,74,74	0
57	MG	AA	3150	1/1	0.19	-	57,57,57,57	0
57	MG	DA	3435	1/1	0.15	-	50,50,50,50	0
57	MG	CA	3107	1/1	0.30	-	80,80,80,80	0
57	MG	BA	3734	1/1	0.12	-	52,52,52,52	0
57	MG	DA	3207	1/1	0.47	-	63,63,63,63	0
57	MG	DA	3531	1/1	0.31	-	61,61,61,61	0
57	MG	CA	3003	1/1	0.14	-	57,57,57,57	0
57	MG	DA	3514	1/1	0.12	-	42,42,42,42	0
57	MG	AA	3156	1/1	0.14	-	63,63,63,63	0
57	MG	AA	3176	1/1	0.11	-	67,67,67,67	0
57	MG	CA	3158	1/1	0.08	-	67,67,67,67	0
57	MG	BA	3808	1/1	0.28	-	42,42,42,42	0
57	MG	AA	3159	1/1	0.11	-	66,66,66,66	0
57	MG	BA	3668	1/1	0.14	-	53,53,53,53	0
57	MG	DA	3448	1/1	0.21	-	70,70,70,70	0
57	MG	AE	202	1/1	0.14	-	80,80,80,80	0
57	MG	BA	3274	1/1	0.10	-	49,49,49,49	0
57	MG	AA	3149	1/1	0.09	-	46,46,46,46	0
57	MG	BA	3080	1/1	0.15	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3092	1/1	0.10	-	50,50,50,50	0
57	MG	BA	3472	1/1	0.12	-	20,20,20,20	0
57	MG	DA	3169	1/1	0.51	-	47,47,47,47	0
57	MG	BA	3401	1/1	0.17	-	35,35,35,35	0
57	MG	BA	3082	1/1	0.21	-	39,39,39,39	0
57	MG	BN	3006	1/1	0.30	-	49,49,49,49	0
57	MG	DA	3258	1/1	0.11	-	48,48,48,48	0
57	MG	BA	3177	1/1	0.20	-	46,46,46,46	0
57	MG	BA	3765	1/1	0.21	-	48,48,48,48	0
57	MG	BA	3434	1/1	0.13	-	55,55,55,55	0
57	MG	BA	3134	1/1	0.13	-	48,48,48,48	0
57	MG	BA	3131	1/1	0.15	-	58,58,58,58	0
57	MG	BA	3688	1/1	0.14	-	46,46,46,46	0
57	MG	CK	3001	1/1	0.16	-	45,45,45,45	0
57	MG	DA	3099	1/1	0.13	-	32,32,32,32	0
57	MG	BA	3489	1/1	0.07	-	59,59,59,59	0
57	MG	BB	204	1/1	0.15	-	41,41,41,41	0
57	MG	DA	3090	1/1	0.09	-	52,52,52,52	0
57	MG	BA	3461	1/1	0.13	-	62,62,62,62	0
57	MG	BA	3479	1/1	0.05	-	50,50,50,50	0
57	MG	CA	3065	1/1	0.15	-	49,49,49,49	0
57	MG	BA	3703	1/1	0.20	-	64,64,64,64	0
57	MG	DA	3663	1/1	0.13	-	60,60,60,60	0
57	MG	DA	3320	1/1	0.16	-	55,55,55,55	0
57	MG	DA	3264	1/1	0.14	-	40,40,40,40	0
57	MG	DA	3467	1/1	0.26	-	40,40,40,40	0
57	MG	AX	3015	1/1	0.19	-	42,42,42,42	0
57	MG	DA	3463	1/1	0.13	-	55,55,55,55	0
57	MG	BA	3555	1/1	0.15	-	29,29,29,29	0
57	MG	B7	103	1/1	0.17	-	42,42,42,42	0
57	MG	BA	3595	1/1	0.10	-	51,51,51,51	0
57	MG	AA	3044	1/1	0.26	-	60,60,60,60	0
57	MG	BA	3535	1/1	0.20	-	31,31,31,31	0
57	MG	BA	3148	1/1	0.30	-	44,44,44,44	0
57	MG	DA	3243	1/1	0.19	-	55,55,55,55	0
57	MG	BA	3706	1/1	0.13	-	53,53,53,53	0
57	MG	DA	3489	1/1	0.12	-	51,51,51,51	0
57	MG	AX	3005	1/1	0.10	-	47,47,47,47	0
57	MG	AA	3191	1/1	0.12	-	47,47,47,47	0
57	MG	DA	3643	1/1	0.11	-	61,61,61,61	0
57	MG	DA	3271	1/1	0.15	-	48,48,48,48	0
57	MG	BB	219	1/1	0.10	-	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3659	1/1	0.20	-	61,61,61,61	0
57	MG	BA	3617	1/1	0.12	-	51,51,51,51	0
57	MG	BA	3167	1/1	0.11	-	41,41,41,41	0
57	MG	BA	3495	1/1	0.10	-	37,37,37,37	0
57	MG	AA	3112	1/1	0.07	-	63,63,63,63	0
57	MG	DA	3066	1/1	0.11	-	42,42,42,42	0
57	MG	DA	3232	1/1	0.06	-	62,62,62,62	0
57	MG	BA	3694	1/1	0.08	-	51,51,51,51	0
57	MG	DA	3102	1/1	0.25	-	40,40,40,40	0
57	MG	BA	3019	1/1	0.11	-	42,42,42,42	0
57	MG	CF	3001	1/1	0.09	-	46,46,46,46	0
57	MG	DA	3570	1/1	0.11	-	31,31,31,31	0
57	MG	DA	3045	1/1	0.23	-	51,51,51,51	0
57	MG	CA	3081	1/1	0.07	-	46,46,46,46	0
57	MG	BA	3043	1/1	0.12	-	48,48,48,48	0
57	MG	BA	3418	1/1	0.13	-	30,30,30,30	0
57	MG	AA	3104	1/1	0.24	-	59,59,59,59	0
57	MG	BA	3795	1/1	0.15	-	35,35,35,35	0
57	MG	B6	102	1/1	0.15	-	68,68,68,68	0
57	MG	DA	3183	1/1	0.16	-	38,38,38,38	0
57	MG	CA	3154	1/1	0.19	-	56,56,56,56	0
57	MG	BA	3419	1/1	0.24	-	37,37,37,37	0
57	MG	BA	3518	1/1	0.18	-	44,44,44,44	0
57	MG	BA	3740	1/1	0.16	-	28,28,28,28	0
57	MG	DA	3423	1/1	0.11	-	49,49,49,49	0
57	MG	CA	3027	1/1	0.21	-	64,64,64,64	0
57	MG	DA	3629	1/1	0.18	-	62,62,62,62	0
57	MG	BA	3327	1/1	0.14	-	38,38,38,38	0
57	MG	DA	3006	1/1	0.07	-	38,38,38,38	0
57	MG	DA	3052	1/1	0.15	-	61,61,61,61	0
57	MG	DA	3486	1/1	0.08	-	47,47,47,47	0
57	MG	DA	3658	1/1	0.10	-	62,62,62,62	0
57	MG	AA	3089	1/1	0.14	-	60,60,60,60	0
57	MG	AW	3002	1/1	0.17	-	53,53,53,53	0
57	MG	BA	3642	1/1	0.11	-	48,48,48,48	0
57	MG	BA	3285	1/1	0.21	-	50,50,50,50	0
57	MG	BA	3023	1/1	0.18	-	36,36,36,36	0
57	MG	AA	3037	1/1	0.14	-	55,55,55,55	0
57	MG	DA	3161	1/1	0.14	-	38,38,38,38	0
57	MG	DA	3515	1/1	0.14	-	45,45,45,45	0
57	MG	DA	3420	1/1	0.24	-	60,60,60,60	0
57	MG	DA	3642	1/1	0.47	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3708	1/1	0.28	-	50,50,50,50	0
57	MG	CA	3050	1/1	0.08	-	61,61,61,61	0
57	MG	BU	206	1/1	0.68	-	35,35,35,35	0
57	MG	BA	3648	1/1	0.11	-	65,65,65,65	0
57	MG	BA	3742	1/1	0.22	-	65,65,65,65	0
57	MG	CJ	5001	1/1	0.18	-	73,73,73,73	0
57	MG	AA	3170	1/1	0.13	-	75,75,75,75	0
57	MG	BA	3573	1/1	0.13	-	51,51,51,51	0
57	MG	AA	3099	1/1	0.14	-	51,51,51,51	0
57	MG	BA	3437	1/1	0.16	-	36,36,36,36	0
57	MG	DA	3312	1/1	0.11	-	54,54,54,54	0
57	MG	DA	3078	1/1	0.15	-	57,57,57,57	0
57	MG	CA	3077	1/1	0.07	-	66,66,66,66	0
57	MG	BA	3272	1/1	0.45	-	48,48,48,48	0
57	MG	BA	3737	1/1	0.26	-	43,43,43,43	0
57	MG	DA	3044	1/1	0.43	-	62,62,62,62	0
57	MG	DA	3472	1/1	0.15	-	44,44,44,44	0
57	MG	BA	3374	1/1	0.23	-	40,40,40,40	0
57	MG	DA	3220	1/1	0.18	-	46,46,46,46	0
57	MG	BA	3801	1/1	0.35	-	50,50,50,50	0
57	MG	AA	3094	1/1	0.11	-	59,59,59,59	0
57	MG	BA	3319	1/1	0.16	-	46,46,46,46	0
57	MG	DA	3261	1/1	0.12	-	49,49,49,49	0
57	MG	BN	3003	1/1	0.18	-	48,48,48,48	0
57	MG	BA	3583	1/1	0.21	-	45,45,45,45	0
57	MG	DA	3067	1/1	0.19	-	57,57,57,57	0
57	MG	DA	3370	1/1	0.09	-	51,51,51,51	0
57	MG	AA	3106	1/1	0.07	-	57,57,57,57	0
57	MG	DA	3273	1/1	0.11	-	47,47,47,47	0
57	MG	BA	3050	1/1	0.14	-	38,38,38,38	0
57	MG	DA	3061	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3689	1/1	0.21	-	42,42,42,42	0
57	MG	BB	201	1/1	0.14	-	55,55,55,55	0
57	MG	BA	3633	1/1	0.09	-	49,49,49,49	0
57	MG	DW	3003	1/1	0.24	-	72,72,72,72	0
57	MG	DA	3024	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3384	1/1	0.07	-	49,49,49,49	0
57	MG	CA	3099	1/1	0.14	-	44,44,44,44	0
57	MG	AA	3035	1/1	0.20	-	56,56,56,56	0
57	MG	CA	3015	1/1	0.15	-	56,56,56,56	0
57	MG	DA	3130	1/1	0.14	-	52,52,52,52	0
57	MG	DA	3009	1/1	0.22	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3421	1/1	0.17	-	32,32,32,32	0
57	MG	BA	3408	1/1	0.19	-	36,36,36,36	0
57	MG	DA	3605	1/1	0.14	-	58,58,58,58	0
57	MG	BA	3267	1/1	0.15	-	65,65,65,65	0
57	MG	DA	3038	1/1	0.10	-	47,47,47,47	0
57	MG	BA	3030	1/1	0.16	-	46,46,46,46	0
57	MG	BA	3161	1/1	0.12	-	52,52,52,52	0
57	MG	DA	3245	1/1	0.08	-	54,54,54,54	0
57	MG	DA	3137	1/1	0.14	-	54,54,54,54	0
57	MG	DA	3500	1/1	0.35	-	49,49,49,49	0
57	MG	BA	3094	1/1	0.16	-	36,36,36,36	0
57	MG	BA	3486	1/1	0.14	-	57,57,57,57	0
57	MG	DA	3665	1/1	0.09	-	42,42,42,42	0
57	MG	DA	3135	1/1	0.10	-	38,38,38,38	0
57	MG	BA	3415	1/1	0.15	-	28,28,28,28	0
57	MG	CA	3020	1/1	0.16	-	56,56,56,56	0
57	MG	BA	3169	1/1	0.18	-	45,45,45,45	0
57	MG	BB	215	1/1	0.18	-	73,73,73,73	0
57	MG	DA	3507	1/1	0.10	-	43,43,43,43	0
57	MG	BA	3736	1/1	0.24	-	42,42,42,42	0
57	MG	DA	3498	1/1	0.08	-	51,51,51,51	0
57	MG	DA	3042	1/1	0.20	-	38,38,38,38	0
57	MG	BQ	3001	1/1	0.17	-	45,45,45,45	0
57	MG	DA	3248	1/1	0.12	-	56,56,56,56	0
57	MG	DA	3039	1/1	0.13	-	43,43,43,43	0
57	MG	DA	3369	1/1	0.13	-	28,28,28,28	0
57	MG	CA	3022	1/1	0.13	-	78,78,78,78	0
57	MG	DA	3559	1/1	0.08	-	43,43,43,43	0
57	MG	DA	3461	1/1	0.14	-	62,62,62,62	0
57	MG	DA	3443	1/1	0.12	-	54,54,54,54	0
57	MG	DA	3172	1/1	0.12	-	62,62,62,62	0
57	MG	DA	3361	1/1	0.14	-	44,44,44,44	0
57	MG	BA	3313	1/1	0.06	-	53,53,53,53	0
57	MG	AA	3052	1/1	0.22	-	65,65,65,65	0
57	MG	BA	3193	1/1	0.16	-	48,48,48,48	0
57	MG	DA	3389	1/1	0.12	-	46,46,46,46	0
57	MG	BB	202	1/1	0.25	-	59,59,59,59	0
59	ZN	D9	501	1/1	0.10	-	68,68,68,68	0
57	MG	BA	3020	1/1	0.19	-	53,53,53,53	0
57	MG	DA	3055	1/1	0.15	-	49,49,49,49	0
57	MG	DA	3520	1/1	0.14	-	57,57,57,57	0
57	MG	DA	3537	1/1	0.05	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3106	1/1	0.07	-	56,56,56,56	0
57	MG	BA	3634	1/1	0.18	-	62,62,62,62	0
57	MG	BA	3277	1/1	0.66	-	47,47,47,47	0
57	MG	DA	3089	1/1	0.42	-	52,52,52,52	0
57	MG	DA	3291	1/1	0.18	-	44,44,44,44	0
57	MG	BR	201	1/1	0.19	-	57,57,57,57	0
57	MG	DA	3662	1/1	0.10	-	62,62,62,62	0
57	MG	CA	3122	1/1	0.22	-	64,64,64,64	0
57	MG	BA	3628	1/1	0.17	-	49,49,49,49	0
57	MG	BA	3667	1/1	0.12	-	61,61,61,61	0
57	MG	AA	3162	1/1	0.06	-	66,66,66,66	0
57	MG	BA	3413	1/1	0.13	-	47,47,47,47	0
57	MG	DA	3473	1/1	0.08	-	50,50,50,50	0
57	MG	DU	3001	1/1	0.37	-	55,55,55,55	0
57	MG	DA	3484	1/1	0.12	-	62,62,62,62	0
57	MG	DA	3109	1/1	0.33	-	40,40,40,40	0
57	MG	AA	3214	1/1	0.15	-	73,73,73,73	0
57	MG	DA	3383	1/1	0.15	-	54,54,54,54	0
57	MG	AA	3200	1/1	0.09	-	73,73,73,73	0
57	MG	DA	3239	1/1	0.11	-	56,56,56,56	0
57	MG	DA	3436	1/1	0.09	-	54,54,54,54	0
57	MG	DA	3096	1/1	0.24	-	42,42,42,42	0
57	MG	BA	3028	1/1	0.13	-	51,51,51,51	0
57	MG	BA	3341	1/1	0.11	-	51,51,51,51	0
57	MG	CA	3164	1/1	0.16	-	60,60,60,60	0
57	MG	AA	3103	1/1	0.18	-	73,73,73,73	0
57	MG	BA	3198	1/1	0.47	-	37,37,37,37	0
57	MG	DA	3522	1/1	0.13	-	71,71,71,71	0
57	MG	BA	3170	1/1	0.16	-	38,38,38,38	0
57	MG	CA	3098	1/1	0.10	-	65,65,65,65	0
57	MG	BA	3773	1/1	0.19	-	52,52,52,52	0
57	MG	BA	3257	1/1	0.22	-	53,53,53,53	0
57	MG	BA	3699	1/1	0.19	-	35,35,35,35	0
57	MG	DA	3403	1/1	0.13	-	57,57,57,57	0
57	MG	DA	3201	1/1	0.13	-	61,61,61,61	0
57	MG	BA	3775	1/1	0.21	-	33,33,33,33	0
57	MG	BA	3753	1/1	0.16	-	33,33,33,33	0
57	MG	DA	3209	1/1	0.15	-	53,53,53,53	0
57	MG	DA	3631	1/1	0.10	-	57,57,57,57	0
57	MG	DA	3677	1/1	0.68	-	52,52,52,52	0
57	MG	DA	3225	1/1	0.14	-	49,49,49,49	0
57	MG	DA	3062	1/1	0.34	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3121	1/1	0.10	-	44,44,44,44	0
57	MG	BA	3762	1/1	0.14	-	46,46,46,46	0
57	MG	CA	3058	1/1	0.12	-	68,68,68,68	0
57	MG	BA	3032	1/1	0.19	-	47,47,47,47	0
57	MG	B5	101	1/1	0.51	-	51,51,51,51	0
57	MG	BA	3034	1/1	0.13	-	56,56,56,56	0
57	MG	CA	3135	1/1	0.14	-	63,63,63,63	0
57	MG	DA	3462	1/1	0.25	-	42,42,42,42	0
57	MG	DA	3155	1/1	0.18	-	48,48,48,48	0
57	MG	BA	3718	1/1	0.14	-	71,71,71,71	0
57	MG	BU	204	1/1	0.28	-	35,35,35,35	0
57	MG	BA	3550	1/1	0.17	-	36,36,36,36	0
57	MG	BA	3693	1/1	0.13	-	56,56,56,56	0
57	MG	BP	205	1/1	0.23	-	65,65,65,65	0
57	MG	BA	3782	1/1	0.12	-	65,65,65,65	0
57	MG	DA	3512	1/1	0.10	-	47,47,47,47	0
57	MG	DA	3568	1/1	0.07	-	52,52,52,52	0
57	MG	DA	3150	1/1	0.07	-	56,56,56,56	0
57	MG	AF	3001	1/1	0.16	-	44,44,44,44	0
57	MG	DA	3010	1/1	0.07	-	47,47,47,47	0
57	MG	BA	3350	1/1	0.18	-	28,28,28,28	0
57	MG	AA	3130	1/1	0.09	-	56,56,56,56	0
57	MG	AA	3201	1/1	0.08	-	52,52,52,52	0
57	MG	DA	3158	1/1	0.11	-	60,60,60,60	0
57	MG	AY	3003	1/1	0.39	-	53,53,53,53	0
57	MG	DA	3270	1/1	0.10	-	46,46,46,46	0
57	MG	AA	3107	1/1	0.16	-	64,64,64,64	0
57	MG	AA	3213	1/1	0.21	-	54,54,54,54	0
57	MG	DA	3651	1/1	0.70	-	75,75,75,75	0
57	MG	BA	3680	1/1	0.09	-	68,68,68,68	0
57	MG	AA	3049	1/1	0.17	-	64,64,64,64	0
57	MG	AA	3123	1/1	0.20	-	51,51,51,51	0
57	MG	BA	3143	1/1	0.22	-	45,45,45,45	0
57	MG	CA	3125	1/1	0.06	-	63,63,63,63	0
57	MG	AA	3033	1/1	0.11	-	59,59,59,59	0
57	MG	BA	3013	1/1	0.16	-	32,32,32,32	0
57	MG	BA	3727	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3064	1/1	0.35	-	49,49,49,49	0
57	MG	BA	3153	1/1	0.23	-	47,47,47,47	0
57	MG	DV	3002	1/1	0.61	-	49,49,49,49	0
57	MG	DA	3221	1/1	0.31	-	52,52,52,52	0
57	MG	DF	3004	1/1	0.41	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3605	1/1	0.14	-	43,43,43,43	0
57	MG	DA	3184	1/1	0.12	-	47,47,47,47	0
57	MG	DA	3388	1/1	0.12	-	53,53,53,53	0
57	MG	BA	3781	1/1	0.18	-	41,41,41,41	0
57	MG	BA	3181	1/1	0.16	-	43,43,43,43	0
57	MG	BA	3576	1/1	0.07	-	57,57,57,57	0
57	MG	DA	3046	1/1	0.14	-	47,47,47,47	0
57	MG	BA	3251	1/1	0.13	-	44,44,44,44	0
57	MG	BA	3516	1/1	0.17	-	52,52,52,52	0
57	MG	CA	3166	1/1	0.15	-	66,66,66,66	0
57	MG	AA	3057	1/1	0.23	-	64,64,64,64	0
57	MG	DA	3023	1/1	0.24	-	40,40,40,40	0
57	MG	BA	3044	1/1	0.26	-	20,20,20,20	0
57	MG	BE	303	1/1	0.13	-	51,51,51,51	0
57	MG	BD	304	1/1	0.15	-	32,32,32,32	0
57	MG	AA	3207	1/1	0.07	-	65,65,65,65	0
57	MG	BD	306	1/1	0.21	-	38,38,38,38	0
57	MG	AA	3171	1/1	0.09	-	51,51,51,51	0
57	MG	BA	3785	1/1	0.23	-	59,59,59,59	0
57	MG	BA	3142	1/1	0.30	-	49,49,49,49	0
57	MG	DA	3141	1/1	0.28	-	61,61,61,61	0
57	MG	BA	3380	1/1	0.08	-	48,48,48,48	0
57	MG	BA	3333	1/1	0.18	-	38,38,38,38	0
57	MG	AA	3142	1/1	0.11	-	41,41,41,41	0
57	MG	AA	3120	1/1	0.14	-	45,45,45,45	0
57	MG	DA	3093	1/1	0.10	-	62,62,62,62	0
57	MG	BA	3812	1/1	0.48	-	47,47,47,47	0
57	MG	BA	3236	1/1	0.17	-	49,49,49,49	0
57	MG	DA	3072	1/1	0.14	-	47,47,47,47	0
57	MG	BA	3465	1/1	0.15	-	43,43,43,43	0
57	MG	BA	3346	1/1	0.08	-	27,27,27,27	0
57	MG	BA	3663	1/1	0.15	-	41,41,41,41	0
57	MG	DA	3446	1/1	0.11	-	45,45,45,45	0
57	MG	BA	3409	1/1	0.16	-	30,30,30,30	0
57	MG	BA	3314	1/1	0.16	-	58,58,58,58	0
57	MG	BA	3508	1/1	0.18	-	51,51,51,51	0
57	MG	AA	3132	1/1	0.17	-	55,55,55,55	0
59	ZN	B5	102	1/1	0.21	-	48,48,48,48	0
57	MG	BA	3022	1/1	0.13	-	60,60,60,60	0
57	MG	BA	3156	1/1	0.33	-	41,41,41,41	0
57	MG	AA	3075	1/1	0.09	-	49,49,49,49	0
57	MG	BA	3542	1/1	0.16	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3496	1/1	0.09	-	53,53,53,53	0
57	MG	DA	3254	1/1	0.06	-	52,52,52,52	0
57	MG	DA	3278	1/1	0.07	-	43,43,43,43	0
57	MG	AA	3168	1/1	0.10	-	59,59,59,59	0
57	MG	BA	3484	1/1	0.10	-	54,54,54,54	0
57	MG	BA	3067	1/1	0.10	-	41,41,41,41	0
57	MG	AA	3088	1/1	0.23	-	65,65,65,65	0
57	MG	AA	3064	1/1	0.20	-	60,60,60,60	0
57	MG	BA	3083	1/1	0.10	-	56,56,56,56	0
57	MG	DA	3017	1/1	0.07	-	55,55,55,55	0
57	MG	DA	3340	1/1	0.15	-	58,58,58,58	0
57	MG	DA	3585	1/1	0.10	-	43,43,43,43	0
57	MG	BA	3106	1/1	0.17	-	42,42,42,42	0
57	MG	AA	3066	1/1	0.25	-	60,60,60,60	0
57	MG	BA	3270	1/1	0.19	-	48,48,48,48	0
57	MG	DA	3534	1/1	0.15	-	55,55,55,55	0
57	MG	DA	3068	1/1	0.13	-	58,58,58,58	0
57	MG	DA	3177	1/1	0.15	-	42,42,42,42	0
57	MG	DA	3382	1/1	0.05	-	48,48,48,48	0
57	MG	DA	3289	1/1	0.07	-	53,53,53,53	0
57	MG	AA	3114	1/1	0.10	-	59,59,59,59	0
57	MG	CA	3072	1/1	0.07	-	54,54,54,54	0
59	ZN	BY	501	1/1	0.13	-	58,58,58,58	0
57	MG	AA	3179	1/1	0.14	-	69,69,69,69	0
57	MG	AW	3004	1/1	0.12	-	49,49,49,49	0
57	MG	BF	304	1/1	0.28	-	45,45,45,45	0
57	MG	DA	3293	1/1	0.11	-	54,54,54,54	0
57	MG	B0	101	1/1	0.27	-	36,36,36,36	0
57	MG	DN	5001	1/1	0.10	-	66,66,66,66	0
57	MG	DA	3140	1/1	0.15	-	58,58,58,58	0
57	MG	CA	3143	1/1	0.16	-	64,64,64,64	0
57	MG	BA	3590	1/1	0.15	-	50,50,50,50	0
57	MG	BA	3725	1/1	0.14	-	44,44,44,44	0
57	MG	BA	3163	1/1	0.10	-	55,55,55,55	0
57	MG	BA	3453	1/1	0.35	-	45,45,45,45	0
57	MG	DA	3566	1/1	0.16	-	69,69,69,69	0
57	MG	BA	3710	1/1	0.19	-	57,57,57,57	0
57	MG	CA	3124	1/1	0.13	-	59,59,59,59	0
57	MG	DA	3567	1/1	0.61	-	62,62,62,62	0
57	MG	BA	3417	1/1	0.18	-	38,38,38,38	0
57	MG	AA	3204	1/1	0.16	-	53,53,53,53	0
57	MG	AA	3093	1/1	0.17	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DB	3011	1/1	0.09	-	72,72,72,72	0
57	MG	BA	3602	1/1	0.17	-	53,53,53,53	0
57	MG	BA	3526	1/1	0.10	-	44,44,44,44	0
57	MG	BA	3692	1/1	0.10	-	40,40,40,40	0
57	MG	BA	3600	1/1	0.23	-	44,44,44,44	0
57	MG	DA	3424	1/1	0.09	-	61,61,61,61	0
57	MG	BA	3673	1/1	0.20	-	55,55,55,55	0
57	MG	AA	3152	1/1	0.10	-	62,62,62,62	0
57	MG	BA	3173	1/1	0.13	-	48,48,48,48	0
57	MG	BA	3750	1/1	0.17	-	27,27,27,27	0
57	MG	AX	3004	1/1	0.16	-	64,64,64,64	0
57	MG	BA	3640	1/1	0.20	-	53,53,53,53	0
57	MG	DA	3069	1/1	0.12	-	57,57,57,57	0
57	MG	BA	3462	1/1	0.13	-	36,36,36,36	0
57	MG	BX	3003	1/1	0.15	-	35,35,35,35	0
57	MG	BA	3568	1/1	0.09	-	59,59,59,59	0
57	MG	BA	3770	1/1	0.16	-	45,45,45,45	0
57	MG	BA	3021	1/1	0.12	-	49,49,49,49	0
57	MG	BA	3289	1/1	0.15	-	56,56,56,56	0
57	MG	BA	3091	1/1	0.36	-	56,56,56,56	0
57	MG	DA	3210	1/1	0.08	-	53,53,53,53	0
57	MG	BA	3216	1/1	0.24	-	37,37,37,37	0
57	MG	BA	3062	1/1	0.24	-	42,42,42,42	0
57	MG	BA	3385	1/1	0.13	-	59,59,59,59	0
57	MG	CA	3142	1/1	0.11	-	69,69,69,69	0
57	MG	CA	3086	1/1	0.12	-	64,64,64,64	0
57	MG	AA	3158	1/1	0.15	-	45,45,45,45	0
57	MG	BD	305	1/1	0.13	-	35,35,35,35	0
57	MG	DR	5001	1/1	0.37	-	70,70,70,70	0
57	MG	DA	3398	1/1	0.11	-	45,45,45,45	0
57	MG	AA	3039	1/1	0.17	-	56,56,56,56	0
57	MG	BA	3536	1/1	0.27	-	49,49,49,49	0
57	MG	DA	3215	1/1	0.13	-	59,59,59,59	0
57	MG	BA	3454	1/1	0.24	-	27,27,27,27	0
57	MG	DA	3535	1/1	0.20	-	56,56,56,56	0
57	MG	CA	3090	1/1	0.10	-	67,67,67,67	0
57	MG	BA	3712	1/1	0.18	-	53,53,53,53	0
57	MG	BA	3598	1/1	0.19	-	63,63,63,63	0
57	MG	BA	3488	1/1	0.14	-	60,60,60,60	0
57	MG	DA	3599	1/1	0.16	-	36,36,36,36	0
57	MG	DA	3163	1/1	0.09	-	49,49,49,49	0
57	MG	DD	307	1/1	0.45	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3205	1/1	0.28	-	50,50,50,50	0
57	MG	BD	309	1/1	0.27	-	57,57,57,57	0
57	MG	BA	3705	1/1	0.10	-	62,62,62,62	0
57	MG	BA	3630	1/1	0.13	-	58,58,58,58	0
57	MG	DA	3476	1/1	0.16	-	62,62,62,62	0
57	MG	DA	3346	1/1	0.11	-	48,48,48,48	0
57	MG	AA	3059	1/1	0.11	-	78,78,78,78	0
57	MG	DA	3653	1/1	0.10	-	52,52,52,52	0
57	MG	DA	3336	1/1	0.16	-	40,40,40,40	0
57	MG	AA	3148	1/1	0.20	-	57,57,57,57	0
57	MG	BA	3416	1/1	0.22	-	21,21,21,21	0
57	MG	AA	3072	1/1	0.09	-	66,66,66,66	0
57	MG	DA	3178	1/1	0.20	-	50,50,50,50	0
57	MG	DB	3003	1/1	0.13	-	57,57,57,57	0
57	MG	DA	3129	1/1	0.10	-	46,46,46,46	0
57	MG	BA	3651	1/1	0.13	-	45,45,45,45	0
57	MG	BA	3514	1/1	0.21	-	48,48,48,48	0
57	MG	BA	3164	1/1	0.27	-	48,48,48,48	0
57	MG	BA	3556	1/1	0.22	-	36,36,36,36	0
57	MG	DA	3202	1/1	0.18	-	57,57,57,57	0
57	MG	CA	3140	1/1	0.12	-	67,67,67,67	0
57	MG	DA	3311	1/1	0.18	-	54,54,54,54	0
57	MG	DA	3602	1/1	0.06	-	65,65,65,65	0
57	MG	DA	3134	1/1	0.24	-	41,41,41,41	0
57	MG	BA	3554	1/1	0.10	-	51,51,51,51	0
57	MG	DA	3180	1/1	0.16	-	42,42,42,42	0
57	MG	BA	3139	1/1	0.37	-	40,40,40,40	0
57	MG	BA	3761	1/1	0.16	-	59,59,59,59	0
57	MG	BA	3323	1/1	0.23	-	30,30,30,30	0
57	MG	BA	3601	1/1	0.08	-	55,55,55,55	0
57	MG	BA	3312	1/1	0.20	-	32,32,32,32	0
57	MG	BA	3180	1/1	0.16	-	47,47,47,47	0
57	MG	BA	3371	1/1	0.10	-	35,35,35,35	0
57	MG	BY	502	1/1	0.15	-	40,40,40,40	0
57	MG	BA	3645	1/1	0.17	-	33,33,33,33	0
57	MG	DA	3123	1/1	0.14	-	56,56,56,56	0
57	MG	DA	3418	1/1	0.13	-	52,52,52,52	0
57	MG	DA	3672	1/1	0.29	-	71,71,71,71	0
57	MG	DA	3353	1/1	0.13	-	42,42,42,42	0
57	MG	BP	203	1/1	0.13	-	33,33,33,33	0
57	MG	AA	3029	1/1	0.20	-	53,53,53,53	0
57	MG	DA	3027	1/1	0.36	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3084	1/1	0.20	-	38,38,38,38	0
57	MG	DA	3617	1/1	0.13	-	56,56,56,56	0
57	MG	BA	3228	1/1	0.14	-	59,59,59,59	0
57	MG	DA	3356	1/1	0.10	-	36,36,36,36	0
57	MG	DA	3421	1/1	0.12	-	50,50,50,50	0
57	MG	DA	3206	1/1	0.09	-	50,50,50,50	0
57	MG	DA	3572	1/1	0.08	-	62,62,62,62	0
57	MG	BA	3799	1/1	0.06	-	49,49,49,49	0
57	MG	BA	3593	1/1	0.19	-	38,38,38,38	0
57	MG	DA	3300	1/1	0.19	-	45,45,45,45	0
57	MG	DA	3108	1/1	0.07	-	52,52,52,52	0
57	MG	DA	3647	1/1	0.14	-	54,54,54,54	0
57	MG	BA	3221	1/1	0.12	-	37,37,37,37	0
57	MG	DB	3009	1/1	0.14	-	59,59,59,59	0
57	MG	DA	3058	1/1	0.09	-	29,29,29,29	0
57	MG	BA	3141	1/1	0.50	-	42,42,42,42	0
57	MG	CA	3053	1/1	0.14	-	41,41,41,41	0
57	MG	BA	3060	1/1	0.18	-	30,30,30,30	0
57	MG	BA	3422	1/1	0.21	-	33,33,33,33	0
57	MG	BA	3355	1/1	0.18	-	61,61,61,61	0
57	MG	BA	3432	1/1	0.18	-	58,58,58,58	0
57	MG	DA	3244	1/1	0.09	-	71,71,71,71	0
57	MG	CA	3087	1/1	0.14	-	67,67,67,67	0
57	MG	BA	3424	1/1	0.23	-	39,39,39,39	0
57	MG	DA	3438	1/1	0.16	-	47,47,47,47	0
57	MG	DU	3002	1/1	0.99	-	55,55,55,55	0
57	MG	BA	3637	1/1	0.10	-	39,39,39,39	0
57	MG	BA	3360	1/1	0.14	-	41,41,41,41	0
57	MG	DB	3002	1/1	0.19	-	65,65,65,65	0
57	MG	AA	3174	1/1	0.07	-	50,50,50,50	0
57	MG	DA	3471	1/1	0.39	-	50,50,50,50	0
57	MG	DA	3250	1/1	0.28	-	69,69,69,69	0
57	MG	DA	3625	1/1	0.06	-	69,69,69,69	0
57	MG	DA	3431	1/1	0.25	-	50,50,50,50	0
57	MG	DA	3626	1/1	0.14	-	67,67,67,67	0
57	MG	BA	3196	1/1	0.43	-	38,38,38,38	0
57	MG	AA	3062	1/1	0.28	-	51,51,51,51	0
57	MG	BA	3125	1/1	0.14	-	47,47,47,47	0
57	MG	DA	3284	1/1	0.11	-	47,47,47,47	0
57	MG	DA	3047	1/1	0.10	-	49,49,49,49	0
57	MG	BO	201	1/1	0.18	-	50,50,50,50	0
57	MG	CA	3063	1/1	0.11	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3187	1/1	0.11	-	42,42,42,42	0
57	MG	DA	3168	1/1	0.21	-	45,45,45,45	0
57	MG	DA	3488	1/1	0.08	-	41,41,41,41	0
57	MG	DA	3079	1/1	0.17	-	55,55,55,55	0
57	MG	DA	3454	1/1	0.14	-	56,56,56,56	0
57	MG	DD	304	1/1	0.27	-	52,52,52,52	0
57	MG	BA	3191	1/1	0.14	-	43,43,43,43	0
57	MG	DA	3164	1/1	0.09	-	51,51,51,51	0
57	MG	BA	3768	1/1	0.10	-	47,47,47,47	0
57	MG	BA	3511	1/1	0.12	-	30,30,30,30	0
57	MG	BA	3066	1/1	0.29	-	49,49,49,49	0
57	MG	DA	3392	1/1	0.14	-	70,70,70,70	0
57	MG	BA	3410	1/1	0.17	-	27,27,27,27	0
57	MG	DA	3297	1/1	0.08	-	39,39,39,39	0
57	MG	BN	3001	1/1	0.48	-	53,53,53,53	0
57	MG	BR	202	1/1	0.10	-	31,31,31,31	0
57	MG	BA	3183	1/1	0.19	-	42,42,42,42	0
57	MG	BA	3780	1/1	0.11	-	62,62,62,62	0
57	MG	DA	3267	1/1	0.10	-	49,49,49,49	0
57	MG	DA	3552	1/1	0.07	-	54,54,54,54	0
57	MG	DA	3030	1/1	0.10	-	39,39,39,39	0
57	MG	DA	3104	1/1	0.27	-	53,53,53,53	0
57	MG	DA	3527	1/1	0.10	-	60,60,60,60	0
57	MG	BA	3636	1/1	0.12	-	64,64,64,64	0
57	MG	DA	3262	1/1	0.11	-	65,65,65,65	0
57	MG	AW	3001	1/1	0.09	-	60,60,60,60	0
57	MG	DA	3157	1/1	0.24	-	47,47,47,47	0
57	MG	DA	3162	1/1	0.32	-	50,50,50,50	0
57	MG	DA	3360	1/1	0.15	-	46,46,46,46	0
57	MG	BA	3677	1/1	0.15	-	60,60,60,60	0
57	MG	BA	3103	1/1	0.14	-	38,38,38,38	0
57	MG	BA	3735	1/1	0.62	-	57,57,57,57	0
57	MG	BA	3229	1/1	0.14	-	54,54,54,54	0
57	MG	BA	3713	1/1	0.14	-	33,33,33,33	0
57	MG	CA	3025	1/1	0.13	-	51,51,51,51	0
57	MG	DA	3228	1/1	0.40	-	38,38,38,38	0
57	MG	DA	3546	1/1	0.11	-	71,71,71,71	0
57	MG	BZ	3001	1/1	0.21	-	55,55,55,55	0
57	MG	BA	3557	1/1	0.15	-	33,33,33,33	0
57	MG	AA	3205	1/1	0.19	-	51,51,51,51	0
57	MG	AA	3083	1/1	0.35	-	57,57,57,57	0
57	MG	DA	3536	1/1	0.08	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3208	1/1	0.40	-	58,58,58,58	0
57	MG	BA	3085	1/1	0.20	-	35,35,35,35	0
57	MG	BA	3537	1/1	0.18	-	45,45,45,45	0
57	MG	CA	3028	1/1	0.11	-	41,41,41,41	0
57	MG	BA	3423	1/1	0.18	-	44,44,44,44	0
57	MG	DA	3407	1/1	0.04	-	66,66,66,66	0
57	MG	DA	3573	1/1	0.07	-	43,43,43,43	0
57	MG	BU	207	1/1	0.33	-	38,38,38,38	0
57	MG	BA	3290	1/1	0.24	-	40,40,40,40	0
57	MG	BA	3024	1/1	0.17	-	49,49,49,49	0
57	MG	CA	3129	1/1	0.07	-	43,43,43,43	0
57	MG	BA	3039	1/1	0.13	-	32,32,32,32	0
57	MG	BA	3123	1/1	0.27	-	32,32,32,32	0
57	MG	BA	3115	1/1	0.24	-	59,59,59,59	0
57	MG	BA	3729	1/1	0.14	-	47,47,47,47	0
57	MG	BA	3090	1/1	0.15	-	53,53,53,53	0
57	MG	DA	3571	1/1	0.18	-	56,56,56,56	0
57	MG	DA	3483	1/1	0.46	-	55,55,55,55	0
57	MG	DV	3001	1/1	0.10	-	70,70,70,70	0
57	MG	AA	3082	1/1	0.19	-	46,46,46,46	0
57	MG	DA	3551	1/1	0.06	-	55,55,55,55	0
57	MG	DA	3277	1/1	0.13	-	55,55,55,55	0
57	MG	BA	3232	1/1	0.14	-	52,52,52,52	0
57	MG	CA	3019	1/1	0.07	-	65,65,65,65	0
57	MG	BA	3578	1/1	0.13	-	46,46,46,46	0
57	MG	DA	3323	1/1	0.11	-	50,50,50,50	0
57	MG	DA	3410	1/1	0.12	-	53,53,53,53	0
57	MG	DA	3252	1/1	0.07	-	37,37,37,37	0
57	MG	DA	3321	1/1	0.07	-	48,48,48,48	0
57	MG	BA	3120	1/1	0.17	-	55,55,55,55	0
59	ZN	D5	501	1/1	0.18	-	58,58,58,58	0
57	MG	CA	3108	1/1	0.10	-	68,68,68,68	0
57	MG	AA	3092	1/1	0.11	-	63,63,63,63	0
57	MG	BA	3108	1/1	0.25	-	44,44,44,44	0
57	MG	BA	3683	1/1	0.10	-	73,73,73,73	0
57	MG	BA	3018	1/1	0.53	-	56,56,56,56	0
57	MG	CA	3111	1/1	0.15	-	64,64,64,64	0
57	MG	BA	3529	1/1	0.14	-	56,56,56,56	0
57	MG	BA	3088	1/1	0.35	-	48,48,48,48	0
57	MG	DA	3128	1/1	0.16	-	58,58,58,58	0
57	MG	DA	3174	1/1	0.09	-	44,44,44,44	0
57	MG	DA	3485	1/1	0.09	-	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3402	1/1	0.11	-	40,40,40,40	0
57	MG	BA	3288	1/1	0.27	-	56,56,56,56	0
57	MG	BA	3771	1/1	0.29	-	50,50,50,50	0
57	MG	BA	3297	1/1	0.16	-	43,43,43,43	0
57	MG	BA	3447	1/1	0.08	-	72,72,72,72	0
57	MG	AA	3051	1/1	0.31	-	73,73,73,73	0
57	MG	DA	3185	1/1	0.47	-	68,68,68,68	0
57	MG	BA	3304	1/1	0.15	-	67,67,67,67	0
57	MG	DA	3674	1/1	0.25	-	37,37,37,37	0
57	MG	CD	301	1/1	0.12	-	56,56,56,56	0
57	MG	BA	3300	1/1	0.21	-	57,57,57,57	0
57	MG	DA	3151	1/1	0.07	-	55,55,55,55	0
57	MG	CA	3084	1/1	0.10	-	60,60,60,60	0
57	MG	CA	3132	1/1	0.28	-	66,66,66,66	0
57	MG	DA	3197	1/1	0.11	-	55,55,55,55	0
57	MG	BA	3672	1/1	0.21	-	43,43,43,43	0
57	MG	DA	3041	1/1	0.07	-	38,38,38,38	0
57	MG	BB	213	1/1	0.15	-	60,60,60,60	0
57	MG	BA	3746	1/1	0.13	-	51,51,51,51	0
57	MG	DA	3060	1/1	0.10	-	64,64,64,64	0
57	MG	BD	303	1/1	0.20	-	39,39,39,39	0
57	MG	DA	3432	1/1	0.14	-	37,37,37,37	0
57	MG	BA	3222	1/1	0.17	-	37,37,37,37	0
59	ZN	D6	501	1/1	0.17	-	71,71,71,71	0
57	MG	DA	3035	1/1	0.53	-	52,52,52,52	0
57	MG	DA	3281	1/1	0.14	-	53,53,53,53	0
57	MG	DA	3470	1/1	0.21	-	45,45,45,45	0
57	MG	BA	3500	1/1	0.16	-	56,56,56,56	0
57	MG	DA	3433	1/1	0.20	-	46,46,46,46	0
57	MG	DA	3348	1/1	0.12	-	34,34,34,34	0
57	MG	CA	3117	1/1	0.14	-	71,71,71,71	0
57	MG	AX	3008	1/1	0.17	-	70,70,70,70	0
57	MG	BA	3691	1/1	0.18	-	55,55,55,55	0
57	MG	CA	3024	1/1	0.12	-	74,74,74,74	0
57	MG	DA	3466	1/1	0.16	-	41,41,41,41	0
57	MG	AA	3137	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3635	1/1	0.11	-	38,38,38,38	0
57	MG	BA	3336	1/1	0.12	-	64,64,64,64	0
59	ZN	B9	501	1/1	0.14	-	38,38,38,38	0
57	MG	BA	3353	1/1	0.17	-	50,50,50,50	0
57	MG	DA	3666	1/1	0.12	-	35,35,35,35	0
57	MG	BA	3321	1/1	0.21	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3303	1/1	0.07	-	48,48,48,48	0
57	MG	DA	3212	1/1	0.11	-	45,45,45,45	0
57	MG	BA	3420	1/1	0.15	-	40,40,40,40	0
57	MG	DA	3632	1/1	0.12	-	36,36,36,36	0
57	MG	BA	3763	1/1	0.17	-	24,24,24,24	0
57	MG	DA	3584	1/1	0.18	-	53,53,53,53	0
57	MG	DA	3191	1/1	0.14	-	37,37,37,37	0
57	MG	BA	3179	1/1	0.16	-	50,50,50,50	0
57	MG	DA	3526	1/1	0.11	-	48,48,48,48	0
57	MG	AA	3031	1/1	0.16	-	70,70,70,70	0
57	MG	DA	3367	1/1	0.17	-	61,61,61,61	0
57	MG	BA	3728	1/1	0.33	-	48,48,48,48	0
57	MG	DA	3655	1/1	0.13	-	64,64,64,64	0
57	MG	BA	3287	1/1	0.10	-	42,42,42,42	0
57	MG	BD	302	1/1	0.33	-	50,50,50,50	0
57	MG	DE	302	1/1	0.10	-	33,33,33,33	0
57	MG	BA	3098	1/1	0.21	-	40,40,40,40	0
57	MG	B4	502	1/1	0.14	-	71,71,71,71	0
57	MG	BA	3394	1/1	0.19	-	40,40,40,40	0
57	MG	AA	3125	1/1	0.22	-	37,37,37,37	0
57	MG	BA	3026	1/1	0.12	-	41,41,41,41	0
57	MG	BA	3101	1/1	0.33	-	53,53,53,53	0
57	MG	BA	3140	1/1	0.14	-	47,47,47,47	0
57	MG	CA	3148	1/1	0.13	-	70,70,70,70	0
57	MG	BA	3036	1/1	0.13	-	40,40,40,40	0
57	MG	BA	3096	1/1	0.39	-	54,54,54,54	0
57	MG	BG	202	1/1	0.15	-	41,41,41,41	0
57	MG	BA	3749	1/1	0.11	-	56,56,56,56	0
57	MG	BU	203	1/1	0.31	-	47,47,47,47	0
57	MG	DA	3447	1/1	0.17	-	58,58,58,58	0
57	MG	AX	3011	1/1	0.23	-	78,78,78,78	0
57	MG	BA	3016	1/1	0.13	-	38,38,38,38	0
57	MG	DA	3114	1/1	0.18	-	55,55,55,55	0
57	MG	AA	3084	1/1	0.23	-	51,51,51,51	0
57	MG	BA	3007	1/1	0.18	-	55,55,55,55	0
57	MG	DA	3501	1/1	0.24	-	37,37,37,37	0
57	MG	BA	3064	1/1	0.28	-	43,43,43,43	0
57	MG	DA	3143	1/1	0.15	-	38,38,38,38	0
57	MG	BA	3172	1/1	0.20	-	46,46,46,46	0
57	MG	BA	3426	1/1	0.20	-	37,37,37,37	0
57	MG	BA	3223	1/1	0.10	-	41,41,41,41	0
57	MG	AA	3161	1/1	0.12	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3641	1/1	0.36	-	69,69,69,69	0
57	MG	BA	3225	1/1	0.17	-	61,61,61,61	0
57	MG	CA	3009	1/1	0.10	-	64,64,64,64	0
57	MG	CA	3036	1/1	0.12	-	66,66,66,66	0
57	MG	AX	3016	1/1	0.18	-	56,56,56,56	0
57	MG	B2	3001	1/1	0.34	-	56,56,56,56	0
57	MG	CA	3127	1/1	0.12	-	62,62,62,62	0
57	MG	BA	3318	1/1	0.13	-	41,41,41,41	0
57	MG	BA	3265	1/1	0.17	-	54,54,54,54	0
57	MG	BQ	3002	1/1	0.13	-	43,43,43,43	0
57	MG	DA	3152	1/1	0.18	-	51,51,51,51	0
57	MG	BA	3611	1/1	0.14	-	46,46,46,46	0
57	MG	BA	3618	1/1	0.13	-	65,65,65,65	0
57	MG	BA	3612	1/1	0.14	-	21,21,21,21	0
57	MG	BA	3794	1/1	0.25	-	51,51,51,51	0
57	MG	BA	3695	1/1	0.19	-	67,67,67,67	0
57	MG	BA	3320	1/1	0.17	-	48,48,48,48	0
57	MG	AA	3175	1/1	0.19	-	63,63,63,63	0
57	MG	BA	3256	1/1	0.14	-	40,40,40,40	0
57	MG	BA	3523	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3363	1/1	0.12	-	22,22,22,22	0
57	MG	DA	3338	1/1	0.13	-	61,61,61,61	0
57	MG	AA	3027	1/1	0.21	-	50,50,50,50	0
59	ZN	D4	501	1/1	0.06	-	144,144,144,144	0
57	MG	BA	3476	1/1	0.23	-	55,55,55,55	0
57	MG	BB	216	1/1	0.25	-	51,51,51,51	0
57	MG	DP	202	1/1	0.11	-	53,53,53,53	0
57	MG	CA	3112	1/1	0.10	-	69,69,69,69	0
57	MG	DA	3332	1/1	0.14	-	53,53,53,53	0
57	MG	BA	3118	1/1	0.14	-	48,48,48,48	0
57	MG	BA	3503	1/1	0.12	-	49,49,49,49	0
57	MG	BA	3797	1/1	0.14	-	53,53,53,53	0
57	MG	CA	3155	1/1	0.12	-	53,53,53,53	0
57	MG	AA	3040	1/1	0.08	-	60,60,60,60	0
57	MG	DG	3001	1/1	0.08	-	55,55,55,55	0
57	MG	DA	3582	1/1	0.07	-	56,56,56,56	0
57	MG	CA	3093	1/1	0.09	-	55,55,55,55	0
57	MG	BA	3580	1/1	0.12	-	55,55,55,55	0
57	MG	BA	3722	1/1	0.18	-	47,47,47,47	0
57	MG	AA	3164	1/1	0.11	-	61,61,61,61	0
57	MG	BA	3754	1/1	0.17	-	48,48,48,48	0
57	MG	BA	3609	1/1	0.13	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3400	1/1	0.26	-	33,33,33,33	0
57	MG	BA	3405	1/1	0.21	-	63,63,63,63	0
57	MG	DA	3575	1/1	0.12	-	64,64,64,64	0
57	MG	BB	214	1/1	0.16	-	49,49,49,49	0
57	MG	BA	3302	1/1	0.11	-	69,69,69,69	0
60	K	AX	3001	1/1	0.12	-	65,65,65,65	0
57	MG	DA	3097	1/1	0.15	-	33,33,33,33	0
57	MG	DA	3083	1/1	0.37	-	40,40,40,40	0
57	MG	DA	3676	1/1	0.36	-	67,67,67,67	0
57	MG	DA	3586	1/1	0.13	-	60,60,60,60	0
57	MG	BA	3133	1/1	0.12	-	45,45,45,45	0
57	MG	BA	3670	1/1	0.21	-	61,61,61,61	0
57	MG	DA	3328	1/1	0.10	-	47,47,47,47	0
57	MG	BA	3769	1/1	0.13	-	52,52,52,52	0
57	MG	BA	3113	1/1	0.14	-	53,53,53,53	0
57	MG	DA	3581	1/1	0.21	-	57,57,57,57	0
59	ZN	CN	501	1/1	0.09	-	93,93,93,93	0
57	MG	CA	3031	1/1	0.19	-	68,68,68,68	0
57	MG	AA	3081	1/1	0.18	-	48,48,48,48	0
57	MG	BA	3231	1/1	0.30	-	63,63,63,63	0
57	MG	CA	3026	1/1	0.15	-	63,63,63,63	0
57	MG	DA	3018	1/1	0.25	-	62,62,62,62	0
57	MG	BA	3240	1/1	0.59	-	47,47,47,47	0
57	MG	BA	3452	1/1	0.13	-	55,55,55,55	0
57	MG	BA	3626	1/1	0.20	-	44,44,44,44	0
57	MG	BA	3777	1/1	0.13	-	40,40,40,40	0
57	MG	DA	3116	1/1	0.46	-	52,52,52,52	0
57	MG	BA	3147	1/1	0.17	-	45,45,45,45	0
57	MG	BA	3551	1/1	0.16	-	36,36,36,36	0
57	MG	BA	3505	1/1	0.13	-	55,55,55,55	0
57	MG	DA	3238	1/1	0.18	-	44,44,44,44	0
57	MG	CA	3150	1/1	0.18	-	56,56,56,56	0
57	MG	DA	3444	1/1	0.06	-	44,44,44,44	0
57	MG	AA	3034	1/1	0.12	-	47,47,47,47	0
57	MG	DA	3051	1/1	0.11	-	48,48,48,48	0
57	MG	AA	3166	1/1	0.08	-	69,69,69,69	0
57	MG	DA	3031	1/1	0.41	-	43,43,43,43	0
57	MG	BB	207	1/1	0.17	-	54,54,54,54	0
57	MG	BA	3266	1/1	0.16	-	39,39,39,39	0
57	MG	DA	3650	1/1	0.14	-	67,67,67,67	0
57	MG	DA	3648	1/1	0.20	-	57,57,57,57	0
57	MG	BA	3613	1/1	0.47	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3080	1/1	0.11	-	55,55,55,55	0
57	MG	DA	3404	1/1	0.09	-	48,48,48,48	0
57	MG	CA	3017	1/1	0.19	-	53,53,53,53	0
57	MG	DA	3286	1/1	0.12	-	42,42,42,42	0
57	MG	BA	3041	1/1	0.14	-	40,40,40,40	0
57	MG	BA	3061	1/1	0.23	-	29,29,29,29	0
57	MG	BA	3226	1/1	0.18	-	47,47,47,47	0
57	MG	CA	3054	1/1	0.26	-	69,69,69,69	0
57	MG	BA	3376	1/1	0.17	-	48,48,48,48	0
57	MG	BA	3055	1/1	0.17	-	45,45,45,45	0
57	MG	BQ	3003	1/1	0.22	-	49,49,49,49	0
57	MG	BA	3246	1/1	0.25	-	39,39,39,39	0
57	MG	DA	3458	1/1	0.09	-	52,52,52,52	0
57	MG	CA	3056	1/1	0.17	-	64,64,64,64	0
57	MG	DA	3110	1/1	0.24	-	58,58,58,58	0
57	MG	DB	3013	1/1	0.13	-	64,64,64,64	0
57	MG	DA	3464	1/1	0.11	-	46,46,46,46	0
57	MG	BA	3326	1/1	0.12	-	20,20,20,20	0
57	MG	BA	3442	1/1	0.15	-	44,44,44,44	0
57	MG	DA	3620	1/1	0.08	-	68,68,68,68	0
57	MG	DA	3553	1/1	0.10	-	49,49,49,49	0
57	MG	DA	3419	1/1	0.10	-	32,32,32,32	0
57	MG	AA	3116	1/1	0.11	-	55,55,55,55	0
57	MG	DA	3279	1/1	0.11	-	56,56,56,56	0
57	MG	BA	3406	1/1	0.10	-	50,50,50,50	0
57	MG	BA	3042	1/1	0.13	-	43,43,43,43	0
57	MG	AA	3151	1/1	0.14	-	45,45,45,45	0
57	MG	BF	302	1/1	0.15	-	46,46,46,46	0
57	MG	CA	3046	1/1	0.07	-	69,69,69,69	0
57	MG	BA	3587	1/1	0.21	-	36,36,36,36	0
57	MG	AX	3009	1/1	0.18	-	64,64,64,64	0
57	MG	DA	3357	1/1	0.08	-	50,50,50,50	0
57	MG	BA	3519	1/1	0.08	-	55,55,55,55	0
57	MG	DA	3469	1/1	0.28	-	44,44,44,44	0
57	MG	BA	3539	1/1	0.19	-	52,52,52,52	0
57	MG	DA	3377	1/1	0.08	-	38,38,38,38	0
57	MG	BA	3087	1/1	0.22	-	42,42,42,42	0
57	MG	DA	3199	1/1	0.22	-	47,47,47,47	0
57	MG	BA	3679	1/1	0.14	-	62,62,62,62	0
57	MG	BA	3211	1/1	0.58	-	55,55,55,55	0
57	MG	BA	3621	1/1	0.15	-	53,53,53,53	0
57	MG	DA	3453	1/1	0.18	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3175	1/1	0.14	-	41,41,41,41	0
57	MG	BA	3220	1/1	0.19	-	29,29,29,29	0
57	MG	BA	3811	1/1	0.13	-	65,65,65,65	0
57	MG	AA	3145	1/1	0.20	-	66,66,66,66	0
57	MG	BA	3329	1/1	0.35	-	60,60,60,60	0
57	MG	CA	3165	1/1	0.09	-	45,45,45,45	0
57	MG	BA	3065	1/1	0.25	-	60,60,60,60	0
57	MG	BA	3053	1/1	0.15	-	54,54,54,54	0
57	MG	BA	3507	1/1	0.16	-	49,49,49,49	0
57	MG	CA	3080	1/1	0.09	-	49,49,49,49	0
57	MG	BA	3553	1/1	0.08	-	59,59,59,59	0
57	MG	BA	3704	1/1	0.09	-	77,77,77,77	0
57	MG	BA	3585	1/1	0.06	-	46,46,46,46	0
57	MG	CA	3153	1/1	0.12	-	70,70,70,70	0
57	MG	BA	3152	1/1	0.26	-	43,43,43,43	0
57	MG	DA	3459	1/1	0.16	-	47,47,47,47	0
57	MG	BA	3235	1/1	0.24	-	42,42,42,42	0
57	MG	BA	3009	1/1	0.08	-	28,28,28,28	0
57	MG	AA	3135	1/1	0.20	-	65,65,65,65	0
57	MG	DA	3026	1/1	0.50	-	59,59,59,59	0
57	MG	DA	3614	1/1	0.09	-	65,65,65,65	0
58	SF4	AD	501	8/8	0.17	-	62,68,73,86	0
57	MG	BA	3591	1/1	0.17	-	35,35,35,35	0
57	MG	DA	3402	1/1	0.10	-	66,66,66,66	0
57	MG	BB	205	1/1	0.11	-	60,60,60,60	0
57	MG	DA	3063	1/1	0.32	-	54,54,54,54	0
57	MG	BA	3716	1/1	0.15	-	65,65,65,65	0
57	MG	AA	3115	1/1	0.12	-	79,79,79,79	0
57	MG	DA	3160	1/1	0.13	-	56,56,56,56	0
57	MG	B3	3001	1/1	0.10	-	34,34,34,34	0
57	MG	DA	3292	1/1	0.12	-	30,30,30,30	0
57	MG	CA	3067	1/1	0.29	-	61,61,61,61	0
57	MG	CA	3018	1/1	0.16	-	69,69,69,69	0
57	MG	BE	304	1/1	0.24	-	42,42,42,42	0
57	MG	BA	3589	1/1	0.23	-	27,27,27,27	0
57	MG	AN	502	1/1	0.27	-	63,63,63,63	0
57	MG	CA	3094	1/1	0.16	-	70,70,70,70	0
57	MG	BA	3097	1/1	0.20	-	44,44,44,44	0
57	MG	BA	3678	1/1	0.07	-	65,65,65,65	0
57	MG	DA	3054	1/1	0.25	-	48,48,48,48	0
57	MG	BA	3809	1/1	0.16	-	63,63,63,63	0
57	MG	BA	3383	1/1	0.10	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3035	1/1	0.24	-	39,39,39,39	0
57	MG	DA	3094	1/1	0.16	-	50,50,50,50	0
57	MG	DA	3315	1/1	0.06	-	42,42,42,42	0
57	MG	DA	3033	1/1	0.08	-	42,42,42,42	0
57	MG	DA	3608	1/1	0.12	-	68,68,68,68	0
57	MG	BA	3209	1/1	0.19	-	54,54,54,54	0
57	MG	CA	3068	1/1	0.11	-	48,48,48,48	0
57	MG	BA	3168	1/1	0.14	-	47,47,47,47	0
57	MG	DA	3213	1/1	0.84	-	63,63,63,63	0
57	MG	BA	3244	1/1	0.23	-	53,53,53,53	0
57	MG	BA	3339	1/1	0.18	-	23,23,23,23	0
57	MG	DA	3657	1/1	0.08	-	63,63,63,63	0
57	MG	BA	3281	1/1	0.14	-	60,60,60,60	0
57	MG	CA	3147	1/1	0.12	-	64,64,64,64	0
57	MG	BB	218	1/1	0.13	-	77,77,77,77	0
57	MG	BA	3213	1/1	0.23	-	40,40,40,40	0
57	MG	DA	3304	1/1	0.07	-	48,48,48,48	0
57	MG	CA	3044	1/1	0.20	-	62,62,62,62	0
57	MG	AA	3013	1/1	0.11	-	69,69,69,69	0
57	MG	BA	3330	1/1	0.25	-	37,37,37,37	0
57	MG	BA	3077	1/1	0.12	-	49,49,49,49	0
57	MG	BA	3165	1/1	0.28	-	45,45,45,45	0
57	MG	DA	3115	1/1	0.13	-	40,40,40,40	0
57	MG	DA	3630	1/1	0.11	-	61,61,61,61	0
57	MG	DA	3205	1/1	0.11	-	56,56,56,56	0
57	MG	BA	3610	1/1	0.13	-	61,61,61,61	0
57	MG	DA	3391	1/1	0.09	-	45,45,45,45	0
57	MG	BQ	3004	1/1	0.17	-	42,42,42,42	0
57	MG	BA	3279	1/1	0.23	-	43,43,43,43	0
57	MG	DA	3503	1/1	0.14	-	52,52,52,52	0
57	MG	AA	3019	1/1	0.14	-	66,66,66,66	0
57	MG	AA	3056	1/1	0.19	-	61,61,61,61	0
57	MG	BA	3414	1/1	0.16	-	41,41,41,41	0
57	MG	DA	3560	1/1	0.06	-	40,40,40,40	0
57	MG	BA	3214	1/1	0.12	-	41,41,41,41	0
57	MG	DA	3181	1/1	0.09	-	50,50,50,50	0
57	MG	DA	3422	1/1	0.09	-	46,46,46,46	0
57	MG	AA	3202	1/1	0.17	-	57,57,57,57	0
57	MG	BA	3582	1/1	0.22	-	74,74,74,74	0
57	MG	DA	3532	1/1	0.20	-	69,69,69,69	0
57	MG	CA	3114	1/1	0.10	-	57,57,57,57	0
57	MG	DA	3556	1/1	0.18	-	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3147	1/1	0.09	-	56,56,56,56	0
57	MG	BA	3089	1/1	0.15	-	19,19,19,19	0
57	MG	AA	3032	1/1	0.23	-	67,67,67,67	0
57	MG	BA	3469	1/1	0.13	-	49,49,49,49	0
57	MG	DA	3621	1/1	0.07	-	44,44,44,44	0
57	MG	AE	203	1/1	0.18	-	63,63,63,63	0
57	MG	AA	3086	1/1	0.11	-	57,57,57,57	0
57	MG	BA	3110	1/1	0.14	-	41,41,41,41	0
57	MG	BA	3054	1/1	0.23	-	36,36,36,36	0
57	MG	BA	3399	1/1	0.20	-	45,45,45,45	0
57	MG	BA	3249	1/1	0.32	-	49,49,49,49	0
57	MG	DA	3194	1/1	0.22	-	56,56,56,56	0
57	MG	CA	3169	1/1	0.14	-	51,51,51,51	0
57	MG	BA	3702	1/1	0.18	-	51,51,51,51	0
57	MG	BA	3107	1/1	0.14	-	53,53,53,53	0
57	MG	AA	3042	1/1	0.06	-	57,57,57,57	0
57	MG	BA	3562	1/1	0.13	-	37,37,37,37	0
57	MG	AX	3006	1/1	0.09	-	65,65,65,65	0
57	MG	B0	102	1/1	0.14	-	48,48,48,48	0
57	MG	DA	3105	1/1	0.15	-	48,48,48,48	0
57	MG	DA	3022	1/1	0.17	-	51,51,51,51	0
57	MG	DA	3525	1/1	0.16	-	59,59,59,59	0
57	MG	CA	3095	1/1	0.10	-	64,64,64,64	0
57	MG	DA	3558	1/1	0.15	-	61,61,61,61	0
57	MG	AA	3010	1/1	0.09	-	52,52,52,52	0
57	MG	DA	3451	1/1	0.13	-	55,55,55,55	0
57	MG	DA	3122	1/1	0.10	-	49,49,49,49	0
57	MG	DA	3493	1/1	0.20	-	66,66,66,66	0
57	MG	BA	3348	1/1	0.18	-	36,36,36,36	0
57	MG	BA	3620	1/1	0.11	-	40,40,40,40	0
57	MG	DA	3333	1/1	0.13	-	41,41,41,41	0
57	MG	DA	3371	1/1	0.11	-	58,58,58,58	0
57	MG	CA	3160	1/1	0.17	-	62,62,62,62	0
57	MG	BA	3175	1/1	0.19	-	20,20,20,20	0
57	MG	CA	3048	1/1	0.33	-	67,67,67,67	0
57	MG	CA	3096	1/1	0.06	-	44,44,44,44	0
57	MG	CA	3170	1/1	0.12	-	58,58,58,58	0
57	MG	DB	3006	1/1	0.12	-	57,57,57,57	0
57	MG	BA	3682	1/1	0.18	-	53,53,53,53	0
57	MG	BA	3701	1/1	0.16	-	43,43,43,43	0
57	MG	AA	3167	1/1	0.15	-	57,57,57,57	0
59	ZN	B4	501	1/1	0.13	-	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3014	1/1	0.10	-	58,58,58,58	0
57	MG	BA	3571	1/1	0.18	-	58,58,58,58	0
57	MG	AA	3212	1/1	0.12	-	42,42,42,42	0
57	MG	BA	3078	1/1	0.16	-	51,51,51,51	0
57	MG	BA	3510	1/1	0.14	-	46,46,46,46	0
57	MG	BA	3631	1/1	0.23	-	42,42,42,42	0
57	MG	AA	3126	1/1	0.06	-	49,49,49,49	0
57	MG	DA	3437	1/1	0.14	-	52,52,52,52	0
57	MG	DA	3050	1/1	0.13	-	59,59,59,59	0
57	MG	BD	308	1/1	0.36	-	46,46,46,46	0
57	MG	DA	3229	1/1	0.15	-	50,50,50,50	0
57	MG	BA	3430	1/1	0.15	-	37,37,37,37	0
57	MG	CA	3139	1/1	0.13	-	62,62,62,62	0
57	MG	DA	3310	1/1	0.15	-	38,38,38,38	0
57	MG	DA	3380	1/1	0.10	-	55,55,55,55	0
57	MG	AA	3060	1/1	0.22	-	46,46,46,46	0
57	MG	DA	3275	1/1	0.17	-	42,42,42,42	0
57	MG	D3	3001	1/1	0.30	-	57,57,57,57	0
57	MG	DA	3487	1/1	0.25	-	62,62,62,62	0
57	MG	BA	3111	1/1	0.13	-	54,54,54,54	0
57	MG	AA	3178	1/1	0.15	-	59,59,59,59	0
57	MG	BA	3739	1/1	0.23	-	40,40,40,40	0
57	MG	DA	3145	1/1	0.24	-	43,43,43,43	0
57	MG	CA	3157	1/1	0.11	-	58,58,58,58	0
57	MG	DA	3211	1/1	0.09	-	48,48,48,48	0
57	MG	CA	3035	1/1	0.10	-	59,59,59,59	0
57	MG	DA	3364	1/1	0.17	-	40,40,40,40	0
57	MG	DA	3379	1/1	0.10	-	63,63,63,63	0
57	MG	BA	3756	1/1	0.17	-	48,48,48,48	0
57	MG	BP	202	1/1	0.22	-	36,36,36,36	0
57	MG	DA	3529	1/1	0.09	-	38,38,38,38	0
57	MG	BA	3352	1/1	0.23	-	53,53,53,53	0
57	MG	BA	3068	1/1	0.13	-	43,43,43,43	0
57	MG	DA	3288	1/1	0.15	-	52,52,52,52	0
57	MG	BA	3124	1/1	0.18	-	19,19,19,19	0
57	MG	BA	3075	1/1	0.19	-	45,45,45,45	0
57	MG	DA	3591	1/1	0.12	-	55,55,55,55	0
57	MG	BB	208	1/1	0.12	-	45,45,45,45	0
57	MG	AA	3193	1/1	0.09	-	72,72,72,72	0
57	MG	DA	3179	1/1	0.09	-	52,52,52,52	0
57	MG	AA	3050	1/1	0.19	-	33,33,33,33	0
57	MG	BA	3596	1/1	0.13	-	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3513	1/1	0.10	-	59,59,59,59	0
57	MG	BA	3247	1/1	0.31	-	25,25,25,25	0
57	MG	BA	3293	1/1	0.22	-	50,50,50,50	0
57	MG	AX	3003	1/1	0.10	-	71,71,71,71	0
57	MG	DA	3399	1/1	0.14	-	59,59,59,59	0
57	MG	BA	3643	1/1	0.17	-	46,46,46,46	0
57	MG	BQ	3005	1/1	0.11	-	49,49,49,49	0
57	MG	AA	3002	1/1	0.13	-	71,71,71,71	0
57	MG	DA	3387	1/1	0.08	-	42,42,42,42	0
57	MG	BA	3440	1/1	0.08	-	42,42,42,42	0
57	MG	DA	3015	1/1	0.32	-	52,52,52,52	0
57	MG	BA	3639	1/1	0.36	-	48,48,48,48	0
57	MG	DA	3481	1/1	0.60	-	55,55,55,55	0
57	MG	DA	3428	1/1	0.17	-	37,37,37,37	0
57	MG	BP	204	1/1	0.09	-	46,46,46,46	0
57	MG	CA	3074	1/1	0.23	-	64,64,64,64	0
57	MG	DA	3368	1/1	0.23	-	50,50,50,50	0
57	MG	DA	3668	1/1	0.22	-	60,60,60,60	0
57	MG	DA	3148	1/1	0.14	-	54,54,54,54	0
57	MG	AE	201	1/1	0.16	-	59,59,59,59	0
57	MG	BA	3723	1/1	0.08	-	47,47,47,47	0
57	MG	AM	201	1/1	0.12	-	51,51,51,51	0
57	MG	BA	3757	1/1	0.19	-	76,76,76,76	0
57	MG	CA	3088	1/1	0.17	-	74,74,74,74	0
57	MG	DA	3219	1/1	0.15	-	53,53,53,53	0
57	MG	BA	3253	1/1	0.26	-	55,55,55,55	0
57	MG	DA	3670	1/1	0.29	-	60,60,60,60	0
57	MG	DA	3495	1/1	0.10	-	47,47,47,47	0
57	MG	BA	3102	1/1	0.11	-	44,44,44,44	0
57	MG	DA	3189	1/1	0.21	-	41,41,41,41	0
57	MG	DW	3002	1/1	0.20	-	45,45,45,45	0
57	MG	BA	3572	1/1	0.19	-	61,61,61,61	0
57	MG	BA	3463	1/1	0.24	-	48,48,48,48	0
57	MG	BA	3194	1/1	0.15	-	47,47,47,47	0
57	MG	BA	3278	1/1	0.14	-	34,34,34,34	0
57	MG	BA	3776	1/1	0.16	-	43,43,43,43	0
57	MG	BD	307	1/1	0.30	-	40,40,40,40	0
57	MG	BA	3301	1/1	0.11	-	60,60,60,60	0
57	MG	DA	3057	1/1	0.16	-	42,42,42,42	0
57	MG	DA	3465	1/1	0.13	-	46,46,46,46	0
57	MG	DA	3008	1/1	0.08	-	36,36,36,36	0
57	MG	BA	3052	1/1	0.15	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3037	1/1	0.18	-	34,34,34,34	0
57	MG	DA	3492	1/1	0.10	-	55,55,55,55	0
57	MG	AA	3005	1/1	0.14	-	62,62,62,62	0
57	MG	BA	3810	1/1	0.26	-	41,41,41,41	0
57	MG	BA	3492	1/1	0.14	-	46,46,46,46	0
57	MG	BF	307	1/1	0.34	-	37,37,37,37	0
57	MG	AA	3007	1/1	0.15	-	57,57,57,57	0
57	MG	CA	3113	1/1	0.08	-	67,67,67,67	0
57	MG	BA	3308	1/1	0.15	-	43,43,43,43	0
57	MG	DA	3381	1/1	0.11	-	56,56,56,56	0
57	MG	BA	3456	1/1	0.19	-	49,49,49,49	0
57	MG	CA	3032	1/1	0.18	-	62,62,62,62	0
57	MG	DA	3095	1/1	0.25	-	58,58,58,58	0
57	MG	BA	3092	1/1	0.14	-	37,37,37,37	0
57	MG	BA	3744	1/1	0.10	-	39,39,39,39	0
57	MG	BA	3354	1/1	0.08	-	48,48,48,48	0
57	MG	DA	3673	1/1	0.13	-	69,69,69,69	0
57	MG	BA	3473	1/1	0.24	-	56,56,56,56	0
57	MG	DA	3583	1/1	0.16	-	51,51,51,51	0
57	MG	BA	3045	1/1	0.23	-	36,36,36,36	0
60	K	CX	3001	1/1	0.33	-	82,82,82,82	0
57	MG	BA	3714	1/1	0.21	-	57,57,57,57	0
57	MG	BA	3584	1/1	0.24	-	63,63,63,63	0
57	MG	BA	3448	1/1	0.23	-	32,32,32,32	0
57	MG	CX	3004	1/1	0.15	-	63,63,63,63	0
57	MG	BE	302	1/1	0.29	-	39,39,39,39	0
57	MG	DA	3636	1/1	0.15	-	63,63,63,63	0
57	MG	DA	3217	1/1	0.11	-	38,38,38,38	0
57	MG	DA	3378	1/1	0.12	-	57,57,57,57	0
57	MG	DA	3098	1/1	0.16	-	53,53,53,53	0
57	MG	BA	3652	1/1	0.10	-	67,67,67,67	0
57	MG	AA	3038	1/1	0.25	-	68,68,68,68	0
57	MG	DW	3004	1/1	0.28	-	52,52,52,52	0
57	MG	BA	3807	1/1	0.13	-	47,47,47,47	0
57	MG	BA	3298	1/1	0.11	-	51,51,51,51	0
57	MG	DA	3117	1/1	0.52	-	52,52,52,52	0
57	MG	AA	3074	1/1	0.13	-	50,50,50,50	0
57	MG	DF	3002	1/1	0.08	-	48,48,48,48	0
57	MG	DA	3412	1/1	0.14	-	50,50,50,50	0
57	MG	BA	3031	1/1	0.14	-	52,52,52,52	0
57	MG	CA	3073	1/1	0.15	-	57,57,57,57	0
57	MG	DA	3324	1/1	0.11	-	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3197	1/1	0.29	-	70,70,70,70	0
57	MG	BA	3370	1/1	0.21	-	39,39,39,39	0
57	MG	BA	3579	1/1	0.10	-	49,49,49,49	0
57	MG	BA	3606	1/1	0.13	-	61,61,61,61	0
57	MG	BA	3243	1/1	0.11	-	53,53,53,53	0
57	MG	DA	3597	1/1	0.05	-	51,51,51,51	0
57	MG	DA	3592	1/1	0.10	-	51,51,51,51	0
57	MG	AA	3053	1/1	0.15	-	61,61,61,61	0
57	MG	BU	201	1/1	0.24	-	43,43,43,43	0
57	MG	BA	3561	1/1	0.11	-	45,45,45,45	0
57	MG	DA	3519	1/1	0.09	-	63,63,63,63	0
57	MG	AA	3067	1/1	0.24	-	57,57,57,57	0
57	MG	CA	3163	1/1	0.08	-	63,63,63,63	0
57	MG	DA	3365	1/1	0.07	-	36,36,36,36	0
57	MG	CA	3033	1/1	0.17	-	71,71,71,71	0
57	MG	CA	3146	1/1	0.17	-	66,66,66,66	0
57	MG	CA	3006	1/1	0.08	-	64,64,64,64	0
57	MG	DA	3165	1/1	0.14	-	57,57,57,57	0
57	MG	DA	3521	1/1	0.13	-	58,58,58,58	0
57	MG	B0	103	1/1	0.12	-	53,53,53,53	0
57	MG	BA	3190	1/1	0.15	-	52,52,52,52	0
57	MG	DA	3628	1/1	0.18	-	76,76,76,76	0
57	MG	AA	3008	1/1	0.15	-	73,73,73,73	0
57	MG	DA	3092	1/1	0.13	-	45,45,45,45	0
57	MG	DA	3414	1/1	0.13	-	43,43,43,43	0
57	MG	CA	3097	1/1	0.11	-	69,69,69,69	0
57	MG	BA	3664	1/1	0.13	-	55,55,55,55	0
57	MG	DA	3173	1/1	0.27	-	53,53,53,53	0
57	MG	CA	3057	1/1	0.17	-	76,76,76,76	0
57	MG	DA	3337	1/1	0.15	-	41,41,41,41	0
57	MG	DA	3283	1/1	0.09	-	51,51,51,51	0
57	MG	BA	3112	1/1	0.22	-	30,30,30,30	0
57	MG	BA	3261	1/1	0.12	-	61,61,61,61	0
57	MG	BA	3185	1/1	0.13	-	57,57,57,57	0
57	MG	BA	3666	1/1	0.18	-	50,50,50,50	0
57	MG	BA	3806	1/1	0.12	-	30,30,30,30	0
57	MG	DA	3235	1/1	0.12	-	45,45,45,45	0
57	MG	BA	3603	1/1	0.11	-	53,53,53,53	0
57	MG	BA	3509	1/1	0.20	-	31,31,31,31	0
57	MG	AA	3143	1/1	0.09	-	60,60,60,60	0
57	MG	DA	3190	1/1	0.22	-	54,54,54,54	0
57	MG	DA	3237	1/1	0.10	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3482	1/1	0.12	-	51,51,51,51	0
57	MG	BA	3178	1/1	0.13	-	46,46,46,46	0
57	MG	DA	3053	1/1	0.08	-	47,47,47,47	0
57	MG	DA	3574	1/1	0.11	-	53,53,53,53	0
57	MG	B7	102	1/1	0.18	-	47,47,47,47	0
57	MG	DD	305	1/1	0.13	-	36,36,36,36	0
57	MG	CA	3168	1/1	0.09	-	56,56,56,56	0
57	MG	DA	3490	1/1	0.10	-	47,47,47,47	0
57	MG	BA	3793	1/1	0.21	-	40,40,40,40	0
57	MG	DA	3139	1/1	0.13	-	53,53,53,53	0
57	MG	DA	3524	1/1	0.12	-	61,61,61,61	0
57	MG	BA	3743	1/1	0.19	-	44,44,44,44	0
57	MG	DA	3071	1/1	0.15	-	59,59,59,59	0
57	MG	CA	3004	1/1	0.13	-	66,66,66,66	0
57	MG	DA	3604	1/1	0.26	-	59,59,59,59	0
57	MG	BA	3614	1/1	0.09	-	63,63,63,63	0
57	MG	CE	3001	1/1	0.09	-	79,79,79,79	0
57	MG	DA	3002	1/1	0.07	-	48,48,48,48	0
57	MG	DA	3606	1/1	0.13	-	71,71,71,71	0
57	MG	DA	3298	1/1	0.12	-	59,59,59,59	0
57	MG	BA	3273	1/1	0.17	-	54,54,54,54	0
57	MG	DA	3561	1/1	0.07	-	57,57,57,57	0
57	MG	BA	3174	1/1	0.20	-	37,37,37,37	0
57	MG	BA	3033	1/1	0.30	-	53,53,53,53	0
57	MG	DA	3557	1/1	0.17	-	51,51,51,51	0
57	MG	AA	3117	1/1	0.12	-	79,79,79,79	0
57	MG	DQ	3003	1/1	0.18	-	51,51,51,51	0
57	MG	AA	3192	1/1	0.11	-	71,71,71,71	0
57	MG	DA	3032	1/1	0.12	-	48,48,48,48	0
57	MG	DF	3003	1/1	0.36	-	43,43,43,43	0
57	MG	DA	3396	1/1	0.10	-	40,40,40,40	0
57	MG	DA	3251	1/1	0.14	-	62,62,62,62	0
57	MG	BA	3570	1/1	0.14	-	42,42,42,42	0
57	MG	DA	3227	1/1	0.17	-	41,41,41,41	0
57	MG	BA	3436	1/1	0.15	-	40,40,40,40	0
57	MG	BA	3264	1/1	0.14	-	58,58,58,58	0
57	MG	DA	3528	1/1	0.11	-	62,62,62,62	0
57	MG	BA	3335	1/1	0.18	-	52,52,52,52	0
57	MG	DE	304	1/1	0.14	-	43,43,43,43	0
57	MG	DA	3508	1/1	0.33	-	44,44,44,44	0
57	MG	DA	3637	1/1	0.85	-	58,58,58,58	0
57	MG	CA	3102	1/1	0.12	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3322	1/1	0.15	-	52,52,52,52	0
57	MG	B7	105	1/1	0.13	-	56,56,56,56	0
57	MG	CA	3062	1/1	0.15	-	64,64,64,64	0
57	MG	BA	3309	1/1	0.14	-	41,41,41,41	0
57	MG	BA	3224	1/1	0.22	-	65,65,65,65	0
57	MG	BA	3238	1/1	0.14	-	62,62,62,62	0
57	MG	BA	3014	1/1	0.64	-	42,42,42,42	0
57	MG	AA	3134	1/1	0.44	-	66,66,66,66	0
57	MG	BA	3760	1/1	0.17	-	44,44,44,44	0
57	MG	CA	3128	1/1	0.09	-	65,65,65,65	0
57	MG	DA	3076	1/1	0.11	-	58,58,58,58	0
57	MG	BA	3351	1/1	0.15	-	30,30,30,30	0
57	MG	BA	3392	1/1	0.16	-	53,53,53,53	0
57	MG	BA	3202	1/1	0.17	-	60,60,60,60	0
57	MG	CA	3110	1/1	0.09	-	65,65,65,65	0
57	MG	DA	3479	1/1	0.19	-	43,43,43,43	0
57	MG	BA	3305	1/1	0.09	-	62,62,62,62	0
57	MG	BA	3564	1/1	0.15	-	44,44,44,44	0
57	MG	CA	3041	1/1	0.15	-	59,59,59,59	0
57	MG	AA	3021	1/1	0.13	-	63,63,63,63	0
57	MG	BA	3515	1/1	0.27	-	53,53,53,53	0
57	MG	CA	3023	1/1	0.12	-	44,44,44,44	0
57	MG	BF	301	1/1	0.13	-	35,35,35,35	0
57	MG	BA	3291	1/1	0.18	-	33,33,33,33	0
57	MG	BA	3792	1/1	0.15	-	54,54,54,54	0
57	MG	DA	3562	1/1	0.10	-	64,64,64,64	0
57	MG	CA	3001	1/1	0.15	-	75,75,75,75	0
57	MG	DA	3652	1/1	0.57	-	67,67,67,67	0
57	MG	AA	3054	1/1	0.14	-	53,53,53,53	0
57	MG	BA	3373	1/1	0.16	-	48,48,48,48	0
57	MG	CA	3091	1/1	0.10	-	55,55,55,55	0
57	MG	BA	3451	1/1	0.19	-	31,31,31,31	0
57	MG	BA	3192	1/1	0.19	-	46,46,46,46	0
57	MG	BA	3460	1/1	0.13	-	62,62,62,62	0
57	MG	AA	3105	1/1	0.22	-	69,69,69,69	0
57	MG	DA	3246	1/1	0.14	-	43,43,43,43	0
57	MG	DA	3359	1/1	0.12	-	47,47,47,47	0
57	MG	DE	303	1/1	0.13	-	54,54,54,54	0
57	MG	AA	3061	1/1	0.30	-	55,55,55,55	0
57	MG	DA	3616	1/1	0.11	-	71,71,71,71	0
57	MG	DA	3196	1/1	0.19	-	49,49,49,49	0
57	MG	DA	3299	1/1	0.18	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3214	1/1	0.18	-	59,59,59,59	0
57	MG	AA	3047	1/1	0.12	-	63,63,63,63	0
57	MG	AA	3012	1/1	0.17	-	46,46,46,46	0
57	MG	BA	3546	1/1	0.23	-	40,40,40,40	0
57	MG	BA	3804	1/1	0.50	-	53,53,53,53	0
57	MG	AA	3155	1/1	0.21	-	48,48,48,48	0
57	MG	CA	3115	1/1	0.12	-	63,63,63,63	0
57	MG	BA	3779	1/1	0.19	-	66,66,66,66	0
57	MG	AX	3007	1/1	0.18	-	67,67,67,67	0
57	MG	DA	3430	1/1	0.10	-	37,37,37,37	0
57	MG	BA	3367	1/1	0.16	-	29,29,29,29	0
57	MG	AA	3077	1/1	0.18	-	56,56,56,56	0
57	MG	BA	3073	1/1	0.15	-	61,61,61,61	0
57	MG	AA	3136	1/1	0.15	-	70,70,70,70	0
57	MG	DA	3073	1/1	0.10	-	42,42,42,42	0
57	MG	BA	3669	1/1	0.08	-	62,62,62,62	0
57	MG	AA	3079	1/1	0.12	-	68,68,68,68	0
57	MG	DA	3477	1/1	0.08	-	43,43,43,43	0
57	MG	DA	3334	1/1	0.12	-	52,52,52,52	0
57	MG	BA	3715	1/1	0.16	-	63,63,63,63	0
57	MG	BA	3342	1/1	0.10	-	46,46,46,46	0
57	MG	DA	3171	1/1	0.13	-	31,31,31,31	0
57	MG	DA	3132	1/1	0.21	-	52,52,52,52	0
57	MG	BA	3530	1/1	0.23	-	49,49,49,49	0
57	MG	BA	3477	1/1	0.15	-	61,61,61,61	0
57	MG	CA	3105	1/1	0.15	-	52,52,52,52	0
57	MG	BA	3565	1/1	0.18	-	40,40,40,40	0
57	MG	BA	3581	1/1	0.19	-	30,30,30,30	0
57	MG	AA	3108	1/1	0.25	-	67,67,67,67	0
57	MG	DA	3549	1/1	0.11	-	57,57,57,57	0
57	MG	DA	3125	1/1	0.20	-	70,70,70,70	0
57	MG	B1	101	1/1	0.59	-	51,51,51,51	0
57	MG	DA	3671	1/1	0.25	-	74,74,74,74	0
57	MG	BD	301	1/1	0.22	-	40,40,40,40	0
57	MG	BA	3623	1/1	0.28	-	55,55,55,55	0
57	MG	BA	3332	1/1	0.13	-	38,38,38,38	0
57	MG	DA	3100	1/1	0.13	-	43,43,43,43	0
57	MG	DA	3513	1/1	0.15	-	52,52,52,52	0
57	MG	DA	3124	1/1	0.08	-	57,57,57,57	0
57	MG	BA	3207	1/1	0.23	-	54,54,54,54	0
57	MG	BV	202	1/1	0.13	-	50,50,50,50	0
57	MG	BA	3201	1/1	0.10	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3788	1/1	0.14	-	51,51,51,51	0
57	MG	BA	3093	1/1	0.16	-	56,56,56,56	0
57	MG	CA	3060	1/1	0.08	-	65,65,65,65	0
57	MG	DA	3405	1/1	0.15	-	46,46,46,46	0
57	MG	BA	3081	1/1	0.15	-	46,46,46,46	0
57	MG	BA	3296	1/1	0.12	-	53,53,53,53	0
57	MG	BA	3364	1/1	0.21	-	60,60,60,60	0
57	MG	BA	3747	1/1	0.14	-	52,52,52,52	0
57	MG	BA	3324	1/1	0.20	-	45,45,45,45	0
57	MG	DD	308	1/1	0.52	-	48,48,48,48	0
57	MG	AA	3131	1/1	0.06	-	71,71,71,71	0
57	MG	BA	3002	1/1	0.12	-	50,50,50,50	0
57	MG	DA	3475	1/1	0.28	-	51,51,51,51	0
57	MG	BA	3372	1/1	0.19	-	28,28,28,28	0
57	MG	CA	3136	1/1	0.15	-	72,72,72,72	0
57	MG	AA	3111	1/1	0.21	-	79,79,79,79	0
57	MG	BA	3443	1/1	0.25	-	37,37,37,37	0
57	MG	DA	3468	1/1	0.54	-	66,66,66,66	0
57	MG	BA	3721	1/1	0.27	-	82,82,82,82	0
57	MG	BA	3563	1/1	0.16	-	36,36,36,36	0
57	MG	DA	3456	1/1	0.05	-	50,50,50,50	0
57	MG	DB	3001	1/1	0.19	-	64,64,64,64	0
57	MG	DA	3131	1/1	0.19	-	46,46,46,46	0
57	MG	BA	3497	1/1	0.17	-	28,28,28,28	0
57	MG	CA	3010	1/1	0.11	-	56,56,56,56	0
57	MG	DA	3253	1/1	0.05	-	45,45,45,45	0
57	MG	DA	3256	1/1	0.16	-	62,62,62,62	0
57	MG	DA	3240	1/1	0.12	-	48,48,48,48	0
57	MG	BA	3121	1/1	0.15	-	64,64,64,64	0
57	MG	AA	3073	1/1	0.12	-	56,56,56,56	0
57	MG	DA	3329	1/1	0.13	-	54,54,54,54	0
57	MG	DA	3005	1/1	0.07	-	57,57,57,57	0
57	MG	DA	3020	1/1	0.20	-	55,55,55,55	0
57	MG	DA	3231	1/1	0.13	-	62,62,62,62	0
57	MG	BA	3649	1/1	0.08	-	40,40,40,40	0
57	MG	AA	3022	1/1	0.11	-	71,71,71,71	0
57	MG	BA	3389	1/1	0.11	-	55,55,55,55	0
57	MG	BA	3395	1/1	0.14	-	38,38,38,38	0
57	MG	BA	3575	1/1	0.09	-	48,48,48,48	0
57	MG	AA	3173	1/1	0.14	-	54,54,54,54	0
57	MG	DD	303	1/1	0.52	-	87,87,87,87	0
57	MG	DA	3623	1/1	0.10	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3394	1/1	0.10	-	65,65,65,65	0
57	MG	DA	3234	1/1	0.12	-	63,63,63,63	0
57	MG	AA	3055	1/1	0.21	-	57,57,57,57	0
57	MG	BA	3532	1/1	0.21	-	52,52,52,52	0
57	MG	BA	3588	1/1	0.22	-	31,31,31,31	0
57	MG	BA	3644	1/1	0.11	-	35,35,35,35	0
57	MG	DA	3309	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3660	1/1	0.17	-	61,61,61,61	0
57	MG	AA	3009	1/1	0.11	-	57,57,57,57	0
57	MG	DA	3272	1/1	0.07	-	41,41,41,41	0
57	MG	AA	3046	1/1	0.17	-	55,55,55,55	0
57	MG	AX	3002	1/1	0.16	-	58,58,58,58	0
57	MG	DA	3016	1/1	0.42	-	50,50,50,50	0
57	MG	DB	3004	1/1	0.12	-	55,55,55,55	0
57	MG	BA	3783	1/1	0.12	-	56,56,56,56	0
57	MG	BA	3368	1/1	0.13	-	40,40,40,40	0
57	MG	DP	201	1/1	0.50	-	70,70,70,70	0
57	MG	DA	3142	1/1	0.26	-	47,47,47,47	0
57	MG	BA	3517	1/1	0.13	-	45,45,45,45	0
57	MG	AA	3133	1/1	0.11	-	56,56,56,56	0
57	MG	BA	3056	1/1	0.18	-	40,40,40,40	0
57	MG	BA	3381	1/1	0.12	-	46,46,46,46	0
57	MG	BA	3331	1/1	0.14	-	49,49,49,49	0
57	MG	AA	3185	1/1	0.13	-	82,82,82,82	0
57	MG	BN	3004	1/1	0.09	-	60,60,60,60	0
57	MG	DA	3343	1/1	0.18	-	50,50,50,50	0
57	MG	BA	3512	1/1	0.15	-	52,52,52,52	0
57	MG	BA	3790	1/1	0.15	-	34,34,34,34	0
57	MG	BA	3502	1/1	0.12	-	56,56,56,56	0
57	MG	BA	3130	1/1	0.08	-	44,44,44,44	0
57	MG	BA	3079	1/1	0.17	-	39,39,39,39	0
57	MG	BA	3558	1/1	0.14	-	32,32,32,32	0
57	MG	BB	220	1/1	0.12	-	57,57,57,57	0
57	MG	BU	205	1/1	0.34	-	47,47,47,47	0
57	MG	BA	3230	1/1	0.14	-	53,53,53,53	0
57	MG	BA	3687	1/1	0.22	-	22,22,22,22	0
57	MG	BA	3001	1/1	0.13	-	53,53,53,53	0
57	MG	AX	3013	1/1	0.12	-	58,58,58,58	0
57	MG	DQ	3002	1/1	0.27	-	51,51,51,51	0
57	MG	BA	3386	1/1	0.24	-	53,53,53,53	0
57	MG	AA	3018	1/1	0.25	-	56,56,56,56	0
57	MG	AA	3006	1/1	0.14	-	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3110	1/1	0.11	-	48,48,48,48	0
57	MG	BA	3632	1/1	0.08	-	50,50,50,50	0
57	MG	BA	3534	1/1	0.16	-	44,44,44,44	0
57	MG	BA	3307	1/1	0.16	-	29,29,29,29	0
57	MG	BA	3635	1/1	0.09	-	58,58,58,58	0
57	MG	BA	3206	1/1	0.15	-	49,49,49,49	0
57	MG	BA	3382	1/1	0.06	-	63,63,63,63	0
57	MG	BA	3493	1/1	0.12	-	58,58,58,58	0
57	MG	BA	3071	1/1	0.23	-	59,59,59,59	0
57	MG	DA	3119	1/1	0.18	-	39,39,39,39	0
57	MG	BE	307	1/1	0.35	-	62,62,62,62	0
57	MG	AA	3128	1/1	0.07	-	57,57,57,57	0
57	MG	BA	3199	1/1	0.12	-	46,46,46,46	0
57	MG	DA	3255	1/1	0.08	-	51,51,51,51	0
57	MG	CA	3039	1/1	0.09	-	68,68,68,68	0
57	MG	BA	3435	1/1	0.22	-	45,45,45,45	0
57	MG	DA	3103	1/1	0.10	-	58,58,58,58	0
57	MG	BA	3268	1/1	0.53	-	55,55,55,55	0
57	MG	DB	3010	1/1	0.14	-	57,57,57,57	0
57	MG	DA	3417	1/1	0.11	-	52,52,52,52	0
57	MG	DA	3268	1/1	0.21	-	51,51,51,51	0
57	MG	BA	3487	1/1	0.17	-	50,50,50,50	0
57	MG	BA	3741	1/1	0.60	-	64,64,64,64	0
57	MG	BA	3398	1/1	0.22	-	32,32,32,32	0
57	MG	CX	3003	1/1	0.20	-	54,54,54,54	0
57	MG	DA	3319	1/1	0.09	-	41,41,41,41	0
57	MG	AA	3045	1/1	0.09	-	58,58,58,58	0
57	MG	AA	3209	1/1	0.10	-	59,59,59,59	0
57	MG	BA	3299	1/1	0.14	-	25,25,25,25	0
57	MG	BB	206	1/1	0.24	-	47,47,47,47	0
57	MG	BA	3752	1/1	0.18	-	32,32,32,32	0
57	MG	DA	3548	1/1	0.07	-	60,60,60,60	0
57	MG	DA	3386	1/1	0.12	-	35,35,35,35	0
57	MG	BA	3390	1/1	0.23	-	38,38,38,38	0
57	MG	DA	3091	1/1	0.09	-	48,48,48,48	0
57	MG	BA	3126	1/1	0.13	-	54,54,54,54	0
57	MG	BA	3099	1/1	0.19	-	41,41,41,41	0
57	MG	DA	3081	1/1	0.22	-	55,55,55,55	0
57	MG	BF	308	1/1	0.28	-	46,46,46,46	0
57	MG	DA	3021	1/1	0.07	-	31,31,31,31	0
57	MG	BA	3428	1/1	0.20	-	46,46,46,46	0
57	MG	AA	3129	1/1	0.12	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3524	1/1	0.14	-	42,42,42,42	0
57	MG	AA	3165	1/1	0.21	-	54,54,54,54	0
57	MG	CA	3043	1/1	0.17	-	47,47,47,47	0
57	MG	BA	3592	1/1	0.21	-	28,28,28,28	0
57	MG	CA	3089	1/1	0.11	-	47,47,47,47	0
57	MG	BA	3567	1/1	0.14	-	34,34,34,34	0
57	MG	DA	3075	1/1	0.15	-	59,59,59,59	0
57	MG	DB	3008	1/1	0.17	-	67,67,67,67	0
57	MG	BA	3379	1/1	0.18	-	31,31,31,31	0
57	MG	BA	3227	1/1	0.21	-	57,57,57,57	0
57	MG	B6	101	1/1	0.28	-	48,48,48,48	0
57	MG	DA	3138	1/1	0.09	-	55,55,55,55	0
57	MG	DA	3565	1/1	0.07	-	59,59,59,59	0
57	MG	AA	3127	1/1	0.16	-	65,65,65,65	0
57	MG	BA	3697	1/1	0.11	-	61,61,61,61	0
57	MG	BA	3615	1/1	0.16	-	68,68,68,68	0
57	MG	BA	3494	1/1	0.09	-	49,49,49,49	0
57	MG	CA	3123	1/1	0.14	-	58,58,58,58	0
57	MG	AA	3078	1/1	0.26	-	66,66,66,66	0
57	MG	BA	3294	1/1	0.30	-	61,61,61,61	0
57	MG	AA	3140	1/1	0.14	-	53,53,53,53	0
57	MG	DA	3580	1/1	0.15	-	36,36,36,36	0
57	MG	DA	3316	1/1	0.13	-	45,45,45,45	0
57	MG	BA	3029	1/1	0.61	-	37,37,37,37	0
57	MG	BA	3252	1/1	0.32	-	60,60,60,60	0
57	MG	DA	3627	1/1	0.15	-	63,63,63,63	0
57	MG	BA	3145	1/1	0.08	-	44,44,44,44	0
57	MG	AN	503	1/1	0.15	-	54,54,54,54	0
57	MG	AA	3190	1/1	0.09	-	58,58,58,58	0
57	MG	AA	3160	1/1	0.17	-	59,59,59,59	0
57	MG	DQ	3001	1/1	0.14	-	47,47,47,47	0
57	MG	BA	3748	1/1	0.11	-	29,29,29,29	0
57	MG	AA	3090	1/1	0.24	-	66,66,66,66	0
57	MG	BA	3204	1/1	0.18	-	36,36,36,36	0
57	MG	BA	3263	1/1	0.47	-	49,49,49,49	0
57	MG	BA	3676	1/1	0.22	-	33,33,33,33	0
57	MG	BA	3467	1/1	0.23	-	50,50,50,50	0
57	MG	DA	3415	1/1	0.12	-	68,68,68,68	0
57	MG	BA	3772	1/1	0.14	-	33,33,33,33	0
57	MG	BW	203	1/1	0.15	-	44,44,44,44	0
57	MG	AA	3199	1/1	0.19	-	73,73,73,73	0
57	MG	BA	3787	1/1	0.29	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3211	1/1	0.12	-	47,47,47,47	0
57	MG	AA	3098	1/1	0.23	-	55,55,55,55	0
57	MG	CA	3121	1/1	0.07	-	63,63,63,63	0
57	MG	BA	3397	1/1	0.16	-	30,30,30,30	0
57	MG	BA	3531	1/1	0.21	-	26,26,26,26	0
57	MG	BA	3344	1/1	0.19	-	66,66,66,66	0
57	MG	D8	5001	1/1	0.21	-	66,66,66,66	0
57	MG	DA	3059	1/1	0.28	-	43,43,43,43	0
57	MG	BA	3439	1/1	0.10	-	33,33,33,33	0
57	MG	BA	3128	1/1	0.22	-	69,69,69,69	0
57	MG	DA	3596	1/1	0.09	-	56,56,56,56	0
57	MG	AA	3003	1/1	0.14	-	72,72,72,72	0
57	MG	DA	3416	1/1	0.12	-	50,50,50,50	0
57	MG	BB	210	1/1	0.10	-	61,61,61,61	0
57	MG	AA	3030	1/1	0.14	-	60,60,60,60	0
57	MG	DA	3607	1/1	0.14	-	65,65,65,65	0
57	MG	DA	3640	1/1	0.25	-	43,43,43,43	0
57	MG	BA	3116	1/1	0.30	-	50,50,50,50	0
57	MG	DA	3345	1/1	0.08	-	44,44,44,44	0
57	MG	DA	3355	1/1	0.09	-	58,58,58,58	0
57	MG	CA	3076	1/1	0.13	-	57,57,57,57	0
57	MG	DA	3638	1/1	0.10	-	51,51,51,51	0
57	MG	BE	308	1/1	0.14	-	40,40,40,40	0
57	MG	BA	3218	1/1	0.16	-	47,47,47,47	0
57	MG	BA	3766	1/1	0.12	-	28,28,28,28	0
57	MG	DX	101	1/1	0.11	-	51,51,51,51	0
57	MG	DA	3341	1/1	0.14	-	51,51,51,51	0
57	MG	DA	3307	1/1	0.10	-	42,42,42,42	0
57	MG	BA	3137	1/1	0.23	-	39,39,39,39	0
57	MG	DA	3344	1/1	0.13	-	31,31,31,31	0
57	MG	CA	3134	1/1	0.12	-	69,69,69,69	0
57	MG	AA	3070	1/1	0.13	-	52,52,52,52	0
57	MG	DA	3610	1/1	0.34	-	64,64,64,64	0
57	MG	CA	3119	1/1	0.09	-	64,64,64,64	0
57	MG	DA	3204	1/1	0.19	-	46,46,46,46	0
57	MG	DA	3390	1/1	0.12	-	43,43,43,43	0
57	MG	BA	3255	1/1	0.21	-	47,47,47,47	0
57	MG	AA	3139	1/1	0.15	-	59,59,59,59	0
57	MG	BA	3362	1/1	0.19	-	41,41,41,41	0
57	MG	BA	3404	1/1	0.18	-	59,59,59,59	0
57	MG	BA	3008	1/1	0.12	-	47,47,47,47	0
57	MG	AA	3183	1/1	0.14	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3120	1/1	0.07	-	49,49,49,49	0
57	MG	BA	3047	1/1	0.09	-	60,60,60,60	0
57	MG	BB	212	1/1	0.11	-	55,55,55,55	0
57	MG	CA	3052	1/1	0.17	-	72,72,72,72	0
57	MG	BA	3046	1/1	0.23	-	41,41,41,41	0
57	MG	BA	3396	1/1	0.12	-	50,50,50,50	0
57	MG	BB	203	1/1	0.25	-	43,43,43,43	0
57	MG	DA	3086	1/1	0.16	-	43,43,43,43	0
57	MG	BA	3711	1/1	0.15	-	54,54,54,54	0
57	MG	CA	3103	1/1	0.12	-	46,46,46,46	0
57	MG	BE	306	1/1	0.16	-	26,26,26,26	0
57	MG	DA	3084	1/1	0.08	-	39,39,39,39	0
57	MG	BA	3619	1/1	0.25	-	58,58,58,58	0
57	MG	AA	3097	1/1	0.34	-	56,56,56,56	0
57	MG	CA	3152	1/1	0.18	-	76,76,76,76	0
57	MG	CA	3034	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3195	1/1	0.08	-	43,43,43,43	0
57	MG	BA	3574	1/1	0.18	-	66,66,66,66	0
57	MG	AA	3206	1/1	0.17	-	64,64,64,64	0
57	MG	BA	3657	1/1	0.27	-	47,47,47,47	0
57	MG	BA	3119	1/1	0.13	-	45,45,45,45	0
57	MG	BA	3276	1/1	0.31	-	54,54,54,54	0
57	MG	BA	3241	1/1	0.11	-	36,36,36,36	0
57	MG	BA	3388	1/1	0.16	-	48,48,48,48	0
57	MG	CA	3145	1/1	0.12	-	66,66,66,66	0
57	MG	CA	3083	1/1	0.11	-	79,79,79,79	0
57	MG	BA	3188	1/1	0.25	-	49,49,49,49	0
57	MG	BA	3520	1/1	0.18	-	61,61,61,61	0
57	MG	DA	3460	1/1	0.10	-	41,41,41,41	0
57	MG	BA	3345	1/1	0.11	-	38,38,38,38	0
57	MG	BA	3069	1/1	0.20	-	22,22,22,22	0
57	MG	BA	3475	1/1	0.15	-	42,42,42,42	0
57	MG	DA	3287	1/1	0.07	-	41,41,41,41	0
57	MG	BA	3504	1/1	0.12	-	56,56,56,56	0
57	MG	BA	3144	1/1	0.14	-	41,41,41,41	0
57	MG	DA	3013	1/1	0.07	-	40,40,40,40	0
57	MG	D0	101	1/1	0.11	-	71,71,71,71	0
57	MG	DA	3074	1/1	0.10	-	37,37,37,37	0
57	MG	BA	3755	1/1	0.13	-	55,55,55,55	0
57	MG	BA	3284	1/1	0.34	-	43,43,43,43	0
57	MG	DA	3622	1/1	0.13	-	61,61,61,61	0
57	MG	DD	301	1/1	0.14	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3499	1/1	0.11	-	58,58,58,58	0
57	MG	BA	3655	1/1	0.09	-	50,50,50,50	0
57	MG	BA	3707	1/1	0.28	-	44,44,44,44	0
57	MG	DA	3236	1/1	0.19	-	47,47,47,47	0
57	MG	DA	3533	1/1	0.10	-	43,43,43,43	0
57	MG	AA	3011	1/1	0.28	-	57,57,57,57	0
57	MG	AA	3138	1/1	0.18	-	71,71,71,71	0
57	MG	DA	3576	1/1	0.09	-	53,53,53,53	0
57	MG	CA	3071	1/1	0.13	-	68,68,68,68	0
57	MG	DA	3296	1/1	0.11	-	28,28,28,28	0
57	MG	CA	3012	1/1	0.15	-	60,60,60,60	0
57	MG	DA	3167	1/1	0.11	-	41,41,41,41	0
57	MG	BA	3805	1/1	0.12	-	44,44,44,44	0
57	MG	DA	3545	1/1	0.11	-	35,35,35,35	0
57	MG	DA	3290	1/1	0.16	-	59,59,59,59	0
57	MG	AY	3002	1/1	0.18	-	56,56,56,56	0
57	MG	AA	3141	1/1	0.24	-	61,61,61,61	0
57	MG	BV	205	1/1	0.12	-	38,38,38,38	0
57	MG	BA	3155	1/1	0.62	-	44,44,44,44	0
57	MG	BA	3259	1/1	0.22	-	25,25,25,25	0
57	MG	BA	3449	1/1	0.17	-	35,35,35,35	0
57	MG	BA	3292	1/1	0.11	-	48,48,48,48	0
57	MG	AA	3203	1/1	0.11	-	59,59,59,59	0
57	MG	BA	3086	1/1	0.15	-	22,22,22,22	0
57	MG	BA	3638	1/1	0.13	-	63,63,63,63	0
57	MG	CA	3059	1/1	0.17	-	72,72,72,72	0
57	MG	BA	3004	1/1	0.17	-	33,33,33,33	0
57	MG	DA	3331	1/1	0.16	-	37,37,37,37	0
57	MG	BA	3543	1/1	0.23	-	37,37,37,37	0
57	MG	BA	3438	1/1	0.15	-	60,60,60,60	0
57	MG	AA	3113	1/1	0.12	-	58,58,58,58	0
57	MG	AA	3026	1/1	0.13	-	70,70,70,70	0
57	MG	DA	3242	1/1	0.13	-	52,52,52,52	0
57	MG	DA	3085	1/1	0.10	-	53,53,53,53	0
57	MG	DO	5001	1/1	0.12	-	59,59,59,59	0
57	MG	BA	3135	1/1	0.17	-	43,43,43,43	0
57	MG	DA	3101	1/1	0.13	-	49,49,49,49	0
57	MG	DA	3373	1/1	0.10	-	44,44,44,44	0
57	MG	DA	3659	1/1	0.11	-	48,48,48,48	0
57	MG	DV	3003	1/1	0.09	-	65,65,65,65	0
57	MG	BA	3100	1/1	0.14	-	39,39,39,39	0
57	MG	BA	3586	1/1	0.06	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3800	1/1	0.18	-	38,38,38,38	0
57	MG	DA	3457	1/1	0.09	-	54,54,54,54	0
57	MG	CA	3013	1/1	0.12	-	69,69,69,69	0
57	MG	DA	3600	1/1	0.39	-	70,70,70,70	0
57	MG	DA	3400	1/1	0.12	-	54,54,54,54	0
57	MG	AW	3003	1/1	0.14	-	72,72,72,72	0
57	MG	BA	3541	1/1	0.18	-	38,38,38,38	0
57	MG	DA	3516	1/1	0.10	-	67,67,67,67	0
57	MG	BA	3105	1/1	0.11	-	37,37,37,37	0
57	MG	DA	3182	1/1	0.25	-	51,51,51,51	0
57	MG	DA	3154	1/1	0.12	-	48,48,48,48	0
57	MG	AA	3036	1/1	0.14	-	61,61,61,61	0
57	MG	CA	3066	1/1	0.08	-	66,66,66,66	0
57	MG	CA	3126	1/1	0.10	-	67,67,67,67	0
57	MG	BX	3002	1/1	0.30	-	46,46,46,46	0
57	MG	DA	3118	1/1	0.40	-	77,77,77,77	0
57	MG	BA	3027	1/1	0.09	-	26,26,26,26	0
57	MG	BA	3548	1/1	0.17	-	40,40,40,40	0
57	MG	BA	3306	1/1	0.14	-	37,37,37,37	0
57	MG	BA	3552	1/1	0.22	-	29,29,29,29	0
57	MG	BA	3271	1/1	0.14	-	58,58,58,58	0
57	MG	AA	3208	1/1	0.13	-	60,60,60,60	0
57	MG	DA	3106	1/1	0.13	-	52,52,52,52	0
57	MG	BA	3325	1/1	0.12	-	48,48,48,48	0
57	MG	AA	3025	1/1	0.09	-	62,62,62,62	0
57	MG	DA	3504	1/1	0.21	-	47,47,47,47	0
57	MG	BA	3700	1/1	0.14	-	61,61,61,61	0
57	MG	DA	3274	1/1	0.17	-	58,58,58,58	0
57	MG	AA	3069	1/1	0.45	-	68,68,68,68	0
57	MG	DA	3578	1/1	0.18	-	59,59,59,59	0
57	MG	BF	306	1/1	0.22	-	31,31,31,31	0
57	MG	DA	3149	1/1	0.07	-	56,56,56,56	0
57	MG	DA	3230	1/1	0.54	-	73,73,73,73	0
57	MG	DA	3656	1/1	0.11	-	58,58,58,58	0
57	MG	BA	3709	1/1	0.20	-	62,62,62,62	0
57	MG	AA	3109	1/1	0.08	-	62,62,62,62	0
57	MG	BA	3717	1/1	0.13	-	50,50,50,50	0
57	MG	BA	3365	1/1	0.13	-	62,62,62,62	0
57	MG	BA	3005	1/1	0.13	-	30,30,30,30	0
57	MG	BA	3010	1/1	0.14	-	39,39,39,39	0
57	MG	BA	3311	1/1	0.20	-	48,48,48,48	0
57	MG	BG	201	1/1	0.16	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3411	1/1	0.18	-	53,53,53,53	0
57	MG	BA	3215	1/1	0.28	-	36,36,36,36	0
57	MG	BA	3566	1/1	0.20	-	67,67,67,67	0
57	MG	DA	3056	1/1	0.08	-	51,51,51,51	0
57	MG	DA	3003	1/1	0.13	-	27,27,27,27	0
57	MG	CA	3120	1/1	0.18	-	64,64,64,64	0
57	MG	BA	3653	1/1	0.13	-	39,39,39,39	0
57	MG	DA	3170	1/1	0.14	-	53,53,53,53	0
57	MG	BA	3533	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3530	1/1	0.11	-	74,74,74,74	0
57	MG	CA	3138	1/1	0.20	-	80,80,80,80	0
57	MG	AA	3016	1/1	0.07	-	63,63,63,63	0
57	MG	BA	3006	1/1	0.35	-	48,48,48,48	0
57	MG	DA	3661	1/1	0.10	-	62,62,62,62	0
57	MG	BA	3481	1/1	0.18	-	41,41,41,41	0
57	MG	BA	3444	1/1	0.19	-	29,29,29,29	0
57	MG	DA	3366	1/1	0.14	-	42,42,42,42	0
57	MG	BA	3458	1/1	0.15	-	18,18,18,18	0
57	MG	AA	3014	1/1	0.16	-	32,32,32,32	0
57	MG	DA	3019	1/1	0.30	-	37,37,37,37	0
57	MG	BA	3726	1/1	0.14	-	63,63,63,63	0
57	MG	BA	3429	1/1	0.09	-	65,65,65,65	0
57	MG	BV	204	1/1	0.15	-	49,49,49,49	0
57	MG	BA	3724	1/1	0.19	-	62,62,62,62	0
57	MG	BA	3357	1/1	0.21	-	25,25,25,25	0
57	MG	DA	3542	1/1	0.14	-	24,24,24,24	0
57	MG	DA	3499	1/1	0.12	-	53,53,53,53	0
57	MG	DA	3136	1/1	0.09	-	52,52,52,52	0
57	MG	BA	3347	1/1	0.18	-	44,44,44,44	0
57	MG	DA	3502	1/1	0.09	-	55,55,55,55	0
57	MG	DA	3615	1/1	0.13	-	65,65,65,65	0
57	MG	DA	3077	1/1	0.19	-	61,61,61,61	0
57	MG	CA	3118	1/1	0.10	-	68,68,68,68	0
57	MG	DA	3350	1/1	0.11	-	51,51,51,51	0
57	MG	BA	3540	1/1	0.22	-	37,37,37,37	0
57	MG	DA	3241	1/1	0.11	-	45,45,45,45	0
57	MG	AA	3122	1/1	0.10	-	56,56,56,56	0
57	MG	BA	3498	1/1	0.17	-	36,36,36,36	0
57	MG	DA	3541	1/1	0.11	-	44,44,44,44	0
57	MG	DA	3014	1/1	0.16	-	46,46,46,46	0
57	MG	DA	3004	1/1	0.19	-	40,40,40,40	0
57	MG	DA	3587	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
57	MG	BA	3258	1/1	0.14	-	44,44,44,44	0
57	MG	DA	3176	1/1	0.16	-	41,41,41,41	0
57	MG	DA	3426	1/1	0.24	-	49,49,49,49	0
57	MG	DD	302	1/1	0.20	-	42,42,42,42	0
57	MG	BA	3577	1/1	0.15	-	51,51,51,51	0
57	MG	BA	3425	1/1	0.13	-	40,40,40,40	0
57	MG	DA	3601	1/1	0.08	-	44,44,44,44	0
57	MG	DA	3588	1/1	0.32	-	65,65,65,65	0
57	MG	DA	3474	1/1	0.09	-	51,51,51,51	0
57	MG	DA	3305	1/1	0.19	-	50,50,50,50	0
57	MG	AA	3210	1/1	0.25	-	59,59,59,59	0
57	MG	BA	3197	1/1	0.43	-	41,41,41,41	0
57	MG	BA	3483	1/1	0.12	-	28,28,28,28	0
57	MG	BA	3260	1/1	0.24	-	39,39,39,39	0
57	MG	AA	3041	1/1	0.17	-	46,46,46,46	0
57	MG	BA	3072	1/1	0.27	-	47,47,47,47	0
57	MG	DE	301	1/1	0.36	-	46,46,46,46	0
57	MG	DA	3669	1/1	0.22	-	55,55,55,55	0
57	MG	DA	3040	1/1	0.08	-	31,31,31,31	0
57	MG	AA	3020	1/1	0.13	-	76,76,76,76	0
57	MG	BA	3361	1/1	0.09	-	49,49,49,49	0
57	MG	AA	3102	1/1	0.21	-	59,59,59,59	0
57	MG	BA	3646	1/1	0.13	-	42,42,42,42	0
57	MG	DA	3478	1/1	0.23	-	59,59,59,59	0
57	MG	AA	3184	1/1	0.12	-	60,60,60,60	0
57	MG	DA	3523	1/1	0.08	-	59,59,59,59	0
57	MG	BA	3203	1/1	0.42	-	40,40,40,40	0
57	MG	DA	3449	1/1	0.08	-	54,54,54,54	0
57	MG	DA	3203	1/1	0.40	-	50,50,50,50	0
57	MG	DA	3374	1/1	0.14	-	56,56,56,56	0
57	MG	BA	3166	1/1	0.11	-	38,38,38,38	0
57	MG	CA	3104	1/1	0.10	-	68,68,68,68	0
57	MG	DB	3005	1/1	0.06	-	59,59,59,59	0
57	MG	BA	3471	1/1	0.21	-	53,53,53,53	0
57	MG	AA	3015	1/1	0.12	-	65,65,65,65	0
57	MG	BA	3242	1/1	0.18	-	55,55,55,55	0
57	MG	BA	3158	1/1	0.18	-	41,41,41,41	0
57	MG	AA	3146	1/1	0.12	-	66,66,66,66	0
57	MG	BA	3685	1/1	0.16	-	53,53,53,53	0
57	MG	AA	3085	1/1	0.13	-	48,48,48,48	0
57	MG	DA	3667	1/1	0.14	-	50,50,50,50	0
57	MG	DA	3547	1/1	0.11	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3778	1/1	0.09	-	48,48,48,48	0
57	MG	BA	3665	1/1	0.11	-	49,49,49,49	0
57	MG	AA	3091	1/1	0.18	-	60,60,60,60	0
57	MG	BA	3393	1/1	0.15	-	51,51,51,51	0
57	MG	BA	3280	1/1	0.10	-	37,37,37,37	0
57	MG	DA	3295	1/1	0.18	-	44,44,44,44	0
57	MG	BA	3151	1/1	0.25	-	52,52,52,52	0
57	MG	DA	3127	1/1	0.12	-	35,35,35,35	0
57	MG	DA	3594	1/1	0.31	-	54,54,54,54	0
57	MG	BA	3391	1/1	0.24	-	63,63,63,63	0
57	MG	CA	3167	1/1	0.10	-	60,60,60,60	0
57	MG	BA	3521	1/1	0.22	-	39,39,39,39	0
57	MG	BA	3431	1/1	0.15	-	59,59,59,59	0
57	MG	DA	3302	1/1	0.14	-	70,70,70,70	0
57	MG	BA	3063	1/1	0.09	-	59,59,59,59	0
57	MG	DA	3409	1/1	0.18	-	57,57,57,57	0
57	MG	DA	3664	1/1	0.36	-	48,48,48,48	0
57	MG	BA	3675	1/1	0.20	-	67,67,67,67	0
57	MG	DA	3011	1/1	0.08	-	48,48,48,48	0
57	MG	DA	3111	1/1	0.10	-	61,61,61,61	0
57	MG	DA	3491	1/1	0.12	-	51,51,51,51	0
57	MG	BA	3378	1/1	0.07	-	28,28,28,28	0
57	MG	BA	3698	1/1	0.23	-	31,31,31,31	0
57	MG	DA	3505	1/1	0.13	-	56,56,56,56	0
57	MG	BA	3338	1/1	0.11	-	40,40,40,40	0
57	MG	CA	3078	1/1	0.13	-	44,44,44,44	0
57	MG	CA	3042	1/1	0.07	-	59,59,59,59	0
57	MG	BA	3146	1/1	0.18	-	40,40,40,40	0
57	MG	DA	3330	1/1	0.17	-	45,45,45,45	0
57	MG	BA	3210	1/1	0.20	-	49,49,49,49	0
57	MG	DA	3480	1/1	0.06	-	40,40,40,40	0
57	MG	DA	3579	1/1	0.09	-	48,48,48,48	0
57	MG	BF	303	1/1	0.51	-	49,49,49,49	0
57	MG	AA	3001	1/1	0.19	-	61,61,61,61	0
57	MG	BA	3650	1/1	0.14	-	52,52,52,52	0
57	MG	BA	3239	1/1	0.23	-	48,48,48,48	0
57	MG	BA	3182	1/1	0.16	-	55,55,55,55	0
57	MG	AA	3154	1/1	0.10	-	69,69,69,69	0
57	MG	BE	305	1/1	0.20	-	43,43,43,43	0
57	MG	DA	3509	1/1	0.12	-	59,59,59,59	0
57	MG	BA	3127	1/1	0.17	-	57,57,57,57	0
57	MG	DA	3375	1/1	0.15	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3276	1/1	0.11	-	49,49,49,49	0
57	MG	CA	3055	1/1	0.08	-	69,69,69,69	0
57	MG	BA	3608	1/1	0.27	-	62,62,62,62	0
57	MG	BA	3058	1/1	0.09	-	49,49,49,49	0
57	MG	DA	3619	1/1	0.18	-	69,69,69,69	0
57	MG	AA	3187	1/1	0.21	-	62,62,62,62	0
57	MG	DA	3198	1/1	0.10	-	40,40,40,40	0
57	MG	AA	3186	1/1	0.07	-	42,42,42,42	0
57	MG	AA	3028	1/1	0.22	-	76,76,76,76	0
57	MG	BA	3048	1/1	0.08	-	47,47,47,47	0
57	MG	BA	3283	1/1	0.12	-	35,35,35,35	0
57	MG	BA	3789	1/1	0.14	-	12,12,12,12	0
57	MG	AX	3010	1/1	0.12	-	59,59,59,59	0
57	MG	AA	3063	1/1	0.07	-	35,35,35,35	0
57	MG	DA	3088	1/1	0.13	-	47,47,47,47	0
57	MG	DA	3376	1/1	0.23	-	61,61,61,61	0
57	MG	BA	3237	1/1	0.13	-	45,45,45,45	0
57	MG	CA	3109	1/1	0.17	-	67,67,67,67	0
57	MG	BA	3070	1/1	0.31	-	59,59,59,59	0
57	MG	BA	3138	1/1	0.37	-	42,42,42,42	0
57	MG	BA	3684	1/1	0.30	-	68,68,68,68	0
57	MG	B9	502	1/1	0.14	-	48,48,48,48	0
57	MG	CA	3131	1/1	0.06	-	55,55,55,55	0
57	MG	BA	3641	1/1	0.20	-	68,68,68,68	0
57	MG	BW	202	1/1	0.07	-	54,54,54,54	0
57	MG	BN	3005	1/1	0.14	-	36,36,36,36	0
57	MG	DA	3188	1/1	0.12	-	48,48,48,48	0
57	MG	DA	3216	1/1	0.14	-	56,56,56,56	0
57	MG	DA	3441	1/1	0.11	-	45,45,45,45	0
57	MG	BA	3733	1/1	0.10	-	58,58,58,58	0
57	MG	CA	3069	1/1	0.21	-	60,60,60,60	0
57	MG	CA	3040	1/1	0.10	-	51,51,51,51	0
57	MG	BA	3132	1/1	0.20	-	40,40,40,40	0
57	MG	DA	3352	1/1	0.17	-	63,63,63,63	0
57	MG	BA	3662	1/1	0.10	-	61,61,61,61	0
57	MG	AA	3048	1/1	0.13	-	57,57,57,57	0
57	MG	BA	3076	1/1	0.19	-	43,43,43,43	0
57	MG	DA	3445	1/1	0.08	-	32,32,32,32	0
57	MG	BA	3387	1/1	0.15	-	54,54,54,54	0
57	MG	DA	3633	1/1	0.25	-	58,58,58,58	0
57	MG	CA	3021	1/1	0.12	-	61,61,61,61	0
57	MG	BA	3730	1/1	0.20	-	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3445	1/1	0.14	-	63,63,63,63	0
57	MG	BP	201	1/1	0.27	-	41,41,41,41	0
57	MG	BA	3457	1/1	0.21	-	32,32,32,32	0
57	MG	DA	3025	1/1	0.13	-	54,54,54,54	0
57	MG	BB	217	1/1	0.16	-	29,29,29,29	0
57	MG	DA	3427	1/1	0.12	-	45,45,45,45	0
57	MG	AA	3017	1/1	0.26	-	71,71,71,71	0
57	MG	BF	309	1/1	0.19	-	53,53,53,53	0
57	MG	BA	3660	1/1	0.09	-	61,61,61,61	0
57	MG	DA	3294	1/1	0.11	-	43,43,43,43	0
57	MG	CA	3162	1/1	0.06	-	66,66,66,66	0
57	MG	DA	3634	1/1	0.22	-	60,60,60,60	0
57	MG	DA	3538	1/1	0.09	-	58,58,58,58	0
57	MG	CA	3082	1/1	0.18	-	79,79,79,79	0
57	MG	DA	3200	1/1	0.14	-	66,66,66,66	0
57	MG	BA	3802	1/1	0.76	-	54,54,54,54	0
57	MG	BA	3758	1/1	0.10	-	45,45,45,45	0
57	MG	BA	3262	1/1	0.13	-	41,41,41,41	0
57	MG	BA	3751	1/1	0.15	-	26,26,26,26	0
57	MG	BA	3485	1/1	0.07	-	42,42,42,42	0
57	MG	BE	301	1/1	0.14	-	35,35,35,35	0
57	MG	BA	3049	1/1	0.25	-	36,36,36,36	0
57	MG	BA	3559	1/1	0.08	-	47,47,47,47	0
57	MG	DA	3554	1/1	0.09	-	62,62,62,62	0
57	MG	DA	3497	1/1	0.21	-	55,55,55,55	0
57	MG	BA	3160	1/1	0.28	-	55,55,55,55	0
57	MG	AA	3144	1/1	0.15	-	46,46,46,46	0
57	MG	DY	502	1/1	0.11	-	50,50,50,50	0
57	MG	DA	3133	1/1	0.14	-	50,50,50,50	0
57	MG	BA	3129	1/1	0.22	-	58,58,58,58	0
57	MG	CA	3007	1/1	0.08	-	57,57,57,57	0
57	MG	CA	3047	1/1	0.16	-	53,53,53,53	0
57	MG	AA	3172	1/1	0.12	-	72,72,72,72	0
57	MG	AA	3153	1/1	0.15	-	74,74,74,74	0
57	MG	BV	201	1/1	0.37	-	33,33,33,33	0
57	MG	B8	101	1/1	0.17	-	44,44,44,44	0
57	MG	BA	3597	1/1	0.16	-	25,25,25,25	0
57	MG	DA	3455	1/1	0.11	-	47,47,47,47	0
57	MG	DA	3589	1/1	0.08	-	68,68,68,68	0
57	MG	CA	3005	1/1	0.10	-	62,62,62,62	0
57	MG	BA	3803	1/1	0.22	-	44,44,44,44	0
57	MG	DA	3037	1/1	0.15	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3647	1/1	0.06	-	56,56,56,56	0
57	MG	BA	3455	1/1	0.11	-	64,64,64,64	0
57	MG	B7	101	1/1	0.25	-	39,39,39,39	0
57	MG	BA	3607	1/1	0.19	-	38,38,38,38	0
57	MG	DA	3569	1/1	0.21	-	49,49,49,49	0

6.5 Other polymers

There are no such residues in this entry.