



Full wwPDB X-ray Structure Validation Report

Sep 10, 2014 – 10:54 PM EDT

PDB ID : 1VY4
Title : Crystal structure of the Thermus thermophilus 70S ribosome in the pre-attack state of peptide bond formation containing acylated tRNA-substrates in the A and P sites.
Authors : Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on : 2014-05-13
Resolution : 2.60 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>

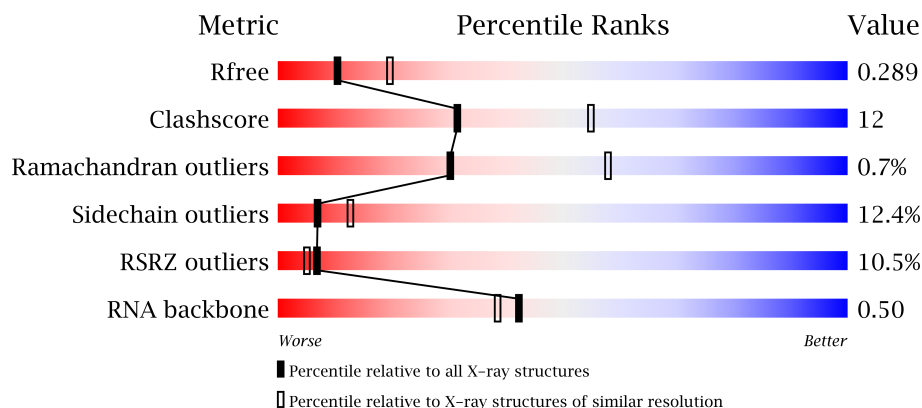
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.60 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	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)
RNA backbone	1838	1002 (3.12-2.08)

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 297127 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	1497	Total	C	N	O	P	0	0	0
			32185	14324	5968	10396	1497			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1552	976	302	273	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1544	970	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
			1678	1052	333	286	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
			812	514	146	149	3			
6	CF	100	Total	C	N	O	S	0	0	0
			820	518	147	152	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
			986	626	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			
			833	519	156	155	3	0	0	0
11	CK	114	Total	C	N	O	S			
			833	519	156	155	3	0	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	0
12	CL	122	Total	C	N	O	S			
			930	585	185	159	1	0	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			
			966	598	200	166	2	0	0	0
13	CM	122	Total	C	N	O	S			
			950	586	197	165	2	0	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	0
14	CN	60	Total	C	N	O	S			
			492	312	104	72	4	0	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	0
15	CO	88	Total	C	N	O	S			
			728	456	144	126	2	0	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	84	Total	C	N	O	S	0	0	0
			661	423	122	114	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
			731	449	156	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
			1599	722	287	515	73	2			
23	CW	72	Total	C	N	O	P	S	0	0	0
			1552	697	280	502	72	1			

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

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

- Molecule 25 is a RNA chain called 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
			2142	1352	426	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
			1073	688	188	196	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
			1139	709	231	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
			517	331	102	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	814	Total	Mg	0	0
			814	814		
57	AK	1	Total	Mg	0	0
			1	1		
57	DQ	3	Total	Mg	0	0
			3	3		
57	D3	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AB	1	Total 1	Mg 1	0	0
57	DF	5	Total 5	Mg 5	0	0
57	B8	2	Total 2	Mg 2	0	0
57	BE	6	Total 6	Mg 6	0	0
57	AW	2	Total 2	Mg 2	0	0
57	DU	1	Total 1	Mg 1	0	0
57	AN	2	Total 2	Mg 2	0	0
57	BP	2	Total 2	Mg 2	0	0
57	AX	15	Total 15	Mg 15	0	0
57	DN	1	Total 1	Mg 1	0	0
57	CA	169	Total 169	Mg 169	0	0
57	B5	3	Total 3	Mg 3	0	0
57	BB	23	Total 23	Mg 23	0	0
57	D8	1	Total 1	Mg 1	0	0
57	AE	1	Total 1	Mg 1	0	0
57	DB	13	Total 13	Mg 13	0	0
57	CF	1	Total 1	Mg 1	0	0
57	B9	1	Total 1	Mg 1	0	0
57	BF	11	Total 11	Mg 11	0	0
57	BX	1	Total 1	Mg 1	0	0
57	B2	1	Total 1	Mg 1	0	0

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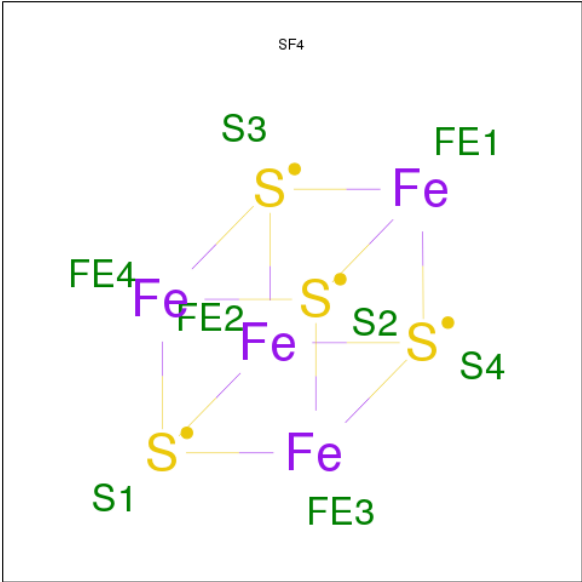
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AA	216	Total 216	Mg 216	0	0
57	BQ	2	Total 2	Mg 2	0	0
57	CX	2	Total 2	Mg 2	0	0
57	DV	1	Total 1	Mg 1	0	0
57	B6	2	Total 2	Mg 2	0	0
57	AM	2	Total 2	Mg 2	0	0
57	BU	4	Total 4	Mg 4	0	0
57	DR	1	Total 1	Mg 1	0	0
57	BN	3	Total 3	Mg 3	0	0
57	CT	1	Total 1	Mg 1	0	0
57	D0	1	Total 1	Mg 1	0	0
57	BG	2	Total 2	Mg 2	0	0
57	BY	1	Total 1	Mg 1	0	0
57	DE	7	Total 7	Mg 7	0	0
57	CJ	1	Total 1	Mg 1	0	0
57	BR	2	Total 2	Mg 2	0	0
57	DA	664	Total 664	Mg 664	0	0
57	AU	1	Total 1	Mg 1	0	0
57	DW	1	Total 1	Mg 1	0	0
57	B7	5	Total 5	Mg 5	0	0
57	AL	2	Total 2	Mg 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	BV	5	Total 5	Mg 5	0	0
57	DP	2	Total 2	Mg 2	0	0
57	DO	2	Total 2	Mg 2	0	0
57	BO	1	Total 1	Mg 1	0	0
57	BZ	2	Total 2	Mg 2	0	0
57	DY	1	Total 1	Mg 1	0	0
57	CW	1	Total 1	Mg 1	0	0
57	DG	1	Total 1	Mg 1	0	0
57	CD	1	Total 1	Mg 1	0	0
57	BD	10	Total 10	Mg 10	0	0
57	AT	1	Total 1	Mg 1	0	0
57	B0	2	Total 2	Mg 2	0	0
57	CE	2	Total 2	Mg 2	0	0
57	BW	4	Total 4	Mg 4	0	0
57	AY	3	Total 3	Mg 3	0	0
57	DD	4	Total 4	Mg 4	0	0
57	CK	1	Total 1	Mg 1	0	0
57	AF	1	Total 1	Mg 1	0	0
57	BH	1	Total 1	Mg 1	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

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AA	210	Total 210	O 210	0	0
61	AD	1	Total 1	O 1	0	0
61	AE	2	Total 2	O 2	0	0
61	AJ	1	Total 1	O 1	0	0
61	AL	2	Total 2	O 2	0	0
61	AM	2	Total 2	O 2	0	0
61	AV	2	Total 2	O 2	0	0
61	AW	4	Total 4	O 4	0	0
61	AX	4	Total 4	O 4	0	0
61	AY	1	Total 1	O 1	0	0
61	BA	1405	Total 1406	O 1406	0	1
61	BB	37	Total 37	O 37	0	0
61	BD	15	Total 15	O 15	0	0
61	BE	17	Total 17	O 17	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BF	11	Total 11	O 11	0	0
61	BG	3	Total 3	O 3	0	0
61	BH	1	Total 1	O 1	0	0
61	BI	1	Total 1	O 1	0	0
61	BN	1	Total 1	O 1	0	0
61	BO	2	Total 2	O 2	0	0
61	BP	13	Total 13	O 13	0	0
61	BQ	4	Total 4	O 4	0	0
61	BR	2	Total 2	O 2	0	0
61	BS	2	Total 2	O 2	0	0
61	BT	2	Total 2	O 2	0	0
61	BU	4	Total 4	O 4	0	0
61	BV	2	Total 2	O 2	0	0
61	BW	3	Total 3	O 3	0	0
61	BX	3	Total 3	O 3	0	0
61	BZ	1	Total 1	O 1	0	0
61	B0	6	Total 6	O 6	0	0
61	B1	2	Total 2	O 2	0	0
61	B3	2	Total 2	O 2	0	0
61	B5	4	Total 4	O 4	0	0
61	B6	2	Total 2	O 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	B7	3	Total 3	O 3	0	0
61	B8	13	Total 13	O 13	0	0
61	B9	1	Total 1	O 1	0	0
61	CA	156	Total 156	O 156	0	0
61	CE	2	Total 2	O 2	0	0
61	CH	1	Total 1	O 1	0	0
61	CJ	1	Total 1	O 1	0	0
61	CK	1	Total 1	O 1	0	0
61	CL	1	Total 1	O 1	0	0
61	CT	1	Total 1	O 1	0	0
61	CW	2	Total 2	O 2	0	0
61	CX	2	Total 2	O 2	0	0
61	CY	1	Total 1	O 1	0	0
61	DA	989	Total 989	O 989	0	0
61	DB	9	Total 9	O 9	0	0
61	DD	18	Total 18	O 18	0	0
61	DE	5	Total 5	O 5	0	0
61	DF	4	Total 4	O 4	0	0
61	DN	2	Total 2	O 2	0	0
61	DP	12	Total 12	O 12	0	0
61	DQ	1	Total 1	O 1	0	0

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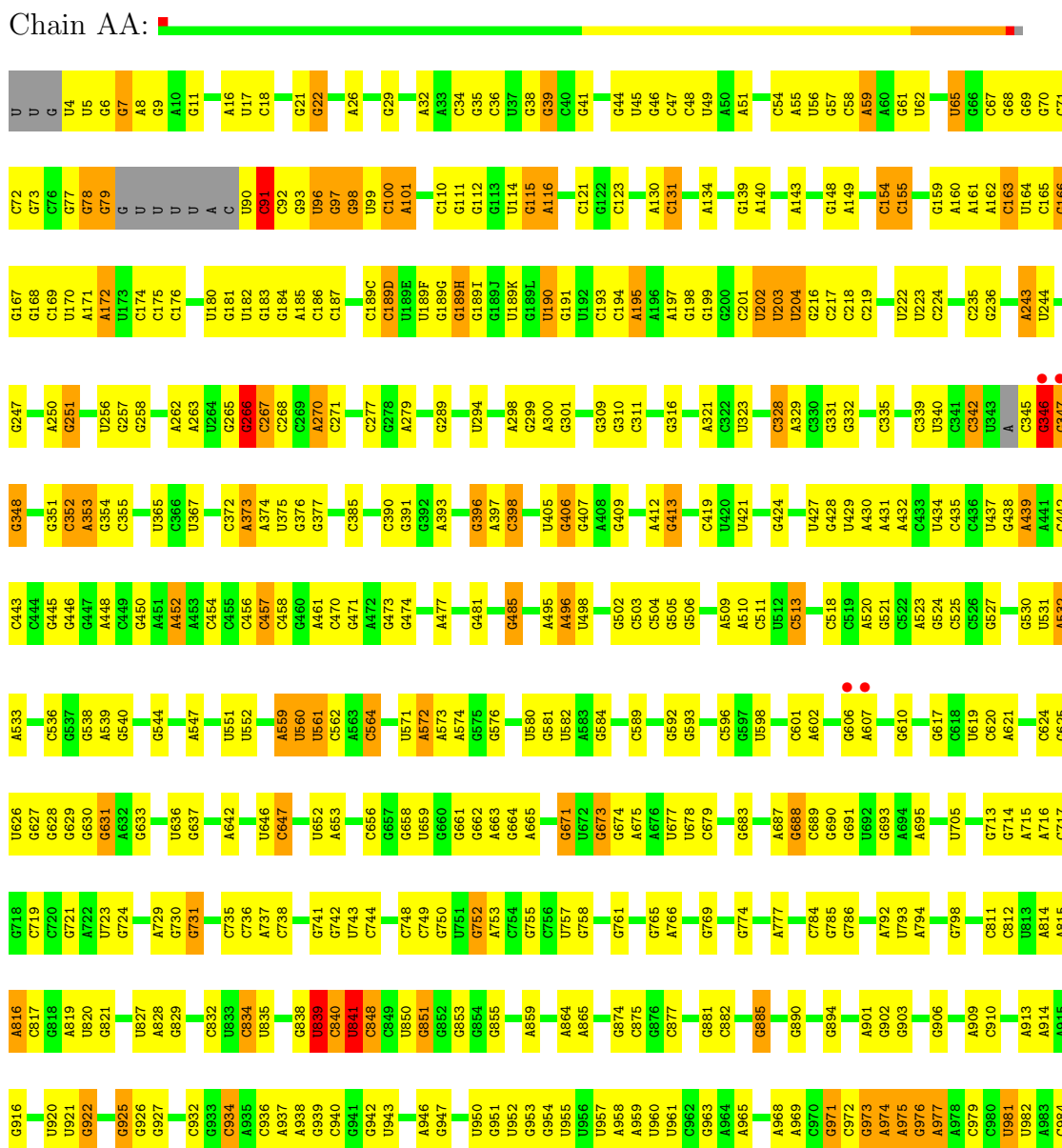
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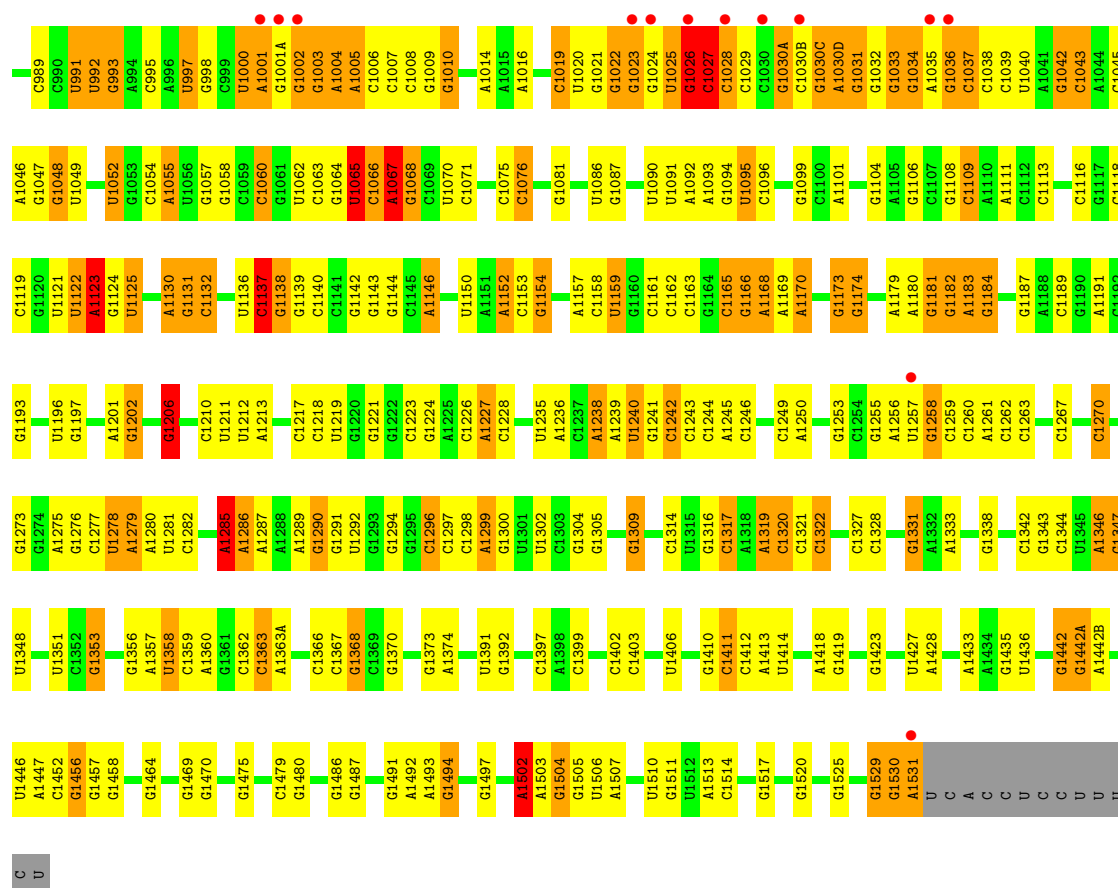
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	DT	4	Total 4	O 4	0	0
61	DU	1	Total 1	O 1	0	0
61	DV	1	Total 1	O 1	0	0
61	DW	1	Total 1	O 1	0	0
61	DX	2	Total 2	O 2	0	0
61	DY	1	Total 1	O 1	0	0
61	D0	4	Total 4	O 4	0	0
61	D1	1	Total 1	O 1	0	0
61	D3	2	Total 2	O 2	0	0
61	D5	1	Total 1	O 1	0	0
61	D6	1	Total 1	O 1	0	0
61	D8	3	Total 3	O 3	0	0

3 Residue-property plots

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

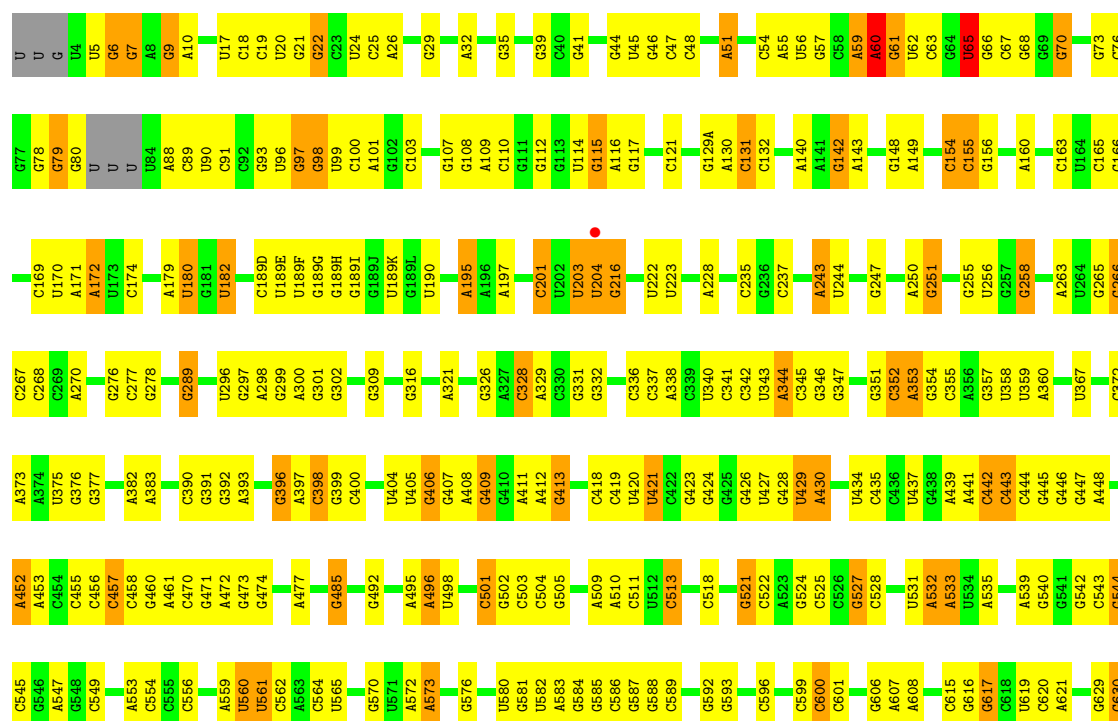
• Molecule 1: 16S Ribosomal RNA

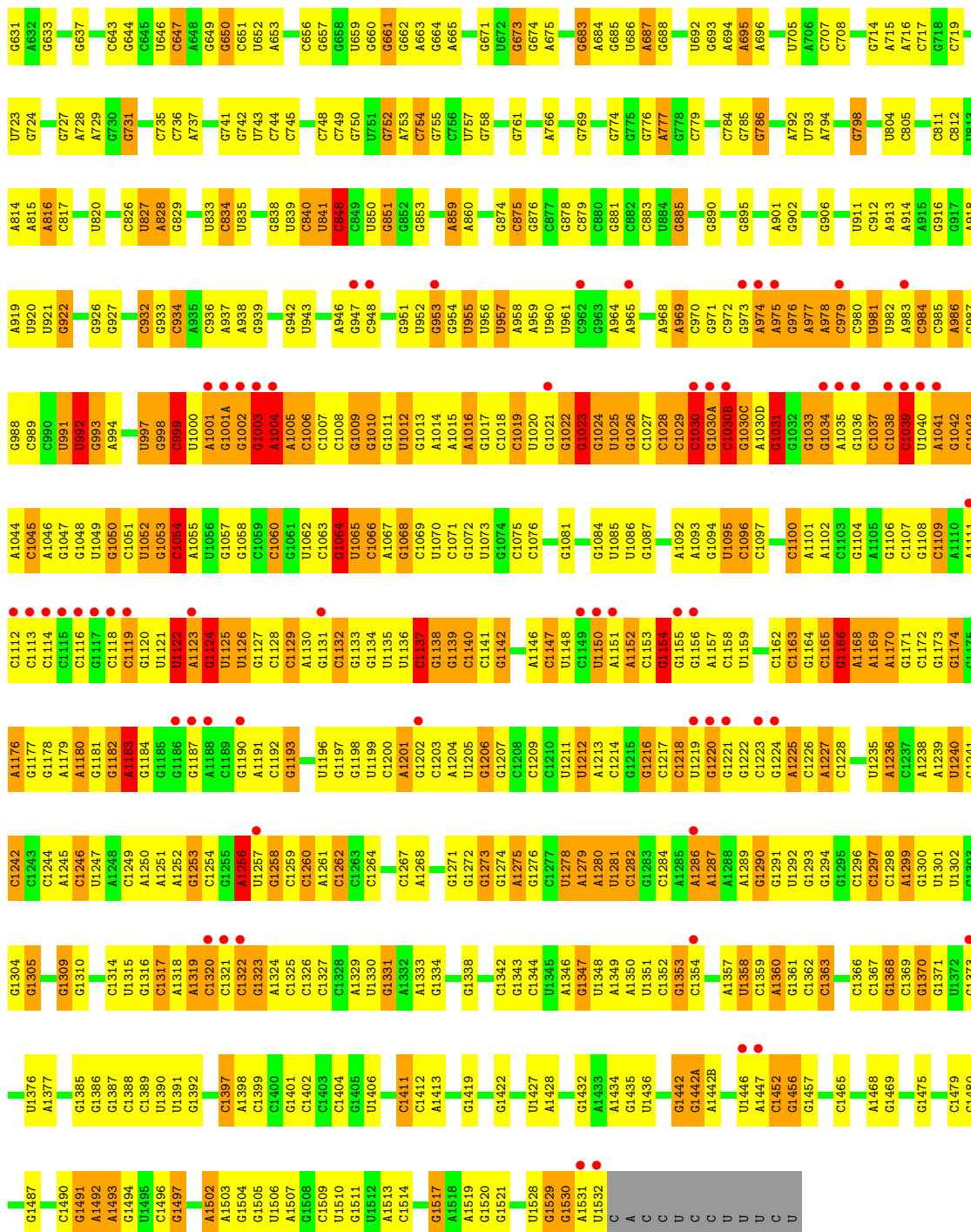




Molecule 1: 16S Ribosomal RNA

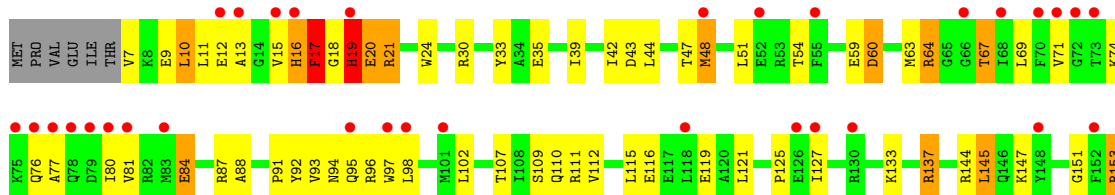
Chain CA:

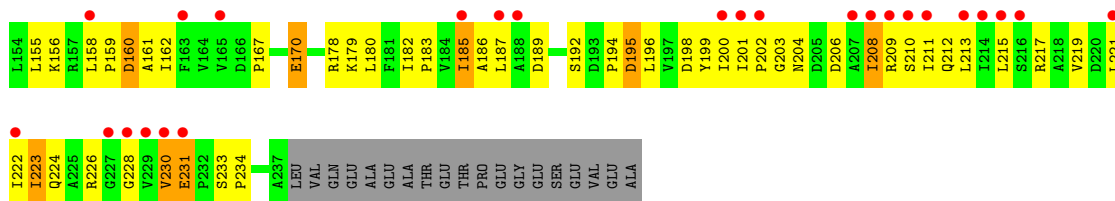




- Molecule 2: 30S ribosomal protein S2

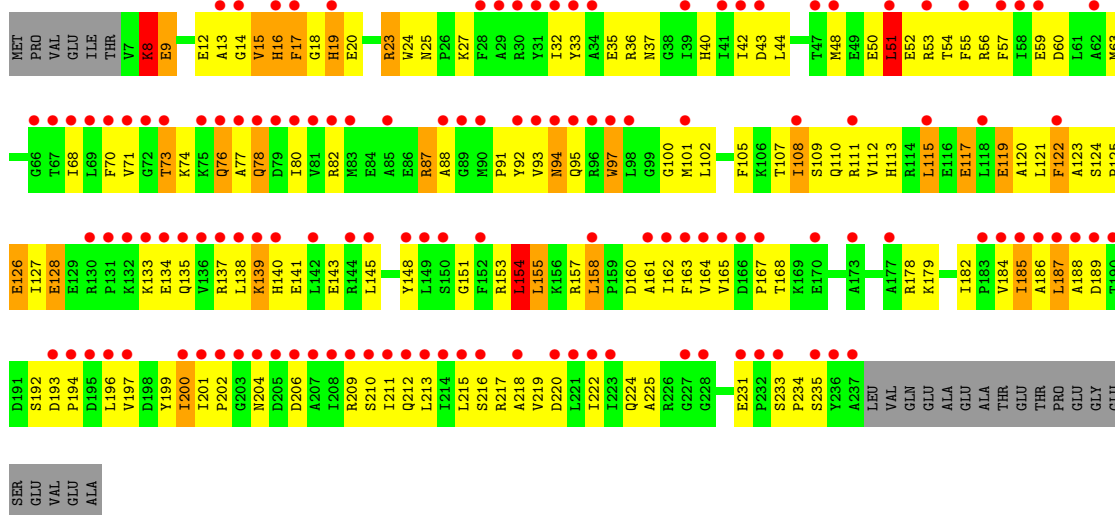
Chain AB:





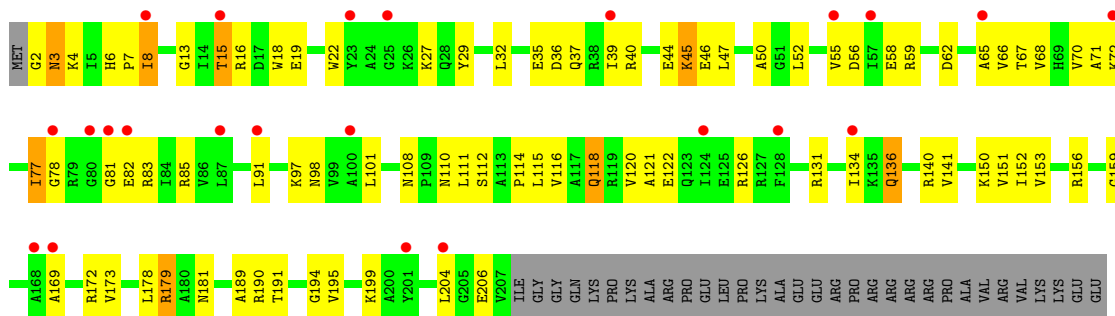
• Molecule 2: 30S ribosomal protein S2

Chain CB:



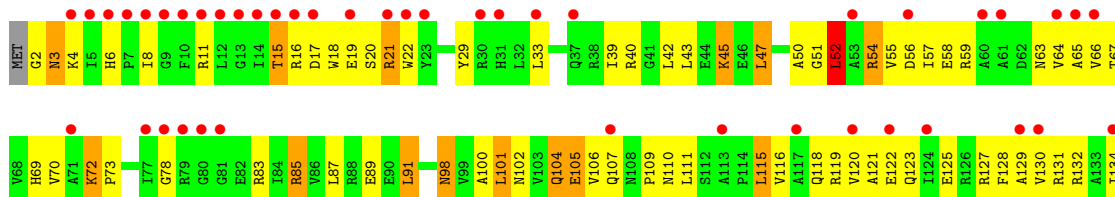
• Molecule 3: 30S ribosomal protein S3

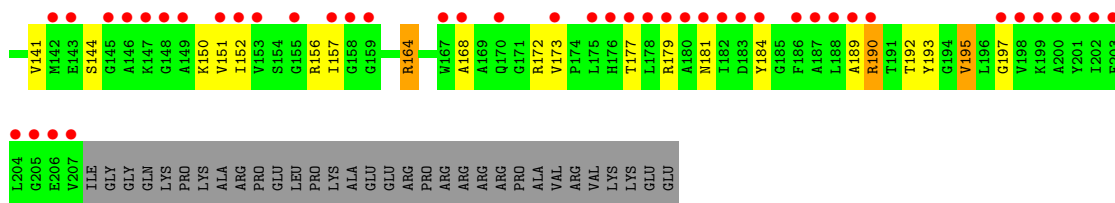
Chain AC:



• Molecule 3: 30S ribosomal protein S3

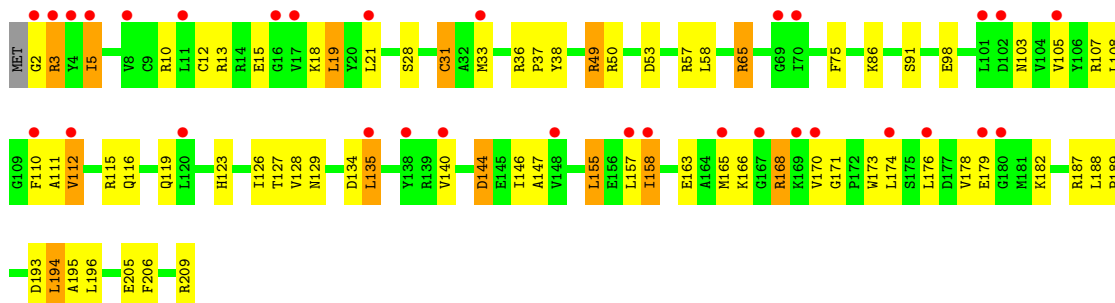
Chain CC:





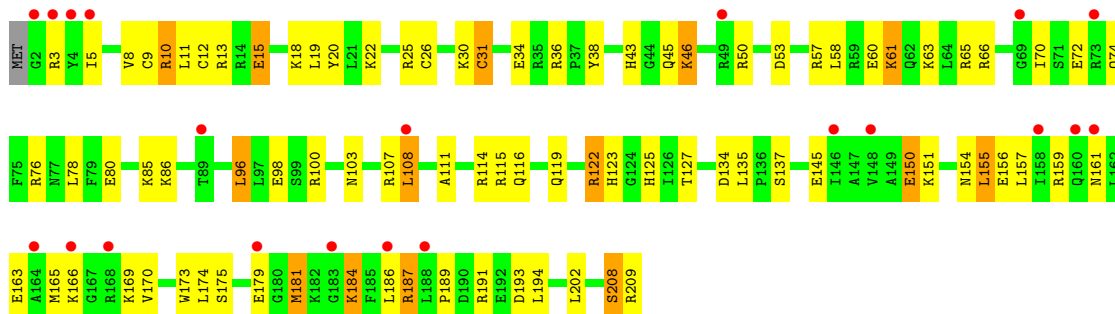
- Molecule 4: 30S ribosomal protein S4

Chain AD:



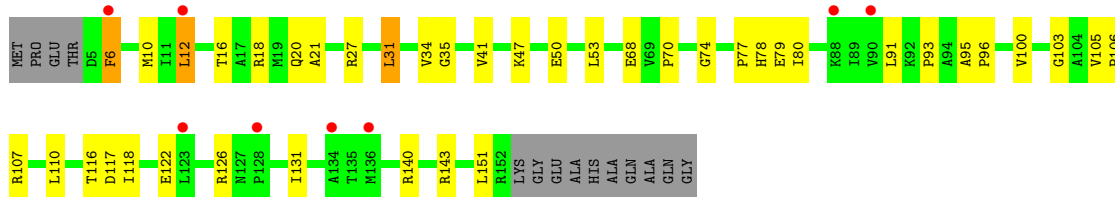
- Molecule 4: 30S ribosomal protein S4

Chain CD:



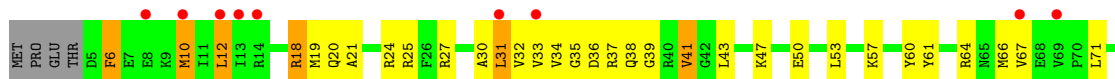
- Molecule 5: 30S ribosomal protein S5

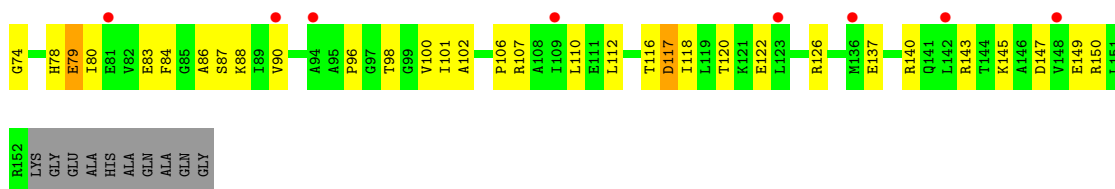
Chain AE:



- Molecule 5: 30S ribosomal protein S5

Chain CE:





- Molecule 6: 30S ribosomal protein S6

Chain AF:



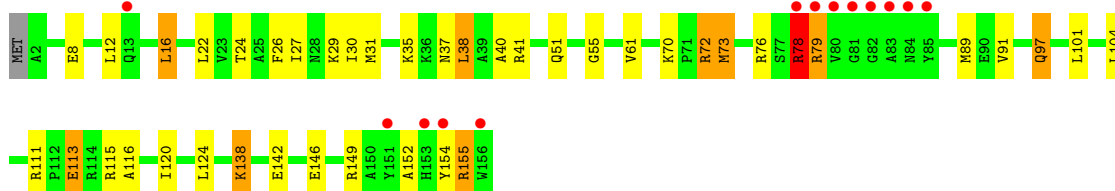
- Molecule 6: 30S ribosomal protein S6

Chain CF:



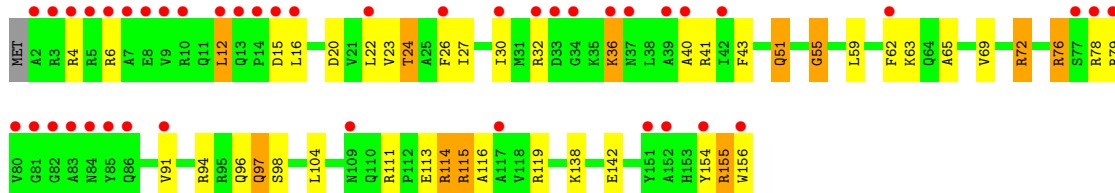
- Molecule 7: 30S ribosomal protein S7

Chain AG:



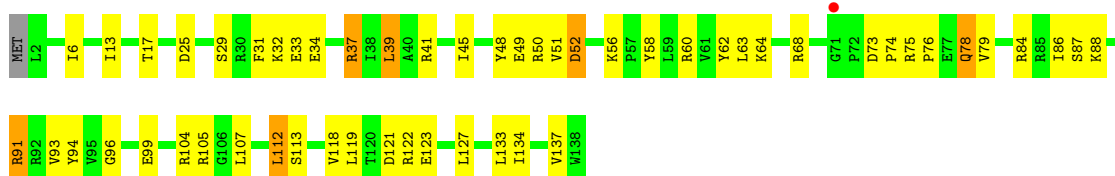
- Molecule 7: 30S ribosomal protein S7

Chain CG:



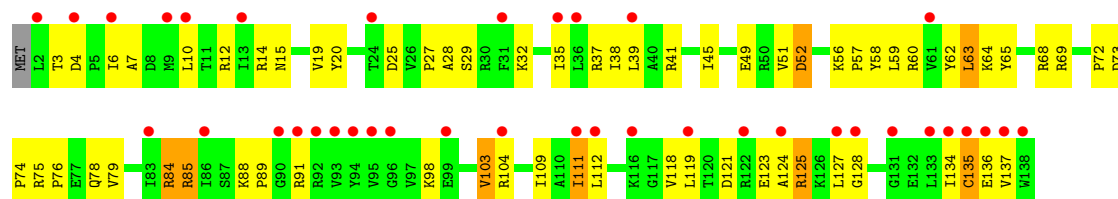
- Molecule 8: 30S ribosomal protein S8

Chain AH:



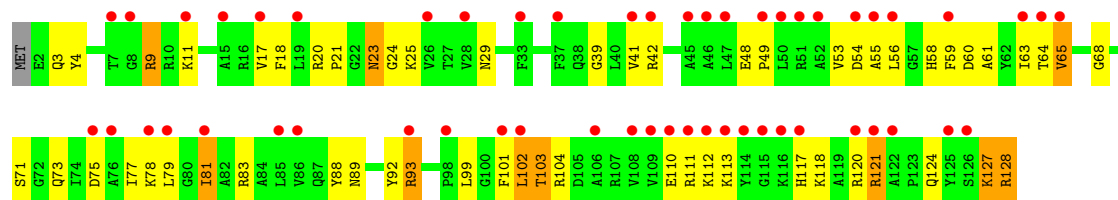
- Molecule 8: 30S ribosomal protein S8

Chain CH:



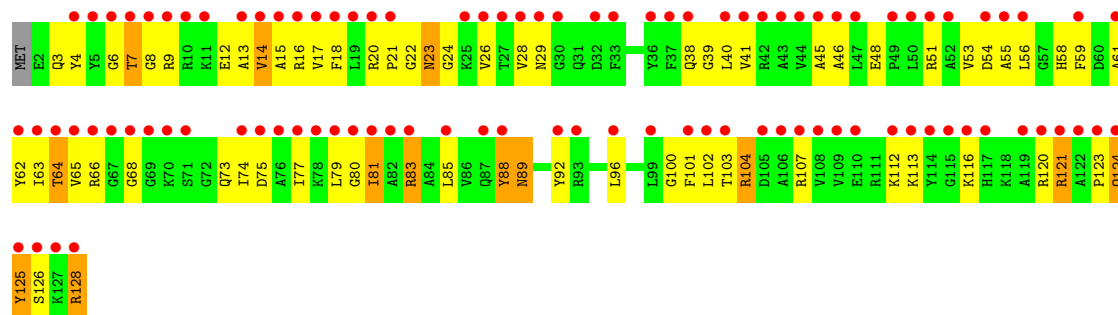
- Molecule 9: 30S ribosomal protein S9

Chain AI:



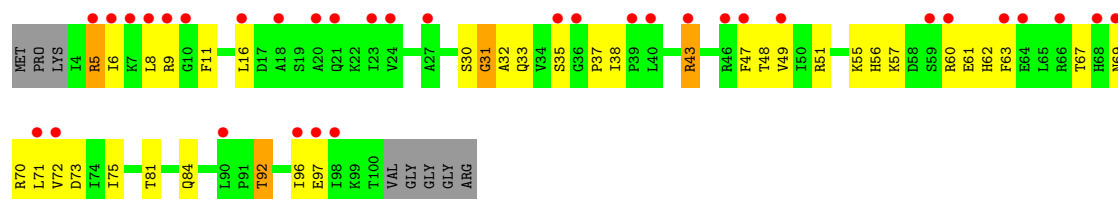
- Molecule 9: 30S ribosomal protein S9

Chain CI:



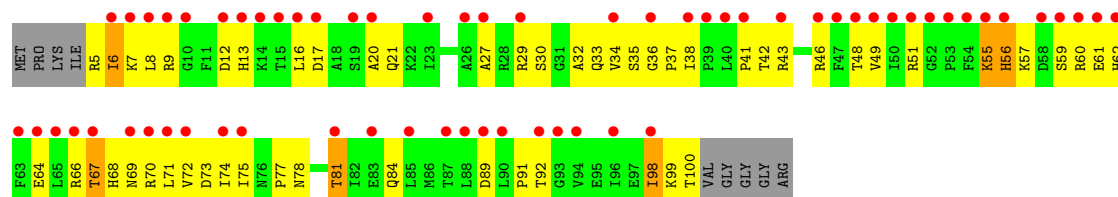
- Molecule 10: 30S ribosomal protein S10

Chain AJ:



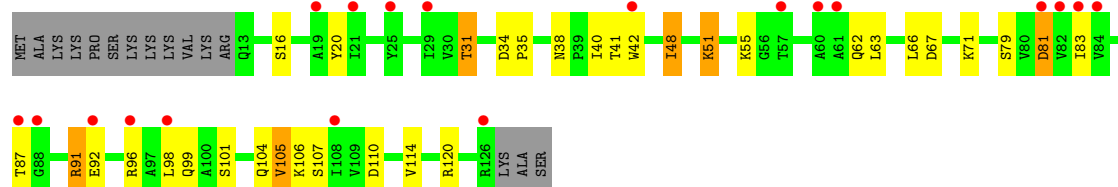
- Molecule 10: 30S ribosomal protein S10

Chain CJ:



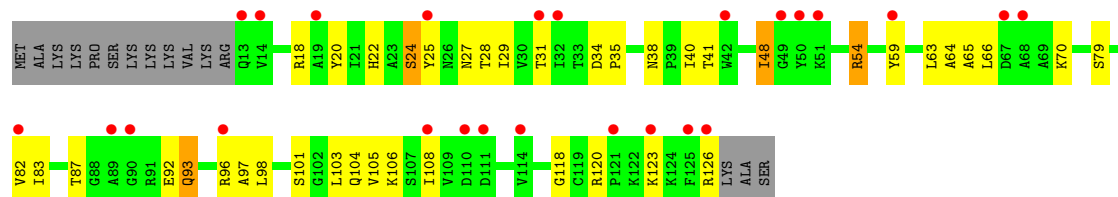
- Molecule 11: 30S ribosomal protein S11

Chain AK:



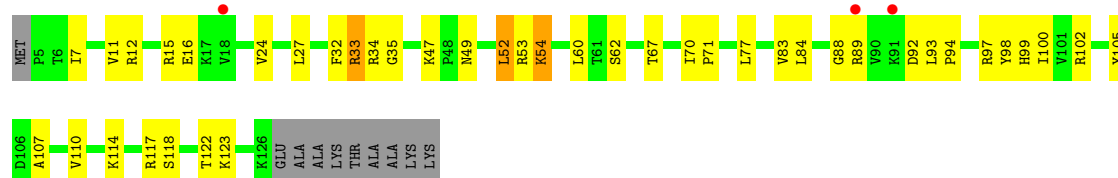
- Molecule 11: 30S ribosomal protein S11

Chain CK:



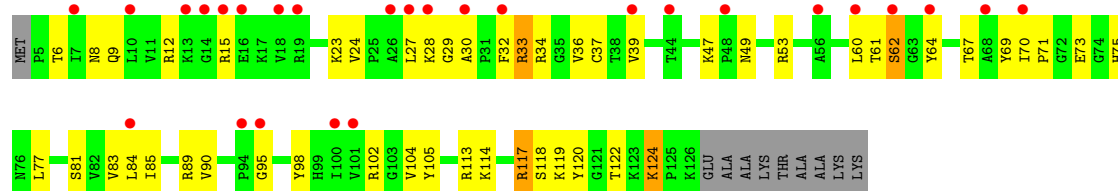
- Molecule 12: 30S ribosomal protein S12

Chain AL:



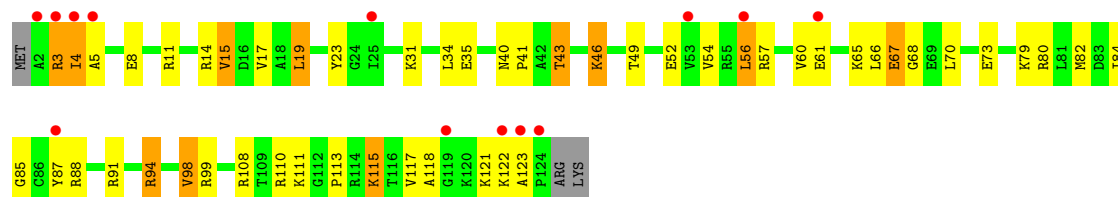
- Molecule 12: 30S ribosomal protein S12

Chain CL:



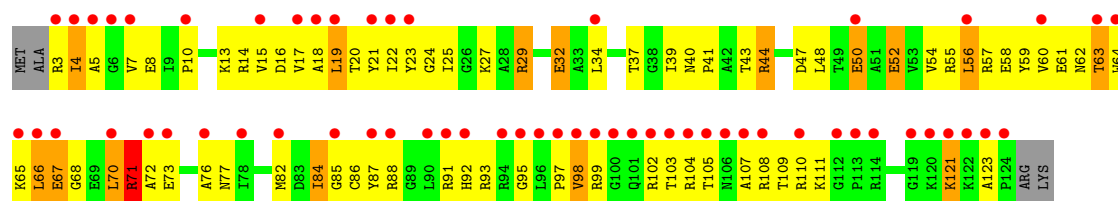
- Molecule 13: 30S ribosomal protein S13

Chain AM:



- Molecule 13: 30S ribosomal protein S13

Chain CM:



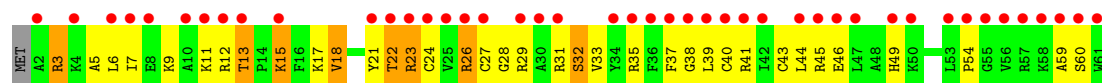
- Molecule 14: 30S ribosomal protein S14 type Z

Chain AN:



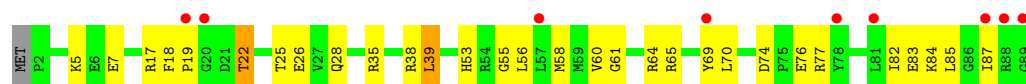
- Molecule 14: 30S ribosomal protein S14 type Z

Chain CN:



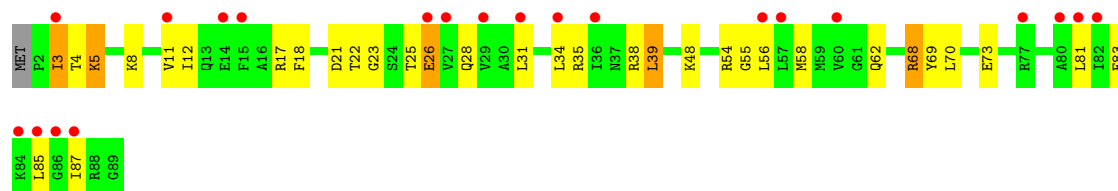
- Molecule 15: 30S ribosomal protein S15

Chain AO:



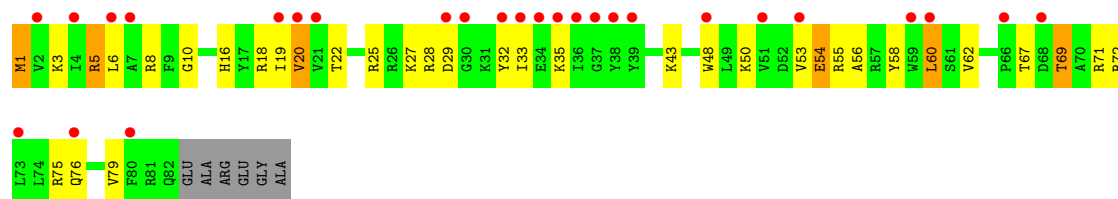
- Molecule 15: 30S ribosomal protein S15

Chain CO:



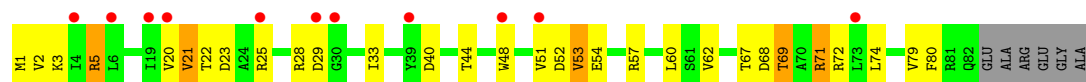
- Molecule 16: 30S ribosomal protein S16

Chain AP:



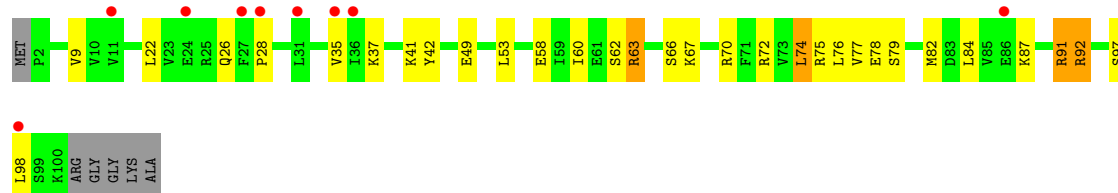
- Molecule 16: 30S ribosomal protein S16

Chain CP:



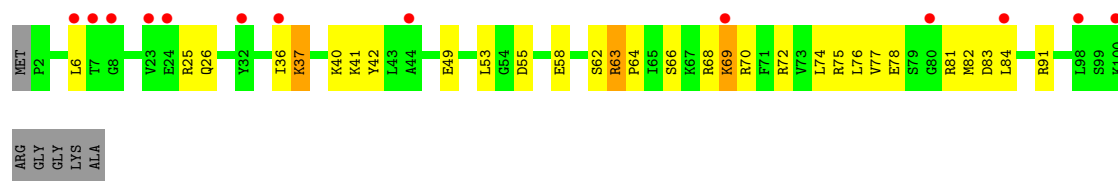
- Molecule 17: 30S ribosomal protein S17

Chain AQ:



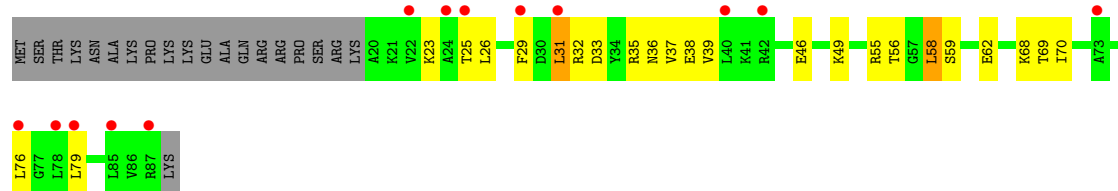
- Molecule 17: 30S ribosomal protein S17

Chain CQ:



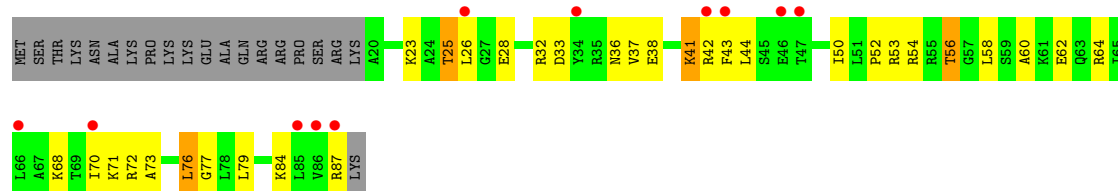
- Molecule 18: 30S ribosomal protein S18

Chain AR:



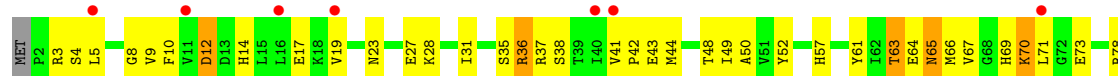
- Molecule 18: 30S ribosomal protein S18

Chain CR:



- Molecule 19: 30S ribosomal protein S19

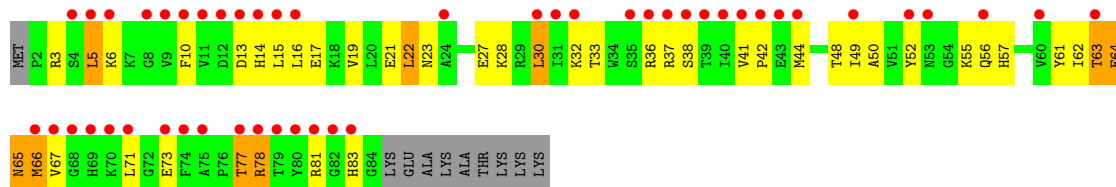
Chain AS:





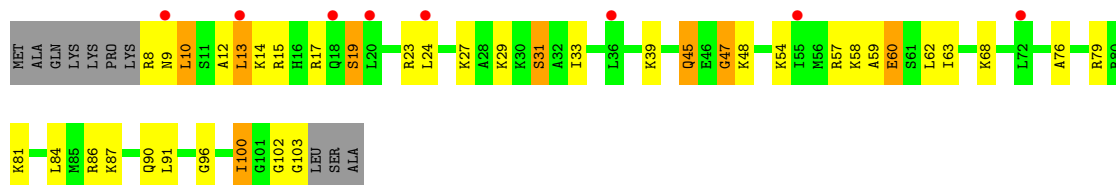
- Molecule 19: 30S ribosomal protein S19

Chain CS:



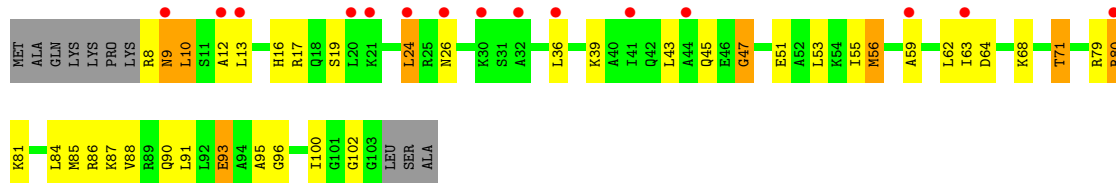
- Molecule 20: 30S ribosomal protein S20

Chain AT:



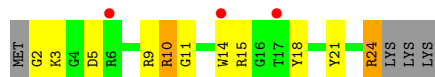
- Molecule 20: 30S ribosomal protein S20

Chain CT:



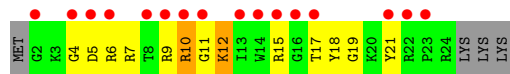
- Molecule 21: 30S ribosomal protein Thx

Chain AU:



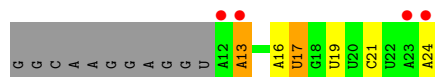
- Molecule 21: 30S ribosomal protein Thx

Chain CU:



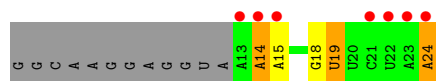
- Molecule 22: mRNA

Chain AV:



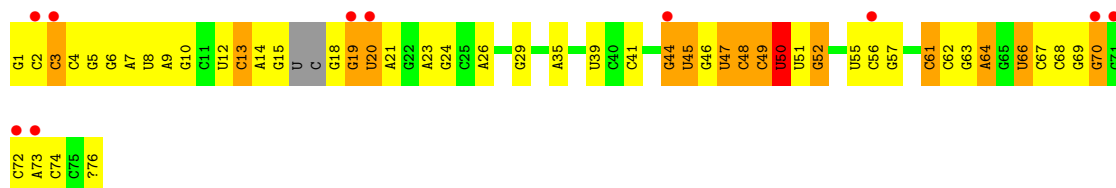
- Molecule 22: mRNA

Chain CV:



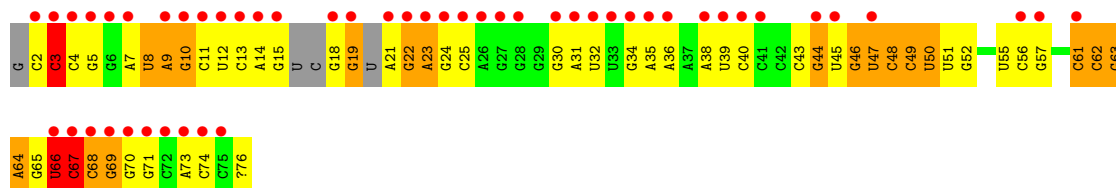
- Molecule 23: A-site tRNA

Chain AW:



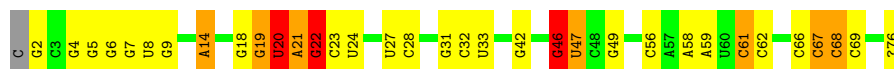
- Molecule 23: A-site tRNA

Chain CW:



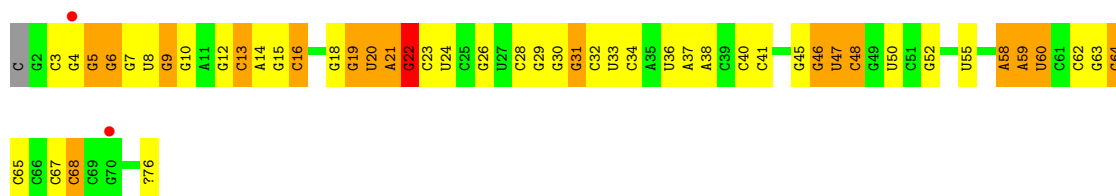
- Molecule 24: P-site tRNA

Chain AX:



- Molecule 24: P-site tRNA

Chain CX:



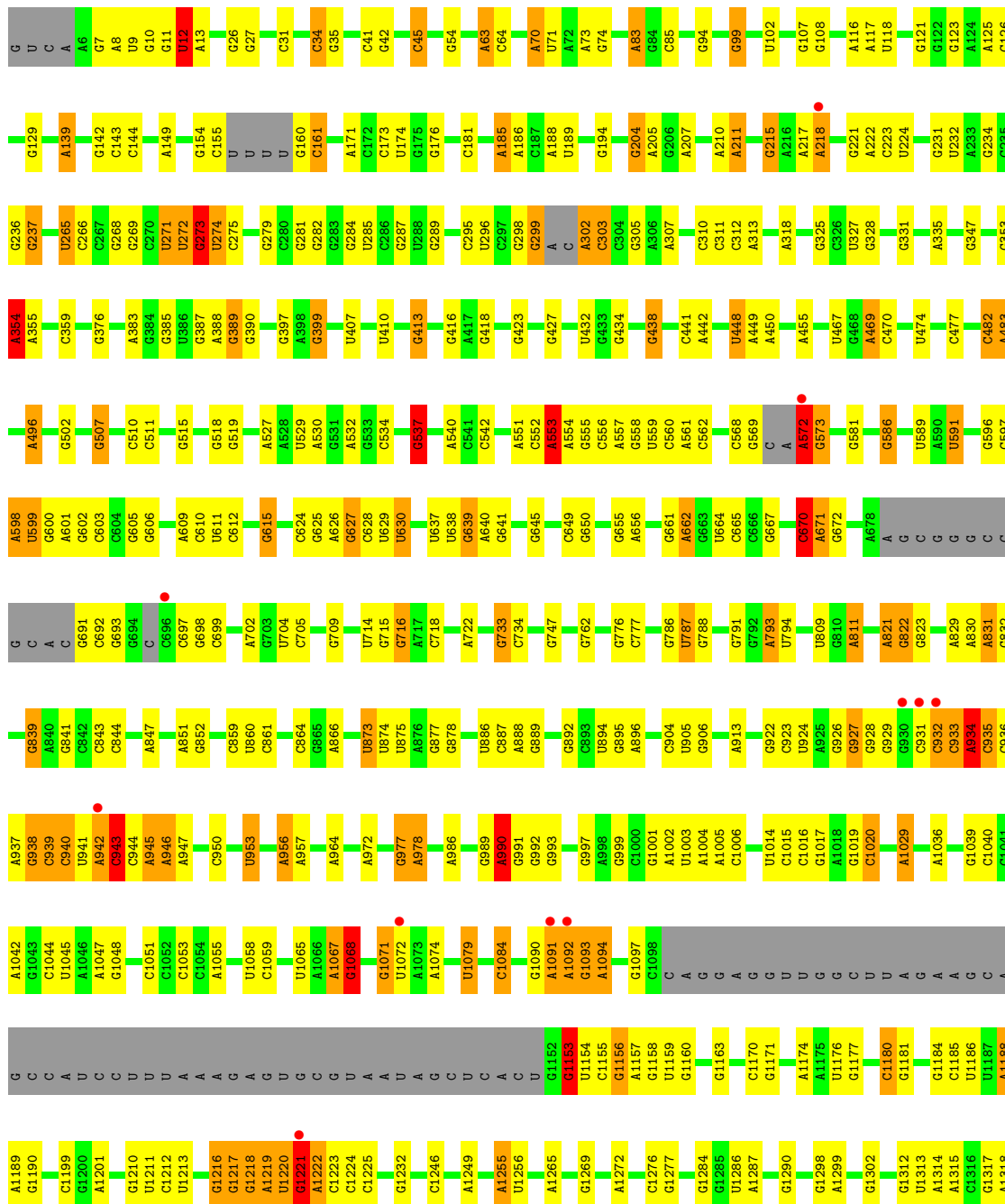
- Molecule 25: E-site tRNA

Chain CY:



- Molecule 26: 23S Ribosomal RNA

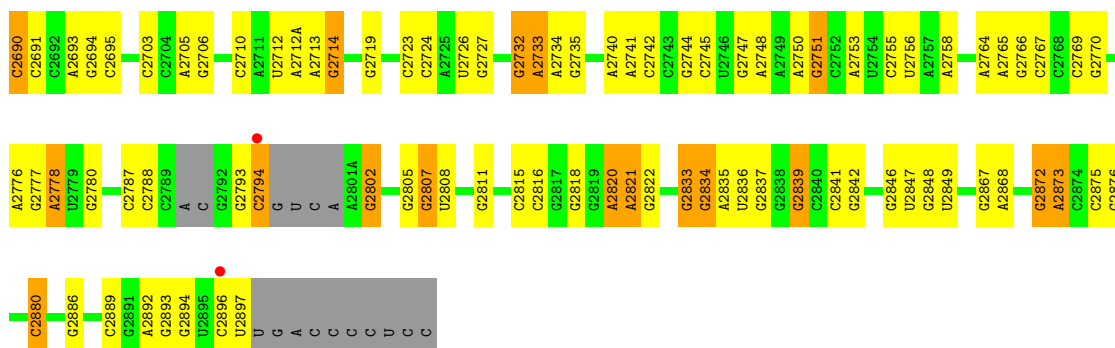
Chain BA:





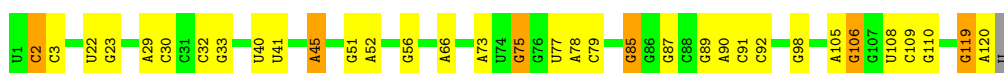


U1288	U1396	U1487	A1566	G1792	G1899	A2014	G2110	A2170	G2267	G2334	C2494	U2511	A2602
U1291	U1397	G1488	A1567	G1793	A1900	A2019	C2111	A2171	A2268	A2335	A2425	C2512	G2603
U1292	U1405	U1489	G1568	G1794	G1906	A2020	U1213	U2172	A2269	A2336	G2429	G2513	U2604
C1293	U1406	A1490	A1569	U1796	G1907	G2021	U1214	A2173	A2273	C2343	A2430	G2516	U2605
G1297	C1407	C1493	C1575	U1797	G1908	U2022	G2115	C2175	A2274	U2344	U2431	A2518	C2606
G1298	C1408	C1496	U1576	U1798	A1913	G2023	G2116	A2176	C2276	C2347	A2434	U2519	U2609
G1299	G1409	U1497	U1577	G1799	C2024	G2024	A2117	C2177	G2277	U2348	A2435	C2520	G2610
A1300	G1410	U1498	A1579	C1800	U1915	C2025	U1218	C2178	C2279	G2349	G2439	G2521	U2611
U1301	C1411	C1501	A1580	G1801	U1916	C2026	G2119	C2179	C2280	G2350	A2440	U2522	C2612
A1302	A1412	C1502	G1581	A1802	U1917	G2027	G2120	U2180	C2281	G2351	C2441	C2525	C2617
G1303	G1413	A1507	C1582	U1803	U1918	A2030	U2121	G2182	C2282	G2354	G2441	G2526	G2618
A1308	G1416	A1508	A1583	U1804	A1919	A2031	G2123	C2183	C2283	C2355	G2445	G2527	G2625
G1309	C1417	A1509	C1584	A1812	C1924	G2032	G2124	G2185	A2286	C2356	G2446	U2528	G2626
G1310	G1418	A1509A	A1586	G1813	A1927	A2033	A2126	G2186	G2287	U2357	A2447	G2529	
U1313	U1420	A1510	A1587	U1699	A1928	C2036	G2127	G2187	U2289	C2364	U2449	G2532	A2629
C1314	G1421	U1514	C1588	A1700	G1929	G2037	C2128	G2188	G2290	G2365	U2450	A2533	G2630
C1315	A1427	U1515	A1592	A1701	G1930	G2038	U1229	U2189	U2291	G2366	G2455	U2537	A2632
U1316	G1428	U1518	G1594	U1720	U1931	C2039	U1330	G2191	C2292	G2367	G2456	C2538	G2633
A1317	G1429	U1519	G1594	G1721	G1935	C2040	U1232	G2192	G2293	G2368	G2457	U2539	G2634
C1318	C1430	G1520	G1600	A1722	U1936	U2041	U1233	G2193	C2295	A2369	C2461	A2542	
G1325	U1431	G1523	G1601	G1740	A1937	A2042	A2134	G2194	C2296	G2370	U2462	G2543	A2639
G1332	A1434	U1524	U1602	G1741	A1938	G2043	A2135	A2198	C2297	G2372	C2465	G2544	
G1339	G1436	G1525	A1603	G1742	U1939	G2046	C2136	U2203	A2298	G2373	G2468	U2547	G2645
U1340	C1437	G1526	C1604	C1743	A1962	C2055	C2138	G2205	G2300	A2376	G2469	G2548	G2646
U1341	A1445	G1527	G1607	G1746	U1965	A2057	C2140	G2206	C2301	A2377	C2474	G2549	U2647
U1352	C1445A	A1528	A1608	U1739	U1966	G2058	G2141	G2207	G2302	A2378	C2475	G2552	G2648
U1357	G1446	A1529	A1610	G1750	U1963	A2059	C2142	A2208	G2303	G2379	A2476	U2553	U2649
G1358	A1449	C1532	G1615	G1754	U1964	G2061	C2143	U2218	A2305	G2382	G2481	U2554	C2652
A1359	G1450	U1533	A1616	A1755	G1967	A2062	C2145	G2224	G2308	G2383	G2482	U2555	A2654
A1360	U1453	A	G1622	G1756	G1968		G2146	A2225	C2309	G2384	C2483	C2556	
G1364	G1459	G1539	G1628	G1758	A1969	G2069	G2147	C2226	A2310	C2385	G2484	G2557	A2657
A1365	A1460	U1540	U1629	G1759	A1970	G2070	G2148	G2227	A2311	C2386	G2485	C2558	C2658
A1366	C1462	G1541	C1636	G1763	A1971	G2072	U2150	G2228	U2312	U2387	G2486	U2562	G2659
G1367	C1463	A1542	A1637	G1764	C1983	U2074	G2151	U2232	C2313	G2391	A2488	U2563	A2660
G1368	C1464	G1543	C1638	U1765	G1984	U2075	G2152	G2238	C2314	A2392	G2489	A2566	A2661
G1369	G1465	A1545	U1639	A1773	U1991	G2093	G2153	G2239	G2315	A2393	G2490	G2567	A2662
G1370	G1466	C1546	C1640	U1777	G1992	G2096	G2154	C2240	C2317	C2394	U2491	C2568	G2663
U1372	C1467	C1547	G1645	U1778	U1993	U2097	G2155	G2241	G2318	G2400	G2494	G2569	A2665
A1378	G1470		G1646	U1779	G1997	U2098	G2156	C2242	G2319	U2401	C2498	C2573	G2669
A1379	A1471	C1560	G1647	A1780	G1998	U2099	G2157	U2243	A2320	U2402	C2499	A2577	A2670
G1380	C1474	A1554	C1648	C1781	G1999	G2101	A2158	G2248	G2321	C2403	C2502	G2578	G2673
A1384	G1479	G1555	A1652	C1782	G2000	G2102	G2159	G2252	G2322	C2404	G2503	U2585	G2674
G1385	G1480	C1557	G1653	A1783	A2001	C2103	G2160	G2253	G2323	G2405	U2504	C2586	A2675
C1386	U1481	A1558	A1654	A1784	G2002	G2104	C2161	G2254	G2324	U2406	U2505	U2587	G2680
U1394	G1482	C1559	C1657	A1789	C2006	G2105	C2162	G2255	G2325	G2407	U2506	U2588	C2681
A1395				C1790	G2009	G2106	G2163	U2261	G2326	U2408	U2507	C2591	U2682
				A1791			G2164	G2262	C2327	G2409	C2507	G2592	C2683
							G2165	G2263	C2328	G2410	G2508	G2593	
							G2166	G2264	C2329	A2422	G2509	G2594	U2689
							U2167	U2265	U2332	C2510		G2595	
							A2169	A2266	A2333	U2423			



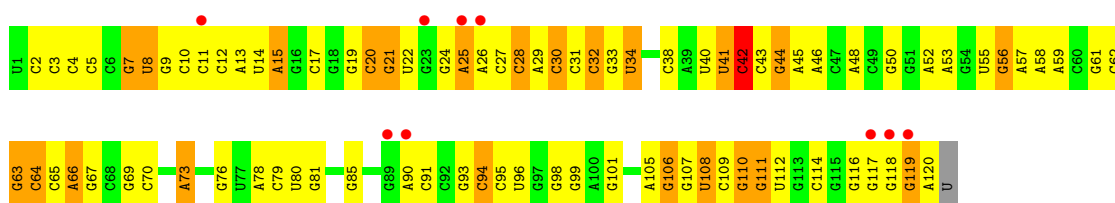
• Molecule 27: 5S Ribosomal RNA

Chain BB:



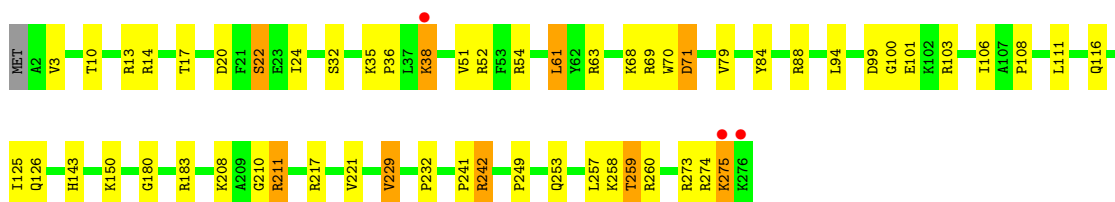
• Molecule 27: 5S Ribosomal RNA

Chain DB:



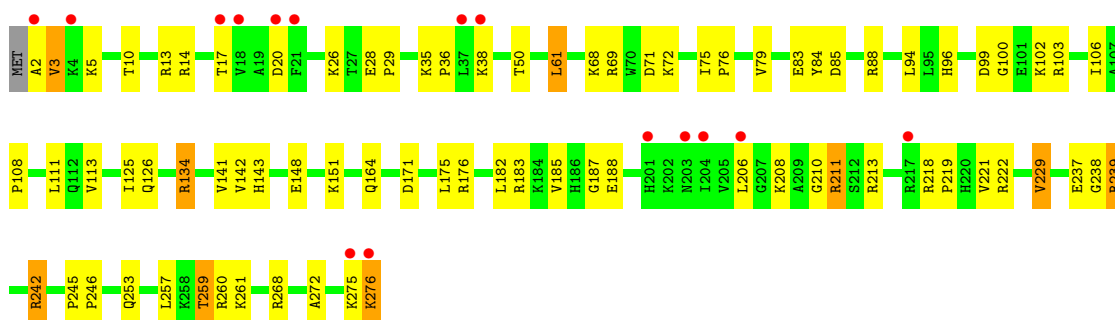
• Molecule 28: 50S ribosomal protein L2

Chain BD:



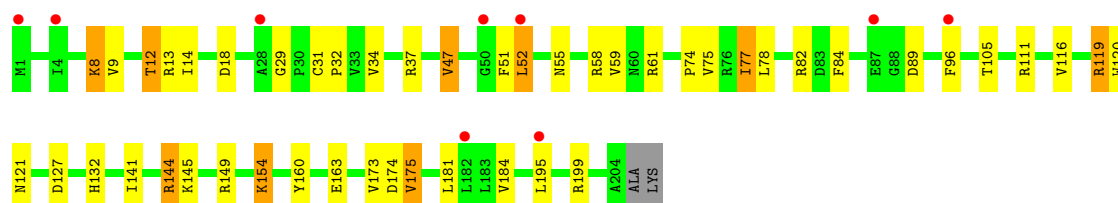
• Molecule 28: 50S ribosomal protein L2

Chain DD:



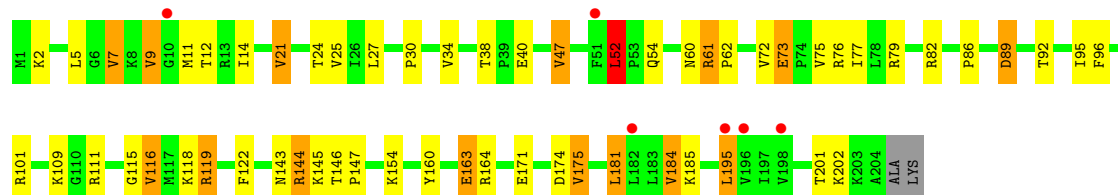
• Molecule 29: 50S ribosomal protein L3

Chain BE:



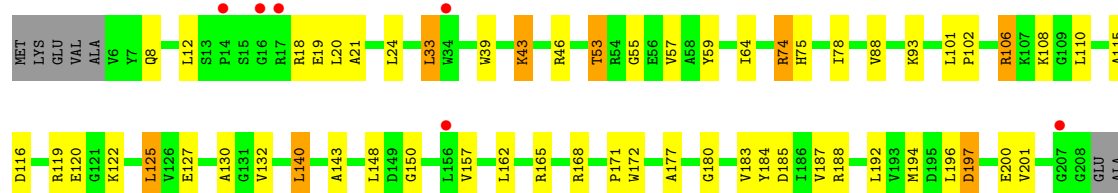
- Molecule 29: 50S ribosomal protein L3

Chain DE:



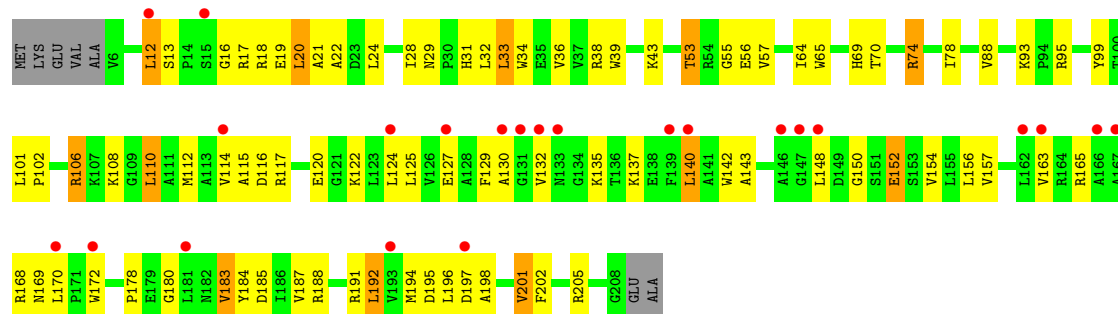
- Molecule 30: 50S ribosomal protein L4

Chain BF:



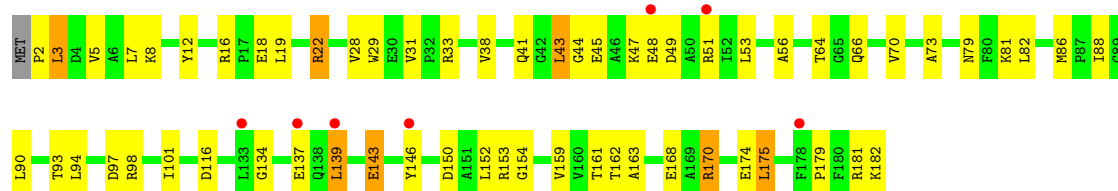
- Molecule 30: 50S ribosomal protein L4

Chain DF:



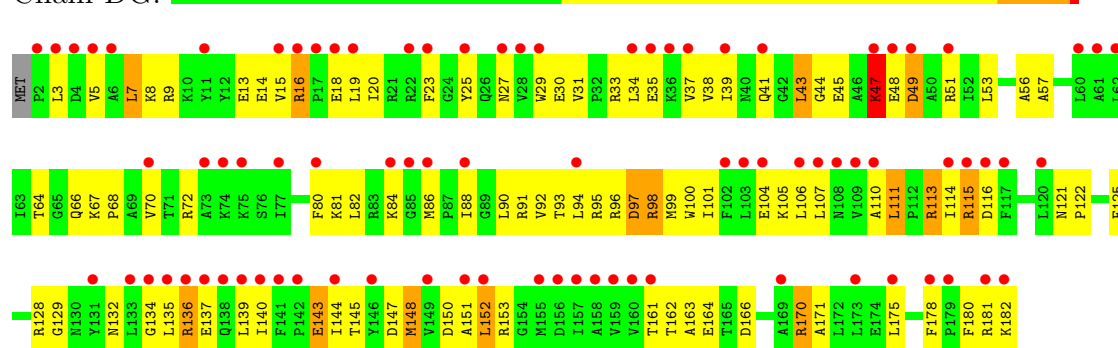
- Molecule 31: 50S ribosomal protein L5

Chain BG:



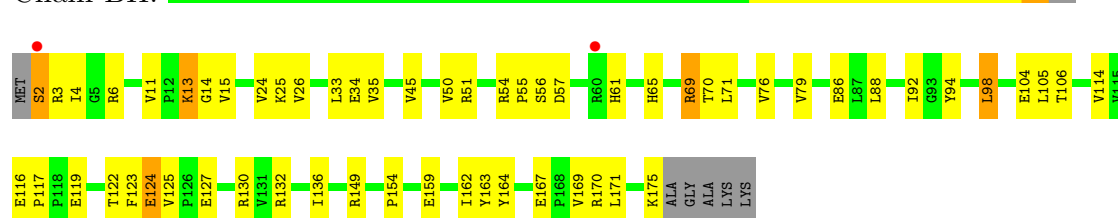
- Molecule 31: 50S ribosomal protein L5

Chain DG:



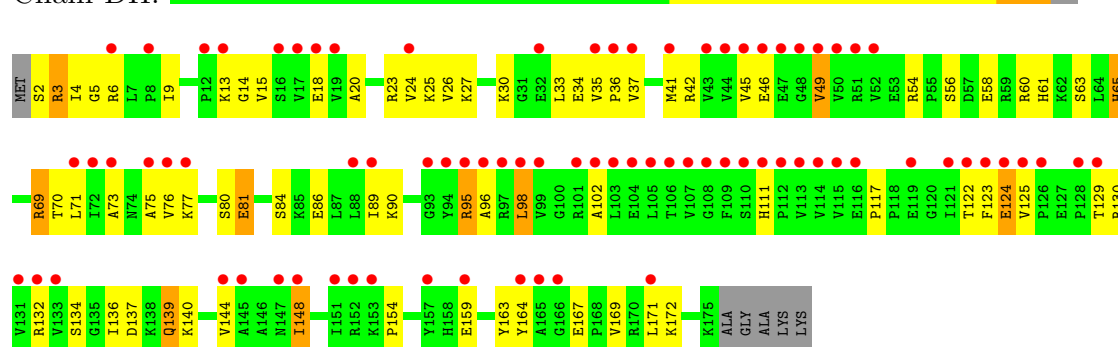
- Molecule 32: 50S ribosomal protein L6

Chain BH:



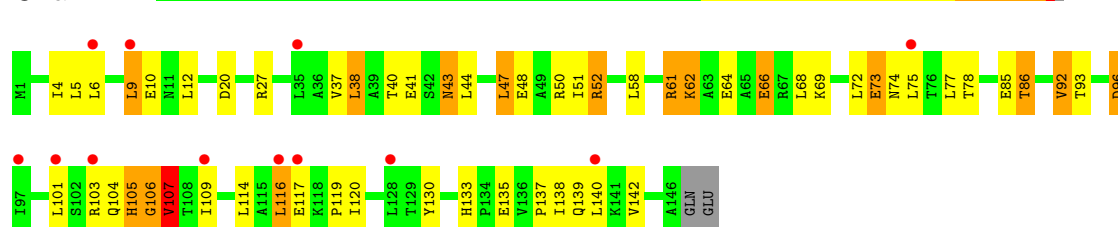
- Molecule 32: 50S ribosomal protein L6

Chain DH:



- Molecule 33: 50S ribosomal protein L9

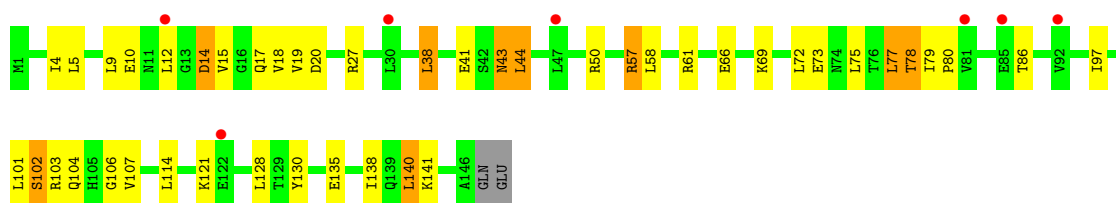
Chain BI:



- Molecule 33: 50S ribosomal protein L9

Chain DI:





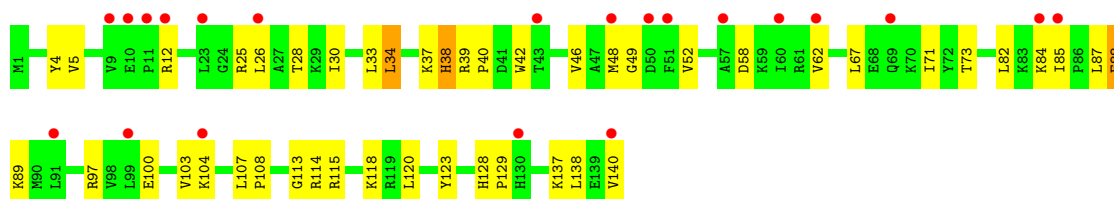
- Molecule 34: 50S ribosomal protein L13

Chain BN:



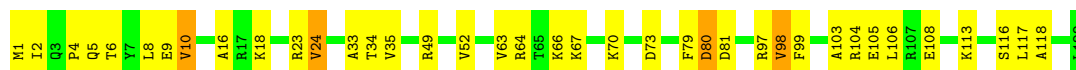
- Molecule 34: 50S ribosomal protein L13

Chain DN:



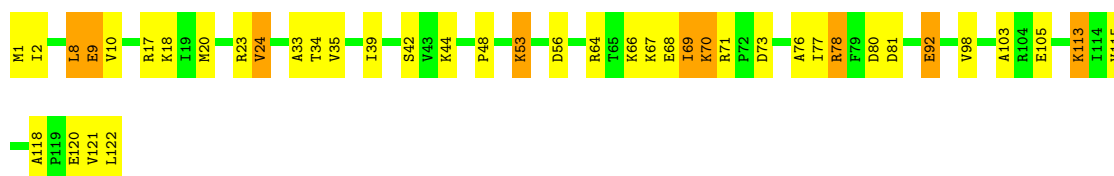
- Molecule 35: 50S ribosomal protein L14

Chain BO:



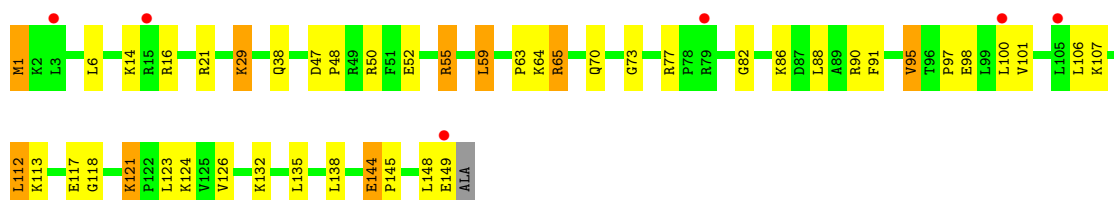
- Molecule 35: 50S ribosomal protein L14

Chain DO:



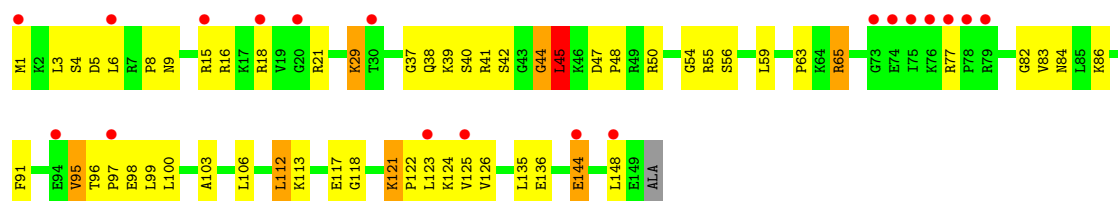
- Molecule 36: 50S ribosomal protein L15

Chain BP:



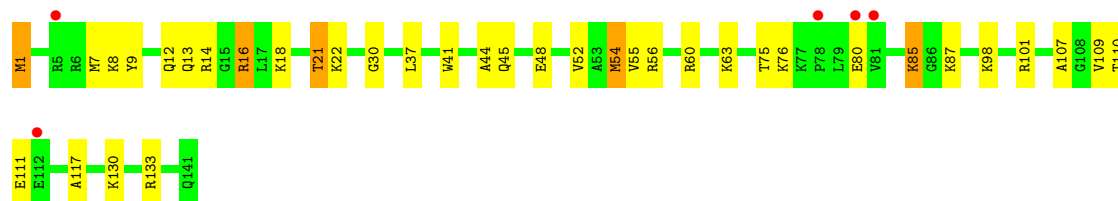
- Molecule 36: 50S ribosomal protein L15

Chain DP:



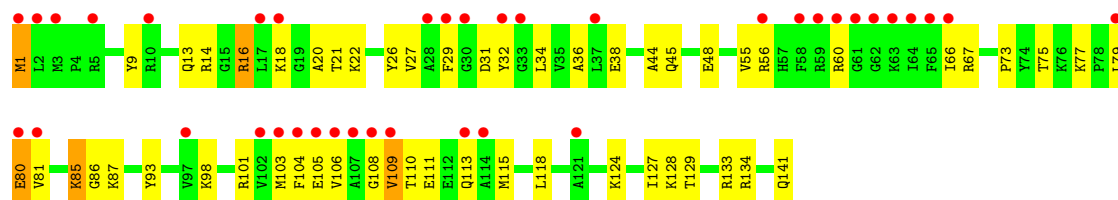
- Molecule 37: 50S ribosomal protein L16

Chain BQ:



- Molecule 37: 50S ribosomal protein L16

Chain DQ:



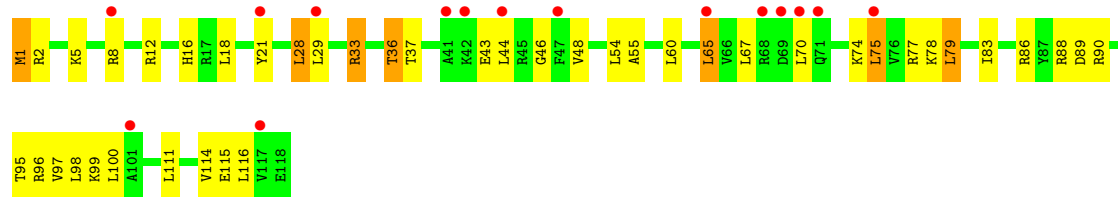
- Molecule 38: 50S ribosomal protein L17

Chain BR:



- Molecule 38: 50S ribosomal protein L17

Chain DR:



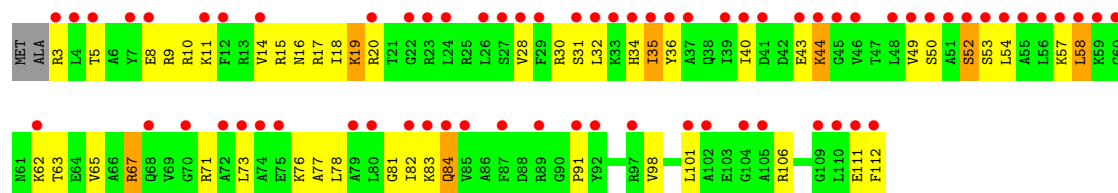
- Molecule 39: 50S ribosomal protein L18

Chain BS:



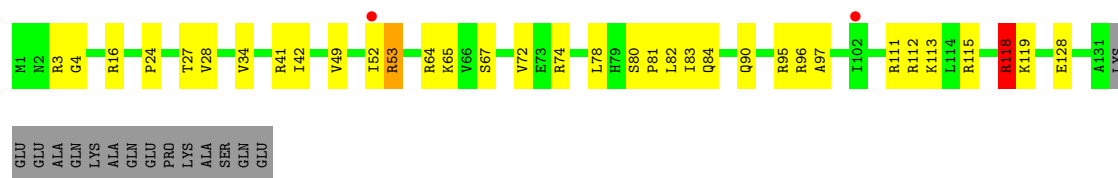
- Molecule 39: 50S ribosomal protein L18

Chain DS:



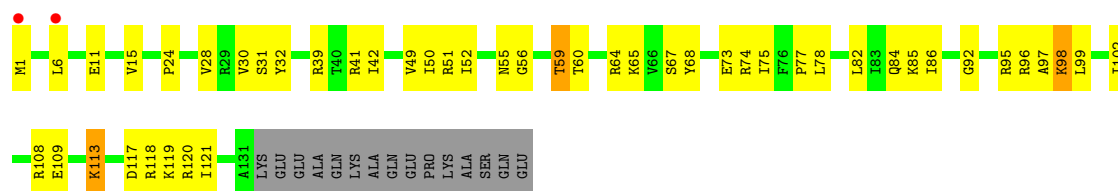
- Molecule 40: 50S ribosomal protein L19

Chain BT:



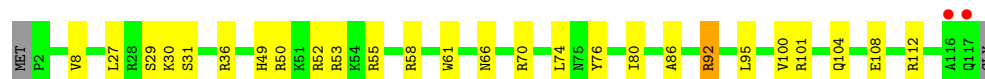
- Molecule 40: 50S ribosomal protein L19

Chain DT:



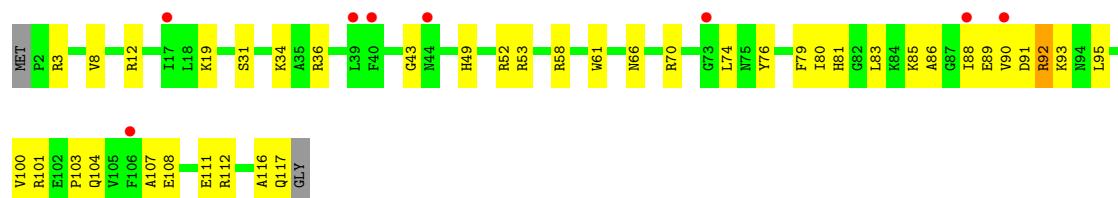
- Molecule 41: 50S ribosomal protein L20

Chain BU:



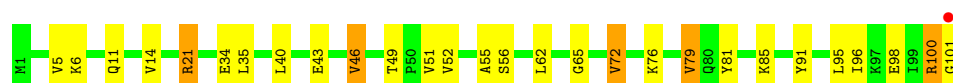
- Molecule 41: 50S ribosomal protein L20

Chain DU:



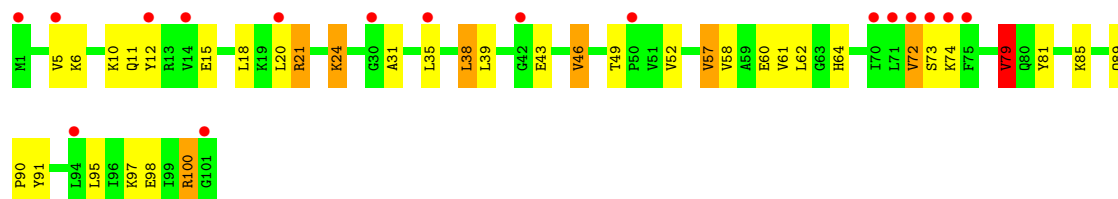
- Molecule 42: 50S ribosomal protein L21

Chain BV:



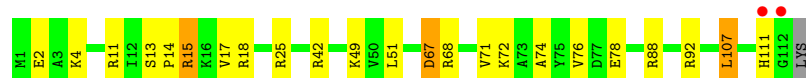
- Molecule 42: 50S ribosomal protein L21

Chain DV: 



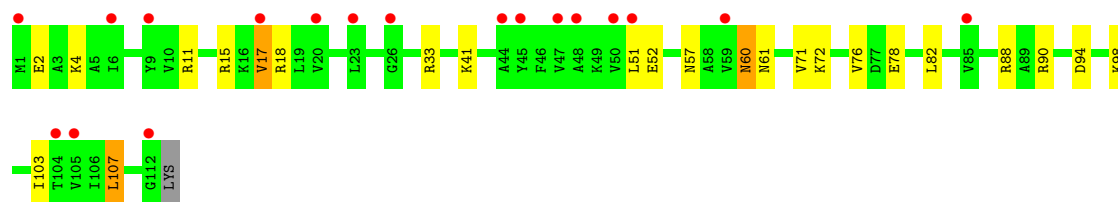
- Molecule 43: 50S ribosomal protein L22

Chain BW: 



- Molecule 43: 50S ribosomal protein L22

Chain DW: 



- Molecule 44: 50S ribosomal protein L23

Chain BX: 



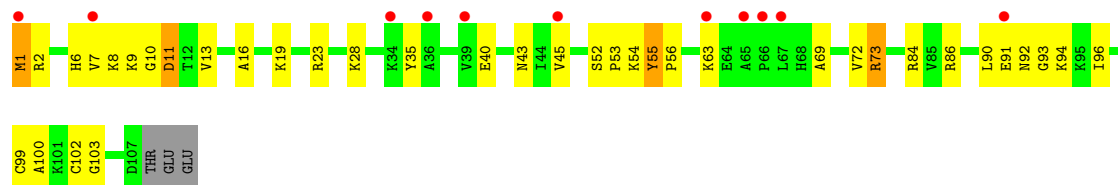
- Molecule 44: 50S ribosomal protein L23

Chain DX: 



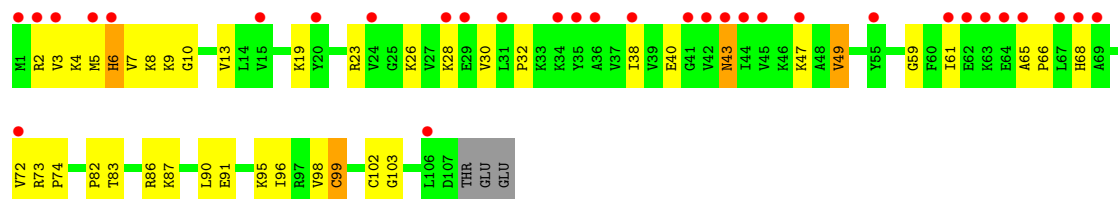
- Molecule 45: 50S ribosomal protein L24

Chain BY: 



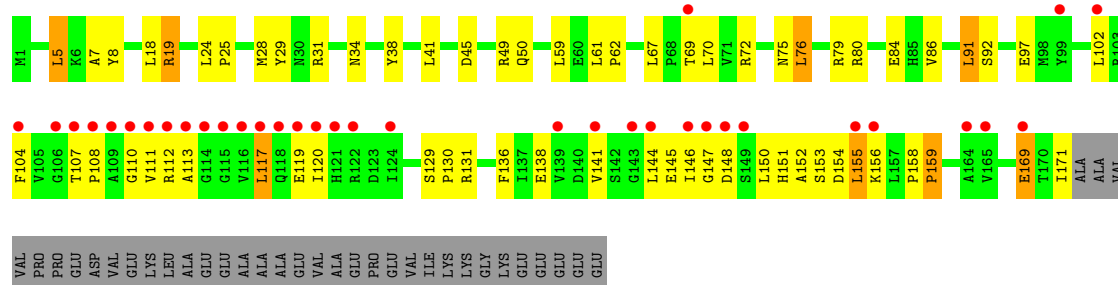
- Molecule 45: 50S ribosomal protein L24

Chain DY: 



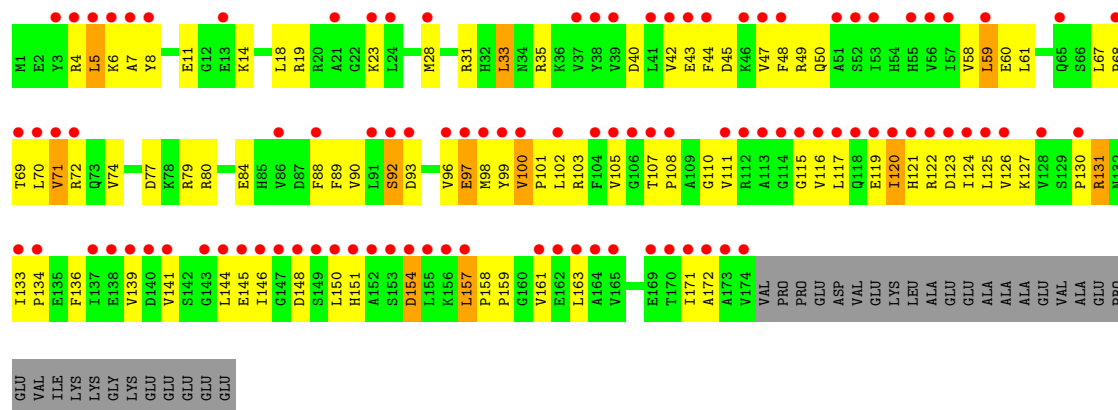
- Molecule 46: 50S ribosomal protein L25

Chain BZ: 



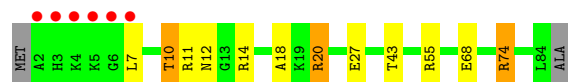
- Molecule 46: 50S ribosomal protein L25

Chain DZ: 



- Molecule 47: 50S ribosomal protein L27

Chain B0: 



- Molecule 47: 50S ribosomal protein L27

Chain D0: 





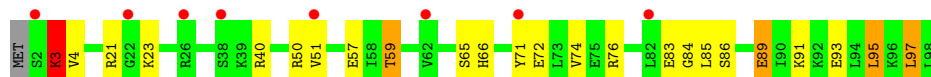
- Molecule 48: 50S ribosomal protein L28

Chain B1:



- Molecule 48: 50S ribosomal protein L28

Chain D1:



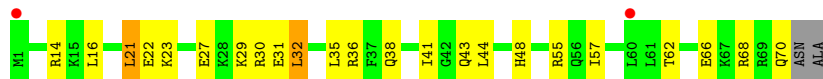
- Molecule 49: 50S ribosomal protein L29

Chain B2:



- Molecule 49: 50S ribosomal protein L29

Chain D2:



- Molecule 50: 50S ribosomal protein L30

Chain B3:



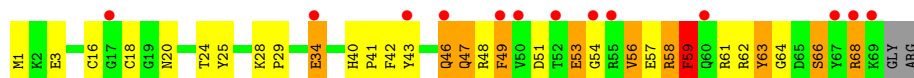
- Molecule 50: 50S ribosomal protein L30

Chain D3:



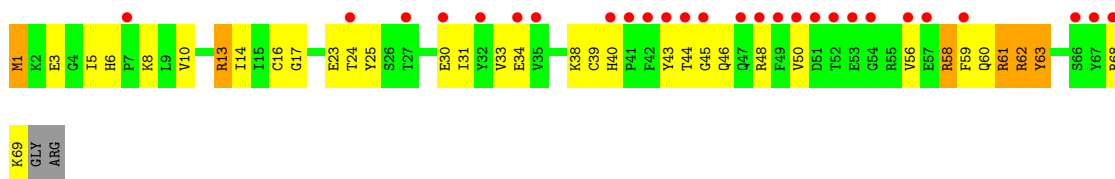
- Molecule 51: 50S ribosomal protein L31

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	209.45Å 448.85Å 619.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	151.90 – 2.60 224.43 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (151.90-2.60) 99.9 (224.43-2.60)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 2.62Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.223 , 0.264 0.248 , 0.289	Depositor DCC
R_{free} test set	43531 reflections (2.47%)	DCC
Wilson B-factor (Å ²)	56.4	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Outliers	0 of 1760092 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	297127	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% 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, MIA, SF4, MG, F3N, 31H, 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	0.38	0/36027	0.91	43/56227 (0.1%)
1	CA	0.41	8/36170 (0.0%)	1.01	101/56452 (0.2%)
2	AB	0.30	0/1881	0.62	0/2542
2	CB	0.33	0/1860	0.67	2/2518 (0.1%)
3	AC	0.27	0/1576	0.52	0/2130
3	CC	0.31	0/1568	0.61	1/2122 (0.0%)
4	AD	0.29	0/1689	0.55	0/2267
4	CD	0.30	0/1708	0.55	0/2289
5	AE	0.30	0/1145	0.54	0/1543
5	CE	0.33	0/1149	0.61	0/1548
6	AF	0.30	0/825	0.52	0/1118
6	CF	0.32	0/833	0.55	0/1128
7	AG	0.28	0/1250	0.50	0/1679
7	CG	0.27	0/1254	0.53	0/1683
8	AH	0.28	0/1108	0.52	0/1494
8	CH	0.29	0/1108	0.54	0/1494
9	AI	0.29	0/1005	0.57	0/1350
9	CI	0.31	0/997	0.64	0/1343
10	AJ	0.27	0/722	0.54	0/982
10	CJ	0.33	0/727	0.62	0/988
11	AK	0.28	0/848	0.51	0/1149
11	CK	0.28	0/848	0.53	0/1149
12	AL	0.33	0/946	0.52	0/1274
12	CL	0.30	0/946	0.58	0/1274
13	AM	0.31	0/977	0.60	0/1310
13	CM	0.31	0/961	0.62	1/1291 (0.1%)
14	AN	0.32	0/501	0.53	0/664
14	CN	0.33	0/501	0.57	0/664
15	AO	0.28	0/739	0.52	0/985
15	CO	0.29	0/739	0.54	0/985
16	AP	0.31	0/697	0.54	0/939
16	CP	0.29	0/693	0.51	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.29	0/836	0.53	0/1117
17	CQ	0.29	0/836	0.50	0/1117
18	AR	0.27	0/560	0.54	0/746
18	CR	0.29	0/560	0.56	0/746
19	AS	0.30	0/676	0.58	0/911
19	CS	0.33	0/661	0.71	0/893
20	AT	0.29	0/730	0.57	0/965
20	CT	0.28	0/733	0.55	0/969
21	AU	0.27	0/203	0.50	0/266
21	CU	0.33	0/203	0.53	0/266
22	AV	0.39	0/310	0.96	1/480 (0.2%)
22	CV	0.42	0/282	0.99	2/437 (0.5%)
23	AW	0.47	0/1577	1.20	7/2454 (0.3%)
23	CW	0.53	0/1531	1.28	9/2379 (0.4%)
24	AX	0.53	2/1700 (0.1%)	1.20	22/2650 (0.8%)
24	CX	0.46	0/1700	1.15	6/2650 (0.2%)
25	AY	0.58	0/1602	1.35	20/2493 (0.8%)
25	CY	0.59	0/1579	1.40	25/2455 (1.0%)
26	BA	0.50	1/68013 (0.0%)	0.93	91/106165 (0.1%)
26	DA	0.41	1/67542 (0.0%)	0.92	74/105428 (0.1%)
27	BB	0.41	0/2878	0.86	1/4490 (0.0%)
27	DB	0.44	0/2878	0.92	2/4490 (0.0%)
28	BD	0.37	0/2186	0.59	0/2944
28	DD	0.33	0/2192	0.57	0/2951
29	BE	0.37	0/1592	0.57	0/2149
29	DE	0.33	0/1592	0.55	0/2149
30	BF	0.34	0/1619	0.55	0/2193
30	DF	0.32	0/1615	0.55	0/2188
31	BG	0.31	0/1450	0.54	1/1959 (0.1%)
31	DG	0.33	0/1449	0.60	0/1958
32	BH	0.33	0/1356	0.54	0/1834
32	DH	0.29	0/1356	0.54	0/1834
33	BI	0.28	0/1100	0.56	0/1501
33	DI	0.29	0/1088	0.55	0/1484
34	BN	0.34	0/1144	0.53	0/1543
34	DN	0.31	0/1144	0.52	0/1543
35	BO	0.37	0/943	0.57	0/1269
35	DO	0.31	0/943	0.55	1/1269 (0.1%)
36	BP	0.35	0/1156	0.57	0/1537
36	DP	0.32	0/1152	0.61	1/1533 (0.1%)
37	BQ	0.35	0/1143	0.53	0/1527
37	DQ	0.32	0/1143	0.53	0/1527
38	BR	0.36	0/982	0.58	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DR	0.30	0/982	0.53	0/1312
39	BS	0.31	0/887	0.56	0/1180
39	DS	0.28	0/880	0.56	0/1172
40	BT	0.34	0/1105	0.56	1/1477 (0.1%)
40	DT	0.31	0/1097	0.53	0/1468
41	BU	0.39	0/977	0.56	0/1301
41	DU	0.30	0/977	0.54	0/1301
42	BV	0.36	0/782	0.58	0/1049
42	DV	0.32	0/782	0.57	1/1049 (0.1%)
43	BW	0.39	0/897	0.56	0/1205
43	DW	0.31	0/897	0.52	0/1205
44	BX	0.38	0/764	0.57	1/1025 (0.1%)
44	DX	0.33	0/764	0.58	1/1025 (0.1%)
45	BY	0.35	0/819	0.57	0/1095
45	DY	0.32	0/819	0.55	0/1095
46	BZ	0.32	0/1379	0.58	0/1873
46	DZ	0.30	0/1390	0.56	0/1890
47	B0	0.35	0/662	0.55	0/881
47	D0	0.32	0/662	0.53	0/881
48	B1	0.35	0/762	0.54	0/1014
48	D1	0.31	0/762	0.53	0/1014
49	B2	0.31	0/590	0.53	0/781
49	D2	0.28	0/590	0.46	0/781
50	B3	0.34	0/474	0.57	0/635
50	D3	0.27	0/469	0.55	0/630
51	B4	0.31	0/571	0.70	0/768
51	D4	0.32	0/545	0.67	0/737
52	B5	0.35	0/469	0.65	0/635
52	D5	0.31	0/469	0.50	0/635
53	B6	0.37	0/460	0.52	0/613
53	D6	0.29	0/456	0.49	0/608
54	B7	0.40	0/426	0.57	0/561
54	D7	0.33	0/426	0.54	0/561
55	B8	0.37	0/525	0.59	0/691
55	D8	0.32	0/525	0.51	0/691
56	B9	0.37	0/310	0.50	0/407
56	D9	0.33	0/310	0.52	0/407
All	All	0.41	12/316594 (0.0%)	0.87	415/473940 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	2
2	CB	0	1
7	AG	0	2
20	CT	0	1
33	BI	0	1
35	BO	0	1
39	BS	0	1
51	B4	0	1
All	All	0	10

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	1154	G	N1-C2	-10.90	1.29	1.37
1	CA	1119	C	N3-C4	-10.71	1.26	1.33
1	CA	1154	G	C6-N1	-10.47	1.32	1.39
26	DA	528	A	N9-C4	-6.80	1.33	1.37
1	CA	1154	G	N7-C5	-6.78	1.35	1.39
1	CA	1119	C	C2-N3	-6.04	1.30	1.35
26	BA	1188	A	N9-C4	-5.97	1.34	1.37
1	CA	1154	G	C5-C4	5.82	1.42	1.38
24	AX	22	G	N7-C5	5.60	1.42	1.39
24	AX	14	A	N7-C5	-5.36	1.36	1.39
1	CA	1154	G	C8-N7	-5.29	1.27	1.30
1	CA	1119	C	N1-C2	5.25	1.45	1.40

All (415) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1119	C	N1-C2-O2	35.97	140.48	118.90
1	CA	1154	G	C5-C6-O6	25.44	143.86	128.60
1	CA	1154	G	N3-C2-N2	24.34	136.94	119.90
1	CA	1154	G	N1-C2-N2	-21.83	96.56	116.20
1	CA	1119	C	N3-C2-O2	-21.82	106.63	121.90
1	CA	1154	G	C5-C6-N1	-18.28	102.36	111.50
1	CA	1119	C	C2-N3-C4	17.80	128.80	119.90
1	CA	1154	G	C6-N1-C2	16.98	135.29	125.10
1	CA	1119	C	C2-N1-C1'	15.84	136.22	118.80
1	CA	1119	C	N3-C4-N4	-15.07	107.45	118.00
1	CA	1119	C	C5-C4-N4	15.04	130.73	120.20
1	CA	1119	C	C6-N1-C1'	-12.88	105.34	120.80
25	CY	66	U	C5-C4-O4	-11.57	118.96	125.90
1	CA	1154	G	C2-N3-C4	-11.37	106.22	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	46	G	C6-N1-C2	-11.23	118.36	125.10
1	CA	1154	G	C4-N9-C1'	10.50	140.15	126.50
26	DA	2139	C	N1-C2-O2	10.43	125.16	118.90
1	CA	1154	G	N1-C6-O6	-10.31	113.72	119.90
24	AX	14	A	C4-C5-C6	10.16	122.08	117.00
1	CA	1180	A	C5-C6-N1	-9.83	112.78	117.70
26	DA	2139	C	C2-N1-C1'	9.76	129.53	118.80
1	CA	1119	C	N1-C2-N3	-9.72	112.40	119.20
1	CA	1154	G	C8-N9-C1'	-9.27	114.95	127.00
26	DA	34	C	N1-C2-O2	9.06	124.33	118.90
24	AX	14	A	C5-N7-C8	8.99	108.39	103.90
26	DA	2102	U	N1-C2-O2	8.93	129.05	122.80
26	DA	528	A	C2-N3-C4	-8.89	106.15	110.60
25	CY	7	A	C6-N1-C2	-8.88	113.27	118.60
26	DA	2187	G	C5-C6-O6	-8.86	123.28	128.60
26	DA	2174	C	C2-N1-C1'	8.85	128.54	118.80
24	AX	22	G	C5-N7-C8	-8.78	99.91	104.30
25	AY	50	U	C5-C4-O4	8.74	131.15	125.90
1	CA	1004	A	O4'-C1'-N9	8.59	115.08	108.20
1	CA	1119	C	C5-C6-N1	8.58	125.29	121.00
26	BA	537	G	O4'-C1'-N9	8.51	115.01	108.20
24	CX	14	A	C4-C5-C6	8.43	121.22	117.00
25	AY	68	C	N1-C2-O2	8.36	123.92	118.90
26	DA	2682	U	O5'-P-OP2	-8.36	98.18	105.70
1	CA	1119	C	C4-C5-C6	-8.35	113.23	117.40
26	DA	2136	C	N1-C2-O2	8.32	123.89	118.90
25	AY	50	U	C2-N3-C4	8.32	131.99	127.00
1	CA	1180	A	C2-N3-C4	-8.29	106.46	110.60
26	BA	943	C	C5-C6-N1	8.26	125.13	121.00
26	DA	2139	C	C6-N1-C1'	-8.07	111.12	120.80
26	DA	2152	G	N1-C6-O6	8.07	124.74	119.90
26	DA	2061	G	O5'-P-OP2	-8.04	98.47	105.70
25	AY	64	A	C6-N1-C2	8.01	123.41	118.60
26	BA	2162	C	C2-N1-C1'	7.97	127.56	118.80
24	AX	22	G	C4-C5-C6	-7.92	114.05	118.80
1	AA	1027	C	N1-C2-O2	7.92	123.65	118.90
24	AX	14	A	C5-C6-N1	-7.91	113.75	117.70
25	CY	68	C	N1-C2-O2	7.88	123.62	118.90
26	DA	34	C	C2-N1-C1'	7.84	127.43	118.80
26	DA	2152	G	C5-C6-O6	-7.69	123.99	128.60
26	DA	897	C	C2-N1-C1'	7.61	127.17	118.80
25	CY	66	U	N3-C4-O4	7.57	124.69	119.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	79	G	C5-C6-O6	7.50	133.10	128.60
25	AY	64	A	C5-C6-N6	7.47	129.67	123.70
26	BA	2162	C	C6-N1-C2	-7.46	117.32	120.30
24	AX	46	G	N3-C2-N2	-7.39	114.72	119.90
25	CY	7	A	C5-C6-N1	7.38	121.39	117.70
1	CA	1154	G	C4-C5-C6	7.34	123.20	118.80
26	BA	1985	U	C2-N1-C1'	7.32	126.48	117.70
26	DA	2136	C	N3-C2-O2	-7.30	116.79	121.90
26	BA	1045	U	O5'-P-OP2	-7.28	99.14	105.70
23	AW	50	U	C5-C6-N1	7.27	126.33	122.70
1	AA	1042	G	O4'-C1'-N9	7.24	114.00	108.20
25	AY	56	C	N1-C2-O2	7.24	123.25	118.90
26	BA	553	A	C2-N3-C4	-7.23	106.98	110.60
26	BA	12	U	C2-N1-C1'	7.20	126.34	117.70
1	CA	1137	C	O4'-C1'-N1	7.20	113.96	108.20
1	AA	997	U	C5-C4-O4	7.14	130.18	125.90
1	CA	1004	A	N1-C6-N6	-7.13	114.32	118.60
26	DA	2153	G	C5-C6-O6	-7.12	124.33	128.60
25	CY	68	C	N3-C2-O2	-7.12	116.92	121.90
1	AA	1030(B)	C	C2-N1-C1'	7.02	126.52	118.80
23	AW	70	G	C4-N9-C1'	-7.01	117.39	126.50
26	BA	943	C	C2-N1-C1'	6.97	126.47	118.80
26	BA	2162	C	N1-C2-O2	6.97	123.08	118.90
1	CA	1119	C	C6-N1-C2	-6.92	117.53	120.30
26	DA	2155	G	C6-N1-C2	6.92	129.25	125.10
26	DA	2174	C	C6-N1-C1'	-6.90	112.52	120.80
44	DX	57	LEU	CA-CB-CG	6.87	131.10	115.30
25	CY	66	U	C2-N3-C4	-6.86	122.88	127.00
26	BA	139	A	N7-C8-N9	6.84	117.22	113.80
1	AA	1067	A	P-O3'-C3'	6.84	127.91	119.70
26	BA	2281	A	O5'-P-OP1	-6.84	99.55	105.70
26	BA	2163	G	C5-C6-O6	6.83	132.70	128.60
1	CA	1225	A	C5-C6-N6	6.82	129.16	123.70
25	CY	7	A	N3-C4-N9	6.81	132.85	127.40
26	BA	1418	U	C5-C4-O4	-6.80	121.82	125.90
1	AA	1042	G	C8-N9-C1'	6.74	135.76	127.00
26	BA	354	A	C2-N3-C4	-6.73	107.23	110.60
23	AW	70	G	C8-N9-C1'	6.71	135.72	127.00
24	AX	46	G	N1-C2-N3	6.71	127.92	123.90
26	BA	1067	A	C2-N3-C4	-6.70	107.25	110.60
1	AA	1002	G	N3-C4-N9	6.69	130.01	126.00
1	CA	1150	U	C5-C4-O4	6.68	129.91	125.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1002	G	C4-N9-C1'	6.68	135.18	126.50
26	BA	2162	C	N3-C2-O2	-6.67	117.23	121.90
26	DA	2139	C	N3-C2-O2	-6.66	117.24	121.90
26	BA	2014	G	P-O3'-C3'	6.64	127.67	119.70
26	BA	1020	C	N1-C2-O2	-6.64	114.92	118.90
25	AY	4	C	N3-C2-O2	-6.61	117.27	121.90
1	CA	1042	G	N3-C4-C5	6.58	131.89	128.60
1	CA	65	U	P-O3'-C3'	6.58	127.59	119.70
25	CY	18	G	C4-N9-C1'	6.57	135.04	126.50
1	AA	1150	U	C5-C4-O4	6.57	129.84	125.90
26	BA	1188	A	C2-N3-C4	-6.56	107.32	110.60
25	CY	18	G	C8-N9-C1'	-6.55	118.48	127.00
26	BA	990	A	C2-N3-C4	-6.55	107.33	110.60
24	AX	22	G	C8-N9-C1'	6.54	135.50	127.00
1	AA	346	G	C4-N9-C1'	6.52	134.98	126.50
24	CX	14	A	C5-N7-C8	6.52	107.16	103.90
24	CX	46	G	C6-N1-C2	-6.52	121.19	125.10
26	DA	2139	C	N3-C4-C5	6.52	124.51	121.90
26	BA	1418	U	N3-C4-O4	6.52	123.96	119.40
26	DA	34	C	N3-C2-O2	-6.51	117.34	121.90
1	AA	1026	G	C8-N9-C4	-6.47	103.81	106.40
1	CA	848	C	C5-C6-N1	6.46	124.23	121.00
26	DA	2153	G	N1-C6-O6	6.45	123.77	119.90
1	CA	754	C	C2-N1-C1'	6.44	125.89	118.80
1	AA	841	U	C5-C6-N1	6.44	125.92	122.70
25	AY	4	C	C6-N1-C2	-6.43	117.73	120.30
1	CA	1030	C	C2-N1-C1'	6.41	125.84	118.80
26	DA	1614	A	O5'-P-OP1	-6.40	99.94	105.70
1	AA	1002	G	C8-N9-C1'	-6.36	118.73	127.00
26	DA	897	C	C6-N1-C1'	-6.34	113.19	120.80
44	BX	57	LEU	CA-CB-CG	6.32	129.82	115.30
26	BA	1359	U	N3-C2-O2	-6.30	117.79	122.20
25	CY	23	A	N1-C6-N6	6.30	122.38	118.60
25	AY	64	A	C5-C6-N1	-6.29	114.56	117.70
26	BA	1359	U	C2-N1-C1'	6.25	125.20	117.70
1	CA	1256	A	O4'-C1'-N9	-6.24	103.20	108.20
1	AA	839	U	P-O3'-C3'	6.23	127.18	119.70
23	CW	69	G	O4'-C1'-N9	-6.23	103.22	108.20
1	CA	1003	G	N7-C8-N9	6.22	116.21	113.10
1	AA	1042	G	C4-N9-C1'	-6.21	118.42	126.50
24	AX	22	G	C5-C6-N1	6.21	114.60	111.50
26	BA	2122	G	C5-C6-O6	-6.21	124.88	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AY	23	A	N1-C6-N6	-6.20	114.88	118.60
1	CA	955	U	C5-C4-O4	6.19	129.62	125.90
23	AW	70	G	N3-C4-N9	-6.18	122.29	126.00
26	BA	2858	G	O4'-C1'-N9	6.16	113.12	108.20
1	CA	984	C	C2-N3-C4	6.15	122.98	119.90
25	CY	68	C	C2-N1-C1'	6.13	125.55	118.80
1	CA	1003	G	C4-N9-C1'	6.13	134.47	126.50
13	CM	71	ARG	NE-CZ-NH1	6.12	123.36	120.30
31	BG	3	LEU	CA-CB-CG	6.12	129.38	115.30
26	BA	670	C	C2-N1-C1'	6.12	125.53	118.80
26	BA	1686	U	O5'-P-OP2	-6.12	100.20	105.70
1	AA	1027	C	N3-C2-O2	-6.10	117.63	121.90
26	BA	2627	U	O5'-P-OP1	-6.10	100.21	105.70
1	CA	1225	A	N1-C6-N6	-6.09	114.94	118.60
26	BA	1660	A	O5'-P-OP1	-6.09	100.22	105.70
26	DA	512	G	O4'-C1'-N9	6.09	113.07	108.20
1	CA	1126	U	C2-N1-C1'	6.08	125.00	117.70
26	DA	801	G	O5'-P-OP2	-6.08	100.23	105.70
25	CY	10	G	N1-C6-O6	6.06	123.53	119.90
1	CA	1452	C	C6-N1-C2	-6.05	117.88	120.30
26	DA	1992	G	C8-N9-C4	-6.05	103.98	106.40
26	BA	978	A	O4'-C1'-N9	6.02	113.02	108.20
24	AX	46	G	C5-C6-N1	6.02	114.51	111.50
1	CA	1039	C	C5-C6-N1	6.01	124.01	121.00
26	DA	2102	U	C2-N3-C4	6.00	130.60	127.00
26	BA	2185	C	C6-N1-C2	-6.00	117.90	120.30
23	CW	10	G	N3-C2-N2	-5.99	115.71	119.90
26	DA	1531	C	C2-N1-C1'	5.99	125.38	118.80
26	BA	2260	C	O5'-P-OP2	-5.98	100.31	105.70
26	DA	2187	G	N3-C4-N9	5.98	129.59	126.00
26	DA	2160	G	C5-C6-O6	5.98	132.19	128.60
26	DA	2128	C	C2-N3-C4	5.97	122.89	119.90
26	DA	2167	U	N3-C2-O2	-5.97	118.02	122.20
1	AA	991	U	P-O3'-C3'	5.95	126.83	119.70
26	BA	215	G	O4'-C1'-N9	5.94	112.95	108.20
1	CA	998	G	N9-C4-C5	5.94	107.78	105.40
26	DA	34	C	C6-N1-C1'	-5.94	113.67	120.80
24	AX	22	G	N3-C4-N9	-5.94	122.44	126.00
26	BA	1346	U	P-O3'-C3'	5.94	126.82	119.70
26	BA	31	C	O5'-P-OP1	-5.93	100.36	105.70
42	DV	38	LEU	CA-CB-CG	5.93	128.94	115.30
26	BA	354	A	N1-C2-N3	5.93	132.26	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	501	C	O5'-P-OP1	-5.93	100.36	105.70
26	BA	139	A	C5-N7-C8	-5.92	100.94	103.90
1	AA	1026	G	N7-C8-N9	5.91	116.06	113.10
24	AX	22	G	N1-C6-O6	-5.91	116.35	119.90
26	BA	1539	C	N1-C2-O2	5.91	122.44	118.90
1	CA	1003	G	C8-N9-C4	-5.91	104.04	106.40
1	CA	1220	G	N3-C2-N2	-5.91	115.77	119.90
26	DA	528	A	N1-C2-N3	5.91	132.25	129.30
26	BA	1221	G	OP1-P-O3'	5.90	118.17	105.20
1	CA	955	U	C2-N3-C4	5.90	130.54	127.00
26	DA	2190	G	C5-C6-O6	5.90	132.14	128.60
26	BA	139	A	O4'-C1'-N9	5.89	112.92	108.20
26	BA	1361	C	O5'-P-OP2	-5.88	100.41	105.70
1	AA	1123	A	C6-N1-C2	5.87	122.12	118.60
26	BA	2083	G	O5'-P-OP2	-5.86	100.43	105.70
25	AY	15	G	N3-C2-N2	5.85	124.00	119.90
26	BA	978	A	N7-C8-N9	5.85	116.72	113.80
1	CA	1001(A)	G	C5-C6-O6	-5.85	125.09	128.60
1	AA	1137	C	O4'-C1'-N1	-5.84	103.53	108.20
26	DA	1204	A	O4'-C1'-N9	5.84	112.87	108.20
1	CA	1166	G	N7-C8-N9	5.84	116.02	113.10
1	CA	1323	G	N3-C4-N9	5.82	129.49	126.00
1	CA	1180	A	C4-C5-C6	5.81	119.91	117.00
26	DA	2167	U	N1-C2-O2	5.81	126.87	122.80
26	BA	2802	C	C2-N1-C1'	-5.80	112.42	118.80
25	CY	4	C	N1-C2-O2	5.79	122.38	118.90
25	CY	10	G	C5-C6-O6	-5.79	125.12	128.60
1	CA	1031	G	C5-C6-O6	-5.79	125.13	128.60
24	CX	14	A	N1-C6-N6	5.78	122.07	118.60
26	BA	273	G	P-O3'-C3'	5.77	126.62	119.70
26	BA	553	A	N3-C4-N9	-5.74	122.81	127.40
23	CW	66	U	P-O3'-C3'	5.74	126.58	119.70
26	BA	934	A	O4'-C1'-N9	5.73	112.79	108.20
27	DB	30	C	C6-N1-C2	-5.73	118.01	120.30
26	BA	2604	G	O5'-P-OP1	-5.71	100.56	105.70
24	AX	22	G	C4-N9-C1'	-5.71	119.08	126.50
1	AA	1052	U	N1-C2-O2	5.71	126.80	122.80
25	AY	60	U	C2-N1-C1'	5.70	124.54	117.70
1	AA	204	U	C2-N1-C1'	5.69	124.53	117.70
26	BA	1020	C	C2-N1-C1'	-5.69	112.54	118.80
26	BA	1807	G	O5'-P-OP2	-5.69	100.58	105.70
26	DA	897	C	N1-C2-O2	5.69	122.31	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	572	A	P-O3'-C3'	5.69	126.52	119.70
25	CY	7	A	N3-C4-C5	-5.68	122.82	126.80
26	BA	1985	U	N1-C2-O2	5.68	126.78	122.80
26	DA	2248	C	O5'-P-OP2	-5.68	100.59	105.70
1	CA	1154	G	N3-C4-N9	5.67	129.41	126.00
26	DA	1300	U	P-O3'-C3'	5.67	126.51	119.70
24	AX	20	U	C2-N1-C1'	5.67	124.51	117.70
26	BA	1815	A	O5'-P-OP2	-5.67	100.59	105.70
1	AA	1150	U	C2-N3-C4	5.66	130.40	127.00
26	DA	2155	G	N3-C2-N2	5.66	123.86	119.90
26	DA	2102	U	N3-C2-O2	-5.65	118.24	122.20
26	BA	273	G	OP1-P-O3'	5.64	117.62	105.20
26	DA	784	A	O4'-C1'-N9	5.64	112.71	108.20
1	CA	182	U	N1-C2-O2	-5.64	118.85	122.80
23	CW	36	A	C6-N1-C2	5.63	121.98	118.60
1	CA	1126	U	N1-C2-O2	5.63	126.74	122.80
25	AY	56	C	N3-C2-O2	-5.62	117.96	121.90
1	CA	1137	C	C2-N1-C1'	-5.61	112.62	118.80
1	CA	204	U	C2-N1-C1'	5.61	124.43	117.70
24	AX	22	G	N3-C4-C5	5.61	131.41	128.60
24	AX	46	G	N9-C4-C5	5.61	107.64	105.40
1	CA	1023	G	C4-N9-C1'	5.61	133.79	126.50
1	AA	346	G	O4'-C1'-N9	5.60	112.68	108.20
25	AY	68	C	C5-C6-N1	5.60	123.80	121.00
26	BA	793	A	O4'-C1'-N9	5.60	112.68	108.20
26	DA	1313	U	C2-N1-C1'	5.60	124.42	117.70
1	AA	1502	A	N1-C2-N3	5.59	132.09	129.30
25	CY	31	A	N1-C6-N6	5.58	121.95	118.60
1	AA	1206	G	C5-C6-O6	-5.58	125.25	128.60
1	CA	998	G	C6-C5-N7	5.58	133.75	130.40
25	AY	68	C	N3-C2-O2	-5.57	118.00	121.90
26	DA	1992	G	P-O3'-C3'	5.57	126.38	119.70
1	CA	1039	C	C2-N1-C1'	5.56	124.92	118.80
1	AA	91	C	C2-N1-C1'	5.56	124.91	118.80
1	CA	1047	G	N3-C4-N9	5.55	129.33	126.00
26	DA	2155	G	N1-C2-N3	-5.54	120.57	123.90
23	CW	67	C	C2-N3-C4	5.54	122.67	119.90
1	AA	1165	C	P-O3'-C3'	5.54	126.34	119.70
26	BA	1067	A	N1-C2-N3	5.53	132.06	129.30
26	BA	2605	U	N3-C4-O4	-5.53	115.53	119.40
1	CA	986	A	C6-N1-C2	-5.53	115.28	118.60
1	CA	1039	C	C5-C4-N4	-5.53	116.33	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	DA	2128	C	N1-C2-O2	5.52	122.21	118.90
26	BA	1398	U	O5'-P-OP1	-5.52	100.73	105.70
24	CX	22	G	C5-N7-C8	-5.51	101.54	104.30
1	CA	1042	G	N3-C4-N9	-5.51	122.69	126.00
1	CA	992	U	C5-C6-N1	5.50	125.45	122.70
25	CY	62	C	C2-N3-C4	5.50	122.65	119.90
26	BA	1985	U	C6-N1-C1'	-5.50	113.51	121.20
27	BB	85	G	O4'-C1'-N9	-5.49	103.81	108.20
1	CA	1180	A	N1-C2-N3	5.48	132.04	129.30
1	CA	1154	G	C5-N7-C8	5.48	107.04	104.30
26	BA	990	A	C5-N7-C8	-5.48	101.16	103.90
24	AX	14	A	C4-N9-C1'	5.47	136.16	126.30
1	CA	1030(B)	C	C6-N1-C2	-5.47	118.11	120.30
1	CA	998	G	C4-C5-N7	-5.47	108.61	110.80
26	DA	277	C	N1-C2-O2	5.47	122.18	118.90
1	AA	1065	U	P-O3'-C3'	5.47	126.26	119.70
26	DA	2160	G	C6-N1-C2	5.46	128.38	125.10
26	DA	2139	C	C5-C6-N1	5.45	123.73	121.00
40	BT	118	ARG	NE-CZ-NH1	5.45	123.02	120.30
26	BA	989	G	C4-N9-C1'	5.44	133.57	126.50
26	BA	1068	G	N3-C2-N2	-5.44	116.09	119.90
26	BA	1177	G	O4'-C1'-N9	5.44	112.55	108.20
26	DA	2187	G	C6-N1-C2	-5.43	121.84	125.10
1	AA	1131	G	C6-C5-N7	-5.43	127.14	130.40
1	CA	997	U	C5-C4-O4	5.42	129.15	125.90
26	DA	2187	G	N1-C6-O6	5.42	123.15	119.90
1	CA	1183	A	P-O3'-C3'	5.41	126.20	119.70
22	CV	19	U	C2-N3-C4	5.41	130.25	127.00
23	CW	3	C	C6-N1-C2	-5.41	118.14	120.30
1	AA	841	U	C6-N1-C2	-5.41	117.75	121.00
24	AX	14	A	C8-N9-C1'	-5.40	117.99	127.70
1	AA	1030(B)	C	N1-C2-O2	5.39	122.14	118.90
23	AW	44	G	C5-C6-O6	5.39	131.84	128.60
24	AX	46	G	C4-C5-N7	-5.39	108.64	110.80
26	BA	2189	U	C2-N1-C1'	5.39	124.16	117.70
26	BA	2156	A	C3'-C2'-C1'	5.38	105.81	101.50
1	CA	998	G	N3-C4-N9	-5.38	122.77	126.00
2	CB	154	LEU	CA-CB-CG	5.38	127.67	115.30
1	CA	942	G	C5-C6-O6	5.38	131.83	128.60
1	AA	1285	A	P-O3'-C3'	5.34	126.11	119.70
26	BA	139	A	C8-N9-C4	-5.34	103.66	105.80
23	CW	25	C	C5-C4-N4	5.34	123.94	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	DA	2153	G	C8-N9-C1'	-5.33	120.07	127.00
1	AA	925	G	C5-C6-O6	-5.33	125.40	128.60
1	CA	1123	A	C5-C6-N6	5.33	127.96	123.70
1	CA	1216	G	C4-N9-C1'	-5.33	119.58	126.50
26	DA	2153	G	N3-C4-N9	5.32	129.19	126.00
24	AX	22	G	N7-C8-N9	5.32	115.76	113.10
26	BA	1221	G	P-O3'-C3'	5.32	126.08	119.70
1	CA	1054	C	O4'-C1'-N1	5.31	112.45	108.20
3	CC	52	LEU	CA-CB-CG	5.31	127.50	115.30
26	BA	553	A	N3-C4-C5	5.30	130.51	126.80
1	CA	1122	U	C5-C4-O4	5.30	129.08	125.90
1	CA	1004	A	C6-C5-N7	5.30	136.01	132.30
26	DA	528	A	N3-C4-C5	5.30	130.51	126.80
26	DA	2153	G	N9-C4-C5	-5.30	103.28	105.40
26	DA	748	G	O4'-C1'-N9	5.29	112.43	108.20
26	BA	2359	C	N1-C2-O2	5.29	122.07	118.90
1	CA	992	U	P-O3'-C3'	5.28	126.04	119.70
26	DA	2313	C	N1-C2-O2	5.26	122.06	118.90
26	BA	2442	A	C2-N3-C4	5.26	113.23	110.60
1	CA	1220	G	N3-C4-N9	-5.25	122.85	126.00
1	CA	1452	C	C5-C6-N1	5.25	123.63	121.00
1	AA	1010	G	N3-C4-N9	5.25	129.15	126.00
1	CA	79	G	N1-C6-O6	-5.25	116.75	119.90
25	AY	23	A	C4-C5-C6	-5.25	114.38	117.00
25	CY	50	U	C5-C4-O4	5.24	129.05	125.90
26	BA	2213	G	N7-C8-N9	5.24	115.72	113.10
26	DA	2889	C	N1-C2-O2	5.24	122.05	118.90
24	CX	34	C	C2-N1-C1'	5.24	124.56	118.80
1	CA	998	G	N1-C6-O6	-5.22	116.77	119.90
26	BA	978	A	C5-N7-C8	-5.22	101.29	103.90
26	DA	2297	C	C6-N1-C2	-5.22	118.21	120.30
1	CA	687	A	P-O3'-C3'	5.21	125.96	119.70
1	AA	266	G	P-O3'-C3'	5.21	125.96	119.70
1	CA	992	U	C2-N1-C1'	5.21	123.95	117.70
1	CA	182	U	C2-N1-C1'	-5.21	111.45	117.70
26	BA	599	U	O5'-P-OP1	-5.20	101.02	105.70
22	AV	17	U	C5-C4-O4	5.20	129.02	125.90
26	BA	1462	G	O4'-C1'-N9	5.20	112.36	108.20
26	BA	2227	G	C5-C6-O6	-5.19	125.48	128.60
25	AY	50	U	N3-C4-C5	-5.19	111.49	114.60
26	DA	1937	A	O4'-C1'-N9	5.19	112.35	108.20
2	CB	51	LEU	CA-CB-CG	5.17	127.20	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	598	A	O5'-P-OP1	-5.17	101.05	105.70
23	CW	44	G	N3-C4-N9	5.17	129.10	126.00
26	DA	2689	U	P-O3'-C3'	5.16	125.89	119.70
35	DO	8	LEU	CA-CB-CG	5.16	127.16	115.30
1	CA	754	C	N1-C2-O2	5.16	121.99	118.90
25	CY	9	A	C4-C5-C6	-5.16	114.42	117.00
26	BA	2621	U	C2-N1-C1'	-5.15	111.52	117.70
26	BA	1153	G	N3-C4-C5	-5.15	126.02	128.60
1	CA	1012	U	N1-C2-N3	5.15	117.99	114.90
26	BA	2701	U	P-O3'-C3'	5.14	125.87	119.70
26	DA	2153	G	C6-C5-N7	-5.14	127.32	130.40
26	DA	2174	C	C5-C6-N1	5.14	123.57	121.00
36	DP	44	GLY	C-N-CA	5.14	134.54	121.70
1	CA	1030	C	C6-N1-C1'	-5.13	114.64	120.80
26	BA	873	U	OP1-P-O3'	5.13	116.49	105.20
1	CA	999	C	C2-N3-C4	5.13	122.47	119.90
26	DA	2178	C	N1-C2-O2	5.13	121.98	118.90
1	AA	1042	G	N3-C4-N9	-5.13	122.92	126.00
24	AX	14	A	C4-C5-N7	-5.12	108.14	110.70
1	CA	1124	G	N3-C4-N9	5.12	129.07	126.00
1	AA	1036	G	C4-N9-C1'	5.11	133.14	126.50
26	BA	2163	G	C6-N1-C2	5.11	128.16	125.10
25	CY	25	C	C2-N1-C1'	5.11	124.42	118.80
26	BA	2196	C	C2-N1-C1'	5.09	124.40	118.80
1	CA	1221	G	C6-N1-C2	5.09	128.16	125.10
22	CV	19	U	C5-C4-O4	5.09	128.96	125.90
1	CA	953	G	N3-C4-N9	5.09	129.06	126.00
26	BA	1067	A	C8-N9-C4	-5.09	103.77	105.80
27	DB	42	C	N1-C2-O2	5.09	121.95	118.90
25	AY	9	A	N1-C6-N6	5.08	121.65	118.60
1	CA	1166	G	C8-N9-C4	-5.08	104.37	106.40
1	CA	1064	G	P-O3'-C3'	5.08	125.79	119.70
26	DA	1038	C	C2-N1-C1'	5.07	124.38	118.80
1	CA	1126	U	C6-N1-C1'	-5.07	114.10	121.20
26	DA	2206	G	C4-N9-C1'	-5.07	119.91	126.50
26	DA	2155	G	N9-C4-C5	-5.07	103.37	105.40
23	AW	70	G	C6-C5-N7	5.06	133.44	130.40
26	BA	892	G	O4'-C1'-N9	5.06	112.25	108.20
26	DA	2174	C	N1-C2-O2	5.06	121.93	118.90
26	BA	2802	C	O4'-C1'-N1	5.06	112.25	108.20
25	CY	68	C	C6-N1-C2	-5.05	118.28	120.30
26	DA	2153	G	C4-N9-C1'	5.05	133.07	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1067	A	O4'-C1'-N9	-5.05	104.16	108.20
26	BA	1068	G	N3-C4-N9	-5.05	122.97	126.00
26	BA	2331	G	O4'-C1'-N9	5.05	112.24	108.20
23	CW	25	C	C6-N1-C1'	5.05	126.86	120.80
1	CA	65	U	OP2-P-O3'	5.04	116.30	105.20
26	BA	2205	C	N1-C2-O2	-5.04	115.88	118.90
25	AY	15	G	N1-C2-N2	-5.04	111.66	116.20
25	CY	50	U	O4'-C1'-N1	5.04	112.23	108.20
26	BA	2298	A	N7-C8-N9	5.03	116.31	113.80
1	AA	1173	G	N3-C4-N9	5.03	129.02	126.00
1	AA	1019	C	N1-C2-O2	5.03	121.92	118.90
26	DA	1558	A	P-O3'-C3'	5.03	125.73	119.70
1	CA	204	U	O4'-C1'-N1	5.03	112.22	108.20
1	AA	1026	G	N3-C4-C5	-5.02	126.09	128.60
1	CA	60	A	P-O3'-C3'	5.02	125.73	119.70
1	CA	998	G	C8-N9-C1'	5.02	133.53	127.00
25	AY	4	C	N1-C2-O2	5.02	121.91	118.90
25	CY	7	A	C6-C5-N7	-5.02	128.79	132.30
26	DA	2139	C	C4-C5-C6	-5.02	114.89	117.40
1	AA	1502	A	N7-C8-N9	5.01	116.30	113.80
25	CY	18	G	N3-C4-N9	5.01	129.01	126.00
26	BA	410	U	C2-N1-C1'	-5.00	111.70	117.70
23	AW	49	C	C6-N1-C2	-5.00	118.30	120.30

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	231	GLU	Peptide
2	AB	9	GLU	Peptide
7	AG	78	ARG	Peptide
7	AG	79	ARG	Peptide
51	B4	59	PHE	Peptide
33	BI	9	LEU	Peptide
35	BO	80	ASP	Peptide
39	BS	58	LEU	Peptide
2	CB	9	GLU	Peptide
20	CT	9	ASN	Peptide

5.2 Close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32185	0	16245	536	0
1	CA	32312	0	16307	762	0
2	AB	1846	0	1867	81	0
2	CB	1825	0	1828	119	0
3	AC	1552	0	1546	60	0
3	CC	1544	0	1524	70	0
4	AD	1659	0	1676	56	0
4	CD	1678	0	1718	67	0
5	AE	1129	0	1185	27	0
5	CE	1133	0	1191	46	0
6	AF	812	0	804	18	0
6	CF	820	0	814	19	0
7	AG	1231	0	1238	21	0
7	CG	1235	0	1249	39	0
8	AH	1088	0	1126	35	0
8	CH	1088	0	1126	40	0
9	AI	986	0	995	43	0
9	CI	978	0	966	55	0
10	AJ	709	0	650	34	0
10	CJ	714	0	672	44	0
11	AK	833	0	836	19	0
11	CK	833	0	836	22	0
12	AL	930	0	980	27	0
12	CL	930	0	980	33	0
13	AM	966	0	1024	40	0
13	CM	950	0	988	74	0
14	AN	492	0	529	26	0
14	CN	492	0	529	34	0
15	AO	728	0	760	20	0
15	CO	728	0	760	22	0
16	AP	681	0	697	27	0
16	CP	677	0	686	22	0
17	AQ	823	0	891	26	0
17	CQ	823	0	891	19	0
18	AR	555	0	618	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	CR	555	0	618	24	0
19	AS	661	0	675	31	0
19	CS	646	0	644	40	0
20	AT	728	0	798	26	0
20	CT	731	0	807	26	0
21	AU	199	0	208	8	0
21	CU	199	0	208	9	0
22	AV	277	0	140	3	0
22	CV	252	0	130	6	0
23	AW	1599	0	808	42	0
23	CW	1552	0	772	51	0
24	AX	1635	0	817	23	0
24	CX	1635	0	817	36	0
25	AY	1581	0	805	82	0
25	CY	1561	0	796	94	0
26	BA	60729	0	30622	666	0
26	DA	60311	0	30412	876	0
27	BB	2573	0	1306	20	0
27	DB	2573	0	1306	76	0
28	BD	2136	0	2218	42	0
28	DD	2142	0	2229	58	0
29	BE	1559	0	1618	25	0
29	DE	1559	0	1618	39	0
30	BF	1584	0	1625	39	0
30	DF	1580	0	1619	60	0
31	BG	1425	0	1443	38	0
31	DG	1424	0	1434	90	0
32	BH	1330	0	1407	34	0
32	DH	1330	0	1407	44	0
33	BI	1085	0	1114	37	0
33	DI	1073	0	1106	22	0
34	BN	1117	0	1184	23	0
34	DN	1117	0	1184	26	0
35	BO	933	0	996	25	0
35	DO	933	0	996	32	0
36	BP	1139	0	1223	41	0
36	DP	1135	0	1212	52	0
37	BQ	1122	0	1179	28	0
37	DQ	1122	0	1179	40	0
38	BR	968	0	1033	22	0
38	DR	968	0	1033	28	0
39	BS	877	0	938	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	DS	870	0	923	33	0
40	BT	1091	0	1151	26	0
40	DT	1083	0	1136	37	0
41	BU	959	0	1019	18	0
41	DU	959	0	1018	30	0
42	BV	771	0	830	13	0
42	DV	771	0	830	24	0
43	BW	886	0	940	17	0
43	DW	886	0	940	13	0
44	BX	750	0	814	15	0
44	DX	750	0	814	27	0
45	BY	806	0	881	27	0
45	DY	806	0	881	30	0
46	BZ	1349	0	1355	44	0
46	DZ	1360	0	1363	70	0
47	B0	653	0	674	13	0
47	D0	653	0	674	22	0
48	B1	755	0	826	16	0
48	D1	755	0	826	18	0
49	B2	588	0	643	11	0
49	D2	588	0	643	14	0
50	B3	469	0	518	6	0
50	D3	464	0	514	13	0
51	B4	558	0	544	37	0
51	D4	532	0	503	25	0
52	B5	455	0	465	14	0
52	D5	455	0	465	13	0
53	B6	453	0	473	13	0
53	D6	449	0	469	12	0
54	B7	418	0	467	10	0
54	D7	418	0	467	13	0
55	B8	517	0	582	17	0
55	D8	517	0	582	15	0
56	B9	307	0	335	7	0
56	D9	307	0	335	11	0
57	AA	216	0	0	0	0
57	AB	1	0	0	0	0
57	AE	1	0	0	0	0
57	AF	1	0	0	0	0
57	AK	1	0	0	0	0
57	AL	2	0	0	0	0
57	AM	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	AN	2	0	0	0	0
57	AT	1	0	0	0	0
57	AU	1	0	0	0	0
57	AW	2	0	0	0	0
57	AX	15	0	0	0	0
57	AY	3	0	0	0	0
57	B0	2	0	0	0	0
57	B2	1	0	0	0	0
57	B4	1	0	0	0	0
57	B5	3	0	0	0	0
57	B6	2	0	0	0	0
57	B7	5	0	0	0	0
57	B8	2	0	0	0	0
57	B9	1	0	0	0	0
57	BA	814	0	0	0	0
57	BB	23	0	0	0	0
57	BD	10	0	0	0	0
57	BE	6	0	0	0	0
57	BF	11	0	0	0	0
57	BG	2	0	0	0	0
57	BH	1	0	0	0	0
57	BN	3	0	0	0	0
57	BO	1	0	0	0	0
57	BP	2	0	0	0	0
57	BQ	2	0	0	0	0
57	BR	2	0	0	0	0
57	BU	4	0	0	0	0
57	BV	5	0	0	0	0
57	BW	4	0	0	0	0
57	BX	1	0	0	0	0
57	BY	1	0	0	0	0
57	BZ	2	0	0	0	0
57	CA	169	0	0	0	0
57	CD	1	0	0	0	0
57	CE	2	0	0	0	0
57	CF	1	0	0	0	0
57	CJ	1	0	0	0	0
57	CK	1	0	0	0	0
57	CT	1	0	0	0	0
57	CW	1	0	0	0	0
57	CX	2	0	0	0	0
57	D0	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	D3	1	0	0	0	0
57	D8	1	0	0	0	0
57	DA	664	0	0	0	0
57	DB	13	0	0	0	0
57	DD	4	0	0	0	0
57	DE	7	0	0	0	0
57	DF	5	0	0	0	0
57	DG	1	0	0	0	0
57	DN	1	0	0	0	0
57	DO	2	0	0	0	0
57	DP	2	0	0	0	0
57	DQ	3	0	0	0	0
57	DR	1	0	0	0	0
57	DU	1	0	0	0	0
57	DV	1	0	0	0	0
57	DW	1	0	0	0	0
57	DY	1	0	0	0	0
58	AD	8	0	0	1	0
58	CD	8	0	0	1	0
59	AN	1	0	0	0	0
59	B4	1	0	0	0	0
59	B5	1	0	0	0	0
59	B6	1	0	0	0	0
59	B9	1	0	0	0	0
59	BY	1	0	0	0	0
59	CN	1	0	0	0	0
59	D4	1	0	0	0	0
59	D5	1	0	0	0	0
59	D6	1	0	0	0	0
59	D9	1	0	0	0	0
59	DY	1	0	0	0	0
60	AX	1	0	0	0	0
61	AA	210	0	0	13	0
61	AD	1	0	0	0	0
61	AE	2	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	2	0	0	1	0
61	AM	2	0	0	0	0
61	AV	2	0	0	0	0
61	AW	4	0	0	0	0
61	AX	4	0	0	0	0
61	AY	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	B0	6	0	0	0	0
61	B1	2	0	0	0	0
61	B3	2	0	0	0	0
61	B5	4	0	0	0	0
61	B6	2	0	0	0	0
61	B7	3	0	0	2	0
61	B8	13	0	0	0	0
61	B9	1	0	0	0	0
61	BA	1406	0	0	56	0
61	BB	37	0	0	1	0
61	BD	15	0	0	2	0
61	BE	17	0	0	4	0
61	BF	11	0	0	0	0
61	BG	3	0	0	0	0
61	BH	1	0	0	0	0
61	BI	1	0	0	0	0
61	BN	1	0	0	0	0
61	BO	2	0	0	0	0
61	BP	13	0	0	0	0
61	BQ	4	0	0	0	0
61	BR	2	0	0	0	0
61	BS	2	0	0	0	0
61	BT	2	0	0	0	0
61	BU	4	0	0	0	0
61	BV	2	0	0	0	0
61	BW	3	0	0	1	0
61	BX	3	0	0	0	0
61	BZ	1	0	0	0	0
61	CA	156	0	0	11	0
61	CE	2	0	0	0	0
61	CH	1	0	0	0	0
61	CJ	1	0	0	0	0
61	CK	1	0	0	0	0
61	CL	1	0	0	1	0
61	CT	1	0	0	0	0
61	CW	2	0	0	2	0
61	CX	2	0	0	0	0
61	CY	1	0	0	0	0
61	D0	4	0	0	0	0
61	D1	1	0	0	0	0
61	D3	2	0	0	0	0
61	D5	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	D6	1	0	0	0	0
61	D8	3	0	0	0	0
61	DA	989	0	0	44	0
61	DB	9	0	0	0	0
61	DD	18	0	0	3	0
61	DE	5	0	0	0	0
61	DF	4	0	0	0	0
61	DN	2	0	0	0	0
61	DP	12	0	0	4	0
61	DQ	1	0	0	0	0
61	DT	4	0	0	0	0
61	DU	1	0	0	0	0
61	DV	1	0	0	0	0
61	DW	1	0	0	0	0
61	DX	2	0	0	0	0
61	DY	1	0	0	0	0
All	All	297127	0	196316	5502	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 12.

All (5502) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2139:C:N4	26:DA:2152:G:H1	1.46	1.14
1:CA:999:C:N4	1:CA:1042:G:H1	1.48	1.12
25:AY:49:C:N4	25:AY:65:G:H1	1.51	1.09
1:CA:985:C:N4	1:CA:1220:G:H1	1.50	1.09
1:CA:998:G:H1	1:CA:1043:C:N4	1.51	1.09
25:CY:7:A:N6	25:CY:66:U:H3	1.54	1.06
26:DA:2138:C:N4	26:DA:2153:G:H1	1.53	1.04
25:AY:53:G:H1	25:AY:61:C:N4	1.56	1.04
26:BA:2158:C:N4	26:BA:2177:G:H1	1.57	1.02
45:BY:92:ASN:HB2	45:BY:94:LYS:H	1.21	1.02
26:BA:2124:U:H3	26:BA:2209:G:H1	1.06	1.00
1:CA:1245:A:H61	1:CA:1292:U:H3	1.09	1.00
1:CA:985:C:H42	1:CA:1220:G:H1	0.99	0.99
1:CA:1162:C:N4	1:CA:1174:G:H1	1.60	0.99
25:CY:10:G:H1	25:CY:25:C:H42	1.09	0.98
26:BA:2511:C:OP1	61:BA:5135:HOH:O	1.83	0.97
4:CD:15:GLU:HG3	4:CD:63:LYS:HG3	1.47	0.96
26:BA:2160:C:H42	26:BA:2175:G:H1	1.09	0.96
1:CA:1000:U:H3	1:CA:1041:A:N6	1.63	0.95

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:CY:50:U:H3	25:CY:64:A:H61	1.02	0.95
26:DA:2127:G:C6	26:DA:2161:C:N4	2.34	0.95
23:AW:26:A:H61	23:AW:44:G:H1	1.06	0.94
47:B0:11:ARG:O	47:B0:14:ARG:NH2	1.99	0.94
25:AY:29:G:H1	25:AY:41:C:N4	1.65	0.94
1:CA:76:C:N4	1:CA:93:G:H1	1.64	0.94
1:CA:1025:U:H3	1:CA:1036:G:H1	1.03	0.94
25:CY:22:G:N7	25:CY:46:7MG:N2	2.14	0.94
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.31	0.94
1:CA:501:C:OP1	12:CL:124:LYS:NZ	2.01	0.93
1:CA:1162:C:H42	1:CA:1174:G:H1	1.14	0.93
40:DT:55:ASN:H	40:DT:59:THR:HG22	1.29	0.93
26:BA:1829:U:H5'	28:BD:259:THR:HG22	1.50	0.93
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.47	0.93
23:AW:19:G:H1	23:AW:56:C:H42	1.17	0.93
1:CA:838:G:H1	1:CA:848:C:H42	1.10	0.93
35:BO:35:VAL:HG11	35:BO:103:ALA:HB3	1.51	0.92
26:BA:2143:G:H1	26:BA:2199:C:H42	1.13	0.92
46:DZ:5:LEU:HG	46:DZ:47:VAL:HG21	1.50	0.92
25:CY:19:G:H1	25:CY:56:C:H42	1.12	0.92
25:CY:51:U:H3	25:CY:63:G:H1	1.17	0.91
23:AW:1:G:O6	23:AW:72:C:N3	2.04	0.91
26:DA:2121:G:H1	26:DA:2177:C:N4	1.68	0.91
26:DA:631:A:OP1	36:DP:65:ARG:NH1	2.04	0.91
1:CA:985:C:N3	1:CA:1220:G:N2	2.17	0.91
19:CS:42:PRO:HG3	51:D4:61:ARG:HG3	1.53	0.91
26:DA:2139:C:N4	26:DA:2152:G:N1	2.12	0.91
1:CA:1165:C:H42	1:CA:1171:G:H1	1.19	0.90
25:AY:53:G:H1	25:AY:61:C:H42	0.91	0.90
25:AY:29:G:H1	25:AY:41:C:H42	0.90	0.90
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.06	0.89
26:DA:2121:G:H1	26:DA:2177:C:H42	0.95	0.89
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.55	0.89
1:CA:1244:C:H42	1:CA:1293:G:H1	1.12	0.89
25:AY:49:C:N3	25:AY:65:G:N2	2.21	0.89
1:CA:999:C:N3	1:CA:1042:G:N2	2.21	0.89
25:CY:19:G:N2	25:CY:56:C:N3	2.20	0.89
26:DA:1798:U:H5'	28:DD:259:THR:HG22	1.55	0.89
25:CY:9:A:N6	25:CY:23:A:OP2	2.06	0.88
1:CA:998:G:N2	1:CA:1043:C:N3	2.20	0.88
1:AA:78:G:C6	1:AA:91:C:N4	2.40	0.88
25:AY:5:G:H1	25:AY:68:C:H42	1.16	0.88

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:DZ:110:GLY:HA3	46:DZ:145:GLU:HA	1.55	0.88
1:AA:1316:G:H22	1:AA:1319:A:H5''	1.39	0.88
27:DB:41:U:H5	31:DG:70:VAL:H	1.22	0.88
1:AA:78:G:C2	1:AA:91:C:N3	2.43	0.87
46:BZ:138:GLU:H	46:BZ:156:LYS:HD3	1.36	0.87
1:AA:1166:G:N2	1:AA:1170:A:OP2	2.06	0.87
23:AW:1:G:N1	23:AW:72:C:O2	2.07	0.87
41:DU:76:TYR:OH	41:DU:92:ARG:NH1	2.08	0.87
26:BA:1221:G:H1'	26:BA:1222:A:H5'	1.55	0.87
25:CY:15:G:H22	25:CY:48:C:H42	1.16	0.87
9:AI:17:VAL:HG21	9:AI:81:ILE:HG22	1.55	0.87
11:AK:48:ILE:HD12	11:AK:63:LEU:HB2	1.54	0.86
1:AA:1502:A:H2	1:AA:1505:G:H1	1.21	0.86
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.06	0.86
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.57	0.86
25:CY:50:U:H3	25:CY:64:A:N6	1.74	0.86
26:BA:2212:G:H2'	26:BA:2213:G:H5''	1.56	0.86
26:DA:2139:C:N3	26:DA:2152:G:N2	2.23	0.86
1:AA:664:G:H22	1:AA:741:G:H1	1.23	0.86
19:AS:63:THR:H	19:AS:66:MET:HE2	1.41	0.86
26:DA:2136:C:N3	26:DA:2155:G:N2	2.24	0.86
1:CA:76:C:H42	1:CA:93:G:H1	0.91	0.86
26:DA:2136:C:N4	26:DA:2155:G:N1	2.24	0.85
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.10	0.85
26:DA:2807:G:N1	26:DA:2893:G:O6	2.08	0.85
26:BA:1356:G:OP2	54:B7:9:ARG:NH1	2.09	0.85
1:CA:1166:G:N2	1:CA:1170:A:OP2	2.09	0.85
46:BZ:72:ARG:NH2	46:BZ:97:GLU:O	2.10	0.84
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.58	0.84
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.42	0.84
26:DA:2297:C:N3	26:DA:2321:G:N1	2.25	0.84
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.59	0.84
26:BA:2156:A:H2'	26:BA:2157:A:C8	2.13	0.84
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.10	0.84
26:BA:656:A:OP1	36:BP:65:ARG:NH1	2.10	0.84
1:CA:1075:C:OP1	2:CB:179:LYS:NZ	2.10	0.84
26:DA:880:G:H22	26:DA:898:C:H1'	1.40	0.84
32:DH:46:GLU:HB2	32:DH:49:VAL:HG12	1.58	0.84
37:DQ:109:VAL:HG13	37:DQ:113:GLN:HB3	1.60	0.84
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.11	0.84
1:CA:958:A:N6	19:CS:77:THR:O	2.11	0.84
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.11	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1039:G:O6	26:DA:1116:C:N4	2.11	0.83
1:CA:201:C:H42	1:CA:216:G:H1	1.21	0.83
1:CA:1286:A:H8	1:CA:1287:A:H4'	1.43	0.83
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.11	0.83
30:DF:53:THR:HG22	30:DF:56:GLU:HG3	1.59	0.83
42:DV:24:LYS:HG2	42:DV:64:HIS:HD2	1.43	0.83
26:DA:1204:A:H2	26:DA:1241:A:H62	1.22	0.83
19:CS:30:LEU:HD11	19:CS:32:LYS:HG3	1.60	0.83
23:CW:49:C:N4	23:CW:65:G:O6	2.12	0.83
25:CY:31:A:N1	25:CY:39:PSU:O2	2.12	0.83
1:CA:1162:C:N3	1:CA:1174:G:N2	2.26	0.83
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.12	0.83
13:AM:122:LYS:HD3	13:AM:123:ALA:H	1.43	0.83
26:DA:2165:G:H22	26:DA:2172:U:H5	1.24	0.82
26:DA:2136:C:N4	26:DA:2155:G:H1	1.77	0.82
26:DA:652(D):C:N4	26:DA:652(U):G:O6	2.09	0.82
1:CA:1106:G:H5''	3:CC:172:ARG:HG2	1.62	0.82
4:CD:122:ARG:NH1	4:CD:134:ASP:O	2.12	0.82
26:BA:2158:C:N3	26:BA:2177:G:N2	2.27	0.82
40:BT:118:ARG:HH11	40:BT:118:ARG:HG3	1.45	0.82
1:CA:70:G:H1	1:CA:99:U:H3	1.28	0.82
1:CA:975:A:H4'	1:CA:976:G:H5''	1.60	0.82
26:DA:1019:U:H3	26:DA:1142(A):A:H62	1.26	0.82
26:DA:2136:C:C4	26:DA:2155:G:N1	2.47	0.82
26:BA:1360:C:OP1	61:BA:4634:HOH:O	1.98	0.82
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.12	0.82
1:CA:983:A:N1	1:CA:1222:G:N2	2.28	0.81
27:DB:22:U:H3	27:DB:61:G:H1	1.24	0.81
36:DP:96:THR:H	36:DP:99:LEU:HD21	1.43	0.81
1:CA:1133:G:H1	1:CA:1141:C:H42	1.24	0.81
2:AB:16:HIS:O	2:AB:18:GLY:N	2.13	0.81
9:CI:53:VAL:O	9:CI:55:ALA:N	2.12	0.81
26:DA:994:C:OP1	41:DU:53:ARG:NH2	2.12	0.81
1:AA:78:G:N1	1:AA:91:C:N4	2.29	0.81
25:AY:5:G:H1	25:AY:68:C:N4	1.78	0.81
3:AC:35:GLU:OE2	3:AC:59:ARG:NH2	2.14	0.81
1:CA:1030:C:H42	1:CA:1031:G:H1	1.24	0.81
1:CA:1318:A:H5''	19:CS:3:ARG:HH22	1.46	0.81
40:BT:16:ARG:NH2	40:BT:83:ILE:O	2.14	0.81
1:CA:1000:U:H3	1:CA:1041:A:H61	0.87	0.81
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.62	0.81
28:DD:276:LYS:H	28:DD:276:LYS:HD3	1.45	0.81

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2166:G:H3'	26:DA:2167:U:H5''	1.62	0.81
23:AW:26:A:N6	23:AW:44:G:H1	1.78	0.80
26:BA:2877:G:OP2	40:BT:119:LYS:NZ	2.14	0.80
25:CY:10:G:H1	25:CY:25:C:N4	1.78	0.80
1:AA:839:U:O2'	1:AA:840:C:OP1	2.00	0.80
25:AY:8:4SU:H4'	25:AY:48:C:H4'	1.64	0.80
26:BA:1810:U:OP2	61:BA:5167:HOH:O	1.99	0.80
25:CY:38:A:H3'	25:CY:39:PSU:H5'	1.62	0.80
46:DZ:45:ASP:OD2	46:DZ:49:ARG:NH1	2.14	0.80
1:AA:90:U:H2'	1:AA:91:C:H5''	1.63	0.80
23:CW:4:C:N3	23:CW:69:G:N2	2.29	0.80
31:DG:145:THR:HG23	31:DG:147:ASP:H	1.46	0.80
38:DR:97:VAL:HG22	38:DR:114:VAL:HG22	1.62	0.80
46:DZ:119:GLU:O	46:DZ:122:ARG:NH1	2.15	0.80
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.15	0.80
27:DB:7:G:O6	27:DB:114:C:N4	2.14	0.80
25:AY:53:G:N2	25:AY:61:C:N3	2.29	0.80
25:AY:68:C:H2'	25:AY:69:G:H5'	1.63	0.80
26:BA:181:C:OP1	61:BA:4000:HOH:O	1.99	0.80
1:CA:878:G:H5'	8:CH:89:PRO:HG2	1.64	0.80
30:DF:53:THR:HG23	30:DF:55:GLY:H	1.47	0.79
1:AA:347:G:O2'	1:AA:348:G:OP1	2.00	0.79
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.16	0.79
1:CA:838:G:H1	1:CA:848:C:N4	1.79	0.79
26:BA:1001:G:OP2	37:BQ:14:ARG:NH2	2.15	0.79
26:BA:2695:C:O2	35:BO:70:LYS:NZ	2.14	0.79
1:CA:589:C:O2	1:CA:650:G:N2	2.13	0.79
26:BA:2124:U:O2	26:BA:2209:G:N2	2.13	0.79
28:DD:238:GLY:O	61:DD:409:HOH:O	2.00	0.79
25:AY:15:G:H22	25:AY:48:C:H42	1.30	0.79
23:CW:4:C:N4	23:CW:69:G:N1	2.29	0.79
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.64	0.79
1:CA:1055:A:N7	1:CA:1200:C:N4	2.30	0.79
25:CY:4:C:H42	25:CY:69:G:H1	1.28	0.79
1:CA:1245:A:N6	1:CA:1292:U:H3	1.80	0.79
36:DP:100:LEU:HD12	36:DP:112:LEU:HD11	1.65	0.79
7:AG:38:LEU:HA	7:AG:41:ARG:HD2	1.65	0.78
26:DA:2127:G:C2	26:DA:2161:C:N3	2.52	0.78
1:AA:1027:C:C2	1:AA:1034:G:N1	2.52	0.78
26:BA:1831:C:OP2	28:BD:183:ARG:NH2	2.17	0.78
33:BI:92:VAL:HG13	33:BI:120:ILE:HB	1.65	0.78
6:CF:81:ILE:HD11	28:DD:125:ILE:HB	1.64	0.78

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
44:BX:31:HIS:HD2	44:BX:33:LYS:H	1.29	0.78
4:AD:155:LEU:HB3	4:AD:158:ILE:HD11	1.66	0.78
46:DZ:19:ARG:NH1	46:DZ:84:GLU:O	2.17	0.78
1:AA:266:G:H5'	1:AA:268:C:H41	1.47	0.78
1:CA:1028:C:N3	1:CA:1033:G:C6	2.52	0.78
1:CA:838:G:N2	1:CA:848:C:N3	2.30	0.78
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.64	0.78
26:BA:2158:C:H42	26:BA:2177:G:H1	0.83	0.78
1:CA:664:G:H22	1:CA:741:G:H1	1.29	0.78
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.65	0.77
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.84	0.77
31:BG:12:TYR:HA	31:BG:16:ARG:HG3	1.66	0.77
26:DA:2839:G:H5'	38:DR:46:GLY:HA2	1.64	0.77
27:DB:20:C:N4	27:DB:63:G:O6	2.17	0.77
1:AA:78:G:N2	1:AA:91:C:N3	2.33	0.77
26:BA:2160:C:N4	26:BA:2175:G:H1	1.81	0.77
33:BI:104:GLN:O	33:BI:106:GLY:N	2.16	0.77
44:DX:60:ARG:HH12	54:D7:47:ARG:HH22	1.30	0.77
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.67	0.77
23:AW:50:U:H5'	23:AW:50:U:H6	1.48	0.77
25:AY:7:A:O2'	25:AY:49:C:H5'	1.85	0.77
1:AA:1027:C:N3	1:AA:1034:G:C6	2.53	0.77
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.66	0.77
25:AY:5:G:N2	25:AY:68:C:N3	2.31	0.77
26:BA:542:C:OP1	52:B5:16:ARG:NH2	2.18	0.77
26:DA:2037:G:O6	61:DA:4191:HOH:O	2.02	0.77
37:DQ:31:ASP:OD1	37:DQ:134:ARG:NH1	2.18	0.77
26:BA:1736:A:H62	26:BA:1745:A:H2	1.33	0.77
1:CA:1338:G:H21	24:CX:41:C:H1'	1.49	0.77
1:AA:1025:U:O2'	1:AA:1026:G:O4'	2.02	0.77
25:CY:19:G:H1	25:CY:56:C:N4	1.82	0.77
32:DH:24:VAL:HG13	32:DH:37:VAL:HG21	1.66	0.77
26:BA:2152:U:H4'	26:BA:2155:G:H4'	1.67	0.76
1:CA:1134:G:H1	1:CA:1140:C:H42	1.29	0.76
51:D4:40:HIS:HB3	51:D4:43:TYR:HB2	1.67	0.76
26:DA:370:G:N7	61:DA:3786:HOH:O	2.18	0.76
35:DO:35:VAL:HG11	35:DO:103:ALA:HB3	1.67	0.76
19:AS:27:GLU:HB3	19:AS:28:LYS:HA	1.65	0.76
1:CA:1128:C:O2	1:CA:1147:C:N4	2.18	0.76
1:CA:504:C:OP1	61:CA:3202:HOH:O	2.02	0.76
25:CY:51:U:O2	25:CY:63:G:N2	2.15	0.76
39:BS:39:ILE:HB	39:BS:49:VAL:HG13	1.68	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1060:C:HO2'	10:CJ:56:HIS:HD1	1.34	0.76
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.65	0.76
26:BA:2184:G:H2'	26:BA:2185:C:H5''	1.65	0.76
44:BX:88:LYS:NZ	44:BX:90:GLU:OE1	2.18	0.76
24:CX:7:G:H5''	24:CX:8:4SU:H5	1.65	0.76
1:CA:1030:C:N4	1:CA:1031:G:H1	1.84	0.76
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.18	0.76
13:CM:84:ILE:O	13:CM:86:CYS:N	2.17	0.76
25:CY:49:C:H42	25:CY:65:G:H1	1.33	0.76
39:BS:25:ARG:NH1	39:BS:42:ASP:OD1	2.18	0.76
1:AA:998:G:H1	1:AA:1043:C:H42	1.30	0.76
26:BA:1552:C:H2'	26:BA:1553:A:H8	1.48	0.76
1:CA:1134:G:H1	1:CA:1140:C:N4	1.84	0.76
1:CA:76:C:N3	1:CA:93:G:N2	2.32	0.76
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.67	0.76
1:CA:694:A:HO2'	25:CY:38:A:HO2'	1.32	0.76
26:DA:1169:G:H1	26:DA:1180:C:H42	1.31	0.76
26:DA:2134:A:N3	26:DA:2159:G:O2'	2.17	0.76
31:DG:64:THR:HB	31:DG:94:LEU:HD21	1.67	0.76
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.18	0.75
26:BA:610:C:OP2	36:BP:21:ARG:NH2	2.20	0.75
55:D8:32:LEU:O	55:D8:36:LYS:NZ	2.18	0.75
26:BA:2143:G:H1	26:BA:2199:C:N4	1.84	0.75
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.19	0.75
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.51	0.75
46:DZ:126:VAL:HG11	46:DZ:161:VAL:HG23	1.67	0.75
36:BP:124:LYS:HG3	36:BP:144:GLU:HG2	1.69	0.75
26:DA:2113:U:H3	26:DA:2170:A:H61	1.33	0.75
25:CY:34:G:H2'	25:CY:35:A:C8	2.21	0.75
1:CA:35:G:O2'	12:CL:118:SER:O	2.05	0.75
4:AD:166:LYS:NZ	4:AD:179:GLU:OE2	2.20	0.75
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.15	0.75
1:CA:1244:C:N4	1:CA:1293:G:H1	1.83	0.75
1:CA:1502:A:H2	1:CA:1505:G:H1	1.32	0.75
48:D1:51:VAL:HG11	48:D1:74:VAL:HG21	1.68	0.75
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.19	0.75
25:AY:67:C:H2'	25:AY:68:C:C6	2.21	0.75
26:BA:2156:A:H2'	26:BA:2157:A:H8	1.49	0.75
25:CY:68:C:H2'	25:CY:69:G:H5'	1.69	0.75
26:DA:2122:U:O4	26:DA:2176:A:N1	2.20	0.75
3:CC:100:ALA:O	3:CC:102:ASN:ND2	2.20	0.75
1:CA:664:G:OP1	18:CR:64:ARG:NH2	2.19	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:953:G:H5'	1:CA:965:A:H61	1.51	0.74
3:CC:59:ARG:HG2	3:CC:64:VAL:HG13	1.68	0.74
1:CA:528:C:N4	12:CL:49:ASN:OD1	2.20	0.74
25:CY:38:A:C3'	25:CY:39:PSU:H5'	2.16	0.74
26:DA:1842:G:O2'	28:DD:253:GLN:NE2	2.20	0.74
36:DP:42:SER:O	61:DP:303:HOH:O	2.05	0.74
46:DZ:77:ASP:OD1	46:DZ:80:ARG:NH1	2.18	0.74
26:BA:2138:G:N2	26:BA:2184:G:OP1	2.19	0.74
26:BA:932:C:H3'	26:BA:933:C:H5''	1.70	0.74
2:CB:125:PRO:O	2:CB:127:ILE:N	2.20	0.74
38:DR:33:ARG:NH2	52:D5:57:VAL:O	2.20	0.74
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.53	0.74
1:CA:1153:C:H42	1:CA:1154:G:H21	1.35	0.74
26:BA:1094:A:OP2	26:BA:1155:C:N4	2.21	0.74
26:BA:303:C:H42	26:BA:385:G:H1	1.33	0.74
1:AA:1007:C:N3	1:AA:1022:G:O6	2.19	0.74
26:BA:2299:A:H62	26:BA:2356:U:H3	1.31	0.74
26:BA:2365:G:N7	61:BA:4441:HOH:O	2.20	0.74
37:BQ:111:GLU:OE1	37:BQ:133:ARG:NH2	2.19	0.74
1:CA:1011:G:H1	1:CA:1018:C:H42	1.33	0.74
26:DA:2357:U:OP1	47:D0:20:ARG:NH1	2.19	0.74
46:DZ:154:ASP:N	46:DZ:154:ASP:OD1	2.20	0.74
1:AA:1086:U:H3	1:AA:1099:G:H22	1.35	0.74
26:BA:1873:G:O2'	28:BD:253:GLN:NE2	2.20	0.74
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.21	0.74
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.68	0.74
25:AY:49:C:H42	25:AY:65:G:H1	0.79	0.74
26:BA:2297:C:OP2	53:B6:6:ARG:NH1	2.20	0.74
1:CA:532:A:H61	3:CC:193:TYR:HB3	1.52	0.74
13:CM:5:ALA:HB1	13:CM:66:LEU:HD13	1.70	0.74
23:CW:30:G:H1	23:CW:40:C:H42	1.34	0.74
26:DA:11:G:N7	61:DA:4269:HOH:O	2.21	0.74
26:DA:2138:C:H42	26:DA:2153:G:H1	0.77	0.74
31:DG:106:LEU:HA	31:DG:110:ALA:HB3	1.70	0.74
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.20	0.73
30:DF:120:GLU:HB2	30:DF:122:LYS:HG2	1.68	0.73
1:CA:1005:A:OP2	1:CA:1024:G:N2	2.19	0.73
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.68	0.73
1:CA:992:U:H6	1:CA:992:U:H5''	1.53	0.73
2:CB:119:GLU:OE2	2:CB:153:ARG:NH1	2.22	0.73
24:CX:67:C:H2'	24:CX:68:C:H5'	1.69	0.73
1:AA:376:G:H5''	16:AP:5:ARG:HB3	1.70	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:BH:159:GLU:HG3	32:BH:169:VAL:HG11	1.68	0.73
1:CA:1054:C:C4	23:CW:34:G:H1'	2.23	0.73
26:DA:2632:A:HO2'	26:DA:2811:G:HO2'	1.32	0.73
52:B5:40:LYS:NZ	52:B5:44:THR:O	2.18	0.73
1:CA:345:C:OP2	40:DT:39:ARG:NH2	2.21	0.73
26:BA:1039:G:OP1	41:BU:50:ARG:NH2	2.22	0.73
26:BA:1648:U:O4	61:BA:4209:HOH:O	2.06	0.73
26:BA:894:U:OP2	61:BA:4392:HOH:O	2.06	0.73
45:BY:92:ASN:HB2	45:BY:94:LYS:N	2.01	0.73
9:CI:8:GLY:HA3	9:CI:15:ALA:HB3	1.71	0.73
26:DA:952:G:OP1	37:DQ:16:ARG:NH2	2.21	0.73
23:AW:18:G:O2'	23:AW:57:G:N2	2.14	0.73
1:CA:1321:C:H5''	1:CA:1322:C:H2'	1.69	0.73
26:BA:232:U:OP1	55:B8:6:THR:OG1	2.07	0.73
56:B9:17:ILE:HG22	56:B9:24:TYR:HB2	1.70	0.73
1:AA:812:C:N3	61:AA:4038:HOH:O	2.20	0.73
23:AW:19:G:N2	23:AW:56:C:N3	2.36	0.73
26:DA:2127:G:N1	26:DA:2161:C:C4	2.57	0.73
27:BB:33:G:H5'	31:BG:2:PRO:HD3	1.70	0.73
1:CA:1323:G:N2	1:CA:1361:G:O2'	2.22	0.73
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.21	0.72
25:AY:56:C:H2'	25:AY:57:G:O4'	1.88	0.72
1:AA:504:C:OP1	61:AA:4184:HOH:O	2.07	0.72
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.06	0.72
1:CA:26:A:O2'	4:CD:209:ARG:NH2	2.22	0.72
26:DA:2138:C:N3	26:DA:2153:G:N2	2.34	0.72
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.07	0.72
1:CA:117:G:OP2	61:CA:3236:HOH:O	2.07	0.72
2:CB:95:GLN:HB2	2:CB:148:TYR:HD1	1.54	0.72
26:DA:191:A:N1	61:DA:4214:HOH:O	2.22	0.72
1:AA:975:A:H4'	1:AA:976:G:H5''	1.70	0.72
25:AY:33:U:H3'	25:AY:34:G:H5''	1.71	0.72
23:CW:19:G:H1	23:CW:56:C:H42	1.37	0.72
26:DA:740:U:OP2	61:DA:4209:HOH:O	2.07	0.72
44:DX:53:LYS:HB3	44:DX:82:GLN:HB3	1.69	0.72
51:B4:57:GLU:HB2	51:B4:58:ARG:HA	1.72	0.72
13:CM:5:ALA:HB3	13:CM:22:ILE:HD12	1.69	0.72
42:DV:98:GLU:OE1	42:DV:100:ARG:NH1	2.23	0.72
26:BA:64:C:O2	26:BA:482:C:N4	2.20	0.72
23:CW:50:U:O4	23:CW:64:A:N1	2.22	0.72
25:CY:7:A:H61	25:CY:66:U:H3	0.79	0.72
43:BW:15:ARG:NH1	61:BW:4002:HOH:O	2.21	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1431:G:O2'	26:BA:1442:U:O2	2.07	0.72
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.23	0.72
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.70	0.72
28:BD:17:THR:O	28:BD:211:ARG:NH2	2.23	0.72
46:BZ:117:LEU:HD11	46:BZ:144:LEU:HD22	1.71	0.72
23:CW:61:C:O2'	23:CW:62:C:O5'	2.07	0.72
25:CY:15:G:H22	25:CY:48:C:N4	1.87	0.72
26:DA:1250:G:OP2	36:DP:21:ARG:NH1	2.23	0.72
1:AA:934:C:OP1	61:AA:4086:HOH:O	2.08	0.71
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	1.71	0.71
1:AA:310:G:OP2	16:AP:27:LYS:NZ	2.22	0.71
2:CB:212:GLN:NE2	2:CB:234:PRO:O	2.23	0.71
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.72	0.71
23:AW:7:A:H61	23:AW:66:U:H3	1.36	0.71
26:BA:2071:G:N7	61:BA:5132:HOH:O	2.23	0.71
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.73	0.71
49:D2:38:GLN:HB3	49:D2:44:LEU:HB2	1.72	0.71
26:DA:2206:G:H3'	26:DA:2207:G:C8	2.25	0.71
48:B1:86:SER:OG	48:B1:89:GLU:OE1	2.08	0.71
26:BA:627:G:OP2	36:BP:90:ARG:NH1	2.24	0.71
1:CA:1011:G:H1	1:CA:1018:C:N4	1.89	0.71
26:DA:143:G:H4'	44:DX:35:THR:HG21	1.73	0.71
20:AT:57:ARG:HH12	20:AT:100:ILE:HD12	1.55	0.71
23:AW:19:G:H1	23:AW:56:C:N4	1.89	0.71
1:AA:1027:C:O2	1:AA:1034:G:C2	2.43	0.71
26:BA:1740:U:O2'	28:BD:14:ARG:NH2	2.23	0.71
26:DA:1449:A:O2'	26:DA:1529:G:N2	2.17	0.71
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.71	0.71
19:CS:77:THR:HG22	19:CS:78:ARG:HG2	1.71	0.71
26:DA:1800:C:OP2	28:DD:183:ARG:NH2	2.23	0.71
26:BA:1185:C:O3'	34:BN:25:ARG:NH1	2.23	0.71
1:CA:1465:C:OP2	40:DT:108:ARG:NH2	2.22	0.71
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.72	0.71
26:BA:945:A:O2'	26:BA:946:A:O5'	2.08	0.71
1:CA:986:A:O2'	19:CS:55:LYS:O	2.08	0.71
28:DD:85:ASP:OD2	28:DD:88:ARG:NH1	2.21	0.71
26:DA:2788:C:OP1	29:DE:61:ARG:NH2	2.23	0.71
4:CD:57:ARG:HH22	5:CE:107:ARG:HD3	1.55	0.71
5:CE:50:GLU:HB2	5:CE:53:LEU:HD13	1.73	0.71
27:DB:5:C:H42	27:DB:116:G:H1	1.39	0.71
6:AF:70:ASP:OD1	6:AF:70:ASP:N	2.24	0.70
39:DS:15:ARG:O	39:DS:19:LYS:HD3	1.90	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1426:G:OP2	61:BA:5119:HOH:O	2.09	0.70
1:CA:1366:C:O2'	10:CJ:60:ARG:NH2	2.24	0.70
31:DG:80:PHE:O	31:DG:82:LEU:N	2.22	0.70
33:DI:72:LEU:HD21	33:DI:107:VAL:HG11	1.74	0.70
54:B7:24:THR:HG22	54:B7:27:GLY:H	1.56	0.70
26:BA:2251:G:OP2	61:BA:4313:HOH:O	2.08	0.70
26:BA:2460:A:OP1	61:BA:5135:HOH:O	2.09	0.70
1:CA:999:C:H42	1:CA:1042:G:H1	0.74	0.70
26:DA:1038:C:H42	26:DA:1117:G:H1	1.38	0.70
26:DA:2148:G:H2'	26:DA:2149:G:C8	2.27	0.70
17:AQ:75:ARG:NH1	17:AQ:76:LEU:O	2.25	0.70
1:CA:993:G:O6	1:CA:1045:C:N4	2.15	0.70
26:DA:1689:A:H62	26:DA:1698:A:H2	1.40	0.70
26:DA:900:A:H2'	26:DA:901:A:H8	1.57	0.70
3:AC:19:GLU:HB3	3:AC:40:ARG:HH22	1.57	0.70
25:AY:51:U:H2'	25:AY:52:G:H8	1.56	0.70
36:BP:126:VAL:HG12	36:BP:148:LEU:HD22	1.72	0.70
32:DH:159:GLU:HG3	32:DH:169:VAL:HG11	1.74	0.70
33:DI:78:THR:O	33:DI:104:GLN:NE2	2.25	0.70
25:AY:22:G:N7	25:AY:46:7MG:O6	2.25	0.70
25:AY:15:G:N1	25:AY:48:C:N3	2.39	0.70
23:CW:4:C:N4	23:CW:69:G:C6	2.59	0.70
1:AA:1304:G:OP2	61:AA:4111:HOH:O	2.10	0.70
5:AE:6:PHE:HB2	5:AE:34:VAL:HG22	1.73	0.70
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.72	0.70
1:CA:953:G:H5'	1:CA:965:A:N6	2.07	0.70
27:DB:28:C:H2'	27:DB:29:A:H8	1.57	0.70
1:CA:582:U:OP1	15:CO:68:ARG:NH1	2.24	0.70
46:DZ:44:PHE:O	46:DZ:48:PHE:N	2.21	0.70
1:AA:1159:U:OP1	2:AB:133:LYS:NZ	2.25	0.69
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.20	0.69
26:BA:1284:G:OP2	61:BA:4983:HOH:O	2.10	0.69
1:CA:812:C:N3	61:CA:3212:HOH:O	2.25	0.69
2:CB:161:ALA:HB1	2:CB:185:ILE:HD11	1.74	0.69
10:CJ:5:ARG:N	10:CJ:73:ASP:HA	2.07	0.69
26:DA:2404:C:O3'	36:DP:77:ARG:NH2	2.25	0.69
28:BD:71:ASP:HB3	28:BD:103:ARG:HH22	1.57	0.69
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	1.72	0.69
26:DA:1033:U:OP1	56:D9:9:ARG:NH2	2.26	0.69
46:DZ:72:ARG:NH1	46:DZ:97:GLU:O	2.25	0.69
26:BA:1480:A:H61	26:BA:1605:A:H62	1.39	0.69
1:CA:798:G:O6	61:CA:3223:HOH:O	2.09	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:300:A:OP1	45:DY:86:ARG:NH2	2.25	0.69
30:DF:197:ASP:OD1	30:DF:198:ALA:N	2.25	0.69
36:DP:91:PHE:O	36:DP:121:LYS:NZ	2.21	0.69
9:AI:110:GLU:OE2	9:AI:113:LYS:NZ	2.25	0.69
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.75	0.69
15:AO:55:GLY:HA2	15:AO:58:MET:HE2	1.73	0.69
26:BA:1343:C:OP1	61:BA:4340:HOH:O	2.09	0.69
31:BG:41:GLN:NE2	31:BG:154:GLY:O	2.25	0.69
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.56	0.69
1:CA:1359:C:O2	61:CA:3330:HOH:O	2.09	0.69
1:CA:67:C:H2'	1:CA:68:G:C8	2.28	0.69
8:CH:12:ARG:HH12	8:CH:27:PRO:HD2	1.58	0.69
25:CY:26:A:N1	25:CY:44:G:O6	2.26	0.69
26:DA:987:G:O2'	26:DA:1000:A:N3	2.25	0.69
1:AA:1423:G:OP1	35:BO:49:ARG:NH2	2.24	0.69
4:AD:49:ARG:HE	4:AD:49:ARG:H	1.38	0.69
23:CW:56:C:H5	26:DA:897:C:H1'	1.56	0.69
26:DA:2166:G:H3'	26:DA:2167:U:C5'	2.22	0.69
26:DA:2176:A:H2'	26:DA:2177:C:C6	2.27	0.69
28:DD:275:LYS:HG3	28:DD:276:LYS:HA	1.73	0.69
30:BF:185:ASP:HA	30:BF:188:ARG:HD3	1.73	0.69
25:CY:69:G:H2'	25:CY:70:G:O4'	1.92	0.69
26:DA:2119:A:H2	26:DA:2171:A:H5'	1.58	0.69
26:DA:2135:A:H2'	26:DA:2136:C:C6	2.27	0.69
26:DA:878:A:N6	26:DA:899:A:O2'	2.22	0.69
19:AS:27:GLU:HB2	19:AS:28:LYS:HD2	1.74	0.69
44:BX:35:THR:HG22	44:BX:38:GLU:H	1.57	0.69
17:CQ:53:LEU:HD23	17:CQ:82:MET:HE1	1.75	0.69
19:CS:27:GLU:HB3	19:CS:28:LYS:HA	1.75	0.69
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.58	0.69
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.75	0.69
26:BA:271:U:H1'	33:BI:50:ARG:HD2	1.74	0.69
12:CL:124:LYS:HB2	12:CL:124:LYS:HZ2	1.57	0.69
29:BE:8:LYS:NZ	61:BE:416:HOH:O	2.18	0.69
1:CA:1060:C:O2'	10:CJ:56:HIS:ND1	2.24	0.69
1:CA:1329:A:OP2	21:CU:7:ARG:NH2	2.22	0.69
1:CA:460:G:O6	1:CA:470:C:H5''	1.93	0.69
1:CA:1320:C:O4'	19:CS:73:GLU:HG2	1.93	0.69
25:CY:5:G:H1	25:CY:68:C:H42	1.40	0.69
26:DA:89:G:H3'	26:DA:90:U:H5''	1.75	0.69
26:DA:568:U:H5'	26:DA:945:A:N1	2.08	0.69
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.23	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:AY:76:A:N6	26:BA:2434:A:O4'	2.26	0.69
26:DA:1420:U:O2'	26:DA:1421:G:OP1	2.10	0.69
2:AB:21:ARG:HB3	2:AB:39:ILE:HG12	1.75	0.69
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.74	0.69
26:BA:997:G:OP1	37:BQ:16:ARG:NH2	2.26	0.69
46:DZ:93:ASP:HA	46:DZ:131:ARG:HH22	1.57	0.69
23:AW:50:U:H3	23:AW:64:A:H61	1.39	0.68
26:BA:1871:G:N7	61:BA:4310:HOH:O	2.26	0.68
47:B0:10:THR:HG22	47:B0:12:ASN:H	1.57	0.68
20:CT:43:LEU:O	20:CT:47:GLY:N	2.17	0.68
1:AA:838:G:H1	1:AA:848:C:H42	1.40	0.68
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.27	0.68
31:DG:113:ARG:NH1	31:DG:139:LEU:O	2.26	0.68
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.40	0.68
14:AN:3:ARG:HH21	14:AN:3:ARG:HB3	1.57	0.68
26:BA:1189:A:OP1	34:BN:25:ARG:NH2	2.26	0.68
26:BA:1761:G:H1	26:BA:1775:C:H42	1.41	0.68
33:BI:38:LEU:HD12	33:BI:38:LEU:H	1.58	0.68
25:CY:62:C:H2'	25:CY:63:G:H8	1.58	0.68
51:D4:44:THR:O	51:D4:46:GLN:N	2.27	0.68
26:DA:1816:G:O6	28:DD:35:LYS:NZ	2.20	0.68
26:DA:741:G:OP2	61:DA:4210:HOH:O	2.12	0.68
1:AA:953:G:H5'	1:AA:965:A:H61	1.56	0.68
37:BQ:18:LYS:O	37:BQ:98:LYS:NZ	2.22	0.68
8:CH:12:ARG:NH1	8:CH:27:PRO:HD2	2.09	0.68
47:D0:40:GLN:HE21	47:D0:57:PHE:HB3	1.58	0.68
26:DA:2128:C:H42	26:DA:2160:G:H1	1.42	0.68
26:DA:2502:G:N7	61:DA:4405:HOH:O	2.26	0.68
26:DA:2689:U:H4'	26:DA:2690:C:H5'	1.75	0.68
30:DF:143:ALA:HB1	30:DF:148:LEU:HB2	1.74	0.68
25:AY:69:G:H2'	25:AY:70:G:O4'	1.94	0.68
26:BA:2145:G:H1	26:BA:2197:C:H42	1.40	0.68
1:CA:1002:G:H1	1:CA:1038:C:N4	1.91	0.68
1:CA:1166:G:H5''	1:CA:1166:G:H8	1.59	0.68
26:DA:1593:G:H2'	26:DA:1594:G:C8	2.28	0.68
26:DA:2171:A:N3	26:DA:2172:U:N3	2.41	0.68
38:DR:33:ARG:NH1	38:DR:115:GLU:OE2	2.26	0.68
1:AA:339:C:OP2	35:BO:97:ARG:NH1	2.26	0.68
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.26	0.68
26:BA:1814:A:N7	61:BA:5029:HOH:O	2.27	0.68
26:BA:568:C:N4	26:BA:573:G:O6	2.18	0.68
26:DA:1019:U:HO2'	26:DA:1021:A:H2	1.42	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2183:C:H2'	26:DA:2184:G:H8	1.59	0.68
30:DF:21:ALA:HB3	30:DF:22:ALA:HA	1.75	0.68
1:AA:838:G:H1	1:AA:848:C:N4	1.91	0.68
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.76	0.68
26:BA:572:A:O2'	26:BA:573:G:OP1	2.10	0.68
27:BB:2:C:O2	27:BB:119:G:N2	2.20	0.68
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.93	0.68
23:CW:43:C:H2'	23:CW:44:G:C8	2.29	0.68
1:AA:123:C:OP1	1:AA:311:C:O2'	2.11	0.68
26:BA:2459:G:OP2	61:BA:4544:HOH:O	2.11	0.68
46:BZ:145:GLU:O	46:BZ:148:ASP:N	2.26	0.68
1:CA:750:G:N3	15:CO:23:GLY:HA3	2.08	0.68
26:DA:1189:A:OP2	61:DA:4174:HOH:O	2.12	0.68
29:DE:111:ARG:HG3	29:DE:160:TYR:CD2	2.29	0.68
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.26	0.68
1:CA:344:A:H5''	1:CA:345:C:H5	1.59	0.68
27:DB:55:U:O2'	31:DG:27:ASN:ND2	2.26	0.68
39:DS:58:LEU:HD11	39:DS:65:VAL:HA	1.75	0.68
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.12	0.67
50:B3:8:LEU:HD13	50:B3:31:LEU:HD23	1.75	0.67
26:BA:625:G:O2'	26:BA:702:A:N6	2.27	0.67
33:BI:106:GLY:HA2	33:BI:107:VAL:O	1.93	0.67
35:BO:2:ILE:HD12	35:BO:6:THR:HG21	1.73	0.67
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.57	0.67
1:CA:1309:G:OP1	13:CM:88:ARG:NH1	2.26	0.67
4:CD:173:TRP:HB3	4:CD:187:ARG:HE	1.59	0.67
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.42	0.67
1:AA:572:A:OP1	61:AA:4084:HOH:O	2.11	0.67
26:BA:2081:A:OP2	61:BA:4315:HOH:O	2.11	0.67
26:BA:2340:A:H2'	26:BA:2341:G:C8	2.28	0.67
12:CL:124:LYS:HB2	12:CL:124:LYS:NZ	2.08	0.67
24:CX:31:G:H3'	24:CX:32:5MC:HM51	1.76	0.67
1:AA:1158:C:H5	1:AA:1181:G:H1	1.42	0.67
9:AI:53:VAL:O	9:AI:55:ALA:N	2.27	0.67
19:CS:27:GLU:HB2	19:CS:28:LYS:HD3	1.77	0.67
25:CY:15:G:N2	25:CY:48:C:H42	1.90	0.67
52:D5:16:ARG:NH1	52:D5:17:ASP:OD1	2.27	0.67
42:DV:43:GLU:OE2	42:DV:43:GLU:N	2.27	0.67
1:AA:347:G:H2'	1:AA:348:G:O4'	1.94	0.67
16:AP:1:MET:N	16:AP:1:MET:SD	2.62	0.67
3:CC:91:LEU:HD23	3:CC:101:LEU:HD22	1.76	0.67
8:CH:4:ASP:OD2	8:CH:85:ARG:NH1	2.27	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2121:G:N2	26:DA:2177:C:N3	2.36	0.67
26:DA:526:A:OP1	61:DA:4183:HOH:O	2.12	0.67
1:AA:1028:C:H2'	1:AA:1029:C:H4'	1.77	0.67
3:CC:129:ALA:HB3	3:CC:132:ARG:HB2	1.77	0.67
26:DA:2518:A:OP2	61:DA:3991:HOH:O	2.12	0.67
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.76	0.67
26:BA:1500:A:OP2	61:BA:3995:HOH:O	2.12	0.67
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.77	0.67
1:CA:1310:G:OP1	13:CM:77:ASN:ND2	2.27	0.67
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.77	0.67
26:DA:2224:G:OP1	28:DD:268:ARG:NE	2.28	0.67
26:DA:2562:U:H1'	35:DO:23:ARG:HH11	1.60	0.67
1:AA:160:A:N6	1:AA:345:C:OP2	2.27	0.67
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.29	0.67
13:CM:121:LYS:HZ2	13:CM:121:LYS:H	1.43	0.67
1:AA:67:C:H2'	1:AA:68:G:C8	2.30	0.67
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.76	0.67
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.27	0.67
51:D4:38:LYS:O	51:D4:40:HIS:N	2.21	0.67
26:DA:1783:A:N7	61:DA:4510:HOH:O	2.26	0.67
1:AA:1022:G:H2'	1:AA:1023:G:H8	1.60	0.67
46:BZ:108:PRO:HB3	46:BZ:117:LEU:HD13	1.75	0.67
1:CA:560:U:O2'	1:CA:561:U:OP2	2.13	0.67
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.58	0.67
26:DA:131:G:OP1	61:DA:3791:HOH:O	2.11	0.67
26:DA:2126:A:H61	26:DA:2172:U:H3'	1.60	0.67
26:DA:2287:A:H62	26:DA:2344:U:H3	1.40	0.67
34:DN:115:ARG:HA	34:DN:118:LYS:HE3	1.75	0.67
25:CY:9:A:OP2	25:CY:13:C:N4	2.26	0.67
26:DA:2148:G:H2'	26:DA:2149:G:H8	1.58	0.67
26:DA:2127:G:N1	26:DA:2161:C:N4	2.42	0.67
26:DA:7:G:N2	26:DA:2896:C:O2	2.23	0.67
31:DG:13:GLU:O	31:DG:15:VAL:N	2.27	0.67
1:CA:673:G:H2'	1:CA:674:G:C8	2.30	0.66
25:CY:62:C:H2'	25:CY:63:G:C8	2.30	0.66
3:AC:70:VAL:HG22	3:AC:72:LYS:H	1.59	0.66
26:BA:1016:C:OP2	61:BA:5252:HOH:O	2.11	0.66
2:CB:87:ARG:HH21	2:CB:233:SER:HB3	1.60	0.66
1:CA:951:G:OP2	13:CM:102:ARG:NH1	2.29	0.66
19:CS:49:ILE:HG13	19:CS:62:ILE:HD11	1.76	0.66
27:DB:50:G:OP1	39:DS:63:THR:N	2.27	0.66
1:CA:1155:G:H2'	1:CA:1156:G:C8	2.29	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1191:A:OP1	3:CC:3:ASN:ND2	2.28	0.66
3:CC:22:TRP:CD2	3:CC:59:ARG:HD2	2.30	0.66
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.60	0.66
37:BQ:54:MET:HG3	37:BQ:117:ALA:HB1	1.76	0.66
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.27	0.66
7:CG:59:LEU:HG	7:CG:63:LYS:HE2	1.77	0.66
26:DA:2400:G:O3'	53:D6:18:ARG:NH1	2.27	0.66
27:DB:76:G:N2	27:DB:101:G:O6	2.25	0.66
1:AA:1245:A:H61	1:AA:1292:U:H3	1.44	0.66
2:AB:93:VAL:HG21	2:AB:97:TRP:CD1	2.30	0.66
13:AM:34:LEU:HD13	13:AM:41:PRO:HA	1.77	0.66
25:AY:6:G:O6	25:AY:7:A:N6	2.29	0.66
26:BA:121:G:OP2	61:BA:3977:HOH:O	2.14	0.66
26:BA:2289:G:OP2	47:B0:10:THR:HG21	1.96	0.66
26:BA:2772:G:N7	61:BA:4108:HOH:O	2.27	0.66
42:BV:34:GLU:HB3	42:BV:56:SER:HB2	1.75	0.66
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.13	0.66
20:AT:15:ARG:O	20:AT:19:SER:OG	2.13	0.66
1:CA:1316:G:H4'	14:CN:18:VAL:HG13	1.77	0.66
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.28	0.66
26:DA:1278:A:OP1	38:DR:36:THR:HG23	1.96	0.66
1:CA:1348:U:H4'	9:CI:120:ARG:HD3	1.78	0.66
3:CC:150:LYS:HB2	3:CC:173:VAL:HG21	1.77	0.66
26:BA:237:G:OP1	61:BA:4977:HOH:O	2.13	0.66
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.29	0.66
26:BA:927:G:H2'	26:BA:928:G:C8	2.30	0.66
1:CA:660:G:H1	1:CA:745:C:H42	1.43	0.66
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.29	0.66
26:BA:1044:C:OP1	61:BA:4644:HOH:O	2.14	0.66
26:BA:1451:U:H2'	26:BA:1452:U:C6	2.31	0.66
26:BA:2102:G:O6	61:BA:4418:HOH:O	2.12	0.66
26:BA:2162:C:C2	26:BA:2173:G:N2	2.64	0.66
26:BA:786:G:OP1	61:BA:5169:HOH:O	2.13	0.66
26:BA:630:U:OP1	30:BF:102:PRO:HA	1.96	0.66
35:BO:64:ARG:NH1	35:BO:81:ASP:OD1	2.29	0.66
1:AA:193:C:H2'	1:AA:194:C:H6	1.59	0.65
1:CA:649:G:H2'	1:CA:650:G:H5''	1.78	0.65
24:CX:9:G:O2'	24:CX:10:G:N7	2.20	0.65
50:D3:7:LYS:NZ	50:D3:32:GLN:O	2.29	0.65
31:DG:16:ARG:O	31:DG:20:ILE:HG13	1.95	0.65
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.78	0.65
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.77	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AW:5:G:H2'	23:AW:6:G:H8	1.60	0.65
26:BA:1219:A:H4'	26:BA:1220:U:OP1	1.95	0.65
26:BA:2735:G:OP2	61:BA:4098:HOH:O	2.14	0.65
29:BE:105:THR:OG1	29:BE:199:ARG:NH2	2.30	0.65
26:BA:1785:C:H5''	40:BT:113:LYS:HE3	1.77	0.65
1:CA:1026:G:O6	1:CA:1036:G:N2	2.28	0.65
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.30	0.65
1:AA:1239:A:H62	1:AA:1299:A:N6	1.94	0.65
1:CA:977:A:O2'	1:CA:981:U:N3	2.29	0.65
1:CA:1320:C:N3	19:CS:36:ARG:NH2	2.44	0.65
1:CA:1022:G:H2'	1:CA:1023:G:H8	1.60	0.65
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.76	0.65
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.70	0.65
25:CY:4:C:N4	25:CY:69:G:H1	1.94	0.65
30:DF:184:TYR:CE2	30:DF:188:ARG:HD2	2.32	0.65
36:DP:44:GLY:O	61:DP:301:HOH:O	2.14	0.65
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.32	0.65
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.12	0.65
25:AY:29:G:N2	25:AY:41:C:N3	2.36	0.65
26:BA:927:G:H2'	26:BA:928:G:H8	1.61	0.65
26:DA:323:G:HO2'	26:DA:1205:U:H3	1.43	0.65
26:DA:857:C:OP2	47:D0:77:ARG:NH2	2.29	0.65
2:AB:93:VAL:HG21	2:AB:97:TRP:HD1	1.59	0.65
26:BA:302:A:H2'	26:BA:303:C:C6	2.31	0.65
1:CA:954:G:H21	1:CA:1227:A:H62	1.44	0.65
26:BA:1388:A:OP2	61:BA:4209:HOH:O	2.13	0.65
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.62	0.65
1:CA:1359:C:H1'	1:CA:1362:C:H41	1.61	0.65
1:CA:501:C:H2'	1:CA:502:G:C8	2.31	0.65
23:CW:3:C:N3	23:CW:70:G:O6	2.29	0.65
26:DA:500:G:N1	26:DA:503:A:OP2	2.30	0.65
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.32	0.65
27:BB:106:G:H5'	46:BZ:31:ARG:HG2	1.79	0.65
26:DA:1693:U:O2'	28:DD:14:ARG:NH2	2.29	0.65
31:DG:44:GLY:O	31:DG:47:LYS:HB2	1.95	0.65
46:DZ:130:PRO:HA	46:DZ:133:ILE:HD11	1.77	0.65
1:AA:1030(D):A:N6	1:AA:1031:G:H21	1.95	0.65
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.32	0.65
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	1.78	0.65
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.79	0.65
26:BA:1249:A:H2	26:BA:1287:A:H62	1.43	0.65
26:BA:129:G:OP1	61:BA:4045:HOH:O	2.13	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2490:A:OP2	56:B9:2:LYS:NZ	2.29	0.65
38:BR:67:LEU:HD13	38:BR:76:VAL:HG21	1.79	0.65
4:CD:157:LEU:O	4:CD:161:ASN:ND2	2.29	0.65
8:CH:49:GLU:OE2	8:CH:62:TYR:OH	2.14	0.65
3:AC:150:LYS:HG3	3:AC:169:ALA:HB2	1.79	0.64
26:DA:1803:A:O2'	28:DD:259:THR:HG21	1.97	0.64
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.30	0.64
1:AA:942:G:H21	9:AI:124:GLN:NE2	1.95	0.64
25:AY:51:U:H2'	25:AY:52:G:C8	2.32	0.64
51:B4:59:PHE:HA	51:B4:61:ARG:H	1.63	0.64
53:B6:6:ARG:NH1	53:B6:26:ASN:HB2	2.12	0.64
26:BA:1827:U:H2'	26:BA:1828:C:C6	2.32	0.64
26:BA:929:G:N2	26:BA:941:U:O2	2.27	0.64
27:BB:23:G:O6	61:BB:3133:HOH:O	2.10	0.64
47:D0:10:THR:HG22	47:D0:12:ASN:H	1.61	0.64
26:DA:2794:C:N4	26:DA:2802:G:O6	2.30	0.64
40:BT:112:ARG:HG3	40:BT:115:ARG:HH21	1.62	0.64
51:D4:1:MET:HG2	51:D4:6:HIS:CD2	2.32	0.64
39:DS:28:VAL:HG13	39:DS:35:ILE:HD11	1.79	0.64
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.32	0.64
26:BA:1361:C:OP2	61:BA:4634:HOH:O	2.14	0.64
26:BA:2184:G:C2'	26:BA:2185:C:H5''	2.28	0.64
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.33	0.64
1:CA:599:C:H2'	1:CA:600:C:H5''	1.80	0.64
2:CB:218:ALA:O	2:CB:222:ILE:HG23	1.97	0.64
26:DA:1648:C:OP1	61:DA:4201:HOH:O	2.14	0.64
27:DB:24:G:N7	27:DB:56:G:H2'	2.12	0.64
30:DF:116:ASP:OD2	36:DP:1:MET:N	2.30	0.64
2:AB:13:ALA:HB2	2:AB:44:LEU:HG	1.80	0.64
26:BA:2146:G:H1	26:BA:2196:C:H42	1.45	0.64
26:BA:791:G:OP1	61:BA:4683:HOH:O	2.15	0.64
11:CK:98:LEU:O	11:CK:101:SER:OG	2.14	0.64
1:CA:664:G:P	18:CR:64:ARG:HH22	2.19	0.64
26:DA:528:A:O2'	26:DA:529:A:H5''	1.96	0.64
39:DS:10:ARG:NH2	39:DS:91:PRO:O	2.27	0.64
26:BA:2015:U:OP2	61:BA:5277:HOH:O	2.15	0.64
1:CA:1323:G:H4'	1:CA:1363:C:C2	2.32	0.64
26:DA:236:C:H2'	26:DA:237:C:H6	1.63	0.64
27:DB:66:A:H61	27:DB:109:C:H5''	1.63	0.64
33:DI:12:LEU:HD22	33:DI:19:VAL:HG21	1.78	0.64
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.77	0.64
48:B1:23:LYS:HB3	48:B1:29:GLY:HA3	1.78	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1002:G:C4	1:CA:1003:G:H8	2.15	0.64
26:DA:1792:G:O2'	26:DA:1830:C:OP1	2.15	0.64
30:DF:101:LEU:HD12	30:DF:102:PRO:HD2	1.80	0.64
1:AA:195:A:OP1	20:AT:68:LYS:NZ	2.30	0.64
23:AW:5:G:H2'	23:AW:6:G:C8	2.33	0.64
45:BY:54:LYS:HA	45:BY:56:PRO:HD3	1.80	0.64
1:CA:1309:G:OP2	13:CM:99:ARG:NH2	2.28	0.64
5:CE:20:GLN:NE2	5:CE:21:ALA:O	2.31	0.64
26:DA:2323:G:O6	26:DA:2332:U:N3	2.18	0.64
33:DI:102:SER:O	33:DI:106:GLY:N	2.30	0.64
11:AK:98:LEU:O	11:AK:101:SER:OG	2.16	0.64
12:AL:33:ARG:HH11	12:AL:62:SER:HB3	1.62	0.64
26:BA:2859:U:OP2	40:BT:95:ARG:NH1	2.30	0.64
1:CA:1004:A:H2'	1:CA:1038:C:H1'	1.80	0.64
1:CA:1133:G:H1	1:CA:1141:C:N4	1.95	0.64
1:CA:1507:A:N6	1:CA:1528:U:O4	2.16	0.64
1:CA:444:C:H2'	1:CA:445:G:H8	1.62	0.64
1:AA:56:U:H2'	1:AA:57:G:C8	2.33	0.64
3:AC:37:GLN:NE2	14:AN:52:GLN:OE1	2.31	0.64
24:AX:19:G:H4'	24:AX:20:U:OP2	1.97	0.64
32:BH:86:GLU:OE2	32:BH:132:ARG:NH2	2.30	0.64
32:BH:149:ARG:NH1	32:BH:167:GLU:OE2	2.30	0.64
43:BW:88:ARG:HG3	43:BW:92:ARG:HH21	1.61	0.64
1:AA:1464:G:OP2	40:BT:111:ARG:NH2	2.30	0.63
1:AA:405:U:OP2	4:AD:3:ARG:NH2	2.32	0.63
26:BA:467:U:O2	30:BF:46:ARG:NH2	2.26	0.63
44:BX:31:HIS:CD2	44:BX:33:LYS:H	2.14	0.63
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.11	0.63
1:CA:1165:C:N4	1:CA:1171:G:H1	1.93	0.63
2:CB:178:ARG:NH2	8:CH:68:ARG:HH22	1.95	0.63
29:DE:101:ARG:CZ	29:DE:171:GLU:HB2	2.28	0.63
1:AA:1027:C:C2	1:AA:1034:G:C6	2.86	0.63
1:AA:894:G:N7	61:AA:4110:HOH:O	2.30	0.63
23:AW:55:PSU:O3'	26:BA:943:C:H4'	1.98	0.63
25:AY:25:C:O2'	25:AY:26:A:H8	1.82	0.63
26:BA:1211:U:H2'	26:BA:1212:C:C6	2.33	0.63
26:BA:1464:G:OP2	61:BA:4561:HOH:O	2.16	0.63
46:BZ:7:ALA:HB2	46:BZ:59:LEU:HD22	1.78	0.63
1:CA:1216:G:H5''	14:CN:5:ALA:HB2	1.79	0.63
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.31	0.63
1:CA:1318:A:OP1	19:CS:3:ARG:NH1	2.32	0.63
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.63	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1521:G:N3	61:CA:3217:HOH:O	2.30	0.63
1:CA:562:C:H1'	12:CL:15:ARG:HB3	1.80	0.63
7:CG:72:ARG:HH22	7:CG:138:LYS:HZ1	1.45	0.63
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.79	0.63
25:CY:31:A:N1	25:CY:39:PSU:C2	2.65	0.63
26:DA:971:C:OP2	61:DA:4615:HOH:O	2.15	0.63
35:DO:115:VAL:HG13	35:DO:121:VAL:HG21	1.79	0.63
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.31	0.63
3:AC:181:ASN:ND2	3:AC:204:LEU:HD12	2.13	0.63
26:BA:388:A:H2'	26:BA:389:G:C8	2.34	0.63
1:CA:1013:G:N2	1:CA:1016:A:OP2	2.25	0.63
1:CA:533:A:O2'	1:CA:535:A:OP2	2.17	0.63
26:DA:2127:G:C2	26:DA:2161:C:C4	2.87	0.63
26:DA:2805:G:H2'	26:DA:2807:G:C8	2.34	0.63
26:DA:2880:C:O3'	38:DR:90:ARG:NH1	2.30	0.63
27:DB:19:G:H2'	27:DB:20:C:O4'	1.99	0.63
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	1.79	0.63
25:AY:15:G:H22	25:AY:48:C:N4	1.96	0.63
26:BA:2324:U:H5'	31:BG:88:ILE:HD11	1.81	0.63
7:CG:113:GLU:HB2	7:CG:119:ARG:HG2	1.81	0.63
16:CP:23:ASP:OD2	16:CP:25:ARG:NH1	2.32	0.63
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	1.81	0.63
20:AT:87:LYS:O	20:AT:91:LEU:HG	1.98	0.63
26:BA:2695:C:OP1	40:BT:53:ARG:NH2	2.31	0.63
26:DA:2206:G:H3'	26:DA:2207:G:N7	2.13	0.63
28:DD:206:LEU:HD22	28:DD:211:ARG:HG2	1.80	0.63
32:DH:3:ARG:HH22	32:DH:5:GLY:H	1.47	0.63
46:DZ:157:LEU:HD13	46:DZ:161:VAL:HG13	1.80	0.63
8:AH:34:GLU:OE2	8:AH:37:ARG:NH1	2.31	0.63
19:AS:64:GLU:O	19:AS:67:VAL:HG23	1.98	0.63
25:AY:5:G:N1	25:AY:68:C:N4	2.31	0.63
33:BI:93:THR:OG1	33:BI:96:ASP:OD1	2.17	0.63
26:DA:1038:C:N4	26:DA:1117:G:H1	1.97	0.63
1:AA:1036:G:H3'	1:AA:1037:C:H6	1.63	0.63
1:CA:539:A:H2'	1:CA:540:G:C8	2.33	0.63
1:CA:957:U:O2'	1:CA:959:A:N7	2.30	0.63
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.30	0.63
23:CW:76:F3N:OP2	61:CW:3102:HOH:O	2.15	0.63
1:AA:1321:C:H5''	1:AA:1322:C:H2'	1.78	0.63
1:CA:1002:G:H1	1:CA:1038:C:H42	1.44	0.63
1:CA:1402:C:N4	22:CV:18:G:OP2	2.31	0.63
23:CW:76:F3N:O2'	26:DA:2585:U:O4	2.15	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1021:A:H62	26:DA:1141:U:H3	1.44	0.63
26:DA:1637:A:OP2	61:DA:4544:HOH:O	2.16	0.63
26:DA:1939:U:OP1	26:DA:2604:U:O2'	2.17	0.63
26:DA:2173:A:H2'	26:DA:2174:C:O4'	1.99	0.63
1:CA:1150:U:O4	1:CA:1151:A:N6	2.32	0.63
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.31	0.63
8:CH:37:ARG:HH21	8:CH:38:ILE:HD11	1.63	0.63
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.31	0.63
26:DA:1602:U:O4	61:DA:3879:HOH:O	2.11	0.63
31:DG:145:THR:HG22	31:DG:148:MET:SD	2.38	0.63
1:AA:1025:U:O2	1:AA:1036:G:O6	2.16	0.62
23:AW:47:U:H5'	23:AW:47:U:H6	1.64	0.62
26:BA:1613:A:OP1	28:BD:211:ARG:NH1	2.32	0.62
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.33	0.62
1:CA:1120:G:C6	1:CA:1154:G:N2	2.67	0.62
2:CB:216:SER:O	2:CB:220:ASP:N	2.21	0.62
29:DE:14:ILE:HG13	29:DE:21:VAL:HG13	1.80	0.62
1:AA:673:G:H2'	1:AA:674:G:C8	2.34	0.62
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.82	0.62
26:BA:2544:G:O2'	26:BA:2669:A:N1	2.31	0.62
26:BA:1201:A:OP1	41:BU:55:ARG:HD3	1.99	0.62
3:CC:125:GLU:OE2	3:CC:125:GLU:N	2.26	0.62
11:CK:93:GLN:HA	11:CK:93:GLN:HE21	1.64	0.62
13:CM:32:GLU:OE1	13:CM:59:TYR:OH	2.16	0.62
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.62	0.62
37:DQ:67:ARG:O	37:DQ:101:ARG:NH2	2.30	0.62
47:B0:27:GLU:HG3	47:B0:68:GLU:HA	1.81	0.62
1:CA:981:U:H5'	14:CN:21:TYR:CZ	2.35	0.62
3:CC:16:ARG:NH1	3:CC:181:ASN:OD1	2.31	0.62
5:CE:36:ASP:O	5:CE:38:GLN:N	2.27	0.62
26:DA:1300:U:H4'	26:DA:1301:A:C5'	2.29	0.62
25:CY:76:A:O2'	26:DA:2394:C:N3	2.31	0.62
1:CA:1023:G:H3'	1:CA:1024:G:H8	1.63	0.62
25:CY:31:A:C6	25:CY:39:PSU:O2	2.52	0.62
26:DA:902:C:H2'	26:DA:903:C:C6	2.35	0.62
26:DA:322:A:OP2	30:DF:169:ASN:HB2	1.98	0.62
42:DV:72:VAL:HG13	42:DV:85:LYS:HB3	1.80	0.62
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.81	0.62
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.80	0.62
36:BP:65:ARG:HG3	55:B8:25:MET:HG3	1.80	0.62
1:CA:946:A:H2'	1:CA:947:G:C8	2.35	0.62
1:CA:951:G:N3	1:CA:970:C:O2'	2.29	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:CM:20:THR:HA	13:CM:25:ILE:HG22	1.81	0.62
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.33	0.62
37:DQ:85:LYS:HB2	47:D0:7:LEU:HD12	1.82	0.62
26:DA:1890:A:OP2	61:DA:4438:HOH:O	2.16	0.62
24:AX:21:A:H61	24:AX:46:G:H2'	1.64	0.62
1:CA:56:U:H2'	1:CA:57:G:C8	2.35	0.62
1:CA:975:A:N1	10:CJ:48:THR:HB	2.13	0.62
16:CP:28:ARG:NH1	16:CP:29:ASP:OD1	2.31	0.62
30:DF:122:LYS:NZ	30:DF:152:GLU:OE2	2.30	0.62
43:DW:88:ARG:NH1	43:DW:94:ASP:OD2	2.32	0.62
45:DY:102:CYS:SG	45:DY:103:GLY:N	2.72	0.62
1:AA:1414:U:H3	1:AA:1486:G:H1	1.46	0.62
1:AA:1187:G:H4'	9:AI:111:ARG:HH11	1.64	0.62
51:B4:63:TYR:N	51:B4:64:GLY:HA2	2.15	0.62
1:CA:661:G:H1	1:CA:744:C:H42	1.46	0.62
1:CA:957:U:H2'	1:CA:959:A:OP2	2.00	0.62
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.23	0.62
31:DG:101:ILE:HD13	51:D4:25:TYR:HB2	1.82	0.62
26:DA:577:G:O2'	26:DA:1254:A:OP1	2.18	0.62
26:DA:658:C:H2'	26:DA:659:C:C6	2.34	0.62
1:AA:97:G:O2'	1:AA:98:G:H5''	2.00	0.62
23:AW:76:F3N:N	24:AX:76:31H:O2'	2.33	0.62
1:CA:54:C:N4	1:CA:353:A:OP2	2.32	0.62
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.81	0.62
26:DA:2096:U:H3	26:DA:2193:G:H1	1.48	0.62
30:DF:28:ILE:HG23	30:DF:112:MET:HE3	1.81	0.62
1:AA:984:C:H42	1:AA:1221:G:H1	1.48	0.62
3:AC:39:ILE:HG23	3:AC:91:LEU:HD11	1.82	0.62
3:AC:82:GLU:HG2	3:AC:85:ARG:HH21	1.63	0.62
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.82	0.62
1:CA:1404:C:O2	1:CA:1519:A:O2'	2.14	0.62
10:CJ:6:ILE:HG23	10:CJ:98:ILE:HG13	1.82	0.62
26:DA:2379:G:O2'	39:DS:17:ARG:NH2	2.30	0.62
25:AY:25:C:O2'	25:AY:26:A:O5'	2.18	0.62
26:BA:272:U:OP1	33:BI:50:ARG:NH2	2.29	0.62
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.33	0.62
55:D8:33:ASN:HA	55:D8:36:LYS:HD2	1.82	0.62
26:DA:1149:G:H2'	26:DA:1150:C:C6	2.35	0.62
33:DI:38:LEU:HD12	33:DI:38:LEU:H	1.64	0.62
36:DP:39:LYS:HB2	36:DP:45:LEU:HG	1.81	0.62
26:DA:2816:C:O3'	38:DR:99:LYS:NZ	2.32	0.62
26:BA:1890:A:N6	26:BA:1905:G:O2'	2.32	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:18:ARG:NH2	30:DF:127:GLU:OE1	2.31	0.61
31:DG:5:VAL:HG22	31:DG:8:LYS:H	1.64	0.61
37:BQ:21:THR:HG21	37:BQ:101:ARG:HB2	1.82	0.61
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.81	0.61
26:DA:881:G:H1	26:DA:895:U:H3	1.48	0.61
1:AA:62:U:OP1	1:AA:385:C:O2'	2.17	0.61
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.15	0.61
51:B4:53:GLU:HB3	51:B4:54:GLY:HA2	1.82	0.61
26:BA:671:A:H2'	26:BA:672:G:O4'	2.01	0.61
30:BF:184:TYR:O	30:BF:188:ARG:HG3	2.00	0.61
1:CA:662:G:H2'	1:CA:663:A:C8	2.34	0.61
2:CB:101:MET:HA	2:CB:108:ILE:HG13	1.82	0.61
1:CA:1376:U:H3'	7:CG:94:ARG:HH21	1.65	0.61
10:CJ:49:VAL:HG12	10:CJ:61:GLU:O	2.00	0.61
26:BA:1494:G:N7	61:BA:4947:HOH:O	2.31	0.61
29:BE:29:GLY:HA3	61:BE:408:HOH:O	1.99	0.61
31:BG:43:LEU:HD11	31:BG:153:ARG:HG2	1.83	0.61
45:BY:102:CYS:SG	45:BY:103:GLY:N	2.73	0.61
1:CA:1397:C:OP2	5:CE:24:ARG:NH2	2.33	0.61
26:DA:1031:G:H5''	56:D9:8:LYS:HE3	1.80	0.61
26:DA:1028:A:N6	26:DA:1125:G:H2'	2.15	0.61
26:DA:796:C:H2'	26:DA:797:C:C6	2.34	0.61
27:DB:45:A:O4'	31:DG:95:ARG:NH1	2.33	0.61
41:DU:83:LEU:HD12	41:DU:88:ILE:HD12	1.81	0.61
1:AA:1036:G:H3'	1:AA:1037:C:C6	2.34	0.61
1:AA:139:G:N2	1:AA:224:C:O2	2.28	0.61
11:AK:91:ARG:HG3	11:AK:92:GLU:N	2.15	0.61
42:BV:40:LEU:HB2	42:BV:46:VAL:HG13	1.81	0.61
46:BZ:24:LEU:HB2	46:BZ:41:LEU:HD23	1.81	0.61
1:CA:1297:C:OP1	13:CM:44:ARG:NH2	2.27	0.61
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.82	0.61
26:DA:1371:G:O6	61:DA:3964:HOH:O	2.12	0.61
23:AW:26:A:N1	23:AW:44:G:N2	2.44	0.61
26:BA:2442:A:N3	26:BA:2442:A:H2'	2.15	0.61
30:BF:101:LEU:O	30:BF:106:ARG:NH1	2.32	0.61
1:CA:1193:G:O2'	5:CE:25:ARG:NH2	2.34	0.61
2:CB:16:HIS:CD2	2:CB:17:PHE:H	2.18	0.61
6:CF:61:LEU:HB3	6:CF:63:TYR:HE1	1.65	0.61
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.36	0.61
12:CL:113:ARG:NH2	61:CL:201:HOH:O	2.33	0.61
13:CM:91:ARG:HB2	13:CM:98:VAL:HG13	1.82	0.61
26:DA:958:U:OP2	37:DQ:14:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:DB:106:G:H5'	46:DZ:31:ARG:HG2	1.83	0.61
26:BA:1159:U:H2'	26:BA:1160:G:C8	2.36	0.61
26:BA:1874:C:H5'	28:BD:253:GLN:NE2	2.15	0.61
27:BB:105:A:OP1	46:BZ:72:ARG:NH1	2.34	0.61
8:CH:45:ILE:HG22	8:CH:63:LEU:HA	1.83	0.61
44:DX:60:ARG:HH12	54:D7:47:ARG:NH2	1.98	0.61
36:BP:59:LEU:HD21	55:B8:10:ALA:HA	1.82	0.61
26:BA:2317:A:H5''	31:BG:134:GLY:HA3	1.83	0.61
4:CD:154:ASN:HA	4:CD:159:ARG:HH21	1.65	0.61
10:CJ:29:ARG:HB2	10:CJ:84:GLN:HE22	1.65	0.61
56:D9:25:VAL:HB	56:D9:34:GLN:HB2	1.81	0.61
26:DA:2114:A:N6	26:DA:2119:A:N7	2.48	0.61
35:DO:71:ARG:NE	35:DO:105:GLU:OE2	2.32	0.61
25:AY:15:G:N2	25:AY:48:C:H42	1.99	0.61
30:BF:8:GLN:HA	30:BF:8:GLN:HE21	1.65	0.61
1:CA:1240:U:OP2	7:CG:116:ALA:N	2.34	0.61
1:CA:735:C:H2'	1:CA:736:C:H6	1.64	0.61
2:CB:113:HIS:O	2:CB:117:GLU:N	2.32	0.61
26:DA:2169:A:H2'	26:DA:2170:A:C8	2.35	0.61
1:AA:69:G:H2'	1:AA:70:G:C8	2.36	0.61
11:AK:51:LYS:HD3	11:AK:55:LYS:HE2	1.83	0.61
1:CA:1128:C:O2'	1:CA:1147:C:N3	2.23	0.61
2:CB:13:ALA:N	2:CB:14:GLY:HA3	2.16	0.61
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.19	0.61
9:CI:3:GLN:OE1	9:CI:20:ARG:NH2	2.34	0.61
26:DA:1140:C:O3'	34:DN:25:ARG:NH1	2.34	0.61
26:DA:1557:C:OP2	26:DA:1558:A:O2'	2.17	0.61
26:DA:2022:U:O2'	26:DA:2617:C:H5'	2.01	0.61
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.20	0.60
1:AA:1502:A:H2	1:AA:1505:G:N1	1.95	0.60
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.82	0.60
13:AM:23:TYR:HB3	13:AM:67:GLU:HA	1.83	0.60
18:AR:26:LEU:HD21	18:AR:39:VAL:HG13	1.82	0.60
54:B7:34:ARG:NH1	54:B7:41:ARG:O	2.34	0.60
26:BA:1935:A:H4'	26:BA:1936:C:H5''	1.83	0.60
27:BB:41:U:H5	31:BG:70:VAL:H	1.49	0.60
1:CA:728:A:H2'	1:CA:729:A:C8	2.36	0.60
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.82	0.60
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.19	0.60
26:DA:1550:C:OP1	26:DA:1720:U:O2'	2.17	0.60
26:DA:821:A:N1	61:DA:4084:HOH:O	2.31	0.60
26:DA:93:G:H2'	26:DA:94:C:C6	2.36	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:AL:32:PHE:HB3	12:AL:84:LEU:HD11	1.82	0.60
14:AN:21:TYR:OH	14:AN:23:ARG:NH2	2.33	0.60
1:CA:1329:A:H5'	13:CM:29:ARG:HD2	1.82	0.60
26:DA:1231:G:H2'	26:DA:1232:G:C8	2.36	0.60
26:DA:1250:G:N7	36:DP:18:ARG:NH2	2.49	0.60
26:DA:2312:U:H5'	31:DG:88:ILE:HD11	1.83	0.60
26:BA:1224:C:H2'	26:BA:1225:C:H6	1.66	0.60
26:BA:2118:U:H3	26:BA:2215:G:H1	1.49	0.60
26:BA:2832:G:N7	61:BA:5279:HOH:O	2.32	0.60
1:CA:1297:C:O3'	7:CG:114:ARG:NH2	2.34	0.60
1:CA:222:U:H2'	1:CA:223:U:C6	2.35	0.60
1:CA:289:G:OP2	61:CA:3236:HOH:O	2.16	0.60
4:CD:100:ARG:NH1	4:CD:137:SER:OG	2.34	0.60
19:AS:31:ILE:HB	19:AS:49:ILE:HG23	1.83	0.60
25:AY:62:C:H2'	25:AY:63:G:H8	1.66	0.60
26:BA:312:C:H2'	26:BA:313:A:H8	1.66	0.60
26:BA:591:U:H5'	26:BA:990:A:N1	2.16	0.60
30:BF:116:ASP:OD1	30:BF:119:ARG:NH2	2.34	0.60
54:D7:34:ARG:NH1	54:D7:41:ARG:O	2.34	0.60
1:AA:243:A:H4'	1:AA:244:U:H5''	1.82	0.60
1:AA:26:A:O2'	4:AD:209:ARG:NH2	2.34	0.60
26:BA:1324:A:OP1	38:BR:36:THR:HG23	2.02	0.60
1:CA:1135:U:H2'	1:CA:1137:C:C2	2.36	0.60
17:CQ:81:ARG:HB3	17:CQ:84:LEU:HD12	1.83	0.60
26:DA:2130:U:H4'	26:DA:2133:G:H4'	1.82	0.60
1:AA:1106:G:H5''	3:AC:172:ARG:HG2	1.82	0.60
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.84	0.60
1:CA:501:C:H2'	1:CA:502:G:H8	1.67	0.60
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.37	0.60
9:CI:14:VAL:HG23	9:CI:66:ARG:HB3	1.83	0.60
25:CY:15:G:N1	25:CY:48:C:N3	2.46	0.60
46:DZ:111:VAL:HG21	46:DZ:117:LEU:HB2	1.84	0.60
26:BA:1071:G:C4	26:BA:1180:C:H1'	2.37	0.60
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.00	0.60
1:AA:1241:G:OP1	7:AG:35:LYS:NZ	2.35	0.60
1:AA:1351:U:O4	9:AI:118:LYS:NZ	2.35	0.60
13:CM:14:ARG:HB2	13:CM:17:VAL:HG23	1.83	0.60
49:D2:29:LYS:HG2	49:D2:57:ILE:HD13	1.84	0.60
26:DA:2185:C:H2'	26:DA:2186:G:O4'	2.01	0.60
35:DO:53:LYS:NZ	35:DO:56:ASP:OD1	2.34	0.60
26:DA:483:A:O2'	45:DY:49:VAL:O	2.10	0.60
46:DZ:93:ASP:HA	46:DZ:131:ARG:NH2	2.17	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.83	0.60
26:BA:661:G:OP1	36:BP:132:LYS:HE2	2.02	0.60
33:BI:104:GLN:HB3	33:BI:105:HIS:HD2	1.67	0.60
1:CA:148:G:H2'	1:CA:149:A:H8	1.66	0.60
18:AR:70:ILE:HG23	18:AR:79:LEU:HD12	1.84	0.60
23:AW:7:A:N6	23:AW:66:U:H3	2.00	0.60
26:BA:1553:A:O2'	26:BA:1554:A:O4'	2.20	0.60
26:BA:70:A:H3'	26:BA:70:A:OP2	2.02	0.60
28:BD:108:PRO:HB3	28:BD:143:HIS:CE1	2.37	0.60
38:BR:97:VAL:HG22	38:BR:114:VAL:HG13	1.84	0.60
46:BZ:117:LEU:HD21	46:BZ:144:LEU:HD13	1.84	0.60
46:BZ:138:GLU:N	46:BZ:156:LYS:HD3	2.13	0.60
1:CA:19:C:H5''	5:CE:86:ALA:HB3	1.83	0.60
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.67	0.60
1:CA:1456:G:N1	20:CT:51:GLU:OE2	2.30	0.60
51:D4:16:CYS:HA	51:D4:33:VAL:HB	1.83	0.60
26:DA:2836:U:H2'	26:DA:2837:G:C8	2.37	0.60
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.34	0.59
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.37	0.59
1:CA:662:G:H2'	1:CA:663:A:H8	1.67	0.59
3:CC:70:VAL:HG22	3:CC:72:LYS:H	1.66	0.59
26:DA:307:G:N1	26:DA:310:A:OP2	2.33	0.59
31:DG:41:GLN:HB3	31:DG:43:LEU:HD22	1.83	0.59
33:DI:4:ILE:HG12	33:DI:18:VAL:HG22	1.84	0.59
46:DZ:59:LEU:HD11	46:DZ:69:THR:HG21	1.81	0.59
1:AA:1125:U:H4'	10:AJ:5:ARG:HH22	1.67	0.59
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.59
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.34	0.59
7:AG:37:ASN:ND2	9:AI:39:GLY:O	2.33	0.59
9:AI:49:PRO:HG3	9:AI:101:PHE:HD2	1.65	0.59
2:CB:92:TYR:N	2:CB:151:GLY:O	2.32	0.59
9:CI:96:LEU:HD22	9:CI:101:PHE:HB2	1.84	0.59
26:DA:2815:C:H5'	52:D5:29:THR:HG21	1.83	0.59
26:DA:144:C:H2'	26:DA:145:G:H8	1.67	0.59
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.25	0.59
23:AW:9:A:OP2	23:AW:13:C:N4	2.30	0.59
26:BA:1405:A:H61	26:BA:1418:U:H3	1.49	0.59
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.37	0.59
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.36	0.59
25:CY:50:U:O2	25:CY:64:A:N1	2.35	0.59
26:DA:1310:G:OP2	54:D7:9:ARG:NH1	2.35	0.59
26:DA:2127:G:N2	26:DA:2161:C:N3	2.50	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
40:DT:30:VAL:HG22	40:DT:86:ILE:HG12	1.83	0.59
46:DZ:5:LEU:HD22	46:DZ:6:LYS:H	1.68	0.59
1:AA:262:A:H2'	1:AA:263:A:C8	2.38	0.59
9:AI:117:HIS:HB2	9:AI:121:ARG:HG3	1.84	0.59
11:CK:54:ARG:NH1	25:CY:39:PSU:O2'	2.35	0.59
12:CL:117:ARG:CZ	12:CL:117:ARG:HB2	2.32	0.59
26:DA:2336:A:H61	47:D0:43:THR:HG22	1.67	0.59
3:AC:50:ALA:HB1	3:AC:70:VAL:HG21	1.84	0.59
4:AD:173:TRP:CZ3	4:AD:174:LEU:HG	2.38	0.59
26:BA:1405:A:N6	26:BA:1418:U:H3	2.00	0.59
28:BD:68:LYS:HD2	28:BD:70:TRP:CZ2	2.38	0.59
1:CA:646:U:H2'	1:CA:647:C:C6	2.37	0.59
26:DA:668:G:H5'	26:DA:669:G:OP2	2.01	0.59
26:BA:2158:C:N4	26:BA:2177:G:N1	2.30	0.59
36:BP:91:PHE:O	36:BP:121:LYS:NZ	2.35	0.59
1:CA:1070:U:H2'	1:CA:1071:C:H6	1.67	0.59
1:CA:986:A:N3	19:CS:52:TYR:OH	2.33	0.59
2:CB:133:LYS:O	2:CB:137:ARG:N	2.32	0.59
2:CB:15:VAL:HG12	2:CB:209:ARG:HB3	1.85	0.59
39:DS:43:GLU:HB3	39:DS:44:LYS:HE2	1.82	0.59
39:DS:5:THR:OG1	39:DS:8:GLU:OE2	2.13	0.59
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	1.84	0.59
36:BP:52:GLU:OE1	36:BP:55:ARG:NH1	2.31	0.59
46:BZ:111:VAL:HG12	46:BZ:112:ARG:H	1.68	0.59
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.17	0.59
2:CB:91:PRO:HB3	2:CB:154:LEU:HB3	1.83	0.59
26:DA:2140:C:H2'	26:DA:2141:G:H5'	1.85	0.59
26:DA:2745:C:O2'	32:DH:139:GLN:O	2.20	0.59
1:AA:1025:U:O2'	1:AA:1026:G:H8	1.86	0.59
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.35	0.59
9:AI:17:VAL:HG23	9:AI:63:ILE:HG12	1.83	0.59
50:B3:3:ARG:NH1	50:B3:60:GLU:OE2	2.35	0.59
1:CA:1298:C:P	7:CG:114:ARG:HH22	2.26	0.59
10:CJ:46:ARG:HG2	10:CJ:64:GLU:HB3	1.83	0.59
16:CP:52:ASP:O	16:CP:54:GLU:N	2.36	0.59
26:DA:2315:G:H2'	26:DA:2316:C:C6	2.37	0.59
26:DA:2646:C:OP2	26:DA:2732:G:O2'	2.20	0.59
30:DF:185:ASP:HA	30:DF:188:ARG:HD3	1.84	0.59
37:DQ:34:LEU:HB2	37:DQ:118:LEU:HD22	1.84	0.59
40:DT:56:GLY:O	40:DT:59:THR:HG23	2.02	0.59
26:DA:481:G:O5'	45:DY:47:LYS:NZ	2.35	0.59
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.36	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:AQ:9:VAL:HG21	17:AQ:84:LEU:HD13	1.84	0.59
26:BA:2163:G:H22	26:BA:2171:G:H22	1.51	0.59
26:BA:331:G:H21	26:BA:354:A:H62	1.49	0.59
35:BO:63:VAL:HG12	35:BO:106:LEU:HD11	1.84	0.59
1:CA:375:U:OP1	16:CP:69:THR:HG21	2.02	0.59
7:CG:72:ARG:N	7:CG:142:GLU:OE2	2.30	0.59
8:CH:4:ASP:OD1	8:CH:7:ALA:N	2.25	0.59
26:DA:2273:A:H2'	26:DA:2274:A:C8	2.38	0.59
34:DN:38:HIS:CE1	34:DN:39:ARG:HG3	2.37	0.59
1:AA:1320:C:H5''	19:AS:70:LYS:HG3	1.84	0.59
26:BA:1065:U:H3	26:BA:1188:A:H62	1.51	0.59
26:BA:1525:G:O2'	26:BA:1605:A:N1	2.35	0.59
1:CA:573:A:N3	1:CA:883:C:O2'	2.29	0.59
1:CA:1104:G:O5'	2:CB:111:ARG:HD2	2.02	0.59
2:CB:121:LEU:H	2:CB:125:PRO:HG2	1.68	0.59
26:DA:1025:G:C4	26:DA:1135:C:H1'	2.38	0.59
36:DP:86:LYS:HB3	36:DP:118:GLY:HA3	1.83	0.59
1:AA:46:G:O2'	1:AA:365:U:O2	2.21	0.58
26:BA:1216:G:C2	26:BA:1217:G:H1'	2.38	0.58
39:BS:15:ARG:O	39:BS:19:LYS:HG2	2.02	0.58
1:CA:1049:U:C5	1:CA:1201:A:H5'	2.37	0.58
1:CA:1120:G:C6	1:CA:1121:U:C4	2.91	0.58
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.38	0.58
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.84	0.58
2:CB:57:PHE:HE2	2:CB:185:ILE:HD12	1.67	0.58
2:CB:73:THR:HA	2:CB:94:ASN:O	2.02	0.58
19:CS:38:SER:HB2	19:CS:71:LEU:HD22	1.84	0.58
49:D2:22:GLU:OE2	49:D2:68:ARG:NH2	2.35	0.58
13:AM:3:ARG:HG3	13:AM:4:ILE:N	2.18	0.58
2:CB:55:PHE:O	2:CB:59:GLU:N	2.25	0.58
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.51	0.58
27:DB:11:C:OP2	27:DB:12:C:N4	2.30	0.58
2:AB:19:HIS:HE1	2:AB:189:ASP:HB3	1.69	0.58
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.86	0.58
50:D3:5:LYS:NZ	50:D3:34:GLU:OE2	2.19	0.58
26:DA:888:C:H2'	26:DA:889:C:C4	2.38	0.58
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.68	0.58
26:BA:1091:A:H1'	26:BA:1093:G:N3	2.18	0.58
26:BA:2195:A:H3'	26:BA:2196:C:H6	1.69	0.58
26:BA:2227:G:H5'	26:BA:2228:G:N7	2.18	0.58
28:BD:79:VAL:HG21	28:BD:111:LEU:HD11	1.85	0.58
40:BT:65:LYS:HE2	40:BT:67:SER:HB2	1.85	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:BZ:110:GLY:N	46:BZ:144:LEU:O	2.32	0.58
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.18	0.58
1:CA:396:G:O2'	1:CA:398:C:OP1	2.11	0.58
2:CB:87:ARG:NH2	2:CB:233:SER:HB3	2.18	0.58
13:CM:121:LYS:H	13:CM:121:LYS:NZ	2.01	0.58
18:CR:60:ALA:O	18:CR:64:ARG:HG3	2.02	0.58
25:CY:8:4SU:H1'	25:CY:48:C:O2	2.04	0.58
47:D0:11:ARG:O	47:D0:14:ARG:NH2	2.36	0.58
26:DA:1639:U:H2'	26:DA:1640:C:H5''	1.85	0.58
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.18	0.58
1:AA:1309:G:OP2	13:AM:99:ARG:NH2	2.33	0.58
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.03	0.58
25:AY:60:U:H5''	25:AY:61:C:H5	1.69	0.58
45:BY:90:LEU:HD21	45:BY:96:ILE:HG12	1.85	0.58
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.84	0.58
26:DA:1371:G:H2'	26:DA:1372:U:H5	1.69	0.58
26:DA:2680:C:OP2	29:DE:111:ARG:NH2	2.36	0.58
35:DO:24:VAL:HA	35:DO:39:ILE:HG22	1.86	0.58
1:AA:473:G:H2'	1:AA:474:G:H8	1.68	0.58
1:AA:731:G:H5'	1:AA:766:A:H4'	1.85	0.58
13:AM:11:ARG:HB2	13:AM:46:LYS:HB3	1.86	0.58
26:BA:1067:A:H62	26:BA:1186:U:H3	1.49	0.58
26:BA:927:G:N2	26:BA:944:C:N3	2.44	0.58
42:BV:72:VAL:HG13	42:BV:85:LYS:HB3	1.85	0.58
1:CA:1028:C:C2	1:CA:1033:G:N1	2.72	0.58
1:CA:1122:U:C4	1:CA:1123:A:N7	2.72	0.58
1:CA:1298:C:H4'	1:CA:1299:A:H5'	1.85	0.58
13:CM:92:HIS:CD2	13:CM:98:VAL:HG21	2.39	0.58
26:DA:362:U:O2'	26:DA:363:G:H5''	2.03	0.58
1:AA:1026:G:C2	1:AA:1027:C:H4'	2.38	0.58
5:AE:53:LEU:HD12	5:AE:53:LEU:H	1.68	0.58
26:BA:325:G:OP2	45:BY:84:ARG:NH2	2.37	0.58
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.20	0.58
36:DP:63:PRO:HG2	55:D8:25:MET:HB2	1.86	0.58
32:DH:58:GLU:OE2	32:DH:60:ARG:NH1	2.37	0.58
1:AA:998:G:H1	1:AA:1043:C:N4	1.98	0.58
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.38	0.58
1:AA:78:G:N2	1:AA:92:C:N3	2.51	0.58
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.36	0.58
26:BA:929:G:H1	26:BA:940:C:H42	1.50	0.58
1:CA:148:G:H2'	1:CA:149:A:C8	2.39	0.58
1:CA:328:C:H4'	1:CA:329:A:H5'	1.86	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:54:ARG:HH11	3:CC:54:ARG:HB3	1.68	0.58
10:CJ:89:ASP:O	10:CJ:91:PRO:HD3	2.04	0.58
26:DA:1412:A:H2'	26:DA:1413:G:H8	1.68	0.58
26:DA:2127:G:C5	26:DA:2161:C:N4	2.71	0.58
31:DG:15:VAL:HG22	31:DG:175:LEU:HB3	1.85	0.58
46:DZ:150:LEU:H	46:DZ:172:ALA:HB3	1.68	0.58
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.18	0.58
26:BA:1846:A:OP2	28:BD:54:ARG:NH2	2.35	0.58
26:BA:2416:C:O3'	36:BP:77:ARG:NH2	2.37	0.58
1:CA:407:G:OP1	4:CD:115:ARG:NH2	2.35	0.58
26:DA:1166:C:H2'	26:DA:1167:U:C6	2.39	0.58
26:DA:858:U:H1'	26:DA:2268:A:H2'	1.84	0.58
26:DA:903:C:H2'	26:DA:904:C:C6	2.38	0.58
1:AA:72:C:H2'	1:AA:73:G:O4'	2.03	0.58
2:AB:158:LEU:HD21	2:AB:180:LEU:HD13	1.86	0.58
28:BD:180:GLY:HA3	28:BD:275:LYS:HB2	1.86	0.58
30:BF:116:ASP:OD2	36:BP:1:MET:N	2.29	0.58
45:BY:92:ASN:N	45:BY:93:GLY:HA2	2.18	0.58
1:CA:964:A:N3	1:CA:969:A:O2'	2.33	0.58
1:CA:978:A:O2'	1:CA:1321:C:N4	2.36	0.58
3:CC:65:ALA:HA	3:CC:100:ALA:HB3	1.86	0.58
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.85	0.58
24:CX:16:C:H5'	24:CX:59:A:N1	2.19	0.58
25:CY:56:C:O4'	26:DA:2169:A:H1'	2.04	0.58
28:DD:28:GLU:OE2	61:DD:416:HOH:O	2.17	0.58
31:DG:43:LEU:HD12	31:DG:45:GLU:HG3	1.86	0.58
43:DW:57:ASN:HA	43:DW:61:ASN:HD22	1.69	0.58
1:AA:1456:G:O6	20:AT:54:LYS:NZ	2.30	0.57
1:AA:21:G:OP1	61:AA:4104:HOH:O	2.17	0.57
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	1.86	0.57
56:B9:25:VAL:HB	56:B9:34:GLN:HB2	1.86	0.57
26:BA:2135:U:N3	26:BA:2136:A:N7	2.52	0.57
1:CA:998:G:H1	1:CA:1043:C:H42	0.74	0.57
2:CB:52:GLU:O	2:CB:56:ARG:HG2	2.04	0.57
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.04	0.57
42:DV:6:LYS:HG2	42:DV:11:GLN:HG2	1.85	0.57
2:AB:95:GLN:HG3	2:AB:147:LYS:HD3	1.85	0.57
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HB3	1.86	0.57
35:BO:80:ASP:OD1	40:BT:64:ARG:NH2	2.36	0.57
1:CA:114:U:H2'	1:CA:115:G:C8	2.39	0.57
2:CB:25:ASN:OD1	2:CB:27:LYS:HG2	2.04	0.57
23:CW:21:A:N6	23:CW:46:7MG:C4	2.72	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:CY:49:C:N3	25:CY:65:G:N2	2.46	0.57
26:DA:1857:G:O2'	26:DA:1885:A:N6	2.32	0.57
26:DA:2144:U:N3	26:DA:2146:C:N3	2.52	0.57
26:DA:848:G:H2'	26:DA:849:A:C8	2.39	0.57
1:AA:1392:G:H21	1:AA:1502:A:H8	1.53	0.57
2:AB:71:VAL:HG11	2:AB:170:GLU:HG2	1.86	0.57
54:B7:34:ARG:NH2	61:B7:202:HOH:O	2.36	0.57
26:BA:655:G:OP2	55:B8:15:LYS:NZ	2.30	0.57
35:BO:64:ARG:NH2	35:BO:99:PHE:O	2.37	0.57
26:BA:878:G:O2'	36:BP:38:GLN:NE2	2.38	0.57
43:BW:68:ARG:HH11	43:BW:111:HIS:HA	1.67	0.57
1:CA:1119:C:N3	1:CA:1154:G:O6	2.36	0.57
1:CA:45:U:H2'	1:CA:46:G:C8	2.39	0.57
3:CC:47:LEU:O	3:CC:51:GLY:N	2.34	0.57
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.86	0.57
7:CG:27:ILE:HD13	7:CG:40:ALA:HA	1.86	0.57
23:CW:4:C:N3	23:CW:69:G:C2	2.72	0.57
26:DA:1022:G:H22	26:DA:1142(A):A:H2	1.50	0.57
26:BA:1313:U:OP1	61:BA:5075:HOH:O	2.17	0.57
26:BA:715:G:H5'	26:BA:716:G:OP2	2.05	0.57
23:AW:52:G:H4'	37:BQ:56:ARG:NH2	2.20	0.57
1:CA:1097:C:H1'	1:CA:1170:A:H1'	1.86	0.57
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.36	0.57
7:CG:111:ARG:NH1	7:CG:113:GLU:OE1	2.37	0.57
23:CW:30:G:H1	23:CW:40:C:N4	2.03	0.57
26:DA:2070:G:OP2	61:DA:4461:HOH:O	2.17	0.57
26:DA:643:A:N1	26:DA:2369:A:O2'	2.36	0.57
28:DD:108:PRO:HG2	28:DD:111:LEU:HB2	1.87	0.57
35:DO:92:GLU:OE2	35:DO:113:LYS:HD3	2.05	0.57
42:DV:60:GLU:HB2	42:DV:97:LYS:HE2	1.85	0.57
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.43	0.57
2:AB:137:ARG:NH1	2:AB:137:ARG:HB3	2.19	0.57
12:AL:34:ARG:NH2	61:AL:301:HOH:O	2.36	0.57
26:BA:2145:G:H1	26:BA:2197:C:N4	2.02	0.57
1:CA:1051:C:H2'	1:CA:1052:U:C6	2.40	0.57
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.04	0.57
1:CA:1168:A:H2'	1:CA:1169:A:C8	2.39	0.57
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.20	0.57
1:CA:998:G:H2'	1:CA:999:C:O4'	2.04	0.57
4:CD:61:LYS:NZ	4:CD:72:GLU:OE1	2.35	0.57
13:CM:93:ARG:NH1	26:DA:888:C:O5'	2.37	0.57
23:CW:3:C:O2	23:CW:70:G:N1	2.29	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:CX:55:PSU:N3	24:CX:58:A:OP2	2.26	0.57
29:DE:30:PRO:HB3	29:DE:92:THR:HG22	1.86	0.57
37:DQ:111:GLU:O	37:DQ:115:MET:HG2	2.05	0.57
1:AA:1000:U:O2	1:AA:1042:G:N2	2.37	0.57
26:BA:2209:G:O2'	26:BA:2210:C:OP1	2.20	0.57
38:BR:28:LEU:HD12	38:BR:48:VAL:HG21	1.86	0.57
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.38	0.57
1:CA:444:C:H2'	1:CA:445:G:C8	2.39	0.57
16:CP:57:ARG:NH2	16:CP:79:VAL:O	2.38	0.57
30:DF:195:ASP:OD1	30:DF:196:LEU:N	2.38	0.57
1:AA:184:G:H2'	1:AA:185:A:H8	1.70	0.57
25:AY:33:U:H2'	25:AY:34:G:H3'	1.86	0.57
54:B7:33:ARG:NH2	61:B7:201:HOH:O	2.38	0.57
6:AF:81:ILE:HD11	28:BD:125:ILE:HB	1.87	0.57
45:BY:86:ARG:HD2	45:BY:100:ALA:HA	1.87	0.57
1:CA:1154:G:N7	1:CA:1155:G:C4	2.72	0.57
2:CB:16:HIS:O	2:CB:18:GLY:N	2.37	0.57
26:DA:686:G:N2	26:DA:788:A:H61	2.02	0.57
28:DD:3:VAL:HG13	28:DD:17:THR:HB	1.86	0.57
30:DF:13:SER:OG	30:DF:16:GLY:O	2.21	0.57
26:DA:674:G:H1'	30:DF:74:ARG:HD3	1.85	0.57
26:DA:1188:U:H4'	42:DV:79:VAL:HG22	1.86	0.57
1:AA:1057:G:OP2	61:AA:4024:HOH:O	2.16	0.57
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.05	0.57
1:AA:159:G:H2'	1:AA:161:A:OP2	2.05	0.57
26:BA:938:G:H3'	26:BA:939:C:C6	2.39	0.57
31:BG:5:VAL:HG22	31:BG:8:LYS:H	1.69	0.57
1:CA:1001:A:H2'	1:CA:1001(A):G:C8	2.39	0.57
1:CA:1012:U:O2	1:CA:1017:G:O6	2.23	0.57
3:CC:18:TRP:H	3:CC:18:TRP:HE3	1.52	0.57
1:CA:619:U:N3	4:CD:134:ASP:OD1	2.32	0.57
26:DA:479:A:N3	26:DA:481:G:H5''	2.19	0.57
27:DB:3:C:H2'	27:DB:4:C:C6	2.39	0.57
13:AM:40:ASN:O	13:AM:43:THR:OG1	2.23	0.57
25:AY:15:G:O6	25:AY:48:C:O2	2.23	0.57
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.15	0.57
1:CA:297:G:N2	1:CA:300:A:OP2	2.38	0.57
15:CO:55:GLY:HA2	15:CO:58:MET:HE2	1.86	0.57
31:DG:151:ALA:HB3	31:DG:153:ARG:HH11	1.70	0.57
46:DZ:159:PRO:HA	46:DZ:161:VAL:N	2.20	0.57
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.34	0.57
1:AA:375:U:OP1	16:AP:69:THR:HG21	2.05	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1218:G:O2'	26:BA:1219:A:O4'	2.17	0.57
26:BA:2369:U:OP1	47:B0:20:ARG:NH1	2.38	0.57
1:CA:588:G:O6	1:CA:651:C:N4	2.33	0.57
3:CC:3:ASN:HD22	3:CC:4:LYS:HG3	1.69	0.57
1:CA:1204:A:OP1	14:CN:3:ARG:NH1	2.37	0.57
24:CX:21:A:N6	24:CX:46:G:H2'	2.19	0.57
26:DA:1169:G:H1	26:DA:1180:C:N4	2.01	0.57
26:DA:614(C):A:C4	30:DF:180:GLY:HA2	2.40	0.57
45:DY:28:LYS:HD2	45:DY:40:GLU:HG3	1.87	0.57
46:DZ:92:SER:O	46:DZ:130:PRO:HG2	2.05	0.57
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.70	0.56
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.86	0.56
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.26	0.56
49:B2:65:ASN:OD1	49:B2:69:ARG:NH1	2.38	0.56
26:DA:2137:C:H2'	26:DA:2138:C:C6	2.40	0.56
26:DA:247:G:H4'	26:DA:386:G:C5	2.40	0.56
35:DO:1:MET:HG3	35:DO:67:LYS:HG2	1.86	0.56
36:DP:96:THR:H	36:DP:99:LEU:CD2	2.17	0.56
45:DY:6:HIS:CD2	45:DY:7:VAL:HG23	2.40	0.56
26:BA:211:A:H5''	26:BA:448:U:OP1	2.05	0.56
1:CA:1183:A:H5'	1:CA:1183:A:H8	1.69	0.56
8:CH:41:ARG:NH2	8:CH:123:GLU:OE2	2.38	0.56
13:CM:16:ASP:HB3	13:CM:34:LEU:HD11	1.87	0.56
47:D0:27:GLU:HG3	47:D0:68:GLU:HA	1.86	0.56
26:DA:2062:A:OP1	61:DA:3826:HOH:O	2.17	0.56
26:DA:2522:U:O2'	26:DA:2647:U:OP1	2.18	0.56
26:DA:2532:G:O2'	26:DA:2657:A:N1	2.36	0.56
26:DA:422:A:OP2	61:DA:3787:HOH:O	2.17	0.56
26:DA:740:U:H2'	26:DA:741:G:C8	2.39	0.56
31:DG:101:ILE:HG22	31:DG:105:LYS:HE2	1.86	0.56
36:DP:99:LEU:O	36:DP:103:ALA:N	2.37	0.56
44:DX:35:THR:HG22	44:DX:38:GLU:H	1.70	0.56
1:AA:1392:G:N2	1:AA:1502:A:H8	2.03	0.56
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.27	0.56
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.70	0.56
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.70	0.56
26:BA:1346:U:H4'	26:BA:1347:A:C5'	2.36	0.56
26:BA:2160:C:N3	26:BA:2175:G:N2	2.52	0.56
26:BA:847:A:H8	26:BA:847:A:OP1	1.88	0.56
26:BA:9:U:H3	26:BA:2641:A:H2	1.54	0.56
42:BV:76:LYS:HB2	42:BV:81:TYR:HB3	1.87	0.56
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.86	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2184:G:H2'	26:DA:2185:C:C6	2.39	0.56
26:DA:614(A):U:H4'	26:DA:614(B):G:H5'	1.86	0.56
46:DZ:150:LEU:N	46:DZ:172:ALA:HB3	2.20	0.56
1:AA:93:G:H2'	1:AA:96:U:O4'	2.06	0.56
9:AI:23:ASN:ND2	9:AI:60:ASP:OD2	2.38	0.56
13:AM:88:ARG:HG3	13:AM:98:VAL:HG12	1.87	0.56
26:BA:2149:G:H21	26:BA:2195:A:H1'	1.71	0.56
1:CA:1247:U:H1'	1:CA:1291:G:N2	2.20	0.56
2:CB:134:GLU:HA	2:CB:137:ARG:HB2	1.87	0.56
10:CJ:55:LYS:HE3	10:CJ:56:HIS:NE2	2.20	0.56
13:CM:29:ARG:HG3	13:CM:64:TRP:CZ3	2.39	0.56
13:CM:71:ARG:CG	13:CM:71:ARG:HH11	2.18	0.56
17:CQ:78:GLU:OE2	17:CQ:81:ARG:NH1	2.37	0.56
18:CR:43:PHE:HD1	18:CR:56:THR:HG22	1.69	0.56
26:DA:1412:A:H2'	26:DA:1413:G:C8	2.41	0.56
26:DA:236:C:H2'	26:DA:237:C:C6	2.41	0.56
27:DB:28:C:H2'	27:DB:29:A:C8	2.39	0.56
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.88	0.56
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.41	0.56
1:AA:1328:C:OP1	21:AU:21:TYR:OH	2.23	0.56
1:AA:198:G:O6	1:AA:219:C:N4	2.39	0.56
2:AB:54:THR:HG23	2:AB:199:TYR:HB3	1.87	0.56
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.22	0.56
26:BA:2291:G:N7	47:B0:14:ARG:NH1	2.53	0.56
26:BA:1827:U:H2'	26:BA:1828:C:H6	1.68	0.56
26:BA:2658:C:OP2	26:BA:2745:G:O2'	2.20	0.56
26:BA:2849:G:H5'	38:BR:46:GLY:HA2	1.87	0.56
26:BA:388:A:H2'	26:BA:389:G:H8	1.71	0.56
31:BG:28:VAL:O	31:BG:31:VAL:HG12	2.05	0.56
43:BW:14:PRO:HG2	43:BW:78:GLU:HG2	1.86	0.56
7:CG:15:ASP:HB3	7:CG:24:THR:HG23	1.86	0.56
26:DA:2112:G:C5	26:DA:2113:U:H1'	2.40	0.56
26:DA:518:G:H2'	26:DA:519:U:C6	2.41	0.56
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.87	0.56
26:BA:1218:G:O2'	26:BA:1219:A:O5'	2.23	0.56
26:BA:2255:U:H2'	26:BA:2256:U:C6	2.40	0.56
26:BA:2732:G:OP2	61:BA:4851:HOH:O	2.18	0.56
40:BT:24:PRO:HD3	40:BT:52:ILE:HD12	1.88	0.56
26:BA:1232:G:H5''	42:BV:81:TYR:CE1	2.39	0.56
1:CA:532:A:H61	3:CC:193:TYR:CB	2.16	0.56
23:CW:18:G:O2'	23:CW:57:G:N2	2.26	0.56
26:DA:1231:G:H2'	26:DA:1232:G:H8	1.69	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:84:A:H5'	45:DY:8:LYS:HG2	1.86	0.56
27:DB:42:C:O2'	31:DG:67:LYS:O	2.16	0.56
26:DA:2867:G:OP2	40:DT:119:LYS:NZ	2.39	0.56
1:AA:45:U:H2'	1:AA:46:G:C8	2.40	0.56
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.88	0.56
10:AJ:35:SER:N	10:AJ:73:ASP:O	2.33	0.56
25:AY:33:U:C3'	25:AY:34:G:H5''	2.35	0.56
26:BA:1091:A:OP1	26:BA:1092:A:H3'	2.05	0.56
29:BE:55:ASN:HB3	29:BE:58:ARG:HG3	1.87	0.56
26:DA:2142:C:N3	26:DA:2149:G:O6	2.39	0.56
26:DA:2061:G:H5''	26:DA:2503:A:C2	2.40	0.56
26:DA:330:A:H2	26:DA:1210:A:HO2'	1.54	0.56
1:AA:1278:U:H5'	1:AA:1279:A:O4'	2.06	0.56
1:AA:976:G:H5'	1:AA:1358:U:O2'	2.06	0.56
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.06	0.56
13:AM:122:LYS:HD3	13:AM:123:ALA:N	2.18	0.56
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.38	0.56
26:BA:2152:U:O2	26:BA:2153:G:N2	2.38	0.56
44:BX:53:LYS:HB3	44:BX:82:GLN:HB3	1.88	0.56
1:CA:587:G:N2	1:CA:754:C:OP2	2.37	0.56
4:CD:191:ARG:NH1	4:CD:191:ARG:O	2.38	0.56
15:CO:17:ARG:HG3	15:CO:17:ARG:HH11	1.69	0.56
26:DA:1579:A:H2'	26:DA:1580:A:C8	2.41	0.56
1:AA:1003:G:C2	1:AA:1004:A:N3	2.73	0.56
3:AC:29:TYR:OH	14:AN:54:PRO:O	2.20	0.56
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.05	0.56
25:AY:38:A:C2'	25:AY:39:PSU:H5''	2.35	0.56
26:BA:1217:G:H3'	26:BA:1218:G:H5'	1.88	0.56
1:CA:1154:G:N7	1:CA:1155:G:N9	2.54	0.56
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.39	0.56
6:CF:50:TYR:CE2	18:CR:77:GLY:HA2	2.41	0.56
9:CI:8:GLY:O	9:CI:15:ALA:N	2.35	0.56
1:AA:78:G:C2	1:AA:91:C:C4	2.94	0.56
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.86	0.56
9:AI:29:ASN:OD1	9:AI:65:VAL:N	2.37	0.56
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.06	0.56
39:BS:14:VAL:O	39:BS:18:ILE:HG12	2.06	0.56
2:CB:8:LYS:HD2	2:CB:9:GLU:H	1.71	0.56
5:CE:84:PHE:N	5:CE:87:SER:O	2.33	0.56
13:CM:71:ARG:HH11	13:CM:71:ARG:HG3	1.69	0.56
37:DQ:77:LYS:NZ	37:DQ:86:GLY:O	2.39	0.56
1:AA:193:C:H2'	1:AA:194:C:C6	2.41	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.73	0.56
24:AX:21:A:H5'	24:AX:22:G:OP1	2.05	0.56
49:B2:23:LYS:O	49:B2:27:GLU:HG3	2.06	0.56
26:BA:1634:C:H2'	26:BA:1635:C:C6	2.40	0.56
26:BA:482:C:H4'	61:BA:3937:HOH:O	2.04	0.56
35:BO:1:MET:HG3	35:BO:67:LYS:HG2	1.87	0.56
26:BA:63:A:O3'	44:BX:71:GLY:HA3	2.05	0.56
1:CA:1057:G:H2'	1:CA:1058:G:O4'	2.05	0.56
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.06	0.56
1:CA:1095:U:H5''	1:CA:1109:C:O2	2.05	0.56
25:CY:19:G:N1	25:CY:56:C:N4	2.41	0.56
26:DA:1316:U:H2'	26:DA:1317:A:H8	1.71	0.56
26:DA:2327:A:H2'	26:DA:2328:A:C8	2.41	0.56
46:DZ:100:VAL:HG21	46:DZ:134:PRO:HG2	1.88	0.56
1:AA:946:A:H2'	1:AA:947:G:C8	2.40	0.55
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.32	0.55
10:AJ:8:LEU:HB2	10:AJ:70:ARG:HB2	1.88	0.55
26:BA:1079:U:OP1	56:B9:9:ARG:NH2	2.39	0.55
26:BA:2045:G:H5'	26:BA:2629:C:H4'	1.87	0.55
26:BA:302:A:O2'	26:BA:303:C:OP1	2.16	0.55
26:BA:957:A:H2'	37:BQ:9:TYR:OH	2.05	0.55
1:CA:757:U:H2'	1:CA:758:G:O4'	2.06	0.55
4:CD:43:HIS:ND1	4:CD:46:LYS:HE2	2.20	0.55
23:CW:51:U:H3	23:CW:63:G:H1	1.54	0.55
44:DX:60:ARG:NH1	54:D7:47:ARG:HH22	2.01	0.55
26:DA:2723:C:H5''	38:DR:1:MET:HE2	1.88	0.55
26:DA:299:A:N1	26:DA:322:A:O2'	2.30	0.55
26:DA:478:A:N1	26:DA:500:G:H4'	2.21	0.55
41:DU:76:TYR:CZ	41:DU:80:ILE:HG13	2.42	0.55
1:AA:68:G:C2	1:AA:69:G:H1'	2.42	0.55
26:BA:416:G:N1	36:BP:70:GLN:HG3	2.22	0.55
1:CA:1028:C:C4	1:CA:1033:G:O6	2.59	0.55
20:CT:10:LEU:HD23	20:CT:12:ALA:HB2	1.88	0.55
23:CW:44:G:H2'	23:CW:45:U:H5'	1.88	0.55
26:DA:2776:A:H4'	26:DA:2777:G:H5''	1.87	0.55
26:DA:586:A:N1	26:DA:809:G:O2'	2.31	0.55
1:AA:167:G:H2'	1:AA:168:G:H8	1.72	0.55
1:AA:181:G:O2'	1:AA:183:G:O6	2.18	0.55
1:AA:652:U:O4	1:AA:752:G:O2'	2.13	0.55
1:AA:674:G:H2'	1:AA:675:A:H8	1.69	0.55
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.06	0.55
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.39	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
36:BP:63:PRO:HG2	55:B8:25:MET:HB2	1.87	0.55
26:BA:2858:G:C8	40:BT:97:ALA:HB2	2.41	0.55
26:BA:611:U:H2'	26:BA:612:C:C6	2.40	0.55
3:CC:56:ASP:HB2	3:CC:67:THR:HB	1.88	0.55
27:DB:55:U:H1'	31:DG:29:TRP:CD1	2.42	0.55
29:DE:116:VAL:HG13	29:DE:122:PHE:HB2	1.88	0.55
29:DE:163:GLU:HG2	29:DE:164:ARG:N	2.20	0.55
1:AA:222:U:H2'	1:AA:223:U:C6	2.42	0.55
10:AJ:30:SER:O	10:AJ:81:THR:HG21	2.07	0.55
26:BA:560:C:O3'	41:BU:53:ARG:NH1	2.39	0.55
33:BI:114:LEU:HD12	33:BI:130:TYR:HA	1.87	0.55
1:CA:1023:G:H3'	1:CA:1024:G:C8	2.41	0.55
1:CA:420:U:O2'	1:CA:423:G:O6	2.13	0.55
1:CA:521:G:H4'	12:CL:73:GLU:HG2	1.87	0.55
1:CA:527:G:O2'	1:CA:535:A:N1	2.34	0.55
18:CR:43:PHE:CD1	18:CR:56:THR:HG22	2.41	0.55
26:DA:1446:C:H42	26:DA:1465:G:H1	1.52	0.55
26:DA:2674:G:H2'	26:DA:2675:A:C8	2.41	0.55
26:DA:2753:A:N3	56:D9:15:LYS:NZ	2.43	0.55
26:DA:888:C:H5''	26:DA:889:C:OP2	2.07	0.55
28:DD:71:ASP:HB3	28:DD:103:ARG:HH22	1.71	0.55
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.89	0.55
26:BA:1587:U:H2'	26:BA:1588:G:O4'	2.07	0.55
26:BA:2228:G:O2'	26:BA:2229:A:OP1	2.24	0.55
26:BA:2579:G:H2'	26:BA:2580:C:C6	2.41	0.55
1:CA:1223:C:H5''	1:CA:1224:G:H5''	1.88	0.55
1:CA:984:C:O5'	1:CA:984:C:H6	1.88	0.55
2:CB:162:ILE:O	2:CB:185:ILE:HG12	2.06	0.55
5:CE:137:GLU:HG2	5:CE:140:ARG:HH11	1.71	0.55
6:CF:97:PHE:HE1	18:CR:62:GLU:HG2	1.71	0.55
48:D1:59:THR:O	48:D1:91:LYS:NZ	2.26	0.55
26:DA:39:C:H2'	26:DA:40:C:C6	2.42	0.55
26:DA:848:G:C4	26:DA:933:A:H8	2.24	0.55
26:DA:2787:C:H1'	29:DE:62:PRO:HG3	1.88	0.55
38:DR:55:ALA:HB2	38:DR:79:LEU:HD13	1.88	0.55
40:DT:50:ILE:HA	40:DT:99:LEU:HD12	1.89	0.55
2:AB:167:PRO:HG3	2:AB:186:ALA:HB1	1.88	0.55
26:BA:1067:A:H8	26:BA:1068:G:H5''	1.71	0.55
26:BA:354:A:H2	26:BA:1255:A:H2'	1.71	0.55
26:BA:2130:C:H2'	26:BA:2131:U:H6	1.71	0.55
33:BI:93:THR:HG22	33:BI:119:PRO:HB3	1.88	0.55
1:CA:1028:C:N3	1:CA:1033:G:O6	2.40	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1316:G:H22	1:CA:1319:A:H5''	1.72	0.55
23:CW:19:G:H1	23:CW:56:C:N4	2.03	0.55
26:DA:1434:A:H61	26:DA:1558:A:H62	1.54	0.55
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.07	0.55
1:AA:750:G:O2'	15:AO:22:THR:O	2.14	0.55
23:AW:50:U:H3	23:AW:64:A:N6	2.05	0.55
1:CA:1299:A:H2'	1:CA:1299:A:N3	2.21	0.55
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.41	0.55
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.21	0.55
2:CB:122:PHE:CE2	2:CB:139:LYS:HG2	2.42	0.55
2:CB:87:ARG:NH1	2:CB:220:ASP:OD1	2.39	0.55
5:CE:6:PHE:HB2	5:CE:34:VAL:HG22	1.89	0.55
48:D1:76:ARG:HH11	48:D1:97:LEU:HD22	1.71	0.55
26:DA:2126:A:N6	26:DA:2162:G:O2'	2.39	0.55
26:DA:2630:G:H2'	26:DA:2631:G:C8	2.42	0.55
26:DA:84:A:H5''	45:DY:8:LYS:HE3	1.89	0.55
3:AC:58:GLU:HB2	3:AC:65:ALA:HB3	1.88	0.55
27:BB:66:A:H61	27:BB:108:U:H2'	1.72	0.55
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.47	0.55
26:DA:1528:A:OP2	61:DA:3982:HOH:O	2.18	0.55
26:DA:528:A:C2	26:DA:2042:A:H2'	2.42	0.55
26:DA:2098:U:H3	26:DA:2191:G:H1	1.53	0.55
26:DA:566:U:H5''	36:DP:29:LYS:HE3	1.87	0.55
26:DA:2303:G:O2'	31:DG:132:ASN:HB2	2.07	0.55
1:AA:814:A:H2'	1:AA:816:A:H5''	1.89	0.55
18:CR:25:THR:O	18:CR:25:THR:OG1	2.19	0.55
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.06	0.55
48:D1:83:GLU:OE1	48:D1:83:GLU:N	2.39	0.55
50:D3:7:LYS:HB2	50:D3:34:GLU:HG3	1.89	0.55
55:D8:6:THR:HG22	55:D8:63:PRO:HD2	1.88	0.55
26:DA:1889:A:H2'	26:DA:1890:A:C8	2.42	0.55
26:DA:900:A:H2'	26:DA:901:A:C8	2.41	0.55
38:DR:36:THR:HG22	38:DR:37:THR:H	1.72	0.55
44:DX:4:ALA:HB1	44:DX:42:ALA:HA	1.89	0.55
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.21	0.55
1:AA:79:G:C2	1:AA:90:U:O2	2.60	0.55
1:AA:954:G:H21	1:AA:1227:A:H62	1.55	0.55
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.38	0.55
26:BA:1466:U:O2'	26:BA:1467:G:OP1	2.22	0.55
26:BA:2212:G:C2'	26:BA:2213:G:H5''	2.34	0.55
37:BQ:14:ARG:HG2	37:BQ:41:TRP:HH2	1.71	0.55
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.42	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:692:U:O2'	1:CA:694:A:N7	2.34	0.55
23:CW:11:C:H42	23:CW:24:G:H1	1.54	0.55
47:D0:32:ARG:H	47:D0:35:ASN:ND2	2.05	0.55
26:DA:1292:U:H2'	26:DA:1293:C:C6	2.42	0.55
26:DA:2298:A:H1'	26:DA:2321:G:H21	1.72	0.55
28:DD:10:THR:OG1	28:DD:13:ARG:HG2	2.07	0.55
36:DP:48:PRO:O	55:D8:57:ARG:NH2	2.37	0.55
37:DQ:36:ALA:HA	37:DQ:129:THR:HG22	1.89	0.55
26:DA:2848:G:C8	40:DT:97:ALA:HB2	2.42	0.55
14:AN:33:VAL:HA	14:AN:40:CYS:HA	1.89	0.54
51:B4:53:GLU:HB3	51:B4:54:GLY:CA	2.37	0.54
26:BA:354:A:HO2'	26:BA:355:A:H8	1.56	0.54
32:BH:154:PRO:HB3	32:BH:163:TYR:CZ	2.42	0.54
33:BI:116:LEU:HD21	33:BI:119:PRO:HA	1.89	0.54
1:CA:1004:A:H62	1:CA:1037:C:H2'	1.71	0.54
1:CA:1262:C:H42	1:CA:1273:G:H1	1.53	0.54
1:CA:1359:C:H3'	14:CN:35:ARG:HH21	1.72	0.54
26:DA:2592:G:OP1	61:DA:4233:HOH:O	2.18	0.54
26:DA:2595:G:N7	61:DA:4305:HOH:O	2.34	0.54
26:DA:297:C:H2'	26:DA:298:G:O4'	2.07	0.54
26:DA:1011:G:OP2	41:DU:66:ASN:ND2	2.39	0.54
1:AA:757:U:H2'	1:AA:758:G:O4'	2.08	0.54
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.75	0.54
19:AS:67:VAL:HG21	51:B4:59:PHE:CD1	2.42	0.54
26:BA:2699:U:H2'	26:BA:2700:U:O4'	2.07	0.54
36:BP:50:ARG:HD3	55:B8:7:HIS:CD2	2.42	0.54
1:CA:1055:A:N3	3:CC:156:ARG:NH1	2.51	0.54
1:CA:1118:C:C2	1:CA:1119:C:H5	2.26	0.54
1:CA:1376:U:O5'	7:CG:94:ARG:NH2	2.40	0.54
2:CB:63:MET:HG2	2:CB:225:ALA:HB1	1.89	0.54
19:CS:19:VAL:O	19:CS:23:ASN:ND2	2.40	0.54
24:CX:19:G:H4'	24:CX:20:U:OP2	2.07	0.54
26:DA:1796:U:H2'	26:DA:1797:C:C6	2.42	0.54
28:DD:36:PRO:HA	28:DD:61:LEU:HD12	1.88	0.54
30:DF:34:TRP:CE2	36:DP:8:PRO:HG3	2.43	0.54
37:DQ:18:LYS:O	37:DQ:98:LYS:NZ	2.33	0.54
5:AE:68:GLU:HG2	5:AE:70:PRO:HD3	1.87	0.54
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.42	0.54
1:CA:1165:C:N3	1:CA:1171:G:N2	2.56	0.54
1:CA:920:U:H2'	1:CA:921:U:C6	2.41	0.54
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.89	0.54
26:DA:2113:U:H3	26:DA:2170:A:N6	2.03	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:DG:18:GLU:HG2	31:DG:175:LEU:HD21	1.89	0.54
31:DG:41:GLN:HE22	31:DG:153:ARG:HB3	1.71	0.54
33:DI:61:ARG:HA	33:DI:61:ARG:NE	2.22	0.54
36:DP:44:GLY:CA	36:DP:45:LEU:HB2	2.37	0.54
38:DR:95:THR:HG22	38:DR:116:LEU:HD23	1.90	0.54
1:AA:1026:G:C6	1:AA:1027:C:H1'	2.42	0.54
1:AA:456:C:C2'	1:AA:457:C:H5'	2.37	0.54
12:AL:97:ARG:HB2	12:AL:98:TYR:CE1	2.42	0.54
26:BA:2348:A:H61	47:B0:43:THR:CG2	2.21	0.54
26:BA:1817:A:H1'	26:BA:1960:A:N6	2.22	0.54
26:BA:2339:A:H2'	26:BA:2340:A:C8	2.42	0.54
26:BA:645:G:H5'	26:BA:645:G:N3	2.23	0.54
26:BA:718:C:N4	61:BA:4880:HOH:O	2.39	0.54
46:BZ:75:ASN:O	46:BZ:84:GLU:HG2	2.08	0.54
1:CA:674:G:H2'	1:CA:675:A:H8	1.72	0.54
4:CD:70:ILE:HG12	4:CD:74:GLN:HB3	1.88	0.54
26:DA:1005:C:H2'	26:DA:1006:C:C6	2.43	0.54
26:DA:1805:U:O2	28:DD:50:THR:HB	2.08	0.54
26:DA:2533:A:OP1	26:DA:2665:A:O2'	2.20	0.54
26:BA:347:G:C8	30:BF:171:PRO:HG3	2.43	0.54
26:BA:776:G:C6	28:BD:208:LYS:HB2	2.42	0.54
26:BA:933:C:H4'	26:BA:933:C:OP1	2.08	0.54
30:BF:18:ARG:NH2	30:BF:127:GLU:OE1	2.37	0.54
26:BA:640:A:C4	30:BF:180:GLY:HA2	2.42	0.54
36:BP:97:PRO:HD3	36:BP:126:VAL:O	2.08	0.54
42:BV:98:GLU:OE2	42:BV:100:ARG:NH1	2.41	0.54
1:CA:1132:C:H42	1:CA:1142:G:H1	1.55	0.54
1:CA:991:U:C4	1:CA:1212:U:H1'	2.42	0.54
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.73	0.54
1:CA:430:A:P	4:CD:22:LYS:HZ1	2.31	0.54
2:CB:16:HIS:HB2	2:CB:204:ASN:CB	2.30	0.54
4:CD:150:GLU:OE2	4:CD:151:LYS:N	2.41	0.54
50:D3:3:ARG:HH21	50:D3:36:VAL:HG11	1.73	0.54
51:D4:59:PHE:HA	51:D4:61:ARG:N	2.23	0.54
52:D5:49:CYS:O	52:D5:56:LYS:NZ	2.40	0.54
26:DA:590:A:OP1	30:DF:95:ARG:NH1	2.41	0.54
30:DF:165:ARG:HG2	30:DF:168:ARG:HH21	1.73	0.54
37:DQ:1:MET:HB2	37:DQ:44:ALA:HB1	1.89	0.54
4:AD:178:VAL:HG12	4:AD:179:GLU:H	1.72	0.54
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.07	0.54
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.55	0.54
10:AJ:5:ARG:NH2	10:AJ:73:ASP:OD2	2.24	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:99:G:O2'	49:B2:7:ARG:NH2	2.40	0.54
1:CA:1348:U:OP2	1:CA:1373:G:N2	2.32	0.54
1:CA:266:G:H5''	1:CA:268:C:H41	1.73	0.54
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.88	0.54
23:CW:7:A:H5'	23:CW:8:4SU:H5	1.88	0.54
24:CX:23:C:H2'	24:CX:24:U:C6	2.43	0.54
26:DA:1639:U:OP1	61:DA:4007:HOH:O	2.19	0.54
26:DA:954:G:H5''	37:DQ:13:GLN:HB3	1.89	0.54
31:DG:44:GLY:N	31:DG:88:ILE:O	2.40	0.54
37:DQ:32:TYR:HB2	37:DQ:106:VAL:HG23	1.88	0.54
1:AA:1399:C:C2	1:AA:1502:A:N6	2.76	0.54
5:AE:78:HIS:HD1	8:AH:104:ARG:HD2	1.72	0.54
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.08	0.54
25:AY:63:G:H2'	25:AY:64:A:O4'	2.08	0.54
26:BA:1810:U:H2'	61:BA:5029:HOH:O	2.07	0.54
26:BA:2825:C:H5'	52:B5:29:THR:HG21	1.88	0.54
26:BA:2457:G:OP1	30:BF:74:ARG:NH2	2.41	0.54
34:BN:75:TYR:CE2	34:BN:77:GLY:HA2	2.43	0.54
1:CA:1153:C:H42	1:CA:1154:G:N2	2.04	0.54
2:CB:12:GLU:O	2:CB:15:VAL:N	2.34	0.54
11:CK:48:ILE:HD11	11:CK:64:ALA:HA	1.89	0.54
26:DA:2139:C:C4	26:DA:2153:G:C2	2.96	0.54
26:DA:2285:C:OP2	53:D6:6:ARG:NH1	2.38	0.54
26:DA:370:G:OP2	61:DA:3787:HOH:O	2.18	0.54
33:DI:27:ARG:HD2	48:D1:71:TYR:CE2	2.43	0.54
38:DR:21:TYR:OH	38:DR:43:GLU:HG2	2.08	0.54
1:AA:1298:C:H4'	1:AA:1299:A:H5''	1.89	0.54
1:AA:79:G:N1	1:AA:90:U:N3	2.56	0.54
19:AS:65:ASN:HD22	19:AS:65:ASN:N	2.05	0.54
37:BQ:85:LYS:HB2	47:B0:7:LEU:HD12	1.90	0.54
26:BA:1090:G:HO2'	26:BA:1157:A:H61	1.56	0.54
26:BA:1830:G:H4'	26:BA:1831:C:H5''	1.89	0.54
1:CA:1003:G:H2'	1:CA:1004:A:H1'	1.89	0.54
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.07	0.54
26:DA:1859:A:N6	26:DA:1883:G:O2'	2.41	0.54
26:DA:2552:U:OP2	61:DA:4518:HOH:O	2.18	0.54
26:DA:305:U:H2'	26:DA:306:U:C6	2.42	0.54
35:DO:80:ASP:OD1	40:DT:64:ARG:NH2	2.41	0.54
1:AA:1258:G:O2'	1:AA:1259:C:H5'	2.08	0.54
1:AA:560:U:O2'	1:AA:561:U:OP2	2.21	0.54
13:AM:57:ARG:O	13:AM:61:GLU:HG2	2.08	0.54
2:CB:105:PHE:CE1	2:CB:155:LEU:HD12	2.42	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:130:VAL:O	3:CC:134:ILE:HG12	2.07	0.54
4:CD:108:LEU:HD13	4:CD:174:LEU:HD13	1.88	0.54
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.89	0.54
26:DA:1010:A:OP2	61:DA:4178:HOH:O	2.18	0.54
26:DA:1514:U:H2'	26:DA:1515:G:H8	1.73	0.54
26:DA:2153:G:C6	26:DA:2154:G:C6	2.96	0.54
26:DA:289:A:H2'	26:DA:290:G:O4'	2.08	0.54
30:DF:101:LEU:O	30:DF:106:ARG:NH1	2.34	0.54
30:DF:192:LEU:HD13	30:DF:194:MET:HE2	1.89	0.54
32:DH:3:ARG:NH2	32:DH:5:GLY:H	2.05	0.54
46:DZ:69:THR:HG22	46:DZ:90:VAL:HA	1.90	0.54
1:AA:1316:G:N2	1:AA:1319:A:H5''	2.17	0.54
1:AA:950:U:H2'	1:AA:951:G:H8	1.73	0.54
2:AB:69:LEU:HD12	2:AB:91:PRO:HB2	1.90	0.54
12:AL:53:ARG:HG3	12:AL:93:LEU:HD21	1.90	0.54
25:AY:58:A:HO2'	25:AY:60:U:H5	1.55	0.54
26:BA:2123:G:H2'	26:BA:2124:U:C6	2.43	0.54
26:BA:2163:G:N7	26:BA:2173:G:N2	2.56	0.54
26:BA:2702:C:OP1	38:BR:17:ARG:NH1	2.38	0.54
26:BA:956:A:H62	37:BQ:12:GLN:HA	1.73	0.54
34:BN:21:LYS:HE3	34:BN:140:VAL:OXT	2.08	0.54
1:CA:1120:G:O6	1:CA:1154:G:N2	2.41	0.54
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.42	0.54
2:CB:115:LEU:HD11	2:CB:153:ARG:HD2	1.90	0.54
9:CI:23:ASN:HD22	9:CI:23:ASN:N	2.06	0.54
19:CS:48:THR:HG22	19:CS:61:TYR:HA	1.88	0.54
25:CY:5:G:H1	25:CY:68:C:N4	2.06	0.54
31:DG:39:ILE:HB	31:DG:92:VAL:HG13	1.90	0.54
1:AA:78:G:N1	1:AA:91:C:C4	2.76	0.53
4:AD:173:TRP:NE1	4:AD:193:ASP:OD2	2.38	0.53
5:AE:80:ILE:HG22	5:AE:91:LEU:HB2	1.89	0.53
25:AY:19:G:H4'	25:AY:20:U:OP2	2.06	0.53
51:B4:57:GLU:CB	51:B4:58:ARG:HA	2.38	0.53
26:BA:1276:C:H2'	26:BA:1277:G:C8	2.43	0.53
26:BA:215:G:H21	26:BA:217:A:H62	1.56	0.53
31:BG:170:ARG:NH2	31:BG:182:LYS:O	2.41	0.53
1:CA:1033:G:C2'	1:CA:1034:G:H5'	2.38	0.53
10:CJ:81:THR:HA	10:CJ:84:GLN:HB2	1.89	0.53
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.19	0.53
26:DA:2144:U:H1'	26:DA:2148:G:N2	2.23	0.53
1:AA:202:U:O2'	1:AA:203:U:O5'	2.13	0.53
19:AS:65:ASN:HA	51:B4:58:ARG:HG3	1.89	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1065:U:HO2'	26:BA:1067:A:H2	1.55	0.53
26:BA:1424:A:OP1	54:B7:10:ARG:NH2	2.42	0.53
26:BA:2164:C:O2'	26:BA:2165:C:H5'	2.08	0.53
26:BA:2173:G:H2'	26:BA:2174:G:C8	2.42	0.53
26:BA:639:G:OP1	61:BA:5228:HOH:O	2.19	0.53
44:BX:94:GLY:N	44:BX:95:LEU:HA	2.23	0.53
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.08	0.53
1:CA:890:G:O2'	1:CA:906:G:O6	2.21	0.53
1:CA:952:U:H2'	1:CA:953:G:C8	2.43	0.53
1:CA:951:G:HO2'	1:CA:972:C:H5	1.56	0.53
2:CB:186:ALA:O	2:CB:201:ILE:N	2.40	0.53
6:CF:69:GLU:H	6:CF:69:GLU:CD	2.09	0.53
7:CG:72:ARG:NH1	7:CG:142:GLU:OE2	2.41	0.53
8:CH:51:VAL:HG11	8:CH:60:ARG:HH11	1.73	0.53
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.09	0.53
23:CW:50:U:H3	23:CW:64:A:H2	1.54	0.53
61:CW:3102:HOH:O	47:D0:2:ALA:N	2.41	0.53
26:DA:144:C:H2'	26:DA:145:G:C8	2.44	0.53
26:DA:973:A:H8	26:DA:973:A:OP1	1.92	0.53
27:DB:28:C:OP1	39:DS:36:TYR:OH	2.16	0.53
26:BA:139:A:H8	26:BA:1454:C:HO2'	1.55	0.53
5:CE:6:PHE:HD1	5:CE:36:ASP:HB3	1.72	0.53
26:DA:2261:C:O2'	26:DA:2262:U:H5'	2.08	0.53
39:DS:67:ARG:O	39:DS:71:ARG:HG3	2.08	0.53
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.08	0.53
1:AA:646:U:H2'	1:AA:647:C:C6	2.43	0.53
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.89	0.53
26:BA:714:U:O2	55:B8:2:PRO:HD2	2.08	0.53
26:BA:186:A:N6	26:BA:2442:A:O2'	2.40	0.53
26:BA:667:G:H21	26:BA:671:A:H2	1.56	0.53
31:BG:161:THR:HG22	31:BG:163:ALA:H	1.73	0.53
26:BA:2671:G:O2'	32:BH:175:LYS:NZ	2.41	0.53
1:CA:1250:A:N3	1:CA:1370:G:O2'	2.35	0.53
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.41	0.53
20:CT:36:LEU:HD12	20:CT:55:ILE:HG23	1.90	0.53
26:DA:2590:A:OP2	28:DD:238:GLY:HA2	2.08	0.53
1:AA:1028:C:H2'	1:AA:1029:C:C4'	2.37	0.53
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.43	0.53
1:AA:1270:C:OP2	21:AU:24:ARG:NH2	2.42	0.53
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	1.89	0.53
20:AT:27:LYS:O	20:AT:31:SER:OG	2.27	0.53
33:BI:27:ARG:HD2	48:B1:71:TYR:CE1	2.44	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:70:A:N7	44:BX:31:HIS:HE1	2.05	0.53
46:BZ:28:MET:HE1	46:BZ:67:LEU:HD12	1.91	0.53
1:CA:1152:A:H2'	1:CA:1153:C:H6	1.73	0.53
1:CA:243:A:H4'	1:CA:244:U:H5''	1.90	0.53
1:CA:1057:G:O3'	3:CC:197:GLY:HA3	2.09	0.53
3:CC:52:LEU:HD13	3:CC:118:GLN:HE22	1.73	0.53
9:CI:17:VAL:HG23	9:CI:63:ILE:HG12	1.89	0.53
25:CY:70:G:H2'	25:CY:71:G:H5'	1.91	0.53
26:DA:2128:C:H5'	26:DA:2173:A:N3	2.23	0.53
26:DA:2364:C:OP1	47:D0:55:ARG:NH1	2.41	0.53
35:DO:120:GLU:HB2	40:DT:68:TYR:HE2	1.74	0.53
39:DS:77:ALA:HB1	39:DS:82:ILE:HB	1.89	0.53
46:DZ:50:GLN:OE1	46:DZ:50:GLN:N	2.34	0.53
1:AA:1239:A:H62	1:AA:1299:A:H62	1.57	0.53
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.44	0.53
26:BA:1153:G:H2'	26:BA:1153:G:N3	2.23	0.53
26:BA:1093:G:H2'	26:BA:1156:G:H22	1.74	0.53
30:BF:20:LEU:HD22	30:BF:21:ALA:H	1.73	0.53
1:CA:1166:G:H5'	1:CA:1168:A:OP2	2.08	0.53
1:CA:316:G:OP2	1:CA:351:G:O2'	2.24	0.53
1:CA:97:G:O2'	1:CA:98:G:H5''	2.08	0.53
25:CY:68:C:C2'	25:CY:69:G:H5'	2.38	0.53
53:D6:35:GLU:OE2	53:D6:50:ARG:NH1	2.42	0.53
26:DA:1593:G:H2'	26:DA:1594:G:H8	1.73	0.53
26:DA:2302:G:H2'	26:DA:2303:G:H5'	1.91	0.53
31:DG:97:ASP:HA	31:DG:100:TRP:HD1	1.73	0.53
40:DT:28:VAL:HG13	40:DT:86:ILE:HG23	1.89	0.53
41:DU:92:ARG:HA	41:DU:95:LEU:HB2	1.91	0.53
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.91	0.53
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.37	0.53
25:AY:60:U:H5''	25:AY:61:C:C5	2.43	0.53
26:BA:1735:U:O2	26:BA:1747:A:H5'	2.09	0.53
26:BA:2897:U:H2'	26:BA:2898:C:C6	2.44	0.53
26:BA:649:C:O2'	26:BA:704:U:OP1	2.24	0.53
30:BF:197:ASP:OD1	30:BF:197:ASP:N	2.41	0.53
31:BG:179:PRO:HB2	51:B4:42:PHE:HE1	1.73	0.53
41:BU:66:ASN:O	41:BU:70:ARG:HG3	2.09	0.53
1:CA:1173:G:H2'	1:CA:1174:G:H8	1.73	0.53
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.43	0.53
1:CA:142:G:H2'	1:CA:143:A:C8	2.44	0.53
1:CA:876:G:O5'	8:CH:14:ARG:NH1	2.41	0.53
12:CL:32:PHE:HB3	12:CL:84:LEU:HD11	1.89	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:CR:53:ARG:HA	18:CR:56:THR:OG1	2.08	0.53
26:DA:1309:G:H3'	54:D7:9:ARG:HH12	1.73	0.53
26:DA:1645:G:H5''	26:DA:1646:C:H5'	1.89	0.53
26:DA:2430:A:H2'	26:DA:2430:A:N3	2.23	0.53
27:DB:110:G:H2'	27:DB:111:G:H5'	1.90	0.53
32:DH:154:PRO:HB3	32:DH:163:TYR:CE2	2.43	0.53
34:DN:67:LEU:O	34:DN:88:GLU:HG2	2.08	0.53
40:DT:60:THR:HG22	40:DT:77:PRO:HA	1.90	0.53
35:DO:77:ILE:HB	40:DT:74:ARG:HD3	1.91	0.53
1:AA:1238:A:OP2	61:AA:4136:HOH:O	2.18	0.53
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.91	0.53
17:AQ:53:LEU:HD23	17:AQ:82:MET:HE1	1.91	0.53
23:AW:47:U:H5'	23:AW:47:U:C6	2.44	0.53
26:BA:231:G:C8	55:B8:5:LYS:HG2	2.44	0.53
26:BA:1014:U:H2'	26:BA:1015:C:C6	2.44	0.53
1:CA:1119:C:C4	1:CA:1154:G:O6	2.62	0.53
1:CA:522:C:H41	12:CL:53:ARG:NH2	2.07	0.53
2:CB:70:PHE:HE1	2:CB:163:PHE:HD2	1.56	0.53
4:CD:159:ARG:O	4:CD:163:GLU:N	2.40	0.53
4:CD:78:LEU:HD22	4:CD:96:LEU:HB3	1.90	0.53
26:DA:1405:U:H2'	26:DA:1406:U:C6	2.43	0.53
26:DA:1839:G:C8	26:DA:1927:A:H1'	2.44	0.53
26:DA:2127:G:N2	26:DA:2161:C:C2	2.77	0.53
26:DA:2206:G:H5'	26:DA:2207:G:N7	2.24	0.53
26:DA:852:G:H2'	26:DA:853:G:C8	2.44	0.53
26:DA:8:A:H2'	26:DA:9:U:H6	1.74	0.53
27:DB:66:A:N6	27:DB:109:C:H5''	2.24	0.53
31:DG:7:LEU:HD13	31:DG:104:GLU:HA	1.91	0.53
46:DZ:145:GLU:H	46:DZ:148:ASP:HB2	1.73	0.53
1:AA:877:C:H5''	8:AH:88:LYS:HD3	1.90	0.53
26:BA:1221:G:H1'	26:BA:1222:A:C5'	2.33	0.53
26:BA:2346:G:O6	47:B0:74:ARG:NH2	2.42	0.53
33:BI:104:GLN:HB3	33:BI:105:HIS:CD2	2.43	0.53
39:BS:46:VAL:HG12	39:BS:48:LEU:HD12	1.91	0.53
1:CA:1023:G:C4	1:CA:1024:G:C8	2.97	0.53
1:CA:1133:G:C4	1:CA:1134:G:C8	2.97	0.53
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.49	0.53
26:DA:1688:U:O2	26:DA:1700:A:H5'	2.09	0.53
26:DA:2023:G:H5'	26:DA:2617:C:H4'	1.91	0.53
26:DA:601:C:OP1	30:DF:108:LYS:NZ	2.23	0.53
26:DA:90:U:H1'	26:DA:92:A:C8	2.44	0.53
1:AA:1241:G:C2'	1:AA:1242:C:H5'	2.38	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:79:G:C6	1:AA:90:U:N3	2.77	0.53
1:AA:841:U:P	1:AA:841:U:H6	2.32	0.53
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.44	0.53
27:BB:2:C:H2'	27:BB:3:C:C6	2.43	0.53
32:BH:88:LEU:HD13	32:BH:130:ARG:HG2	1.91	0.53
42:BV:14:VAL:HB	42:BV:96:ILE:HG13	1.90	0.53
1:CA:1330:U:H4'	13:CM:23:TYR:CE1	2.43	0.53
1:CA:309:G:O2'	1:CA:607:A:N1	2.42	0.53
2:CB:33:TYR:HB2	2:CB:43:ASP:HA	1.91	0.53
8:CH:103:VAL:HG11	8:CH:136:GLU:HB2	1.91	0.53
9:CI:29:ASN:OD1	9:CI:64:THR:HA	2.09	0.53
51:D4:58:ARG:HB3	51:D4:59:PHE:HD1	1.74	0.53
32:DH:26:VAL:HG21	32:DH:75:ALA:HB1	1.90	0.53
34:DN:4:TYR:HB2	41:DU:101:ARG:HH12	1.74	0.53
41:DU:79:PHE:CZ	41:DU:83:LEU:HD21	2.43	0.53
1:AA:539:A:H2'	1:AA:540:G:C8	2.42	0.52
8:AH:51:VAL:HG12	8:AH:52:ASP:H	1.74	0.52
26:BA:1269:G:N2	26:BA:1272:A:OP2	2.35	0.52
26:BA:2623:U:C4	52:B5:3:LYS:HG2	2.44	0.52
1:CA:714:G:H2'	1:CA:715:A:C8	2.44	0.52
1:CA:952:U:H2'	1:CA:953:G:H8	1.73	0.52
7:CG:78:ARG:NH1	7:CG:154:TYR:O	2.41	0.52
20:CT:13:LEU:O	20:CT:17:ARG:HG3	2.09	0.52
1:CA:263:A:OP1	20:CT:79:ARG:NH1	2.41	0.52
27:DB:56:G:OP1	31:DG:27:ASN:ND2	2.42	0.52
46:DZ:111:VAL:HA	46:DZ:115:GLY:HA3	1.91	0.52
1:AA:1035:A:H8	1:AA:1035:A:O5'	1.92	0.52
1:AA:714:G:H2'	1:AA:715:A:C8	2.44	0.52
23:AW:47:U:O2'	23:AW:48:C:OP1	2.23	0.52
53:B6:35:GLU:OE2	53:B6:50:ARG:NH1	2.43	0.52
26:BA:2190:G:C6	26:BA:2193:A:H8	2.27	0.52
26:BA:265:U:H2'	26:BA:266:C:C6	2.44	0.52
46:BZ:144:LEU:HD21	46:BZ:148:ASP:O	2.08	0.52
1:CA:1066:C:H2'	1:CA:1067:A:C8	2.45	0.52
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.45	0.52
1:CA:952:U:O2'	1:CA:965:A:N6	2.41	0.52
1:CA:975:A:H4'	1:CA:976:G:C5'	2.35	0.52
3:CC:43:LEU:HD11	3:CC:91:LEU:HD11	1.91	0.52
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.09	0.52
25:CY:27:G:O6	25:CY:43:C:N3	2.42	0.52
55:D8:26:LYS:HB2	55:D8:44:LYS:O	2.10	0.52
26:DA:589:C:H2'	26:DA:590:A:C8	2.44	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
45:DY:49:VAL:HG21	45:DY:61:ILE:HG23	1.91	0.52
46:DZ:33:LEU:HD21	46:DZ:90:VAL:HG21	1.90	0.52
1:AA:662:G:H2'	1:AA:663:A:C8	2.44	0.52
4:AD:49:ARG:NE	4:AD:49:ARG:H	2.07	0.52
5:AE:79:GLU:HG3	5:AE:93:PRO:HD2	1.92	0.52
19:AS:48:THR:HG22	19:AS:61:TYR:HA	1.91	0.52
26:BA:2148:A:N3	26:BA:2149:G:H1'	2.24	0.52
26:BA:2880:C:H2'	26:BA:2881:C:O4'	2.09	0.52
1:CA:1095:U:C4	1:CA:1096:C:C4	2.98	0.52
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.09	0.52
1:CA:1264:C:O2	1:CA:1272:G:N2	2.41	0.52
26:DA:646:A:H2'	26:DA:647:G:O4'	2.09	0.52
26:DA:885:C:H1'	26:DA:892:G:H22	1.75	0.52
46:DZ:6:LYS:HD2	46:DZ:8:TYR:OH	2.10	0.52
3:AC:40:ARG:O	3:AC:44:GLU:HB2	2.10	0.52
26:BA:2132:G:C2	26:BA:2142:G:H1'	2.44	0.52
35:BO:104:ARG:CZ	40:BT:34:VAL:HG21	2.39	0.52
1:CA:1039:C:H2'	1:CA:1040:U:O4'	2.09	0.52
1:CA:1318:A:H5''	19:CS:3:ARG:NH2	2.20	0.52
1:CA:302:G:N3	1:CA:556:C:H4'	2.24	0.52
1:CA:56:U:H2'	1:CA:57:G:H8	1.74	0.52
26:DA:83:G:OP1	45:DY:95:LYS:NZ	2.32	0.52
27:DB:66:A:N6	27:DB:108:U:H3'	2.25	0.52
29:DE:111:ARG:HA	38:DR:1:MET:SD	2.50	0.52
39:DS:14:VAL:O	39:DS:18:ILE:HG12	2.10	0.52
46:DZ:105:VAL:N	46:DZ:139:VAL:O	2.39	0.52
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.41	0.52
1:AA:626:U:H2'	1:AA:627:G:C8	2.45	0.52
16:AP:58:TYR:O	16:AP:62:VAL:HG23	2.09	0.52
31:BG:48:GLU:HA	31:BG:51:ARG:HG2	1.91	0.52
1:CA:1004:A:N6	1:CA:1037:C:C2	2.77	0.52
3:CC:119:ARG:HG2	3:CC:123:GLN:HE21	1.75	0.52
13:CM:29:ARG:HG3	13:CM:64:TRP:CH2	2.45	0.52
1:CA:1286:A:N1	21:CU:18:TYR:OH	2.42	0.52
25:CY:9:A:H5'	25:CY:46:7MG:H1'	1.91	0.52
26:DA:2815:C:C5'	52:D5:29:THR:HG21	2.39	0.52
26:DA:2117:A:O2'	26:DA:2118:U:H5''	2.09	0.52
26:DA:2126:A:N6	26:DA:2172:U:H3'	2.24	0.52
26:DA:2128:C:H2'	26:DA:2129:C:O4'	2.10	0.52
26:DA:2350:C:H2'	26:DA:2351:G:O4'	2.10	0.52
26:DA:729:G:H5'	26:DA:730:C:H5''	1.91	0.52
27:DB:110:G:C2'	27:DB:111:G:H5'	2.39	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DD:175:LEU:HD12	28:DD:185:VAL:HG21	1.92	0.52
35:DO:73:ASP:HB2	40:DT:82:LEU:HD13	1.92	0.52
1:AA:1279:A:H4'	1:AA:1281:U:H5	1.75	0.52
1:AA:946:A:O2'	1:AA:1333:A:N3	2.35	0.52
20:AT:9:ASN:O	20:AT:10:LEU:HB2	2.10	0.52
53:B6:13:CYS:SG	53:B6:47:THR:HG21	2.49	0.52
53:B6:6:ARG:NE	53:B6:24:GLU:OE1	2.32	0.52
26:BA:1074:A:H61	26:BA:1171:G:H2'	1.75	0.52
26:BA:2195:A:H3'	26:BA:2196:C:C6	2.45	0.52
26:BA:895:G:C4	26:BA:978:A:H8	2.26	0.52
31:BG:143:GLU:O	51:B4:28:LYS:NZ	2.32	0.52
37:BQ:30:GLY:HA2	37:BQ:107:ALA:HB2	1.92	0.52
26:BA:1199:C:OP1	41:BU:92:ARG:NH1	2.43	0.52
45:BY:35:TYR:CE2	45:BY:69:ALA:HB3	2.44	0.52
2:CB:100:GLY:O	2:CB:108:ILE:HD11	2.10	0.52
2:CB:158:LEU:HD23	2:CB:182:ILE:HD11	1.91	0.52
3:CC:125:GLU:HG3	3:CC:190:ARG:O	2.10	0.52
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.09	0.52
23:CW:76:F3N:N	24:CX:76:31H:O2'	2.43	0.52
25:CY:33:U:C3'	25:CY:34:G:H5''	2.40	0.52
26:DA:200:U:O4	26:DA:250:G:N2	2.43	0.52
34:DN:38:HIS:ND1	34:DN:39:ARG:HG3	2.25	0.52
1:AA:1144:G:N2	1:AA:1146:A:H62	2.08	0.52
1:AA:353:A:H5'	1:AA:353:A:H8	1.74	0.52
1:AA:950:U:H2'	1:AA:951:G:C8	2.45	0.52
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.43	0.52
30:BF:53:THR:CG2	30:BF:55:GLY:H	2.22	0.52
35:BO:73:ASP:HB2	40:BT:82:LEU:HD13	1.91	0.52
1:CA:171:A:H2'	1:CA:172:A:C8	2.45	0.52
1:CA:448:A:P	1:CA:485:G:H22	2.33	0.52
18:CR:70:ILE:HG23	18:CR:79:LEU:HD12	1.92	0.52
1:CA:1353:G:OP1	21:CU:10:ARG:NH1	2.43	0.52
26:DA:79:G:H1	26:DA:107:C:H42	1.58	0.52
26:DA:77:C:H42	26:DA:109:G:H1	1.57	0.52
26:DA:2155:G:H2'	26:DA:2156:G:O4'	2.10	0.52
27:DB:17:C:O2	27:DB:67:G:N2	2.35	0.52
30:DF:184:TYR:O	30:DF:188:ARG:HG3	2.09	0.52
1:AA:677:U:H3	1:AA:713:G:H22	1.58	0.52
6:AF:10:LEU:HB2	6:AF:59:TYR:HB3	1.92	0.52
1:AA:1125:U:H4'	10:AJ:5:ARG:NH2	2.24	0.52
23:AW:52:G:H4'	37:BQ:56:ARG:CZ	2.39	0.52
24:AX:21:A:N6	24:AX:46:G:H2'	2.24	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1700:G:H3'	38:BR:2:ARG:HD3	1.90	0.52
26:BA:938:G:H3'	26:BA:939:C:H6	1.74	0.52
29:BE:111:ARG:HG3	29:BE:160:TYR:CD2	2.44	0.52
1:CA:142:G:H2'	1:CA:143:A:H8	1.74	0.52
1:CA:457:C:H2'	1:CA:458:C:H6	1.75	0.52
26:DA:1341:U:OP1	26:DA:1397:U:N3	2.35	0.52
26:DA:1608:A:H1'	26:DA:1610:A:OP2	2.10	0.52
26:DA:263:C:H2'	26:DA:264:C:O4'	2.10	0.52
26:DA:528:A:OP2	34:DN:114:ARG:NH1	2.43	0.52
26:DA:1827:C:OP2	28:DD:222:ARG:NH1	2.43	0.52
39:DS:34:HIS:ND1	39:DS:53:SER:OG	2.35	0.52
1:AA:1024:G:H2'	1:AA:1025:U:H5''	1.92	0.52
1:AA:69:G:H2'	1:AA:70:G:H8	1.74	0.52
4:AD:128:VAL:HG12	4:AD:129:ASN:ND2	2.25	0.52
1:AA:619:U:N3	4:AD:134:ASP:OD2	2.38	0.52
9:AI:9:ARG:H	9:AI:79:LEU:HD23	1.75	0.52
26:BA:1452:U:H2'	26:BA:1453:C:C6	2.45	0.52
26:BA:664:U:H2'	26:BA:665:C:C6	2.45	0.52
1:CA:1030(A):G:N2	1:CA:1030(C):G:H3'	2.25	0.52
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.45	0.52
3:CC:22:TRP:CB	3:CC:59:ARG:HB2	2.40	0.52
12:CL:34:ARG:HG3	12:CL:105:TYR:CE2	2.44	0.52
19:CS:17:GLU:O	19:CS:21:GLU:N	2.36	0.52
25:CY:18:G:N2	25:CY:55:PSU:C4	2.77	0.52
56:D9:17:ILE:HG22	56:D9:24:TYR:HB2	1.92	0.52
26:DA:2114:A:N6	26:DA:2115:G:H21	2.08	0.52
26:DA:637:A:H8	36:DP:117:GLU:HG3	1.75	0.52
1:CA:346:G:OP1	40:DT:41:ARG:NH2	2.42	0.52
1:AA:347:G:HO2'	1:AA:348:G:P	2.33	0.52
12:AL:77:LEU:HD21	12:AL:107:ALA:HA	1.92	0.52
13:AM:15:VAL:HB	13:AM:34:LEU:HD11	1.92	0.52
1:AA:582:U:OP1	15:AO:64:ARG:NH1	2.43	0.52
52:B5:55:ARG:NH1	52:B5:57:VAL:HG22	2.25	0.52
28:BD:101:GLU:OE1	28:BD:103:ARG:NH1	2.42	0.52
29:BE:77:ILE:HD13	29:BE:195:LEU:HD12	1.92	0.52
1:CA:545:C:O2'	1:CA:549:C:OP1	2.22	0.52
6:CF:3:ARG:HD3	6:CF:64:GLN:NE2	2.25	0.52
12:CL:69:TYR:HE2	12:CL:71:PRO:HA	1.73	0.52
20:CT:56:MET:HE3	20:CT:85:MET:HA	1.90	0.52
22:CV:14:A:C2	22:CV:15:A:C4	2.98	0.52
26:DA:93:G:H2'	26:DA:94:C:H6	1.74	0.52
30:DF:32:LEU:O	30:DF:36:VAL:HG23	2.09	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
38:DR:74:LYS:HG2	38:DR:77:ARG:HH21	1.74	0.52
40:DT:51:ARG:HG3	40:DT:98:LYS:HZ3	1.75	0.52
42:DV:21:ARG:HG2	42:DV:91:TYR:CD2	2.45	0.52
43:DW:60:ASN:HD22	43:DW:60:ASN:N	2.07	0.52
1:AA:1022:G:H2'	1:AA:1023:G:C8	2.44	0.51
8:AH:112:LEU:HA	8:AH:134:ILE:HG12	1.92	0.51
25:AY:13:C:H2'	25:AY:14:A:C8	2.45	0.51
26:BA:1074:A:N6	26:BA:1171:G:H2'	2.25	0.51
26:BA:1391:C:OP2	61:BA:4016:HOH:O	2.18	0.51
26:BA:2885:C:OP1	40:BT:3:ARG:NH1	2.42	0.51
46:BZ:29:TYR:HB3	46:BZ:34:ASN:HD22	1.75	0.51
46:BZ:92:SER:O	46:BZ:130:PRO:HG2	2.10	0.51
1:CA:1250:A:H4'	9:CI:68:GLY:N	2.25	0.51
2:CB:135:GLN:O	2:CB:139:LYS:HB2	2.10	0.51
24:CX:67:C:C2'	24:CX:68:C:H5'	2.40	0.51
26:DA:1032:A:H2	26:DA:1122:G:H22	1.59	0.51
26:DA:2124:G:H1	26:DA:2174:C:H42	1.58	0.51
26:DA:2400:G:H2'	26:DA:2401:U:H6	1.74	0.51
26:DA:323:G:O2'	26:DA:1205:U:N3	2.35	0.51
26:DA:956:G:H5''	37:DQ:77:LYS:HD2	1.92	0.51
31:DG:106:LEU:O	31:DG:111:LEU:HD22	2.10	0.51
31:DG:48:GLU:HA	31:DG:51:ARG:HG2	1.90	0.51
1:AA:524:G:H2'	1:AA:525:C:C6	2.46	0.51
1:AA:606:G:N2	1:AA:631:G:N7	2.58	0.51
24:AX:61:C:H2'	24:AX:62:C:H6	1.76	0.51
24:AX:66:C:H2'	24:AX:67:C:O4'	2.10	0.51
53:B6:14:THR:HG21	53:B6:48:VAL:HG22	1.92	0.51
26:BA:2213:G:H8	26:BA:2213:G:H5'	1.74	0.51
26:BA:85:C:H4'	26:BA:102:U:H1'	1.92	0.51
23:AW:19:G:C5	26:BA:929:G:H4'	2.45	0.51
39:BS:11:LYS:O	39:BS:15:ARG:HG3	2.10	0.51
43:BW:2:GLU:OE2	43:BW:72:LYS:HE2	2.10	0.51
1:CA:1028:C:H2'	1:CA:1029:C:C6	2.45	0.51
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.45	0.51
1:CA:1359:C:H3'	14:CN:35:ARG:NH2	2.25	0.51
2:CB:219:VAL:O	2:CB:222:ILE:HG12	2.11	0.51
4:CD:18:LYS:NZ	4:CD:31:CYS:SG	2.84	0.51
8:CH:15:ASN:O	8:CH:19:VAL:HG23	2.10	0.51
19:CS:33:THR:HG21	19:CS:71:LEU:HD21	1.91	0.51
26:DA:1721:G:N1	26:DA:1739:U:OP2	2.43	0.51
26:DA:2537:U:H2'	26:DA:2538:C:C6	2.45	0.51
26:DA:2645:G:N2	26:DA:2767:C:OP2	2.43	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:DB:48:A:P	39:DS:30:ARG:HH12	2.33	0.51
29:DE:115:GLY:O	29:DE:119:ARG:HB2	2.11	0.51
44:DX:11:PRO:HB3	44:DX:92:LEU:HD11	1.91	0.51
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.58	0.51
11:AK:16:SER:O	11:AK:35:PRO:HD3	2.11	0.51
13:AM:14:ARG:HB2	13:AM:17:VAL:HG23	1.91	0.51
26:BA:2132:G:OP1	26:BA:2140:U:N3	2.27	0.51
26:BA:2764:G:C2	32:BH:2:SER:HB3	2.45	0.51
26:BA:41:C:H2'	26:BA:42:G:O4'	2.10	0.51
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.45	0.51
24:CX:48:C:C2	24:CX:59:A:H1'	2.45	0.51
26:DA:1366:A:OP1	48:D1:3:LYS:NZ	2.30	0.51
27:DB:7:G:N1	27:DB:114:C:N3	2.48	0.51
27:DB:94:C:H2'	27:DB:95:C:H6	1.75	0.51
1:AA:265:G:H2'	1:AA:267:C:H5	1.74	0.51
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.46	0.51
24:AX:8:4SU:H6	24:AX:8:4SU:O5'	2.11	0.51
48:B1:51:VAL:HG11	48:B1:74:VAL:HG21	1.92	0.51
26:BA:734:C:H5''	54:B7:2:LYS:HE2	1.91	0.51
26:BA:354:A:H2	26:BA:1255:A:HO2'	1.58	0.51
46:BZ:59:LEU:HD12	46:BZ:69:THR:HG21	1.92	0.51
1:CA:1134:G:N2	1:CA:1140:C:N3	2.54	0.51
14:CN:6:LEU:HB3	14:CN:23:ARG:HH22	1.75	0.51
25:CY:31:A:C2	25:CY:39:PSU:N3	2.79	0.51
26:DA:1325:G:OP1	26:DA:1647:G:O2'	2.15	0.51
26:DA:708:C:H42	26:DA:723:G:H1	1.57	0.51
46:DZ:108:PRO:HG3	46:DZ:141:VAL:HB	1.91	0.51
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.30	0.51
25:AY:7:A:HO2'	25:AY:49:C:H5'	1.72	0.51
26:BA:273:G:H4'	26:BA:274:U:OP1	2.10	0.51
26:BA:624:C:OP1	30:BF:108:LYS:HE3	2.11	0.51
1:CA:1011:G:N2	1:CA:1018:C:N3	2.53	0.51
1:CA:1028:C:O2	1:CA:1033:G:N1	2.44	0.51
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.10	0.51
51:D4:59:PHE:HA	51:D4:60:GLN:C	2.29	0.51
26:DA:2394:C:OP2	55:D8:30:ARG:NH1	2.43	0.51
26:DA:392:C:H5''	26:DA:409:C:H5''	1.93	0.51
26:DA:528:A:C2'	26:DA:529:A:H5''	2.40	0.51
31:DG:105:LYS:NZ	31:DG:143:GLU:OE1	2.43	0.51
34:DN:58:ASP:OD1	34:DN:58:ASP:N	2.41	0.51
26:DA:1187:G:H5'	42:DV:81:TYR:CE1	2.45	0.51
46:DZ:59:LEU:HD21	46:DZ:69:THR:OG1	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:309:G:O2'	1:AA:607:A:N1	2.44	0.51
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.46	0.51
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.26	0.51
25:AY:38:A:H2'	25:AY:39:PSU:H5''	1.91	0.51
43:BW:25:ARG:NH2	43:BW:74:ALA:O	2.40	0.51
1:CA:1120:G:C6	1:CA:1154:G:C2	2.99	0.51
9:CI:125:TYR:HD1	9:CI:126:SER:N	2.09	0.51
9:CI:85:LEU:HB3	9:CI:92:TYR:CD2	2.40	0.51
13:CM:71:ARG:NH1	13:CM:71:ARG:HG3	2.25	0.51
26:DA:667:U:O2	55:D8:2:PRO:HD2	2.10	0.51
26:DA:184:C:H2'	26:DA:185:U:C6	2.45	0.51
27:DB:95:C:H2'	27:DB:96:U:C6	2.46	0.51
28:DD:20:ASP:OD1	28:DD:20:ASP:N	2.44	0.51
42:DV:35:LEU:HB2	42:DV:57:VAL:HG23	1.93	0.51
1:AA:625:G:H4'	16:AP:16:HIS:CD2	2.45	0.51
36:BP:59:LEU:HD11	55:B8:10:ALA:HB2	1.91	0.51
26:BA:2205:C:H2'	26:BA:2206:G:H8	1.76	0.51
26:BA:483:A:H5''	61:BA:3937:HOH:O	2.10	0.51
45:BY:86:ARG:HH11	45:BY:100:ALA:HB1	1.76	0.51
1:CA:1347:G:HO2'	1:CA:1373:G:H1	1.59	0.51
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.92	0.51
24:CX:23:C:H2'	24:CX:24:U:H6	1.75	0.51
25:CY:33:U:H3'	25:CY:34:G:H5''	1.92	0.51
26:DA:1378:A:OP1	54:D7:10:ARG:NH2	2.44	0.51
26:DA:1246:A:OP1	30:DF:38:ARG:NH1	2.43	0.51
26:DA:2126:A:N3	26:DA:2127:G:H1'	2.26	0.51
26:DA:872:A:H2'	26:DA:873:G:C8	2.45	0.51
27:DB:80:U:H2'	27:DB:81:G:C8	2.44	0.51
32:DH:30:LYS:HG3	32:DH:80:SER:O	2.10	0.51
41:DU:49:HIS:HA	41:DU:52:ARG:HB3	1.91	0.51
43:DW:18:ARG:NH1	43:DW:76:VAL:O	2.44	0.51
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.32	0.51
1:AA:328:C:H4'	1:AA:329:A:H5'	1.93	0.51
1:AA:78:G:N2	1:AA:91:C:C2	2.79	0.51
1:AA:841:U:C4	1:AA:848:C:H1'	2.45	0.51
2:AB:137:ARG:CZ	2:AB:137:ARG:HB3	2.41	0.51
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.92	0.51
9:AI:99:LEU:HB3	9:AI:101:PHE:CD1	2.44	0.51
13:AM:19:LEU:HD21	13:AM:56:LEU:HD11	1.92	0.51
25:AY:68:C:C2'	25:AY:69:G:H5'	2.40	0.51
33:BI:140:LEU:HD22	33:BI:142:VAL:HG22	1.92	0.51
3:CC:63:ASN:HB2	3:CC:98:ASN:HB2	1.93	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:CF:87:ARG:HH11	6:CF:87:ARG:HB2	1.75	0.51
11:CK:101:SER:HB2	11:CK:103:LEU:HD23	1.92	0.51
13:CM:25:ILE:HG23	13:CM:29:ARG:HB3	1.92	0.51
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.92	0.51
1:CA:1517:G:H1'	26:DA:1919:A:O3'	2.11	0.51
26:DA:71:A:N7	44:DX:31:HIS:HE1	2.08	0.51
1:AA:1001:A:H2'	1:AA:1001(A):G:C8	2.46	0.51
1:AA:1022:G:H4'	1:AA:1022:G:OP1	2.11	0.51
1:AA:1068:G:N2	1:AA:1191:A:N3	2.47	0.51
1:AA:1226:C:O2'	13:AM:111:LYS:NZ	2.41	0.51
20:AT:76:ALA:HA	20:AT:79:ARG:NH1	2.26	0.51
13:AM:123:ALA:HB2	23:AW:39:PSU:H1'	1.93	0.51
51:B4:63:TYR:CD1	51:B4:63:TYR:N	2.77	0.51
29:BE:47:VAL:HG22	29:BE:84:PHE:O	2.11	0.51
1:CA:1038:C:H2'	1:CA:1039:C:H5''	1.91	0.51
1:CA:1264:C:H42	1:CA:1271:G:H1	1.58	0.51
8:CH:69:ARG:HG3	8:CH:76:PRO:HA	1.93	0.51
26:DA:1410:G:H2'	26:DA:1411:C:C6	2.46	0.51
26:DA:218:A:C2	26:DA:235:U:H4'	2.46	0.51
27:DB:3:C:H2'	27:DB:4:C:H6	1.76	0.51
27:DB:42:C:O2'	31:DG:66:GLN:HG2	2.11	0.51
34:DN:30:ILE:HG22	34:DN:34:LEU:HD22	1.93	0.51
46:DZ:145:GLU:HG2	46:DZ:146:ILE:HD12	1.93	0.51
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.27	0.51
9:AI:48:GLU:HB3	9:AI:101:PHE:HE2	1.76	0.51
18:AR:56:THR:HB	18:AR:58:LEU:HD22	1.93	0.51
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.92	0.51
24:AX:19:G:H3'	24:AX:20:U:H6	1.76	0.51
26:BA:1094:A:P	26:BA:1155:C:H42	2.32	0.51
26:BA:2331:G:N2	39:BS:3:ARG:HA	2.26	0.51
26:BA:939:C:O2'	26:BA:940:C:H5'	2.10	0.51
26:BA:927:G:N2	26:BA:944:C:C2	2.79	0.51
33:BI:96:ASP:OD1	33:BI:96:ASP:N	2.44	0.51
26:BA:953:U:HO2'	37:BQ:101:ARG:HH22	1.58	0.51
1:CA:982:U:O2	1:CA:1222:G:N1	2.43	0.51
1:CA:160:A:H61	1:CA:347:G:H1'	1.76	0.51
1:CA:839:U:O2'	1:CA:840:C:OP1	2.27	0.51
2:CB:19:HIS:CE1	2:CB:206:ASP:HB2	2.44	0.51
3:CC:125:GLU:O	3:CC:127:ARG:NH1	2.41	0.51
8:CH:73:ASP:OD1	8:CH:75:ARG:HD3	2.10	0.51
26:DA:2376:A:H3'	26:DA:2377:A:H8	1.76	0.51
26:DA:2769:C:H2'	26:DA:2770:G:O4'	2.11	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DD:79:VAL:HG21	28:DD:111:LEU:HD11	1.93	0.51
30:DF:24:LEU:HD23	30:DF:115:ALA:HA	1.93	0.51
30:DF:150:GLY:HA2	30:DF:172:TRP:CE3	2.46	0.51
32:DH:154:PRO:HB3	32:DH:163:TYR:CZ	2.46	0.51
32:DH:20:ALA:HB3	32:DH:23:ARG:HG3	1.93	0.51
40:DT:24:PRO:HD3	40:DT:52:ILE:HD12	1.93	0.51
26:DA:997:G:OP1	41:DU:92:ARG:HG2	2.10	0.51
1:AA:46:G:O6	61:AA:4164:HOH:O	2.16	0.50
1:AA:735:C:H2'	1:AA:736:C:H6	1.76	0.50
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.21	0.50
1:AA:96:U:O2'	1:AA:97:G:H5'	2.11	0.50
25:AY:28:G:H2'	25:AY:29:G:C8	2.46	0.50
52:B5:16:ARG:NH1	52:B5:17:ASP:OD1	2.44	0.50
40:BT:118:ARG:HG3	40:BT:118:ARG:NH1	2.14	0.50
1:CA:344:A:H4'	1:CA:345:C:OP2	2.11	0.50
1:CA:707:C:H2'	1:CA:708:C:C6	2.46	0.50
1:CA:735:C:H2'	1:CA:736:C:C6	2.45	0.50
4:CD:12:CYS:SG	4:CD:19:LEU:HB2	2.51	0.50
5:CE:18:ARG:HG2	5:CE:19:MET:N	2.27	0.50
8:CH:20:TYR:CE2	8:CH:76:PRO:HG2	2.46	0.50
18:CR:38:GLU:O	18:CR:41:LYS:NZ	2.45	0.50
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.11	0.50
21:CU:7:ARG:NH1	21:CU:21:TYR:OH	2.43	0.50
23:CW:21:A:H1'	23:CW:48:C:N4	2.26	0.50
26:DA:1299:G:OP1	61:DA:4540:HOH:O	2.19	0.50
26:DA:2103:C:C2'	26:DA:2104:G:H5'	2.40	0.50
26:DA:656:G:H2'	26:DA:657:U:O4'	2.10	0.50
26:DA:662:G:H5''	36:DP:16:ARG:HG2	1.92	0.50
1:AA:523:A:H61	12:AL:92:ASP:HB2	1.76	0.50
26:BA:173:C:H2'	26:BA:174:U:C6	2.47	0.50
26:BA:1834:A:O2'	28:BD:259:THR:HG21	2.11	0.50
26:BA:2018:C:H4'	26:BA:2019:G:OP1	2.11	0.50
26:BA:2198:A:H2'	26:BA:2199:C:C6	2.46	0.50
26:BA:895:G:H2'	26:BA:896:A:C8	2.46	0.50
26:BA:2761:A:H5'	32:BH:4:ILE:HD12	1.93	0.50
38:BR:38:VAL:HG12	38:BR:42:LYS:HE3	1.92	0.50
1:CA:1164:G:C2'	1:CA:1165:C:H5'	2.40	0.50
1:CA:580:U:H5''	15:CO:58:MET:HG2	1.92	0.50
2:CB:120:ALA:O	2:CB:121:LEU:HB3	2.11	0.50
20:CT:86:ARG:NH1	20:CT:90:GLN:HE22	2.10	0.50
26:DA:2611:U:C4	52:D5:3:LYS:HG2	2.46	0.50
26:DA:2139:C:N4	26:DA:2152:G:C6	2.79	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DD:148:GLU:HB2	28:DD:151:LYS:HD2	1.91	0.50
31:DG:5:VAL:HG22	31:DG:8:LYS:HB2	1.93	0.50
44:DX:31:HIS:CD2	44:DX:33:LYS:H	2.29	0.50
26:BA:2155:G:O2'	26:BA:2178:G:N2	2.43	0.50
26:BA:2826:C:O3'	38:BR:99:LYS:NZ	2.40	0.50
26:BA:2879:G:H2'	26:BA:2880:C:O4'	2.11	0.50
26:BA:704:U:H2'	26:BA:705:C:C6	2.45	0.50
35:BO:34:THR:OG1	35:BO:35:VAL:N	2.43	0.50
1:CA:1007:C:H2'	1:CA:1008:C:H6	1.75	0.50
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.46	0.50
26:DA:2046:G:H5'	52:D5:19:ARG:HA	1.92	0.50
26:DA:272(A):U:H5	26:DA:272(C):G:OP1	1.95	0.50
26:DA:571:A:H5'	26:DA:2030:A:N7	2.27	0.50
27:DB:27:C:H5''	39:DS:54:LEU:HD21	1.94	0.50
1:AA:1034:G:H3'	1:AA:1035:A:C8	2.46	0.50
1:AA:551:U:H2'	1:AA:552:U:C6	2.47	0.50
1:AA:642:A:N3	8:AH:113:SER:OG	2.38	0.50
1:AA:752:G:H4'	15:AO:69:TYR:OH	2.12	0.50
51:B4:46:GLN:O	51:B4:48:ARG:N	2.44	0.50
53:B6:9:LEU:HD13	53:B6:51:GLU:HG3	1.92	0.50
26:BA:2902:G:H4'	26:BA:2903:G:O5'	2.11	0.50
26:BA:691:G:H1	26:BA:699:C:H42	1.59	0.50
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.46	0.50
1:CA:1154:G:N7	1:CA:1155:G:C8	2.80	0.50
1:CA:473:G:H2'	1:CA:474:G:H8	1.76	0.50
4:CD:155:LEU:O	4:CD:159:ARG:HG3	2.11	0.50
25:CY:59:U:H3'	25:CY:60:U:O2	2.12	0.50
26:DA:271(R):G:H5''	48:D1:97:LEU:HD21	1.93	0.50
50:D3:18:ASP:N	50:D3:18:ASP:OD1	2.44	0.50
26:DA:361:G:O2'	26:DA:362:U:H5'	2.12	0.50
26:DA:866:A:H2	26:DA:867:C:C4	2.29	0.50
26:DA:873:G:N2	26:DA:905:U:C2	2.80	0.50
41:DU:61:TRP:CH2	41:DU:93:LYS:HB2	2.47	0.50
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.26	0.50
1:AA:186:C:H2'	1:AA:187:C:C6	2.47	0.50
4:AD:65:ARG:HG2	4:AD:75:PHE:CD1	2.47	0.50
20:AT:45:GLN:HA	20:AT:91:LEU:HB3	1.94	0.50
26:BA:1159:U:H2'	26:BA:1160:G:H8	1.75	0.50
26:BA:1222:A:O2'	26:BA:1223:C:O4'	2.24	0.50
26:BA:2250:G:H2'	26:BA:2250:G:N3	2.25	0.50
26:BA:589:U:H5''	36:BP:29:LYS:HE3	1.93	0.50
45:BY:16:ALA:HB2	45:BY:73:ARG:HD3	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1033:G:H2'	1:CA:1034:G:H5'	1.93	0.50
1:CA:1119:C:OP2	9:CI:9:ARG:NH1	2.35	0.50
1:CA:1492:A:H2'	1:CA:1493:A:C8	2.46	0.50
1:CA:344:A:H5''	1:CA:345:C:C5	2.43	0.50
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.93	0.50
3:CC:22:TRP:HB3	3:CC:59:ARG:HB2	1.93	0.50
25:CY:1:G:H1	25:CY:72:C:H42	1.60	0.50
25:CY:26:A:N1	25:CY:44:G:C6	2.80	0.50
26:DA:1166:C:H1'	26:DA:1184:G:N2	2.27	0.50
26:DA:2252:G:H2'	26:DA:2253:G:C8	2.47	0.50
26:DA:2364:C:H2'	26:DA:2365:G:O4'	2.12	0.50
26:DA:2528:U:O2'	26:DA:2529:G:H3'	2.12	0.50
26:DA:289:A:H62	26:DA:351:G:H21	1.59	0.50
29:DE:174:ASP:OD1	29:DE:175:VAL:N	2.44	0.50
32:DH:73:ALA:O	32:DH:76:VAL:HG12	2.11	0.50
35:DO:78:ARG:HG2	40:DT:73:GLU:HB2	1.93	0.50
7:AG:78:ARG:NH2	7:AG:154:TYR:O	2.43	0.50
25:AY:25:C:C2	25:AY:26:A:C8	3.00	0.50
25:AY:44:G:H8	25:AY:44:G:OP2	1.95	0.50
26:BA:2172:U:C2'	26:BA:2173:G:H5'	2.41	0.50
26:BA:2576:A:C2	26:BA:2659:U:H4'	2.46	0.50
1:CA:1342:C:H2'	1:CA:1343:G:C8	2.46	0.50
6:CF:15:ASP:OD1	6:CF:18:GLN:N	2.24	0.50
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.39	0.50
13:CM:57:ARG:NH1	51:D4:34:GLU:HA	2.27	0.50
13:CM:121:LYS:HZ3	23:CW:40:C:H4'	1.77	0.50
23:CW:61:C:O2'	23:CW:62:C:H6	1.95	0.50
26:DA:1379:A:H4'	26:DA:1380:G:OP2	2.11	0.50
26:DA:601:C:O2	26:DA:605:C:H4'	2.11	0.50
27:DB:66:A:H61	27:DB:108:U:H3'	1.76	0.50
26:BA:211:A:H3'	26:BA:448:U:H5'	1.94	0.50
26:BA:904:C:N4	26:BA:905:U:O4	2.45	0.50
34:BN:73:THR:OG1	34:BN:82:LEU:HD11	2.11	0.50
26:BA:709:G:H5''	36:BP:16:ARG:HG2	1.94	0.50
38:BR:21:TYR:OH	38:BR:43:GLU:HG2	2.11	0.50
1:CA:109:A:C6	1:CA:326:G:C6	3.00	0.50
1:CA:811:C:O2'	1:CA:901:A:N1	2.40	0.50
2:CB:134:GLU:O	2:CB:138:LEU:HG	2.11	0.50
4:CD:38:TYR:CZ	4:CD:45:GLN:HG3	2.47	0.50
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.94	0.50
10:CJ:27:ALA:HA	10:CJ:81:THR:CG2	2.41	0.50
12:CL:71:PRO:O	12:CL:102:ARG:HD2	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1038:C:N3	26:DA:1117:G:N2	2.50	0.50
26:DA:2001:A:H2'	26:DA:2002:G:C8	2.46	0.50
26:DA:304:G:O6	61:DA:4181:HOH:O	2.18	0.50
26:DA:570:G:H5''	61:DA:3844:HOH:O	2.11	0.50
26:DA:2748:A:O2'	32:DH:63:SER:O	2.18	0.50
33:DI:14:ASP:N	33:DI:17:GLN:OE1	2.44	0.50
37:DQ:38:GLU:HG3	37:DQ:127:ILE:HB	1.94	0.50
1:AA:1064:G:N2	1:AA:1191:A:OP2	2.41	0.50
1:AA:977:A:H1'	1:AA:982:U:O4	2.12	0.50
2:AB:185:ILE:HG23	2:AB:199:TYR:HB2	1.93	0.50
26:BA:2701:U:H4'	26:BA:2702:C:H5'	1.93	0.50
33:BI:72:LEU:C	33:BI:74:ASN:H	2.14	0.50
26:BA:83:A:H5''	45:BY:8:LYS:HG3	1.93	0.50
1:CA:1035:A:H2'	1:CA:1036:G:C8	2.46	0.50
1:CA:1137:C:H5''	1:CA:1138:G:OP1	2.12	0.50
1:CA:1049:U:C6	1:CA:1201:A:H5'	2.47	0.50
1:CA:457:C:H2'	1:CA:458:C:C6	2.46	0.50
24:CX:8:4SU:O2'	24:CX:21:A:N1	2.28	0.50
25:CY:34:G:C6	25:CY:35:A:C6	3.00	0.50
26:DA:2240:C:OP2	61:DA:3953:HOH:O	2.19	0.50
29:DE:89:ASP:N	29:DE:89:ASP:OD1	2.43	0.50
30:DF:137:LYS:HA	30:DF:140:LEU:HD23	1.93	0.50
31:DG:125:PHE:CZ	31:DG:170:ARG:HA	2.47	0.50
39:DS:50:SER:O	39:DS:76:LYS:NZ	2.45	0.50
1:AA:1002:G:C4	1:AA:1003:G:H1'	2.47	0.50
1:AA:250:A:H4'	1:AA:251:G:O5'	2.10	0.50
2:AB:30:ARG:HH21	2:AB:194:PRO:HB2	1.76	0.50
26:BA:2624:C:OP2	52:B5:2:ALA:N	2.45	0.50
26:BA:2856:G:H2'	26:BA:2857:U:O4'	2.11	0.50
27:BB:87:G:N2	27:BB:90:A:OP2	2.30	0.50
41:BU:58:ARG:HA	41:BU:61:TRP:CE3	2.46	0.50
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.26	0.50
1:CA:1342:C:O2'	9:CI:124:GLN:HG2	2.12	0.50
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.12	0.50
5:CE:137:GLU:HA	5:CE:140:ARG:HB3	1.94	0.50
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.92	0.50
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.94	0.50
23:CW:66:U:H2'	23:CW:67:C:O4'	2.12	0.50
26:DA:1184:G:H5'	50:D3:29:ARG:HH11	1.77	0.50
26:DA:2305:A:H5''	31:DG:134:GLY:HA3	1.94	0.50
26:DA:2750:A:H8	26:DA:2750:A:OP1	1.95	0.50
26:DA:686:G:H21	26:DA:788:A:H61	1.58	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DD:17:THR:O	28:DD:211:ARG:NH2	2.43	0.50
30:DF:110:LEU:HD12	30:DF:202:PHE:CE1	2.47	0.50
31:DG:37:VAL:O	31:DG:94:LEU:N	2.41	0.50
35:DO:24:VAL:HB	35:DO:33:ALA:HB2	1.92	0.50
1:AA:1027:C:C4	1:AA:1034:G:O6	2.64	0.49
1:AA:79:G:N1	1:AA:90:U:C2	2.80	0.49
1:AA:92:C:H2'	1:AA:93:G:C8	2.47	0.49
3:AC:47:LEU:HD13	3:AC:68:VAL:HG11	1.94	0.49
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.75	0.49
17:AQ:28:PRO:HA	17:AQ:35:VAL:HA	1.94	0.49
51:B4:59:PHE:CA	51:B4:61:ARG:H	2.24	0.49
26:BA:1320:A:N3	26:BA:1343:C:H1'	2.27	0.49
26:BA:1553:A:O2'	26:BA:1554:A:O5'	2.26	0.49
26:BA:2658:C:H2'	26:BA:2659:U:O4'	2.12	0.49
26:BA:2703:C:O3'	26:BA:2881:C:H4'	2.12	0.49
26:BA:282:G:O6	61:BA:4929:HOH:O	2.19	0.49
26:BA:638:U:H5''	61:BA:5227:HOH:O	2.12	0.49
36:BP:82:GLY:HA2	36:BP:113:LYS:O	2.11	0.49
46:BZ:111:VAL:C	46:BZ:113:ALA:H	2.15	0.49
1:CA:1016:A:C5	1:CA:1017:G:H1'	2.47	0.49
1:CA:1128:C:H4'	1:CA:1148:U:O2	2.12	0.49
1:CA:1316:G:O2'	1:CA:1318:A:N7	2.37	0.49
1:CA:54:C:H2'	1:CA:352:C:H41	1.77	0.49
1:CA:404:U:H5'	4:CD:122:ARG:HD3	1.94	0.49
25:CY:4:C:H2'	25:CY:5:G:H5'	1.92	0.49
26:DA:1357:U:H2'	26:DA:1358:G:O4'	2.12	0.49
26:DA:2025:C:N4	61:DA:4191:HOH:O	2.45	0.49
26:DA:526:A:O2'	26:DA:2043:C:O2	2.24	0.49
27:DB:44:G:OP1	31:DG:98:ARG:NH2	2.45	0.49
27:DB:98:G:H2'	27:DB:99:G:O4'	2.12	0.49
34:DN:4:TYR:CD2	41:DU:100:VAL:HG11	2.47	0.49
1:AA:1007:C:O2	1:AA:1022:G:N1	2.31	0.49
1:AA:1366:C:O2'	10:AJ:60:ARG:NH2	2.44	0.49
4:AD:53:ASP:O	4:AD:57:ARG:HG3	2.12	0.49
5:AE:18:ARG:HE	5:AE:27:ARG:HH21	1.60	0.49
50:B3:18:ASP:OD1	50:B3:18:ASP:N	2.40	0.49
26:BA:1897:C:H2'	26:BA:1898:A:O4'	2.12	0.49
26:BA:236:G:H4'	26:BA:413:G:C5	2.47	0.49
1:CA:1028:C:C2	1:CA:1033:G:C6	3.00	0.49
1:CA:1152:A:H2'	1:CA:1153:C:C6	2.46	0.49
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.26	0.49
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	1.93	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1452:C:H6	1:CA:1452:C:O5'	1.95	0.49
1:CA:195:A:OP1	20:CT:68:LYS:NZ	2.44	0.49
1:CA:441:A:H3'	1:CA:442:C:C6	2.48	0.49
1:CA:65:U:H5'	1:CA:65:U:C6	2.47	0.49
1:CA:954:G:H21	1:CA:1227:A:N6	2.10	0.49
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.94	0.49
1:CA:992:U:C6	1:CA:992:U:H5''	2.41	0.49
1:CA:716:A:N3	11:CK:118:GLY:HA2	2.27	0.49
13:CM:3:ARG:HB2	51:D4:34:GLU:HG2	1.94	0.49
26:DA:141:A:C8	26:DA:1408:C:O2'	2.64	0.49
26:DA:2153:G:H3'	26:DA:2154:G:H8	1.77	0.49
26:DA:443:A:H5''	26:DA:444:C:OP1	2.13	0.49
26:DA:900:A:O2'	26:DA:901:A:OP1	2.29	0.49
30:DF:178:PRO:HB2	30:DF:201:VAL:HG21	1.94	0.49
32:DH:69:ARG:HG3	32:DH:70:THR:N	2.27	0.49
34:DN:30:ILE:HG23	34:DN:52:VAL:HG11	1.94	0.49
1:AA:279:A:C4	17:AQ:98:LEU:HD23	2.47	0.49
2:AB:112:VAL:O	2:AB:116:GLU:HG3	2.11	0.49
13:AM:79:LYS:HA	13:AM:82:MET:HE2	1.95	0.49
51:B4:53:GLU:HG2	51:B4:56:VAL:HG22	1.94	0.49
26:BA:670:C:H5'	26:BA:671:A:OP2	2.12	0.49
29:BE:52:LEU:HD12	29:BE:77:ILE:HD11	1.94	0.49
31:BG:139:LEU:HD12	31:BG:139:LEU:H	1.75	0.49
33:BI:6:LEU:HD11	33:BI:37:VAL:HG23	1.93	0.49
1:CA:1249:C:O2'	9:CI:73:GLN:NE2	2.44	0.49
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.47	0.49
1:CA:1324:A:H4'	1:CA:1362:C:O3'	2.12	0.49
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.47	0.49
3:CC:6:HIS:ND1	14:CN:49:HIS:HB3	2.27	0.49
13:CM:19:LEU:HD21	13:CM:56:LEU:HD11	1.94	0.49
25:CY:61:C:H2'	25:CY:62:C:C6	2.48	0.49
26:DA:1991:U:H2'	26:DA:1992:G:H5''	1.93	0.49
26:DA:2557:G:H2'	26:DA:2558:C:C6	2.47	0.49
28:DD:108:PRO:HB3	28:DD:143:HIS:CE1	2.47	0.49
35:DO:64:ARG:NH1	35:DO:81:ASP:OD1	2.45	0.49
1:AA:131:C:O2'	1:AA:262:A:N3	2.41	0.49
26:BA:287:G:N7	26:BA:448:U:H2'	2.27	0.49
46:BZ:45:ASP:OD2	46:BZ:49:ARG:NH1	2.45	0.49
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.42	0.49
1:CA:814:A:H2'	1:CA:816:A:H5''	1.94	0.49
13:CM:60:VAL:HA	13:CM:63:THR:OG1	2.11	0.49
23:CW:70:G:H2'	23:CW:71:G:H8	1.76	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
55:D8:15:LYS:HG2	55:D8:16:ILE:N	2.26	0.49
26:DA:1509(B):A:H2'	26:DA:1510:G:H8	1.76	0.49
26:DA:1264:G:H2'	26:DA:2014:A:N6	2.28	0.49
26:DA:2135:A:H2'	26:DA:2136:C:C5	2.47	0.49
26:DA:2314:C:H2'	26:DA:2315:G:C8	2.47	0.49
26:DA:624:C:OP1	61:DA:3854:HOH:O	2.20	0.49
28:DD:182:LEU:HB2	28:DD:272:ALA:HB3	1.95	0.49
29:DE:73:GLU:OE2	29:DE:73:GLU:N	2.41	0.49
30:DF:29:ASN:O	30:DF:112:MET:HE1	2.12	0.49
39:DS:58:LEU:HD21	39:DS:65:VAL:HG13	1.94	0.49
44:DX:31:HIS:HD2	44:DX:33:LYS:H	1.59	0.49
46:DZ:108:PRO:HB2	46:DZ:111:VAL:HG23	1.94	0.49
1:AA:335:C:O2'	1:AA:1433:A:N3	2.41	0.49
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.43	0.49
26:BA:1090:G:H5'	26:BA:1091:A:OP2	2.12	0.49
26:BA:469:A:H1'	26:BA:1246:C:O4'	2.12	0.49
26:BA:1760:U:H2'	26:BA:1761:G:H8	1.77	0.49
26:BA:2545:A:H2'	26:BA:2546:A:O4'	2.13	0.49
26:BA:650:G:O6	36:BP:107:LYS:NZ	2.46	0.49
33:BI:66:GLU:HA	33:BI:69:LYS:HB3	1.93	0.49
34:BN:4:TYR:HB2	41:BU:101:ARG:NH1	2.28	0.49
36:BP:121:LYS:HB3	36:BP:123:LEU:HG	1.95	0.49
36:BP:138:LEU:HD23	36:BP:145:PRO:HB3	1.94	0.49
46:BZ:152:ALA:HA	46:BZ:155:LEU:HD22	1.93	0.49
3:CC:110:ASN:O	3:CC:141:VAL:HG22	2.12	0.49
3:CC:157:ILE:HD12	3:CC:164:ARG:HB3	1.94	0.49
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.48	0.49
10:CJ:51:ARG:O	14:CN:45:ARG:NH1	2.45	0.49
13:CM:34:LEU:HD13	13:CM:41:PRO:HB3	1.94	0.49
15:CO:8:LYS:O	15:CO:12:ILE:HG13	2.12	0.49
23:CW:68:C:H2'	23:CW:69:G:H8	1.76	0.49
25:C'Y:74:C:H4'	48:D1:23:LYS:HE3	1.93	0.49
26:DA:2343:C:O2'	26:DA:2373:G:O2'	2.22	0.49
26:DA:2602:A:H4'	26:DA:2603:G:O5'	2.12	0.49
27:DB:45:A:H2'	27:DB:46:A:C8	2.47	0.49
30:DF:64:ILE:HG21	30:DF:78:ILE:HG23	1.95	0.49
26:DA:335:C:H4'	45:DY:73:ARG:NE	2.27	0.49
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.47	0.49
8:AH:64:LYS:HG2	8:AH:79:VAL:HG21	1.94	0.49
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.48	0.49
1:AA:110:C:O2'	16:AP:25:ARG:O	2.26	0.49
23:AW:69:G:H2'	23:AW:69:G:N3	2.28	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:AX:7:G:O2'	24:AX:49:G:H5'	2.13	0.49
26:BA:2534:U:O2'	26:BA:2659:U:OP1	2.20	0.49
26:BA:704:U:H2'	26:BA:705:C:H6	1.77	0.49
41:BU:29:SER:OG	41:BU:30:LYS:NZ	2.40	0.49
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.27	0.49
1:CA:585:G:OP1	17:CQ:37:LYS:NZ	2.45	0.49
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.12	0.49
2:CB:105:PHE:HE1	2:CB:155:LEU:HD12	1.78	0.49
5:CE:80:ILE:HD11	8:CH:104:ARG:HH21	1.77	0.49
25:CY:19:G:C2	25:CY:57:G:C6	3.01	0.49
26:DA:1514:U:H2'	26:DA:1515:G:C8	2.48	0.49
26:DA:2164:C:H5	26:DA:2165:G:N3	2.11	0.49
26:DA:692:C:O2'	28:DD:38:LYS:NZ	2.44	0.49
44:DX:52:VAL:HG12	44:DX:82:GLN:O	2.13	0.49
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.43	0.49
1:AA:256:U:H2'	1:AA:257:G:H8	1.77	0.49
2:AB:42:ILE:HD12	2:AB:203:GLY:HA2	1.93	0.49
3:AC:181:ASN:HD21	3:AC:204:LEU:HD12	1.77	0.49
16:AP:22:THR:HA	16:AP:33:ILE:HG12	1.93	0.49
1:AA:266:G:O3'	17:AQ:67:LYS:HB2	2.13	0.49
1:AA:1014:A:H4'	19:AS:14:HIS:CE1	2.46	0.49
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.45	0.49
25:AY:50:U:H2'	25:AY:51:U:C6	2.46	0.49
26:BA:1091:A:OP1	26:BA:1091:A:H4'	2.12	0.49
26:BA:2451:A:C8	26:BA:2451:A:H5'	2.48	0.49
26:BA:427:G:N7	61:BA:4974:HOH:O	2.34	0.49
26:BA:602:G:H2'	26:BA:603:C:C6	2.48	0.49
45:BY:28:LYS:HD2	45:BY:40:GLU:HG3	1.94	0.49
1:CA:1324:A:O4'	1:CA:1362:C:H4'	2.13	0.49
1:CA:343:U:H2'	1:CA:345:C:C5	2.47	0.49
2:CB:140:HIS:O	2:CB:143:GLU:HB2	2.12	0.49
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.11	0.49
37:DQ:85:LYS:HG2	47:D0:7:LEU:HB3	1.94	0.49
26:DA:1508:A:H4'	26:DA:1509(A):A:C5	2.47	0.49
26:DA:1952:A:OP1	35:DO:42:SER:OG	2.29	0.49
26:DA:2528:U:H5''	56:D9:31:LYS:HE2	1.94	0.49
26:DA:2602:A:H4'	26:DA:2603:G:C5'	2.42	0.49
26:DA:854:G:H2'	26:DA:855:G:H8	1.77	0.49
33:DI:130:TYR:HB3	33:DI:138:ILE:HB	1.94	0.49
39:DS:31:SER:OG	39:DS:32:LEU:N	2.46	0.49
40:DT:24:PRO:HA	40:DT:49:VAL:HG23	1.95	0.49
1:AA:346:G:C4	1:AA:347:G:H1'	2.48	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:115:LEU:HD13	2:AB:145:LEU:HB3	1.93	0.49
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.77	0.49
8:AH:6:ILE:HD11	8:AH:31:PHE:HD2	1.78	0.49
44:BX:5:TYR:CZ	49:B2:30:ARG:HB2	2.48	0.49
53:B6:6:ARG:HH12	53:B6:26:ASN:HB2	1.78	0.49
31:BG:66:GLN:HG3	51:B4:1:MET:HE1	1.94	0.49
33:BI:109:ILE:HG23	33:BI:130:TYR:CZ	2.48	0.49
1:CA:1003:G:N2	1:CA:1025:U:O4	2.46	0.49
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.30	0.49
1:CA:834:C:H2'	1:CA:835:U:C6	2.47	0.49
1:CA:1151:A:H5'	10:CJ:41:PRO:HA	1.95	0.49
26:DA:242:G:N2	26:DA:255:A:OP2	2.38	0.49
30:DF:183:VAL:O	30:DF:187:VAL:HG23	2.13	0.49
1:AA:1137:C:H5''	1:AA:1138:G:OP1	2.13	0.49
1:AA:628:G:H2'	1:AA:629:G:C8	2.48	0.49
13:AM:65:LYS:NZ	51:B4:53:GLU:OE1	2.45	0.49
19:AS:27:GLU:CB	19:AS:28:LYS:HA	2.38	0.49
26:BA:934:A:O2'	26:BA:935:C:OP2	2.28	0.49
31:BG:170:ARG:HD3	31:BG:174:GLU:HG3	1.94	0.49
32:BH:154:PRO:HD3	32:BH:162:ILE:O	2.12	0.49
32:BH:154:PRO:HB3	32:BH:163:TYR:CE2	2.48	0.49
1:CA:1010:G:N2	1:CA:1020:U:O2	2.46	0.49
1:CA:250:A:H4'	1:CA:251:G:O5'	2.12	0.49
1:CA:392:G:H2'	1:CA:393:A:C8	2.48	0.49
1:CA:429:U:H1'	1:CA:430:A:H5''	1.95	0.49
1:CA:589:C:N3	1:CA:650:G:N1	2.41	0.49
1:CA:976:G:C8	1:CA:1362:C:N4	2.80	0.49
25:CY:35:A:N6	25:CY:36:A:N1	2.61	0.49
26:DA:1300:U:H4'	26:DA:1301:A:H5'	1.94	0.49
26:DA:1313:U:H4'	26:DA:1332:G:H4'	1.95	0.49
26:DA:1652:A:OP1	38:DR:8:ARG:NH1	2.46	0.49
26:DA:1657:C:H2'	26:DA:1658:C:C6	2.48	0.49
26:DA:465:G:OP1	54:D7:12:ARG:NH2	2.41	0.49
42:DV:24:LYS:HG2	42:DV:64:HIS:CD2	2.35	0.49
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.48	0.49
1:AA:111:G:H5''	16:AP:27:LYS:HG2	1.93	0.49
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.46	0.49
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.48	0.49
1:AA:262:A:C6	1:AA:263:A:C6	3.00	0.49
1:AA:736:C:H2'	1:AA:737:A:C8	2.48	0.49
9:AI:93:ARG:HB2	9:AI:93:ARG:HH11	1.78	0.49
19:AS:38:SER:HB2	19:AS:71:LEU:HD13	1.95	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:AX:7:G:H1	24:AX:66:C:H42	1.61	0.49
51:B4:24:THR:OG1	51:B4:25:TYR:N	2.45	0.49
26:BA:2146:G:H1	26:BA:2196:C:N4	2.11	0.49
26:BA:2044:U:O2'	26:BA:2629:C:H5'	2.13	0.49
26:BA:599:U:H2'	26:BA:600:G:C8	2.47	0.49
32:BH:11:VAL:HG21	32:BH:50:VAL:HG23	1.94	0.49
39:BS:65:VAL:O	39:BS:69:VAL:HG13	2.13	0.49
1:CA:434:U:H2'	1:CA:435:C:C6	2.48	0.49
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.77	0.49
5:CE:12:LEU:O	5:CE:30:ALA:HA	2.13	0.49
23:CW:21:A:N6	23:CW:46:7MG:N3	2.61	0.49
26:DA:1339:G:N2	26:DA:1603:A:H1'	2.27	0.49
26:DA:648:G:O2'	26:DA:2351:G:OP1	2.23	0.49
26:DA:724:U:H2'	26:DA:725:G:O4'	2.13	0.49
27:DB:118:G:H2'	27:DB:119:G:H5'	1.95	0.49
27:DB:20:C:H2'	27:DB:21:G:H5'	1.93	0.49
30:DF:154:VAL:HG22	30:DF:191:ARG:HB2	1.94	0.49
36:DP:84:ASN:OD1	36:DP:117:GLU:HB2	2.13	0.49
1:AA:1027:C:C2	1:AA:1034:G:C2	3.01	0.48
1:AA:1131:G:O5'	1:AA:1131:G:H8	1.96	0.48
3:AC:81:GLY:O	3:AC:85:ARG:HG3	2.13	0.48
6:AF:69:GLU:CD	6:AF:69:GLU:H	2.12	0.48
13:AM:80:ARG:NH2	19:AS:69:HIS:HE1	2.11	0.48
23:AW:1:G:C6	23:AW:72:C:N3	2.79	0.48
49:B2:31:GLU:HB3	49:B2:53:LEU:HD11	1.94	0.48
26:BA:1067:A:H3'	26:BA:1067:A:C8	2.47	0.48
26:BA:1634:C:H2'	26:BA:1635:C:H6	1.78	0.48
26:BA:2776:G:OP2	61:BA:4693:HOH:O	2.20	0.48
26:BA:601:A:OP2	61:BA:4085:HOH:O	2.20	0.48
32:BH:86:GLU:OE2	32:BH:130:ARG:NH1	2.46	0.48
34:BN:67:LEU:O	34:BN:88:GLU:HG3	2.13	0.48
36:BP:121:LYS:O	36:BP:123:LEU:N	2.42	0.48
42:BV:21:ARG:HG2	42:BV:91:TYR:CD1	2.48	0.48
1:CA:976:G:C8	1:CA:1358:U:C2	3.01	0.48
15:CO:26:GLU:N	15:CO:26:GLU:OE2	2.43	0.48
15:CO:25:THR:HG21	15:CO:70:LEU:HB2	1.94	0.48
26:DA:196:A:H2'	26:DA:196:A:N3	2.28	0.48
26:DA:2693:A:H2'	26:DA:2694:G:H8	1.78	0.48
26:DA:539:G:H2'	26:DA:540:C:H6	1.78	0.48
29:DE:9:VAL:HG13	29:DE:25:VAL:O	2.13	0.48
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.13	0.48
4:AD:165:MET:C	4:AD:168:ARG:HH12	2.17	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.13	0.48
9:AI:77:ILE:O	9:AI:81:ILE:HG23	2.13	0.48
26:BA:1210:G:H2'	26:BA:1211:U:C6	2.49	0.48
26:BA:1633:A:H2'	26:BA:1634:C:C6	2.49	0.48
26:BA:2163:G:C2	26:BA:2164:C:C2	3.02	0.48
26:BA:2298:A:H4'	26:BA:2299:A:O4'	2.13	0.48
30:BF:64:ILE:HD11	30:BF:75:HIS:HB2	1.94	0.48
1:CA:834:C:H2'	1:CA:835:U:H6	1.78	0.48
1:CA:936:C:H2'	1:CA:937:A:O4'	2.13	0.48
1:CA:938:A:C6	1:CA:939:G:C5	3.01	0.48
2:CB:210:SER:OG	2:CB:211:ILE:N	2.46	0.48
4:CD:175:SER:OG	4:CD:184:LYS:HB2	2.12	0.48
14:CN:29:ARG:HD3	14:CN:40:CYS:HB2	1.94	0.48
23:CW:8:4SU:H1'	23:CW:48:C:H1'	1.95	0.48
26:DA:1434:A:H61	26:DA:1558:A:N6	2.11	0.48
26:DA:191:A:H2'	26:DA:192:C:C6	2.48	0.48
26:DA:2552:U:H2'	26:DA:2554:U:H5''	1.96	0.48
26:DA:607:U:OP1	30:DF:102:PRO:HA	2.13	0.48
36:DP:39:LYS:CB	36:DP:45:LEU:HG	2.43	0.48
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.35	0.48
17:AQ:58:GLU:O	17:AQ:74:LEU:N	2.41	0.48
54:B7:46:VAL:HG13	54:B7:48:LYS:HE3	1.95	0.48
56:B9:2:LYS:HE2	56:B9:31:LYS:O	2.12	0.48
26:BA:1065:U:O2'	26:BA:1067:A:H2	1.96	0.48
26:BA:1425:A:H4'	26:BA:1426:G:OP2	2.13	0.48
26:BA:809:U:H5''	61:BA:4793:HOH:O	2.13	0.48
35:BO:24:VAL:HB	35:BO:33:ALA:HB2	1.95	0.48
45:BY:6:HIS:CD2	45:BY:6:HIS:H	2.30	0.48
1:CA:1053:G:O5'	1:CA:1054:C:H5'	2.13	0.48
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.48	0.48
1:CA:1181:G:O2'	1:CA:1182:G:N7	2.38	0.48
1:CA:979:C:H2'	1:CA:980:C:H5'	1.95	0.48
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.81	0.48
2:CB:27:LYS:HG3	2:CB:194:PRO:HD2	1.95	0.48
1:CA:1060:C:C5	3:CC:2:GLY:HA3	2.49	0.48
7:CG:76:ARG:HB3	7:CG:156:TRP:HH2	1.78	0.48
7:CG:20:ASP:OD2	7:CG:23:VAL:HG23	2.14	0.48
8:CH:134:ILE:HG22	8:CH:135:CYS:SG	2.54	0.48
54:D7:9:ARG:HE	54:D7:47:ARG:HB2	1.78	0.48
26:DA:1218:C:H42	26:DA:1231:G:H1	1.61	0.48
26:DA:1998:G:O2'	26:DA:2724:C:O2'	2.25	0.48
26:DA:2183:C:H2'	26:DA:2184:G:C8	2.46	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:223:A:O2'	26:DA:420:C:O2	2.31	0.48
26:DA:531:C:H4'	26:DA:532:A:H5''	1.95	0.48
26:DA:858:U:OP1	47:D0:44:ARG:NH2	2.44	0.48
35:DO:98:VAL:HG22	35:DO:118:ALA:HA	1.95	0.48
1:AA:1243:C:H2'	1:AA:1244:C:C6	2.48	0.48
1:AA:963:G:H5'	61:AA:4173:HOH:O	2.12	0.48
3:AC:181:ASN:HD22	3:AC:204:LEU:HB2	1.78	0.48
1:AA:1525:G:OP1	11:AK:120:ARG:NH2	2.46	0.48
19:AS:19:VAL:O	19:AS:23:ASN:ND2	2.47	0.48
48:B1:85:LEU:HB3	48:B1:89:GLU:CG	2.43	0.48
26:BA:1761:G:H1	26:BA:1775:C:N4	2.11	0.48
26:BA:223:C:H2'	26:BA:224:U:H6	1.79	0.48
26:BA:2705:A:H2'	26:BA:2706:G:H8	1.77	0.48
27:BB:22:U:H2'	27:BB:23:G:C8	2.49	0.48
1:CA:988:G:H1	1:CA:1217:C:H42	1.60	0.48
1:CA:1376:U:OP1	7:CG:98:SER:OG	2.29	0.48
1:CA:1399:C:C2	1:CA:1502:A:N6	2.81	0.48
1:CA:17:U:H2'	1:CA:18:C:C6	2.49	0.48
1:CA:736:C:H2'	1:CA:737:A:C8	2.48	0.48
1:CA:73:G:C6	1:CA:97:G:C6	3.01	0.48
1:CA:1126:U:O4	10:CJ:71:LEU:HD13	2.14	0.48
17:CQ:40:LYS:HD2	17:CQ:42:TYR:CZ	2.49	0.48
5:CE:24:ARG:NH1	22:CV:24:A:OP2	2.46	0.48
23:CW:22:G:H2'	23:CW:23:A:C8	2.48	0.48
26:DA:2348:U:O4	26:DA:2382:G:N1	2.47	0.48
26:DA:250:G:C6	26:DA:251:A:C6	3.01	0.48
26:DA:894:C:H2'	26:DA:895:U:C6	2.48	0.48
27:DB:43:C:OP1	51:D4:6:HIS:NE2	2.42	0.48
46:DZ:103:ARG:O	46:DZ:139:VAL:N	2.45	0.48
10:AJ:5:ARG:HD3	10:AJ:71:LEU:HD11	1.95	0.48
3:AC:13:GLY:HA3	14:AN:57:ARG:NH2	2.27	0.48
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	1.95	0.48
24:AX:67:C:H2'	24:AX:68:C:H5'	1.94	0.48
26:BA:2149:G:C6	26:BA:2150:C:C4	3.01	0.48
26:BA:946:A:H2'	26:BA:947:A:C8	2.49	0.48
1:CA:1030:C:N3	1:CA:1031:G:N2	2.54	0.48
1:CA:203:U:OP2	1:CA:203:U:H2'	2.13	0.48
10:CJ:55:LYS:O	10:CJ:57:LYS:N	2.46	0.48
12:CL:67:THR:OG1	12:CL:95:GLY:O	2.31	0.48
36:DP:50:ARG:HD3	55:D8:7:HIS:CD2	2.49	0.48
26:DA:2839:G:H5'	38:DR:46:GLY:CA	2.37	0.48
26:DA:455:C:N3	26:DA:472:A:H2'	2.28	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:539:G:H2'	26:DA:540:C:C6	2.48	0.48
39:DS:11:LYS:O	39:DS:15:ARG:HG3	2.13	0.48
40:DT:109:GLU:O	40:DT:113:LYS:HB2	2.13	0.48
44:DX:12:VAL:HG22	44:DX:29:TRP:CE2	2.48	0.48
1:AA:36:C:OP1	12:AL:123:LYS:NZ	2.24	0.48
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.96	0.48
4:AD:107:ARG:HH22	4:AD:194:LEU:HD11	1.78	0.48
4:AD:3:ARG:O	4:AD:5:ILE:HG22	2.12	0.48
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.46	0.48
7:AG:73:MET:HG3	7:AG:89:MET:O	2.14	0.48
8:AH:96:GLY:N	8:AH:99:GLU:OE2	2.33	0.48
1:AA:584:G:H5'	17:AQ:91:ARG:HH22	1.78	0.48
25:AY:35:A:H5''	25:AY:35:A:H8	1.78	0.48
26:BA:1249:A:N6	26:BA:1286:U:H2'	2.28	0.48
26:BA:1829:U:OP2	28:BD:274:ARG:NH2	2.43	0.48
26:BA:2187:G:H1	26:BA:2194:U:H5	1.61	0.48
26:BA:2846:U:H2'	26:BA:2847:G:C8	2.49	0.48
26:BA:791:G:OP1	29:BE:132:HIS:ND1	2.37	0.48
26:BA:1856:A:OP1	28:BD:249:PRO:HD3	2.14	0.48
41:BU:49:HIS:HA	41:BU:52:ARG:HB3	1.94	0.48
1:CA:1030:C:N4	1:CA:1031:G:N1	2.58	0.48
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.49	0.48
1:CA:130:A:N3	1:CA:263:A:O2'	2.32	0.48
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.94	0.48
13:CM:108:ARG:HD3	13:CM:108:ARG:HA	1.74	0.48
13:CM:86:CYS:SG	13:CM:87:TYR:N	2.86	0.48
26:DA:597:U:H2'	26:DA:598:G:H8	1.79	0.48
26:DA:8:A:H2'	26:DA:9:U:C6	2.49	0.48
33:DI:128:LEU:O	33:DI:140:LEU:N	2.34	0.48
46:DZ:144:LEU:HD21	46:DZ:172:ALA:HB1	1.95	0.48
46:DZ:40:ASP:OD2	46:DZ:42:VAL:HG12	2.14	0.48
1:AA:175:C:H2'	1:AA:176:C:C6	2.48	0.48
1:AA:390:C:H2'	1:AA:391:G:C8	2.49	0.48
1:AA:520:A:N1	1:AA:536:C:H1'	2.28	0.48
1:AA:688:G:H2'	1:AA:689:C:H6	1.79	0.48
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.43	0.48
3:AC:45:LYS:HG3	3:AC:46:GLU:N	2.28	0.48
25:AY:58:A:O2'	25:AY:60:U:H5	1.96	0.48
51:B4:64:GLY:C	51:B4:66:SER:H	2.16	0.48
26:BA:2304:C:P	39:BS:17:ARG:HH12	2.35	0.48
26:BA:2830:A:OP2	38:BR:2:ARG:NH2	2.47	0.48
30:BF:157:VAL:HB	30:BF:194:MET:HG2	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
34:BN:58:ASP:OD1	34:BN:58:ASP:N	2.45	0.48
1:CA:1013:G:N2	1:CA:1015:A:H3'	2.28	0.48
1:CA:1236:A:O2'	1:CA:1304:G:H4'	2.13	0.48
1:CA:524:G:H2'	1:CA:525:C:C6	2.49	0.48
20:CT:16:HIS:O	20:CT:19:SER:OG	2.22	0.48
25:CY:9:A:H8	25:CY:11:C:N4	2.11	0.48
25:CY:64:A:C2'	25:CY:65:G:H5'	2.43	0.48
26:DA:752:A:P	54:D7:3:ARG:HH22	2.37	0.48
26:DA:1721:G:H2'	26:DA:1740:G:O6	2.14	0.48
26:DA:2036:C:H2'	26:DA:2037:G:C8	2.48	0.48
26:DA:2291:U:H2'	26:DA:2292:C:C6	2.49	0.48
31:DG:57:ALA:HA	31:DG:90:LEU:HD13	1.94	0.48
36:DP:121:LYS:HG2	36:DP:122:PRO:HD2	1.96	0.48
46:DZ:43:GLU:O	46:DZ:47:VAL:HG23	2.13	0.48
1:AA:1144:G:H21	1:AA:1146:A:H62	1.61	0.48
23:AW:2:C:H2'	23:AW:3:C:C6	2.48	0.48
26:BA:268:G:H5''	48:B1:81:LYS:HE3	1.96	0.48
26:BA:1834:A:H4'	28:BD:259:THR:HG23	1.95	0.48
32:BH:104:GLU:HG3	32:BH:114:VAL:HG22	1.95	0.48
41:BU:108:GLU:O	41:BU:112:ARG:HG2	2.13	0.48
1:CA:1268:A:N3	1:CA:1326:C:O2'	2.38	0.48
1:CA:359:U:H2'	1:CA:360:A:C8	2.49	0.48
1:CA:421:U:O2'	1:CA:423:G:N7	2.47	0.48
1:CA:442:C:H42	1:CA:492:G:H1	1.61	0.48
1:CA:683:G:H2'	1:CA:684:A:C8	2.49	0.48
2:CB:16:HIS:HD2	2:CB:204:ASN:N	2.11	0.48
14:CN:24:CYS:O	14:CN:28:GLY:N	2.33	0.48
25:CY:22:G:N7	25:CY:46:7MG:C2	2.82	0.48
26:DA:1899:G:N3	26:DA:1899:G:H2'	2.28	0.48
26:DA:2144:U:H1'	26:DA:2148:G:H22	1.79	0.48
26:DA:622:G:H2'	26:DA:623:G:H8	1.78	0.48
26:DA:2591:C:OP1	28:DD:239:ARG:HD2	2.14	0.48
32:DH:3:ARG:HB3	32:DH:3:ARG:NH1	2.29	0.48
34:DN:34:LEU:O	34:DN:49:GLY:HA3	2.13	0.48
41:DU:108:GLU:O	41:DU:112:ARG:HG2	2.14	0.48
43:DW:33:ARG:NE	43:DW:52:GLU:OE1	2.47	0.48
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.13	0.48
1:AA:1162:C:H42	1:AA:1174:G:H1	1.59	0.48
1:AA:270:A:H2'	1:AA:271:C:C6	2.49	0.48
1:AA:574:A:HO2'	1:AA:882:C:HO2'	1.60	0.48
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.49	0.48
51:B4:16:CYS:HB3	51:B4:20:ASN:HB3	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1712:A:H2'	26:BA:1713:G:O4'	2.13	0.48
1:CA:1000:U:O2	1:CA:1041:A:N1	2.47	0.48
7:CG:12:LEU:HD12	7:CG:12:LEU:H	1.78	0.48
13:CM:50:GLU:O	13:CM:54:VAL:HG22	2.14	0.48
26:DA:1466:G:O2'	26:DA:1546:C:O2'	2.16	0.48
26:DA:2483:C:H2'	26:DA:2484:G:O4'	2.14	0.48
26:DA:340:A:H2'	26:DA:341:G:O4'	2.14	0.48
30:DF:56:GLU:OE2	30:DF:93:LYS:NZ	2.46	0.48
32:DH:122:THR:O	32:DH:134:SER:OG	2.29	0.48
32:DH:69:ARG:O	32:DH:73:ALA:N	2.31	0.48
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.47	0.48
25:AY:22:G:C8	25:AY:46:7MG:O6	2.67	0.48
26:BA:1314:A:H2'	26:BA:1315:A:O4'	2.14	0.48
26:BA:2348:A:H61	47:B0:43:THR:HG21	1.79	0.48
26:BA:2376:C:H2'	26:BA:2377:G:O4'	2.14	0.48
26:BA:821:A:H2'	26:BA:821:A:N3	2.29	0.48
26:BA:939:C:H2'	26:BA:940:C:C6	2.49	0.48
31:BG:41:GLN:HB2	31:BG:90:LEU:HB2	1.94	0.48
1:CA:1434:A:H2'	1:CA:1435:G:O4'	2.14	0.48
1:CA:392:G:H2'	1:CA:393:A:H8	1.78	0.48
1:CA:991:U:H4'	1:CA:992:U:OP1	2.14	0.48
4:CD:53:ASP:O	4:CD:57:ARG:HG3	2.13	0.48
8:CH:119:LEU:HB3	8:CH:123:GLU:HB3	1.94	0.48
11:CK:66:LEU:HB3	11:CK:70:LYS:NZ	2.29	0.48
13:CM:4:ILE:HG22	13:CM:7:VAL:O	2.13	0.48
13:CM:91:ARG:NE	13:CM:97:PRO:O	2.43	0.48
14:CN:12:ARG:HG2	14:CN:13:THR:N	2.29	0.48
23:CW:9:A:O2'	23:CW:10:G:N7	2.47	0.48
26:DA:2031:A:N3	26:DA:2455:G:O2'	2.38	0.48
26:DA:2314:C:H2'	26:DA:2315:G:H8	1.79	0.48
26:DA:898:C:H2'	26:DA:899:A:C8	2.49	0.48
30:DF:116:ASP:O	30:DF:120:GLU:HG3	2.14	0.48
35:DO:68:GLU:OE2	35:DO:78:ARG:NH1	2.47	0.48
43:DW:82:LEU:HB2	43:DW:98:LYS:HB2	1.95	0.48
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.28	0.47
17:AQ:22:LEU:HD13	17:AQ:41:LYS:HG3	1.96	0.47
23:AW:29:G:H1	23:AW:41:C:H42	1.62	0.47
26:BA:2859:U:H4'	26:BA:2878:A:C2	2.49	0.47
30:BF:101:LEU:HD12	30:BF:102:PRO:HD2	1.95	0.47
35:BO:16:ALA:HB2	35:BO:52:VAL:HG21	1.95	0.47
45:BY:45:VAL:HG23	45:BY:63:LYS:HG2	1.95	0.47
1:CA:1162:C:N4	1:CA:1174:G:N1	2.36	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1490:C:H2'	1:CA:1491:G:C8	2.49	0.47
1:CA:583:A:H2'	1:CA:584:G:O4'	2.14	0.47
2:CB:153:ARG:HE	2:CB:153:ARG:HB2	1.53	0.47
2:CB:71:VAL:CG2	2:CB:164:VAL:HA	2.44	0.47
4:CD:57:ARG:NH2	5:CE:107:ARG:HD3	2.26	0.47
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.14	0.47
10:CJ:38:ILE:HG13	10:CJ:71:LEU:HB3	1.96	0.47
48:D1:76:ARG:NH1	48:D1:97:LEU:O	2.46	0.47
26:DA:1453:U:O4	38:DR:67:LEU:HD21	2.14	0.47
26:DA:1509(B):A:H2'	26:DA:1510:G:C8	2.49	0.47
26:DA:863:A:H2'	26:DA:864:G:H8	1.79	0.47
26:DA:947:G:H2'	26:DA:948:G:C8	2.49	0.47
27:DB:42:C:H1'	31:DG:68:PRO:HA	1.96	0.47
43:DW:71:VAL:HA	43:DW:107:LEU:HD12	1.96	0.47
45:DY:13:VAL:HB	45:DY:72:VAL:HG13	1.95	0.47
1:AA:1104:G:O5'	2:AB:111:ARG:HD2	2.14	0.47
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.96	0.47
14:AN:14:PRO:HB2	14:AN:16:PHE:O	2.14	0.47
26:BA:1921:G:H2'	26:BA:1921:G:N3	2.29	0.47
26:BA:2164:C:H2'	26:BA:2165:C:C6	2.49	0.47
26:BA:207:A:C2	26:BA:224:U:H4'	2.50	0.47
37:BQ:21:THR:HG21	37:BQ:101:ARG:HD3	1.96	0.47
1:CA:1017:G:H2'	1:CA:1018:C:C6	2.49	0.47
1:CA:1502:A:H2	1:CA:1505:G:N1	2.07	0.47
1:CA:59:A:H3'	1:CA:331:G:H22	1.79	0.47
1:CA:659:U:H2'	1:CA:660:G:O4'	2.14	0.47
1:CA:811:C:N3	61:CA:3210:HOH:O	2.35	0.47
5:CE:6:PHE:CD1	5:CE:36:ASP:HB3	2.49	0.47
13:CM:40:ASN:HB3	13:CM:43:THR:HG23	1.95	0.47
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.14	0.47
48:D1:65:SER:OG	48:D1:66:HIS:ND1	2.41	0.47
53:D6:21:TYR:CE1	53:D6:38:LYS:HG2	2.49	0.47
26:DA:2124:G:H1	26:DA:2174:C:N4	2.13	0.47
26:DA:2321:G:N3	26:DA:2321:G:H2'	2.28	0.47
30:DF:36:VAL:HG11	30:DF:183:VAL:HG11	1.96	0.47
32:DH:35:VAL:HG11	32:DH:71:LEU:HG	1.97	0.47
33:DI:102:SER:OG	33:DI:103:ARG:N	2.47	0.47
36:DP:21:ARG:HA	36:DP:21:ARG:HD3	1.50	0.47
26:DA:863:A:P	37:DQ:22:LYS:HG3	2.54	0.47
39:DS:77:ALA:O	39:DS:81:GLY:N	2.46	0.47
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.79	0.47
1:AA:346:G:P	40:BT:41:ARG:HH22	2.36	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.50	0.47
15:AO:84:LYS:HD3	15:AO:84:LYS:O	2.13	0.47
17:AQ:78:GLU:HG2	17:AQ:79:SER:N	2.29	0.47
26:BA:354:A:H2	26:BA:1255:A:C2'	2.26	0.47
26:BA:2152:U:H1'	26:BA:2180:A:N1	2.29	0.47
45:BY:11:ASP:OD1	45:BY:11:ASP:N	2.40	0.47
1:CA:1267:C:H6	1:CA:1267:C:O5'	1.97	0.47
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.96	0.47
1:CA:664:G:N2	1:CA:741:G:H1	2.04	0.47
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.95	0.47
49:D2:16:LEU:HB2	49:D2:21:LEU:HD23	1.97	0.47
26:DA:62:C:H42	26:DA:93:G:H1	1.62	0.47
26:DA:885:C:H2'	26:DA:886:C:H4'	1.96	0.47
27:DB:24:G:H4'	27:DB:25:A:C8	2.49	0.47
30:DF:33:LEU:HD13	30:DF:112:MET:HE2	1.95	0.47
31:DG:111:LEU:HA	31:DG:114:ILE:HD13	1.96	0.47
31:DG:15:VAL:HG13	31:DG:175:LEU:HD23	1.97	0.47
36:DP:82:GLY:HA2	36:DP:113:LYS:O	2.14	0.47
39:DS:84:GLN:H	39:DS:111:GLU:HB2	1.79	0.47
39:DS:30:ARG:HD3	39:DS:98:VAL:HG22	1.97	0.47
40:DT:99:LEU:O	40:DT:102:ILE:HG12	2.14	0.47
1:AA:1033:G:H2'	1:AA:1034:G:C8	2.45	0.47
1:AA:1255:G:N7	10:AJ:43:ARG:NH2	2.62	0.47
1:AA:1479:C:H2'	1:AA:1480:G:C8	2.49	0.47
51:B4:18:CYS:SG	51:B4:20:ASN:HB2	2.55	0.47
51:B4:59:PHE:C	51:B4:61:ARG:H	2.13	0.47
26:BA:873:U:H4'	36:BP:55:ARG:HB2	1.96	0.47
45:BY:13:VAL:HB	45:BY:72:VAL:HG13	1.95	0.47
1:CA:1004:A:H62	1:CA:1037:C:C2'	2.28	0.47
1:CA:1179:A:H2'	1:CA:1180:A:O4'	2.13	0.47
1:CA:1225:A:OP1	13:CM:103:THR:OG1	2.30	0.47
1:CA:353:A:H8	1:CA:353:A:H5'	1.78	0.47
4:CD:20:TYR:HD1	4:CD:26:CYS:HB3	1.78	0.47
2:CB:178:ARG:HH21	8:CH:74:PRO:HG3	1.80	0.47
11:CK:24:SER:OG	11:CK:25:TYR:N	2.45	0.47
25:CY:66:U:H2'	25:CY:67:C:O4'	2.14	0.47
26:DA:1029:A:N6	26:DA:1125:G:O2'	2.44	0.47
26:DA:1639:U:C2'	26:DA:1640:C:H5''	2.42	0.47
26:DA:212:G:H2'	26:DA:213:A:O4'	2.13	0.47
26:DA:571:A:N6	26:DA:2499:C:O3'	2.46	0.47
26:DA:2646:C:H2'	26:DA:2647:U:O4'	2.15	0.47
31:DG:144:ILE:HG23	31:DG:148:MET:HE1	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
39:DS:53:SER:O	39:DS:57:LYS:N	2.47	0.47
1:AA:167:G:H2'	1:AA:168:G:C8	2.49	0.47
1:AA:457:C:H2'	1:AA:458:C:H6	1.79	0.47
1:AA:741:G:H2'	1:AA:742:G:O4'	2.15	0.47
1:AA:952:U:H2'	1:AA:953:G:C8	2.50	0.47
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.96	0.47
1:AA:428:G:OP2	4:AD:10:ARG:NH1	2.47	0.47
8:AH:33:GLU:HG2	8:AH:48:TYR:OH	2.14	0.47
24:AX:56:C:O5'	24:AX:56:C:H6	1.97	0.47
33:BI:85:GLU:HB3	33:BI:86:THR:H	1.55	0.47
46:BZ:108:PRO:HB3	46:BZ:117:LEU:HD22	1.97	0.47
2:CB:91:PRO:HG3	2:CB:155:LEU:HD23	1.95	0.47
5:CE:10:MET:HG3	5:CE:32:VAL:HG22	1.96	0.47
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.50	0.47
18:CR:41:LYS:HB3	18:CR:41:LYS:NZ	2.29	0.47
18:CR:73:ALA:HB3	18:CR:79:LEU:HG	1.96	0.47
26:DA:1220:A:OP2	41:DU:19:LYS:NZ	2.34	0.47
26:DA:1316:U:H2'	26:DA:1317:A:C8	2.49	0.47
26:DA:1420:U:HO2'	26:DA:1421:G:P	2.37	0.47
26:DA:2136:C:H1'	26:DA:2137:C:H5'	1.96	0.47
26:DA:641:C:H42	26:DA:647:G:H1	1.62	0.47
26:DA:657:U:H2'	26:DA:658:C:C6	2.49	0.47
28:DD:2:ALA:O	28:DD:3:VAL:HB	2.15	0.47
30:DF:178:PRO:HB3	30:DF:198:ALA:HA	1.97	0.47
44:DX:35:THR:HB	44:DX:38:GLU:HB2	1.97	0.47
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.96	0.47
4:AD:12:CYS:SG	4:AD:19:LEU:HB2	2.54	0.47
16:AP:28:ARG:NE	16:AP:29:ASP:OD1	2.29	0.47
16:AP:20:VAL:HG23	16:AP:35:LYS:HA	1.96	0.47
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.13	0.47
25:AY:15:G:C6	25:AY:48:C:O2	2.68	0.47
25:AY:2:C:H42	25:AY:71:G:H1	1.63	0.47
26:BA:2203:G:HO2'	26:BA:2204:G:P	2.37	0.47
26:BA:2228:G:H2'	26:BA:2229:A:C2	2.50	0.47
26:BA:559:U:H2'	26:BA:560:C:C6	2.49	0.47
33:BI:48:GLU:O	33:BI:52:ARG:HB3	2.14	0.47
1:CA:1362:C:C2'	1:CA:1363:C:H5''	2.45	0.47
1:CA:601:C:H42	1:CA:637:G:H1	1.63	0.47
2:CB:17:PHE:CD2	2:CB:44:LEU:HD11	2.49	0.47
8:CH:84:ARG:O	8:CH:84:ARG:HG3	2.14	0.47
20:CT:56:MET:HE2	20:CT:56:MET:HB2	1.71	0.47
23:CW:50:U:H2'	23:CW:51:U:O4'	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:CX:12:G:H4'	26:DA:1908:C:O2	2.14	0.47
24:CX:37:A:H2'	24:CX:38:A:O4'	2.14	0.47
50:D3:50:VAL:O	50:D3:54:VAL:HB	2.15	0.47
26:DA:1019:U:O2'	26:DA:1021:A:H2	1.97	0.47
28:DD:164:GLN:NE2	28:DD:176:ARG:HH22	2.12	0.47
35:DO:120:GLU:HG2	35:DO:122:LEU:HG	1.97	0.47
45:DY:28:LYS:HE2	45:DY:28:LYS:HB3	1.67	0.47
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.50	0.47
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.50	0.47
1:AA:162:A:H3'	1:AA:163:C:C4'	2.45	0.47
1:AA:620:C:H2'	1:AA:621:A:O4'	2.15	0.47
3:AC:62:ASP:HA	3:AC:97:LYS:HD3	1.96	0.47
16:AP:48:TRP:HH2	16:AP:76:GLN:NE2	2.12	0.47
19:AS:23:ASN:HA	19:AS:27:GLU:CD	2.35	0.47
24:AX:2:G:H2'	24:AX:2:G:N3	2.29	0.47
26:BA:2162:C:C4	26:BA:2173:G:N1	2.83	0.47
26:BA:2357:G:H4'	26:BA:2358:A:H5''	1.97	0.47
30:BF:39:TRP:O	30:BF:43:LYS:HD3	2.14	0.47
31:BG:19:LEU:HG	31:BG:175:LEU:HD23	1.97	0.47
1:CA:1256:A:N1	1:CA:1278:U:H1'	2.29	0.47
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.78	0.47
1:CA:24:U:OP1	12:CL:23:LYS:NZ	2.47	0.47
13:CM:39:ILE:HG12	13:CM:52:GLU:HG2	1.96	0.47
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.55	0.47
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.96	0.47
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	2.15	0.47
22:CV:14:A:C4	25:CY:34:G:C6	3.02	0.47
50:D3:8:LEU:HD13	50:D3:31:LEU:HD23	1.97	0.47
26:DA:1239:G:H2'	26:DA:1240:U:O4'	2.14	0.47
28:DD:134:ARG:NH1	28:DD:188:GLU:OE2	2.47	0.47
32:DH:98:LEU:HD13	32:DH:102:ALA:O	2.13	0.47
26:DA:2547:U:O2	35:DO:23:ARG:NH2	2.47	0.47
36:DP:16:ARG:HG3	61:DP:305:HOH:O	2.13	0.47
1:AA:1007:C:N3	1:AA:1022:G:C6	2.83	0.47
1:AA:1285:A:H4'	1:AA:1286:A:O5'	2.15	0.47
1:AA:1392:G:N2	1:AA:1502:A:C8	2.83	0.47
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.15	0.47
1:AA:564:C:O2'	8:AH:91:ARG:NH2	2.38	0.47
26:BA:2569:G:H2'	26:BA:2570:C:C6	2.50	0.47
26:BA:284:G:C2	26:BA:285:U:O4	2.68	0.47
1:CA:1392:G:H21	1:CA:1502:A:H8	1.63	0.47
1:CA:22:G:H4'	1:CA:885:G:C8	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:643:C:H2'	1:CA:644:G:H8	1.79	0.47
4:CD:22:LYS:HG3	58:CD:501:SF4:S4	2.55	0.47
8:CH:103:VAL:HG21	8:CH:109:ILE:C	2.35	0.47
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.14	0.47
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	1.96	0.47
19:CS:41:VAL:O	19:CS:44:MET:HB2	2.14	0.47
26:DA:1270:C:H5''	26:DA:1271:G:O5'	2.15	0.47
26:DA:1528(A):A:H2'	26:DA:1529:G:O4'	2.15	0.47
26:DA:1592:C:H2'	26:DA:1593:G:H8	1.79	0.47
26:DA:2128:C:N4	26:DA:2160:G:H1	2.09	0.47
27:DB:70:C:H42	27:DB:107:G:H1	1.61	0.47
27:DB:94:C:H2'	27:DB:95:C:C6	2.50	0.47
28:DD:26:LYS:HE2	28:DD:28:GLU:O	2.15	0.47
1:AA:1122:U:C4	1:AA:1123:A:N7	2.83	0.47
1:AA:346:G:OP1	40:BT:41:ARG:NH1	2.42	0.47
9:AI:4:TYR:CE2	9:AI:88:TYR:HD1	2.33	0.47
1:AA:1250:A:H4'	9:AI:68:GLY:N	2.30	0.47
26:BA:1462:G:O2'	26:BA:1463:C:OP2	2.24	0.47
26:BA:1529:G:O6	26:BA:1553:A:N6	2.48	0.47
26:BA:1733:C:H2'	26:BA:1734:G:O4'	2.15	0.47
26:BA:2159:C:N3	26:BA:2176:G:O6	2.48	0.47
26:BA:2190:G:C6	26:BA:2193:A:C8	3.02	0.47
26:BA:34:C:H5''	26:BA:35:G:OP2	2.15	0.47
26:BA:831:A:N6	28:BD:229:VAL:HG11	2.30	0.47
30:BF:53:THR:HG23	30:BF:55:GLY:H	1.80	0.47
1:CA:1360:A:O5'	1:CA:1360:A:H8	1.97	0.47
5:CE:145:LYS:HE3	5:CE:149:GLU:OE2	2.15	0.47
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.30	0.47
11:CK:65:ALA:HB3	11:CK:97:ALA:HB3	1.97	0.47
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.97	0.47
51:D4:16:CYS:SG	51:D4:17:GLY:N	2.87	0.47
26:DA:1127:A:H2'	26:DA:1128:A:H5''	1.97	0.47
26:DA:2059:A:O2'	30:DF:69:HIS:HD2	1.98	0.47
26:DA:251:A:C5	26:DA:252:G:H1'	2.50	0.47
26:DA:2820:A:O2'	26:DA:2821:A:OP1	2.29	0.47
26:DA:602:G:O2'	26:DA:655:A:N6	2.48	0.47
26:DA:782:A:H5'	26:DA:783:A:N7	2.30	0.47
27:DB:8:U:O2'	39:DS:40:ILE:HD13	2.15	0.47
1:AA:1095:U:H5''	1:AA:1109:C:O2	2.14	0.47
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.42	0.47
1:AA:256:U:H2'	1:AA:257:G:C8	2.49	0.47
1:AA:413:G:N2	1:AA:428:G:H1'	2.30	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:626:U:H2'	1:AA:627:G:H8	1.78	0.47
1:AA:743:U:H2'	1:AA:744:C:C6	2.50	0.47
2:AB:59:GLU:O	2:AB:63:MET:HG3	2.14	0.47
4:AD:98:GLU:HG2	4:AD:189:PRO:HG2	1.96	0.47
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.15	0.47
1:AA:1525:G:P	11:AK:120:ARG:HH22	2.37	0.47
18:AR:26:LEU:HD23	18:AR:29:PHE:CE2	2.50	0.47
33:BI:12:LEU:HD23	33:BI:12:LEU:HA	1.79	0.47
33:BI:47:LEU:HA	33:BI:47:LEU:HD23	1.75	0.47
26:BA:950:C:H4'	46:BZ:169:GLU:OE2	2.15	0.47
46:BZ:7:ALA:HB3	46:BZ:61:LEU:HD12	1.97	0.47
1:CA:1314:C:OP1	19:CS:6:LYS:NZ	2.24	0.47
1:CA:258:G:OP1	20:CT:86:ARG:NH1	2.48	0.47
25:CY:35:A:H2'	25:CY:36:A:O4'	2.15	0.47
25:CY:50:U:H2'	25:CY:51:U:C6	2.50	0.47
26:DA:1600:C:OP1	44:DX:58:HIS:NE2	2.37	0.47
26:DA:1794:U:H2'	26:DA:1795:C:C6	2.50	0.47
26:DA:2136:C:N4	26:DA:2155:G:C6	2.82	0.47
26:DA:2391:G:O6	26:DA:2425:A:H8	1.98	0.47
26:DA:272:G:H4'	26:DA:272(A):U:H5''	1.97	0.47
30:DF:20:LEU:HD12	30:DF:125:LEU:HD13	1.97	0.47
1:AA:502:G:H2'	1:AA:503:C:O4'	2.14	0.47
2:AB:80:ILE:O	2:AB:84:GLU:HB2	2.15	0.47
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.45	0.47
19:AS:41:VAL:HG12	19:AS:43:GLU:H	1.80	0.47
26:BA:1170:C:H1'	56:B9:36:GLN:NE2	2.30	0.47
26:BA:1775:C:H5'	26:BA:1776:G:OP2	2.15	0.47
26:BA:1809:U:H2'	26:BA:1815:A:N6	2.29	0.47
26:BA:2185:C:H5'	26:BA:2185:C:C6	2.49	0.47
26:BA:922:G:H2'	26:BA:923:C:O4'	2.15	0.47
26:BA:895:G:N9	26:BA:978:A:H8	2.11	0.47
32:BH:25:LYS:HG2	32:BH:34:GLU:HG2	1.97	0.47
1:CA:107:G:H2'	1:CA:108:G:O4'	2.15	0.47
1:CA:827:U:H5''	1:CA:828:A:OP2	2.15	0.47
2:CB:219:VAL:HA	2:CB:222:ILE:HG12	1.96	0.47
3:CC:127:ARG:NH2	3:CC:192:THR:HG23	2.29	0.47
3:CC:54:ARG:H	3:CC:69:HIS:HB2	1.79	0.47
4:CD:103:ASN:OD1	4:CD:114:ARG:NE	2.39	0.47
6:CF:97:PHE:CE1	18:CR:62:GLU:HG2	2.50	0.47
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	1.96	0.47
49:D2:29:LYS:HE2	49:D2:57:ILE:HG21	1.96	0.47
26:DA:1027:A:C6	26:DA:1126:A:C4	3.03	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2153:G:C2	26:DA:2154:G:C4	3.03	0.47
26:DA:2841:C:H2'	26:DA:2842:G:C8	2.51	0.47
26:DA:613:G:O2'	26:DA:614(C):A:N1	2.40	0.47
26:DA:900:A:C8	26:DA:901:A:N7	2.83	0.47
26:DA:955:C:OP1	37:DQ:87:LYS:HE3	2.15	0.47
34:DN:108:PRO:O	34:DN:113:GLY:HA3	2.15	0.47
1:AA:116:A:H8	1:AA:116:A:O5'	1.97	0.46
1:AA:1367:C:H4'	10:AJ:48:THR:HG21	1.96	0.46
1:AA:664:G:N2	1:AA:741:G:H1	2.03	0.46
1:AA:890:G:O2'	1:AA:906:G:O6	2.19	0.46
1:AA:992:U:H4'	1:AA:993:G:H5''	1.97	0.46
2:AB:60:ASP:OD1	2:AB:64:ARG:NH2	2.49	0.46
3:AC:122:GLU:O	3:AC:126:ARG:NH1	2.41	0.46
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.96	0.46
6:AF:86:ARG:O	6:AF:87:ARG:HG2	2.14	0.46
9:AI:79:LEU:O	9:AI:83:ARG:HG3	2.15	0.46
1:AA:1458:G:H5''	20:AT:31:SER:HB2	1.96	0.46
24:AX:32:5MC:HM53	24:AX:33:U:O4	2.15	0.46
25:AY:57:G:H2'	25:AY:58:A:H5'	1.97	0.46
25:AY:58:A:N6	25:AY:61:C:C2	2.83	0.46
52:B5:11:THR:HG23	52:B5:15:ARG:HB3	1.96	0.46
26:BA:1517:G:N2	26:BA:1568:G:OP2	2.36	0.46
26:BA:2156:A:HO2'	26:BA:2157:A:C5'	2.28	0.46
1:CA:1129:C:H2'	1:CA:1139:G:C5	2.49	0.46
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.50	0.46
1:CA:447:G:O6	1:CA:485:G:O2'	2.23	0.46
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.14	0.46
3:CC:121:ALA:HB1	3:CC:189:ALA:HB2	1.96	0.46
20:CT:87:LYS:O	20:CT:91:LEU:HG	2.15	0.46
26:DA:1628:G:H2'	26:DA:1629:U:C6	2.50	0.46
26:DA:2136:C:O2'	26:DA:2137:C:O5'	2.22	0.46
26:DA:2577:A:OP2	52:D5:3:LYS:NZ	2.43	0.46
26:DA:908:C:OP2	37:DQ:22:LYS:NZ	2.48	0.46
31:DG:107:LEU:HD21	31:DG:178:PHE:CE1	2.50	0.46
31:DG:122:PRO:HG3	31:DG:180:PHE:HB3	1.96	0.46
31:DG:41:GLN:NE2	31:DG:153:ARG:HB3	2.30	0.46
34:DN:104:LYS:HA	34:DN:107:LEU:HD12	1.97	0.46
36:DP:54:GLY:O	61:DP:308:HOH:O	2.20	0.46
39:DS:106:ARG:HG3	39:DS:112:PHE:CZ	2.50	0.46
1:AA:405:U:H5''	1:AA:495:A:H2	1.80	0.46
1:AA:955:U:O2'	19:AS:83:HIS:HD2	1.98	0.46
2:AB:10:LEU:C	2:AB:12:GLU:H	2.17	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:AD:107:ARG:NH2	4:AD:194:LEU:HD21	2.31	0.46
5:AE:110:LEU:HD13	5:AE:118:ILE:HD13	1.97	0.46
12:AL:88:GLY:O	12:AL:99:HIS:HD2	1.99	0.46
15:AO:82:ILE:HB	15:AO:87:ILE:HB	1.96	0.46
23:AW:50:U:H2'	23:AW:51:U:O4'	2.14	0.46
31:BG:66:GLN:HG3	51:B4:1:MET:CE	2.46	0.46
26:BA:1974:A:C6	26:BA:1975:A:N1	2.83	0.46
26:BA:2181:G:H2'	26:BA:2182:G:C8	2.50	0.46
26:BA:389:G:H2'	26:BA:390:G:H5'	1.97	0.46
26:BA:886:U:H2'	26:BA:887:C:C6	2.51	0.46
27:BB:77:U:OP1	46:BZ:19:ARG:NH2	2.39	0.46
36:BP:135:LEU:HD23	36:BP:135:LEU:HA	1.71	0.46
38:BR:44:LEU:HD22	38:BR:48:VAL:HG23	1.97	0.46
38:BR:55:ALA:HB2	38:BR:79:LEU:HD13	1.97	0.46
39:BS:10:ARG:O	39:BS:14:VAL:HG13	2.16	0.46
43:BW:71:VAL:HA	43:BW:107:LEU:HD12	1.96	0.46
44:BX:60:ARG:HA	44:BX:75:ASP:OD2	2.16	0.46
1:CA:1256:A:C6	1:CA:1278:U:H1'	2.51	0.46
1:CA:1279:A:O2'	1:CA:1282:C:N4	2.49	0.46
1:CA:1291:G:O2'	9:CI:38:GLN:HG3	2.14	0.46
1:CA:59:A:H5"	1:CA:60:A:H5"	1.96	0.46
1:CA:1320:C:C1'	19:CS:73:GLU:HG2	2.46	0.46
25:CY:35:A:C6	25:CY:36:A:C2	3.03	0.46
47:D0:14:ARG:NH1	47:D0:14:ARG:HB2	2.30	0.46
26:DA:1430:C:H2'	26:DA:1431:U:C6	2.50	0.46
26:DA:1916:A:H2'	26:DA:1917:U:O4'	2.16	0.46
26:DA:293:U:H5"	26:DA:294:A:OP2	2.15	0.46
1:AA:154:C:C2'	1:AA:155:C:H5'	2.45	0.46
1:AA:65:U:H6	1:AA:65:U:H5'	1.80	0.46
4:AD:18:LYS:HG2	58:AD:501:SF4:S1	2.55	0.46
10:AJ:8:LEU:N	10:AJ:70:ARG:O	2.33	0.46
26:BA:1053:C:OP1	34:BN:37:LYS:NZ	2.46	0.46
26:BA:831:A:C6	28:BD:229:VAL:HG11	2.50	0.46
32:BH:69:ARG:HG3	32:BH:70:THR:N	2.29	0.46
45:BY:28:LYS:HB3	45:BY:28:LYS:HE2	1.75	0.46
2:CB:71:VAL:HG12	2:CB:93:VAL:CG2	2.45	0.46
7:CG:72:ARG:NH2	7:CG:138:LYS:HZ1	2.12	0.46
13:CM:25:ILE:HG13	13:CM:29:ARG:HG2	1.97	0.46
26:DA:1006:C:C2	26:DA:1138:G:N2	2.84	0.46
26:DA:2127:G:OP1	26:DA:2127:G:H4'	2.15	0.46
26:DA:857:C:H4'	47:D0:23:VAL:HG21	1.98	0.46
1:AA:1002:G:N3	1:AA:1003:G:H1'	2.30	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1090:U:H2'	1:AA:1091:U:C6	2.50	0.46
1:AA:1296:C:H5''	13:AM:14:ARG:HD2	1.96	0.46
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.80	0.46
1:AA:316:G:OP2	1:AA:351:G:O2'	2.30	0.46
1:AA:448:A:OP2	1:AA:485:G:N1	2.33	0.46
4:AD:187:ARG:HG2	4:AD:188:LEU:N	2.31	0.46
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.68	0.46
25:AY:5:G:H2'	25:AY:6:G:C8	2.51	0.46
26:BA:1212:C:H2'	26:BA:1213:U:C6	2.51	0.46
26:BA:2123:G:H2'	26:BA:2124:U:H6	1.80	0.46
26:BA:2148:A:H4'	26:BA:2149:G:OP1	2.16	0.46
26:BA:2184:G:C3'	26:BA:2185:C:H5''	2.46	0.46
26:BA:441:C:H2'	26:BA:442:A:C8	2.51	0.46
31:BG:66:GLN:OE1	31:BG:98:ARG:NE	2.43	0.46
26:BA:2574:U:O2'	35:BO:23:ARG:HD3	2.15	0.46
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.50	0.46
1:CA:1164:G:O2'	1:CA:1165:C:H5'	2.15	0.46
9:CI:18:PHE:HD2	9:CI:62:TYR:HD2	1.63	0.46
24:CX:47:U:N3	24:CX:50:U:OP1	2.49	0.46
26:DA:1199:U:H2'	26:DA:1200:C:C6	2.51	0.46
26:DA:1789:A:H2'	26:DA:1790:C:C6	2.50	0.46
26:DA:2296:U:OP2	39:DS:9:ARG:NH2	2.46	0.46
26:DA:242:G:C8	55:D8:5:LYS:HG2	2.51	0.46
26:DA:2689:U:P	26:DA:2719:G:H22	2.39	0.46
31:DG:96:ARG:O	31:DG:99:MET:HB3	2.15	0.46
36:DP:121:LYS:O	36:DP:123:LEU:N	2.44	0.46
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.51	0.46
1:AA:601:C:H2'	1:AA:602:A:C8	2.50	0.46
1:AA:8:A:N6	4:AD:205:GLU:O	2.49	0.46
12:AL:52:LEU:O	12:AL:54:LYS:NZ	2.34	0.46
26:BA:1797:U:H2'	26:BA:1798:C:C6	2.51	0.46
26:BA:1800:G:O2'	26:BA:1980:C:OP1	2.24	0.46
26:BA:1985:U:H4'	26:BA:1986:G:OP1	2.15	0.46
26:BA:223:C:H2'	26:BA:224:U:C6	2.51	0.46
26:BA:2881:C:N3	61:BA:4761:HOH:O	2.35	0.46
30:BF:183:VAL:O	30:BF:187:VAL:HG23	2.15	0.46
30:BF:33:LEU:HB3	36:BP:6:LEU:HD21	1.98	0.46
39:BS:110:LEU:HD12	39:BS:110:LEU:HA	1.74	0.46
26:BA:2858:G:H8	40:BT:97:ALA:HB2	1.79	0.46
1:CA:1241:G:C2'	1:CA:1242:C:H5'	2.45	0.46
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.47	0.46
1:CA:1390:U:H2'	1:CA:1391:U:C6	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:390:C:H2'	1:CA:391:G:C8	2.50	0.46
2:CB:137:ARG:HB3	2:CB:137:ARG:CZ	2.45	0.46
2:CB:87:ARG:HD3	2:CB:219:VAL:HG11	1.98	0.46
23:CW:31:A:H2'	23:CW:32:PSU:O4'	2.16	0.46
24:CX:33:U:N3	24:CX:36:U:OP2	2.48	0.46
26:DA:2712:U:OP1	26:DA:2714:G:H4'	2.16	0.46
26:DA:852:G:H2'	26:DA:853:G:H8	1.80	0.46
1:AA:1286:A:H3'	1:AA:1286:A:H8	1.81	0.46
1:AA:1245:A:N6	1:AA:1292:U:H3	2.11	0.46
1:AA:627:G:H2'	1:AA:628:G:H8	1.81	0.46
2:AB:67:THR:N	2:AB:160:ASP:OD1	2.47	0.46
2:AB:80:ILE:HD11	2:AB:212:GLN:CA	2.44	0.46
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.51	0.46
7:AG:22:LEU:HD11	7:AG:101:LEU:HD21	1.96	0.46
11:AK:91:ARG:NH1	11:AK:110:ASP:OD2	2.48	0.46
26:BA:2108:U:H2'	26:BA:2109:G:C8	2.51	0.46
26:BA:2860:A:OP2	26:BA:2876:U:H5	1.98	0.46
36:BP:86:LYS:HB3	36:BP:118:GLY:HA3	1.96	0.46
45:BY:6:HIS:HE1	45:BY:72:VAL:O	1.99	0.46
1:CA:841:U:H6	1:CA:841:U:OP1	1.98	0.46
2:CB:76:GLN:H	2:CB:76:GLN:HG2	1.49	0.46
10:CJ:12:ASP:OD1	10:CJ:13:HIS:N	2.48	0.46
15:CO:11:VAL:HG21	15:CO:34:LEU:HD22	1.97	0.46
16:CP:53:VAL:O	16:CP:57:ARG:HB2	2.15	0.46
20:CT:26:ASN:HA	20:CT:71:THR:HG23	1.97	0.46
26:DA:2648:C:H2'	26:DA:2649:U:C6	2.50	0.46
27:DB:90:A:C5	27:DB:91:C:H1'	2.51	0.46
46:DZ:141:VAL:HG12	46:DZ:144:LEU:HD13	1.98	0.46
46:DZ:5:LEU:O	46:DZ:59:LEU:HA	2.16	0.46
2:AB:16:HIS:C	2:AB:18:GLY:H	2.14	0.46
7:AG:138:LYS:NZ	7:AG:142:GLU:OE2	2.48	0.46
24:AX:23:C:H2'	24:AX:24:U:C6	2.51	0.46
25:AY:19:G:N2	25:AY:56:C:N3	2.64	0.46
26:BA:1093:G:H2'	26:BA:1156:G:H1	1.81	0.46
26:BA:2371:C:H2'	26:BA:2372:A:O4'	2.15	0.46
36:BP:6:LEU:HD23	36:BP:6:LEU:HA	1.71	0.46
41:BU:76:TYR:CZ	41:BU:80:ILE:HG13	2.51	0.46
1:CA:296:U:O2'	1:CA:556:C:O2	2.25	0.46
4:CD:157:LEU:HD22	4:CD:161:ASN:HD21	1.80	0.46
5:CE:39:GLY:HA2	5:CE:71:LEU:HD13	1.98	0.46
5:CE:53:LEU:HD12	5:CE:53:LEU:H	1.80	0.46
8:CH:111:ILE:HD11	8:CH:118:VAL:HG12	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:CI:116:LYS:HA	9:CI:123:PRO:HD3	1.97	0.46
11:CK:79:SER:OG	11:CK:106:LYS:HE3	2.15	0.46
13:CM:23:TYR:CE2	13:CM:70:LEU:HB3	2.50	0.46
13:CM:65:LYS:N	51:D4:50:VAL:HG21	2.31	0.46
47:D0:82:ARG:HA	47:D0:83:PRO:HD3	1.67	0.46
26:DA:1027:A:C2	26:DA:2488:A:H5'	2.51	0.46
26:DA:1790:C:H5''	26:DA:1791:A:OP1	2.15	0.46
26:DA:1833:U:O2'	26:DA:1969:A:N1	2.38	0.46
26:DA:2302:G:C2'	26:DA:2303:G:H5'	2.46	0.46
26:DA:82:G:H5''	26:DA:296:C:H5'	1.96	0.46
26:DA:699:A:H4'	26:DA:1554:A:N6	2.29	0.46
26:DA:848:G:N9	26:DA:933:A:H8	2.13	0.46
27:DB:20:C:C2'	27:DB:21:G:H5'	2.45	0.46
31:DG:8:LYS:HG3	31:DG:100:TRP:CE2	2.51	0.46
32:DH:98:LEU:HD23	32:DH:125:VAL:HG23	1.97	0.46
36:DP:38:GLN:O	36:DP:39:LYS:HB3	2.15	0.46
37:DQ:108:GLY:HA3	46:DZ:116:VAL:HG13	1.96	0.46
46:DZ:67:LEU:HA	46:DZ:68:PRO:HD3	1.83	0.46
1:AA:1036:G:N3	1:AA:1036:G:H2'	2.31	0.46
1:AA:532:A:H2	1:AA:1206:G:H21	1.63	0.46
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.45	0.46
1:AA:473:G:H2'	1:AA:474:G:C8	2.50	0.46
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	1.98	0.46
26:BA:1730:C:H2'	26:BA:1731:C:C6	2.51	0.46
26:BA:2023:A:H2'	26:BA:2024:G:C8	2.51	0.46
26:BA:45:C:OP2	26:BA:204:G:H2'	2.16	0.46
1:CA:1135:U:H2'	1:CA:1137:C:N3	2.31	0.46
1:CA:1251:A:N1	1:CA:1354:C:O2'	2.47	0.46
1:CA:1392:G:N2	1:CA:1502:A:H8	2.14	0.46
1:CA:472:A:H5''	16:CP:80:PHE:HB3	1.98	0.46
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.30	0.46
16:CP:3:LYS:O	16:CP:21:VAL:HA	2.15	0.46
1:CA:276:G:O3'	17:CQ:68:ARG:NH1	2.48	0.46
23:CW:4:C:C4	23:CW:69:G:N1	2.84	0.46
26:DA:375:C:H2'	26:DA:376:C:C6	2.51	0.46
33:DI:43:ASN:C	33:DI:43:ASN:HD22	2.19	0.46
33:DI:66:GLU:HA	33:DI:69:LYS:HB3	1.97	0.46
36:DP:124:LYS:HA	36:DP:144:GLU:O	2.16	0.46
1:AA:715:A:H2'	1:AA:716:A:C8	2.51	0.46
2:AB:119:GLU:OE1	2:AB:153:ARG:NH2	2.49	0.46
4:AD:168:ARG:H	4:AD:168:ARG:NH1	2.13	0.46
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	1.97	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.16	0.46
26:BA:354:A:H2	26:BA:1255:A:O2'	1.99	0.46
28:BD:10:THR:OG1	28:BD:13:ARG:HG2	2.16	0.46
37:BQ:1:MET:HB2	37:BQ:44:ALA:HB1	1.96	0.46
39:BS:41:ASP:OD2	39:BS:44:LYS:NZ	2.42	0.46
1:CA:1064:G:H4'	1:CA:1065:U:O5'	2.16	0.46
1:CA:991:U:H3'	1:CA:1212:U:C4	2.51	0.46
1:CA:1368:G:C2'	1:CA:1369:C:H5'	2.46	0.46
2:CB:23:ARG:H	2:CB:23:ARG:HG2	1.53	0.46
1:CA:1321:C:H4'	13:CM:87:TYR:CE2	2.50	0.46
20:CT:63:ILE:HD13	20:CT:80:ARG:HB3	1.98	0.46
24:CX:40:C:H2'	24:CX:41:C:H6	1.81	0.46
55:D8:8:LYS:HB3	55:D8:12:LYS:HE3	1.98	0.46
26:DA:1015:G:O2'	26:DA:1016:G:H5'	2.15	0.46
26:DA:1418:G:O5'	26:DA:1418:G:H8	1.99	0.46
26:DA:1467:C:C5	26:DA:1546:C:H2'	2.51	0.46
26:DA:2114:A:N1	26:DA:2117:A:N6	2.64	0.46
26:DA:2724:C:OP1	29:DE:118:LYS:NZ	2.33	0.46
26:DA:476:G:H4'	26:DA:502:A:N1	2.31	0.46
28:DD:242:ARG:N	28:DD:242:ARG:HD3	2.31	0.46
28:DD:5:LYS:HE3	28:DD:5:LYS:HB3	1.66	0.46
36:DP:121:LYS:HD2	36:DP:123:LEU:HG	1.97	0.46
39:DS:62:LYS:HA	39:DS:65:VAL:HB	1.98	0.46
1:AA:99:U:H2'	1:AA:100:C:C6	2.50	0.46
18:AR:32:ARG:HA	18:AR:69:THR:HG21	1.97	0.46
23:AW:2:C:H2'	23:AW:3:C:H6	1.81	0.46
48:B1:3:LYS:HB2	48:B1:61:ARG:HH12	1.81	0.46
26:BA:1067:A:H3'	26:BA:1067:A:H8	1.79	0.46
26:BA:1466:U:HO2'	26:BA:1467:G:P	2.38	0.46
26:BA:926:G:O5'	26:BA:926:G:H8	1.98	0.46
31:BG:163:ALA:HB1	31:BG:168:GLU:HB2	1.98	0.46
38:BR:36:THR:HG22	38:BR:37:THR:H	1.81	0.46
46:BZ:70:LEU:HG	46:BZ:91:LEU:HD21	1.98	0.46
1:CA:337:C:H2'	1:CA:338:A:H8	1.81	0.46
2:CB:122:PHE:HA	2:CB:127:ILE:HD12	1.98	0.46
5:CE:41:VAL:O	5:CE:66:MET:HA	2.15	0.46
10:CJ:7:LYS:HA	10:CJ:71:LEU:HD12	1.98	0.46
1:CA:1310:G:P	13:CM:88:ARG:HH22	2.39	0.46
26:DA:330:A:H2	26:DA:1210:A:H2'	1.80	0.46
26:DA:1366:A:H2'	26:DA:1367:A:O4'	2.16	0.46
26:DA:2191:G:H2'	26:DA:2192:G:O4'	2.16	0.46
26:DA:27:G:N2	26:DA:512:G:H1'	2.31	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2846:G:H2'	26:DA:2847:U:O4'	2.15	0.46
26:DA:855:G:H2'	26:DA:856:C:C6	2.51	0.46
26:DA:863:A:H2'	26:DA:864:G:C8	2.51	0.46
27:DB:14:U:O3'	27:DB:108:U:O2'	2.33	0.46
29:DE:143:ASN:HD22	29:DE:147:PRO:HD3	1.80	0.46
39:DS:35:ILE:HD12	39:DS:101:LEU:HD12	1.98	0.46
40:DT:6:LEU:HA	40:DT:6:LEU:HD12	1.80	0.46
44:DX:94:GLY:N	44:DX:95:LEU:HA	2.30	0.46
1:AA:198:G:H2'	1:AA:199:G:H8	1.81	0.45
1:AA:373:A:H2'	1:AA:374:A:H8	1.80	0.45
1:AA:864:A:H2'	1:AA:865:A:C8	2.51	0.45
1:AA:134:A:N1	16:AP:25:ARG:NH1	2.65	0.45
21:AU:18:TYR:CD1	21:AU:24:ARG:HG2	2.51	0.45
26:BA:1001:G:OP2	37:BQ:87:LYS:NZ	2.42	0.45
26:BA:1845:G:H4'	28:BD:51:VAL:HG21	1.99	0.45
26:BA:2096:U:H2'	26:BA:2097:U:C6	2.51	0.45
26:BA:2136:A:H2'	26:BA:2137:G:O4'	2.16	0.45
28:BD:68:LYS:O	28:BD:69:ARG:HB2	2.16	0.45
33:BI:61:ARG:HD2	33:BI:61:ARG:N	2.31	0.45
34:BN:4:TYR:HB2	41:BU:101:ARG:HH12	1.81	0.45
1:CA:1126:U:C4'	1:CA:1281:U:H1'	2.45	0.45
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.15	0.45
2:CB:112:VAL:O	2:CB:115:LEU:HD23	2.17	0.45
1:CA:532:A:N6	3:CC:193:TYR:HB3	2.25	0.45
3:CC:50:ALA:HB1	3:CC:70:VAL:HG21	1.98	0.45
1:CA:427:U:P	4:CD:13:ARG:HH22	2.39	0.45
5:CE:110:LEU:HD13	5:CE:118:ILE:HD13	1.97	0.45
10:CJ:5:ARG:N	10:CJ:72:VAL:O	2.48	0.45
11:CK:20:TYR:CZ	11:CK:83:ILE:HD12	2.51	0.45
19:CS:22:LEU:O	19:CS:27:GLU:HG3	2.16	0.45
25:CY:33:U:H2'	25:CY:35:A:OP2	2.16	0.45
50:D3:5:LYS:HB3	50:D3:57:GLU:HG2	1.98	0.45
26:DA:1913:A:H4'	26:DA:1914:C:C5'	2.45	0.45
26:DA:2378:A:H8	26:DA:2378:A:O5'	1.98	0.45
26:DA:2507:C:H5''	26:DA:2573:C:N4	2.31	0.45
26:DA:992:C:OP1	42:DV:74:LYS:NZ	2.33	0.45
29:DE:47:VAL:HG11	29:DE:86:PRO:HD2	1.98	0.45
40:DT:42:ILE:HG12	40:DT:84:GLN:NE2	2.31	0.45
1:AA:1039:C:H2'	1:AA:1040:U:C6	2.51	0.45
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.46	0.45
1:AA:166:G:H2'	1:AA:167:G:H8	1.79	0.45
1:AA:236:G:H5''	17:AQ:42:TYR:OH	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:AM:68:GLY:HA3	31:BG:116:ASP:OD1	2.16	0.45
13:AM:3:ARG:HG2	13:AM:8:GLU:HA	1.98	0.45
1:AA:323:U:H5'	20:AT:23:ARG:HB2	1.98	0.45
25:AY:48:C:OP1	25:AY:48:C:H2'	2.16	0.45
55:B8:6:THR:HG22	55:B8:62:LEU:HA	1.98	0.45
26:BA:2745:G:H3'	26:BA:2746:A:O4'	2.17	0.45
26:BA:2804:C:H2'	26:BA:2805:G:H8	1.81	0.45
26:BA:787:U:H2'	26:BA:788:G:C8	2.51	0.45
26:BA:932:C:H3'	26:BA:933:C:C5'	2.44	0.45
33:BI:130:TYR:HB3	33:BI:138:ILE:HB	1.98	0.45
1:CA:1008:C:H2'	1:CA:1009:G:O4'	2.16	0.45
1:CA:1096:C:H2'	1:CA:1097:C:H6	1.81	0.45
1:CA:1315:U:H2'	1:CA:1316:G:O4'	2.16	0.45
1:CA:696:A:H8	1:CA:696:A:O5'	1.99	0.45
1:CA:727:G:P	1:CA:742:G:H21	2.39	0.45
6:CF:87:ARG:CB	6:CF:87:ARG:HH11	2.29	0.45
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.98	0.45
26:DA:2167:U:H2'	26:DA:2167:U:O2	2.15	0.45
26:DA:288:C:H2'	26:DA:289:A:H8	1.80	0.45
26:DA:597:U:H2'	26:DA:598:G:C8	2.51	0.45
26:DA:921:G:C6	26:DA:922:U:C4	3.04	0.45
34:DN:39:ARG:HA	34:DN:40:PRO:HD3	1.88	0.45
35:DO:103:ALA:HB1	35:DO:105:GLU:OE1	2.16	0.45
29:DE:27:LEU:HD22	40:DT:1:MET:CE	2.46	0.45
1:AA:1038:C:O2'	1:AA:1039:C:H5'	2.17	0.45
1:AA:11:G:O2'	1:AA:506:G:N2	2.46	0.45
2:AB:20:GLU:HA	2:AB:21:ARG:NH2	2.30	0.45
2:AB:222:ILE:O	2:AB:226:ARG:HG2	2.16	0.45
4:AD:187:ARG:HB3	4:AD:187:ARG:HE	1.53	0.45
8:AH:51:VAL:HG21	8:AH:60:ARG:HB2	1.98	0.45
25:AY:2:C:N4	25:AY:71:G:H1	2.14	0.45
26:BA:1312:G:O5'	43:BW:15:ARG:NH2	2.49	0.45
26:BA:139:A:H8	26:BA:1454:C:O2'	1.99	0.45
26:BA:2202:U:H2'	26:BA:2203:G:O4'	2.17	0.45
26:BA:2760:G:O6	26:BA:2768:C:H5''	2.16	0.45
30:BF:64:ILE:HG21	30:BF:78:ILE:HG23	1.96	0.45
26:BA:2032:G:H5''	43:BW:42:ARG:HB2	1.97	0.45
1:CA:67:C:O2'	1:CA:171:A:N3	2.37	0.45
1:CA:456:C:C2'	1:CA:457:C:H5'	2.46	0.45
1:CA:620:C:H2'	1:CA:621:A:O4'	2.17	0.45
9:CI:45:ALA:O	9:CI:48:GLU:HB2	2.16	0.45
13:CM:3:ARG:HA	51:D4:34:GLU:HG2	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:CS:63:THR:O	19:CS:66:MET:HG3	2.16	0.45
23:CW:22:G:C2	23:CW:23:A:C5	3.04	0.45
25:CY:10:G:N2	25:CY:25:C:N3	2.54	0.45
25:CY:35:A:H8	25:CY:35:A:O5'	1.98	0.45
26:DA:1213:A:N3	26:DA:1238:G:O2'	2.46	0.45
26:DA:1417:C:H3'	61:DA:4108:HOH:O	2.16	0.45
26:DA:2149:G:H5''	26:DA:2150:U:OP2	2.17	0.45
26:DA:2543:G:H2'	26:DA:2544:G:C8	2.51	0.45
26:DA:271(H):G:O2'	26:DA:271(I):G:H8	2.00	0.45
29:DE:144:ARG:HB3	29:DE:145:LYS:H	1.53	0.45
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.80	0.45
1:AA:163:C:H2'	1:AA:164:U:C6	2.51	0.45
1:AA:189(D):C:O2	1:AA:189(H):G:C6	2.69	0.45
1:AA:735:C:H2'	1:AA:736:C:C6	2.52	0.45
1:AA:1055:A:H2'	3:AC:156:ARG:HD2	1.99	0.45
3:AC:71:ALA:HB2	3:AC:115:LEU:HD21	1.97	0.45
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.85	0.45
8:AH:49:GLU:OE2	8:AH:62:TYR:OH	2.26	0.45
10:AJ:8:LEU:HD21	10:AJ:96:ILE:HG23	1.98	0.45
13:AM:113:PRO:O	13:AM:115:LYS:NZ	2.50	0.45
51:B4:41:PRO:HA	51:B4:47:GLN:HB3	1.98	0.45
53:B6:40:CYS:HA	53:B6:41:PRO:HD3	1.80	0.45
26:BA:2121:U:H2'	26:BA:2122:G:C8	2.51	0.45
26:BA:2352:G:H2'	26:BA:2353:G:H8	1.81	0.45
35:BO:98:VAL:HG13	35:BO:117:LEU:HB3	1.97	0.45
41:BU:76:TYR:CE1	41:BU:80:ILE:HG13	2.52	0.45
43:BW:88:ARG:HD2	43:BW:88:ARG:HA	1.76	0.45
1:CA:1009:G:C2	1:CA:1010:G:C4	3.04	0.45
1:CA:1062:U:H2'	1:CA:1063:C:C5	2.51	0.45
1:CA:652:U:O4	1:CA:752:G:O2'	2.21	0.45
1:CA:859:A:H2'	1:CA:860:A:O4'	2.16	0.45
11:CK:34:ASP:OD2	11:CK:38:ASN:HB2	2.16	0.45
12:CL:37:CYS:SG	12:CL:81:SER:HB2	2.56	0.45
1:CA:110:C:O2'	16:CP:25:ARG:O	2.27	0.45
49:D2:62:THR:O	49:D2:66:GLU:HG3	2.16	0.45
51:D4:62:ARG:HB2	51:D4:63:TYR:CE1	2.51	0.45
56:D9:3:VAL:HA	56:D9:35:ARG:O	2.17	0.45
26:DA:1654:A:OP1	38:DR:1:MET:HA	2.15	0.45
26:DA:2659:G:O2'	26:DA:2661:G:N7	2.38	0.45
26:DA:536:A:H2'	26:DA:537:C:C6	2.51	0.45
28:DD:218:ARG:HB3	28:DD:219:PRO:HD2	1.99	0.45
31:DG:66:GLN:HE21	31:DG:92:VAL:HG23	1.82	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
40:DT:51:ARG:HG3	40:DT:98:LYS:NZ	2.32	0.45
26:DA:996:A:H4'	41:DU:91:ASP:OD2	2.16	0.45
46:DZ:23:LYS:NZ	46:DZ:40:ASP:OD1	2.48	0.45
46:DZ:43:GLU:O	46:DZ:47:VAL:N	2.50	0.45
1:AA:161:A:H2'	1:AA:162:A:C8	2.52	0.45
1:AA:811:C:O2'	1:AA:901:A:N1	2.43	0.45
8:AH:29:SER:OG	8:AH:32:LYS:HG3	2.17	0.45
17:AQ:78:GLU:HG2	17:AQ:79:SER:H	1.81	0.45
24:AX:4:G:H1	24:AX:69:C:H42	1.64	0.45
26:BA:1091:A:H1'	26:BA:1093:G:C2	2.51	0.45
26:BA:2213:G:C8	26:BA:2213:G:H5'	2.50	0.45
26:BA:605:G:H2'	26:BA:606:G:C8	2.52	0.45
28:BD:24:ILE:HD13	28:BD:84:TYR:HB2	1.99	0.45
43:BW:18:ARG:NH1	43:BW:76:VAL:O	2.50	0.45
1:CA:1347:G:O2'	1:CA:1373:G:N1	2.47	0.45
1:CA:399:G:H2'	1:CA:400:C:C6	2.51	0.45
1:CA:920:U:H2'	1:CA:921:U:H6	1.80	0.45
12:CL:8:ASN:O	12:CL:12:ARG:HG3	2.16	0.45
24:CX:22:G:H8	24:CX:22:G:OP2	2.00	0.45
25:CY:36:A:H2'	25:CY:37:MIA:O4'	2.16	0.45
26:DA:1667:G:O2'	26:DA:1991:U:O4	2.31	0.45
26:DA:2153:G:H3'	26:DA:2154:G:C8	2.51	0.45
26:DA:527:C:H4'	26:DA:528:A:O5'	2.15	0.45
26:DA:652:C:C2'	26:DA:652(A):A:H5'	2.46	0.45
26:DA:71:A:H5''	26:DA:73:A:C8	2.51	0.45
30:DF:12:LEU:HB2	30:DF:124:LEU:HD11	1.97	0.45
31:DG:106:LEU:HA	31:DG:110:ALA:CB	2.45	0.45
33:DI:69:LYS:HG3	33:DI:73:GLU:OE1	2.16	0.45
38:DR:70:LEU:HD13	38:DR:75:LEU:HD13	1.98	0.45
42:DV:89:GLN:HA	42:DV:90:PRO:HD3	1.83	0.45
1:AA:175:C:H2'	1:AA:176:C:H6	1.80	0.45
1:AA:17:U:H2'	1:AA:18:C:C6	2.52	0.45
1:AA:850:U:H2'	1:AA:851:G:H5''	1.98	0.45
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.97	0.45
23:AW:9:A:O2'	23:AW:10:G:N7	2.49	0.45
26:BA:27:G:N2	26:BA:537:G:H1'	2.32	0.45
26:BA:2814:C:H2'	26:BA:2815:C:C6	2.51	0.45
26:BA:794:U:O2	26:BA:2036:A:H1'	2.17	0.45
26:BA:8:A:H2'	26:BA:9:U:C6	2.52	0.45
46:BZ:146:ILE:HA	46:BZ:147:GLY:HA2	1.70	0.45
1:CA:1121:U:C4	1:CA:1122:U:C5	3.05	0.45
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.80	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1320:C:H2'	1:CA:1321:C:O4'	2.17	0.45
1:CA:1385:G:H2'	1:CA:1386:G:C8	2.51	0.45
1:CA:429:U:O3'	4:CD:22:LYS:NZ	2.45	0.45
9:CI:9:ARG:HA	9:CI:13:ALA:O	2.17	0.45
13:CM:57:ARG:O	13:CM:61:GLU:HB2	2.17	0.45
14:CN:32:SER:OG	14:CN:32:SER:O	2.28	0.45
21:CU:12:LYS:HZ2	21:CU:19:GLY:HA3	1.81	0.45
52:D5:40:LYS:NZ	52:D5:44:THR:O	2.34	0.45
52:D5:49:CYS:SG	52:D5:51:TYR:HB2	2.57	0.45
54:D7:5:TRP:CD1	54:D7:7:PRO:HD3	2.50	0.45
26:DA:1527:G:H5''	26:DA:1528:A:OP1	2.16	0.45
26:DA:1876:A:H2'	26:DA:1877:A:C8	2.52	0.45
26:DA:2120:G:O6	26:DA:2178:C:N3	2.49	0.45
26:DA:2207:G:H8	26:DA:2207:G:P	2.40	0.45
26:DA:2468:G:C4	26:DA:2481:G:C2	3.05	0.45
26:DA:784:A:N6	28:DD:229:VAL:HG11	2.31	0.45
28:DD:141:VAL:HG12	28:DD:164:GLN:HG3	1.99	0.45
29:DE:54:GLN:HB2	29:DE:76:ARG:HG2	1.98	0.45
26:DA:2494:G:O2'	37:DQ:80:GLU:HA	2.16	0.45
40:DT:11:GLU:O	40:DT:15:VAL:HG23	2.16	0.45
42:DV:12:TYR:CG	42:DV:20:LEU:HD21	2.52	0.45
44:DX:44:GLU:OE2	44:DX:51:VAL:N	2.45	0.45
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.17	0.45
1:AA:445:G:H2'	1:AA:446:G:C8	2.52	0.45
1:AA:688:G:H2'	1:AA:689:C:C6	2.52	0.45
2:AB:19:HIS:CD2	2:AB:206:ASP:HB2	2.52	0.45
2:AB:48:MET:HA	2:AB:51:LEU:HD12	1.97	0.45
1:AA:407:G:O2'	4:AD:116:GLN:HG3	2.17	0.45
4:AD:144:ASP:N	4:AD:144:ASP:OD1	2.49	0.45
1:AA:881:G:P	12:AL:12:ARG:HH22	2.40	0.45
1:AA:375:U:O2'	16:AP:6:LEU:O	2.32	0.45
24:AX:4:G:H2'	24:AX:5:G:C8	2.52	0.45
26:BA:1410:G:OP2	48:B1:3:LYS:HG3	2.17	0.45
26:BA:1476:C:H2'	26:BA:1477:U:C6	2.51	0.45
26:BA:1639:G:H2'	26:BA:1640:G:C8	2.52	0.45
26:BA:432:U:O5'	26:BA:432:U:H6	1.99	0.45
26:BA:615:G:O6	61:BA:4916:HOH:O	2.15	0.45
30:BF:125:LEU:HD12	30:BF:194:MET:HB2	1.98	0.45
1:CA:1036:G:N7	1:CA:1037:C:C2	2.85	0.45
1:CA:411:A:OP1	4:CD:30:LYS:HD3	2.16	0.45
1:CA:419:C:OP1	1:CA:513:C:O2'	2.25	0.45
1:CA:660:G:H1	1:CA:745:C:N4	2.12	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:985:C:N4	1:CA:1220:G:N1	2.29	0.45
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.99	0.45
23:CW:10:G:N2	23:CW:11:C:C2	2.84	0.45
24:CX:5:G:H2'	24:CX:6:G:H5'	1.99	0.45
25:CY:71:G:H4'	26:DA:1851:U:H4'	1.99	0.45
26:DA:620:G:H5'	26:DA:620:G:N3	2.31	0.45
26:DA:848:G:C2	26:DA:933:A:H1'	2.52	0.45
32:DH:95:ARG:HG2	32:DH:96:ALA:N	2.32	0.45
44:DX:31:HIS:CD2	44:DX:33:LYS:HB2	2.52	0.45
45:DY:90:LEU:HD11	45:DY:96:ILE:HG23	1.98	0.45
46:DZ:158:PRO:HA	46:DZ:159:PRO:HD3	1.71	0.45
1:AA:1290:G:H2'	1:AA:1291:G:H8	1.82	0.45
1:AA:217:C:C2'	1:AA:218:C:H5'	2.46	0.45
3:AC:8:ILE:HG23	3:AC:16:ARG:HG2	1.98	0.45
48:B1:3:LYS:HB3	48:B1:4:VAL:H	1.50	0.45
26:BA:94:G:O2'	49:B2:48:HIS:ND1	2.38	0.45
55:B8:33:ASN:HA	55:B8:36:LYS:HD2	1.99	0.45
26:BA:2190:G:O6	26:BA:2193:A:H2'	2.16	0.45
26:BA:2221:A:OP2	26:BA:2222:C:H5	1.99	0.45
26:BA:2324:U:OP1	31:BG:73:ALA:HA	2.17	0.45
26:BA:2652:G:OP1	34:BN:97:ARG:NH2	2.49	0.45
26:BA:722:A:C8	26:BA:851:A:C6	3.05	0.45
28:BD:70:TRP:CE2	28:BD:150:LYS:HD3	2.52	0.45
28:BD:232:PRO:O	61:BD:3103:HOH:O	2.21	0.45
29:BE:31:CYS:HA	29:BE:32:PRO:HD2	1.89	0.45
30:BF:150:GLY:HA2	30:BF:172:TRP:CE3	2.52	0.45
34:BN:68:GLU:H	34:BN:68:GLU:HG2	1.46	0.45
26:BA:2033:U:OP1	43:BW:42:ARG:HD3	2.17	0.45
1:CA:1035:A:H2'	1:CA:1036:G:H8	1.82	0.45
1:CA:1490:C:H2'	1:CA:1491:G:O4'	2.17	0.45
1:CA:826:C:H2'	1:CA:827:U:C6	2.51	0.45
2:CB:70:PHE:HB2	2:CB:92:TYR:CB	2.47	0.45
1:CA:1205:U:H4'	3:CC:195:VAL:HG23	1.98	0.45
4:CD:8:VAL:O	4:CD:11:LEU:HB2	2.17	0.45
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.17	0.45
9:CI:17:VAL:HG11	9:CI:80:GLY:C	2.37	0.45
48:D1:83:GLU:HA	48:D1:84:GLY:HA2	1.70	0.45
51:D4:40:HIS:O	51:D4:44:THR:N	2.24	0.45
52:D5:33:CYS:HA	52:D5:34:PRO:HD3	1.85	0.45
26:DA:2138:C:N4	26:DA:2153:G:N1	2.32	0.45
26:DA:2328:A:H2'	26:DA:2329:G:C8	2.52	0.45
26:DA:2461:C:H2'	26:DA:2462:U:C6	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:271(K):U:O2	33:DI:50:ARG:HG3	2.17	0.45
27:DB:34:U:O4	27:DB:44:G:O2'	2.29	0.45
28:DD:171:ASP:O	28:DD:187:GLY:N	2.49	0.45
32:DH:148:ILE:HG12	32:DH:148:ILE:H	1.54	0.45
1:AA:678:U:H2'	1:AA:679:C:C6	2.52	0.45
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.52	0.45
3:AC:108:ASN:HB3	3:AC:111:LEU:HD12	1.99	0.45
3:AC:121:ALA:HB1	3:AC:189:ALA:HB2	1.99	0.45
3:AC:156:ARG:HE	3:AC:156:ARG:HB3	1.50	0.45
26:BA:125:A:H5''	26:BA:126:C:C6	2.52	0.45
26:BA:1547:C:O4'	28:BD:100:GLY:HA2	2.17	0.45
28:BD:52:ARG:NH2	61:BD:3112:HOH:O	2.42	0.45
26:BA:234:G:O5'	36:BP:73:GLY:HA2	2.16	0.45
1:CA:1253:G:H2'	1:CA:1254:C:C6	2.52	0.45
1:CA:376:G:O2'	16:CP:5:ARG:NH2	2.50	0.45
1:CA:6:G:H4'	1:CA:298:A:H4'	1.98	0.45
1:CA:982:U:H4'	1:CA:983:A:O5'	2.17	0.45
3:CC:40:ARG:NH1	3:CC:57:ILE:HD13	2.32	0.45
9:CI:81:ILE:O	9:CI:85:LEU:HG	2.17	0.45
19:CS:30:LEU:HA	19:CS:48:THR:O	2.16	0.45
24:CX:10:G:N2	24:CX:26:G:H1'	2.31	0.45
26:DA:1165:U:H2'	26:DA:1166:C:C6	2.51	0.45
26:DA:1287:A:C5	26:DA:1288:U:C4	3.05	0.45
26:DA:2263:C:H2'	26:DA:2264:C:O4'	2.17	0.45
26:DA:2365:G:P	47:D0:55:ARG:HG2	2.57	0.45
26:DA:2683:C:O2	35:DO:70:LYS:NZ	2.44	0.45
26:DA:2872:G:C2	26:DA:2873:A:N6	2.85	0.45
26:DA:34:C:H2'	26:DA:34:C:O2	2.17	0.45
26:DA:862:G:H2'	26:DA:863:A:O4'	2.16	0.45
29:DE:24:THR:HG22	29:DE:184:VAL:HG12	1.98	0.45
30:DF:156:LEU:HD21	30:DF:163:VAL:HG12	1.98	0.45
31:DG:171:ALA:O	31:DG:175:LEU:N	2.37	0.45
33:DI:141:LYS:HZ2	33:DI:141:LYS:HB2	1.82	0.45
26:DA:297:C:OP1	45:DY:87:LYS:HG3	2.17	0.45
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.05	0.45
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.17	0.45
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.99	0.45
13:AM:108:ARG:HD3	13:AM:108:ARG:HA	1.66	0.45
13:AM:15:VAL:O	13:AM:19:LEU:HD22	2.17	0.45
20:AT:9:ASN:ND2	20:AT:10:LEU:H	2.15	0.45
25:AY:13:C:H2'	25:AY:14:A:H8	1.82	0.45
37:BQ:85:LYS:HG2	47:B0:7:LEU:HB3	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
48:B1:67:ILE:N	48:B1:68:PRO:HD2	2.31	0.45
26:BA:11:G:H2'	26:BA:12:U:H5''	1.98	0.45
26:BA:2102:G:OP1	48:B1:35:THR:HG21	2.17	0.45
26:BA:2258:G:H2'	26:BA:2259:A:C8	2.52	0.45
26:BA:597:C:N3	29:BE:145:LYS:NZ	2.51	0.45
28:BD:20:ASP:OD2	28:BD:22:SER:HB2	2.17	0.45
30:BF:184:TYR:CE2	30:BF:188:ARG:HD2	2.52	0.45
31:BG:150:ASP:OD1	31:BG:150:ASP:N	2.46	0.45
26:BA:610:C:P	36:BP:21:ARG:HH22	2.40	0.45
1:CA:1206:G:C6	1:CA:1207:G:C5	3.05	0.45
1:CA:502:G:C2	1:CA:503:C:C2	3.05	0.45
1:CA:25:C:H5'	1:CA:524:G:H1'	1.98	0.45
1:CA:65:U:H5'	1:CA:65:U:H6	1.81	0.45
2:CB:71:VAL:HG23	2:CB:71:VAL:O	2.17	0.45
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.52	0.45
17:CQ:63:ARG:HG2	17:CQ:64:PRO:HD2	1.99	0.45
23:CW:38:A:H5'	26:DA:1913:A:N6	2.32	0.45
53:D6:23:THR:OG1	53:D6:24:GLU:N	2.48	0.45
26:DA:1031:G:H21	56:D9:36:GLN:HE22	1.63	0.45
26:DA:1427:A:H4'	26:DA:1428:C:O5'	2.17	0.45
26:DA:1588:C:H2'	26:DA:1589:C:H6	1.82	0.45
26:DA:1131:G:O6	26:DA:2040:C:H1'	2.17	0.45
27:DB:73:A:C4	27:DB:105:A:C2	3.04	0.45
31:DG:166:ASP:O	31:DG:170:ARG:N	2.46	0.45
41:DU:85:LYS:HB2	41:DU:116:ALA:HB1	1.99	0.45
43:DW:2:GLU:OE2	43:DW:72:LYS:HE2	2.17	0.45
44:DX:31:HIS:HA	44:DX:32:PRO:HD3	1.87	0.45
1:AA:1161:C:O2'	1:AA:1162:C:H5'	2.18	0.44
1:AA:345:C:O5'	1:AA:345:C:H6	2.00	0.44
6:AF:55:ASP:HA	6:AF:56:PRO:HD3	1.84	0.44
14:AN:14:PRO:HG2	14:AN:20:ALA:HB2	1.98	0.44
1:AA:750:G:H1'	15:AO:22:THR:HG23	1.99	0.44
18:AR:59:SER:OG	18:AR:62:GLU:HG2	2.18	0.44
19:AS:36:ARG:NH1	19:AS:52:TYR:O	2.48	0.44
23:AW:61:C:H2'	23:AW:62:C:H6	1.82	0.44
23:AW:4:C:N3	23:AW:69:G:O6	2.50	0.44
51:B4:48:ARG:HB3	51:B4:51:ASP:O	2.17	0.44
26:BA:864:C:H4'	26:BA:977:G:C5	2.52	0.44
36:BP:65:ARG:HG3	55:B8:25:MET:CG	2.46	0.44
38:BR:53:HIS:O	38:BR:56:LYS:HB2	2.18	0.44
1:CA:1084:G:C5	1:CA:1085:U:C4	3.05	0.44
1:CA:1120:G:N1	1:CA:1154:G:N3	2.65	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1258:G:O2'	1:CA:1259:C:H5'	2.17	0.44
1:CA:154:C:H2'	1:CA:155:C:C6	2.52	0.44
1:CA:382:A:H2'	1:CA:383:A:C8	2.52	0.44
1:CA:606:G:H5''	1:CA:607:A:H5'	1.99	0.44
1:CA:986:A:H2'	1:CA:987:G:O4'	2.17	0.44
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.51	0.44
7:CG:155:ARG:HG2	7:CG:156:TRP:N	2.32	0.44
1:CA:1015:A:H4'	14:CN:15:LYS:NZ	2.33	0.44
23:CW:47:U:O2'	23:CW:48:C:OP1	2.29	0.44
26:DA:1913:A:H4'	26:DA:1914:C:H5''	1.98	0.44
26:DA:2356:C:O3'	47:D0:20:ARG:HD3	2.17	0.44
26:DA:2727:G:O2'	35:DO:70:LYS:NZ	2.51	0.44
26:DA:751:A:H5'	43:DW:90:ARG:HA	1.98	0.44
26:DA:971:C:H2'	26:DA:972:G:O4'	2.17	0.44
31:DG:152:LEU:HD12	31:DG:152:LEU:H	1.82	0.44
32:DH:13:LYS:HA	32:DH:14:GLY:HA2	1.55	0.44
36:DP:95:VAL:HG13	36:DP:125:VAL:HG12	1.98	0.44
41:DU:76:TYR:HH	41:DU:92:ARG:NH1	2.12	0.44
43:DW:17:VAL:HG11	43:DW:103:ILE:HD11	1.98	0.44
45:DY:3:VAL:HB	45:DY:32:PRO:HB3	2.00	0.44
1:AA:100:C:H2'	1:AA:101:A:C8	2.52	0.44
1:AA:1027:C:H2'	1:AA:1028:C:C6	2.52	0.44
1:AA:114:U:H1'	1:AA:353:A:H1'	1.99	0.44
1:AA:431:A:H2'	1:AA:432:A:O4'	2.18	0.44
4:AD:112:VAL:HG23	4:AD:116:GLN:OE1	2.16	0.44
8:AH:56:LYS:HB2	8:AH:58:TYR:HE1	1.81	0.44
9:AI:102:LEU:HD22	9:AI:102:LEU:HA	1.85	0.44
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.51	0.44
17:AQ:92:ARG:HD2	17:AQ:92:ARG:HA	1.92	0.44
19:AS:9:VAL:HG21	51:B4:61:ARG:HH12	1.82	0.44
25:AY:6:G:C6	25:AY:7:A:C5	3.05	0.44
26:BA:399:G:H8	48:B1:65:SER:O	2.00	0.44
26:BA:1016:C:O2'	26:BA:1029:A:N3	2.40	0.44
26:BA:1825:U:H2'	26:BA:1826:C:H6	1.81	0.44
26:BA:2152:U:H2'	26:BA:2153:G:H21	1.82	0.44
26:BA:2272:C:H2'	26:BA:2273:C:H6	1.82	0.44
26:BA:733:G:H8	54:B7:6:GLN:O	2.00	0.44
27:BB:91:C:OP1	37:BQ:16:ARG:HG3	2.18	0.44
29:BE:149:ARG:O	61:BE:406:HOH:O	2.21	0.44
30:BF:8:GLN:HA	30:BF:8:GLN:NE2	2.32	0.44
32:BH:13:LYS:HA	32:BH:14:GLY:HA2	1.58	0.44
39:BS:27:SER:HA	39:BS:88:ASP:HB3	1.98	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:683:G:H2'	1:CA:684:A:H8	1.81	0.44
1:CA:848:C:O5'	1:CA:848:C:H6	2.00	0.44
2:CB:162:ILE:HG13	2:CB:162:ILE:O	2.15	0.44
2:CB:167:PRO:HG3	2:CB:188:ALA:HB2	1.98	0.44
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.98	0.44
3:CC:85:ARG:O	3:CC:89:GLU:HG3	2.17	0.44
9:CI:16:ARG:HB2	9:CI:64:THR:HG23	1.99	0.44
12:CL:6:THR:HG23	12:CL:9:GLN:OE1	2.17	0.44
16:CP:40:ASP:O	16:CP:48:TRP:HB2	2.18	0.44
6:CF:100:ASN:HD21	18:CR:23:LYS:HG2	1.83	0.44
26:DA:1021:A:C8	26:DA:1021:A:H3'	2.52	0.44
26:DA:1127:A:N7	26:DA:2488:A:O2'	2.50	0.44
26:DA:1583:A:H4'	26:DA:1586:A:C4	2.52	0.44
26:DA:921:G:H4'	26:DA:2269:A:C5	2.51	0.44
26:DA:774:A:N3	26:DA:774:A:H2'	2.33	0.44
26:DA:776:G:H4'	26:DA:777:A:O5'	2.17	0.44
33:DI:77:LEU:HD11	33:DI:97:ILE:HG23	1.99	0.44
34:DN:73:THR:OG1	34:DN:82:LEU:HD11	2.16	0.44
35:DO:76:ALA:HB3	40:DT:75:ILE:HB	1.99	0.44
46:DZ:79:ARG:HD2	46:DZ:80:ARG:NH2	2.32	0.44
1:AA:110:C:H2'	1:AA:111:G:O4'	2.18	0.44
2:AB:219:VAL:O	2:AB:223:ILE:HG12	2.16	0.44
2:AB:223:ILE:HD12	2:AB:230:VAL:HG12	2.00	0.44
4:AD:18:LYS:HD2	4:AD:31:CYS:SG	2.57	0.44
24:AX:46:G:H5''	24:AX:47:U:OP2	2.16	0.44
26:BA:215:G:N2	26:BA:217:A:H62	2.15	0.44
26:BA:2803:A:N3	26:BA:2803:A:H2'	2.31	0.44
26:BA:843:C:H2'	26:BA:844:C:C6	2.52	0.44
30:BF:165:ARG:HG2	30:BF:168:ARG:HH21	1.82	0.44
31:BG:43:LEU:HD12	31:BG:43:LEU:HA	1.81	0.44
32:BH:124:GLU:OE1	32:BH:132:ARG:HD2	2.18	0.44
33:BI:75:LEU:HD22	33:BI:105:HIS:ND1	2.31	0.44
39:BS:6:ALA:O	39:BS:10:ARG:HB2	2.17	0.44
1:CA:1001(A):G:H5''	1:CA:1002:G:OP2	2.17	0.44
1:CA:1131:G:H2'	1:CA:1132:C:H6	1.82	0.44
1:CA:1132:C:H2'	1:CA:1133:G:H8	1.83	0.44
1:CA:1239:A:H4'	1:CA:1240:U:H5''	1.98	0.44
1:CA:437:U:O2'	4:CD:125:HIS:HE1	1.99	0.44
1:CA:543:C:O2'	1:CA:544:G:H5'	2.17	0.44
1:CA:715:A:H5''	1:CA:805:C:H1'	1.99	0.44
1:CA:743:U:H2'	1:CA:744:C:C6	2.52	0.44
11:CK:66:LEU:O	11:CK:70:LYS:HD2	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:CN:40:CYS:O	14:CN:44:LEU:HB3	2.18	0.44
14:CN:45:ARG:O	14:CN:49:HIS:HD2	1.99	0.44
19:CS:33:THR:HG22	19:CS:50:ALA:O	2.17	0.44
25:CY:51:U:N3	25:CY:63:G:N1	2.41	0.44
25:CY:67:C:H2'	25:CY:68:C:C6	2.52	0.44
26:DA:1030:G:OP2	37:DQ:128:LYS:HD3	2.17	0.44
26:DA:2355:C:H4'	47:D0:24:LYS:HD3	1.99	0.44
26:DA:2441:C:OP2	26:DA:2586:C:O2'	2.31	0.44
26:DA:2849:U:H4'	26:DA:2868:A:C2	2.51	0.44
26:DA:752:A:H4'	26:DA:753:C:H5'	1.99	0.44
26:DA:902:C:H2'	26:DA:903:C:H6	1.82	0.44
27:DB:45:A:H2'	27:DB:46:A:H8	1.82	0.44
28:DD:96:HIS:CD2	28:DD:102:LYS:HG2	2.53	0.44
31:DG:3:LEU:HD23	31:DG:3:LEU:H	1.81	0.44
36:DP:37:GLY:O	36:DP:40:SER:OG	2.22	0.44
37:DQ:29:PHE:HB2	37:DQ:105:GLU:OE2	2.18	0.44
37:DQ:134:ARG:CZ	46:DZ:122:ARG:HE	2.30	0.44
1:AA:1057:G:H2'	1:AA:1058:G:O4'	2.17	0.44
1:AA:1131:G:H2'	1:AA:1132:C:H6	1.83	0.44
1:AA:217:C:O2'	1:AA:218:C:H5'	2.17	0.44
1:AA:21:G:H2'	1:AA:22:G:C8	2.53	0.44
1:AA:435:C:H6	1:AA:435:C:O5'	2.01	0.44
5:AE:27:ARG:HB2	5:AE:27:ARG:HE	1.53	0.44
10:AJ:33:GLN:O	10:AJ:75:ILE:N	2.44	0.44
17:AQ:60:ILE:O	17:AQ:62:SER:OG	2.34	0.44
26:BA:1055:A:OP2	34:BN:37:LYS:NZ	2.50	0.44
26:BA:1223:C:O5'	26:BA:1223:C:H6	2.00	0.44
27:BB:91:C:OP2	37:BQ:16:ARG:NH1	2.51	0.44
33:BI:38:LEU:H	33:BI:38:LEU:CD1	2.23	0.44
1:CA:1016:A:O2'	1:CA:1217:C:O2'	2.14	0.44
1:CA:1004:A:C2	1:CA:1038:C:C4	3.05	0.44
1:CA:1085:U:H3'	1:CA:1086:U:C5	2.52	0.44
1:CA:1134:G:C6	1:CA:1135:U:C2	3.05	0.44
1:CA:994:A:C5	1:CA:1216:G:H4'	2.53	0.44
1:CA:814:A:N7	1:CA:816:A:C4	2.85	0.44
1:CA:90:U:O2'	1:CA:91:C:H5'	2.18	0.44
4:CD:173:TRP:CE2	4:CD:189:PRO:HG3	2.53	0.44
7:CG:78:ARG:CZ	7:CG:79:ARG:HH22	2.30	0.44
8:CH:125:ARG:HE	8:CH:125:ARG:HB2	1.49	0.44
9:CI:24:GLY:HA2	9:CI:59:PHE:O	2.17	0.44
13:CM:13:LYS:HA	13:CM:44:ARG:NH1	2.33	0.44
47:D0:14:ARG:HH11	47:D0:14:ARG:HB2	1.83	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1406:U:H2'	26:DA:1407:C:C6	2.52	0.44
26:DA:2192:G:H5'	26:DA:2193:G:OP2	2.17	0.44
26:DA:1129:A:N6	26:DA:2491:U:OP1	2.50	0.44
26:DA:2611:U:OP2	26:DA:2611:U:H3'	2.18	0.44
26:DA:1999:C:H4'	26:DA:2723:C:O2	2.17	0.44
26:DA:87:C:H5''	26:DA:88:G:H5'	1.99	0.44
27:DB:33:G:N3	27:DB:50:G:N2	2.66	0.44
30:DF:187:VAL:HG12	36:DP:3:LEU:HD12	1.99	0.44
30:DF:24:LEU:HD21	30:DF:114:VAL:HG12	1.99	0.44
34:DN:103:VAL:O	34:DN:107:LEU:HG	2.17	0.44
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.63	0.44
1:AA:1152:A:H2'	1:AA:1153:C:H6	1.82	0.44
2:AB:107:THR:O	2:AB:110:GLN:HB2	2.18	0.44
3:AC:156:ARG:NH2	3:AC:159:GLY:O	2.48	0.44
11:AK:34:ASP:HB3	11:AK:40:ILE:HD11	1.99	0.44
25:AY:57:G:H2'	25:AY:58:A:C5'	2.48	0.44
49:B2:2:LYS:O	49:B2:6:VAL:HG23	2.17	0.44
52:B5:16:ARG:HD2	52:B5:20:ARG:NH1	2.31	0.44
26:BA:176:G:OP2	61:BA:4447:HOH:O	2.21	0.44
26:BA:2050:U:H2'	26:BA:2051:G:O4'	2.18	0.44
26:BA:2213:G:H2'	26:BA:2214:G:O4'	2.17	0.44
26:BA:2417:G:O2'	26:BA:2423:A:N6	2.50	0.44
32:BH:125:VAL:HG12	32:BH:127:GLU:O	2.18	0.44
33:BI:62:LYS:HE3	33:BI:133:HIS:CE1	2.53	0.44
26:BA:662:A:H8	36:BP:117:GLU:HG3	1.82	0.44
1:CA:1132:C:H2'	1:CA:1133:G:C8	2.52	0.44
1:CA:1113:C:H42	1:CA:1187:G:H1	1.65	0.44
1:CA:1360:A:H2'	1:CA:1361:G:O4'	2.18	0.44
1:CA:1371:G:OP1	9:CI:12:GLU:HB2	2.18	0.44
1:CA:947:G:C6	1:CA:948:C:C4	3.06	0.44
2:CB:36:ARG:O	2:CB:37:ASN:HB2	2.17	0.44
3:CC:83:ARG:O	3:CC:87:LEU:HG	2.18	0.44
5:CE:57:LYS:O	5:CE:61:TYR:HD2	2.00	0.44
5:CE:6:PHE:HB3	5:CE:35:GLY:C	2.37	0.44
1:CA:878:G:OP1	8:CH:88:LYS:HB3	2.17	0.44
11:CK:66:LEU:HB3	11:CK:70:LYS:HZ2	1.82	0.44
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.16	0.44
44:DX:8:ILE:O	49:D2:36:ARG:NH2	2.51	0.44
26:DA:1235:G:C6	26:DA:1236:G:N1	2.85	0.44
26:DA:2131:G:H5''	26:DA:2131:G:N3	2.32	0.44
26:DA:2274:A:C5	26:DA:2276:G:C8	3.05	0.44
26:DA:2286:A:H4'	26:DA:2287:A:O4'	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:140:LEU:HD13	30:DF:170:LEU:HD21	1.99	0.44
31:DG:161:THR:HG22	31:DG:163:ALA:H	1.83	0.44
32:DH:137:ASP:HB3	32:DH:140:LYS:HB3	1.98	0.44
26:DA:2748:A:H5'	32:DH:4:ILE:HD12	1.99	0.44
1:AA:1479:C:H2'	1:AA:1480:G:H8	1.82	0.44
8:AH:119:LEU:HB3	8:AH:123:GLU:HB3	1.99	0.44
13:AM:49:THR:OG1	13:AM:52:GLU:HG3	2.18	0.44
25:AY:71:G:H2'	25:AY:72:C:C6	2.53	0.44
26:BA:1423:G:H2'	61:BA:3925:HOH:O	2.18	0.44
26:BA:1451:U:H2'	26:BA:1452:U:H6	1.78	0.44
26:BA:553:A:N1	26:BA:2064:A:H2'	2.32	0.44
26:BA:2156:A:OP2	26:BA:2179:G:N2	2.50	0.44
26:BA:2830:A:P	38:BR:2:ARG:HH22	2.41	0.44
26:BA:305:G:O2'	26:BA:383:A:N6	2.47	0.44
26:BA:637:U:H5'	26:BA:640:A:N6	2.33	0.44
26:BA:811:A:H5'	28:BD:210:GLY:HA2	1.99	0.44
29:BE:174:ASP:OD1	29:BE:175:VAL:N	2.50	0.44
30:BF:24:LEU:HD23	30:BF:115:ALA:HA	2.00	0.44
31:BG:43:LEU:HB3	31:BG:44:GLY:H	1.50	0.44
33:BI:4:ILE:HD13	33:BI:47:LEU:HG	2.00	0.44
26:BA:997:G:P	37:BQ:16:ARG:HH21	2.40	0.44
1:CA:1002:G:C2	1:CA:1003:G:C8	3.06	0.44
1:CA:1286:A:H2'	1:CA:1287:A:H5'	1.99	0.44
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.30	0.44
1:CA:727:G:OP1	1:CA:742:G:N2	2.43	0.44
3:CC:98:ASN:N	3:CC:98:ASN:OD1	2.49	0.44
5:CE:90:VAL:O	5:CE:120:THR:HA	2.17	0.44
7:CG:72:ARG:HH22	7:CG:138:LYS:NZ	2.15	0.44
10:CJ:69:ASN:O	10:CJ:70:ARG:HD3	2.18	0.44
23:CW:61:C:HO2'	23:CW:62:C:P	2.37	0.44
25:CY:8:4SU:S4	25:CY:14:A:N7	2.90	0.44
26:DA:2165:G:H2'	26:DA:2166:G:O4'	2.17	0.44
26:DA:492:A:H2'	26:DA:493:G:O4'	2.18	0.44
13:CM:93:ARG:HD3	26:DA:888:C:OP1	2.18	0.44
27:DB:33:G:C6	27:DB:34:U:C4	3.06	0.44
1:CA:1432:G:OP2	40:DT:108:ARG:HD2	2.18	0.44
29:DE:27:LEU:HD22	40:DT:1:MET:HE1	1.98	0.44
46:DZ:120:ILE:HD13	46:DZ:171:ILE:HA	1.99	0.44
1:AA:1223:C:H5''	1:AA:1224:G:H5''	2.00	0.44
1:AA:1469:G:H2'	1:AA:1470:G:C8	2.53	0.44
1:AA:589:C:H5''	8:AH:29:SER:HB3	1.99	0.44
1:AA:834:C:H2'	1:AA:835:U:C6	2.53	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.53	0.44
7:AG:72:ARG:HG3	7:AG:142:GLU:OE2	2.18	0.44
1:AA:35:G:O2'	12:AL:118:SER:O	2.29	0.44
13:AM:31:LYS:O	13:AM:35:GLU:HG3	2.18	0.44
13:AM:60:VAL:HG12	13:AM:66:LEU:HD11	2.00	0.44
16:AP:56:ALA:O	16:AP:60:LEU:HB2	2.18	0.44
17:AQ:74:LEU:HD13	17:AQ:75:ARG:HG2	2.00	0.44
23:AW:56:C:H5	26:BA:943:C:O4'	2.00	0.44
51:B4:40:HIS:HB3	51:B4:43:TYR:HB2	2.00	0.44
26:BA:1188:A:C4	26:BA:1190:G:C8	3.06	0.44
26:BA:1501:U:OP1	38:BR:77:ARG:NH1	2.39	0.44
31:BG:97:ASP:O	31:BG:101:ILE:HG13	2.17	0.44
46:BZ:108:PRO:HB2	46:BZ:111:VAL:HG23	1.99	0.44
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.33	0.44
2:CB:16:HIS:CD2	2:CB:17:PHE:N	2.85	0.44
7:CG:16:LEU:HD23	9:CI:41:VAL:HG12	1.99	0.44
26:DA:1410:G:H2'	26:DA:1411:C:H6	1.82	0.44
26:DA:2104:G:H2'	26:DA:2105:C:C6	2.53	0.44
26:DA:2136:C:HO2'	26:DA:2137:C:C5'	2.27	0.44
26:DA:2302:G:C2	26:DA:2303:G:C8	3.06	0.44
26:DA:2344:U:H3'	53:D6:37:ARG:O	2.18	0.44
26:DA:483:A:H1'	45:DY:59:GLY:O	2.18	0.44
26:DA:784:A:C8	26:DA:792:G:C5	3.06	0.44
31:DG:129:GLY:O	31:DG:161:THR:HB	2.18	0.44
36:DP:6:LEU:HA	36:DP:6:LEU:HD23	1.73	0.44
36:DP:83:VAL:HG11	36:DP:100:LEU:HD13	1.99	0.44
38:DR:28:LEU:HD12	38:DR:48:VAL:HG21	2.00	0.44
40:DT:50:ILE:HG22	40:DT:102:ILE:HD11	1.99	0.44
26:DA:994:C:H1'	42:DV:10:LYS:HE3	1.98	0.44
46:DZ:99:TYR:HA	46:DZ:124:ILE:O	2.17	0.44
1:AA:1025:U:O2'	1:AA:1026:G:C8	2.67	0.44
1:AA:1130:A:H5'	9:AI:18:PHE:CE2	2.52	0.44
1:AA:1261:A:H3'	1:AA:1262:C:C6	2.52	0.44
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.87	0.44
2:AB:158:LEU:HG	2:AB:182:ILE:HD11	2.00	0.44
10:AJ:69:ASN:O	10:AJ:70:ARG:HD3	2.17	0.44
25:AY:4:C:H3'	25:AY:5:G:H5''	2.00	0.44
26:BA:2283:G:OP1	47:B0:18:ALA:HB1	2.18	0.44
26:BA:1797:U:H2'	26:BA:1798:C:H6	1.83	0.44
26:BA:2389:A:H2'	26:BA:2390:A:C8	2.53	0.44
26:BA:2705:A:H2'	26:BA:2706:G:C8	2.53	0.44
26:BA:2859:U:P	40:BT:95:ARG:HH12	2.40	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:938:G:N3	26:BA:938:G:H2'	2.32	0.44
26:BA:939:C:H2'	26:BA:940:C:H6	1.81	0.44
33:BI:103:ARG:HG3	33:BI:104:GLN:H	1.82	0.44
33:BI:43:ASN:C	33:BI:43:ASN:HD22	2.20	0.44
1:CA:1000:U:H2'	1:CA:1001:A:H8	1.83	0.44
1:CA:1014:A:O2'	1:CA:1219:U:H4'	2.17	0.44
1:CA:1245:A:N1	1:CA:1292:U:O2	2.51	0.44
1:CA:1291:G:C6	1:CA:1292:U:C4	3.05	0.44
1:CA:6:G:O2'	1:CA:7:G:H5'	2.17	0.44
1:CA:570:G:H1'	1:CA:820:U:C4	2.53	0.44
2:CB:109:SER:O	2:CB:112:VAL:HB	2.17	0.44
2:CB:15:VAL:HG21	2:CB:213:LEU:HD13	1.99	0.44
4:CD:111:ALA:HB1	4:CD:116:GLN:HB3	2.00	0.44
6:CF:37:VAL:HA	6:CF:65:VAL:HG12	2.00	0.44
9:CI:16:ARG:CB	9:CI:64:THR:HG23	2.47	0.44
10:CJ:43:ARG:HB2	10:CJ:67:THR:HG23	2.00	0.44
19:CS:67:VAL:H	51:D4:58:ARG:HD3	1.82	0.44
22:CV:14:A:C2	25:CY:34:G:C2	3.06	0.44
25:CY:40:C:H2'	25:CY:41:C:C6	2.53	0.44
26:DA:1268:A:H2'	26:DA:1269:A:O4'	2.17	0.44
26:DA:1983:C:H4'	26:DA:2606:C:H4'	1.99	0.44
26:DA:2127:G:N1	26:DA:2128:C:C4	2.85	0.44
26:DA:2617:C:H2'	26:DA:2618:G:O4'	2.17	0.44
26:DA:2805:G:H2'	26:DA:2807:G:H8	1.79	0.44
26:DA:2313:C:H4'	31:DG:91:ARG:HG3	2.00	0.44
32:DH:18:GLU:HB3	32:DH:25:LYS:HB2	2.00	0.44
40:DT:117:ASP:O	40:DT:121:ILE:HG13	2.18	0.44
41:DU:66:ASN:O	41:DU:70:ARG:HG3	2.18	0.44
1:AA:1153:C:H2'	1:AA:1154:G:O4'	2.18	0.44
1:AA:1179:A:H4'	9:AI:103:THR:HA	2.00	0.44
1:AA:166:G:H2'	1:AA:167:G:C8	2.53	0.44
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	2.00	0.44
7:AG:16:LEU:HD23	9:AI:41:VAL:O	2.18	0.44
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.33	0.44
52:B5:35:GLU:HG3	52:B5:51:TYR:CD2	2.53	0.44
26:BA:1343:C:OP1	26:BA:2722:C:H4'	2.18	0.44
26:BA:139:A:C8	26:BA:1454:C:O2'	2.68	0.44
26:BA:2126:G:H2'	26:BA:2127:C:C6	2.53	0.44
28:BD:35:LYS:HB2	28:BD:36:PRO:HD2	1.99	0.44
32:BH:26:VAL:HG12	32:BH:79:VAL:HG21	1.99	0.44
42:BV:65:GLY:HA3	42:BV:91:TYR:CZ	2.53	0.44
1:CA:1151:A:O2'	1:CA:1152:A:H8	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1154:G:O6	1:CA:1155:G:N1	2.51	0.44
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.18	0.44
1:CA:44:G:H2'	1:CA:45:U:O4'	2.18	0.44
2:CB:71:VAL:HG22	2:CB:163:PHE:O	2.18	0.44
5:CE:96:PRO:HA	5:CE:117:ASP:OD2	2.18	0.44
53:D6:14:THR:HG22	53:D6:15:GLU:HG3	2.00	0.44
26:DA:1185:C:H5''	26:DA:1186:G:OP1	2.18	0.44
26:DA:1308:A:H2'	26:DA:1309:G:O4'	2.18	0.44
26:DA:172:C:H2'	26:DA:173:G:H8	1.83	0.44
24:CX:13:C:O2'	26:DA:1924:C:H4'	2.17	0.44
26:DA:2439:A:H5'	26:DA:2439:A:C8	2.52	0.44
26:DA:2567:G:H2'	26:DA:2568:C:C6	2.53	0.44
26:DA:861:A:N3	27:DB:79:C:O2'	2.43	0.44
27:DB:42:C:C2	31:DG:92:VAL:HA	2.53	0.44
26:DA:764:A:H5'	28:DD:210:GLY:HA2	2.00	0.44
26:DA:1826:G:H4'	28:DD:242:ARG:CZ	2.47	0.44
30:DF:39:TRP:CZ2	30:DF:43:LYS:HE2	2.52	0.44
1:AA:1014:A:C2	1:AA:1219:U:H1'	2.53	0.43
1:AA:973:G:OP1	10:AJ:57:LYS:HE3	2.18	0.43
2:AB:21:ARG:H	2:AB:21:ARG:HD2	1.83	0.43
4:AD:107:ARG:HD2	4:AD:107:ARG:HA	1.78	0.43
4:AD:163:GLU:O	4:AD:166:LYS:HG2	2.18	0.43
4:AD:19:LEU:HB3	4:AD:21:LEU:HD21	2.00	0.43
5:AE:131:ILE:HD13	5:AE:131:ILE:HA	1.79	0.43
7:AG:146:GLU:OE2	7:AG:149:ARG:NE	2.51	0.43
11:AK:81:ASP:OD1	11:AK:81:ASP:N	2.50	0.43
12:AL:24:VAL:HG13	12:AL:98:TYR:HE2	1.84	0.43
23:AW:19:G:N1	23:AW:56:C:N4	2.53	0.43
25:AY:36:A:H2'	25:AY:37:MIA:O4'	2.18	0.43
56:B9:32:HIS:O	56:B9:34:GLN:HG3	2.18	0.43
26:BA:1848:G:OP1	28:BD:88:ARG:NH2	2.43	0.43
26:BA:2163:G:N1	26:BA:2164:C:C2	2.86	0.43
26:BA:2357:G:OP2	53:B6:38:LYS:NZ	2.46	0.43
26:BA:2573:A:H2'	26:BA:2574:U:O4'	2.17	0.43
26:BA:2762:A:P	32:BH:3:ARG:HH21	2.41	0.43
26:BA:144:C:H5'	44:BX:2:LYS:HE2	2.00	0.43
1:CA:1177:G:H3'	1:CA:1178:G:H8	1.83	0.43
1:CA:1226:C:C5	13:CM:104:ARG:HA	2.52	0.43
1:CA:1278:U:H5'	1:CA:1279:A:O4'	2.18	0.43
1:CA:685:G:C2	1:CA:686:U:C4	3.06	0.43
1:CA:954:G:H2'	1:CA:955:U:O4'	2.17	0.43
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:111:LEU:HD11	3:CC:144:SER:O	2.17	0.43
4:CD:20:TYR:CD1	4:CD:26:CYS:HB3	2.52	0.43
7:CG:22:LEU:HD13	7:CG:97:GLN:OE1	2.17	0.43
9:CI:4:TYR:CD2	9:CI:88:TYR:HB2	2.53	0.43
9:CI:89:ASN:C	9:CI:89:ASN:HD22	2.22	0.43
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.36	0.43
12:CL:34:ARG:O	12:CL:61:THR:HG23	2.18	0.43
13:CM:16:ASP:O	13:CM:20:THR:HG23	2.17	0.43
13:CM:54:VAL:HA	13:CM:57:ARG:HB3	2.00	0.43
15:CO:58:MET:O	15:CO:62:GLN:N	2.45	0.43
23:CW:69:G:N2	23:CW:70:G:C4	2.86	0.43
48:D1:91:LYS:HG2	48:D1:95:LEU:HD22	2.00	0.43
50:D3:10:LYS:HB3	50:D3:53:LEU:HA	2.00	0.43
26:DA:1274:A:N3	26:DA:1297:C:H1'	2.33	0.43
26:DA:2318:G:H21	39:DS:3:ARG:HD2	1.83	0.43
26:DA:298:G:H5''	26:DA:299:A:OP1	2.18	0.43
29:DE:21:VAL:HG23	29:DE:185:LYS:HD2	1.99	0.43
29:DE:77:ILE:CD1	29:DE:195:LEU:HD13	2.49	0.43
31:DG:115:ARG:NH1	31:DG:137:GLU:OE2	2.51	0.43
33:DI:44:LEU:HA	33:DI:44:LEU:HD13	1.77	0.43
34:DN:88:GLU:H	34:DN:88:GLU:HG2	1.56	0.43
45:DY:19:LYS:HB3	45:DY:19:LYS:HE2	1.74	0.43
45:DY:86:ARG:HB2	45:DY:98:VAL:HG23	1.99	0.43
1:AA:1131:G:H22	1:AA:1143:G:H21	1.65	0.43
1:AA:1191:A:H5''	3:AC:4:LYS:HZ2	1.83	0.43
1:AA:737:A:H2'	1:AA:738:C:C6	2.53	0.43
2:AB:208:ILE:H	2:AB:208:ILE:HG13	1.43	0.43
2:AB:219:VAL:HA	2:AB:222:ILE:HD12	2.00	0.43
12:AL:92:ASP:O	12:AL:94:PRO:HD3	2.18	0.43
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.84	0.43
21:AU:3:LYS:HB3	21:AU:14:TRP:CG	2.54	0.43
26:BA:217:A:H8	26:BA:218:A:H5'	1.83	0.43
45:BY:52:SER:HB2	45:BY:53:PRO:HD2	2.00	0.43
1:CA:1005:A:O2'	1:CA:1006:C:OP1	2.32	0.43
1:CA:448:A:O5'	1:CA:485:G:N2	2.45	0.43
1:CA:999:C:N4	1:CA:1042:G:N1	2.30	0.43
2:CB:97:TRP:HH2	2:CB:102:LEU:HD13	1.83	0.43
2:CB:53:ARG:HB3	2:CB:53:ARG:NH1	2.33	0.43
7:CG:113:GLU:O	7:CG:119:ARG:HD3	2.19	0.43
13:CM:82:MET:HE2	13:CM:92:HIS:HB3	2.00	0.43
15:CO:26:GLU:HB3	15:CO:81:LEU:HD13	1.99	0.43
15:CO:3:ILE:O	15:CO:3:ILE:HG12	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:CY:71:G:H2'	25:CY:72:C:C6	2.53	0.43
51:D4:46:GLN:C	51:D4:48:ARG:H	2.21	0.43
26:DA:122:G:OP1	26:DA:149:A:O2'	2.29	0.43
26:DA:1805:U:C2	26:DA:1813:G:N2	2.86	0.43
26:DA:2112:G:C4	26:DA:2113:U:H1'	2.53	0.43
26:DA:2115:G:O2'	26:DA:2167:U:O4	2.35	0.43
26:DA:2119:A:C2	26:DA:2171:A:H5'	2.46	0.43
35:DO:34:THR:OG1	35:DO:35:VAL:N	2.50	0.43
36:DP:44:GLY:HA3	36:DP:45:LEU:HB2	2.00	0.43
36:DP:1:MET:HG2	36:DP:5:ASP:HB2	1.99	0.43
1:AA:1320:C:H2'	1:AA:1321:C:O4'	2.19	0.43
2:AB:189:ASP:O	2:AB:192:SER:OG	2.35	0.43
2:AB:96:ARG:HD2	2:AB:98:LEU:HD23	2.00	0.43
4:AD:105:VAL:HG21	4:AD:126:ILE:HG13	2.00	0.43
49:B2:53:LEU:HD23	49:B2:53:LEU:HA	1.83	0.43
55:B8:6:THR:HG23	55:B8:63:PRO:HD2	2.00	0.43
26:BA:1093:G:H2'	26:BA:1156:G:N2	2.33	0.43
26:BA:1417:G:H2'	26:BA:1418:U:H5	1.82	0.43
26:BA:1496:A:H5'	26:BA:1497:G:OP2	2.18	0.43
26:BA:1604:C:OP2	26:BA:1605:A:O2'	2.28	0.43
26:BA:586:G:H22	26:BA:601:A:H2	1.65	0.43
27:BB:29:A:H2'	27:BB:30:C:O4'	2.18	0.43
33:BI:68:LEU:HA	33:BI:68:LEU:HD23	1.77	0.43
38:BR:54:LEU:HD12	38:BR:54:LEU:HA	1.88	0.43
1:CA:1106:G:OP1	3:CC:172:ARG:HD3	2.18	0.43
1:CA:1106:G:C6	1:CA:1107:C:C4	3.07	0.43
1:CA:1172:C:H2'	1:CA:1173:G:C8	2.53	0.43
1:CA:1442:G:H8	1:CA:1442:G:H3'	1.84	0.43
2:CB:16:HIS:HB3	2:CB:210:SER:HB3	1.99	0.43
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.54	0.43
9:CI:23:ASN:HD22	9:CI:23:ASN:H	1.66	0.43
10:CJ:42:THR:HG21	10:CJ:66:ARG:HB3	1.99	0.43
26:DA:1607:C:N4	26:DA:1622:G:OP2	2.45	0.43
26:DA:2512:C:H2'	26:DA:2513:G:O4'	2.17	0.43
26:DA:493:G:H2'	26:DA:494:G:O4'	2.17	0.43
26:DA:522:G:H2'	26:DA:523:C:C6	2.54	0.43
26:DA:868:U:C4	26:DA:869:G:N7	2.87	0.43
34:DN:37:LYS:HG3	34:DN:42:TRP:NE1	2.33	0.43
26:DA:875:G:O2'	46:DZ:151:HIS:HE1	2.00	0.43
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.53	0.43
1:AA:419:C:OP1	1:AA:513:C:O2'	2.21	0.43
1:AA:44:G:H2'	1:AA:45:U:O4'	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:87:ARG:NE	2:AB:233:SER:HB3	2.33	0.43
9:AI:4:TYR:CD1	9:AI:88:TYR:HA	2.53	0.43
20:AT:60:GLU:HG2	20:AT:81:LYS:HD3	2.00	0.43
26:BA:1047:A:H2'	26:BA:1048:G:O4'	2.19	0.43
26:BA:510:C:H2'	26:BA:511:C:C6	2.53	0.43
26:BA:553:A:C2	26:BA:2065:C:H4'	2.53	0.43
26:BA:860:U:H2'	26:BA:861:C:C6	2.53	0.43
28:BD:13:ARG:HD2	28:BD:13:ARG:HA	1.82	0.43
26:BA:999:G:H5''	37:BQ:13:GLN:HB3	2.00	0.43
26:BA:1001:G:P	37:BQ:14:ARG:HH22	2.35	0.43
46:BZ:104:PHE:HB3	46:BZ:141:VAL:HG21	1.99	0.43
1:CA:1011:G:C6	1:CA:1012:U:C2	3.06	0.43
1:CA:1304:G:C6	1:CA:1305:G:N1	2.86	0.43
1:CA:1342:C:H2'	1:CA:1343:G:H8	1.83	0.43
1:CA:934:C:H5	1:CA:1344:C:H2'	1.84	0.43
1:CA:404:U:H2'	1:CA:405:U:C6	2.53	0.43
1:CA:881:G:OP2	12:CL:12:ARG:NH2	2.51	0.43
7:CG:23:VAL:HG13	7:CG:43:PHE:CE2	2.54	0.43
19:CS:65:ASN:N	19:CS:65:ASN:OD1	2.51	0.43
23:CW:2:C:N3	23:CW:71:G:O6	2.52	0.43
25:C'Y:58:A:H4'	25:C'Y:59:U:OP1	2.18	0.43
26:DA:2156:G:O5'	26:DA:2156:G:H8	2.01	0.43
26:DA:2393:A:H2'	26:DA:2394:C:O4'	2.19	0.43
26:DA:2485:G:C2	26:DA:2486:G:C8	3.06	0.43
26:DA:2519:U:O4'	26:DA:2542:A:N6	2.51	0.43
26:DA:2821:A:H2'	26:DA:2822:G:C8	2.54	0.43
26:DA:880:G:N2	26:DA:898:C:H1'	2.21	0.43
26:DA:862:G:O2'	27:DB:78:A:N3	2.51	0.43
29:DE:60:ASN:OD1	29:DE:62:PRO:HD2	2.18	0.43
37:DQ:66:ILE:HG12	37:DQ:104:PHE:CE1	2.53	0.43
45:DY:43:ASN:CG	45:DY:65:ALA:HB3	2.39	0.43
1:AA:841:U:OP2	1:AA:841:U:H6	2.02	0.43
2:AB:211:ILE:O	2:AB:215:LEU:HB2	2.19	0.43
9:AI:55:ALA:HA	9:AI:58:HIS:CD2	2.54	0.43
9:AI:18:PHE:O	9:AI:61:ALA:HA	2.19	0.43
11:AK:34:ASP:OD2	11:AK:38:ASN:HB2	2.19	0.43
11:AK:41:THR:OG1	11:AK:42:TRP:N	2.52	0.43
1:AA:1049:U:OP1	14:AN:3:ARG:HB2	2.19	0.43
26:BA:1756:U:H2'	26:BA:1757:C:C6	2.54	0.43
26:BA:185:A:H2'	26:BA:185:A:N3	2.34	0.43
26:BA:2143:G:N2	26:BA:2199:C:N3	2.50	0.43
26:BA:709:G:H5'	36:BP:14:LYS:O	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:BH:164:TYR:HB2	32:BH:167:GLU:HB2	2.00	0.43
39:BS:34:HIS:ND1	39:BS:53:SER:OG	2.42	0.43
46:BZ:79:ARG:HB3	46:BZ:80:ARG:NH1	2.33	0.43
1:CA:988:G:H1'	1:CA:1014:A:N1	2.32	0.43
1:CA:731:G:H5'	1:CA:766:A:H4'	2.00	0.43
5:CE:41:VAL:HG23	5:CE:67:VAL:HG13	2.01	0.43
1:CA:1240:U:N3	7:CG:30:ILE:O	2.44	0.43
26:DA:1652:A:O2'	26:DA:1653:G:H5'	2.17	0.43
26:DA:1778:U:H2'	26:DA:1784:A:N6	2.34	0.43
26:DA:1847:A:H4'	26:DA:1848:A:OP2	2.18	0.43
26:DA:2036:C:H2'	26:DA:2037:G:H8	1.83	0.43
26:DA:2639:A:C2	26:DA:2778:A:C8	3.07	0.43
26:DA:373:U:H2'	26:DA:374:A:H8	1.83	0.43
26:DA:647:G:H8	26:DA:647:G:O5'	2.02	0.43
26:DA:949:C:H2'	26:DA:950:G:C8	2.54	0.43
30:DF:129:PHE:HA	30:DF:142:TRP:NE1	2.33	0.43
31:DG:43:LEU:HB3	31:DG:44:GLY:H	1.48	0.43
41:DU:58:ARG:HA	41:DU:61:TRP:CE3	2.53	0.43
41:DU:43:GLY:HA3	42:DV:73:SER:HB3	2.01	0.43
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.19	0.43
1:AA:164:U:H2'	1:AA:165:C:C6	2.54	0.43
1:AA:202:U:HO2'	1:AA:203:U:P	2.39	0.43
1:AA:658:G:H2'	1:AA:659:U:C6	2.54	0.43
1:AA:71:C:N3	1:AA:98:G:O6	2.51	0.43
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	2.00	0.43
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.19	0.43
14:AN:13:THR:HA	14:AN:14:PRO:HD3	1.81	0.43
1:AA:1217:C:OP1	14:AN:9:LYS:HE2	2.18	0.43
24:AX:31:G:N7	24:AX:32:5MC:HM52	2.34	0.43
26:BA:1716:A:H5''	26:BA:2562:G:OP1	2.18	0.43
26:BA:1759:C:H2'	26:BA:1760:U:O4'	2.18	0.43
26:BA:449:A:H2'	26:BA:450:A:C8	2.53	0.43
26:BA:568:C:N3	26:BA:573:G:N1	2.49	0.43
26:BA:1701:A:OP1	38:BR:1:MET:HA	2.19	0.43
46:BZ:111:VAL:CG2	46:BZ:117:LEU:HB2	2.48	0.43
1:CA:1187:G:OP1	9:CI:113:LYS:NZ	2.50	0.43
1:CA:396:G:H2'	1:CA:397:A:H5''	1.99	0.43
1:CA:553:A:H2'	1:CA:554:C:C6	2.53	0.43
1:CA:953:G:N7	13:CM:104:ARG:NH2	2.67	0.43
1:CA:1187:G:H5''	9:CI:113:LYS:HE3	1.99	0.43
19:CS:13:ASP:HA	19:CS:16:LEU:HB2	2.01	0.43
20:CT:59:ALA:O	20:CT:63:ILE:HG13	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1588:C:H2'	26:DA:1589:C:C6	2.53	0.43
26:DA:1853:A:H2'	26:DA:1854:A:C8	2.54	0.43
26:DA:2172:U:O2'	26:DA:2173:A:OP1	2.36	0.43
26:DA:2180:U:H2'	26:DA:2181:G:O4'	2.17	0.43
26:DA:2526:G:H2'	26:DA:2527:C:H6	1.83	0.43
26:DA:286:C:H2'	26:DA:287:C:C6	2.54	0.43
26:DA:910:A:C6	26:DA:911:A:C6	3.06	0.43
27:DB:15:A:C8	27:DB:110:G:C4	3.07	0.43
31:DG:150:ASP:OD1	31:DG:150:ASP:N	2.44	0.43
37:DQ:20:ALA:HB2	46:DZ:79:ARG:HG2	2.00	0.43
38:DR:88:ARG:NH2	38:DR:89:ASP:OD1	2.50	0.43
44:DX:35:THR:HG22	44:DX:37:THR:N	2.34	0.43
44:DX:55:ASN:O	44:DX:79:ALA:HA	2.19	0.43
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.18	0.43
1:AA:434:U:H2'	1:AA:435:C:C6	2.54	0.43
2:AB:21:ARG:HH21	2:AB:21:ARG:H	1.65	0.43
3:AC:78:GLY:HA3	3:AC:83:ARG:H	1.84	0.43
11:AK:67:ASP:OD1	11:AK:71:LYS:HE3	2.18	0.43
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.80	0.43
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.99	0.43
31:BG:179:PRO:HG3	51:B4:43:TYR:OH	2.19	0.43
51:B4:46:GLN:O	51:B4:46:GLN:HG2	2.19	0.43
36:BP:64:LYS:HE3	55:B8:12:LYS:HD3	2.01	0.43
26:BA:1475:G:H2'	26:BA:1476:C:C6	2.53	0.43
28:BD:20:ASP:OD1	28:BD:20:ASP:N	2.39	0.43
41:BU:86:ALA:O	42:BV:49:THR:HG23	2.19	0.43
1:CA:1321:C:H3'	1:CA:1322:C:H6	1.82	0.43
1:CA:20:U:H2'	1:CA:21:G:O4'	2.18	0.43
1:CA:21:G:H2'	1:CA:22:G:C8	2.54	0.43
1:CA:299:G:H2'	1:CA:300:A:C8	2.53	0.43
1:CA:427:U:H3'	1:CA:428:G:H2'	2.01	0.43
1:CA:62:U:H2'	1:CA:63:C:C6	2.54	0.43
1:CA:707:C:H2'	1:CA:708:C:H6	1.83	0.43
3:CC:104:GLN:NE2	3:CC:105:GLU:HG3	2.34	0.43
3:CC:19:GLU:HB3	3:CC:55:VAL:O	2.18	0.43
4:CD:53:ASP:HB3	4:CD:57:ARG:NH1	2.34	0.43
8:CH:124:ALA:O	8:CH:128:GLY:N	2.52	0.43
8:CH:56:LYS:HB2	8:CH:58:TYR:HE1	1.83	0.43
9:CI:22:GLY:N	9:CI:58:HIS:O	2.30	0.43
16:CP:74:LEU:O	16:CP:79:VAL:HG23	2.19	0.43
1:CA:719:C:N4	18:CR:71:LYS:NZ	2.66	0.43
25:C'Y:19:G:C4'	25:C'Y:57:G:H22	2.32	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1836:C:H2'	26:DA:1837:C:H6	1.84	0.43
26:DA:2125:G:H1	26:DA:2172:U:P	2.41	0.43
26:DA:2406:U:OP2	26:DA:2406:U:H2'	2.19	0.43
26:DA:272(D):G:C2	26:DA:272(E):G:C8	3.07	0.43
26:DA:839:U:H2'	26:DA:840:C:C6	2.53	0.43
34:DN:71:ILE:HG21	34:DN:84:LYS:HB3	2.01	0.43
40:DT:92:GLY:O	40:DT:120:ARG:NH2	2.51	0.43
41:DU:81:HIS:HB3	41:DU:117:GLN:HE22	1.83	0.43
41:DU:8:VAL:O	41:DU:12:ARG:HG3	2.18	0.43
42:DV:5:VAL:HG11	42:DV:57:VAL:HG21	2.00	0.43
46:DZ:4:ARG:HG3	46:DZ:58:VAL:HB	2.01	0.43
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.83	0.43
1:AA:984:C:N4	1:AA:1221:G:H1	2.13	0.43
1:AA:942:G:C2	1:AA:1342:C:C2	3.06	0.43
1:AA:1362:C:H2'	1:AA:1363:C:H5''	2.01	0.43
1:AA:339:C:H2'	1:AA:340:U:C6	2.54	0.43
11:AK:62:GLN:O	11:AK:66:LEU:HG	2.19	0.43
18:AR:31:LEU:H	18:AR:31:LEU:HD23	1.83	0.43
25:AY:23:A:H2'	25:AY:24:G:C8	2.54	0.43
25:AY:3:C:H2'	25:AY:4:C:O4'	2.18	0.43
51:B4:68:ARG:HD2	51:B4:68:ARG:HA	1.84	0.43
26:BA:2623:U:H2'	52:B5:2:ALA:O	2.19	0.43
26:BA:1487:G:H2'	26:BA:1488:G:H8	1.83	0.43
26:BA:747:G:O2'	26:BA:1679:A:N3	2.43	0.43
26:BA:2059:G:H2'	26:BA:2060:G:C8	2.54	0.43
26:BA:2347:A:C8	26:BA:2349:G:C5	3.07	0.43
26:BA:502:G:H4'	26:BA:527:A:N1	2.34	0.43
30:BF:106:ARG:H	30:BF:106:ARG:HG2	1.67	0.43
43:BW:67:ASP:N	43:BW:67:ASP:OD1	2.50	0.43
45:BY:19:LYS:HB3	45:BY:19:LYS:HE2	1.60	0.43
46:BZ:151:HIS:HA	46:BZ:169:GLU:O	2.19	0.43
1:CA:1051:C:H2'	1:CA:1052:U:H6	1.82	0.43
1:CA:1119:C:C2	1:CA:1154:G:O6	2.71	0.43
1:CA:1368:G:OP2	9:CI:112:LYS:HG3	2.19	0.43
1:CA:988:G:O2'	1:CA:1014:A:N6	2.52	0.43
2:CB:178:ARG:NH1	2:CB:196:LEU:O	2.52	0.43
2:CB:73:THR:HG22	2:CB:95:GLN:O	2.18	0.43
3:CC:20:SER:OG	3:CC:22:TRP:NE1	2.52	0.43
7:CG:72:ARG:HH12	7:CG:138:LYS:NZ	2.17	0.43
10:CJ:99:LYS:O	10:CJ:100:THR:OG1	2.32	0.43
13:CM:123:ALA:HB2	23:CW:39:PSU:H1'	2.00	0.43
14:CN:37:PHE:HB2	14:CN:39:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
49:D2:32:LEU:HD12	49:D2:57:ILE:HD12	2.00	0.43
36:DP:59:LEU:HD21	55:D8:10:ALA:HA	2.01	0.43
26:DA:1364:G:OP2	48:D1:3:LYS:HG3	2.19	0.43
26:DA:1652:A:C2'	26:DA:1653:G:H5'	2.48	0.43
26:DA:1720:U:H2'	26:DA:1721:G:O4'	2.19	0.43
26:DA:2152:G:H2'	26:DA:2153:G:O4'	2.18	0.43
26:DA:2031:A:C6	26:DA:2498:C:H1'	2.54	0.43
26:DA:2526:G:H2'	26:DA:2527:C:C6	2.53	0.43
26:DA:2682:U:H5'	29:DE:11:MET:O	2.19	0.43
26:DA:1999:C:H5''	26:DA:2723:C:O2'	2.19	0.43
26:DA:2732:G:H3'	26:DA:2733:A:O4'	2.19	0.43
26:DA:2741:A:H2'	26:DA:2742:C:O4'	2.18	0.43
26:DA:289:A:H62	26:DA:351:G:N2	2.15	0.43
35:DO:69:ILE:HG12	35:DO:69:ILE:H	1.61	0.43
37:DQ:16:ARG:NH2	37:DQ:18:LYS:HD3	2.33	0.43
37:DQ:26:TYR:O	37:DQ:67:ARG:NH1	2.42	0.43
46:DZ:159:PRO:HA	46:DZ:161:VAL:HG12	2.01	0.43
1:AA:909:A:H2'	1:AA:910:C:O4'	2.19	0.43
1:AA:438:G:H4'	4:AD:123:HIS:CE1	2.54	0.43
4:AD:33:MET:O	4:AD:37:PRO:HB3	2.19	0.43
1:AA:671:G:H5'	6:AF:77:ARG:HH12	1.83	0.43
12:AL:117:ARG:HB3	12:AL:122:THR:HB	2.00	0.43
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.18	0.43
26:BA:1440:U:H2'	26:BA:1441:A:O4'	2.18	0.43
26:BA:2122:G:H1	26:BA:2211:U:H3	1.66	0.43
26:BA:1814:A:H5'	26:BA:2620:G:H4'	2.00	0.43
29:BE:121:ASN:ND2	61:BE:411:HOH:O	2.40	0.43
32:BH:117:PRO:HG3	32:BH:123:PHE:CD2	2.54	0.43
34:BN:9:VAL:HG11	34:BN:39:ARG:HH22	1.83	0.43
45:BY:54:LYS:CA	45:BY:56:PRO:HD3	2.48	0.43
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.34	0.43
1:CA:1261:A:C6	1:CA:1262:C:C2	3.07	0.43
1:CA:664:G:H5''	18:CR:64:ARG:NH2	2.34	0.43
1:CA:776:G:HO2'	1:CA:777:A:H8	1.66	0.43
1:CA:955:U:H2'	1:CA:956:U:O4'	2.19	0.43
4:CD:13:ARG:HD2	4:CD:38:TYR:O	2.18	0.43
5:CE:83:GLU:HA	5:CE:88:LYS:HA	2.00	0.43
6:CF:91:VAL:HG11	18:CR:72:ARG:NH1	2.34	0.43
1:CA:1317:C:O2	19:CS:37:ARG:NH1	2.52	0.43
26:DA:1636:C:H2'	26:DA:1637:A:C8	2.54	0.43
26:DA:2171:A:C4	26:DA:2172:U:C4	3.06	0.43
26:DA:2173:A:OP2	26:DA:2173:A:H3'	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2193:G:H2'	26:DA:2194:G:H8	1.84	0.43
25:CY:76:A:H62	26:DA:2422:A:C5'	2.31	0.43
26:DA:2439:A:H8	26:DA:2439:A:H5'	1.84	0.43
26:DA:2516:G:C6	26:DA:2517:C:C4	3.07	0.43
26:DA:2557:G:H2'	26:DA:2558:C:H6	1.83	0.43
26:DA:2693:A:H2'	26:DA:2694:G:C8	2.54	0.43
26:DA:322:A:C5	26:DA:340:A:C2	3.06	0.43
26:DA:770:G:OP2	61:DA:4255:HOH:O	2.21	0.43
27:DB:15:A:OP2	27:DB:69:G:N2	2.49	0.43
30:DF:195:ASP:HB3	30:DF:197:ASP:OD1	2.18	0.43
31:DG:145:THR:HG23	31:DG:147:ASP:N	2.23	0.43
31:DG:64:THR:OG1	31:DG:66:GLN:O	2.37	0.43
45:DY:5:MET:HE1	45:DY:32:PRO:HA	2.01	0.43
1:AA:1505:G:O2'	22:AV:13:A:O2'	2.33	0.43
1:AA:936:C:H2'	1:AA:937:A:O4'	2.19	0.43
3:AC:116:VAL:O	3:AC:120:VAL:HG23	2.19	0.43
3:AC:6:HIS:CD2	3:AC:8:ILE:HB	2.54	0.43
9:AI:20:ARG:HA	9:AI:21:PRO:HD3	1.92	0.43
12:AL:110:VAL:O	12:AL:122:THR:OG1	2.32	0.43
14:AN:23:ARG:HH11	14:AN:30:ALA:HB2	1.83	0.43
20:AT:29:LYS:O	20:AT:33:ILE:HG13	2.18	0.43
52:B5:59:GLU:HG2	52:B5:60:VAL:H	1.83	0.43
26:BA:2176:G:C2'	26:BA:2177:G:H5'	2.49	0.43
26:BA:2724:U:OP1	26:BA:2727:G:H4'	2.19	0.43
32:BH:11:VAL:HG13	32:BH:15:VAL:HG22	2.00	0.43
26:BA:1051:C:O2'	34:BN:28:THR:HG21	2.19	0.43
35:BO:98:VAL:HG22	35:BO:118:ALA:HA	2.01	0.43
37:BQ:56:ARG:HD2	37:BQ:56:ARG:HA	1.72	0.43
1:CA:1112:C:N3	3:CC:177:THR:HA	2.34	0.43
1:CA:1176:A:H2'	1:CA:1177:G:H8	1.84	0.43
1:CA:1216:G:H5''	14:CN:5:ALA:CB	2.47	0.43
2:CB:115:LEU:HD21	2:CB:153:ARG:NE	2.34	0.43
3:CC:42:LEU:HA	3:CC:45:LYS:NZ	2.33	0.43
5:CE:110:LEU:HD13	5:CE:118:ILE:HG21	2.00	0.43
13:CM:66:LEU:O	13:CM:68:GLY:N	2.52	0.43
19:CS:71:LEU:HD12	19:CS:71:LEU:HA	1.91	0.43
25:CY:1:G:H2'	25:CY:2:C:C6	2.54	0.43
25:CY:51:U:H2'	25:CY:52:G:O4'	2.18	0.43
50:D3:46:ASN:O	50:D3:50:VAL:HG22	2.19	0.43
26:DA:1010:A:H1'	26:DA:1153:C:H1'	2.00	0.43
26:DA:1394:U:C4	26:DA:1395:A:C5	3.07	0.43
26:DA:1899:G:O2'	26:DA:1900:A:OP2	2.35	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2265:U:C4	26:DA:2266:A:C5	3.07	0.43
26:DA:2461:C:H2'	26:DA:2462:U:H6	1.84	0.43
26:DA:2740:A:H2'	26:DA:2741:A:C8	2.54	0.43
26:DA:2747:G:O6	26:DA:2755:C:H5''	2.19	0.43
27:DB:24:G:O4'	27:DB:26:A:N6	2.47	0.43
32:DH:124:GLU:OE1	32:DH:132:ARG:HD2	2.19	0.43
36:DP:99:LEU:HD23	36:DP:99:LEU:H	1.83	0.43
37:DQ:36:ALA:HB2	37:DQ:103:MET:SD	2.59	0.43
38:DR:2:ARG:NH1	38:DR:5:LYS:O	2.52	0.43
26:DA:2019:A:H4'	41:DU:34:LYS:HD2	2.01	0.43
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.53	0.42
1:AA:294:U:OP1	1:AA:610:G:O2'	2.30	0.42
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.48	0.42
2:AB:224:GLN:HA	2:AB:228:GLY:O	2.19	0.42
3:AC:77:ILE:HG22	3:AC:81:GLY:HA2	2.01	0.42
3:AC:82:GLU:HA	3:AC:85:ARG:NE	2.34	0.42
4:AD:170:VAL:HG12	4:AD:171:GLY:N	2.34	0.42
7:AG:70:LYS:O	7:AG:138:LYS:NZ	2.49	0.42
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.34	0.42
23:AW:51:U:H2'	23:AW:52:G:C8	2.54	0.42
48:B1:62:VAL:HG22	48:B1:63:ALA:O	2.18	0.42
26:BA:1400:A:H2'	26:BA:1401:G:O4'	2.19	0.42
26:BA:1550:C:H2'	26:BA:1551:C:C6	2.54	0.42
26:BA:1825:U:H2'	26:BA:1826:C:C6	2.54	0.42
26:BA:1904:C:H2'	26:BA:1905:G:O4'	2.19	0.42
26:BA:1935:A:H4'	26:BA:1936:C:C5'	2.49	0.42
26:BA:2221:A:H5''	26:BA:2222:C:OP2	2.19	0.42
33:BI:40:THR:O	33:BI:44:LEU:HB2	2.19	0.42
36:BP:100:LEU:HD12	36:BP:112:LEU:HD11	2.01	0.42
43:BW:14:PRO:HG2	43:BW:78:GLU:CG	2.48	0.42
45:BY:1:MET:HB2	45:BY:2:ARG:H	1.53	0.42
1:CA:1025:U:H1'	1:CA:1026:G:C8	2.54	0.42
1:CA:103:C:P	20:CT:17:ARG:HH21	2.42	0.42
1:CA:228:A:H5'	16:CP:62:VAL:HG21	2.01	0.42
1:CA:495:A:H4'	1:CA:496:A:OP1	2.18	0.42
1:CA:993:G:H2'	1:CA:993:G:N3	2.33	0.42
2:CB:115:LEU:HG	2:CB:119:GLU:OE2	2.19	0.42
2:CB:122:PHE:HE2	2:CB:139:LYS:HG2	1.84	0.42
10:CJ:30:SER:OG	10:CJ:84:GLN:OE1	2.29	0.42
13:CM:4:ILE:HG23	13:CM:22:ILE:HD11	2.01	0.42
18:CR:76:LEU:HA	18:CR:76:LEU:HD12	1.81	0.42
26:DA:1463:C:H2'	26:DA:1464:C:C6	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:150:C:H2'	26:DA:151:C:C6	2.54	0.42
26:DA:2302:G:C6	26:DA:2303:G:N7	2.88	0.42
26:DA:2302:G:H1	26:DA:2314:C:H42	1.67	0.42
26:DA:2316:C:O2'	31:DG:128:ARG:NH1	2.52	0.42
26:DA:2529:G:O6	56:D9:31:LYS:NZ	2.51	0.42
26:DA:2591:C:H2'	26:DA:2592:G:C8	2.54	0.42
26:DA:2723:C:OP2	29:DE:109:LYS:NZ	2.52	0.42
26:DA:272(E):G:C2	26:DA:364:C:C2	3.07	0.42
26:DA:524:U:H2'	26:DA:525:U:C6	2.54	0.42
26:DA:563:G:OP2	61:DA:4169:HOH:O	2.21	0.42
26:DA:660:G:H5'	30:DF:99:TYR:CE2	2.53	0.42
28:DD:75:ILE:HA	28:DD:76:PRO:HD3	1.93	0.42
29:DE:181:LEU:HD12	29:DE:181:LEU:HA	1.76	0.42
30:DF:31:HIS:HB2	36:DP:9:ASN:OD1	2.19	0.42
31:DG:135:LEU:HD13	31:DG:135:LEU:HA	1.89	0.42
31:DG:23:PHE:HB2	31:DG:25:TYR:CE1	2.54	0.42
32:DH:164:TYR:HB2	32:DH:167:GLU:HB2	2.00	0.42
32:DH:2:SER:O	32:DH:3:ARG:HG2	2.19	0.42
32:DH:56:SER:HB3	32:DH:61:HIS:ND1	2.33	0.42
35:DO:17:ARG:HD3	35:DO:17:ARG:HA	1.69	0.42
38:DR:12:ARG:HG2	38:DR:16:HIS:ND1	2.34	0.42
41:DU:107:ALA:O	41:DU:111:GLU:HG2	2.18	0.42
42:DV:31:ALA:O	42:DV:61:VAL:HG12	2.18	0.42
1:AA:1286:A:H3'	1:AA:1286:A:C8	2.54	0.42
1:AA:405:U:O4	4:AD:2:GLY:N	2.53	0.42
1:AA:373:A:H1'	1:AA:481:G:N3	2.34	0.42
1:AA:54:C:H2'	1:AA:352:C:H41	1.84	0.42
3:AC:191:THR:OG1	3:AC:194:GLY:O	2.33	0.42
4:AD:170:VAL:HG11	4:AD:174:LEU:HD12	2.01	0.42
5:AE:6:PHE:HB3	5:AE:35:GLY:C	2.40	0.42
8:AH:78:GLN:HE21	8:AH:78:GLN:HB2	1.47	0.42
26:BA:1154:U:O2'	26:BA:1155:C:C6	2.72	0.42
26:BA:2303:U:H2'	26:BA:2304:C:C6	2.54	0.42
32:BH:24:VAL:HG22	32:BH:35:VAL:HB	2.01	0.42
44:BX:64:LYS:HA	44:BX:64:LYS:HD3	1.83	0.42
1:CA:1154:G:C8	1:CA:1155:G:C8	3.07	0.42
1:CA:850:U:H2'	1:CA:851:G:H5''	2.01	0.42
4:CD:163:GLU:C	4:CD:165:MET:H	2.22	0.42
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	2.01	0.42
19:CS:41:VAL:HG13	19:CS:42:PRO:HD2	2.01	0.42
26:DA:1204:A:N6	26:DA:1240:U:H2'	2.34	0.42
26:DA:1556:C:H2'	26:DA:1557:C:H6	1.84	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1877:A:H5'	26:DA:1878:G:OP2	2.19	0.42
26:DA:39:C:H2'	26:DA:40:C:H6	1.84	0.42
31:DG:47:LYS:HE2	31:DG:47:LYS:HB3	1.56	0.42
45:DY:5:MET:HG2	45:DY:30:VAL:HG11	2.00	0.42
1:AA:1002:G:C6	1:AA:1003:G:N3	2.88	0.42
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.34	0.42
1:AA:539:A:H2'	1:AA:540:G:H8	1.84	0.42
1:AA:59:A:H3'	1:AA:331:G:H22	1.84	0.42
1:AA:78:G:C2	1:AA:91:C:N4	2.87	0.42
2:AB:12:GLU:HA	2:AB:213:LEU:HD11	2.01	0.42
5:AE:103:GLY:O	5:AE:106:PRO:HD2	2.19	0.42
6:AF:10:LEU:HD23	6:AF:61:LEU:HD23	2.02	0.42
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.34	0.42
13:AM:84:ILE:HG13	13:AM:85:GLY:CA	2.44	0.42
1:AA:530:G:O6	22:AV:21:C:H1'	2.19	0.42
25:AY:5:G:C2	25:AY:6:G:C4	3.07	0.42
25:AY:7:A:C6	25:AY:49:C:C4	3.07	0.42
26:BA:1016:C:H2'	26:BA:1017:G:O4'	2.19	0.42
26:BA:1222:A:H3'	26:BA:1223:C:C6	2.54	0.42
26:BA:1298:G:OP1	41:BU:36:ARG:NH2	2.52	0.42
26:BA:1314:A:C2	26:BA:2035:A:C4	3.08	0.42
26:BA:554:A:H62	26:BA:2063:U:H3	1.67	0.42
27:BB:32:C:C2	27:BB:51:G:N2	2.86	0.42
31:BG:53:LEU:HD23	31:BG:53:LEU:HA	1.84	0.42
1:CA:1122:U:H2'	1:CA:1123:A:O4'	2.19	0.42
3:CC:39:ILE:O	3:CC:43:LEU:HG	2.19	0.42
1:CA:1124:G:H5'	10:CJ:36:GLY:H	1.84	0.42
13:CM:47:ASP:O	13:CM:48:LEU:HD23	2.18	0.42
18:CR:44:LEU:HD23	18:CR:50:ILE:HA	2.02	0.42
23:CW:4:C:N4	23:CW:5:G:C6	2.87	0.42
24:CX:9:G:H21	24:CX:45:G:H3'	1.84	0.42
26:DA:1021:A:H3'	26:DA:1021:A:H8	1.84	0.42
26:DA:2386:C:H2'	26:DA:2387:U:C6	2.54	0.42
26:DA:2705:A:H2'	26:DA:2706:G:O4'	2.20	0.42
26:DA:735:A:N7	26:DA:761:A:H2	2.17	0.42
27:DB:11:C:H3'	27:DB:12:C:C6	2.55	0.42
29:DE:96:PHE:O	29:DE:175:VAL:HG11	2.19	0.42
42:DV:5:VAL:CG1	42:DV:57:VAL:HG21	2.49	0.42
26:DA:1188:U:C4'	42:DV:79:VAL:HG22	2.50	0.42
45:DY:7:VAL:HG21	45:DY:72:VAL:HG12	2.00	0.42
45:DY:83:THR:HG21	45:DY:99:CYS:HB2	2.01	0.42
46:DZ:100:VAL:HA	46:DZ:101:PRO:HD3	1.91	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:DZ:28:MET:HA	46:DZ:88:PHE:O	2.18	0.42
1:AA:1004:A:N7	1:AA:1036:G:C2	2.87	0.42
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.55	0.42
1:AA:658:G:H2'	1:AA:659:U:H6	1.85	0.42
4:AD:176:LEU:HD12	4:AD:182:LYS:O	2.19	0.42
9:AI:127:LYS:O	9:AI:128:ARG:HG2	2.19	0.42
11:AK:20:TYR:CZ	11:AK:83:ILE:HD12	2.52	0.42
1:AA:1187:G:N3	14:AN:60:SER:OG	2.53	0.42
17:AQ:76:LEU:HD12	17:AQ:77:VAL:H	1.84	0.42
20:AT:13:LEU:O	20:AT:17:ARG:HG3	2.19	0.42
49:B2:3:LEU:O	49:B2:7:ARG:HG3	2.19	0.42
26:BA:2359:C:O2'	53:B6:21:TYR:OH	2.35	0.42
26:BA:1338:U:H2'	26:BA:1339:C:C6	2.54	0.42
26:BA:160:G:O2'	26:BA:161:C:H5'	2.19	0.42
26:BA:2451:A:H8	26:BA:2451:A:H5'	1.85	0.42
26:BA:2721:G:H2'	26:BA:2722:C:C6	2.54	0.42
26:BA:831:A:C8	26:BA:839:G:C5	3.07	0.42
26:BA:888:A:H2'	26:BA:889:G:C8	2.54	0.42
26:BA:964:A:H5''	27:BB:98:G:O2'	2.19	0.42
29:BE:18:ASP:HB3	40:BT:82:LEU:HD21	2.01	0.42
34:BN:20:GLY:HA2	34:BN:61:ARG:HD2	2.01	0.42
26:BA:515:G:N7	43:BW:49:LYS:NZ	2.68	0.42
1:CA:1009:G:C4	1:CA:1021:G:C2	3.08	0.42
1:CA:1320:C:H5'	1:CA:1320:C:H6	1.85	0.42
1:CA:156:G:H1	1:CA:165:C:H42	1.67	0.42
1:CA:933:G:C6	1:CA:1385:G:C6	3.07	0.42
1:CA:985:C:C2	1:CA:1220:G:N2	2.80	0.42
2:CB:51:LEU:HA	2:CB:54:THR:HB	2.01	0.42
3:CC:134:ILE:HG22	3:CC:168:ALA:HB3	2.01	0.42
5:CE:57:LYS:HG2	5:CE:61:TYR:HE2	1.84	0.42
7:CG:114:ARG:HB2	7:CG:115:ARG:NH2	2.35	0.42
7:CG:155:ARG:CZ	7:CG:155:ARG:HB3	2.48	0.42
24:CX:21:A:H61	24:CX:46:G:H2'	1.84	0.42
26:DA:2203:U:H2'	26:DA:2205:C:C6	2.54	0.42
26:DA:2510:C:C4	26:DA:2511:U:C4	3.07	0.42
27:DB:117:G:C2	27:DB:118:G:C5	3.07	0.42
31:DG:43:LEU:HD11	31:DG:153:ARG:HG2	2.01	0.42
32:DH:89:ILE:O	32:DH:129:THR:HG23	2.18	0.42
34:DN:123:TYR:CZ	34:DN:129:PRO:HD2	2.54	0.42
37:DQ:73:PRO:HA	37:DQ:93:TYR:CD1	2.54	0.42
1:AA:1004:A:C5	1:AA:1037:C:N3	2.87	0.42
1:AA:1029:C:N4	1:AA:1030(A):G:C2	2.88	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:580:U:H5''	15:AO:58:MET:HG2	2.01	0.42
1:AA:79:G:C2	1:AA:90:U:C2	3.07	0.42
2:AB:18:GLY:O	2:AB:19:HIS:HB3	2.19	0.42
3:AC:136:GLN:O	3:AC:140:ARG:HG3	2.18	0.42
9:AI:4:TYR:CE1	9:AI:88:TYR:HA	2.55	0.42
51:B4:28:LYS:HA	51:B4:29:PRO:HD3	1.84	0.42
53:B6:50:ARG:HB2	53:B6:50:ARG:HE	1.67	0.42
26:BA:1766:G:H3'	26:BA:1767:A:H5''	2.01	0.42
26:BA:2051:G:H2'	26:BA:2053:A:OP1	2.19	0.42
26:BA:2245:U:H2'	26:BA:2246:G:C8	2.55	0.42
26:BA:2408:G:OP1	48:B1:25:LYS:NZ	2.30	0.42
31:BG:28:VAL:HG23	31:BG:29:TRP:CD1	2.54	0.42
32:BH:170:ARG:O	32:BH:171:LEU:HD23	2.19	0.42
35:BO:113:LYS:O	35:BO:116:SER:OG	2.34	0.42
36:BP:112:LEU:HA	36:BP:112:LEU:HD23	1.85	0.42
1:CA:1067:A:N3	1:CA:1068:G:H1'	2.33	0.42
1:CA:1388:C:H2'	1:CA:1389:C:C6	2.54	0.42
1:CA:1422:G:H5'	35:DO:48:PRO:HB3	2.01	0.42
1:CA:357:G:O2'	1:CA:358:U:H5'	2.18	0.42
1:CA:560:U:OP2	61:CA:3313:HOH:O	2.21	0.42
1:CA:911:U:O2'	1:CA:912:C:H5'	2.20	0.42
3:CC:69:HIS:HB3	3:CC:106:VAL:CG2	2.50	0.42
4:CD:150:GLU:HG3	4:CD:150:GLU:H	1.68	0.42
12:CL:62:SER:HB2	12:CL:64:TYR:HD1	1.85	0.42
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.55	0.42
17:CQ:62:SER:CB	17:CQ:72:ARG:HD3	2.49	0.42
20:CT:93:GLU:C	20:CT:95:ALA:H	2.23	0.42
48:D1:89:GLU:O	48:D1:93:GLU:HG2	2.19	0.42
50:D3:6:VAL:HG13	50:D3:56:VAL:HG22	2.02	0.42
26:DA:1127:A:C2'	26:DA:1128:A:H5''	2.50	0.42
26:DA:117:G:C6	26:DA:119:A:C6	3.07	0.42
26:DA:1317:A:H2'	26:DA:1318:C:C6	2.55	0.42
26:DA:1341:U:O4	44:DX:16:LYS:HE2	2.19	0.42
26:DA:2130:U:H3	26:DA:2159:G:N2	2.17	0.42
26:DA:829:A:N7	26:DA:2248:C:H5'	2.34	0.42
26:DA:954:G:O2'	26:DA:2274:A:N1	2.45	0.42
26:DA:2408:U:H2'	26:DA:2409:G:C8	2.55	0.42
26:DA:64:A:O3'	44:DX:71:GLY:HA3	2.19	0.42
26:DA:764:A:H5'	28:DD:210:GLY:CA	2.49	0.42
27:DB:62:C:H2'	27:DB:63:G:C8	2.55	0.42
27:DB:91:C:OP1	37:DQ:16:ARG:HG3	2.19	0.42
31:DG:53:LEU:HD23	31:DG:53:LEU:HA	1.88	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
41:DU:92:ARG:H	41:DU:92:ARG:HG2	1.44	0.42
1:AA:162:A:N7	1:AA:163:C:H1'	2.35	0.42
1:AA:299:G:H2'	1:AA:300:A:C8	2.55	0.42
1:AA:765:G:N1	1:AA:812:C:O2'	2.42	0.42
7:AG:120:ILE:O	7:AG:124:LEU:HB2	2.20	0.42
9:AI:20:ARG:O	9:AI:60:ASP:N	2.30	0.42
15:AO:85:LEU:HD23	15:AO:85:LEU:HA	1.75	0.42
26:BA:2115:G:C6	26:BA:2237:A:C8	3.08	0.42
26:BA:2541:G:H5''	26:BA:2542:A:H5''	2.01	0.42
26:BA:691:G:H1	26:BA:699:C:N4	2.18	0.42
26:BA:822:G:C4	26:BA:841:G:C8	3.07	0.42
26:BA:928:G:N1	26:BA:943:C:N4	2.67	0.42
29:BE:12:THR:HG22	29:BE:13:ARG:H	1.85	0.42
32:BH:98:LEU:HA	32:BH:98:LEU:HD12	1.91	0.42
33:BI:73:GLU:HG3	33:BI:139:GLN:O	2.19	0.42
1:CA:1118:C:C2	1:CA:1119:C:C5	3.06	0.42
1:CA:336:C:H2'	1:CA:337:C:C6	2.55	0.42
2:CB:107:THR:O	2:CB:110:GLN:HB3	2.19	0.42
2:CB:82:ARG:HG3	2:CB:92:TYR:OH	2.18	0.42
3:CC:52:LEU:HD23	3:CC:55:VAL:HG23	2.01	0.42
1:CA:921:U:O2	5:CE:19:MET:HB2	2.19	0.42
9:CI:28:VAL:HA	9:CI:63:ILE:O	2.20	0.42
11:CK:59:TYR:O	11:CK:63:LEU:HG	2.20	0.42
20:CT:56:MET:HE2	20:CT:88:VAL:HG21	2.00	0.42
53:D6:13:CYS:SG	53:D6:47:THR:HG21	2.60	0.42
53:D6:18:ARG:HD2	53:D6:42:TRP:CG	2.55	0.42
26:DA:2006:C:O5'	26:DA:2006:C:H6	2.02	0.42
26:DA:2320:A:N3	26:DA:2320:A:H2'	2.33	0.42
26:DA:925:C:H2'	26:DA:926:A:H8	1.85	0.42
26:DA:935:C:C2'	26:DA:936:C:H5'	2.50	0.42
27:DB:31:C:H4'	31:DG:29:TRP:CZ2	2.54	0.42
27:DB:55:U:H1'	31:DG:29:TRP:HD1	1.81	0.42
28:DD:245:PRO:HA	28:DD:246:PRO:HD3	1.91	0.42
26:DA:2228:G:OP1	28:DD:261:LYS:HE3	2.19	0.42
31:DG:121:ASN:HA	31:DG:181:ARG:HH21	1.84	0.42
27:DB:57:A:N3	31:DG:29:TRP:HB3	2.33	0.42
32:DH:84:SER:HB3	32:DH:132:ARG:HH11	1.85	0.42
1:AA:171:A:H2'	1:AA:172:A:C8	2.54	0.42
1:AA:396:G:O2'	1:AA:398:C:OP1	2.23	0.42
2:AB:111:ARG:HG2	2:AB:111:ARG:HH11	1.84	0.42
8:AH:13:ILE:O	8:AH:17:THR:HG23	2.20	0.42
20:AT:13:LEU:HD12	20:AT:14:LYS:N	2.35	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:AY:18:G:N2	25:AY:58:A:C8	2.88	0.42
36:BP:63:PRO:HD3	55:B8:27:THR:HG22	2.00	0.42
26:BA:1405:A:H2'	26:BA:1406:A:H5'	2.02	0.42
26:BA:1961:U:OP1	26:BA:2616:U:O2'	2.33	0.42
26:BA:2161:C:H2'	26:BA:2162:C:H4'	2.01	0.42
26:BA:2718:G:N7	61:BA:4712:HOH:O	2.37	0.42
26:BA:624:C:O2'	26:BA:628:C:H5''	2.19	0.42
39:BS:58:LEU:HD23	39:BS:58:LEU:HA	1.71	0.42
34:BN:4:TYR:CE2	41:BU:100:VAL:HG11	2.55	0.42
46:BZ:108:PRO:CB	46:BZ:117:LEU:HD13	2.46	0.42
1:CA:1002:G:N2	1:CA:1038:C:N3	2.55	0.42
1:CA:1065:U:H1'	1:CA:1066:C:OP2	2.20	0.42
1:CA:1279:A:OP2	10:CJ:9:ARG:NH1	2.53	0.42
1:CA:1126:U:H4'	1:CA:1281:U:H1'	2.01	0.42
1:CA:1357:A:N7	1:CA:1358:U:C4	2.88	0.42
1:CA:1368:G:H2'	1:CA:1369:C:H5'	2.01	0.42
1:CA:695:A:H2'	1:CA:696:A:C8	2.55	0.42
5:CE:98:THR:HB	5:CE:117:ASP:HB3	2.01	0.42
8:CH:51:VAL:HG12	8:CH:52:ASP:H	1.84	0.42
1:CA:779:C:O2'	11:CK:120:ARG:HD3	2.20	0.42
19:CS:52:TYR:HB2	19:CS:57:HIS:CE1	2.55	0.42
26:DA:1019:U:H3	26:DA:1142(A):A:N6	2.06	0.42
26:DA:108:U:H2'	26:DA:109:G:H8	1.83	0.42
26:DA:1248:G:C5	41:DU:3:ARG:HB2	2.55	0.42
26:DA:1449:A:OP2	26:DA:1449:A:H8	2.02	0.42
26:DA:2055:C:H1'	29:DE:145:LYS:HE2	2.01	0.42
26:DA:2187:G:C6	26:DA:2188:C:N3	2.87	0.42
26:DA:2262:U:H4'	26:DA:2328:A:C2	2.54	0.42
31:DG:43:LEU:C	31:DG:45:GLU:H	2.21	0.42
33:DI:77:LEU:HG	33:DI:101:LEU:HD12	2.02	0.42
34:DN:128:HIS:HA	34:DN:129:PRO:HD3	1.81	0.42
26:DA:296:C:O3'	45:DY:95:LYS:NZ	2.52	0.42
46:DZ:121:HIS:HB3	46:DZ:123:ASP:O	2.20	0.42
46:DZ:71:VAL:HG13	46:DZ:88:PHE:CD1	2.54	0.42
1:AA:1304:G:C6	1:AA:1305:G:N1	2.88	0.42
1:AA:1493:A:H5''	1:AA:1494:G:OP2	2.20	0.42
1:AA:457:C:H2'	1:AA:458:C:C6	2.54	0.42
1:AA:636:U:H2'	1:AA:637:G:H8	1.84	0.42
4:AD:36:ARG:HB3	4:AD:38:TYR:CZ	2.55	0.42
8:AH:73:ASP:OD1	8:AH:75:ARG:NH1	2.49	0.42
10:AJ:8:LEU:CD2	10:AJ:96:ILE:HG23	2.50	0.42
16:AP:18:ARG:NH1	16:AP:32:TYR:OH	2.52	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2230:U:O4'	48:B1:52:ARG:NH2	2.53	0.42
51:B4:49:PHE:HA	51:B4:49:PHE:HD1	1.72	0.42
53:B6:8:LYS:HD3	55:B8:34:TRP:CD2	2.55	0.42
26:BA:1090:G:HO2'	26:BA:1157:A:N6	2.17	0.42
26:BA:1346:U:H4'	26:BA:1347:A:H5''	2.01	0.42
26:BA:1517:G:H5''	26:BA:1518:A:OP1	2.20	0.42
26:BA:1698:G:OP1	38:BR:40:LYS:HE3	2.20	0.42
26:BA:1699:A:C2'	26:BA:1700:G:H5'	2.49	0.42
26:BA:2331:G:C2	39:BS:3:ARG:HA	2.54	0.42
26:BA:2340:A:H2'	26:BA:2341:G:H8	1.80	0.42
26:BA:941:U:H5'	26:BA:942:A:OP1	2.20	0.42
31:BG:79:ASN:OD1	31:BG:79:ASN:N	2.52	0.42
26:BA:1002:A:H5'	37:BQ:76:LYS:HG2	2.02	0.42
42:BV:55:ALA:HB2	42:BV:101:GLY:HA2	2.02	0.42
46:BZ:19:ARG:HD3	46:BZ:25:PRO:CD	2.50	0.42
1:CA:1268:A:H2	1:CA:1326:C:O2	2.02	0.42
1:CA:1362:C:H2'	1:CA:1363:C:H5''	2.00	0.42
2:CB:70:PHE:HE1	2:CB:163:PHE:CD2	2.36	0.42
2:CB:95:GLN:HB2	2:CB:148:TYR:CD1	2.44	0.42
5:CE:79:GLU:HG2	5:CE:79:GLU:O	2.18	0.42
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.20	0.42
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HA	2.01	0.42
18:CR:73:ALA:CB	18:CR:79:LEU:HG	2.49	0.42
24:CX:21:A:H3'	24:CX:46:G:O6	2.19	0.42
26:DA:1242:A:N1	36:DP:4:SER:OG	2.41	0.42
26:DA:1262:A:H2	52:D5:10:LYS:HD2	1.84	0.42
26:DA:1266:G:O5'	43:DW:15:ARG:NH2	2.52	0.42
26:DA:11:G:H2'	26:DA:12:U:H5''	2.02	0.42
26:DA:1445(A):C:H2'	26:DA:1446:C:H6	1.83	0.42
26:DA:271(K):U:H4'	26:DA:271(L):U:OP1	2.20	0.42
26:DA:479:A:H4'	26:DA:480:A:OP1	2.19	0.42
26:DA:740:U:H2'	26:DA:741:G:H8	1.81	0.42
26:DA:807:U:OP2	36:DP:41:ARG:NH2	2.53	0.42
26:DA:820:A:N3	26:DA:943:U:H4'	2.35	0.42
28:DD:29:PRO:HA	28:DD:83:GLU:OE1	2.19	0.42
30:DF:117:ARG:HH12	36:DP:1:MET:N	2.18	0.42
37:DQ:141:GLN:NE2	46:DZ:74:VAL:O	2.39	0.42
1:AA:1262:C:H2'	1:AA:1263:C:C6	2.55	0.42
1:AA:1267:C:H6	1:AA:1267:C:O5'	2.02	0.42
1:AA:377:G:OP1	16:AP:3:LYS:HD3	2.20	0.42
1:AA:393:A:OP1	61:AA:4195:HOH:O	2.21	0.42
1:AA:627:G:O2'	1:AA:628:G:H5'	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:71:VAL:CG1	2:AB:170:GLU:HG2	2.49	0.42
5:AE:116:THR:HG23	5:AE:117:ASP:OD2	2.19	0.42
25:AY:24:G:C6	25:AY:25:C:C4	3.08	0.42
25:AY:53:G:N1	25:AY:61:C:N4	2.38	0.42
26:BA:160:G:C2'	26:BA:161:C:H5'	2.49	0.42
26:BA:174:U:H4'	26:BA:207:A:H4'	2.02	0.42
26:BA:2272:C:H2'	26:BA:2273:C:C6	2.55	0.42
26:BA:2820:A:N6	26:BA:2900:G:O2'	2.39	0.42
29:BE:141:ILE:HA	29:BE:154:LYS:HE2	2.02	0.42
32:BH:56:SER:HB3	32:BH:61:HIS:ND1	2.35	0.42
34:BN:4:TYR:CD2	41:BU:100:VAL:HG11	2.54	0.42
37:BQ:37:LEU:HD21	37:BQ:130:LYS:HD3	2.01	0.42
46:BZ:24:LEU:HD21	46:BZ:86:VAL:HG13	2.01	0.42
1:CA:1118:C:N1	1:CA:1119:C:H5	2.18	0.42
1:CA:255:G:C6	1:CA:256:U:C4	3.08	0.42
1:CA:456:C:H2'	1:CA:457:C:H5'	2.00	0.42
1:CA:586:C:O2'	1:CA:878:G:H4'	2.19	0.42
5:CE:80:ILE:HA	5:CE:80:ILE:HD12	1.87	0.42
6:CF:2:ARG:HG3	6:CF:69:GLU:HG3	2.02	0.42
13:CM:3:ARG:HG2	13:CM:8:GLU:HA	2.01	0.42
1:CA:1048:G:OP1	14:CN:3:ARG:HD2	2.19	0.42
17:CQ:76:LEU:HD12	17:CQ:77:VAL:H	1.84	0.42
6:CF:100:ASN:ND2	18:CR:23:LYS:HE3	2.34	0.42
25:CY:19:G:N3	25:CY:57:G:N1	2.68	0.42
25:CY:37:MIA:H2'	25:CY:38:A:O4'	2.20	0.42
53:D6:35:GLU:HA	53:D6:49:HIS:O	2.20	0.42
26:DA:1237:A:OP1	61:DA:4484:HOH:O	2.21	0.42
26:DA:1371:G:H2'	26:DA:1372:U:C5	2.51	0.42
26:DA:1748:G:H2'	26:DA:1749:A:O4'	2.20	0.42
26:DA:211:A:H2'	26:DA:212:G:O4'	2.20	0.42
26:DA:2140:C:C2	26:DA:2152:G:C2	3.07	0.42
26:DA:2150:U:H2'	26:DA:2151:G:C8	2.55	0.42
26:DA:644:A:C2	26:DA:2369:A:H1'	2.55	0.42
25:CY:76:A:N6	26:DA:2422:A:H5'	2.35	0.42
26:DA:708:C:N4	26:DA:723:G:H1	2.18	0.42
26:DA:848:G:C4	26:DA:933:A:C8	3.06	0.42
27:DB:40:U:N3	27:DB:44:G:OP2	2.48	0.42
28:DD:68:LYS:O	28:DD:69:ARG:HB2	2.20	0.42
30:DF:196:LEU:HA	30:DF:196:LEU:HD23	1.86	0.42
35:DO:73:ASP:OD2	40:DT:32:TYR:OH	2.35	0.42
41:DU:90:VAL:HG12	41:DU:95:LEU:HD12	2.02	0.42
46:DZ:97:GLU:HB2	46:DZ:125:LEU:HD11	2.02	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1210:C:C2'	1:AA:1211:U:H5'	2.50	0.42
1:AA:342:C:C2	1:AA:348:G:N2	2.88	0.42
1:AA:56:U:H2'	1:AA:57:G:H8	1.79	0.42
1:AA:674:G:H2'	1:AA:675:A:C8	2.53	0.42
1:AA:729:A:H2'	1:AA:730:G:H8	1.84	0.42
1:AA:820:U:H4'	1:AA:821:G:OP2	2.20	0.42
1:AA:16:A:O2'	5:AE:16:THR:HB	2.20	0.42
8:AH:49:GLU:HG2	8:AH:62:TYR:HE1	1.84	0.42
12:AL:34:ARG:HG3	12:AL:105:TYR:CE2	2.55	0.42
1:AA:584:G:H5'	17:AQ:91:ARG:NH2	2.35	0.42
18:AR:25:THR:OG1	18:AR:25:THR:O	2.32	0.42
26:BA:1903:C:H2'	26:BA:1904:C:C6	2.55	0.42
26:BA:2119:C:H2'	26:BA:2120:U:O4'	2.19	0.42
28:BD:242:ARG:HD3	28:BD:242:ARG:N	2.34	0.42
29:BE:14:ILE:HD11	29:BE:173:VAL:HG11	2.01	0.42
31:BG:18:GLU:OE1	31:BG:22:ARG:HD3	2.20	0.42
32:BH:54:ARG:HD3	32:BH:65:HIS:ND1	2.35	0.42
32:BH:98:LEU:HD13	32:BH:125:VAL:HG23	2.00	0.42
35:BO:4:PRO:O	35:BO:5:GLN:HB2	2.20	0.42
42:BV:5:VAL:HG21	42:BV:35:LEU:HD23	2.02	0.42
1:CA:1011:G:H21	1:CA:1019:C:H1'	1.84	0.42
1:CA:1162:C:H2'	1:CA:1163:C:O4'	2.20	0.42
1:CA:1203:C:H2'	1:CA:1204:A:O4'	2.20	0.42
1:CA:1323:G:O2'	1:CA:1362:C:O2'	2.23	0.42
1:CA:452:A:O2'	1:CA:453:A:OP2	2.34	0.42
2:CB:57:PHE:CE2	2:CB:185:ILE:HD12	2.50	0.42
2:CB:193:ASP:HA	2:CB:194:PRO:HD2	1.89	0.42
9:CI:20:ARG:HA	9:CI:21:PRO:HD3	1.92	0.42
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.46	0.42
14:CN:26:ARG:HD2	14:CN:43:CYS:HB3	2.01	0.42
14:CN:24:CYS:HA	14:CN:38:GLY:O	2.20	0.42
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.20	0.42
17:CQ:78:GLU:OE1	17:CQ:81:ARG:HD3	2.19	0.42
48:D1:72:GLU:OE1	48:D1:76:ARG:NH2	2.53	0.42
26:DA:1221(A):C:C2	26:DA:1229:G:C2	3.08	0.42
26:DA:1927:A:OP1	26:DA:1927:A:H8	2.03	0.42
26:DA:2110:G:H4'	26:DA:2111:C:OP2	2.20	0.42
26:DA:271(D):G:C6	26:DA:271(E):U:C4	3.08	0.42
26:DA:30:G:H2'	26:DA:31:C:O4'	2.19	0.42
26:DA:847:U:OP2	61:DA:4017:HOH:O	2.22	0.42
31:DG:49:ASP:N	31:DG:49:ASP:OD1	2.53	0.42
31:DG:72:ARG:HA	31:DG:86:MET:O	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
38:DR:65:LEU:HA	38:DR:65:LEU:HD12	1.87	0.42
42:DV:21:ARG:HG2	42:DV:91:TYR:CE2	2.55	0.42
1:AA:1362:C:C2'	1:AA:1363:C:H5''	2.49	0.41
1:AA:571:U:H5''	1:AA:819:A:C5	2.55	0.41
1:AA:841:U:C5	1:AA:848:C:H1'	2.54	0.41
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.34	0.41
15:AO:53:HIS:O	15:AO:56:LEU:HB3	2.20	0.41
21:AU:15:ARG:HH11	21:AU:15:ARG:HB2	1.85	0.41
25:AY:5:G:H2'	25:AY:6:G:H8	1.85	0.41
26:BA:2417:G:O2'	26:BA:2418:U:OP1	2.29	0.41
26:BA:312:C:H2'	26:BA:313:A:C8	2.49	0.41
26:BA:26:G:H1'	26:BA:540:A:H61	1.85	0.41
27:BB:40:U:H1'	27:BB:45:A:H61	1.84	0.41
28:BD:61:LEU:O	28:BD:63:ARG:NH1	2.53	0.41
46:BZ:104:PHE:CZ	46:BZ:119:GLU:HG2	2.55	0.41
46:BZ:5:LEU:O	46:BZ:59:LEU:HA	2.20	0.41
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.55	0.41
1:CA:337:C:H2'	1:CA:338:A:C8	2.54	0.41
1:CA:583:A:N6	1:CA:758:G:O2'	2.53	0.41
1:CA:804:U:OP1	61:CA:3206:HOH:O	2.21	0.41
1:CA:981:U:O5'	1:CA:981:U:H6	2.03	0.41
10:CJ:16:LEU:O	10:CJ:20:ALA:N	2.34	0.41
47:D0:52:GLY:O	47:D0:59:LEU:HA	2.20	0.41
26:DA:2093:G:C6	26:DA:2225:A:C8	3.08	0.41
26:DA:2147:G:C4	26:DA:2148:G:H1'	2.55	0.41
26:DA:2135:A:OP1	26:DA:2160:G:H1'	2.20	0.41
26:DA:2100:G:C6	26:DA:2190:G:C6	3.08	0.41
26:DA:2370:G:C6	26:DA:2371:G:C6	3.07	0.41
26:DA:2483:C:O2	37:DQ:124:LYS:NZ	2.52	0.41
26:DA:2833:G:H4'	26:DA:2834:G:OP2	2.20	0.41
26:DA:460:A:C2	26:DA:470:A:C4	3.08	0.41
26:DA:812:C:H2'	26:DA:813:U:H6	1.85	0.41
27:DB:19:G:H1	27:DB:64:C:H42	1.67	0.41
27:DB:80:U:H2'	27:DB:81:G:H8	1.85	0.41
28:DD:276:LYS:H	28:DD:276:LYS:CD	2.15	0.41
29:DE:146:THR:HA	29:DE:147:PRO:HA	1.90	0.41
31:DG:137:GLU:HB3	31:DG:139:LEU:HG	2.02	0.41
31:DG:33:ARG:O	31:DG:34:LEU:HD23	2.19	0.41
45:DY:2:ARG:NH1	45:DY:4:LYS:HA	2.35	0.41
45:DY:38:ILE:HD11	45:DY:66:PRO:HG3	2.01	0.41
45:DY:9:LYS:HA	45:DY:10:GLY:HA2	1.49	0.41
1:AA:690:G:C6	1:AA:691:G:C6	3.08	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:78:G:O2'	1:AA:79:G:H8	2.03	0.41
13:AM:5:ALA:HA	13:AM:61:GLU:OE2	2.18	0.41
1:AA:454:C:OP1	16:AP:75:ARG:NH2	2.53	0.41
17:AQ:87:LYS:HA	17:AQ:87:LYS:HD3	1.73	0.41
19:AS:12:ASP:OD1	19:AS:35:SER:HB3	2.19	0.41
19:AS:65:ASN:N	19:AS:65:ASN:ND2	2.66	0.41
19:AS:69:HIS:HD2	19:AS:73:GLU:OE1	2.03	0.41
25:AY:20:U:C4'	25:AY:21:A:H5'	2.50	0.41
25:AY:21:A:H8	25:AY:21:A:OP2	2.03	0.41
51:B4:46:GLN:N	51:B4:46:GLN:HE21	2.18	0.41
26:BA:1084:C:H42	26:BA:1163:G:H1	1.68	0.41
26:BA:1563:G:H2'	26:BA:1564:C:C6	2.55	0.41
26:BA:1925:G:OP1	28:BD:241:PRO:HB2	2.20	0.41
26:BA:2157:A:N6	26:BA:2178:G:O2'	2.53	0.41
26:BA:2172:U:H2'	26:BA:2172:U:O2	2.19	0.41
26:BA:2430:A:H2'	26:BA:2431:U:C6	2.54	0.41
26:BA:2797:C:H1'	29:BE:37:ARG:NH1	2.36	0.41
26:BA:7:G:H2'	26:BA:8:A:O4'	2.20	0.41
30:BF:140:LEU:HA	30:BF:140:LEU:HD13	1.86	0.41
32:BH:54:ARG:HA	32:BH:55:PRO:HD3	1.87	0.41
40:BT:27:THR:HB	40:BT:90:GLN:HB3	2.01	0.41
1:CA:1030(A):G:H2'	1:CA:1030(B):C:H5''	2.02	0.41
1:CA:1133:G:N2	1:CA:1141:C:N3	2.61	0.41
1:CA:1274:G:N2	1:CA:1275:A:H62	2.17	0.41
1:CA:1279:A:H5''	1:CA:1280:A:OP1	2.20	0.41
1:CA:266:G:H8	1:CA:266:G:H2'	1.68	0.41
1:CA:60:A:H4'	1:CA:61:G:O5'	2.21	0.41
2:CB:16:HIS:HD2	2:CB:204:ASN:H	1.67	0.41
13:CM:72:ALA:O	13:CM:76:ALA:N	2.48	0.41
20:CT:64:ASP:OD2	20:CT:81:LYS:NZ	2.44	0.41
24:CX:30:G:C6	24:CX:31:G:N7	2.89	0.41
25:C'Y:56:C:H2'	25:C'Y:57:G:O4'	2.20	0.41
49:D2:23:LYS:O	49:D2:27:GLU:HG3	2.20	0.41
26:DA:2297:C:N3	26:DA:2321:G:N2	2.66	0.41
26:DA:2875:C:H2'	26:DA:2876:G:O4'	2.20	0.41
26:DA:373:U:H2'	26:DA:374:A:C8	2.55	0.41
26:DA:382:G:OP2	61:DA:4359:HOH:O	2.22	0.41
26:DA:732:C:H2'	26:DA:733:G:O4'	2.20	0.41
26:DA:878:A:H61	26:DA:899:A:HO2'	1.59	0.41
36:DP:47:ASP:HA	36:DP:48:PRO:HD3	1.84	0.41
46:DZ:96:VAL:O	46:DZ:127:LYS:HA	2.20	0.41
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:114:U:H2'	1:AA:115:G:C8	2.54	0.41
1:AA:160:A:H61	1:AA:345:C:H5'	1.86	0.41
1:AA:456:C:H2'	1:AA:457:C:H5'	2.02	0.41
1:AA:624:C:O3'	16:AP:10:GLY:HA2	2.20	0.41
1:AA:6:G:O2'	1:AA:7:G:H5'	2.20	0.41
1:AA:812:C:OP1	1:AA:903:G:H1'	2.19	0.41
4:AD:194:LEU:HD12	4:AD:195:ALA:N	2.36	0.41
10:AJ:11:PHE:CE1	10:AJ:67:THR:HG22	2.51	0.41
13:AM:56:LEU:O	13:AM:60:VAL:HG23	2.19	0.41
20:AT:48:LYS:HA	20:AT:48:LYS:HD3	1.77	0.41
25:AY:22:G:N7	25:AY:46:7MG:C6	2.87	0.41
26:BA:2157:A:N1	26:BA:2178:G:O2'	2.44	0.41
26:BA:2164:C:C2	26:BA:2165:C:C5	3.08	0.41
26:BA:691:G:N2	26:BA:699:C:N3	2.64	0.41
26:BA:809:U:OP1	61:BA:4794:HOH:O	2.21	0.41
30:BF:120:GLU:HB2	30:BF:122:LYS:HG2	2.01	0.41
34:BN:67:LEU:HD12	34:BN:67:LEU:HA	1.82	0.41
23:AW:52:G:H4'	37:BQ:56:ARG:NH1	2.35	0.41
39:BS:59:LYS:HB2	39:BS:59:LYS:HE3	1.64	0.41
45:BY:9:LYS:HA	45:BY:10:GLY:HA2	1.68	0.41
46:BZ:150:LEU:O	46:BZ:171:ILE:HG13	2.19	0.41
1:CA:1044:A:C5	1:CA:1045:C:H1'	2.55	0.41
1:CA:1096:C:H2'	1:CA:1097:C:C6	2.55	0.41
1:CA:51:A:N7	1:CA:114:U:O2'	2.53	0.41
1:CA:617:G:H4'	16:CP:44:THR:O	2.19	0.41
2:CB:70:PHE:CD1	2:CB:163:PHE:HB3	2.55	0.41
7:CG:65:ALA:O	7:CG:69:VAL:HG23	2.20	0.41
8:CH:58:TYR:O	8:CH:59:LEU:HD23	2.19	0.41
23:CW:18:G:O6	23:CW:55:PSU:H1'	2.20	0.41
25:C'Y:35:A:H3'	25:C'Y:36:A:C8	2.55	0.41
25:C'Y:18:G:N2	25:C'Y:55:PSU:N3	2.68	0.41
48:D1:86:SER:OG	48:D1:89:GLU:OE2	2.19	0.41
49:D2:41:ILE:HG13	49:D2:43:GLN:HB2	2.02	0.41
26:DA:1291:C:H2'	26:DA:1292:U:C6	2.55	0.41
26:DA:1463:C:H2'	26:DA:1464:C:H6	1.86	0.41
26:DA:1860:G:C6	26:DA:1883:G:N2	2.88	0.41
26:DA:2137:C:C2	26:DA:2138:C:C5	3.09	0.41
26:DA:2366:A:H2'	26:DA:2367:G:O4'	2.20	0.41
26:DA:38:A:H2'	26:DA:39:C:C6	2.55	0.41
26:DA:565:C:H4'	26:DA:1253:A:N6	2.35	0.41
26:DA:956:G:OP2	37:DQ:14:ARG:NH2	2.53	0.41
26:DA:980:A:C4	26:DA:1136:G:O4'	2.73	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:DB:32:C:H2'	27:DB:33:G:O4'	2.20	0.41
29:DE:7:VAL:HG12	29:DE:27:LEU:HB3	2.01	0.41
30:DF:20:LEU:HD23	30:DF:20:LEU:HA	1.90	0.41
46:DZ:159:PRO:HA	46:DZ:161:VAL:H	1.84	0.41
46:DZ:124:ILE:HD11	46:DZ:163:LEU:HD11	2.02	0.41
46:DZ:98:MET:SD	46:DZ:100:VAL:HG23	2.60	0.41
23:AW:66:U:H2'	23:AW:67:C:C6	2.55	0.41
25:AY:68:C:C4	25:AY:69:G:N7	2.89	0.41
29:BE:96:PHE:O	29:BE:175:VAL:HG11	2.20	0.41
32:BH:56:SER:OG	32:BH:57:ASP:N	2.54	0.41
34:BN:61:ARG:HE	34:BN:61:ARG:HA	1.85	0.41
1:CA:1050:G:C6	1:CA:1051:C:C4	3.09	0.41
1:CA:1070:U:H2'	1:CA:1071:C:C6	2.52	0.41
1:CA:1183:A:H5'	1:CA:1183:A:C8	2.53	0.41
1:CA:1272:G:H2'	1:CA:1273:G:O4'	2.20	0.41
1:CA:1290:G:C4	1:CA:1291:G:C8	3.08	0.41
1:CA:922:G:N3	1:CA:1398:A:H2	2.19	0.41
1:CA:1412:C:H2'	1:CA:1413:A:H8	1.81	0.41
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.21	0.41
1:CA:1496:C:H2'	1:CA:1497:G:O4'	2.21	0.41
1:CA:445:G:H2'	1:CA:446:G:C8	2.55	0.41
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.68	0.41
1:CA:607:A:H2'	1:CA:608:A:O4'	2.20	0.41
1:CA:839:U:H5''	1:CA:840:C:C5	2.56	0.41
2:CB:32:ILE:HD13	2:CB:40:HIS:CG	2.55	0.41
3:CC:66:VAL:HB	3:CC:101:LEU:HA	2.02	0.41
3:CC:116:VAL:O	3:CC:120:VAL:HG23	2.21	0.41
8:CH:28:ALA:HB3	8:CH:57:PRO:HB2	2.03	0.41
9:CI:96:LEU:O	9:CI:100:GLY:N	2.54	0.41
13:CM:91:ARG:HH22	13:CM:103:THR:CG2	2.33	0.41
1:CA:1114:C:O2'	14:CN:60:SER:O	2.32	0.41
1:CA:237:C:H5''	17:CQ:25:ARG:CZ	2.49	0.41
19:CS:5:LEU:HG	19:CS:5:LEU:H	1.48	0.41
37:DQ:81:VAL:HB	47:D0:7:LEU:HD21	2.01	0.41
26:DA:108:U:H2'	26:DA:109:G:C8	2.56	0.41
26:DA:1638:C:H5''	26:DA:2710:C:O2'	2.21	0.41
26:DA:859:G:O2'	26:DA:916:G:O6	2.24	0.41
26:DA:96:G:H4'	49:D2:48:HIS:CD2	2.55	0.41
30:DF:178:PRO:HB2	30:DF:201:VAL:CG2	2.49	0.41
31:DG:38:VAL:HG22	31:DG:93:THR:HG23	2.02	0.41
32:DH:117:PRO:HG3	32:DH:123:PHE:CD2	2.55	0.41
32:DH:90:LYS:HD2	32:DH:163:TYR:CD1	2.54	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
34:DN:4:TYR:HB2	41:DU:101:ARG:NH1	2.35	0.41
36:DP:97:PRO:HD3	36:DP:126:VAL:O	2.19	0.41
37:DQ:18:LYS:HE3	37:DQ:18:LYS:HB2	1.68	0.41
40:DT:65:LYS:HE2	40:DT:67:SER:HB2	2.02	0.41
1:AA:1152:A:H2'	1:AA:1153:C:C6	2.55	0.41
1:AA:971:G:N2	1:AA:1363(A):A:OP2	2.46	0.41
1:AA:266:G:H4'	1:AA:267:C:C5	2.55	0.41
1:AA:374:A:C6	1:AA:375:U:C4	3.08	0.41
1:AA:975:A:H4'	1:AA:976:G:C5'	2.46	0.41
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	2.03	0.41
4:AD:111:ALA:HB1	4:AD:116:GLN:HB3	2.03	0.41
11:AK:81:ASP:HB3	11:AK:107:SER:OG	2.21	0.41
13:AM:40:ASN:HA	13:AM:41:PRO:HD3	1.84	0.41
13:AM:54:VAL:HA	13:AM:57:ARG:HB3	2.03	0.41
24:AX:27:U:H2'	24:AX:28:C:C6	2.56	0.41
25:AY:62:C:H2'	25:AY:63:G:C8	2.51	0.41
25:AY:6:G:C6	25:AY:7:A:C6	3.08	0.41
26:BA:1405:A:N1	26:BA:1418:U:O4	2.54	0.41
26:BA:2710:U:H2'	26:BA:2711:C:C6	2.55	0.41
26:BA:518:G:H2'	26:BA:519:G:O4'	2.20	0.41
26:BA:27:G:C2	26:BA:537:G:N3	2.88	0.41
30:BF:143:ALA:HB1	30:BF:148:LEU:HB2	2.02	0.41
44:BX:12:VAL:HG21	44:BX:27:THR:HG22	2.03	0.41
44:BX:31:HIS:HA	44:BX:32:PRO:HD3	1.96	0.41
46:BZ:8:TYR:HB2	46:BZ:38:TYR:CE2	2.56	0.41
1:CA:1030(A):G:N3	1:CA:1030(C):G:C8	2.88	0.41
1:CA:1128:C:H1'	1:CA:1147:C:N4	2.31	0.41
1:CA:411:A:C8	1:CA:413:G:C8	3.09	0.41
1:CA:932:C:H4'	7:CG:4:ARG:NH2	2.35	0.41
3:CC:11:ARG:HD3	3:CC:15:THR:HG21	2.01	0.41
1:CA:1373:G:H5''	7:CG:36:LYS:HD2	2.03	0.41
8:CH:6:ILE:O	8:CH:10:LEU:HG	2.19	0.41
10:CJ:6:ILE:O	10:CJ:71:LEU:HD12	2.21	0.41
12:CL:33:ARG:O	12:CL:85:ILE:HG12	2.21	0.41
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.53	0.41
25:CY:38:A:C2'	25:CY:39:PSU:H5'	2.50	0.41
26:DA:120:U:H5''	26:DA:122:G:OP2	2.20	0.41
26:DA:1857:G:C6	26:DA:1858:G:C6	3.08	0.41
25:CY:76:A:H62	26:DA:2422:A:H5'	1.86	0.41
26:DA:328:U:H4'	45:DY:68:HIS:CG	2.56	0.41
26:DA:266:G:N2	26:DA:427:U:H1'	2.35	0.41
26:DA:443:A:H1'	26:DA:1201:C:O4'	2.19	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:DG:136:ARG:HD2	31:DG:137:GLU:HG3	2.03	0.41
36:DP:126:VAL:HG12	36:DP:148:LEU:HD22	2.03	0.41
1:AA:1002:G:H3'	1:AA:1003:G:O4'	2.20	0.41
1:AA:1241:G:O2'	1:AA:1242:C:H5'	2.20	0.41
1:AA:992:U:H4'	1:AA:993:G:C5'	2.50	0.41
2:AB:20:GLU:HA	2:AB:21:ARG:HH21	1.86	0.41
2:AB:92:TYR:CE1	2:AB:151:GLY:HA3	2.55	0.41
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.20	0.41
3:AC:179:ARG:NH1	3:AC:206:GLU:OE1	2.54	0.41
5:AE:77:PRO:HG2	5:AE:78:HIS:HD2	1.85	0.41
1:AA:1368:G:OP2	9:AI:112:LYS:HG3	2.20	0.41
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.36	0.41
20:AT:59:ALA:O	20:AT:63:ILE:HG13	2.21	0.41
48:B1:85:LEU:HB3	48:B1:89:GLU:HG3	2.03	0.41
26:BA:107:G:H2'	26:BA:108:G:O4'	2.20	0.41
26:BA:1566:U:H2'	26:BA:1567:G:O4'	2.20	0.41
29:BE:59:VAL:HG21	29:BE:74:PRO:HB3	2.02	0.41
30:BF:196:LEU:HA	30:BF:196:LEU:HD23	1.91	0.41
31:BG:33:ARG:N	31:BG:162:THR:OG1	2.52	0.41
32:BH:33:LEU:HD21	32:BH:136:ILE:HG13	2.02	0.41
38:BR:118:GLU:H	38:BR:118:GLU:CD	2.23	0.41
39:BS:83:LYS:HB2	39:BS:83:LYS:HE2	1.88	0.41
40:BT:42:ILE:HG12	40:BT:84:GLN:NE2	2.36	0.41
45:BY:55:TYR:CD1	45:BY:55:TYR:N	2.88	0.41
1:CA:1179:A:C2	1:CA:1180:A:H1'	2.55	0.41
1:CA:1401:G:C2	1:CA:1402:C:H1'	2.55	0.41
1:CA:615:C:H2'	1:CA:616:G:O4'	2.20	0.41
1:CA:918:A:H2'	1:CA:919:A:O4'	2.21	0.41
13:CM:50:GLU:HG3	13:CM:50:GLU:O	2.20	0.41
21:CU:6:ARG:HG2	21:CU:15:ARG:HD2	2.02	0.41
51:D4:60:GLN:O	51:D4:63:TYR:HE2	2.03	0.41
26:DA:1153:C:H2'	26:DA:1154:G:O4'	2.20	0.41
26:DA:1446:C:N4	26:DA:1465:G:H1	2.19	0.41
26:DA:1968:G:OP1	61:DA:4233:HOH:O	2.22	0.41
26:DA:2238:G:H2'	26:DA:2238:G:N3	2.35	0.41
26:DA:2507:C:H2'	26:DA:2508:G:O4'	2.21	0.41
26:DA:2751:G:C8	32:DH:2:SER:HA	2.56	0.41
26:DA:431:U:H6	26:DA:431:U:O5'	2.02	0.41
26:DA:79:G:H1	26:DA:107:C:N4	2.19	0.41
26:DA:1567:A:H2'	28:DD:84:TYR:HE2	1.86	0.41
31:DG:68:PRO:HB3	31:DG:92:VAL:HB	2.02	0.41
34:DN:97:ARG:HA	34:DN:100:GLU:HB2	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1754:C:OP2	40:DT:113:LYS:HE2	2.21	0.41
1:AA:190:U:H3'	1:AA:190:U:H6	1.85	0.41
2:AB:47:THR:HA	2:AB:202:PRO:HG2	2.02	0.41
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.30	0.41
4:AD:57:ARG:HB3	4:AD:206:PHE:HB2	2.01	0.41
1:AA:4:U:O4	8:AH:105:ARG:HD3	2.20	0.41
8:AH:87:SER:HB2	8:AH:93:VAL:H	1.85	0.41
1:AA:1317:C:OP1	14:AN:17:LYS:HG2	2.19	0.41
26:BA:142:G:H2'	26:BA:143:C:C6	2.55	0.41
26:BA:2346:G:H4'	26:BA:2347:A:OP2	2.20	0.41
26:BA:2378:A:H2'	26:BA:2379:G:O4'	2.21	0.41
26:BA:2724:U:O2'	26:BA:2726:A:H5'	2.21	0.41
26:BA:2885:C:O2'	40:BT:4:GLY:HA3	2.21	0.41
27:BB:75:G:H5''	27:BB:75:G:H8	1.85	0.41
32:BH:11:VAL:CG2	32:BH:50:VAL:HG23	2.50	0.41
1:CA:1070:U:O2'	1:CA:1071:C:H5'	2.21	0.41
1:CA:278:G:OP2	17:CQ:41:LYS:NZ	2.36	0.41
1:CA:340:U:H2'	1:CA:341:C:C6	2.56	0.41
1:CA:418:C:H2'	1:CA:419:C:C6	2.56	0.41
3:CC:70:VAL:HG13	3:CC:73:PRO:HA	2.02	0.41
6:CF:55:ASP:HA	6:CF:56:PRO:HD3	1.83	0.41
9:CI:17:VAL:HG11	9:CI:81:ILE:N	2.36	0.41
11:CK:82:VAL:HB	11:CK:108:ILE:HG12	2.02	0.41
13:CM:3:ARG:CB	51:D4:34:GLU:HG2	2.50	0.41
23:CW:11:C:N4	23:CW:24:G:H1	2.17	0.41
25:CY:27:G:N1	25:CY:43:C:O2	2.49	0.41
55:D8:34:TRP:CG	55:D8:35:GLN:N	2.89	0.41
26:DA:1470:G:N2	26:DA:1523:U:C4	2.88	0.41
26:DA:2161:C:H2'	26:DA:2162:G:O4'	2.20	0.41
26:DA:624:C:O2'	26:DA:657:U:OP1	2.36	0.41
27:DB:118:G:C2'	27:DB:119:G:H5'	2.51	0.41
28:DD:61:LEU:HA	28:DD:61:LEU:HD12	1.93	0.41
27:DB:57:A:C4	31:DG:29:TRP:HB3	2.55	0.41
32:DH:15:VAL:HG23	32:DH:27:LYS:O	2.21	0.41
26:DA:1012:U:C4	34:DN:25:ARG:HG2	2.56	0.41
34:DN:26:LEU:O	34:DN:30:ILE:HG13	2.21	0.41
46:DZ:4:ARG:HD3	46:DZ:60:GLU:OE1	2.21	0.41
1:AA:1418:A:H2	26:BA:1970:G:N3	2.19	0.41
1:AA:1469:G:H2'	1:AA:1470:G:H8	1.86	0.41
1:AA:154:C:N3	1:AA:168:G:C2	2.88	0.41
1:AA:839:U:HO2'	1:AA:840:C:P	2.35	0.41
1:AA:920:U:H2'	1:AA:921:U:C6	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:938:A:C6	1:AA:939:G:C5	3.09	0.41
1:AA:958:A:C6	1:AA:959:A:N1	2.88	0.41
1:AA:995:C:H5'	14:AN:8:GLU:HG2	2.02	0.41
3:AC:32:LEU:HD13	3:AC:59:ARG:HD3	2.02	0.41
8:AH:75:ARG:HA	8:AH:76:PRO:HD2	1.87	0.41
14:AN:25:VAL:HG22	14:AN:38:GLY:O	2.20	0.41
24:AX:61:C:H2'	24:AX:62:C:C6	2.56	0.41
50:B3:16:PRO:HB2	50:B3:18:ASP:OD1	2.20	0.41
51:B4:34:GLU:HG3	51:B4:34:GLU:H	1.56	0.41
51:B4:53:GLU:HB3	51:B4:54:GLY:O	2.21	0.41
26:BA:1224:C:H2'	26:BA:1225:C:C6	2.52	0.41
26:BA:2153:G:H5'	26:BA:2155:G:O4'	2.21	0.41
26:BA:2299:A:H2	26:BA:2358:A:H62	1.64	0.41
26:BA:2092:G:C2	26:BA:2454:C:C2	3.09	0.41
26:BA:581:G:OP1	34:BN:111:PRO:HD2	2.21	0.41
26:BA:928:G:H1	26:BA:943:C:N4	2.19	0.41
29:BE:119:ARG:HD2	29:BE:120:TRP:CE2	2.55	0.41
45:BY:91:GLU:OE2	45:BY:91:GLU:N	2.54	0.41
1:CA:1084:G:OP1	1:CA:1086:U:C2	2.73	0.41
1:CA:1134:G:C2	1:CA:1135:U:H1'	2.56	0.41
1:CA:1427:U:H2'	1:CA:1428:A:C8	2.55	0.41
1:CA:443:C:H2'	1:CA:444:C:H6	1.85	0.41
8:CH:35:ILE:HG22	8:CH:39:LEU:HD23	2.03	0.41
1:CA:972:C:O2'	10:CJ:55:LYS:O	2.39	0.41
13:CM:37:THR:HG21	13:CM:56:LEU:HA	2.03	0.41
14:CN:22:THR:HB	14:CN:33:VAL:HG21	2.03	0.41
14:CN:45:ARG:O	14:CN:49:HIS:CD2	2.74	0.41
1:CA:265:G:H5'	17:CQ:64:PRO:O	2.20	0.41
26:DA:1165:U:H6	26:DA:1165:U:O5'	2.04	0.41
26:DA:1445(A):C:H2'	26:DA:1446:C:C6	2.56	0.41
26:DA:889:C:O2'	26:DA:890:A:O5'	2.36	0.41
26:DA:899:A:C2'	26:DA:900:A:H5''	2.51	0.41
28:DD:72:LYS:HE3	28:DD:72:LYS:HB3	1.85	0.41
29:DE:5:LEU:HD21	29:DE:79:ARG:HB2	2.03	0.41
30:DF:64:ILE:HG13	30:DF:65:TRP:N	2.36	0.41
31:DG:122:PRO:HG2	31:DG:182:LYS:O	2.20	0.41
31:DG:33:ARG:NH2	31:DG:162:THR:HG21	2.35	0.41
32:DH:86:GLU:CD	32:DH:130:ARG:HD3	2.41	0.41
26:DA:637:A:C8	36:DP:117:GLU:HG3	2.55	0.41
46:DZ:50:GLN:CD	46:DZ:50:GLN:N	2.73	0.41
46:DZ:70:LEU:O	46:DZ:89:PHE:N	2.44	0.41
1:AA:1427:U:H2'	1:AA:1428:A:C8	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:571:U:H5''	1:AA:819:A:C4	2.56	0.41
1:AA:925:G:H1'	1:AA:1502:A:C4	2.55	0.41
1:AA:1060:C:C4	3:AC:2:GLY:HA3	2.56	0.41
6:AF:9:VAL:HA	6:AF:59:TYR:O	2.20	0.41
16:AP:72:ARG:O	16:AP:76:GLN:N	2.30	0.41
17:AQ:9:VAL:CG2	17:AQ:84:LEU:HD13	2.50	0.41
23:AW:9:A:H1'	23:AW:45:U:H2'	2.03	0.41
50:B3:31:LEU:O	50:B3:32:GLN:HB2	2.21	0.41
52:B5:35:GLU:HG3	52:B5:51:TYR:CG	2.56	0.41
26:BA:1398:U:OP2	61:BA:4017:HOH:O	2.22	0.41
26:BA:2151:C:C2	26:BA:2152:U:H5	2.39	0.41
26:BA:418:G:H1'	26:BA:438:G:O4'	2.20	0.41
26:BA:992:G:H2'	26:BA:993:G:C8	2.56	0.41
33:BI:106:GLY:N	33:BI:107:VAL:HG23	2.36	0.41
34:BN:39:ARG:HA	34:BN:40:PRO:HD3	1.84	0.41
1:CA:1011:G:C2	1:CA:1019:C:C2	3.09	0.41
1:CA:1252:A:H2'	1:CA:1253:G:O4'	2.21	0.41
1:CA:1321:C:H3'	1:CA:1322:C:C6	2.56	0.41
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.21	0.41
1:CA:1529:G:H4'	1:CA:1530:G:OP2	2.21	0.41
1:CA:784:C:H4'	26:DA:1837:C:OP1	2.20	0.41
2:CB:48:MET:HA	2:CB:51:LEU:CD2	2.51	0.41
4:CD:163:GLU:O	4:CD:166:LYS:HG2	2.20	0.41
7:CG:91:VAL:HB	7:CG:96:GLN:HG2	2.02	0.41
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.54	0.41
9:CI:7:THR:OG1	9:CI:83:ARG:NH1	2.54	0.41
1:CA:974:A:P	14:CN:29:ARG:HH21	2.44	0.41
15:CO:85:LEU:HA	15:CO:85:LEU:HD23	1.82	0.41
19:CS:23:ASN:HA	19:CS:27:GLU:CD	2.41	0.41
50:D3:4:LEU:O	50:D3:36:VAL:HA	2.21	0.41
51:D4:24:THR:OG1	51:D4:25:TYR:N	2.54	0.41
26:DA:1257:C:H2'	26:DA:1258:C:C6	2.56	0.41
26:DA:2009:G:OP1	43:DW:41:LYS:HE2	2.20	0.41
26:DA:854:G:H2'	26:DA:855:G:C8	2.54	0.41
26:DA:899:A:O2'	26:DA:900:A:H5''	2.21	0.41
26:DA:923:C:H2'	26:DA:924:C:H6	1.84	0.41
29:DE:2:LYS:NZ	29:DE:95:ILE:O	2.40	0.41
32:DH:84:SER:CB	32:DH:132:ARG:HH11	2.33	0.41
32:DH:35:VAL:HA	32:DH:36:PRO:HD2	1.94	0.41
26:DA:25:U:H5'	43:DW:78:GLU:O	2.21	0.41
46:DZ:70:LEU:HA	46:DZ:70:LEU:HD23	1.80	0.41
1:AA:1026:G:N3	1:AA:1026:G:H2'	2.35	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:34:C:H2'	1:AA:35:G:C8	2.56	0.41
1:AA:953:G:H5'	1:AA:965:A:N6	2.31	0.41
1:AA:981:U:H6	1:AA:981:U:O5'	2.04	0.41
8:AH:118:VAL:O	8:AH:119:LEU:HD23	2.21	0.41
13:AM:84:ILE:CG1	13:AM:85:GLY:HA2	2.44	0.41
13:AM:94:ARG:CZ	19:AS:80:TYR:HD2	2.34	0.41
1:AA:1457:G:P	20:AT:39:LYS:NZ	2.94	0.41
1:AA:1305:G:OP2	21:AU:2:GLY:N	2.53	0.41
49:B2:13:ALA:HA	49:B2:16:LEU:HD12	2.03	0.41
50:B3:31:LEU:HD23	50:B3:31:LEU:HA	1.87	0.41
26:BA:2160:C:C2	26:BA:2176:G:C2	3.08	0.41
26:BA:2178:G:H21	26:BA:2179:G:H22	1.69	0.41
26:BA:2801:C:OP1	29:BE:61:ARG:NH2	2.48	0.41
15:AO:56:LEU:HD21	26:BA:762:G:C2	2.56	0.41
28:BD:108:PRO:HB3	28:BD:143:HIS:HE1	1.84	0.41
31:BG:137:GLU:HG2	31:BG:152:LEU:HD22	2.03	0.41
26:BA:2653:G:H5'	34:BN:83:LYS:HE2	2.03	0.41
35:BO:10:VAL:HG21	35:BO:16:ALA:HB3	2.03	0.41
35:BO:9:GLU:H	35:BO:9:GLU:HG2	1.72	0.41
44:BX:61:GLY:HA3	44:BX:73:ARG:O	2.21	0.41
1:CA:131:C:H2'	1:CA:132:C:C6	2.55	0.41
1:CA:1401:G:OP1	22:CV:18:G:O2'	2.28	0.41
1:CA:1442:G:HO2'	1:CA:1442(A):G:P	2.39	0.41
3:CC:122:GLU:HA	3:CC:125:GLU:OE1	2.21	0.41
4:CD:191:ARG:HD2	4:CD:191:ARG:HA	1.94	0.41
1:CA:875:C:O2'	8:CH:14:ARG:HD2	2.21	0.41
13:CM:24:GLY:C	13:CM:25:ILE:HD12	2.41	0.41
13:CM:47:ASP:C	13:CM:48:LEU:HD23	2.41	0.41
1:CA:974:A:O4'	14:CN:31:ARG:HD3	2.21	0.41
49:D2:31:GLU:O	49:D2:35:LEU:HG	2.21	0.41
31:DG:105:LYS:NZ	51:D4:25:TYR:O	2.53	0.41
53:D6:43:CYS:O	53:D6:45:LYS:HG2	2.21	0.41
54:D7:8:ASN:HB3	54:D7:11:LYS:HB3	2.02	0.41
26:DA:1116:C:H2'	26:DA:1117:G:C8	2.55	0.41
26:DA:116:C:H2'	26:DA:117:G:O4'	2.21	0.41
26:DA:819:A:C4	26:DA:1189:A:C2	3.09	0.41
26:DA:793:A:OP2	26:DA:2072:G:H5'	2.20	0.41
26:DA:2193:G:H2'	26:DA:2194:G:C8	2.56	0.41
28:DD:213:ARG:HD2	28:DD:213:ARG:HA	1.86	0.41
33:DI:79:ILE:HA	33:DI:80:PRO:HD2	1.90	0.41
37:DQ:79:LEU:C	37:DQ:80:GLU:HG2	2.42	0.41
39:DS:15:ARG:HB3	39:DS:19:LYS:NZ	2.36	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
39:DS:16:ASN:O	39:DS:19:LYS:HG2	2.21	0.41
44:DX:1:MET:N	49:D2:29:LYS:HE3	2.36	0.41
1:AA:976:G:N2	1:AA:1363:C:OP2	2.45	0.41
1:AA:439:A:C8	1:AA:496:A:C6	3.09	0.41
3:AC:8:ILE:HD12	3:AC:8:ILE:HA	1.94	0.41
4:AD:105:VAL:HG13	4:AD:110:PHE:HB2	2.02	0.41
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.21	0.41
6:AF:61:LEU:HD13	6:AF:61:LEU:HA	1.86	0.41
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.53	0.41
22:AV:16:A:H2'	22:AV:17:U:O4'	2.21	0.41
25:AY:5:G:C6	25:AY:6:G:C6	3.08	0.41
51:B4:53:GLU:O	51:B4:56:VAL:HG13	2.21	0.41
26:BA:1067:A:C8	26:BA:1068:G:H5''	2.55	0.41
26:BA:1454:C:H2'	26:BA:1455:C:C6	2.56	0.41
26:BA:1524:A:C2	26:BA:1563:G:C2	3.09	0.41
26:BA:2176:G:H2'	26:BA:2177:G:H5'	2.03	0.41
26:BA:2285:A:H2'	26:BA:2286:A:C8	2.55	0.41
26:BA:2308:U:OP2	39:BS:9:ARG:NH2	2.49	0.41
26:BA:507:G:C4	26:BA:532:A:C2	3.09	0.41
26:BA:629:U:H4'	26:BA:705:C:H4'	2.03	0.41
27:BB:92:C:OP1	46:BZ:79:ARG:NH1	2.54	0.41
30:BF:165:ARG:HG2	30:BF:168:ARG:NH2	2.36	0.41
31:BG:56:ALA:HA	31:BG:153:ARG:HH21	1.86	0.41
33:BI:47:LEU:O	33:BI:51:ILE:HG13	2.21	0.41
37:BQ:48:GLU:O	37:BQ:52:VAL:HG23	2.20	0.41
26:BA:1696:G:O2'	38:BR:107:ASP:OD2	2.32	0.41
1:CA:1163:C:C2	1:CA:1174:G:C2	3.09	0.41
1:CA:1267:C:N4	1:CA:1268:A:C6	2.89	0.41
1:CA:423:G:H3'	1:CA:423:G:N3	2.35	0.41
1:CA:61:G:C5	1:CA:107:G:C2	3.08	0.41
1:CA:757:U:O2'	1:CA:879:C:O2	2.38	0.41
8:CH:64:LYS:HB3	8:CH:79:VAL:HG21	2.02	0.41
12:CL:89:ARG:HG2	12:CL:90:VAL:N	2.36	0.41
20:CT:36:LEU:HA	20:CT:36:LEU:HD13	1.90	0.41
24:CX:3:C:H2'	24:CX:4:G:C8	2.56	0.41
26:DA:1005:C:H2'	26:DA:1006:C:H6	1.83	0.41
26:DA:1518:U:H2'	26:DA:1519:G:O4'	2.20	0.41
26:DA:1575:C:H2'	26:DA:1576:U:O4'	2.21	0.41
26:DA:2135:A:H61	26:DA:2157:G:N2	2.19	0.41
26:DA:25:U:C4	26:DA:26:G:C6	3.09	0.41
26:DA:2669:G:C2	26:DA:2670:A:C8	3.09	0.41
26:DA:642:G:H21	26:DA:646:A:H2	1.68	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:706:A:H2'	26:DA:707:G:O4'	2.21	0.41
26:DA:77:C:O2'	49:D2:14:ARG:NH2	2.52	0.41
28:DD:237:GLU:OE2	61:DD:401:HOH:O	2.22	0.41
26:DA:590:A:P	30:DF:95:ARG:HH11	2.44	0.41
31:DG:56:ALA:HA	31:DG:153:ARG:HH21	1.85	0.41
32:DH:54:ARG:HB3	32:DH:65:HIS:CD2	2.56	0.41
35:DO:20:MET:HE3	35:DO:44:LYS:HE3	2.03	0.41
41:DU:86:ALA:O	42:DV:49:THR:HG23	2.20	0.41
1:AA:1028:C:C2	1:AA:1029:C:H1'	2.56	0.40
1:AA:1047:G:C2'	1:AA:1048:G:H5'	2.51	0.40
1:AA:165:C:H2'	1:AA:166:G:C8	2.56	0.40
1:AA:183:G:H1	1:AA:194:C:H42	1.69	0.40
1:AA:44:G:N7	61:AA:4044:HOH:O	2.37	0.40
2:AB:161:ALA:HB1	2:AB:185:ILE:HD11	2.02	0.40
2:AB:183:PRO:HA	2:AB:198:ASP:OD2	2.21	0.40
3:AC:110:ASN:O	3:AC:141:VAL:HG22	2.21	0.40
4:AD:178:VAL:HG12	4:AD:179:GLU:N	2.35	0.40
14:AN:50:LYS:HB2	14:AN:50:LYS:HE2	1.76	0.40
19:AS:42:PRO:HD2	51:B4:61:ARG:HH21	1.86	0.40
26:BA:231:G:H5''	55:B8:64:TYR:CZ	2.57	0.40
26:BA:1153:G:N2	26:BA:1154:U:O4	2.54	0.40
26:BA:1217:G:N7	26:BA:1218:G:C8	2.89	0.40
26:BA:1891:G:N2	26:BA:1904:C:O2	2.49	0.40
26:BA:2159:C:H2'	26:BA:2160:C:C6	2.56	0.40
26:BA:2213:G:H8	26:BA:2213:G:C5'	2.33	0.40
26:BA:2459:G:N2	26:BA:2462:A:OP2	2.53	0.40
26:BA:298:G:H2'	26:BA:299:G:C8	2.56	0.40
29:BE:144:ARG:HB3	29:BE:145:LYS:H	1.53	0.40
29:BE:51:PHE:CD2	29:BE:52:LEU:HG	2.56	0.40
30:BF:177:ALA:O	30:BF:180:GLY:N	2.45	0.40
26:BA:496:A:OP1	30:BF:59:TYR:HE1	2.03	0.40
31:BG:64:THR:HB	31:BG:94:LEU:HD21	2.03	0.40
32:BH:94:TYR:HA	32:BH:106:THR:O	2.21	0.40
26:BA:1040:C:OP1	41:BU:53:ARG:NH2	2.54	0.40
46:BZ:158:PRO:HA	46:BZ:159:PRO:HD3	1.90	0.40
46:BZ:76:LEU:HA	46:BZ:76:LEU:HD12	1.87	0.40
46:BZ:7:ALA:O	46:BZ:62:PRO:HD3	2.21	0.40
1:CA:130:A:H1'	1:CA:263:A:O2'	2.20	0.40
1:CA:1350:A:OP1	9:CI:121:ARG:HD3	2.22	0.40
1:CA:629:G:H2'	1:CA:630:G:O4'	2.21	0.40
1:CA:895:G:N7	61:CA:3246:HOH:O	2.37	0.40
1:CA:9:G:H2'	1:CA:10:A:C8	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:CB:48:MET:HA	2:CB:51:LEU:HD21	2.02	0.40
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.46	0.40
4:CD:179:GLU:O	4:CD:181:MET:HE2	2.21	0.40
10:CJ:42:THR:HG23	10:CJ:68:HIS:HD2	1.86	0.40
12:CL:119:LYS:O	12:CL:120:TYR:HB2	2.21	0.40
15:CO:31:LEU:HD23	15:CO:31:LEU:HA	1.89	0.40
15:CO:3:ILE:H	15:CO:3:ILE:HD13	1.86	0.40
16:CP:68:ASP:O	16:CP:71:ARG:HG2	2.21	0.40
19:CS:3:ARG:NH2	19:CS:10:PHE:HB2	2.36	0.40
1:CA:1325:C:H4'	21:CU:17:THR:HG21	2.02	0.40
25:CY:36:A:C2	25:CY:37:MIA:C4	3.04	0.40
26:DA:1479:G:C2	26:DA:1480:G:C4	3.09	0.40
26:DA:195:A:H2'	26:DA:198:C:N4	2.36	0.40
26:DA:2037:G:O2'	26:DA:2038:G:H5'	2.22	0.40
26:DA:2058:A:N7	61:DA:3874:HOH:O	2.37	0.40
26:DA:2142:C:H2'	26:DA:2143:C:C6	2.56	0.40
26:DA:2694:G:C6	26:DA:2695:C:C4	3.08	0.40
26:DA:271(H):G:O2'	26:DA:271(I):G:C8	2.74	0.40
26:DA:528:A:C2	26:DA:2043:C:H4'	2.57	0.40
26:DA:531:C:OP1	26:DA:561:G:N1	2.50	0.40
26:DA:953:A:OP2	37:DQ:16:ARG:NE	2.50	0.40
29:DE:72:VAL:HG12	29:DE:73:GLU:O	2.21	0.40
36:DP:135:LEU:HD23	36:DP:135:LEU:HA	1.79	0.40
26:DA:911:A:H2'	37:DQ:9:TYR:OH	2.22	0.40
26:DA:2848:G:H8	40:DT:97:ALA:HB2	1.85	0.40
42:DV:58:VAL:O	42:DV:97:LYS:N	2.45	0.40
45:DY:74:PRO:O	45:DY:82:PRO:HA	2.20	0.40
1:AA:993:G:N3	1:AA:993:G:H2'	2.35	0.40
2:AB:17:PHE:HD2	2:AB:44:LEU:HD21	1.86	0.40
2:AB:47:THR:HG22	2:AB:51:LEU:HD11	2.03	0.40
3:AC:150:LYS:HB2	3:AC:173:VAL:HG21	2.02	0.40
3:AC:134:ILE:HD11	3:AC:153:VAL:HG23	2.04	0.40
8:AH:123:GLU:O	8:AH:127:LEU:HD13	2.22	0.40
23:AW:19:G:H4'	23:AW:20:U:OP1	2.20	0.40
25:AY:18:G:O6	25:AY:55:PSU:H1'	2.21	0.40
52:B5:40:LYS:HE2	52:B5:46:CYS:HA	2.04	0.40
26:BA:1068:G:C6	26:BA:1186:U:C5	3.09	0.40
26:BA:1467:G:C2	26:BA:1468:G:C8	3.10	0.40
26:BA:2160:C:C4	26:BA:2176:G:C6	3.10	0.40
27:BB:78:A:H2'	27:BB:79:C:O4'	2.21	0.40
36:BP:88:LEU:HD22	36:BP:95:VAL:HG21	2.03	0.40
1:CA:1118:C:N4	1:CA:1119:C:H41	2.19	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1350:A:C2	1:CA:1351:U:C2	3.09	0.40
1:CA:981:U:H5'	14:CN:21:TYR:CE2	2.56	0.40
2:CB:77:ALA:HB2	2:CB:165:VAL:HG11	2.03	0.40
2:CB:201:ILE:HA	2:CB:202:PRO:HD2	1.97	0.40
2:CB:80:ILE:HD13	2:CB:211:ILE:HB	2.02	0.40
3:CC:105:GLU:OE1	3:CC:107:GLN:N	2.55	0.40
3:CC:70:VAL:HG22	3:CC:72:LYS:N	2.35	0.40
4:CD:108:LEU:HD12	4:CD:108:LEU:HA	1.74	0.40
4:CD:76:ARG:NE	4:CD:80:GLU:OE1	2.50	0.40
11:CK:18:ARG:NH2	11:CK:35:PRO:O	2.49	0.40
11:CK:87:THR:OG1	11:CK:87:THR:O	2.37	0.40
13:CM:10:PRO:HD2	13:CM:18:ALA:HB1	2.03	0.40
16:CP:69:THR:O	16:CP:72:ARG:HB2	2.22	0.40
19:CS:36:ARG:HD2	19:CS:52:TYR:O	2.21	0.40
23:CW:23:A:H2'	23:CW:24:G:C8	2.56	0.40
25:CY:9:A:H5'	25:CY:46:7MG:C1'	2.52	0.40
48:D1:50:ARG:NH1	48:D1:57:GLU:OE2	2.54	0.40
26:DA:1359:A:N1	26:DA:1372:U:C4	2.89	0.40
26:DA:1482:G:C6	26:DA:1507:A:C2	3.08	0.40
26:DA:1539:G:H2'	26:DA:1540:U:O4'	2.20	0.40
26:DA:2074:U:H2'	26:DA:2075:U:C6	2.56	0.40
26:DA:2137:C:N3	26:DA:2138:C:N4	2.68	0.40
26:DA:2542:A:H4'	26:DA:2543:G:C8	2.56	0.40
26:DA:2542:A:H4'	26:DA:2543:G:H8	1.87	0.40
26:DA:511:U:H4'	26:DA:1235:G:H4'	2.03	0.40
26:DA:581:C:H2'	26:DA:582:G:C8	2.56	0.40
26:DA:885:C:H2'	26:DA:886:C:C4'	2.51	0.40
29:DE:52:LEU:O	29:DE:76:ARG:N	2.33	0.40
32:DH:144:VAL:O	32:DH:148:ILE:HG12	2.21	0.40
32:DH:9:ILE:HG12	32:DH:69:ARG:HD2	2.04	0.40
27:DB:50:G:OP1	39:DS:63:THR:HG22	2.21	0.40
1:AA:1003:G:N3	1:AA:1004:A:H1'	2.36	0.40
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.21	0.40
1:AA:1358:U:OP2	1:AA:1359:C:N4	2.54	0.40
2:AB:192:SER:O	2:AB:194:PRO:HD3	2.22	0.40
2:AB:77:ALA:O	2:AB:81:VAL:HG22	2.20	0.40
6:AF:95:GLU:HA	6:AF:96:PRO:HD3	1.98	0.40
7:AG:29:LYS:HD3	7:AG:29:LYS:HA	1.92	0.40
13:AM:117:VAL:HG12	13:AM:118:ALA:O	2.21	0.40
17:AQ:75:ARG:HH12	17:AQ:77:VAL:HA	1.86	0.40
26:BA:2343:G:O2'	47:B0:43:THR:HG22	2.21	0.40
49:B2:64:LEU:CD2	49:B2:68:ARG:HE	2.34	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1882:U:H2'	26:BA:1883:C:O4'	2.21	0.40
26:BA:2518:U:C2	26:BA:2597:U:O4	2.75	0.40
35:BO:10:VAL:HG11	35:BO:16:ALA:HB1	2.04	0.40
36:BP:47:ASP:HA	36:BP:48:PRO:HD3	1.92	0.40
42:BV:6:LYS:HG2	42:BV:11:GLN:HG2	2.03	0.40
1:CA:9:G:H2'	1:CA:10:A:H8	1.85	0.40
1:CA:426:G:OP1	4:CD:36:ARG:NH1	2.42	0.40
1:CA:300:A:H1'	1:CA:565:U:O2	2.20	0.40
2:CB:197:VAL:HB	2:CB:200:ILE:HG12	2.03	0.40
3:CC:109:PRO:HB3	3:CC:115:LEU:HD23	2.03	0.40
3:CC:70:VAL:N	3:CC:106:VAL:HG23	2.37	0.40
4:CD:3:ARG:O	4:CD:5:ILE:HG22	2.21	0.40
1:CA:1347:G:H5''	9:CI:107:ARG:HB3	2.02	0.40
13:CM:95:GLY:HA2	13:CM:110:ARG:NH1	2.36	0.40
1:CA:255:G:P	17:CQ:69:LYS:HZ1	2.42	0.40
24:CX:47:U:H3'	24:CX:48:C:C5'	2.51	0.40
24:CX:58:A:O2'	24:CX:60:U:OP2	2.34	0.40
54:D7:10:ARG:O	54:D7:14:LYS:HB2	2.22	0.40
56:D9:29:ASN:HA	56:D9:30:PRO:HD3	1.88	0.40
26:DA:1487:G:H2'	26:DA:1488:G:H5''	2.04	0.40
26:DA:1777:U:O2'	26:DA:1778:U:H5'	2.20	0.40
26:DA:2136:C:O2'	26:DA:2137:C:H6	2.05	0.40
26:DA:2447:G:N2	26:DA:2450:A:OP2	2.54	0.40
26:DA:2689:U:C4'	26:DA:2690:C:H5'	2.48	0.40
26:DA:565:C:H2'	26:DA:566:U:O4'	2.21	0.40
26:DA:587:C:OP2	36:DP:21:ARG:NH2	2.55	0.40
27:DB:57:A:O4'	31:DG:30:GLU:HG3	2.21	0.40
38:DR:78:LYS:HE2	38:DR:83:ILE:HD11	2.04	0.40
39:DS:36:TYR:CD2	39:DS:52:SER:HB3	2.56	0.40
41:DU:103:PRO:O	41:DU:107:ALA:N	2.50	0.40
46:DZ:7:ALA:HB3	46:DZ:61:LEU:HD12	2.03	0.40
46:DZ:79:ARG:HD2	46:DZ:80:ARG:CZ	2.51	0.40
46:DZ:97:GLU:HA	46:DZ:126:VAL:O	2.21	0.40
1:AA:1006:C:H2'	1:AA:1007:C:C6	2.56	0.40
1:AA:1001:A:N1	1:AA:1040:U:O4	2.54	0.40
1:AA:1118:C:OP1	9:AI:9:ARG:NH1	2.53	0.40
1:AA:1166:G:H5'	1:AA:1168:A:OP2	2.21	0.40
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.17	0.40
1:AA:1457:G:H2'	1:AA:1458:G:C8	2.57	0.40
1:AA:201:C:H2'	1:AA:202:U:H2'	2.03	0.40
1:AA:7:G:H5''	1:AA:298:A:O4'	2.22	0.40
1:AA:49:U:O4	1:AA:365:U:H5	2.05	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:57:G:H2'	1:AA:58:C:C6	2.57	0.40
1:AA:784:C:H2'	1:AA:785:G:O4'	2.22	0.40
4:AD:147:ALA:HB2	4:AD:182:LYS:HA	2.04	0.40
1:AA:737:A:OP1	6:AF:92:LYS:HG3	2.21	0.40
14:AN:27:CYS:SG	14:AN:29:ARG:HB2	2.61	0.40
1:AA:376:G:O2'	16:AP:5:ARG:NH2	2.54	0.40
19:AS:41:VAL:O	19:AS:44:MET:HB2	2.21	0.40
51:B4:40:HIS:HA	51:B4:41:PRO:HD2	1.88	0.40
26:BA:1683:C:H2'	26:BA:1684:A:C8	2.56	0.40
26:BA:2274:U:H4'	26:BA:2340:A:C2	2.56	0.40
26:BA:310:C:H2'	26:BA:311:C:C6	2.57	0.40
26:BA:327:U:O4	61:BA:4656:HOH:O	2.22	0.40
26:BA:551:A:H5''	26:BA:552:C:OP1	2.21	0.40
26:BA:561:A:H2'	26:BA:562:C:C6	2.56	0.40
28:BD:38:LYS:HD2	28:BD:38:LYS:HA	1.98	0.40
30:BF:93:LYS:HD3	30:BF:93:LYS:HA	1.91	0.40
33:BI:135:GLU:C	33:BI:137:PRO:HD3	2.42	0.40
35:BO:23:ARG:HG3	35:BO:24:VAL:N	2.36	0.40
40:BT:80:SER:HA	40:BT:81:PRO:HD3	1.89	0.40
26:BA:359:C:H5'	45:BY:73:ARG:NH2	2.36	0.40
1:CA:1442:G:C8	1:CA:1442:G:H3'	2.56	0.40
2:CB:168:THR:OG1	2:CB:192:SER:HA	2.22	0.40
2:CB:42:ILE:HG21	2:CB:202:PRO:HB2	2.03	0.40
2:CB:15:VAL:CG1	2:CB:209:ARG:HB3	2.49	0.40
24:CX:28:C:H2'	24:CX:29:G:C8	2.56	0.40
24:CX:28:C:H2'	24:CX:29:G:H8	1.85	0.40
24:CX:50:U:H3	24:CX:64:G:H1	1.68	0.40
48:D1:23:LYS:HB2	48:D1:23:LYS:HE3	1.79	0.40
52:D5:11:THR:HG22	52:D5:12:SER:O	2.21	0.40
26:DA:1653:G:H3'	38:DR:2:ARG:HD3	2.04	0.40
26:DA:1773:A:H5''	61:DA:4357:HOH:O	2.21	0.40
26:DA:19:C:H2'	26:DA:20:C:H6	1.86	0.40
26:DA:2224:G:H4'	26:DA:2226:C:C2	2.56	0.40
26:DA:2273:A:H2'	26:DA:2274:A:H8	1.85	0.40
26:DA:2755:C:HO2'	26:DA:2756:U:H6	1.69	0.40
26:DA:469:G:H2'	26:DA:470:A:H5''	2.02	0.40
26:DA:478:A:H62	26:DA:502:A:N6	2.19	0.40
26:DA:1501:C:O4'	28:DD:100:GLY:HA2	2.21	0.40
29:DE:24:THR:CG2	29:DE:184:VAL:HG12	2.52	0.40
32:DH:77:LYS:HG3	32:DH:81:GLU:OE2	2.21	0.40
35:DO:9:GLU:OE2	35:DO:18:LYS:HE3	2.21	0.40
42:DV:39:LEU:HG	42:DV:46:VAL:O	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
44:DX:64:LYS:HA	44:DX:64:LYS:HD2	1.88	0.40
44:DX:84:ALA:HB3	44:DX:87:GLN:NE2	2.37	0.40
1:AA:1121:U:C2'	1:AA:1122:U:H5'	2.52	0.40
1:AA:1261:A:H3'	1:AA:1262:C:H6	1.87	0.40
1:AA:1410:G:H2'	1:AA:1411:C:C6	2.57	0.40
1:AA:1529:G:H4'	1:AA:1530:G:OP2	2.22	0.40
1:AA:22:G:H4'	1:AA:885:G:C8	2.57	0.40
1:AA:38:G:O2'	1:AA:39:G:H5''	2.21	0.40
1:AA:719:C:H1'	18:AR:49:LYS:HB3	2.03	0.40
1:AA:881:G:H2'	1:AA:882:C:O4'	2.21	0.40
7:AG:97:GLN:HB2	7:AG:97:GLN:HE21	1.66	0.40
12:AL:24:VAL:HG13	12:AL:98:TYR:CE2	2.57	0.40
12:AL:7:ILE:O	12:AL:11:VAL:HG23	2.21	0.40
16:AP:54:GLU:HG3	16:AP:55:ARG:N	2.37	0.40
26:BA:123:G:N2	54:B7:48:LYS:HA	2.36	0.40
26:BA:1068:G:N2	26:BA:1188:A:C2	2.80	0.40
26:BA:1276:C:H2'	26:BA:1277:G:H8	1.86	0.40
26:BA:1784:G:N1	26:BA:1787:G:OP2	2.53	0.40
26:BA:1848:G:C6	26:BA:1849:U:C4	3.10	0.40
26:BA:2169:G:H2'	26:BA:2170:G:O4'	2.22	0.40
26:BA:327:U:H2'	26:BA:328:G:C8	2.56	0.40
26:BA:510:C:H2'	26:BA:511:C:H6	1.87	0.40
28:BD:258:LYS:HE2	28:BD:273:ARG:CZ	2.51	0.40
31:BG:38:VAL:HG22	31:BG:93:THR:HG23	2.03	0.40
35:BO:79:PHE:CD2	40:BT:72:VAL:HG22	2.56	0.40
43:BW:13:SER:HA	43:BW:14:PRO:HD3	1.82	0.40
43:BW:14:PRO:HG2	43:BW:78:GLU:CD	2.42	0.40
1:CA:1028:C:O2	1:CA:1034:G:H1'	2.21	0.40
1:CA:1065:U:P	1:CA:1190:G:H22	2.45	0.40
1:CA:1100:C:H2'	1:CA:1102:A:O5'	2.22	0.40
1:CA:1133:G:H2'	1:CA:1134:G:O4'	2.22	0.40
1:CA:179:A:C2'	1:CA:180:U:H5'	2.52	0.40
1:CA:377:G:H5'	16:CP:5:ARG:NH2	2.37	0.40
1:CA:407:G:H5''	4:CD:115:ARG:HB3	2.03	0.40
1:CA:408:A:H2'	1:CA:409:G:O4'	2.21	0.40
1:CA:643:C:H2'	1:CA:644:G:C8	2.57	0.40
1:CA:785:G:C2'	1:CA:786:G:H5'	2.51	0.40
2:CB:12:GLU:C	2:CB:14:GLY:HA3	2.41	0.40
2:CB:189:ASP:O	2:CB:192:SER:OG	2.40	0.40
6:CF:82:ARG:HD2	6:CF:82:ARG:HA	1.71	0.40
6:CF:95:GLU:HA	6:CF:96:PRO:HD3	1.85	0.40
8:CH:27:PRO:O	8:CH:32:LYS:HD2	2.22	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1014:A:H4'	19:CS:14:HIS:CE1	2.57	0.40
20:CT:24:LEU:HA	20:CT:24:LEU:HD13	1.71	0.40
51:D4:13:ARG:O	51:D4:30:GLU:HA	2.20	0.40
53:D6:8:LYS:HD3	55:D8:34:TRP:CD2	2.56	0.40
56:D9:12:ASP:OD1	56:D9:13:LYS:HG2	2.21	0.40
26:DA:1011:G:C2	26:DA:1151:G:N3	2.90	0.40
26:DA:1604:C:O2'	26:DA:1610:A:N1	2.38	0.40
26:DA:195:A:H2'	26:DA:198:C:H41	1.86	0.40
26:DA:1935:G:H1'	26:DA:1964:G:N2	2.37	0.40
26:DA:2625:G:H2'	26:DA:2626:C:O4'	2.22	0.40
26:DA:2734:A:H2'	26:DA:2735:G:O4'	2.21	0.40
26:DA:463:G:N2	26:DA:466:A:OP2	2.49	0.40
26:DA:661:C:H2'	26:DA:662:G:C8	2.56	0.40
27:DB:5:C:N4	27:DB:116:G:H1	2.13	0.40
26:DA:729:G:C6	28:DD:208:LYS:HB2	2.56	0.40
29:DE:201:THR:OG1	29:DE:202:LYS:N	2.55	0.40
31:DG:51:ARG:H	31:DG:51:ARG:HG3	1.69	0.40
31:DG:97:ASP:O	31:DG:101:ILE:HG13	2.21	0.40
33:DI:57:ARG:O	33:DI:61:ARG:HG2	2.21	0.40
35:DO:2:ILE:HB	35:DO:33:ALA:HB3	2.03	0.40
38:DR:1:MET:HB2	38:DR:2:ARG:H	1.71	0.40
38:DR:96:ARG:HD3	38:DR:98:LEU:HD11	2.04	0.40
26:DA:2849:U:P	40:DT:95:ARG:HH12	2.44	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%)	13 (6%)	8 (4%)	6 8
2	CB	229/256 (90%)	208 (91%)	14 (6%)	7 (3%)	7 10
3	AC	204/239 (85%)	193 (95%)	10 (5%)	1 (0%)	38 67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CC	204/239 (85%)	191 (94%)	13 (6%)	0	100	100
4	AD	206/209 (99%)	197 (96%)	9 (4%)	0	100	100
4	CD	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	38	67
5	AE	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
5	CE	146/162 (90%)	142 (97%)	3 (2%)	1 (1%)	30	58
6	AF	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
6	CF	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
7	AG	153/156 (98%)	149 (97%)	3 (2%)	1 (1%)	30	58
7	CG	153/156 (98%)	149 (97%)	3 (2%)	1 (1%)	30	58
8	AH	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
8	CH	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
9	AI	125/128 (98%)	119 (95%)	5 (4%)	1 (1%)	27	53
9	CI	125/128 (98%)	120 (96%)	4 (3%)	1 (1%)	27	53
10	AJ	95/105 (90%)	85 (90%)	8 (8%)	2 (2%)	11	19
10	CJ	94/105 (90%)	84 (89%)	6 (6%)	4 (4%)	4	5
11	AK	112/129 (87%)	107 (96%)	4 (4%)	1 (1%)	25	49
11	CK	112/129 (87%)	107 (96%)	4 (4%)	1 (1%)	25	49
12	AL	120/132 (91%)	118 (98%)	2 (2%)	0	100	100
12	CL	120/132 (91%)	117 (98%)	2 (2%)	1 (1%)	27	53
13	AM	121/126 (96%)	116 (96%)	4 (3%)	1 (1%)	27	53
13	CM	120/126 (95%)	113 (94%)	4 (3%)	3 (2%)	9	14
14	AN	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
14	CN	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
15	AO	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
15	CO	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
16	AP	80/88 (91%)	78 (98%)	2 (2%)	0	100	100
16	CP	80/88 (91%)	78 (98%)	1 (1%)	1 (1%)	18	35
17	AQ	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
17	CQ	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
18	AR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
18	CR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	AS	82/93 (88%)	76 (93%)	5 (6%)	1 (1%)	19	39
19	CS	81/93 (87%)	75 (93%)	6 (7%)	0	100	100
20	AT	94/106 (89%)	85 (90%)	4 (4%)	5 (5%)	3	3
20	CT	94/106 (89%)	85 (90%)	4 (4%)	5 (5%)	3	3
21	AU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
21	CU	21/27 (78%)	21 (100%)	0	0	100	100
28	BD	273/276 (99%)	263 (96%)	9 (3%)	1 (0%)	43	72
28	DD	273/276 (99%)	261 (96%)	10 (4%)	2 (1%)	30	58
29	BE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	38	67
29	DE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	38	67
30	BF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	38	67
30	DF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	38	67
31	BG	179/182 (98%)	171 (96%)	7 (4%)	1 (1%)	33	63
31	DG	179/182 (98%)	168 (94%)	8 (4%)	3 (2%)	14	26
32	BH	172/180 (96%)	166 (96%)	6 (4%)	0	100	100
32	DH	172/180 (96%)	166 (96%)	6 (4%)	0	100	100
33	BI	144/148 (97%)	132 (92%)	7 (5%)	5 (4%)	6	8
33	DI	144/148 (97%)	135 (94%)	8 (6%)	1 (1%)	30	58
34	BN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
34	DN	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
35	BO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
35	DO	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
36	BP	147/150 (98%)	142 (97%)	4 (3%)	1 (1%)	30	58
36	DP	147/150 (98%)	139 (95%)	6 (4%)	2 (1%)	16	32
37	BQ	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
37	DQ	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	30	58
38	BR	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
38	DR	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
39	BS	108/112 (96%)	106 (98%)	2 (2%)	0	100	100
39	DS	108/112 (96%)	107 (99%)	0	1 (1%)	25	49
40	BT	129/146 (88%)	123 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	DT	129/146 (88%)	126 (98%)	3 (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%)	5 (5%)	1 (1%)	22	45
42	DV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	22	45
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%)	91 (98%)	2 (2%)	0	100	100
44	DX	93/96 (97%)	91 (98%)	1 (1%)	1 (1%)	21	42
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	63
46	DZ	172/206 (84%)	159 (92%)	13 (8%)	0	100	100
47	B0	81/85 (95%)	81 (100%)	0	0	100	100
47	D0	81/85 (95%)	79 (98%)	1 (1%)	1 (1%)	19	39
48	B1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	21	42
48	D1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	21	42
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%)	54 (81%)	9 (13%)	4 (6%)	2	2
51	D4	67/71 (94%)	53 (79%)	11 (16%)	3 (4%)	4	4
52	B5	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
52	D5	57/60 (95%)	56 (98%)	1 (2%)	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%)	45 (98%)	1 (2%)	0	100	100
54	D7	46/49 (94%)	45 (98%)	0	1 (2%)	10	18
55	B8	62/65 (95%)	62 (100%)	0	0	100	100
55	D8	62/65 (95%)	62 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	B9	35/37 (95%)	35 (100%)	0	0	100	100
56	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11410/12128 (94%)	10945 (96%)	381 (3%)	84 (1%)	30	58

All (84) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	17	PHE
2	AB	19	HIS
2	AB	231	GLU
9	AI	54	ASP
10	AJ	56	HIS
28	BD	275	LYS
30	BF	130	ALA
33	BI	106	GLY
33	BI	107	VAL
48	B1	3	LYS
51	B4	53	GLU
51	B4	62	ARG
2	CB	8	LYS
2	CB	16	HIS
2	CB	17	PHE
2	CB	123	ALA
2	CB	126	GLU
2	CB	231	GLU
9	CI	54	ASP
10	CJ	56	HIS
10	CJ	75	ILE
13	CM	67	GLU
13	CM	85	GLY
31	DG	14	GLU
51	D4	39	CYS
51	D4	45	GLY
51	D4	62	ARG
54	D7	46	VAL
2	AB	10	LEU
2	AB	16	HIS
3	AC	66	VAL
7	AG	55	GLY
10	AJ	31	GLY
19	AS	84	GLY

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Mol	Chain	Res	Type
20	AT	10	LEU
20	AT	47	GLY
20	AT	96	GLY
20	AT	100	ILE
33	BI	105	HIS
42	BV	79	VAL
51	B4	47	GLN
2	CB	20	GLU
4	CD	46	LYS
5	CE	37	ARG
7	CG	55	GLY
10	CJ	78	ASN
20	CT	47	GLY
31	DG	81	LYS
42	DV	79	VAL
48	D1	3	LYS
13	AM	67	GLU
29	BE	52	LEU
33	BI	10	GLU
10	CJ	55	LYS
20	CT	102	GLY
28	DD	239	ARG
31	DG	47	LYS
33	DI	10	GLU
39	DS	84	GLN
2	AB	125	PRO
11	AK	105	VAL
20	CT	10	LEU
28	DD	3	VAL
29	DE	52	LEU
36	DP	45	LEU
47	D0	4	LYS
2	AB	11	LEU
31	BG	47	LYS
46	BZ	159	PRO
51	B4	59	PHE
11	CK	105	VAL
30	DF	130	ALA
44	DX	2	LYS
33	BI	73	GLU
36	BP	29	LYS
36	DP	29	LYS

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Mol	Chain	Res	Type
37	DQ	27	VAL
20	AT	102	GLY
16	CP	53	VAL
20	CT	100	ILE
13	CM	4	ILE
12	CL	30	ALA
20	CT	96	GLY
2	AB	234	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%)	155 (81%)	37 (19%)	2	3
2	CB	187/220 (85%)	151 (81%)	36 (19%)	2	3
3	AC	143/188 (76%)	127 (89%)	16 (11%)	9	16
3	CC	141/188 (75%)	116 (82%)	25 (18%)	3	4
4	AD	170/181 (94%)	147 (86%)	23 (14%)	6	10
4	CD	174/181 (96%)	147 (84%)	27 (16%)	4	6
5	AE	113/123 (92%)	106 (94%)	7 (6%)	26	49
5	CE	114/123 (93%)	99 (87%)	15 (13%)	6	10
6	AF	84/90 (93%)	74 (88%)	10 (12%)	8	14
6	CF	86/90 (96%)	79 (92%)	7 (8%)	17	32
7	AG	119/127 (94%)	99 (83%)	20 (17%)	3	5
7	CG	120/127 (94%)	106 (88%)	14 (12%)	8	14
8	AH	114/119 (96%)	101 (89%)	13 (11%)	8	15
8	CH	114/119 (96%)	97 (85%)	17 (15%)	4	7
9	AI	91/99 (92%)	73 (80%)	18 (20%)	2	3
9	CI	89/99 (90%)	69 (78%)	20 (22%)	1	2
10	AJ	66/92 (72%)	60 (91%)	6 (9%)	14	25
10	CJ	69/92 (75%)	61 (88%)	8 (12%)	8	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AK	83/99 (84%)	74 (89%)	9 (11%)	9	17
11	CK	83/99 (84%)	72 (87%)	11 (13%)	6	10
12	AL	97/109 (89%)	88 (91%)	9 (9%)	13	24
12	CL	97/109 (89%)	85 (88%)	12 (12%)	7	13
13	AM	95/101 (94%)	81 (85%)	14 (15%)	4	8
13	CM	92/101 (91%)	74 (80%)	18 (20%)	2	3
14	AN	49/50 (98%)	40 (82%)	9 (18%)	2	4
14	CN	49/50 (98%)	37 (76%)	12 (24%)	1	2
15	AO	78/80 (98%)	70 (90%)	8 (10%)	10	19
15	CO	78/80 (98%)	67 (86%)	11 (14%)	5	9
16	AP	69/74 (93%)	58 (84%)	11 (16%)	4	6
16	CP	68/74 (92%)	59 (87%)	9 (13%)	6	10
17	AQ	94/97 (97%)	87 (93%)	7 (7%)	20	38
17	CQ	94/97 (97%)	84 (89%)	10 (11%)	10	18
18	AR	59/77 (77%)	50 (85%)	9 (15%)	4	7
18	CR	59/77 (77%)	46 (78%)	13 (22%)	1	2
19	AS	70/80 (88%)	59 (84%)	11 (16%)	4	6
19	CS	67/80 (84%)	54 (81%)	13 (19%)	2	3
20	AT	70/82 (85%)	60 (86%)	10 (14%)	5	8
20	CT	71/82 (87%)	62 (87%)	9 (13%)	6	12
21	AU	18/22 (82%)	15 (83%)	3 (17%)	3	5
21	CU	18/22 (82%)	15 (83%)	3 (17%)	3	5
28	BD	215/218 (99%)	196 (91%)	19 (9%)	14	27
28	DD	216/218 (99%)	200 (93%)	16 (7%)	20	38
29	BE	164/166 (99%)	145 (88%)	19 (12%)	8	14
29	DE	164/166 (99%)	141 (86%)	23 (14%)	5	9
30	BF	160/166 (96%)	142 (89%)	18 (11%)	9	15
30	DF	159/166 (96%)	138 (87%)	21 (13%)	6	10
31	BG	143/156 (92%)	127 (89%)	16 (11%)	9	16
31	DG	142/156 (91%)	119 (84%)	23 (16%)	3	6
32	BH	144/148 (97%)	129 (90%)	15 (10%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	DH	144/148 (97%)	124 (86%)	20 (14%)	5	9
33	BI	110/124 (89%)	88 (80%)	22 (20%)	2	3
33	DI	107/124 (86%)	87 (81%)	20 (19%)	2	3
34	BN	118/119 (99%)	101 (86%)	17 (14%)	5	8
34	DN	118/119 (99%)	101 (86%)	17 (14%)	5	8
35	BO	100/100 (100%)	92 (92%)	8 (8%)	17	33
35	DO	100/100 (100%)	89 (89%)	11 (11%)	9	16
36	BP	116/116 (100%)	104 (90%)	12 (10%)	10	19
36	DP	115/116 (99%)	103 (90%)	12 (10%)	10	18
37	BQ	111/111 (100%)	95 (86%)	16 (14%)	5	8
37	DQ	111/111 (100%)	97 (87%)	14 (13%)	7	12
38	BR	101/101 (100%)	83 (82%)	18 (18%)	2	4
38	DR	101/101 (100%)	86 (85%)	15 (15%)	4	7
39	BS	87/88 (99%)	79 (91%)	8 (9%)	13	24
39	DS	85/88 (97%)	74 (87%)	11 (13%)	6	11
40	BT	115/127 (91%)	107 (93%)	8 (7%)	21	41
40	DT	113/127 (89%)	105 (93%)	8 (7%)	21	40
41	BU	93/94 (99%)	86 (92%)	7 (8%)	19	36
41	DU	93/94 (99%)	87 (94%)	6 (6%)	24	46
42	BV	80/82 (98%)	70 (88%)	10 (12%)	7	12
42	DV	80/82 (98%)	67 (84%)	13 (16%)	3	6
43	BW	90/92 (98%)	83 (92%)	7 (8%)	18	34
43	DW	90/92 (98%)	84 (93%)	6 (7%)	23	44
44	BX	77/78 (99%)	72 (94%)	5 (6%)	24	46
44	DX	77/78 (99%)	70 (91%)	7 (9%)	14	25
45	BY	85/91 (93%)	77 (91%)	8 (9%)	13	23
45	DY	85/91 (93%)	78 (92%)	7 (8%)	17	31
46	BZ	145/179 (81%)	128 (88%)	17 (12%)	8	14
46	DZ	145/179 (81%)	127 (88%)	18 (12%)	7	13
47	B0	65/67 (97%)	61 (94%)	4 (6%)	26	49
47	D0	65/67 (97%)	59 (91%)	6 (9%)	13	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	B1	80/83 (96%)	72 (90%)	8 (10%)	11	20
48	D1	80/83 (96%)	71 (89%)	9 (11%)	9	15
49	B2	65/67 (97%)	59 (91%)	6 (9%)	13	24
49	D2	65/67 (97%)	60 (92%)	5 (8%)	18	35
50	B3	51/52 (98%)	47 (92%)	4 (8%)	18	34
50	D3	50/52 (96%)	47 (94%)	3 (6%)	27	51
51	B4	60/63 (95%)	51 (85%)	9 (15%)	4	7
51	D4	53/63 (84%)	38 (72%)	15 (28%)	0	1
52	B5	50/52 (96%)	46 (92%)	4 (8%)	17	33
52	D5	50/52 (96%)	48 (96%)	2 (4%)	42	73
53	B6	51/52 (98%)	45 (88%)	6 (12%)	8	14
53	D6	50/52 (96%)	47 (94%)	3 (6%)	27	51
54	B7	41/42 (98%)	39 (95%)	2 (5%)	35	62
54	D7	41/42 (98%)	39 (95%)	2 (5%)	35	62
55	B8	54/55 (98%)	50 (93%)	4 (7%)	20	38
55	D8	54/55 (98%)	50 (93%)	4 (7%)	20	38
56	B9	34/34 (100%)	33 (97%)	1 (3%)	55	83
56	D9	34/34 (100%)	33 (97%)	1 (3%)	55	83
All	All	9336/10066 (93%)	8180 (88%)	1156 (12%)	7	13

All (1156) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	7	VAL
2	AB	15	VAL
2	AB	17	PHE
2	AB	19	HIS
2	AB	20	GLU
2	AB	21	ARG
2	AB	24	TRP
2	AB	35	GLU
2	AB	48	MET
2	AB	60	ASP
2	AB	64	ARG
2	AB	67	THR
2	AB	74	LYS

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Mol	Chain	Res	Type
2	AB	76	GLN
2	AB	84	GLU
2	AB	94	ASN
2	AB	121	LEU
2	AB	127	ILE
2	AB	137	ARG
2	AB	144	ARG
2	AB	145	LEU
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	160	ASP
2	AB	170	GLU
2	AB	185	ILE
2	AB	187	LEU
2	AB	195	ASP
2	AB	196	LEU
2	AB	200	ILE
2	AB	208	ILE
2	AB	209	ARG
2	AB	217	ARG
2	AB	221	LEU
2	AB	223	ILE
2	AB	230	VAL
3	AC	3	ASN
3	AC	8	ILE
3	AC	15	THR
3	AC	27	LYS
3	AC	45	LYS
3	AC	52	LEU
3	AC	77	ILE
3	AC	98	ASN
3	AC	101	LEU
3	AC	118	GLN
3	AC	131	ARG
3	AC	136	GLN
3	AC	178	LEU
3	AC	179	ARG
3	AC	190	ARG
3	AC	195	VAL
4	AD	3	ARG
4	AD	5	ILE

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Mol	Chain	Res	Type
4	AD	15	GLU
4	AD	19	LEU
4	AD	28	SER
4	AD	31	CYS
4	AD	49	ARG
4	AD	50	ARG
4	AD	58	LEU
4	AD	65	ARG
4	AD	86	LYS
4	AD	91	SER
4	AD	108	LEU
4	AD	112	VAL
4	AD	115	ARG
4	AD	127	THR
4	AD	135	LEU
4	AD	144	ASP
4	AD	155	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	194	LEU
4	AD	196	LEU
5	AE	6	PHE
5	AE	10	MET
5	AE	12	LEU
5	AE	31	LEU
5	AE	41	VAL
5	AE	47	LYS
5	AE	151	LEU
6	AF	10	LEU
6	AF	17	SER
6	AF	28	ARG
6	AF	40	VAL
6	AF	45	LEU
6	AF	55	ASP
6	AF	61	LEU
6	AF	70	ASP
6	AF	75	LEU
6	AF	82	ARG
7	AG	8	GLU
7	AG	12	LEU
7	AG	16	LEU
7	AG	24	THR

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Mol	Chain	Res	Type
7	AG	31	MET
7	AG	38	LEU
7	AG	51	GLN
7	AG	61	VAL
7	AG	72	ARG
7	AG	73	MET
7	AG	76	ARG
7	AG	78	ARG
7	AG	79	ARG
7	AG	91	VAL
7	AG	97	GLN
7	AG	104	LEU
7	AG	113	GLU
7	AG	115	ARG
7	AG	138	LYS
7	AG	155	ARG
8	AH	25	ASP
8	AH	37	ARG
8	AH	39	LEU
8	AH	50	ARG
8	AH	52	ASP
8	AH	63	LEU
8	AH	78	GLN
8	AH	84	ARG
8	AH	91	ARG
8	AH	107	LEU
8	AH	112	LEU
8	AH	122	ARG
8	AH	137	VAL
9	AI	9	ARG
9	AI	11	LYS
9	AI	23	ASN
9	AI	42	ARG
9	AI	56	LEU
9	AI	64	THR
9	AI	65	VAL
9	AI	71	SER
9	AI	75	ASP
9	AI	78	LYS
9	AI	81	ILE
9	AI	89	ASN
9	AI	93	ARG

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Mol	Chain	Res	Type
9	AI	102	LEU
9	AI	103	THR
9	AI	121	ARG
9	AI	127	LYS
9	AI	128	ARG
10	AJ	5	ARG
10	AJ	9	ARG
10	AJ	16	LEU
10	AJ	43	ARG
10	AJ	84	GLN
10	AJ	92	THR
11	AK	31	THR
11	AK	48	ILE
11	AK	51	LYS
11	AK	81	ASP
11	AK	87	THR
11	AK	91	ARG
11	AK	96	ARG
11	AK	106	LYS
11	AK	114	VAL
12	AL	16	GLU
12	AL	33	ARG
12	AL	47	LYS
12	AL	52	LEU
12	AL	54	LYS
12	AL	60	LEU
12	AL	67	THR
12	AL	83	VAL
12	AL	89	ARG
13	AM	3	ARG
13	AM	4	ILE
13	AM	15	VAL
13	AM	19	LEU
13	AM	43	THR
13	AM	46	LYS
13	AM	56	LEU
13	AM	70	LEU
13	AM	73	GLU
13	AM	94	ARG
13	AM	98	VAL
13	AM	110	ARG
13	AM	115	LYS

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Mol	Chain	Res	Type
13	AM	121	LYS
14	AN	3	ARG
14	AN	6	LEU
14	AN	7	ILE
14	AN	9	LYS
14	AN	12	ARG
14	AN	13	THR
14	AN	18	VAL
14	AN	32	SER
14	AN	50	LYS
15	AO	5	LYS
15	AO	7	GLU
15	AO	22	THR
15	AO	26	GLU
15	AO	38	ARG
15	AO	39	LEU
15	AO	76	GLU
15	AO	83	GLU
16	AP	1	MET
16	AP	5	ARG
16	AP	8	ARG
16	AP	19	ILE
16	AP	20	VAL
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	67	THR
16	AP	69	THR
16	AP	71	ARG
17	AQ	49	GLU
17	AQ	63	ARG
17	AQ	72	ARG
17	AQ	74	LEU
17	AQ	91	ARG
17	AQ	92	ARG
17	AQ	97	SER
18	AR	31	LEU
18	AR	35	ARG
18	AR	37	VAL
18	AR	38	GLU
18	AR	46	GLU
18	AR	55	ARG

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Mol	Chain	Res	Type
18	AR	58	LEU
18	AR	68	LYS
18	AR	76	LEU
19	AS	5	LEU
19	AS	12	ASP
19	AS	17	GLU
19	AS	36	ARG
19	AS	37	ARG
19	AS	63	THR
19	AS	65	ASN
19	AS	70	LYS
19	AS	78	ARG
19	AS	81	ARG
19	AS	85	LYS
20	AT	8	ARG
20	AT	13	LEU
20	AT	19	SER
20	AT	24	LEU
20	AT	31	SER
20	AT	45	GLN
20	AT	58	LYS
20	AT	60	GLU
20	AT	62	LEU
20	AT	84	LEU
21	AU	9	ARG
21	AU	10	ARG
21	AU	24	ARG
28	BD	3	VAL
28	BD	22	SER
28	BD	32	SER
28	BD	38	LYS
28	BD	61	LEU
28	BD	71	ASP
28	BD	94	LEU
28	BD	99	ASP
28	BD	106	ILE
28	BD	116	GLN
28	BD	126	GLN
28	BD	211	ARG
28	BD	217	ARG
28	BD	221	VAL
28	BD	229	VAL

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Mol	Chain	Res	Type
28	BD	242	ARG
28	BD	257	LEU
28	BD	259	THR
28	BD	260	ARG
29	BE	8	LYS
29	BE	9	VAL
29	BE	12	THR
29	BE	34	VAL
29	BE	47	VAL
29	BE	75	VAL
29	BE	77	ILE
29	BE	78	LEU
29	BE	82	ARG
29	BE	89	ASP
29	BE	116	VAL
29	BE	119	ARG
29	BE	127	ASP
29	BE	144	ARG
29	BE	154	LYS
29	BE	163	GLU
29	BE	175	VAL
29	BE	181	LEU
29	BE	184	VAL
30	BF	12	LEU
30	BF	19	GLU
30	BF	33	LEU
30	BF	43	LYS
30	BF	53	THR
30	BF	57	VAL
30	BF	74	ARG
30	BF	88	VAL
30	BF	106	ARG
30	BF	110	LEU
30	BF	125	LEU
30	BF	132	VAL
30	BF	140	LEU
30	BF	162	LEU
30	BF	192	LEU
30	BF	197	ASP
30	BF	200	GLU
30	BF	201	VAL
31	BG	3	LEU

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Mol	Chain	Res	Type
31	BG	7	LEU
31	BG	22	ARG
31	BG	43	LEU
31	BG	45	GLU
31	BG	49	ASP
31	BG	81	LYS
31	BG	82	LEU
31	BG	86	MET
31	BG	139	LEU
31	BG	143	GLU
31	BG	146	TYR
31	BG	159	VAL
31	BG	170	ARG
31	BG	175	LEU
31	BG	181	ARG
32	BH	2	SER
32	BH	6	ARG
32	BH	13	LYS
32	BH	45	VAL
32	BH	51	ARG
32	BH	69	ARG
32	BH	71	LEU
32	BH	76	VAL
32	BH	92	ILE
32	BH	98	LEU
32	BH	105	LEU
32	BH	116	GLU
32	BH	119	GLU
32	BH	122	THR
32	BH	124	GLU
33	BI	5	LEU
33	BI	9	LEU
33	BI	20	ASP
33	BI	38	LEU
33	BI	41	GLU
33	BI	43	ASN
33	BI	47	LEU
33	BI	52	ARG
33	BI	58	LEU
33	BI	61	ARG
33	BI	62	LYS
33	BI	64	GLU

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Mol	Chain	Res	Type
33	BI	66	GLU
33	BI	77	LEU
33	BI	78	THR
33	BI	86	THR
33	BI	92	VAL
33	BI	96	ASP
33	BI	101	LEU
33	BI	107	VAL
33	BI	116	LEU
33	BI	117	GLU
34	BN	1	MET
34	BN	5	VAL
34	BN	8	GLN
34	BN	9	VAL
34	BN	12	ARG
34	BN	28	THR
34	BN	33	LEU
34	BN	34	LEU
34	BN	48	MET
34	BN	61	ARG
34	BN	67	LEU
34	BN	68	GLU
34	BN	87	LEU
34	BN	99	LEU
34	BN	120	LEU
34	BN	138	LEU
34	BN	140	VAL
35	BO	8	LEU
35	BO	10	VAL
35	BO	18	LYS
35	BO	24	VAL
35	BO	66	LYS
35	BO	98	VAL
35	BO	105	GLU
35	BO	108	GLU
36	BP	1	MET
36	BP	55	ARG
36	BP	59	LEU
36	BP	65	ARG
36	BP	95	VAL
36	BP	98	GLU
36	BP	101	VAL

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Mol	Chain	Res	Type
36	BP	106	LEU
36	BP	112	LEU
36	BP	121	LYS
36	BP	144	GLU
36	BP	149	GLU
37	BQ	1	MET
37	BQ	7	MET
37	BQ	8	LYS
37	BQ	16	ARG
37	BQ	21	THR
37	BQ	22	LYS
37	BQ	45	GLN
37	BQ	54	MET
37	BQ	55	VAL
37	BQ	60	ARG
37	BQ	63	LYS
37	BQ	75	THR
37	BQ	80	GLU
37	BQ	85	LYS
37	BQ	109	VAL
37	BQ	110	THR
38	BR	1	MET
38	BR	18	LEU
38	BR	28	LEU
38	BR	29	LEU
38	BR	33	ARG
38	BR	36	THR
38	BR	44	LEU
38	BR	54	LEU
38	BR	60	LEU
38	BR	65	LEU
38	BR	67	LEU
38	BR	75	LEU
38	BR	79	LEU
38	BR	86	ARG
38	BR	100	LEU
38	BR	102	GLU
38	BR	111	LEU
38	BR	114	VAL
39	BS	3	ARG
39	BS	20	ARG
39	BS	49	VAL

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Mol	Chain	Res	Type
39	BS	52	SER
39	BS	59	LYS
39	BS	69	VAL
39	BS	73	LEU
39	BS	83	LYS
40	BT	28	VAL
40	BT	49	VAL
40	BT	53	ARG
40	BT	74	ARG
40	BT	78	LEU
40	BT	96	ARG
40	BT	118	ARG
40	BT	128	GLU
41	BU	8	VAL
41	BU	27	LEU
41	BU	31	SER
41	BU	74	LEU
41	BU	92	ARG
41	BU	95	LEU
41	BU	104	GLN
42	BV	21	ARG
42	BV	43	GLU
42	BV	46	VAL
42	BV	51	VAL
42	BV	52	VAL
42	BV	62	LEU
42	BV	72	VAL
42	BV	79	VAL
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	107	LEU
44	BX	2	LYS
44	BX	35	THR
44	BX	57	LEU
44	BX	65	ARG
44	BX	88	LYS

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Mol	Chain	Res	Type
45	BY	1	MET
45	BY	7	VAL
45	BY	11	ASP
45	BY	23	ARG
45	BY	43	ASN
45	BY	55	TYR
45	BY	73	ARG
45	BY	99	CYS
46	BZ	5	LEU
46	BZ	18	LEU
46	BZ	19	ARG
46	BZ	50	GLN
46	BZ	76	LEU
46	BZ	91	LEU
46	BZ	102	LEU
46	BZ	107	THR
46	BZ	117	LEU
46	BZ	120	ILE
46	BZ	129	SER
46	BZ	131	ARG
46	BZ	136	PHE
46	BZ	153	SER
46	BZ	154	ASP
46	BZ	155	LEU
46	BZ	169	GLU
47	B0	10	THR
47	B0	20	ARG
47	B0	55	ARG
47	B0	74	ARG
48	B1	3	LYS
48	B1	21	ARG
48	B1	23	LYS
48	B1	35	THR
48	B1	40	ARG
48	B1	59	THR
48	B1	78	LYS
48	B1	95	LEU
49	B2	19	VAL
49	B2	30	ARG
49	B2	32	LEU
49	B2	40	SER
49	B2	55	ARG

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Mol	Chain	Res	Type
49	B2	70	GLN
50	B3	3	ARG
50	B3	8	LEU
50	B3	23	LEU
50	B3	54	VAL
51	B4	3	GLU
51	B4	34	GLU
51	B4	46	GLN
51	B4	49	PHE
51	B4	56	VAL
51	B4	58	ARG
51	B4	63	TYR
51	B4	66	SER
51	B4	68	ARG
52	B5	6	VAL
52	B5	29	THR
52	B5	40	LYS
52	B5	55	ARG
53	B6	4	GLU
53	B6	6	ARG
53	B6	14	THR
53	B6	28	ARG
53	B6	38	LYS
53	B6	48	VAL
54	B7	9	ARG
54	B7	43	THR
55	B8	6	THR
55	B8	31	HIS
55	B8	46	ARG
55	B8	59	LYS
56	B9	4	ARG
2	CB	8	LYS
2	CB	15	VAL
2	CB	19	HIS
2	CB	23	ARG
2	CB	24	TRP
2	CB	35	GLU
2	CB	50	GLU
2	CB	51	LEU
2	CB	60	ASP
2	CB	73	THR
2	CB	74	LYS

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Mol	Chain	Res	Type
2	CB	76	GLN
2	CB	78	GLN
2	CB	87	ARG
2	CB	94	ASN
2	CB	97	TRP
2	CB	108	ILE
2	CB	115	LEU
2	CB	117	GLU
2	CB	119	GLU
2	CB	122	PHE
2	CB	124	SER
2	CB	126	GLU
2	CB	128	GLU
2	CB	139	LYS
2	CB	154	LEU
2	CB	155	LEU
2	CB	157	ARG
2	CB	158	LEU
2	CB	160	ASP
2	CB	185	ILE
2	CB	187	LEU
2	CB	200	ILE
2	CB	217	ARG
2	CB	224	GLN
2	CB	235	SER
3	CC	3	ASN
3	CC	15	THR
3	CC	17	ASP
3	CC	21	ARG
3	CC	33	LEU
3	CC	45	LYS
3	CC	47	LEU
3	CC	52	LEU
3	CC	54	ARG
3	CC	72	LYS
3	CC	85	ARG
3	CC	91	LEU
3	CC	98	ASN
3	CC	101	LEU
3	CC	104	GLN
3	CC	105	GLU
3	CC	115	LEU

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Mol	Chain	Res	Type
3	CC	128	PHE
3	CC	131	ARG
3	CC	151	VAL
3	CC	152	ILE
3	CC	164	ARG
3	CC	179	ARG
3	CC	190	ARG
3	CC	195	VAL
4	CD	10	ARG
4	CD	15	GLU
4	CD	31	CYS
4	CD	34	GLU
4	CD	50	ARG
4	CD	58	LEU
4	CD	61	LYS
4	CD	65	ARG
4	CD	85	LYS
4	CD	86	LYS
4	CD	96	LEU
4	CD	107	ARG
4	CD	108	LEU
4	CD	122	ARG
4	CD	127	THR
4	CD	135	LEU
4	CD	145	GLU
4	CD	150	GLU
4	CD	155	LEU
4	CD	156	GLU
4	CD	169	LYS
4	CD	170	VAL
4	CD	181	MET
4	CD	184	LYS
4	CD	187	ARG
4	CD	194	LEU
4	CD	208	SER
5	CE	6	PHE
5	CE	10	MET
5	CE	12	LEU
5	CE	18	ARG
5	CE	27	ARG
5	CE	31	LEU
5	CE	41	VAL

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Mol	Chain	Res	Type
5	CE	47	LYS
5	CE	60	TYR
5	CE	64	ARG
5	CE	78	HIS
5	CE	79	GLU
5	CE	117	ASP
5	CE	147	ASP
5	CE	150	ARG
6	CF	17	SER
6	CF	21	LEU
6	CF	27	GLN
6	CF	28	ARG
6	CF	45	LEU
6	CF	82	ARG
6	CF	87	ARG
7	CG	6	ARG
7	CG	12	LEU
7	CG	24	THR
7	CG	32	ARG
7	CG	36	LYS
7	CG	41	ARG
7	CG	51	GLN
7	CG	72	ARG
7	CG	76	ARG
7	CG	97	GLN
7	CG	104	LEU
7	CG	114	ARG
7	CG	115	ARG
7	CG	155	ARG
8	CH	3	THR
8	CH	25	ASP
8	CH	29	SER
8	CH	52	ASP
8	CH	63	LEU
8	CH	78	GLN
8	CH	84	ARG
8	CH	85	ARG
8	CH	91	ARG
8	CH	98	LYS
8	CH	103	VAL
8	CH	111	ILE
8	CH	112	LEU

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Mol	Chain	Res	Type
8	CH	125	ARG
8	CH	127	LEU
8	CH	135	CYS
8	CH	137	VAL
9	CI	7	THR
9	CI	14	VAL
9	CI	23	ASN
9	CI	40	LEU
9	CI	51	ARG
9	CI	56	LEU
9	CI	64	THR
9	CI	65	VAL
9	CI	75	ASP
9	CI	81	ILE
9	CI	83	ARG
9	CI	88	TYR
9	CI	89	ASN
9	CI	102	LEU
9	CI	103	THR
9	CI	104	ARG
9	CI	121	ARG
9	CI	124	GLN
9	CI	125	TYR
9	CI	128	ARG
10	CJ	6	ILE
10	CJ	21	GLN
10	CJ	34	VAL
10	CJ	59	SER
10	CJ	67	THR
10	CJ	74	ILE
10	CJ	81	THR
10	CJ	98	ILE
11	CK	24	SER
11	CK	31	THR
11	CK	41	THR
11	CK	48	ILE
11	CK	54	ARG
11	CK	92	GLU
11	CK	93	GLN
11	CK	96	ARG
11	CK	104	GLN
11	CK	123	LYS

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Mol	Chain	Res	Type
11	CK	126	ARG
12	CL	33	ARG
12	CL	36	VAL
12	CL	39	VAL
12	CL	47	LYS
12	CL	60	LEU
12	CL	62	SER
12	CL	75	HIS
12	CL	83	VAL
12	CL	104	VAL
12	CL	114	LYS
12	CL	117	ARG
12	CL	124	LYS
13	CM	15	VAL
13	CM	19	LEU
13	CM	27	LYS
13	CM	29	ARG
13	CM	32	GLU
13	CM	44	ARG
13	CM	50	GLU
13	CM	52	GLU
13	CM	56	LEU
13	CM	63	THR
13	CM	66	LEU
13	CM	70	LEU
13	CM	71	ARG
13	CM	73	GLU
13	CM	84	ILE
13	CM	98	VAL
13	CM	105	THR
13	CM	121	LYS
14	CN	3	ARG
14	CN	7	ILE
14	CN	11	LYS
14	CN	13	THR
14	CN	15	LYS
14	CN	17	LYS
14	CN	18	VAL
14	CN	22	THR
14	CN	23	ARG
14	CN	26	ARG
14	CN	32	SER

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Mol	Chain	Res	Type
14	CN	46	GLU
15	CO	3	ILE
15	CO	4	THR
15	CO	5	LYS
15	CO	22	THR
15	CO	26	GLU
15	CO	38	ARG
15	CO	39	LEU
15	CO	48	LYS
15	CO	68	ARG
15	CO	83	GLU
15	CO	87	ILE
16	CP	1	MET
16	CP	2	VAL
16	CP	5	ARG
16	CP	20	VAL
16	CP	21	VAL
16	CP	60	LEU
16	CP	67	THR
16	CP	69	THR
16	CP	71	ARG
17	CQ	36	ILE
17	CQ	37	LYS
17	CQ	49	GLU
17	CQ	55	ASP
17	CQ	63	ARG
17	CQ	69	LYS
17	CQ	74	LEU
17	CQ	75	ARG
17	CQ	83	ASP
17	CQ	91	ARG
18	CR	25	THR
18	CR	26	LEU
18	CR	28	GLU
18	CR	32	ARG
18	CR	37	VAL
18	CR	41	LYS
18	CR	42	ARG
18	CR	56	THR
18	CR	58	LEU
18	CR	68	LYS
18	CR	76	LEU

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Mol	Chain	Res	Type
18	CR	84	LYS
18	CR	87	ARG
19	CS	5	LEU
19	CS	15	LEU
19	CS	22	LEU
19	CS	30	LEU
19	CS	56	GLN
19	CS	63	THR
19	CS	64	GLU
19	CS	65	ASN
19	CS	66	MET
19	CS	77	THR
19	CS	78	ARG
19	CS	81	ARG
19	CS	83	HIS
20	CT	8	ARG
20	CT	24	LEU
20	CT	45	GLN
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	84	LEU
20	CT	93	GLU
21	CU	9	ARG
21	CU	10	ARG
21	CU	12	LYS
28	DD	61	LEU
28	DD	94	LEU
28	DD	99	ASP
28	DD	106	ILE
28	DD	113	VAL
28	DD	126	GLN
28	DD	134	ARG
28	DD	142	VAL
28	DD	211	ARG
28	DD	221	VAL
28	DD	229	VAL
28	DD	242	ARG
28	DD	257	LEU
28	DD	259	THR
28	DD	260	ARG

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Mol	Chain	Res	Type
28	DD	276	LYS
29	DE	7	VAL
29	DE	9	VAL
29	DE	12	THR
29	DE	21	VAL
29	DE	34	VAL
29	DE	38	THR
29	DE	40	GLU
29	DE	47	VAL
29	DE	52	LEU
29	DE	61	ARG
29	DE	73	GLU
29	DE	75	VAL
29	DE	82	ARG
29	DE	89	ASP
29	DE	116	VAL
29	DE	119	ARG
29	DE	144	ARG
29	DE	154	LYS
29	DE	163	GLU
29	DE	175	VAL
29	DE	181	LEU
29	DE	184	VAL
29	DE	195	LEU
30	DF	12	LEU
30	DF	17	ARG
30	DF	19	GLU
30	DF	20	LEU
30	DF	33	LEU
30	DF	53	THR
30	DF	57	VAL
30	DF	70	THR
30	DF	74	ARG
30	DF	88	VAL
30	DF	106	ARG
30	DF	110	LEU
30	DF	132	VAL
30	DF	135	LYS
30	DF	140	LEU
30	DF	152	GLU
30	DF	157	VAL
30	DF	183	VAL

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Mol	Chain	Res	Type
30	DF	192	LEU
30	DF	201	VAL
30	DF	205	ARG
31	DG	7	LEU
31	DG	9	ARG
31	DG	16	ARG
31	DG	19	LEU
31	DG	31	VAL
31	DG	35	GLU
31	DG	43	LEU
31	DG	47	LYS
31	DG	49	ASP
31	DG	84	LYS
31	DG	97	ASP
31	DG	98	ARG
31	DG	111	LEU
31	DG	113	ARG
31	DG	115	ARG
31	DG	116	ASP
31	DG	136	ARG
31	DG	140	ILE
31	DG	143	GLU
31	DG	148	MET
31	DG	152	LEU
31	DG	164	GLU
31	DG	170	ARG
32	DH	3	ARG
32	DH	6	ARG
32	DH	33	LEU
32	DH	34	GLU
32	DH	41	MET
32	DH	42	ARG
32	DH	45	VAL
32	DH	49	VAL
32	DH	65	HIS
32	DH	69	ARG
32	DH	81	GLU
32	DH	95	ARG
32	DH	98	LEU
32	DH	111	HIS
32	DH	124	GLU
32	DH	136	ILE

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Mol	Chain	Res	Type
32	DH	139	GLN
32	DH	148	ILE
32	DH	171	LEU
32	DH	172	LYS
33	DI	5	LEU
33	DI	9	LEU
33	DI	14	ASP
33	DI	15	VAL
33	DI	20	ASP
33	DI	38	LEU
33	DI	41	GLU
33	DI	43	ASN
33	DI	44	LEU
33	DI	57	ARG
33	DI	58	LEU
33	DI	75	LEU
33	DI	77	LEU
33	DI	78	THR
33	DI	86	THR
33	DI	102	SER
33	DI	114	LEU
33	DI	121	LYS
33	DI	135	GLU
33	DI	140	LEU
34	DN	5	VAL
34	DN	12	ARG
34	DN	28	THR
34	DN	33	LEU
34	DN	34	LEU
34	DN	38	HIS
34	DN	46	VAL
34	DN	48	MET
34	DN	62	VAL
34	DN	85	ILE
34	DN	87	LEU
34	DN	88	GLU
34	DN	89	LYS
34	DN	120	LEU
34	DN	137	LYS
34	DN	138	LEU
34	DN	140	VAL
35	DO	8	LEU

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Mol	Chain	Res	Type
35	DO	9	GLU
35	DO	10	VAL
35	DO	24	VAL
35	DO	53	LYS
35	DO	66	LYS
35	DO	69	ILE
35	DO	70	LYS
35	DO	78	ARG
35	DO	92	GLU
35	DO	113	LYS
36	DP	15	ARG
36	DP	45	LEU
36	DP	55	ARG
36	DP	56	SER
36	DP	65	ARG
36	DP	95	VAL
36	DP	98	GLU
36	DP	106	LEU
36	DP	112	LEU
36	DP	121	LYS
36	DP	136	GLU
36	DP	144	GLU
37	DQ	1	MET
37	DQ	16	ARG
37	DQ	21	THR
37	DQ	45	GLN
37	DQ	48	GLU
37	DQ	55	VAL
37	DQ	56	ARG
37	DQ	60	ARG
37	DQ	75	THR
37	DQ	80	GLU
37	DQ	85	LYS
37	DQ	109	VAL
37	DQ	110	THR
37	DQ	133	ARG
38	DR	1	MET
38	DR	18	LEU
38	DR	28	LEU
38	DR	29	LEU
38	DR	33	ARG
38	DR	36	THR

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Mol	Chain	Res	Type
38	DR	44	LEU
38	DR	54	LEU
38	DR	60	LEU
38	DR	65	LEU
38	DR	75	LEU
38	DR	79	LEU
38	DR	86	ARG
38	DR	100	LEU
38	DR	111	LEU
39	DS	19	LYS
39	DS	20	ARG
39	DS	35	ILE
39	DS	44	LYS
39	DS	49	VAL
39	DS	52	SER
39	DS	58	LEU
39	DS	67	ARG
39	DS	73	LEU
39	DS	78	LEU
39	DS	83	LYS
40	DT	31	SER
40	DT	59	THR
40	DT	78	LEU
40	DT	85	LYS
40	DT	96	ARG
40	DT	98	LYS
40	DT	113	LYS
40	DT	118	ARG
41	DU	31	SER
41	DU	36	ARG
41	DU	74	LEU
41	DU	89	GLU
41	DU	92	ARG
41	DU	104	GLN
42	DV	15	GLU
42	DV	18	LEU
42	DV	21	ARG
42	DV	24	LYS
42	DV	38	LEU
42	DV	46	VAL
42	DV	52	VAL
42	DV	57	VAL

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Mol	Chain	Res	Type
42	DV	62	LEU
42	DV	72	VAL
42	DV	79	VAL
42	DV	95	LEU
42	DV	100	ARG
43	DW	4	LYS
43	DW	11	ARG
43	DW	17	VAL
43	DW	51	LEU
43	DW	60	ASN
43	DW	107	LEU
44	DX	44	GLU
44	DX	52	VAL
44	DX	57	LEU
44	DX	64	LYS
44	DX	66	LEU
44	DX	70	LEU
44	DX	92	LEU
45	DY	6	HIS
45	DY	23	ARG
45	DY	26	LYS
45	DY	43	ASN
45	DY	49	VAL
45	DY	91	GLU
45	DY	99	CYS
46	DZ	5	LEU
46	DZ	11	GLU
46	DZ	14	LYS
46	DZ	18	LEU
46	DZ	33	LEU
46	DZ	35	ARG
46	DZ	59	LEU
46	DZ	71	VAL
46	DZ	92	SER
46	DZ	97	GLU
46	DZ	100	VAL
46	DZ	102	LEU
46	DZ	107	THR
46	DZ	120	ILE
46	DZ	131	ARG
46	DZ	136	PHE
46	DZ	154	ASP

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Mol	Chain	Res	Type
46	DZ	157	LEU
47	D0	19	LYS
47	D0	20	ARG
47	D0	24	LYS
47	D0	55	ARG
47	D0	68	GLU
47	D0	74	ARG
48	D1	3	LYS
48	D1	4	VAL
48	D1	21	ARG
48	D1	40	ARG
48	D1	59	THR
48	D1	85	LEU
48	D1	89	GLU
48	D1	95	LEU
48	D1	97	LEU
49	D2	21	LEU
49	D2	30	ARG
49	D2	32	LEU
49	D2	55	ARG
49	D2	70	GLN
50	D3	8	LEU
50	D3	30	ARG
50	D3	55	ARG
51	D4	1	MET
51	D4	3	GLU
51	D4	5	ILE
51	D4	8	LYS
51	D4	10	VAL
51	D4	13	ARG
51	D4	14	ILE
51	D4	23	GLU
51	D4	31	ILE
51	D4	56	VAL
51	D4	58	ARG
51	D4	61	ARG
51	D4	63	TYR
51	D4	68	ARG
51	D4	69	LYS
52	D5	6	VAL
52	D5	40	LYS
53	D6	6	ARG

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Mol	Chain	Res	Type
53	D6	14	THR
53	D6	38	LYS
54	D7	1	MET
54	D7	14	LYS
55	D8	26	LYS
55	D8	31	HIS
55	D8	34	TRP
55	D8	50	LEU
56	D9	4	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (127) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	76	GLN
2	AB	94	ASN
3	AC	6	HIS
3	AC	28	GLN
3	AC	118	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	42	GLN
4	AD	77	ASN
4	AD	123	HIS
5	AE	20	GLN
5	AE	38	GLN
5	AE	73	ASN
5	AE	141	GLN
6	AF	73	ASN
6	AF	94	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	97	GLN
9	AI	23	ASN
9	AI	31	GLN
9	AI	58	HIS
9	AI	73	GLN
9	AI	89	ASN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	104	GLN
12	AL	78	GLN
13	AM	92	HIS

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Mol	Chain	Res	Type
15	AO	28	GLN
17	AQ	16	GLN
19	AS	23	ASN
19	AS	65	ASN
19	AS	69	HIS
20	AT	9	ASN
20	AT	26	ASN
20	AT	45	GLN
20	AT	73	HIS
28	BD	164	GLN
28	BD	166	GLN
28	BD	253	GLN
30	BF	8	GLN
30	BF	69	HIS
30	BF	169	ASN
30	BF	203	GLN
31	BG	40	ASN
33	BI	43	ASN
33	BI	105	HIS
34	BN	8	GLN
34	BN	133	GLN
36	BP	38	GLN
43	BW	60	ASN
44	BX	31	HIS
44	BX	82	GLN
45	BY	6	HIS
45	BY	92	ASN
46	BZ	34	ASN
51	B4	46	GLN
56	B9	36	GLN
2	CB	16	HIS
2	CB	40	HIS
2	CB	76	GLN
2	CB	94	ASN
2	CB	224	GLN
3	CC	3	ASN
3	CC	6	HIS
3	CC	28	GLN
3	CC	37	GLN
3	CC	104	GLN
3	CC	118	GLN
3	CC	123	GLN

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Mol	Chain	Res	Type
4	CD	77	ASN
4	CD	123	HIS
4	CD	125	HIS
4	CD	161	ASN
5	CE	20	GLN
5	CE	141	GLN
6	CF	27	GLN
6	CF	73	ASN
6	CF	100	ASN
7	CG	28	ASN
8	CH	78	GLN
9	CI	23	ASN
9	CI	31	GLN
9	CI	58	HIS
9	CI	73	GLN
9	CI	89	ASN
9	CI	124	GLN
10	CJ	21	GLN
10	CJ	62	HIS
10	CJ	68	HIS
11	CK	93	GLN
12	CL	78	GLN
12	CL	99	HIS
13	CM	77	ASN
13	CM	92	HIS
14	CN	49	HIS
15	CO	28	GLN
16	CP	16	HIS
17	CQ	16	GLN
19	CS	69	HIS
20	CT	90	GLN
28	DD	164	GLN
28	DD	253	GLN
30	DF	69	HIS
30	DF	169	ASN
30	DF	203	GLN
31	DG	40	ASN
31	DG	41	GLN
31	DG	108	ASN
33	DI	43	ASN
34	DN	8	GLN
36	DP	38	GLN

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Mol	Chain	Res	Type
37	DQ	123	HIS
39	DS	68	GLN
40	DT	43	GLN
40	DT	58	ASN
42	DV	64	HIS
43	DW	60	ASN
44	DX	31	HIS
45	DY	43	ASN
46	DZ	55	HIS
46	DZ	151	HIS
47	D0	35	ASN
49	D2	38	GLN
50	D3	32	GLN
56	D9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1494/1521 (98%)	361 (24%)	19 (1%)
1	CA	1501/1521 (98%)	370 (24%)	25 (1%)
22	AV	12/24 (50%)	3 (25%)	0
22	CV	11/24 (45%)	3 (27%)	0
23	AW	70/76 (92%)	27 (38%)	2 (2%)
23	CW	67/76 (88%)	26 (38%)	3 (4%)
24	AX	74/77 (96%)	16 (21%)	0
24	CX	74/77 (96%)	23 (31%)	0
25	AY	71/76 (93%)	37 (52%)	3 (4%)
25	CY	69/76 (90%)	36 (52%)	1 (1%)
26	BA	2812/2915 (96%)	444 (15%)	36 (1%)
26	DA	2791/2915 (95%)	563 (20%)	24 (0%)
27	BB	119/121 (98%)	13 (10%)	0
27	DB	119/121 (98%)	38 (31%)	0
All	All	9284/9620 (96%)	1960 (21%)	113 (1%)

All (1960) RNA backbone outliers are listed below:

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

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Mol	Chain	Res	Type
1	AA	29	G
1	AA	32	A
1	AA	39	G
1	AA	41	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	55	A
1	AA	59	A
1	AA	61	G
1	AA	65	U
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	100	C
1	AA	101	A
1	AA	112	G
1	AA	115	G
1	AA	116	A
1	AA	121	C
1	AA	131	C
1	AA	140	A
1	AA	143	A
1	AA	154	C
1	AA	155	C
1	AA	163	C
1	AA	166	G
1	AA	169	C
1	AA	170	U
1	AA	172	A
1	AA	174	C
1	AA	180	U
1	AA	182	U
1	AA	189(C)	C
1	AA	189(D)	C
1	AA	189(F)	U
1	AA	189(G)	G
1	AA	189(H)	G

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Mol	Chain	Res	Type
1	AA	189(I)	G
1	AA	189(K)	U
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	243	A
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C
1	AA	270	A
1	AA	277	C
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	342	C
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	396	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	409	G
1	AA	412	A
1	AA	413	G
1	AA	421	U
1	AA	424	G

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Mol	Chain	Res	Type
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	457	C
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	477	A
1	AA	485	G
1	AA	496	A
1	AA	498	U
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	521	G
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	544	G
1	AA	547	A
1	AA	559	A
1	AA	561	U
1	AA	564	C
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	581	G
1	AA	592	G
1	AA	593	G
1	AA	596	C
1	AA	617	G
1	AA	630	G
1	AA	631	G
1	AA	633	G
1	AA	647	C

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Mol	Chain	Res	Type
1	AA	653	A
1	AA	661	G
1	AA	665	A
1	AA	671	G
1	AA	673	G
1	AA	683	G
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	695	A
1	AA	705	U
1	AA	717	C
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	752	G
1	AA	753	A
1	AA	755	G
1	AA	761	G
1	AA	774	G
1	AA	777	A
1	AA	786	G
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	798	G
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	827	U
1	AA	828	A
1	AA	829	G
1	AA	832	C
1	AA	834	C
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	851	G
1	AA	853	G
1	AA	855	G

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Mol	Chain	Res	Type
1	AA	859	A
1	AA	874	G
1	AA	875	C
1	AA	885	G
1	AA	902	G
1	AA	914	A
1	AA	916	G
1	AA	922	G
1	AA	926	G
1	AA	927	G
1	AA	932	C
1	AA	934	C
1	AA	943	U
1	AA	957	U
1	AA	960	U
1	AA	961	U
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	973	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	979	C
1	AA	981	U
1	AA	989	C
1	AA	992	U
1	AA	993	G
1	AA	997	U
1	AA	1000	U
1	AA	1001	A
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1009	G
1	AA	1010	G
1	AA	1016	A
1	AA	1019	C
1	AA	1022	G
1	AA	1023	G

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Mol	Chain	Res	Type
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1033	G
1	AA	1034	G
1	AA	1037	C
1	AA	1043	C
1	AA	1045	C
1	AA	1046	A
1	AA	1048	G
1	AA	1052	U
1	AA	1054	C
1	AA	1055	A
1	AA	1060	C
1	AA	1065	U
1	AA	1066	C
1	AA	1067	A
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1087	G
1	AA	1092	A
1	AA	1093	A
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1101	A
1	AA	1108	G
1	AA	1109	C
1	AA	1111	A
1	AA	1113	C
1	AA	1116	C
1	AA	1122	U
1	AA	1123	A
1	AA	1124	G
1	AA	1125	U
1	AA	1130	A

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Mol	Chain	Res	Type
1	AA	1132	C
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1142	G
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1159	U
1	AA	1163	C
1	AA	1165	C
1	AA	1166	G
1	AA	1168	A
1	AA	1169	A
1	AA	1170	A
1	AA	1173	G
1	AA	1174	G
1	AA	1181	G
1	AA	1182	G
1	AA	1183	A
1	AA	1184	G
1	AA	1193	G
1	AA	1196	U
1	AA	1197	G
1	AA	1201	A
1	AA	1202	G
1	AA	1206	G
1	AA	1212	U
1	AA	1213	A
1	AA	1218	C
1	AA	1227	A
1	AA	1228	C
1	AA	1235	U
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1242	C
1	AA	1246	C
1	AA	1253	G
1	AA	1256	A

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Mol	Chain	Res	Type
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1270	C
1	AA	1273	G
1	AA	1275	A
1	AA	1276	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1282	C
1	AA	1286	A
1	AA	1287	A
1	AA	1289	A
1	AA	1290	G
1	AA	1294	G
1	AA	1296	C
1	AA	1297	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1309	G
1	AA	1317	C
1	AA	1319	A
1	AA	1320	C
1	AA	1322	C
1	AA	1327	C
1	AA	1331	G
1	AA	1338	G
1	AA	1346	A
1	AA	1347	G
1	AA	1353	G
1	AA	1358	U
1	AA	1360	A
1	AA	1363	C
1	AA	1368	G
1	AA	1370	G
1	AA	1397	C
1	AA	1406	U
1	AA	1411	C
1	AA	1419	G
1	AA	1442	G

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Mol	Chain	Res	Type
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1456	G
1	AA	1475	G
1	AA	1487	G
1	AA	1491	G
1	AA	1492	A
1	AA	1494	G
1	AA	1497	G
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
22	AV	13	A
22	AV	19	U
22	AV	24	A
23	AW	3	C
23	AW	8	4SU
23	AW	12	U
23	AW	13	C
23	AW	14	A
23	AW	15	G
23	AW	19	G
23	AW	20	U
23	AW	21	A
23	AW	23	A
23	AW	24	G
23	AW	35	A
23	AW	45	U
23	AW	46	7MG
23	AW	47	U
23	AW	48	C
23	AW	49	C
23	AW	50	U

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Mol	Chain	Res	Type
23	AW	52	G
23	AW	61	C
23	AW	63	G
23	AW	64	A
23	AW	66	U
23	AW	68	C
23	AW	70	G
23	AW	73	A
23	AW	74	C
24	AX	6	G
24	AX	9	G
24	AX	14	A
24	AX	18	G
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	22	G
24	AX	42	G
24	AX	46	G
24	AX	47	U
24	AX	58	A
24	AX	59	A
24	AX	61	C
24	AX	67	C
24	AX	68	C
25	AY	2	C
25	AY	4	C
25	AY	5	G
25	AY	7	A
25	AY	9	A
25	AY	10	G
25	AY	11	C
25	AY	14	A
25	AY	19	G
25	AY	20	U
25	AY	21	A
25	AY	23	A
25	AY	25	C
25	AY	26	A
25	AY	32	PSU
25	AY	34	G
25	AY	39	PSU

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Mol	Chain	Res	Type
25	AY	41	C
25	AY	42	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	56	C
25	AY	57	G
25	AY	58	A
25	AY	59	U
25	AY	60	U
25	AY	61	C
25	AY	62	C
25	AY	67	C
25	AY	68	C
25	AY	69	G
25	AY	73	A
26	BA	10	G
26	BA	12	U
26	BA	13	A
26	BA	34	C
26	BA	45	C
26	BA	54	G
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	99	G
26	BA	116	A
26	BA	117	A
26	BA	118	U
26	BA	149	A
26	BA	154	G
26	BA	155	C
26	BA	161	C
26	BA	171	A
26	BA	185	A

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Mol	Chain	Res	Type
26	BA	188	A
26	BA	189	U
26	BA	194	G
26	BA	204	G
26	BA	205	A
26	BA	210	A
26	BA	211	A
26	BA	218	A
26	BA	221	G
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	275	C
26	BA	279	G
26	BA	281	G
26	BA	289	G
26	BA	295	C
26	BA	296	U
26	BA	299	G
26	BA	303	C
26	BA	307	A
26	BA	318	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	397	G
26	BA	399	G
26	BA	407	U
26	BA	413	G
26	BA	423	G
26	BA	434	G
26	BA	438	G
26	BA	448	U
26	BA	455	A

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Mol	Chain	Res	Type
26	BA	469	A
26	BA	470	C
26	BA	474	U
26	BA	477	C
26	BA	482	C
26	BA	483	A
26	BA	496	A
26	BA	507	G
26	BA	529	U
26	BA	530	A
26	BA	534	C
26	BA	537	G
26	BA	553	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	591	U
26	BA	596	G
26	BA	598	A
26	BA	609	A
26	BA	615	G
26	BA	626	A
26	BA	627	G
26	BA	630	U
26	BA	639	G
26	BA	641	G
26	BA	662	A
26	BA	670	C
26	BA	671	A
26	BA	692	C
26	BA	693	G
26	BA	697	C
26	BA	698	G
26	BA	716	G
26	BA	733	G
26	BA	777	C
26	BA	787	U
26	BA	811	A

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Mol	Chain	Res	Type
26	BA	822	G
26	BA	823	G
26	BA	829	A
26	BA	830	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	874	U
26	BA	875	U
26	BA	877	G
26	BA	906	G
26	BA	913	A
26	BA	924	U
26	BA	927	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	942	A
26	BA	943	C
26	BA	945	A
26	BA	946	A
26	BA	953	U
26	BA	956	A
26	BA	972	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

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Mol	Chain	Res	Type
26	BA	1020	C
26	BA	1029	A
26	BA	1036	A
26	BA	1042	A
26	BA	1058	U
26	BA	1059	C
26	BA	1068	G
26	BA	1071	G
26	BA	1072	U
26	BA	1079	U
26	BA	1084	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	1156	G
26	BA	1158	G
26	BA	1174	A
26	BA	1176	U
26	BA	1180	C
26	BA	1181	G
26	BA	1184	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	1255	A
26	BA	1256	U
26	BA	1265	A
26	BA	1290	G
26	BA	1299	A
26	BA	1302	G
26	BA	1317	G
26	BA	1318	A
26	BA	1319	U
26	BA	1346	U
26	BA	1347	A

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Mol	Chain	Res	Type
26	BA	1349	G
26	BA	1360	C
26	BA	1398	U
26	BA	1405	A
26	BA	1406	A
26	BA	1411	A
26	BA	1426	G
26	BA	1430	A
26	BA	1431	G
26	BA	1441	A
26	BA	1462	G
26	BA	1463	C
26	BA	1467	G
26	BA	1468	G
26	BA	1474	C
26	BA	1491	A
26	BA	1496	A
26	BA	1497	G
26	BA	1502	G
26	BA	1514	C
26	BA	1518	A
26	BA	1525	G
26	BA	1529	G
26	BA	1536	A
26	BA	1539	C
26	BA	1550	C
26	BA	1554	A
26	BA	1555	C
26	BA	1556	A
26	BA	1578	C
26	BA	1586	G
26	BA	1587	U
26	BA	1589	A
26	BA	1590	C
26	BA	1601	A
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

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Mol	Chain	Res	Type
26	BA	1632	A
26	BA	1654	A
26	BA	1656	A
26	BA	1695	C
26	BA	1701	A
26	BA	1721	G
26	BA	1743	G
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	1787	G
26	BA	1793	A
26	BA	1794	G
26	BA	1795	G
26	BA	1804	A
26	BA	1811	A
26	BA	1822	A
26	BA	1831	C
26	BA	1847	G
26	BA	1859	G
26	BA	1870	G
26	BA	1878	A
26	BA	1889	G
26	BA	1892	G
26	BA	1900	G
26	BA	1911	A
26	BA	1922	A
26	BA	1928	G
26	BA	1941	A
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

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Mol	Chain	Res	Type
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	2071	G
26	BA	2077	C
26	BA	2078	G
26	BA	2082	A
26	BA	2083	G
26	BA	2084	A
26	BA	2089	G
26	BA	2091	G
26	BA	2115	G
26	BA	2120	U
26	BA	2122	G
26	BA	2123	G
26	BA	2126	G
26	BA	2133	C
26	BA	2138	G
26	BA	2141	A
26	BA	2144	U
26	BA	2147	G
26	BA	2149	G
26	BA	2151	C
26	BA	2152	U
26	BA	2153	G
26	BA	2154	U
26	BA	2155	G
26	BA	2156	A
26	BA	2157	A
26	BA	2158	C
26	BA	2159	C
26	BA	2160	C
26	BA	2162	C
26	BA	2163	G
26	BA	2164	C

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Mol	Chain	Res	Type
26	BA	2165	C
26	BA	2167	C
26	BA	2169	G
26	BA	2173	G
26	BA	2174	G
26	BA	2175	G
26	BA	2177	G
26	BA	2179	G
26	BA	2180	A
26	BA	2181	G
26	BA	2182	G
26	BA	2183	C
26	BA	2185	C
26	BA	2186	C
26	BA	2187	G
26	BA	2188	G
26	BA	2189	U
26	BA	2190	G
26	BA	2191	A
26	BA	2193	A
26	BA	2194	U
26	BA	2196	C
26	BA	2197	C
26	BA	2200	C
26	BA	2203	G
26	BA	2204	G
26	BA	2205	C
26	BA	2206	G
26	BA	2210	C
26	BA	2211	U
26	BA	2213	G
26	BA	2220	A
26	BA	2221	A
26	BA	2227	G
26	BA	2228	G
26	BA	2229	A
26	BA	2230	U
26	BA	2237	A
26	BA	2250	G
26	BA	2251	G
26	BA	2280	A
26	BA	2285	A

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Mol	Chain	Res	Type
26	BA	2287	C
26	BA	2292	G
26	BA	2295	C
26	BA	2298	A
26	BA	2299	A
26	BA	2301	G
26	BA	2310	A
26	BA	2317	A
26	BA	2320	G
26	BA	2325	C
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	2408	G
26	BA	2418	U
26	BA	2426	G
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	2480	G
26	BA	2481	A
26	BA	2486	C
26	BA	2488	A
26	BA	2490	A
26	BA	2514	G
26	BA	2517	G
26	BA	2530	A
26	BA	2541	G
26	BA	2566	U
26	BA	2578	A

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Mol	Chain	Res	Type
26	BA	2579	G
26	BA	2585	C
26	BA	2594	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	2701	U
26	BA	2702	C
26	BA	2703	C
26	BA	2715	C
26	BA	2725	A
26	BA	2726	A
26	BA	2727	G
26	BA	2739	U
26	BA	2746	A
26	BA	2770	A
26	BA	2771	A
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	2806	G
26	BA	2813	G
26	BA	2818	U
26	BA	2828	G
26	BA	2830	A
26	BA	2831	A
26	BA	2834	C
26	BA	2843	G
26	BA	2845	A
26	BA	2882	G
26	BA	2883	A
26	BA	2884	C
26	BA	2885	C
26	BA	2890	C
26	BA	2901	A

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Mol	Chain	Res	Type
26	BA	2902	G
26	BA	2903	G
27	BB	2	C
27	BB	45	A
27	BB	52	A
27	BB	56	G
27	BB	73	A
27	BB	75	G
27	BB	85	G
27	BB	89	G
27	BB	106	G
27	BB	109	C
27	BB	110	G
27	BB	119	G
27	BB	120	A
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	41	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	55	A
1	CA	59	A
1	CA	61	G
1	CA	65	U
1	CA	66	G
1	CA	70	G
1	CA	78	G
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	96	U
1	CA	97	G
1	CA	98	G
1	CA	100	C

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Mol	Chain	Res	Type
1	CA	101	A
1	CA	112	G
1	CA	116	A
1	CA	121	C
1	CA	131	C
1	CA	140	A
1	CA	142	G
1	CA	154	C
1	CA	155	C
1	CA	163	C
1	CA	166	G
1	CA	169	C
1	CA	170	U
1	CA	172	A
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(D)	C
1	CA	189(F)	U
1	CA	189(G)	G
1	CA	189(H)	G
1	CA	189(I)	G
1	CA	189(K)	U
1	CA	190	U
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	243	A
1	CA	247	G
1	CA	251	G
1	CA	258	G
1	CA	266	G
1	CA	267	C
1	CA	270	A
1	CA	277	C
1	CA	289	G
1	CA	301	G
1	CA	321	A
1	CA	328	C

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Mol	Chain	Res	Type
1	CA	332	G
1	CA	342	C
1	CA	344	A
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	396	G
1	CA	398	C
1	CA	406	G
1	CA	409	G
1	CA	412	A
1	CA	413	G
1	CA	421	U
1	CA	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	455	C
1	CA	457	C
1	CA	461	A
1	CA	471	G
1	CA	477	A
1	CA	485	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	521	G
1	CA	527	G
1	CA	531	U
1	CA	532	A

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Mol	Chain	Res	Type
1	CA	533	A
1	CA	544	G
1	CA	547	A
1	CA	559	A
1	CA	561	U
1	CA	564	C
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	581	G
1	CA	592	G
1	CA	593	G
1	CA	596	C
1	CA	600	C
1	CA	617	G
1	CA	630	G
1	CA	631	G
1	CA	633	G
1	CA	647	C
1	CA	650	G
1	CA	653	A
1	CA	657	G
1	CA	661	G
1	CA	665	A
1	CA	671	G
1	CA	673	G
1	CA	683	G
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	695	A
1	CA	705	U
1	CA	717	C
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	749	C
1	CA	752	G
1	CA	753	A
1	CA	755	G
1	CA	761	G
1	CA	774	G

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Mol	Chain	Res	Type
1	CA	777	A
1	CA	786	G
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	798	G
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	827	U
1	CA	828	A
1	CA	829	G
1	CA	833	U
1	CA	834	C
1	CA	840	C
1	CA	841	U
1	CA	848	C
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	874	G
1	CA	875	C
1	CA	885	G
1	CA	902	G
1	CA	914	A
1	CA	916	G
1	CA	922	G
1	CA	926	G
1	CA	927	G
1	CA	932	C
1	CA	934	C
1	CA	943	U
1	CA	957	U
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	973	G
1	CA	974	A
1	CA	975	A
1	CA	976	G

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Mol	Chain	Res	Type
1	CA	977	A
1	CA	978	A
1	CA	979	C
1	CA	981	U
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	997	U
1	CA	999	C
1	CA	1001	A
1	CA	1002	G
1	CA	1003	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1009	G
1	CA	1010	G
1	CA	1016	A
1	CA	1019	C
1	CA	1022	G
1	CA	1023	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1029	C
1	CA	1030	C
1	CA	1030(A)	G
1	CA	1030(B)	C
1	CA	1030(C)	G
1	CA	1031	G
1	CA	1033	G
1	CA	1034	G
1	CA	1037	C
1	CA	1038	C
1	CA	1039	C
1	CA	1041	A
1	CA	1043	C
1	CA	1045	C
1	CA	1046	A
1	CA	1050	G

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Mol	Chain	Res	Type
1	CA	1052	U
1	CA	1053	G
1	CA	1054	C
1	CA	1060	C
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1087	G
1	CA	1092	A
1	CA	1093	A
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1100	C
1	CA	1101	A
1	CA	1108	G
1	CA	1109	C
1	CA	1111	A
1	CA	1116	C
1	CA	1122	U
1	CA	1124	G
1	CA	1125	U
1	CA	1127	G
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1142	G
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1159	U
1	CA	1163	C
1	CA	1165	C
1	CA	1166	G

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Mol	Chain	Res	Type
1	CA	1168	A
1	CA	1169	A
1	CA	1170	A
1	CA	1174	G
1	CA	1176	A
1	CA	1182	G
1	CA	1183	A
1	CA	1184	G
1	CA	1193	G
1	CA	1196	U
1	CA	1197	G
1	CA	1202	G
1	CA	1206	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1218	C
1	CA	1227	A
1	CA	1228	C
1	CA	1235	U
1	CA	1236	A
1	CA	1238	A
1	CA	1240	U
1	CA	1242	C
1	CA	1246	C
1	CA	1253	G
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1262	C
1	CA	1273	G
1	CA	1275	A
1	CA	1276	G
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	1289	A

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Mol	Chain	Res	Type
1	CA	1290	G
1	CA	1294	G
1	CA	1296	C
1	CA	1297	C
1	CA	1299	A
1	CA	1300	G
1	CA	1305	G
1	CA	1309	G
1	CA	1317	C
1	CA	1319	A
1	CA	1320	C
1	CA	1322	C
1	CA	1327	C
1	CA	1331	G
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1358	U
1	CA	1360	A
1	CA	1363	C
1	CA	1368	G
1	CA	1370	G
1	CA	1397	C
1	CA	1406	U
1	CA	1411	C
1	CA	1419	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1446	U
1	CA	1447	A
1	CA	1456	G
1	CA	1475	G
1	CA	1487	G
1	CA	1491	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

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Mol	Chain	Res	Type
1	CA	1506	U
1	CA	1517	G
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	14	A
22	CV	19	U
22	CV	24	A
23	CW	3	C
23	CW	8	4SU
23	CW	9	A
23	CW	12	U
23	CW	13	C
23	CW	14	A
23	CW	15	G
23	CW	19	G
23	CW	22	G
23	CW	23	A
23	CW	35	A
23	CW	46	7MG
23	CW	47	U
23	CW	48	C
23	CW	49	C
23	CW	50	U
23	CW	52	G
23	CW	61	C
23	CW	62	C
23	CW	63	G
23	CW	64	A
23	CW	66	U
23	CW	67	C
23	CW	68	C
23	CW	73	A
23	CW	74	C
24	CX	5	G
24	CX	6	G
24	CX	9	G
24	CX	13	C
24	CX	15	G
24	CX	16	C

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Mol	Chain	Res	Type
24	CX	18	G
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	22	G
24	CX	31	G
24	CX	47	U
24	CX	48	C
24	CX	52	G
24	CX	58	A
24	CX	59	A
24	CX	60	U
24	CX	62	C
24	CX	63	G
24	CX	64	G
24	CX	65	C
24	CX	68	C
25	CY	2	C
25	CY	7	A
25	CY	9	A
25	CY	10	G
25	CY	11	C
25	CY	14	A
25	CY	15	G
25	CY	19	G
25	CY	23	A
25	CY	25	C
25	CY	26	A
25	CY	32	PSU
25	CY	33	U
25	CY	34	G
25	CY	39	PSU
25	CY	41	C
25	CY	42	C
25	CY	45	U
25	CY	46	7MG
25	CY	47	U
25	CY	49	C
25	CY	52	G
25	CY	54	5MU
25	CY	55	PSU
25	CY	56	C

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Mol	Chain	Res	Type
25	CY	57	G
25	CY	58	A
25	CY	59	U
25	CY	61	C
25	CY	62	C
25	CY	65	G
25	CY	67	C
25	CY	68	C
25	CY	69	G
25	CY	70	G
25	CY	73	A
26	DA	10	G
26	DA	12	U
26	DA	13	A
26	DA	15	G
26	DA	34	C
26	DA	35	G
26	DA	45	C
26	DA	59	U
26	DA	71	A
26	DA	74	A
26	DA	75	G
26	DA	79	G
26	DA	83	G
26	DA	84	A
26	DA	90	U
26	DA	94	C
26	DA	100	G
26	DA	102	G
26	DA	118	A
26	DA	119	A
26	DA	120	U
26	DA	125	G
26	DA	140	G
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

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Mol	Chain	Res	Type
26	DA	205	G
26	DA	214	G
26	DA	215	G
26	DA	216	A
26	DA	221	A
26	DA	222	A
26	DA	228	A
26	DA	229	A
26	DA	232	G
26	DA	233	A
26	DA	248	G
26	DA	266	G
26	DA	271	A
26	DA	271(D)	G
26	DA	271(I)	G
26	DA	271(J)	C
26	DA	271(L)	U
26	DA	271(M)	G
26	DA	271(N)	U
26	DA	271(O)	C
26	DA	272(A)	U
26	DA	272(B)	G
26	DA	274	G
26	DA	277	C
26	DA	278	A
26	DA	292	C
26	DA	293	U
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	338	G
26	DA	342	G
26	DA	352	G
26	DA	353	G
26	DA	354	G
26	DA	362	U
26	DA	363	G
26	DA	363(A)	A

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Mol	Chain	Res	Type
26	DA	363(C)	G
26	DA	364	C
26	DA	372	G
26	DA	380	U
26	DA	386	G
26	DA	389	G
26	DA	396	G
26	DA	405	U
26	DA	406	G
26	DA	411	G
26	DA	412	A
26	DA	428	A
26	DA	442	G
26	DA	443	A
26	DA	444	C
26	DA	454	A
26	DA	455	C
26	DA	457	A
26	DA	470	A
26	DA	479	A
26	DA	481	G
26	DA	504	U
26	DA	505	A
26	DA	508	G
26	DA	509	C
26	DA	512	G
26	DA	521	G
26	DA	528	A
26	DA	529	A
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	575	A
26	DA	586	A
26	DA	588	U
26	DA	592	G
26	DA	599	G

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Mol	Chain	Res	Type
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
26	DA	616	G
26	DA	627	A
26	DA	637	A
26	DA	645	C
26	DA	646	A
26	DA	651	G
26	DA	652(A)	A
26	DA	652(B)	A
26	DA	652(C)	G
26	DA	652(U)	G
26	DA	669	G
26	DA	686	G
26	DA	715	G
26	DA	717	G
26	DA	726	G
26	DA	730	C
26	DA	753	C
26	DA	765	G
26	DA	774	A
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	792	G
26	DA	805	G
26	DA	812	C
26	DA	819	A
26	DA	827	U
26	DA	828	U
26	DA	847	U
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	867	C
26	DA	872	A
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	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	902	C
26	DA	903	C
26	DA	910	A
26	DA	911	A
26	DA	917	A
26	DA	923	C
26	DA	932	G
26	DA	933	A
26	DA	936	C
26	DA	938	G
26	DA	941	A
26	DA	943	U
26	DA	945	A
26	DA	946	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	980	A
26	DA	983	A
26	DA	996	A
26	DA	1005	C
26	DA	1006	C

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Mol	Chain	Res	Type
26	DA	1012	U
26	DA	1013	C
26	DA	1018	C
26	DA	1020	A
26	DA	1021	A
26	DA	1022	G
26	DA	1025	G
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	1113	U
26	DA	1114	G
26	DA	1116	C
26	DA	1121	C
26	DA	1126	A
26	DA	1128	A
26	DA	1129	A
26	DA	1130	U
26	DA	1135	C
26	DA	1136	G
26	DA	1137	G
26	DA	1139	G
26	DA	1144	G
26	DA	1159	U
26	DA	1171	G
26	DA	1204	A
26	DA	1210	A
26	DA	1211	U
26	DA	1212	G
26	DA	1220	A
26	DA	1244	G
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	1292	U

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Mol	Chain	Res	Type
26	DA	1300	U
26	DA	1301	A
26	DA	1303	G
26	DA	1314	C
26	DA	1332	G
26	DA	1352	U
26	DA	1359	A
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	1386	C
26	DA	1413	G
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	1435	G
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	1461	G
26	DA	1467	C
26	DA	1471	A
26	DA	1474	C
26	DA	1482	G
26	DA	1488	G
26	DA	1489	U
26	DA	1490	A
26	DA	1493	C
26	DA	1496	A
26	DA	1497	U
26	DA	1508	A
26	DA	1509	C

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Mol	Chain	Res	Type
26	DA	1509(A)	A
26	DA	1525	G
26	DA	1531	C
26	DA	1533	G
26	DA	1539	G
26	DA	1541	G
26	DA	1542	A
26	DA	1543	C
26	DA	1545	A
26	DA	1547	C
26	DA	1558	A
26	DA	1559	G
26	DA	1566	A
26	DA	1569	A
26	DA	1578	U
26	DA	1582	C
26	DA	1584	C
26	DA	1586	A
26	DA	1608	A
26	DA	1609	A
26	DA	1610	A
26	DA	1616	A
26	DA	1640	C
26	DA	1648	C
26	DA	1653	G
26	DA	1654	A
26	DA	1669	A
26	DA	1674	G
26	DA	1695	G
26	DA	1696	G
26	DA	1700	A
26	DA	1701	A
26	DA	1721	G
26	DA	1722	A
26	DA	1739	U
26	DA	1740	G
26	DA	1741	A
26	DA	1743	C
26	DA	1746	G
26	DA	1750	G
26	DA	1756	G
26	DA	1758	G

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Mol	Chain	Res	Type
26	DA	1762	A
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	1828	G
26	DA	1829	A
26	DA	1835	G
26	DA	1847	A
26	DA	1848	A
26	DA	1877	A
26	DA	1878	G
26	DA	1889	A
26	DA	1900	A
26	DA	1906	G
26	DA	1913	A
26	DA	1914	C
26	DA	1927	A
26	DA	1929	G
26	DA	1930	G
26	DA	1931	U
26	DA	1937	A
26	DA	1938	A
26	DA	1955	U
26	DA	1963	U
26	DA	1967	C
26	DA	1970	A
26	DA	1971	A
26	DA	1972	A
26	DA	1984	G
26	DA	1993	U
26	DA	1997	G
26	DA	2020	A
26	DA	2023	G
26	DA	2027	G
26	DA	2031	A

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Mol	Chain	Res	Type
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	2096	U
26	DA	2099	U
26	DA	2102	U
26	DA	2104	G
26	DA	2105	C
26	DA	2106	G
26	DA	2110	G
26	DA	2111	C
26	DA	2112	G
26	DA	2113	U
26	DA	2115	G
26	DA	2116	G
26	DA	2119	A
26	DA	2122	U
26	DA	2124	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	2142	C
26	DA	2144	U
26	DA	2146	C
26	DA	2148	G

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Mol	Chain	Res	Type
26	DA	2150	U
26	DA	2151	G
26	DA	2154	G
26	DA	2155	G
26	DA	2158	A
26	DA	2159	G
26	DA	2160	G
26	DA	2161	C
26	DA	2162	G
26	DA	2164	C
26	DA	2165	G
26	DA	2166	G
26	DA	2167	U
26	DA	2168	G
26	DA	2169	A
26	DA	2170	A
26	DA	2171	A
26	DA	2172	U
26	DA	2173	A
26	DA	2177	C
26	DA	2178	C
26	DA	2181	G
26	DA	2185	C
26	DA	2186	G
26	DA	2187	G
26	DA	2188	C
26	DA	2189	U
26	DA	2192	G
26	DA	2198	A
26	DA	2206	G
26	DA	2207	G
26	DA	2208	A
26	DA	2218	U
26	DA	2225	A
26	DA	2232	U
26	DA	2238	G
26	DA	2239	G
26	DA	2243	U
26	DA	2269	A
26	DA	2275	C
26	DA	2279	G
26	DA	2283	C

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Mol	Chain	Res	Type
26	DA	2287	A
26	DA	2289	G
26	DA	2294	C
26	DA	2297	C
26	DA	2299	G
26	DA	2301	C
26	DA	2303	G
26	DA	2305	A
26	DA	2308	G
26	DA	2312	U
26	DA	2318	G
26	DA	2319	G
26	DA	2320	A
26	DA	2321	G
26	DA	2322	A
26	DA	2325	G
26	DA	2327	A
26	DA	2334	G
26	DA	2336	A
26	DA	2343	C
26	DA	2347	C
26	DA	2354	G
26	DA	2372	G
26	DA	2376	A
26	DA	2377	A
26	DA	2383	G
26	DA	2385	C
26	DA	2387	U
26	DA	2402	C
26	DA	2406	U
26	DA	2410	G
26	DA	2422	A
26	DA	2423	U
26	DA	2425	A
26	DA	2429	G
26	DA	2430	A
26	DA	2431	U
26	DA	2434	A
26	DA	2435	A
26	DA	2439	A
26	DA	2441	C
26	DA	2445	G

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Mol	Chain	Res	Type
26	DA	2448	A
26	DA	2465	C
26	DA	2474	C
26	DA	2476	A
26	DA	2490	G
26	DA	2494	G
26	DA	2502	G
26	DA	2505	G
26	DA	2506	U
26	DA	2518	A
26	DA	2520	C
26	DA	2525	G
26	DA	2532	G
26	DA	2549	G
26	DA	2554	U
26	DA	2555	U
26	DA	2566	A
26	DA	2567	G
26	DA	2569	G
26	DA	2573	C
26	DA	2578	G
26	DA	2602	A
26	DA	2603	G
26	DA	2609	U
26	DA	2611	U
26	DA	2612	C
26	DA	2629	A
26	DA	2630	G
26	DA	2634	G
26	DA	2652	C
26	DA	2654	A
26	DA	2663	G
26	DA	2673	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	2732	G

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Mol	Chain	Res	Type
26	DA	2733	A
26	DA	2744	G
26	DA	2751	G
26	DA	2758	A
26	DA	2764	A
26	DA	2765	A
26	DA	2766	G
26	DA	2778	A
26	DA	2780	G
26	DA	2793	G
26	DA	2794	C
26	DA	2802	G
26	DA	2807	G
26	DA	2808	U
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	2839	G
26	DA	2872	G
26	DA	2873	A
26	DA	2880	C
26	DA	2886	G
26	DA	2892	A
26	DA	2894	G
26	DA	2897	U
27	DB	2	C
27	DB	7	G
27	DB	8	U
27	DB	9	G
27	DB	10	C
27	DB	13	A
27	DB	15	A
27	DB	20	C
27	DB	21	G
27	DB	25	A
27	DB	28	C
27	DB	30	C
27	DB	32	C
27	DB	34	U

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Mol	Chain	Res	Type
27	DB	38	C
27	DB	41	U
27	DB	42	C
27	DB	44	G
27	DB	52	A
27	DB	53	A
27	DB	56	G
27	DB	58	A
27	DB	59	A
27	DB	63	G
27	DB	64	C
27	DB	65	C
27	DB	66	A
27	DB	73	A
27	DB	85	G
27	DB	93	G
27	DB	94	C
27	DB	106	G
27	DB	108	U
27	DB	110	G
27	DB	111	G
27	DB	112	U
27	DB	119	G
27	DB	120	A

All (113) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	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	1065	U
1	AA	1067	A

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Mol	Chain	Res	Type
1	AA	1165	C
1	AA	1201	A
1	AA	1256	A
1	AA	1285	A
1	AA	1442	G
23	AW	13	C
23	AW	45	U
25	AY	19	G
25	AY	44	G
25	AY	58	A
26	BA	70	A
26	BA	185	A
26	BA	273	G
26	BA	302	A
26	BA	572	A
26	BA	793	A
26	BA	821	A
26	BA	874	U
26	BA	945	A
26	BA	1003	U
26	BA	1005	A
26	BA	1019	G
26	BA	1093	G
26	BA	1219	A
26	BA	1220	U
26	BA	1221	G
26	BA	1255	A
26	BA	1346	U
26	BA	1347	A
26	BA	1466	U
26	BA	1577	C
26	BA	1654	A
26	BA	1700	G
26	BA	2014	G
26	BA	2148	A
26	BA	2156	A
26	BA	2185	C
26	BA	2203	G
26	BA	2205	C
26	BA	2209	G
26	BA	2250	G
26	BA	2418	U

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Mol	Chain	Res	Type
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	560	U
1	CA	687	A
1	CA	748	C
1	CA	793	U
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1005	A
1	CA	1027	C
1	CA	1064	G
1	CA	1065	U
1	CA	1129	C
1	CA	1183	A
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1331	G
1	CA	1442	G
1	CA	1492	A
23	CW	13	C
23	CW	14	A
23	CW	66	U
25	CY	46	7MG
26	DA	196	A
26	DA	271(M)	G
26	DA	277	C
26	DA	614(B)	G
26	DA	752	A
26	DA	774	A
26	DA	856	C
26	DA	888	C
26	DA	900	A

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Mol	Chain	Res	Type
26	DA	1210	A
26	DA	1300	U
26	DA	1379	A
26	DA	1420	U
26	DA	1427	A
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	2318	G
26	DA	2422	A
26	DA	2430	A
26	DA	2689	U

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

40 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	57,23	19,21,22	1.82	4 (21%)	23,30,33	0.99	2 (8%)
23	MIA	AW	37	23	29,31,32	1.82	5 (17%)	41,44,47	1.86	7 (17%)
23	PSU	AW	39	23	19,21,22	1.81	4 (21%)	23,30,33	0.98	2 (8%)
23	7MG	AW	46	23	24,26,27	1.97	7 (29%)	34,39,42	2.45	10 (29%)
23	5MU	AW	54	23	20,22,23	1.67	4 (20%)	25,32,35	2.09	4 (16%)
23	PSU	AW	55	23	19,21,22	1.89	4 (21%)	23,30,33	1.39	1 (4%)
23	F3N	AW	76	23	34,36,37	1.45	4 (11%)	48,51,54	2.02	6 (12%)
23	4SU	AW	8	23	19,21,22	1.88	4 (21%)	23,30,33	3.02	4 (17%)
24	5MC	AX	32	24	20,22,23	1.73	4 (20%)	26,32,35	1.46	4 (15%)
24	5MU	AX	54	24,57	20,22,23	1.58	5 (25%)	25,32,35	2.03	4 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	PSU	AX	55	24	19,21,22	2.01	5 (26%)	23,30,33	1.03	3 (13%)
24	31H	AX	76	24,57	32,34,35	1.22	3 (9%)	44,47,50	2.33	11 (25%)
24	4SU	AX	8	24	19,21,22	1.89	4 (21%)	23,30,33	33.54	2 (8%)
25	PSU	AY	32	25	19,21,22	1.78	4 (21%)	23,30,33	1.04	3 (13%)
25	MIA	AY	37	25	20,24,32	1.76	5 (25%)	27,35,47	1.92	4 (14%)
25	PSU	AY	39	25	19,21,22	1.84	5 (26%)	23,30,33	1.07	2 (8%)
25	7MG	AY	46	25	24,26,27	1.98	6 (25%)	34,39,42	2.64	12 (35%)
25	5MU	AY	54	25	20,22,23	1.90	4 (20%)	25,32,35	2.70	5 (20%)
25	PSU	AY	55	25	19,21,22	1.90	4 (21%)	23,30,33	0.86	2 (8%)
25	4SU	AY	8	25	19,21,22	1.70	4 (21%)	23,30,33	4.73	4 (17%)
23	PSU	CW	32	23	19,21,22	1.83	4 (21%)	23,30,33	1.21	2 (8%)
23	MIA	CW	37	23	20,24,32	1.73	5 (25%)	27,35,47	1.93	4 (14%)
23	PSU	CW	39	23	19,21,22	1.95	4 (21%)	23,30,33	1.19	1 (4%)
23	7MG	CW	46	23	24,26,27	2.05	6 (25%)	34,39,42	2.25	9 (26%)
23	5MU	CW	54	23	20,22,23	1.65	4 (20%)	25,32,35	1.79	3 (12%)
23	PSU	CW	55	23	19,21,22	1.87	4 (21%)	23,30,33	1.29	2 (8%)
23	F3N	CW	76	23	34,36,37	1.49	4 (11%)	48,51,54	2.08	7 (14%)
23	4SU	CW	8	23	19,21,22	1.81	4 (21%)	23,30,33	6.41	4 (17%)
24	5MC	CX	32	24	20,22,23	1.74	4 (20%)	26,32,35	1.55	5 (19%)
24	5MU	CX	54	24	20,22,23	1.61	4 (20%)	25,32,35	2.30	4 (16%)
24	PSU	CX	55	24	19,21,22	1.84	4 (21%)	23,30,33	0.96	2 (8%)
24	31H	CX	76	24,57	32,34,35	1.24	3 (9%)	44,47,50	2.62	12 (27%)
24	4SU	CX	8	24	19,21,22	1.84	4 (21%)	23,30,33	23.31	2 (8%)
25	PSU	CY	32	25	19,21,22	1.79	4 (21%)	23,30,33	1.11	2 (8%)
25	MIA	CY	37	25	20,24,32	1.79	5 (25%)	27,35,47	1.95	5 (18%)
25	PSU	CY	39	25	19,21,22	2.04	5 (26%)	23,30,33	1.55	3 (13%)
25	7MG	CY	46	25	24,26,27	2.03	8 (33%)	34,39,42	2.61	10 (29%)
25	5MU	CY	54	25	20,22,23	1.67	4 (20%)	25,32,35	2.03	4 (16%)
25	PSU	CY	55	25	19,21,22	1.78	4 (21%)	23,30,33	1.17	2 (8%)
25	4SU	CY	8	25	19,21,22	1.96	4 (21%)	23,30,33	4.24	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	57,23	-	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	F3N	AW	76	23	-	0/20/37/38	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	-	0/8/25/26	0/2/2/2
24	31H	AX	76	24,57	-	1/23/40/41	0/3/3/3
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	-	0/6/25/26	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	-	0/8/37/38	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
23	F3N	CW	76	23	-	0/20/37/38	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	31H	CX	76	24,57	-	1/23/40/41	0/3/3/3
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	-	0/6/25/26	0/2/2/2

All (177) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C2-S10	-6.26	1.70	1.75
23	CW	46	7MG	C6-C5	6.20	1.49	1.41
25	CY	46	7MG	C6-C5	5.42	1.48	1.41
23	AW	46	7MG	C6-C5	5.33	1.48	1.41
24	AX	55	PSU	C5-C1'	-5.20	1.47	1.52
25	CY	39	PSU	C5-C1'	-5.11	1.47	1.52
23	AW	76	F3N	CB-CG	-4.82	1.39	1.51
25	AY	46	7MG	P-OP1	4.72	1.52	1.46
23	CW	46	7MG	P-OP1	4.70	1.52	1.46
25	AY	54	5MU	C2-N1	4.69	1.43	1.38
23	CW	55	PSU	P-OP1	4.67	1.52	1.46
24	AX	32	5MC	C5-C4	4.67	1.48	1.41
25	AY	8	4SU	P-OP1	4.66	1.52	1.46
25	AY	55	PSU	C5-C1'	-4.65	1.48	1.52
25	CY	39	PSU	P-OP1	4.62	1.52	1.46
25	CY	46	7MG	P-OP1	4.60	1.52	1.46
25	CY	55	PSU	P-OP1	4.54	1.51	1.46
25	CY	54	5MU	P-OP1	4.52	1.51	1.46
25	AY	46	7MG	C6-C5	4.50	1.47	1.41
24	AX	8	4SU	O2-C2	4.47	1.27	1.21
25	CY	8	4SU	P-OP1	4.46	1.51	1.46
25	AY	54	5MU	P-OP1	4.46	1.51	1.46
24	AX	8	4SU	P-OP1	4.45	1.51	1.46
23	CW	8	4SU	P-OP1	4.45	1.51	1.46
24	CX	54	5MU	P-OP1	4.39	1.51	1.46
25	CY	32	PSU	P-OP1	4.39	1.51	1.46
24	AX	55	PSU	P-OP1	4.38	1.51	1.46
23	CW	76	F3N	CB-CG	-4.38	1.40	1.51
24	CX	8	4SU	P-OP1	4.37	1.51	1.46
23	CW	37	MIA	P-OP1	4.37	1.51	1.46
23	CW	39	PSU	P-OP1	4.36	1.51	1.46
24	CX	32	5MC	C5-C4	4.36	1.48	1.41
25	AY	37	MIA	P-OP1	4.36	1.51	1.46
25	CY	8	4SU	C2-N1	4.36	1.43	1.38
25	CY	37	MIA	P-OP1	4.36	1.51	1.46
24	AX	32	5MC	P-OP1	4.33	1.51	1.46
23	AW	46	7MG	P-OP1	4.33	1.51	1.46
23	AW	55	PSU	P-OP1	4.30	1.51	1.46
23	AW	55	PSU	C5-C1'	-4.30	1.48	1.52
23	CW	39	PSU	C5-C1'	-4.28	1.48	1.52
25	AY	55	PSU	P-OP1	4.24	1.51	1.46
23	AW	39	PSU	P-OP1	4.24	1.51	1.46
23	AW	32	PSU	P-OP1	4.23	1.51	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CX	55	PSU	C5-C1'	-4.23	1.48	1.52
23	AW	8	4SU	P-OP1	4.21	1.51	1.46
23	CW	32	PSU	P-OP1	4.20	1.51	1.46
24	CX	8	4SU	O2-C2	4.16	1.27	1.21
23	AW	37	MIA	P-OP1	4.16	1.51	1.46
25	AY	39	PSU	P-OP1	4.15	1.51	1.46
25	AY	32	PSU	P-OP1	4.08	1.51	1.46
23	CW	54	5MU	P-OP1	4.06	1.51	1.46
24	CX	32	5MC	P-OP1	4.05	1.51	1.46
23	AW	8	4SU	C2-N1	4.04	1.42	1.38
24	AX	54	5MU	P-OP1	4.03	1.51	1.46
24	CX	55	PSU	P-OP1	4.01	1.51	1.46
25	CY	8	4SU	C4-S4	-3.99	1.59	1.67
23	CW	55	PSU	C5-C1'	-3.98	1.48	1.52
23	CW	32	PSU	C5-C1'	-3.97	1.48	1.52
23	CW	8	4SU	C2-N1	3.97	1.42	1.38
23	AW	8	4SU	C4-S4	-3.92	1.59	1.67
23	AW	54	5MU	P-OP1	3.91	1.51	1.46
23	AW	32	PSU	C5-C1'	-3.90	1.48	1.52
25	AY	8	4SU	C4-S4	-3.84	1.60	1.67
25	AY	39	PSU	C5-C1'	-3.78	1.48	1.52
25	AY	32	PSU	C4-C5	3.77	1.49	1.40
24	CX	32	5MC	C2-N1	3.74	1.42	1.38
23	AW	39	PSU	C5-C1'	-3.73	1.48	1.52
23	CW	76	F3N	O4'-C1'	3.70	1.45	1.41
24	AX	8	4SU	C4-S4	-3.67	1.60	1.67
24	CX	76	31H	C5-C4	-3.64	1.32	1.40
23	CW	8	4SU	C4-S4	-3.64	1.60	1.67
23	CW	39	PSU	O2-C2	3.61	1.26	1.21
23	AW	8	4SU	O2-C2	3.59	1.26	1.21
23	AW	76	F3N	O4'-C1'	3.58	1.45	1.41
24	CX	8	4SU	C4-S4	-3.56	1.60	1.67
25	CY	32	PSU	C4-C5	3.56	1.49	1.40
25	CY	37	MIA	C5-C4	3.52	1.48	1.40
25	AY	46	7MG	C2-N3	3.50	1.37	1.33
24	CX	54	5MU	C4-C5	3.48	1.48	1.40
25	AY	37	MIA	C5-C4	3.48	1.48	1.40
23	CW	76	F3N	C5-C4	-3.47	1.32	1.40
23	CW	54	5MU	C4-C5	3.46	1.48	1.40
25	AY	54	5MU	C4-C5	3.45	1.48	1.40
23	AW	39	PSU	C4-C5	3.45	1.48	1.40
25	AY	39	PSU	C4-C5	3.44	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CW	32	PSU	C4-C5	3.43	1.48	1.40
23	AW	54	5MU	C4-C5	3.42	1.48	1.40
25	CY	39	PSU	C4-C5	3.42	1.48	1.40
23	AW	55	PSU	C4-C5	3.41	1.48	1.40
23	AW	32	PSU	C4-C5	3.40	1.48	1.40
23	AW	54	5MU	C2-N1	3.39	1.42	1.38
25	CY	8	4SU	O2-C2	3.39	1.26	1.21
24	CX	55	PSU	C4-C5	3.38	1.48	1.40
25	CY	37	MIA	C6-N6	3.37	1.35	1.28
25	AY	55	PSU	C4-C5	3.34	1.48	1.40
25	CY	32	PSU	C5-C1'	-3.34	1.49	1.52
24	AX	54	5MU	C4-C5	3.34	1.48	1.40
23	CW	37	MIA	C5-C4	3.33	1.48	1.40
24	CX	8	4SU	C2-N1	3.33	1.42	1.38
25	CY	54	5MU	C4-C5	3.32	1.48	1.40
23	CW	55	PSU	C4-C5	3.30	1.48	1.40
25	AY	37	MIA	C6-N6	3.30	1.35	1.28
23	CW	37	MIA	C6-N6	3.25	1.35	1.28
24	AX	55	PSU	C4-C5	3.24	1.48	1.40
25	AY	39	PSU	O2-C2	3.24	1.26	1.21
25	CY	55	PSU	C4-C5	3.20	1.48	1.40
23	AW	37	MIA	C5-C4	3.18	1.47	1.40
23	AW	76	F3N	C5-C4	-3.14	1.33	1.40
23	AW	54	5MU	O2-C2	3.13	1.25	1.21
24	AX	76	31H	C5-C4	-3.12	1.33	1.40
23	CW	39	PSU	C4-C5	3.11	1.48	1.40
25	AY	32	PSU	O2-C2	3.11	1.25	1.21
25	CY	55	PSU	C5-C1'	-3.08	1.49	1.52
23	CW	54	5MU	C2-N1	3.08	1.41	1.38
25	AY	46	7MG	C5-N7	-3.06	1.33	1.39
25	AY	32	PSU	C5-C1'	-3.05	1.49	1.52
23	CW	54	5MU	O2-C2	3.03	1.25	1.21
25	CY	54	5MU	C2-N1	3.00	1.41	1.38
25	CY	32	PSU	O2-C2	2.98	1.25	1.21
23	CW	55	PSU	O2-C2	2.97	1.25	1.21
23	CW	32	PSU	O2-C2	2.97	1.25	1.21
25	CY	46	7MG	C2-N2	2.96	1.36	1.32
23	AW	32	PSU	O2-C2	2.96	1.25	1.21
25	CY	54	5MU	O2-C2	2.96	1.25	1.21
23	AW	55	PSU	O2-C2	2.93	1.25	1.21
25	AY	54	5MU	O2-C2	2.91	1.25	1.21
24	CX	55	PSU	O2-C2	2.90	1.25	1.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	CY	55	PSU	O2-C2	2.89	1.25	1.21
24	AX	32	5MC	C2-N1	2.87	1.41	1.38
25	AY	55	PSU	O2-C2	2.87	1.25	1.21
24	AX	55	PSU	O2-C2	2.82	1.25	1.21
24	CX	54	5MU	C2-N1	2.82	1.41	1.38
23	CW	8	4SU	O2-C2	2.81	1.25	1.21
23	CW	46	7MG	C5-N7	-2.74	1.34	1.39
25	CY	46	7MG	C5-C4	2.73	1.48	1.39
25	CY	37	MIA	C6-C5	2.73	1.49	1.44
23	AW	46	7MG	C5-N7	-2.72	1.34	1.39
23	AW	39	PSU	O2-C2	2.71	1.25	1.21
23	AW	46	7MG	C2-N2	2.70	1.36	1.32
23	AW	46	7MG	C5-C4	2.70	1.48	1.39
24	CX	32	5MC	O2-C2	2.70	1.25	1.21
24	AX	54	5MU	C2-N1	2.69	1.41	1.38
25	AY	8	4SU	O2-C2	2.67	1.25	1.21
25	AY	46	7MG	C5-C4	2.64	1.47	1.39
25	AY	37	MIA	C6-C5	2.59	1.49	1.44
23	AW	37	MIA	C6-C5	2.55	1.49	1.44
24	CX	76	31H	CA-N	2.55	1.48	1.45
23	AW	37	MIA	C4-N9	-2.54	1.34	1.37
25	CY	46	7MG	C5-N7	-2.53	1.34	1.39
23	AW	46	7MG	C2-N3	2.53	1.36	1.33
24	AX	32	5MC	O2-C2	2.52	1.25	1.21
24	AX	76	31H	C5-N7	-2.49	1.31	1.39
25	AY	46	7MG	C2-N2	2.48	1.36	1.32
24	AX	54	5MU	O2-C2	2.48	1.25	1.21
24	AX	8	4SU	C2-N1	2.46	1.41	1.38
23	CW	37	MIA	C6-C5	2.46	1.49	1.44
25	AY	8	4SU	C2-N1	2.45	1.41	1.38
24	AX	76	31H	C8-N9	-2.44	1.33	1.36
23	CW	46	7MG	C5-C4	2.35	1.47	1.39
24	CX	54	5MU	O2-C2	2.34	1.24	1.21
25	CY	37	MIA	C4-N9	-2.34	1.34	1.37
23	AW	76	F3N	C5-N7	-2.32	1.31	1.39
25	CY	46	7MG	C4-N9	-2.31	1.33	1.37
23	AW	46	7MG	C4-N9	-2.30	1.33	1.37
23	CW	37	MIA	C4-N9	-2.28	1.34	1.37
25	AY	37	MIA	C4-N9	-2.27	1.34	1.37
23	CW	46	7MG	C4-N9	-2.26	1.33	1.37
24	CX	76	31H	C3'-N3'	2.24	1.49	1.45
25	CY	39	PSU	O4'-C1'	-2.21	1.40	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CW	46	7MG	C2-N2	2.21	1.35	1.32
24	AX	54	5MU	C4-N3	-2.15	1.33	1.36
25	CY	46	7MG	CM7-N7	2.12	1.49	1.46
23	CW	76	F3N	C5-N7	-2.05	1.32	1.39
25	CY	46	7MG	C2-N3	2.05	1.36	1.33
25	AY	39	PSU	C4-N3	-2.03	1.33	1.36
25	CY	39	PSU	C6-N1	-2.01	1.32	1.35
24	AX	55	PSU	O4'-C1'	-2.01	1.41	1.44

All (179) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	8	4SU	C4-N3-C2	160.78	128.48	121.60
24	CX	8	4SU	C4-N3-C2	111.46	126.37	121.60
23	CW	8	4SU	C4-N3-C2	-29.19	120.35	121.60
25	AY	8	4SU	C4-N3-C2	-21.05	120.70	121.60
25	CY	8	4SU	C4-N3-C2	-17.66	120.85	121.60
23	AW	8	4SU	C4-N3-C2	12.04	122.12	121.60
24	CX	76	31H	N3-C2-N1	-10.06	120.04	128.89
23	CW	76	F3N	N3-C2-N1	-10.04	120.06	128.89
23	AW	76	F3N	N3-C2-N1	-9.90	120.18	128.89
24	AX	76	31H	N3-C2-N1	-9.87	120.20	128.89
25	AY	54	5MU	C6-N1-C2	-9.51	119.71	122.41
25	AY	46	7MG	N3-C4-N9	9.26	141.42	126.80
24	CX	8	4SU	C2-N1-C1'	8.42	123.49	118.21
25	CY	8	4SU	C2-N1-C1'	8.07	123.27	118.21
25	CY	46	7MG	C6-N1-C2	7.55	124.47	120.20
24	CX	54	5MU	C6-N1-C2	-7.51	120.27	122.41
24	CX	54	5MU	N3-C2-N1	7.34	122.09	115.97
23	CW	8	4SU	C2-N1-C1'	7.14	122.68	118.21
23	AW	46	7MG	N3-C4-N9	7.07	137.97	126.80
23	AW	46	7MG	C6-N1-C2	7.07	124.19	120.20
23	AW	54	5MU	C6-N1-C2	-6.93	120.44	122.41
25	AY	54	5MU	N3-C2-N1	6.91	121.74	115.97
25	CY	46	7MG	N3-C4-N9	6.87	137.66	126.80
24	CX	76	31H	O4'-C1'-N9	6.70	122.69	108.10
25	CY	54	5MU	N3-C2-N1	6.64	121.52	115.97
23	AW	37	MIA	C5-C4-N3	-6.55	118.53	126.07
24	AX	54	5MU	N3-C2-N1	6.54	121.44	115.97
23	CW	37	MIA	C5-C4-N3	-6.45	118.64	126.07
23	AW	8	4SU	C2-N1-C1'	6.45	122.25	118.21
25	AY	37	MIA	C5-C4-N3	-6.35	118.75	126.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	54	5MU	C6-N1-C2	-6.33	120.61	122.41
25	CY	37	MIA	C5-C4-N3	-6.29	118.82	126.07
23	CW	76	F3N	C5-C4-N3	-6.16	119.98	125.98
24	CX	76	31H	C4'-O4'-C1'	-6.13	102.99	109.72
23	AW	54	5MU	N3-C2-N1	5.94	120.93	115.97
25	AY	46	7MG	C5-C4-N3	-5.93	116.23	126.61
23	CW	46	7MG	N3-C4-N9	5.86	136.05	126.80
23	CW	46	7MG	N7-C8-N9	-5.70	95.56	103.13
23	CW	37	MIA	N3-C4-N9	5.66	135.21	126.91
23	AW	76	F3N	C5-C4-N3	-5.64	120.48	125.98
23	CW	54	5MU	C6-N1-C2	-5.63	120.81	122.41
23	AW	46	7MG	N7-C8-N9	-5.62	95.67	103.13
23	CW	8	4SU	N3-C2-N1	5.53	120.59	115.97
25	CY	37	MIA	N3-C4-N9	5.52	135.00	126.91
25	AY	37	MIA	N3-C4-N9	5.52	135.00	126.91
25	CY	46	7MG	N7-C8-N9	-5.51	95.81	103.13
25	AY	8	4SU	C2-N1-C1'	5.46	121.63	118.21
24	CX	76	31H	C5-C4-N3	-5.44	120.68	125.98
23	CW	54	5MU	N3-C2-N1	5.42	120.50	115.97
23	AW	55	PSU	C5-C1'-C2'	-5.39	105.73	115.73
23	AW	37	MIA	N3-C4-N9	5.17	134.50	126.91
24	CX	32	5MC	C2-N3-C4	5.17	120.45	115.50
25	AY	8	4SU	N3-C2-N1	5.13	120.26	115.97
25	AY	46	7MG	N7-C8-N9	-5.11	96.35	103.13
24	AX	76	31H	C4'-O4'-C1'	-5.05	104.17	109.72
24	CX	76	31H	C4'-C3'-N3'	-4.86	103.33	113.56
23	CW	46	7MG	C5-C4-N3	-4.83	118.15	126.61
25	CY	39	PSU	C5-C1'-C2'	-4.73	106.96	115.73
23	AW	37	MIA	C2-N3-C4	4.62	121.73	115.22
24	AX	76	31H	C5-C4-N3	-4.61	121.49	125.98
25	AY	54	5MU	C2-N1-C1'	4.59	121.08	118.21
24	AX	32	5MC	C2-N3-C4	4.58	119.88	115.50
25	CY	54	5MU	C6-N1-C2	-4.57	121.11	122.41
25	CY	8	4SU	N3-C2-N1	4.35	119.60	115.97
24	AX	76	31H	C4'-C3'-N3'	-4.23	104.66	113.56
23	AW	46	7MG	C5-C4-N3	-4.22	119.21	126.61
25	CY	46	7MG	C5-C4-N3	-4.22	119.22	126.61
23	CW	39	PSU	C5-C1'-C2'	-4.14	108.06	115.73
23	CW	76	F3N	C5'-C4'-C3'	-4.02	108.72	115.85
23	CW	46	7MG	C8-N7-C5	3.85	116.52	108.83
25	AY	46	7MG	C8-N9-C1'	-3.85	110.43	121.06
23	AW	76	F3N	C5'-C4'-C3'	-3.80	109.12	115.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CW	46	7MG	C6-N1-C2	3.75	122.32	120.20
23	CW	32	PSU	C5-C1'-C2'	-3.75	108.77	115.73
23	CW	55	PSU	C5-C1'-C2'	-3.71	108.85	115.73
25	AY	46	7MG	C6-N1-C2	3.67	122.28	120.20
23	AW	8	4SU	N3-C2-N1	3.62	119.00	115.97
25	CY	55	PSU	C5-C1'-C2'	-3.61	109.03	115.73
24	AX	8	4SU	C2-N1-C1'	3.48	120.39	118.21
25	AY	46	7MG	C8-N7-C5	3.46	115.73	108.83
25	AY	46	7MG	C6-C5-C4	3.44	120.69	116.01
23	AW	37	MIA	C4-C5-N7	-3.44	106.08	109.41
23	AW	46	7MG	C8-N7-C5	3.44	115.70	108.83
25	CY	54	5MU	C5-C6-N1	-3.37	118.99	122.02
25	CY	46	7MG	C8-N7-C5	3.37	115.55	108.83
25	CY	39	PSU	O4'-C1'-C5	-3.33	104.22	109.80
23	AW	54	5MU	C2-N1-C1'	3.29	120.27	118.21
24	AX	76	31H	N3-C4-N9	3.26	130.98	125.39
23	CW	76	F3N	N3-C4-N9	3.23	130.93	125.39
25	CY	37	MIA	C4-C5-N7	-3.18	106.34	109.41
24	AX	76	31H	O4'-C1'-N9	3.17	114.99	108.10
24	CX	76	31H	N3-C4-N9	3.15	130.80	125.39
23	AW	76	F3N	N3-C4-N9	3.15	130.79	125.39
23	CW	46	7MG	N2-C2-N3	-3.15	116.20	120.29
24	AX	32	5MC	C5-C6-N1	-3.13	119.20	122.02
24	AX	76	31H	C5'-C4'-C3'	-3.06	110.43	115.85
25	AY	37	MIA	C4-C5-N7	-3.04	106.47	109.41
23	AW	37	MIA	C2-N1-C6	3.00	122.22	113.31
25	CY	46	7MG	N2-C2-N1	3.00	121.04	117.82
24	CX	76	31H	C5'-C4'-C3'	-2.99	110.56	115.85
23	CW	37	MIA	C4-C5-N7	-2.97	106.54	109.41
25	CY	37	MIA	C5-C6-N1	-2.97	117.52	120.10
24	AX	32	5MC	C6-N1-C2	2.97	120.99	118.86
25	CY	46	7MG	N2-C2-N3	-2.92	116.51	120.29
24	AX	76	31H	O4'-C1'-C2'	-2.90	102.47	106.69
24	CX	32	5MC	N4-C4-N3	2.88	121.10	116.99
25	AY	37	MIA	C5-C6-N1	-2.84	117.63	120.10
23	AW	46	7MG	C8-N9-C1'	-2.82	113.28	121.06
23	AW	39	PSU	C5-C1'-C2'	-2.80	110.53	115.73
25	CY	32	PSU	O4'-C1'-C5	-2.79	105.12	109.80
25	CY	39	PSU	C4-N3-C2	-2.79	119.70	125.36
23	AW	37	MIA	C5-C6-N1	-2.71	117.57	120.46
23	AW	76	F3N	C4'-C3'-N3'	-2.71	107.85	113.56
23	CW	76	F3N	C6-C5-C4	2.69	120.57	117.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	54	5MU	C5-C6-N1	-2.68	119.61	122.02
25	CY	46	7MG	C8-N9-C1'	-2.67	113.68	121.06
24	CX	54	5MU	C5-C6-N1	-2.67	119.62	122.02
23	CW	46	7MG	N2-C2-N1	2.61	120.61	117.82
25	CY	8	4SU	C5-C4-N3	2.59	120.52	116.04
24	AX	55	PSU	C5-C1'-C2'	-2.56	110.97	115.73
24	CX	76	31H	C2'-C3'-N3'	2.56	119.02	113.08
23	CW	37	MIA	C5-C6-N1	-2.56	117.88	120.10
25	AY	32	PSU	O4'-C1'-C5	2.55	114.08	109.80
25	AY	54	5MU	C5-C6-N1	-2.55	119.73	122.02
25	CY	54	5MU	C4-N3-C2	-2.53	120.19	125.39
23	AW	46	7MG	C8-N9-C4	2.51	118.62	110.66
24	CX	76	31H	O4'-C1'-C2'	-2.49	103.06	106.69
23	AW	37	MIA	N3-C2-N1	-2.49	122.37	126.87
25	AY	46	7MG	C5-C4-N9	-2.49	102.35	106.08
23	AW	32	PSU	C5-C1'-C2'	-2.48	111.12	115.73
23	CW	55	PSU	C4-N3-C2	-2.47	120.36	125.36
25	CY	46	7MG	C8-N9-C4	2.45	118.42	110.66
24	CX	54	5MU	C4-N3-C2	-2.43	120.41	125.39
25	AY	39	PSU	C5-C1'-C2'	-2.41	111.26	115.73
23	CW	32	PSU	C4-N3-C2	-2.39	120.51	125.36
23	AW	8	4SU	C5-C4-N3	2.36	120.13	116.04
25	AY	46	7MG	CM7-N7-C5	2.36	132.04	123.46
23	CW	76	F3N	C4'-C3'-N3'	-2.35	108.61	113.56
25	CY	46	7MG	CM7-N7-C5	2.35	132.01	123.46
24	AX	76	31H	O2'-C2'-C3'	2.34	116.46	110.69
23	AW	46	7MG	C6-C5-C4	2.33	119.18	116.01
25	AY	8	4SU	C5-C4-N3	2.32	120.05	116.04
23	CW	46	7MG	O4'-C1'-N9	2.31	112.19	108.93
23	CW	8	4SU	C5-C4-N3	2.29	120.01	116.04
25	AY	55	PSU	C4-N3-C2	-2.28	120.74	125.36
25	AY	32	PSU	C4-N3-C2	-2.27	120.75	125.36
24	CX	76	31H	C6-C5-C4	2.27	120.10	117.55
23	AW	46	7MG	CM7-N7-C5	2.27	131.71	123.46
24	CX	55	PSU	C4-N3-C2	-2.26	120.78	125.36
23	CW	76	F3N	C2-N3-C4	2.25	119.75	113.27
24	AX	55	PSU	C4-N3-C2	-2.23	120.85	125.36
23	AW	32	PSU	C4-N3-C2	-2.22	120.86	125.36
25	AY	46	7MG	C8-N9-C4	2.21	117.67	110.66
24	AX	32	5MC	N4-C4-N3	2.21	120.14	116.99
23	AW	54	5MU	C5-C6-N1	-2.19	120.05	122.02
24	AX	54	5MU	C4-N3-C2	-2.19	120.90	125.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	46	7MG	C5-C4-N9	-2.18	102.81	106.08
24	CX	32	5MC	C2-N1-C1'	2.17	121.98	119.03
24	CX	55	PSU	C5-C1'-C2'	-2.16	111.73	115.73
23	CW	54	5MU	C5-C6-N1	-2.16	120.08	122.02
25	AY	46	7MG	C4-N9-C1'	2.15	131.90	126.62
24	CX	32	5MC	C5-C6-N1	-2.14	120.09	122.02
23	AW	39	PSU	C4-N3-C2	-2.14	121.03	125.36
25	CY	32	PSU	O4'-C1'-C2'	2.13	108.08	104.43
24	CX	76	31H	C2-N3-C4	2.13	119.40	113.27
23	AW	76	F3N	C2-N3-C4	2.12	119.38	113.27
25	CY	37	MIA	C8-N9-C4	2.12	108.68	106.96
24	CX	76	31H	O2'-C2'-C3'	2.09	115.83	110.69
24	AX	76	31H	CA-N-CN	-2.08	119.62	122.82
25	AY	54	5MU	C4-N3-C2	-2.06	121.17	125.39
25	AY	55	PSU	O4'-C1'-C2'	2.05	107.94	104.43
25	CY	55	PSU	C4-N3-C2	-2.05	121.20	125.36
24	AX	55	PSU	O4'-C1'-C2'	2.04	107.92	104.43
25	AY	32	PSU	C5-C1'-C2'	-2.03	111.97	115.73
24	AX	76	31H	C2-N3-C4	2.02	119.09	113.27
23	CW	46	7MG	C6-C5-C4	2.02	118.76	116.01
25	AY	46	7MG	CM7-N7-C8	-2.02	112.22	119.61
24	CX	32	5MC	C6-N1-C2	2.02	120.31	118.86
25	AY	39	PSU	C4-N3-C2	-2.01	121.28	125.36

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	AX	76	31H	OCN-CN-N-CA
24	CX	76	31H	OCN-CN-N-CA
25	AY	46	7MG	OP2-P-O5'-C5'
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 2063 ligands modelled in this entry, 2061 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	22.24	12 (100%)	0,24,24	0.00	-
58	SF4	CD	501	4	12,12,12	21.71	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	501	4	-	0/0/48/48	0/6/5/5

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	AD	501	SF4	S1-FE2	-23.30	2.17	2.33
58	AD	501	SF4	S3-FE4	-22.80	2.17	2.33
58	AD	501	SF4	S4-FE2	-22.72	2.18	2.33
58	AD	501	SF4	S2-FE4	-22.43	2.18	2.33
58	AD	501	SF4	S2-FE1	-22.18	2.18	2.33
58	AD	501	SF4	S2-FE3	-22.16	2.18	2.33
58	CD	501	SF4	S4-FE1	-22.09	2.18	2.33
58	AD	501	SF4	S3-FE2	-22.09	2.18	2.33
58	CD	501	SF4	S3-FE2	-22.03	2.18	2.33
58	CD	501	SF4	S2-FE4	-21.99	2.18	2.33
58	AD	501	SF4	S4-FE3	-21.98	2.18	2.33
58	CD	501	SF4	S3-FE4	-21.97	2.18	2.33
58	AD	501	SF4	S1-FE3	-21.88	2.18	2.33
58	AD	501	SF4	S1-FE4	-21.87	2.18	2.33
58	CD	501	SF4	S1-FE2	-21.87	2.18	2.33
58	CD	501	SF4	S4-FE2	-21.86	2.18	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	CD	501	SF4	S3-FE1	-21.81	2.18	2.33
58	AD	501	SF4	S3-FE1	-21.78	2.18	2.33
58	CD	501	SF4	S4-FE3	-21.61	2.18	2.33
58	AD	501	SF4	S4-FE1	-21.58	2.18	2.33
58	CD	501	SF4	S1-FE4	-21.52	2.18	2.33
58	CD	501	SF4	S2-FE1	-21.41	2.18	2.33
58	CD	501	SF4	S1-FE3	-21.31	2.18	2.33
58	CD	501	SF4	S2-FE3	-21.04	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	1497/1521 (98%)	0.08	17 (1%) 77 79	41, 72, 93, 106	0
1	CA	1503/1521 (98%)	0.17	64 (4%) 34 30	43, 75, 94, 106	0
2	AB	231/256 (90%)	1.23	57 (24%) 1 1	68, 82, 89, 95	0
2	CB	231/256 (90%)	2.90	131 (56%) 0 0	68, 83, 90, 96	0
3	AC	206/239 (86%)	0.81	23 (11%) 6 4	69, 79, 87, 94	0
3	CC	206/239 (86%)	1.84	88 (42%) 1 0	70, 82, 90, 94	0
4	AD	208/209 (99%)	0.78	32 (15%) 3 2	57, 72, 81, 87	0
4	CD	208/209 (99%)	0.68	21 (10%) 7 5	60, 72, 81, 89	0
5	AE	148/162 (91%)	0.57	8 (5%) 25 21	58, 71, 81, 85	0
5	CE	148/162 (91%)	0.98	17 (11%) 5 4	60, 74, 83, 86	0
6	AF	100/101 (99%)	0.21	1 (1%) 79 81	52, 67, 75, 85	0
6	CF	100/101 (99%)	0.25	3 (3%) 48 45	57, 71, 81, 85	0
7	AG	155/156 (99%)	0.50	13 (8%) 11 8	66, 76, 85, 96	0
7	CG	155/156 (99%)	1.31	43 (27%) 1 1	68, 77, 86, 97	0
8	AH	137/138 (99%)	0.18	1 (0%) 84 86	62, 72, 79, 83	0
8	CH	137/138 (99%)	1.45	38 (27%) 1 1	64, 74, 80, 85	0
9	AI	127/128 (99%)	1.86	53 (41%) 1 0	62, 80, 87, 89	0
9	CI	127/128 (99%)	3.66	97 (76%) 0 0	69, 82, 89, 91	0
10	AJ	97/105 (92%)	1.63	34 (35%) 1 1	66, 83, 91, 92	0
10	CJ	96/105 (91%)	2.94	63 (65%) 0 0	68, 84, 91, 93	0
11	AK	114/129 (88%)	0.92	19 (16%) 2 1	51, 70, 80, 84	0
11	CK	114/129 (88%)	1.15	25 (21%) 1 1	52, 72, 81, 85	0
12	AL	122/132 (92%)	0.16	3 (2%) 54 52	41, 56, 71, 75	0
12	CL	122/132 (92%)	1.13	27 (22%) 1 1	58, 73, 82, 87	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	123/126 (97%)	0.57	13 (10%) 7 5	57, 72, 83, 88	0
13	CM	122/126 (96%)	2.61	59 (48%) 1 0	69, 85, 92, 97	0
14	AN	60/61 (98%)	0.96	9 (15%) 3 2	70, 76, 83, 84	0
14	CN	60/61 (98%)	3.39	44 (73%) 0 0	73, 79, 85, 87	0
15	AO	88/89 (98%)	0.84	9 (10%) 7 5	54, 68, 79, 83	0
15	CO	88/89 (98%)	1.34	21 (23%) 1 1	56, 70, 81, 84	0
16	AP	82/88 (93%)	1.81	27 (32%) 1 1	59, 71, 79, 84	0
16	CP	82/88 (93%)	0.94	11 (13%) 4 3	59, 70, 79, 83	0
17	AQ	99/105 (94%)	0.58	9 (9%) 9 7	57, 70, 79, 84	0
17	CQ	99/105 (94%)	0.90	13 (13%) 4 3	60, 71, 79, 84	0
18	AR	68/88 (77%)	0.93	13 (19%) 2 1	59, 69, 81, 84	0
18	CR	68/88 (77%)	0.91	11 (16%) 2 1	58, 70, 81, 85	0
19	AS	84/93 (90%)	0.48	8 (9%) 8 6	70, 81, 87, 92	0
19	CS	83/93 (89%)	2.44	48 (57%) 0 0	74, 83, 90, 94	0
20	AT	96/106 (90%)	0.57	8 (8%) 11 8	59, 71, 80, 83	0
20	CT	96/106 (90%)	0.92	15 (15%) 3 2	59, 71, 80, 83	0
21	AU	23/27 (85%)	0.84	3 (13%) 4 3	70, 75, 78, 82	0
21	CU	23/27 (85%)	3.35	16 (69%) 0 0	71, 78, 81, 82	0
22	AV	13/24 (54%)	1.54	4 (30%) 1 1	58, 77, 95, 100	0
22	CV	12/24 (50%)	3.21	7 (58%) 0 0	64, 81, 93, 95	0
23	AW	72/76 (94%)	0.77	10 (13%) 4 2	66, 95, 102, 105	0
23	CW	70/76 (92%)	2.86	50 (71%) 0 0	70, 96, 101, 106	0
24	AX	75/77 (97%)	0.04	0 100 100	42, 71, 90, 96	0
24	CX	75/77 (97%)	0.13	2 (2%) 52 49	55, 86, 95, 98	0
25	AY	73/76 (96%)	0.45	9 (12%) 5 4	44, 97, 101, 105	0
25	CY	72/76 (94%)	1.48	20 (27%) 1 1	48, 98, 102, 103	0
26	BA	2819/2915 (96%)	0.56	24 (0%) 81 82	23, 43, 87, 106	0
26	DA	2800/2915 (96%)	-0.09	60 (2%) 60 58	27, 48, 90, 108	0
27	BB	120/121 (99%)	0.66	0 100 100	41, 64, 76, 88	0
27	DB	120/121 (99%)	0.12	9 (7%) 14 11	48, 70, 80, 91	0
28	BD	275/276 (99%)	0.19	3 (1%) 77 79	24, 41, 58, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DD	275/276 (99%)	0.40	15 (5%) 24 20	28, 44, 61, 79	0
29	BE	204/206 (99%)	0.59	9 (4%) 33 29	23, 46, 65, 83	0
29	DE	204/206 (99%)	0.32	6 (2%) 49 46	26, 50, 67, 84	0
30	BF	203/210 (96%)	0.58	6 (2%) 48 45	25, 51, 76, 86	0
30	DF	203/210 (96%)	0.75	23 (11%) 6 4	28, 56, 78, 88	0
31	BG	181/182 (99%)	0.56	7 (3%) 37 33	55, 72, 83, 93	0
31	DG	181/182 (99%)	2.10	84 (46%) 1 0	64, 76, 85, 93	0
32	BH	174/180 (96%)	0.53	2 (1%) 77 79	50, 66, 75, 82	0
32	DH	174/180 (96%)	2.10	80 (45%) 1 0	56, 71, 79, 83	0
33	BI	146/148 (98%)	0.51	12 (8%) 12 9	49, 74, 83, 87	0
33	DI	146/148 (98%)	0.32	7 (4%) 29 26	50, 74, 83, 87	0
34	BN	140/140 (100%)	0.56	0 100 100	29, 48, 67, 79	0
34	DN	140/140 (100%)	1.17	21 (15%) 3 2	35, 53, 70, 82	0
35	BO	122/122 (100%)	0.04	0 100 100	25, 40, 57, 67	0
35	DO	122/122 (100%)	0.27	0 100 100	44, 58, 74, 79	0
36	BP	149/150 (99%)	0.59	6 (4%) 36 32	25, 55, 75, 80	0
36	DP	149/150 (99%)	0.85	19 (12%) 4 3	28, 58, 78, 83	0
37	BQ	141/141 (100%)	0.67	5 (3%) 42 38	37, 52, 68, 77	0
37	DQ	141/141 (100%)	1.44	38 (26%) 1 1	41, 58, 72, 79	0
38	BR	118/118 (100%)	0.25	0 100 100	22, 34, 50, 59	0
38	DR	118/118 (100%)	0.90	15 (12%) 4 3	38, 53, 64, 75	0
39	BS	110/112 (98%)	0.33	2 (1%) 65 64	34, 50, 64, 70	0
39	DS	110/112 (98%)	2.83	69 (62%) 0 0	70, 79, 87, 91	0
40	BT	131/146 (89%)	0.37	2 (1%) 70 71	38, 51, 73, 82	0
40	DT	131/146 (89%)	0.17	2 (1%) 70 71	40, 54, 75, 81	0
41	BU	116/118 (98%)	0.34	2 (1%) 67 66	17, 30, 50, 63	0
41	DU	116/118 (98%)	0.75	8 (6%) 17 14	40, 59, 79, 85	0
42	BV	101/101 (100%)	0.12	1 (0%) 79 81	16, 38, 58, 68	0
42	DV	101/101 (100%)	0.91	17 (16%) 2 1	44, 73, 81, 92	0
43	BW	112/113 (99%)	0.40	2 (1%) 65 64	22, 30, 49, 83	0
43	DW	112/113 (99%)	1.08	18 (16%) 2 1	35, 50, 66, 86	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BX	95/96 (98%)	0.50	0 100 100	31, 46, 67, 83	0
44	DX	95/96 (98%)	0.93	11 (11%) 5 4	36, 50, 68, 83	0
45	BY	107/110 (97%)	0.74	11 (10%) 7 5	42, 59, 73, 84	0
45	DY	107/110 (97%)	1.50	32 (29%) 1 1	47, 61, 75, 84	0
46	BZ	171/206 (83%)	1.16	35 (20%) 1 1	40, 66, 91, 95	0
46	DZ	174/206 (84%)	2.66	101 (58%) 0 0	69, 85, 94, 101	0
47	B0	83/85 (97%)	0.88	6 (7%) 15 12	34, 50, 67, 75	0
47	D0	83/85 (97%)	1.54	22 (26%) 1 1	40, 56, 71, 76	0
48	B1	97/98 (98%)	0.29	1 (1%) 79 81	31, 49, 72, 76	0
48	D1	97/98 (98%)	0.59	8 (8%) 12 9	34, 53, 73, 78	0
49	B2	70/72 (97%)	0.32	1 (1%) 72 72	33, 49, 64, 82	0
49	D2	70/72 (97%)	0.58	2 (2%) 49 46	58, 69, 78, 82	0
50	B3	59/60 (98%)	0.08	0 100 100	24, 37, 63, 74	0
50	D3	59/60 (98%)	1.24	12 (20%) 1 1	52, 65, 79, 87	0
51	B4	69/71 (97%)	0.83	13 (18%) 2 1	49, 76, 89, 91	0
51	D4	69/71 (97%)	1.73	27 (39%) 1 0	74, 89, 95, 99	0
52	B5	59/60 (98%)	0.14	1 (1%) 67 66	16, 30, 46, 68	0
52	D5	59/60 (98%)	0.36	1 (1%) 67 66	35, 49, 65, 77	0
53	B6	53/54 (98%)	0.19	0 100 100	32, 44, 57, 72	0
53	D6	53/54 (98%)	0.62	5 (9%) 9 6	49, 64, 74, 79	0
54	B7	48/49 (97%)	0.50	4 (8%) 11 8	23, 32, 58, 70	0
54	D7	48/49 (97%)	1.16	6 (12%) 5 3	26, 35, 61, 70	0
55	B8	64/65 (98%)	0.48	1 (1%) 68 69	34, 42, 50, 65	0
55	D8	64/65 (98%)	0.61	3 (4%) 30 27	37, 46, 54, 65	0
56	B9	37/37 (100%)	1.18	6 (16%) 2 1	36, 51, 65, 73	0
56	D9	37/37 (100%)	0.53	4 (10%) 6 5	43, 55, 68, 76	0
All	All	20927/21748 (96%)	0.65	2204 (10%) 7 5	16, 64, 90, 108	0

All (2204) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	CB	165	VAL	16.5
13	CM	124	PRO	15.2

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Mol	Chain	Res	Type	RSRZ
13	CM	123	ALA	13.6
13	CM	122	LYS	13.0
46	DZ	171	ILE	11.8
46	DZ	155	LEU	10.9
2	CB	214	ILE	10.5
2	CB	211	ILE	10.4
2	CB	81	VAL	9.8
2	CB	163	PHE	9.6
2	CB	187	LEU	9.5
14	CN	25	VAL	9.4
46	DZ	114	GLY	9.3
2	CB	77	ALA	9.3
39	DS	32	LEU	9.3
13	CM	102	ARG	9.2
2	CB	200	ILE	9.2
2	CB	207	ALA	8.8
39	DS	56	LEU	8.8
2	CB	70	PHE	8.8
39	DS	58	LEU	8.7
14	CN	53	LEU	8.7
10	CJ	71	LEU	8.7
10	CJ	63	PHE	8.6
46	DZ	172	ALA	8.5
13	CM	121	LYS	8.4
54	D7	48	LYS	8.4
10	CJ	47	PHE	8.4
23	CW	31	A	8.3
7	CG	83	ALA	8.3
9	CI	9	ARG	8.3
13	AM	2	ALA	8.3
9	AI	19	LEU	8.3
2	CB	164	VAL	8.2
7	CG	81	GLY	8.2
9	CI	5	TYR	8.2
9	CI	14	VAL	8.1
9	CI	19	LEU	8.1
47	D0	2	ALA	8.0
2	CB	215	LEU	8.0
46	DZ	170	THR	7.9
46	BZ	118	GLN	7.8
9	CI	7	THR	7.8
9	AI	47	LEU	7.8

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Mol	Chain	Res	Type	RSRZ
32	DH	107	VAL	7.8
3	CC	13	GLY	7.8
13	CM	95	GLY	7.8
9	CI	79	LEU	7.8
37	DQ	104	PHE	7.7
39	DS	54	LEU	7.7
8	CH	2	LEU	7.6
2	CB	83	MET	7.6
21	CU	6	ARG	7.6
19	CS	41	VAL	7.6
46	DZ	108	PRO	7.6
47	B0	7	LEU	7.6
9	CI	36	TYR	7.5
7	CG	80	VAL	7.5
9	CI	4	TYR	7.4
9	AI	106	ALA	7.4
31	DG	102	PHE	7.4
7	AG	85	TYR	7.4
32	DH	94	TYR	7.4
13	CM	120	LYS	7.3
47	B0	6	GLY	7.3
7	AG	83	ALA	7.2
46	DZ	121	HIS	7.2
7	CG	82	GLY	7.2
13	CM	4	ILE	7.2
46	DZ	107	THR	7.1
46	BZ	120	ILE	7.1
9	CI	76	ALA	7.1
23	CW	32	PSU	7.1
39	DS	35	ILE	7.0
10	CJ	49	VAL	7.0
9	CI	106	ALA	7.0
13	CM	90	LEU	7.0
32	DH	113	VAL	7.0
47	D0	7	LEU	7.0
9	CI	61	ALA	6.9
43	BW	112	GLY	6.9
31	DG	140	ILE	6.9
2	AB	215	LEU	6.9
12	CL	18	VAL	6.9
21	CU	14	TRP	6.9
13	CM	94	ARG	6.9

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Mol	Chain	Res	Type	RSRZ
25	CY	54	5MU	6.9
3	CC	80	GLY	6.8
39	DS	26	LEU	6.8
39	DS	57	LYS	6.8
32	DH	115	VAL	6.8
31	DG	19	LEU	6.8
46	DZ	125	LEU	6.8
16	AP	19	ILE	6.7
3	CC	12	LEU	6.7
2	CB	222	ILE	6.7
54	D7	46	VAL	6.7
9	CI	80	GLY	6.7
2	CB	132	LYS	6.7
45	DY	5	MET	6.7
13	CM	66	LEU	6.6
26	DA	896	A	6.6
39	DS	34	HIS	6.6
46	DZ	113	ALA	6.6
2	AB	214	ILE	6.6
9	CI	18	PHE	6.6
13	CM	60	VAL	6.6
2	CB	152	PHE	6.6
3	CC	145	GLY	6.6
46	BZ	144	LEU	6.6
46	DZ	139	VAL	6.6
46	DZ	144	LEU	6.5
46	DZ	116	VAL	6.5
22	CV	13	A	6.5
9	CI	123	PRO	6.5
2	CB	92	TYR	6.5
10	CJ	50	ILE	6.5
3	CC	134	ILE	6.5
14	CN	59	ALA	6.4
14	CN	34	TYR	6.4
10	CJ	65	LEU	6.4
2	CB	72	GLY	6.4
9	CI	26	VAL	6.4
28	DD	2	ALA	6.4
2	CB	201	ILE	6.3
14	CN	44	LEU	6.3
3	CC	8	ILE	6.3
9	CI	64	THR	6.3

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Mol	Chain	Res	Type	RSRZ
14	CN	57	ARG	6.3
26	DA	229	A	6.3
46	DZ	115	GLY	6.3
39	DS	40	ILE	6.2
46	BZ	113	ALA	6.2
9	CI	81	ILE	6.2
46	BZ	114	GLY	6.2
7	AG	82	GLY	6.2
31	DG	142	PRO	6.2
3	CC	124	ILE	6.2
2	CB	71	VAL	6.2
34	DN	140	VAL	6.2
13	CM	7	VAL	6.1
39	DS	52	SER	6.1
1	CA	1030(B)	C	6.1
10	CJ	38	ILE	6.1
9	CI	17	VAL	6.1
9	CI	101	PHE	6.1
2	CB	196	LEU	6.1
31	DG	146	TYR	6.1
13	CM	5	ALA	6.1
2	CB	203	GLY	6.1
22	CV	14	A	6.1
37	DQ	63	LYS	6.1
22	AV	12	A	6.0
21	CU	11	GLY	6.0
2	CB	131	PRO	6.0
7	CG	84	ASN	6.0
9	CI	105	ASP	6.0
2	CB	228	GLY	6.0
31	DG	157	ILE	6.0
10	CJ	85	LEU	6.0
44	DX	92	LEU	6.0
2	CB	136	VAL	6.0
19	CS	80	TYR	5.9
46	DZ	122	ARG	5.9
9	AI	59	PHE	5.9
39	DS	82	ILE	5.9
9	CI	109	VAL	5.9
9	CI	115	GLY	5.9
19	CS	38	SER	5.9
46	DZ	119	GLU	5.9

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Mol	Chain	Res	Type	RSRZ
46	DZ	149	SER	5.9
2	CB	69	LEU	5.9
14	CN	39	LEU	5.9
9	CI	15	ALA	5.9
2	CB	133	LYS	5.9
46	DZ	163	LEU	5.9
5	CE	94	ALA	5.9
31	DG	34	LEU	5.9
10	AJ	98	ILE	5.8
26	DA	883	G	5.8
3	CC	184	TYR	5.8
9	CI	62	TYR	5.8
46	DZ	96	VAL	5.8
14	CN	37	PHE	5.8
46	DZ	173	ALA	5.7
2	AB	221	LEU	5.7
26	BA	942	A	5.7
31	BG	146	TYR	5.7
23	CW	73	A	5.7
46	DZ	124	ILE	5.7
2	CB	185	ILE	5.7
39	DS	39	ILE	5.7
9	CI	110	GLU	5.7
51	D4	49	PHE	5.7
23	CW	23	A	5.7
2	CB	188	ALA	5.7
2	CB	90	MET	5.7
31	DG	173	LEU	5.7
32	DH	45	VAL	5.6
13	AM	123	ALA	5.6
2	AB	213	LEU	5.6
25	CY	18	G	5.6
32	DH	97	ARG	5.6
19	CS	40	ILE	5.6
46	BZ	111	VAL	5.6
15	CO	15	PHE	5.6
47	B0	2	ALA	5.6
31	DG	139	LEU	5.6
13	CM	6	GLY	5.6
51	D4	54	GLY	5.5
32	DH	105	LEU	5.5
31	DG	11	TYR	5.5

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Mol	Chain	Res	Type	RSRZ
31	DG	17	PRO	5.5
46	BZ	108	PRO	5.5
3	CC	6	HIS	5.5
1	CA	1131	G	5.5
14	CN	58	LYS	5.5
14	CN	38	GLY	5.5
2	CB	101	MET	5.5
32	DH	43	VAL	5.5
32	DH	114	VAL	5.5
46	DZ	111	VAL	5.5
31	DG	133	LEU	5.4
32	DH	96	ALA	5.4
30	DF	131	GLY	5.4
46	DZ	52	SER	5.4
46	DZ	137	ILE	5.4
2	CB	76	GLN	5.4
2	CB	66	GLY	5.4
3	CC	189	ALA	5.4
46	DZ	174	VAL	5.4
14	CN	36	PHE	5.4
2	CB	31	TYR	5.4
46	DZ	150	LEU	5.4
50	D3	26	LEU	5.4
15	CO	87	ILE	5.4
19	CS	49	ILE	5.4
13	AM	124	PRO	5.4
10	CJ	8	LEU	5.4
46	BZ	106	GLY	5.4
21	CU	15	ARG	5.3
51	D4	51	ASP	5.3
32	DH	48	GLY	5.3
31	DG	149	VAL	5.3
9	CI	75	ASP	5.3
50	D3	60	GLU	5.3
19	CS	35	SER	5.3
9	AI	8	GLY	5.3
25	CY	61	C	5.3
10	CJ	46	ARG	5.3
9	CI	50	LEU	5.3
47	B0	4	LYS	5.3
31	DG	39	ILE	5.3
10	CJ	27	ALA	5.3

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Mol	Chain	Res	Type	RSRZ
19	CS	82	GLY	5.3
3	CC	14	ILE	5.3
42	DV	73	SER	5.3
14	CN	2	ALA	5.3
39	DS	51	ALA	5.3
46	DZ	161	VAL	5.3
2	CB	118	LEU	5.2
46	DZ	102	LEU	5.2
10	AJ	72	VAL	5.2
23	CW	30	G	5.2
14	CN	29	ARG	5.2
26	BA	2183	C	5.2
2	AB	15	VAL	5.2
13	CM	15	VAL	5.2
13	CM	64	TRP	5.1
2	CB	162	ILE	5.1
10	CJ	6	ILE	5.1
12	CL	28	LYS	5.1
31	DG	141	PHE	5.1
8	CH	135	CYS	5.1
46	DZ	5	LEU	5.1
2	CB	206	ASP	5.1
1	CA	1112	C	5.1
23	CW	3	C	5.1
46	DZ	99	TYR	5.1
3	CC	182	ILE	5.0
9	AI	50	LEU	5.0
2	AB	165	VAL	5.0
9	CI	116	LYS	5.0
14	CN	56	VAL	5.0
7	CG	16	LEU	5.0
48	B1	98	LEU	5.0
39	DS	5	THR	5.0
39	DS	55	ALA	5.0
45	DY	45	VAL	5.0
54	D7	47	ARG	5.0
46	DZ	118	GLN	5.0
22	CV	24	A	5.0
30	DF	139	PHE	5.0
9	CI	27	THR	5.0
2	CB	197	VAL	4.9
44	DX	68	ARG	4.9

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Mol	Chain	Res	Type	RSRZ
27	DB	118	G	4.9
2	CB	16	HIS	4.9
12	CL	64	TYR	4.9
9	AI	49	PRO	4.9
10	CJ	72	VAL	4.9
14	CN	41	ARG	4.9
31	DG	178	PHE	4.9
7	AG	84	ASN	4.9
2	AB	163	PHE	4.9
8	CH	93	VAL	4.9
2	CB	68	ILE	4.9
7	CG	79	ARG	4.9
9	CI	92	TYR	4.9
54	B7	48	LYS	4.9
9	CI	126	SER	4.9
2	CB	88	ALA	4.9
27	DB	119	G	4.9
13	CM	98	VAL	4.9
19	CS	10	PHE	4.9
51	D4	57	GLU	4.9
21	CU	10	ARG	4.9
3	CC	159	GLY	4.9
31	DG	106	LEU	4.9
23	AW	73	A	4.9
21	CU	2	GLY	4.8
2	AB	126	GLU	4.8
3	CC	206	GLU	4.8
7	CG	4	ARG	4.8
32	DH	106	THR	4.8
2	CB	58	ILE	4.8
7	CG	2	ALA	4.8
11	CK	125	PHE	4.8
13	CM	3	ARG	4.8
1	CA	1532	U	4.8
9	CI	66	ARG	4.8
2	CB	122	PHE	4.8
9	CI	33	PHE	4.8
13	AM	56	LEU	4.8
39	DS	36	TYR	4.8
47	B0	3	HIS	4.8
46	BZ	141	VAL	4.8
16	AP	36	ILE	4.8

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Mol	Chain	Res	Type	RSRZ
51	D4	40	HIS	4.8
32	DH	102	ALA	4.8
9	CI	28	VAL	4.8
51	D4	42	PHE	4.8
23	CW	2	C	4.8
45	DY	44	ILE	4.8
10	AJ	71	LEU	4.7
30	DF	12	LEU	4.7
39	DS	53	SER	4.7
14	CN	42	ILE	4.7
10	CJ	40	LEU	4.7
25	CY	34	G	4.7
25	CY	53	G	4.7
10	CJ	60	ARG	4.7
2	CB	223	ILE	4.7
10	CJ	41	PRO	4.7
23	CW	13	C	4.7
3	AC	39	ILE	4.7
9	CI	125	TYR	4.7
20	CT	24	LEU	4.7
23	AW	72	C	4.7
25	CY	36	A	4.7
26	DA	2155	G	4.7
2	CB	232	PRO	4.7
9	CI	114	TYR	4.7
25	AY	36	A	4.7
2	CB	210	SER	4.6
9	CI	83	ARG	4.6
2	AB	48	MET	4.6
31	DG	28	VAL	4.6
31	DG	159	VAL	4.6
46	DZ	147	GLY	4.6
32	DH	13	LYS	4.6
47	D0	3	HIS	4.6
32	DH	98	LEU	4.6
2	CB	218	ALA	4.6
14	AN	2	ALA	4.6
25	CY	35	A	4.6
44	DX	89	ILE	4.6
46	DZ	146	ILE	4.6
32	DH	124	GLU	4.6
39	DS	33	LYS	4.6

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Mol	Chain	Res	Type	RSRZ
14	AN	16	PHE	4.6
2	CB	89	GLY	4.6
10	CJ	34	VAL	4.6
13	CM	119	GLY	4.6
46	BZ	116	VAL	4.6
13	CM	105	THR	4.6
23	CW	24	G	4.6
26	DA	2146	C	4.6
48	D1	2	SER	4.6
3	CC	10	PHE	4.6
47	D0	5	LYS	4.6
31	DG	15	VAL	4.6
39	DS	46	VAL	4.6
46	DZ	4	ARG	4.5
32	DH	151	ILE	4.5
39	DS	83	LYS	4.5
9	CI	42	ARG	4.5
2	CB	41	ILE	4.5
43	DW	112	GLY	4.5
7	AG	153	HIS	4.5
3	CC	23	TYR	4.5
51	D4	43	TYR	4.5
3	CC	204	LEU	4.5
2	CB	233	SER	4.5
10	CJ	88	LEU	4.5
22	CV	23	A	4.5
8	CH	94	TYR	4.5
53	D6	54	ILE	4.5
1	CA	1001	A	4.5
46	BZ	107	THR	4.4
32	DH	36	PRO	4.4
47	B0	5	LYS	4.4
31	DG	35	GLU	4.4
31	DG	120	LEU	4.4
45	DY	65	ALA	4.4
26	DA	2145	C	4.4
8	CH	133	LEU	4.4
26	DA	2160	G	4.4
46	DZ	104	PHE	4.4
14	CN	31	ARG	4.4
7	AG	80	VAL	4.4
23	CW	39	PSU	4.4

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Mol	Chain	Res	Type	RSRZ
14	CN	55	GLY	4.4
3	CC	16	ARG	4.4
15	AO	87	ILE	4.4
23	CW	10	G	4.4
46	BZ	146	ILE	4.4
10	CJ	10	GLY	4.4
19	CS	71	LEU	4.4
47	D0	75	LEU	4.4
22	CV	15	A	4.4
46	DZ	152	ALA	4.4
10	CJ	12	ASP	4.4
39	DS	73	LEU	4.4
51	D4	67	TYR	4.4
3	CC	9	GLY	4.4
3	CC	178	LEU	4.3
26	DA	1509	C	4.4
39	DS	110	LEU	4.3
10	CJ	15	THR	4.3
10	CJ	67	THR	4.3
19	CS	69	HIS	4.3
45	DY	35	TYR	4.3
44	DX	1	MET	4.3
19	CS	13	ASP	4.3
3	CC	153	VAL	4.3
12	CL	27	LEU	4.3
46	BZ	117	LEU	4.3
3	CC	158	GLY	4.3
10	AJ	20	ALA	4.3
46	DZ	88	PHE	4.3
2	AB	80	ILE	4.3
9	CI	47	LEU	4.3
51	D4	44	THR	4.3
2	CB	209	ARG	4.3
3	CC	21	ARG	4.3
46	BZ	104	PHE	4.3
14	AN	15	LYS	4.3
25	CY	55	PSU	4.3
37	DQ	2	LEU	4.3
51	D4	50	VAL	4.3
23	AW	20	U	4.3
26	BA	932	C	4.3
37	DQ	106	VAL	4.3

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Mol	Chain	Res	Type	RSRZ
39	DS	3	ARG	4.3
21	CU	16	GLY	4.3
37	DQ	33	GLY	4.3
2	CB	186	ALA	4.3
10	CJ	19	SER	4.3
26	BA	2167	C	4.3
19	CS	43	GLU	4.2
26	BA	931	C	4.2
34	DN	23	LEU	4.2
3	CC	17	ASP	4.2
23	CW	71	G	4.2
34	DN	85	ILE	4.2
14	CN	6	LEU	4.2
45	DY	106	LEU	4.2
51	D4	56	VAL	4.2
25	CY	62	C	4.2
2	CB	205	ASP	4.2
5	CE	12	LEU	4.2
10	CJ	93	GLY	4.2
26	BA	218	A	4.2
9	AI	113	LYS	4.2
13	CM	92	HIS	4.2
39	DS	29	PHE	4.2
9	CI	127	LYS	4.2
32	DH	116	GLU	4.2
46	DZ	156	LYS	4.2
33	DI	12	LEU	4.2
9	AI	114	TYR	4.2
14	CN	50	LYS	4.2
10	CJ	61	GLU	4.2
46	DZ	143	GLY	4.2
15	CO	31	LEU	4.2
36	DP	125	VAL	4.2
52	B5	60	VAL	4.2
30	DF	146	ALA	4.2
2	AB	68	ILE	4.2
14	CN	12	ARG	4.2
21	CU	8	THR	4.2
46	DZ	97	GLU	4.2
22	CV	22	U	4.2
14	CN	23	ARG	4.2
5	CE	10	MET	4.2

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Mol	Chain	Res	Type	RSRZ
12	CL	100	ILE	4.2
23	AW	71	G	4.1
9	AI	109	VAL	4.1
7	CG	13	GLN	4.1
32	DH	145	ALA	4.1
46	BZ	164	ALA	4.1
2	CB	48	MET	4.1
32	DH	148	ILE	4.1
37	DQ	103	MET	4.1
2	CB	202	PRO	4.1
23	CW	44	G	4.1
26	DA	2156	G	4.1
32	DH	95	ARG	4.1
7	CG	33	ASP	4.1
19	CS	52	TYR	4.1
21	CU	5	ASP	4.1
26	DA	2132	U	4.1
45	DY	29	GLU	4.1
9	CI	107	ARG	4.1
10	CJ	55	LYS	4.1
11	CK	126	ARG	4.1
9	CI	54	ASP	4.1
1	CA	1220	G	4.1
3	CC	207	VAL	4.1
19	CS	32	LYS	4.1
42	DV	71	LEU	4.1
5	CE	109	ILE	4.1
12	CL	39	VAL	4.1
10	CJ	48	THR	4.1
25	CY	63	G	4.1
32	DH	111	HIS	4.1
2	CB	237	ALA	4.1
3	AC	91	LEU	4.1
7	CG	85	TYR	4.1
32	DH	101	ARG	4.1
51	D4	68	ARG	4.1
9	CI	108	VAL	4.1
10	AJ	6	ILE	4.1
15	CO	80	ALA	4.1
37	DQ	65	PHE	4.1
41	DU	40	PHE	4.1
8	CH	10	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
23	CW	14	A	4.1
2	CB	170	GLU	4.1
20	CT	9	ASN	4.1
38	DR	69	ASP	4.1
45	DY	43	ASN	4.0
1	AA	1001(A)	G	4.0
12	CL	48	PRO	4.0
11	CK	31	THR	4.0
21	CU	17	THR	4.0
31	DG	41	GLN	4.0
3	AC	87	LEU	4.0
9	AI	108	VAL	4.0
16	AP	33	ILE	4.0
22	AV	24	A	4.0
39	DS	24	LEU	4.0
32	DH	72	ILE	4.0
14	CN	35	ARG	4.0
2	CB	67	THR	4.0
47	D0	45	PHE	4.0
7	CG	109	ASN	4.0
23	CW	72	C	4.0
2	AB	230	VAL	4.0
8	CH	83	ILE	4.0
20	AT	55	ILE	4.0
32	DH	17	VAL	4.0
19	CS	14	HIS	4.0
29	BE	1	MET	4.0
3	CC	53	ALA	4.0
16	AP	59	TRP	4.0
28	BD	276	LYS	4.0
4	AD	138	TYR	4.0
8	CH	95	VAL	4.0
46	DZ	120	ILE	4.0
1	CA	1531	A	4.0
2	CB	140	HIS	4.0
2	CB	62	ALA	4.0
9	CI	10	ARG	4.0
13	CM	19	LEU	4.0
39	DS	41	ASP	4.0
46	BZ	155	LEU	4.0
46	DZ	141	VAL	4.0
51	D4	32	TYR	4.0

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Mol	Chain	Res	Type	RSRZ
46	BZ	115	GLY	4.0
2	AB	77	ALA	4.0
9	CI	74	ILE	3.9
15	CO	27	VAL	3.9
13	CM	103	THR	3.9
16	AP	32	TYR	3.9
9	CI	6	GLY	3.9
9	CI	45	ALA	3.9
10	CJ	26	ALA	3.9
13	CM	97	PRO	3.9
3	CC	5	ILE	3.9
1	AA	1257	U	3.9
1	CA	1116	C	3.9
3	AC	201	TYR	3.9
51	D4	52	THR	3.9
14	CN	47	LEU	3.9
12	CL	62	SER	3.9
13	CM	65	LYS	3.9
26	BA	2182	G	3.9
31	DG	48	GLU	3.9
32	DH	76	VAL	3.9
33	DI	85	GLU	3.9
7	CG	12	LEU	3.9
22	CV	21	C	3.9
23	CW	56	C	3.9
26	DA	2111	C	3.9
2	CB	97	TRP	3.9
12	CL	13	LYS	3.9
10	CJ	74	ILE	3.9
51	B4	50	VAL	3.9
10	CJ	92	THR	3.9
26	DA	2158	A	3.9
32	DH	123	PHE	3.9
46	DZ	98	MET	3.9
9	CI	124	GLN	3.9
9	CI	65	VAL	3.9
31	DG	161	THR	3.9
18	CR	87	ARG	3.9
9	CI	37	PHE	3.9
32	DH	103	LEU	3.9
37	DQ	32	TYR	3.9
2	CB	29	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
31	DG	182	LYS	3.9
31	DG	2	PRO	3.9
9	CI	20	ARG	3.9
19	CS	70	LYS	3.9
3	CC	71	ALA	3.9
7	CG	154	TYR	3.9
34	DN	11	PRO	3.8
13	CM	106	ASN	3.8
46	DZ	69	THR	3.8
2	CB	85	ALA	3.8
23	CW	40	C	3.8
34	DN	62	VAL	3.8
3	CC	181	ASN	3.8
16	CP	19	ILE	3.8
18	AR	25	THR	3.8
1	CA	1111	A	3.8
46	DZ	70	LEU	3.8
2	AB	207	ALA	3.8
31	DG	115	ARG	3.8
1	CA	1001(A)	G	3.8
32	DH	144	VAL	3.8
1	CA	1219	U	3.8
23	CW	75	C	3.8
19	CS	8	GLY	3.8
9	CI	88	TYR	3.8
32	DH	37	VAL	3.8
32	DH	133	VAL	3.8
32	DH	89	ILE	3.8
2	CB	177	ALA	3.8
41	DU	73	GLY	3.8
23	CW	27	G	3.8
8	CH	99	GLU	3.8
9	CI	63	ILE	3.8
18	AR	85	LEU	3.8
9	CI	122	ALA	3.8
22	AV	13	A	3.8
2	AB	12	GLU	3.8
46	BZ	119	GLU	3.8
21	CU	9	ARG	3.8
10	AJ	8	LEU	3.8
46	DZ	106	GLY	3.8
39	DS	37	ALA	3.8

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Mol	Chain	Res	Type	RSRZ
39	DS	20	ARG	3.7
36	DP	1	MET	3.7
19	CS	9	VAL	3.7
2	AB	201	ILE	3.7
2	CB	80	ILE	3.7
16	AP	35	LYS	3.7
19	CS	79	THR	3.7
23	CW	4	C	3.7
1	CA	973	G	3.7
26	DA	2110	G	3.7
38	DR	68	ARG	3.7
46	BZ	149	SER	3.7
2	AB	211	ILE	3.7
2	AB	222	ILE	3.7
23	CW	38	A	3.7
39	DS	12	PHE	3.7
9	CI	128	ARG	3.7
32	DH	112	PRO	3.7
2	CB	148	TYR	3.7
42	DV	12	TYR	3.7
2	CB	93	VAL	3.7
9	CI	87	GLN	3.7
30	DF	147	GLY	3.7
50	D3	9	VAL	3.7
16	AP	4	ILE	3.7
56	B9	17	ILE	3.7
31	DG	181	ARG	3.7
47	D0	74	ARG	3.7
2	AB	75	LYS	3.7
39	DS	79	ALA	3.7
9	CI	49	PRO	3.7
43	BW	111	HIS	3.7
26	DA	2144	U	3.7
2	CB	130	ARG	3.7
9	CI	120	ARG	3.7
9	CI	82	ALA	3.7
7	CG	42	ILE	3.7
16	AP	7	ALA	3.7
46	BZ	109	ALA	3.7
2	CB	216	SER	3.7
3	CC	198	VAL	3.7
45	DY	1	MET	3.7

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Mol	Chain	Res	Type	RSRZ
3	CC	152	ILE	3.7
10	AJ	23	ILE	3.7
32	DH	128	PRO	3.7
9	CI	56	LEU	3.7
40	DT	1	MET	3.7
44	DX	69	TYR	3.7
2	CB	32	ILE	3.7
25	CY	6	G	3.7
13	CM	110	ARG	3.6
47	D0	76	GLY	3.6
10	CJ	59	SER	3.6
4	AD	176	LEU	3.6
2	AB	101	MET	3.6
13	CM	21	TYR	3.6
2	CB	57	PHE	3.6
2	CB	78	GLN	3.6
17	AQ	27	PHE	3.6
3	CC	179	ARG	3.6
7	AG	79	ARG	3.6
9	CI	46	ALA	3.6
46	BZ	121	HIS	3.6
1	CA	1002	G	3.6
23	AW	44	G	3.6
18	CR	85	LEU	3.6
31	BG	139	LEU	3.6
41	BU	117	GLN	3.6
19	AS	40	ILE	3.6
46	DZ	133	ILE	3.6
34	DN	91	LEU	3.6
31	DG	136	ARG	3.6
14	CN	30	ALA	3.6
10	CJ	62	HIS	3.6
30	DF	148	LEU	3.6
45	DY	41	GLY	3.6
31	DG	60	LEU	3.6
46	DZ	59	LEU	3.6
32	DH	125	VAL	3.6
19	CS	39	THR	3.6
10	CJ	66	ARG	3.6
30	DF	172	TRP	3.6
2	CB	139	LYS	3.6
15	CO	29	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
41	DU	90	VAL	3.6
2	CB	55	PHE	3.6
37	DQ	62	GLY	3.6
21	CU	13	ILE	3.6
26	DA	885	C	3.6
32	DH	159	GLU	3.6
9	CI	59	PHE	3.6
15	CO	82	ILE	3.5
23	CW	45	U	3.5
1	AA	1002	G	3.5
24	CX	70	G	3.5
2	AB	231	GLU	3.5
23	CW	7	A	3.5
3	CC	205	GLY	3.5
10	CJ	54	PHE	3.5
25	CY	47	U	3.5
37	DQ	66	ILE	3.5
3	CC	142	MET	3.5
16	AP	39	TYR	3.5
32	DH	47	GLU	3.5
2	CB	193	ASP	3.5
14	CN	61	TRP	3.5
19	CS	12	ASP	3.5
23	CW	28	G	3.5
26	DA	2131	G	3.5
8	CH	61	VAL	3.5
32	DH	49	VAL	3.5
39	DS	60	GLY	3.5
46	DZ	6	LYS	3.5
8	CH	134	ILE	3.5
2	AB	79	ASP	3.5
33	BI	140	LEU	3.5
7	CG	32	ARG	3.5
32	DH	52	VAL	3.5
12	CL	32	PHE	3.5
5	CE	13	ILE	3.5
2	CB	13	ALA	3.5
9	CI	112	LYS	3.5
31	DG	156	ASP	3.5
13	CM	88	ARG	3.5
18	AR	78	LEU	3.5
36	DP	15	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
12	CL	56	ALA	3.5
13	CM	82	MET	3.5
1	CA	1224	G	3.5
23	CW	5	G	3.5
25	CY	57	G	3.5
9	AI	26	VAL	3.5
46	DZ	162	GLU	3.5
51	D4	48	ARG	3.5
2	CB	220	ASP	3.5
4	AD	11	LEU	3.5
38	DR	70	LEU	3.5
42	DV	94	LEU	3.5
39	DS	11	LYS	3.5
16	AP	2	VAL	3.5
31	DG	160	VAL	3.5
43	DW	50	VAL	3.5
1	CA	1156	G	3.5
2	CB	17	PHE	3.5
2	CB	135	GLN	3.5
1	CA	1257	U	3.5
46	DZ	123	ASP	3.5
4	AD	169	LYS	3.5
31	DG	137	GLU	3.5
7	CG	37	ASN	3.5
7	CG	156	TRP	3.5
16	AP	48	TRP	3.5
34	DN	9	VAL	3.5
1	CA	1114	C	3.4
10	AJ	5	ARG	3.4
13	CM	78	ILE	3.4
3	AC	81	GLY	3.4
15	CO	84	LYS	3.4
10	AJ	35	SER	3.4
32	DH	166	GLY	3.4
39	DS	74	ALA	3.4
45	BY	65	ALA	3.4
11	AK	25	TYR	3.4
13	CM	87	TYR	3.4
13	CM	101	GLN	3.4
39	DS	111	GLU	3.4
7	CG	40	ALA	3.4
9	AI	55	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
31	DG	73	ALA	3.4
2	AB	228	GLY	3.4
1	CA	1030(A)	G	3.4
54	D7	45	ALA	3.4
9	AI	125	TYR	3.4
10	CJ	94	VAL	3.4
8	CH	31	PHE	3.4
8	CH	96	GLY	3.4
23	AW	3	C	3.4
9	AI	116	LYS	3.4
31	DG	110	ALA	3.4
14	CN	15	LYS	3.4
19	CS	68	GLY	3.4
28	DD	204	ILE	3.4
23	CW	74	C	3.4
31	DG	108	ASN	3.4
9	CI	96	LEU	3.4
37	DQ	79	LEU	3.4
50	D3	53	LEU	3.4
5	CE	90	VAL	3.4
47	D0	4	LYS	3.4
31	DG	74	LYS	3.4
8	CH	9	MET	3.4
5	CE	33	VAL	3.4
9	CI	67	GLY	3.4
14	CN	22	THR	3.3
32	DH	109	PHE	3.3
12	CL	10	LEU	3.3
1	CA	965	A	3.3
3	CC	30	ARG	3.3
2	CB	19	HIS	3.3
5	CE	8	GLU	3.3
10	CJ	56	HIS	3.3
18	CR	43	PHE	3.3
1	CA	1115	C	3.3
31	DG	169	ALA	3.3
13	CM	56	LEU	3.3
18	AR	79	LEU	3.3
36	DP	148	LEU	3.3
2	CB	53	ARG	3.3
13	CM	104	ARG	3.3
2	CB	231	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
4	AD	180	GLY	3.3
8	CH	128	GLY	3.3
11	AK	82	VAL	3.3
19	CS	53	ASN	3.3
13	AM	4	ILE	3.3
12	CL	60	LEU	3.3
32	DH	35	VAL	3.3
3	AC	65	ALA	3.3
14	CN	10	ALA	3.3
51	D4	41	PRO	3.3
2	CB	137	ARG	3.3
37	DQ	5	ARG	3.3
47	D0	8	GLY	3.3
23	CW	11	C	3.3
7	CG	7	ALA	3.3
9	AI	15	ALA	3.3
36	DP	79	ARG	3.3
3	CC	147	LYS	3.3
10	AJ	16	LEU	3.3
15	AO	57	LEU	3.3
20	CT	20	LEU	3.3
8	CH	131	GLY	3.3
9	AI	75	ASP	3.3
23	CW	6	G	3.3
25	CY	64	A	3.3
26	BA	2184	G	3.3
26	DA	2147	G	3.3
19	CS	66	MET	3.3
46	DZ	128	VAL	3.3
8	CH	92	ARG	3.3
10	CJ	64	GLU	3.3
26	DA	884	C	3.3
31	BG	137	GLU	3.3
45	DY	64	GLU	3.3
19	CS	75	ALA	3.3
46	DZ	164	ALA	3.3
9	AI	56	LEU	3.3
15	CO	81	LEU	3.3
10	CJ	13	HIS	3.3
3	CC	130	VAL	3.3
10	AJ	69	ASN	3.3
37	DQ	109	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
39	DS	112	PHE	3.3
46	DZ	71	VAL	3.3
3	CC	149	ALA	3.3
7	AG	81	GLY	3.3
11	CK	25	TYR	3.3
31	DG	138	GLN	3.3
23	CW	41	C	3.3
46	BZ	102	LEU	3.3
14	CN	8	GLU	3.3
7	CG	26	PHE	3.2
9	CI	119	ALA	3.2
16	AP	38	TYR	3.2
30	DF	140	LEU	3.2
32	BH	2	SER	3.2
16	AP	34	GLU	3.2
25	CY	52	G	3.2
4	AD	170	VAL	3.2
5	CE	31	LEU	3.2
19	AS	71	LEU	3.2
10	AJ	43	ARG	3.2
39	DS	92	TYR	3.2
2	AB	70	PHE	3.2
1	CA	1149	C	3.2
16	AP	21	VAL	3.2
46	DZ	65	GLN	3.2
51	D4	35	VAL	3.2
45	DY	63	LYS	3.2
26	DA	2149	G	3.2
26	DA	2159	G	3.2
9	AI	102	LEU	3.2
31	DG	3	LEU	3.2
38	DR	29	LEU	3.2
49	D2	60	LEU	3.2
3	CC	201	TYR	3.2
14	CN	24	CYS	3.2
51	B4	54	GLY	3.2
55	D8	2	PRO	3.2
3	CC	188	LEU	3.2
18	AR	40	LEU	3.2
39	DS	102	ALA	3.2
4	AD	70	ILE	3.2
1	CA	1117	G	3.2

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Mol	Chain	Res	Type	RSRZ
9	CI	117	HIS	3.2
4	CD	179	GLU	3.2
2	CB	79	ASP	3.2
8	CH	35	ILE	3.2
19	CS	83	HIS	3.2
23	CW	26	A	3.2
45	DY	62	GLU	3.2
9	AI	33	PHE	3.2
30	BF	207	GLY	3.2
1	CA	1202	G	3.2
23	CW	70	G	3.2
12	CL	26	ALA	3.2
18	CR	66	LEU	3.2
30	DF	124	LEU	3.2
10	AJ	97	GLU	3.2
46	DZ	169	GLU	3.2
46	BZ	112	ARG	3.2
9	CI	41	VAL	3.2
29	DE	196	VAL	3.2
9	CI	102	LEU	3.2
10	AJ	18	ALA	3.2
7	AG	156	TRP	3.2
54	B7	47	ARG	3.2
9	CI	11	LYS	3.2
48	D1	22	GLY	3.2
9	CI	103	THR	3.1
10	CJ	89	ASP	3.1
2	CB	149	LEU	3.1
4	AD	120	LEU	3.1
9	AI	52	ALA	3.1
31	DG	103	LEU	3.1
9	CI	16	ARG	3.1
42	BV	101	GLY	3.1
2	CB	98	LEU	3.1
9	CI	40	LEU	3.1
3	CC	4	LYS	3.1
4	AD	3	ARG	3.1
4	CD	49	ARG	3.1
46	DZ	57	ILE	3.1
1	CA	1321	C	3.1
42	DV	42	GLY	3.1
2	AB	55	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
44	DX	49	VAL	3.1
4	CD	188	LEU	3.1
9	CI	99	LEU	3.1
1	CA	1150	U	3.1
12	CL	7	ILE	3.1
23	CW	47	U	3.1
2	AB	152	PHE	3.1
2	CB	144	ARG	3.1
19	CS	37	ARG	3.1
32	DH	99	VAL	3.1
50	D3	29	ARG	3.1
2	CB	138	LEU	3.1
19	CS	4	SER	3.1
31	DG	135	LEU	3.1
31	DG	152	LEU	3.1
2	AB	200	ILE	3.1
9	AI	117	HIS	3.1
3	CC	167	TRP	3.1
10	CJ	7	LYS	3.1
26	DA	2148	G	3.1
26	DA	2157	G	3.1
17	AQ	28	PRO	3.1
3	CC	168	ALA	3.1
11	AK	19	ALA	3.1
41	BU	116	ALA	3.1
9	CI	8	GLY	3.1
3	CC	19	GLU	3.1
8	CH	136	GLU	3.1
14	CN	11	LYS	3.1
19	CS	6	LYS	3.1
46	BZ	124	ILE	3.1
32	DH	152	ARG	3.1
5	AE	6	PHE	3.1
9	AI	79	LEU	3.1
31	DG	179	PRO	3.1
32	DH	88	LEU	3.1
46	DZ	24	LEU	3.1
12	CL	14	GLY	3.1
8	CH	91	ARG	3.1
28	DD	217	ARG	3.1
26	DA	645	C	3.1
7	CG	22	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
46	DZ	47	VAL	3.1
15	CO	86	GLY	3.1
26	DA	887	A	3.1
37	DQ	107	ALA	3.1
2	CB	96	ARG	3.1
1	CA	1036	G	3.1
25	AY	20	U	3.0
7	CG	62	PHE	3.0
3	CC	33	LEU	3.0
37	DQ	37	LEU	3.0
20	CT	26	ASN	3.0
31	DG	6	ALA	3.0
2	AB	208	ILE	3.0
2	CB	189	ASP	3.0
45	DY	38	ILE	3.0
13	CM	73	GLU	3.0
2	AB	78	GLN	3.0
8	CH	36	LEU	3.0
10	AJ	40	LEU	3.0
1	AA	1026	G	3.0
36	BP	79	ARG	3.0
14	AN	59	ALA	3.0
37	DQ	18	LYS	3.0
9	AI	81	ILE	3.0
19	CS	44	MET	3.0
16	AP	20	VAL	3.0
18	AR	87	ARG	3.0
23	CW	36	A	3.0
32	DH	50	VAL	3.0
39	DS	89	ARG	3.0
13	CM	107	ALA	3.0
15	CO	3	ILE	3.0
10	AJ	21	GLN	3.0
15	AO	88	ARG	3.0
3	AC	72	LYS	3.0
3	CC	7	PRO	3.0
10	AJ	7	LYS	3.0
42	DV	74	LYS	3.0
46	DZ	68	PRO	3.0
46	DZ	100	VAL	3.0
46	DZ	157	LEU	3.0
9	AI	54	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
7	CG	78	ARG	3.0
46	BZ	143	GLY	3.0
9	CI	29	ASN	3.0
13	CM	70	LEU	3.0
17	AQ	11	VAL	3.0
46	BZ	99	TYR	3.0
4	AD	102	ASP	3.0
2	AB	209	ARG	3.0
13	AM	122	LYS	3.0
14	CN	26	ARG	3.0
14	CN	45	ARG	3.0
31	DG	16	ARG	3.0
9	CI	77	ILE	3.0
32	DH	108	GLY	3.0
2	AB	229	VAL	3.0
10	AJ	64	GLU	3.0
13	CM	34	LEU	3.0
55	B8	65	GLU	3.0
9	AI	46	ALA	3.0
26	DA	886	C	3.0
39	DS	7	TYR	3.0
45	BY	36	ALA	3.0
7	AG	78	ARG	3.0
16	CP	25	ARG	3.0
17	CQ	36	ILE	3.0
14	CN	46	GLU	3.0
37	DQ	58	PHE	3.0
11	CK	121	PRO	3.0
26	DA	958	U	3.0
8	CH	116	LYS	3.0
9	AI	78	LYS	3.0
7	CG	3	ARG	3.0
9	CI	32	ASP	3.0
10	CJ	17	ASP	3.0
14	CN	27	CYS	3.0
14	CN	40	CYS	3.0
30	DF	130	ALA	3.0
30	DF	166	ALA	3.0
45	DY	55	TYR	3.0
1	CA	1118	C	3.0
49	D2	1	MET	2.9
2	CB	212	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
3	CC	65	ALA	2.9
20	CT	44	ALA	2.9
13	CM	85	GLY	2.9
2	CB	39	ILE	2.9
8	CH	6	ILE	2.9
17	CQ	100	LYS	2.9
4	AD	174	LEU	2.9
8	CH	112	LEU	2.9
20	AT	20	LEU	2.9
26	DA	2164	C	2.9
36	DP	123	LEU	2.9
1	AA	1023	G	2.9
3	AC	168	ALA	2.9
3	CC	187	ALA	2.9
46	DZ	55	HIS	2.9
2	AB	227	GLY	2.9
3	AC	78	GLY	2.9
11	CK	49	GLY	2.9
31	DG	47	LYS	2.9
2	AB	127	ILE	2.9
2	CB	208	ILE	2.9
9	AI	63	ILE	2.9
10	AJ	46	ARG	2.9
32	DH	12	PRO	2.9
2	CB	43	ASP	2.9
43	DW	104	THR	2.9
31	DG	29	TRP	2.9
9	CI	113	LYS	2.9
12	CL	68	ALA	2.9
13	CM	72	ALA	2.9
10	AJ	10	GLY	2.9
11	AK	126	ARG	2.9
1	AA	1036	G	2.9
23	CW	57	G	2.9
4	AD	157	LEU	2.9
16	AP	6	LEU	2.9
45	BY	67	LEU	2.9
32	DH	104	GLU	2.9
9	AI	126	SER	2.9
19	CS	81	ARG	2.9
16	AP	73	LEU	2.9
42	DV	20	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
2	AB	73	THR	2.9
11	AK	57	THR	2.9
28	DD	18	VAL	2.9
8	CH	124	ALA	2.9
46	DZ	21	ALA	2.9
2	AB	76	GLN	2.9
39	DS	27	SER	2.9
20	CT	30	LYS	2.9
45	BY	63	LYS	2.9
4	AD	110	PHE	2.9
26	DA	888	C	2.9
3	AC	15	THR	2.9
31	DG	155	MET	2.9
42	DV	72	VAL	2.9
3	CC	190	ARG	2.9
9	CI	69	GLY	2.9
30	BF	17	ARG	2.9
23	CW	15	G	2.9
26	DA	2154	G	2.9
7	AG	154	TYR	2.9
12	CL	70	ILE	2.9
14	AN	7	ILE	2.9
16	AP	29	ASP	2.9
16	AP	68	ASP	2.9
19	CS	30	LEU	2.9
17	CQ	80	GLY	2.9
34	DN	12	ARG	2.9
42	DV	5	VAL	2.9
42	DV	14	VAL	2.9
1	CA	1041	A	2.9
2	CB	161	ALA	2.9
3	CC	146	ALA	2.9
26	DA	2310	A	2.9
46	DZ	7	ALA	2.9
2	CB	108	ILE	2.8
18	AR	76	LEU	2.8
20	AT	72	LEU	2.8
45	DY	61	ILE	2.8
2	CB	183	PRO	2.8
4	CD	168	ARG	2.8
32	DH	126	PRO	2.8
10	CJ	81	THR	2.8

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Mol	Chain	Res	Type	RSRZ
28	DD	276	LYS	2.8
45	DY	3	VAL	2.8
31	DG	49	ASP	2.8
4	AD	21	LEU	2.8
34	DN	84	LYS	2.8
37	DQ	60	ARG	2.8
39	DS	97	ARG	2.8
32	DH	8	PRO	2.8
2	AB	81	VAL	2.8
3	CC	15	THR	2.8
51	D4	66	SER	2.8
34	DN	50	ASP	2.8
8	CH	111	ILE	2.8
31	DG	107	LEU	2.8
46	DZ	117	LEU	2.8
1	AA	1030(B)	C	2.8
26	BA	2157	A	2.8
7	CG	9	VAL	2.8
14	AN	56	VAL	2.8
31	DG	37	VAL	2.8
2	AB	188	ALA	2.8
6	CF	89	MET	2.8
10	CJ	20	ALA	2.8
26	BA	1072	U	2.8
3	AC	204	LEU	2.8
13	CM	67	GLU	2.8
34	DN	99	LEU	2.8
7	CG	14	PRO	2.8
37	DQ	64	ILE	2.8
7	CG	39	ALA	2.8
39	DS	31	SER	2.8
1	CA	1286	A	2.8
10	CJ	69	ASN	2.8
43	DW	1	MET	2.8
29	BE	195	LEU	2.8
19	CS	42	PRO	2.8
54	B7	46	VAL	2.8
3	AC	100	ALA	2.8
3	CC	200	ALA	2.8
8	CH	122	ARG	2.8
23	CW	34	G	2.8
26	BA	2181	G	2.8

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Mol	Chain	Res	Type	RSRZ
26	DA	2127	G	2.8
37	BQ	112	GLU	2.8
9	CI	85	LEU	2.8
20	AT	24	LEU	2.8
31	DG	80	PHE	2.8
4	AD	4	TYR	2.8
4	AD	140	VAL	2.8
11	AK	87	THR	2.8
11	CK	59	TYR	2.8
12	CL	15	ARG	2.8
2	CB	150	SER	2.8
37	BQ	80	GLU	2.8
4	CD	183	GLY	2.8
32	DH	93	GLY	2.8
41	DU	39	LEU	2.8
16	AP	80	PHE	2.8
26	DA	2319	G	2.8
26	BA	1555	C	2.8
26	DA	894	C	2.8
31	DG	144	ILE	2.8
46	DZ	112	ARG	2.8
3	CC	173	VAL	2.8
51	D4	24	THR	2.8
26	DA	2134	A	2.8
34	DN	57	ALA	2.8
31	DG	134	GLY	2.7
3	CC	175	LEU	2.7
42	DV	35	LEU	2.7
13	CM	108	ARG	2.7
46	BZ	169	GLU	2.7
2	CB	75	LYS	2.7
4	AD	17	VAL	2.7
7	CG	36	LYS	2.7
45	DY	34	LYS	2.7
46	DZ	151	HIS	2.7
56	B9	13	LYS	2.7
23	AW	56	C	2.7
23	CW	22	G	2.7
26	DA	2138	C	2.7
26	DA	2153	G	2.7
47	D0	54	GLY	2.7
49	B2	1	MET	2.7

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Mol	Chain	Res	Type	RSRZ
1	AA	1035	A	2.7
2	AB	118	LEU	2.7
9	AI	120	ARG	2.7
2	CB	59	GLU	2.7
45	BY	91	GLU	2.7
39	DS	62	LYS	2.7
4	CD	161	ASN	2.7
10	AJ	24	VAL	2.7
39	DS	85	VAL	2.7
2	CB	34	ALA	2.7
4	AD	2	GLY	2.7
10	AJ	36	GLY	2.7
9	AI	42	ARG	2.7
9	AI	121	ARG	2.7
5	AE	12	LEU	2.7
23	CW	19	G	2.7
11	CK	13	GLN	2.7
32	DH	110	SER	2.7
4	AD	8	VAL	2.7
5	CE	67	VAL	2.7
11	AK	84	VAL	2.7
17	CQ	23	VAL	2.7
43	DW	59	VAL	2.7
46	DZ	148	ASP	2.7
4	CD	2	GLY	2.7
33	BI	117	GLU	2.7
6	CF	79	LEU	2.7
19	CS	16	LEU	2.7
37	DQ	17	LEU	2.7
45	DY	31	LEU	2.7
2	CB	167	PRO	2.7
1	CA	1322	C	2.7
26	BA	2185	C	2.7
2	CB	184	VAL	2.7
9	AI	28	VAL	2.7
16	CP	20	VAL	2.7
31	DG	70	VAL	2.7
3	CC	122	GLU	2.7
31	DG	36	LYS	2.7
3	CC	170	GLN	2.7
33	BI	75	LEU	2.7
2	CB	94	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
9	CI	71	SER	2.7
28	BD	275	LYS	2.7
41	DU	17	ILE	2.7
29	DE	10	GLY	2.7
36	DP	20	GLY	2.7
9	CI	55	ALA	2.7
20	CT	32	ALA	2.7
31	DG	25	TYR	2.7
4	CD	108	LEU	2.7
16	AP	60	LEU	2.7
51	D4	59	PHE	2.7
2	CB	82	ARG	2.7
10	CJ	51	ARG	2.7
11	AK	81	ASP	2.7
3	AC	55	VAL	2.7
9	AI	86	VAL	2.7
38	DR	117	VAL	2.7
3	CC	129	ALA	2.7
13	CM	76	ALA	2.7
19	CS	24	ALA	2.7
38	DR	41	ALA	2.7
10	CJ	16	LEU	2.7
18	AR	31	LEU	2.7
10	AJ	66	ARG	2.7
13	CM	99	ARG	2.7
37	DQ	59	ARG	2.7
37	DQ	105	GLU	2.7
19	CS	31	ILE	2.7
26	BA	2154	U	2.7
56	B9	12	ASP	2.7
46	DZ	105	VAL	2.7
5	AE	134	ALA	2.7
9	CI	43	ALA	2.7
9	CI	51	ARG	2.6
12	CL	84	LEU	2.6
20	AT	9	ASN	2.6
46	DZ	92	SER	2.6
20	CT	41	ILE	2.6
31	DG	85	GLY	2.6
21	AU	17	THR	2.6
15	CO	60	VAL	2.6
37	DQ	97	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
45	BY	34	LYS	2.6
13	CM	50	GLU	2.6
13	CM	91	ARG	2.6
18	AR	42	ARG	2.6
26	BA	930	G	2.6
15	AO	81	LEU	2.6
15	CO	57	LEU	2.6
21	CU	21	TYR	2.6
26	DA	2135	A	2.6
4	CD	160	GLN	2.6
10	AJ	96	ILE	2.6
51	B4	60	GLN	2.6
13	AM	53	VAL	2.6
16	CP	51	VAL	2.6
19	CS	11	VAL	2.6
23	CW	12	U	2.6
23	CW	66	U	2.6
25	CY	49	C	2.6
37	DQ	102	VAL	2.6
12	CL	30	ALA	2.6
54	D7	41	ARG	2.6
2	CB	51	LEU	2.6
39	DS	101	LEU	2.6
10	CJ	58	ASP	2.6
36	DP	78	PRO	2.6
1	CA	953	G	2.6
3	AC	80	GLY	2.6
13	CM	112	GLY	2.6
16	AP	37	GLY	2.6
46	DZ	44	PHE	2.6
51	D4	45	GLY	2.6
51	B4	46	GLN	2.6
3	CC	177	THR	2.6
27	DB	25	A	2.6
27	DB	90	A	2.6
2	CB	30	ARG	2.6
4	CD	148	VAL	2.6
10	CJ	9	ARG	2.6
16	AP	51	VAL	2.6
32	DH	46	GLU	2.6
43	DW	17	VAL	2.6
31	DG	158	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	CA	1039	C	2.6
2	CB	221	LEU	2.6
23	AW	2	C	2.6
26	DA	2139	C	2.6
38	DR	65	LEU	2.6
46	DZ	46	LYS	2.6
2	CB	95	GLN	2.6
15	AO	20	GLY	2.6
5	CE	81	GLU	2.6
15	CO	14	GLU	2.6
2	AB	185	ILE	2.6
2	CB	73	THR	2.6
33	BI	103	ARG	2.6
46	DZ	72	ARG	2.6
18	CR	86	VAL	2.6
19	CS	60	VAL	2.6
45	DY	42	VAL	2.6
14	CN	4	LYS	2.6
3	CC	155	GLY	2.6
3	CC	143	GLU	2.6
10	AJ	59	SER	2.6
45	DY	20	TYR	2.6
39	DS	87	PHE	2.6
47	D0	69	PHE	2.6
38	DR	8	ARG	2.6
54	D7	1	MET	2.6
34	DN	43	THR	2.6
19	AS	41	VAL	2.6
3	CC	117	ALA	2.6
39	BS	37	ALA	2.6
5	AE	123	LEU	2.6
28	DD	37	LEU	2.6
36	BP	105	LEU	2.6
39	DS	68	GLN	2.6
39	DS	104	GLY	2.6
51	B4	17	GLY	2.6
23	AW	70	G	2.6
23	CW	18	G	2.6
37	DQ	10	ARG	2.6
42	DV	75	PHE	2.6
5	AE	88	LYS	2.6
23	CW	25	C	2.6

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Mol	Chain	Res	Type	RSRZ
31	DG	5	VAL	2.6
3	CC	60	ALA	2.6
11	CK	19	ALA	2.6
17	CQ	84	LEU	2.6
32	DH	18	GLU	2.6
51	D4	30	GLU	2.6
2	CB	227	GLY	2.6
9	CI	25	LYS	2.6
12	CL	19	ARG	2.6
46	BZ	122	ARG	2.6
47	D0	44	ARG	2.6
2	AB	19	HIS	2.6
14	CN	49	HIS	2.6
32	DH	164	TYR	2.6
10	CJ	98	ILE	2.6
11	AK	108	ILE	2.6
1	CA	983	A	2.6
5	AE	90	VAL	2.6
23	CW	69	G	2.6
13	AM	5	ALA	2.6
19	CS	73	GLU	2.6
39	DS	72	ALA	2.6
19	AS	81	ARG	2.5
42	DV	101	GLY	2.5
16	CP	48	TRP	2.5
18	CR	70	ILE	2.5
3	CC	64	VAL	2.5
31	DG	151	ALA	2.5
46	DZ	86	VAL	2.5
11	AK	96	ARG	2.5
2	CB	195	ASP	2.5
31	DG	116	ASP	2.5
1	AA	1001	A	2.5
1	CA	1155	G	2.5
14	CN	60	SER	2.5
9	AI	98	PRO	2.5
51	D4	7	PRO	2.5
23	CW	61	C	2.5
25	AY	56	C	2.5
26	DA	2136	C	2.5
16	AP	76	GLN	2.5
38	DR	71	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
3	AC	134	ILE	2.5
3	CC	79	ARG	2.5
2	AB	13	ALA	2.5
3	CC	197	GLY	2.5
11	CK	89	ALA	2.5
43	DW	105	VAL	2.5
15	CO	34	LEU	2.5
20	CT	13	LEU	2.5
34	DN	26	LEU	2.5
46	BZ	148	ASP	2.5
46	DZ	153	SER	2.5
31	DG	75	LYS	2.5
31	DG	117	PHE	2.5
7	AG	151	TYR	2.5
19	CS	36	ARG	2.5
26	DA	2119	A	2.5
51	B4	67	TYR	2.5
11	CK	96	ARG	2.5
3	CC	77	ILE	2.5
7	CG	30	ILE	2.5
18	AR	22	VAL	2.5
37	DQ	108	GLY	2.5
43	DW	20	VAL	2.5
46	DZ	51	ALA	2.5
4	AD	135	LEU	2.5
31	BG	133	LEU	2.5
46	DZ	93	ASP	2.5
10	CJ	53	PRO	2.5
36	DP	144	GLU	2.5
31	DG	23	PHE	2.5
2	AB	130	ARG	2.5
9	CI	93	ARG	2.5
36	BP	15	ARG	2.5
51	B4	43	TYR	2.5
8	CH	13	ILE	2.5
3	CC	113	ALA	2.5
3	CC	180	ALA	2.5
17	CQ	44	ALA	2.5
31	DG	109	VAL	2.5
46	BZ	165	VAL	2.5
1	AA	1531	A	2.5
29	DE	195	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
30	DF	181	LEU	2.5
38	DR	75	LEU	2.5
43	DW	51	LEU	2.5
2	AB	52	GLU	2.5
29	BE	87	GLU	2.5
36	DP	74	GLU	2.5
1	CA	204	U	2.5
13	AM	3	ARG	2.5
31	DG	51	ARG	2.5
47	D0	6	GLY	2.5
19	AS	11	VAL	2.5
31	DG	86	MET	2.5
32	DH	147	ASN	2.5
39	BS	49	VAL	2.5
36	DP	94	GLU	2.5
9	AI	111	ARG	2.5
26	DA	1026	U	2.5
2	CB	28	PHE	2.5
23	CW	35	A	2.5
26	DA	6	A	2.5
4	AD	167	GLY	2.5
44	DX	94	GLY	2.5
9	AI	110	GLU	2.5
13	CM	23	TYR	2.5
39	DS	8	GLU	2.5
19	AS	5	LEU	2.5
19	CS	5	LEU	2.5
30	DF	162	LEU	2.5
44	DX	42	ALA	2.5
34	DN	104	LYS	2.5
19	CS	63	THR	2.5
26	BA	696	C	2.5
51	B4	52	THR	2.5
16	AP	53	VAL	2.5
29	BE	28	ALA	2.5
46	DZ	37	VAL	2.5
4	CD	186	LEU	2.4
51	B4	68	ARG	2.4
29	DE	51	PHE	2.4
3	AC	169	ALA	2.4
17	CQ	32	TYR	2.4
38	DR	21	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
13	CM	96	LEU	2.4
48	D1	51	VAL	2.4
20	CT	21	LYS	2.4
1	CA	1119	C	2.4
25	CY	48	C	2.4
2	AB	16	HIS	2.4
32	DH	32	GLU	2.4
24	CX	4	G	2.4
3	CC	37	GLN	2.4
11	CK	67	ASP	2.4
19	CS	56	GLN	2.4
10	CJ	87	THR	2.4
32	DH	129	THR	2.4
2	CB	173	ALA	2.4
3	CC	157	ILE	2.4
4	AD	112	VAL	2.4
4	CD	4	TYR	2.4
15	AO	69	TYR	2.4
17	CQ	6	LEU	2.4
29	BE	52	LEU	2.4
31	DG	62	LEU	2.4
39	DS	80	LEU	2.4
56	D9	16	VAL	2.4
37	DQ	1	MET	2.4
33	DI	122	GLU	2.4
36	BP	149	GLU	2.4
30	BF	14	PRO	2.4
3	CC	81	GLY	2.4
3	CC	203	PHE	2.4
42	DV	30	GLY	2.4
25	AY	13	C	2.4
2	CB	166	ASP	2.4
3	CC	183	ASP	2.4
9	AI	112	LYS	2.4
46	BZ	156	LYS	2.4
26	DA	2173	A	2.4
1	CA	1187	G	2.4
9	CI	13	ALA	2.4
18	CR	26	LEU	2.4
19	CS	15	LEU	2.4
26	DA	2112	G	2.4
48	D1	82	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
30	DF	127	GLU	2.4
9	CI	38	GLN	2.4
1	CA	1113	C	2.4
9	AI	64	THR	2.4
8	CH	137	VAL	2.4
11	AK	61	ALA	2.4
11	AK	98	LEU	2.4
11	CK	108	ILE	2.4
47	D0	68	GLU	2.4
13	CM	18	ALA	2.4
44	DX	91	ALA	2.4
45	DY	72	VAL	2.4
2	AB	148	TYR	2.4
26	BA	1092	A	2.4
56	D9	13	LYS	2.4
5	CE	14	ARG	2.4
9	AI	93	ARG	2.4
37	BQ	5	ARG	2.4
39	DS	70	GLY	2.4
39	DS	43	GLU	2.4
2	CB	42	ILE	2.4
4	AD	158	ILE	2.4
11	CK	114	VAL	2.4
16	CP	4	ILE	2.4
16	CP	6	LEU	2.4
20	AT	36	LEU	2.4
36	BP	100	LEU	2.4
37	DQ	114	ALA	2.4
39	DS	44	LYS	2.4
45	DY	15	VAL	2.4
47	D0	37	LEU	2.4
56	B9	26	ILE	2.4
1	CA	1038	C	2.4
4	CD	73	ARG	2.4
7	CG	10	ARG	2.4
16	CP	39	TYR	2.4
31	BG	51	ARG	2.4
53	D6	50	ARG	2.4
46	BZ	110	GLY	2.4
14	CN	54	PRO	2.4
10	AJ	47	PHE	2.4
1	CA	1188	A	2.4

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Mol	Chain	Res	Type	RSRZ
8	CH	4	ASP	2.4
38	DR	47	PHE	2.4
22	AV	23	A	2.4
1	CA	1186	G	2.4
8	CH	24	THR	2.4
25	AY	34	G	2.4
2	CB	145	LEU	2.4
3	CC	11	ARG	2.4
8	CH	86	ILE	2.4
8	CH	127	LEU	2.4
10	CJ	75	ILE	2.4
15	CO	85	LEU	2.4
12	AL	89	ARG	2.4
18	AR	24	ALA	2.4
48	D1	62	VAL	2.4
37	DQ	61	GLY	2.4
3	CC	176	HIS	2.4
46	DZ	3	TYR	2.4
16	AP	66	PRO	2.4
31	DG	104	GLU	2.4
34	DN	10	GLU	2.4
2	CB	204	ASN	2.4
28	DD	275	LYS	2.4
13	CM	114	ARG	2.4
51	B4	55	ARG	2.4
5	CE	148	VAL	2.3
15	CO	11	VAL	2.3
33	DI	92	VAL	2.3
45	BY	45	VAL	2.3
56	B9	7	VAL	2.3
13	CM	100	GLY	2.3
37	DQ	30	GLY	2.3
29	BE	96	PHE	2.3
46	DZ	48	PHE	2.3
9	AI	51	ARG	2.3
7	CG	77	SER	2.3
23	CW	33	U	2.3
26	DA	2161	C	2.3
27	DB	11	C	2.3
30	BF	156	LEU	2.3
3	AC	124	ILE	2.3
20	CT	59	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
20	CT	63	ILE	2.3
29	BE	50	GLY	2.3
32	DH	44	VAL	2.3
32	DH	121	ILE	2.3
36	DP	75	ILE	2.3
11	CK	123	LYS	2.3
30	DF	197	ASP	2.3
3	CC	186	PHE	2.3
26	DA	2308	G	2.3
34	DN	69	GLN	2.3
1	CA	1040	U	2.3
15	CO	56	LEU	2.3
17	CQ	7	THR	2.3
30	BF	16	GLY	2.3
32	DH	77	LYS	2.3
50	D3	23	LEU	2.3
6	CF	9	VAL	2.3
10	CJ	96	ILE	2.3
11	CK	32	ILE	2.3
43	DW	6	ILE	2.3
45	DY	36	ALA	2.3
45	DY	69	ALA	2.3
46	DZ	42	VAL	2.3
46	DZ	53	ILE	2.3
50	D3	6	VAL	2.3
1	CA	962	C	2.3
9	CI	121	ARG	2.3
31	DG	131	TYR	2.3
32	DH	132	ARG	2.3
1	CA	1447	A	2.3
17	AQ	86	GLU	2.3
46	DZ	138	GLU	2.3
4	CD	69	GLY	2.3
9	CI	30	GLY	2.3
17	AQ	31	LEU	2.3
17	CQ	8	GLY	2.3
32	DH	122	THR	2.3
33	BI	9	LEU	2.3
38	DR	44	LEU	2.3
52	D5	29	THR	2.3
13	AM	25	ILE	2.3
47	D0	79	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
55	D8	16	ILE	2.3
1	CA	1003	G	2.3
25	AY	24	G	2.3
34	DN	130	HIS	2.3
1	CA	1320	C	2.3
2	CB	236	TYR	2.3
14	AN	17	LYS	2.3
39	DS	59	LYS	2.3
42	DV	1	MET	2.3
51	B4	49	PHE	2.3
26	DA	2143	C	2.3
4	AD	69	GLY	2.3
8	CH	39	LEU	2.3
32	DH	71	LEU	2.3
51	D4	27	THR	2.3
4	CD	5	ILE	2.3
9	AI	45	ALA	2.3
19	CS	67	VAL	2.3
30	DF	163	VAL	2.3
23	CW	21	A	2.3
9	CI	21	PRO	2.3
10	CJ	83	GLU	2.3
32	DH	119	GLU	2.3
1	AA	1024	G	2.3
1	CA	1190	G	2.3
2	AB	187	LEU	2.3
23	CW	68	C	2.3
26	DA	2128	C	2.3
26	DA	2174	C	2.3
45	DY	67	LEU	2.3
10	CJ	70	ARG	2.3
15	CO	77	ARG	2.3
21	CU	22	ARG	2.3
16	CP	29	ASP	2.3
28	DD	20	ASP	2.3
31	DG	84	LYS	2.3
43	DW	44	ALA	2.3
40	BT	52	ILE	2.3
23	CW	9	A	2.3
33	BI	128	LEU	2.3
33	DI	47	LEU	2.3
39	DS	23	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
9	AI	17	VAL	2.3
10	AJ	49	VAL	2.3
26	DA	2318	G	2.3
32	DH	24	VAL	2.3
37	DQ	28	ALA	2.3
39	DS	105	ALA	2.3
10	CJ	23	ILE	2.3
41	DU	88	ILE	2.3
44	DX	43	VAL	2.3
21	CU	23	PRO	2.3
26	DA	2896	C	2.3
2	CB	33	TYR	2.3
28	BD	38	LYS	2.3
28	DD	4	LYS	2.3
43	DW	26	GLY	2.3
48	D1	71	TYR	2.3
10	CJ	43	ARG	2.3
39	DS	4	LEU	2.3
1	CA	1035	A	2.2
1	CA	1151	A	2.2
12	CL	44	THR	2.2
2	AB	95	GLN	2.2
12	AL	18	VAL	2.2
18	AR	73	ALA	2.2
30	DF	132	VAL	2.2
32	DH	73	ALA	2.2
38	DR	101	ALA	2.2
51	D4	34	GLU	2.2
3	CC	202	ILE	2.2
10	AJ	39	PRO	2.2
1	CA	1373	G	2.2
9	CI	78	LYS	2.2
12	AL	91	LYS	2.2
26	DA	2125	G	2.2
37	DQ	29	PHE	2.2
3	CC	148	GLY	2.2
16	CP	30	GLY	2.2
47	D0	72	ARG	2.2
47	D0	73	GLY	2.2
13	AM	87	TYR	2.2
2	AB	158	LEU	2.2
12	CL	16	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
51	D4	53	GLU	2.2
37	DQ	113	GLN	2.2
39	DS	49	VAL	2.2
46	DZ	56	VAL	2.2
3	AC	8	ILE	2.2
11	AK	83	ILE	2.2
25	AY	47	U	2.2
31	DG	77	ILE	2.2
42	DV	70	ILE	2.2
1	CA	1004	A	2.2
25	AY	23	A	2.2
26	DA	2602	A	2.2
8	CH	90	GLY	2.2
14	AN	37	PHE	2.2
17	CQ	24	GLU	2.2
30	DF	170	LEU	2.2
36	BP	3	LEU	2.2
46	DZ	8	TYR	2.2
46	DZ	38	TYR	2.2
13	CM	63	THR	2.2
17	CQ	69	LYS	2.2
32	DH	153	LYS	2.2
32	BH	60	ARG	2.2
37	BQ	78	PRO	2.2
8	AH	71	GLY	2.2
2	AB	98	LEU	2.2
7	CG	151	TYR	2.2
10	CJ	90	LEU	2.2
20	CT	36	LEU	2.2
21	AU	14	TRP	2.2
27	DB	26	A	2.2
43	DW	45	TYR	2.2
46	DZ	41	LEU	2.2
50	D3	28	LEU	2.2
51	B4	69	LYS	2.2
32	DH	165	ALA	2.2
26	DA	2140	C	2.2
32	DH	6	ARG	2.2
33	DI	81	VAL	2.2
47	D0	80	HIS	2.2
1	CA	948	C	2.2
2	CB	111	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
5	AE	128	PRO	2.2
10	CJ	39	PRO	2.2
15	CO	36	ILE	2.2
37	DQ	56	ARG	2.2
39	DS	91	PRO	2.2
1	CA	947	G	2.2
2	CB	14	GLY	2.2
7	CG	8	GLU	2.2
16	AP	30	GLY	2.2
21	CU	4	GLY	2.2
26	DA	2120	G	2.2
26	DA	2133	G	2.2
31	BG	48	GLU	2.2
7	AG	13	GLN	2.2
48	D1	38	SER	2.2
9	CI	70	LYS	2.2
3	CC	22	TRP	2.2
5	CE	123	LEU	2.2
17	CQ	98	LEU	2.2
29	DE	182	LEU	2.2
46	DZ	140	ASP	2.2
11	CK	50	TYR	2.2
18	CR	47	THR	2.2
19	CS	77	THR	2.2
2	AB	71	VAL	2.2
10	AJ	68	HIS	2.2
32	DH	51	ARG	2.2
36	DP	18	ARG	2.2
26	BA	2195	A	2.2
32	DH	19	VAL	2.2
41	DU	44	ASN	2.2
3	AC	57	ILE	2.2
13	CM	10	PRO	2.2
29	BE	4	ILE	2.2
40	BT	102	ILE	2.2
2	CB	235	SER	2.2
4	CD	166	LYS	2.2
9	AI	11	LYS	2.2
31	BG	178	PHE	2.2
39	DS	50	SER	2.2
45	DY	28	LYS	2.2
26	BA	2196	C	2.2

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Mol	Chain	Res	Type	RSRZ
31	DG	175	LEU	2.2
1	CA	1034	G	2.2
4	AD	165	MET	2.2
4	CD	3	ARG	2.2
27	DB	23	G	2.2
27	DB	89	G	2.2
27	DB	117	G	2.2
4	CD	164	ALA	2.2
7	CG	152	ALA	2.2
45	DY	68	HIS	2.2
12	CL	101	VAL	2.2
28	DD	38	LYS	2.2
56	D9	25	VAL	2.2
4	CD	158	ILE	2.2
7	CG	86	GLN	2.2
14	CN	7	ILE	2.2
1	CA	1123	A	2.2
20	CT	80	ARG	2.2
29	BE	182	LEU	2.2
39	DS	48	LEU	2.2
8	CH	138	TRP	2.2
26	DA	2142	C	2.2
26	DA	2794	C	2.2
51	B4	34	GLU	2.2
47	D0	78	TYR	2.2
3	CC	120	VAL	2.2
4	AD	148	VAL	2.2
5	CE	69	VAL	2.2
7	CG	34	GLY	2.2
7	CG	117	ALA	2.2
9	AI	76	ALA	2.2
9	CI	68	GLY	2.2
13	CM	17	VAL	2.2
30	DF	193	VAL	2.2
39	DS	84	GLN	2.2
46	DZ	39	VAL	2.2
1	AA	606	G	2.2
1	CA	1221	G	2.2
14	AN	14	PRO	2.2
23	AW	19	G	2.2
34	DN	60	ILE	2.2
18	AR	29	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
7	CG	15	ASP	2.2
46	DZ	23	LYS	2.2
53	D6	34	LEU	2.2
1	CA	975	A	2.1
25	AY	35	A	2.1
30	DF	133	ASN	2.1
3	CC	61	ALA	2.1
9	CI	52	ALA	2.1
11	CK	68	ALA	2.1
1	CA	1354	C	2.1
7	CG	91	VAL	2.1
2	AB	202	PRO	2.1
23	CW	67	C	2.1
2	AB	210	SER	2.1
30	DF	15	SER	2.1
9	AI	37	PHE	2.1
46	DZ	43	GLU	2.1
17	AQ	98	LEU	2.1
25	CY	22	G	2.1
43	DW	23	LEU	2.1
2	CB	190	THR	2.1
4	CD	89	THR	2.1
20	AT	18	GLN	2.1
39	DS	45	GLY	2.1
30	DF	167	ALA	2.1
9	CI	44	VAL	2.1
46	DZ	126	VAL	2.1
3	CC	199	LYS	2.1
17	AQ	36	ILE	2.1
32	DH	16	SER	2.1
33	BI	109	ILE	2.1
4	AD	179	GLU	2.1
50	D3	17	LYS	2.1
1	AA	1030	C	2.1
25	CY	51	U	2.1
26	BA	2168	C	2.1
32	DH	171	LEU	2.1
33	BI	6	LEU	2.1
33	BI	35	LEU	2.1
11	CK	42	TRP	2.1
28	DD	17	THR	2.1
30	BF	34	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
36	DP	30	THR	2.1
1	CA	1021	G	2.1
2	CB	134	GLU	2.1
7	CG	5	ARG	2.1
8	CH	104	ARG	2.1
9	AI	65	VAL	2.1
13	CM	113	PRO	2.1
25	CY	65	G	2.1
26	DA	614(B)	G	2.1
31	DG	18	GLU	2.1
32	DH	157	TYR	2.1
36	DP	76	LYS	2.1
42	DV	50	PRO	2.1
46	DZ	134	PRO	2.1
4	AD	5	ILE	2.1
11	AK	21	ILE	2.1
31	DG	114	ILE	2.1
44	DX	8	ILE	2.1
19	CS	74	PHE	2.1
34	DN	51	PHE	2.1
47	D0	71	ASP	2.1
8	CH	119	LEU	2.1
10	AJ	90	LEU	2.1
33	BI	116	LEU	2.1
1	CA	1223	C	2.1
2	AB	66	GLY	2.1
9	AI	115	GLY	2.1
2	AB	97	TRP	2.1
10	AJ	60	ARG	2.1
2	AB	83	MET	2.1
3	AC	82	GLU	2.1
13	AM	61	GLU	2.1
17	AQ	35	VAL	2.1
30	DF	114	VAL	2.1
45	DY	24	VAL	2.1
56	B9	16	VAL	2.1
26	BA	1221	G	2.1
20	AT	13	LEU	2.1
33	DI	30	LEU	2.1
2	AB	72	GLY	2.1
15	AO	89	GLY	2.1
45	DY	47	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
2	CB	47	THR	2.1
15	CO	26	GLU	2.1
50	D3	35	ARG	2.1
46	BZ	69	THR	2.1
11	AK	60	ALA	2.1
20	CT	12	ALA	2.1
32	DH	75	ALA	2.1
37	DQ	121	ALA	2.1
2	AB	216	SER	2.1
26	BA	572	A	2.1
37	DQ	3	MET	2.1
45	BY	66	PRO	2.1
46	DZ	165	VAL	2.1
3	CC	56	ASP	2.1
4	CD	146	ILE	2.1
38	DR	42	LYS	2.1
3	AC	25	GLY	2.1
7	CG	6	ARG	2.1
10	CJ	36	GLY	2.1
46	BZ	147	GLY	2.1
55	D8	46	ARG	2.1
28	DD	201	HIS	2.1
50	D3	21	ALA	2.1
4	AD	33	MET	2.1
11	CK	82	VAL	2.1
19	AS	19	VAL	2.1
32	DH	41	MET	2.1
43	DW	47	VAL	2.1
45	BY	1	MET	2.1
45	BY	7	VAL	2.1
11	CK	111	ASP	2.1
31	DG	88	ILE	2.1
41	DU	106	PHE	2.1
1	CA	974	A	2.1
2	CB	142	LEU	2.1
3	CC	78	GLY	2.1
9	AI	85	LEU	2.1
11	AK	88	GLY	2.1
18	CR	42	ARG	2.1
19	AS	16	LEU	2.1
39	DS	109	GLY	2.1
9	AI	41	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
11	AK	42	TRP	2.1
11	CK	110	ASP	2.1
36	DP	97	PRO	2.1
34	DN	48	MET	2.1
37	DQ	81	VAL	2.1
45	BY	39	VAL	2.1
51	D4	47	GLN	2.1
3	AC	23	TYR	2.1
11	AK	29	ILE	2.1
1	AA	346	G	2.1
10	AJ	9	ARG	2.1
15	AO	78	TYR	2.1
18	CR	34	TYR	2.1
56	D9	17	ILE	2.1
26	DA	2100	G	2.1
2	CB	115	LEU	2.1
4	AD	101	LEU	2.1
6	AF	98	LEU	2.1
13	AM	119	GLY	2.1
36	DP	6	LEU	2.1
39	DS	22	GLY	2.1
40	DT	6	LEU	2.1
1	CA	1030	C	2.0
14	CN	13	THR	2.0
3	CC	107	GLN	2.0
26	BA	1091	A	2.0
9	AI	122	ALA	2.0
10	AJ	27	ALA	2.0
29	DE	198	VAL	2.0
31	DG	4	ASP	2.0
43	DW	48	ALA	2.0
11	CK	14	VAL	2.0
37	BQ	81	VAL	2.0
46	DZ	130	PRO	2.0
46	DZ	154	ASP	2.0
5	CE	136	MET	2.0
17	AQ	24	GLU	2.0
37	DQ	80	GLU	2.0
39	DS	75	GLU	2.0
46	DZ	145	GLU	2.0
50	D3	59	VAL	2.0
48	D1	26	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
9	AI	101	PHE	2.0
10	AJ	63	PHE	2.0
14	CN	21	TYR	2.0
36	DP	73	GLY	2.0
43	DW	9	TYR	2.0
2	CB	158	LEU	2.0
2	CB	213	LEU	2.0
5	CE	142	LEU	2.0
28	DD	203	ASN	2.0
28	DD	206	LEU	2.0
31	DG	27	ASN	2.0
1	AA	1028	C	2.0
2	CB	194	PRO	2.0
4	AD	105	VAL	2.0
15	AO	19	PRO	2.0
32	DH	131	VAL	2.0
39	DS	14	VAL	2.0
45	DY	2	ARG	2.0
53	D6	52	VAL	2.0
1	AA	607	A	2.0
46	DZ	28	MET	2.0
4	AD	16	GLY	2.0
10	CJ	52	GLY	2.0
11	CK	90	GLY	2.0
12	CL	95	GLY	2.0
13	CM	22	ILE	2.0
33	BI	97	ILE	2.0
46	DZ	91	LEU	2.0
53	D6	11	LEU	2.0
3	CC	31	HIS	2.0
45	DY	6	HIS	2.0
9	AI	7	THR	2.0
11	AK	92	GLU	2.0
10	CJ	29	ARG	2.0
31	DG	22	ARG	2.0
3	CC	66	VAL	2.0
10	CJ	14	LYS	2.0
1	AA	347	G	2.0
3	AC	128	PHE	2.0
5	AE	136	MET	2.0
26	BA	2134	G	2.0
28	DD	21	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	CA	979	C	2.0
16	CP	73	LEU	2.0
31	DG	94	LEU	2.0
33	BI	101	LEU	2.0
18	CR	46	GLU	2.0
46	DZ	13	GLU	2.0
19	CS	78	ARG	2.0
21	AU	6	ARG	2.0
36	DP	77	ARG	2.0
1	CA	1446	U	2.0
11	CK	51	LYS	2.0
12	CL	94	PRO	2.0
31	DG	61	ALA	2.0
54	B7	45	ALA	2.0
3	CC	151	VAL	2.0
39	DS	28	VAL	2.0
43	DW	85	VAL	2.0
46	BZ	139	VAL	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
23	PSU	AW	32	20/21	0.23	-	77,84,98,106	0
23	MIA	AW	37	29/30	0.22	-	56,65,80,82	0
23	MIA	CW	37	22/30	0.29	-	72,86,92,96	0
24	31H	AX	76	32/33	0.31	-	31,57,76,77	10
23	7MG	AW	46	24/25	0.17	-	80,97,112,135	0
25	7MG	AY	46	24/25	0.20	-	80,99,107,116	0
24	4SU	CX	8	20/21	0.13	-	84,92,105,111	0
25	PSU	CY	32	20/21	0.23	-	77,91,109,114	0
23	PSU	CW	32	20/21	0.55	-	77,86,95,106	0
23	PSU	AW	55	20/21	0.20	-	76,88,103,105	0
25	PSU	CY	55	20/21	0.40	-	86,100,107,118	0
25	PSU	AY	55	20/21	0.18	-	85,96,106,117	0
23	5MU	AW	54	21/22	0.17	-	66,80,87,93	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
24	5MC	AX	32	21/22	0.16	-	50,57,69,76	0
23	4SU	AW	8	20/21	0.12	-	83,89,107,110	0
23	PSU	AW	39	20/21	0.18	-	71,82,92,93	0
25	MIA	AY	37	22/30	0.18	-	79,89,101,116	0
24	5MU	CX	54	21/22	0.15	-	71,85,94,104	0
24	5MC	CX	32	21/22	0.16	-	63,77,85,87	0
23	F3N	CW	76	33/34	0.45	-	53,69,79,80	0
25	PSU	AY	32	20/21	0.21	-	76,92,107,110	0
24	PSU	CX	55	20/21	0.12	-	81,87,92,97	0
23	5MU	CW	54	21/22	0.17	-	76,87,97,99	0
23	PSU	CW	55	20/21	0.24	-	76,90,103,106	0
25	4SU	CY	8	20/21	0.14	-	88,102,112,128	0
23	F3N	AW	76	33/34	0.33	-	44,58,72,77	0
24	PSU	AX	55	20/21	0.15	-	52,69,77,77	0
25	4SU	AY	8	20/21	0.12	-	83,95,104,129	0
25	5MU	CY	54	21/22	0.52	-	89,99,105,136	0
23	4SU	CW	8	20/21	0.23	-	85,96,117,121	0
25	PSU	CY	39	20/21	0.23	-	86,91,104,110	0
25	MIA	CY	37	22/30	0.26	-	79,95,102,124	0
25	5MU	AY	54	21/22	0.15	-	81,89,99,128	0
24	4SU	AX	8	20/21	0.16	-	59,69,79,85	0
23	7MG	CW	46	24/25	0.27	-	81,97,101,125	0
25	7MG	CY	46	24/25	0.21	-	87,101,108,135	0
23	PSU	CW	39	20/21	0.41	-	76,85,92,95	0
24	5MU	AX	54	21/22	0.15	-	46,72,77,86	0
25	PSU	AY	39	20/21	0.20	-	84,90,102,107	0
24	31H	CX	76	32/33	0.34	-	48,68,88,99	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(\AA^2)	Q<0.9
57	MG	BA	3605	1/1	0.17	-	47,47,47,47	0
57	MG	BA	3126	1/1	0.22	-	36,36,36,36	0
57	MG	DA	3442	1/1	0.16	-	64,64,64,64	0
57	MG	DA	3401	1/1	0.05	-	69,69,69,69	0
57	MG	DA	3487	1/1	0.11	-	55,55,55,55	0
57	MG	AA	1643	1/1	0.15	-	58,58,58,58	0
57	MG	BA	3583	1/1	0.12	-	33,33,33,33	0
57	MG	DA	3007	1/1	0.10	-	30,30,30,30	0
57	MG	DA	3207	1/1	0.12	-	48,48,48,48	0
57	MG	DA	3014	1/1	0.23	-	44,44,44,44	0
57	MG	DA	3482	1/1	0.13	-	60,60,60,60	0
57	MG	AX	3011	1/1	0.11	-	60,60,60,60	0
57	MG	BA	3688	1/1	0.25	-	61,61,61,61	0
57	MG	DA	3523	1/1	0.13	-	39,39,39,39	0
57	MG	BF	310	1/1	0.20	-	56,56,56,56	0
57	MG	AA	1656	1/1	0.18	-	63,63,63,63	0
57	MG	BA	3016	1/1	0.26	-	67,67,67,67	0
57	MG	DA	3345	1/1	0.11	-	58,58,58,58	0
57	MG	BA	3285	1/1	0.12	-	58,58,58,58	0
57	MG	DA	3552	1/1	0.12	-	34,34,34,34	0
57	MG	DA	3532	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3568	1/1	0.23	-	24,24,24,24	0
57	MG	DA	3652	1/1	0.12	-	31,31,31,31	0
57	MG	CA	3100	1/1	0.10	-	59,59,59,59	0
57	MG	DA	3296	1/1	0.08	-	60,60,60,60	0
57	MG	BA	3570	1/1	0.18	-	31,31,31,31	0
57	MG	AA	1746	1/1	0.12	-	56,56,56,56	0
57	MG	DA	3174	1/1	0.15	-	52,52,52,52	0
57	MG	AA	1672	1/1	0.19	-	45,45,45,45	0
57	MG	BB	3005	1/1	0.21	-	51,51,51,51	0
57	MG	CA	3073	1/1	0.17	-	55,55,55,55	0
57	MG	CA	3169	1/1	0.30	-	62,62,62,62	0
57	MG	B9	502	1/1	0.33	-	46,46,46,46	0
57	MG	DA	3312	1/1	0.12	-	42,42,42,42	0
57	MG	BA	3586	1/1	0.09	-	55,55,55,55	0
57	MG	BA	3512	1/1	0.18	-	23,23,23,23	0
57	MG	CA	3013	1/1	0.10	-	67,67,67,67	0
57	MG	DA	3261	1/1	0.14	-	39,39,39,39	0
57	MG	CA	3041	1/1	0.10	-	57,57,57,57	0
57	MG	BA	3603	1/1	0.25	-	42,42,42,42	0
57	MG	DA	3194	1/1	0.14	-	48,48,48,48	0
57	MG	DW	3001	1/1	0.21	-	41,41,41,41	0
57	MG	BV	203	1/1	0.18	-	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3679	1/1	0.18	-	52,52,52,52	0
57	MG	AA	1742	1/1	0.13	-	52,52,52,52	0
57	MG	BA	3013	1/1	0.14	-	28,28,28,28	0
57	MG	BA	3007	1/1	0.17	-	21,21,21,21	0
57	MG	BA	3290	1/1	0.17	-	57,57,57,57	0
57	MG	BA	3019	1/1	0.24	-	54,54,54,54	0
57	MG	BB	3019	1/1	0.17	-	70,70,70,70	0
57	MG	DA	3051	1/1	0.08	-	44,44,44,44	0
57	MG	BR	5002	1/1	0.17	-	50,50,50,50	0
57	MG	AA	1807	1/1	0.07	-	68,68,68,68	0
57	MG	BA	3425	1/1	0.22	-	48,48,48,48	0
57	MG	BA	3734	1/1	0.13	-	65,65,65,65	0
57	MG	DA	3445	1/1	0.10	-	52,52,52,52	0
57	MG	AA	1654	1/1	0.23	-	65,65,65,65	0
57	MG	DA	3348	1/1	0.21	-	53,53,53,53	0
57	MG	BA	3357	1/1	0.05	-	34,34,34,34	0
57	MG	BA	3757	1/1	0.28	-	43,43,43,43	0
57	MG	BA	3494	1/1	0.08	-	38,38,38,38	0
57	MG	CA	3034	1/1	0.18	-	66,66,66,66	0
57	MG	BA	3694	1/1	0.22	-	53,53,53,53	0
57	MG	BA	3783	1/1	0.13	-	37,37,37,37	0
57	MG	DA	3175	1/1	0.09	-	41,41,41,41	0
57	MG	AA	1801	1/1	0.06	-	71,71,71,71	0
57	MG	AA	1798	1/1	0.12	-	62,62,62,62	0
57	MG	DA	3213	1/1	0.21	-	37,37,37,37	0
57	MG	DA	3291	1/1	0.13	-	36,36,36,36	0
57	MG	BA	3747	1/1	0.22	-	55,55,55,55	0
57	MG	BA	3323	1/1	0.18	-	57,57,57,57	0
57	MG	AA	1731	1/1	0.13	-	56,56,56,56	0
57	MG	DA	3350	1/1	0.15	-	31,31,31,31	0
57	MG	DA	3252	1/1	0.09	-	50,50,50,50	0
57	MG	BA	3057	1/1	0.16	-	48,48,48,48	0
57	MG	DA	3278	1/1	0.07	-	39,39,39,39	0
57	MG	BA	3071	1/1	0.20	-	59,59,59,59	0
57	MG	DA	3551	1/1	0.16	-	49,49,49,49	0
57	MG	DA	3074	1/1	0.04	-	59,59,59,59	0
57	MG	BB	3021	1/1	0.20	-	41,41,41,41	0
57	MG	DA	3574	1/1	0.06	-	61,61,61,61	0
57	MG	BA	3356	1/1	0.20	-	31,31,31,31	0
57	MG	BA	3225	1/1	0.12	-	46,46,46,46	0
57	MG	DA	3583	1/1	0.16	-	52,52,52,52	0
57	MG	CA	3063	1/1	0.21	-	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	AA	1697	1/1	0.11	-	65,65,65,65	0
57	MG	AA	1757	1/1	0.25	-	68,68,68,68	0
57	MG	BA	3529	1/1	0.23	-	24,24,24,24	0
57	MG	BA	3183	1/1	0.58	-	49,49,49,49	0
57	MG	BB	3008	1/1	0.29	-	59,59,59,59	0
57	MG	BA	3123	1/1	0.09	-	43,43,43,43	0
57	MG	CK	5001	1/1	0.11	-	61,61,61,61	0
57	MG	BA	3206	1/1	0.13	-	34,34,34,34	0
57	MG	BA	3760	1/1	0.14	-	50,50,50,50	0
57	MG	BA	3358	1/1	0.15	-	52,52,52,52	0
57	MG	CA	3096	1/1	0.15	-	43,43,43,43	0
57	MG	DA	3571	1/1	0.29	-	45,45,45,45	0
57	MG	DA	3173	1/1	0.22	-	62,62,62,62	0
59	ZN	B6	102	1/1	0.23	-	50,50,50,50	0
57	MG	AA	1815	1/1	0.12	-	47,47,47,47	0
57	MG	BA	3027	1/1	0.37	-	64,64,64,64	0
57	MG	DA	3032	1/1	0.20	-	57,57,57,57	0
57	MG	DA	3361	1/1	0.08	-	33,33,33,33	0
57	MG	AA	1710	1/1	0.13	-	64,64,64,64	0
57	MG	BA	3547	1/1	0.14	-	45,45,45,45	0
57	MG	AA	1795	1/1	0.17	-	55,55,55,55	0
57	MG	AU	101	1/1	0.09	-	56,56,56,56	0
57	MG	BA	3588	1/1	0.10	-	43,43,43,43	0
57	MG	BA	3054	1/1	0.19	-	30,30,30,30	0
57	MG	DN	5001	1/1	0.11	-	63,63,63,63	0
57	MG	AA	1639	1/1	0.06	-	54,54,54,54	0
57	MG	AA	1677	1/1	0.22	-	43,43,43,43	0
57	MG	BA	3593	1/1	0.15	-	55,55,55,55	0
57	MG	DR	3001	1/1	0.15	-	49,49,49,49	0
57	MG	DA	3527	1/1	0.13	-	52,52,52,52	0
57	MG	DA	3304	1/1	0.15	-	42,42,42,42	0
57	MG	BA	3219	1/1	0.49	-	58,58,58,58	0
57	MG	AA	1606	1/1	0.12	-	54,54,54,54	0
57	MG	DA	3314	1/1	0.11	-	43,43,43,43	0
57	MG	BZ	302	1/1	0.11	-	60,60,60,60	0
57	MG	DA	3419	1/1	0.09	-	50,50,50,50	0
57	MG	DA	3573	1/1	0.06	-	61,61,61,61	0
57	MG	B0	3002	1/1	0.18	-	63,63,63,63	0
57	MG	BF	303	1/1	0.21	-	33,33,33,33	0
57	MG	DA	3117	1/1	0.06	-	56,56,56,56	0
57	MG	BA	3791	1/1	0.33	-	49,49,49,49	0
57	MG	BA	3431	1/1	0.26	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3383	1/1	0.14	-	37,37,37,37	0
57	MG	BA	3558	1/1	0.13	-	51,51,51,51	0
57	MG	CA	3010	1/1	0.06	-	49,49,49,49	0
57	MG	CA	3040	1/1	0.11	-	56,56,56,56	0
57	MG	BA	3811	1/1	0.20	-	48,48,48,48	0
57	MG	BA	3714	1/1	0.09	-	46,46,46,46	0
57	MG	BA	3049	1/1	0.16	-	46,46,46,46	0
57	MG	BA	3669	1/1	0.19	-	28,28,28,28	0
57	MG	BF	309	1/1	0.21	-	31,31,31,31	0
57	MG	DA	3232	1/1	0.17	-	56,56,56,56	0
57	MG	DB	3010	1/1	0.08	-	75,75,75,75	0
57	MG	DA	3366	1/1	0.10	-	44,44,44,44	0
57	MG	BA	3061	1/1	0.24	-	25,25,25,25	0
57	MG	DA	3101	1/1	0.22	-	56,56,56,56	0
57	MG	DA	3335	1/1	0.19	-	49,49,49,49	0
57	MG	BA	3627	1/1	0.15	-	56,56,56,56	0
57	MG	BA	3134	1/1	0.18	-	40,40,40,40	0
57	MG	AA	1716	1/1	0.15	-	50,50,50,50	0
57	MG	DA	3103	1/1	0.17	-	56,56,56,56	0
57	MG	BA	3424	1/1	0.25	-	31,31,31,31	0
57	MG	AA	1651	1/1	0.24	-	58,58,58,58	0
57	MG	DA	3609	1/1	0.17	-	61,61,61,61	0
57	MG	DA	3030	1/1	0.11	-	44,44,44,44	0
57	MG	BA	3042	1/1	0.08	-	37,37,37,37	0
57	MG	BA	3261	1/1	0.14	-	18,18,18,18	0
57	MG	BA	3463	1/1	0.24	-	56,56,56,56	0
57	MG	BA	3191	1/1	0.16	-	40,40,40,40	0
57	MG	CA	3139	1/1	0.33	-	81,81,81,81	0
57	MG	CA	3114	1/1	0.12	-	71,71,71,71	0
57	MG	AA	1814	1/1	0.18	-	57,57,57,57	0
57	MG	BA	3346	1/1	0.07	-	39,39,39,39	0
57	MG	DA	3464	1/1	0.28	-	54,54,54,54	0
57	MG	DA	3039	1/1	0.11	-	38,38,38,38	0
57	MG	B6	103	1/1	0.12	-	52,52,52,52	0
57	MG	DA	3203	1/1	0.14	-	53,53,53,53	0
57	MG	AA	1741	1/1	0.12	-	86,86,86,86	0
57	MG	DA	3381	1/1	0.10	-	40,40,40,40	0
57	MG	BA	3288	1/1	0.16	-	44,44,44,44	0
57	MG	DA	3170	1/1	0.11	-	35,35,35,35	0
57	MG	DA	3560	1/1	0.15	-	60,60,60,60	0
57	MG	CA	3002	1/1	0.17	-	77,77,77,77	0
57	MG	DA	3512	1/1	0.11	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3539	1/1	0.08	-	55,55,55,55	0
57	MG	DA	3042	1/1	0.27	-	49,49,49,49	0
57	MG	BD	3008	1/1	0.27	-	45,45,45,45	0
57	MG	DA	3662	1/1	0.19	-	50,50,50,50	0
59	ZN	B4	501	1/1	0.09	-	118,118,118,118	0
57	MG	DA	3558	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3159	1/1	0.13	-	27,27,27,27	0
57	MG	BA	3370	1/1	0.14	-	50,50,50,50	0
57	MG	DA	3410	1/1	0.20	-	40,40,40,40	0
57	MG	DA	3623	1/1	0.12	-	45,45,45,45	0
57	MG	AA	1684	1/1	0.11	-	54,54,54,54	0
57	MG	BA	3788	1/1	0.18	-	44,44,44,44	0
57	MG	AA	1721	1/1	0.14	-	57,57,57,57	0
57	MG	AA	1806	1/1	0.16	-	74,74,74,74	0
59	ZN	AN	501	1/1	0.16	-	77,77,77,77	0
57	MG	BA	3034	1/1	0.17	-	35,35,35,35	0
57	MG	AA	1601	1/1	0.14	-	81,81,81,81	0
57	MG	DO	201	1/1	0.08	-	49,49,49,49	0
57	MG	BA	3680	1/1	0.31	-	42,42,42,42	0
57	MG	CA	3039	1/1	0.09	-	64,64,64,64	0
57	MG	DA	3288	1/1	0.14	-	39,39,39,39	0
57	MG	AL	201	1/1	0.11	-	63,63,63,63	0
57	MG	DA	3629	1/1	0.12	-	57,57,57,57	0
57	MG	AN	503	1/1	0.15	-	52,52,52,52	0
57	MG	DA	3298	1/1	0.15	-	55,55,55,55	0
57	MG	BA	3636	1/1	0.13	-	66,66,66,66	0
57	MG	BA	3109	1/1	0.08	-	56,56,56,56	0
57	MG	BA	3545	1/1	0.18	-	28,28,28,28	0
57	MG	BA	3270	1/1	0.22	-	56,56,56,56	0
57	MG	DA	3599	1/1	0.09	-	48,48,48,48	0
57	MG	BG	202	1/1	0.13	-	52,52,52,52	0
57	MG	BA	3340	1/1	0.15	-	27,27,27,27	0
57	MG	BA	3119	1/1	0.09	-	46,46,46,46	0
57	MG	CA	3113	1/1	0.13	-	47,47,47,47	0
57	MG	AA	1767	1/1	0.09	-	67,67,67,67	0
57	MG	AA	1788	1/1	0.06	-	75,75,75,75	0
57	MG	BA	3589	1/1	0.20	-	59,59,59,59	0
57	MG	DA	3465	1/1	0.17	-	42,42,42,42	0
57	MG	DA	3272	1/1	0.14	-	49,49,49,49	0
57	MG	CA	3032	1/1	0.11	-	53,53,53,53	0
57	MG	DA	3130	1/1	0.12	-	52,52,52,52	0
59	ZN	BY	501	1/1	0.16	-	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	3468	1/1	0.15	-	45,45,45,45	0
57	MG	AA	1754	1/1	0.16	-	58,58,58,58	0
57	MG	BA	3291	1/1	0.25	-	53,53,53,53	0
57	MG	DA	3480	1/1	0.11	-	58,58,58,58	0
57	MG	BA	3447	1/1	0.24	-	52,52,52,52	0
57	MG	DA	3239	1/1	0.10	-	49,49,49,49	0
57	MG	DB	3004	1/1	0.20	-	63,63,63,63	0
57	MG	BA	3347	1/1	0.16	-	38,38,38,38	0
57	MG	BA	3229	1/1	0.20	-	52,52,52,52	0
57	MG	CA	3095	1/1	0.10	-	71,71,71,71	0
57	MG	DA	3146	1/1	0.06	-	54,54,54,54	0
57	MG	BA	3417	1/1	0.21	-	24,24,24,24	0
57	MG	BA	3384	1/1	0.10	-	45,45,45,45	0
57	MG	BA	3571	1/1	0.22	-	28,28,28,28	0
57	MG	BA	3794	1/1	0.11	-	37,37,37,37	0
57	MG	BA	3211	1/1	0.14	-	43,43,43,43	0
57	MG	BA	3656	1/1	0.12	-	45,45,45,45	0
57	MG	CA	3166	1/1	0.14	-	55,55,55,55	0
57	MG	AA	1706	1/1	0.18	-	60,60,60,60	0
57	MG	CA	3036	1/1	0.17	-	73,73,73,73	0
57	MG	DA	3229	1/1	0.12	-	38,38,38,38	0
57	MG	DA	3388	1/1	0.22	-	47,47,47,47	0
57	MG	DA	3467	1/1	0.23	-	52,52,52,52	0
57	MG	DE	3004	1/1	0.15	-	31,31,31,31	0
57	MG	BA	3276	1/1	0.49	-	44,44,44,44	0
57	MG	CA	3054	1/1	0.32	-	69,69,69,69	0
57	MG	DB	3002	1/1	0.26	-	63,63,63,63	0
57	MG	DA	3233	1/1	0.14	-	65,65,65,65	0
57	MG	BA	3576	1/1	0.20	-	30,30,30,30	0
57	MG	BA	3079	1/1	0.30	-	58,58,58,58	0
57	MG	BA	3487	1/1	0.11	-	54,54,54,54	0
57	MG	BA	3224	1/1	0.24	-	59,59,59,59	0
57	MG	DG	3001	1/1	0.09	-	66,66,66,66	0
57	MG	DA	3514	1/1	0.13	-	47,47,47,47	0
57	MG	CA	3031	1/1	0.10	-	58,58,58,58	0
57	MG	BA	3155	1/1	0.17	-	40,40,40,40	0
57	MG	BB	3009	1/1	0.07	-	57,57,57,57	0
57	MG	DA	3456	1/1	0.24	-	38,38,38,38	0
57	MG	BA	3502	1/1	0.16	-	30,30,30,30	0
57	MG	AA	1653	1/1	0.21	-	54,54,54,54	0
57	MG	DA	3548	1/1	0.15	-	66,66,66,66	0
57	MG	DA	3302	1/1	0.18	-	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	3813	1/1	0.19	-	29,29,29,29	0
57	MG	CA	3052	1/1	0.09	-	71,71,71,71	0
57	MG	BA	3452	1/1	0.11	-	56,56,56,56	0
57	MG	BA	3264	1/1	0.16	-	51,51,51,51	0
57	MG	CA	3066	1/1	0.08	-	48,48,48,48	0
57	MG	DA	3561	1/1	0.11	-	52,52,52,52	0
57	MG	BA	3194	1/1	0.19	-	39,39,39,39	0
57	MG	DA	3370	1/1	0.12	-	59,59,59,59	0
57	MG	BA	3069	1/1	0.24	-	48,48,48,48	0
57	MG	DA	3510	1/1	0.23	-	64,64,64,64	0
59	ZN	DY	501	1/1	0.11	-	90,90,90,90	0
57	MG	DA	3579	1/1	0.14	-	62,62,62,62	0
57	MG	BA	3102	1/1	0.24	-	57,57,57,57	0
57	MG	DA	3050	1/1	0.21	-	44,44,44,44	0
57	MG	BA	3727	1/1	0.22	-	53,53,53,53	0
57	MG	DB	3003	1/1	0.09	-	78,78,78,78	0
57	MG	BA	3199	1/1	0.27	-	64,64,64,64	0
57	MG	DA	3092	1/1	0.12	-	57,57,57,57	0
57	MG	DA	3435	1/1	0.11	-	44,44,44,44	0
57	MG	BA	3310	1/1	0.20	-	26,26,26,26	0
57	MG	BA	3204	1/1	0.26	-	67,67,67,67	0
57	MG	DA	3075	1/1	0.07	-	55,55,55,55	0
57	MG	BA	3400	1/1	0.23	-	39,39,39,39	0
57	MG	DA	3185	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3212	1/1	0.20	-	62,62,62,62	0
57	MG	BA	3768	1/1	0.09	-	57,57,57,57	0
57	MG	BA	3133	1/1	0.25	-	37,37,37,37	0
57	MG	BA	3036	1/1	0.10	-	56,56,56,56	0
59	ZN	D5	501	1/1	0.17	-	57,57,57,57	0
57	MG	BA	3657	1/1	0.10	-	38,38,38,38	0
57	MG	BA	3022	1/1	0.10	-	25,25,25,25	0
57	MG	DA	3642	1/1	0.13	-	62,62,62,62	0
57	MG	BA	3500	1/1	0.16	-	57,57,57,57	0
57	MG	DA	3486	1/1	0.25	-	57,57,57,57	0
57	MG	BQ	3001	1/1	0.19	-	37,37,37,37	0
57	MG	BD	3005	1/1	0.19	-	44,44,44,44	0
57	MG	BA	3331	1/1	0.17	-	53,53,53,53	0
57	MG	DA	3422	1/1	0.26	-	62,62,62,62	0
57	MG	BA	3336	1/1	0.12	-	20,20,20,20	0
57	MG	BA	3230	1/1	0.22	-	58,58,58,58	0
57	MG	DQ	3003	1/1	0.66	-	62,62,62,62	0
57	MG	BA	3365	1/1	0.13	-	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	DA	3144	1/1	0.10	-	41,41,41,41	0
57	MG	BA	3437	1/1	0.21	-	62,62,62,62	0
57	MG	BA	3597	1/1	0.20	-	55,55,55,55	0
57	MG	DA	3107	1/1	0.08	-	61,61,61,61	0
57	MG	DA	3002	1/1	0.12	-	64,64,64,64	0
57	MG	DA	3585	1/1	0.30	-	55,55,55,55	0
57	MG	BA	3564	1/1	0.08	-	44,44,44,44	0
57	MG	DA	3004	1/1	0.14	-	53,53,53,53	0
57	MG	AA	1712	1/1	0.13	-	69,69,69,69	0
57	MG	CA	3046	1/1	0.17	-	61,61,61,61	0
57	MG	BA	3611	1/1	0.16	-	59,59,59,59	0
57	MG	CA	3135	1/1	0.09	-	59,59,59,59	0
57	MG	BA	3009	1/1	0.13	-	31,31,31,31	0
57	MG	BA	3325	1/1	0.13	-	45,45,45,45	0
57	MG	AA	1714	1/1	0.16	-	56,56,56,56	0
57	MG	DB	3005	1/1	0.14	-	68,68,68,68	0
57	MG	DA	3451	1/1	0.07	-	55,55,55,55	0
57	MG	BA	3538	1/1	0.14	-	68,68,68,68	0
57	MG	CA	3120	1/1	0.10	-	68,68,68,68	0
57	MG	DA	3383	1/1	0.13	-	28,28,28,28	0
57	MG	CA	3020	1/1	0.15	-	45,45,45,45	0
57	MG	BA	3227	1/1	0.14	-	33,33,33,33	0
57	MG	DA	3397	1/1	0.12	-	42,42,42,42	0
57	MG	BA	3212	1/1	0.21	-	57,57,57,57	0
57	MG	AA	1657	1/1	0.09	-	64,64,64,64	0
57	MG	AA	1621	1/1	0.11	-	44,44,44,44	0
57	MG	BA	3446	1/1	0.08	-	59,59,59,59	0
57	MG	BA	3258	1/1	0.45	-	44,44,44,44	0
57	MG	DA	3041	1/1	0.28	-	60,60,60,60	0
57	MG	B7	105	1/1	0.21	-	28,28,28,28	0
57	MG	DA	3242	1/1	0.07	-	52,52,52,52	0
57	MG	BA	3277	1/1	0.50	-	52,52,52,52	0
57	MG	BA	3519	1/1	0.16	-	45,45,45,45	0
57	MG	BA	3218	1/1	0.11	-	45,45,45,45	0
57	MG	AA	1709	1/1	0.22	-	55,55,55,55	0
57	MG	AA	1664	1/1	0.17	-	62,62,62,62	0
57	MG	BA	3806	1/1	0.14	-	43,43,43,43	0
57	MG	CA	3115	1/1	0.19	-	82,82,82,82	0
57	MG	BP	3002	1/1	0.15	-	60,60,60,60	0
57	MG	DA	3414	1/1	0.14	-	42,42,42,42	0
57	MG	DA	3582	1/1	0.04	-	53,53,53,53	0
57	MG	BA	3106	1/1	0.24	-	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	3298	1/1	0.13	-	27,27,27,27	0
57	MG	CA	3028	1/1	0.25	-	48,48,48,48	0
57	MG	DA	3379	1/1	0.14	-	46,46,46,46	0
57	MG	DA	3008	1/1	0.08	-	45,45,45,45	0
57	MG	AA	1816	1/1	0.21	-	59,59,59,59	0
57	MG	B7	103	1/1	0.31	-	40,40,40,40	0
57	MG	DA	3171	1/1	0.13	-	40,40,40,40	0
57	MG	DA	3491	1/1	0.22	-	43,43,43,43	0
57	MG	DA	3323	1/1	0.20	-	49,49,49,49	0
57	MG	DA	3614	1/1	0.14	-	55,55,55,55	0
57	MG	DA	3640	1/1	0.08	-	62,62,62,62	0
57	MG	DA	3349	1/1	0.14	-	34,34,34,34	0
57	MG	DA	3468	1/1	0.17	-	62,62,62,62	0
57	MG	DA	3369	1/1	0.13	-	55,55,55,55	0
57	MG	DA	3374	1/1	0.18	-	62,62,62,62	0
57	MG	CA	3025	1/1	0.16	-	53,53,53,53	0
57	MG	AA	1792	1/1	0.07	-	47,47,47,47	0
57	MG	BA	3472	1/1	0.19	-	24,24,24,24	0
57	MG	BA	3536	1/1	0.11	-	32,32,32,32	0
57	MG	DA	3329	1/1	0.09	-	47,47,47,47	0
57	MG	DA	3555	1/1	0.17	-	46,46,46,46	0
57	MG	AA	1612	1/1	0.15	-	63,63,63,63	0
57	MG	DA	3215	1/1	0.19	-	40,40,40,40	0
57	MG	DA	3306	1/1	0.25	-	65,65,65,65	0
57	MG	D0	101	1/1	0.15	-	71,71,71,71	0
57	MG	DA	3067	1/1	0.12	-	63,63,63,63	0
57	MG	AA	1802	1/1	0.06	-	54,54,54,54	0
57	MG	DA	3327	1/1	0.17	-	45,45,45,45	0
57	MG	BA	3201	1/1	0.11	-	48,48,48,48	0
57	MG	DA	3235	1/1	0.10	-	48,48,48,48	0
57	MG	DA	3646	1/1	0.12	-	56,56,56,56	0
57	MG	DA	3615	1/1	0.05	-	62,62,62,62	0
57	MG	AT	3001	1/1	0.11	-	63,63,63,63	0
57	MG	CA	3014	1/1	0.09	-	62,62,62,62	0
57	MG	DA	3251	1/1	0.11	-	40,40,40,40	0
57	MG	AA	1689	1/1	0.19	-	71,71,71,71	0
57	MG	DA	3098	1/1	0.05	-	66,66,66,66	0
57	MG	BA	3718	1/1	0.14	-	47,47,47,47	0
57	MG	CA	3105	1/1	0.05	-	75,75,75,75	0
57	MG	AA	1770	1/1	0.15	-	51,51,51,51	0
57	MG	DA	3049	1/1	0.06	-	47,47,47,47	0
57	MG	DA	3276	1/1	0.15	-	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	1618	1/1	0.17	-	68,68,68,68	0
57	MG	BA	3303	1/1	0.23	-	26,26,26,26	0
57	MG	AA	1607	1/1	0.12	-	55,55,55,55	0
57	MG	DA	3071	1/1	0.27	-	47,47,47,47	0
57	MG	BA	3070	1/1	0.20	-	41,41,41,41	0
57	MG	BB	3002	1/1	0.26	-	55,55,55,55	0
57	MG	BB	3007	1/1	0.14	-	41,41,41,41	0
57	MG	AA	1698	1/1	0.16	-	58,58,58,58	0
57	MG	AA	1702	1/1	0.25	-	47,47,47,47	0
57	MG	DA	3021	1/1	0.16	-	50,50,50,50	0
57	MG	BA	3569	1/1	0.20	-	56,56,56,56	0
57	MG	DA	3502	1/1	0.23	-	48,48,48,48	0
57	MG	DA	3168	1/1	0.13	-	44,44,44,44	0
57	MG	CA	3001	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3161	1/1	0.18	-	50,50,50,50	0
57	MG	DA	3299	1/1	0.09	-	46,46,46,46	0
57	MG	AX	3008	1/1	0.14	-	76,76,76,76	0
57	MG	AA	1615	1/1	0.20	-	51,51,51,51	0
57	MG	BA	3128	1/1	0.13	-	42,42,42,42	0
57	MG	AX	3003	1/1	0.20	-	56,56,56,56	0
57	MG	BA	3125	1/1	0.22	-	38,38,38,38	0
57	MG	BA	3466	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3147	1/1	0.10	-	44,44,44,44	0
57	MG	BA	3662	1/1	0.20	-	62,62,62,62	0
57	MG	BA	3436	1/1	0.11	-	57,57,57,57	0
57	MG	BA	3666	1/1	0.18	-	74,74,74,74	0
57	MG	CA	3008	1/1	0.27	-	47,47,47,47	0
57	MG	DA	3218	1/1	0.09	-	52,52,52,52	0
57	MG	BA	3284	1/1	0.08	-	57,57,57,57	0
57	MG	AA	1634	1/1	0.12	-	64,64,64,64	0
57	MG	BA	3250	1/1	0.15	-	68,68,68,68	0
57	MG	DA	3280	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3279	1/1	0.23	-	52,52,52,52	0
57	MG	DA	3273	1/1	0.09	-	62,62,62,62	0
57	MG	DA	3405	1/1	0.06	-	47,47,47,47	0
57	MG	BA	3726	1/1	0.17	-	31,31,31,31	0
57	MG	BA	3245	1/1	0.24	-	59,59,59,59	0
57	MG	DA	3192	1/1	0.27	-	34,34,34,34	0
57	MG	DA	3047	1/1	0.12	-	45,45,45,45	0
57	MG	DA	3378	1/1	0.10	-	52,52,52,52	0
57	MG	DA	3224	1/1	0.08	-	39,39,39,39	0
57	MG	BA	3130	1/1	0.43	-	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	3779	1/1	0.16	-	17,17,17,17	0
57	MG	CA	3029	1/1	0.09	-	50,50,50,50	0
57	MG	BA	3691	1/1	0.06	-	43,43,43,43	0
57	MG	DA	3110	1/1	0.06	-	49,49,49,49	0
57	MG	BA	3809	1/1	0.41	-	61,61,61,61	0
57	MG	CA	3058	1/1	0.10	-	66,66,66,66	0
57	MG	BA	3515	1/1	0.14	-	27,27,27,27	0
57	MG	DA	3575	1/1	0.12	-	56,56,56,56	0
57	MG	BA	3077	1/1	0.17	-	15,15,15,15	0
57	MG	BA	3485	1/1	0.23	-	26,26,26,26	0
57	MG	AA	1810	1/1	0.06	-	86,86,86,86	0
57	MG	AA	1661	1/1	0.32	-	54,54,54,54	0
57	MG	BA	3104	1/1	0.18	-	24,24,24,24	0
57	MG	DA	3371	1/1	0.14	-	34,34,34,34	0
57	MG	BA	3785	1/1	0.15	-	56,56,56,56	0
57	MG	B7	102	1/1	0.13	-	41,41,41,41	0
57	MG	BA	3659	1/1	0.09	-	47,47,47,47	0
57	MG	BA	3501	1/1	0.11	-	42,42,42,42	0
57	MG	DA	3125	1/1	0.13	-	56,56,56,56	0
57	MG	DA	3062	1/1	0.06	-	53,53,53,53	0
57	MG	BV	201	1/1	0.39	-	31,31,31,31	0
57	MG	BA	3058	1/1	0.26	-	54,54,54,54	0
57	MG	AA	1715	1/1	0.18	-	45,45,45,45	0
57	MG	BA	3594	1/1	0.13	-	45,45,45,45	0
57	MG	DA	3496	1/1	0.11	-	56,56,56,56	0
57	MG	BA	3135	1/1	0.33	-	56,56,56,56	0
57	MG	DA	3621	1/1	0.54	-	52,52,52,52	0
57	MG	BA	3801	1/1	0.17	-	71,71,71,71	0
57	MG	AA	1803	1/1	0.10	-	46,46,46,46	0
57	MG	BA	3631	1/1	0.25	-	46,46,46,46	0
57	MG	CA	3064	1/1	0.15	-	55,55,55,55	0
57	MG	BA	3051	1/1	0.18	-	37,37,37,37	0
57	MG	AA	1663	1/1	0.10	-	50,50,50,50	0
57	MG	AA	1718	1/1	0.09	-	66,66,66,66	0
57	MG	CA	3145	1/1	0.07	-	65,65,65,65	0
57	MG	BA	3360	1/1	0.21	-	37,37,37,37	0
57	MG	DA	3001	1/1	0.15	-	57,57,57,57	0
57	MG	BA	3304	1/1	0.15	-	39,39,39,39	0
57	MG	BA	3777	1/1	0.10	-	41,41,41,41	0
57	MG	BA	3146	1/1	0.15	-	41,41,41,41	0
57	MG	AA	1733	1/1	0.14	-	50,50,50,50	0
57	MG	BA	3573	1/1	0.22	-	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	CA	3033	1/1	0.05	-	54,54,54,54	0
57	MG	BB	3014	1/1	0.12	-	67,67,67,67	0
57	MG	BW	3002	1/1	0.12	-	58,58,58,58	0
57	MG	DA	3313	1/1	0.11	-	39,39,39,39	0
57	MG	AA	1738	1/1	0.39	-	68,68,68,68	0
57	MG	DA	3613	1/1	0.10	-	56,56,56,56	0
57	MG	BA	3690	1/1	0.10	-	39,39,39,39	0
57	MG	DA	3223	1/1	0.14	-	39,39,39,39	0
57	MG	DA	3392	1/1	0.16	-	53,53,53,53	0
57	MG	CA	3153	1/1	0.10	-	69,69,69,69	0
57	MG	DA	3597	1/1	0.11	-	48,48,48,48	0
57	MG	BA	3248	1/1	0.12	-	67,67,67,67	0
57	MG	BA	3674	1/1	0.38	-	48,48,48,48	0
57	MG	BE	303	1/1	0.11	-	43,43,43,43	0
57	MG	DA	3630	1/1	0.13	-	69,69,69,69	0
57	MG	BA	3008	1/1	0.11	-	28,28,28,28	0
57	MG	BA	3306	1/1	0.13	-	15,15,15,15	0
57	MG	CA	3004	1/1	0.07	-	69,69,69,69	0
57	MG	AA	1687	1/1	0.22	-	46,46,46,46	0
57	MG	CA	3086	1/1	0.18	-	93,93,93,93	0
57	MG	BA	3423	1/1	0.14	-	69,69,69,69	0
57	MG	DA	3256	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3351	1/1	0.16	-	56,56,56,56	0
57	MG	BA	3232	1/1	0.20	-	49,49,49,49	0
57	MG	DA	3148	1/1	0.21	-	49,49,49,49	0
57	MG	BA	3321	1/1	0.11	-	53,53,53,53	0
57	MG	BA	3484	1/1	0.10	-	40,40,40,40	0
57	MG	BA	3023	1/1	0.12	-	41,41,41,41	0
57	MG	BA	3711	1/1	0.18	-	44,44,44,44	0
57	MG	DA	3052	1/1	0.07	-	49,49,49,49	0
57	MG	DA	3602	1/1	0.24	-	62,62,62,62	0
57	MG	DA	3634	1/1	0.13	-	68,68,68,68	0
57	MG	BA	3256	1/1	0.36	-	34,34,34,34	0
57	MG	BA	3171	1/1	0.45	-	35,35,35,35	0
57	MG	BA	3648	1/1	0.20	-	58,58,58,58	0
57	MG	CA	3161	1/1	0.12	-	76,76,76,76	0
57	MG	BA	3741	1/1	0.10	-	57,57,57,57	0
57	MG	DA	3206	1/1	0.06	-	50,50,50,50	0
57	MG	BA	3460	1/1	0.10	-	52,52,52,52	0
57	MG	AA	1692	1/1	0.12	-	65,65,65,65	0
57	MG	DA	3255	1/1	0.20	-	47,47,47,47	0
57	MG	BA	3260	1/1	0.11	-	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3775	1/1	0.28	-	39,39,39,39	0
57	MG	CA	3158	1/1	0.16	-	55,55,55,55	0
57	MG	BA	3116	1/1	0.23	-	46,46,46,46	0
57	MG	BA	3746	1/1	0.11	-	78,78,78,78	0
57	MG	BA	3608	1/1	0.25	-	58,58,58,58	0
57	MG	BA	3759	1/1	0.11	-	70,70,70,70	0
57	MG	DA	3457	1/1	0.14	-	44,44,44,44	0
57	MG	DA	3624	1/1	0.45	-	59,59,59,59	0
57	MG	DA	3368	1/1	0.08	-	67,67,67,67	0
57	MG	AA	1809	1/1	0.16	-	42,42,42,42	0
57	MG	BE	306	1/1	0.07	-	38,38,38,38	0
57	MG	BA	3405	1/1	0.14	-	52,52,52,52	0
57	MG	DA	3113	1/1	0.09	-	35,35,35,35	0
57	MG	DA	3149	1/1	0.08	-	46,46,46,46	0
57	MG	BA	3664	1/1	0.20	-	69,69,69,69	0
57	MG	DA	3188	1/1	0.23	-	35,35,35,35	0
57	MG	AA	1673	1/1	0.11	-	48,48,48,48	0
57	MG	DA	3246	1/1	0.05	-	46,46,46,46	0
57	MG	DA	3332	1/1	0.15	-	46,46,46,46	0
57	MG	DA	3338	1/1	0.08	-	44,44,44,44	0
57	MG	DA	3542	1/1	0.26	-	60,60,60,60	0
57	MG	DA	3412	1/1	0.10	-	41,41,41,41	0
57	MG	AA	1793	1/1	0.15	-	63,63,63,63	0
57	MG	BA	3792	1/1	0.15	-	52,52,52,52	0
57	MG	BA	3739	1/1	0.07	-	21,21,21,21	0
57	MG	AA	1679	1/1	0.20	-	51,51,51,51	0
57	MG	BA	3324	1/1	0.16	-	60,60,60,60	0
57	MG	DA	3141	1/1	0.10	-	51,51,51,51	0
57	MG	BA	3426	1/1	0.14	-	46,46,46,46	0
57	MG	DA	3616	1/1	0.16	-	63,63,63,63	0
57	MG	DA	3119	1/1	0.17	-	50,50,50,50	0
57	MG	BA	3467	1/1	0.10	-	46,46,46,46	0
57	MG	DA	3347	1/1	0.11	-	35,35,35,35	0
57	MG	CA	3121	1/1	0.07	-	67,67,67,67	0
57	MG	DA	3477	1/1	0.08	-	53,53,53,53	0
57	MG	CA	3123	1/1	0.24	-	61,61,61,61	0
57	MG	AA	1691	1/1	0.27	-	62,62,62,62	0
57	MG	CA	3048	1/1	0.12	-	58,58,58,58	0
57	MG	DA	3167	1/1	0.20	-	40,40,40,40	0
57	MG	BA	3012	1/1	0.20	-	25,25,25,25	0
57	MG	DA	3515	1/1	0.09	-	55,55,55,55	0
57	MG	BF	301	1/1	0.29	-	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3447	1/1	0.15	-	59,59,59,59	0
57	MG	DA	3065	1/1	0.12	-	56,56,56,56	0
57	MG	DA	3309	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3004	1/1	0.16	-	36,36,36,36	0
57	MG	DA	3034	1/1	0.09	-	42,42,42,42	0
57	MG	DA	3564	1/1	0.25	-	53,53,53,53	0
57	MG	AA	1640	1/1	0.17	-	54,54,54,54	0
57	MG	CA	3061	1/1	0.16	-	66,66,66,66	0
57	MG	BA	3168	1/1	0.25	-	45,45,45,45	0
57	MG	BA	3647	1/1	0.10	-	53,53,53,53	0
57	MG	DB	3011	1/1	0.19	-	67,67,67,67	0
57	MG	DA	3645	1/1	0.12	-	64,64,64,64	0
57	MG	BA	3765	1/1	0.21	-	49,49,49,49	0
57	MG	BA	3579	1/1	0.09	-	63,63,63,63	0
57	MG	BA	3239	1/1	0.21	-	47,47,47,47	0
57	MG	DA	3432	1/1	0.17	-	52,52,52,52	0
57	MG	BA	3543	1/1	0.25	-	52,52,52,52	0
57	MG	AA	1680	1/1	0.14	-	51,51,51,51	0
57	MG	CA	3111	1/1	0.19	-	72,72,72,72	0
57	MG	AA	1628	1/1	0.10	-	65,65,65,65	0
57	MG	DA	3430	1/1	0.14	-	47,47,47,47	0
57	MG	AA	1769	1/1	0.19	-	50,50,50,50	0
57	MG	DA	3503	1/1	0.25	-	38,38,38,38	0
57	MG	BA	3482	1/1	0.10	-	51,51,51,51	0
57	MG	BA	3715	1/1	0.19	-	52,52,52,52	0
57	MG	BA	3732	1/1	0.22	-	33,33,33,33	0
57	MG	DA	3198	1/1	0.12	-	52,52,52,52	0
57	MG	DA	3557	1/1	0.14	-	57,57,57,57	0
57	MG	DA	3134	1/1	0.19	-	52,52,52,52	0
57	MG	BA	3401	1/1	0.22	-	26,26,26,26	0
57	MG	BA	3255	1/1	0.15	-	55,55,55,55	0
57	MG	DA	3053	1/1	0.09	-	47,47,47,47	0
57	MG	AA	1608	1/1	0.13	-	43,43,43,43	0
57	MG	DA	3389	1/1	0.13	-	59,59,59,59	0
57	MG	DA	3193	1/1	0.10	-	47,47,47,47	0
57	MG	CE	201	1/1	0.15	-	65,65,65,65	0
57	MG	BA	3808	1/1	0.13	-	38,38,38,38	0
57	MG	BA	3040	1/1	0.21	-	33,33,33,33	0
57	MG	AA	1804	1/1	0.12	-	70,70,70,70	0
57	MG	DB	3001	1/1	0.15	-	63,63,63,63	0
57	MG	BA	3766	1/1	0.11	-	47,47,47,47	0
57	MG	DF	305	1/1	0.45	-	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	BA	3514	1/1	0.16	-	43,43,43,43	0
57	MG	CX	3001	1/1	0.11	-	57,57,57,57	0
57	MG	DA	3322	1/1	0.14	-	42,42,42,42	0
59	ZN	D6	501	1/1	0.17	-	65,65,65,65	0
57	MG	DA	3159	1/1	0.10	-	62,62,62,62	0
57	MG	BA	3505	1/1	0.17	-	53,53,53,53	0
57	MG	DA	3089	1/1	0.11	-	52,52,52,52	0
57	MG	AY	3001	1/1	0.30	-	63,63,63,63	0
57	MG	DA	3509	1/1	0.07	-	49,49,49,49	0
57	MG	AX	3015	1/1	0.24	-	51,51,51,51	0
57	MG	BA	3616	1/1	0.18	-	59,59,59,59	0
57	MG	BA	3546	1/1	0.11	-	68,68,68,68	0
57	MG	DU	201	1/1	0.70	-	58,58,58,58	0
57	MG	DA	3649	1/1	0.14	-	71,71,71,71	0
57	MG	BA	3645	1/1	0.18	-	47,47,47,47	0
57	MG	CA	3168	1/1	0.13	-	41,41,41,41	0
57	MG	DA	3154	1/1	0.06	-	51,51,51,51	0
57	MG	BA	3371	1/1	0.07	-	49,49,49,49	0
57	MG	BA	3148	1/1	0.34	-	38,38,38,38	0
57	MG	DA	3474	1/1	0.11	-	53,53,53,53	0
57	MG	BA	3082	1/1	0.14	-	28,28,28,28	0
57	MG	BA	3029	1/1	0.21	-	36,36,36,36	0
57	MG	DA	3260	1/1	0.14	-	39,39,39,39	0
57	MG	DA	3586	1/1	0.10	-	50,50,50,50	0
57	MG	DD	301	1/1	0.31	-	44,44,44,44	0
57	MG	BA	3736	1/1	0.14	-	22,22,22,22	0
57	MG	BA	3053	1/1	0.22	-	23,23,23,23	0
57	MG	BA	3451	1/1	0.20	-	44,44,44,44	0
57	MG	DA	3301	1/1	0.10	-	63,63,63,63	0
57	MG	CA	3092	1/1	0.21	-	51,51,51,51	0
57	MG	BO	5001	1/1	0.13	-	61,61,61,61	0
57	MG	DA	3547	1/1	0.06	-	48,48,48,48	0
57	MG	BA	3043	1/1	0.18	-	31,31,31,31	0
57	MG	BA	3572	1/1	0.23	-	39,39,39,39	0
57	MG	DA	3627	1/1	0.18	-	57,57,57,57	0
57	MG	CA	3081	1/1	0.15	-	44,44,44,44	0
57	MG	CA	3015	1/1	0.10	-	64,64,64,64	0
57	MG	BA	3458	1/1	0.18	-	59,59,59,59	0
57	MG	BA	3144	1/1	0.22	-	41,41,41,41	0
57	MG	DA	3417	1/1	0.14	-	52,52,52,52	0
57	MG	BA	3406	1/1	0.10	-	56,56,56,56	0
57	MG	CA	3099	1/1	0.10	-	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	BQ	3002	1/1	0.21	-	46,46,46,46	0
57	MG	DA	3123	1/1	0.09	-	54,54,54,54	0
57	MG	DA	3316	1/1	0.22	-	57,57,57,57	0
57	MG	AA	1768	1/1	0.10	-	53,53,53,53	0
57	MG	AA	1670	1/1	0.14	-	67,67,67,67	0
57	MG	BA	3099	1/1	0.22	-	61,61,61,61	0
57	MG	BA	3441	1/1	0.18	-	39,39,39,39	0
57	MG	BA	3422	1/1	0.15	-	36,36,36,36	0
57	MG	DA	3420	1/1	0.10	-	49,49,49,49	0
57	MG	DA	3162	1/1	0.15	-	57,57,57,57	0
57	MG	BA	3607	1/1	0.14	-	36,36,36,36	0
57	MG	BF	306	1/1	0.27	-	49,49,49,49	0
57	MG	CA	3062	1/1	0.14	-	64,64,64,64	0
57	MG	DA	3460	1/1	0.15	-	37,37,37,37	0
57	MG	BA	3002	1/1	0.21	-	53,53,53,53	0
57	MG	BA	3710	1/1	0.69	-	65,65,65,65	0
57	MG	BA	3037	1/1	0.25	-	42,42,42,42	0
57	MG	DA	3010	1/1	0.07	-	41,41,41,41	0
57	MG	BA	3167	1/1	0.08	-	45,45,45,45	0
57	MG	AA	1739	1/1	0.17	-	72,72,72,72	0
57	MG	CA	3035	1/1	0.08	-	53,53,53,53	0
57	MG	BB	3012	1/1	0.18	-	56,56,56,56	0
57	MG	AK	3101	1/1	0.09	-	69,69,69,69	0
57	MG	DA	3181	1/1	0.09	-	49,49,49,49	0
57	MG	BY	502	1/1	0.17	-	46,46,46,46	0
57	MG	BA	3549	1/1	0.13	-	66,66,66,66	0
57	MG	DA	3595	1/1	0.12	-	57,57,57,57	0
57	MG	BA	3122	1/1	0.12	-	35,35,35,35	0
57	MG	DA	3176	1/1	0.21	-	38,38,38,38	0
57	MG	BA	3498	1/1	0.17	-	45,45,45,45	0
57	MG	AA	1787	1/1	0.13	-	49,49,49,49	0
57	MG	B5	102	1/1	0.24	-	43,43,43,43	0
57	MG	DA	3140	1/1	0.08	-	64,64,64,64	0
57	MG	BA	3439	1/1	0.17	-	36,36,36,36	0
57	MG	DA	3611	1/1	0.11	-	53,53,53,53	0
57	MG	AA	1671	1/1	0.10	-	60,60,60,60	0
57	MG	B7	101	1/1	0.09	-	41,41,41,41	0
57	MG	DA	3394	1/1	0.05	-	60,60,60,60	0
57	MG	AA	1629	1/1	0.29	-	68,68,68,68	0
57	MG	BA	3032	1/1	0.22	-	33,33,33,33	0
57	MG	CA	3164	1/1	0.22	-	76,76,76,76	0
57	MG	DA	3282	1/1	0.10	-	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	BA	3271	1/1	0.14	-	60,60,60,60	0
57	MG	AA	1622	1/1	0.17	-	69,69,69,69	0
57	MG	AA	1647	1/1	0.23	-	44,44,44,44	0
57	MG	DA	3635	1/1	0.11	-	43,43,43,43	0
57	MG	BA	3114	1/1	0.20	-	39,39,39,39	0
57	MG	BA	3139	1/1	0.14	-	44,44,44,44	0
57	MG	BA	3307	1/1	0.17	-	28,28,28,28	0
57	MG	AA	1620	1/1	0.09	-	59,59,59,59	0
57	MG	BA	3554	1/1	0.09	-	51,51,51,51	0
57	MG	BA	3640	1/1	0.17	-	57,57,57,57	0
57	MG	DA	3158	1/1	0.33	-	56,56,56,56	0
57	MG	DA	3196	1/1	0.13	-	54,54,54,54	0
57	MG	CA	3098	1/1	0.15	-	54,54,54,54	0
57	MG	DA	3493	1/1	0.09	-	51,51,51,51	0
57	MG	CA	3042	1/1	0.09	-	57,57,57,57	0
57	MG	BA	3281	1/1	0.19	-	50,50,50,50	0
57	MG	BA	3496	1/1	0.09	-	51,51,51,51	0
57	MG	BA	3164	1/1	0.21	-	46,46,46,46	0
57	MG	BA	3614	1/1	0.17	-	53,53,53,53	0
57	MG	DA	3341	1/1	0.12	-	55,55,55,55	0
57	MG	DA	3488	1/1	0.09	-	53,53,53,53	0
57	MG	BA	3362	1/1	0.19	-	47,47,47,47	0
57	MG	BA	3409	1/1	0.21	-	22,22,22,22	0
57	MG	DA	3497	1/1	0.13	-	58,58,58,58	0
57	MG	DA	3267	1/1	0.10	-	44,44,44,44	0
57	MG	BA	3653	1/1	0.19	-	57,57,57,57	0
57	MG	BA	3560	1/1	0.12	-	63,63,63,63	0
57	MG	BA	3247	1/1	0.16	-	29,29,29,29	0
57	MG	BE	305	1/1	0.23	-	48,48,48,48	0
57	MG	DA	3265	1/1	0.13	-	57,57,57,57	0
57	MG	CA	3137	1/1	0.14	-	78,78,78,78	0
57	MG	BA	3584	1/1	0.09	-	55,55,55,55	0
57	MG	AA	1603	1/1	0.10	-	64,64,64,64	0
57	MG	DA	3620	1/1	0.09	-	53,53,53,53	0
57	MG	DA	3490	1/1	0.11	-	33,33,33,33	0
57	MG	CA	3019	1/1	0.13	-	68,68,68,68	0
57	MG	DA	3400	1/1	0.14	-	62,62,62,62	0
57	MG	CA	3069	1/1	0.17	-	58,58,58,58	0
57	MG	DA	3498	1/1	0.17	-	35,35,35,35	0
57	MG	AX	3012	1/1	0.14	-	52,52,52,52	0
57	MG	BA	3052	1/1	0.24	-	50,50,50,50	0
57	MG	BZ	301	1/1	0.15	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3393	1/1	0.16	-	37,37,37,37	0
57	MG	AA	1775	1/1	0.11	-	73,73,73,73	0
57	MG	DA	3399	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3070	1/1	0.14	-	65,65,65,65	0
57	MG	DA	3121	1/1	0.09	-	40,40,40,40	0
57	MG	BA	3598	1/1	0.12	-	33,33,33,33	0
57	MG	DA	3064	1/1	0.10	-	46,46,46,46	0
57	MG	BB	3013	1/1	0.18	-	39,39,39,39	0
57	MG	BE	302	1/1	0.17	-	35,35,35,35	0
57	MG	BA	3388	1/1	0.19	-	25,25,25,25	0
57	MG	CA	3044	1/1	0.14	-	47,47,47,47	0
57	MG	BA	3266	1/1	0.16	-	44,44,44,44	0
57	MG	DE	3005	1/1	0.11	-	35,35,35,35	0
57	MG	DA	3197	1/1	0.19	-	59,59,59,59	0
57	MG	BA	3553	1/1	0.14	-	45,45,45,45	0
57	MG	BA	3782	1/1	0.12	-	38,38,38,38	0
57	MG	DA	3022	1/1	0.38	-	60,60,60,60	0
57	MG	DA	3105	1/1	0.18	-	45,45,45,45	0
57	MG	AA	1637	1/1	0.07	-	61,61,61,61	0
57	MG	AX	3006	1/1	0.13	-	68,68,68,68	0
57	MG	DA	3479	1/1	0.13	-	42,42,42,42	0
57	MG	BA	3427	1/1	0.14	-	33,33,33,33	0
57	MG	DA	3231	1/1	0.13	-	61,61,61,61	0
57	MG	BA	3278	1/1	0.91	-	54,54,54,54	0
57	MG	DA	3572	1/1	0.14	-	65,65,65,65	0
57	MG	DA	3531	1/1	0.06	-	48,48,48,48	0
57	MG	DA	3211	1/1	0.17	-	51,51,51,51	0
57	MG	BA	3289	1/1	0.14	-	49,49,49,49	0
57	MG	AA	1681	1/1	0.09	-	38,38,38,38	0
57	MG	DA	3470	1/1	0.05	-	61,61,61,61	0
57	MG	BV	204	1/1	0.22	-	39,39,39,39	0
57	MG	DA	3097	1/1	0.15	-	47,47,47,47	0
57	MG	DA	3656	1/1	0.33	-	41,41,41,41	0
57	MG	CA	3043	1/1	0.13	-	44,44,44,44	0
57	MG	BA	3738	1/1	0.13	-	41,41,41,41	0
57	MG	AA	1704	1/1	0.10	-	57,57,57,57	0
57	MG	BA	3709	1/1	0.34	-	48,48,48,48	0
57	MG	BA	3802	1/1	0.15	-	46,46,46,46	0
57	MG	DA	3453	1/1	0.13	-	54,54,54,54	0
57	MG	DA	3036	1/1	0.12	-	35,35,35,35	0
57	MG	DA	3549	1/1	0.18	-	49,49,49,49	0
57	MG	AA	1703	1/1	0.28	-	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	DA	3501	1/1	0.10	-	49,49,49,49	0
57	MG	DA	3587	1/1	0.11	-	51,51,51,51	0
57	MG	CA	3142	1/1	0.14	-	50,50,50,50	0
57	MG	DA	3448	1/1	0.10	-	55,55,55,55	0
57	MG	BA	3326	1/1	0.12	-	24,24,24,24	0
57	MG	DA	3395	1/1	0.14	-	58,58,58,58	0
57	MG	BA	3124	1/1	0.19	-	57,57,57,57	0
57	MG	CA	3030	1/1	0.08	-	74,74,74,74	0
57	MG	AA	1611	1/1	0.11	-	20,20,20,20	0
57	MG	AA	1722	1/1	0.16	-	57,57,57,57	0
57	MG	DA	3577	1/1	0.06	-	60,60,60,60	0
57	MG	BA	3414	1/1	0.12	-	54,54,54,54	0
57	MG	BA	3396	1/1	0.21	-	25,25,25,25	0
57	MG	DA	3264	1/1	0.12	-	51,51,51,51	0
57	MG	BA	3152	1/1	0.21	-	23,23,23,23	0
57	MG	AA	1645	1/1	0.12	-	61,61,61,61	0
57	MG	BA	3689	1/1	0.15	-	59,59,59,59	0
57	MG	DA	3380	1/1	0.06	-	66,66,66,66	0
57	MG	DA	3237	1/1	0.10	-	59,59,59,59	0
57	MG	BA	3015	1/1	0.17	-	47,47,47,47	0
57	MG	DA	3191	1/1	0.27	-	54,54,54,54	0
57	MG	CA	3079	1/1	0.11	-	49,49,49,49	0
57	MG	DA	3589	1/1	0.06	-	29,29,29,29	0
57	MG	BA	3196	1/1	0.21	-	56,56,56,56	0
57	MG	AA	1808	1/1	0.12	-	49,49,49,49	0
57	MG	BA	3683	1/1	0.32	-	62,62,62,62	0
57	MG	DA	3626	1/1	0.08	-	81,81,81,81	0
57	MG	CA	3085	1/1	0.11	-	41,41,41,41	0
57	MG	DA	3294	1/1	0.08	-	40,40,40,40	0
57	MG	BA	3193	1/1	0.11	-	37,37,37,37	0
57	MG	BA	3062	1/1	0.22	-	59,59,59,59	0
57	MG	DA	3324	1/1	0.08	-	54,54,54,54	0
57	MG	BA	3282	1/1	0.16	-	57,57,57,57	0
57	MG	DQ	3001	1/1	0.06	-	50,50,50,50	0
57	MG	DA	3209	1/1	0.13	-	49,49,49,49	0
57	MG	BA	3097	1/1	0.06	-	41,41,41,41	0
57	MG	BA	3577	1/1	0.19	-	58,58,58,58	0
57	MG	CA	3071	1/1	0.12	-	56,56,56,56	0
57	MG	BA	3667	1/1	0.19	-	58,58,58,58	0
57	MG	DA	3651	1/1	0.13	-	48,48,48,48	0
57	MG	BA	3795	1/1	0.18	-	19,19,19,19	0
57	MG	DA	3506	1/1	0.11	-	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	BA	3391	1/1	0.14	-	41,41,41,41	0
59	ZN	D9	501	1/1	0.12	-	64,64,64,64	0
57	MG	BA	3733	1/1	0.14	-	42,42,42,42	0
57	MG	BA	3273	1/1	0.15	-	45,45,45,45	0
57	MG	AA	1772	1/1	0.14	-	47,47,47,47	0
57	MG	BA	3393	1/1	0.18	-	23,23,23,23	0
57	MG	BA	3504	1/1	0.21	-	56,56,56,56	0
57	MG	BA	3731	1/1	0.12	-	32,32,32,32	0
57	MG	CW	3001	1/1	0.23	-	66,66,66,66	0
57	MG	CA	3091	1/1	0.15	-	69,69,69,69	0
57	MG	BA	3233	1/1	0.23	-	40,40,40,40	0
57	MG	BA	3649	1/1	0.15	-	55,55,55,55	0
57	MG	BD	3007	1/1	0.29	-	46,46,46,46	0
57	MG	BA	3319	1/1	0.21	-	23,23,23,23	0
57	MG	BA	3309	1/1	0.15	-	65,65,65,65	0
57	MG	BA	3761	1/1	0.07	-	36,36,36,36	0
57	MG	BA	3789	1/1	0.14	-	47,47,47,47	0
57	MG	DA	3375	1/1	0.09	-	57,57,57,57	0
57	MG	AA	1655	1/1	0.10	-	53,53,53,53	0
57	MG	DA	3505	1/1	0.07	-	51,51,51,51	0
57	MG	BA	3149	1/1	0.14	-	42,42,42,42	0
57	MG	DA	3271	1/1	0.14	-	30,30,30,30	0
57	MG	BA	3085	1/1	0.24	-	31,31,31,31	0
57	MG	AA	1652	1/1	0.13	-	62,62,62,62	0
57	MG	AA	1707	1/1	0.10	-	57,57,57,57	0
57	MG	BA	3798	1/1	0.24	-	22,22,22,22	0
57	MG	BA	3314	1/1	0.16	-	39,39,39,39	0
57	MG	AA	1719	1/1	0.15	-	63,63,63,63	0
57	MG	BA	3198	1/1	0.11	-	44,44,44,44	0
57	MG	DA	3099	1/1	0.18	-	63,63,63,63	0
57	MG	BA	3312	1/1	0.14	-	31,31,31,31	0
57	MG	BA	3382	1/1	0.10	-	55,55,55,55	0
57	MG	DA	3568	1/1	0.12	-	43,43,43,43	0
57	MG	BA	3118	1/1	0.22	-	35,35,35,35	0
57	MG	DA	3657	1/1	0.39	-	54,54,54,54	0
57	MG	DA	3485	1/1	0.10	-	56,56,56,56	0
57	MG	BA	3684	1/1	0.17	-	51,51,51,51	0
57	MG	BA	3699	1/1	0.19	-	67,67,67,67	0
57	MG	DA	3650	1/1	0.11	-	61,61,61,61	0
57	MG	DA	3578	1/1	0.12	-	43,43,43,43	0
57	MG	BA	3522	1/1	0.16	-	44,44,44,44	0
57	MG	CA	3141	1/1	0.12	-	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	CA	3126	1/1	0.07	-	45,45,45,45	0
57	MG	CE	202	1/1	0.22	-	95,95,95,95	0
57	MG	BA	3127	1/1	0.22	-	45,45,45,45	0
57	MG	BA	3327	1/1	0.15	-	39,39,39,39	0
57	MG	DA	3102	1/1	0.28	-	40,40,40,40	0
57	MG	BV	205	1/1	0.07	-	34,34,34,34	0
57	MG	CA	3037	1/1	0.20	-	53,53,53,53	0
57	MG	BA	3803	1/1	0.27	-	55,55,55,55	0
57	MG	BB	3011	1/1	0.19	-	47,47,47,47	0
57	MG	BA	3668	1/1	0.16	-	75,75,75,75	0
57	MG	DA	3461	1/1	0.12	-	51,51,51,51	0
57	MG	BA	3363	1/1	0.14	-	52,52,52,52	0
57	MG	BA	3580	1/1	0.11	-	48,48,48,48	0
57	MG	BA	3138	1/1	0.10	-	43,43,43,43	0
57	MG	AA	1688	1/1	0.14	-	66,66,66,66	0
57	MG	DA	3530	1/1	0.14	-	55,55,55,55	0
57	MG	DA	3277	1/1	0.10	-	50,50,50,50	0
57	MG	AA	1676	1/1	0.14	-	58,58,58,58	0
57	MG	BA	3415	1/1	0.21	-	35,35,35,35	0
57	MG	CA	3060	1/1	0.10	-	71,71,71,71	0
57	MG	BH	201	1/1	0.23	-	56,56,56,56	0
57	MG	BA	3693	1/1	0.15	-	77,77,77,77	0
57	MG	BA	3544	1/1	0.15	-	52,52,52,52	0
57	MG	BA	3378	1/1	0.23	-	39,39,39,39	0
57	MG	DA	3520	1/1	0.10	-	57,57,57,57	0
57	MG	DA	3431	1/1	0.17	-	42,42,42,42	0
57	MG	BA	3623	1/1	0.17	-	43,43,43,43	0
57	MG	BA	3527	1/1	0.16	-	24,24,24,24	0
57	MG	BA	3221	1/1	0.14	-	29,29,29,29	0
57	MG	DA	3522	1/1	0.09	-	51,51,51,51	0
57	MG	AA	1636	1/1	0.22	-	52,52,52,52	0
57	MG	DA	3069	1/1	0.10	-	43,43,43,43	0
57	MG	BA	3774	1/1	0.28	-	27,27,27,27	0
57	MG	DA	3152	1/1	0.20	-	45,45,45,45	0
57	MG	BA	3101	1/1	0.19	-	37,37,37,37	0
57	MG	DA	3359	1/1	0.14	-	40,40,40,40	0
59	ZN	B5	103	1/1	0.18	-	40,40,40,40	0
57	MG	BA	3503	1/1	0.08	-	51,51,51,51	0
57	MG	BA	3080	1/1	0.11	-	31,31,31,31	0
57	MG	AA	1699	1/1	0.23	-	58,58,58,58	0
57	MG	DA	3195	1/1	0.09	-	42,42,42,42	0
57	MG	BA	3086	1/1	0.29	-	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	3639	1/1	0.15	-	59,59,59,59	0
57	MG	DA	3377	1/1	0.10	-	50,50,50,50	0
57	MG	CA	3165	1/1	0.07	-	42,42,42,42	0
57	MG	AA	1659	1/1	0.15	-	65,65,65,65	0
57	MG	BA	3618	1/1	0.09	-	35,35,35,35	0
57	MG	BA	3369	1/1	0.22	-	62,62,62,62	0
57	MG	BA	3389	1/1	0.18	-	37,37,37,37	0
57	MG	DA	3576	1/1	0.12	-	67,67,67,67	0
57	MG	BA	3778	1/1	0.07	-	40,40,40,40	0
57	MG	BA	3793	1/1	0.16	-	11,11,11,11	0
57	MG	DA	3142	1/1	0.09	-	51,51,51,51	0
57	MG	BA	3366	1/1	0.15	-	52,52,52,52	0
57	MG	DA	3321	1/1	0.16	-	29,29,29,29	0
57	MG	DA	3285	1/1	0.13	-	50,50,50,50	0
57	MG	BA	3334	1/1	0.19	-	56,56,56,56	0
57	MG	DA	3454	1/1	0.10	-	43,43,43,43	0
57	MG	BA	3236	1/1	0.18	-	52,52,52,52	0
57	MG	CA	3009	1/1	0.14	-	73,73,73,73	0
57	MG	DA	3297	1/1	0.16	-	51,51,51,51	0
57	MG	CA	3005	1/1	0.15	-	73,73,73,73	0
57	MG	BA	3373	1/1	0.18	-	34,34,34,34	0
57	MG	BA	3499	1/1	0.15	-	39,39,39,39	0
57	MG	DA	3584	1/1	0.05	-	31,31,31,31	0
57	MG	BA	3469	1/1	0.13	-	61,61,61,61	0
57	MG	BA	3041	1/1	0.18	-	63,63,63,63	0
57	MG	BU	201	1/1	0.44	-	43,43,43,43	0
57	MG	AA	1760	1/1	0.15	-	65,65,65,65	0
57	MG	BA	3525	1/1	0.14	-	43,43,43,43	0
57	MG	BA	3214	1/1	0.36	-	43,43,43,43	0
57	MG	BA	3599	1/1	0.12	-	60,60,60,60	0
57	MG	CA	3068	1/1	0.12	-	58,58,58,58	0
57	MG	BA	3471	1/1	0.15	-	27,27,27,27	0
57	MG	DA	3541	1/1	0.08	-	59,59,59,59	0
57	MG	AA	1690	1/1	0.38	-	52,52,52,52	0
57	MG	DA	3054	1/1	0.06	-	27,27,27,27	0
57	MG	DA	3550	1/1	0.04	-	60,60,60,60	0
57	MG	BA	3352	1/1	0.17	-	68,68,68,68	0
57	MG	BA	3585	1/1	0.15	-	29,29,29,29	0
57	MG	BA	3486	1/1	0.10	-	41,41,41,41	0
57	MG	DA	3352	1/1	0.10	-	34,34,34,34	0
57	MG	DA	3458	1/1	0.09	-	41,41,41,41	0
57	MG	DA	3407	1/1	0.09	-	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	3418	1/1	0.07	-	47,47,47,47	0
57	MG	AA	1667	1/1	0.17	-	55,55,55,55	0
57	MG	BA	3376	1/1	0.18	-	29,29,29,29	0
57	MG	DA	3484	1/1	0.05	-	46,46,46,46	0
57	MG	CA	3053	1/1	0.09	-	41,41,41,41	0
57	MG	BA	3234	1/1	0.10	-	52,52,52,52	0
57	MG	DA	3354	1/1	0.07	-	41,41,41,41	0
57	MG	DA	3283	1/1	0.06	-	27,27,27,27	0
57	MG	BA	3262	1/1	0.32	-	31,31,31,31	0
57	MG	BA	3474	1/1	0.21	-	33,33,33,33	0
57	MG	BA	3129	1/1	0.14	-	54,54,54,54	0
57	MG	BA	3663	1/1	0.17	-	50,50,50,50	0
57	MG	BA	3177	1/1	0.29	-	46,46,46,46	0
57	MG	DA	3567	1/1	0.24	-	44,44,44,44	0
57	MG	AA	1613	1/1	0.14	-	75,75,75,75	0
57	MG	DA	3061	1/1	0.17	-	60,60,60,60	0
57	MG	BA	3120	1/1	0.29	-	45,45,45,45	0
57	MG	AX	3010	1/1	0.41	-	68,68,68,68	0
57	MG	BA	3686	1/1	0.15	-	27,27,27,27	0
57	MG	DA	3472	1/1	0.11	-	25,25,25,25	0
57	MG	DA	3631	1/1	0.11	-	49,49,49,49	0
57	MG	DA	3269	1/1	0.10	-	50,50,50,50	0
57	MG	AA	1786	1/1	0.11	-	69,69,69,69	0
57	MG	BA	3354	1/1	0.10	-	47,47,47,47	0
57	MG	AA	1609	1/1	0.09	-	63,63,63,63	0
57	MG	DA	3104	1/1	0.09	-	57,57,57,57	0
57	MG	DA	3157	1/1	0.11	-	34,34,34,34	0
57	MG	BA	3228	1/1	0.09	-	65,65,65,65	0
57	MG	BA	3453	1/1	0.23	-	50,50,50,50	0
57	MG	AA	1648	1/1	0.15	-	56,56,56,56	0
57	MG	DA	3339	1/1	0.24	-	52,52,52,52	0
57	MG	BE	301	1/1	0.17	-	31,31,31,31	0
57	MG	BA	3166	1/1	0.15	-	33,33,33,33	0
57	MG	BA	3068	1/1	0.16	-	49,49,49,49	0
57	MG	BA	3619	1/1	0.11	-	28,28,28,28	0
57	MG	BA	3243	1/1	0.68	-	44,44,44,44	0
57	MG	BA	3596	1/1	0.15	-	59,59,59,59	0
57	MG	DB	3006	1/1	0.10	-	55,55,55,55	0
57	MG	BA	3381	1/1	0.09	-	49,49,49,49	0
57	MG	DA	3326	1/1	0.08	-	46,46,46,46	0
57	MG	CA	3102	1/1	0.12	-	71,71,71,71	0
57	MG	AA	1642	1/1	0.23	-	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	3204	1/1	0.26	-	68,68,68,68	0
57	MG	BA	3317	1/1	0.18	-	43,43,43,43	0
57	MG	DA	3244	1/1	0.24	-	55,55,55,55	0
57	MG	AA	1668	1/1	0.08	-	63,63,63,63	0
57	MG	CA	3133	1/1	0.19	-	82,82,82,82	0
57	MG	BA	3432	1/1	0.20	-	32,32,32,32	0
57	MG	BA	3542	1/1	0.17	-	44,44,44,44	0
57	MG	BA	3005	1/1	0.12	-	44,44,44,44	0
57	MG	CA	3093	1/1	0.14	-	55,55,55,55	0
57	MG	CA	3108	1/1	0.08	-	72,72,72,72	0
57	MG	DA	3390	1/1	0.08	-	58,58,58,58	0
57	MG	BA	3010	1/1	0.18	-	53,53,53,53	0
57	MG	BA	3459	1/1	0.13	-	31,31,31,31	0
57	MG	BA	3274	1/1	0.18	-	66,66,66,66	0
57	MG	BA	3740	1/1	0.20	-	65,65,65,65	0
57	MG	AA	1602	1/1	0.08	-	68,68,68,68	0
57	MG	BA	3429	1/1	0.25	-	50,50,50,50	0
57	MG	BA	3551	1/1	0.12	-	44,44,44,44	0
57	MG	BA	3035	1/1	0.14	-	49,49,49,49	0
57	MG	DA	3289	1/1	0.14	-	52,52,52,52	0
57	MG	DA	3020	1/1	0.08	-	26,26,26,26	0
57	MG	BA	3339	1/1	0.17	-	43,43,43,43	0
57	MG	BA	3622	1/1	0.18	-	43,43,43,43	0
57	MG	BA	3209	1/1	0.17	-	48,48,48,48	0
57	MG	BA	3265	1/1	0.24	-	72,72,72,72	0
57	MG	BA	3435	1/1	0.19	-	53,53,53,53	0
57	MG	DA	3600	1/1	0.12	-	72,72,72,72	0
57	MG	BA	3756	1/1	0.15	-	18,18,18,18	0
57	MG	DA	3112	1/1	0.14	-	56,56,56,56	0
57	MG	BA	3720	1/1	0.13	-	38,38,38,38	0
57	MG	DA	3330	1/1	0.15	-	36,36,36,36	0
57	MG	DA	3013	1/1	0.09	-	39,39,39,39	0
57	MG	BA	3729	1/1	0.12	-	46,46,46,46	0
57	MG	DA	3489	1/1	0.07	-	48,48,48,48	0
57	MG	BA	3723	1/1	0.17	-	30,30,30,30	0
57	MG	AA	1732	1/1	0.22	-	63,63,63,63	0
57	MG	DA	3428	1/1	0.10	-	38,38,38,38	0
57	MG	BA	3641	1/1	0.14	-	68,68,68,68	0
57	MG	DA	3015	1/1	0.19	-	60,60,60,60	0
57	MG	DB	3009	1/1	0.13	-	58,58,58,58	0
57	MG	AA	1614	1/1	0.13	-	75,75,75,75	0
57	MG	DA	3281	1/1	0.13	-	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BU	202	1/1	0.22	-	40,40,40,40	0
57	MG	BA	3480	1/1	0.16	-	47,47,47,47	0
57	MG	DA	3180	1/1	0.15	-	48,48,48,48	0
57	MG	B8	5001	1/1	0.15	-	42,42,42,42	0
57	MG	BA	3548	1/1	0.10	-	35,35,35,35	0
57	MG	DA	3408	1/1	0.17	-	55,55,55,55	0
57	MG	DA	3622	1/1	0.07	-	49,49,49,49	0
57	MG	DA	3025	1/1	0.51	-	47,47,47,47	0
57	MG	BA	3322	1/1	0.15	-	38,38,38,38	0
57	MG	DA	3219	1/1	0.15	-	50,50,50,50	0
57	MG	DA	3058	1/1	0.07	-	61,61,61,61	0
57	MG	BA	3428	1/1	0.16	-	51,51,51,51	0
57	MG	DA	3156	1/1	0.12	-	52,52,52,52	0
57	MG	BA	3205	1/1	0.34	-	57,57,57,57	0
57	MG	BA	3047	1/1	0.18	-	43,43,43,43	0
57	MG	AA	1780	1/1	0.13	-	69,69,69,69	0
57	MG	DA	3109	1/1	0.09	-	49,49,49,49	0
57	MG	BA	3259	1/1	0.18	-	25,25,25,25	0
57	MG	BA	3267	1/1	0.23	-	61,61,61,61	0
57	MG	BA	3531	1/1	0.12	-	60,60,60,60	0
57	MG	BA	3677	1/1	0.10	-	44,44,44,44	0
57	MG	BA	3613	1/1	0.20	-	53,53,53,53	0
57	MG	BA	3654	1/1	0.09	-	59,59,59,59	0
57	MG	DA	3303	1/1	0.11	-	43,43,43,43	0
57	MG	BA	3719	1/1	0.13	-	41,41,41,41	0
57	MG	BA	3083	1/1	0.24	-	60,60,60,60	0
57	MG	DA	3384	1/1	0.08	-	38,38,38,38	0
57	MG	DA	3598	1/1	0.07	-	55,55,55,55	0
57	MG	DA	3166	1/1	0.17	-	55,55,55,55	0
57	MG	CA	3021	1/1	0.07	-	61,61,61,61	0
57	MG	BA	3385	1/1	0.19	-	30,30,30,30	0
57	MG	BA	3530	1/1	0.23	-	33,33,33,33	0
57	MG	DA	3087	1/1	0.20	-	55,55,55,55	0
57	MG	AA	1784	1/1	0.28	-	72,72,72,72	0
57	MG	DA	3139	1/1	0.12	-	44,44,44,44	0
57	MG	AA	1728	1/1	0.21	-	49,49,49,49	0
57	MG	BA	3174	1/1	0.46	-	38,38,38,38	0
57	MG	BA	3587	1/1	0.12	-	46,46,46,46	0
57	MG	DA	3566	1/1	0.18	-	37,37,37,37	0
57	MG	BA	3025	1/1	0.14	-	43,43,43,43	0
57	MG	AA	1783	1/1	0.12	-	35,35,35,35	0
57	MG	BA	3620	1/1	0.07	-	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3121	1/1	0.26	-	42,42,42,42	0
57	MG	DA	3238	1/1	0.13	-	48,48,48,48	0
57	MG	CA	3157	1/1	0.14	-	60,60,60,60	0
57	MG	DA	3186	1/1	0.12	-	49,49,49,49	0
57	MG	BA	3145	1/1	0.19	-	48,48,48,48	0
57	MG	BA	3301	1/1	0.14	-	62,62,62,62	0
57	MG	BB	3020	1/1	0.15	-	65,65,65,65	0
57	MG	AA	1725	1/1	0.20	-	51,51,51,51	0
57	MG	BB	3016	1/1	0.16	-	34,34,34,34	0
57	MG	CA	3007	1/1	0.14	-	51,51,51,51	0
57	MG	BA	3110	1/1	0.18	-	36,36,36,36	0
57	MG	DA	3037	1/1	0.08	-	26,26,26,26	0
57	MG	DA	3403	1/1	0.05	-	49,49,49,49	0
57	MG	BA	3651	1/1	0.13	-	66,66,66,66	0
57	MG	BA	3241	1/1	0.15	-	56,56,56,56	0
57	MG	BA	3479	1/1	0.12	-	53,53,53,53	0
57	MG	DA	3643	1/1	0.07	-	54,54,54,54	0
57	MG	AA	1796	1/1	0.09	-	64,64,64,64	0
57	MG	BA	3403	1/1	0.25	-	33,33,33,33	0
57	MG	DA	3017	1/1	0.10	-	59,59,59,59	0
57	MG	BA	3404	1/1	0.32	-	59,59,59,59	0
57	MG	DA	3603	1/1	0.06	-	65,65,65,65	0
57	MG	DA	3066	1/1	0.09	-	58,58,58,58	0
57	MG	BA	3722	1/1	0.15	-	64,64,64,64	0
57	MG	CA	3022	1/1	0.18	-	76,76,76,76	0
57	MG	BA	3563	1/1	0.12	-	50,50,50,50	0
57	MG	DA	3315	1/1	0.12	-	44,44,44,44	0
57	MG	BA	3635	1/1	0.09	-	42,42,42,42	0
57	MG	DA	3637	1/1	0.14	-	72,72,72,72	0
57	MG	BA	3311	1/1	0.18	-	56,56,56,56	0
57	MG	DA	3127	1/1	0.07	-	52,52,52,52	0
57	MG	BA	3392	1/1	0.16	-	26,26,26,26	0
57	MG	BA	3413	1/1	0.14	-	37,37,37,37	0
57	MG	BA	3046	1/1	0.10	-	43,43,43,43	0
57	MG	CA	3055	1/1	0.08	-	63,63,63,63	0
57	MG	DA	3569	1/1	0.15	-	45,45,45,45	0
57	MG	BA	3292	1/1	0.23	-	26,26,26,26	0
57	MG	DA	3005	1/1	0.15	-	54,54,54,54	0
57	MG	BA	3208	1/1	0.15	-	43,43,43,43	0
57	MG	BA	3661	1/1	0.24	-	25,25,25,25	0
57	MG	BA	3215	1/1	0.43	-	37,37,37,37	0
57	MG	DA	3132	1/1	0.10	-	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	BP	3001	1/1	0.13	-	34,34,34,34	0
57	MG	CA	3138	1/1	0.10	-	65,65,65,65	0
57	MG	BA	3074	1/1	0.18	-	69,69,69,69	0
57	MG	DA	3016	1/1	0.08	-	66,66,66,66	0
57	MG	AX	3002	1/1	0.31	-	71,71,71,71	0
57	MG	AA	1735	1/1	0.11	-	45,45,45,45	0
57	MG	DA	3227	1/1	0.17	-	56,56,56,56	0
57	MG	DA	3653	1/1	0.13	-	33,33,33,33	0
57	MG	BA	3705	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3084	1/1	0.18	-	44,44,44,44	0
57	MG	AA	1626	1/1	0.23	-	59,59,59,59	0
57	MG	BA	3670	1/1	0.13	-	54,54,54,54	0
57	MG	AA	1778	1/1	0.07	-	51,51,51,51	0
57	MG	CA	3167	1/1	0.23	-	57,57,57,57	0
57	MG	BA	3192	1/1	0.15	-	19,19,19,19	0
57	MG	BA	3238	1/1	0.37	-	44,44,44,44	0
57	MG	DA	3317	1/1	0.09	-	54,54,54,54	0
57	MG	BA	3338	1/1	0.15	-	55,55,55,55	0
57	MG	AA	1736	1/1	0.06	-	49,49,49,49	0
57	MG	BA	3625	1/1	0.10	-	33,33,33,33	0
57	MG	AA	1638	1/1	0.22	-	60,60,60,60	0
57	MG	BD	3002	1/1	0.15	-	28,28,28,28	0
57	MG	BA	3799	1/1	0.20	-	42,42,42,42	0
57	MG	DA	3183	1/1	0.12	-	41,41,41,41	0
57	MG	DA	3287	1/1	0.19	-	52,52,52,52	0
57	MG	DA	3076	1/1	0.08	-	52,52,52,52	0
57	MG	DA	3415	1/1	0.16	-	43,43,43,43	0
57	MG	DA	3343	1/1	0.14	-	34,34,34,34	0
57	MG	CA	3128	1/1	0.14	-	52,52,52,52	0
57	MG	DA	3336	1/1	0.08	-	49,49,49,49	0
57	MG	BA	3178	1/1	0.12	-	32,32,32,32	0
57	MG	AA	1700	1/1	0.06	-	71,71,71,71	0
57	MG	DA	3122	1/1	0.29	-	60,60,60,60	0
57	MG	BA	3095	1/1	0.17	-	53,53,53,53	0
57	MG	BA	3113	1/1	0.11	-	50,50,50,50	0
57	MG	CA	3050	1/1	0.13	-	73,73,73,73	0
57	MG	B5	101	1/1	0.32	-	30,30,30,30	0
57	MG	AA	1790	1/1	0.08	-	81,81,81,81	0
57	MG	DA	3446	1/1	0.12	-	50,50,50,50	0
57	MG	DA	3202	1/1	0.31	-	62,62,62,62	0
57	MG	CT	3001	1/1	0.11	-	60,60,60,60	0
57	MG	DP	201	1/1	0.27	-	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3672	1/1	0.20	-	44,44,44,44	0
57	MG	BF	311	1/1	0.11	-	52,52,52,52	0
57	MG	AA	1675	1/1	0.20	-	61,61,61,61	0
57	MG	AA	1708	1/1	0.14	-	60,60,60,60	0
57	MG	DA	3660	1/1	0.56	-	46,46,46,46	0
57	MG	BA	3786	1/1	0.15	-	51,51,51,51	0
57	MG	BA	3011	1/1	0.12	-	30,30,30,30	0
57	MG	DA	3426	1/1	0.09	-	49,49,49,49	0
57	MG	DA	3136	1/1	0.13	-	48,48,48,48	0
57	MG	CA	3084	1/1	0.07	-	56,56,56,56	0
57	MG	BA	3280	1/1	0.16	-	25,25,25,25	0
57	MG	DA	3068	1/1	0.14	-	53,53,53,53	0
57	MG	AA	1794	1/1	0.15	-	58,58,58,58	0
57	MG	DA	3535	1/1	0.17	-	44,44,44,44	0
57	MG	DA	3024	1/1	0.52	-	61,61,61,61	0
57	MG	BA	3489	1/1	0.21	-	50,50,50,50	0
57	MG	AE	3001	1/1	0.07	-	63,63,63,63	0
57	MG	BA	3604	1/1	0.17	-	43,43,43,43	0
57	MG	DA	3088	1/1	0.30	-	50,50,50,50	0
57	MG	BA	3465	1/1	0.06	-	48,48,48,48	0
57	MG	CA	3152	1/1	0.07	-	71,71,71,71	0
57	MG	DA	3205	1/1	0.18	-	62,62,62,62	0
57	MG	AA	1616	1/1	0.11	-	73,73,73,73	0
57	MG	BA	3108	1/1	0.17	-	42,42,42,42	0
57	MG	CA	3107	1/1	0.10	-	68,68,68,68	0
57	MG	DE	3003	1/1	0.06	-	43,43,43,43	0
57	MG	BA	3293	1/1	0.08	-	58,58,58,58	0
57	MG	DA	3199	1/1	0.22	-	62,62,62,62	0
57	MG	DA	3165	1/1	0.19	-	55,55,55,55	0
57	MG	BV	202	1/1	0.39	-	32,32,32,32	0
57	MG	BA	3394	1/1	0.27	-	40,40,40,40	0
57	MG	DA	3416	1/1	0.12	-	52,52,52,52	0
57	MG	AA	1730	1/1	0.22	-	27,27,27,27	0
57	MG	BA	3014	1/1	0.10	-	35,35,35,35	0
57	MG	BA	3590	1/1	0.14	-	33,33,33,33	0
57	MG	B5	104	1/1	0.08	-	58,58,58,58	0
57	MG	BA	3601	1/1	0.40	-	40,40,40,40	0
57	MG	BA	3305	1/1	0.13	-	46,46,46,46	0
57	MG	BA	3526	1/1	0.20	-	41,41,41,41	0
57	MG	BA	3073	1/1	0.12	-	32,32,32,32	0
57	MG	CA	3150	1/1	0.12	-	65,65,65,65	0
57	MG	DA	3376	1/1	0.14	-	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	DA	3293	1/1	0.14	-	61,61,61,61	0
57	MG	BA	3316	1/1	0.15	-	54,54,54,54	0
57	MG	BB	3015	1/1	0.21	-	45,45,45,45	0
57	MG	BA	3555	1/1	0.15	-	50,50,50,50	0
57	MG	DF	301	1/1	0.22	-	48,48,48,48	0
57	MG	AA	1705	1/1	0.20	-	70,70,70,70	0
57	MG	CA	3127	1/1	0.08	-	59,59,59,59	0
57	MG	BA	3257	1/1	0.23	-	43,43,43,43	0
57	MG	BA	3495	1/1	0.15	-	43,43,43,43	0
57	MG	BA	3721	1/1	0.10	-	47,47,47,47	0
57	MG	DA	3082	1/1	0.08	-	47,47,47,47	0
57	MG	BA	3658	1/1	0.12	-	61,61,61,61	0
57	MG	BA	3397	1/1	0.14	-	28,28,28,28	0
57	MG	BA	3320	1/1	0.16	-	55,55,55,55	0
57	MG	DA	3618	1/1	0.14	-	46,46,46,46	0
57	MG	DA	3044	1/1	0.08	-	53,53,53,53	0
57	MG	BA	3742	1/1	0.20	-	48,48,48,48	0
57	MG	DA	3310	1/1	0.14	-	35,35,35,35	0
57	MG	DA	3546	1/1	0.08	-	47,47,47,47	0
57	MG	BA	3087	1/1	0.47	-	43,43,43,43	0
57	MG	BA	3796	1/1	0.18	-	47,47,47,47	0
57	MG	BA	3675	1/1	0.22	-	56,56,56,56	0
57	MG	BU	204	1/1	0.34	-	47,47,47,47	0
57	MG	DA	3364	1/1	0.10	-	45,45,45,45	0
57	MG	BA	3039	1/1	0.19	-	36,36,36,36	0
57	MG	DA	3208	1/1	0.07	-	54,54,54,54	0
57	MG	DA	3462	1/1	0.21	-	50,50,50,50	0
57	MG	BA	3737	1/1	0.14	-	34,34,34,34	0
57	MG	B2	3001	1/1	0.27	-	53,53,53,53	0
57	MG	BA	3351	1/1	0.17	-	45,45,45,45	0
57	MG	DA	3469	1/1	0.07	-	50,50,50,50	0
57	MG	BA	3150	1/1	0.14	-	39,39,39,39	0
57	MG	BA	3386	1/1	0.13	-	28,28,28,28	0
57	MG	BA	3455	1/1	0.14	-	52,52,52,52	0
57	MG	BA	3643	1/1	0.09	-	52,52,52,52	0
57	MG	CA	3080	1/1	0.09	-	49,49,49,49	0
57	MG	BE	304	1/1	0.19	-	23,23,23,23	0
57	MG	AA	1695	1/1	0.16	-	59,59,59,59	0
57	MG	DA	3222	1/1	0.15	-	58,58,58,58	0
57	MG	DA	3319	1/1	0.13	-	33,33,33,33	0
57	MG	BA	3103	1/1	0.29	-	63,63,63,63	0
57	MG	DE	3001	1/1	0.47	-	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3763	1/1	0.12	-	44,44,44,44	0
57	MG	BF	308	1/1	0.06	-	43,43,43,43	0
57	MG	CA	3129	1/1	0.09	-	69,69,69,69	0
57	MG	DA	3434	1/1	0.12	-	60,60,60,60	0
57	MG	DA	3028	1/1	0.09	-	39,39,39,39	0
57	MG	BA	3762	1/1	0.15	-	20,20,20,20	0
57	MG	BA	3521	1/1	0.17	-	40,40,40,40	0
57	MG	DA	3079	1/1	0.10	-	72,72,72,72	0
57	MG	DA	3249	1/1	0.13	-	65,65,65,65	0
57	MG	DA	3443	1/1	0.15	-	51,51,51,51	0
57	MG	AA	1605	1/1	0.17	-	50,50,50,50	0
57	MG	BB	3022	1/1	0.16	-	60,60,60,60	0
57	MG	BA	3341	1/1	0.19	-	18,18,18,18	0
57	MG	BA	3562	1/1	0.14	-	55,55,55,55	0
57	MG	BA	3638	1/1	0.16	-	65,65,65,65	0
57	MG	DA	3254	1/1	0.15	-	68,68,68,68	0
57	MG	DA	3257	1/1	0.20	-	44,44,44,44	0
57	MG	DA	3406	1/1	0.17	-	70,70,70,70	0
57	MG	BA	3421	1/1	0.13	-	62,62,62,62	0
57	MG	DY	502	1/1	0.09	-	55,55,55,55	0
57	MG	BA	3136	1/1	0.53	-	49,49,49,49	0
57	MG	DA	3344	1/1	0.13	-	38,38,38,38	0
57	MG	DA	3475	1/1	0.17	-	56,56,56,56	0
57	MG	BA	3708	1/1	0.22	-	33,33,33,33	0
57	MG	BA	3655	1/1	0.15	-	55,55,55,55	0
57	MG	DA	3270	1/1	0.15	-	42,42,42,42	0
57	MG	DA	3172	1/1	0.13	-	61,61,61,61	0
57	MG	BA	3517	1/1	0.21	-	33,33,33,33	0
57	MG	DA	3033	1/1	0.68	-	68,68,68,68	0
57	MG	DD	304	1/1	0.06	-	36,36,36,36	0
57	MG	CA	3148	1/1	0.11	-	68,68,68,68	0
57	MG	DA	3664	1/1	0.08	-	51,51,51,51	0
57	MG	BA	3644	1/1	0.11	-	64,64,64,64	0
57	MG	BA	3367	1/1	0.19	-	52,52,52,52	0
57	MG	BA	3142	1/1	0.23	-	46,46,46,46	0
57	MG	BA	3703	1/1	0.31	-	28,28,28,28	0
57	MG	BA	3066	1/1	0.22	-	58,58,58,58	0
57	MG	BA	3507	1/1	0.25	-	43,43,43,43	0
57	MG	DA	3396	1/1	0.16	-	46,46,46,46	0
57	MG	BA	3157	1/1	0.14	-	46,46,46,46	0
57	MG	BA	3165	1/1	0.25	-	52,52,52,52	0
57	MG	DA	3138	1/1	0.16	-	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	3540	1/1	0.15	-	31,31,31,31	0
57	MG	DA	3081	1/1	0.09	-	51,51,51,51	0
57	MG	BA	3217	1/1	0.07	-	50,50,50,50	0
57	MG	DA	3145	1/1	0.31	-	48,48,48,48	0
57	MG	DA	3055	1/1	0.12	-	53,53,53,53	0
57	MG	BA	3478	1/1	0.10	-	54,54,54,54	0
57	MG	DB	3012	1/1	0.21	-	66,66,66,66	0
57	MG	BX	3001	1/1	0.31	-	44,44,44,44	0
57	MG	AA	1799	1/1	0.09	-	78,78,78,78	0
57	MG	BA	3707	1/1	0.19	-	39,39,39,39	0
57	MG	DA	3463	1/1	0.17	-	44,44,44,44	0
57	MG	BA	3084	1/1	0.14	-	42,42,42,42	0
57	MG	DA	3540	1/1	0.06	-	50,50,50,50	0
57	MG	AA	1610	1/1	0.14	-	81,81,81,81	0
57	MG	BA	3287	1/1	0.14	-	27,27,27,27	0
57	MG	DA	3508	1/1	0.20	-	57,57,57,57	0
57	MG	DA	3177	1/1	0.09	-	58,58,58,58	0
57	MG	BA	3606	1/1	0.11	-	36,36,36,36	0
57	MG	DA	3495	1/1	0.08	-	50,50,50,50	0
57	MG	BA	3045	1/1	0.17	-	39,39,39,39	0
57	MG	BA	3170	1/1	0.20	-	38,38,38,38	0
57	MG	BA	3535	1/1	0.18	-	39,39,39,39	0
57	MG	BA	3700	1/1	0.24	-	36,36,36,36	0
57	MG	BB	3018	1/1	0.05	-	54,54,54,54	0
57	MG	DA	3221	1/1	0.06	-	41,41,41,41	0
57	MG	BA	3361	1/1	0.08	-	56,56,56,56	0
57	MG	BA	3612	1/1	0.06	-	60,60,60,60	0
57	MG	BA	3449	1/1	0.19	-	62,62,62,62	0
57	MG	DA	3439	1/1	0.10	-	40,40,40,40	0
57	MG	DA	3150	1/1	0.11	-	50,50,50,50	0
57	MG	AA	1646	1/1	0.12	-	58,58,58,58	0
57	MG	BA	3753	1/1	0.22	-	68,68,68,68	0
57	MG	DA	3423	1/1	0.20	-	37,37,37,37	0
57	MG	DA	3248	1/1	0.24	-	58,58,58,58	0
57	MG	DA	3459	1/1	0.12	-	49,49,49,49	0
57	MG	DA	3628	1/1	0.21	-	77,77,77,77	0
57	MG	AA	1734	1/1	0.11	-	43,43,43,43	0
57	MG	AA	1696	1/1	0.11	-	83,83,83,83	0
57	MG	DA	3038	1/1	0.13	-	56,56,56,56	0
57	MG	DA	3619	1/1	0.14	-	40,40,40,40	0
57	MG	BA	3412	1/1	0.13	-	30,30,30,30	0
57	MG	BA	3185	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	DA	3517	1/1	0.08	-	48,48,48,48	0
57	MG	CA	3016	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3660	1/1	0.12	-	60,60,60,60	0
57	MG	DA	3563	1/1	0.09	-	70,70,70,70	0
57	MG	AA	1711	1/1	0.11	-	51,51,51,51	0
57	MG	BA	3210	1/1	0.14	-	41,41,41,41	0
57	MG	DA	3647	1/1	0.08	-	52,52,52,52	0
57	MG	DA	3133	1/1	0.20	-	60,60,60,60	0
57	MG	DA	3026	1/1	0.47	-	50,50,50,50	0
57	MG	DA	3625	1/1	0.09	-	60,60,60,60	0
57	MG	AA	1623	1/1	0.19	-	65,65,65,65	0
57	MG	DA	3373	1/1	0.07	-	31,31,31,31	0
57	MG	DA	3131	1/1	0.41	-	49,49,49,49	0
57	MG	BA	3481	1/1	0.08	-	54,54,54,54	0
57	MG	BA	3173	1/1	0.26	-	32,32,32,32	0
57	MG	BU	203	1/1	0.31	-	34,34,34,34	0
57	MG	DA	3592	1/1	0.11	-	67,67,67,67	0
57	MG	DA	3500	1/1	0.28	-	55,55,55,55	0
57	MG	BA	3539	1/1	0.12	-	42,42,42,42	0
57	MG	DA	3164	1/1	0.12	-	44,44,44,44	0
57	MG	DA	3200	1/1	0.12	-	41,41,41,41	0
57	MG	AA	1665	1/1	0.08	-	55,55,55,55	0
57	MG	DA	3295	1/1	0.22	-	67,67,67,67	0
57	MG	BA	3491	1/1	0.20	-	56,56,56,56	0
57	MG	AA	1781	1/1	0.11	-	59,59,59,59	0
57	MG	BG	201	1/1	0.12	-	39,39,39,39	0
57	MG	BA	3213	1/1	0.11	-	43,43,43,43	0
57	MG	DA	3537	1/1	0.07	-	45,45,45,45	0
57	MG	BA	3673	1/1	0.23	-	61,61,61,61	0
57	MG	CA	3067	1/1	0.13	-	46,46,46,46	0
57	MG	DA	3243	1/1	0.13	-	48,48,48,48	0
57	MG	BW	3004	1/1	0.16	-	45,45,45,45	0
57	MG	DA	3153	1/1	0.17	-	44,44,44,44	0
57	MG	DA	3169	1/1	0.28	-	41,41,41,41	0
57	MG	DA	3638	1/1	0.15	-	47,47,47,47	0
57	MG	BA	3275	1/1	0.14	-	66,66,66,66	0
57	MG	BA	3758	1/1	0.14	-	41,41,41,41	0
57	MG	AX	3016	1/1	0.53	-	86,86,86,86	0
57	MG	AA	1765	1/1	0.10	-	65,65,65,65	0
57	MG	BA	3162	1/1	0.26	-	41,41,41,41	0
57	MG	BA	3089	1/1	0.11	-	36,36,36,36	0
57	MG	BA	3800	1/1	0.16	-	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AX	3014	1/1	0.20	-	61,61,61,61	0
57	MG	DA	3518	1/1	0.09	-	56,56,56,56	0
57	MG	BA	3160	1/1	0.14	-	49,49,49,49	0
57	MG	DA	3263	1/1	0.11	-	65,65,65,65	0
57	MG	AA	1756	1/1	0.30	-	45,45,45,45	0
57	MG	DA	3543	1/1	0.14	-	64,64,64,64	0
57	MG	BA	3717	1/1	0.13	-	72,72,72,72	0
57	MG	BA	3402	1/1	0.14	-	27,27,27,27	0
57	MG	BA	3557	1/1	0.10	-	53,53,53,53	0
57	MG	DA	3328	1/1	0.19	-	42,42,42,42	0
57	MG	DA	3440	1/1	0.10	-	36,36,36,36	0
57	MG	DA	3648	1/1	0.06	-	62,62,62,62	0
57	MG	BA	3231	1/1	0.14	-	57,57,57,57	0
57	MG	DA	3659	1/1	0.13	-	41,41,41,41	0
57	MG	DA	3594	1/1	0.09	-	58,58,58,58	0
57	MG	BA	3450	1/1	0.28	-	54,54,54,54	0
57	MG	BA	3642	1/1	0.26	-	64,64,64,64	0
57	MG	BD	3010	1/1	0.14	-	46,46,46,46	0
57	MG	BA	3056	1/1	0.40	-	46,46,46,46	0
57	MG	BA	3784	1/1	0.14	-	52,52,52,52	0
57	MG	DA	3163	1/1	0.15	-	34,34,34,34	0
57	MG	DA	3391	1/1	0.10	-	45,45,45,45	0
57	MG	DA	3258	1/1	0.13	-	45,45,45,45	0
57	MG	DF	304	1/1	0.05	-	51,51,51,51	0
57	MG	DA	3120	1/1	0.27	-	56,56,56,56	0
57	MG	DA	3078	1/1	0.09	-	47,47,47,47	0
57	MG	AA	1776	1/1	0.15	-	73,73,73,73	0
57	MG	AA	1743	1/1	0.16	-	66,66,66,66	0
57	MG	AA	1753	1/1	0.20	-	55,55,55,55	0
57	MG	DA	3604	1/1	0.15	-	61,61,61,61	0
57	MG	CA	3130	1/1	0.24	-	64,64,64,64	0
57	MG	BA	3448	1/1	0.14	-	17,17,17,17	0
57	MG	DA	3266	1/1	0.09	-	37,37,37,37	0
57	MG	DA	3187	1/1	0.20	-	47,47,47,47	0
57	MG	BA	3443	1/1	0.17	-	59,59,59,59	0
57	MG	DA	3292	1/1	0.09	-	29,29,29,29	0
57	MG	BA	3355	1/1	0.11	-	35,35,35,35	0
57	MG	DQ	3002	1/1	0.09	-	47,47,47,47	0
57	MG	DA	3358	1/1	0.17	-	50,50,50,50	0
57	MG	DA	3040	1/1	0.11	-	28,28,28,28	0
57	MG	BA	3117	1/1	0.42	-	38,38,38,38	0
57	MG	BA	3438	1/1	0.17	-	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	BA	3524	1/1	0.19	-	33,33,33,33	0
57	MG	CA	3124	1/1	0.20	-	69,69,69,69	0
57	MG	BA	3634	1/1	0.13	-	55,55,55,55	0
57	MG	BA	3176	1/1	0.24	-	55,55,55,55	0
57	MG	DA	3355	1/1	0.09	-	43,43,43,43	0
57	MG	AA	1727	1/1	0.14	-	50,50,50,50	0
57	MG	BA	3600	1/1	0.23	-	44,44,44,44	0
57	MG	BA	3272	1/1	0.20	-	64,64,64,64	0
57	MG	DA	3023	1/1	0.11	-	58,58,58,58	0
57	MG	AA	1662	1/1	0.12	-	58,58,58,58	0
57	MG	BA	3246	1/1	0.26	-	55,55,55,55	0
57	MG	AA	1650	1/1	0.12	-	74,74,74,74	0
57	MG	AA	1777	1/1	0.07	-	71,71,71,71	0
57	MG	B4	502	1/1	0.21	-	70,70,70,70	0
57	MG	CA	3109	1/1	0.19	-	74,74,74,74	0
57	MG	CA	3070	1/1	0.10	-	69,69,69,69	0
57	MG	BA	3650	1/1	0.16	-	45,45,45,45	0
57	MG	BA	3725	1/1	0.15	-	31,31,31,31	0
57	MG	AA	1762	1/1	0.16	-	66,66,66,66	0
57	MG	AA	1813	1/1	0.18	-	38,38,38,38	0
57	MG	BA	3161	1/1	0.28	-	44,44,44,44	0
57	MG	DA	3308	1/1	0.19	-	62,62,62,62	0
57	MG	BA	3493	1/1	0.17	-	38,38,38,38	0
57	MG	DA	3612	1/1	0.09	-	58,58,58,58	0
57	MG	DA	3320	1/1	0.13	-	49,49,49,49	0
57	MG	DA	3290	1/1	0.10	-	33,33,33,33	0
57	MG	AA	1604	1/1	0.11	-	58,58,58,58	0
57	MG	DA	3521	1/1	0.06	-	57,57,57,57	0
57	MG	DA	3210	1/1	0.06	-	52,52,52,52	0
57	MG	DA	3178	1/1	0.12	-	40,40,40,40	0
57	MG	BA	3179	1/1	0.20	-	43,43,43,43	0
57	MG	AA	1644	1/1	0.13	-	56,56,56,56	0
57	MG	AA	1641	1/1	0.14	-	65,65,65,65	0
57	MG	AA	1751	1/1	0.19	-	53,53,53,53	0
57	MG	BA	3445	1/1	0.18	-	54,54,54,54	0
57	MG	BA	3203	1/1	0.27	-	61,61,61,61	0
57	MG	BA	3240	1/1	0.13	-	53,53,53,53	0
57	MG	CA	3147	1/1	0.06	-	70,70,70,70	0
57	MG	BA	3263	1/1	0.26	-	60,60,60,60	0
57	MG	DA	3003	1/1	0.20	-	36,36,36,36	0
57	MG	BA	3295	1/1	0.23	-	23,23,23,23	0
57	MG	DA	3644	1/1	0.20	-	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	BA	3343	1/1	0.19	-	54,54,54,54	0
57	MG	CA	3090	1/1	0.16	-	76,76,76,76	0
57	MG	DA	3601	1/1	0.09	-	55,55,55,55	0
57	MG	BA	3735	1/1	0.18	-	50,50,50,50	0
57	MG	BA	3509	1/1	0.20	-	50,50,50,50	0
57	MG	DA	3085	1/1	0.15	-	28,28,28,28	0
57	MG	BA	3749	1/1	0.07	-	52,52,52,52	0
57	MG	CA	3163	1/1	0.14	-	62,62,62,62	0
57	MG	CA	3077	1/1	0.18	-	60,60,60,60	0
57	MG	DA	3529	1/1	0.05	-	76,76,76,76	0
57	MG	DA	3593	1/1	0.08	-	60,60,60,60	0
59	ZN	CN	501	1/1	0.06	-	100,100,100,100	0
57	MG	CA	3075	1/1	0.17	-	65,65,65,65	0
57	MG	AA	1789	1/1	0.12	-	60,60,60,60	0
57	MG	CA	3017	1/1	0.14	-	54,54,54,54	0
57	MG	BA	3407	1/1	0.15	-	32,32,32,32	0
57	MG	BA	3186	1/1	0.17	-	41,41,41,41	0
57	MG	DA	3236	1/1	0.08	-	55,55,55,55	0
57	MG	BA	3153	1/1	0.11	-	45,45,45,45	0
59	ZN	B9	501	1/1	0.20	-	49,49,49,49	0
57	MG	BA	3395	1/1	0.17	-	30,30,30,30	0
57	MG	DA	3478	1/1	0.14	-	58,58,58,58	0
57	MG	BA	3226	1/1	0.17	-	25,25,25,25	0
57	MG	DA	3190	1/1	0.14	-	63,63,63,63	0
57	MG	DA	3090	1/1	0.26	-	50,50,50,50	0
57	MG	AF	3001	1/1	0.13	-	50,50,50,50	0
57	MG	BA	3348	1/1	0.14	-	37,37,37,37	0
57	MG	DA	3019	1/1	0.07	-	42,42,42,42	0
57	MG	BA	3552	1/1	0.16	-	55,55,55,55	0
57	MG	BA	3296	1/1	0.14	-	55,55,55,55	0
57	MG	DA	3433	1/1	0.17	-	59,59,59,59	0
57	MG	AA	1625	1/1	0.21	-	73,73,73,73	0
57	MG	DA	3544	1/1	0.15	-	53,53,53,53	0
57	MG	DA	3641	1/1	0.08	-	46,46,46,46	0
57	MG	DA	3346	1/1	0.12	-	49,49,49,49	0
57	MG	BA	3158	1/1	0.16	-	41,41,41,41	0
57	MG	BA	3063	1/1	0.25	-	47,47,47,47	0
57	MG	BA	3626	1/1	0.11	-	50,50,50,50	0
57	MG	DA	3106	1/1	0.15	-	50,50,50,50	0
57	MG	DA	3365	1/1	0.12	-	19,19,19,19	0
57	MG	CA	3104	1/1	0.18	-	37,37,37,37	0
57	MG	BA	3353	1/1	0.10	-	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	3334	1/1	0.22	-	57,57,57,57	0
57	MG	AA	1720	1/1	0.13	-	55,55,55,55	0
57	MG	BA	3093	1/1	0.21	-	41,41,41,41	0
57	MG	BD	3006	1/1	0.07	-	34,34,34,34	0
57	MG	DA	3387	1/1	0.07	-	59,59,59,59	0
57	MG	DA	3421	1/1	0.11	-	56,56,56,56	0
57	MG	DA	3562	1/1	0.10	-	31,31,31,31	0
57	MG	DA	3654	1/1	0.16	-	35,35,35,35	0
57	MG	DA	3413	1/1	0.19	-	62,62,62,62	0
57	MG	DA	3632	1/1	0.12	-	52,52,52,52	0
57	MG	AA	1724	1/1	0.15	-	39,39,39,39	0
57	MG	DA	3526	1/1	0.09	-	52,52,52,52	0
57	MG	BA	3697	1/1	0.13	-	41,41,41,41	0
57	MG	DA	3253	1/1	0.10	-	54,54,54,54	0
57	MG	BA	3812	1/1	0.17	-	42,42,42,42	0
57	MG	DA	3536	1/1	0.07	-	52,52,52,52	0
57	MG	AA	1737	1/1	0.11	-	60,60,60,60	0
57	MG	BA	3702	1/1	0.11	-	39,39,39,39	0
57	MG	BF	302	1/1	0.24	-	30,30,30,30	0
57	MG	DA	3126	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3455	1/1	0.12	-	64,64,64,64	0
57	MG	AA	1631	1/1	0.12	-	64,64,64,64	0
57	MG	AA	1771	1/1	0.18	-	75,75,75,75	0
57	MG	DA	3018	1/1	0.07	-	31,31,31,31	0
57	MG	BA	3772	1/1	0.10	-	36,36,36,36	0
57	MG	DA	3570	1/1	0.14	-	43,43,43,43	0
57	MG	BA	3676	1/1	0.15	-	70,70,70,70	0
57	MG	BA	3561	1/1	0.26	-	34,34,34,34	0
57	MG	CA	3122	1/1	0.11	-	69,69,69,69	0
57	MG	DA	3080	1/1	0.07	-	49,49,49,49	0
57	MG	BA	3187	1/1	0.15	-	38,38,38,38	0
57	MG	BA	3475	1/1	0.07	-	49,49,49,49	0
57	MG	BA	3163	1/1	0.31	-	55,55,55,55	0
57	MG	DA	3524	1/1	0.15	-	52,52,52,52	0
57	MG	BA	3181	1/1	0.07	-	40,40,40,40	0
57	MG	BA	3375	1/1	0.20	-	39,39,39,39	0
57	MG	DB	3007	1/1	0.12	-	67,67,67,67	0
57	MG	AA	1805	1/1	0.07	-	48,48,48,48	0
57	MG	DA	3559	1/1	0.12	-	67,67,67,67	0
57	MG	DA	3241	1/1	0.09	-	55,55,55,55	0
57	MG	DA	3095	1/1	0.13	-	60,60,60,60	0
57	MG	BA	3048	1/1	0.16	-	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3093	1/1	0.17	-	47,47,47,47	0
57	MG	DA	3201	1/1	0.09	-	52,52,52,52	0
57	MG	BA	3410	1/1	0.13	-	55,55,55,55	0
57	MG	BA	3559	1/1	0.20	-	26,26,26,26	0
57	MG	BA	3078	1/1	0.28	-	54,54,54,54	0
57	MG	BA	3692	1/1	0.10	-	58,58,58,58	0
57	MG	AA	1666	1/1	0.31	-	63,63,63,63	0
57	MG	BA	3379	1/1	0.18	-	35,35,35,35	0
57	MG	BA	3140	1/1	0.09	-	58,58,58,58	0
57	MG	BA	3532	1/1	0.11	-	55,55,55,55	0
57	MG	BA	3024	1/1	0.16	-	58,58,58,58	0
57	MG	BA	3687	1/1	0.16	-	64,64,64,64	0
57	MG	DA	3554	1/1	0.08	-	50,50,50,50	0
57	MG	DA	3363	1/1	0.10	-	50,50,50,50	0
57	MG	BA	3610	1/1	0.10	-	61,61,61,61	0
57	MG	DA	3473	1/1	0.18	-	50,50,50,50	0
57	MG	BA	3088	1/1	0.21	-	43,43,43,43	0
57	MG	CX	3002	1/1	0.10	-	67,67,67,67	0
57	MG	CA	3003	1/1	0.13	-	58,58,58,58	0
57	MG	AA	1726	1/1	0.11	-	58,58,58,58	0
57	MG	BA	3235	1/1	0.15	-	44,44,44,44	0
57	MG	BA	3156	1/1	0.15	-	35,35,35,35	0
57	MG	AA	1740	1/1	0.13	-	41,41,41,41	0
57	MG	BA	3105	1/1	0.11	-	46,46,46,46	0
57	MG	BA	3050	1/1	0.14	-	32,32,32,32	0
57	MG	CA	3082	1/1	0.10	-	66,66,66,66	0
57	MG	DF	302	1/1	0.15	-	53,53,53,53	0
57	MG	DA	3367	1/1	0.22	-	49,49,49,49	0
57	MG	BA	3090	1/1	0.23	-	38,38,38,38	0
57	MG	DA	3360	1/1	0.10	-	31,31,31,31	0
57	MG	BA	3810	1/1	0.16	-	35,35,35,35	0
57	MG	AA	1774	1/1	0.17	-	51,51,51,51	0
57	MG	DA	3268	1/1	0.09	-	41,41,41,41	0
57	MG	DA	3429	1/1	0.17	-	36,36,36,36	0
57	MG	AN	502	1/1	0.23	-	62,62,62,62	0
57	MG	DA	3545	1/1	0.11	-	62,62,62,62	0
57	MG	BA	3508	1/1	0.19	-	20,20,20,20	0
57	MG	DO	202	1/1	0.09	-	60,60,60,60	0
57	MG	AA	1633	1/1	0.29	-	59,59,59,59	0
57	MG	BA	3332	1/1	0.07	-	54,54,54,54	0
57	MG	DA	3275	1/1	0.19	-	65,65,65,65	0
57	MG	AB	3001	1/1	0.11	-	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3682	1/1	0.08	-	60,60,60,60	0
57	MG	AX	3013	1/1	0.17	-	70,70,70,70	0
57	MG	AA	1758	1/1	0.06	-	37,37,37,37	0
57	MG	DA	3333	1/1	0.16	-	47,47,47,47	0
57	MG	BA	3773	1/1	0.16	-	32,32,32,32	0
57	MG	AY	3003	1/1	0.06	-	79,79,79,79	0
57	MG	DA	3331	1/1	0.15	-	47,47,47,47	0
57	MG	CA	3088	1/1	0.12	-	43,43,43,43	0
57	MG	BA	3637	1/1	0.16	-	38,38,38,38	0
57	MG	BA	3399	1/1	0.17	-	41,41,41,41	0
57	MG	BA	3098	1/1	0.16	-	23,23,23,23	0
57	MG	BB	3017	1/1	0.16	-	81,81,81,81	0
57	MG	DA	3494	1/1	0.18	-	45,45,45,45	0
57	MG	AA	1658	1/1	0.11	-	64,64,64,64	0
57	MG	BD	3003	1/1	0.24	-	37,37,37,37	0
57	MG	BB	3006	1/1	0.09	-	62,62,62,62	0
57	MG	DA	3424	1/1	0.16	-	41,41,41,41	0
57	MG	BA	3345	1/1	0.17	-	51,51,51,51	0
57	MG	BN	3003	1/1	0.13	-	38,38,38,38	0
57	MG	BA	3003	1/1	0.13	-	33,33,33,33	0
57	MG	CA	3149	1/1	0.10	-	54,54,54,54	0
57	MG	CA	3110	1/1	0.10	-	63,63,63,63	0
57	MG	BA	3797	1/1	0.23	-	51,51,51,51	0
57	MG	AA	1745	1/1	0.17	-	36,36,36,36	0
57	MG	DA	3100	1/1	0.06	-	47,47,47,47	0
57	MG	AX	3009	1/1	0.35	-	65,65,65,65	0
57	MG	BA	3440	1/1	0.16	-	35,35,35,35	0
57	MG	DA	3636	1/1	0.11	-	62,62,62,62	0
57	MG	BA	3143	1/1	0.08	-	41,41,41,41	0
57	MG	BA	3430	1/1	0.20	-	34,34,34,34	0
57	MG	BA	3470	1/1	0.11	-	57,57,57,57	0
57	MG	BA	3182	1/1	0.56	-	52,52,52,52	0
57	MG	CA	3059	1/1	0.17	-	75,75,75,75	0
57	MG	DE	3006	1/1	0.15	-	38,38,38,38	0
57	MG	DA	3311	1/1	0.12	-	46,46,46,46	0
57	MG	BA	3646	1/1	0.14	-	50,50,50,50	0
57	MG	BA	3754	1/1	0.11	-	42,42,42,42	0
57	MG	AA	1682	1/1	0.21	-	59,59,59,59	0
57	MG	AA	1635	1/1	0.11	-	65,65,65,65	0
57	MG	BA	3313	1/1	0.18	-	38,38,38,38	0
57	MG	CA	3146	1/1	0.14	-	72,72,72,72	0
57	MG	AX	3004	1/1	0.15	-	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	DA	3094	1/1	0.06	-	39,39,39,39	0
57	MG	DE	3002	1/1	0.10	-	33,33,33,33	0
57	MG	BA	3716	1/1	0.25	-	45,45,45,45	0
57	MG	DA	3151	1/1	0.10	-	37,37,37,37	0
57	MG	BA	3115	1/1	0.16	-	33,33,33,33	0
57	MG	BA	3411	1/1	0.18	-	50,50,50,50	0
57	MG	BA	3330	1/1	0.16	-	27,27,27,27	0
57	MG	BA	3566	1/1	0.22	-	31,31,31,31	0
57	MG	BA	3374	1/1	0.18	-	50,50,50,50	0
57	MG	DA	3372	1/1	0.11	-	53,53,53,53	0
57	MG	DB	3008	1/1	0.20	-	56,56,56,56	0
57	MG	BA	3329	1/1	0.10	-	60,60,60,60	0
57	MG	DA	3035	1/1	0.13	-	37,37,37,37	0
57	MG	BA	3141	1/1	0.28	-	38,38,38,38	0
57	MG	BA	3752	1/1	0.09	-	34,34,34,34	0
57	MG	BA	3111	1/1	0.34	-	53,53,53,53	0
57	MG	DA	3449	1/1	0.10	-	34,34,34,34	0
57	MG	BA	3001	1/1	0.11	-	43,43,43,43	0
57	MG	DA	3590	1/1	0.21	-	51,51,51,51	0
57	MG	BA	3513	1/1	0.30	-	50,50,50,50	0
57	MG	DA	3608	1/1	0.06	-	57,57,57,57	0
57	MG	DA	3466	1/1	0.08	-	48,48,48,48	0
57	MG	CA	3132	1/1	0.11	-	64,64,64,64	0
57	MG	AA	1660	1/1	0.19	-	51,51,51,51	0
57	MG	BA	3184	1/1	0.10	-	42,42,42,42	0
57	MG	CA	3112	1/1	0.08	-	72,72,72,72	0
57	MG	CA	3078	1/1	0.17	-	65,65,65,65	0
57	MG	BA	3764	1/1	0.12	-	66,66,66,66	0
57	MG	AA	1797	1/1	0.13	-	59,59,59,59	0
57	MG	AA	1678	1/1	0.22	-	47,47,47,47	0
57	MG	BA	3681	1/1	0.15	-	61,61,61,61	0
57	MG	DA	3160	1/1	0.31	-	62,62,62,62	0
57	MG	BA	3380	1/1	0.12	-	40,40,40,40	0
57	MG	CA	3023	1/1	0.09	-	39,39,39,39	0
57	MG	DA	3043	1/1	0.13	-	53,53,53,53	0
57	MG	DA	3565	1/1	0.05	-	52,52,52,52	0
57	MG	BA	3064	1/1	0.21	-	45,45,45,45	0
57	MG	AA	1701	1/1	0.22	-	73,73,73,73	0
57	MG	CA	3083	1/1	0.12	-	50,50,50,50	0
57	MG	DA	3411	1/1	0.17	-	37,37,37,37	0
57	MG	DA	3128	1/1	0.24	-	56,56,56,56	0
57	MG	BA	3072	1/1	0.12	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3283	1/1	0.31	-	57,57,57,57	0
57	MG	BA	3518	1/1	0.19	-	46,46,46,46	0
57	MG	BA	3523	1/1	0.19	-	41,41,41,41	0
57	MG	AA	1694	1/1	0.06	-	47,47,47,47	0
57	MG	BA	3805	1/1	0.11	-	48,48,48,48	0
57	MG	BA	3457	1/1	0.17	-	48,48,48,48	0
57	MG	BA	3724	1/1	0.14	-	20,20,20,20	0
57	MG	BA	3511	1/1	0.12	-	50,50,50,50	0
57	MG	BA	3055	1/1	0.22	-	37,37,37,37	0
57	MG	DA	3274	1/1	0.27	-	40,40,40,40	0
57	MG	BA	3031	1/1	0.22	-	36,36,36,36	0
57	MG	BR	5001	1/1	0.11	-	50,50,50,50	0
57	MG	AA	1782	1/1	0.11	-	54,54,54,54	0
57	MG	DA	3143	1/1	0.10	-	62,62,62,62	0
57	MG	AA	1683	1/1	0.16	-	62,62,62,62	0
57	MG	B0	3001	1/1	0.30	-	47,47,47,47	0
57	MG	BA	3652	1/1	0.08	-	58,58,58,58	0
57	MG	CA	3056	1/1	0.08	-	64,64,64,64	0
57	MG	CA	3065	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3009	1/1	0.13	-	61,61,61,61	0
57	MG	DA	3077	1/1	0.09	-	38,38,38,38	0
57	MG	BD	3004	1/1	0.32	-	28,28,28,28	0
57	MG	B7	104	1/1	0.19	-	62,62,62,62	0
57	MG	BB	3010	1/1	0.19	-	53,53,53,53	0
57	MG	DA	3427	1/1	0.15	-	47,47,47,47	0
57	MG	AA	1669	1/1	0.17	-	69,69,69,69	0
57	MG	AA	1752	1/1	0.13	-	48,48,48,48	0
58	SF4	AD	501	8/8	0.17	-	59,68,73,79	0
57	MG	BA	3169	1/1	0.14	-	50,50,50,50	0
57	MG	DA	3096	1/1	0.08	-	68,68,68,68	0
57	MG	BA	3377	1/1	0.19	-	51,51,51,51	0
57	MG	DA	3606	1/1	0.17	-	74,74,74,74	0
57	MG	AA	1729	1/1	0.13	-	35,35,35,35	0
57	MG	BA	3581	1/1	0.11	-	59,59,59,59	0
57	MG	BA	3698	1/1	0.09	-	47,47,47,47	0
57	MG	BA	3151	1/1	0.14	-	36,36,36,36	0
57	MG	CA	3049	1/1	0.26	-	65,65,65,65	0
57	MG	BA	3092	1/1	0.28	-	40,40,40,40	0
57	MG	AA	1630	1/1	0.09	-	53,53,53,53	0
57	MG	BA	3704	1/1	0.21	-	26,26,26,26	0
57	MG	BF	304	1/1	0.40	-	41,41,41,41	0
57	MG	BA	3390	1/1	0.07	-	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3537	1/1	0.07	-	43,43,43,43	0
57	MG	BA	3344	1/1	0.09	-	71,71,71,71	0
57	MG	BA	3172	1/1	0.32	-	40,40,40,40	0
57	MG	AA	1749	1/1	0.17	-	50,50,50,50	0
57	MG	BA	3220	1/1	0.11	-	35,35,35,35	0
57	MG	BA	3006	1/1	0.41	-	54,54,54,54	0
57	MG	BA	3456	1/1	0.27	-	37,37,37,37	0
58	SF4	CD	501	8/8	0.16	-	64,67,74,91	0
57	MG	AA	1785	1/1	0.12	-	72,72,72,72	0
57	MG	BA	3268	1/1	0.17	-	54,54,54,54	0
57	MG	CA	3119	1/1	0.10	-	59,59,59,59	0
57	MG	BA	3713	1/1	0.26	-	33,33,33,33	0
57	MG	BA	3190	1/1	0.27	-	54,54,54,54	0
57	MG	BA	3444	1/1	0.10	-	48,48,48,48	0
57	MG	DA	3337	1/1	0.06	-	48,48,48,48	0
57	MG	AA	1617	1/1	0.11	-	58,58,58,58	0
57	MG	BA	3335	1/1	0.11	-	40,40,40,40	0
57	MG	AA	1773	1/1	0.09	-	61,61,61,61	0
57	MG	DA	3059	1/1	0.06	-	50,50,50,50	0
57	MG	BA	3188	1/1	0.16	-	32,32,32,32	0
57	MG	DA	3108	1/1	0.09	-	50,50,50,50	0
57	MG	CA	3089	1/1	0.21	-	74,74,74,74	0
57	MG	DA	3137	1/1	0.15	-	52,52,52,52	0
57	MG	DA	3450	1/1	0.06	-	50,50,50,50	0
57	MG	BB	3001	1/1	0.27	-	68,68,68,68	0
57	MG	DA	3556	1/1	0.08	-	55,55,55,55	0
57	MG	DA	3525	1/1	0.10	-	28,28,28,28	0
57	MG	DA	3116	1/1	0.13	-	53,53,53,53	0
57	MG	CA	3117	1/1	0.07	-	63,63,63,63	0
57	MG	BA	3318	1/1	0.14	-	54,54,54,54	0
57	MG	BA	3528	1/1	0.18	-	36,36,36,36	0
57	MG	AM	3002	1/1	0.09	-	68,68,68,68	0
57	MG	BA	3252	1/1	0.17	-	36,36,36,36	0
57	MG	B8	5002	1/1	0.23	-	53,53,53,53	0
57	MG	AA	1755	1/1	0.09	-	80,80,80,80	0
57	MG	CA	3006	1/1	0.07	-	68,68,68,68	0
57	MG	CA	3045	1/1	0.21	-	62,62,62,62	0
57	MG	BN	3002	1/1	0.20	-	51,51,51,51	0
57	MG	CA	3024	1/1	0.11	-	67,67,67,67	0
57	MG	BA	3408	1/1	0.20	-	51,51,51,51	0
57	MG	DD	302	1/1	0.14	-	49,49,49,49	0
57	MG	CA	3074	1/1	0.11	-	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	BA	3249	1/1	0.18	-	53,53,53,53	0
57	MG	DA	3234	1/1	0.10	-	54,54,54,54	0
57	MG	BA	3398	1/1	0.20	-	32,32,32,32	0
57	MG	CA	3026	1/1	0.13	-	66,66,66,66	0
57	MG	BA	3621	1/1	0.14	-	43,43,43,43	0
57	MG	DA	3045	1/1	0.10	-	51,51,51,51	0
57	MG	BA	3223	1/1	0.15	-	41,41,41,41	0
57	MG	BA	3294	1/1	0.13	-	43,43,43,43	0
57	MG	BA	3728	1/1	0.13	-	52,52,52,52	0
57	MG	BA	3454	1/1	0.15	-	46,46,46,46	0
57	MG	BA	3755	1/1	0.18	-	43,43,43,43	0
57	MG	BA	3804	1/1	0.14	-	36,36,36,36	0
57	MG	BA	3628	1/1	0.24	-	52,52,52,52	0
57	MG	BA	3189	1/1	0.16	-	39,39,39,39	0
57	MG	BA	3473	1/1	0.18	-	28,28,28,28	0
57	MG	BA	3359	1/1	0.06	-	60,60,60,60	0
57	MG	DA	3661	1/1	0.08	-	62,62,62,62	0
57	MG	BA	3350	1/1	0.07	-	34,34,34,34	0
57	MG	DA	3325	1/1	0.19	-	45,45,45,45	0
57	MG	DA	3617	1/1	0.21	-	51,51,51,51	0
57	MG	DA	3012	1/1	0.08	-	43,43,43,43	0
57	MG	BA	3574	1/1	0.16	-	42,42,42,42	0
57	MG	BA	3091	1/1	0.34	-	42,42,42,42	0
57	MG	DD	303	1/1	0.32	-	51,51,51,51	0
57	MG	DA	3179	1/1	0.05	-	59,59,59,59	0
57	MG	BA	3665	1/1	0.14	-	42,42,42,42	0
57	MG	BF	305	1/1	0.20	-	36,36,36,36	0
57	MG	BA	3021	1/1	0.08	-	43,43,43,43	0
57	MG	B6	101	1/1	0.19	-	60,60,60,60	0
57	MG	CA	3134	1/1	0.14	-	64,64,64,64	0
57	MG	DA	3357	1/1	0.12	-	33,33,33,33	0
57	MG	DA	3111	1/1	0.10	-	56,56,56,56	0
57	MG	BA	3678	1/1	0.10	-	67,67,67,67	0
57	MG	BA	3200	1/1	0.16	-	48,48,48,48	0
57	MG	BA	3730	1/1	0.17	-	68,68,68,68	0
57	MG	BA	3595	1/1	0.08	-	61,61,61,61	0
57	MG	BA	3242	1/1	0.68	-	55,55,55,55	0
57	MG	AA	1811	1/1	0.14	-	49,49,49,49	0
57	MG	CA	3151	1/1	0.08	-	64,64,64,64	0
57	MG	BA	3387	1/1	0.18	-	29,29,29,29	0
57	MG	BA	3520	1/1	0.23	-	29,29,29,29	0
57	MG	DP	202	1/1	0.08	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3685	1/1	0.22	-	61,61,61,61	0
57	MG	DA	3072	1/1	0.24	-	47,47,47,47	0
57	MG	DA	3318	1/1	0.10	-	45,45,45,45	0
57	MG	AA	1744	1/1	0.15	-	44,44,44,44	0
57	MG	CA	3038	1/1	0.10	-	57,57,57,57	0
57	MG	BA	3776	1/1	0.16	-	60,60,60,60	0
57	MG	DA	3124	1/1	0.16	-	43,43,43,43	0
57	MG	DA	3220	1/1	0.22	-	50,50,50,50	0
57	MG	AA	1748	1/1	0.17	-	64,64,64,64	0
57	MG	CA	3144	1/1	0.10	-	82,82,82,82	0
57	MG	AA	1624	1/1	0.23	-	66,66,66,66	0
57	MG	BB	3023	1/1	0.13	-	47,47,47,47	0
57	MG	DA	3507	1/1	0.12	-	59,59,59,59	0
57	MG	AA	1693	1/1	0.22	-	76,76,76,76	0
57	MG	BA	3701	1/1	0.28	-	39,39,39,39	0
57	MG	BA	3060	1/1	0.16	-	51,51,51,51	0
57	MG	AA	1649	1/1	0.13	-	28,28,28,28	0
57	MG	CA	3154	1/1	0.13	-	68,68,68,68	0
57	MG	DA	3056	1/1	0.10	-	49,49,49,49	0
57	MG	AM	3001	1/1	0.10	-	66,66,66,66	0
57	MG	AA	1619	1/1	0.08	-	64,64,64,64	0
57	MG	CA	3027	1/1	0.10	-	65,65,65,65	0
57	MG	BB	3003	1/1	0.13	-	30,30,30,30	0
57	MG	CA	3156	1/1	0.06	-	59,59,59,59	0
57	MG	DA	3029	1/1	0.46	-	45,45,45,45	0
57	MG	DA	3129	1/1	0.15	-	56,56,56,56	0
57	MG	BA	3418	1/1	0.19	-	38,38,38,38	0
57	MG	CA	3072	1/1	0.18	-	62,62,62,62	0
57	MG	BA	3244	1/1	0.23	-	31,31,31,31	0
57	MG	DA	3063	1/1	0.14	-	47,47,47,47	0
57	MG	DA	3226	1/1	0.18	-	57,57,57,57	0
57	MG	CA	3103	1/1	0.12	-	73,73,73,73	0
57	MG	DA	3214	1/1	0.07	-	51,51,51,51	0
57	MG	BA	3337	1/1	0.23	-	44,44,44,44	0
57	MG	BA	3671	1/1	0.16	-	24,24,24,24	0
57	MG	DA	3476	1/1	0.07	-	45,45,45,45	0
57	MG	DA	3031	1/1	0.08	-	42,42,42,42	0
57	MG	D3	3001	1/1	0.34	-	63,63,63,63	0
57	MG	BA	3477	1/1	0.13	-	68,68,68,68	0
57	MG	AA	1800	1/1	0.12	-	59,59,59,59	0
57	MG	BA	3624	1/1	0.11	-	38,38,38,38	0
57	MG	BA	3254	1/1	0.10	-	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	CA	3076	1/1	0.17	-	77,77,77,77	0
60	K	AX	3001	1/1	0.11	-	77,77,77,77	0
57	MG	DA	3382	1/1	0.10	-	41,41,41,41	0
57	MG	DA	3499	1/1	0.17	-	52,52,52,52	0
59	ZN	D4	501	1/1	0.10	-	162,162,162,162	0
57	MG	DB	3013	1/1	0.09	-	66,66,66,66	0
57	MG	CA	3143	1/1	0.15	-	74,74,74,74	0
57	MG	BA	3253	1/1	0.20	-	31,31,31,31	0
57	MG	AX	3005	1/1	0.10	-	65,65,65,65	0
57	MG	DA	3006	1/1	0.10	-	41,41,41,41	0
57	MG	DA	3610	1/1	0.06	-	47,47,47,47	0
57	MG	DA	3452	1/1	0.09	-	45,45,45,45	0
57	MG	BW	3003	1/1	0.13	-	35,35,35,35	0
57	MG	BA	3018	1/1	0.36	-	39,39,39,39	0
57	MG	DA	3385	1/1	0.06	-	60,60,60,60	0
57	MG	AX	3007	1/1	0.30	-	68,68,68,68	0
57	MG	DA	3437	1/1	0.23	-	48,48,48,48	0
57	MG	BA	3222	1/1	0.15	-	42,42,42,42	0
57	MG	DA	3240	1/1	0.06	-	52,52,52,52	0
57	MG	BA	3745	1/1	0.27	-	61,61,61,61	0
57	MG	CA	3106	1/1	0.10	-	58,58,58,58	0
57	MG	BA	3639	1/1	0.14	-	49,49,49,49	0
57	MG	CA	3057	1/1	0.15	-	84,84,84,84	0
57	MG	BA	3771	1/1	0.10	-	41,41,41,41	0
57	MG	AA	1747	1/1	0.17	-	55,55,55,55	0
57	MG	DA	3216	1/1	0.15	-	35,35,35,35	0
57	MG	DA	3362	1/1	0.20	-	42,42,42,42	0
57	MG	BA	3488	1/1	0.12	-	20,20,20,20	0
57	MG	BA	3420	1/1	0.17	-	25,25,25,25	0
57	MG	CA	3140	1/1	0.15	-	57,57,57,57	0
57	MG	BA	3630	1/1	0.23	-	39,39,39,39	0
57	MG	DA	3534	1/1	0.07	-	46,46,46,46	0
57	MG	AA	1766	1/1	0.13	-	71,71,71,71	0
57	MG	BA	3100	1/1	0.22	-	61,61,61,61	0
57	MG	AA	1761	1/1	0.21	-	70,70,70,70	0
57	MG	DA	3633	1/1	0.14	-	58,58,58,58	0
57	MG	BA	3696	1/1	0.10	-	46,46,46,46	0
57	MG	DA	3118	1/1	0.11	-	39,39,39,39	0
57	MG	BA	3067	1/1	0.21	-	43,43,43,43	0
57	MG	BA	3602	1/1	0.07	-	47,47,47,47	0
57	MG	BA	3372	1/1	0.09	-	40,40,40,40	0
57	MG	BA	3342	1/1	0.28	-	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	AA	1632	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3107	1/1	0.23	-	57,57,57,57	0
57	MG	DA	3340	1/1	0.13	-	27,27,27,27	0
57	MG	BA	3464	1/1	0.05	-	44,44,44,44	0
57	MG	BA	3419	1/1	0.16	-	25,25,25,25	0
57	MG	DA	3342	1/1	0.15	-	53,53,53,53	0
57	MG	AW	3002	1/1	0.09	-	79,79,79,79	0
57	MG	BA	3787	1/1	0.11	-	45,45,45,45	0
57	MG	DA	3471	1/1	0.34	-	54,54,54,54	0
57	MG	DA	3011	1/1	0.07	-	35,35,35,35	0
57	MG	BA	3617	1/1	0.07	-	42,42,42,42	0
57	MG	DA	3300	1/1	0.10	-	38,38,38,38	0
57	MG	DA	3086	1/1	0.11	-	47,47,47,47	0
57	MG	DA	3504	1/1	0.13	-	52,52,52,52	0
57	MG	BA	3333	1/1	0.15	-	57,57,57,57	0
57	MG	DA	3663	1/1	0.15	-	73,73,73,73	0
57	MG	DA	3279	1/1	0.10	-	36,36,36,36	0
57	MG	CA	3051	1/1	0.12	-	77,77,77,77	0
57	MG	BA	3615	1/1	0.12	-	71,71,71,71	0
57	MG	DA	3184	1/1	0.09	-	52,52,52,52	0
57	MG	BA	3038	1/1	0.20	-	20,20,20,20	0
57	MG	AW	3001	1/1	0.10	-	59,59,59,59	0
57	MG	AA	1791	1/1	0.07	-	54,54,54,54	0
57	MG	BA	3706	1/1	0.16	-	47,47,47,47	0
57	MG	DA	3083	1/1	0.16	-	41,41,41,41	0
57	MG	BF	307	1/1	0.09	-	34,34,34,34	0
57	MG	BA	3743	1/1	0.59	-	47,47,47,47	0
57	MG	DA	3492	1/1	0.05	-	48,48,48,48	0
57	MG	CA	3160	1/1	0.08	-	73,73,73,73	0
57	MG	BA	3308	1/1	0.17	-	39,39,39,39	0
57	MG	BA	3195	1/1	0.14	-	36,36,36,36	0
57	MG	AA	1763	1/1	0.05	-	79,79,79,79	0
57	MG	BA	3017	1/1	0.27	-	65,65,65,65	0
57	MG	DA	3057	1/1	0.15	-	44,44,44,44	0
57	MG	BA	3364	1/1	0.14	-	47,47,47,47	0
57	MG	DA	3425	1/1	0.15	-	51,51,51,51	0
57	MG	BA	3302	1/1	0.13	-	49,49,49,49	0
57	MG	DA	3404	1/1	0.08	-	43,43,43,43	0
57	MG	DA	3305	1/1	0.11	-	53,53,53,53	0
57	MG	DA	3250	1/1	0.10	-	50,50,50,50	0
57	MG	CF	3001	1/1	0.09	-	51,51,51,51	0
57	MG	BA	3300	1/1	0.14	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3483	1/1	0.06	-	53,53,53,53	0
57	MG	BW	3001	1/1	0.25	-	44,44,44,44	0
57	MG	DA	3386	1/1	0.07	-	44,44,44,44	0
57	MG	DA	3481	1/1	0.10	-	40,40,40,40	0
57	MG	DA	3605	1/1	0.08	-	45,45,45,45	0
57	MG	BA	3094	1/1	0.17	-	52,52,52,52	0
57	MG	AA	1750	1/1	0.13	-	49,49,49,49	0
57	MG	BA	3175	1/1	0.25	-	57,57,57,57	0
57	MG	BA	3075	1/1	0.12	-	24,24,24,24	0
57	MG	DA	3538	1/1	0.09	-	60,60,60,60	0
57	MG	AA	1713	1/1	0.11	-	67,67,67,67	0
57	MG	BA	3251	1/1	0.29	-	43,43,43,43	0
57	MG	BA	3751	1/1	0.21	-	37,37,37,37	0
57	MG	BA	3020	1/1	0.15	-	25,25,25,25	0
57	MG	CA	3155	1/1	0.12	-	57,57,57,57	0
57	MG	DA	3091	1/1	0.22	-	54,54,54,54	0
57	MG	DF	303	1/1	0.29	-	42,42,42,42	0
57	MG	BD	3009	1/1	0.13	-	37,37,37,37	0
57	MG	DA	3048	1/1	0.07	-	59,59,59,59	0
57	MG	CA	3097	1/1	0.22	-	60,60,60,60	0
57	MG	AA	1717	1/1	0.14	-	75,75,75,75	0
57	MG	BA	3575	1/1	0.13	-	50,50,50,50	0
57	MG	DA	3245	1/1	0.07	-	58,58,58,58	0
57	MG	CA	3162	1/1	0.08	-	79,79,79,79	0
57	MG	DA	3115	1/1	0.21	-	55,55,55,55	0
57	MG	DA	3516	1/1	0.19	-	67,67,67,67	0
57	MG	CA	3131	1/1	0.17	-	69,69,69,69	0
57	MG	BA	3299	1/1	0.18	-	60,60,60,60	0
57	MG	BA	3609	1/1	0.19	-	56,56,56,56	0
57	MG	DA	3189	1/1	0.15	-	47,47,47,47	0
57	MG	BA	3462	1/1	0.09	-	53,53,53,53	0
57	MG	DA	3356	1/1	0.16	-	39,39,39,39	0
57	MG	BA	3712	1/1	0.22	-	51,51,51,51	0
57	MG	BA	3506	1/1	0.18	-	61,61,61,61	0
57	MG	BA	3328	1/1	0.16	-	27,27,27,27	0
57	MG	BA	3131	1/1	0.22	-	44,44,44,44	0
57	MG	BA	3695	1/1	0.10	-	40,40,40,40	0
57	MG	BA	3591	1/1	0.39	-	41,41,41,41	0
57	MG	DA	3307	1/1	0.09	-	51,51,51,51	0
57	MG	AA	1779	1/1	0.11	-	59,59,59,59	0
57	MG	BA	3315	1/1	0.12	-	40,40,40,40	0
57	MG	AA	1685	1/1	0.18	-	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	3490	1/1	0.14	-	43,43,43,43	0
57	MG	DA	3444	1/1	0.18	-	44,44,44,44	0
57	MG	AA	1674	1/1	0.14	-	58,58,58,58	0
57	MG	AL	202	1/1	0.23	-	56,56,56,56	0
57	MG	DA	3225	1/1	0.08	-	55,55,55,55	0
57	MG	CA	3047	1/1	0.12	-	50,50,50,50	0
57	MG	DA	3658	1/1	0.43	-	62,62,62,62	0
57	MG	BA	3578	1/1	0.30	-	39,39,39,39	0
57	MG	DA	3135	1/1	0.28	-	63,63,63,63	0
57	MG	DA	3228	1/1	0.13	-	44,44,44,44	0
57	MG	BA	3065	1/1	0.25	-	50,50,50,50	0
57	MG	BA	3629	1/1	0.19	-	58,58,58,58	0
57	MG	BA	3269	1/1	0.17	-	45,45,45,45	0
57	MG	BA	3461	1/1	0.07	-	45,45,45,45	0
57	MG	AA	1759	1/1	0.16	-	55,55,55,55	0
57	MG	BA	3416	1/1	0.28	-	60,60,60,60	0
57	MG	BA	3112	1/1	0.24	-	41,41,41,41	0
57	MG	BA	3582	1/1	0.11	-	31,31,31,31	0
57	MG	BA	3059	1/1	0.11	-	36,36,36,36	0
57	MG	AA	1764	1/1	0.06	-	66,66,66,66	0
57	MG	DA	3409	1/1	0.09	-	54,54,54,54	0
57	MG	BA	3368	1/1	0.25	-	32,32,32,32	0
57	MG	DA	3511	1/1	0.09	-	44,44,44,44	0
57	MG	BA	3533	1/1	0.18	-	23,23,23,23	0
57	MG	BA	3565	1/1	0.14	-	61,61,61,61	0
57	MG	BA	3744	1/1	0.15	-	55,55,55,55	0
57	MG	BA	3180	1/1	0.24	-	46,46,46,46	0
57	MG	BA	3633	1/1	0.16	-	57,57,57,57	0
57	MG	DA	3513	1/1	0.15	-	69,69,69,69	0
57	MG	BA	3567	1/1	0.23	-	32,32,32,32	0
57	MG	BA	3044	1/1	0.30	-	43,43,43,43	0
57	MG	BA	3770	1/1	0.43	-	49,49,49,49	0
57	MG	CA	3125	1/1	0.21	-	64,64,64,64	0
57	MG	DA	3438	1/1	0.06	-	42,42,42,42	0
57	MG	DA	3247	1/1	0.09	-	49,49,49,49	0
57	MG	AY	3002	1/1	0.36	-	52,52,52,52	0
57	MG	BA	3147	1/1	0.16	-	36,36,36,36	0
57	MG	BA	3632	1/1	0.26	-	55,55,55,55	0
57	MG	AA	1627	1/1	0.09	-	54,54,54,54	0
57	MG	DA	3581	1/1	0.05	-	44,44,44,44	0
57	MG	BA	3137	1/1	0.23	-	52,52,52,52	0
57	MG	DA	3073	1/1	0.05	-	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	BA	3748	1/1	0.08	-	61,61,61,61	0
57	MG	DA	3519	1/1	0.14	-	58,58,58,58	0
57	MG	BA	3434	1/1	0.08	-	19,19,19,19	0
57	MG	AA	1686	1/1	0.16	-	61,61,61,61	0
57	MG	BA	3767	1/1	0.32	-	45,45,45,45	0
57	MG	BD	3001	1/1	0.10	-	34,34,34,34	0
57	MG	CA	3159	1/1	0.12	-	62,62,62,62	0
57	MG	DA	3286	1/1	0.12	-	55,55,55,55	0
57	MG	DA	3259	1/1	0.09	-	42,42,42,42	0
57	MG	BA	3592	1/1	0.07	-	65,65,65,65	0
57	MG	CD	502	1/1	0.19	-	53,53,53,53	0
57	MG	BA	3433	1/1	0.22	-	27,27,27,27	0
57	MG	DA	3155	1/1	0.19	-	53,53,53,53	0
57	MG	DA	3060	1/1	0.22	-	60,60,60,60	0
57	MG	BA	3483	1/1	0.12	-	44,44,44,44	0
57	MG	BA	3030	1/1	0.20	-	39,39,39,39	0
57	MG	DA	3217	1/1	0.15	-	57,57,57,57	0
57	MG	BA	3541	1/1	0.19	-	38,38,38,38	0
57	MG	BA	3442	1/1	0.19	-	65,65,65,65	0
57	MG	AA	1723	1/1	0.13	-	63,63,63,63	0
57	MG	BA	3081	1/1	0.20	-	48,48,48,48	0
57	MG	DA	3553	1/1	0.06	-	72,72,72,72	0
57	MG	DA	3114	1/1	0.10	-	51,51,51,51	0
57	MG	CA	3118	1/1	0.14	-	60,60,60,60	0
57	MG	BA	3790	1/1	0.72	-	66,66,66,66	0
57	MG	BA	3750	1/1	0.18	-	46,46,46,46	0
57	MG	DA	3230	1/1	0.09	-	46,46,46,46	0
57	MG	DA	3436	1/1	0.11	-	35,35,35,35	0
57	MG	DA	3402	1/1	0.07	-	48,48,48,48	0
57	MG	BA	3028	1/1	0.18	-	37,37,37,37	0
57	MG	BA	3349	1/1	0.17	-	34,34,34,34	0
57	MG	DA	3046	1/1	0.13	-	56,56,56,56	0
57	MG	BB	3004	1/1	0.18	-	69,69,69,69	0
57	MG	BA	3096	1/1	0.14	-	60,60,60,60	0
57	MG	DA	3284	1/1	0.10	-	58,58,58,58	0
57	MG	BA	3197	1/1	0.21	-	58,58,58,58	0
57	MG	BA	3216	1/1	0.27	-	39,39,39,39	0
57	MG	BA	3814	1/1	0.21	-	39,39,39,39	0
57	MG	BA	3026	1/1	0.25	-	60,60,60,60	0
57	MG	BA	3237	1/1	0.13	-	44,44,44,44	0
57	MG	DE	3007	1/1	0.08	-	58,58,58,58	0
57	MG	BA	3154	1/1	0.18	-	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	3510	1/1	0.18	-	45,45,45,45	0
57	MG	BN	3001	1/1	0.15	-	48,48,48,48	0
57	MG	BA	3534	1/1	0.23	-	26,26,26,26	0
57	MG	CA	3087	1/1	0.07	-	57,57,57,57	0
57	MG	BA	3780	1/1	0.08	-	42,42,42,42	0
57	MG	D8	5001	1/1	0.18	-	44,44,44,44	0
57	MG	BA	3202	1/1	0.09	-	62,62,62,62	0
57	MG	BA	3076	1/1	0.22	-	42,42,42,42	0
57	MG	DA	3441	1/1	0.19	-	58,58,58,58	0
57	MG	BA	3297	1/1	0.22	-	42,42,42,42	0
57	MG	DV	201	1/1	0.78	-	58,58,58,58	0
57	MG	DA	3655	1/1	0.14	-	38,38,38,38	0
57	MG	CA	3136	1/1	0.14	-	48,48,48,48	0
57	MG	CA	3094	1/1	0.08	-	61,61,61,61	0
57	MG	BA	3550	1/1	0.15	-	50,50,50,50	0
57	MG	CA	3011	1/1	0.23	-	66,66,66,66	0
57	MG	DA	3607	1/1	0.09	-	64,64,64,64	0
57	MG	DA	3398	1/1	0.07	-	40,40,40,40	0
57	MG	CA	3018	1/1	0.11	-	63,63,63,63	0
57	MG	CA	3012	1/1	0.25	-	64,64,64,64	0
57	MG	BA	3476	1/1	0.14	-	48,48,48,48	0
57	MG	CA	3116	1/1	0.18	-	57,57,57,57	0
57	MG	CA	3101	1/1	0.09	-	65,65,65,65	0
57	MG	DA	3182	1/1	0.20	-	52,52,52,52	0
57	MG	DA	3528	1/1	0.14	-	36,36,36,36	0
57	MG	DA	3533	1/1	0.16	-	56,56,56,56	0
57	MG	BA	3132	1/1	0.10	-	50,50,50,50	0
57	MG	BA	3769	1/1	0.17	-	47,47,47,47	0
57	MG	DA	3596	1/1	0.29	-	69,69,69,69	0
57	MG	BA	3207	1/1	0.21	-	36,36,36,36	0
57	MG	DA	3353	1/1	0.12	-	47,47,47,47	0
57	MG	BA	3286	1/1	0.14	-	44,44,44,44	0
57	MG	BA	3781	1/1	0.15	-	56,56,56,56	0
57	MG	DA	3027	1/1	0.46	-	43,43,43,43	0
57	MG	DA	3591	1/1	0.07	-	66,66,66,66	0
57	MG	BA	3033	1/1	0.47	-	31,31,31,31	0
57	MG	BA	3556	1/1	0.09	-	46,46,46,46	0
57	MG	AA	1812	1/1	0.13	-	63,63,63,63	0
57	MG	CJ	5001	1/1	0.12	-	77,77,77,77	0
57	MG	BA	3516	1/1	0.23	-	46,46,46,46	0
57	MG	DA	3588	1/1	0.18	-	59,59,59,59	0
57	MG	BA	3492	1/1	0.06	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3497	1/1	0.16	-	50,50,50,50	0
57	MG	DA	3580	1/1	0.20	-	62,62,62,62	0
57	MG	DA	3262	1/1	0.09	-	20,20,20,20	0
57	MG	BA	3807	1/1	0.20	-	66,66,66,66	0

6.5 Other polymers

There are no such residues in this entry.