Full wwPDB X-ray Structure Validation Report

Mar 12, 2026 – 07:51 AM UTC

PDB ID	:	1VY7 / pdb_00001vy7
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in the pre-attack state of peptide bond formation containing short substrate-mimic Cytidine-Cytidine-Puromycin in the A site and acylated tRNA in the P site.
Authors	:	Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on	:	2014-05-13
Resolution	:	2.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

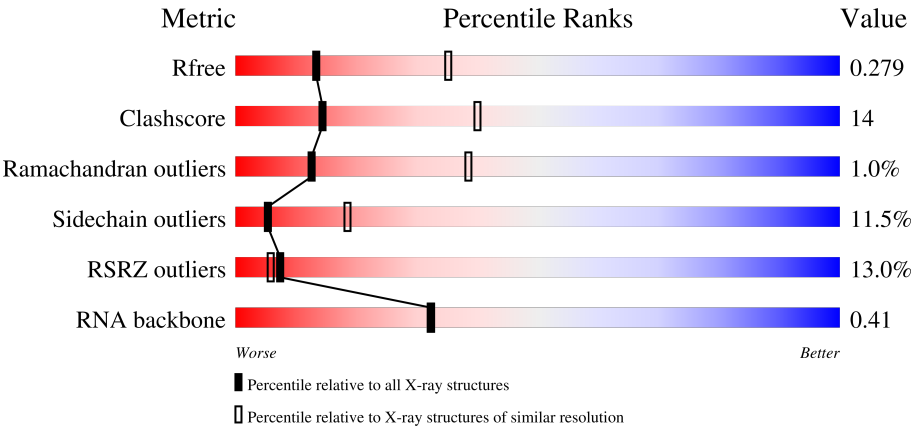
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1521	7% 38% 44% 16% ·
1	CA	1521	16% 33% 48% 17% ·
2	AB	256	20% 46% 35% 9% 10%
2	CB	256	39% 46% 34% 9% · 10%

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Mol	Chain	Length	Quality of chain
3	AC	239	19% 56% 26% 14%
3	CC	239	31% 50% 31% 5% 14%
4	AD	209	27% 56% 39% 5%
4	CD	209	46% 51% 41% 7%
5	AE	162	16% 56% 33% 9%
5	CE	162	26% 54% 33% 9%
6	AF	101	10% 69% 26%
6	CF	101	15% 61% 33% 5%
7	AG	156	19% 59% 35% 6%
7	CG	156	28% 62% 31% 6%
8	AH	138	20% 64% 35%
8	CH	138	20% 57% 37% 6%
9	AI	128	37% 51% 38% 10%
9	CI	128	75% 41% 53% 5%
10	AJ	105	45% 56% 30% 6% 8%
10	CJ	105	53% 46% 41% 5% 9%
11	AK	129	13% 60% 27% 12%
11	CK	129	19% 62% 26% 12%
12	AL	132	8% 67% 20% 5% 8%
12	CL	132	12% 58% 32% 8%
13	AM	126	22% 60% 32% 5%
13	CM	126	64% 47% 46%
14	AN	61	39% 56% 38% 5%
14	CN	61	72% 54% 39% 5%
15	AO	89	15% 61% 33% 6%

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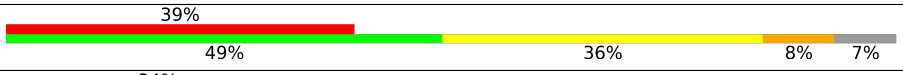
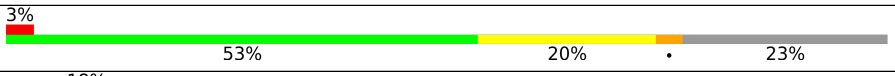
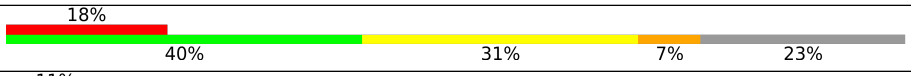
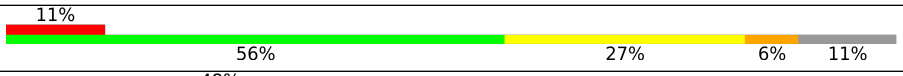
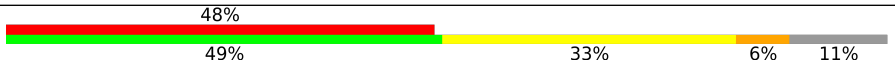
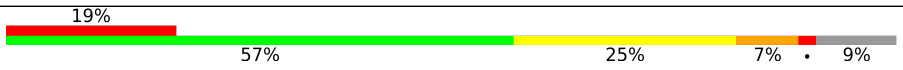
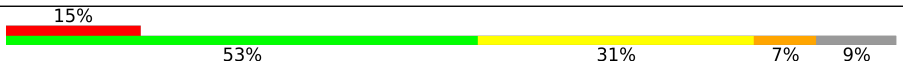
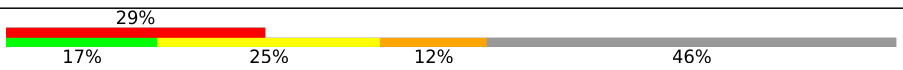
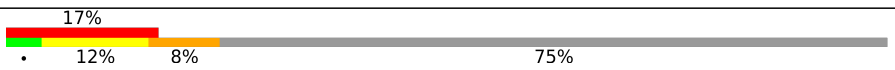
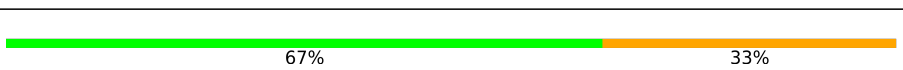
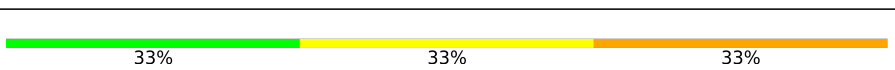
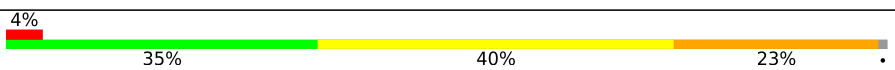
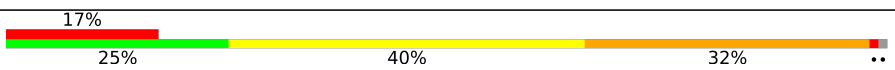
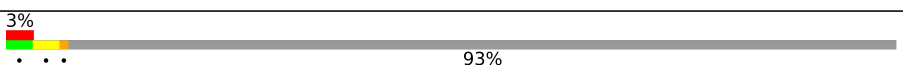
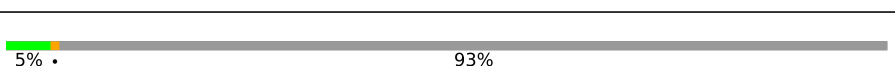
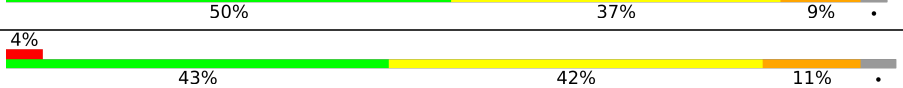
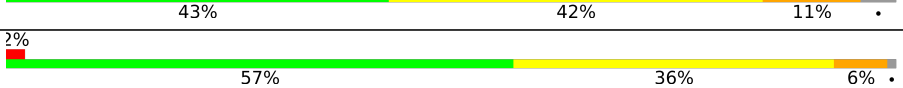
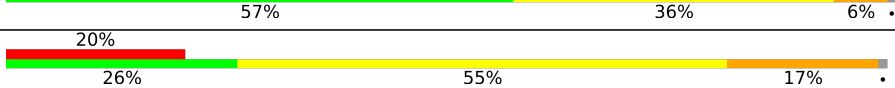
Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AW	3	
23	CW	3	
24	AX	77	
24	CX	77	
25	AY	76	
25	CY	76	
26	BA	2915	
26	DA	2915	
27	BB	121	
27	DB	121	

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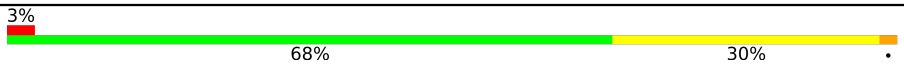
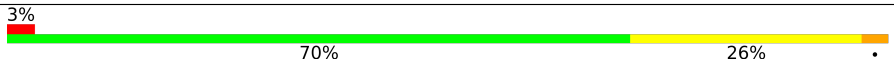
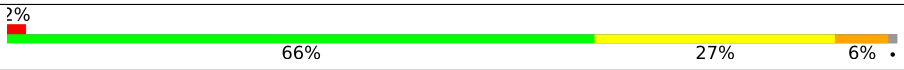
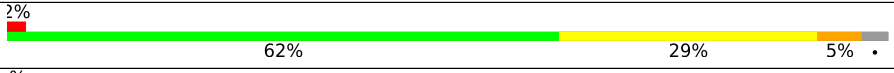
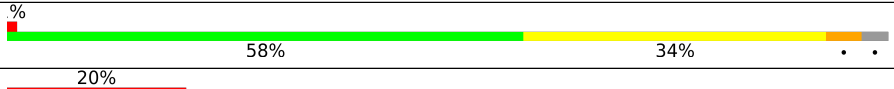
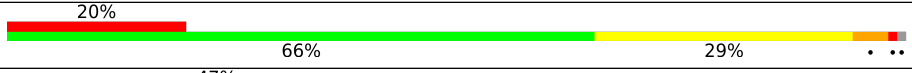
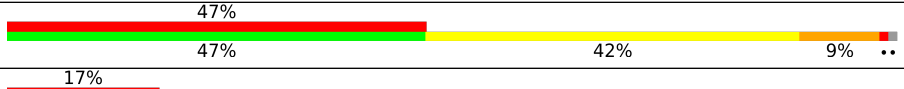
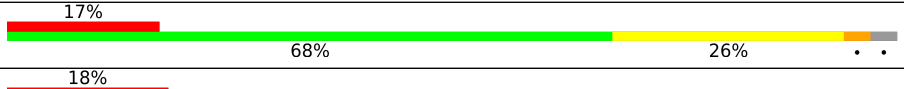
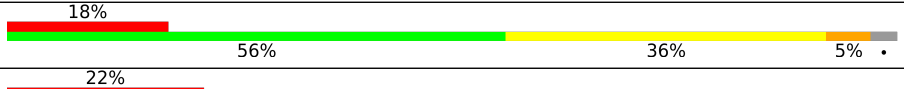
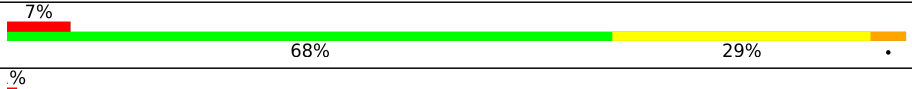
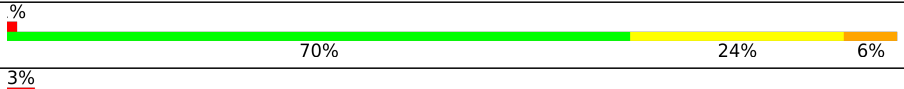
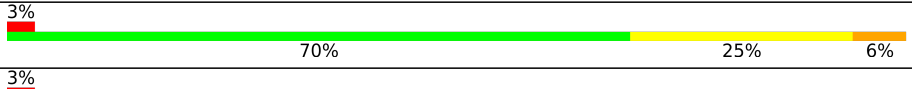
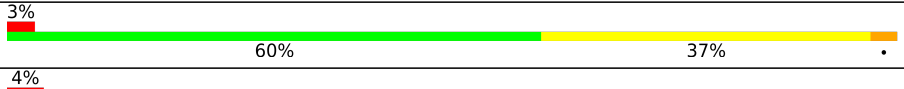
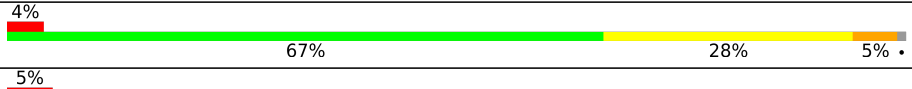
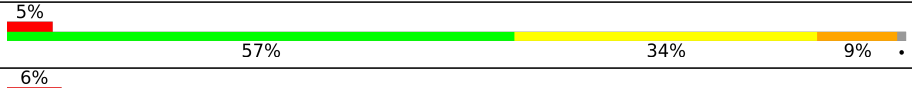
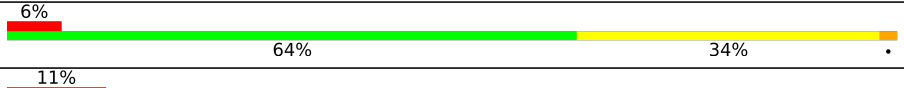
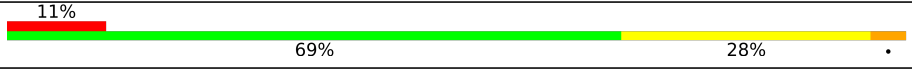
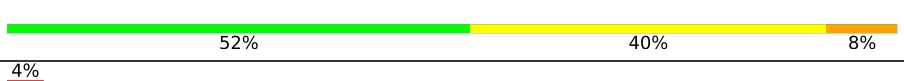
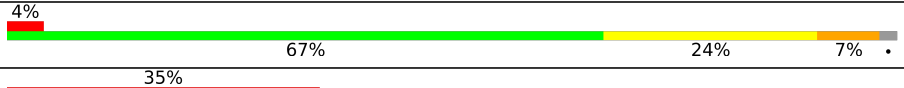
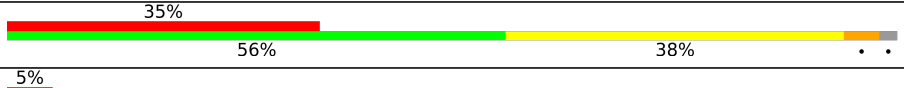
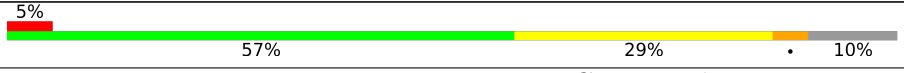
Mol	Chain	Length	Quality of chain
28	BD	276	
28	DD	276	
29	BE	206	
29	DE	206	
30	BF	210	
30	DF	210	
31	BG	182	
31	DG	182	
32	BH	180	
32	DH	180	
33	BI	148	
33	DI	148	
34	BN	140	
34	DN	140	
35	BO	122	
35	DO	122	
36	BP	150	
36	DP	150	
37	BQ	141	
37	DQ	141	
38	BR	118	
38	DR	118	
39	BS	112	
39	DS	112	
40	BT	146	

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Mol	Chain	Length	Quality of chain
40	DT	146	7% 54% 29% 6% 10%
41	BU	118	% 69% 26%
41	DU	118	2% 69% 28%
42	BV	101	% 59% 34% 6%
42	DV	101	6% 66% 27% 6%
43	BW	113	71% 25%
43	DW	113	2% 65% 31%
44	BX	96	% 67% 30%
44	DX	96	9% 67% 29%
45	BY	110	2% 64% 32%
45	DY	110	11% 65% 31%
46	BZ	206	8% 50% 29% 17%
46	DZ	206	30% 48% 31% 6% 16%
47	B0	85	% 72% 21% 5%
47	D0	85	15% 69% 24% 5%
48	B1	98	4% 69% 26%
48	D1	98	9% 70% 23% 5%
49	B2	72	3% 69% 24%
49	D2	72	4% 74% 21%
50	B3	60	2% 65% 25% 8%
50	D3	60	5% 57% 37% 5%
51	B4	71	24% 45% 35% 14%
51	D4	71	37% 35% 49% 10%
52	B5	60	2% 80% 13% 5%
52	D5	60	77% 20%

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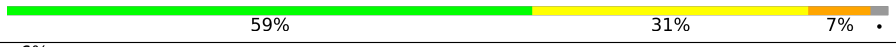
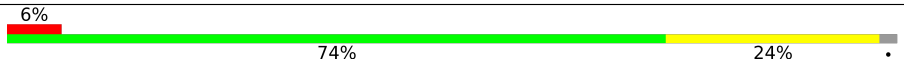
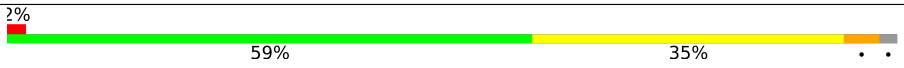
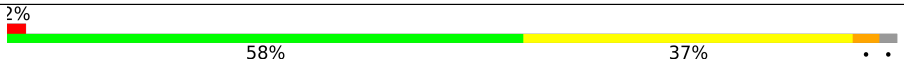
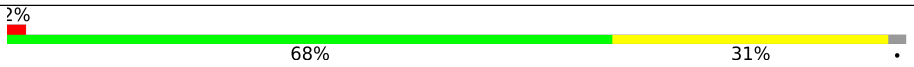
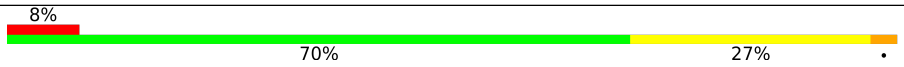
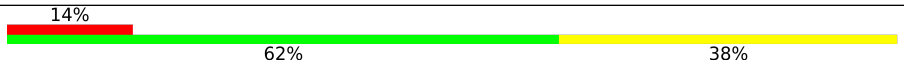
Mol	Chain	Length	Quality of chain
53	B6	54	
53	D6	54	
54	B7	49	
54	D7	49	
55	B8	65	
55	D8	65	
56	B9	37	
56	D9	37	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	AA	3145	-	-	-	X
57	MG	CA	3062	-	-	-	X
57	MG	DR	3001	-	-	-	X

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 290205 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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	0	0	0
			829	516	155	155	3			
11	CK	114	Total	C	N	O	S	0	0	0
			833	519	156	155	3			

- 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	0	0	0
			930	585	185	159	1			
12	CL	122	Total	C	N	O	S	0	0	0
			930	585	185	159	1			

- 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	0	0	0
			958	592	198	166	2			
13	CM	122	Total	C	N	O	S	0	0	0
			950	586	197	165	2			

- 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	0	0	0
			492	312	104	72	4			
14	CN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- 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	0	0	0
			728	456	144	126	2			
15	CO	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
22	CV	6	Total	C	N	O	P	0	0	0
			129	58	24	41	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AW	3	Total	C	N	O	P	0	0	0
			74	40	13	19	2			
23	CW	3	Total	C	N	O	P	0	0	0
			74	40	13	19	2			

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
24	AX	76	Total	C	N	O	P	S	0	0	0
			1633	730	296	529	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	5	Total	C	N	O	P	0	0	0
			104	47	19	33	5			
25	CY	5	Total	C	N	O	P	0	0	0
			104	47	19	33	5			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B4	69	Total	C	N	O	S	0	0	0
			552	349	99	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 453	C 281	N 91	O 77	S 4	0	0	0
53	D6	53	Total 449	C 279	N 91	O 75	S 4	0	0	0

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

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

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

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

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

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

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AA	207	Total 207	Mg 207	0	0
57	AD	2	Total 2	Mg 2	0	0
57	AE	2	Total 2	Mg 2	0	0
57	AF	1	Total 1	Mg 1	0	0
57	AJ	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	AK	1	Total Mg 1 1	0	0
57	AM	1	Total Mg 1 1	0	0
57	AN	2	Total Mg 2 2	0	0
57	AS	1	Total Mg 1 1	0	0
57	AV	1	Total Mg 1 1	0	0
57	AW	1	Total Mg 1 1	0	0
57	AX	11	Total Mg 11 11	0	0
57	BA	720	Total Mg 720 720	0	0
57	BB	20	Total Mg 20 20	0	0
57	BD	11	Total Mg 11 11	0	0
57	BE	7	Total Mg 7 7	0	0
57	BF	10	Total Mg 10 10	0	0
57	BG	2	Total Mg 2 2	0	0
57	BN	6	Total Mg 6 6	0	0
57	BO	1	Total Mg 1 1	0	0
57	BP	4	Total Mg 4 4	0	0
57	BQ	5	Total Mg 5 5	0	0
57	BR	3	Total Mg 3 3	0	0
57	BU	8	Total Mg 8 8	0	0
57	BV	4	Total Mg 4 4	0	0
57	BW	5	Total Mg 5 5	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	BX	1	Total Mg 1 1	0	0
57	BY	1	Total Mg 1 1	0	0
57	BZ	1	Total Mg 1 1	0	0
57	B0	4	Total Mg 4 4	0	0
57	B1	1	Total Mg 1 1	0	0
57	B2	1	Total Mg 1 1	0	0
57	B3	2	Total Mg 2 2	0	0
57	B5	2	Total Mg 2 2	0	0
57	B7	3	Total Mg 3 3	0	0
57	B8	1	Total Mg 1 1	0	0
57	B9	1	Total Mg 1 1	0	0
57	CA	160	Total Mg 160 160	0	0
57	CE	1	Total Mg 1 1	0	0
57	CF	1	Total Mg 1 1	0	0
57	CJ	1	Total Mg 1 1	0	0
57	CK	1	Total Mg 1 1	0	0
57	CT	1	Total Mg 1 1	0	0
57	CW	1	Total Mg 1 1	0	0
57	CX	2	Total Mg 2 2	0	0
57	DA	629	Total Mg 629 629	0	0
57	DB	10	Total Mg 10 10	0	0

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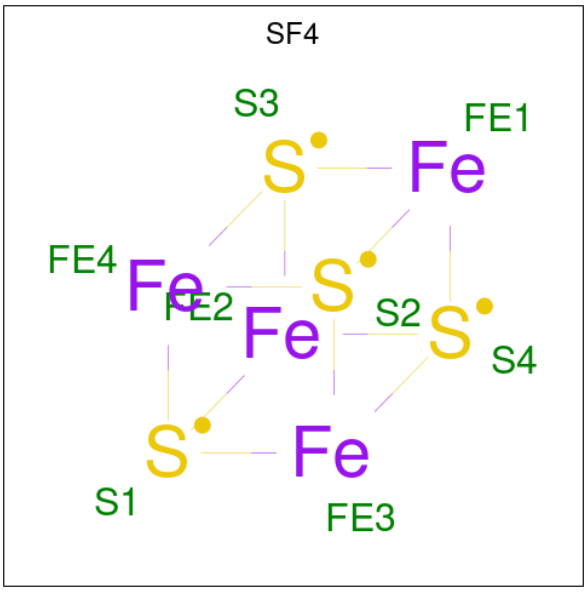
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	DD	7	Total Mg 7 7	0	0
57	DE	4	Total Mg 4 4	0	0
57	DF	4	Total Mg 4 4	0	0
57	DG	1	Total Mg 1 1	0	0
57	DN	1	Total Mg 1 1	0	0
57	DO	1	Total Mg 1 1	0	0
57	DP	2	Total Mg 2 2	0	0
57	DQ	3	Total Mg 3 3	0	0
57	DR	2	Total Mg 2 2	0	0
57	DU	4	Total Mg 4 4	0	0
57	DV	2	Total Mg 2 2	0	0
57	DW	2	Total Mg 2 2	0	0
57	DY	1	Total Mg 1 1	0	0
57	D3	1	Total Mg 1 1	0	0
57	D5	1	Total Mg 1 1	0	0
57	D8	2	Total Mg 2 2	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



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

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	D6	1	Total Zn 1 1	0	0
59	D9	1	Total Zn 1 1	0	0

- Molecule 60 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 61 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	AA	170	Total O 170 170	0	0
61	AL	2	Total O 2 2	0	0
61	AO	1	Total O 1 1	0	0
61	AU	1	Total O 1 1	0	0
61	AV	2	Total O 2 2	0	0
61	AW	3	Total O 3 3	0	0
61	BA	1102	Total O 1102 1102	0	0
61	BB	36	Total O 36 36	0	0
61	BD	8	Total O 8 8	0	0
61	BE	13	Total O 13 13	0	0
61	BF	4	Total O 4 4	0	0
61	BG	3	Total O 3 3	0	0
61	BI	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	BP	15	Total O 15 15	0	0
61	BQ	3	Total O 3 3	0	0
61	BR	1	Total O 1 1	0	0
61	BS	1	Total O 1 1	0	0
61	BT	3	Total O 3 3	0	0
61	BU	1	Total O 1 1	0	0
61	BV	4	Total O 4 4	0	0
61	BW	2	Total O 2 2	0	0
61	BX	2	Total O 2 2	0	0
61	B0	4	Total O 4 4	0	0
61	B1	1	Total O 1 1	0	0
61	B3	1	Total O 1 1	0	0
61	B5	5	Total O 5 5	0	0
61	B7	1	Total O 1 1	0	0
61	B8	7	Total O 7 7	0	0
61	CA	130	Total O 130 130	0	0
61	CE	1	Total O 1 1	0	0
61	CJ	2	Total O 2 2	0	0
61	CN	1	Total O 1 1	0	0
61	CT	1	Total O 1 1	0	0
61	CV	1	Total O 1 1	0	0

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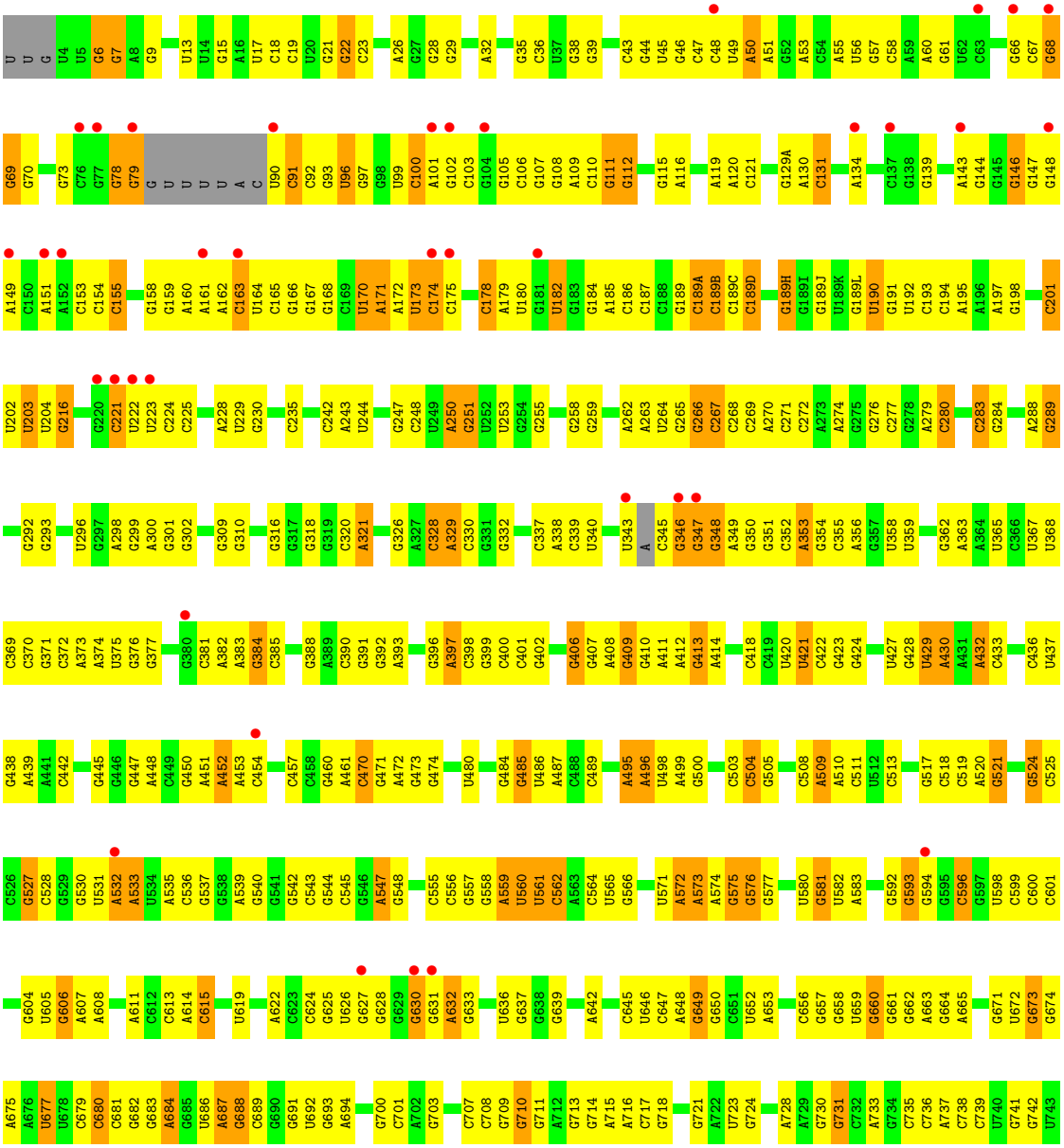
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	CW	1	Total O 1 1	0	0
61	CX	1	Total O 1 1	0	0
61	DA	767	Total O 767 767	0	0
61	DB	9	Total O 9 9	0	0
61	DD	9	Total O 9 9	0	0
61	DE	5	Total O 5 5	0	0
61	DF	6	Total O 6 6	0	0
61	DN	2	Total O 2 2	0	0
61	DP	12	Total O 12 12	0	0
61	DR	2	Total O 2 2	0	0
61	DT	1	Total O 1 1	0	0
61	DU	2	Total O 2 2	0	0
61	DV	1	Total O 1 1	0	0
61	DX	2	Total O 2 2	0	0
61	DY	1	Total O 1 1	0	0
61	D0	5	Total O 5 5	0	0
61	D1	1	Total O 1 1	0	0
61	D3	2	Total O 2 2	0	0
61	D7	1	Total O 1 1	0	0
61	D8	4	Total O 4 4	0	0

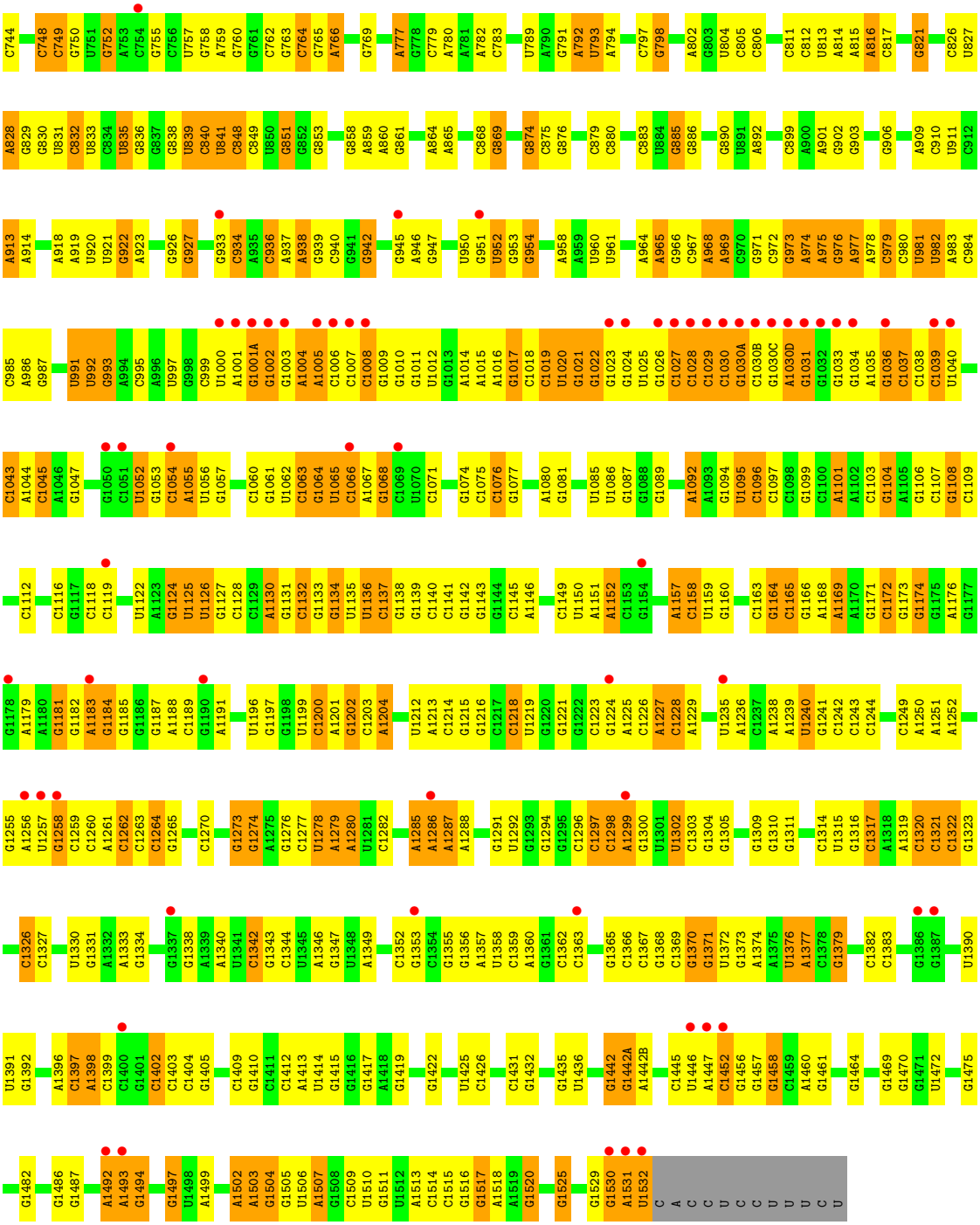
3 Residue-property plots (i)

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

- Molecule 1: 16S Ribosomal RNA

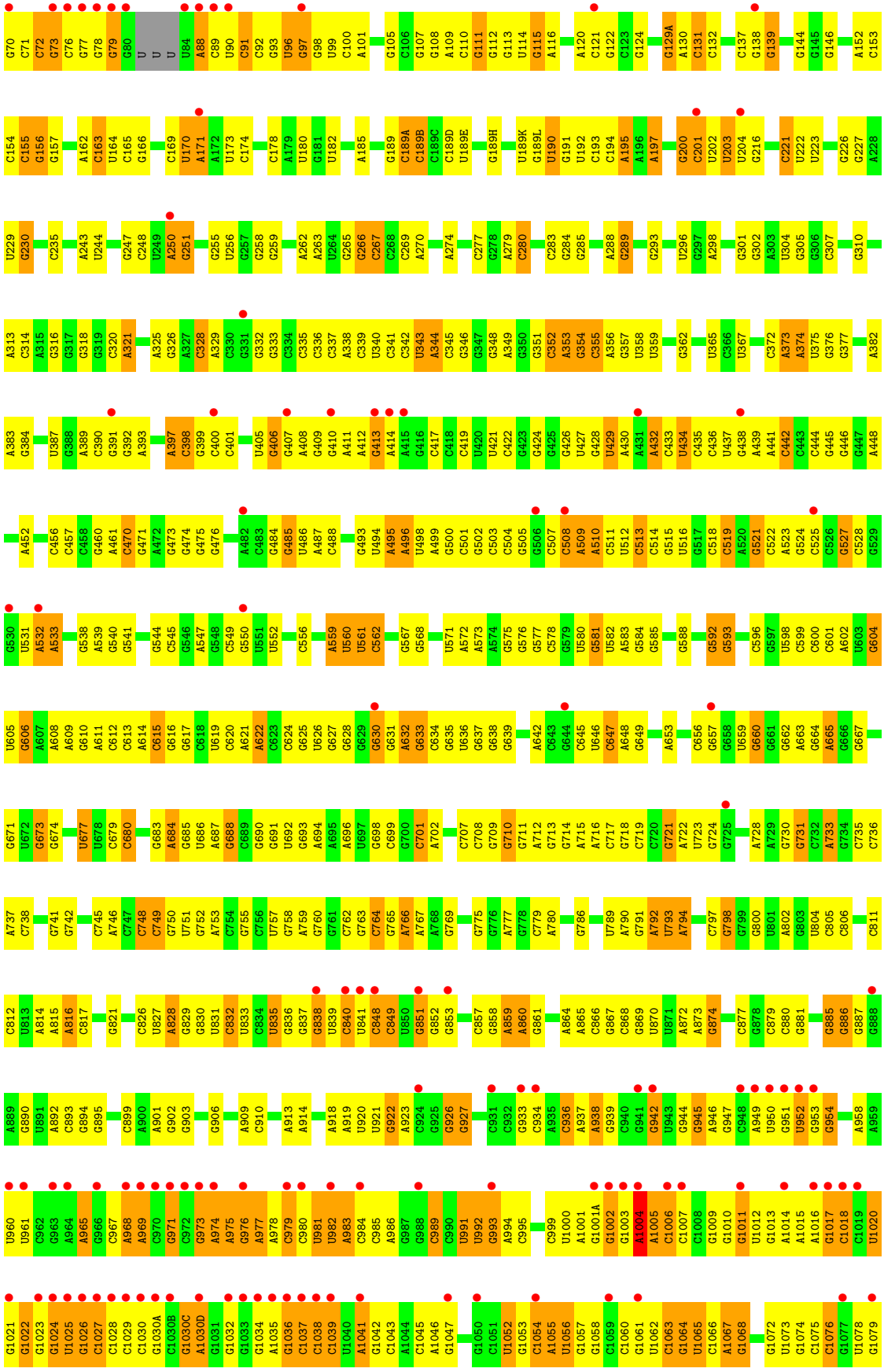
Chain AA:

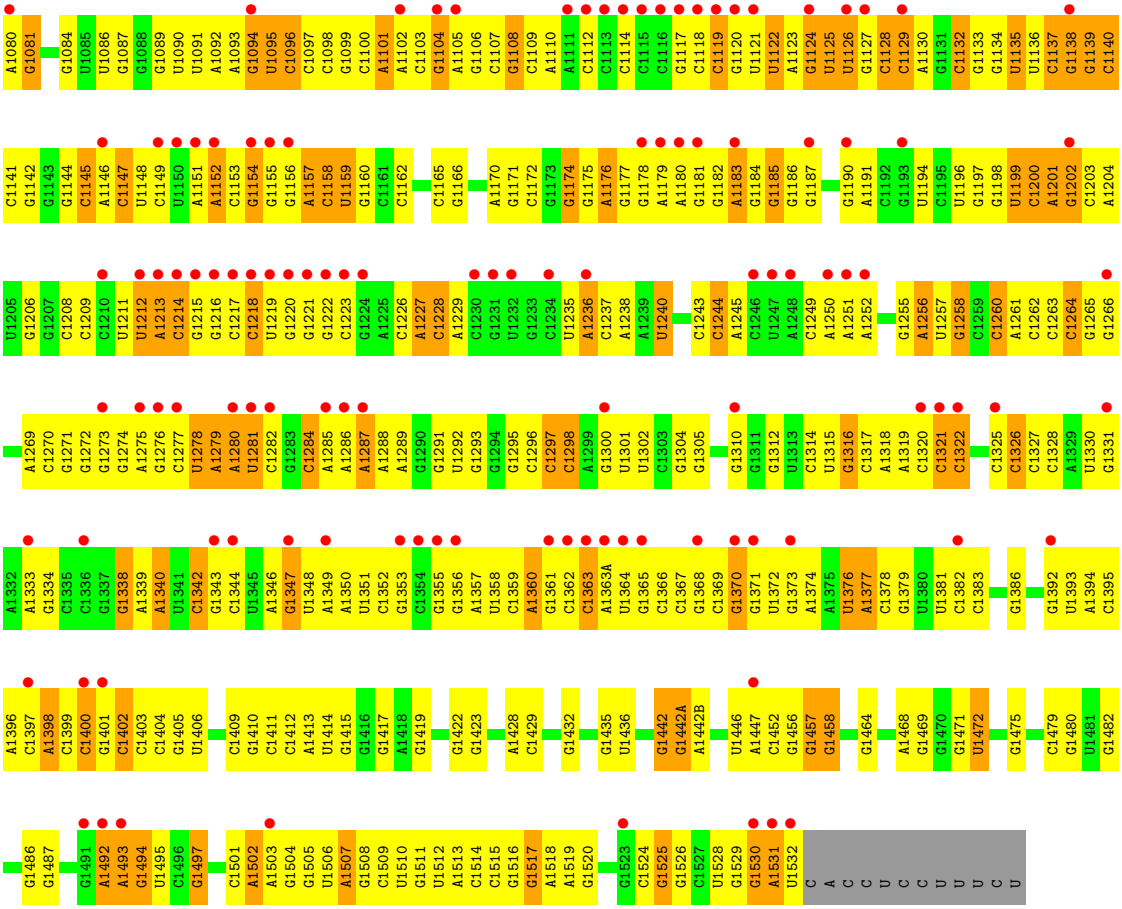




• Molecule 1: 16S Ribosomal RNA

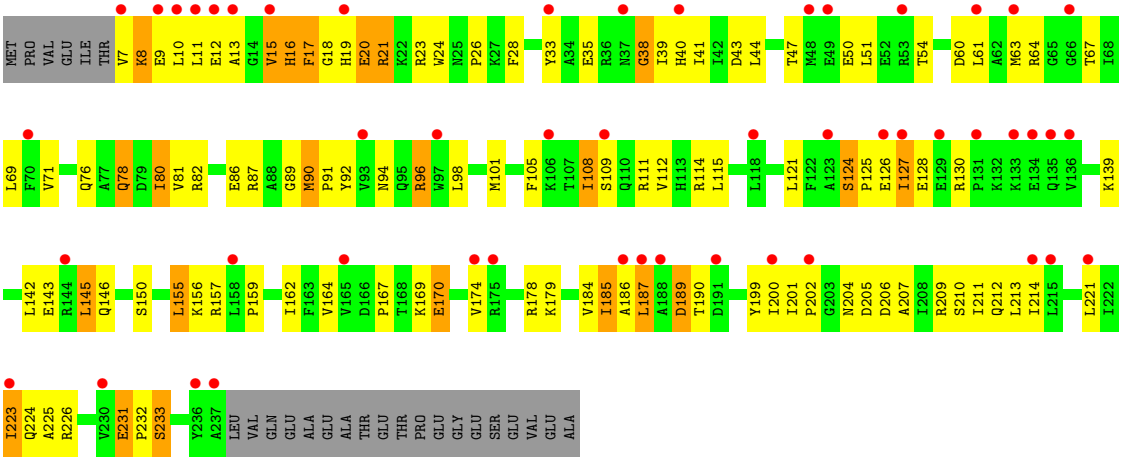
Chain CA:





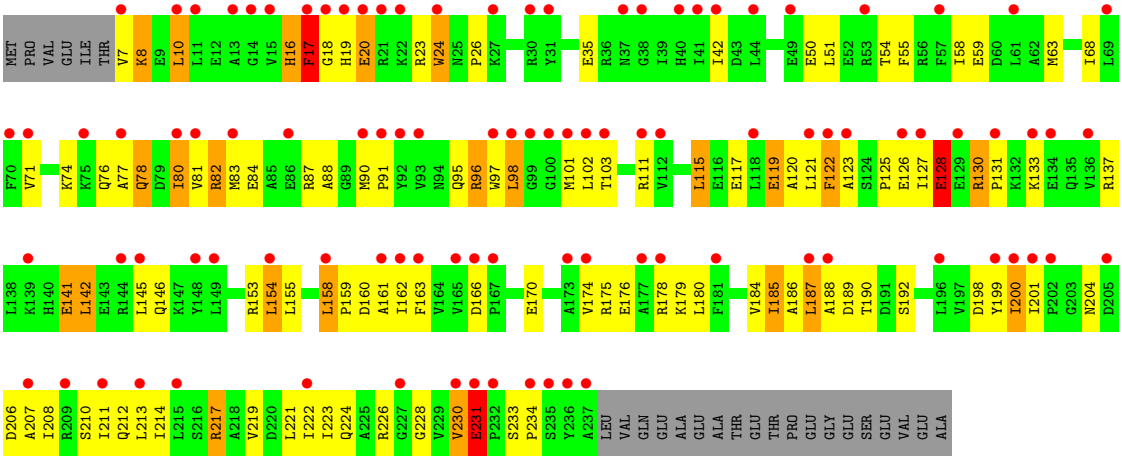
• Molecule 2: 30S ribosomal protein S2

Chain AB:

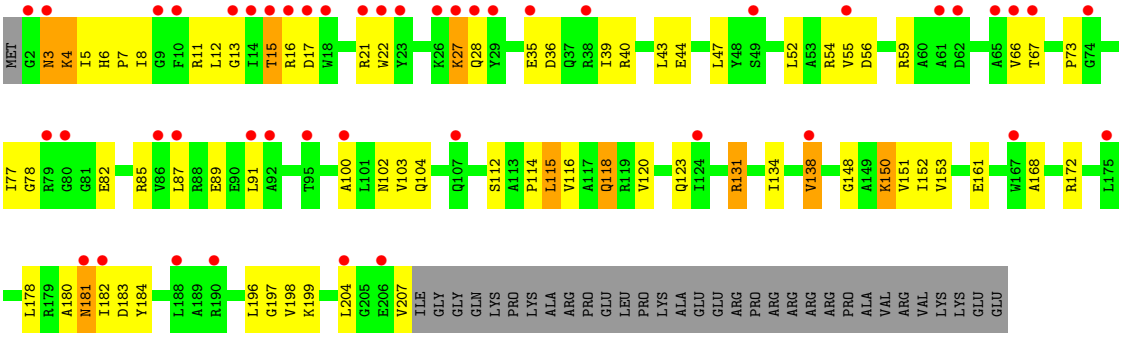


• Molecule 2: 30S ribosomal protein S2

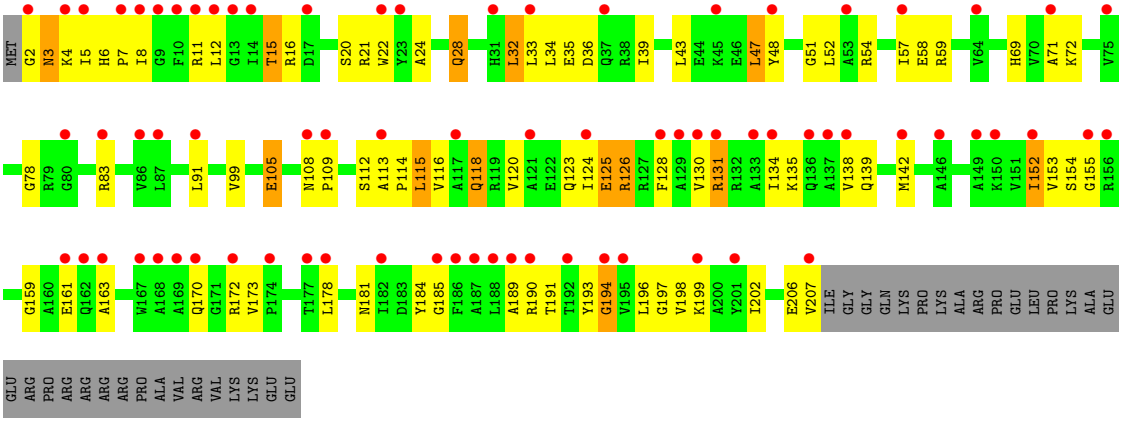
Chain CB:



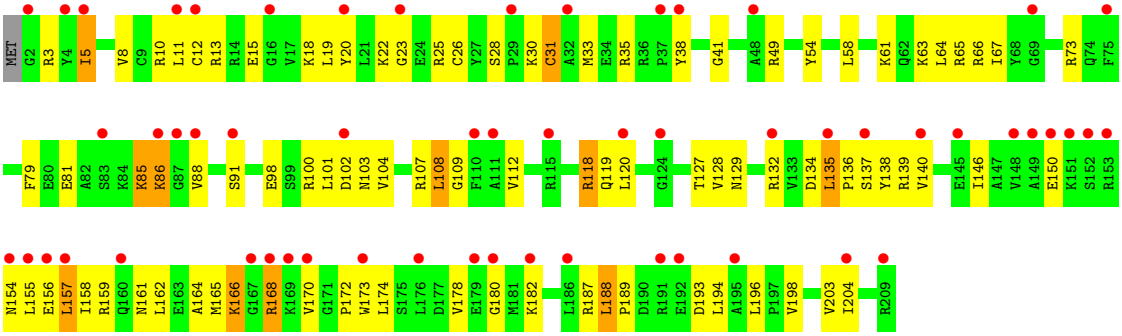
• Molecule 3: 30S ribosomal protein S3



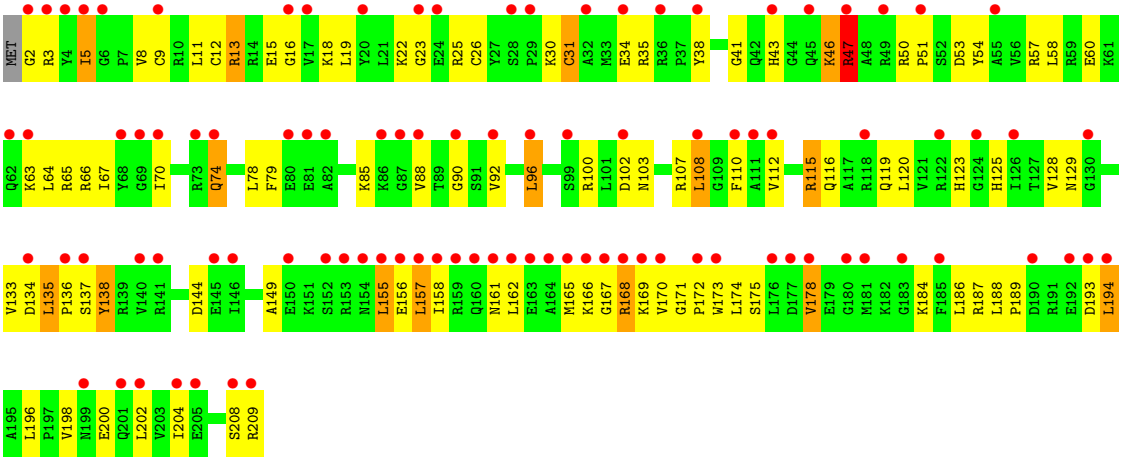
• Molecule 3: 30S ribosomal protein S3



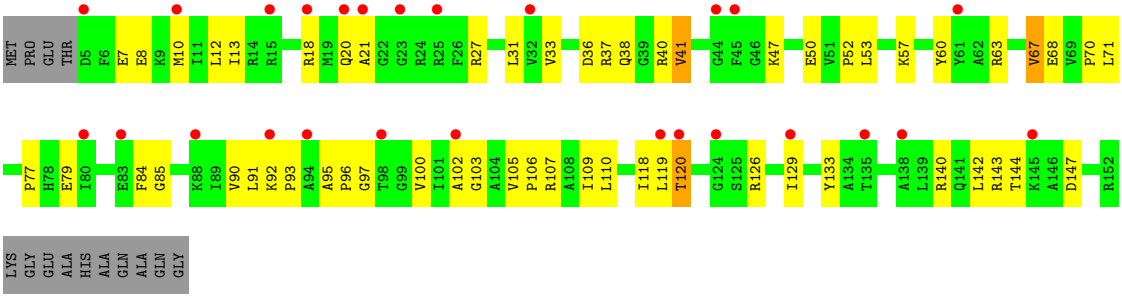
• Molecule 4: 30S ribosomal protein S4



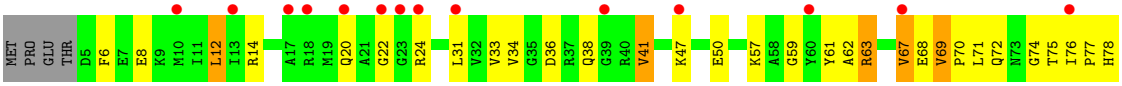
• Molecule 4: 30S ribosomal protein S4

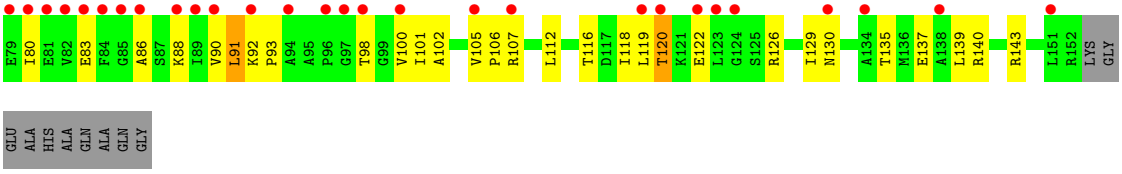


• Molecule 5: 30S ribosomal protein S5

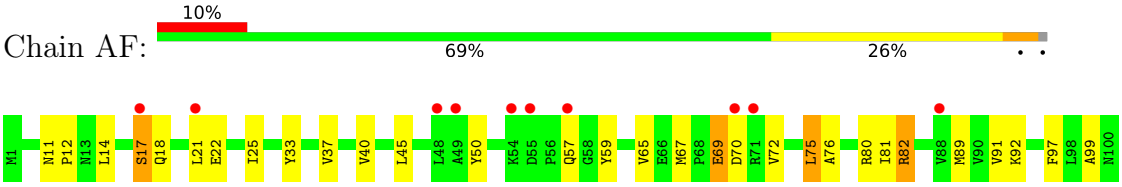


• Molecule 5: 30S ribosomal protein S5

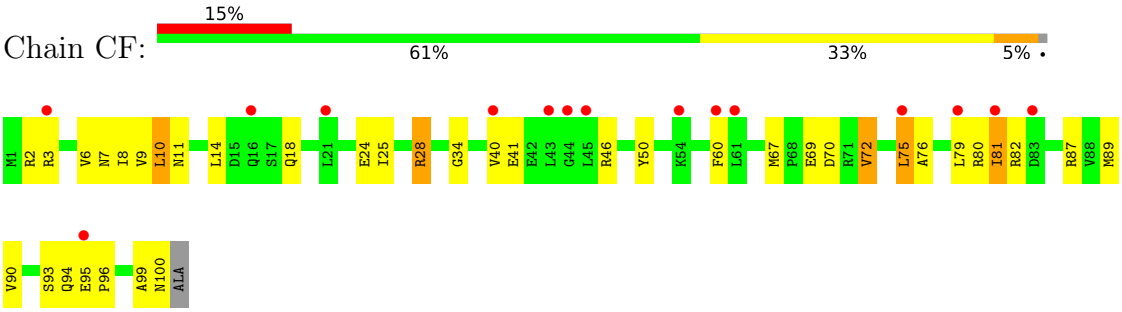




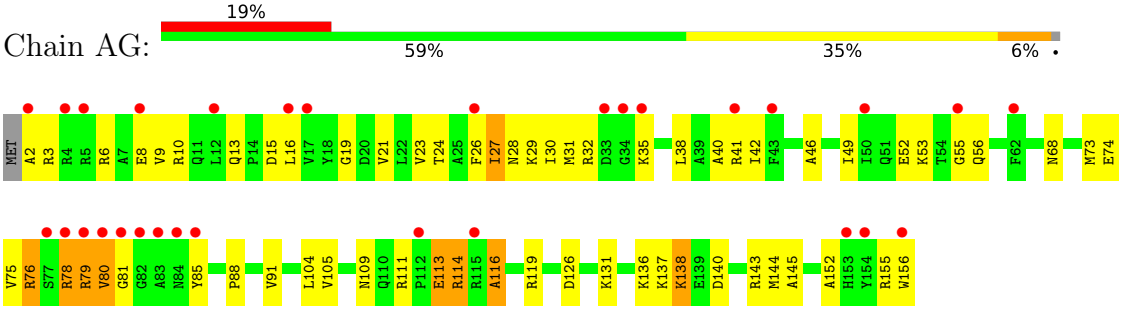
• Molecule 6: 30S ribosomal protein S6



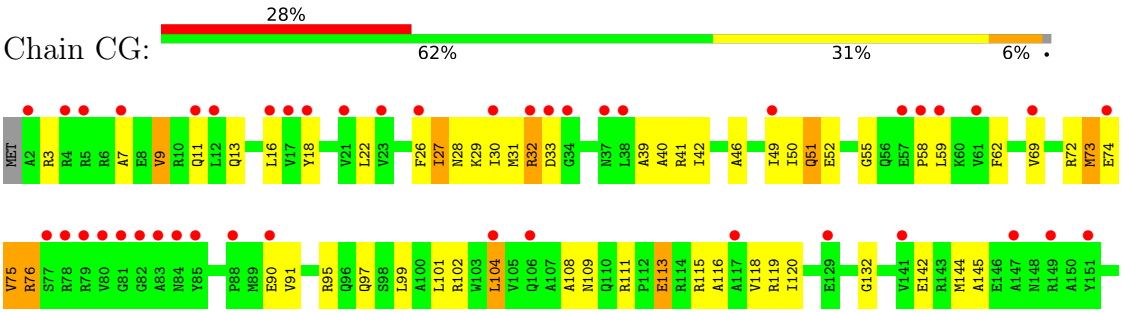
• Molecule 6: 30S ribosomal protein S6



• Molecule 7: 30S ribosomal protein S7

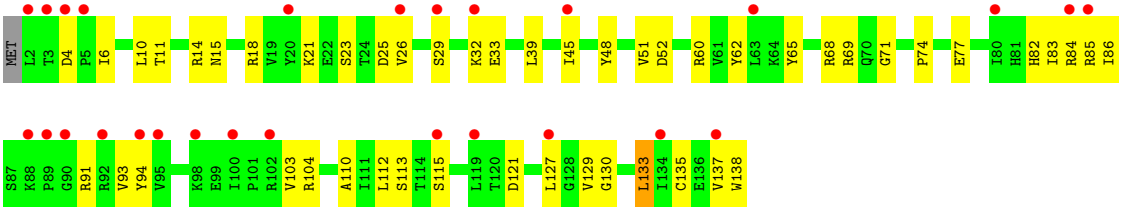


• Molecule 7: 30S ribosomal protein S7



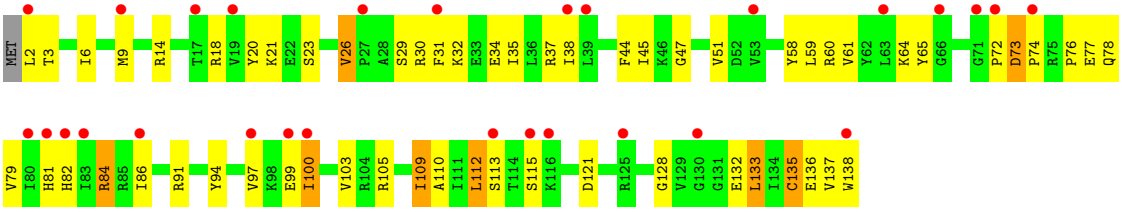
• Molecule 8: 30S ribosomal protein S8

Chain AH:



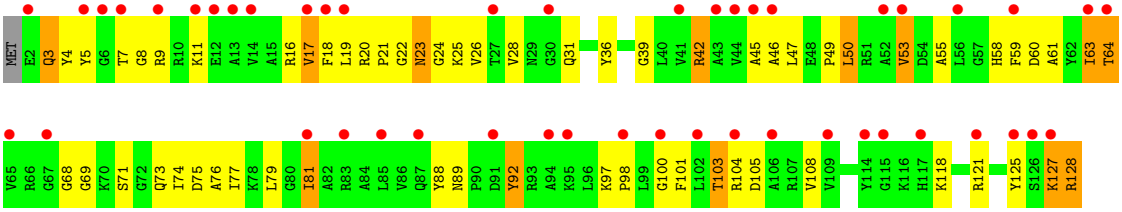
• Molecule 8: 30S ribosomal protein S8

Chain CH:



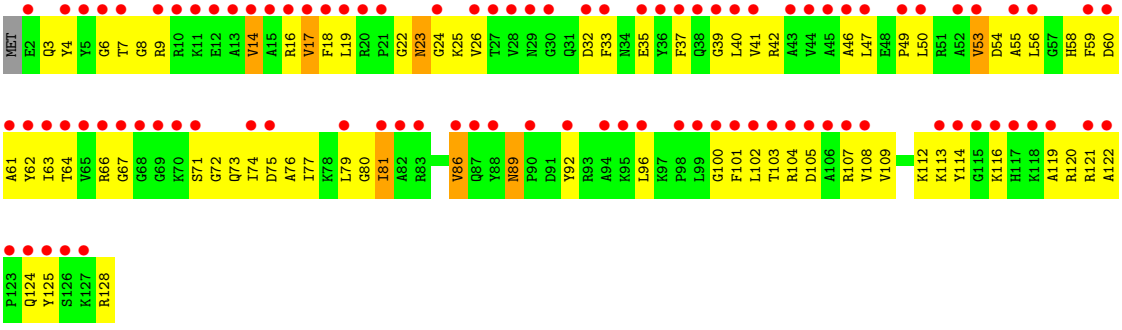
• Molecule 9: 30S ribosomal protein S9

Chain AI:



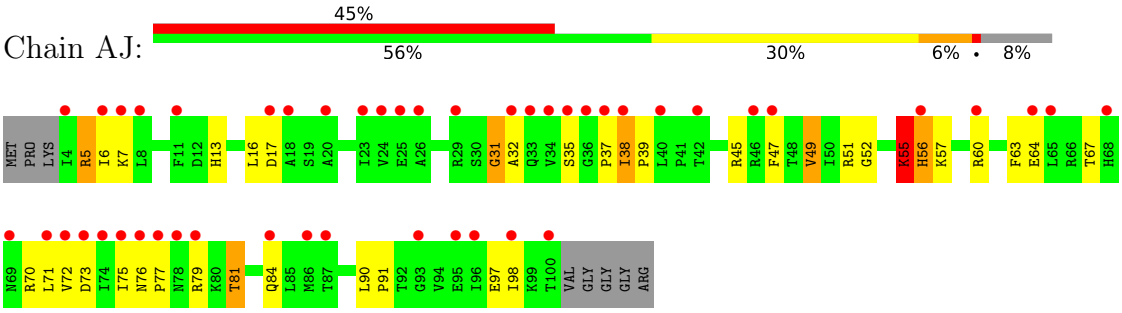
• Molecule 9: 30S ribosomal protein S9

Chain CI:



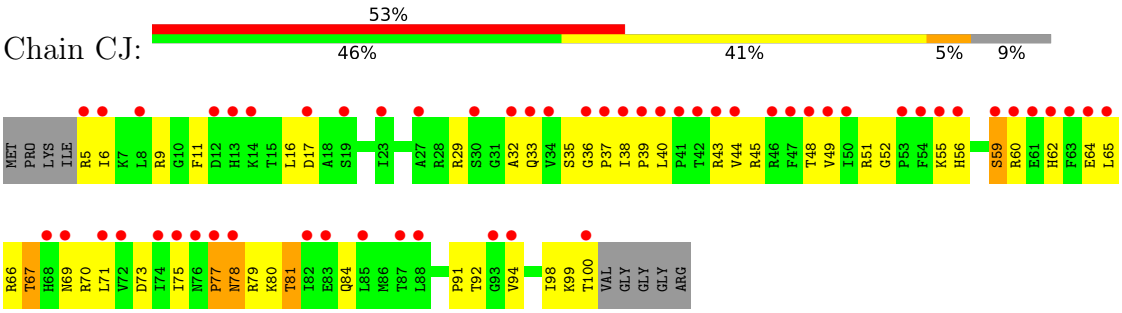
• Molecule 10: 30S ribosomal protein S10

Chain AJ:



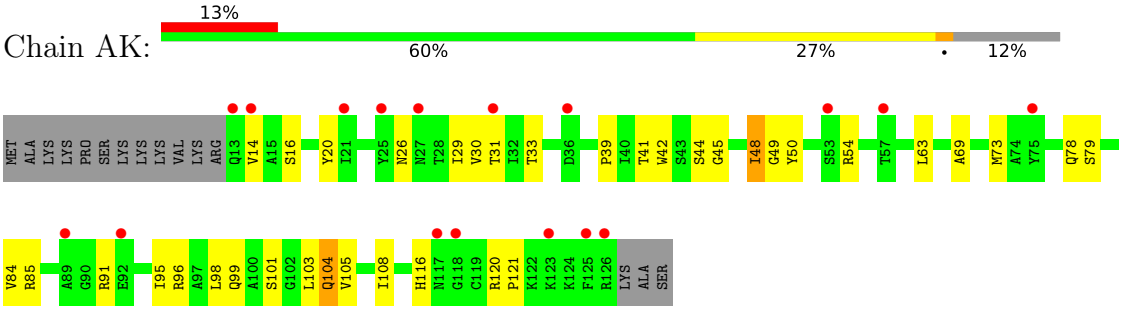
• Molecule 10: 30S ribosomal protein S10

Chain CJ:



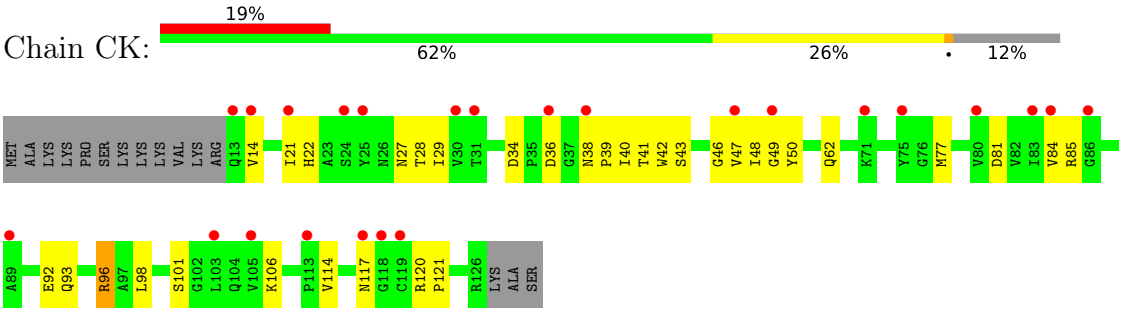
• Molecule 11: 30S ribosomal protein S11

Chain AK:



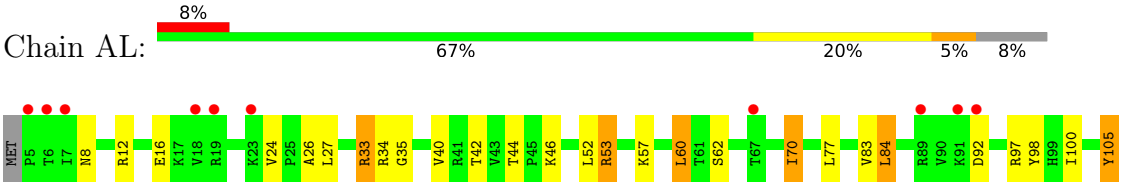
• Molecule 11: 30S ribosomal protein S11

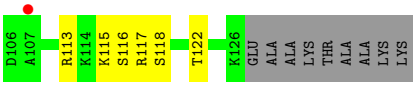
Chain CK:



• Molecule 12: 30S ribosomal protein S12

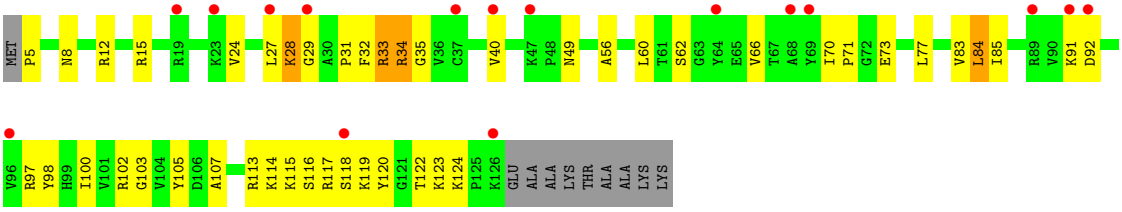
Chain AL:





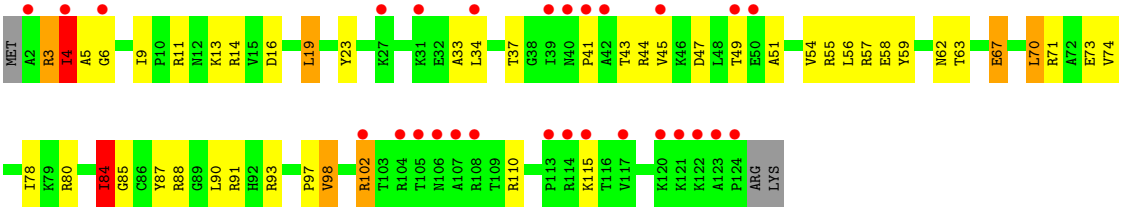
• Molecule 12: 30S ribosomal protein S12

Chain CL:



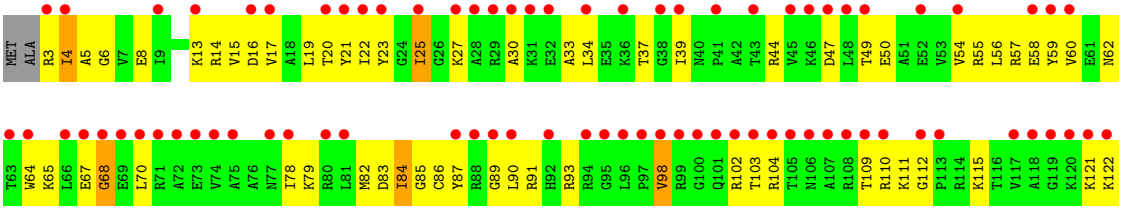
• Molecule 13: 30S ribosomal protein S13

Chain AM:



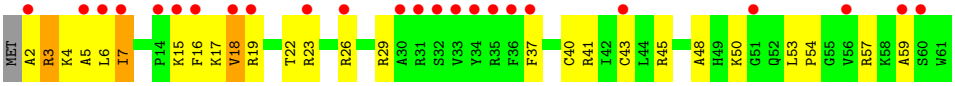
• Molecule 13: 30S ribosomal protein S13

Chain CM:



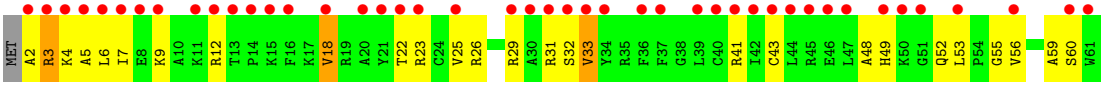
• Molecule 14: 30S ribosomal protein S14 type Z

Chain AN:



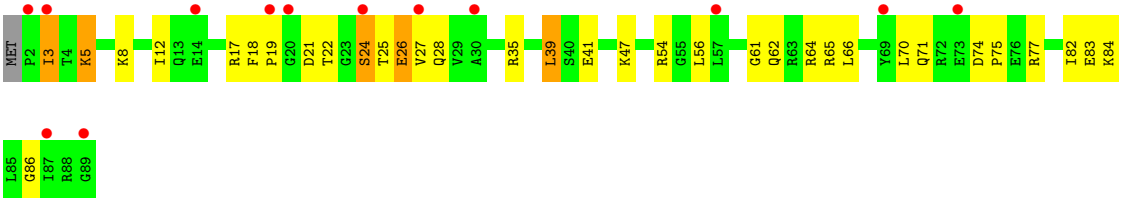
• Molecule 14: 30S ribosomal protein S14 type Z

Chain CN:



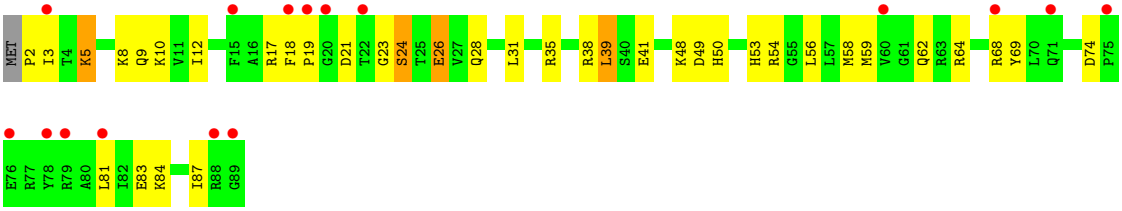
• Molecule 15: 30S ribosomal protein S15

Chain AO:



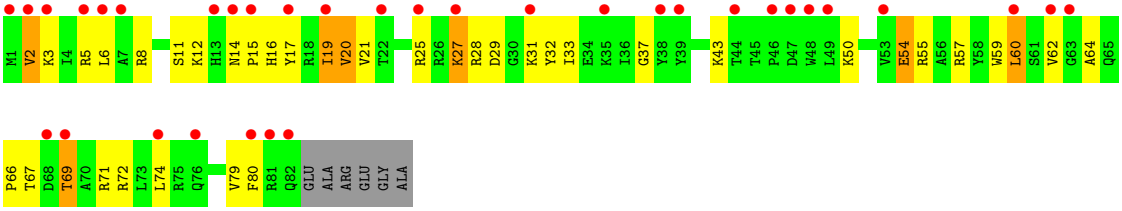
• Molecule 15: 30S ribosomal protein S15

Chain CO:



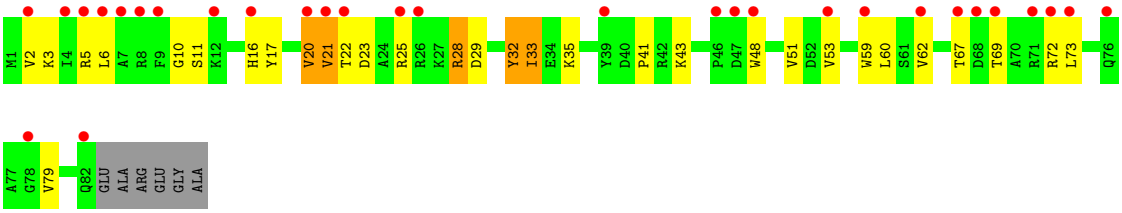
• Molecule 16: 30S ribosomal protein S16

Chain AP:



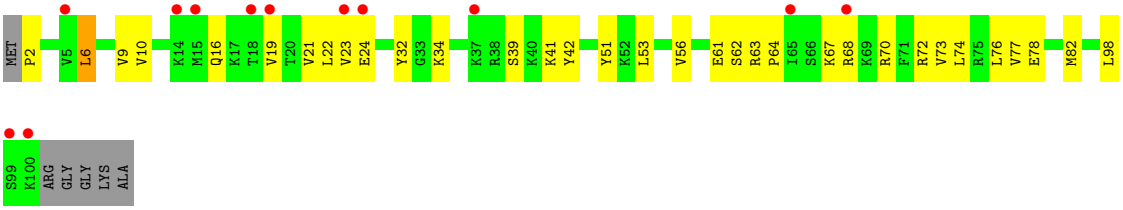
• Molecule 16: 30S ribosomal protein S16

Chain CP:

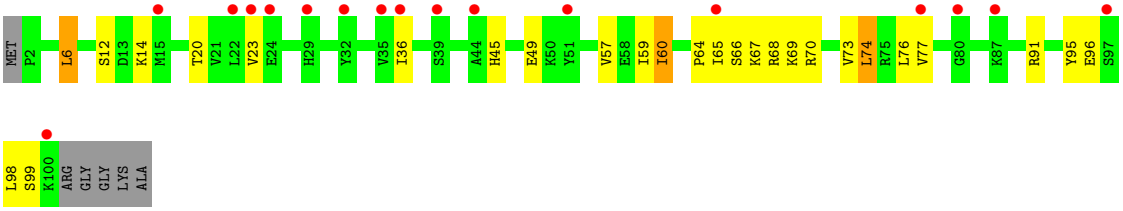


• Molecule 17: 30S ribosomal protein S17

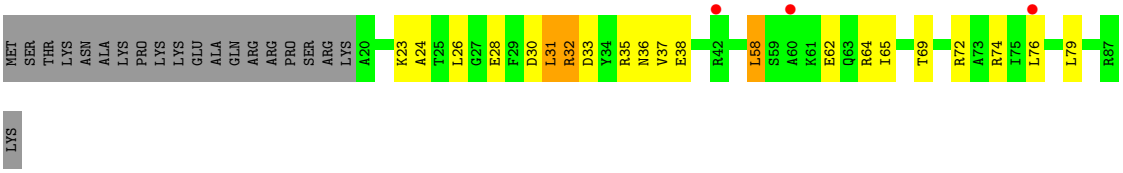
Chain AQ:



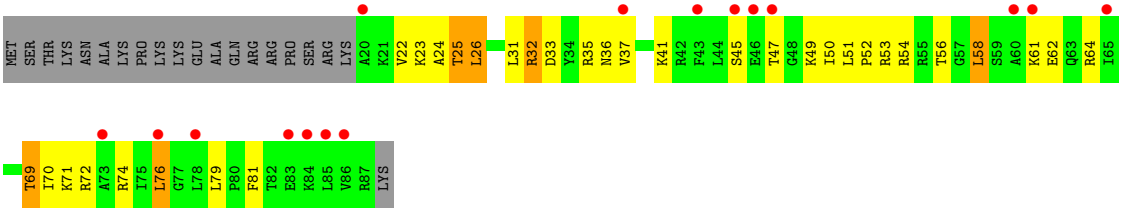
• Molecule 17: 30S ribosomal protein S17



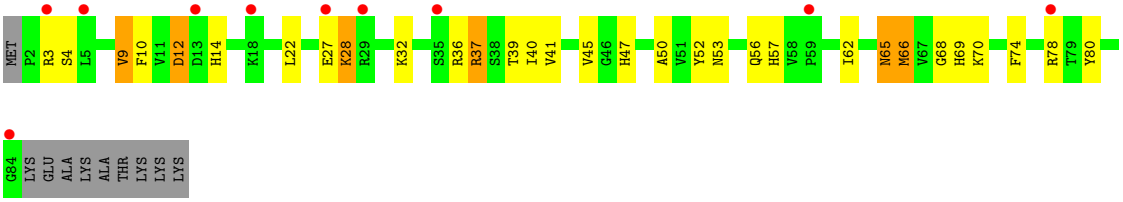
• Molecule 18: 30S ribosomal protein S18



• Molecule 18: 30S ribosomal protein S18

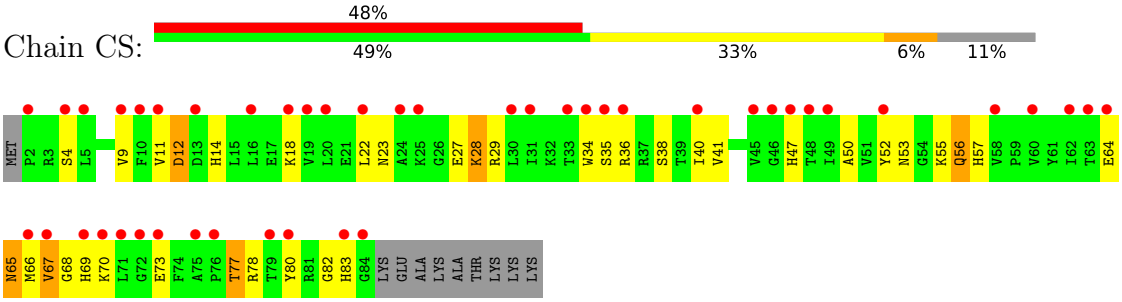


• Molecule 19: 30S ribosomal protein S19



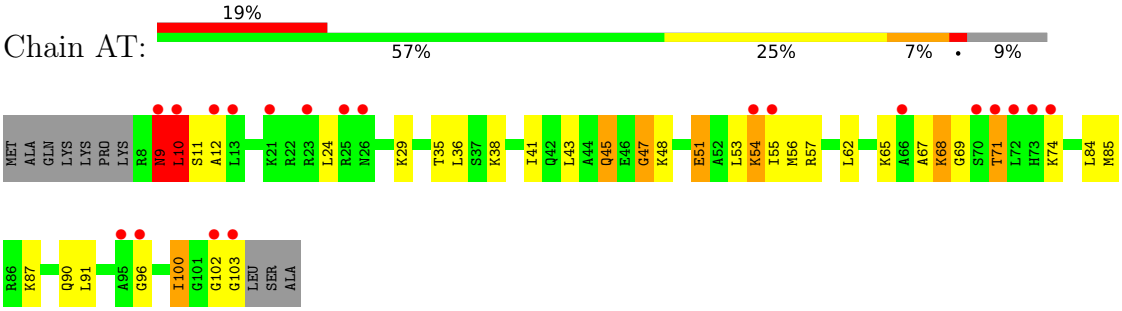
• Molecule 19: 30S ribosomal protein S19

Chain CS:



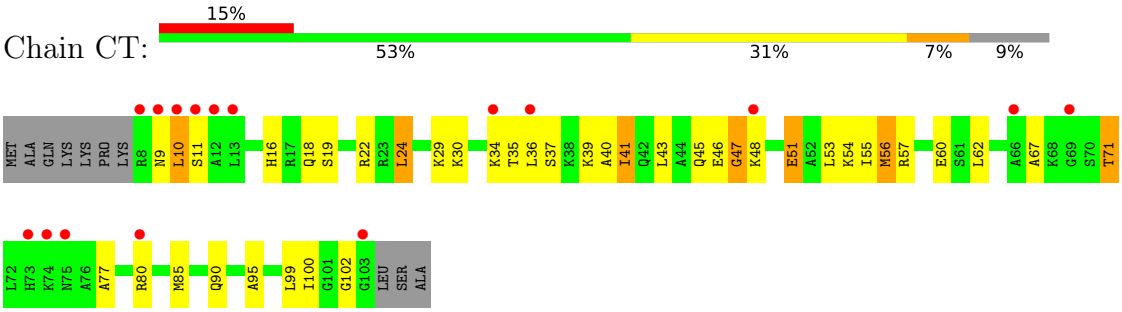
• Molecule 20: 30S ribosomal protein S20

Chain AT:



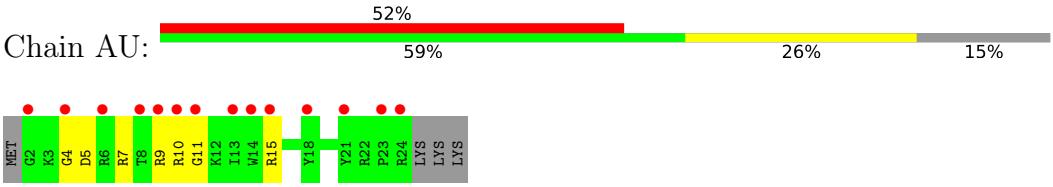
• Molecule 20: 30S ribosomal protein S20

Chain CT:



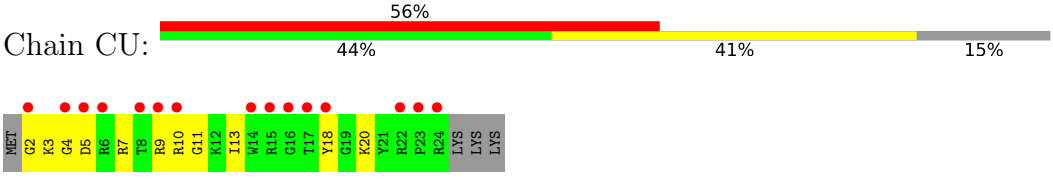
• Molecule 21: 30S ribosomal protein Thx

Chain AU:



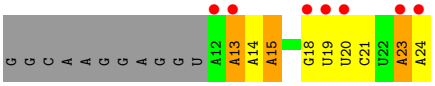
• Molecule 21: 30S ribosomal protein Thx

Chain CU:



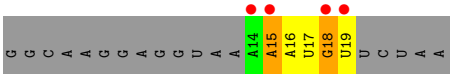
• Molecule 22: mRNA

Chain AV:



• Molecule 22: mRNA

Chain CV:

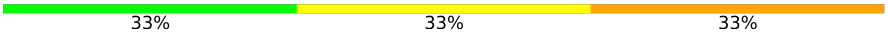


• Molecule 23: Cytidine-Puromycin

Chain AW:

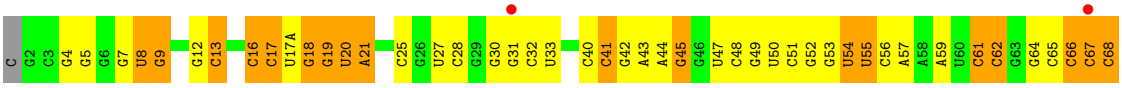
• Molecule 23: Cytidine-Puromycin

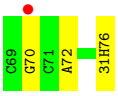
Chain CW:



• Molecule 24: P-site tRNA

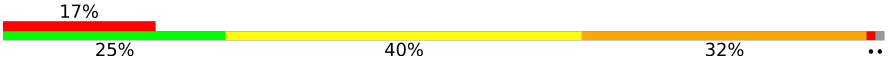
Chain AX:

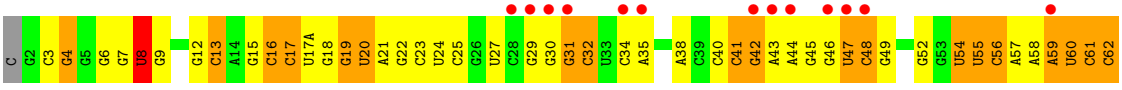


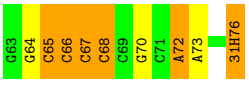


• Molecule 24: P-site tRNA

Chain CX:

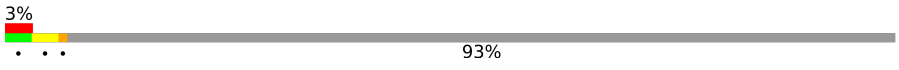






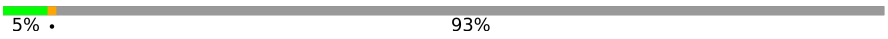
• Molecule 25: E-site tRNA

Chain AY:



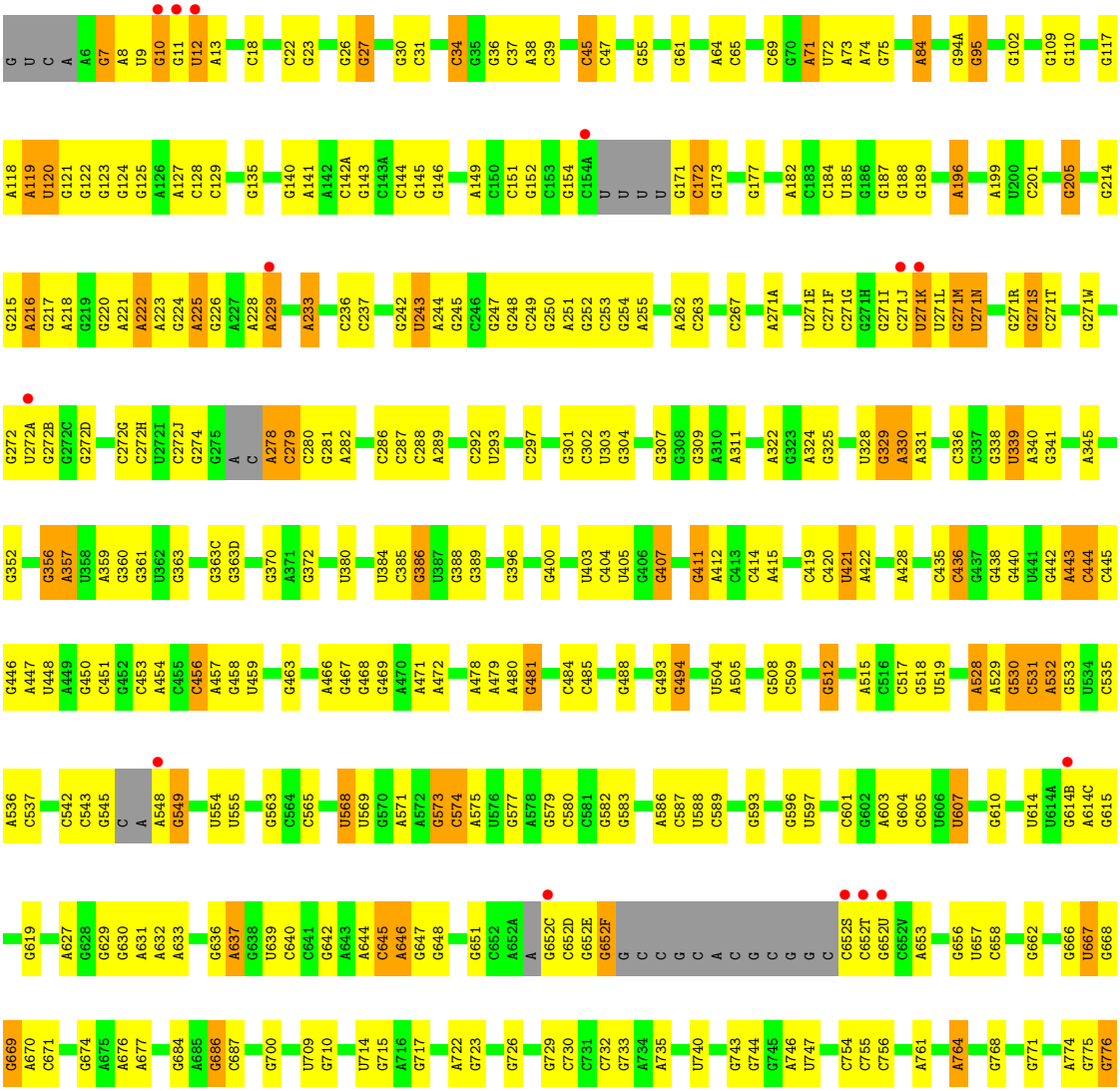
• Molecule 25: E-site tRNA

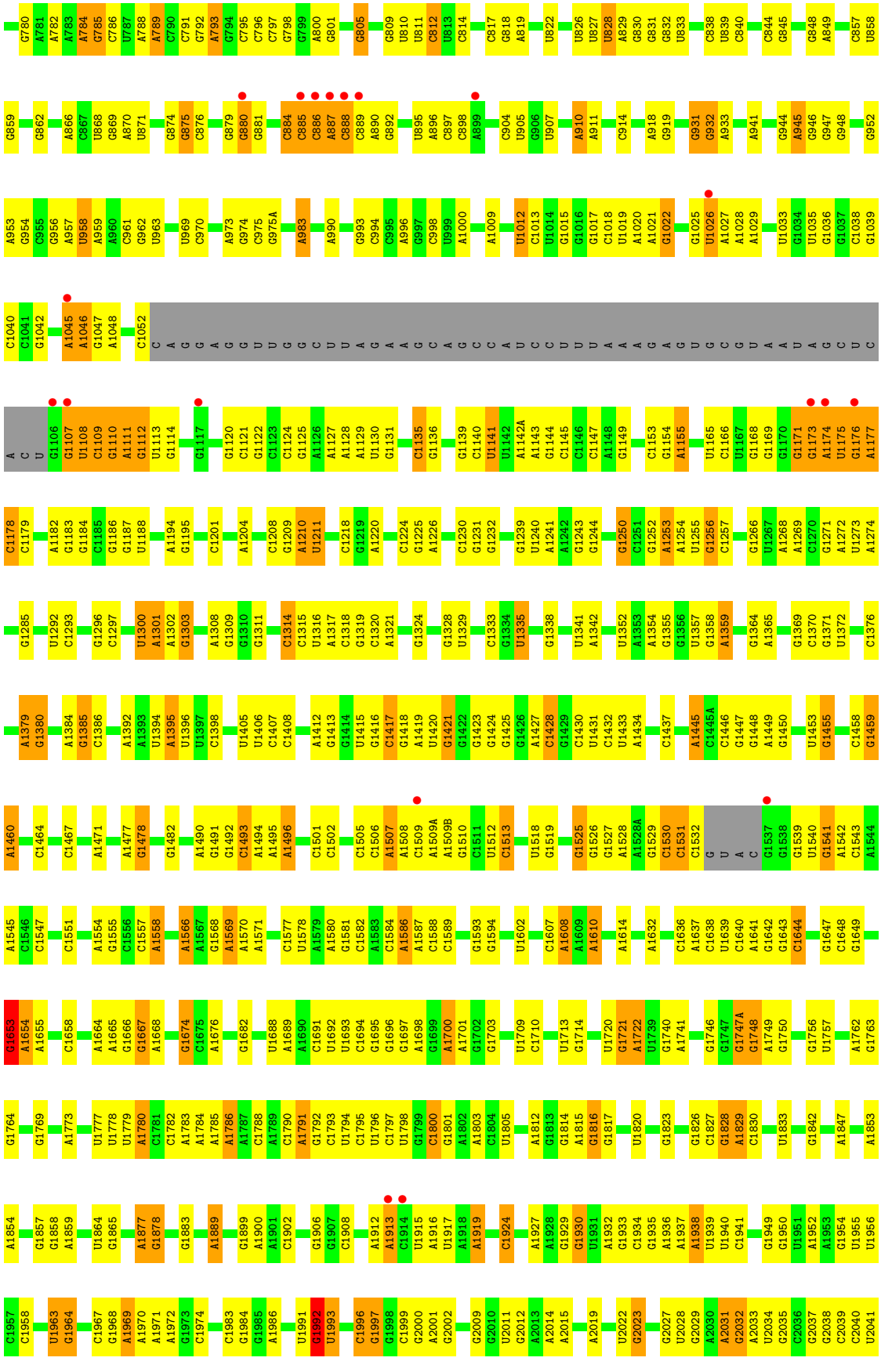
Chain CY:

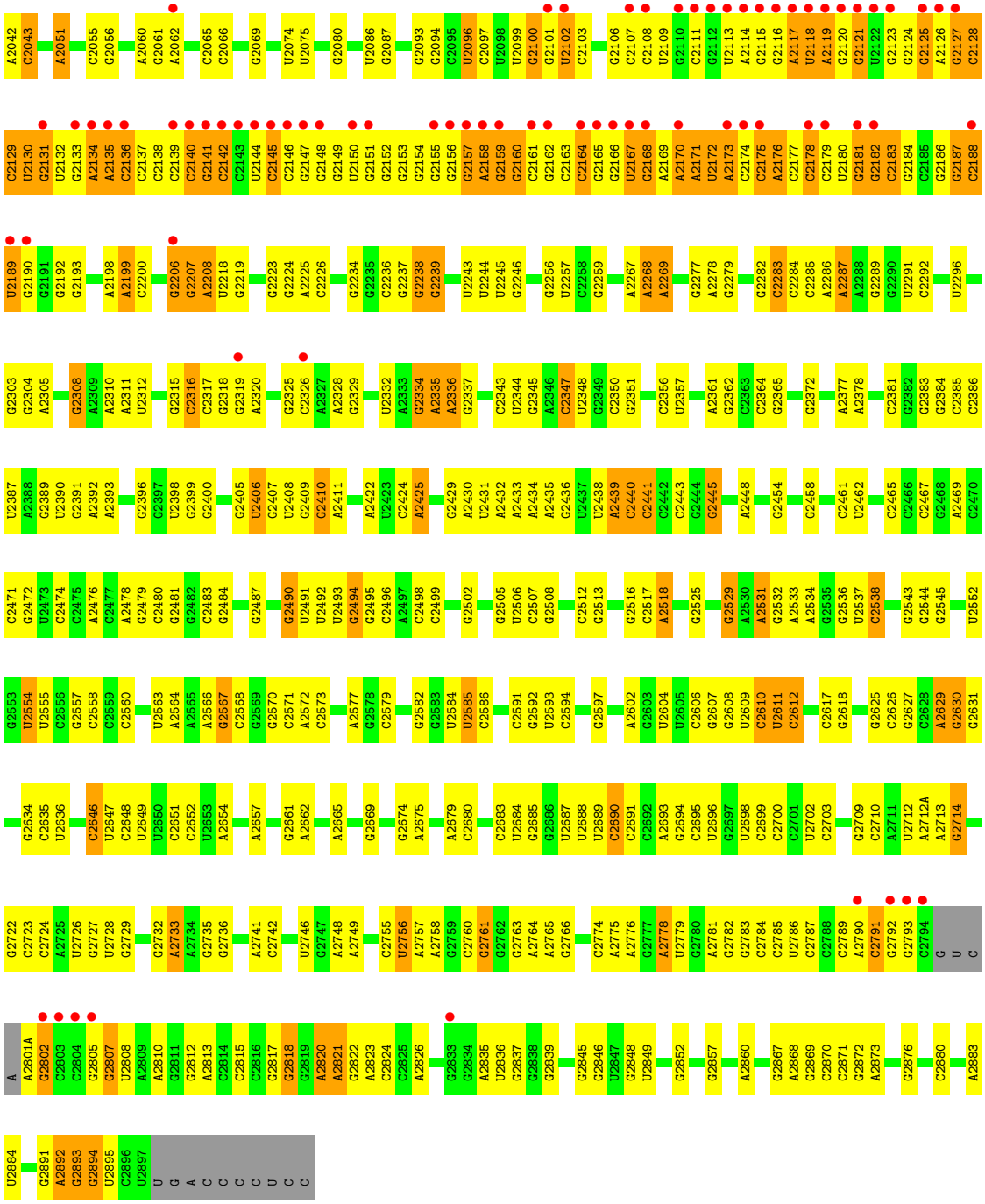


• Molecule 26: 23S Ribosomal RNA

Chain BA:

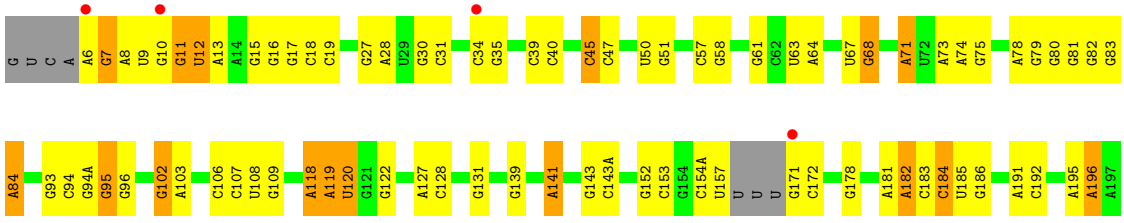


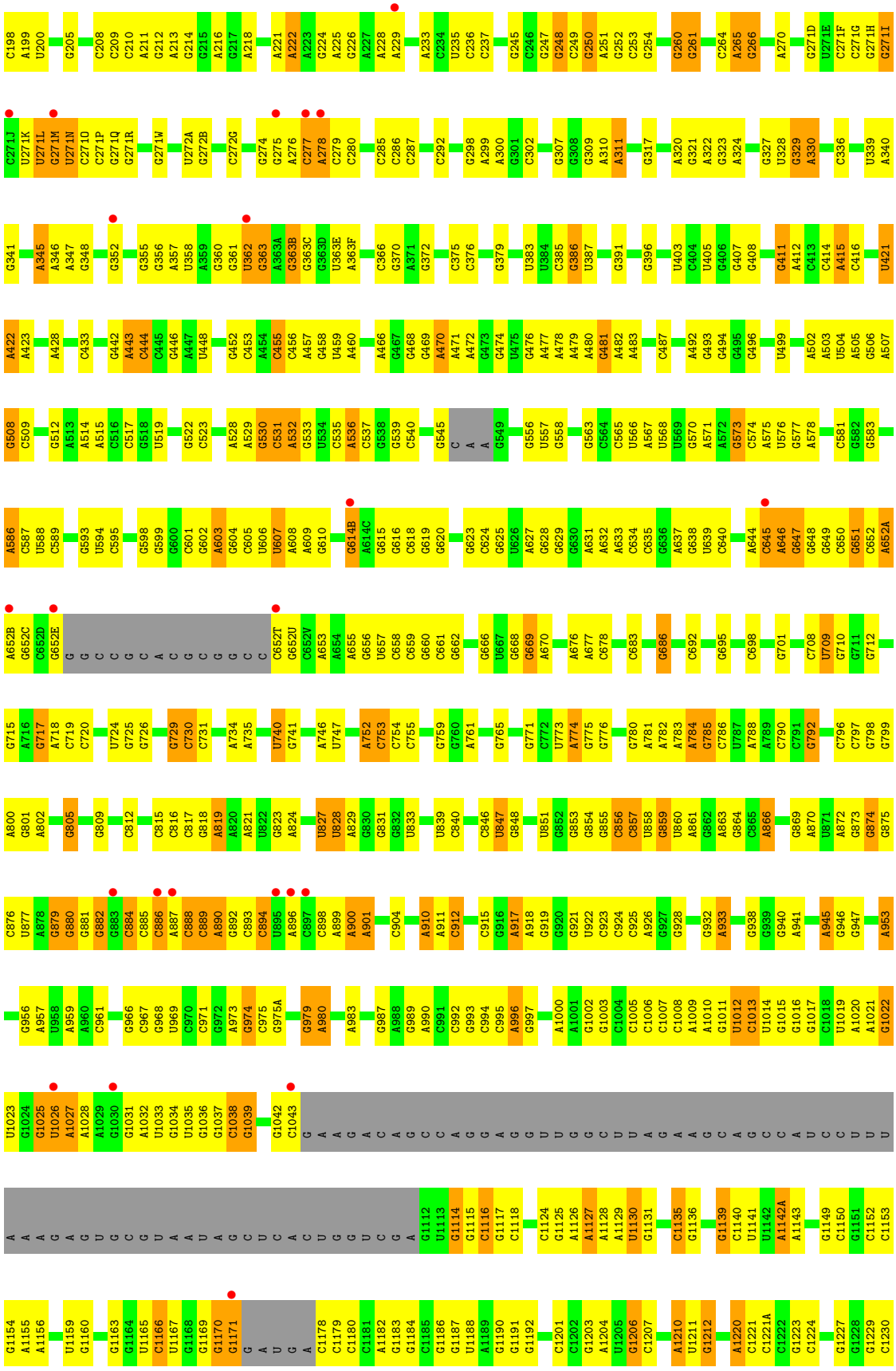


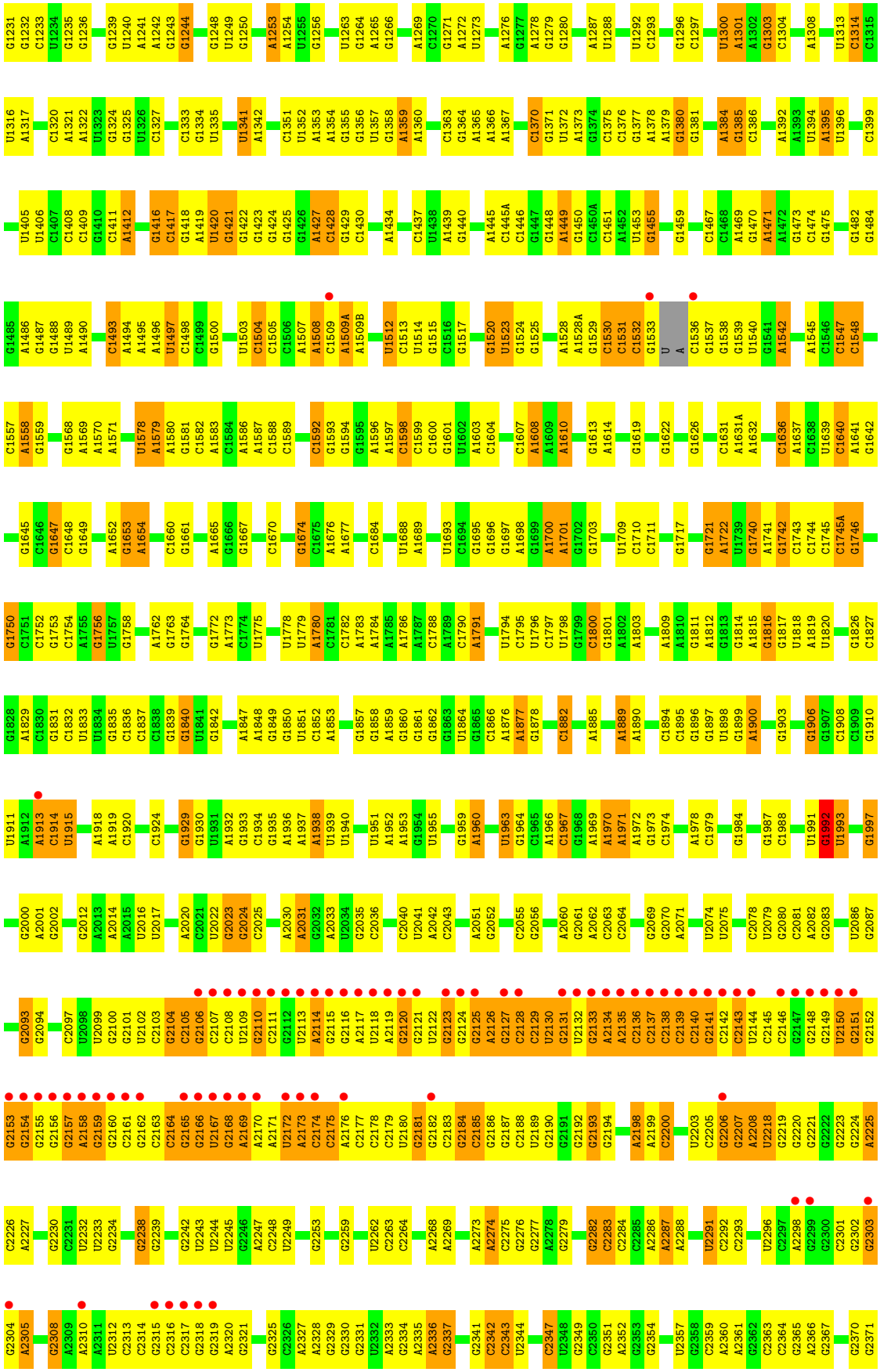


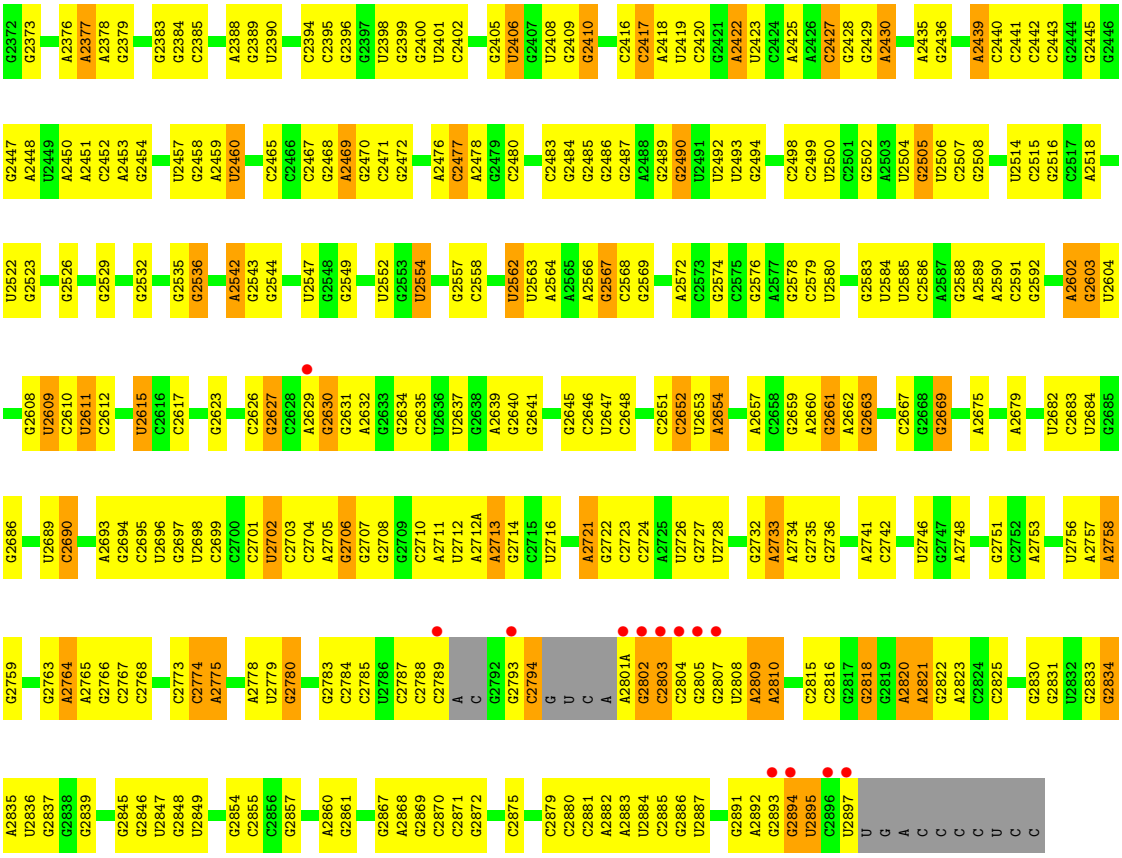
• Molecule 26: 23S Ribosomal RNA

Chain DA:



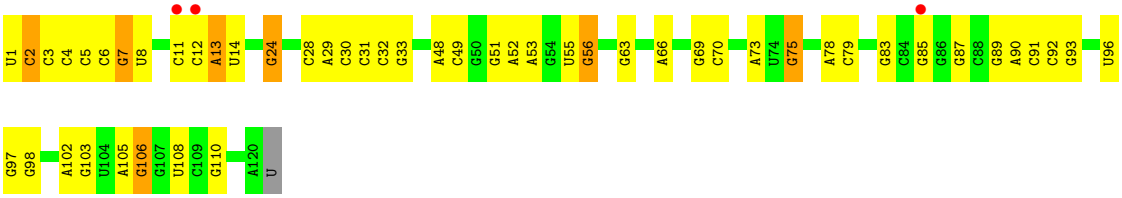






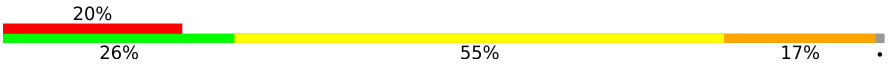
• Molecule 27: 5S Ribosomal RNA

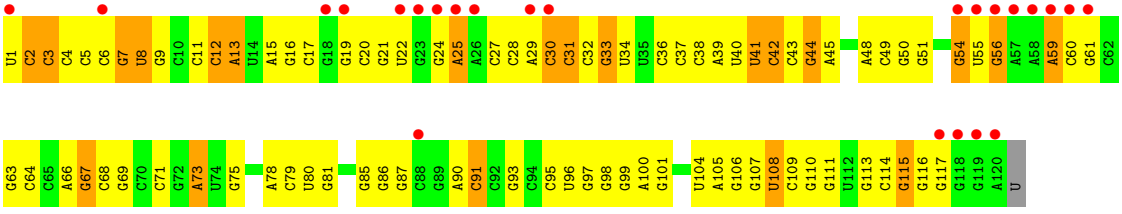
Chain BB:



• Molecule 27: 5S Ribosomal RNA

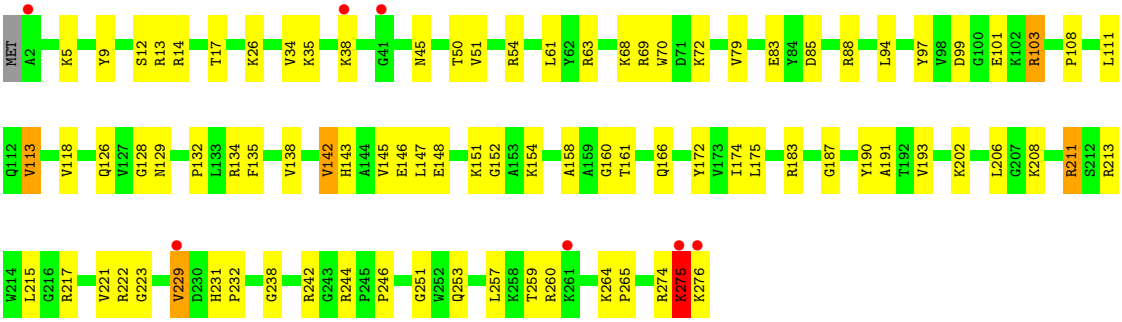
Chain DB:



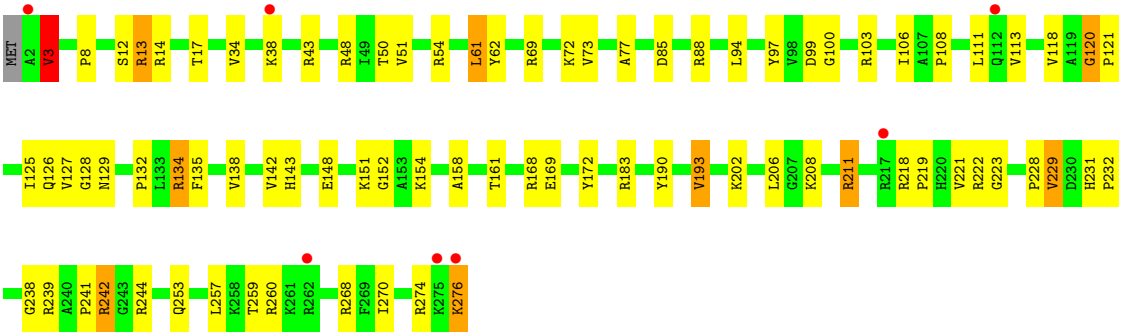


• Molecule 28: 50S ribosomal protein L2

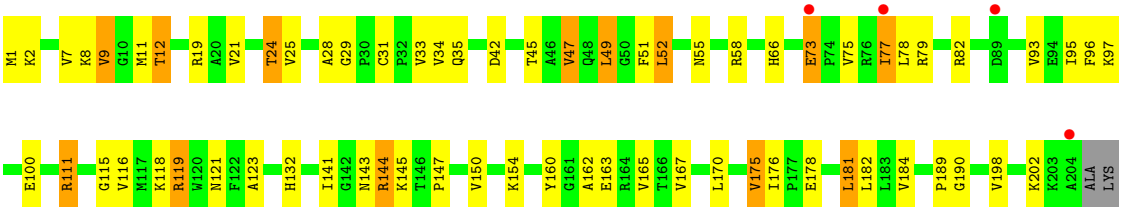
Chain BD:



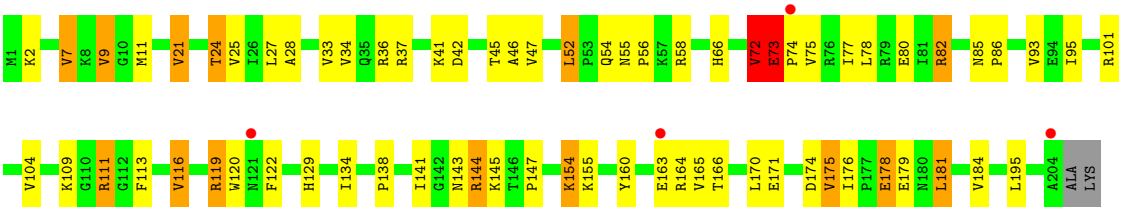
• Molecule 28: 50S ribosomal protein L2



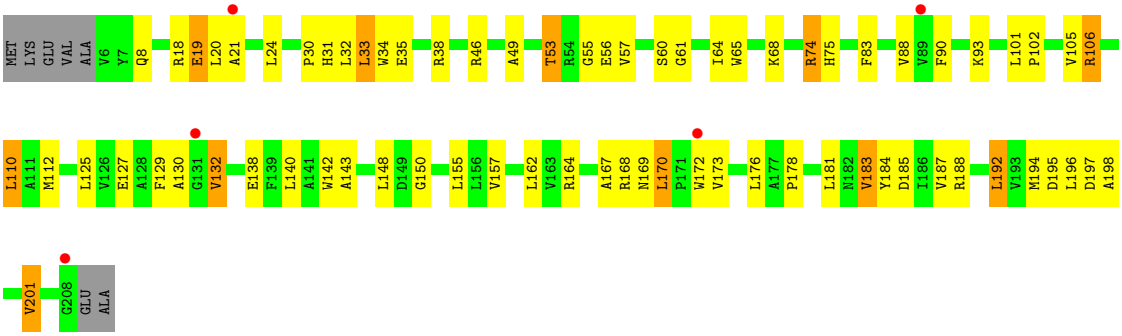
• Molecule 29: 50S ribosomal protein L3



• Molecule 29: 50S ribosomal protein L3

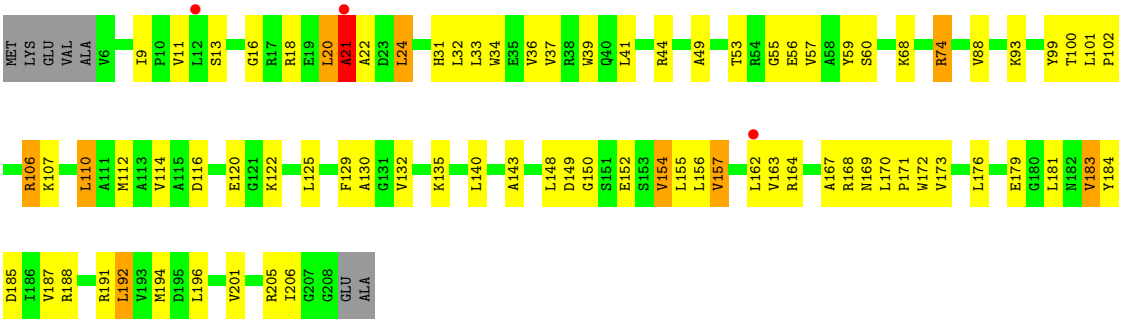


• Molecule 30: 50S ribosomal protein L4



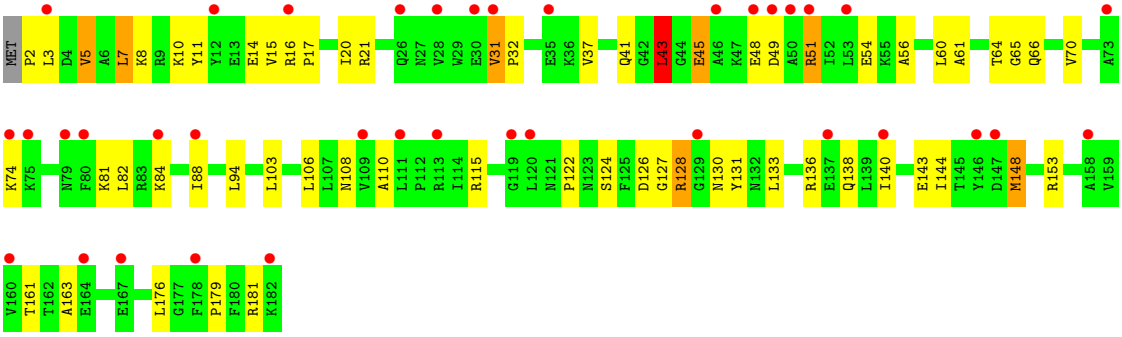
• Molecule 30: 50S ribosomal protein L4

Chain DF:



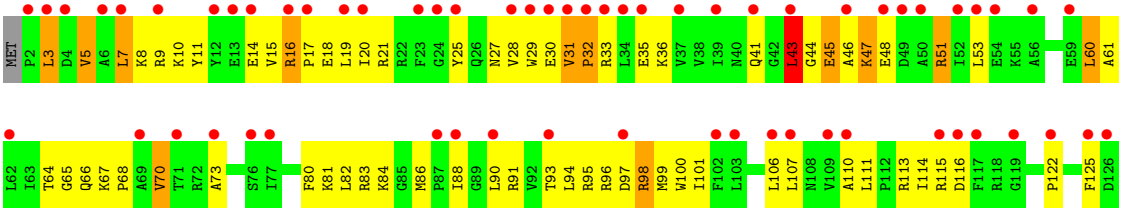
• Molecule 31: 50S ribosomal protein L5

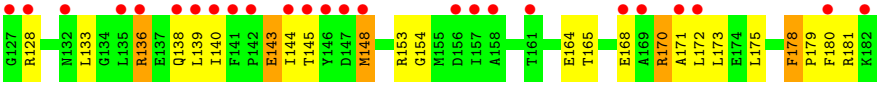
Chain BG:



• Molecule 31: 50S ribosomal protein L5

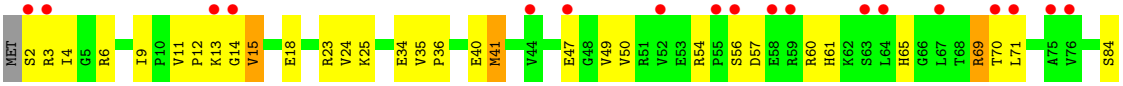
Chain DG:

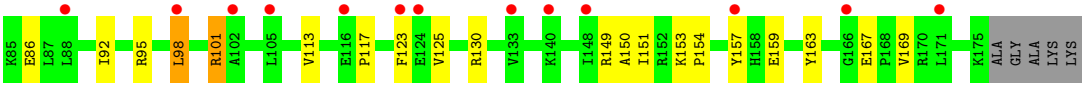




• Molecule 32: 50S ribosomal protein L6

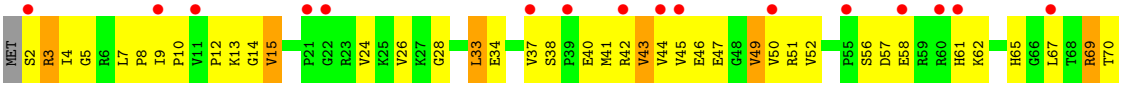
Chain BH:

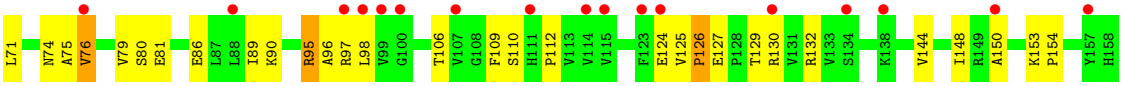


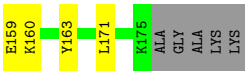


• Molecule 32: 50S ribosomal protein L6

Chain DH:

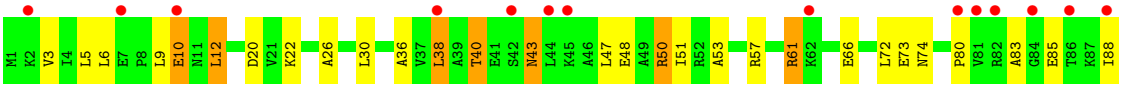


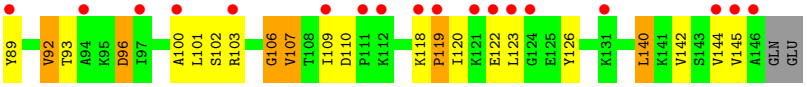




• Molecule 33: 50S ribosomal protein L9

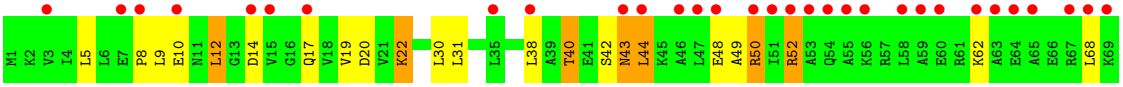
Chain BI:

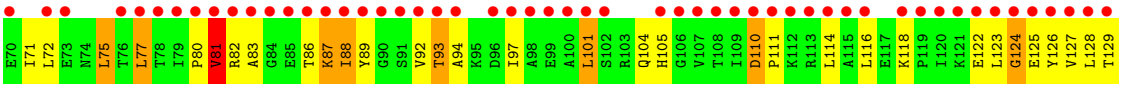


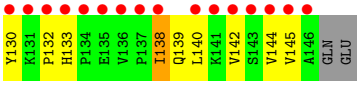


• Molecule 33: 50S ribosomal protein L9

Chain DI:

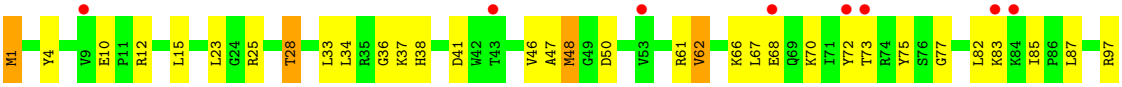


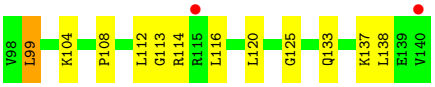




• Molecule 34: 50S ribosomal protein L13

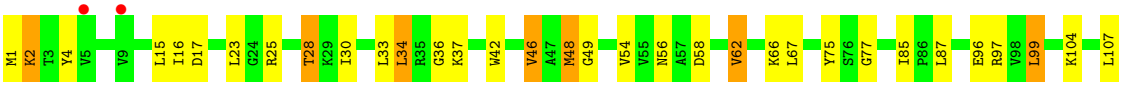
Chain BN:

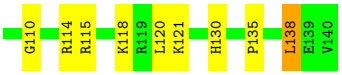




• Molecule 34: 50S ribosomal protein L13

Chain DN:



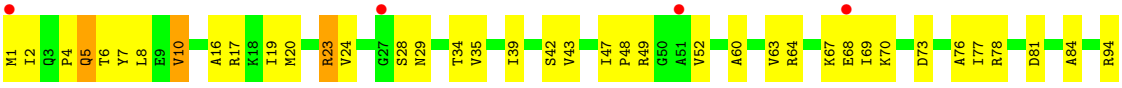


• Molecule 35: 50S ribosomal protein L14

Chain BO:

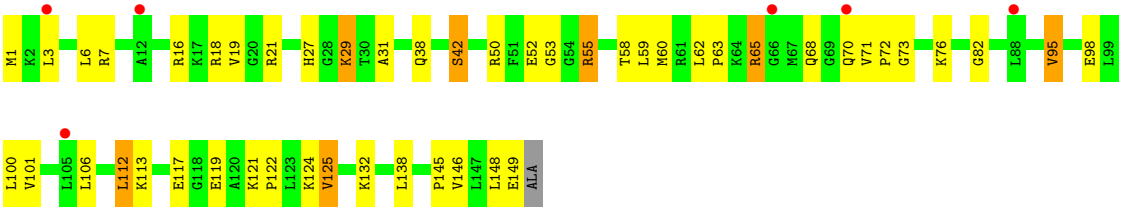
• Molecule 35: 50S ribosomal protein L14

Chain DO:

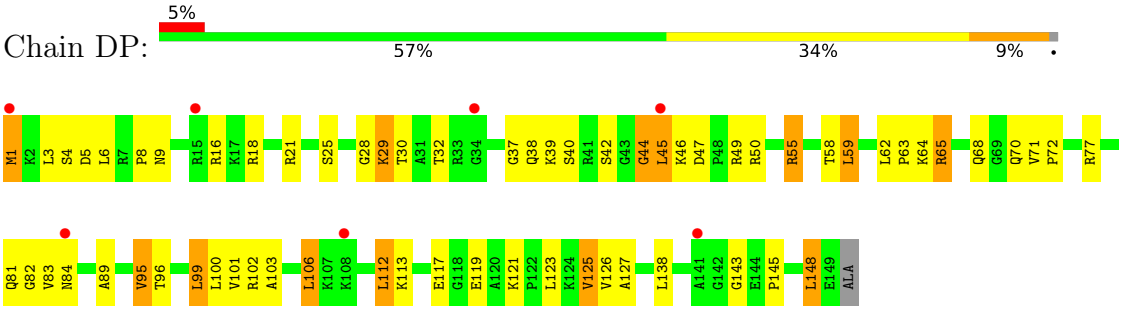


• Molecule 36: 50S ribosomal protein L15

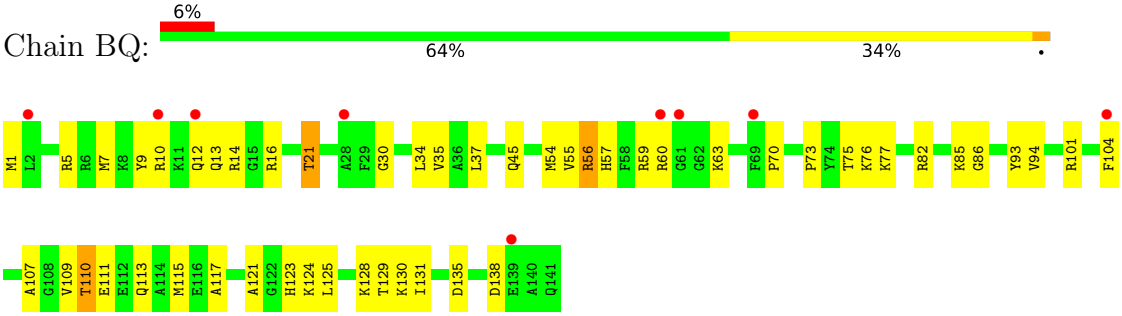
Chain BP:



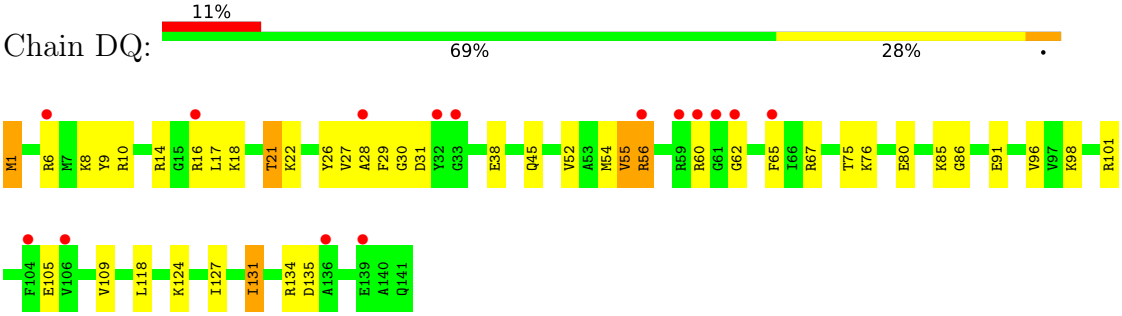
• Molecule 36: 50S ribosomal protein L15



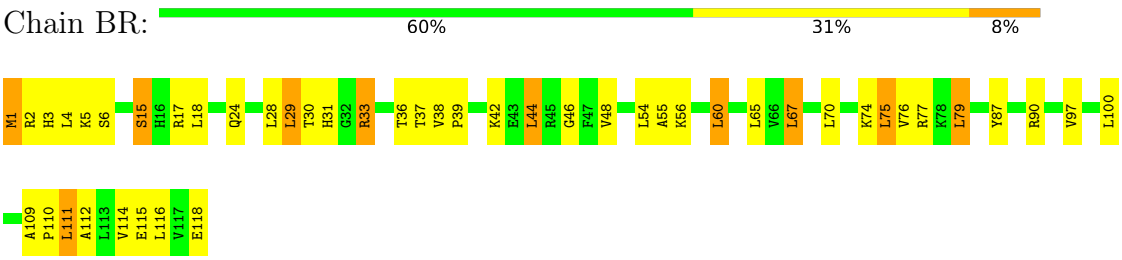
• Molecule 37: 50S ribosomal protein L16



• Molecule 37: 50S ribosomal protein L16

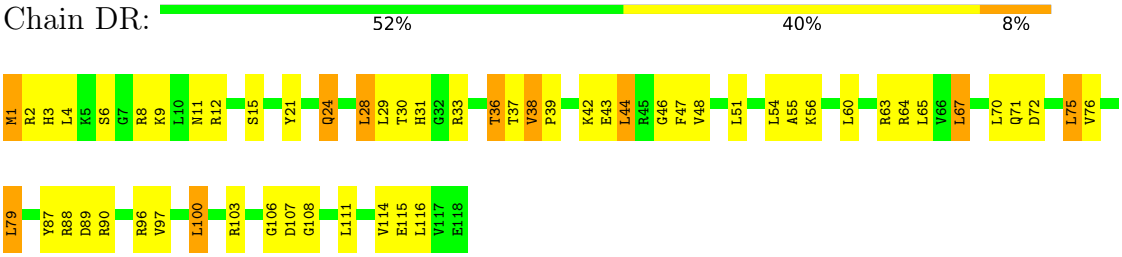


• Molecule 38: 50S ribosomal protein L17



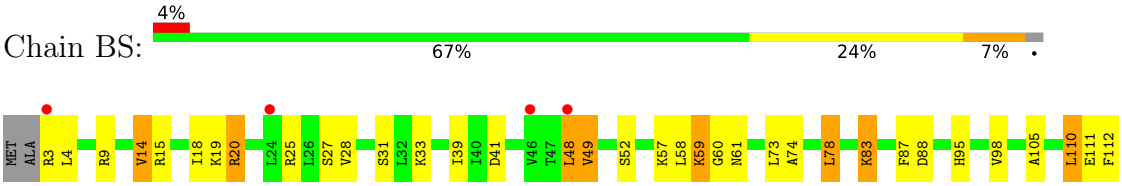
• Molecule 38: 50S ribosomal protein L17

Chain DR:



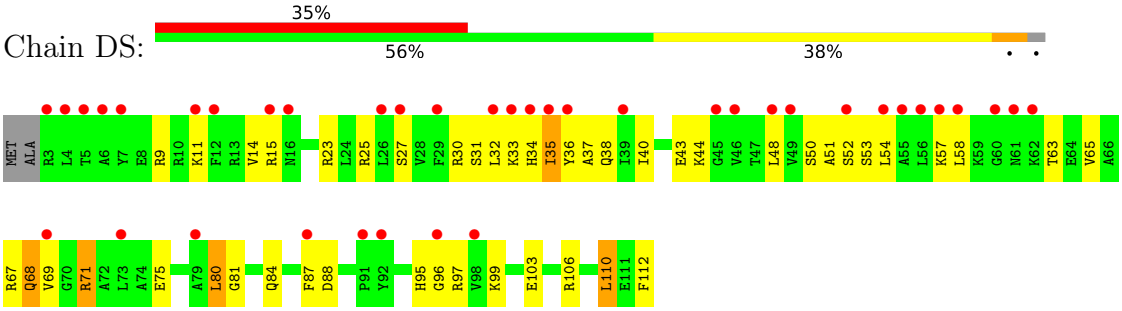
• Molecule 39: 50S ribosomal protein L18

Chain BS:



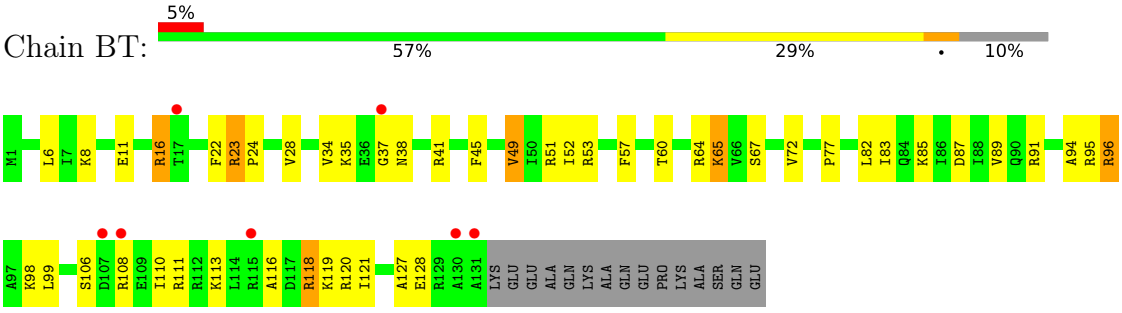
• Molecule 39: 50S ribosomal protein L18

Chain DS:



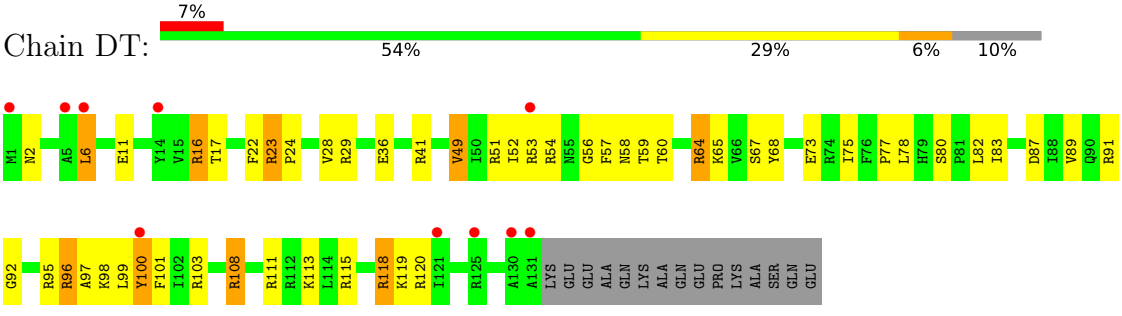
• Molecule 40: 50S ribosomal protein L19

Chain BT:



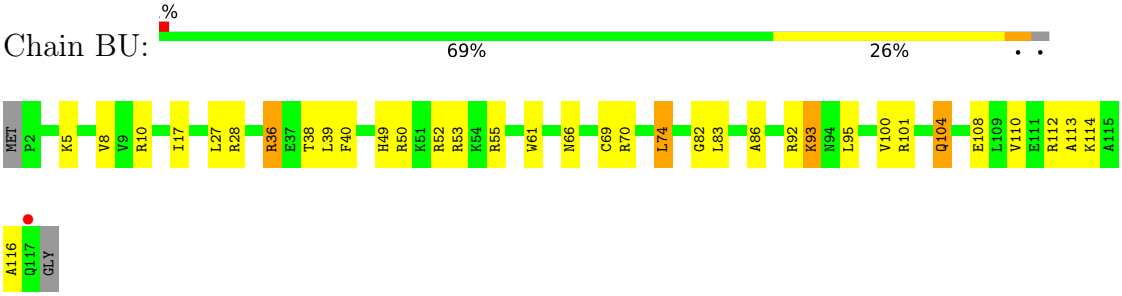
• Molecule 40: 50S ribosomal protein L19

Chain DT:



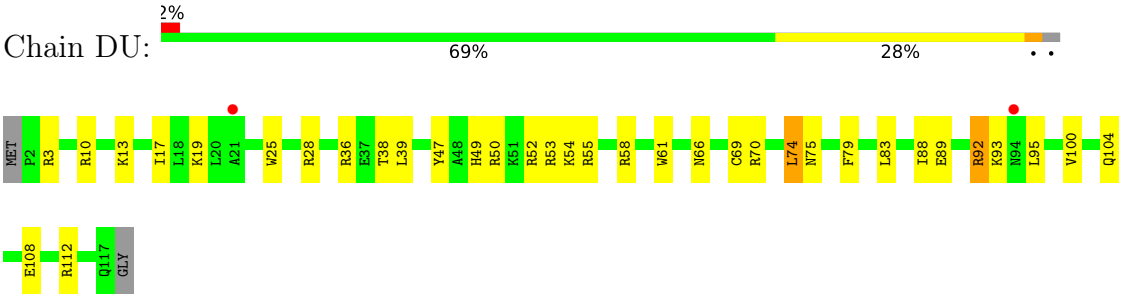
• Molecule 41: 50S ribosomal protein L20

Chain BU:



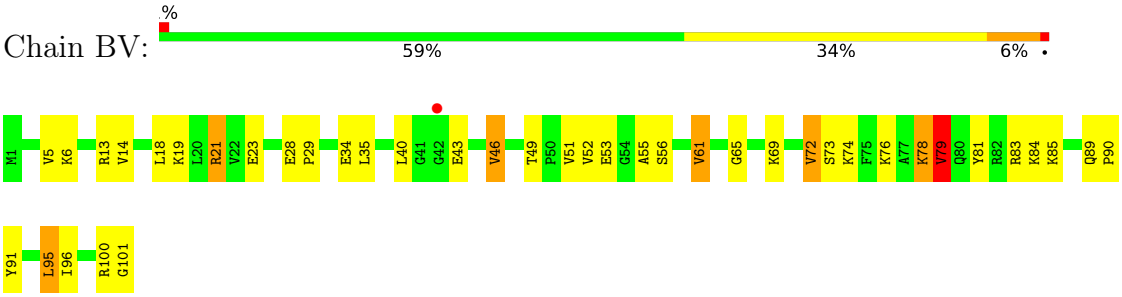
• Molecule 41: 50S ribosomal protein L20

Chain DU:



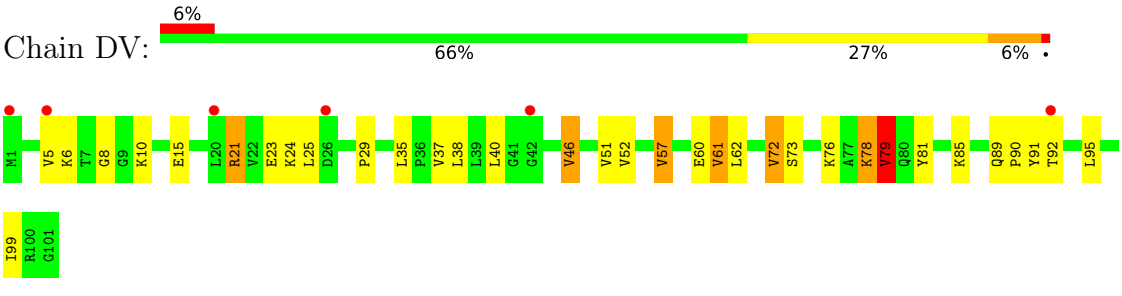
• Molecule 42: 50S ribosomal protein L21

Chain BV:



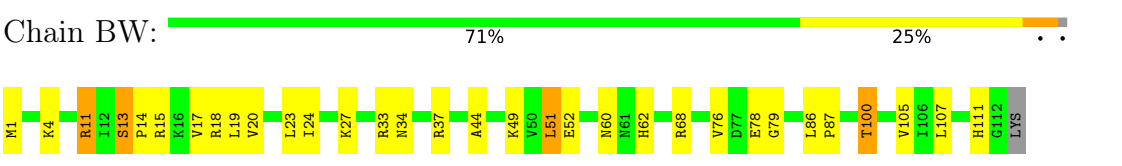
• Molecule 42: 50S ribosomal protein L21

Chain DV:



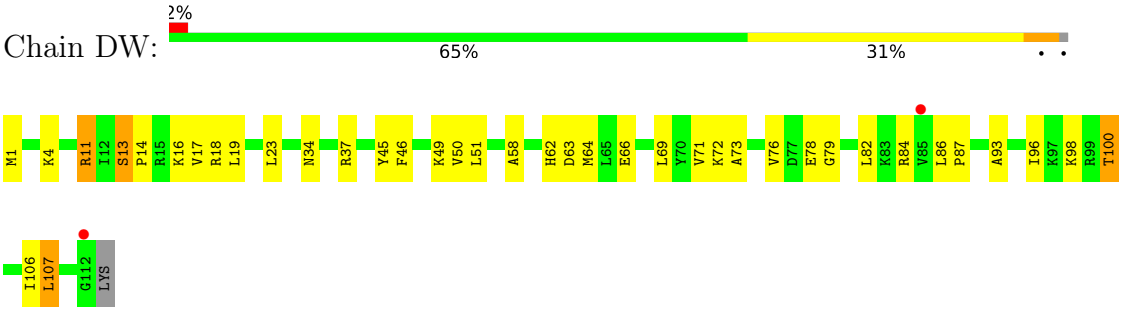
• Molecule 43: 50S ribosomal protein L22

Chain BW:



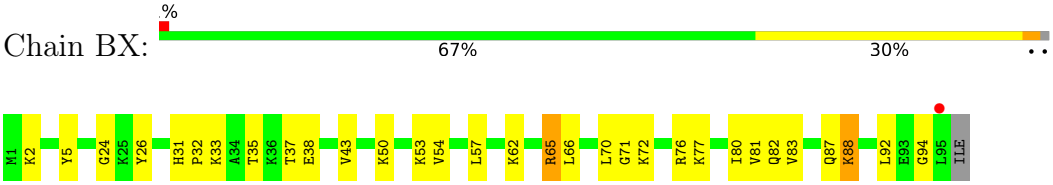
• Molecule 43: 50S ribosomal protein L22

Chain DW:



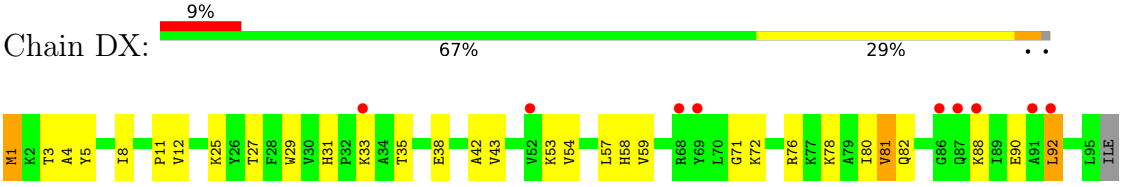
• Molecule 44: 50S ribosomal protein L23

Chain BX:



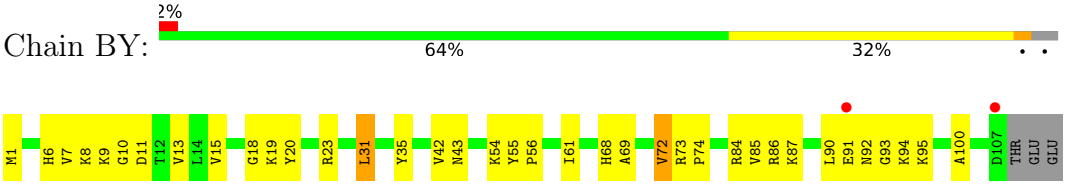
• Molecule 44: 50S ribosomal protein L23

Chain DX:



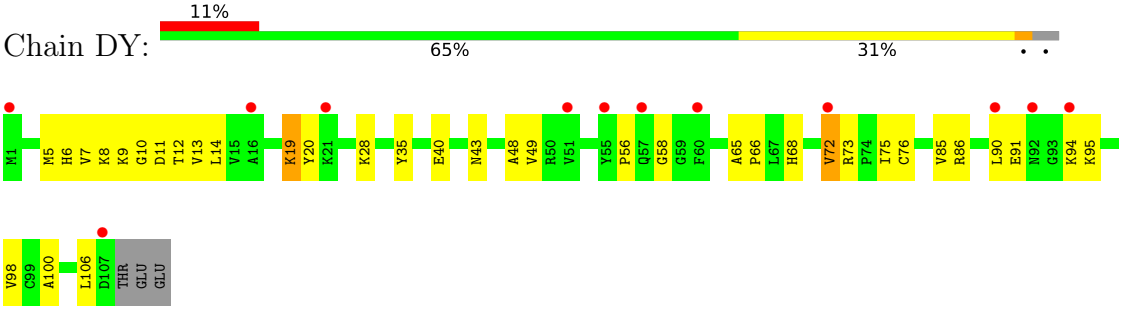
• Molecule 45: 50S ribosomal protein L24

Chain BY:



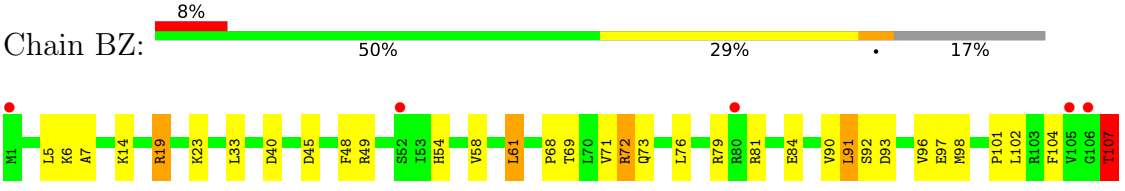
• Molecule 45: 50S ribosomal protein L24

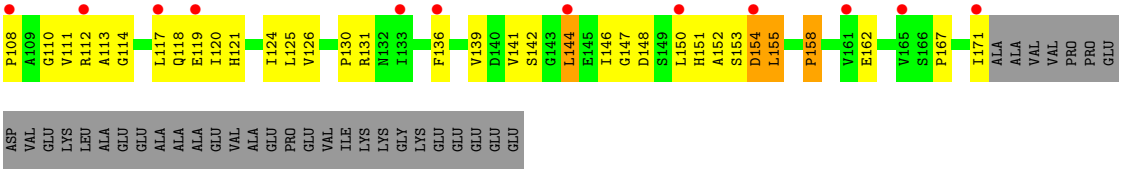
Chain DY:



• Molecule 46: 50S ribosomal protein L25

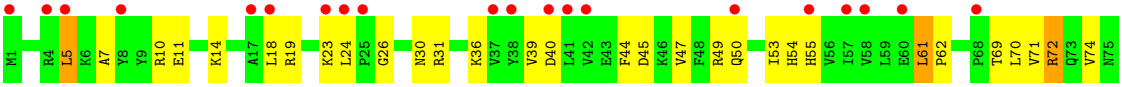
Chain BZ:

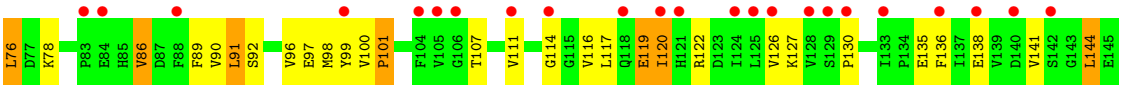


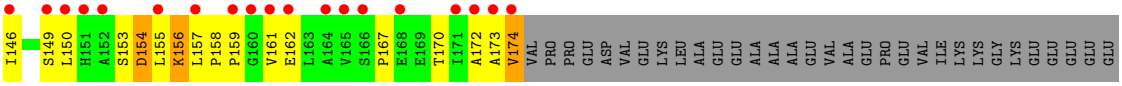


• Molecule 46: 50S ribosomal protein L25

Chain DZ:

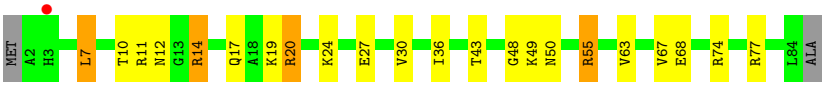






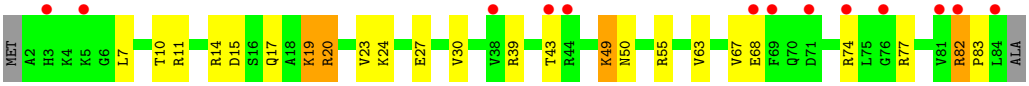
• Molecule 47: 50S ribosomal protein L27

Chain B0:



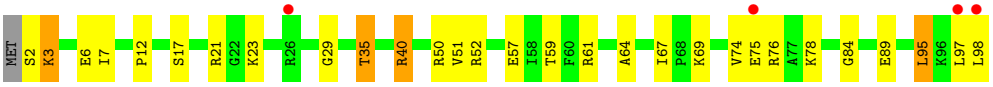
• Molecule 47: 50S ribosomal protein L27

Chain D0:



• Molecule 48: 50S ribosomal protein L28

Chain B1:

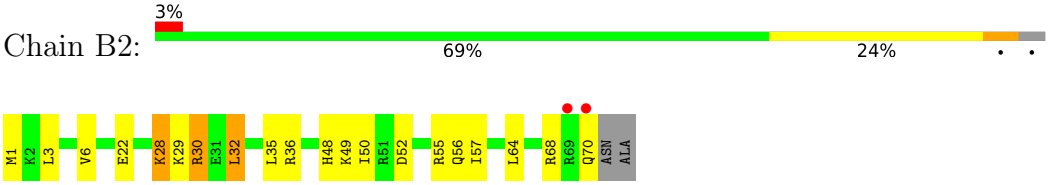


• Molecule 48: 50S ribosomal protein L28

Chain D1:

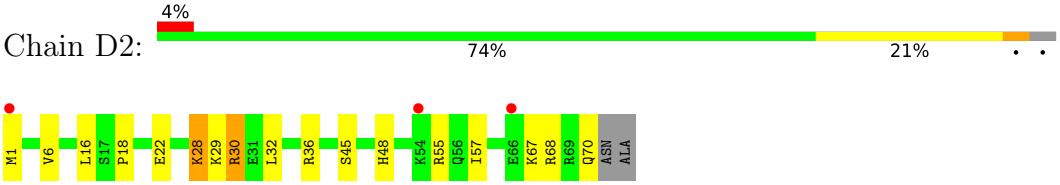
• Molecule 49: 50S ribosomal protein L29

Chain B2:



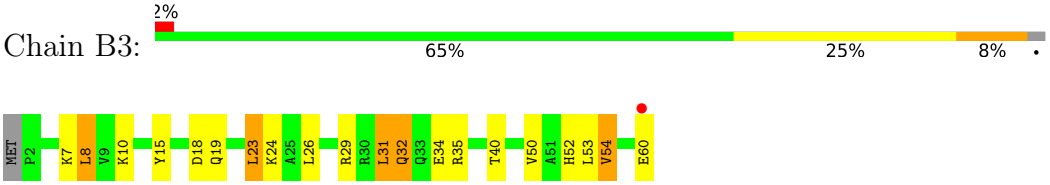
• Molecule 49: 50S ribosomal protein L29

Chain D2:



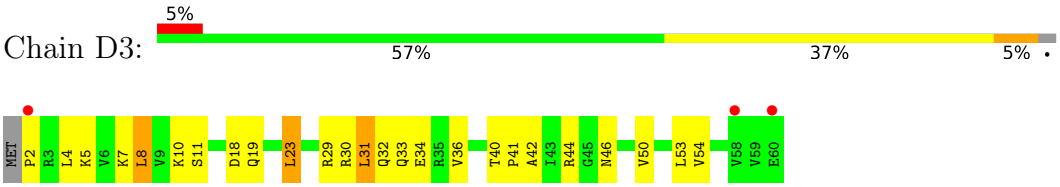
• Molecule 50: 50S ribosomal protein L30

Chain B3:



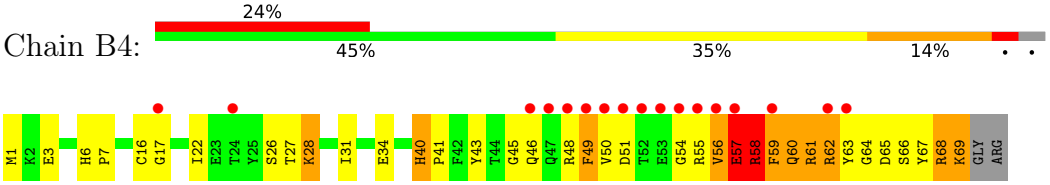
• Molecule 50: 50S ribosomal protein L30

Chain D3:



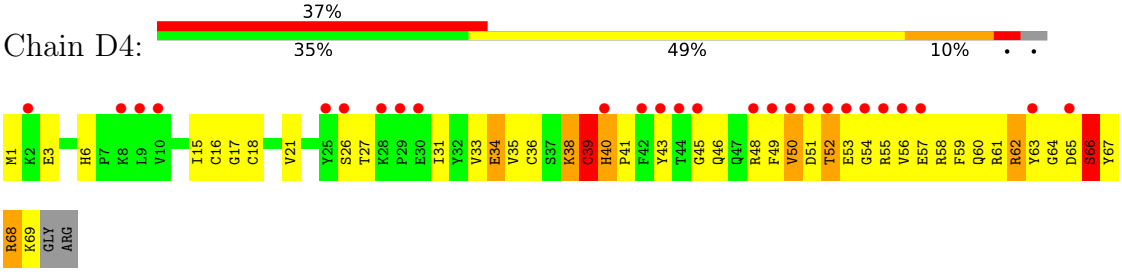
• Molecule 51: 50S ribosomal protein L31

Chain B4:



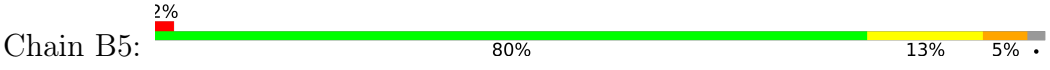
• Molecule 51: 50S ribosomal protein L31

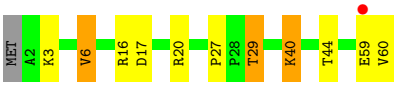
Chain D4:



• Molecule 52: 50S ribosomal protein L32

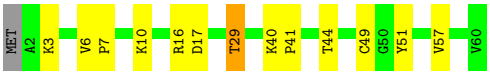
Chain B5:





• Molecule 52: 50S ribosomal protein L32

Chain D5:

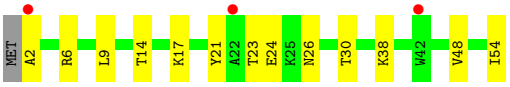


• Molecule 53: 50S ribosomal protein L33

Chain B6:

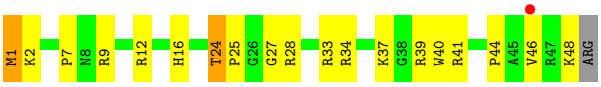
• Molecule 53: 50S ribosomal protein L33

Chain D6:



• Molecule 54: 50S ribosomal protein L34

Chain B7:

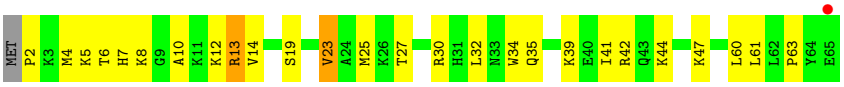


• Molecule 54: 50S ribosomal protein L34

Chain D7:

• Molecule 55: 50S ribosomal protein L35

Chain B8:



• Molecule 55: 50S ribosomal protein L35

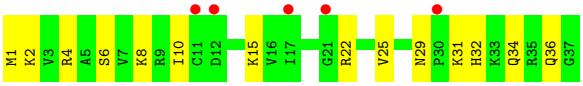
Chain D8:

• Molecule 56: 50S ribosomal protein L36

Chain B9:

• Molecule 56: 50S ribosomal protein L36

Chain D9:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	207.56Å 444.23Å 613.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	150.38 – 2.80 150.38 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.0 (150.38-2.80) 98.0 (150.38-2.80)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.29 (at 2.82Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.234 , 0.280 0.234 , 0.279	Depositor DCC
R_{free} test set	67651 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	50.1	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 58.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	290205	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.56% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.23	0/36049	0.47	2/56261 (0.0%)
1	CA	0.24	0/36170	0.50	7/56452 (0.0%)
2	AB	0.39	0/1881	1.00	6/2542 (0.2%)
2	CB	0.44	0/1860	1.05	11/2518 (0.4%)
3	AC	0.39	0/1576	0.86	1/2130 (0.0%)
3	CC	0.40	0/1566	0.94	5/2119 (0.2%)
4	AD	0.38	0/1689	0.89	2/2267 (0.1%)
4	CD	0.39	0/1704	0.93	7/2284 (0.3%)
5	AE	0.39	0/1145	0.85	2/1543 (0.1%)
5	CE	0.40	0/1149	0.97	3/1548 (0.2%)
6	AF	0.35	0/819	0.79	0/1111
6	CF	0.36	0/829	0.81	0/1123
7	AG	0.36	0/1250	0.88	2/1679 (0.1%)
7	CG	0.37	0/1254	0.95	1/1683 (0.1%)
8	AH	0.36	0/1108	0.90	2/1494 (0.1%)
8	CH	0.35	0/1108	0.94	6/1494 (0.4%)
9	AI	0.38	0/1002	0.90	1/1346 (0.1%)
9	CI	0.42	0/997	0.92	3/1343 (0.2%)
10	AJ	0.38	0/722	1.06	7/982 (0.7%)
10	CJ	0.42	0/727	0.96	2/988 (0.2%)
11	AK	0.38	0/844	0.84	0/1145
11	CK	0.36	0/848	0.85	0/1149
12	AL	0.38	0/946	0.82	3/1274 (0.2%)
12	CL	0.36	0/946	0.85	2/1274 (0.2%)
13	AM	0.38	0/969	0.92	1/1302 (0.1%)
13	CM	0.41	0/961	0.95	3/1291 (0.2%)
14	AN	0.38	0/501	0.81	0/664
14	CN	0.41	0/501	0.86	1/664 (0.2%)
15	AO	0.38	0/739	0.86	1/985 (0.1%)
15	CO	0.40	0/739	0.88	2/985 (0.2%)
16	AP	0.39	0/697	0.86	1/939 (0.1%)
16	CP	0.38	0/693	0.82	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	AQ	0.34	0/836	0.84	0/1117
17	CQ	0.32	0/836	0.85	0/1117
18	AR	0.35	0/560	0.81	0/746
18	CR	0.37	0/560	0.83	0/746
19	AS	0.38	0/667	0.85	0/900
19	CS	0.40	0/661	1.04	1/893 (0.1%)
20	AT	0.36	0/730	0.94	0/965
20	CT	0.35	0/729	0.87	1/965 (0.1%)
21	AU	0.32	0/203	0.94	0/266
21	CU	0.38	0/203	0.80	0/266
22	AV	0.27	0/310	0.46	0/480
22	CV	0.61	0/144	0.83	0/222
23	AW	0.29	0/40	0.52	0/60
23	CW	0.21	0/40	0.51	0/60
24	AX	0.29	0/1700	0.50	0/2650
24	CX	0.30	0/1700	0.59	0/2650
25	AY	0.20	0/115	0.41	0/176
25	CY	0.19	0/115	0.36	0/176
26	BA	0.28	0/68013	0.45	2/106165 (0.0%)
26	DA	0.24	0/67542	0.45	1/105428 (0.0%)
27	BB	0.24	0/2878	0.48	0/4490
27	DB	0.23	0/2878	0.47	0/4490
28	BD	0.49	0/2186	0.87	2/2944 (0.1%)
28	DD	0.42	0/2186	0.92	5/2944 (0.2%)
29	BE	0.48	0/1592	0.87	0/2149
29	DE	0.43	0/1592	0.94	6/2149 (0.3%)
30	BF	0.46	0/1619	0.83	0/2193
30	DF	0.43	0/1615	0.93	5/2188 (0.2%)
31	BG	0.38	0/1450	0.90	4/1959 (0.2%)
31	DG	0.41	0/1449	1.01	4/1958 (0.2%)
32	BH	0.42	0/1356	0.86	1/1834 (0.1%)
32	DH	0.39	0/1356	0.92	3/1834 (0.2%)
33	BI	0.43	0/1100	0.98	7/1501 (0.5%)
33	DI	0.55	0/1076	1.27	12/1471 (0.8%)
34	BN	0.45	0/1144	0.90	2/1543 (0.1%)
34	DN	0.41	0/1144	0.95	2/1543 (0.1%)
35	BO	0.45	0/943	0.84	0/1269
35	DO	0.40	0/943	0.84	0/1269
36	BP	0.44	0/1152	0.84	0/1533
36	DP	0.40	0/1152	0.93	2/1533 (0.1%)
37	BQ	0.46	0/1143	0.84	0/1527
37	DQ	0.41	0/1143	0.83	0/1527
38	BR	0.48	0/982	0.84	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	DR	0.40	0/982	0.86	2/1312 (0.2%)
39	BS	0.40	0/887	0.89	0/1180
39	DS	0.38	0/880	0.88	1/1172 (0.1%)
40	BT	0.43	0/1105	0.87	0/1477
40	DT	0.39	0/1097	0.79	0/1468
41	BU	0.46	0/977	0.79	0/1301
41	DU	0.37	0/977	0.82	0/1301
42	BV	0.45	0/782	0.80	0/1049
42	DV	0.37	0/782	0.79	0/1049
43	BW	0.48	0/897	0.89	2/1205 (0.2%)
43	DW	0.40	0/897	0.83	2/1205 (0.2%)
44	BX	0.47	0/764	0.87	0/1025
44	DX	0.37	0/764	0.79	0/1025
45	BY	0.44	0/819	0.93	2/1095 (0.2%)
45	DY	0.37	0/819	0.90	1/1095 (0.1%)
46	BZ	0.41	0/1379	0.96	4/1873 (0.2%)
46	DZ	0.36	0/1390	0.90	4/1890 (0.2%)
47	B0	0.44	0/662	0.87	1/881 (0.1%)
47	D0	0.36	0/662	0.82	2/881 (0.2%)
48	B1	0.42	0/762	0.85	1/1014 (0.1%)
48	D1	0.40	0/762	0.83	0/1014
49	B2	0.43	0/590	0.84	0/781
49	D2	0.35	0/590	0.80	0/781
50	B3	0.46	0/474	0.88	0/635
50	D3	0.39	0/469	0.94	0/630
51	B4	0.42	0/565	1.10	5/761 (0.7%)
51	D4	0.40	0/545	1.17	8/737 (1.1%)
52	B5	0.50	0/469	0.95	3/635 (0.5%)
52	D5	0.42	0/469	0.77	0/635
53	B6	0.47	0/460	0.78	0/613
53	D6	0.40	0/456	0.75	0/608
54	B7	0.48	0/426	0.85	0/561
54	D7	0.47	0/426	0.88	2/561 (0.4%)
55	B8	0.47	0/519	0.81	0/684
55	D8	0.40	0/525	0.75	0/691
56	B9	0.48	0/310	0.95	0/407
56	D9	0.36	0/310	0.89	0/407
All	All	0.31	0/310421	0.61	184/464361 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	1
7	AG	0	1
20	AT	0	1
29	DE	0	1
33	DI	0	1
39	BS	0	1
46	BZ	0	1
51	B4	0	2
51	D4	0	1
All	All	0	10

There are no bond length outliers.

All (184) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
33	DI	88	ILE	N-CA-C	11.06	124.26	109.21
33	DI	71	ILE	N-CA-C	9.08	119.06	110.53
51	D4	52	THR	N-CA-C	-8.91	102.42	113.38
51	B4	60	GLN	N-CA-C	-8.37	103.17	112.72
3	CC	194	GLY	N-CA-C	8.30	120.91	110.29
2	AB	9	GLU	N-CA-C	8.11	122.67	109.94
1	AA	1172	C	N1-C2-O2	7.95	142.76	118.90
33	DI	118	LYS	CA-C-N	7.95	129.78	119.84
33	DI	118	LYS	C-N-CA	7.95	129.78	119.84
46	BZ	107	THR	CA-C-N	7.84	127.84	119.76
46	BZ	107	THR	C-N-CA	7.84	127.84	119.76
51	D4	66	SER	N-CA-C	-7.84	103.29	113.17
4	AD	188	LEU	CA-C-N	7.71	129.48	119.84
4	AD	188	LEU	C-N-CA	7.71	129.48	119.84
2	AB	23	ARG	N-CA-C	-7.54	104.12	112.72
31	DG	31	VAL	CA-C-N	7.37	129.05	119.84
31	DG	31	VAL	C-N-CA	7.37	129.05	119.84
2	CB	130	ARG	CA-C-N	7.27	127.30	119.89
2	CB	130	ARG	C-N-CA	7.27	127.30	119.89
46	BZ	158	PRO	CA-C-N	7.25	128.91	119.84
46	BZ	158	PRO	C-N-CA	7.25	128.91	119.84
33	DI	138	ILE	N-CA-C	7.19	118.47	108.12
29	DE	72	VAL	CA-C-N	7.14	134.55	121.70
29	DE	72	VAL	C-N-CA	7.14	134.55	121.70
13	AM	84	ILE	N-CA-C	7.08	123.71	113.16
1	CA	1154	G	N1-C2-N2	-7.08	94.95	116.20
46	DZ	14	LYS	CA-C-N	7.08	128.69	119.84
46	DZ	14	LYS	C-N-CA	7.08	128.69	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	BA	1992	G	C2'-C3'-O3'	6.97	119.96	109.50
7	CG	132	GLY	N-CA-C	6.96	119.14	112.04
45	BY	31	LEU	CA-C-N	6.89	126.70	119.05
45	BY	31	LEU	C-N-CA	6.89	126.70	119.05
30	DF	9	ILE	N-CA-C	6.89	115.49	107.77
33	DI	88	ILE	CB-CA-C	-6.89	101.56	111.34
8	CH	73	ASP	CA-C-N	6.88	126.51	119.56
8	CH	73	ASP	C-N-CA	6.88	126.51	119.56
31	DG	178	PHE	CA-C-N	6.86	127.88	120.13
31	DG	178	PHE	C-N-CA	6.86	127.88	120.13
10	AJ	52	GLY	CA-C-N	6.80	126.43	119.56
10	AJ	52	GLY	C-N-CA	6.80	126.43	119.56
43	BW	13	SER	CA-C-N	6.78	127.05	119.32
43	BW	13	SER	C-N-CA	6.78	127.05	119.32
31	BG	31	VAL	CA-C-N	6.69	128.20	119.84
31	BG	31	VAL	C-N-CA	6.69	128.20	119.84
9	CI	63	ILE	N-CA-C	6.68	117.75	108.12
51	D4	40	HIS	CA-C-N	6.66	128.17	119.84
51	D4	40	HIS	C-N-CA	6.66	128.17	119.84
8	AH	71	GLY	CA-C-N	6.64	126.33	119.56
8	AH	71	GLY	C-N-CA	6.64	126.33	119.56
33	DI	124	GLY	N-CA-C	6.62	120.24	110.63
47	D0	82	ARG	CA-C-N	6.61	126.99	119.92
47	D0	82	ARG	C-N-CA	6.61	126.99	119.92
33	DI	110	ASP	CA-C-N	6.59	128.07	119.84
33	DI	110	ASP	C-N-CA	6.59	128.07	119.84
34	DN	110	GLY	CA-C-N	6.57	126.07	119.24
34	DN	110	GLY	C-N-CA	6.57	126.07	119.24
13	CM	68	GLY	N-CA-C	6.48	120.34	112.49
2	CB	119	GLU	N-CA-C	-6.48	104.30	111.82
8	CH	100	ILE	CA-C-N	6.48	126.66	120.31
8	CH	100	ILE	C-N-CA	6.48	126.66	120.31
32	DH	9	ILE	N-CA-C	6.46	113.95	107.55
36	DP	44	GLY	CA-C-N	6.42	133.27	121.70
36	DP	44	GLY	C-N-CA	6.42	133.27	121.70
5	CE	105	VAL	CA-C-N	-6.39	113.10	119.56
5	CE	105	VAL	C-N-CA	-6.39	113.10	119.56
32	DH	9	ILE	CA-C-N	6.39	126.34	119.76
32	DH	9	ILE	C-N-CA	6.39	126.34	119.76
33	BI	118	LYS	CA-C-N	6.34	127.77	119.84
33	BI	118	LYS	C-N-CA	6.34	127.77	119.84
4	CD	171	GLY	CA-C-N	6.31	126.51	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	CD	171	GLY	C-N-CA	6.31	126.51	119.32
2	AB	128	GLU	N-CA-C	-6.29	104.92	112.59
51	D4	65	ASP	N-CA-C	-6.27	104.85	113.56
33	BI	110	ASP	CA-C-N	6.18	126.08	119.28
33	BI	110	ASP	C-N-CA	6.18	126.08	119.28
9	AI	55	ALA	N-CA-C	-6.09	106.52	112.97
4	CD	166	LYS	N-CA-C	-6.06	105.54	113.12
10	AJ	90	LEU	CA-C-N	6.05	127.41	119.84
10	AJ	90	LEU	C-N-CA	6.05	127.41	119.84
34	BN	125	GLY	CA-C-N	6.04	125.74	119.64
34	BN	125	GLY	C-N-CA	6.04	125.74	119.64
2	CB	231	GLU	CA-C-N	-6.04	113.46	119.92
2	CB	231	GLU	C-N-CA	-6.04	113.46	119.92
10	AJ	76	ASN	CA-C-N	6.02	127.36	119.84
10	AJ	76	ASN	C-N-CA	6.02	127.36	119.84
54	D7	6	GLN	CA-C-N	6.02	126.04	119.90
54	D7	6	GLN	C-N-CA	6.02	126.04	119.90
31	BG	54	GLU	N-CA-C	-5.93	105.81	113.16
29	DE	21	VAL	CA-C-N	5.92	126.12	119.90
29	DE	21	VAL	C-N-CA	5.92	126.12	119.90
1	AA	1172	C	N3-C2-O2	-5.91	104.18	121.90
33	BI	106	GLY	CA-C-N	5.90	132.31	121.70
33	BI	106	GLY	C-N-CA	5.90	132.31	121.70
52	B5	27	PRO	O-C-N	5.89	124.02	121.31
12	AL	44	THR	CA-C-N	5.88	126.34	120.52
12	AL	44	THR	C-N-CA	5.88	126.34	120.52
33	BI	51	ILE	N-CA-C	-5.88	104.78	110.72
28	DD	244	ARG	CA-C-N	-5.86	114.34	120.38
28	DD	244	ARG	C-N-CA	-5.86	114.34	120.38
1	CA	1119	C	C2-N1-C1'	5.85	136.34	118.80
1	CA	1004	A	O4'-C1'-N9	5.84	117.26	108.50
26	DA	1992	G	C2'-C3'-O3'	5.82	118.22	109.50
19	CS	67	VAL	N-CA-C	5.78	115.85	110.42
51	B4	51	ASP	N-CA-C	5.76	118.55	109.39
2	CB	23	ARG	NE-CZ-NH1	-5.71	115.79	121.50
51	D4	39	CYS	N-CA-C	5.68	122.90	110.80
51	B4	40	HIS	CA-C-N	5.67	126.93	119.84
51	B4	40	HIS	C-N-CA	5.67	126.93	119.84
51	B4	58	ARG	N-CA-C	5.67	122.88	110.80
2	AB	16	HIS	N-CA-C	5.67	116.93	108.31
10	AJ	55	LYS	N-CA-C	5.61	122.75	110.80
12	AL	105	TYR	CB-CA-C	-5.61	109.60	117.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	DY	91	GLU	N-CA-C	-5.59	105.33	111.82
2	AB	16	HIS	CB-CA-C	-5.57	110.13	116.54
29	DE	85	ASN	CA-C-N	5.56	125.47	119.85
29	DE	85	ASN	C-N-CA	5.56	125.47	119.85
26	BA	1653	G	P-O3'-C3'	5.55	128.52	120.20
30	DF	21	ALA	CA-C-N	5.54	131.67	121.70
30	DF	21	ALA	C-N-CA	5.54	131.67	121.70
5	AE	105	VAL	CA-C-N	-5.54	113.97	119.56
5	AE	105	VAL	C-N-CA	-5.54	113.97	119.56
2	AB	38	GLY	N-CA-C	-5.51	106.59	115.08
2	CB	24	TRP	N-CA-C	5.50	117.02	110.19
20	CT	11	SER	N-CA-C	-5.49	106.17	112.92
52	B5	6	VAL	CA-C-N	-5.47	114.15	119.90
52	B5	6	VAL	C-N-CA	-5.47	114.15	119.90
3	CC	99	VAL	N-CA-C	5.47	114.48	106.55
38	DR	106	GLY	N-CA-C	5.45	120.38	113.24
5	CE	98	THR	N-CA-C	5.44	117.66	111.02
32	BH	9	ILE	N-CA-C	5.42	112.92	107.55
1	CA	1154	G	N3-C2-N2	5.41	136.14	119.90
46	DZ	100	VAL	CA-C-N	5.38	126.57	119.84
46	DZ	100	VAL	C-N-CA	5.38	126.57	119.84
8	CH	6	ILE	N-CA-C	5.38	115.47	110.42
43	DW	13	SER	CA-C-N	5.37	124.83	119.24
43	DW	13	SER	C-N-CA	5.37	124.83	119.24
1	CA	1119	C	N1-C2-O2	5.37	135.00	118.90
31	BG	127	GLY	N-CA-C	-5.35	107.29	114.25
28	DD	50	THR	N-CA-C	-5.34	106.70	114.12
30	DF	154	VAL	N-CA-C	5.34	115.58	108.11
28	BD	238	GLY	N-CA-C	-5.33	103.12	112.77
39	DS	81	GLY	N-CA-C	-5.33	108.28	115.21
3	AC	4	LYS	N-CA-C	5.29	117.75	110.35
33	DI	22	LYS	CA-C-N	5.28	125.34	119.32
33	DI	22	LYS	C-N-CA	5.28	125.34	119.32
9	CI	89	ASN	CA-C-N	5.27	125.08	119.28
9	CI	89	ASN	C-N-CA	5.27	125.08	119.28
38	DR	38	VAL	CB-CA-C	-5.26	108.70	113.70
15	AO	21	ASP	N-CA-C	5.24	118.16	110.30
1	CA	1281	U	O4'-C1'-N1	-5.24	100.34	108.20
2	CB	158	LEU	CA-C-N	5.24	125.53	119.92
2	CB	158	LEU	C-N-CA	5.24	125.53	119.92
10	CJ	52	GLY	CA-C-N	5.23	124.84	119.56
10	CJ	52	GLY	C-N-CA	5.23	124.84	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	AG	116	ALA	N-CA-C	5.21	116.64	111.07
28	BD	275	LYS	N-CA-C	5.21	121.89	110.80
4	CD	178	VAL	N-CA-C	5.20	115.93	110.62
28	DD	120	GLY	CA-C-N	5.20	124.83	119.05
28	DD	120	GLY	C-N-CA	5.20	124.83	119.05
3	CC	72	LYS	CA-C-N	5.20	124.81	119.56
3	CC	72	LYS	C-N-CA	5.20	124.81	119.56
51	D4	68	ARG	N-CA-C	5.19	116.63	111.07
3	CC	139	GLN	N-CA-C	5.19	116.79	111.03
12	CL	28	LYS	N-CA-C	5.18	118.54	111.39
15	CO	74	ASP	CA-C-N	5.17	124.79	119.05
15	CO	74	ASP	C-N-CA	5.17	124.79	119.05
30	DF	157	VAL	N-CA-C	5.17	114.19	106.85
1	CA	992	U	P-O3'-C3'	5.17	127.95	120.20
14	CN	55	GLY	N-CA-C	5.15	122.20	115.40
2	CB	141	GLU	N-CA-C	5.13	116.56	110.97
51	D4	36	CYS	N-CA-C	5.12	114.80	108.19
4	CD	168	ARG	N-CA-C	5.11	117.44	110.24
7	AG	78	ARG	N-CA-C	5.10	115.75	107.23
4	CD	188	LEU	CA-C-N	5.09	125.09	119.90
4	CD	188	LEU	C-N-CA	5.09	125.09	119.90
48	B1	84	GLY	N-CA-C	-5.08	107.97	114.37
13	CM	112	GLY	CA-C-N	5.08	125.01	119.78
13	CM	112	GLY	C-N-CA	5.08	125.01	119.78
8	CH	47	GLY	N-CA-C	5.05	117.95	110.63
12	CL	119	LYS	N-CA-C	-5.05	103.38	110.50
16	AP	20	VAL	N-CA-C	5.03	115.61	108.42
2	CB	160	ASP	N-CA-C	-5.02	106.84	113.17
33	DI	30	LEU	N-CA-C	5.02	116.44	110.97
47	B0	14	ARG	N-CA-C	5.01	117.94	110.52

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	8	LYS	Peptide
7	AG	79	ARG	Peptide
20	AT	9	ASN	Peptide
51	B4	57	GLU	Peptide
51	B4	58	ARG	Peptide
39	BS	58	LEU	Peptide
46	BZ	158	PRO	Peptide

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Mol	Chain	Res	Type	Group
51	D4	66	SER	Peptide
29	DE	72	VAL	Peptide
33	DI	81	VAL	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32205	0	16255	758	1
1	CA	32312	0	16307	969	1
2	AB	1846	0	1867	75	0
2	CB	1825	0	1828	76	0
3	AC	1552	0	1546	51	0
3	CC	1542	0	1517	58	0
4	AD	1659	0	1676	77	0
4	CD	1674	0	1714	82	0
5	AE	1129	0	1184	35	0
5	CE	1133	0	1191	39	0
6	AF	806	0	793	20	0
6	CF	816	0	808	26	0
7	AG	1231	0	1238	39	0
7	CG	1235	0	1249	40	0
8	AH	1088	0	1126	36	0
8	CH	1088	0	1126	40	0
9	AI	983	0	986	49	0
9	CI	978	0	966	54	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	38	0
11	AK	829	0	825	23	0
11	CK	833	0	836	22	0
12	AL	930	0	980	22	0
12	CL	930	0	980	33	0
13	AM	958	0	1002	38	0
13	CM	950	0	988	47	0
14	AN	492	0	529	28	0
14	CN	492	0	529	23	0
15	AO	728	0	760	23	0
15	CO	728	0	760	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	AP	681	0	697	28	0
16	CP	677	0	686	26	0
17	AQ	823	0	891	24	0
17	CQ	823	0	891	18	0
18	AR	555	0	618	13	0
18	CR	555	0	618	25	0
19	AS	652	0	662	31	0
19	CS	646	0	644	40	0
20	AT	728	0	798	29	0
20	CT	727	0	796	24	0
21	AU	199	0	208	5	0
21	CU	199	0	208	7	0
22	AV	277	0	140	7	0
22	CV	129	0	65	16	0
23	AW	74	0	51	5	0
23	CW	74	0	51	11	0
24	AX	1633	0	836	33	0
24	CX	1635	0	838	81	0
25	AY	104	0	56	3	0
25	CY	104	0	56	2	0
26	BA	60729	0	30620	968	0
26	DA	60311	0	30412	1244	1
27	BB	2573	0	1306	33	0
27	DB	2573	0	1306	87	0
28	BD	2136	0	2218	68	0
28	DD	2136	0	2218	75	0
29	BE	1559	0	1618	44	0
29	DE	1559	0	1618	53	0
30	BF	1584	0	1625	51	0
30	DF	1580	0	1619	57	0
31	BG	1425	0	1443	38	0
31	DG	1424	0	1434	74	0
32	BH	1330	0	1407	30	0
32	DH	1330	0	1407	47	0
33	BI	1085	0	1114	30	1
33	DI	1061	0	1080	51	0
34	BN	1117	0	1184	22	0
34	DN	1117	0	1184	29	0
35	BO	933	0	996	28	0
35	DO	933	0	996	42	0
36	BP	1135	0	1212	53	0
36	DP	1135	0	1212	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	BQ	1122	0	1179	40	0
37	DQ	1122	0	1179	34	0
38	BR	968	0	1033	28	1
38	DR	968	0	1033	37	0
39	BS	877	0	938	28	0
39	DS	870	0	923	29	0
40	BT	1091	0	1151	37	0
40	DT	1083	0	1136	40	0
41	BU	959	0	1019	25	0
41	DU	959	0	1018	28	0
42	BV	771	0	830	23	1
42	DV	771	0	830	25	0
43	BW	886	0	940	16	0
43	DW	886	0	940	21	0
44	BX	750	0	814	25	0
44	DX	750	0	814	20	0
45	BY	806	0	881	23	0
45	DY	806	0	881	23	0
46	BZ	1349	0	1355	38	0
46	DZ	1360	0	1363	50	0
47	B0	653	0	674	21	0
47	D0	653	0	674	19	0
48	B1	755	0	826	19	0
48	D1	755	0	826	20	0
49	B2	588	0	643	9	0
49	D2	588	0	643	10	0
50	B3	469	0	518	15	0
50	D3	464	0	514	17	0
51	B4	552	0	533	34	0
51	D4	532	0	503	31	0
52	B5	455	0	465	9	0
52	D5	455	0	465	10	0
53	B6	453	0	473	14	0
53	D6	449	0	469	7	0
54	B7	418	0	467	20	0
54	D7	418	0	467	16	0
55	B8	511	0	571	30	0
55	D8	517	0	582	15	0
56	B9	307	0	335	7	0
56	D9	307	0	335	11	0
57	AA	207	0	0	0	0
57	AD	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	AE	2	0	0	0	0
57	AF	1	0	0	0	0
57	AJ	1	0	0	0	0
57	AK	1	0	0	0	0
57	AM	1	0	0	0	0
57	AN	2	0	0	0	0
57	AS	1	0	0	0	0
57	AV	1	0	0	0	0
57	AW	1	0	0	0	0
57	AX	11	0	0	0	0
57	B0	4	0	0	0	0
57	B1	1	0	0	0	0
57	B2	1	0	0	0	0
57	B3	2	0	0	0	0
57	B5	2	0	0	0	0
57	B7	3	0	0	0	0
57	B8	1	0	0	0	0
57	B9	1	0	0	0	0
57	BA	720	0	0	0	0
57	BB	20	0	0	0	0
57	BD	11	0	0	0	0
57	BE	7	0	0	0	0
57	BF	10	0	0	0	0
57	BG	2	0	0	0	0
57	BN	6	0	0	0	0
57	BO	1	0	0	0	0
57	BP	4	0	0	0	0
57	BQ	5	0	0	0	0
57	BR	3	0	0	0	0
57	BU	8	0	0	0	0
57	BV	4	0	0	0	0
57	BW	5	0	0	0	0
57	BX	1	0	0	0	0
57	BY	1	0	0	0	0
57	BZ	1	0	0	0	0
57	CA	160	0	0	0	0
57	CE	1	0	0	0	0
57	CF	1	0	0	0	0
57	CJ	1	0	0	0	0
57	CK	1	0	0	0	0
57	CT	1	0	0	0	0
57	CW	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	CX	2	0	0	0	0
57	D3	1	0	0	0	0
57	D5	1	0	0	0	0
57	D8	2	0	0	0	0
57	DA	629	0	0	0	0
57	DB	10	0	0	0	0
57	DD	7	0	0	0	0
57	DE	4	0	0	0	0
57	DF	4	0	0	0	0
57	DG	1	0	0	0	0
57	DN	1	0	0	0	0
57	DO	1	0	0	0	0
57	DP	2	0	0	0	0
57	DQ	3	0	0	0	0
57	DR	2	0	0	0	0
57	DU	4	0	0	0	0
57	DV	2	0	0	0	0
57	DW	2	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
60	CX	1	0	0	0	0
61	AA	170	0	0	16	0
61	AL	2	0	0	1	0
61	AO	1	0	0	0	0
61	AU	1	0	0	1	0
61	AV	2	0	0	0	0
61	AW	3	0	0	0	0
61	B0	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	B1	1	0	0	0	0
61	B3	1	0	0	0	0
61	B5	5	0	0	0	0
61	B7	1	0	0	1	0
61	B8	7	0	0	0	0
61	BA	1102	0	0	59	0
61	BB	36	0	0	1	0
61	BD	8	0	0	1	0
61	BE	13	0	0	5	0
61	BF	4	0	0	0	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BP	15	0	0	1	0
61	BQ	3	0	0	0	0
61	BR	1	0	0	1	0
61	BS	1	0	0	0	0
61	BT	3	0	0	0	0
61	BU	1	0	0	1	0
61	BV	4	0	0	0	0
61	BW	2	0	0	0	0
61	BX	2	0	0	0	0
61	CA	130	0	0	8	0
61	CE	1	0	0	0	0
61	CJ	2	0	0	0	0
61	CN	1	0	0	0	0
61	CT	1	0	0	0	0
61	CV	1	0	0	0	0
61	CW	1	0	0	0	0
61	CX	1	0	0	1	0
61	D0	5	0	0	1	0
61	D1	1	0	0	0	0
61	D3	2	0	0	0	0
61	D7	1	0	0	0	0
61	D8	4	0	0	0	0
61	DA	767	0	0	55	0
61	DB	9	0	0	0	0
61	DD	9	0	0	3	0
61	DE	5	0	0	0	0
61	DF	6	0	0	0	0
61	DN	2	0	0	0	0
61	DP	12	0	0	3	0
61	DR	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	DT	1	0	0	0	0
61	DU	2	0	0	0	0
61	DV	1	0	0	1	0
61	DX	2	0	0	0	0
61	DY	1	0	0	1	0
All	All	290205	0	193167	6372	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All (6372) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1002:G:H1	1:CA:1038:C:N4	1.48	1.11
26:DA:2121:G:H1	26:DA:2177:C:N4	1.52	1.06
1:AA:1164:G:N2	1:AA:1165:C:C5	2.24	1.06
1:CA:72:C:N4	1:CA:97:G:N1	2.04	1.05
26:DA:2139:C:N4	26:DA:2152:G:H1	1.55	1.04
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.40	1.03
1:CA:1162:C:N4	1:CA:1174:G:H1	1.56	1.03
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.20	1.03
26:DA:2137:C:N4	26:DA:2154:G:H1	1.55	1.02
1:CA:1245:A:H61	1:CA:1292:U:H3	1.07	1.02
1:CA:1244:C:N4	1:CA:1293:G:H1	1.56	1.02
1:CA:76:C:C4	1:CA:93:G:N1	2.28	1.01
1:CA:1114:C:N4	1:CA:1186:G:H1	1.57	1.01
22:CV:18:G:N2	24:CX:34:C:N3	2.07	1.01
1:CA:1355:G:H1	1:CA:1367:C:H42	1.04	1.00
26:DA:2104:G:H1	26:DA:2185:C:N4	1.58	1.00
1:CA:985:C:N4	1:CA:1220:G:H1	1.60	0.99
1:CA:76:C:N4	1:CA:93:G:C6	2.31	0.99
22:CV:18:G:H1	24:CX:34:C:N4	1.60	0.99
1:AA:1164:G:N2	1:AA:1165:C:C6	2.31	0.99
26:BA:2138:C:H42	26:BA:2153:G:H1	1.04	0.99
1:CA:1000:U:H3	1:CA:1041:A:N6	1.61	0.98
26:BA:2102:U:H3	26:BA:2187:G:H1	1.11	0.98
1:CA:1000:U:H3	1:CA:1041:A:H61	0.98	0.97
24:CX:30:G:H1	24:CX:40:C:H42	1.00	0.97
1:AA:1089:G:H1	1:AA:1096:C:N4	1.62	0.97
1:CA:1133:G:H1	1:CA:1141:C:H42	1.10	0.97
1:CA:76:C:N4	1:CA:93:G:N1	2.13	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CX:49:G:N1	24:CX:65:C:N4	2.12	0.96
1:CA:72:C:N3	1:CA:97:G:N2	2.14	0.96
24:CX:49:G:N2	24:CX:65:C:N3	2.13	0.95
26:BA:2096:U:H3	26:BA:2193:G:H1	1.00	0.94
26:DA:2141:G:O6	26:DA:2150:U:O2	1.86	0.94
1:CA:999:C:N3	1:CA:1042:G:N2	2.16	0.94
24:AX:49:G:H1	24:AX:65:C:H42	1.16	0.93
1:CA:989:C:N3	1:CA:1216:G:N1	2.15	0.93
1:CA:1262:C:H42	1:CA:1273:G:H1	1.13	0.93
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.48	0.93
47:B0:11:ARG:O	47:B0:14:ARG:NH2	2.00	0.93
40:BT:16:ARG:NH2	40:BT:83:ILE:O	2.02	0.93
1:CA:70:G:H1	1:CA:99:U:H3	1.17	0.93
1:AA:1502:A:H2	1:AA:1505:G:H1	1.16	0.93
23:CW:76:PPU:H8	23:CW:76:PPU:H5"	1.49	0.92
26:BA:2103:C:H42	26:BA:2186:G:H1	1.11	0.92
26:DA:2141:G:C6	26:DA:2150:U:O2	2.23	0.92
1:CA:407:G:OP1	4:CD:115:ARG:NH2	2.03	0.91
31:DG:41:GLN:HE22	31:DG:153:ARG:HB3	1.35	0.91
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.51	0.91
22:CV:17:U:H3	24:CX:35:A:H61	1.08	0.91
46:BZ:153:SER:HB3	46:BZ:167:PRO:HB3	1.53	0.91
26:BA:1176:G:H1'	26:BA:1177:A:H5'	1.53	0.91
1:CA:1133:G:H1	1:CA:1141:C:N4	1.69	0.91
22:CV:17:U:H3	24:CX:35:A:N6	1.70	0.90
24:AX:28:C:H42	24:AX:42:G:H1	1.19	0.90
26:DA:2139:C:N4	26:DA:2152:G:N1	2.17	0.90
1:CA:1002:G:N2	1:CA:1038:C:N3	2.18	0.89
1:CA:1027:C:C2	1:CA:1034:G:N2	2.40	0.89
26:DA:1607:C:N4	26:DA:1622:G:OP2	2.04	0.89
1:CA:999:C:N4	1:CA:1042:G:N1	2.21	0.89
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.53	0.88
26:BA:2136:C:H42	26:BA:2155:G:H1	1.12	0.88
22:CV:18:G:H1	24:CX:34:C:H42	0.93	0.88
26:DA:2121:G:N1	26:DA:2177:C:N4	2.16	0.88
24:AX:5:G:H1	24:AX:68:C:H42	1.20	0.88
1:AA:1089:G:H1	1:AA:1096:C:H42	0.91	0.88
23:AW:76:PPU:H8	23:AW:76:PPU:H5"	1.53	0.88
26:BA:2140:C:C2	26:BA:2151:G:N2	2.41	0.88
1:CA:1244:C:N3	1:CA:1293:G:N2	2.22	0.87
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.54	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CX:43:A:H2'	24:CX:44:A:H8	1.39	0.87
26:DA:1169:G:H1	26:DA:1180:C:H42	1.14	0.87
26:DA:1689:A:H62	26:DA:1698:A:H2	1.23	0.87
26:BA:2124:G:H1	26:BA:2174:C:H42	1.22	0.87
24:CX:30:G:H1	24:CX:40:C:N4	1.71	0.87
26:BA:993:G:OP1	41:BU:50:ARG:NH2	2.06	0.86
27:DB:32:C:H1'	27:DB:51:G:H22	1.39	0.86
24:CX:49:G:H1	24:CX:65:C:N4	1.72	0.86
26:DA:2121:G:N2	26:DA:2177:C:N3	2.23	0.86
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.11	0.85
1:AA:677:U:H3	1:AA:713:G:H22	1.24	0.85
1:AA:1007:C:H2'	1:AA:1008:C:H5"	1.56	0.85
35:DO:35:VAL:HG11	35:DO:103:ALA:HB3	1.58	0.85
46:DZ:138:GLU:H	46:DZ:156:LYS:HE2	1.40	0.85
1:AA:78:G:N2	1:AA:91:C:N3	2.25	0.85
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.09	0.85
26:BA:1993:U:OP2	61:BA:4878:HOH:O	1.93	0.85
26:BA:2445:G:OP1	30:BF:74:ARG:NH2	2.10	0.85
1:AA:1158:C:H5	1:AA:1181:G:H1	1.19	0.85
1:AA:1164:G:O6	1:AA:1173:G:C4	2.30	0.85
1:CA:985:C:H42	1:CA:1220:G:H1	0.87	0.85
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.09	0.85
32:DH:46:GLU:HB2	32:DH:49:VAL:HG12	1.59	0.85
26:DA:2127:G:O6	26:DA:2161:C:N3	2.10	0.84
26:DA:1604:C:OP1	61:DA:3949:HOH:O	1.95	0.84
51:D4:51:ASP:HA	51:D4:53:GLU:HG2	1.57	0.84
26:BA:2157:G:N3	26:BA:2158:A:N6	2.24	0.84
1:CA:1047:G:HO2'	1:CA:1215:G:HO2'	1.14	0.84
26:DA:2793:G:O6	26:DA:2803:C:N4	2.10	0.84
26:BA:2100:G:H1	26:BA:2189:U:H3	1.25	0.84
35:BO:35:VAL:HG11	35:BO:103:ALA:HB3	1.58	0.84
26:DA:1772:G:OP1	61:DA:4123:HOH:O	1.95	0.84
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.58	0.83
1:CA:76:C:N3	1:CA:93:G:N2	2.27	0.83
1:CA:376:G:H5"	16:CP:5:ARG:HB2	1.60	0.83
26:DA:994:C:OP1	41:DU:53:ARG:NH2	2.10	0.83
1:CA:76:C:C4	1:CA:93:G:C2	2.66	0.83
24:CX:76:31H:OP1	26:DA:2439:A:N6	2.12	0.83
26:DA:731:C:OP1	61:DA:4214:HOH:O	1.94	0.83
26:BA:2120:G:H1	26:BA:2178:C:H42	1.22	0.83
1:CA:1162:C:N3	1:CA:1174:G:N2	2.25	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2849:U:O4	40:BT:23:ARG:NH2	2.13	0.82
1:CA:692:U:O2'	1:CA:694:A:N7	2.12	0.82
1:CA:1114:C:H42	1:CA:1186:G:H1	0.85	0.82
1:CA:1162:C:H42	1:CA:1174:G:H1	0.85	0.82
46:BZ:151:HIS:O	46:BZ:153:SER:N	2.13	0.82
1:CA:985:C:N3	1:CA:1220:G:N2	2.26	0.82
26:DA:652(E):G:N2	26:DA:652(T):C:O2	2.12	0.82
26:DA:1918:A:O2'	26:DA:1920:C:N4	2.11	0.82
26:DA:2137:C:N3	26:DA:2154:G:N2	2.25	0.82
1:AA:982:U:H5"	14:AN:6:LEU:HD21	1.62	0.82
45:BY:92:ASN:HB3	45:BY:94:LYS:H	1.44	0.82
26:DA:2114:A:N1	26:DA:2117:A:N6	2.28	0.82
26:BA:2138:C:N4	26:BA:2153:G:H1	1.76	0.82
26:DA:2104:G:H1	26:DA:2185:C:H42	0.83	0.82
26:DA:2139:C:N3	26:DA:2152:G:N2	2.26	0.82
1:AA:78:G:N1	1:AA:91:C:N4	2.28	0.81
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.13	0.81
26:DA:2206:G:H3'	26:DA:2207:G:C8	2.14	0.81
1:CA:1355:G:H1	1:CA:1367:C:N4	1.76	0.81
1:AA:624:C:H2'	1:AA:625:G:H8	1.45	0.81
26:BA:2136:C:N4	26:BA:2155:G:H1	1.79	0.81
1:CA:1029:C:N3	1:CA:1032:G:N2	2.28	0.81
1:CA:1366:C:O2'	10:CJ:60:ARG:NH2	2.12	0.81
26:DA:1039:G:O6	26:DA:1116:C:N4	2.13	0.81
29:BE:121:ASN:ND2	61:BE:3108:HOH:O	2.14	0.81
2:CB:178:ARG:HE	8:CH:74:PRO:HG3	1.44	0.81
54:B7:24:THR:HG22	54:B7:27:GLY:H	1.45	0.81
1:AA:997:U:H3	1:AA:1044:A:H61	1.28	0.81
13:AM:6:GLY:O	31:BG:115:ARG:NH2	2.14	0.81
26:DA:879:G:H3'	26:DA:880:G:H8	1.46	0.81
47:D0:11:ARG:O	47:D0:14:ARG:NH2	2.13	0.81
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.13	0.81
1:CA:36:C:OP1	12:CL:123:LYS:NZ	2.14	0.80
26:BA:2103:C:N4	26:BA:2186:G:H1	1.79	0.80
1:CA:1245:A:N6	1:CA:1292:U:H3	1.79	0.80
26:BA:453:C:OP1	61:BA:4156:HOH:O	1.98	0.80
26:BA:2285:C:OP2	53:B6:6:ARG:NH1	2.13	0.80
24:CX:43:A:H2'	24:CX:44:A:C8	2.15	0.80
1:CA:1507:A:N6	1:CA:1528:U:O4	2.13	0.80
27:DB:8:U:H3	27:DB:113:G:H1	1.29	0.80
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:301:G:OP2	45:BY:84:ARG:NH2	2.15	0.80
26:BA:2822:G:OP2	61:BA:4874:HOH:O	1.97	0.80
1:CA:1228:C:OP1	13:CM:115:LYS:N	2.13	0.80
26:DA:2137:C:H42	26:DA:2154:G:H1	0.84	0.80
26:DA:2104:G:N2	26:DA:2185:C:N3	2.27	0.80
1:CA:1502:A:H2	1:CA:1505:G:H1	1.28	0.79
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.64	0.79
26:BA:1338:G:N7	44:BX:62:LYS:NZ	2.29	0.79
26:DA:631:A:OP1	36:DP:65:ARG:NH1	2.15	0.79
26:DA:1533:G:N2	26:DA:1536:C:O2	2.16	0.79
27:DB:20:C:N4	27:DB:63:G:O6	2.14	0.79
1:AA:624:C:H2'	1:AA:625:G:C8	2.18	0.79
1:CA:316:G:OP2	1:CA:351:G:O2'	2.01	0.79
40:DT:65:LYS:HE2	40:DT:67:SER:HB2	1.65	0.79
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.15	0.79
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.16	0.79
27:DB:86:G:O6	27:DB:91:C:N4	2.13	0.79
26:BA:303:U:O4	61:BA:4502:HOH:O	2.01	0.79
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.65	0.79
26:BA:2789:C:O2	26:BA:2894:G:N1	2.14	0.79
26:BA:2140:C:C4	26:BA:2151:G:N1	2.51	0.78
1:CA:1400:C:H42	24:CX:34:C:H2'	1.48	0.78
26:DA:182:A:N3	26:DA:433:C:O2'	2.17	0.78
26:DA:2166:G:H3'	26:DA:2167:U:H5"	1.63	0.78
1:AA:1164:G:O6	1:AA:1173:G:C5	2.35	0.78
26:BA:631:A:OP1	36:BP:65:ARG:NH1	2.17	0.78
26:DA:1250:G:OP2	36:DP:21:ARG:NH1	2.16	0.78
26:DA:847:U:O4	26:DA:933:A:N6	2.17	0.78
26:BA:1530:C:O2'	26:BA:1531:C:O5'	2.00	0.78
26:BA:2142:C:N3	26:BA:2149:G:O6	2.16	0.78
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.17	0.78
26:DA:120:U:OP2	61:DA:3738:HOH:O	2.00	0.78
26:DA:1532:C:N4	26:DA:1537:G:O6	2.14	0.78
1:CA:1007:C:N3	1:CA:1022:G:O6	2.17	0.78
24:CX:31:G:H3'	24:CX:32:5MC:HM53	1.64	0.78
1:AA:1252:A:H61	1:AA:1285:A:H61	1.28	0.78
26:BA:1434:A:H61	26:BA:1558:A:H62	1.32	0.78
1:CA:1262:C:N4	1:CA:1273:G:H1	1.81	0.78
1:AA:765:G:H1	1:AA:812:C:HO2'	1.30	0.78
1:AA:347:G:O2'	1:AA:348:G:OP1	2.00	0.77
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.02	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:16:LEU:HD11	9:AI:45:ALA:HB2	1.65	0.77
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.18	0.77
26:BA:2746:U:OP2	61:BA:3988:HOH:O	2.00	0.77
26:BA:2763:G:OP2	61:BA:4535:HOH:O	2.02	0.77
30:BF:53:THR:HG23	30:BF:55:GLY:H	1.49	0.77
1:CA:446:G:H1	1:CA:488:C:H42	1.33	0.77
22:CV:18:G:N1	24:CX:34:C:N4	2.29	0.77
1:CA:838:G:O6	1:CA:848:C:N4	2.18	0.77
12:AL:117:ARG:HB3	12:AL:122:THR:HB	1.67	0.77
46:BZ:72:ARG:NH2	46:BZ:97:GLU:O	2.17	0.77
1:CA:373:A:H61	1:CA:391:G:H1'	1.48	0.77
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.18	0.77
13:CM:6:GLY:O	31:DG:115:ARG:NH2	2.18	0.77
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.67	0.77
26:DA:2116:G:N7	26:DA:2166:G:N2	2.32	0.77
1:CA:401:C:O2'	1:CA:621:A:N3	2.16	0.77
33:BI:92:VAL:HG13	33:BI:120:ILE:HB	1.66	0.77
26:BA:1817:G:OP1	28:BD:88:ARG:NH2	2.18	0.77
26:DA:2126:A:N6	26:DA:2162:G:O2'	2.18	0.77
1:CA:954:G:H21	1:CA:1227:A:H62	1.32	0.77
1:CA:1029:C:N4	1:CA:1032:G:N1	2.32	0.77
1:CA:1114:C:N3	1:CA:1186:G:N2	2.31	0.77
15:CO:17:ARG:HD3	15:CO:26:GLU:HG3	1.66	0.77
24:CX:6:G:H1	24:CX:67:C:H42	1.30	0.77
26:BA:2308:G:O6	26:BA:2311:A:N6	2.15	0.76
1:CA:1183:A:O2'	1:CA:1185:G:OP2	2.01	0.76
1:CA:1256:A:N6	1:CA:1278:U:H1'	1.98	0.76
27:DB:5:C:OP1	27:DB:61:G:O2'	2.01	0.76
26:BA:1689:A:H62	26:BA:1698:A:H2	1.30	0.76
30:BF:185:ASP:HA	30:BF:188:ARG:HD3	1.68	0.76
26:DA:2141:G:O6	26:DA:2150:U:C2	2.37	0.76
28:DD:238:GLY:O	61:DD:405:HOH:O	2.03	0.76
1:AA:966:G:H21	9:AI:127:LYS:HZ1	1.32	0.76
1:AA:1089:G:N2	1:AA:1096:C:N3	2.32	0.76
24:CX:3:C:H2'	24:CX:4:G:H5"	1.67	0.76
28:DD:69:ARG:NH2	28:DD:128:GLY:O	2.18	0.76
1:AA:184:G:H2'	1:AA:185:A:H8	1.51	0.76
28:BD:17:THR:O	28:BD:211:ARG:NH2	2.19	0.76
1:CA:1378:C:O2	7:CG:76:ARG:NH2	2.17	0.76
6:CF:25:ILE:HD13	6:CF:82:ARG:HE	1.50	0.76
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.31	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.66	0.76
26:DA:1470:G:N2	26:DA:1520:G:OP2	2.17	0.76
26:DA:2183:C:H2'	26:DA:2184:G:H8	1.50	0.76
1:AA:766:A:N6	1:AA:813:U:O2	2.18	0.76
1:CA:1356:G:H1	1:CA:1366:C:H42	1.33	0.76
1:CA:1422:G:H5"	35:DO:48:PRO:HB3	1.66	0.76
16:CP:28:ARG:NH1	16:CP:29:ASP:OD2	2.19	0.76
26:DA:586:A:N1	26:DA:809:G:O2'	2.19	0.76
26:DA:1143:A:OP1	34:DN:25:ARG:NH2	2.19	0.76
26:DA:2151:G:H2'	26:DA:2152:G:H8	1.50	0.76
13:CM:84:ILE:O	13:CM:86:CYS:N	2.19	0.76
26:DA:2162:G:H4'	26:DA:2172:U:H2'	1.66	0.76
9:AI:71:SER:HA	9:AI:74:ILE:HD12	1.67	0.76
26:BA:652(F):G:N2	26:BA:652(S):C:O2	2.19	0.76
26:BA:2142:C:O2	26:BA:2149:G:N1	2.18	0.75
1:CA:457:C:N4	1:CA:474:G:O6	2.19	0.75
27:DB:32:C:H1'	27:DB:51:G:N2	2.00	0.75
28:DD:85:ASP:OD2	28:DD:88:ARG:NH1	2.19	0.75
1:CA:1359:C:O2'	1:CA:1361:G:N7	2.20	0.75
2:CB:16:HIS:HB3	2:CB:210:SER:HB2	1.68	0.75
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.66	0.75
1:AA:1422:G:H5"	35:BO:48:PRO:HB3	1.68	0.75
26:BA:1153:C:OP2	61:BA:4487:HOH:O	2.04	0.75
26:BA:2140:C:O2'	26:BA:2152:G:N2	2.19	0.75
31:DG:80:PHE:O	31:DG:82:LEU:N	2.20	0.75
40:DT:16:ARG:NH2	40:DT:83:ILE:O	2.19	0.75
26:BA:1602:U:O4	61:BA:4096:HOH:O	2.04	0.75
26:BA:2386:C:O2'	61:BA:4897:HOH:O	2.03	0.75
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.68	0.75
26:BA:2287:A:H62	26:BA:2344:U:H3	1.34	0.75
26:DA:2314:C:H2'	26:DA:2315:G:C8	2.21	0.75
29:DE:28:ALA:HB3	29:DE:93:VAL:HG12	1.66	0.75
31:DG:43:LEU:HD12	31:DG:45:GLU:HG3	1.67	0.75
30:BF:18:ARG:NH2	30:BF:127:GLU:OE1	2.20	0.75
1:CA:1026:G:O6	1:CA:1036:G:N2	2.19	0.75
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.68	0.75
26:DA:712:G:N2	26:DA:719:C:O2	2.17	0.75
26:DA:1530:C:O2'	26:DA:1531:C:O5'	2.03	0.75
26:DA:1600:C:OP1	44:DX:58:HIS:NE2	2.17	0.75
26:BA:2296:U:OP2	39:BS:9:ARG:NH2	2.20	0.75
15:CO:64:ARG:NH2	26:DA:715:G:OP1	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:D4:38:LYS:O	51:D4:40:HIS:N	2.19	0.75
1:AA:1006:C:H42	1:AA:1023:G:H1	1.32	0.75
1:AA:1303:C:OP1	61:AA:4108:HOH:O	2.04	0.75
1:CA:627:G:H2'	1:CA:628:G:H8	1.52	0.75
26:BA:279:C:H42	26:BA:361:G:H1	1.35	0.74
26:DA:2430:A:OP2	61:DA:4174:HOH:O	2.04	0.74
27:DB:36:C:N4	27:DB:49:C:O2	2.19	0.74
26:BA:1021:A:H62	26:BA:1141:U:H3	1.34	0.74
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.19	0.74
26:BA:65:C:O2	26:BA:456:C:N4	2.19	0.74
26:DA:2793:G:H22	26:DA:2804:C:H1'	1.51	0.74
49:D2:18:PRO:HB3	49:D2:68:ARG:HH12	1.52	0.74
1:AA:78:G:N2	1:AA:92:C:N3	2.35	0.74
1:AA:1243:C:H42	1:AA:1294:G:H1	1.33	0.74
26:BA:2120:G:H1	26:BA:2178:C:N4	1.84	0.74
2:CB:87:ARG:HD3	2:CB:234:PRO:HD2	1.70	0.74
36:BP:59:LEU:HD21	55:B8:10:ALA:HA	1.67	0.74
26:DA:678:C:N4	26:DA:799:G:O6	2.11	0.74
1:AA:448:A:O5'	1:AA:485:G:N2	2.20	0.74
26:BA:9:U:H3	26:BA:2629:A:H2	1.33	0.74
26:BA:568:U:H5'	26:BA:945:A:N1	2.01	0.74
26:BA:887:A:O2'	26:BA:888:C:OP2	2.04	0.74
26:BA:1798:U:H5'	28:BD:259:THR:HG22	1.70	0.74
1:CA:44:G:H1	1:CA:398:C:H42	1.35	0.74
26:DA:1204:A:H2	26:DA:1241:A:H62	1.33	0.74
26:DA:2138:C:H42	26:DA:2153:G:H1	1.34	0.74
1:AA:642:A:N3	8:AH:113:SER:OG	2.20	0.74
26:BA:1371:G:N7	61:BA:4204:HOH:O	2.21	0.74
29:BE:55:ASN:HB3	29:BE:58:ARG:HG3	1.69	0.74
1:CA:1366:C:HO2'	10:CJ:60:ARG:HH22	1.36	0.74
26:DA:792:G:O6	61:DA:4068:HOH:O	2.03	0.74
29:BE:28:ALA:HB3	29:BE:93:VAL:HG12	1.69	0.74
48:D1:51:VAL:HG11	48:D1:74:VAL:HG21	1.69	0.74
1:AA:1183:A:H3'	1:AA:1184:G:H5"	1.68	0.73
24:AX:49:G:H1	24:AX:65:C:N4	1.86	0.73
26:BA:789:A:OP1	61:BA:4147:HOH:O	2.05	0.73
26:BA:2683:C:O2	35:BO:70:LYS:NZ	2.21	0.73
1:CA:532:A:O2'	1:CA:533:A:OP1	2.05	0.73
26:DA:272(G):C:H42	26:DA:363(C):G:H1	1.36	0.73
26:DA:1335:U:O4	61:DA:3860:HOH:O	2.04	0.73
26:DA:1997:G:OP2	61:DA:4145:HOH:O	2.04	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:279:A:H4'	1:AA:280:C:H5"	1.69	0.73
3:CC:120:VAL:HA	3:CC:123:GLN:HE21	1.53	0.73
9:CI:17:VAL:HG11	9:CI:81:ILE:HA	1.71	0.73
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.11	0.73
1:CA:1103:C:H5"	2:CB:98:LEU:HD12	1.70	0.73
1:CA:1133:G:N2	1:CA:1141:C:N3	2.36	0.73
26:DA:2118:U:C4	26:DA:2149:G:H1'	2.23	0.73
26:BA:517:C:OP1	52:B5:16:ARG:NH2	2.20	0.73
1:CA:1126:U:H1'	1:CA:1281:U:C2	2.23	0.73
1:CA:1244:C:H42	1:CA:1293:G:H1	0.80	0.73
33:DI:48:GLU:O	33:DI:52:ARG:NH1	2.21	0.73
36:BP:59:LEU:HD11	55:B8:10:ALA:HB2	1.71	0.73
38:DR:67:LEU:HD13	38:DR:76:VAL:HG21	1.69	0.73
26:BA:422:A:OP2	61:BA:3938:HOH:O	2.05	0.73
25:CY:76:A:O2'	26:DA:2394:C:N3	2.22	0.73
26:DA:1171:G:H22	26:DA:1178:C:H42	1.35	0.73
1:CA:1027:C:C4	1:CA:1034:G:N1	2.56	0.73
26:DA:2576:G:O2'	26:DA:2579:C:OP2	2.07	0.73
1:AA:596:C:OP2	61:AA:4068:HOH:O	2.06	0.73
26:DA:2794:C:N4	26:DA:2802:G:O6	2.17	0.73
1:AA:974:A:OP2	14:AN:29:ARG:NH2	2.22	0.73
19:AS:65:ASN:O	51:B4:58:ARG:NH1	2.21	0.73
28:BD:69:ARG:NH2	28:BD:128:GLY:O	2.21	0.73
31:DG:64:THR:HB	31:DG:94:LEU:HD21	1.69	0.73
1:CA:73:G:H1	1:CA:96:U:H3	1.37	0.72
1:CA:1053:G:N7	1:CA:1200:C:H5"	2.04	0.72
4:CD:31:CYS:HB2	58:CD:501:SF4:S3	2.29	0.72
26:DA:2683:C:OP1	40:DT:53:ARG:NH2	2.21	0.72
46:BZ:69:THR:HG22	46:BZ:90:VAL:HA	1.71	0.72
4:CD:18:LYS:NZ	4:CD:31:CYS:SG	2.62	0.72
26:DA:1970:A:OP1	61:DA:3907:HOH:O	2.07	0.72
26:BA:1019:U:HO2'	26:BA:1021:A:H2	1.35	0.72
26:DA:1316:U:H2'	26:DA:1317:A:H8	1.55	0.72
26:DA:1653:G:H3'	38:DR:2:ARG:HD3	1.71	0.72
37:DQ:22:LYS:O	46:DZ:78:LYS:NZ	2.21	0.72
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.07	0.72
1:CA:72:C:N4	1:CA:97:G:H1	1.85	0.72
1:CA:76:C:N3	1:CA:93:G:C2	2.57	0.72
26:BA:743:G:N7	61:BA:4318:HOH:O	2.22	0.72
42:BV:40:LEU:HB2	42:BV:46:VAL:HG13	1.71	0.72
43:BW:34:ASN:OD1	43:BW:37:ARG:NH1	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:70:ILE:HG12	12:CL:100:ILE:HD12	1.72	0.72
26:DA:1851:U:O4	61:DA:4296:HOH:O	2.06	0.72
46:BZ:107:THR:HG21	46:BZ:112:ARG:HH21	1.55	0.72
1:CA:662:G:O2'	1:CA:836:G:OP1	2.07	0.72
47:B0:27:GLU:HG3	47:B0:68:GLU:HA	1.70	0.72
1:CA:839:U:OP2	1:CA:840:C:N4	2.23	0.72
1:CA:839:U:H5"	1:CA:840:C:H5	1.55	0.72
1:AA:45:U:H2'	1:AA:46:G:C8	2.25	0.72
8:AH:29:SER:HB2	8:AH:32:LYS:HG3	1.72	0.72
16:CP:59:TRP:HA	16:CP:62:VAL:HG12	1.70	0.72
26:DA:1359:A:C6	26:DA:1372:U:C4	2.77	0.72
26:DA:2130:U:H4'	26:DA:2133:G:H4'	1.71	0.72
42:BV:76:LYS:HB2	42:BV:81:TYR:HB3	1.69	0.72
26:DA:2447:G:N2	26:DA:2450:A:OP2	2.23	0.72
27:DB:29:A:C2	27:DB:30:C:H5	2.06	0.72
1:CA:72:C:N4	1:CA:97:G:C6	2.57	0.72
1:CA:989:C:O2	1:CA:1216:G:N2	2.19	0.72
1:CA:1414:U:H3	1:CA:1486:G:H1	1.37	0.72
28:DD:148:GLU:HB2	28:DD:151:LYS:HD2	1.70	0.72
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.72	0.71
24:CX:19:G:N2	24:CX:56:C:N3	2.37	0.71
1:AA:1305:G:H5"	21:AU:4:GLY:HA3	1.70	0.71
27:BB:8:U:O3'	39:BS:25:ARG:NH2	2.20	0.71
26:BA:2336:A:H61	47:B0:43:THR:HG22	1.55	0.71
1:AA:978:A:O2'	1:AA:1322:C:N3	2.22	0.71
3:AC:3:ASN:N	3:AC:3:ASN:OD1	2.24	0.71
36:BP:42:SER:O	61:BP:3102:HOH:O	2.06	0.71
26:DA:2127:G:N1	26:DA:2161:C:O2	2.22	0.71
27:DB:3:C:H2'	27:DB:4:C:C6	2.25	0.71
1:AA:708:C:OP1	11:AK:85:ARG:NH2	2.23	0.71
26:DA:2287:A:H62	26:DA:2344:U:H3	1.39	0.71
26:DA:2526:G:O2'	56:D9:1:MET:N	2.20	0.71
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.71	0.71
31:DG:47:LYS:HE2	31:DG:48:GLU:H	1.56	0.71
1:AA:664:G:H22	1:AA:741:G:H1	1.38	0.71
26:BA:1174:A:H1'	26:BA:1175:U:H5"	1.73	0.71
26:BA:2815:C:H5'	52:B5:29:THR:HG21	1.71	0.71
27:BB:48:A:H4'	39:BS:95:HIS:HD2	1.55	0.71
51:B4:64:GLY:O	51:B4:66:SER:N	2.23	0.71
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.24	0.71
26:BA:1175:U:O2'	26:BA:1176:G:O5'	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:71:SER:HA	9:CI:74:ILE:HD12	1.72	0.71
26:DA:1637:A:OP2	61:DA:4392:HOH:O	2.07	0.71
39:BS:15:ARG:O	39:BS:19:LYS:HG2	1.91	0.71
1:CA:156:G:N2	1:CA:165:C:O2	2.19	0.71
24:CX:19:G:H1	24:CX:56:C:H42	1.39	0.71
46:DZ:23:LYS:NZ	46:DZ:40:ASP:OD1	2.23	0.71
26:BA:245:G:O6	55:B8:8:LYS:NZ	2.22	0.70
1:CA:708:C:H2'	1:CA:709:G:H8	1.55	0.70
1:CA:1027:C:N3	1:CA:1034:G:C2	2.59	0.70
1:CA:1399:C:H4'	1:CA:1400:C:H5"	1.73	0.70
9:CI:42:ARG:NH1	9:CI:75:ASP:OD1	2.24	0.70
1:AA:1304:G:OP2	61:AA:4108:HOH:O	2.09	0.70
26:DA:587:C:OP2	36:DP:21:ARG:NH2	2.23	0.70
46:DZ:55:HIS:HE1	46:DZ:135:GLU:HG3	1.57	0.70
1:AA:221:C:H2'	1:AA:222:U:H6	1.57	0.70
3:AC:11:ARG:HB3	3:AC:15:THR:HB	1.72	0.70
26:BA:1769:G:O2'	26:BA:1958:C:OP1	2.09	0.70
26:BA:2124:G:H1	26:BA:2174:C:N4	1.88	0.70
1:CA:138:G:H2'	1:CA:139:G:H5"	1.74	0.70
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.73	0.70
1:AA:159:G:O2'	1:AA:161:A:N7	2.24	0.70
1:AA:560:U:O2'	1:AA:561:U:OP2	2.10	0.70
4:AD:13:ARG:NH1	4:AD:38:TYR:O	2.24	0.70
1:CA:76:C:C2	1:CA:93:G:N2	2.60	0.70
30:DF:122:LYS:NZ	30:DF:152:GLU:OE2	2.24	0.70
50:D3:7:LYS:HG3	50:D3:34:GLU:HG3	1.73	0.70
1:AA:242:C:N4	1:AA:284:G:O6	2.20	0.70
1:AA:316:G:OP2	1:AA:351:G:O2'	2.09	0.70
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.09	0.70
26:BA:187:G:OP2	61:BA:4313:HOH:O	2.08	0.70
1:AA:60:A:N1	1:AA:107:G:O2'	2.21	0.70
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.56	0.70
26:BA:1551:C:OP2	61:BA:4322:HOH:O	2.08	0.70
26:BA:2618:G:H21	29:BE:150:VAL:HG21	1.56	0.70
26:DA:1417:C:OP2	61:DA:4033:HOH:O	2.08	0.70
38:DR:103:ARG:NH1	38:DR:108:GLY:O	2.24	0.70
1:AA:363:A:OP2	12:AL:34:ARG:NH1	2.24	0.70
1:AA:1288:A:N3	1:AA:1352:C:O2'	2.22	0.70
1:AA:1464:G:OP2	40:BT:111:ARG:NH2	2.23	0.70
8:AH:21:LYS:O	8:AH:65:TYR:OH	2.08	0.70
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CG:99:LEU:HD23	7:CG:102:ARG:HH12	1.56	0.70
7:CG:109:ASN:HA	7:CG:119:ARG:HH21	1.55	0.70
1:AA:661:G:H1	1:AA:744:C:H42	1.39	0.70
20:AT:9:ASN:HD22	20:AT:10:LEU:H	1.40	0.70
26:BA:2107:C:H42	26:BA:2182:G:H1	1.40	0.70
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.36	0.70
26:DA:827:U:OP1	61:DA:4174:HOH:O	2.10	0.70
26:DA:1183:G:O3'	50:D3:29:ARG:NH1	2.24	0.70
26:DA:2107:C:H42	26:DA:2182:G:H1	1.40	0.70
1:AA:1012:U:O2	1:AA:1017:G:O6	2.10	0.70
1:CA:977:A:O2'	1:CA:981:U:N3	2.25	0.70
1:CA:1034:G:H8	1:CA:1034:G:O5'	1.73	0.70
26:DA:1269:A:N7	61:DA:4369:HOH:O	2.25	0.70
26:DA:1300:U:H4'	26:DA:1301:A:H5"	1.74	0.70
31:DG:41:GLN:HG3	31:DG:60:LEU:HD21	1.74	0.70
1:AA:1097:C:O2'	1:AA:1169:A:N3	2.20	0.70
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.74	0.70
24:AX:5:G:H1	24:AX:68:C:N4	1.89	0.69
26:BA:1786:A:H1'	26:BA:1938:A:N6	2.07	0.69
33:BI:38:LEU:HD13	33:BI:40:THR:HG22	1.72	0.69
38:BR:15:SER:OG	61:BR:301:HOH:O	2.08	0.69
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.73	0.69
26:DA:2659:G:O2'	26:DA:2661:G:N7	2.25	0.69
1:CA:1030(C):G:H2'	1:CA:1030(D):A:C8	2.27	0.69
1:CA:1120:G:O6	1:CA:1154:G:N2	2.25	0.69
26:DA:1314:C:OP1	61:DA:4077:HOH:O	2.10	0.69
26:DA:1803:A:O2'	28:DD:259:THR:HG21	1.92	0.69
26:BA:271(A):A:N7	26:BA:271(W):G:N2	2.40	0.69
26:BA:331:A:N1	61:BA:4015:HOH:O	2.25	0.69
27:DB:3:C:H2'	27:DB:4:C:H6	1.55	0.69
1:AA:78:G:C2	1:AA:91:C:N3	2.60	0.69
2:AB:15:VAL:O	2:AB:16:HIS:ND1	2.24	0.69
26:BA:2756:U:O2'	61:BA:4010:HOH:O	2.10	0.69
26:DA:1333:C:OP2	61:DA:3859:HOH:O	2.10	0.69
26:DA:2198:A:O2'	26:DA:2224:G:N2	2.26	0.69
33:DI:129:THR:HG22	33:DI:139:GLN:HE22	1.57	0.69
1:AA:148:G:O6	1:AA:174:C:N4	2.25	0.69
26:BA:400:G:N7	61:BA:4780:HOH:O	2.24	0.69
1:AA:1009:G:H1	1:AA:1020:U:H3	0.76	0.69
1:AA:1086:U:H3	1:AA:1099:G:H22	1.39	0.69
26:BA:2187:G:O2'	26:BA:2188:C:OP1	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:574:C:N3	29:DE:145:LYS:NZ	2.40	0.69
19:AS:12:ASP:OD2	19:AS:37:ARG:NH1	2.24	0.69
29:BE:52:LEU:HD12	29:BE:77:ILE:HD11	1.73	0.69
26:DA:2227:A:OP2	61:DA:4135:HOH:O	2.10	0.69
31:DG:43:LEU:HD21	31:DG:153:ARG:HG2	1.74	0.69
1:AA:148:G:N2	1:AA:175:C:C2	2.61	0.69
8:AH:86:ILE:HG21	8:AH:133:LEU:HD13	1.75	0.69
12:AL:34:ARG:NH2	61:AL:201:HOH:O	2.26	0.69
1:CA:701:C:OP1	1:CA:702:A:O2'	2.10	0.69
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.11	0.69
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.25	0.69
48:D1:50:ARG:HG2	48:D1:59:THR:HB	1.72	0.69
24:AX:28:C:N4	24:AX:42:G:H1	1.88	0.69
26:BA:2156:G:N2	26:BA:2158:A:H62	1.90	0.69
49:B2:28:LYS:NZ	49:B2:56:GLN:OE1	2.26	0.69
1:CA:870:U:OP2	61:CA:4089:HOH:O	2.10	0.69
46:DZ:126:VAL:HG11	46:DZ:161:VAL:HG23	1.73	0.69
26:BA:548:A:O2'	26:BA:549:G:OP1	2.11	0.69
26:BA:833:U:O2	36:BP:55:ARG:NH2	2.26	0.69
28:BD:108:PRO:HB3	28:BD:143:HIS:CE1	2.28	0.69
1:CA:437:U:H5'	4:CD:155:LEU:HD21	1.75	0.69
23:CW:76:PPU:HN1	24:CX:76:31H:HN3'	1.39	0.69
1:AA:1311:G:H1	1:AA:1326:C:H42	1.42	0.68
29:BE:143:ASN:HD22	29:BE:147:PRO:HD3	1.57	0.68
1:CA:1400:C:O4'	22:CV:18:G:N3	2.27	0.68
26:DA:514:A:N3	26:DA:581:C:O2'	2.26	0.68
30:DF:110:LEU:HD21	30:DF:181:LEU:HG	1.75	0.68
47:D0:14:ARG:NH1	61:D0:102:HOH:O	2.26	0.68
26:DA:2313:C:H2'	26:DA:2314:C:H6	1.58	0.68
1:AA:78:G:H1	1:AA:91:C:N4	1.91	0.68
5:AE:102:ALA:O	5:AE:107:ARG:NH1	2.26	0.68
13:AM:11:ARG:HA	13:AM:45:VAL:HB	1.73	0.68
26:BA:2406:U:OP1	61:BA:4116:HOH:O	2.11	0.68
26:DA:2128:C:H5'	26:DA:2173:A:C2	2.27	0.68
26:DA:2136:C:O2'	26:DA:2137:C:H6	1.76	0.68
26:DA:2445:G:OP1	30:DF:74:ARG:NH2	2.27	0.68
1:CA:72:C:C4	1:CA:97:G:N1	2.56	0.68
13:CM:4:ILE:HG23	13:CM:22:ILE:HD11	1.75	0.68
26:DA:1406:U:O4	26:DA:1596:A:N6	2.18	0.68
26:DA:2376:A:N3	39:DS:106:ARG:NH2	2.41	0.68
31:DG:114:ILE:HG23	31:DG:136:ARG:HH22	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:789:U:O2'	1:AA:791:G:N7	2.21	0.68
19:AS:9:VAL:HG21	51:B4:61:ARG:HH21	1.58	0.68
26:BA:1371:G:H2'	26:BA:1372:U:H5	1.59	0.68
26:BA:2400:G:O6	61:BA:4049:HOH:O	2.09	0.68
36:BP:121:LYS:HG2	36:BP:122:PRO:HD2	1.76	0.68
1:CA:376:G:H1	1:CA:387:U:H3	1.41	0.68
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.10	0.68
2:AB:19:HIS:NE2	2:AB:206:ASP:OD2	2.26	0.68
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.75	0.68
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.27	0.68
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.27	0.68
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.57	0.68
2:CB:82:ARG:HD3	2:CB:83:MET:HE2	1.76	0.68
38:DR:33:ARG:NH1	38:DR:115:GLU:OE2	2.26	0.68
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.59	0.68
26:BA:271(R):G:H2'	26:BA:271(S):G:H5"	1.74	0.68
26:BA:370:G:OP2	61:BA:3938:HOH:O	2.12	0.68
26:BA:2111:C:OP2	26:BA:2145:C:N4	2.26	0.68
1:CA:154:C:C2'	1:CA:155:C:H5'	2.23	0.68
1:CA:1256:A:H61	1:CA:1278:U:C1'	2.04	0.68
16:CP:53:VAL:HG13	16:CP:79:VAL:HG22	1.76	0.68
17:CQ:60:ILE:HD12	17:CQ:74:LEU:HG	1.76	0.68
28:DD:232:PRO:O	61:DD:402:HOH:O	2.12	0.68
1:AA:159:G:N2	1:AA:162:A:OP2	2.26	0.68
26:BA:2791:C:N3	26:BA:2805:G:N2	2.36	0.68
46:BZ:45:ASP:OD2	46:BZ:49:ARG:NH1	2.27	0.68
4:CD:172:PRO:HB2	4:CD:187:ARG:HH21	1.58	0.68
12:CL:71:PRO:O	12:CL:102:ARG:NH1	2.23	0.68
26:DA:1169:G:N2	26:DA:1180:C:N3	2.40	0.68
46:DZ:72:ARG:NH2	46:DZ:97:GLU:O	2.27	0.68
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.28	0.68
1:AA:993:G:O6	1:AA:1045:C:N4	2.23	0.67
26:BA:1204:A:H2	26:BA:1241:A:H62	1.40	0.67
26:BA:2810:A:N6	26:BA:2891:G:O2'	2.26	0.67
37:BQ:110:THR:HG23	37:BQ:113:GLN:HB2	1.77	0.67
1:CA:1400:C:OP2	22:CV:18:G:N1	2.26	0.67
28:DD:228:PRO:O	61:DD:401:HOH:O	2.12	0.67
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.27	0.67
37:BQ:30:GLY:HA2	37:BQ:107:ALA:HB2	1.75	0.67
1:CA:72:C:N4	1:CA:73:G:C6	2.62	0.67
26:DA:1695:G:N7	28:DD:14:ARG:NH2	2.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2805:G:H2'	26:DA:2807:G:C8	2.29	0.67
33:DI:40:THR:HG23	33:DI:43:ASN:HD21	1.59	0.67
36:DP:96:THR:H	36:DP:99:LEU:HD21	1.59	0.67
26:BA:801:G:O6	30:BF:53:THR:OG1	2.12	0.67
26:BA:2120:G:N2	26:BA:2178:C:N3	2.41	0.67
33:BI:106:GLY:HA2	33:BI:107:VAL:HG22	1.76	0.67
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.27	0.67
1:CA:1055:A:N7	1:CA:1200:C:N4	2.42	0.67
19:CS:53:ASN:HB2	19:CS:77:THR:HA	1.76	0.67
26:DA:2723:C:H5"	38:DR:1:MET:HE2	1.76	0.67
1:AA:707:C:OP1	11:AK:85:ARG:NH1	2.28	0.67
1:AA:958:A:N3	1:AA:985:C:O2'	2.28	0.67
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.30	0.67
26:BA:2239:G:OP2	28:BD:244:ARG:NH1	2.22	0.67
26:DA:1670:C:O2	29:DE:129:HIS:NE2	2.27	0.67
1:AA:184:G:H2'	1:AA:185:A:C8	2.28	0.67
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.42	0.67
26:BA:1333:C:OP2	61:BA:4097:HOH:O	2.13	0.67
26:DA:2659:G:N2	26:DA:2662:A:OP2	2.27	0.67
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.59	0.67
1:AA:661:G:N2	1:AA:744:C:N3	2.40	0.67
1:AA:975:A:H5'	1:AA:975:A:H8	1.60	0.67
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.27	0.67
10:AJ:5:ARG:NH2	10:AJ:73:ASP:OD2	2.28	0.67
26:BA:740:U:OP2	61:BA:4541:HOH:O	2.12	0.67
26:BA:2141:G:C2	26:BA:2142:C:H1'	2.30	0.67
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.26	0.67
27:DB:49:C:OP1	39:DS:97:ARG:N	2.27	0.67
1:AA:1456:G:O6	20:AT:54:LYS:NZ	2.28	0.67
20:AT:56:MET:HG3	20:AT:84:LEU:HD22	1.76	0.67
40:BT:65:LYS:HE2	40:BT:67:SER:HB2	1.77	0.67
26:DA:2136:C:O2'	26:DA:2137:C:O4'	2.11	0.67
26:BA:330:A:H2	26:BA:1210:A:HO2'	1.41	0.67
26:BA:1250:G:OP2	36:BP:21:ARG:NH1	2.27	0.67
26:BA:2334:G:O6	47:B0:74:ARG:NH2	2.28	0.67
36:BP:62:LEU:O	55:B8:13:ARG:HD3	1.95	0.67
32:DH:124:GLU:HB2	32:DH:132:ARG:HB3	1.77	0.67
26:BA:962:G:OP1	61:BA:4651:HOH:O	2.13	0.67
26:DA:2651:C:H42	26:DA:2669:G:H1	1.43	0.67
30:DF:21:ALA:HB3	30:DF:22:ALA:HA	1.75	0.67
1:AA:103:C:O2'	1:AA:172:A:N1	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:692:U:O2'	1:AA:694:A:N7	2.24	0.67
26:BA:2722:G:OP2	61:BA:3994:HOH:O	2.12	0.67
1:CA:601:C:H2'	1:CA:602:A:C8	2.30	0.67
26:DA:82:G:N1	26:DA:103:A:OP2	2.23	0.67
26:DA:1038:C:H42	26:DA:1117:G:H1	1.43	0.67
1:AA:598:U:O4	61:AA:4068:HOH:O	2.09	0.66
1:AA:652:U:O4	1:AA:752:G:O2'	2.10	0.66
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.23	0.66
1:AA:757:U:O2'	1:AA:879:C:O2	2.13	0.66
1:AA:975:A:H4'	1:AA:976:G:H5"	1.77	0.66
25:AY:76:A:N6	26:BA:2422:A:O4'	2.28	0.66
26:BA:154:G:O6	26:BA:172:C:N4	2.18	0.66
26:BA:2176:A:H2'	26:BA:2177:C:C6	2.30	0.66
1:CA:642:A:N3	8:CH:113:SER:OG	2.28	0.66
1:CA:1153:C:H42	1:CA:1154:G:H21	1.41	0.66
1:CA:1255:G:OP2	10:CJ:45:ARG:NH2	2.27	0.66
52:D5:16:ARG:NH1	52:D5:17:ASP:OD1	2.28	0.66
1:AA:346:G:OP1	40:BT:41:ARG:NH1	2.28	0.66
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.78	0.66
26:BA:243:U:OP1	55:B8:6:THR:OG1	2.11	0.66
1:CA:21:G:OP1	61:CA:4042:HOH:O	2.13	0.66
1:CA:673:G:H2'	1:CA:674:G:C8	2.30	0.66
1:CA:864:A:H5'	5:CE:86:ALA:HB2	1.77	0.66
13:CM:90:LEU:HA	13:CM:93:ARG:HD2	1.77	0.66
1:AA:6:G:H4'	1:AA:298:A:H4'	1.77	0.66
1:AA:56:U:H2'	1:AA:57:G:C8	2.29	0.66
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.77	0.66
2:CB:71:VAL:HG12	2:CB:170:GLU:HG2	1.78	0.66
26:DA:2504:U:OP2	61:DA:4075:HOH:O	2.12	0.66
44:DX:8:ILE:O	49:D2:36:ARG:NH2	2.27	0.66
46:DZ:111:VAL:HG21	46:DZ:117:LEU:HB2	1.77	0.66
26:BA:800:A:H8	26:BA:800:A:OP1	1.78	0.66
26:BA:2779:U:OP1	61:BA:4671:HOH:O	2.13	0.66
26:DA:2494:G:OP2	61:DA:4386:HOH:O	2.13	0.66
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.77	0.66
3:AC:16:ARG:NH2	3:AC:183:ASP:OD1	2.29	0.66
26:BA:2125:G:N1	26:BA:2172:U:OP1	2.29	0.66
29:BE:123:ALA:O	61:BE:3101:HOH:O	2.13	0.66
49:D2:22:GLU:OE2	49:D2:68:ARG:NH2	2.28	0.66
1:AA:574:A:OP2	61:AA:4006:HOH:O	2.12	0.66
35:BO:63:VAL:HG12	35:BO:106:LEU:HD11	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:70:G:N2	1:CA:99:U:O2	2.21	0.66
26:DA:468:G:N7	54:D7:39:ARG:NH2	2.40	0.66
26:DA:2123:G:H1	26:DA:2175:C:H42	1.43	0.66
26:DA:2141:G:O4'	26:DA:2151:G:N2	2.29	0.66
1:AA:1309:G:OP1	13:AM:88:ARG:NH1	2.29	0.66
29:BE:8:LYS:NZ	29:BE:190:GLY:O	2.24	0.66
36:BP:50:ARG:HH21	55:B8:7:HIS:HD2	1.42	0.66
31:DG:171:ALA:O	31:DG:175:LEU:N	2.23	0.66
42:DV:72:VAL:HG22	42:DV:85:LYS:HB3	1.78	0.66
19:AS:68:GLY:N	51:B4:58:ARG:HH21	1.94	0.66
26:DA:1665:A:OP2	61:DA:4367:HOH:O	2.14	0.66
26:DA:1993:U:OP2	61:DA:4451:HOH:O	2.13	0.66
26:DA:2736:G:N2	26:DA:2768:C:O2	2.15	0.66
27:DB:42:C:O2'	31:DG:67:LYS:O	2.10	0.66
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.08	0.66
17:AQ:53:LEU:HD23	17:AQ:82:MET:HE1	1.78	0.66
26:BA:963:U:OP1	61:BA:3878:HOH:O	2.13	0.66
26:BA:2155:G:H2'	26:BA:2156:G:O4'	1.95	0.66
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.60	0.66
26:DA:336:C:O2'	45:DY:35:TYR:OH	2.12	0.66
27:DB:22:U:H3	27:DB:61:G:H1	1.44	0.66
40:DT:51:ARG:HG3	40:DT:98:LYS:HD2	1.78	0.66
1:AA:976:G:H5'	1:AA:1358:U:O2'	1.96	0.66
26:BA:1324:G:N7	61:BA:4100:HOH:O	2.29	0.66
1:CA:1154:G:N7	1:CA:1155:G:C8	2.64	0.66
1:CA:1400:C:C6	22:CV:18:G:N3	2.64	0.66
13:CM:13:LYS:NZ	13:CM:21:TYR:OH	2.25	0.66
26:DA:271(L):U:OP1	33:DI:50:ARG:NH2	2.28	0.66
26:DA:2313:C:H2'	26:DA:2314:C:C6	2.31	0.66
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.29	0.65
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.77	0.65
26:BA:247:G:OP2	26:BA:249:C:N4	2.28	0.65
29:BE:79:ARG:NE	61:BE:3113:HOH:O	2.19	0.65
5:CE:78:HIS:HA	8:CH:105:ARG:HG3	1.77	0.65
26:DA:2815:C:H5'	52:D5:29:THR:HG21	1.76	0.65
27:DB:54:G:H21	31:DG:29:TRP:HZ2	1.42	0.65
32:DH:8:PRO:HB3	32:DH:51:ARG:HG2	1.78	0.65
38:DR:56:LYS:NZ	38:DR:90:ARG:O	2.29	0.65
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.78	0.65
24:CX:76:31H:OP2	61:CX:3101:HOH:O	2.14	0.65
7:AG:126:ASP:OD1	7:AG:131:LYS:NZ	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:67:GLU:OE2	13:AM:71:ARG:NH2	2.28	0.65
26:BA:1342:A:OP2	61:BA:4096:HOH:O	2.13	0.65
38:BR:67:LEU:HD13	38:BR:76:VAL:HG21	1.77	0.65
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.78	0.65
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.95	0.65
26:DA:746:A:N7	61:DA:4449:HOH:O	2.29	0.65
1:AA:1262:C:N3	1:AA:1273:G:O6	2.29	0.65
20:AT:9:ASN:HD22	20:AT:10:LEU:N	1.93	0.65
26:BA:356:G:H2'	26:BA:357:A:H8	1.61	0.65
26:BA:885:C:H3'	26:BA:886:C:H5"	1.77	0.65
28:BD:132:PRO:HD3	28:BD:190:TYR:CZ	2.32	0.65
1:CA:753:A:OP1	15:CO:69:TYR:OH	2.12	0.65
1:CA:975:A:H8	1:CA:975:A:H5'	1.61	0.65
1:CA:1014:A:H1'	19:CS:34:TRP:HB2	1.79	0.65
26:DA:1031:G:H21	56:D9:36:GLN:HE22	1.43	0.65
26:BA:278:A:O2'	26:BA:279:C:OP1	2.14	0.65
26:BA:1184:G:H5'	50:B3:29:ARG:HH11	1.60	0.65
26:BA:2852:G:OP1	61:BA:4891:HOH:O	2.13	0.65
32:BH:149:ARG:NH1	32:BH:167:GLU:OE2	2.29	0.65
1:CA:903:G:OP1	61:CA:4008:HOH:O	2.14	0.65
26:DA:2698:U:H2'	26:DA:2699:C:C6	2.32	0.65
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.78	0.65
1:CA:1190:G:OP1	3:CC:5:ILE:N	2.25	0.65
19:CS:9:VAL:HB	51:D4:67:TYR:HD2	1.60	0.65
1:AA:253:U:OP1	17:AQ:67:LYS:NZ	2.26	0.65
1:AA:580:U:OP2	61:AA:4021:HOH:O	2.14	0.65
1:AA:1261:A:H3'	1:AA:1262:C:H6	1.61	0.65
21:AU:5:ASP:OD2	61:AU:101:HOH:O	2.14	0.65
51:B4:68:ARG:HD2	51:B4:69:LYS:H	1.62	0.65
1:CA:1012:U:O2	1:CA:1017:G:O6	2.14	0.65
4:CD:53:ASP:HB3	4:CD:57:ARG:HH12	1.62	0.65
24:CX:48:C:O2'	24:CX:59:A:H1'	1.97	0.65
29:DE:56:PRO:HG3	29:DE:74:PRO:HG2	1.77	0.65
26:BA:1187:G:H5"	42:BV:81:TYR:CE1	2.31	0.65
32:DH:90:LYS:HD3	32:DH:159:GLU:HG2	1.79	0.65
3:AC:8:ILE:HD13	3:AC:184:TYR:HB3	1.78	0.65
13:CM:65:LYS:HB3	51:D4:50:VAL:HG11	1.77	0.65
55:D8:33:ASN:HA	55:D8:36:LYS:HD2	1.79	0.65
1:AA:1030:C:H3'	1:AA:1030(A):G:H4'	1.79	0.65
2:AB:69:LEU:HD13	2:AB:91:PRO:HB2	1.79	0.65
4:AD:23:GLY:HA3	4:AD:112:VAL:HG12	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:58:GLU:O	13:AM:62:ASN:ND2	2.30	0.65
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.32	0.64
50:B3:10:LYS:NZ	50:B3:15:TYR:OH	2.28	0.64
9:CI:121:ARG:NH1	9:CI:122:ALA:O	2.31	0.64
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.79	0.64
26:BA:529:A:OP2	34:BN:114:ARG:NH2	2.29	0.64
32:BH:98:LEU:HD13	32:BH:125:VAL:HG23	1.79	0.64
1:CA:405:U:O4	4:CD:2:GLY:N	2.30	0.64
9:CI:112:LYS:NZ	9:CI:116:LYS:O	2.30	0.64
26:DA:458:G:O2'	26:DA:469:G:O6	2.13	0.64
35:DO:19:ILE:HG22	35:DO:43:VAL:HA	1.80	0.64
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.20	0.64
26:BA:1823:G:OP1	28:BD:54:ARG:NH1	2.31	0.64
1:CA:827:U:H2'	1:CA:859:A:H61	1.62	0.64
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.80	0.64
13:CM:93:ARG:HD3	26:DA:888:C:OP1	1.97	0.64
26:DA:1169:G:H1	26:DA:1180:C:N4	1.92	0.64
26:DA:2363:C:O2	47:D0:39:ARG:NH2	2.29	0.64
23:AW:76:PPU:H103	26:BA:2584:U:H5'	1.78	0.64
26:BA:1252:G:OP1	41:BU:36:ARG:NH2	2.30	0.64
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.97	0.64
26:DA:1971:A:N1	61:DA:3924:HOH:O	2.30	0.64
26:DA:2779:U:H4'	26:DA:2780:G:H5"	1.78	0.64
27:DB:86:G:N1	27:DB:91:C:N3	2.34	0.64
36:DP:42:SER:O	61:DP:302:HOH:O	2.15	0.64
2:AB:121:LEU:HD13	2:AB:126:GLU:HG2	1.80	0.64
26:BA:2158:A:H2'	26:BA:2158:A:N3	2.12	0.64
27:BB:102:A:N7	61:BB:4020:HOH:O	2.30	0.64
1:CA:600:C:H2'	1:CA:601:C:C6	2.33	0.64
24:CX:6:G:H1	24:CX:67:C:N4	1.94	0.64
1:AA:377:G:OP1	16:AP:3:LYS:HD2	1.97	0.64
1:AA:1392:G:N2	1:AA:1502:A:H8	1.95	0.64
24:AX:55:PSU:O2'	24:AX:57:A:N7	2.24	0.64
26:BA:11:G:H2'	26:BA:12:U:H5"	1.78	0.64
26:BA:1815:A:OP2	28:BD:54:ARG:NH2	2.31	0.64
26:BA:2151:G:H2'	26:BA:2152:G:C8	2.32	0.64
26:DA:2408:U:H2'	26:DA:2409:G:C8	2.32	0.64
14:AN:3:ARG:HB3	14:AN:3:ARG:HH21	1.62	0.64
26:BA:252:G:P	36:BP:50:ARG:HH12	2.21	0.64
26:BA:1800:C:OP2	28:BD:183:ARG:NH2	2.31	0.64
26:BA:2741:A:OP1	56:B9:22:ARG:NH2	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BB:33:G:H5'	31:BG:2:PRO:HD3	1.79	0.64
1:CA:76:C:N4	1:CA:93:G:C2	2.66	0.64
1:CA:582:U:OP1	15:CO:68:ARG:NH1	2.29	0.64
3:CC:11:ARG:HB3	3:CC:15:THR:HB	1.79	0.64
26:DA:1005:C:H2'	26:DA:1006:C:C6	2.32	0.64
26:DA:1276:A:O2'	38:DR:12:ARG:NH2	2.26	0.64
26:BA:2113:U:H3	26:BA:2170:A:H61	1.44	0.64
26:DA:362:U:H1'	26:DA:363:G:H5"	1.80	0.64
26:DA:910:A:N3	26:DA:2264:C:O2'	2.26	0.64
37:DQ:65:PHE:HB2	37:DQ:105:GLU:HB2	1.80	0.64
1:CA:1395:C:O2	1:CA:1398:A:O2'	2.16	0.64
31:DG:20:ILE:HA	31:DG:25:TYR:HD1	1.63	0.64
46:DZ:53:ILE:HD13	46:DZ:99:TYR:HB2	1.80	0.64
1:AA:709:G:H2'	1:AA:710:G:H5'	1.80	0.63
26:BA:1250:G:N7	36:BP:18:ARG:NH2	2.46	0.63
1:CA:302:G:O2'	1:CA:556:C:H5"	1.98	0.63
1:CA:967:C:H3'	1:CA:968:A:H2'	1.79	0.63
1:CA:975:A:N6	1:CA:1367:C:O4'	2.26	0.63
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.63	0.63
8:CH:135:CYS:SG	8:CH:136:GLU:N	2.71	0.63
26:DA:1385:G:O2'	26:DA:1396:U:O2	2.15	0.63
1:AA:175:C:O5'	1:AA:175:C:H6	1.82	0.63
1:AA:709:G:C2'	1:AA:710:G:H5'	2.27	0.63
26:BA:1676:A:N7	61:BA:4171:HOH:O	2.30	0.63
26:BA:2384:G:OP2	47:B0:55:ARG:NH1	2.26	0.63
1:CA:708:C:OP1	11:CK:85:ARG:NH2	2.27	0.63
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.81	0.63
1:AA:1366:C:O2'	10:AJ:60:ARG:NH2	2.31	0.63
1:CA:1120:G:C6	1:CA:1154:G:N2	2.67	0.63
6:CF:11:ASN:HB3	6:CF:14:LEU:HG	1.79	0.63
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.32	0.63
1:AA:600:C:H2'	1:AA:601:C:H6	1.63	0.63
15:AO:5:LYS:H	15:AO:5:LYS:HD2	1.63	0.63
26:BA:71:A:OP2	26:BA:71:A:H3'	1.98	0.63
28:BD:148:GLU:HB2	28:BD:151:LYS:HD2	1.79	0.63
26:DA:1019:U:OP1	26:DA:1035:U:O2'	2.15	0.63
1:AA:96:U:O2'	1:AA:97:G:O4'	2.15	0.63
26:BA:1721:G:H2'	26:BA:1740:G:O6	1.99	0.63
26:BA:2181:G:O2'	26:BA:2182:G:OP1	2.16	0.63
1:CA:1011:G:H1	1:CA:1018:C:H42	1.47	0.63
16:CP:17:TYR:HE2	16:CP:41:PRO:HG3	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1356:G:OP1	61:DA:4383:HOH:O	2.16	0.63
26:DA:2667:C:N3	32:DH:110:SER:OG	2.29	0.63
46:DZ:10:ARG:NH2	46:DZ:26:GLY:O	2.30	0.63
1:AA:545:C:OP2	4:AD:65:ARG:NH2	2.31	0.63
1:CA:521:G:H4'	12:CL:73:GLU:HG2	1.80	0.63
26:DA:588:U:OP2	61:DA:3879:HOH:O	2.16	0.63
26:DA:1359:A:C6	26:DA:1360:A:C5	2.87	0.63
29:DE:72:VAL:HA	29:DE:73:GLU:HB3	1.80	0.63
26:BA:2141:G:N7	26:BA:2151:G:N2	2.47	0.63
26:BA:2518:A:OP2	61:BA:4227:HOH:O	2.15	0.63
61:BA:4874:HOH:O	38:BR:3:HIS:NE2	2.30	0.63
31:BG:37:VAL:HG21	31:BG:103:LEU:HD21	1.80	0.63
1:CA:419:C:OP1	1:CA:513:C:O2'	2.12	0.63
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.39	0.63
26:DA:709:U:H2'	26:DA:710:G:C8	2.34	0.63
26:DA:2138:C:H2'	26:DA:2139:C:H6	1.64	0.63
26:DA:2801(A):A:N3	26:DA:2895:U:H1'	2.13	0.63
41:DU:83:LEU:HD12	41:DU:88:ILE:HB	1.81	0.63
1:AA:1125:U:H4'	10:AJ:5:ARG:HH22	1.64	0.63
26:DA:2193:G:H2'	26:DA:2194:G:H8	1.64	0.63
36:DP:126:VAL:HG12	36:DP:148:LEU:HD22	1.80	0.63
1:AA:148:G:N1	1:AA:175:C:N3	2.47	0.63
1:AA:835:U:H3	1:AA:851:G:H1	1.47	0.63
30:BF:157:VAL:HB	30:BF:194:MET:HG2	1.79	0.63
1:CA:60:A:OP1	1:CA:111:G:N2	2.30	0.63
4:CD:60:GLU:HG3	4:CD:198:VAL:HG13	1.80	0.63
35:DO:102:VAL:HB	35:DO:106:LEU:HD12	1.81	0.63
36:DP:89:ALA:O	36:DP:121:LYS:NZ	2.29	0.63
1:AA:826:C:O2	8:AH:15:ASN:ND2	2.32	0.62
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.81	0.62
26:BA:249:C:O2	55:B8:12:LYS:NZ	2.29	0.62
26:BA:1385:G:O2'	26:BA:1396:U:O2	2.15	0.62
26:BA:1798:U:OP2	28:BD:274:ARG:NH2	2.32	0.62
26:DA:1429:G:H1'	26:DA:1568:G:H1'	1.81	0.62
27:DB:24:G:H5'	27:DB:25:A:H62	1.62	0.62
31:DG:3:LEU:HD12	31:DG:5:VAL:HG12	1.81	0.62
31:DG:122:PRO:HG3	31:DG:180:PHE:HB3	1.79	0.62
26:BA:1243:G:O2'	36:BP:7:ARG:NH2	2.32	0.62
26:BA:2319:G:N2	39:BS:3:ARG:HA	2.15	0.62
1:CA:657:G:H4'	15:CO:28:GLN:HG2	1.81	0.62
1:CA:890:G:O2'	1:CA:906:G:O6	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.79	0.62
28:DD:108:PRO:HB3	28:DD:143:HIS:HE1	1.63	0.62
30:DF:184:TYR:CE2	30:DF:188:ARG:HD2	2.33	0.62
1:AA:946:A:H2'	1:AA:947:G:C8	2.35	0.62
2:AB:185:ILE:HG23	2:AB:199:TYR:HB2	1.82	0.62
31:BG:64:THR:HB	31:BG:94:LEU:HD21	1.82	0.62
18:CR:25:THR:O	18:CR:25:THR:OG1	2.15	0.62
26:DA:1316:U:H2'	26:DA:1317:A:C8	2.34	0.62
26:DA:1817:G:OP1	28:DD:88:ARG:NH2	2.32	0.62
26:DA:2590:A:OP2	28:DD:238:GLY:HA2	1.99	0.62
26:DA:2831:G:OP1	29:DE:58:ARG:NH2	2.29	0.62
30:DF:53:THR:HG23	30:DF:55:GLY:H	1.63	0.62
9:AI:17:VAL:HG11	9:AI:81:ILE:HA	1.82	0.62
26:BA:1314:C:OP1	61:BA:4479:HOH:O	2.15	0.62
26:BA:1713:U:H2'	26:BA:1714:G:H8	1.63	0.62
27:DB:17:C:O2	27:DB:67:G:N2	2.21	0.62
44:DX:53:LYS:HB3	44:DX:82:GLN:HB3	1.81	0.62
26:BA:2303:G:O6	61:BA:3888:HOH:O	2.14	0.62
27:BB:91:C:OP2	37:BQ:16:ARG:NH1	2.32	0.62
37:BQ:138:ASP:OD2	46:BZ:81:ARG:NH1	2.32	0.62
1:CA:1362:C:H2'	1:CA:1363:C:H5"	1.82	0.62
4:CD:162:LEU:HA	4:CD:165:MET:HB2	1.81	0.62
24:CX:42:G:H2'	24:CX:43:A:H8	1.64	0.62
26:DA:1021:A:H62	26:DA:1141:U:H3	1.48	0.62
26:DA:1370:C:HO2'	26:DA:1811:G:HO2'	1.42	0.62
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.14	0.62
7:AG:80:VAL:HB	7:AG:85:TYR:HE2	1.63	0.62
27:BB:28:C:OP1	39:BS:31:SER:OG	2.11	0.62
54:B7:33:ARG:NH2	61:B7:201:HOH:O	2.26	0.62
1:CA:975:A:H4'	1:CA:976:G:H5"	1.82	0.62
24:CX:60:U:H5'	24:CX:61:C:H5	1.63	0.62
26:DA:1230:C:H2'	26:DA:1231:G:H8	1.65	0.62
26:DA:2001:A:H2'	26:DA:2002:G:C8	2.34	0.62
31:DG:7:LEU:HD23	31:DG:100:TRP:HE3	1.65	0.62
1:AA:662:G:H2'	1:AA:663:A:C8	2.34	0.62
1:AA:1297:C:O2'	7:AG:114:ARG:NH2	2.31	0.62
9:AI:49:PRO:HG2	9:AI:81:ILE:HG23	1.81	0.62
25:AY:74:C:H4'	48:B1:23:LYS:HB2	1.81	0.62
26:BA:2127:G:C6	26:BA:2162:G:N1	2.68	0.62
28:BD:12:SER:HB3	28:BD:208:LYS:HB3	1.81	0.62
26:DA:1857:G:O2'	26:DA:1885:A:N6	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:55:U:H4'	31:DG:28:VAL:HG22	1.82	0.62
27:DB:56:G:OP1	31:DG:27:ASN:ND2	2.33	0.62
32:DH:97:ARG:HA	32:DH:125:VAL:HG11	1.81	0.62
26:BA:958:U:OP2	37:BQ:14:ARG:NH1	2.33	0.62
1:CA:977:A:HO2'	1:CA:981:U:H3	1.44	0.62
1:CA:1240:U:C2	7:CG:32:ARG:HD3	2.34	0.62
37:DQ:135:ASP:OD2	46:DZ:49:ARG:NH2	2.31	0.62
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.48	0.62
1:AA:997:U:H3	1:AA:1044:A:N6	1.98	0.62
26:BA:1379:A:H4'	26:BA:1380:G:OP2	1.99	0.62
1:CA:1014:A:OP1	19:CS:18:LYS:NZ	2.33	0.62
1:CA:1346:A:N1	1:CA:1374:A:H5"	2.15	0.62
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.63	0.62
26:DA:953:A:OP1	37:DQ:18:LYS:NZ	2.33	0.62
26:DA:2074:U:H2'	26:DA:2075:U:C6	2.35	0.62
32:DH:4:ILE:HG22	32:DH:69:ARG:HG2	1.81	0.62
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.33	0.62
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.82	0.62
38:BR:55:ALA:HB2	38:BR:79:LEU:HD13	1.82	0.62
1:CA:1120:G:H8	1:CA:1120:G:O5'	1.82	0.62
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.00	0.62
18:CR:74:ARG:HG3	18:CR:79:LEU:HB2	1.82	0.62
26:DA:195:A:OP1	36:DP:46:LYS:NZ	2.31	0.62
26:DA:570:G:H2'	26:DA:2030:A:C5	2.35	0.62
26:DA:2012:G:OP2	43:DW:16:LYS:NZ	2.32	0.62
26:DA:2857:G:N2	26:DA:2860:A:OP2	2.31	0.62
28:DD:108:PRO:HB3	28:DD:143:HIS:CE1	2.35	0.62
30:DF:101:LEU:O	30:DF:106:ARG:NH1	2.28	0.62
1:AA:346:G:C4	1:AA:347:G:H1'	2.35	0.61
1:AA:1261:A:H3'	1:AA:1262:C:C6	2.35	0.61
7:AG:46:ALA:HA	7:AG:49:ILE:HD12	1.82	0.61
12:AL:53:ARG:NH1	12:AL:92:ASP:OD2	2.30	0.61
13:AM:37:THR:O	13:AM:55:ARG:NH1	2.31	0.61
9:CI:53:VAL:O	9:CI:55:ALA:N	2.27	0.61
26:DA:2203:U:H2'	26:DA:2205:C:C6	2.35	0.61
26:DA:2302:G:H2'	26:DA:2303:G:H5'	1.82	0.61
30:DF:53:THR:HG22	30:DF:56:GLU:HG3	1.82	0.61
30:DF:143:ALA:HB1	30:DF:148:LEU:HB2	1.81	0.61
1:AA:1243:C:N4	1:AA:1294:G:H1	1.98	0.61
26:BA:1427:A:H4'	26:BA:1428:C:O5'	2.01	0.61
1:CA:592:G:H1	1:CA:647:C:N4	1.97	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:253:C:OP2	55:D8:5:LYS:NZ	2.28	0.61
26:DA:307:G:N7	61:DA:3912:HOH:O	2.31	0.61
2:AB:204:ASN:OD1	2:AB:206:ASP:N	2.28	0.61
6:AF:37:VAL:HA	6:AF:65:VAL:HG12	1.82	0.61
26:BA:831:G:O2'	36:BP:38:GLN:NE2	2.33	0.61
1:CA:659:U:C2'	1:CA:660:G:H5'	2.30	0.61
1:CA:1002:G:H1	1:CA:1038:C:H42	0.71	0.61
26:DA:30:G:H2'	26:DA:31:C:C6	2.35	0.61
26:DA:2831:G:P	29:DE:58:ARG:HH21	2.23	0.61
26:DA:2839:G:H5'	38:DR:46:GLY:HA2	1.83	0.61
38:DR:28:LEU:HD12	38:DR:48:VAL:HG21	1.82	0.61
39:DS:27:SER:HA	39:DS:88:ASP:HB3	1.82	0.61
46:DZ:45:ASP:OD1	46:DZ:49:ARG:NH1	2.33	0.61
1:CA:411:A:OP2	4:CD:25:ARG:NH2	2.28	0.61
1:CA:1458:G:OP1	20:CT:35:THR:OG1	2.12	0.61
3:CC:126:ARG:HG2	3:CC:126:ARG:HH11	1.65	0.61
10:CJ:81:THR:HA	10:CJ:84:GLN:HB3	1.82	0.61
23:CW:75:C:C5	23:CW:76:PPU:H93	2.36	0.61
26:DA:1528:A:OP2	26:DA:1542:A:N6	2.33	0.61
26:DA:2142:C:H2'	26:DA:2143:C:C6	2.35	0.61
33:DI:87:LYS:HB3	33:DI:122:GLU:HA	1.83	0.61
38:DR:88:ARG:NH2	38:DR:89:ASP:OD1	2.32	0.61
1:AA:147:G:H1	1:AA:148:G:N2	1.99	0.61
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.32	0.61
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.83	0.61
26:BA:1992:G:N7	61:BA:4265:HOH:O	2.31	0.61
1:CA:975:A:N6	10:CJ:60:ARG:HH12	1.99	0.61
26:DA:1840:G:OP2	61:DA:4276:HOH:O	2.16	0.61
31:DG:83:ARG:N	31:DG:86:MET:SD	2.70	0.61
40:DT:60:THR:HG22	40:DT:77:PRO:HA	1.83	0.61
1:AA:600:C:H2'	1:AA:601:C:C6	2.35	0.61
26:BA:1025:G:C4	26:BA:1135:C:H1'	2.36	0.61
1:CA:1356:G:H1	1:CA:1366:C:N4	1.97	0.61
26:DA:2836:U:H2'	26:DA:2837:G:C8	2.35	0.61
33:DI:87:LYS:HA	33:DI:123:LEU:H	1.65	0.61
35:DO:76:ALA:HB3	40:DT:75:ILE:HB	1.81	0.61
39:DS:34:HIS:O	39:DS:97:ARG:NH2	2.34	0.61
43:DW:73:ALA:HB3	43:DW:106:ILE:HD12	1.82	0.61
1:AA:757:U:H2'	1:AA:758:G:O4'	2.00	0.61
3:AC:73:PRO:HB3	3:AC:103:VAL:HG11	1.82	0.61
9:AI:22:GLY:N	9:AI:58:HIS:O	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:372:G:OP2	48:B1:69:LYS:HE2	2.00	0.61
26:BA:1183:G:O2'	50:B3:29:ARG:NH1	2.34	0.61
26:BA:2377:A:H2'	26:BA:2378:A:C8	2.36	0.61
1:CA:1036:G:N7	1:CA:1037:C:C2	2.68	0.61
1:CA:1229:A:O2'	24:CX:30:G:OP1	2.16	0.61
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.36	0.61
1:AA:627:G:H2'	1:AA:628:G:H8	1.66	0.61
19:AS:9:VAL:HG21	51:B4:61:ARG:NH2	2.16	0.61
26:BA:228:A:H8	26:BA:229:A:H5'	1.66	0.61
26:BA:528:A:N1	26:BA:2042:A:H2'	2.16	0.61
26:BA:1315:C:OP2	61:BA:4479:HOH:O	2.16	0.61
26:BA:1693:U:O2'	28:BD:14:ARG:NH2	2.33	0.61
26:BA:2150:U:H2'	26:BA:2151:G:C8	2.36	0.61
26:BA:2454:G:O6	61:BA:4327:HOH:O	2.10	0.61
51:B4:61:ARG:NH1	51:B4:62:ARG:O	2.33	0.61
1:CA:1423:G:OP1	35:DO:49:ARG:NH2	2.26	0.61
9:CI:37:PHE:HD1	9:CI:40:LEU:HD12	1.66	0.61
26:DA:881:G:H2'	26:DA:882:G:O4'	2.00	0.61
26:DA:2223:G:OP1	28:DD:172:TYR:OH	2.17	0.61
1:AA:171:A:H2'	1:AA:172:A:C8	2.36	0.61
5:AE:18:ARG:HE	5:AE:27:ARG:HH21	1.48	0.61
26:BA:196:A:H62	36:BP:38:GLN:HE22	1.49	0.61
1:CA:352:C:O2'	1:CA:354:G:OP1	2.18	0.61
4:CD:64:LEU:HB2	4:CD:198:VAL:HG21	1.83	0.61
33:DI:86:THR:O	33:DI:123:LEU:HB2	2.01	0.61
1:AA:890:G:O2'	1:AA:906:G:O6	2.17	0.61
1:AA:1317:C:OP1	14:AN:17:LYS:HG2	2.01	0.61
26:BA:184:C:H2'	26:BA:185:U:C6	2.36	0.61
53:B6:35:GLU:OE2	53:B6:50:ARG:NH1	2.33	0.61
26:DA:889:C:O2'	26:DA:890:A:O5'	2.18	0.61
26:DA:1324:G:N7	61:DA:3861:HOH:O	2.31	0.61
26:DA:1378:A:OP1	54:D7:10:ARG:NH2	2.33	0.61
26:DA:1632:A:N7	61:DA:4171:HOH:O	2.31	0.61
13:AM:90:LEU:HA	13:AM:93:ARG:HD2	1.83	0.60
24:AX:16:C:O2'	24:AX:61:C:OP1	2.15	0.60
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.16	0.60
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.34	0.60
8:CH:29:SER:HB3	8:CH:32:LYS:HG3	1.82	0.60
26:DA:659:C:H2'	26:DA:660:G:H8	1.66	0.60
26:DA:1587:A:H2'	26:DA:1588:C:C6	2.35	0.60
26:DA:2562:U:H1'	35:DO:23:ARG:HH11	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.32	0.60
4:AD:172:PRO:HB2	4:AD:187:ARG:HH22	1.66	0.60
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.34	0.60
6:AF:89:MET:HE1	18:AR:72:ARG:HB3	1.82	0.60
26:BA:1816:G:O6	28:BD:35:LYS:NZ	2.34	0.60
31:BG:41:GLN:HE22	31:BG:153:ARG:HB3	1.66	0.60
37:BQ:77:LYS:NZ	37:BQ:86:GLY:O	2.33	0.60
1:CA:923:A:O2'	1:CA:1399:C:OP2	2.13	0.60
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.83	0.60
26:DA:271(P):C:O3'	33:DI:42:SER:OG	2.18	0.60
26:DA:1973:G:OP1	61:DA:4133:HOH:O	2.16	0.60
27:DB:30:C:H3'	27:DB:30:C:O2	2.01	0.60
36:DP:50:ARG:HG2	55:D8:61:LEU:HD11	1.83	0.60
42:DV:60:GLU:HB3	42:DV:95:LEU:HB3	1.82	0.60
56:D9:25:VAL:HB	56:D9:34:GLN:HB2	1.82	0.60
1:AA:309:G:O2'	1:AA:607:A:N1	2.33	0.60
1:AA:347:G:H2'	1:AA:348:G:O4'	2.00	0.60
4:AD:162:LEU:HA	4:AD:165:MET:HB2	1.83	0.60
5:AE:8:GLU:OE2	5:AE:63:ARG:NH2	2.34	0.60
26:BA:1986:A:OP1	61:BA:4252:HOH:O	2.15	0.60
28:BD:132:PRO:HG2	28:BD:135:PHE:CD2	2.36	0.60
1:CA:407:G:N2	1:CA:436:C:C2	2.66	0.60
1:CA:1123:A:H4'	10:CJ:36:GLY:HA3	1.83	0.60
1:CA:1275:A:H2'	1:CA:1276:G:O4'	2.01	0.60
26:DA:1012:U:OP1	41:DU:75:ASN:ND2	2.31	0.60
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.83	0.60
19:AS:32:LYS:HA	19:AS:50:ALA:HB3	1.83	0.60
42:BV:19:LYS:HG2	42:BV:95:LEU:HD23	1.84	0.60
1:CA:986:A:O2'	19:CS:55:LYS:O	2.18	0.60
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.01	0.60
2:CB:76:GLN:HG3	2:CB:206:ASP:O	2.00	0.60
24:CX:30:G:N2	24:CX:40:C:N3	2.40	0.60
26:DA:1539:G:H2'	26:DA:1540:U:O4'	2.01	0.60
26:DA:2313:C:H4'	31:DG:91:ARG:HG3	1.84	0.60
30:DF:20:LEU:HD13	30:DF:125:LEU:HD13	1.82	0.60
37:DQ:85:LYS:HD3	47:D0:7:LEU:HD12	1.84	0.60
1:AA:649:G:H2'	1:AA:650:G:H8	1.66	0.60
1:AA:918:A:H2'	1:AA:919:A:C8	2.36	0.60
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.36	0.60
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.83	0.60
26:BA:957:A:H5'	37:BQ:76:LYS:HG3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1495:A:H2'	26:BA:1496:A:C8	2.36	0.60
26:BA:2531:A:H5'	32:BH:157:TYR:CZ	2.36	0.60
1:CA:64:G:H4'	1:CA:65:U:H3'	1.83	0.60
1:CA:757:U:O2'	1:CA:879:C:O2	2.18	0.60
18:CR:45:SER:HB3	18:CR:51:LEU:HD21	1.81	0.60
32:DH:98:LEU:HD13	32:DH:125:VAL:HG23	1.84	0.60
36:DP:29:LYS:HG3	36:DP:30:THR:H	1.64	0.60
36:DP:82:GLY:HA2	36:DP:113:LYS:O	2.01	0.60
1:AA:67:C:H2'	1:AA:68:G:C8	2.37	0.60
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.60
1:AA:473:G:H2'	1:AA:474:G:C8	2.37	0.60
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.02	0.60
31:BG:48:GLU:HA	31:BG:51:ARG:HG3	1.83	0.60
33:BI:72:LEU:C	33:BI:74:ASN:H	2.10	0.60
1:CA:933:G:O6	7:CG:3:ARG:NH2	2.34	0.60
1:CA:1223:C:OP2	19:CS:78:ARG:NH2	2.34	0.60
1:CA:1226:C:H2'	13:CM:103:THR:HB	1.83	0.60
1:CA:1304:G:OP1	21:CU:2:GLY:N	2.35	0.60
30:DF:185:ASP:HA	30:DF:188:ARG:HD3	1.83	0.60
36:DP:63:PRO:HD3	55:D8:27:THR:HG22	1.84	0.60
46:DZ:7:ALA:HB3	46:DZ:61:LEU:HD12	1.83	0.60
1:AA:1223:C:P	19:AS:78:ARG:HH21	2.25	0.60
2:AB:76:GLN:NE2	2:AB:206:ASP:OD1	2.35	0.60
19:AS:27:GLU:HG2	19:AS:47:HIS:NE2	2.17	0.60
26:BA:822:U:O4	26:BA:944:G:H1'	2.01	0.60
31:BG:161:THR:HG22	31:BG:163:ALA:H	1.66	0.60
40:BT:85:LYS:NZ	40:BT:87:ASP:OD2	2.31	0.60
46:BZ:23:LYS:NZ	46:BZ:40:ASP:OD1	2.33	0.60
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.10	0.60
27:DB:49:C:H2'	27:DB:50:G:C8	2.36	0.60
1:AA:1003:G:C2	1:AA:1004:A:N3	2.70	0.60
2:AB:98:LEU:HG	2:AB:101:MET:HE3	1.84	0.60
4:AD:166:LYS:HA	4:AD:178:VAL:HG21	1.83	0.60
26:BA:414:C:H2'	26:BA:415:A:C8	2.37	0.60
26:BA:1165:U:H2'	26:BA:1166:C:C6	2.36	0.60
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.01	0.60
26:DA:2736:G:N1	26:DA:2768:C:N3	2.38	0.60
29:DE:55:ASN:HB3	29:DE:58:ARG:HG3	1.84	0.60
1:AA:662:G:O2'	1:AA:836:G:OP1	2.20	0.60
4:AD:101:LEU:HB2	4:AD:138:TYR:HB3	1.84	0.60
26:BA:1315:C:O2'	26:BA:1392:A:N3	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2086:U:H2'	26:BA:2087:G:C8	2.37	0.60
33:BI:50:ARG:HA	33:BI:53:ALA:HB3	1.83	0.60
1:CA:999:C:N4	1:CA:1042:G:H1	1.95	0.60
26:DA:1028:A:N6	26:DA:1125:G:H2'	2.17	0.60
26:DA:2305:A:H61	31:DG:43:LEU:HD13	1.67	0.60
31:DG:5:VAL:HG22	31:DG:8:LYS:H	1.66	0.60
31:DG:96:ARG:O	31:DG:99:MET:HB3	2.01	0.60
36:DP:63:PRO:HG2	55:D8:25:MET:HB2	1.83	0.60
50:D3:5:LYS:NZ	50:D3:34:GLU:OE2	2.26	0.60
1:AA:804:U:H5"	1:AA:805:C:OP2	2.02	0.60
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.02	0.60
26:BA:1225:G:OP1	42:BV:69:LYS:NZ	2.24	0.60
27:BB:13:A:N1	27:BB:69:G:O2'	2.33	0.60
1:CA:27:G:H2'	1:CA:28:G:H8	1.66	0.60
26:DA:918:A:O2'	27:DB:97:G:N2	2.33	0.60
26:DA:1688:U:O2	26:DA:1700:A:H5'	2.02	0.60
26:DA:1842:G:O2'	28:DD:253:GLN:NE2	2.28	0.60
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.84	0.59
4:AD:166:LYS:HB2	4:AD:168:ARG:HH12	1.65	0.59
26:BA:668:G:H5'	26:BA:669:G:OP2	2.02	0.59
26:BA:1695:G:N7	28:BD:14:ARG:NH2	2.46	0.59
37:BQ:56:ARG:HH11	37:BQ:56:ARG:CG	2.15	0.59
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.67	0.59
1:CA:1129:C:OP1	9:CI:16:ARG:NH1	2.35	0.59
9:CI:96:LEU:HD22	9:CI:101:PHE:HB2	1.84	0.59
26:DA:647:G:H8	26:DA:647:G:O5'	1.85	0.59
26:DA:1971:A:OP2	28:DD:242:ARG:NH2	2.35	0.59
26:DA:2180:U:H2'	26:DA:2181:G:O4'	2.02	0.59
26:DA:2630:G:H2'	26:DA:2631:G:C8	2.37	0.59
26:DA:2820:A:O2'	26:DA:2821:A:OP1	2.20	0.59
39:DS:99:LYS:HE2	39:DS:103:GLU:OE2	2.02	0.59
1:AA:1075:C:H2'	1:AA:1076:C:H5'	1.83	0.59
26:BA:1176:G:H1'	26:BA:1177:A:C5'	2.29	0.59
44:BX:31:HIS:CD2	44:BX:33:LYS:H	2.19	0.59
1:CA:789:U:O2'	1:CA:791:G:N7	2.34	0.59
26:DA:271(M):G:H4'	26:DA:271(N):U:OP1	2.01	0.59
26:DA:657:U:H2'	26:DA:658:C:C6	2.36	0.59
40:DT:59:THR:HG23	40:DT:78:LEU:HB3	1.83	0.59
43:DW:14:PRO:HG2	43:DW:78:GLU:HG2	1.84	0.59
1:AA:148:G:N2	1:AA:175:C:O2	2.35	0.59
1:AA:339:C:OP2	35:BO:97:ARG:NH1	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1228:C:OP1	13:AM:115:LYS:N	2.27	0.59
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.84	0.59
18:AR:31:LEU:HD12	18:AR:65:ILE:HB	1.84	0.59
24:AX:4:G:H2'	24:AX:5:G:C8	2.37	0.59
26:BA:271(R):G:OP1	48:B1:76:ARG:NH2	2.35	0.59
26:BA:1239:G:OP1	61:BA:4617:HOH:O	2.17	0.59
26:BA:2732:G:H3'	26:BA:2733:A:O4'	2.02	0.59
33:BI:61:ARG:HH11	33:BI:61:ARG:HA	1.68	0.59
54:B7:34:ARG:NH1	54:B7:41:ARG:O	2.35	0.59
1:CA:609:A:H2'	1:CA:610:G:H5'	1.84	0.59
1:CA:730:G:C5	1:CA:731:G:H1'	2.36	0.59
26:DA:1453:U:O2'	26:DA:1455:G:N7	2.33	0.59
26:DA:2394:C:OP2	55:D8:30:ARG:NH1	2.35	0.59
26:DA:2408:U:H2'	26:DA:2409:G:H8	1.67	0.59
29:DE:47:VAL:HG11	29:DE:86:PRO:HD2	1.84	0.59
36:DP:99:LEU:HD23	36:DP:99:LEU:H	1.65	0.59
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.83	0.59
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.84	0.59
26:BA:1371:G:H2'	26:BA:1372:U:C5	2.37	0.59
30:BF:33:LEU:HB3	36:BP:6:LEU:HD21	1.84	0.59
1:CA:92:C:C2'	1:CA:93:G:H5'	2.33	0.59
1:CA:545:C:OP2	4:CD:65:ARG:NH2	2.34	0.59
1:CA:958:A:H61	19:CS:77:THR:HG23	1.65	0.59
3:CC:3:ASN:OD1	3:CC:3:ASN:N	2.36	0.59
23:CW:75:C:C4	23:CW:76:PPU:H93	2.37	0.59
26:DA:84:A:H5"	45:DY:8:LYS:HG2	1.84	0.59
26:DA:1005:C:H2'	26:DA:1006:C:H6	1.68	0.59
26:DA:1914:C:H2'	26:DA:1915:U:C6	2.38	0.59
1:AA:763:G:C2'	1:AA:764:C:H5'	2.32	0.59
1:AA:1241:G:OP1	7:AG:35:LYS:NZ	2.33	0.59
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.35	0.59
1:CA:107:G:OP1	1:CA:325:A:N6	2.34	0.59
1:CA:696:A:N3	1:CA:786:G:O2'	2.29	0.59
1:CA:792:A:H4'	1:CA:793:U:H5"	1.83	0.59
1:CA:1068:G:H8	1:CA:1068:G:OP2	1.86	0.59
26:DA:956:G:OP2	37:DQ:14:ARG:NH2	2.35	0.59
26:DA:1448:G:O2'	26:DA:1528(A):A:N1	2.34	0.59
1:AA:448:A:OP2	1:AA:485:G:N1	2.22	0.59
1:AA:977:A:H2'	1:AA:978:A:H5"	1.85	0.59
42:BV:34:GLU:HB3	42:BV:56:SER:HB2	1.85	0.59
26:DA:2136:C:O2'	26:DA:2137:C:O5'	2.21	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2635:C:O2'	29:DE:80:GLU:OE1	2.20	0.59
26:DA:2834:G:O2'	26:DA:2883:A:N6	2.34	0.59
1:AA:1392:G:H21	1:AA:1502:A:H8	1.49	0.59
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.02	0.59
1:CA:284:G:H2'	1:CA:285:G:H8	1.68	0.59
1:CA:588:G:H4'	8:CH:2:LEU:HD12	1.83	0.59
9:CI:105:ASP:HB2	9:CI:107:ARG:HG3	1.84	0.59
36:DP:37:GLY:O	36:DP:40:SER:OG	2.21	0.59
43:DW:71:VAL:HA	43:DW:107:LEU:HD12	1.83	0.59
46:DZ:24:LEU:N	46:DZ:39:VAL:O	2.35	0.59
1:AA:201:C:H42	1:AA:216:G:H1	1.50	0.59
1:AA:1191:A:H5"	3:AC:4:LYS:HZ2	1.66	0.59
4:AD:107:ARG:HH22	4:AD:194:LEU:HD22	1.68	0.59
26:BA:1939:U:OP1	26:BA:2604:U:O2'	2.21	0.59
30:BF:184:TYR:CE2	30:BF:188:ARG:HD2	2.37	0.59
31:BG:11:TYR:CZ	31:BG:16:ARG:HD3	2.38	0.59
35:BO:104:ARG:CZ	40:BT:34:VAL:HG21	2.33	0.59
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.36	0.59
26:DA:276:A:H5"	26:DA:277:C:H5'	1.84	0.59
26:DA:578:A:OP2	61:DA:3804:HOH:O	2.16	0.59
26:DA:861:A:N3	27:DB:79:C:O2'	2.35	0.59
26:DA:892:G:H8	26:DA:892:G:O5'	1.86	0.59
26:DA:1301:A:H2	26:DA:1626:G:N3	2.01	0.59
26:DA:1798:U:H5'	28:DD:259:THR:HG22	1.85	0.59
26:DA:2163:C:OP1	26:DA:2165:G:N1	2.36	0.59
26:DA:2166:G:O6	26:DA:2171:A:N6	2.36	0.59
33:DI:94:ALA:HA	33:DI:97:ILE:HB	1.84	0.59
35:DO:68:GLU:HB3	35:DO:78:ARG:HB2	1.83	0.59
44:DX:43:VAL:HG21	44:DX:81:VAL:HG11	1.84	0.59
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.68	0.59
26:BA:886:C:OP1	26:BA:886:C:H4'	2.01	0.59
1:CA:1352:C:OP1	21:CU:3:LYS:NZ	2.33	0.59
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.38	0.59
18:CR:22:VAL:HB	18:CR:56:THR:HA	1.85	0.59
24:CX:49:G:C6	24:CX:65:C:N4	2.71	0.59
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.85	0.59
7:AG:15:ASP:OD1	7:AG:19:GLY:N	2.36	0.59
26:BA:1173:G:O2'	26:BA:1174:A:O5'	2.21	0.59
26:BA:2893:G:H4'	26:BA:2894:G:O5'	2.01	0.59
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.84	0.59
24:CX:47:U:H3'	24:CX:48:C:C5'	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:309:G:N3	26:DA:329:G:O2'	2.35	0.59
26:DA:336:C:HO2'	45:DY:35:TYR:HH	1.49	0.59
26:DA:857:C:OP2	47:D0:77:ARG:NH2	2.36	0.59
26:DA:2572:A:N7	29:DE:144:ARG:HD2	2.18	0.59
46:DZ:55:HIS:CE1	46:DZ:135:GLU:HG3	2.38	0.59
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.30	0.58
26:BA:1019:U:O2'	26:BA:1021:A:H2	1.86	0.58
30:BF:192:LEU:HD13	30:BF:194:MET:HE2	1.85	0.58
53:B6:34:LEU:HB2	53:B6:51:GLU:HB2	1.84	0.58
26:DA:171:G:H2'	26:DA:172:C:C6	2.37	0.58
26:DA:479:A:N3	26:DA:481:G:H5"	2.18	0.58
26:DA:1860:G:H1	26:DA:1882:C:H42	1.50	0.58
26:DA:2454:G:O6	61:DA:3985:HOH:O	2.15	0.58
42:DV:76:LYS:HB2	42:DV:81:TYR:HB3	1.85	0.58
1:AA:191:G:N2	20:AT:103:GLY:HA2	2.17	0.58
1:AA:1352:C:N4	61:AA:4166:HOH:O	2.33	0.58
26:BA:356:G:H2'	26:BA:357:A:C8	2.37	0.58
26:BA:2687:U:H2'	26:BA:2688:U:O4'	2.03	0.58
26:BA:2869:G:H2'	26:BA:2870:C:O4'	2.03	0.58
33:BI:26:ALA:HA	33:BI:30:LEU:HB2	1.85	0.58
43:BW:18:ARG:NH1	43:BW:76:VAL:O	2.37	0.58
1:CA:1126:U:H1'	1:CA:1281:U:N3	2.18	0.58
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.38	0.58
26:DA:668:G:H5'	26:DA:669:G:OP2	2.01	0.58
26:DA:879:G:H3'	26:DA:880:G:C8	2.34	0.58
38:DR:11:ASN:ND2	61:DR:3101:HOH:O	2.34	0.58
51:D4:46:GLN:O	51:D4:48:ARG:N	2.32	0.58
6:AF:50:TYR:OH	18:AR:74:ARG:O	2.15	0.58
26:BA:330:A:H2	26:BA:1210:A:H2'	1.67	0.58
26:BA:648:G:O2'	26:BA:2351:G:OP1	2.19	0.58
26:BA:1593:G:H2'	26:BA:1594:G:C8	2.38	0.58
29:BE:47:VAL:HG13	29:BE:49:LEU:HD13	1.84	0.58
1:CA:978:A:OP1	1:CA:1361:G:N2	2.35	0.58
1:CA:1004:A:C6	1:CA:1037:C:C2	2.91	0.58
1:CA:1530:G:H2'	1:CA:1531:A:O4'	2.03	0.58
7:CG:99:LEU:HD23	7:CG:102:ARG:NH1	2.17	0.58
26:DA:1019:U:H3	26:DA:1142(A):A:H62	1.49	0.58
26:DA:1166:C:H2'	26:DA:1167:U:C6	2.37	0.58
26:DA:2626:C:H2'	26:DA:2627:G:O4'	2.03	0.58
50:D3:8:LEU:HD13	50:D3:31:LEU:HD23	1.84	0.58
1:AA:613:C:H2'	1:AA:614:A:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:90:VAL:O	5:AE:120:THR:HA	2.04	0.58
9:AI:42:ARG:NH1	9:AI:75:ASP:OD1	2.37	0.58
24:AX:64:G:O2'	37:BQ:10:ARG:NH2	2.37	0.58
26:BA:2155:G:H3'	26:BA:2156:G:H8	1.68	0.58
1:CA:92:C:H2'	1:CA:93:G:H5'	1.83	0.58
1:CA:1058:G:H1	1:CA:1199:U:H3	1.52	0.58
1:CA:1091:U:N3	1:CA:1094:G:OP2	2.25	0.58
1:CA:1428:A:H2'	1:CA:1429:C:C6	2.38	0.58
20:CT:16:HIS:O	20:CT:19:SER:OG	2.21	0.58
26:DA:1149:G:H2'	26:DA:1150:C:C6	2.38	0.58
26:DA:1420:U:O2'	26:DA:1421:G:OP1	2.21	0.58
41:DU:49:HIS:HA	41:DU:52:ARG:HB3	1.84	0.58
1:AA:448:A:P	1:AA:485:G:H22	2.26	0.58
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.38	0.58
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	1.85	0.58
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.84	0.58
26:BA:2332:U:O4	61:BA:4724:HOH:O	2.17	0.58
30:BF:164:ARG:O	30:BF:168:ARG:HB2	2.03	0.58
33:BI:96:ASP:OD1	33:BI:96:ASP:N	2.36	0.58
48:B1:51:VAL:HG11	48:B1:74:VAL:HG21	1.86	0.58
52:B5:59:GLU:HG2	52:B5:60:VAL:N	2.19	0.58
1:CA:953:G:H5'	1:CA:965:A:N6	2.19	0.58
1:CA:1356:G:H2'	1:CA:1357:A:C8	2.38	0.58
2:CB:120:ALA:O	2:CB:122:PHE:N	2.35	0.58
26:DA:1531:C:H42	26:DA:1538:G:H1	1.50	0.58
28:DD:34:VAL:HB	28:DD:61:LEU:HD12	1.85	0.58
28:DD:218:ARG:HB3	28:DD:219:PRO:HD2	1.86	0.58
30:DF:101:LEU:HD12	30:DF:102:PRO:HD2	1.86	0.58
32:DH:3:ARG:NH1	32:DH:3:ARG:HB3	2.18	0.58
43:DW:18:ARG:HG3	43:DW:76:VAL:HB	1.85	0.58
1:AA:13:U:OP1	61:AA:4121:HOH:O	2.17	0.58
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.36	0.58
1:AA:1150:U:O4	1:AA:1151:A:N6	2.37	0.58
2:AB:210:SER:O	2:AB:214:ILE:HG12	2.03	0.58
11:AK:84:VAL:HG21	11:AK:95:ILE:HD11	1.85	0.58
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.86	0.58
13:AM:80:ARG:NH2	51:B4:58:ARG:HD2	2.18	0.58
26:BA:271(A):A:N1	26:BA:272(D):G:O2'	2.30	0.58
26:BA:2820:A:OP2	38:BR:2:ARG:NH2	2.36	0.58
27:BB:75:G:H5"	27:BB:75:G:H8	1.69	0.58
37:BQ:86:GLY:HA3	47:B0:10:THR:HG23	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:592:G:H1	1:CA:647:C:H42	1.50	0.58
26:DA:251:A:C5	26:DA:252:G:H1'	2.37	0.58
26:DA:322:A:OP2	30:DF:169:ASN:HB2	2.03	0.58
26:DA:528:A:OP2	34:DN:114:ARG:NH1	2.37	0.58
26:DA:1427:A:H4'	26:DA:1428:C:O5'	2.04	0.58
26:DA:2263:C:N4	47:D0:15:ASP:OD1	2.36	0.58
26:DA:2637:U:H5"	29:DE:82:ARG:HH21	1.68	0.58
31:DG:113:ARG:NH1	31:DG:139:LEU:O	2.37	0.58
48:D1:3:LYS:HB2	48:D1:61:ARG:NH1	2.19	0.58
1:AA:557:G:OP1	61:AA:4060:HOH:O	2.17	0.58
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.31	0.58
2:AB:189:ASP:N	2:AB:189:ASP:OD1	2.32	0.58
9:AI:28:VAL:HG22	9:AI:63:ILE:HB	1.86	0.58
17:AQ:6:LEU:HG	17:AQ:23:VAL:HG11	1.86	0.58
26:BA:220:G:O2'	26:BA:233:A:N3	2.34	0.58
26:BA:2748:A:H5'	32:BH:4:ILE:HD12	1.84	0.58
42:BV:72:VAL:HG22	42:BV:85:LYS:HB3	1.84	0.58
1:CA:157:G:H1	1:CA:164:U:H3	1.50	0.58
1:CA:708:C:H2'	1:CA:709:G:C8	2.36	0.58
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.39	0.58
2:CB:186:ALA:O	2:CB:201:ILE:N	2.37	0.58
24:CX:23:C:H2'	24:CX:24:U:C6	2.39	0.58
26:DA:2000:G:N7	61:DA:4004:HOH:O	2.32	0.58
26:DA:2079:U:O3'	48:D1:35:THR:OG1	2.21	0.58
33:DI:49:ALA:HA	33:DI:52:ARG:HH22	1.68	0.58
1:AA:984:C:H2'	1:AA:985:C:H6	1.67	0.58
1:AA:1216:G:OP1	14:AN:2:ALA:HA	2.03	0.58
1:AA:1287:A:N1	1:AA:1370:G:N2	2.48	0.58
1:AA:1352:C:H2'	1:AA:1353:G:C8	2.39	0.58
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.85	0.58
26:BA:1954:G:O2'	26:BA:1956:U:O4	2.13	0.58
33:BI:93:THR:OG1	33:BI:96:ASP:OD1	2.14	0.58
44:BX:50:LYS:N	44:BX:87:GLN:OE1	2.33	0.58
46:BZ:117:LEU:HD11	46:BZ:144:LEU:HD13	1.86	0.58
54:B7:12:ARG:NH2	54:B7:44:PRO:HB3	2.19	0.58
1:CA:835:U:H3	1:CA:851:G:H1	1.52	0.58
4:CD:162:LEU:HD22	4:CD:178:VAL:HG13	1.86	0.58
8:CH:51:VAL:HG11	8:CH:60:ARG:HH12	1.67	0.58
26:DA:2586:C:OP2	26:DA:2608:G:N1	2.35	0.58
1:AA:613:C:H2'	1:AA:614:A:H8	1.69	0.58
1:AA:1028:C:H2'	1:AA:1029:C:O4'	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BP:50:ARG:HH21	55:B8:7:HIS:CD2	2.21	0.58
1:CA:21:G:H2'	1:CA:22:G:C8	2.39	0.58
1:CA:27:G:H2'	1:CA:28:G:C8	2.39	0.58
1:CA:516:U:O2'	1:CA:519:C:N3	2.32	0.58
1:CA:814:A:H2'	1:CA:816:A:H5"	1.85	0.58
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.19	0.58
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.85	0.58
26:DA:1169:G:H2'	26:DA:1170:G:C8	2.38	0.58
26:DA:1514:U:H2'	26:DA:1515:G:H8	1.69	0.58
26:DA:2301:C:H2'	26:DA:2302:G:H8	1.69	0.58
29:DE:111:ARG:HG3	29:DE:160:TYR:CD2	2.39	0.58
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.86	0.58
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.86	0.58
26:BA:1747(A):G:H2'	26:BA:1748:G:H5"	1.85	0.58
39:BS:28:VAL:HG11	39:BS:98:VAL:HG13	1.85	0.58
7:CG:27:ILE:HD12	7:CG:40:ALA:HA	1.86	0.58
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.86	0.58
24:CX:64:G:H4'	37:DQ:10:ARG:NH2	2.19	0.58
41:DU:108:GLU:O	41:DU:112:ARG:HG2	2.03	0.58
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.18	0.57
2:AB:87:ARG:NE	2:AB:233:SER:HB3	2.19	0.57
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.33	0.57
26:BA:309:G:N3	26:BA:329:G:O2'	2.36	0.57
26:BA:1300:U:H4'	26:BA:1301:A:C5'	2.33	0.57
1:CA:406:G:N3	4:CD:119:GLN:NE2	2.50	0.57
1:CA:600:C:H2'	1:CA:601:C:H6	1.69	0.57
1:CA:1003:G:H2'	1:CA:1004:A:H1'	1.86	0.57
8:CH:82:HIS:NE2	8:CH:84:ARG:HG2	2.19	0.57
26:DA:678:C:N3	26:DA:799:G:N1	2.42	0.57
26:DA:2233:U:H2'	26:DA:2234:G:C8	2.39	0.57
36:DP:29:LYS:HG3	36:DP:30:THR:N	2.18	0.57
1:AA:154:C:C2'	1:AA:155:C:H5'	2.33	0.57
1:AA:224:C:H2'	1:AA:225:C:C6	2.40	0.57
9:AI:19:LEU:HB3	9:AI:59:PHE:CD1	2.38	0.57
26:BA:2207:G:O2'	26:BA:2208:A:OP1	2.18	0.57
26:BA:2362:G:OP1	55:B8:44:LYS:NZ	2.36	0.57
39:BS:15:ARG:NE	39:BS:88:ASP:OD2	2.35	0.57
40:BT:11:GLU:OE1	40:BT:57:PHE:HB3	2.04	0.57
1:CA:999:C:N4	1:CA:1042:G:C6	2.71	0.57
1:CA:1027:C:N3	1:CA:1035:A:C2	2.72	0.57
20:CT:43:LEU:HD13	20:CT:51:GLU:HB3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:528:A:C2	26:DA:2042:A:H2'	2.39	0.57
26:DA:1014:U:H2'	26:DA:1015:G:C8	2.39	0.57
26:DA:1014:U:H2'	26:DA:1015:G:H8	1.69	0.57
26:DA:2384:G:OP2	47:D0:55:ARG:NH2	2.37	0.57
28:DD:206:LEU:O	28:DD:211:ARG:NE	2.34	0.57
36:DP:44:GLY:CA	36:DP:45:LEU:HB2	2.34	0.57
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.87	0.57
26:BA:1021:A:H3'	26:BA:1021:A:C8	2.38	0.57
43:BW:79:GLY:HA3	43:BW:100:THR:HG22	1.86	0.57
1:CA:279:A:H4'	1:CA:280:C:H5"	1.85	0.57
1:CA:677:U:H3	1:CA:713:G:H22	1.52	0.57
1:CA:880:C:OP1	12:CL:8:ASN:ND2	2.37	0.57
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.37	0.57
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.40	0.57
26:DA:1814:G:H4'	28:DD:51:VAL:HG21	1.86	0.57
35:DO:120:GLU:HB2	40:DT:68:TYR:HE2	1.70	0.57
44:DX:31:HIS:CD2	44:DX:33:LYS:HB2	2.39	0.57
1:AA:170:U:O2'	1:AA:171:A:H5'	2.05	0.57
4:AD:104:VAL:HG11	4:AD:146:ILE:HD13	1.85	0.57
13:AM:34:LEU:HD13	13:AM:41:PRO:HA	1.85	0.57
26:BA:848:G:H2'	26:BA:849:A:C8	2.40	0.57
26:BA:1833:U:O2'	26:BA:1969:A:N1	2.29	0.57
26:BA:2108:C:H2'	26:BA:2109:U:H6	1.69	0.57
1:CA:72:C:N4	1:CA:73:G:C5	2.72	0.57
1:CA:107:G:H2'	1:CA:108:G:O4'	2.05	0.57
1:CA:1029:C:N4	1:CA:1032:G:H1	2.02	0.57
2:CB:207:ALA:O	2:CB:210:SER:HB3	2.04	0.57
34:DN:121:LYS:HG2	34:DN:130:HIS:NE2	2.20	0.57
42:DV:78:LYS:HB3	61:DV:301:HOH:O	2.04	0.57
1:AA:160:A:N6	1:AA:345:C:OP2	2.37	0.57
26:BA:2138:C:C2	26:BA:2154:G:C2	2.93	0.57
27:BB:29:A:H2'	27:BB:30:C:C6	2.38	0.57
43:BW:14:PRO:HG2	43:BW:78:GLU:CD	2.30	0.57
1:CA:54:C:N4	1:CA:353:A:OP2	2.37	0.57
1:CA:1024:G:H2'	1:CA:1025:U:H5"	1.87	0.57
9:CI:23:ASN:ND2	9:CI:60:ASP:OD2	2.37	0.57
26:DA:57:C:H2'	26:DA:58:G:O4'	2.05	0.57
26:DA:2522:U:O2'	26:DA:2647:U:OP1	2.16	0.57
26:DA:2630:G:N2	26:DA:2788:C:O2	2.30	0.57
27:DB:50:G:OP1	39:DS:63:THR:N	2.37	0.57
1:AA:532:A:O2'	1:AA:533:A:OP1	2.16	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.03	0.57
26:BA:1405:U:H2'	26:BA:1406:U:C6	2.39	0.57
26:BA:2243:U:H2'	26:BA:2244:U:C6	2.39	0.57
1:CA:559:A:H4'	1:CA:560:U:H5"	1.87	0.57
1:CA:1027:C:C4	1:CA:1034:G:C2	2.93	0.57
1:CA:1148:U:H2'	1:CA:1149:C:O4'	2.04	0.57
26:DA:1171:G:N2	26:DA:1178:C:H42	2.03	0.57
26:DA:1794:U:H2'	26:DA:1795:C:C6	2.39	0.57
26:DA:2284:C:OP2	53:D6:2:ALA:N	2.38	0.57
33:DI:87:LYS:HA	33:DI:122:GLU:HA	1.86	0.57
1:AA:984:C:H2'	1:AA:985:C:C6	2.40	0.57
1:AA:1125:U:O2'	1:AA:1126:U:H5"	2.04	0.57
9:AI:23:ASN:HB2	9:AI:25:LYS:HE3	1.86	0.57
26:BA:994:C:OP1	41:BU:53:ARG:NH2	2.38	0.57
26:BA:1300:U:H4'	26:BA:1301:A:H5"	1.85	0.57
32:BH:86:GLU:OE2	32:BH:130:ARG:NH1	2.38	0.57
34:BN:70:LYS:HE3	34:BN:72:TYR:CZ	2.39	0.57
36:BP:52:GLU:OE1	36:BP:55:ARG:NH1	2.33	0.57
1:CA:1343:G:O2'	9:CI:121:ARG:HD2	2.04	0.57
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.85	0.57
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.29	0.57
26:DA:2136:C:H42	26:DA:2156:G:H1'	1.68	0.57
26:DA:2206:G:H3'	26:DA:2207:G:N7	2.18	0.57
26:DA:2741:A:H61	26:DA:2763:G:H1'	1.69	0.57
27:DB:29:A:C2	27:DB:30:C:C5	2.91	0.57
1:AA:78:G:N2	1:AA:91:C:C2	2.73	0.57
1:AA:250:A:H4'	1:AA:251:G:O5'	2.05	0.57
1:AA:839:U:H4'	1:AA:840:C:OP2	2.04	0.57
1:AA:1229:A:O2'	24:AX:30:G:OP1	2.23	0.57
9:AI:8:GLY:HA3	9:AI:76:ALA:O	2.05	0.57
49:B2:22:GLU:OE2	49:B2:68:ARG:NH2	2.38	0.57
2:CB:122:PHE:HA	2:CB:127:ILE:HD12	1.86	0.57
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.05	0.57
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.86	0.57
9:CI:22:GLY:N	9:CI:58:HIS:O	2.34	0.57
26:DA:530:G:C5	26:DA:2022:U:H5"	2.39	0.57
26:DA:603:A:N1	26:DA:625:G:O2'	2.37	0.57
26:DA:992:C:OP1	41:DU:47:TYR:OH	2.11	0.57
26:DA:1532:C:N3	26:DA:1537:G:N1	2.40	0.57
26:DA:2138:C:H2'	26:DA:2139:C:C6	2.40	0.57
26:DA:2646:C:OP2	26:DA:2732:G:O2'	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:953:G:H5'	1:AA:965:A:H61	1.69	0.57
1:AA:1036:G:H2'	1:AA:1036:G:N3	2.19	0.57
26:BA:644:A:H4'	26:BA:645:C:H5	1.70	0.57
34:BN:12:ARG:NH1	34:BN:50:ASP:OD2	2.38	0.57
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.86	0.57
26:DA:477:A:H2'	26:DA:478:A:C8	2.40	0.57
28:DD:51:VAL:HG11	28:DD:54:ARG:HH11	1.69	0.57
34:DN:42:TRP:HA	34:DN:48:MET:HE1	1.87	0.57
1:AA:269:C:H2'	1:AA:270:A:C8	2.39	0.57
1:AA:330:C:O2	61:AA:4093:HOH:O	2.15	0.57
1:AA:438:G:N1	1:AA:495:A:OP2	2.29	0.57
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.87	0.57
26:BA:839:U:H2'	26:BA:840:C:C6	2.39	0.57
26:BA:1019:U:H3	26:BA:1142(A):A:H62	1.51	0.57
26:BA:1859:A:N6	26:BA:1883:G:O2'	2.37	0.57
26:BA:2023:G:H5'	26:BA:2617:C:H4'	1.86	0.57
30:BF:195:ASP:HB3	30:BF:198:ALA:H	1.70	0.57
36:BP:63:PRO:HG2	55:B8:25:MET:HB2	1.87	0.57
1:CA:473:G:H2'	1:CA:474:G:C8	2.40	0.57
1:CA:920:U:H2'	1:CA:921:U:C6	2.40	0.57
1:CA:1492:A:H2'	1:CA:1493:A:C4	2.40	0.57
15:CO:64:ARG:HD3	15:CO:68:ARG:NH2	2.20	0.57
26:DA:277:C:O2'	26:DA:278:A:OP1	2.20	0.57
26:DA:286:C:H2'	26:DA:287:C:H6	1.69	0.57
26:DA:827:U:O2'	61:DA:4222:HOH:O	2.18	0.57
26:DA:1991:U:H2'	26:DA:1992:G:H5"	1.87	0.57
31:DG:47:LYS:HG2	31:DG:48:GLU:N	2.19	0.57
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.51	0.56
1:AA:1372:U:H2'	1:AA:1373:G:O4'	2.05	0.56
2:AB:167:PRO:HG3	2:AB:186:ALA:HB1	1.85	0.56
11:AK:48:ILE:O	11:AK:50:TYR:N	2.35	0.56
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.87	0.56
26:BA:1174:A:H4'	26:BA:1175:U:OP1	2.05	0.56
26:BA:2438:U:O2'	26:BA:2440:C:OP1	2.19	0.56
13:CM:68:GLY:HA3	31:DG:116:ASP:OD1	2.05	0.56
26:DA:387:U:OP2	48:D1:20:ARG:NH1	2.32	0.56
26:DA:536:A:H2'	26:DA:537:C:C6	2.40	0.56
26:DA:662:G:H5"	36:DP:16:ARG:HG2	1.86	0.56
26:DA:740:U:H2'	26:DA:741:G:C8	2.40	0.56
26:DA:2103:C:C2'	26:DA:2104:G:H5'	2.35	0.56
36:DP:39:LYS:HB2	36:DP:45:LEU:HG	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DP:64:LYS:HA	55:D8:13:ARG:HB3	1.85	0.56
1:AA:153:C:H42	1:AA:168:G:H1	1.53	0.56
9:AI:16:ARG:HB2	9:AI:64:THR:HB	1.87	0.56
26:BA:36:G:N3	26:BA:450:G:O2'	2.37	0.56
26:BA:831:G:N2	36:BP:53:GLY:O	2.38	0.56
26:BA:1788:C:OP1	28:BD:222:ARG:NH2	2.37	0.56
61:BA:3834:HOH:O	54:B7:34:ARG:NH2	2.38	0.56
45:BY:35:TYR:CE2	45:BY:69:ALA:HB3	2.40	0.56
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.03	0.56
26:DA:888:C:H2'	26:DA:889:C:C4	2.40	0.56
26:DA:889:C:O2'	26:DA:890:A:H8	1.88	0.56
26:DA:2774:C:H2'	26:DA:2775:A:O4'	2.06	0.56
27:DB:12:C:O2'	47:D0:74:ARG:HG2	2.05	0.56
1:AA:376:G:O2'	16:AP:5:ARG:NH2	2.38	0.56
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.05	0.56
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.41	0.56
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.70	0.56
20:AT:57:ARG:HH22	20:AT:100:ILE:HD11	1.70	0.56
26:BA:71:A:N7	44:BX:31:HIS:HE1	2.03	0.56
26:BA:531:C:OP2	61:BA:4510:HOH:O	2.17	0.56
26:BA:1239:G:H2'	26:BA:1240:U:O4'	2.05	0.56
26:BA:1252:G:O6	41:BU:36:ARG:HG2	2.04	0.56
26:BA:2483:C:N3	37:BQ:124:LYS:NZ	2.48	0.56
32:BH:40:GLU:OE1	32:BH:60:ARG:NH1	2.38	0.56
40:BT:95:ARG:HG2	40:BT:95:ARG:HH11	1.71	0.56
45:BY:86:ARG:NH1	45:BY:100:ALA:O	2.38	0.56
50:B3:7:LYS:HG3	50:B3:34:GLU:HG3	1.86	0.56
1:CA:1326:C:H5"	21:CU:18:TYR:O	2.06	0.56
4:CD:155:LEU:HD22	4:CD:157:LEU:H	1.70	0.56
6:CF:2:ARG:HH22	15:CO:2:PRO:HD2	1.71	0.56
6:CF:81:ILE:HD11	28:DD:125:ILE:HB	1.87	0.56
7:CG:9:VAL:O	7:CG:11:GLN:NE2	2.38	0.56
26:DA:752:A:H4'	26:DA:753:C:H5'	1.87	0.56
26:DA:860:U:H1'	26:DA:2268:A:H5'	1.87	0.56
30:DF:11:VAL:HG22	30:DF:125:LEU:HB2	1.86	0.56
1:AA:193:C:H2'	1:AA:194:C:H6	1.71	0.56
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.05	0.56
26:BA:2138:C:N3	26:BA:2153:G:N2	2.45	0.56
26:BA:2159:G:H2'	26:BA:2160:G:C8	2.41	0.56
26:BA:2648:C:H2'	26:BA:2649:U:C6	2.41	0.56
1:CA:93:G:H2'	1:CA:96:U:H6	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:195:A:N3	1:CA:222:U:O2'	2.39	0.56
1:CA:1030:C:N4	1:CA:1032:G:O6	2.38	0.56
3:CC:54:ARG:NH1	3:CC:54:ARG:HB3	2.21	0.56
26:DA:829:A:N7	26:DA:2248:C:H5'	2.21	0.56
26:DA:885:C:H3'	26:DA:886:C:H5"	1.87	0.56
26:DA:1794:U:H2'	26:DA:1795:C:H6	1.69	0.56
26:DA:2166:G:H3'	26:DA:2167:U:C5'	2.33	0.56
26:DA:2224:G:OP1	28:DD:268:ARG:NE	2.39	0.56
1:AA:21:G:H2'	1:AA:22:G:C8	2.40	0.56
1:AA:277:C:H5"	17:AQ:68:ARG:NH2	2.19	0.56
1:AA:858:G:O6	1:AA:869:G:H3'	2.06	0.56
26:BA:1432:C:H2'	26:BA:1433:U:O4'	2.05	0.56
1:CA:93:G:O2'	1:CA:96:U:H5'	2.05	0.56
1:CA:250:A:H4'	1:CA:251:G:O5'	2.04	0.56
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.20	0.56
4:CD:129:ASN:HD21	4:CD:144:ASP:CG	2.13	0.56
9:CI:53:VAL:C	9:CI:55:ALA:H	2.11	0.56
24:CX:15:G:H2'	24:CX:59:A:N6	2.21	0.56
26:DA:880:G:C2	26:DA:898:C:O2	2.59	0.56
26:DA:1131:G:O6	26:DA:2040:C:H1'	2.05	0.56
26:DA:2245:U:O2'	26:DA:2436:G:OP2	2.19	0.56
26:DA:2301:C:H2'	26:DA:2302:G:C8	2.40	0.56
26:DA:2458:G:O2'	26:DA:2460:U:O4	2.21	0.56
31:DG:19:LEU:HD13	31:DG:32:PRO:HG2	1.88	0.56
31:DG:46:ALA:HB2	31:DG:53:LEU:HD12	1.88	0.56
43:DW:11:ARG:HD2	43:DW:82:LEU:HD12	1.86	0.56
1:AA:542:G:H5'	4:AD:41:GLY:HA3	1.86	0.56
24:AX:8:4SU:O5'	24:AX:8:4SU:H6	2.04	0.56
26:BA:1028:A:H61	26:BA:1125:G:H2'	1.70	0.56
26:BA:1865:G:OP1	61:BA:4699:HOH:O	2.17	0.56
26:BA:2000:G:OP1	38:BR:5:LYS:NZ	2.38	0.56
26:BA:2125:G:H22	26:BA:2172:U:P	2.29	0.56
26:BA:2495:G:H5"	37:BQ:82:ARG:HG2	1.85	0.56
29:BE:97:LYS:N	29:BE:100:GLU:OE1	2.29	0.56
35:BO:16:ALA:HB2	35:BO:52:VAL:HG21	1.87	0.56
48:B1:3:LYS:O	48:B1:12:PRO:HD3	2.06	0.56
1:CA:1399:C:H4'	1:CA:1400:C:C5'	2.35	0.56
26:DA:517:C:OP1	52:D5:16:ARG:NH2	2.39	0.56
26:DA:922:U:H2'	26:DA:923:C:C6	2.40	0.56
26:DA:2103:C:H2'	26:DA:2104:G:H5'	1.87	0.56
29:DE:143:ASN:HD22	29:DE:147:PRO:HD3	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:D1:53:VAL:HG22	48:D1:74:VAL:HG13	1.86	0.56
1:AA:545:C:OP1	4:AD:61:LYS:NZ	2.37	0.56
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.40	0.56
26:BA:253:C:O2'	61:BA:4683:HOH:O	2.17	0.56
26:BA:411:G:C5	36:BP:72:PRO:HB3	2.40	0.56
26:BA:577:G:O2'	26:BA:1254:A:OP1	2.23	0.56
26:BA:875:G:H2'	26:BA:876:C:O4'	2.06	0.56
26:BA:1865:G:N2	26:BA:1877:A:OP2	2.34	0.56
26:BA:2690:C:OP1	38:BR:17:ARG:NH1	2.37	0.56
29:BE:111:ARG:HG3	29:BE:160:TYR:CD2	2.41	0.56
34:BN:15:LEU:HD12	34:BN:137:LYS:HG2	1.87	0.56
50:B3:23:LEU:HD13	50:B3:50:VAL:HG11	1.88	0.56
1:CA:601:C:H2'	1:CA:602:A:H8	1.71	0.56
1:CA:757:U:H2'	1:CA:758:G:O4'	2.05	0.56
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.41	0.56
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.86	0.56
26:DA:1366:A:H2'	26:DA:1367:A:O4'	2.06	0.56
27:DB:2:C:O2'	27:DB:3:C:H5'	2.06	0.56
30:DF:107:LYS:HD3	30:DF:206:ILE:HA	1.88	0.56
33:DI:97:ILE:O	33:DI:101:LEU:HB2	2.05	0.56
36:DP:121:LYS:HB3	36:DP:123:LEU:HG	1.87	0.56
26:BA:630:G:N2	26:BA:633:A:OP2	2.30	0.56
26:BA:2135:A:N6	26:BA:2156:G:N2	2.54	0.56
26:BA:2291:U:H2'	26:BA:2292:C:C6	2.41	0.56
40:BT:96:ARG:CZ	40:BT:96:ARG:HB3	2.35	0.56
1:CA:598:U:H2'	1:CA:599:C:C6	2.41	0.56
1:CA:953:G:H5'	1:CA:965:A:H61	1.69	0.56
1:CA:1417:G:O6	61:CA:4029:HOH:O	2.18	0.56
25:CY:76:A:N6	26:DA:2422:A:O4'	2.39	0.56
26:DA:583:G:OP2	41:DU:10:ARG:NH1	2.36	0.56
26:DA:1022:G:N7	34:DN:66:LYS:HE2	2.21	0.56
27:DB:1:U:O2'	27:DB:2:C:O5'	2.20	0.56
33:DI:129:THR:HG22	33:DI:139:GLN:NE2	2.20	0.56
2:AB:105:PHE:CE1	2:AB:155:LEU:HD12	2.40	0.56
2:AB:204:ASN:O	2:AB:210:SER:OG	2.14	0.56
14:AN:4:LYS:HA	14:AN:7:ILE:HG22	1.88	0.56
26:BA:443:A:H1'	26:BA:1201:C:O4'	2.06	0.56
32:BH:24:VAL:HG22	32:BH:35:VAL:HB	1.87	0.56
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.05	0.56
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.24	0.56
4:CD:64:LEU:HA	4:CD:67:ILE:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:49:PRO:HG2	9:CI:81:ILE:HG23	1.88	0.56
9:CI:53:VAL:HG21	9:CI:92:TYR:CZ	2.41	0.56
26:DA:11:G:H2'	26:DA:12:U:H5"	1.87	0.56
26:DA:323:G:C8	30:DF:171:PRO:HG3	2.41	0.56
26:DA:995:C:OP2	41:DU:54:LYS:NZ	2.36	0.56
32:DH:86:GLU:OE2	32:DH:132:ARG:NH2	2.39	0.56
36:DP:95:VAL:HG13	36:DP:125:VAL:HA	1.87	0.56
46:DZ:146:ILE:HA	46:DZ:174:VAL:HG11	1.88	0.56
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.86	0.56
1:AA:1006:C:N4	1:AA:1023:G:H1	2.01	0.56
12:AL:33:ARG:HD3	12:AL:62:SER:HB3	1.88	0.56
26:BA:583:G:OP2	41:BU:10:ARG:HD2	2.06	0.56
26:BA:784:A:C6	28:BD:229:VAL:HG11	2.41	0.56
26:BA:2074:U:H2'	26:BA:2075:U:C6	2.41	0.56
26:BA:2286:A:H4'	26:BA:2287:A:O4'	2.06	0.56
52:B5:16:ARG:NH1	52:B5:17:ASP:OD1	2.38	0.56
52:B5:16:ARG:HD2	52:B5:20:ARG:NH1	2.21	0.56
26:DA:2051:A:H5'	26:DA:2578:G:O4'	2.05	0.56
26:DA:2135:A:N6	26:DA:2156:G:C2	2.74	0.56
28:DD:132:PRO:HG2	28:DD:135:PHE:CD2	2.41	0.56
1:AA:147:G:N1	1:AA:148:G:C2	2.74	0.55
1:AA:473:G:H2'	1:AA:474:G:H8	1.71	0.55
1:AA:1106:G:H5"	3:AC:172:ARG:HG2	1.88	0.55
1:AA:1202:G:H1'	14:AN:29:ARG:HD2	1.88	0.55
1:AA:1320:C:H5'	19:AS:70:LYS:HG3	1.87	0.55
10:AJ:55:LYS:HE3	10:AJ:56:HIS:CE1	2.40	0.55
12:AL:70:ILE:HD13	12:AL:77:LEU:HD12	1.88	0.55
26:BA:2304:G:H22	26:BA:2312:U:H3	1.54	0.55
27:BB:11:C:H3'	27:BB:12:C:H6	1.69	0.55
1:CA:976:G:H22	1:CA:1363(A):A:H2'	1.71	0.55
3:CC:8:ILE:HG22	14:CN:49:HIS:O	2.07	0.55
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.05	0.55
8:CH:86:ILE:HG21	8:CH:133:LEU:HD13	1.88	0.55
15:CO:17:ARG:HH11	15:CO:17:ARG:HG3	1.71	0.55
26:DA:1010:A:H1'	26:DA:1153:C:H1'	1.86	0.55
26:DA:1037:G:H1	26:DA:1118:C:H42	1.54	0.55
26:DA:1710:C:H2'	26:DA:1711:C:C6	2.41	0.55
26:DA:2206:G:H3'	26:DA:2207:G:H8	1.70	0.55
26:DA:2682:U:O2'	40:DT:58:ASN:ND2	2.39	0.55
29:DE:72:VAL:CA	29:DE:73:GLU:HB3	2.36	0.55
33:DI:52:ARG:NH1	33:DI:52:ARG:H	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DY:28:LYS:HD2	45:DY:40:GLU:HG3	1.86	0.55
1:AA:636:U:H2'	1:AA:637:G:H8	1.70	0.55
1:AA:1053:G:N7	1:AA:1200:C:H5"	2.21	0.55
22:AV:15:A:O5'	22:AV:15:A:H8	1.89	0.55
26:BA:607:U:OP1	30:BF:102:PRO:HA	2.06	0.55
26:BA:657:U:H2'	26:BA:658:C:C6	2.41	0.55
26:BA:1012:U:C5	34:BN:28:THR:HG21	2.41	0.55
26:BA:2116:G:H22	26:BA:2162:G:P	2.30	0.55
26:BA:2529:G:O6	56:B9:31:LYS:NZ	2.39	0.55
26:BA:2839:G:H5'	38:BR:46:GLY:HA2	1.87	0.55
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.41	0.55
10:CJ:64:GLU:OE2	10:CJ:66:ARG:NH1	2.39	0.55
26:DA:2802:G:H2'	26:DA:2803:C:O4'	2.06	0.55
34:DN:17:ASP:OD1	34:DN:56:ASN:ND2	2.28	0.55
1:AA:975:A:N6	10:AJ:60:ARG:HH12	2.04	0.55
1:AA:1163:C:H2'	1:AA:1164:G:H5"	1.87	0.55
26:BA:488:G:O2'	43:BW:49:LYS:NZ	2.35	0.55
26:BA:1638:C:O3'	26:BA:2709:G:N2	2.39	0.55
26:BA:2393:A:O2'	55:B8:13:ARG:NH1	2.40	0.55
38:BR:56:LYS:NZ	38:BR:90:ARG:O	2.40	0.55
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.24	0.55
1:CA:877:C:O2	8:CH:3:THR:OG1	2.24	0.55
1:CA:1124:G:H5"	10:CJ:35:SER:OG	2.07	0.55
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.89	0.55
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.35	0.55
8:CH:86:ILE:HG13	8:CH:133:LEU:HD22	1.86	0.55
16:CP:72:ARG:HH21	16:CP:73:LEU:HD21	1.71	0.55
26:DA:618:C:H2'	26:DA:619:G:O4'	2.06	0.55
26:DA:874:G:H5'	26:DA:874:G:H8	1.72	0.55
26:DA:912:C:OP1	37:DQ:8:LYS:NZ	2.36	0.55
26:DA:2552:U:H2'	26:DA:2554:U:OP2	2.06	0.55
28:DD:127:VAL:HA	28:DD:193:VAL:HG22	1.88	0.55
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.06	0.55
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.06	0.55
4:AD:109:GLY:HA3	4:AD:165:MET:HG3	1.88	0.55
26:BA:1021:A:H3'	26:BA:1021:A:H8	1.72	0.55
26:BA:1204:A:N6	26:BA:1240:U:H2'	2.21	0.55
35:BO:10:VAL:HG13	35:BO:17:ARG:C	2.31	0.55
1:CA:93:G:H2'	1:CA:96:U:C6	2.41	0.55
1:CA:406:G:O2'	4:CD:3:ARG:NH2	2.40	0.55
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CE:8:GLU:OE2	5:CE:63:ARG:NH2	2.40	0.55
7:CG:115:ARG:HG2	7:CG:118:VAL:HG23	1.89	0.55
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.05	0.55
24:CX:16:C:H3'	24:CX:17:C:O2	2.06	0.55
24:CX:41:C:H2'	24:CX:42:G:H8	1.71	0.55
26:DA:2869:G:H2'	26:DA:2870:C:O4'	2.05	0.55
35:DO:64:ARG:NH1	35:DO:81:ASP:OD2	2.40	0.55
1:AA:70:G:H1	1:AA:99:U:H3	1.55	0.55
1:AA:562:C:N3	12:AL:16:GLU:HB3	2.22	0.55
9:AI:50:LEU:HD23	9:AI:81:ILE:HD11	1.87	0.55
13:AM:33:ALA:O	13:AM:37:THR:OG1	2.13	0.55
26:BA:651:G:OP1	55:B8:19:SER:OG	2.21	0.55
26:BA:1173:G:N2	26:BA:1177:A:OP2	2.34	0.55
28:BD:118:VAL:N	28:BD:129:ASN:OD1	2.35	0.55
41:BU:17:ILE:HG23	41:BU:39:LEU:HD12	1.87	0.55
1:CA:991:U:H3'	1:CA:1212:U:N3	2.21	0.55
1:CA:1024:G:C2'	1:CA:1025:U:H5"	2.36	0.55
1:CA:1065:U:P	1:CA:1190:G:H22	2.29	0.55
23:CW:76:PPU:H5'	23:CW:76:PPU:O	2.05	0.55
24:CX:66:C:H5"	24:CX:67:C:OP2	2.06	0.55
26:DA:1188:U:H4'	42:DV:79:VAL:HG22	1.88	0.55
26:DA:2296:U:OP2	39:DS:9:ARG:NH2	2.37	0.55
28:DD:242:ARG:N	28:DD:242:ARG:HD3	2.20	0.55
36:DP:55:ARG:HA	61:DP:307:HOH:O	2.06	0.55
1:AA:539:A:OP2	12:AL:115:LYS:NZ	2.40	0.55
1:AA:673:G:H2'	1:AA:674:G:C8	2.42	0.55
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.88	0.55
26:BA:1173:G:H22	26:BA:1177:A:P	2.28	0.55
26:BA:1721:G:H8	26:BA:1741:A:H62	1.53	0.55
44:BX:43:VAL:HG21	44:BX:81:VAL:HG11	1.89	0.55
46:BZ:102:LEU:HD23	46:BZ:139:VAL:HG21	1.89	0.55
1:CA:96:U:O2'	1:CA:97:G:O4'	2.24	0.55
1:CA:113:G:N3	1:CA:353:A:O2'	2.38	0.55
1:CA:971:G:N2	1:CA:1363(A):A:OP2	2.34	0.55
26:DA:796:C:H2'	26:DA:797:C:C6	2.41	0.55
26:DA:892:G:H2'	26:DA:893:C:O4'	2.07	0.55
26:DA:1803:A:H4'	28:DD:259:THR:HG23	1.89	0.55
26:DA:1939:U:OP1	26:DA:2604:U:O2'	2.20	0.55
26:DA:2176:A:H2'	26:DA:2177:C:C5	2.42	0.55
27:DB:40:U:N3	27:DB:44:G:OP2	2.38	0.55
31:DG:16:ARG:O	31:DG:20:ILE:HG13	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:28:G:O2'	1:AA:296:U:OP1	2.20	0.55
26:BA:463:G:N7	61:BA:4346:HOH:O	2.33	0.55
26:BA:645:C:H5'	26:BA:646:A:OP2	2.06	0.55
26:BA:684:G:OP1	54:B7:16:HIS:ND1	2.38	0.55
26:BA:1253:A:N6	61:BA:4106:HOH:O	2.19	0.55
33:BI:93:THR:HG22	33:BI:119:PRO:HB3	1.88	0.55
1:CA:1099:G:C6	1:CA:1100:C:N3	2.75	0.55
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.89	0.55
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.40	0.55
4:CD:161:ASN:O	4:CD:165:MET:N	2.39	0.55
26:DA:800:A:H8	26:DA:800:A:OP1	1.90	0.55
26:DA:2102:U:H3	26:DA:2187:G:H1	1.55	0.55
26:DA:2820:A:C6	38:DR:4:LEU:HD11	2.42	0.55
32:DH:89:ILE:O	32:DH:129:THR:HG23	2.07	0.55
33:DI:12:LEU:HD22	33:DI:19:VAL:HG21	1.89	0.55
1:AA:17:U:H2'	1:AA:18:C:C6	2.42	0.55
1:AA:69:G:H2'	1:AA:70:G:C8	2.41	0.55
1:AA:838:G:H1	1:AA:848:C:H42	1.55	0.55
1:AA:1036:G:H21	1:AA:1037:C:H1'	1.70	0.55
5:AE:7:GLU:OE1	5:AE:37:ARG:NH2	2.39	0.55
9:AI:31:GLN:HE21	9:AI:36:TYR:HA	1.71	0.55
26:BA:784:A:H5'	26:BA:785:G:OP1	2.07	0.55
26:BA:880:G:N2	26:BA:898:C:C2	2.75	0.55
30:BF:101:LEU:O	30:BF:106:ARG:NH1	2.39	0.55
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	1.88	0.55
17:CQ:6:LEU:HG	17:CQ:23:VAL:HG11	1.88	0.55
26:DA:298:G:H5"	26:DA:299:A:OP1	2.07	0.55
26:DA:729:G:H5'	26:DA:730:C:O5'	2.07	0.55
26:DA:1497:U:H5"	26:DA:1498:C:H5	1.71	0.55
26:DA:2867:G:OP2	40:DT:119:LYS:NZ	2.39	0.55
49:D2:18:PRO:HB3	49:D2:68:ARG:NH1	2.20	0.55
1:AA:659:U:C2'	1:AA:660:G:H5'	2.36	0.55
1:AA:1027:C:N3	1:AA:1034:G:C2	2.74	0.55
1:AA:1458:G:OP1	20:AT:35:THR:OG1	2.12	0.55
6:AF:67:MET:HE1	6:AF:75:LEU:HD12	1.89	0.55
20:AT:9:ASN:O	20:AT:10:LEU:HB2	2.05	0.55
26:BA:582:G:H2'	26:BA:583:G:C8	2.42	0.55
26:BA:2156:G:H21	26:BA:2158:A:H62	1.54	0.55
1:CA:97:G:O2'	1:CA:98:G:O4'	2.19	0.55
1:CA:1004:A:H5"	1:CA:1025:U:C5	2.42	0.55
1:CA:1250:A:H2'	1:CA:1251:A:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:43:LEU:HD21	3:CC:91:LEU:HD13	1.89	0.55
3:CC:47:LEU:O	3:CC:51:GLY:N	2.40	0.55
6:CF:70:ASP:OD1	6:CF:70:ASP:N	2.37	0.55
26:DA:1434:A:H61	26:DA:1558:A:N6	2.05	0.55
26:DA:2723:C:OP2	29:DE:109:LYS:NZ	2.40	0.55
44:DX:11:PRO:HB3	44:DX:92:LEU:HD11	1.88	0.55
1:AA:737:A:H2'	1:AA:738:C:C6	2.42	0.55
1:AA:1131:G:H2'	1:AA:1132:C:C6	2.42	0.55
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.05	0.55
2:AB:127:ILE:HD12	2:AB:130:ARG:HD3	1.88	0.55
3:AC:100:ALA:O	3:AC:102:ASN:ND2	2.40	0.55
26:BA:330:A:H2	26:BA:1210:A:C2'	2.20	0.55
46:BZ:19:ARG:NH1	46:BZ:84:GLU:O	2.36	0.55
1:CA:277:C:H5"	17:CQ:68:ARG:NH2	2.22	0.55
1:CA:627:G:H2'	1:CA:628:G:C8	2.39	0.55
1:CA:804:U:H5"	1:CA:805:C:OP2	2.07	0.55
26:DA:480:A:N3	26:DA:499:U:O2'	2.33	0.55
26:DA:784:A:C5	28:DD:229:VAL:HG21	2.41	0.55
27:DB:19:G:H2'	27:DB:20:C:O4'	2.06	0.55
1:AA:527:G:O2'	1:AA:535:A:N1	2.37	0.54
1:AA:954:G:H21	1:AA:1227:A:H62	1.55	0.54
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.07	0.54
2:AB:78:GLN:O	2:AB:94:ASN:ND2	2.40	0.54
26:BA:1899:G:H2'	26:BA:1899:G:N3	2.22	0.54
36:BP:100:LEU:HD12	36:BP:112:LEU:HD11	1.89	0.54
1:CA:979:C:H2'	1:CA:980:C:H5'	1.89	0.54
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.88	0.54
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.43	0.54
26:DA:2507:C:H2'	26:DA:2508:G:O4'	2.07	0.54
33:DI:52:ARG:H	33:DI:52:ARG:HH11	1.53	0.54
1:AA:139:G:N2	1:AA:224:C:O2	2.40	0.54
1:AA:537:G:H5"	12:AL:113:ARG:NH1	2.23	0.54
1:AA:1030:C:H5"	1:AA:1030(A):G:O5'	2.07	0.54
1:AA:1086:U:H2'	1:AA:1087:G:H8	1.72	0.54
24:AX:4:G:H2'	24:AX:5:G:H8	1.72	0.54
26:BA:687:C:H5"	54:B7:2:LYS:HE2	1.89	0.54
26:BA:1557:C:OP2	26:BA:1558:A:O2'	2.21	0.54
26:BA:2364:C:H2'	26:BA:2365:G:O4'	2.07	0.54
26:BA:2572:A:N7	29:BE:144:ARG:HD2	2.21	0.54
36:BP:121:LYS:HG3	50:D3:2:PRO:HG3	1.88	0.54
1:CA:49:U:O4	1:CA:365:U:H5	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1202:G:O4'	14:CN:29:ARG:NH1	2.41	0.54
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.07	0.54
26:DA:1038:C:N4	26:DA:1117:G:H1	2.05	0.54
26:DA:1753:G:OP2	40:DT:115:ARG:NH2	2.41	0.54
26:DA:2183:C:H2'	26:DA:2184:G:C8	2.39	0.54
27:DB:28:C:OP1	39:DS:31:SER:OG	2.17	0.54
31:DG:32:PRO:HB3	31:DG:172:LEU:HD22	1.90	0.54
37:DQ:26:TYR:O	37:DQ:67:ARG:NH1	2.35	0.54
1:AA:1149:C:P	9:AI:9:ARG:HH21	2.30	0.54
4:AD:85:LYS:HG3	4:AD:86:LYS:H	1.73	0.54
26:BA:636:G:OP1	36:BP:132:LYS:HE2	2.07	0.54
26:BA:637:A:H5"	36:BP:117:GLU:HG2	1.89	0.54
26:BA:2531:A:H5'	32:BH:157:TYR:CE1	2.42	0.54
1:CA:72:C:N4	1:CA:97:G:C2	2.73	0.54
1:CA:944:G:O2'	1:CA:1339:A:N6	2.41	0.54
1:CA:1251:A:O2'	1:CA:1369:C:O2'	2.23	0.54
24:CX:17:C:OP1	24:CX:60:U:O2'	2.24	0.54
26:DA:515:A:H1'	26:DA:581:C:H1'	1.89	0.54
26:DA:695:G:H4'	26:DA:1380:G:H5'	1.88	0.54
1:AA:1055:A:H8	1:AA:1055:A:H5'	1.72	0.54
26:BA:1791:A:H5'	28:BD:206:LEU:HD12	1.88	0.54
29:BE:29:GLY:HA3	61:BE:3106:HOH:O	2.07	0.54
34:BN:36:GLY:HA2	34:BN:38:HIS:CE1	2.43	0.54
38:BR:33:ARG:NH1	38:BR:115:GLU:OE2	2.35	0.54
46:BZ:54:HIS:ND1	46:BZ:101:PRO:HG3	2.23	0.54
50:B3:18:ASP:OD1	50:B3:18:ASP:N	2.41	0.54
1:CA:109:A:C6	1:CA:326:G:C6	2.95	0.54
1:CA:562:C:H1'	12:CL:15:ARG:HD2	1.90	0.54
1:CA:1000:U:H2'	1:CA:1001:A:C8	2.43	0.54
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.42	0.54
1:CA:1220:G:H5'	19:CS:34:TRP:O	2.07	0.54
13:CM:87:TYR:N	19:CS:73:GLU:O	2.40	0.54
26:DA:740:U:H2'	26:DA:741:G:H8	1.72	0.54
26:DA:1023:U:OP2	61:DA:4207:HOH:O	2.18	0.54
26:DA:2370:G:H2'	26:DA:2371:G:C8	2.42	0.54
26:DA:2396:G:OP1	48:D1:25:LYS:NZ	2.29	0.54
26:DA:2695:C:H2'	26:DA:2696:U:C6	2.43	0.54
30:DF:167:ALA:HB1	30:DF:173:VAL:HG11	1.87	0.54
40:DT:99:LEU:O	40:DT:101:PHE:N	2.40	0.54
1:AA:636:U:H2'	1:AA:637:G:C8	2.42	0.54
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.75	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:102:ASP:OD1	4:AD:103:ASN:N	2.41	0.54
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.23	0.54
20:AT:67:ALA:C	20:AT:69:GLY:H	2.16	0.54
26:BA:39:C:O2	30:BF:46:ARG:NH2	2.41	0.54
26:BA:330:A:HO2'	26:BA:331:A:H8	1.55	0.54
26:BA:642:G:N2	26:BA:645:C:OP2	2.41	0.54
26:BA:2431:U:O2'	26:BA:2433:A:N7	2.36	0.54
45:BY:15:VAL:HG21	45:BY:42:VAL:HG11	1.89	0.54
6:CF:67:MET:HE1	6:CF:75:LEU:HD12	1.89	0.54
7:CG:69:VAL:HG21	7:CG:104:LEU:HD11	1.89	0.54
26:DA:1889:A:H2'	26:DA:1890:A:C8	2.42	0.54
26:DA:2478:A:O2'	26:DA:2536:G:N2	2.40	0.54
26:DA:2818:G:OP2	38:DR:42:LYS:NZ	2.39	0.54
40:DT:24:PRO:HA	40:DT:49:VAL:HG22	1.89	0.54
46:DZ:154:ASP:OD1	46:DZ:154:ASP:N	2.41	0.54
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.33	0.54
26:BA:1796:U:H2'	26:BA:1797:C:C6	2.43	0.54
51:B4:55:ARG:N	51:B4:56:VAL:HA	2.23	0.54
53:B6:6:ARG:NH1	53:B6:26:ASN:HB2	2.23	0.54
5:CE:31:LEU:HD11	5:CE:129:ILE:HA	1.89	0.54
26:DA:993:G:N2	42:DV:23:GLU:OE2	2.39	0.54
28:DD:77:ALA:HA	28:DD:97:TYR:HA	1.88	0.54
28:DD:108:PRO:HG2	28:DD:111:LEU:HB2	1.89	0.54
29:DE:54:GLN:OE1	29:DE:55:ASN:N	2.40	0.54
1:AA:1460:A:H2'	1:AA:1461:G:O4'	2.07	0.54
11:AK:33:THR:HG22	11:AK:39:PRO:HA	1.90	0.54
26:BA:2532:G:O2'	26:BA:2657:A:N1	2.38	0.54
1:CA:664:G:H22	1:CA:741:G:H1	1.56	0.54
1:CA:1118:C:N3	1:CA:1156:G:N2	2.56	0.54
1:CA:1403:C:N4	22:CV:18:G:OP1	2.41	0.54
3:CC:172:ARG:NH2	3:CC:206:GLU:OE1	2.40	0.54
5:CE:137:GLU:HA	5:CE:140:ARG:HB3	1.89	0.54
26:DA:93:G:H2'	26:DA:94:C:C6	2.43	0.54
26:DA:492:A:H2'	26:DA:493:G:O4'	2.07	0.54
26:DA:2126:A:N3	26:DA:2127:G:H1'	2.22	0.54
44:DX:35:THR:HG22	44:DX:38:GLU:HB2	1.90	0.54
3:AC:153:VAL:HA	3:AC:197:GLY:O	2.08	0.54
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.42	0.54
26:BA:468:G:OP2	54:B7:37:LYS:NZ	2.41	0.54
28:BD:158:ALA:O	28:BD:161:THR:OG1	2.16	0.54
40:BT:24:PRO:HA	40:BT:49:VAL:HG22	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1027:C:N4	1:CA:1034:G:C6	2.76	0.54
1:CA:1262:C:N3	1:CA:1273:G:N2	2.49	0.54
10:CJ:38:ILE:HG13	10:CJ:38:ILE:O	2.07	0.54
26:DA:2138:C:N4	26:DA:2153:G:H1	2.03	0.54
26:DA:2544:G:H1'	26:DA:2646:C:H4'	1.89	0.54
1:AA:165:C:H2'	1:AA:166:G:C8	2.43	0.54
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.41	0.54
1:AA:791:G:N2	1:AA:1497:G:O3'	2.39	0.54
1:AA:975:A:H5'	1:AA:975:A:C8	2.41	0.54
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.72	0.54
18:AR:32:ARG:HA	18:AR:69:THR:HG21	1.90	0.54
26:BA:1107:G:H2'	26:BA:1107:G:N3	2.22	0.54
26:BA:1268:A:H2'	26:BA:1269:A:O4'	2.08	0.54
26:BA:1453:U:O2'	26:BA:1455:G:N7	2.41	0.54
26:BA:2791:C:C2	26:BA:2805:G:N2	2.76	0.54
36:BP:82:GLY:HA2	36:BP:113:LYS:O	2.08	0.54
45:BY:20:TYR:CE1	45:BY:43:ASN:HA	2.43	0.54
1:CA:1000:U:H2'	1:CA:1001:A:H8	1.70	0.54
1:CA:1120:G:N1	1:CA:1154:G:N3	2.55	0.54
13:CM:34:LEU:HD22	13:CM:39:ILE:HB	1.90	0.54
26:DA:880:G:H2'	26:DA:880:G:N3	2.23	0.54
26:DA:2405:G:OP1	36:DP:77:ARG:NH2	2.41	0.54
27:DB:105:A:OP1	46:DZ:72:ARG:NH1	2.41	0.54
1:AA:1151:A:O2'	1:AA:1152:A:H8	1.91	0.54
1:AA:1285:A:H4'	1:AA:1286:A:O5'	2.08	0.54
3:AC:120:VAL:HA	3:AC:123:GLN:HE21	1.73	0.54
26:BA:587:C:OP2	36:BP:21:ARG:NH2	2.41	0.54
26:BA:956:G:OP2	37:BQ:14:ARG:NH2	2.40	0.54
26:BA:2137:C:N3	26:BA:2154:G:O6	2.41	0.54
42:BV:74:LYS:HB2	42:BV:83:ARG:HB2	1.88	0.54
44:BX:54:VAL:HG22	44:BX:81:VAL:HG12	1.89	0.54
1:CA:501:C:H2'	1:CA:502:G:H8	1.72	0.54
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.72	0.54
26:DA:1966:A:H4'	26:DA:1967:C:OP1	2.08	0.54
26:DA:2135:A:H2'	26:DA:2136:C:C6	2.42	0.54
36:DP:99:LEU:HA	36:DP:102:ARG:HB3	1.90	0.54
51:D4:17:GLY:N	51:D4:33:VAL:O	2.41	0.54
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.20	0.53
1:AA:1505:G:O2'	22:AV:13:A:O2'	1.94	0.53
15:AO:24:SER:HB3	15:AO:27:VAL:HG23	1.89	0.53
26:BA:747:U:O2	26:BA:2014:A:H1'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:885:C:H3'	26:BA:886:C:C5'	2.38	0.53
26:BA:2267:A:H5"	26:BA:2268:A:H5'	1.90	0.53
35:BO:23:ARG:HG3	35:BO:24:VAL:N	2.23	0.53
40:BT:53:ARG:HB3	40:BT:53:ARG:NH1	2.23	0.53
1:CA:792:A:H4'	1:CA:793:U:C5'	2.39	0.53
1:CA:999:C:N3	1:CA:1042:G:C2	2.76	0.53
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.41	0.53
22:CV:18:G:N2	24:CX:34:C:C2	2.75	0.53
26:DA:2162:G:H5"	26:DA:2172:U:C6	2.43	0.53
26:DA:2505:G:OP1	61:DA:3855:HOH:O	2.18	0.53
27:DB:13:A:C2	27:DB:16:G:H1'	2.43	0.53
27:DB:54:G:N2	31:DG:29:TRP:HZ2	2.04	0.53
39:DS:58:LEU:HD12	39:DS:65:VAL:HG22	1.89	0.53
19:AS:27:GLU:HB3	19:AS:28:LYS:HB3	1.89	0.53
26:BA:7:G:H2'	26:BA:8:A:O4'	2.07	0.53
26:BA:1020:A:N1	26:BA:1141:U:O2'	2.40	0.53
26:BA:1047:G:N2	26:BA:1110:G:O2'	2.41	0.53
26:BA:2646:C:H2'	26:BA:2647:U:O4'	2.08	0.53
32:BH:3:ARG:HD3	32:BH:54:ARG:HH12	1.74	0.53
1:CA:154:C:H2'	1:CA:155:C:H5'	1.88	0.53
26:DA:71:A:N7	44:DX:31:HIS:HE1	2.06	0.53
36:DP:99:LEU:O	36:DP:103:ALA:N	2.39	0.53
1:AA:148:G:C2	1:AA:175:C:N3	2.77	0.53
1:AA:841:U:C5	1:AA:848:C:H1'	2.43	0.53
1:AA:1149:C:O2'	1:AA:1280:A:N1	2.31	0.53
2:AB:16:HIS:CB	2:AB:204:ASN:HB3	2.33	0.53
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.90	0.53
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	1.89	0.53
26:BA:2337:G:OP1	61:BA:4006:HOH:O	2.18	0.53
26:BA:2801(A):A:H5"	26:BA:2802:G:C8	2.43	0.53
1:CA:229:U:O2'	16:CP:23:ASP:OD2	2.25	0.53
1:CA:578:C:O2'	1:CA:728:A:N3	2.41	0.53
1:CA:636:U:H2'	1:CA:637:G:H8	1.73	0.53
13:CM:62:ASN:HA	51:D4:49:PHE:HD2	1.73	0.53
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.07	0.53
26:DA:299:A:N1	26:DA:322:A:O2'	2.32	0.53
26:DA:307:G:H21	26:DA:330:A:H62	1.55	0.53
26:DA:1009:A:OP2	34:DN:37:LYS:NZ	2.29	0.53
26:DA:1239:G:H2'	26:DA:1240:U:O4'	2.08	0.53
26:DA:1588:C:H2'	26:DA:1589:C:H6	1.74	0.53
26:DA:2023:G:H1	26:DA:2040:C:H42	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2247:A:H2'	26:DA:2248:C:C6	2.44	0.53
38:DR:55:ALA:HB2	38:DR:79:LEU:HD13	1.90	0.53
1:AA:358:U:H2'	1:AA:359:U:C6	2.43	0.53
1:AA:460:G:N1	1:AA:470:C:H5'	2.23	0.53
1:AA:797:C:C2'	1:AA:798:G:H5'	2.38	0.53
1:AA:805:C:OP2	61:AA:4031:HOH:O	2.19	0.53
20:AT:65:LYS:HA	20:AT:68:LYS:HD3	1.89	0.53
26:BA:467:G:OP1	54:B7:33:ARG:NH1	2.41	0.53
26:BA:2782:G:OP2	61:BA:4674:HOH:O	2.18	0.53
1:CA:377:G:OP1	16:CP:3:LYS:HD2	2.07	0.53
1:CA:709:G:C2'	1:CA:710:G:H5'	2.38	0.53
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.24	0.53
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.43	0.53
11:CK:43:SER:HA	11:CK:47:VAL:HG21	1.91	0.53
19:CS:27:GLU:HB3	19:CS:28:LYS:HB3	1.90	0.53
26:DA:698:C:O2'	26:DA:734:A:N6	2.42	0.53
26:DA:1639:U:H2'	26:DA:1640:C:H5"	1.88	0.53
26:DA:1876:A:H2'	26:DA:1877:A:C8	2.44	0.53
26:DA:1933:G:H2'	26:DA:1934:C:O4'	2.08	0.53
27:DB:98:G:H2'	27:DB:99:G:O4'	2.08	0.53
46:DZ:70:LEU:O	46:DZ:89:PHE:N	2.32	0.53
46:DZ:120:ILE:H	46:DZ:120:ILE:HD12	1.72	0.53
1:AA:392:G:H2'	1:AA:393:A:H8	1.73	0.53
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.23	0.53
26:BA:1009:A:OP2	34:BN:37:LYS:NZ	2.29	0.53
26:BA:1175:U:H1'	26:BA:1176:G:OP1	2.08	0.53
1:CA:1178:G:N2	1:CA:1180:A:H3'	2.23	0.53
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.73	0.53
4:CD:173:TRP:CD2	4:CD:189:PRO:HG3	2.43	0.53
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.89	0.53
17:CQ:59:ILE:HG22	17:CQ:73:VAL:HA	1.89	0.53
26:DA:623:G:H2'	26:DA:624:C:C6	2.44	0.53
26:DA:839:U:H2'	26:DA:840:C:C6	2.43	0.53
26:DA:1278:A:OP1	38:DR:36:THR:HG23	2.09	0.53
26:DA:2247:A:H2'	26:DA:2248:C:H6	1.73	0.53
26:DA:2849:U:OP2	40:DT:95:ARG:NH1	2.41	0.53
27:DB:29:A:C2	27:DB:56:G:C2	2.97	0.53
33:DI:81:VAL:O	33:DI:82:ARG:HG3	2.08	0.53
36:DP:100:LEU:HD12	36:DP:112:LEU:HD11	1.89	0.53
37:DQ:52:VAL:O	37:DQ:56:ARG:HB2	2.07	0.53
1:AA:947:G:N2	1:AA:1235:U:O2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1499:A:H1'	1:AA:1520:G:H5'	1.91	0.53
2:AB:231:GLU:HB2	2:AB:232:PRO:HD3	1.91	0.53
3:AC:7:PRO:O	3:AC:11:ARG:NH1	2.42	0.53
7:AG:29:LYS:HB3	7:AG:105:VAL:HG21	1.90	0.53
11:AK:98:LEU:O	11:AK:101:SER:OG	2.15	0.53
26:BA:414:C:H2'	26:BA:415:A:H8	1.73	0.53
26:BA:2031:A:C6	26:BA:2498:C:H1'	2.43	0.53
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.08	0.53
7:CG:72:ARG:NE	7:CG:142:GLU:OE2	2.42	0.53
9:CI:24:GLY:HA2	9:CI:59:PHE:O	2.09	0.53
24:CX:12:G:H4'	26:DA:1908:C:O2	2.08	0.53
26:DA:1750:G:N3	26:DA:2860:A:H2	2.06	0.53
26:DA:1833:U:O2'	26:DA:1969:A:N1	2.35	0.53
26:DA:2086:U:H2'	26:DA:2087:G:C8	2.44	0.53
26:DA:2659:G:N2	26:DA:2661:G:H5"	2.23	0.53
33:DI:124:GLY:O	33:DI:144:VAL:HB	2.08	0.53
36:DP:84:ASN:OD1	36:DP:117:GLU:HB2	2.09	0.53
1:AA:1030(D):A:N6	1:AA:1031:G:H21	2.07	0.53
1:AA:1456:G:H22	20:AT:43:LEU:HD11	1.74	0.53
24:AX:8:4SU:O2	24:AX:21:A:H2	1.91	0.53
26:BA:1587:A:H2'	26:BA:1588:C:C6	2.43	0.53
26:BA:1607:C:H4'	26:BA:1608:A:O5'	2.08	0.53
26:BA:2308:G:O2'	26:BA:2310:A:N7	2.41	0.53
10:CJ:78:ASN:O	10:CJ:80:LYS:N	2.41	0.53
13:CM:122:LYS:HD3	13:CM:123:ALA:H	1.73	0.53
26:DA:18:C:H2'	26:DA:19:C:H6	1.73	0.53
45:DY:14:LEU:N	45:DY:73:ARG:O	2.36	0.53
53:D6:9:LEU:HA	53:D6:54:ILE:HB	1.89	0.53
1:AA:542:G:P	4:AD:10:ARG:HH22	2.32	0.53
1:AA:828:A:H2'	1:AA:829:G:O4'	2.09	0.53
16:AP:19:ILE:HG22	16:AP:37:GLY:C	2.34	0.53
17:AQ:21:VAL:N	17:AQ:42:TYR:O	2.36	0.53
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.07	0.53
26:BA:826:U:H4'	36:BP:55:ARG:HB2	1.90	0.53
26:BA:884:C:H2'	26:BA:885:C:O4'	2.08	0.53
26:BA:1359:A:N6	26:BA:1372:U:C2	2.76	0.53
26:BA:2239:G:H5'	28:BD:251:GLY:HA3	1.90	0.53
26:BA:2441:C:OP2	26:BA:2586:C:O2'	2.23	0.53
26:BA:2695:C:H2'	26:BA:2696:U:H6	1.74	0.53
33:BI:80:PRO:HA	33:BI:145:VAL:O	2.08	0.53
33:BI:102:SER:HA	33:BI:106:GLY:HA3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BY:92:ASN:N	45:BY:93:GLY:HA2	2.23	0.53
1:CA:1003:G:O3'	1:CA:1004:A:H4'	2.09	0.53
1:CA:1027:C:N3	1:CA:1034:G:N2	2.57	0.53
1:CA:1297:C:H4'	1:CA:1298:C:H5"	1.91	0.53
26:DA:143:G:H2'	26:DA:143(A):C:C6	2.43	0.53
26:DA:746:A:O2'	26:DA:2611:U:O2'	2.26	0.53
26:DA:1212:G:H1'	26:DA:1236:G:N2	2.24	0.53
26:DA:1514:U:H2'	26:DA:1515:G:C8	2.44	0.53
26:DA:2312:U:H5'	31:DG:88:ILE:HD11	1.89	0.53
30:DF:192:LEU:HD13	30:DF:194:MET:HE2	1.89	0.53
38:DR:1:MET:HE3	38:DR:3:HIS:CE1	2.43	0.53
38:DR:33:ARG:NH2	52:D5:57:VAL:O	2.37	0.53
1:AA:713:G:H2'	1:AA:714:G:C8	2.43	0.53
1:AA:1025:U:C2	1:AA:1036:G:O6	2.62	0.53
1:AA:1189:C:H5"	3:AC:5:ILE:HD12	1.91	0.53
17:AQ:56:VAL:HB	17:AQ:78:GLU:HB3	1.91	0.53
26:BA:1419:A:O2'	26:BA:1421:G:N7	2.40	0.53
27:BB:30:C:H2'	27:BB:31:C:H5'	1.91	0.53
1:CA:390:C:H2'	1:CA:391:G:C8	2.44	0.53
1:CA:501:C:H2'	1:CA:502:G:C8	2.43	0.53
6:CF:100:ASN:HD21	18:CR:23:LYS:HG2	1.74	0.53
8:CH:103:VAL:HG21	8:CH:110:ALA:HB2	1.89	0.53
18:CR:47:THR:HG23	18:CR:49:LYS:HG3	1.90	0.53
26:DA:307:G:N1	26:DA:310:A:OP2	2.38	0.53
26:DA:531:C:H4'	26:DA:532:A:H5"	1.91	0.53
26:DA:656:G:H2'	26:DA:657:U:O4'	2.09	0.53
26:DA:1276:A:HO2'	38:DR:12:ARG:HH21	1.55	0.53
34:DN:46:VAL:HG23	34:DN:48:MET:HG2	1.91	0.53
43:DW:18:ARG:NH1	43:DW:76:VAL:O	2.42	0.53
1:AA:401:C:OP2	4:AD:73:ARG:NH1	2.42	0.53
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.39	0.53
1:AA:1125:U:C4'	10:AJ:5:ARG:HH22	2.21	0.53
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.08	0.53
4:AD:162:LEU:HB3	4:AD:178:VAL:HG13	1.90	0.53
13:AM:80:ARG:HH21	51:B4:58:ARG:NH1	2.07	0.53
19:AS:69:HIS:H	51:B4:58:ARG:HH21	1.57	0.53
26:BA:667:U:O2	55:B8:2:PRO:HD2	2.09	0.53
26:BA:1786:A:H1'	26:BA:1938:A:H61	1.74	0.53
26:BA:1792:G:O2'	26:BA:1830:C:OP1	2.22	0.53
26:BA:2405:G:O2'	26:BA:2411:A:N6	2.41	0.53
32:BH:101:ARG:NH2	32:BH:117:PRO:HB2	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BS:83:LYS:HD2	39:BS:111:GLU:OE1	2.09	0.53
2:CB:19:HIS:CG	2:CB:20:GLU:H	2.27	0.53
13:CM:4:ILE:HD11	13:CM:60:VAL:HG11	1.91	0.53
26:DA:459:U:H5"	54:D7:40:TRP:CD2	2.44	0.53
26:DA:1292:U:H2'	26:DA:1293:C:C6	2.44	0.53
26:DA:2193:G:H2'	26:DA:2194:G:C8	2.44	0.53
26:DA:2667:C:H1'	32:DH:109:PHE:CD1	2.44	0.53
32:DH:3:ARG:NH2	32:DH:5:GLY:H	2.07	0.53
1:AA:390:C:H2'	1:AA:391:G:C8	2.43	0.52
1:AA:581:G:N2	1:AA:760:G:N7	2.56	0.52
1:AA:861:G:HO2'	1:AA:874:G:HO2'	1.48	0.52
14:AN:29:ARG:HD3	14:AN:40:CYS:SG	2.49	0.52
26:BA:2630:G:H2'	26:BA:2631:G:C8	2.44	0.52
27:BB:105:A:OP1	46:BZ:72:ARG:NH1	2.42	0.52
36:BP:95:VAL:HG13	36:BP:125:VAL:HG12	1.91	0.52
39:BS:14:VAL:O	39:BS:18:ILE:HG12	2.09	0.52
1:CA:97:G:C2	1:CA:98:G:C4	2.97	0.52
1:CA:284:G:H2'	1:CA:285:G:C8	2.44	0.52
8:CH:23:SER:HB2	8:CH:60:ARG:HG2	1.91	0.52
26:DA:470:A:OP1	30:DF:59:TYR:HE1	1.91	0.52
26:DA:571:A:N6	26:DA:2499:C:O3'	2.41	0.52
26:DA:1022:G:H22	26:DA:1142(A):A:H2	1.54	0.52
26:DA:2167:U:H2'	26:DA:2168:G:H21	1.74	0.52
31:DG:73:ALA:HB3	31:DG:84:LYS:HA	1.91	0.52
42:DV:5:VAL:HG11	42:DV:57:VAL:HG21	1.91	0.52
43:DW:34:ASN:OD1	43:DW:37:ARG:NH2	2.42	0.52
1:AA:396:G:O6	61:AA:4041:HOH:O	2.18	0.52
1:AA:524:G:H2'	1:AA:525:C:C6	2.44	0.52
1:AA:1191:A:H5"	3:AC:4:LYS:NZ	2.23	0.52
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.45	0.52
26:BA:34:C:H41	26:BA:447:A:H61	1.56	0.52
26:BA:1035:U:H2'	26:BA:1036:G:C8	2.44	0.52
26:BA:1296:G:OP1	26:BA:2709:G:O2'	2.21	0.52
26:BA:1570:A:H2'	26:BA:1571:A:C8	2.43	0.52
26:BA:1688:U:O2	26:BA:1700:A:H5'	2.09	0.52
26:BA:2224:G:H4'	26:BA:2226:C:C2	2.44	0.52
1:CA:1002:G:H2'	1:CA:1003:G:H8	1.73	0.52
1:CA:1055:A:O2'	3:CC:161:GLU:O	2.24	0.52
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.09	0.52
26:DA:363(B):G:H2'	26:DA:363(C):G:C8	2.43	0.52
26:DA:900:A:H2'	26:DA:901:A:O4'	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1503:U:H2'	26:DA:1504:C:C6	2.45	0.52
26:DA:2343:C:H4'	26:DA:2373:G:O3'	2.09	0.52
26:DA:2523:G:N3	26:DA:2764:A:O2'	2.42	0.52
27:DB:41:U:O4	31:DG:70:VAL:HB	2.09	0.52
33:DI:77:LEU:HA	33:DI:104:GLN:OE1	2.09	0.52
34:DN:58:ASP:OD1	34:DN:58:ASP:N	2.39	0.52
37:DQ:85:LYS:N	37:DQ:85:LYS:HD2	2.24	0.52
45:DY:86:ARG:NH1	45:DY:100:ALA:O	2.42	0.52
47:D0:50:ASN:HB3	47:D0:63:VAL:HG22	1.91	0.52
51:D4:60:GLN:H	51:D4:62:ARG:HE	1.57	0.52
1:AA:154:C:H2'	1:AA:155:C:H5'	1.90	0.52
1:AA:167:G:H2'	1:AA:168:G:H8	1.73	0.52
1:AA:530:G:O6	22:AV:21:C:H1'	2.10	0.52
1:AA:1164:G:N2	1:AA:1165:C:C4	2.75	0.52
1:AA:1349:A:OP2	9:AI:118:LYS:NZ	2.34	0.52
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.44	0.52
4:AD:196:LEU:C	4:AD:198:VAL:H	2.17	0.52
26:BA:1952:A:N3	26:BA:2560:C:O2'	2.40	0.52
26:BA:2199:A:OP2	26:BA:2200:C:H5	1.92	0.52
26:BA:2679:A:H4'	29:BE:165:VAL:HG11	1.92	0.52
45:BY:54:LYS:H	45:BY:56:PRO:HD3	1.73	0.52
1:CA:34:C:H2'	1:CA:35:G:H8	1.73	0.52
1:CA:662:G:H2'	1:CA:663:A:C8	2.44	0.52
1:CA:1216:G:H5"	14:CN:5:ALA:CB	2.39	0.52
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.45	0.52
1:CA:1370:G:N7	9:CI:109:VAL:HG11	2.24	0.52
16:CP:23:ASP:OD1	16:CP:25:ARG:HD3	2.09	0.52
26:DA:537:C:OP1	34:DN:2:LYS:NZ	2.43	0.52
26:DA:2035:G:P	26:DA:2036:C:H41	2.32	0.52
28:DD:17:THR:O	28:DD:211:ARG:NH2	2.42	0.52
28:DD:152:GLY:O	28:DD:154:LYS:HG2	2.10	0.52
30:DF:11:VAL:HB	30:DF:18:ARG:HB3	1.91	0.52
45:DY:13:VAL:HB	45:DY:72:VAL:HG13	1.92	0.52
1:AA:299:G:H2'	1:AA:300:A:C8	2.45	0.52
1:AA:792:A:H4'	1:AA:793:U:H5"	1.92	0.52
14:AN:26:ARG:HD3	14:AN:43:CYS:SG	2.50	0.52
26:BA:253:C:OP2	55:B8:5:LYS:NZ	2.31	0.52
26:BA:302:C:OP2	45:BY:73:ARG:NH2	2.41	0.52
26:BA:796:C:H2'	26:BA:797:C:C6	2.45	0.52
26:BA:1047:G:O2'	26:BA:1109:C:N4	2.42	0.52
26:BA:2135:A:H61	26:BA:2156:G:N2	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2312:U:H5'	31:BG:88:ILE:HD11	1.91	0.52
1:CA:43:C:H2'	1:CA:44:G:O4'	2.10	0.52
1:CA:632:A:H5'	1:CA:633:G:OP2	2.09	0.52
1:CA:1305:G:H5"	21:CU:4:GLY:HA3	1.90	0.52
1:CA:1347:G:HO2'	1:CA:1373:G:H1	1.54	0.52
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.91	0.52
22:CV:15:A:H8	22:CV:15:A:O5'	1.92	0.52
26:DA:275:G:H2'	26:DA:276:A:O4'	2.08	0.52
26:DA:1512:U:H2'	26:DA:1513:C:C6	2.44	0.52
35:DO:2:ILE:HD12	35:DO:6:THR:HG21	1.91	0.52
1:AA:269:C:H2'	1:AA:270:A:H8	1.75	0.52
12:AL:84:LEU:HB2	12:AL:105:TYR:CE2	2.45	0.52
16:AP:57:ARG:HH21	16:AP:79:VAL:HA	1.75	0.52
28:BD:34:VAL:HG12	28:BD:63:ARG:HG3	1.91	0.52
46:BZ:121:HIS:HB2	46:BZ:171:ILE:HG22	1.92	0.52
1:CA:1011:G:H1	1:CA:1018:C:N4	2.08	0.52
1:CA:1029:C:N4	1:CA:1032:G:C6	2.76	0.52
1:CA:1035:A:C2	1:CA:1036:G:N7	2.78	0.52
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.45	0.52
2:CB:96:ARG:CZ	2:CB:98:LEU:HD13	2.40	0.52
8:CH:112:LEU:HB3	8:CH:133:LEU:HA	1.90	0.52
26:DA:529:A:OP2	34:DN:114:ARG:NH2	2.41	0.52
26:DA:1717:G:N2	26:DA:1745:C:O2	2.43	0.52
26:DA:1779:U:H2'	61:DA:4364:HOH:O	2.09	0.52
28:DD:51:VAL:HG11	28:DD:54:ARG:NH1	2.24	0.52
1:AA:911:U:OP2	12:AL:97:ARG:NH1	2.42	0.52
1:AA:1169:A:OP2	1:AA:1169:A:H8	1.92	0.52
1:AA:1224:G:O2'	1:AA:1322:C:OP1	2.21	0.52
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.33	0.52
19:AS:69:HIS:H	51:B4:58:ARG:NH2	2.08	0.52
23:AW:76:PPU:O	23:AW:76:PPU:H5'	2.10	0.52
26:BA:1359:A:N1	26:BA:1372:U:C4	2.76	0.52
26:BA:1826:G:H4'	28:BD:242:ARG:CZ	2.39	0.52
26:BA:2114:A:H2'	26:BA:2115:G:O4'	2.09	0.52
39:BS:39:ILE:HB	39:BS:49:VAL:HG13	1.91	0.52
1:CA:382:A:H2'	1:CA:383:A:C8	2.44	0.52
1:CA:745:C:OP1	1:CA:852:G:H5'	2.10	0.52
1:CA:989:C:N4	1:CA:1216:G:O6	2.43	0.52
1:CA:1107:C:OP1	3:CC:173:VAL:N	2.42	0.52
1:CA:1124:G:H4'	1:CA:1125:U:O2	2.10	0.52
1:CA:1493:A:H5"	1:CA:1494:G:OP2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.91	0.52
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.73	0.52
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.10	0.52
26:DA:781:A:C8	28:DD:219:PRO:HG3	2.44	0.52
26:DA:1032:A:O2'	26:DA:1034:G:OP2	2.24	0.52
26:DA:1405:U:H2'	26:DA:1406:U:C6	2.45	0.52
26:DA:2274:A:O2'	26:DA:2276:G:OP1	2.24	0.52
26:DA:2364:C:H2'	26:DA:2365:G:O4'	2.09	0.52
26:DA:2773:C:OP1	29:DE:166:THR:OG1	2.27	0.52
30:DF:155:LEU:HD11	30:DF:176:LEU:HD12	1.90	0.52
33:DI:88:ILE:HG22	33:DI:123:LEU:HD23	1.92	0.52
38:DR:44:LEU:HD22	38:DR:48:VAL:HG23	1.92	0.52
1:AA:119:A:H4'	1:AA:120:A:C8	2.45	0.52
1:AA:178:C:H2'	1:AA:179:A:H8	1.75	0.52
1:AA:1009:G:O6	1:AA:1020:U:O4	2.27	0.52
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.09	0.52
26:BA:528:A:C2	26:BA:2042:A:H2'	2.45	0.52
26:BA:2805:G:H2'	26:BA:2807:G:H8	1.74	0.52
1:CA:109:A:H2'	1:CA:326:G:N2	2.24	0.52
1:CA:190:U:H2'	1:CA:191:G:C8	2.45	0.52
1:CA:197:A:C6	1:CA:221:C:H4'	2.45	0.52
1:CA:540:G:H2'	1:CA:541:G:O4'	2.10	0.52
1:CA:604:G:H2'	1:CA:605:U:O4'	2.10	0.52
1:CA:1002:G:N3	1:CA:1003:G:H8	2.07	0.52
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.24	0.52
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.27	0.52
5:CE:83:GLU:HG2	5:CE:88:LYS:HG3	1.91	0.52
26:DA:686:G:N2	26:DA:788:A:H61	2.06	0.52
26:DA:1815:A:OP2	28:DD:54:ARG:NH2	2.41	0.52
26:DA:2366:A:H2'	26:DA:2367:G:O4'	2.09	0.52
31:DG:17:PRO:HA	31:DG:20:ILE:HD12	1.91	0.52
34:DN:16:ILE:HB	34:DN:54:VAL:HG22	1.91	0.52
35:DO:115:VAL:HG13	35:DO:121:VAL:HG21	1.91	0.52
45:DY:86:ARG:HB2	45:DY:98:VAL:HG23	1.92	0.52
50:D3:10:LYS:HB3	50:D3:53:LEU:HA	1.91	0.52
1:AA:276:G:O3'	17:AQ:68:ARG:NH1	2.43	0.52
1:AA:663:A:O3'	18:AR:64:ARG:NH2	2.43	0.52
1:AA:683:G:H2'	1:AA:684:A:C8	2.44	0.52
1:AA:973:G:OP1	10:AJ:57:LYS:NZ	2.43	0.52
1:AA:1005:A:C1'	1:AA:1036:G:H22	2.23	0.52
56:B9:7:VAL:HG12	56:B9:34:GLN:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1278:U:H5'	1:CA:1279:A:O4'	2.09	0.52
1:CA:1367:C:HO2'	10:CJ:48:THR:HG1	1.56	0.52
2:CB:137:ARG:O	2:CB:141:GLU:N	2.37	0.52
4:CD:19:LEU:HD21	4:CD:63:LYS:HG3	1.90	0.52
4:CD:128:VAL:HG12	4:CD:129:ASN:HD22	1.75	0.52
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.92	0.52
11:CK:21:ILE:HD12	11:CK:84:VAL:HG22	1.92	0.52
26:DA:2572:A:C8	29:DE:144:ARG:HD2	2.44	0.52
38:DR:31:HIS:C	38:DR:33:ARG:H	2.17	0.52
1:AA:1371:G:O3'	9:AI:69:GLY:HA3	2.10	0.52
26:BA:271(M):G:H4'	26:BA:271(N):U:OP1	2.10	0.52
26:BA:764:A:O4'	28:BD:213:ARG:HG3	2.10	0.52
28:BD:26:LYS:HB3	28:BD:83:GLU:HG2	1.91	0.52
1:CA:152:A:N6	1:CA:169:C:N3	2.56	0.52
1:CA:811:C:O2'	1:CA:901:A:N1	2.39	0.52
1:CA:1399:C:C2	1:CA:1502:A:N6	2.78	0.52
5:CE:6:PHE:HB2	5:CE:34:VAL:HG22	1.91	0.52
5:CE:143:ARG:NH1	8:CH:77:GLU:OE2	2.43	0.52
6:CF:7:ASN:HB2	6:CF:89:MET:HB3	1.92	0.52
26:DA:18:C:H2'	26:DA:19:C:C6	2.45	0.52
26:DA:607:U:OP1	30:DF:102:PRO:HA	2.09	0.52
29:DE:2:LYS:HB2	29:DE:95:ILE:HD12	1.92	0.52
31:DG:106:LEU:HA	31:DG:110:ALA:HB3	1.90	0.52
39:DS:25:ARG:NE	39:DS:88:ASP:OD2	2.29	0.52
40:DT:24:PRO:HD3	40:DT:52:ILE:HD12	1.92	0.52
48:D1:23:LYS:HB3	48:D1:29:GLY:HA3	1.92	0.52
1:AA:1179:A:O3'	9:AI:103:THR:HB	2.09	0.52
3:AC:150:LYS:HD3	3:AC:152:ILE:HD11	1.92	0.52
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.40	0.52
4:AD:157:LEU:HD22	4:AD:161:ASN:HD21	1.75	0.52
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.92	0.52
26:BA:278:A:H2'	26:BA:279:C:C6	2.45	0.52
26:BA:1266:G:O5'	43:BW:15:ARG:NH2	2.43	0.52
26:BA:1653:G:H3'	38:BR:2:ARG:HD3	1.91	0.52
26:BA:2278:A:H5"	47:B0:12:ASN:HD21	1.75	0.52
1:CA:35:G:O2'	12:CL:118:SER:O	2.20	0.52
1:CA:1114:C:O2'	14:CN:60:SER:O	2.14	0.52
2:CB:16:HIS:HB3	2:CB:210:SER:CB	2.39	0.52
3:CC:33:LEU:HD11	14:CN:52:GLN:O	2.10	0.52
4:CD:79:PHE:HE1	4:CD:204:ILE:HD13	1.74	0.52
24:CX:55:PSU:N3	24:CX:58:A:OP2	2.33	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:362:U:H4'	26:DA:363:G:OP1	2.10	0.52
26:DA:817:C:H2'	26:DA:818:G:O4'	2.09	0.52
26:DA:2160:G:H2'	26:DA:2161:C:O4'	2.09	0.52
26:DA:2360:A:H2'	26:DA:2361:A:O4'	2.10	0.52
26:DA:2805:G:C6	26:DA:2807:G:C6	2.98	0.52
32:DH:56:SER:HB3	32:DH:61:HIS:ND1	2.24	0.52
33:DI:104:GLN:O	33:DI:105:HIS:ND1	2.43	0.52
1:AA:356:A:N3	1:AA:368:U:O2'	2.42	0.51
1:AA:576:G:O6	1:AA:880:C:O2'	2.28	0.51
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.44	0.51
24:AX:18:G:O2'	24:AX:19:G:H5'	2.09	0.51
26:BA:2116:G:H2'	26:BA:2117:A:C5	2.45	0.51
26:BA:2627:G:O2'	26:BA:2781:A:N1	2.35	0.51
36:BP:63:PRO:HD3	55:B8:27:THR:HG22	1.93	0.51
41:BU:49:HIS:HA	41:BU:52:ARG:HB3	1.90	0.51
56:B9:16:VAL:HG22	56:B9:25:VAL:HG22	1.92	0.51
1:CA:79:G:OP2	1:CA:79:G:H8	1.92	0.51
1:CA:200:G:H2'	1:CA:201:C:O4'	2.09	0.51
26:DA:94(A):G:H2'	26:DA:95:G:O4'	2.10	0.51
26:DA:196:A:O2'	26:DA:805:G:O6	2.18	0.51
26:DA:271(Q):G:H2'	26:DA:271(R):G:C8	2.45	0.51
26:DA:833:U:O2	36:DP:55:ARG:NH2	2.43	0.51
26:DA:2249:U:N3	26:DA:2253:G:OP2	2.35	0.51
26:DA:2515:C:H2'	26:DA:2516:G:H8	1.75	0.51
26:DA:2645:G:N2	26:DA:2767:C:OP2	2.44	0.51
1:AA:1277:C:H1'	1:AA:1282:C:C2	2.46	0.51
4:AD:128:VAL:HG12	4:AD:129:ASN:HD22	1.75	0.51
5:AE:10:MET:HB2	5:AE:13:ILE:HD11	1.91	0.51
27:BB:11:C:H3'	27:BB:12:C:C6	2.44	0.51
39:BS:74:ALA:O	39:BS:78:LEU:HD23	2.11	0.51
1:CA:1153:C:H42	1:CA:1154:G:N2	2.08	0.51
1:CA:1191:A:OP1	3:CC:4:LYS:HG3	2.10	0.51
4:CD:100:ARG:NH1	4:CD:137:SER:OG	2.39	0.51
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.76	0.51
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.93	0.51
26:DA:7:G:H2'	26:DA:8:A:H8	1.74	0.51
26:DA:539:G:H2'	26:DA:540:C:C6	2.44	0.51
26:DA:660:G:H5'	30:DF:99:TYR:CE2	2.46	0.51
37:DQ:16:ARG:HG2	37:DQ:18:LYS:HE2	1.91	0.51
1:AA:649:G:H2'	1:AA:650:G:C8	2.44	0.51
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2593:U:H2'	26:BA:2594:C:C6	2.45	0.51
33:BI:6:LEU:HG	33:BI:36:ALA:HA	1.93	0.51
37:BQ:86:GLY:HA3	47:B0:10:THR:CG2	2.41	0.51
1:CA:56:U:H2'	1:CA:57:G:C8	2.45	0.51
4:CD:133:VAL:HG11	4:CD:138:TYR:HD2	1.76	0.51
7:CG:116:ALA:O	7:CG:120:ILE:HG13	2.10	0.51
26:DA:2104:G:O2'	26:DA:2105:C:O5'	2.26	0.51
26:DA:2139:C:N4	26:DA:2152:G:C6	2.79	0.51
26:DA:2471:C:H2'	26:DA:2472:G:O4'	2.11	0.51
27:DB:33:G:C2	27:DB:50:G:C2	2.98	0.51
31:DG:41:GLN:NE2	31:DG:154:GLY:O	2.23	0.51
39:DS:68:GLN:O	39:DS:71:ARG:HG3	2.11	0.51
1:AA:406:G:H21	4:AD:119:GLN:HE22	1.58	0.51
1:AA:1061:G:H1'	10:AJ:56:HIS:CE1	2.46	0.51
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.43	0.51
26:BA:862:G:O2'	27:BB:78:A:N3	2.40	0.51
26:BA:1418:G:O2'	26:BA:1580:A:N6	2.42	0.51
26:BA:2134:A:H2'	26:BA:2134:A:N3	2.25	0.51
26:BA:2182:G:H2'	26:BA:2183:C:C6	2.45	0.51
26:BA:2408:U:H2'	26:BA:2409:G:C8	2.45	0.51
30:BF:155:LEU:HD11	30:BF:176:LEU:HD12	1.92	0.51
37:BQ:110:THR:OG1	37:BQ:111:GLU:N	2.44	0.51
38:BR:70:LEU:HD13	38:BR:75:LEU:HD13	1.91	0.51
1:CA:165:C:H2'	1:CA:166:G:C8	2.46	0.51
1:CA:523:A:C2	12:CL:91:LYS:HB3	2.45	0.51
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.43	0.51
1:CA:1348:U:H5"	9:CI:119:ALA:HB3	1.93	0.51
1:CA:1417:G:N2	1:CA:1482:G:H2'	2.25	0.51
1:CA:1511:G:H2'	1:CA:1512:U:O4'	2.11	0.51
1:CA:1516:G:N2	1:CA:1519:A:OP2	2.43	0.51
13:CM:5:ALA:HB3	13:CM:22:ILE:HD12	1.91	0.51
26:DA:383:U:H2'	26:DA:385:C:H5	1.75	0.51
26:DA:747:U:O2	26:DA:2014:A:H1'	2.11	0.51
26:DA:989:G:OP2	50:D3:11:SER:OG	2.28	0.51
26:DA:1155:A:H5"	41:DU:55:ARG:HD3	1.92	0.51
26:DA:1783:A:N7	61:DA:4364:HOH:O	2.34	0.51
26:DA:1899:G:N3	26:DA:1899:G:H2'	2.25	0.51
30:DF:34:TRP:CE2	36:DP:8:PRO:HG3	2.45	0.51
1:AA:270:A:H2'	1:AA:271:C:C6	2.46	0.51
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.46	0.51
1:AA:682:G:H1	1:AA:708:C:H42	1.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:20:ARG:O	9:AI:60:ASP:N	2.32	0.51
26:BA:222:A:N1	26:BA:233:A:H5"	2.25	0.51
26:BA:565:C:H4'	26:BA:1253:A:C6	2.46	0.51
26:BA:1257:C:H5'	30:BF:75:HIS:CE1	2.45	0.51
26:BA:1506:C:C2'	26:BA:1507:A:H5'	2.41	0.51
26:BA:2127:G:C6	26:BA:2162:G:C2	2.99	0.51
32:BH:69:ARG:HG3	32:BH:70:THR:N	2.26	0.51
52:B5:16:ARG:HH11	52:B5:16:ARG:HG2	1.74	0.51
1:CA:427:U:H5'	4:CD:41:GLY:HA2	1.92	0.51
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.42	0.51
2:CB:115:LEU:HD11	2:CB:153:ARG:CZ	2.41	0.51
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.91	0.51
26:DA:375:C:H2'	26:DA:376:C:C6	2.46	0.51
26:DA:646:A:H2'	26:DA:647:G:O4'	2.10	0.51
26:DA:752:A:P	54:D7:3:ARG:HH22	2.34	0.51
26:DA:2602:A:H4'	26:DA:2603:G:O5'	2.09	0.51
30:DF:183:VAL:O	30:DF:187:VAL:HG23	2.10	0.51
33:DI:122:GLU:HB2	33:DI:126:TYR:OH	2.10	0.51
37:DQ:1:MET:SD	37:DQ:1:MET:N	2.82	0.51
40:DT:64:ARG:NH1	40:DT:103:ARG:HA	2.25	0.51
49:D2:29:LYS:HG2	49:D2:57:ILE:HD13	1.91	0.51
1:AA:189(D):C:O2	1:AA:189(H):G:N1	2.44	0.51
1:AA:193:C:H2'	1:AA:194:C:C6	2.45	0.51
1:AA:517:G:N2	1:AA:533:A:OP2	2.39	0.51
1:AA:1276:G:H2'	1:AA:1277:C:H6	1.75	0.51
7:AG:78:ARG:HE	7:AG:156:TRP:HE3	1.57	0.51
19:AS:68:GLY:H	51:B4:58:ARG:HE	1.59	0.51
26:BA:530:G:C5	26:BA:2022:U:H5"	2.45	0.51
26:BA:788:A:OP1	26:BA:791:C:N4	2.40	0.51
26:BA:1026:U:H4'	26:BA:1027:A:OP1	2.10	0.51
34:BN:75:TYR:CE2	34:BN:77:GLY:HA2	2.46	0.51
1:CA:432:A:H5"	1:CA:433:C:OP2	2.11	0.51
1:CA:448:A:O5'	1:CA:485:G:N2	2.34	0.51
1:CA:1243:C:H2'	1:CA:1244:C:C6	2.45	0.51
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	1.93	0.51
11:CK:34:ASP:OD1	11:CK:36:ASP:N	2.44	0.51
13:CM:91:ARG:HB2	13:CM:98:VAL:HG13	1.92	0.51
26:DA:2343:C:O2'	26:DA:2373:G:O2'	2.15	0.51
27:DB:8:U:H6	27:DB:8:U:H5"	1.75	0.51
50:D3:29:ARG:N	50:D3:33:GLN:OE1	2.39	0.51
1:AA:35:G:O2'	12:AL:118:SER:O	2.17	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1136:U:H5”	1:AA:1137:C:N3	2.25	0.51
1:AA:1172:C:N4	1:AA:1173:G:O6	2.44	0.51
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.41	0.51
17:AQ:22:LEU:HD13	17:AQ:41:LYS:HG3	1.91	0.51
26:BA:271(E):U:H2’	26:BA:271(F):C:C6	2.45	0.51
1:CA:376:G:H4’	16:CP:5:ARG:HD3	1.91	0.51
1:CA:1012:U:H2’	1:CA:1013:G:C8	2.46	0.51
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.91	0.51
20:CT:29:LYS:HD2	20:CT:71:THR:HG21	1.93	0.51
26:DA:1469:A:H2’	26:DA:1470:G:O4’	2.10	0.51
26:DA:2023:G:H5’	26:DA:2617:C:H4’	1.93	0.51
26:DA:2080:G:O2’	26:DA:2081:C:H5’	2.10	0.51
43:DW:1:MET:HE2	43:DW:62:HIS:HB3	1.93	0.51
49:D2:16:LEU:O	49:D2:67:LYS:NZ	2.31	0.51
1:AA:57:G:H2’	1:AA:58:C:C6	2.46	0.51
1:AA:731:G:H5’	1:AA:766:A:H4’	1.93	0.51
1:AA:735:C:H2’	1:AA:736:C:H6	1.76	0.51
1:AA:975:A:H4’	1:AA:976:G:C5’	2.38	0.51
1:AA:1005:A:H1’	1:AA:1036:G:H22	1.74	0.51
1:AA:1314:C:H2’	1:AA:1315:U:C6	2.45	0.51
20:AT:38:LYS:HA	20:AT:41:ILE:HD12	1.93	0.51
26:BA:121:G:H4’	26:BA:149:A:H5’	1.93	0.51
26:BA:586:A:N1	26:BA:809:G:O2’	2.37	0.51
26:BA:1178:C:H2’	26:BA:1179:C:C6	2.46	0.51
26:BA:2857:G:N2	26:BA:2860:A:OP2	2.37	0.51
30:BF:53:THR:HG22	30:BF:56:GLU:HG3	1.93	0.51
32:BH:113:VAL:HG11	32:BH:151:ILE:HD13	1.93	0.51
34:BN:47:ALA:HB2	34:BN:112:LEU:HD11	1.93	0.51
1:CA:793:U:C4	1:CA:1517:G:H5”	2.46	0.51
1:CA:1006:C:H2’	1:CA:1007:C:C6	2.45	0.51
1:CA:1340:A:O2’	24:CX:31:G:O2’	2.14	0.51
7:CG:74:GLU:HG2	7:CG:91:VAL:HG22	1.92	0.51
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.11	0.51
15:CO:18:PHE:HB2	15:CO:19:PRO:HD2	1.93	0.51
26:DA:632:A:H2’	26:DA:633:A:C8	2.46	0.51
26:DA:817:C:O2’	26:DA:839:U:OP1	2.25	0.51
26:DA:1186:G:C2	26:DA:1187:G:H1’	2.46	0.51
26:DA:2118:U:OP1	26:DA:2148:G:O2’	2.16	0.51
26:DA:2218:U:O2	48:D1:52:ARG:NH2	2.44	0.51
30:DF:125:LEU:HD22	30:DF:196:LEU:HD23	1.93	0.51
46:DZ:7:ALA:O	46:DZ:62:PRO:HD3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:7:G:H5'	1:AA:298:A:O4'	2.11	0.51
1:AA:369:C:H42	1:AA:392:G:H1	1.59	0.51
1:AA:407:G:OP1	4:AD:3:ARG:NH1	2.43	0.51
1:AA:447:G:O6	1:AA:485:G:O2'	2.27	0.51
1:AA:1125:U:H4'	10:AJ:5:ARG:HH12	1.76	0.51
1:AA:1311:G:H1	1:AA:1326:C:N4	2.09	0.51
15:AO:56:LEU:HD21	26:BA:715:G:C2	2.46	0.51
26:BA:910:A:N1	26:BA:2277:G:H1'	2.25	0.51
26:BA:1028:A:N6	26:BA:1125:G:H2'	2.25	0.51
26:BA:2345:G:OP2	53:B6:38:LYS:NZ	2.37	0.51
26:BA:2433:A:OP2	61:BA:4119:HOH:O	2.19	0.51
1:CA:567:G:O6	12:CL:5:PRO:HD3	2.11	0.51
1:CA:1288:A:N1	1:CA:1371:G:H1'	2.25	0.51
1:CA:1321:C:H5"	1:CA:1322:C:H2'	1.91	0.51
18:CR:58:LEU:HB3	18:CR:62:GLU:HG3	1.93	0.51
26:DA:1011:G:OP2	41:DU:66:ASN:ND2	2.37	0.51
26:DA:1035:U:H2'	26:DA:1036:G:C8	2.45	0.51
26:DA:1710:C:H2'	26:DA:1711:C:H6	1.75	0.51
26:DA:2133:G:HO2'	26:DA:2157:G:H22	1.58	0.51
26:DA:2262:U:H4'	26:DA:2328:A:C2	2.46	0.51
26:DA:2330:G:H2'	26:DA:2331:G:O4'	2.11	0.51
29:DE:179:GLU:HB3	29:DE:181:LEU:HD22	1.93	0.51
35:DO:98:VAL:HG13	35:DO:117:LEU:HB3	1.93	0.51
48:D1:80:LEU:HB3	48:D1:82:LEU:HG	1.93	0.51
1:AA:345:C:H4'	1:AA:346:G:C4	2.46	0.51
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.25	0.51
1:AA:765:G:N1	1:AA:812:C:O2'	2.36	0.51
1:AA:923:A:OP1	5:AE:21:ALA:HB2	2.11	0.51
1:AA:979:C:H2'	1:AA:980:C:H5'	1.93	0.51
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.46	0.51
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.10	0.51
2:AB:115:LEU:HD13	2:AB:145:LEU:HB3	1.93	0.51
24:AX:66:C:H2'	24:AX:67:C:O4'	2.10	0.51
32:BH:159:GLU:HG3	32:BH:169:VAL:HG11	1.93	0.51
1:CA:406:G:H21	4:CD:119:GLN:HE22	1.59	0.51
1:CA:413:G:N2	1:CA:428:G:H1'	2.26	0.51
1:CA:1046:A:H61	1:CA:1213:A:N6	2.09	0.51
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.10	0.51
1:CA:1187:G:N2	14:CN:60:SER:OG	2.36	0.51
1:CA:1206:G:O4'	3:CC:194:GLY:HA2	2.11	0.51
1:CA:1269:A:H2	1:CA:1312:G:N3	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1422:G:O3'	35:DO:49:ARG:NH1	2.40	0.51
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	2.11	0.51
26:DA:208:C:H2'	26:DA:209:C:C6	2.46	0.51
26:DA:2615:U:C2	52:D5:7:PRO:HA	2.46	0.51
29:DE:9:VAL:HG13	29:DE:25:VAL:O	2.11	0.51
31:DG:138:GLN:HB3	31:DG:153:ARG:O	2.11	0.51
41:DU:17:ILE:HG23	41:DU:39:LEU:HD12	1.92	0.51
1:AA:1255:G:H1	1:AA:1282:C:H42	1.58	0.50
1:AA:1291:G:O3'	7:AG:41:ARG:NH2	2.44	0.50
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.92	0.50
26:BA:143:G:H1'	44:BX:37:THR:HG21	1.93	0.50
26:BA:217:G:OP2	61:BA:4821:HOH:O	2.19	0.50
26:BA:1000:A:H62	26:BA:1154:G:H2'	1.77	0.50
26:BA:2611:U:C4	52:B5:3:LYS:HG2	2.45	0.50
31:BG:43:LEU:C	31:BG:45:GLU:H	2.19	0.50
34:BN:1:MET:HE3	42:BV:13:ARG:HB3	1.92	0.50
1:CA:495:A:H4'	1:CA:496:A:OP1	2.12	0.50
1:CA:839:U:H5"	1:CA:840:C:C5	2.42	0.50
1:CA:899:C:O5'	1:CA:899:C:H6	1.94	0.50
1:CA:1288:A:H2'	1:CA:1289:A:C8	2.46	0.50
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.11	0.50
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HG2	1.92	0.50
26:DA:39:C:H2'	26:DA:40:C:C6	2.46	0.50
26:DA:2022:U:O2'	26:DA:2617:C:H5'	2.12	0.50
26:DA:2171:A:H1'	26:DA:2172:U:O4'	2.11	0.50
42:DV:35:LEU:HB2	42:DV:57:VAL:HG23	1.92	0.50
1:AA:130:A:O2'	1:AA:131:C:O5'	2.25	0.50
1:AA:339:C:H2'	1:AA:340:U:C6	2.46	0.50
1:AA:1142:G:H2'	1:AA:1143:G:O4'	2.11	0.50
1:AA:1164:G:N7	1:AA:1173:G:N3	2.59	0.50
28:BD:97:TYR:CE1	28:BD:103:ARG:HG3	2.45	0.50
30:BF:167:ALA:HB1	30:BF:173:VAL:HG11	1.91	0.50
1:CA:438:G:OP1	4:CD:125:HIS:NE2	2.30	0.50
1:CA:763:G:C2'	1:CA:764:C:H5'	2.41	0.50
1:CA:790:A:H2'	1:CA:791:G:C8	2.46	0.50
1:CA:1000:U:O2	1:CA:1041:A:N1	2.45	0.50
1:CA:1310:G:H1	1:CA:1327:C:H42	1.59	0.50
2:CB:51:LEU:HD23	2:CB:201:ILE:HD12	1.92	0.50
4:CD:67:ILE:HD13	4:CD:196:LEU:HD23	1.94	0.50
26:DA:1130:U:O2	26:DA:2025:C:H5"	2.12	0.50
26:DA:1417:C:H2'	26:DA:1418:G:O4'	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1523:U:H2'	26:DA:1524:G:O4'	2.11	0.50
26:DA:1592:C:H2'	26:DA:1593:G:H8	1.76	0.50
26:DA:2148:G:H2'	26:DA:2149:G:C8	2.46	0.50
26:DA:2162:G:H4'	26:DA:2172:U:C2'	2.39	0.50
26:DA:2315:G:H2'	26:DA:2316:C:C6	2.46	0.50
27:DB:45:A:O4'	31:DG:95:ARG:NH1	2.44	0.50
34:DN:15:LEU:HB2	34:DN:135:PRO:HB2	1.94	0.50
44:DX:31:HIS:CD2	44:DX:33:LYS:H	2.29	0.50
54:D7:9:ARG:HH21	54:D7:47:ARG:HD2	1.77	0.50
1:AA:631:G:H2'	1:AA:632:A:C8	2.45	0.50
4:AD:12:CYS:SG	4:AD:19:LEU:HB2	2.52	0.50
19:AS:32:LYS:HE3	19:AS:57:HIS:CD2	2.46	0.50
26:BA:214:G:O2'	26:BA:216:A:O2'	2.20	0.50
26:BA:574:C:N4	26:BA:2034:U:OP1	2.36	0.50
26:BA:1493:C:C5	26:BA:2206:G:H1'	2.46	0.50
26:BA:1666:G:C2'	26:BA:1667:G:H5'	2.40	0.50
26:BA:2127:G:O6	26:BA:2162:G:N1	2.43	0.50
26:BA:2245:U:H5"	26:BA:2246:G:H5'	1.92	0.50
31:BG:144:ILE:HA	31:BG:148:MET:HE1	1.94	0.50
35:BO:73:ASP:HB2	40:BT:82:LEU:HD13	1.93	0.50
1:CA:170:U:O2'	1:CA:171:A:H5'	2.11	0.50
1:CA:791:G:C6	1:CA:792:A:N7	2.79	0.50
6:CF:99:ALA:HB2	18:CR:31:LEU:HD21	1.92	0.50
7:CG:16:LEU:HD23	9:CI:41:VAL:HG12	1.93	0.50
10:CJ:5:ARG:N	10:CJ:99:LYS:O	2.44	0.50
26:DA:1375:C:H2'	26:DA:1376:C:H6	1.76	0.50
31:DG:44:GLY:O	31:DG:47:LYS:HB3	2.12	0.50
1:AA:79:G:C2	1:AA:90:U:O2	2.64	0.50
1:AA:264:U:O2'	17:AQ:64:PRO:O	2.26	0.50
1:AA:432:A:H5"	1:AA:433:C:OP2	2.10	0.50
1:AA:903:G:OP1	61:AA:4029:HOH:O	2.19	0.50
1:AA:1095:U:H5"	1:AA:1109:C:O2	2.12	0.50
26:BA:1124:C:H1'	56:B9:36:GLN:NE2	2.27	0.50
26:BA:1784:A:H4'	26:BA:1785:A:O5'	2.12	0.50
26:BA:2685:G:H5'	35:BO:68:GLU:OE1	2.11	0.50
27:BB:92:C:OP1	46:BZ:79:ARG:NH1	2.43	0.50
31:BG:106:LEU:HA	31:BG:110:ALA:HB3	1.93	0.50
46:BZ:144:LEU:HD23	46:BZ:148:ASP:HB2	1.92	0.50
50:B3:8:LEU:HD13	50:B3:31:LEU:HD23	1.93	0.50
1:CA:1009:G:C2	1:CA:1010:G:C8	2.99	0.50
9:CI:18:PHE:HD2	9:CI:62:TYR:HD2	1.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CJ:55:LYS:HG3	10:CJ:56:HIS:H	1.75	0.50
13:CM:16:ASP:HB2	13:CM:30:ALA:HB1	1.93	0.50
26:DA:12:U:O2	26:DA:2626:C:H4'	2.12	0.50
26:DA:1796:U:H2'	26:DA:1797:C:C6	2.46	0.50
26:DA:2175:C:H2'	26:DA:2176:A:O4'	2.12	0.50
26:DA:2203:U:H4'	28:DD:151:LYS:HG2	1.91	0.50
27:DB:95:C:H2'	27:DB:96:U:C6	2.47	0.50
33:DI:110:ASP:HB3	33:DI:130:TYR:OH	2.12	0.50
38:DR:47:PHE:O	38:DR:51:LEU:HG	2.11	0.50
42:DV:25:LEU:H	42:DV:92:THR:HG1	1.55	0.50
1:AA:189(C):C:H42	1:AA:189(H):G:H1	1.58	0.50
1:AA:521:G:O6	12:AL:53:ARG:NH2	2.44	0.50
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.77	0.50
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.77	0.50
26:BA:222:A:H3'	26:BA:421:U:H5'	1.93	0.50
26:BA:1518:U:H2'	26:BA:1519:G:O4'	2.11	0.50
26:BA:2626:C:H2'	26:BA:2627:G:O4'	2.11	0.50
26:BA:2805:G:H2'	26:BA:2807:G:C8	2.46	0.50
30:BF:30:PRO:HG3	36:BP:1:MET:HE1	1.94	0.50
34:BN:4:TYR:HB2	41:BU:101:ARG:NH1	2.27	0.50
39:BS:27:SER:HA	39:BS:88:ASP:HB3	1.92	0.50
1:CA:354:G:O2'	1:CA:389:A:OP1	2.22	0.50
1:CA:613:C:H2'	1:CA:614:A:H8	1.75	0.50
1:CA:620:C:C2	4:CD:135:LEU:HG	2.46	0.50
1:CA:1321:C:H4'	13:CM:87:TYR:CE2	2.47	0.50
3:CC:113:ALA:HB2	3:CC:202:ILE:HG13	1.92	0.50
9:CI:26:VAL:HG22	9:CI:61:ALA:HB3	1.93	0.50
26:DA:1649:G:O2'	38:DR:107:ASP:OD2	2.21	0.50
27:DB:106:G:H5"	46:DZ:31:ARG:HG2	1.93	0.50
51:D4:15:ILE:HG23	51:D4:21:VAL:HG22	1.92	0.50
1:AA:451:A:N6	1:AA:480:U:H2'	2.26	0.50
1:AA:1493:A:H5"	1:AA:1494:G:OP2	2.11	0.50
4:AD:154:ASN:HA	4:AD:159:ARG:HH21	1.77	0.50
6:AF:89:MET:HE3	6:AF:91:VAL:HG21	1.93	0.50
26:BA:817:C:OP1	61:BA:4091:HOH:O	2.19	0.50
26:BA:1364:G:P	48:B1:3:LYS:HG3	2.51	0.50
30:BF:102:PRO:HB2	30:BF:105:VAL:HG23	1.92	0.50
39:BS:15:ARG:HE	39:BS:88:ASP:CG	2.19	0.50
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.47	0.50
2:CB:24:TRP:CZ3	2:CB:26:PRO:HA	2.46	0.50
13:CM:60:VAL:HG23	13:CM:64:TRP:HZ3	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:648:G:O2'	26:DA:2351:G:OP1	2.17	0.50
26:DA:1266:G:O2'	26:DA:2012:G:O6	2.27	0.50
26:DA:1507:A:O2'	26:DA:1508:A:O5'	2.25	0.50
26:DA:2128:C:H5'	26:DA:2173:A:H2	1.75	0.50
26:DA:2657:A:O3'	32:DH:160:LYS:NZ	2.45	0.50
26:DA:2807:G:C6	26:DA:2808:U:C4	3.00	0.50
27:DB:24:G:H4'	27:DB:25:A:N7	2.26	0.50
33:DI:130:TYR:CE2	33:DI:132:PRO:HB3	2.46	0.50
38:DR:21:TYR:OH	38:DR:43:GLU:HG2	2.12	0.50
45:DY:76:CYS:HA	45:DY:106:LEU:HD22	1.93	0.50
46:DZ:120:ILE:HD11	46:DZ:173:ALA:HB3	1.94	0.50
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.11	0.50
26:BA:2680:C:OP2	29:BE:111:ARG:NH2	2.44	0.50
26:BA:2684:U:H1'	35:BO:70:LYS:HD2	1.94	0.50
30:BF:143:ALA:HB1	30:BF:148:LEU:HB2	1.92	0.50
33:BI:3:VAL:HG12	33:BI:38:LEU:HA	1.93	0.50
34:BN:73:THR:OG1	34:BN:82:LEU:HD11	2.11	0.50
1:CA:137:C:C2	1:CA:227:G:C2	3.00	0.50
1:CA:828:A:H2'	1:CA:829:G:O4'	2.12	0.50
1:CA:1201:A:H4'	1:CA:1202:G:O5'	2.12	0.50
1:CA:1367:C:O2'	10:CJ:62:HIS:HE1	1.94	0.50
15:CO:8:LYS:O	15:CO:12:ILE:HG13	2.12	0.50
26:DA:1786:A:H1'	26:DA:1938:A:N6	2.27	0.50
26:DA:1800:C:OP2	28:DD:183:ARG:NH2	2.45	0.50
26:DA:2001:A:OP1	38:DR:9:LYS:NZ	2.33	0.50
37:DQ:27:VAL:HG21	37:DQ:134:ARG:HA	1.93	0.50
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.47	0.50
1:AA:1007:C:C2'	1:AA:1008:C:H5"	2.34	0.50
24:AX:50:U:H2'	24:AX:51:C:C6	2.46	0.50
26:BA:1184:G:H5'	50:B3:29:ARG:NH1	2.26	0.50
26:BA:1877:A:H5'	26:BA:1878:G:OP2	2.12	0.50
1:CA:17:U:H2'	1:CA:18:C:C6	2.47	0.50
1:CA:338:A:H2	1:CA:351:G:H22	1.60	0.50
1:CA:407:G:H5"	4:CD:115:ARG:HB3	1.93	0.50
1:CA:501:C:H1'	1:CA:549:C:H1'	1.94	0.50
1:CA:613:C:H2'	1:CA:614:A:C8	2.47	0.50
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.42	0.50
1:CA:1162:C:N4	1:CA:1174:G:N1	2.35	0.50
1:CA:1400:C:N4	24:CX:35:A:C8	2.79	0.50
1:CA:1493:A:H2'	26:DA:1913:A:H61	1.76	0.50
20:CT:67:ALA:HB2	20:CT:77:ALA:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:184:C:H2'	26:DA:185:U:C6	2.47	0.50
26:DA:271(W):G:O6	61:DA:4210:HOH:O	2.14	0.50
26:DA:366:C:H5"	26:DA:370:G:H5'	1.92	0.50
26:DA:781:A:P	28:DD:218:ARG:HH22	2.34	0.50
26:DA:1449:A:HO2'	26:DA:1529:G:H21	1.55	0.50
26:DA:1756:G:H4'	26:DA:1758:G:O4'	2.12	0.50
26:DA:2070:G:H2'	26:DA:2071:A:C8	2.47	0.50
26:DA:2130:U:O2	26:DA:2134:A:O2'	2.30	0.50
29:DE:7:VAL:HG13	29:DE:27:LEU:HB3	1.94	0.50
29:DE:77:ILE:HD12	29:DE:195:LEU:HD13	1.93	0.50
36:DP:25:SER:N	61:DP:311:HOH:O	2.40	0.50
5:AE:41:VAL:HG23	5:AE:67:VAL:HG12	1.92	0.50
26:BA:588:U:H1'	30:BF:90:PHE:CG	2.47	0.50
26:BA:601:C:O2'	26:BA:605:C:H5"	2.11	0.50
26:BA:614:U:H5'	26:BA:614(C):A:N6	2.27	0.50
26:BA:2028:U:H2'	26:BA:2029:G:O4'	2.11	0.50
33:BI:100:ALA:HA	33:BI:103:ARG:HG2	1.93	0.50
44:BX:26:TYR:HB3	44:BX:92:LEU:HD22	1.93	0.50
1:CA:91:C:H2'	1:CA:92:C:C6	2.47	0.50
1:CA:1104:G:H4'	2:CB:111:ARG:HD2	1.94	0.50
1:CA:1502:A:H2	1:CA:1505:G:N1	2.03	0.50
18:CR:50:ILE:HG12	18:CR:70:ILE:HG21	1.93	0.50
19:CS:68:GLY:H	51:D4:58:ARG:NH1	2.10	0.50
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.12	0.50
24:CX:65:C:C4	24:CX:66:C:C4	3.00	0.50
26:DA:469:G:C2'	26:DA:470:A:H5"	2.42	0.50
26:DA:588:U:H2'	26:DA:589:C:C6	2.47	0.50
26:DA:1153:C:H2'	26:DA:1154:G:O4'	2.12	0.50
26:DA:1581:G:H2'	26:DA:1582:C:O4'	2.11	0.50
26:DA:1889:A:N1	26:DA:2234:G:H1'	2.26	0.50
26:DA:1987:G:H2'	26:DA:1988:C:C6	2.46	0.50
26:DA:2079:U:H2'	26:DA:2080:G:O4'	2.12	0.50
26:DA:2377:A:H2'	26:DA:2378:A:C8	2.47	0.50
26:DA:2684:U:H1'	35:DO:70:LYS:HD2	1.94	0.50
26:DA:2809:A:H2'	26:DA:2810:A:C8	2.47	0.50
27:DB:7:G:N3	39:DS:38:GLN:NE2	2.38	0.50
28:DD:72:LYS:HD3	28:DD:97:TYR:CE2	2.47	0.50
29:DE:36:ARG:HG2	29:DE:47:VAL:HG12	1.93	0.50
1:AA:302:G:O2'	1:AA:556:C:H5"	2.11	0.49
1:AA:664:G:P	18:AR:64:ARG:HH21	2.35	0.49
4:AD:64:LEU:HA	4:AD:67:ILE:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:48:ILE:HG21	11:AK:63:LEU:HB3	1.93	0.49
24:AX:49:G:N2	24:AX:65:C:N3	2.50	0.49
26:BA:26:G:C6	26:BA:27:G:N1	2.80	0.49
26:BA:55:G:O2'	26:BA:127:A:N1	2.40	0.49
26:BA:729:G:C6	28:BD:208:LYS:HB2	2.47	0.49
26:BA:1047:G:H1'	26:BA:1110:G:N2	2.27	0.49
26:BA:1143:A:OP1	34:BN:25:ARG:NH2	2.45	0.49
26:BA:2386:C:H2'	26:BA:2387:U:C6	2.47	0.49
26:BA:2563:U:H4'	35:BO:28:SER:HA	1.94	0.49
26:BA:2611:U:H5'	26:BA:2611:U:H6	1.77	0.49
32:BH:12:PRO:O	32:BH:15:VAL:HG13	2.12	0.49
1:CA:406:G:N2	4:CD:119:GLN:HE22	2.10	0.49
1:CA:696:A:H8	1:CA:696:A:O5'	1.95	0.49
1:CA:1227:A:N3	19:CS:83:HIS:HB3	2.27	0.49
1:CA:1516:G:H2'	1:CA:1518:A:OP2	2.12	0.49
2:CB:200:ILE:HD13	2:CB:200:ILE:H	1.77	0.49
26:DA:71:A:H5"	26:DA:73:A:C8	2.47	0.49
26:DA:718:A:H3'	26:DA:719:C:H6	1.77	0.49
26:DA:831:G:O2'	36:DP:38:GLN:NE2	2.45	0.49
26:DA:857:C:H4'	47:D0:23:VAL:HG21	1.94	0.49
26:DA:1163:G:OP1	42:DV:24:LYS:NZ	2.34	0.49
26:DA:1500:G:O2'	28:DD:100:GLY:O	2.29	0.49
27:DB:27:C:C4	27:DB:28:C:C4	3.00	0.49
31:DG:179:PRO:HG3	51:D4:43:TYR:OH	2.12	0.49
32:DH:3:ARG:HH22	32:DH:5:GLY:H	1.60	0.49
1:AA:362:G:N1	1:AA:365:U:OP2	2.45	0.49
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.45	0.49
10:AJ:39:PRO:HA	10:AJ:70:ARG:HD3	1.93	0.49
26:BA:10:G:N2	26:BA:2802:G:OP1	2.31	0.49
26:BA:403:U:H4'	26:BA:404:C:H5'	1.93	0.49
26:BA:2086:U:H2'	26:BA:2087:G:H8	1.78	0.49
26:BA:2107:C:N4	26:BA:2182:G:H1	2.07	0.49
26:BA:2206:G:H5'	26:BA:2207:G:N7	2.27	0.49
1:CA:958:A:N6	19:CS:77:THR:O	2.45	0.49
7:CG:76:ARG:HB3	7:CG:156:TRP:HH2	1.77	0.49
8:CH:20:TYR:CE1	8:CH:76:PRO:HG2	2.48	0.49
15:CO:81:LEU:O	15:CO:84:LYS:HG2	2.13	0.49
23:CW:76:PPU:HM2	26:DA:2452:C:N3	2.27	0.49
26:DA:781:A:OP1	28:DD:218:ARG:NH2	2.45	0.49
26:DA:2165:G:O6	26:DA:2171:A:H8	1.95	0.49
37:DQ:31:ASP:OD1	37:DQ:134:ARG:NH1	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:353:A:H8	1:AA:353:A:H5'	1.76	0.49
1:AA:599:C:H4'	8:AH:130:GLY:C	2.37	0.49
1:AA:1024:G:C2'	1:AA:1025:U:H5'	2.41	0.49
4:AD:178:VAL:C	4:AD:180:GLY:H	2.20	0.49
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	1.94	0.49
16:AP:19:ILE:N	16:AP:37:GLY:O	2.45	0.49
26:BA:1012:U:H5	34:BN:28:THR:HG21	1.77	0.49
26:BA:2022:U:O2'	26:BA:2617:C:H5'	2.11	0.49
28:BD:85:ASP:OD2	28:BD:88:ARG:NH1	2.44	0.49
40:BT:45:PHE:CE2	40:BT:65:LYS:HD3	2.47	0.49
1:CA:89:C:H2'	1:CA:90:U:O4'	2.12	0.49
1:CA:1029:C:N3	1:CA:1032:G:C2	2.80	0.49
2:CB:97:TRP:CZ3	2:CB:101:MET:HB2	2.48	0.49
24:CX:47:U:H3'	24:CX:48:C:H5'	1.93	0.49
26:DA:330:A:H2	26:DA:1210:A:H2'	1.78	0.49
26:DA:1212:G:O2'	26:DA:1235:G:O6	2.30	0.49
26:DA:1790:C:H5"	26:DA:1791:A:OP1	2.12	0.49
26:DA:2035:G:H4'	61:DA:4092:HOH:O	2.11	0.49
26:DA:2557:G:H2'	26:DA:2558:C:H6	1.76	0.49
45:DY:94:LYS:NZ	61:DY:601:HOH:O	2.44	0.49
52:D5:41:PRO:O	52:D5:44:THR:OG1	2.24	0.49
1:AA:36:C:O2'	12:AL:117:ARG:NH2	2.45	0.49
1:AA:158:G:N2	1:AA:163:C:O2	2.39	0.49
1:AA:1068:G:N2	1:AA:1191:A:N3	2.56	0.49
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.30	0.49
3:AC:16:ARG:HH22	3:AC:183:ASP:CG	2.20	0.49
3:AC:134:ILE:HG22	3:AC:168:ALA:HB3	1.95	0.49
7:AG:38:LEU:O	7:AG:42:ILE:HG13	2.12	0.49
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.12	0.49
23:AW:76:PPU:H2'	26:BA:2584:U:O2'	2.13	0.49
26:BA:224:G:H2'	26:BA:225:A:O4'	2.12	0.49
26:BA:637:A:H8	36:BP:117:GLU:HG3	1.78	0.49
26:BA:2661:G:H2'	26:BA:2662:A:C8	2.47	0.49
27:BB:89:G:O6	27:BB:90:A:N6	2.46	0.49
29:BE:11:MET:HG2	29:BE:24:THR:HB	1.93	0.49
31:BG:74:LYS:O	31:BG:84:LYS:NZ	2.42	0.49
40:BT:51:ARG:HG3	40:BT:98:LYS:HD2	1.95	0.49
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.12	0.49
17:CQ:12:SER:HB3	17:CQ:20:THR:HB	1.95	0.49
17:CQ:57:VAL:HG12	17:CQ:76:LEU:HA	1.93	0.49
26:DA:469:G:H2'	26:DA:470:A:H5"	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:568:U:H5'	26:DA:945:A:N1	2.26	0.49
26:DA:774:A:N3	26:DA:774:A:H2'	2.27	0.49
26:DA:1798:U:OP2	28:DD:274:ARG:NH2	2.45	0.49
26:DA:2123:G:H1	26:DA:2175:C:N4	2.10	0.49
26:DA:2783:G:H2'	26:DA:2784:C:C6	2.47	0.49
28:DD:118:VAL:N	28:DD:129:ASN:OD1	2.41	0.49
31:DG:14:GLU:O	31:DG:17:PRO:HD2	2.12	0.49
31:DG:98:ARG:HA	31:DG:101:ILE:HB	1.93	0.49
41:DU:92:ARG:HA	41:DU:95:LEU:HB2	1.93	0.49
55:D8:4:MET:HE3	55:D8:63:PRO:HG3	1.93	0.49
1:AA:750:G:O2'	15:AO:22:THR:O	2.24	0.49
1:AA:1494:G:H4'	26:BA:1913:A:C8	2.47	0.49
2:AB:162:ILE:O	2:AB:185:ILE:HG13	2.13	0.49
7:AG:68:ASN:O	7:AG:138:LYS:HE2	2.11	0.49
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.95	0.49
26:BA:65:C:O2'	26:BA:456:C:N3	2.40	0.49
26:BA:1226:A:OP1	42:BV:84:LYS:HE2	2.13	0.49
26:BA:1357:U:H2'	26:BA:1358:G:O4'	2.13	0.49
26:BA:2597:G:OP1	61:BA:4695:HOH:O	2.20	0.49
28:BD:9:TYR:CZ	28:BD:13:ARG:HG2	2.48	0.49
29:BE:2:LYS:HB2	29:BE:95:ILE:HD12	1.93	0.49
37:BQ:85:LYS:N	37:BQ:85:LYS:HD2	2.27	0.49
46:BZ:7:ALA:HB3	46:BZ:61:LEU:HD12	1.95	0.49
1:CA:407:G:N1	1:CA:436:C:N3	2.37	0.49
1:CA:688:G:H5'	11:CK:46:GLY:C	2.37	0.49
1:CA:1376:U:H2'	1:CA:1377:A:H8	1.72	0.49
4:CD:108:LEU:HD13	4:CD:174:LEU:HD13	1.95	0.49
8:CH:82:HIS:HB3	8:CH:138:TRP:NE1	2.26	0.49
16:CP:20:VAL:HG22	16:CP:35:LYS:HA	1.94	0.49
20:CT:46:GLU:O	20:CT:46:GLU:HG2	2.11	0.49
26:DA:644:A:H4'	26:DA:645:C:C5	2.46	0.49
26:DA:1411:C:H2'	26:DA:1412:A:C8	2.47	0.49
26:DA:2808:U:H5"	26:DA:2891:G:O6	2.12	0.49
30:DF:32:LEU:O	30:DF:36:VAL:HG23	2.12	0.49
1:AA:201:C:H42	1:AA:216:G:H22	1.59	0.49
1:AA:1038:C:H2'	1:AA:1039:C:C6	2.48	0.49
3:AC:52:LEU:HD21	3:AC:55:VAL:HG23	1.95	0.49
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	1.93	0.49
13:AM:80:ARG:HH21	51:B4:58:ARG:HH11	1.59	0.49
24:AX:40:C:C2'	24:AX:41:C:H5'	2.43	0.49
26:BA:226:G:H21	26:BA:228:A:H62	1.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1713:U:H2'	26:BA:1714:G:C8	2.46	0.49
26:BA:2849:U:H4'	26:BA:2868:A:C2	2.48	0.49
30:BF:110:LEU:HD21	30:BF:181:LEU:HG	1.93	0.49
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.25	0.49
1:CA:609:A:C2'	1:CA:610:G:H5'	2.42	0.49
1:CA:1004:A:N6	1:CA:1037:C:C2	2.81	0.49
1:CA:1237:C:H5"	1:CA:1238:A:O4'	2.12	0.49
16:CP:22:THR:HA	16:CP:33:ILE:HG12	1.94	0.49
17:CQ:76:LEU:HD12	17:CQ:77:VAL:H	1.78	0.49
24:CX:3:C:C2'	24:CX:4:G:H5"	2.40	0.49
26:DA:286:C:H2'	26:DA:287:C:C6	2.47	0.49
26:DA:443:A:H1'	26:DA:1201:C:O4'	2.12	0.49
26:DA:729:G:C6	28:DD:208:LYS:HB2	2.48	0.49
26:DA:2041:U:H2'	26:DA:2042:A:C8	2.46	0.49
26:DA:2158:A:H4'	26:DA:2159:G:OP1	2.12	0.49
26:DA:2291:U:H2'	26:DA:2292:C:C6	2.48	0.49
26:DA:2728:U:H5'	35:DO:70:LYS:HZ3	1.76	0.49
27:DB:6:C:C2	27:DB:116:G:N2	2.81	0.49
32:DH:70:THR:O	32:DH:74:ASN:N	2.39	0.49
1:AA:49:U:O4	1:AA:365:U:H5	1.95	0.49
1:AA:270:A:H2'	1:AA:271:C:H6	1.78	0.49
1:AA:1200:C:OP1	61:AA:4099:HOH:O	2.20	0.49
1:AA:1258:G:H2'	1:AA:1259:C:C6	2.47	0.49
4:AD:20:TYR:CD2	4:AD:26:CYS:HB3	2.48	0.49
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.93	0.49
26:BA:30:G:H2'	26:BA:31:C:C6	2.47	0.49
26:BA:542:C:H2'	26:BA:543:C:C6	2.48	0.49
26:BA:947:G:H2'	26:BA:948:G:C8	2.48	0.49
26:BA:1692:U:H2'	26:BA:1694:C:C5	2.48	0.49
26:BA:2150:U:H2'	26:BA:2151:G:H8	1.77	0.49
38:BR:37:THR:HA	38:BR:111:LEU:HD12	1.95	0.49
1:CA:539:A:H2'	1:CA:540:G:C8	2.48	0.49
1:CA:1015:A:H1'	1:CA:1219:U:H5'	1.94	0.49
1:CA:1394:A:N6	1:CA:1501:C:H5'	2.28	0.49
3:CC:48:TYR:HE1	3:CC:118:GLN:HB2	1.77	0.49
26:DA:1570:A:H2'	26:DA:1571:A:C8	2.47	0.49
26:DA:1754:C:OP1	40:DT:96:ARG:HD2	2.13	0.49
26:DA:2104:G:H2'	26:DA:2105:C:C6	2.48	0.49
26:DA:2107:C:N4	26:DA:2182:G:H1	2.07	0.49
26:DA:2117:A:N1	26:DA:2171:A:N1	2.60	0.49
26:DA:2121:G:C6	26:DA:2177:C:N4	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2259:G:H1'	26:DA:2427:C:H2'	1.93	0.49
30:DF:13:SER:OG	30:DF:16:GLY:O	2.24	0.49
47:D0:17:GLN:O	47:D0:19:LYS:NZ	2.45	0.49
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.42	0.49
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.93	0.49
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.47	0.49
26:BA:458:G:C8	54:B7:37:LYS:HG2	2.48	0.49
26:BA:518:G:H2'	26:BA:519:U:C6	2.47	0.49
26:BA:1266:G:O2'	26:BA:2012:G:O6	2.30	0.49
26:BA:1820:U:C2	28:BD:202:LYS:HD3	2.47	0.49
26:BA:2127:G:H21	26:BA:2173:A:H1'	1.77	0.49
26:BA:2807:G:H2'	26:BA:2808:U:O4'	2.12	0.49
44:BX:53:LYS:HB3	44:BX:82:GLN:HB3	1.94	0.49
48:B1:50:ARG:HG2	48:B1:59:THR:HB	1.94	0.49
1:CA:22:G:H4'	1:CA:885:G:C8	2.48	0.49
1:CA:460:G:N1	1:CA:470:C:H5'	2.28	0.49
1:CA:999:C:C4	1:CA:1042:G:N1	2.81	0.49
5:CE:69:VAL:HG22	5:CE:71:LEU:HD12	1.94	0.49
13:CM:33:ALA:O	13:CM:37:THR:OG1	2.19	0.49
26:DA:610:G:N2	26:DA:619:G:H1'	2.27	0.49
26:DA:1665:A:H4'	35:DO:67:LYS:HB2	1.94	0.49
26:DA:2173:A:C2	26:DA:2174:C:H1'	2.48	0.49
26:DA:2185:C:H2'	26:DA:2186:G:O4'	2.13	0.49
26:DA:2646:C:H2'	26:DA:2647:U:O4'	2.12	0.49
26:DA:2683:C:O2	35:DO:70:LYS:NZ	2.31	0.49
28:DD:43:ARG:HA	28:DD:48:ARG:O	2.13	0.49
29:DE:116:VAL:HG13	29:DE:122:PHE:HB2	1.95	0.49
39:DS:87:PHE:HB2	39:DS:112:PHE:CE2	2.48	0.49
43:DW:58:ALA:HB1	43:DW:64:MET:HB2	1.95	0.49
1:AA:509:A:N3	1:AA:543:C:O2'	2.35	0.49
1:AA:555:C:H2'	1:AA:556:C:C6	2.47	0.49
1:AA:933:G:O6	7:AG:3:ARG:NH2	2.46	0.49
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.36	0.49
26:BA:484:C:H2'	26:BA:485:C:C6	2.48	0.49
26:BA:2727:G:O2'	35:BO:70:LYS:NZ	2.43	0.49
36:BP:124:LYS:HE3	36:BP:146:VAL:HG21	1.93	0.49
40:BT:116:ALA:HB1	40:BT:121:ILE:HD11	1.94	0.49
43:BW:68:ARG:HD3	43:BW:111:HIS:HA	1.95	0.49
1:CA:713:G:H2'	1:CA:714:G:C8	2.46	0.49
1:CA:715:A:H2'	1:CA:716:A:C8	2.47	0.49
1:CA:1154:G:N7	1:CA:1155:G:N7	2.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1235:U:O2'	1:CA:1305:G:OP1	2.28	0.49
1:CA:1314:C:H2'	1:CA:1315:U:C6	2.48	0.49
4:CD:108:LEU:HD23	4:CD:110:PHE:CZ	2.47	0.49
26:DA:468:G:H5"	30:DF:60:SER:HB2	1.95	0.49
26:DA:997:G:OP1	41:DU:92:ARG:HG2	2.13	0.49
26:DA:1788:C:OP1	28:DD:222:ARG:NH2	2.45	0.49
26:DA:2103:C:C2	26:DA:2187:G:C2	3.01	0.49
26:DA:2734:A:H2'	26:DA:2735:G:O4'	2.13	0.49
27:DB:48:A:P	39:DS:30:ARG:HH12	2.36	0.49
36:DP:38:GLN:HG2	36:DP:45:LEU:H	1.76	0.49
43:DW:45:TYR:CZ	43:DW:49:LYS:HE3	2.47	0.49
1:AA:337:C:H2'	1:AA:338:A:C8	2.48	0.49
1:AA:1027:C:H2'	1:AA:1028:C:C6	2.48	0.49
18:AR:74:ARG:HG3	18:AR:79:LEU:HB2	1.94	0.49
26:BA:735:A:N7	26:BA:761:A:H2	2.11	0.49
26:BA:2570:G:H2'	26:BA:2571:C:O4'	2.13	0.49
26:BA:2572:A:C8	29:BE:144:ARG:HD2	2.47	0.49
30:BF:184:TYR:HE1	36:BP:3:LEU:HD21	1.77	0.49
37:BQ:63:LYS:HE2	46:BZ:118:GLN:NE2	2.27	0.49
37:BQ:135:ASP:OD2	46:BZ:49:ARG:NH2	2.45	0.49
1:CA:392:G:H2'	1:CA:393:A:C8	2.47	0.49
1:CA:1260:C:OP1	1:CA:1284:C:O2'	2.26	0.49
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.94	0.49
4:CD:12:CYS:O	4:CD:16:GLY:N	2.46	0.49
7:CG:31:MET:HA	7:CG:39:ALA:HB2	1.95	0.49
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.39	0.49
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.30	0.49
26:DA:127:A:H5"	26:DA:128:C:O4'	2.13	0.49
26:DA:1445(A):C:H2'	26:DA:1446:C:H6	1.77	0.49
26:DA:1688:U:H1'	26:DA:1701:A:C6	2.47	0.49
26:DA:1752:C:H2'	26:DA:1753:G:C8	2.48	0.49
26:DA:2207:G:H3'	26:DA:2208:A:H5"	1.95	0.49
28:DD:13:ARG:HA	28:DD:13:ARG:HD2	1.59	0.49
30:DF:21:ALA:CB	30:DF:22:ALA:HA	2.42	0.49
32:DH:40:GLU:OE1	32:DH:61:HIS:NE2	2.46	0.49
33:DI:62:LYS:HE2	33:DI:133:HIS:CD2	2.47	0.49
46:DZ:69:THR:HG22	46:DZ:90:VAL:HA	1.95	0.49
1:AA:401:C:H2'	1:AA:402:G:C8	2.48	0.48
1:AA:565:U:OP2	1:AA:566:G:O2'	2.31	0.48
1:AA:1063:C:OP2	1:AA:1064:G:O2'	2.14	0.48
26:BA:644:A:H4'	26:BA:645:C:C5	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1018:C:O3'	26:BA:1120:G:N2	2.46	0.48
26:BA:2037:G:H2'	26:BA:2038:G:C8	2.48	0.48
26:BA:2749:A:P	32:BH:3:ARG:HH21	2.36	0.48
28:BD:108:PRO:HB3	28:BD:143:HIS:HE1	1.75	0.48
30:BF:101:LEU:HD12	30:BF:102:PRO:HD2	1.95	0.48
1:CA:1006:C:OP1	1:CA:1037:C:O2'	2.31	0.48
1:CA:1244:C:N4	1:CA:1293:G:N1	2.34	0.48
1:CA:1355:G:H2'	1:CA:1356:G:C8	2.48	0.48
2:CB:142:LEU:HD21	2:CB:146:GLN:HE21	1.78	0.48
26:DA:709:U:H2'	26:DA:710:G:H8	1.77	0.48
26:DA:994:C:O2'	26:DA:996:A:OP1	2.29	0.48
26:DA:1019:U:O2'	26:DA:1021:A:H2	1.95	0.48
26:DA:1529:G:C6	26:DA:1530:C:N4	2.81	0.48
26:DA:1652:A:OP1	38:DR:8:ARG:NH1	2.41	0.48
26:DA:2398:U:H2'	26:DA:2399:G:H8	1.77	0.48
26:DA:2579:C:H2'	26:DA:2580:U:O4'	2.13	0.48
40:DT:64:ARG:HB2	40:DT:73:GLU:HG2	1.94	0.48
1:AA:153:C:N4	1:AA:168:G:H1	2.10	0.48
1:AA:189:G:C6	1:AA:189(L):G:C6	3.01	0.48
1:AA:413:G:N2	1:AA:428:G:H1'	2.28	0.48
1:AA:619:U:N3	4:AD:134:ASP:OD1	2.32	0.48
1:AA:1002:G:C6	1:AA:1003:G:C2	3.02	0.48
1:AA:1015:A:N3	1:AA:1218:C:O2'	2.44	0.48
9:AI:26:VAL:HG13	9:AI:61:ALA:HB3	1.94	0.48
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.48	0.48
26:BA:548:A:H61	42:BV:19:LYS:H	1.61	0.48
26:BA:944:G:H5"	26:BA:945:A:O5'	2.13	0.48
26:BA:1568:G:N7	61:BD:401:HOH:O	2.35	0.48
26:BA:1949:G:C6	26:BA:1950:G:C6	3.01	0.48
26:BA:2012:G:OP1	43:BW:11:ARG:NH2	2.43	0.48
26:BA:2136:C:N3	26:BA:2155:G:N2	2.53	0.48
29:BE:176:ILE:HB	29:BE:181:LEU:HB2	1.94	0.48
41:BU:82:GLY:HA3	41:BU:113:ALA:HB1	1.95	0.48
48:B1:64:ALA:HA	48:B1:67:ILE:HG13	1.95	0.48
1:CA:16:A:C2'	1:CA:17:U:H5'	2.44	0.48
1:CA:88:A:H4'	1:CA:89:C:O5'	2.13	0.48
1:CA:130:A:O2'	1:CA:131:C:O5'	2.29	0.48
1:CA:189(A):C:H2'	1:CA:189(B):C:H5'	1.94	0.48
1:CA:578:C:OP1	61:CA:4037:HOH:O	2.20	0.48
1:CA:665:A:H1'	1:CA:733:A:O4'	2.13	0.48
1:CA:800:G:O5'	1:CA:800:G:H8	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CP:28:ARG:HH11	16:CP:29:ASP:CG	2.20	0.48
26:DA:27:G:N2	26:DA:512:G:H1'	2.29	0.48
26:DA:218:A:C2	26:DA:235:U:H4'	2.49	0.48
26:DA:968:G:H2'	26:DA:969:U:C6	2.48	0.48
26:DA:968:G:H2'	26:DA:969:U:H6	1.78	0.48
26:DA:1421:G:C2	26:DA:1422:G:N7	2.81	0.48
26:DA:1434:A:H61	26:DA:1558:A:H62	1.60	0.48
26:DA:1860:G:C2	26:DA:1861:G:C8	3.01	0.48
26:DA:2230:G:H1'	48:D1:45:ASN:CG	2.38	0.48
39:DS:15:ARG:HE	39:DS:88:ASP:CG	2.18	0.48
1:AA:346:G:C5	1:AA:347:G:H1'	2.47	0.48
1:AA:452:A:OP1	16:AP:43:LYS:NZ	2.39	0.48
1:AA:728:A:C5	15:AO:54:ARG:HD2	2.49	0.48
1:AA:749:C:H2'	1:AA:750:G:H8	1.78	0.48
2:AB:15:VAL:HG11	2:AB:209:ARG:HG2	1.95	0.48
5:AE:68:GLU:OE1	5:AE:70:PRO:HG3	2.12	0.48
26:BA:565:C:H4'	26:BA:1253:A:N6	2.28	0.48
26:BA:1188:U:H4'	42:BV:79:VAL:HG22	1.96	0.48
26:BA:1354:A:H5"	28:BD:38:LYS:HD3	1.95	0.48
26:BA:1509(B):A:H2'	26:BA:1510:G:O4'	2.13	0.48
26:BA:2127:G:N2	26:BA:2128:C:O2	2.46	0.48
26:BA:2867:G:OP2	40:BT:119:LYS:NZ	2.45	0.48
54:B7:46:VAL:HG13	54:B7:48:LYS:HE3	1.95	0.48
1:CA:692:U:H2'	1:CA:694:A:OP2	2.12	0.48
1:CA:975:A:H5'	1:CA:975:A:C8	2.46	0.48
1:CA:975:A:H4'	1:CA:976:G:C5'	2.43	0.48
1:CA:993:G:H2'	1:CA:995:C:H41	1.78	0.48
1:CA:1038:C:H2'	1:CA:1039:C:H6	1.78	0.48
1:CA:1080:A:H5'	5:CE:14:ARG:NH2	2.28	0.48
1:CA:1223:C:P	19:CS:78:ARG:HH21	2.36	0.48
1:CA:1263:C:H2'	1:CA:1264:C:C6	2.48	0.48
1:CA:1288:A:N3	1:CA:1352:C:O2'	2.42	0.48
1:CA:1355:G:N2	1:CA:1367:C:N3	2.53	0.48
5:CE:80:ILE:HG22	5:CE:91:LEU:HB2	1.95	0.48
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.94	0.48
11:CK:98:LEU:O	11:CK:101:SER:OG	2.30	0.48
18:CR:37:VAL:HG23	18:CR:79:LEU:HD23	1.94	0.48
24:CX:15:G:H2'	24:CX:59:A:H61	1.78	0.48
26:DA:345:A:N3	26:DA:347:A:N6	2.60	0.48
26:DA:993:G:OP1	41:DU:50:ARG:NH2	2.47	0.48
26:DA:1297:C:OP1	26:DA:2710:C:H4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1422:G:H4'	26:DA:1493:C:OP1	2.13	0.48
26:DA:2134:A:O2'	26:DA:2159:G:N3	2.41	0.48
26:DA:2282:G:H4'	26:DA:2389:G:O2'	2.13	0.48
27:DB:5:C:O2'	27:DB:27:C:O2	2.31	0.48
30:DF:120:GLU:HB3	30:DF:122:LYS:HG2	1.95	0.48
1:AA:763:G:H2'	1:AA:764:C:H5'	1.95	0.48
1:AA:811:C:O2'	1:AA:901:A:N1	2.43	0.48
26:BA:918:A:H5"	27:BB:98:G:O2'	2.14	0.48
26:BA:1794:U:H2'	26:BA:1795:C:C6	2.48	0.48
26:BA:2130:U:C2'	26:BA:2131:G:H21	2.26	0.48
29:BE:12:THR:HG21	40:BT:11:GLU:HG2	1.95	0.48
1:CA:255:G:OP1	17:CQ:69:LYS:NZ	2.39	0.48
1:CA:735:C:H2'	1:CA:736:C:H6	1.77	0.48
1:CA:969:A:OP1	10:CJ:55:LYS:NZ	2.38	0.48
1:CA:1316:G:N2	1:CA:1319:A:OP2	2.42	0.48
26:DA:598:G:H2'	26:DA:599:G:O4'	2.13	0.48
26:DA:1139:G:O2'	26:DA:1143:A:N1	2.45	0.48
26:DA:1754:C:N3	26:DA:2716:U:O2'	2.44	0.48
26:DA:2126:A:N6	26:DA:2163:C:O4'	2.47	0.48
26:DA:2238:G:H2'	26:DA:2238:G:N3	2.29	0.48
35:DO:34:THR:OG1	35:DO:35:VAL:N	2.46	0.48
41:DU:50:ARG:HH12	42:DV:72:VAL:HA	1.79	0.48
1:AA:109:A:C6	1:AA:326:G:C6	3.01	0.48
1:AA:657:G:C2	1:AA:658:G:C8	3.02	0.48
1:AA:779:C:OP2	61:AA:4019:HOH:O	2.20	0.48
8:AH:86:ILE:HG22	8:AH:93:VAL:HG21	1.94	0.48
20:AT:43:LEU:O	20:AT:47:GLY:N	2.46	0.48
26:BA:1588:C:H2'	26:BA:1589:C:H6	1.78	0.48
26:BA:2162:G:H4'	26:BA:2172:U:H2'	1.95	0.48
27:BB:2:C:H2'	27:BB:3:C:C6	2.48	0.48
50:B3:19:GLN:OE1	50:B3:52:HIS:NE2	2.45	0.48
1:CA:444:C:H2'	1:CA:445:G:H8	1.79	0.48
1:CA:938:A:C6	1:CA:939:G:C5	3.02	0.48
1:CA:1212:U:H4'	1:CA:1213:A:O5'	2.13	0.48
1:CA:1227:A:OP1	19:CS:80:TYR:OH	2.26	0.48
1:CA:1262:C:H2'	1:CA:1263:C:H5'	1.95	0.48
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.94	0.48
19:CS:12:ASP:OD2	19:CS:35:SER:HB3	2.12	0.48
20:CT:47:GLY:HA2	20:CT:48:LYS:C	2.39	0.48
26:DA:7:G:H5"	34:DN:130:HIS:HE1	1.78	0.48
26:DA:1012:U:OP2	41:DU:70:ARG:NH2	2.33	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1025:G:C4	26:DA:1135:C:H1'	2.48	0.48
26:DA:1449:A:O2'	26:DA:1529:G:N2	2.36	0.48
26:DA:2133:G:C2	26:DA:2157:G:N3	2.81	0.48
26:DA:2741:A:H2'	26:DA:2742:C:O4'	2.13	0.48
44:DX:5:TYR:CZ	49:D2:30:ARG:HB2	2.48	0.48
46:DZ:153:SER:HB3	46:DZ:167:PRO:HB3	1.96	0.48
1:AA:161:A:H8	1:AA:161:A:O5'	1.97	0.48
1:AA:186:C:H2'	1:AA:187:C:C6	2.48	0.48
1:AA:392:G:H2'	1:AA:393:A:C8	2.49	0.48
1:AA:797:C:H2'	1:AA:798:G:H5'	1.94	0.48
1:AA:1239:A:H62	1:AA:1299:A:N6	2.12	0.48
1:AA:1349:A:H5"	9:AI:121:ARG:HB2	1.96	0.48
1:AA:1356:G:H2'	1:AA:1357:A:H8	1.76	0.48
1:AA:1392:G:N2	1:AA:1502:A:C8	2.77	0.48
5:AE:102:ALA:HB1	5:AE:106:PRO:HG2	1.94	0.48
26:BA:84:A:C5'	45:BY:8:LYS:HG2	2.44	0.48
26:BA:568:U:H5'	26:BA:945:A:C6	2.49	0.48
26:BA:1446:C:HO2'	26:BA:1545:A:HO2'	1.59	0.48
26:BA:1812:A:O2'	28:BD:45:ASN:N	2.41	0.48
33:BI:92:VAL:HG22	33:BI:120:ILE:HD12	1.95	0.48
50:B3:50:VAL:O	50:B3:54:VAL:HB	2.14	0.48
1:CA:762:C:H2'	1:CA:763:G:H8	1.78	0.48
1:CA:984:C:H2'	1:CA:985:C:H6	1.79	0.48
1:CA:1075:C:H2'	1:CA:1076:C:H5'	1.95	0.48
1:CA:1078:U:H1'	5:CE:130:ASN:OD1	2.13	0.48
1:CA:1187:G:OP1	9:CI:113:LYS:NZ	2.32	0.48
1:CA:1320:C:OP1	19:CS:70:LYS:HE3	2.12	0.48
8:CH:97:VAL:HG21	8:CH:128:GLY:HA2	1.96	0.48
13:CM:86:CYS:SG	13:CM:89:GLY:N	2.87	0.48
26:DA:1204:A:H2	26:DA:1241:A:N6	2.06	0.48
26:DA:1652:A:C2'	26:DA:1653:G:H5'	2.43	0.48
26:DA:1798:U:H5'	28:DD:259:THR:CG2	2.43	0.48
26:DA:2182:G:H2'	26:DA:2183:C:C6	2.49	0.48
26:DA:2727:G:O2'	35:DO:70:LYS:NZ	2.45	0.48
37:DQ:30:GLY:O	37:DQ:134:ARG:HD3	2.14	0.48
41:DU:79:PHE:CZ	41:DU:83:LEU:HD21	2.48	0.48
46:DZ:97:GLU:HA	46:DZ:127:LYS:HA	1.94	0.48
46:DZ:119:GLU:HG3	46:DZ:122:ARG:HH12	1.78	0.48
1:AA:44:G:C2	1:AA:45:U:H1'	2.49	0.48
1:AA:1085:U:OP2	61:AA:4141:HOH:O	2.20	0.48
1:AA:1116:C:N3	1:AA:1184:G:O6	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1452:C:O2'	1:AA:1456:G:H5"	2.13	0.48
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.14	0.48
4:AD:100:ARG:NH1	4:AD:137:SER:OG	2.46	0.48
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.13	0.48
26:BA:484:C:H2'	26:BA:485:C:H6	1.78	0.48
26:BA:652(C):G:N2	26:BA:653:A:H1'	2.28	0.48
26:BA:1720:U:H2'	26:BA:1721:G:O4'	2.13	0.48
26:BA:2156:G:N2	26:BA:2158:A:N6	2.60	0.48
26:BA:2584:U:H2'	26:BA:2585:U:C6	2.49	0.48
26:BA:2651:C:H2'	26:BA:2652:C:C6	2.48	0.48
26:BA:2836:U:H2'	26:BA:2837:G:C8	2.49	0.48
28:BD:68:LYS:HD3	28:BD:70:TRP:CH2	2.48	0.48
49:B2:1:MET:HE2	49:B2:6:VAL:HG22	1.95	0.48
1:CA:953:G:H8	1:CA:953:G:O5'	1.96	0.48
8:CH:64:LYS:HD2	8:CH:79:VAL:HG21	1.96	0.48
23:CW:76:PPU:H102	26:DA:2584:U:C5'	2.44	0.48
26:DA:385:C:O2	36:DP:71:VAL:HG21	2.13	0.48
26:DA:900:A:H2'	26:DA:901:A:H8	1.79	0.48
26:DA:957:A:H5'	37:DQ:76:LYS:HG3	1.94	0.48
26:DA:1815:A:H8	26:DA:1815:A:OP1	1.96	0.48
26:DA:2690:C:N4	26:DA:2713:A:H1'	2.28	0.48
27:DB:31:C:N4	27:DB:51:G:O6	2.47	0.48
33:DI:31:LEU:HD21	33:DI:38:LEU:HG	1.95	0.48
51:D4:64:GLY:C	51:D4:66:SER:H	2.22	0.48
1:AA:1171:G:C2'	1:AA:1172:C:H5'	2.44	0.48
1:AA:1355:G:H2'	1:AA:1356:G:C8	2.49	0.48
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.48	0.48
3:AC:82:GLU:HG2	3:AC:85:ARG:HH22	1.78	0.48
4:AD:22:LYS:HB2	4:AD:26:CYS:SG	2.53	0.48
5:AE:110:LEU:HD13	5:AE:118:ILE:HD13	1.95	0.48
17:AQ:62:SER:HB3	17:AQ:72:ARG:HD2	1.96	0.48
26:BA:388:G:O2'	26:BA:389:G:N7	2.44	0.48
26:BA:1999:C:H4'	26:BA:2723:C:O2	2.14	0.48
30:BF:34:TRP:HA	36:BP:6:LEU:HD13	1.95	0.48
1:CA:222:U:H2'	1:CA:223:U:C6	2.48	0.48
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.79	0.48
1:CA:567:G:C2	1:CA:568:G:H1'	2.49	0.48
1:CA:922:G:H1	1:CA:1395:C:H42	1.62	0.48
3:CC:71:ALA:HB1	3:CC:109:PRO:HG3	1.96	0.48
3:CC:155:GLY:HA3	3:CC:196:LEU:HD13	1.95	0.48
24:CX:23:C:H2'	24:CX:24:U:H6	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:93:G:H2'	26:DA:94:C:H6	1.78	0.48
26:DA:277:C:HO2'	26:DA:278:A:P	2.34	0.48
26:DA:307:G:N2	26:DA:309:G:H3'	2.29	0.48
26:DA:1416:G:H1	26:DA:1582:C:H42	1.62	0.48
26:DA:2302:G:C2'	26:DA:2303:G:H5'	2.43	0.48
26:DA:2564:A:C2	26:DA:2647:U:H4'	2.49	0.48
27:DB:32:C:C2	27:DB:51:G:N1	2.81	0.48
27:DB:117:G:O2'	39:DS:54:LEU:HD21	2.14	0.48
32:DH:56:SER:OG	32:DH:57:ASP:N	2.45	0.48
37:DQ:21:THR:HG21	37:DQ:101:ARG:HD3	1.95	0.48
1:AA:292:G:N7	1:AA:293:G:H1'	2.29	0.48
1:AA:1516:G:H2'	1:AA:1518:A:OP2	2.13	0.48
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.13	0.48
12:AL:26:ALA:HB1	12:AL:60:LEU:HD23	1.95	0.48
13:AM:19:LEU:HD21	13:AM:56:LEU:HD21	1.96	0.48
26:BA:1341:U:OP2	26:BA:1394:U:O2'	2.23	0.48
26:BA:1494:A:H2'	26:BA:1495:A:C8	2.48	0.48
26:BA:2319:G:H22	39:BS:3:ARG:HA	1.77	0.48
26:BA:2712:U:H2'	26:BA:2714:G:H5"	1.95	0.48
31:BG:16:ARG:O	31:BG:20:ILE:HG13	2.14	0.48
1:CA:434:U:H2'	1:CA:435:C:C6	2.49	0.48
1:CA:659:U:H2'	1:CA:660:G:H5'	1.94	0.48
1:CA:892:A:O2'	1:CA:1415:G:H4'	2.13	0.48
1:CA:1002:G:H2'	1:CA:1003:G:C8	2.49	0.48
1:CA:1404:C:H2'	1:CA:1405:G:C8	2.49	0.48
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.96	0.48
26:DA:7:G:H2'	26:DA:8:A:C8	2.49	0.48
26:DA:476:G:H4'	26:DA:502:A:N1	2.28	0.48
26:DA:1221:C:H2'	26:DA:1221(A):C:C6	2.48	0.48
27:DB:90:A:N7	27:DB:91:C:H1'	2.29	0.48
33:DI:127:VAL:HA	33:DI:140:LEU:O	2.14	0.48
1:AA:339:C:OP2	35:BO:97:ARG:HD3	2.14	0.48
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.36	0.48
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.48	0.48
2:AB:178:ARG:NH2	8:AH:74:PRO:HB3	2.27	0.48
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.96	0.48
9:AI:23:ASN:ND2	9:AI:23:ASN:H	2.12	0.48
12:AL:8:ASN:O	12:AL:12:ARG:HG3	2.14	0.48
15:AO:84:LYS:O	15:AO:84:LYS:HD3	2.13	0.48
26:BA:1029:A:N1	26:BA:2465:C:O2'	2.44	0.48
26:BA:1709:U:H2'	26:BA:1710:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1992:G:H4'	26:BA:1993:U:C5	2.49	0.48
28:BD:134:ARG:HG2	28:BD:187:GLY:O	2.14	0.48
31:BG:5:VAL:HG22	31:BG:8:LYS:H	1.79	0.48
1:CA:441:A:H3'	1:CA:442:C:C6	2.49	0.48
1:CA:1137:C:H5"	1:CA:1138:G:OP1	2.14	0.48
4:CD:90:GLY:HA3	4:CD:200:GLU:HG3	1.94	0.48
4:CD:173:TRP:HB2	4:CD:187:ARG:O	2.14	0.48
7:CG:108:ALA:HA	7:CG:111:ARG:HD2	1.96	0.48
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.95	0.48
26:DA:577:G:H8	26:DA:577:G:O5'	1.97	0.48
26:DA:692:C:O2'	28:DD:38:LYS:NZ	2.32	0.48
26:DA:753:C:H2'	26:DA:754:C:C6	2.49	0.48
26:DA:784:A:H5'	26:DA:785:G:OP1	2.13	0.48
26:DA:1695:G:H8	28:DD:8:PRO:O	1.97	0.48
26:DA:1697:G:OP2	26:DA:1698:A:O2'	2.22	0.48
26:DA:2327:A:H2'	26:DA:2328:A:C8	2.49	0.48
26:DA:2336:A:H61	47:D0:43:THR:CG2	2.27	0.48
33:DI:93:THR:HA	33:DI:116:LEU:HD13	1.96	0.48
1:AA:1024:G:H2'	1:AA:1024:G:N3	2.28	0.47
1:AA:1258:G:H2'	1:AA:1259:C:H6	1.78	0.47
4:AD:85:LYS:HG3	4:AD:86:LYS:N	2.28	0.47
24:AX:61:C:H2'	24:AX:62:C:H6	1.78	0.47
26:BA:952:G:P	37:BQ:16:ARG:HH21	2.37	0.47
26:BA:1292:U:H2'	26:BA:1293:C:C6	2.49	0.47
26:BA:2492:U:H2'	26:BA:2493:U:C6	2.49	0.47
26:BA:2629:A:H1'	26:BA:2630:G:H5"	1.96	0.47
26:BA:2892:A:C5	26:BA:2893:G:C6	3.02	0.47
35:BO:69:ILE:HG12	35:BO:77:ILE:HG22	1.96	0.47
45:BY:6:HIS:H	45:BY:6:HIS:CD2	2.32	0.47
48:B1:3:LYS:HB2	48:B1:61:ARG:NH1	2.29	0.47
51:B4:63:TYR:N	51:B4:64:GLY:HA2	2.29	0.47
54:B7:24:THR:O	54:B7:28:ARG:HG3	2.13	0.47
1:CA:45:U:OP1	1:CA:307:C:O2'	2.27	0.47
1:CA:1089:G:C6	1:CA:1090:U:C2	3.02	0.47
2:CB:8:LYS:HA	2:CB:217:ARG:HE	1.79	0.47
3:CC:35:GLU:OE2	3:CC:59:ARG:NH2	2.47	0.47
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.96	0.47
7:CG:99:LEU:HA	7:CG:102:ARG:NH1	2.29	0.47
7:CG:155:ARG:HB3	7:CG:155:ARG:CZ	2.43	0.47
20:CT:37:SER:O	20:CT:41:ILE:HD13	2.14	0.47
26:DA:80:G:H2'	26:DA:81:G:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1206:G:H2'	26:DA:1207:C:C6	2.48	0.47
26:DA:1951:U:O2'	26:DA:1953:A:N7	2.43	0.47
26:DA:2821:A:H2'	26:DA:2822:G:C8	2.49	0.47
29:DE:37:ARG:HB2	29:DE:46:ALA:N	2.29	0.47
29:DE:119:ARG:HD2	29:DE:120:TRP:CE2	2.49	0.47
31:DG:173:LEU:HB3	31:DG:178:PHE:CG	2.48	0.47
32:DH:13:LYS:HA	32:DH:14:GLY:HA2	1.58	0.47
33:DI:72:LEU:HD13	33:DI:140:LEU:HB2	1.94	0.47
1:AA:406:G:N2	4:AD:119:GLN:HE22	2.13	0.47
2:AB:174:VAL:HG13	2:AB:184:VAL:HG11	1.95	0.47
26:BA:84:A:H5'	45:BY:8:LYS:HG2	1.95	0.47
1:CA:66:G:H8	1:CA:66:G:OP1	1.97	0.47
1:CA:78:G:N2	1:CA:92:C:O2	2.47	0.47
1:CA:974:A:H8	1:CA:974:A:OP1	1.97	0.47
1:CA:1002:G:N2	1:CA:1039:C:C4	2.82	0.47
1:CA:1027:C:N4	1:CA:1034:G:N1	2.61	0.47
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.96	0.47
10:CJ:16:LEU:HD23	10:CJ:94:VAL:HG22	1.95	0.47
26:DA:236:C:H2'	26:DA:237:C:H6	1.79	0.47
26:DA:1899:G:O2'	26:DA:1900:A:OP2	2.31	0.47
26:DA:2150:U:H2'	26:DA:2151:G:C8	2.49	0.47
32:DH:154:PRO:HB3	32:DH:163:TYR:CE2	2.49	0.47
48:D1:3:LYS:HB2	48:D1:61:ARG:HH12	1.79	0.47
51:D4:1:MET:HE2	51:D4:6:HIS:CD2	2.49	0.47
1:AA:221:C:H2'	1:AA:222:U:C6	2.43	0.47
1:AA:381:C:H2'	1:AA:382:A:O4'	2.14	0.47
1:AA:950:U:OP2	13:AM:102:ARG:HD3	2.13	0.47
9:AI:79:LEU:HD22	9:AI:104:ARG:HB2	1.94	0.47
26:BA:548:A:N6	42:BV:19:LYS:H	2.11	0.47
26:BA:1255:U:O5'	26:BA:1256:G:H5"	2.14	0.47
26:BA:1301:A:C8	26:BA:1303:G:C8	3.02	0.47
26:BA:2164:C:H5	26:BA:2165:G:C4	2.32	0.47
26:BA:2698:U:H2'	26:BA:2699:C:C6	2.49	0.47
40:BT:23:ARG:HG3	40:BT:120:ARG:NH1	2.29	0.47
53:B6:14:THR:HB	53:B6:48:VAL:O	2.13	0.47
1:CA:45:U:H2'	1:CA:46:G:C8	2.49	0.47
1:CA:59:A:H5"	1:CA:387:U:H5"	1.95	0.47
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.96	0.47
1:CA:605:U:C2'	1:CA:606:G:H5'	2.44	0.47
1:CA:872:A:O2'	1:CA:873:A:H3'	2.15	0.47
1:CA:953:G:N7	13:CM:104:ARG:NH2	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1060:C:OP1	10:CJ:51:ARG:NH1	2.46	0.47
1:CA:1206:G:N7	61:CA:4001:HOH:O	2.36	0.47
1:CA:1221:G:O3'	19:CS:77:THR:HG21	2.13	0.47
1:CA:1360:A:C4	14:CN:18:VAL:HG12	2.49	0.47
2:CB:184:VAL:N	2:CB:198:ASP:OD2	2.38	0.47
4:CD:31:CYS:O	4:CD:35:ARG:HG3	2.13	0.47
26:DA:83:G:O2'	26:DA:102:G:N2	2.47	0.47
26:DA:236:C:H2'	26:DA:237:C:C6	2.48	0.47
26:DA:987:G:O2'	26:DA:1000:A:N3	2.41	0.47
26:DA:1359:A:C6	26:DA:1360:A:C4	3.02	0.47
26:DA:2400:G:H2'	26:DA:2401:U:C6	2.49	0.47
26:DA:2583:G:OP2	61:DA:3952:HOH:O	2.20	0.47
26:DA:2732:G:H3'	26:DA:2733:A:O4'	2.14	0.47
26:DA:2875:C:O2'	40:DT:2:ASN:OD1	2.21	0.47
38:DR:87:TYR:OH	38:DR:116:LEU:HB3	2.14	0.47
1:AA:58:C:O2'	1:AA:388:G:N7	2.37	0.47
1:AA:687:A:N1	1:AA:700:G:O2'	2.41	0.47
1:AA:964:A:N3	1:AA:969:A:O2'	2.43	0.47
2:AB:28:PHE:CD1	2:AB:190:THR:HA	2.50	0.47
4:AD:11:LEU:HD23	4:AD:66:ARG:HB3	1.97	0.47
4:AD:164:ALA:O	4:AD:168:ARG:NH1	2.45	0.47
4:AD:187:ARG:NH1	4:AD:193:ASP:OD2	2.48	0.47
16:AP:54:GLU:HG3	16:AP:55:ARG:N	2.29	0.47
26:BA:45:C:H2'	26:BA:47:C:C6	2.49	0.47
26:BA:309:G:H4'	45:BY:18:GLY:HA2	1.96	0.47
26:BA:1274:A:N3	26:BA:1297:C:H1'	2.29	0.47
26:BA:1406:U:H2'	26:BA:1407:C:C6	2.50	0.47
26:BA:1643:G:H2'	26:BA:1644:C:O4'	2.14	0.47
26:BA:2493:U:H2'	26:BA:2494:G:O4'	2.14	0.47
26:BA:2552:U:C2	26:BA:2554:U:H5"	2.48	0.47
26:BA:2735:G:H2'	26:BA:2736:G:H8	1.78	0.47
28:BD:146:GLU:HG2	28:BD:152:GLY:C	2.40	0.47
40:BT:108:ARG:HA	40:BT:111:ARG:NH1	2.30	0.47
43:BW:1:MET:HE2	43:BW:62:HIS:HB3	1.96	0.47
46:BZ:33:LEU:HD11	46:BZ:90:VAL:HG21	1.97	0.47
51:B4:26:SER:OG	51:B4:27:THR:N	2.47	0.47
1:CA:165:C:H2'	1:CA:166:G:H8	1.79	0.47
1:CA:1495:U:O2'	26:DA:1919:A:N1	2.40	0.47
2:CB:20:GLU:HB2	2:CB:190:THR:OG1	2.14	0.47
26:DA:191:A:N1	61:DA:4117:HOH:O	2.35	0.47
26:DA:784:A:C8	26:DA:792:G:C5	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1170:G:H1	26:DA:1179:C:H42	1.62	0.47
26:DA:1509(A):A:N3	26:DA:1509(A):A:H5"	2.29	0.47
26:DA:1783:A:H5'	26:DA:2608:G:H4'	1.96	0.47
26:DA:2547:U:O2	35:DO:23:ARG:NH2	2.47	0.47
26:DA:2708:G:H1'	38:DR:71:GLN:HE22	1.79	0.47
31:DG:145:THR:H	31:DG:148:MET:HE3	1.79	0.47
32:DH:69:ARG:HG3	32:DH:70:THR:N	2.26	0.47
54:D7:10:ARG:O	54:D7:14:LYS:HB2	2.14	0.47
1:AA:1321:C:H5"	1:AA:1322:C:H2'	1.97	0.47
2:AB:71:VAL:HB	2:AB:164:VAL:HG22	1.97	0.47
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.14	0.47
8:AH:6:ILE:HB	8:AH:85:ARG:NH1	2.28	0.47
9:AI:100:GLY:O	9:AI:103:THR:HG23	2.14	0.47
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.97	0.47
20:AT:43:LEU:HD13	20:AT:51:GLU:HB3	1.96	0.47
26:BA:1335:U:OP1	44:BX:65:ARG:HD2	2.14	0.47
26:BA:1354:A:H2'	26:BA:1355:G:O4'	2.15	0.47
26:BA:1803:A:O2'	28:BD:259:THR:HG21	2.14	0.47
26:BA:2120:G:C2'	26:BA:2121:G:H5'	2.45	0.47
26:BA:2674:G:H2'	26:BA:2675:A:C8	2.50	0.47
28:BD:108:PRO:HG2	28:BD:111:LEU:HB2	1.96	0.47
32:BH:56:SER:HB3	32:BH:61:HIS:ND1	2.30	0.47
40:BT:106:SER:O	40:BT:110:ILE:HG13	2.14	0.47
46:BZ:111:VAL:C	46:BZ:113:ALA:H	2.22	0.47
50:B3:26:LEU:O	50:B3:35:ARG:NE	2.44	0.47
1:CA:6:G:H4'	1:CA:298:A:H4'	1.96	0.47
1:CA:1052:U:H5"	1:CA:1053:G:OP2	2.13	0.47
1:CA:1392:G:H21	1:CA:1502:A:H8	1.61	0.47
8:CH:45:ILE:HD13	8:CH:61:VAL:HG13	1.96	0.47
11:CK:41:THR:OG1	11:CK:42:TRP:N	2.48	0.47
13:CM:79:LYS:NZ	13:CM:83:ASP:OD2	2.35	0.47
26:DA:608:A:H2'	26:DA:609:A:C8	2.49	0.47
26:DA:1171:G:N2	26:DA:1179:C:N3	2.61	0.47
26:DA:2140:C:O2	26:DA:2140:C:H2'	2.13	0.47
30:DF:157:VAL:HB	30:DF:194:MET:HG2	1.97	0.47
46:DZ:144:LEU:HD11	46:DZ:172:ALA:HB1	1.95	0.47
1:AA:411:A:OP2	4:AD:25:ARG:NH2	2.48	0.47
1:AA:1015:A:H2'	1:AA:1016:A:C8	2.50	0.47
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.42	0.47
1:AA:1127:G:H5'	1:AA:1280:A:O2'	2.13	0.47
26:BA:94(A):G:H2'	26:BA:95:G:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:271(K):U:C2	33:BI:50:ARG:HD3	2.49	0.47
26:BA:1641:A:H2'	26:BA:1642:G:O4'	2.15	0.47
26:BA:1803:A:H4'	28:BD:259:THR:HG23	1.96	0.47
26:BA:2625:G:H2'	26:BA:2626:C:C6	2.49	0.47
37:BQ:85:LYS:HG2	47:B0:7:LEU:HB3	1.96	0.47
38:BR:118:GLU:CD	38:BR:118:GLU:H	2.23	0.47
1:CA:7:G:H5'	1:CA:298:A:O4'	2.15	0.47
1:CA:499:A:H4'	1:CA:500:G:H5'	1.97	0.47
1:CA:624:C:H2'	1:CA:625:G:H8	1.79	0.47
1:CA:721:G:H4'	1:CA:722:A:O4'	2.15	0.47
1:CA:865:A:H5'	1:CA:1078:U:O4	2.14	0.47
6:CF:3:ARG:HB3	6:CF:93:SER:HB2	1.97	0.47
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.29	0.47
24:CX:49:G:C2	24:CX:65:C:N3	2.82	0.47
26:DA:659:C:H2'	26:DA:660:G:C8	2.48	0.47
26:DA:1424:G:H2'	26:DA:1425:G:O4'	2.15	0.47
26:DA:1592:C:H2'	26:DA:1593:G:C8	2.50	0.47
26:DA:2308:G:H5"	26:DA:2310:A:OP2	2.14	0.47
31:DG:43:LEU:HB3	31:DG:44:GLY:H	1.62	0.47
36:DP:28:GLY:O	36:DP:30:THR:N	2.48	0.47
36:DP:143:GLY:O	36:DP:145:PRO:HD3	2.14	0.47
38:DR:97:VAL:HG22	38:DR:114:VAL:HG22	1.97	0.47
40:DT:22:PHE:HA	40:DT:91:ARG:HH12	1.78	0.47
40:DT:36:GLU:OE1	40:DT:41:ARG:NE	2.41	0.47
1:AA:659:U:H2'	1:AA:660:G:H5'	1.96	0.47
1:AA:783:C:OP1	1:AA:1515:C:O2'	2.32	0.47
1:AA:838:G:H1	1:AA:848:C:N4	2.13	0.47
1:AA:936:C:O2	1:AA:1382:C:N4	2.31	0.47
1:AA:979:C:OP1	1:AA:1223:C:N4	2.48	0.47
1:AA:1034:G:H3'	1:AA:1035:A:C8	2.49	0.47
1:AA:1055:A:O2'	3:AC:161:GLU:O	2.23	0.47
1:AA:1112:C:C2	3:AC:178:LEU:HB2	2.49	0.47
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.48	0.47
1:AA:1133:G:H2'	1:AA:1134:G:C8	2.49	0.47
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.47	0.47
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.78	0.47
1:AA:1399:C:C2	1:AA:1502:A:N6	2.82	0.47
4:AD:61:LYS:HA	4:AD:203:VAL:HG22	1.96	0.47
19:AS:39:THR:HG22	19:AS:40:ILE:O	2.15	0.47
26:BA:141:A:C8	26:BA:1408:C:O2'	2.65	0.47
26:BA:242:G:O2'	26:BA:254:G:O6	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:303:U:H2'	26:BA:304:G:C8	2.49	0.47
26:BA:467:G:O6	61:BA:3834:HOH:O	2.19	0.47
26:BA:990:A:C6	26:BA:1186:G:H1'	2.49	0.47
26:BA:1178:C:H2'	26:BA:1179:C:H6	1.80	0.47
26:BA:1297:C:OP1	26:BA:2710:C:H4'	2.14	0.47
26:BA:1668:A:O2'	26:BA:1674:G:N7	2.42	0.47
26:BA:1778:U:H2'	26:BA:1784:A:N6	2.30	0.47
26:BA:2103:C:N3	26:BA:2186:G:N2	2.49	0.47
26:BA:2137:C:H2'	26:BA:2138:C:C6	2.49	0.47
26:BA:2735:G:H2'	26:BA:2736:G:C8	2.50	0.47
26:BA:2848:G:O2'	26:BA:2867:G:N2	2.43	0.47
26:BA:2870:C:H2'	26:BA:2871:C:O4'	2.15	0.47
41:BU:36:ARG:HD2	41:BU:40:PHE:CZ	2.49	0.47
46:BZ:146:ILE:HA	46:BZ:147:GLY:HA2	1.63	0.47
1:CA:545:C:O2'	1:CA:549:C:OP1	2.27	0.47
1:CA:584:G:H5'	17:CQ:91:ARG:NH2	2.30	0.47
1:CA:797:C:C2'	1:CA:798:G:H5'	2.44	0.47
1:CA:811:C:H4'	1:CA:901:A:H61	1.79	0.47
1:CA:986:A:C2	19:CS:52:TYR:HE2	2.32	0.47
1:CA:1004:A:H3'	1:CA:1005:A:C5'	2.45	0.47
1:CA:1097:C:H2'	1:CA:1098:C:O4'	2.15	0.47
1:CA:1099:G:C5	1:CA:1100:C:N3	2.82	0.47
1:CA:1400:C:O5'	22:CV:18:G:C2	2.68	0.47
1:CA:1457:G:H5"	20:CT:35:THR:HG21	1.96	0.47
3:CC:32:LEU:HA	3:CC:35:GLU:HG2	1.96	0.47
5:CE:36:ASP:C	5:CE:38:GLN:H	2.22	0.47
5:CE:93:PRO:HG2	8:CH:105:ARG:NE	2.29	0.47
7:CG:73:MET:HG3	7:CG:90:GLU:HA	1.96	0.47
10:CJ:9:ARG:HG2	10:CJ:69:ASN:OD1	2.14	0.47
26:DA:411:G:C5	36:DP:72:PRO:HB3	2.50	0.47
26:DA:990:A:C6	26:DA:1186:G:H1'	2.50	0.47
26:DA:1579:A:H2'	26:DA:1580:A:C8	2.50	0.47
26:DA:2220:G:H2'	26:DA:2221:G:H8	1.80	0.47
26:DA:2639:A:H2'	26:DA:2640:G:O4'	2.14	0.47
27:DB:55:U:H1'	31:DG:29:TRP:CD1	2.49	0.47
30:DF:150:GLY:HA2	30:DF:172:TRP:CD2	2.50	0.47
32:DH:106:THR:HG22	32:DH:112:PRO:HB3	1.96	0.47
33:DI:83:ALA:C	33:DI:89:TYR:HD2	2.23	0.47
34:DN:4:TYR:CD2	41:DU:100:VAL:HG11	2.49	0.47
34:DN:96:GLU:H	34:DN:96:GLU:CD	2.23	0.47
35:DO:16:ALA:HB2	35:DO:52:VAL:HG21	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DZ:30:ASN:ND2	46:DZ:90:VAL:HB	2.29	0.47
46:DZ:150:LEU:H	46:DZ:172:ALA:HB3	1.80	0.47
56:D9:2:LYS:NZ	56:D9:31:LYS:O	2.28	0.47
1:AA:460:G:O5'	1:AA:460:G:H8	1.97	0.47
1:AA:1425:U:H2'	1:AA:1426:C:C6	2.50	0.47
4:AD:31:CYS:O	4:AD:35:ARG:HG3	2.13	0.47
16:AP:66:PRO:HB2	16:AP:71:ARG:HB3	1.96	0.47
17:AQ:51:TYR:CZ	17:AQ:73:VAL:HG11	2.50	0.47
26:BA:797:C:H2'	26:BA:798:G:O4'	2.15	0.47
26:BA:2160:G:H2'	26:BA:2161:C:C6	2.50	0.47
26:BA:2564:A:C2	26:BA:2647:U:H4'	2.49	0.47
26:BA:2577:A:O4'	52:B5:3:LYS:HB2	2.13	0.47
37:BQ:1:MET:HE2	37:BQ:1:MET:HB3	1.64	0.47
1:CA:76:C:N4	1:CA:96:U:N3	2.62	0.47
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.50	0.47
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.14	0.47
1:CA:1281:U:P	1:CA:1282:C:H41	2.38	0.47
1:CA:1362:C:C2'	1:CA:1363:C:H5"	2.43	0.47
3:CC:134:ILE:HD11	3:CC:153:VAL:HG21	1.96	0.47
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.48	0.47
12:CL:113:ARG:HB3	12:CL:122:THR:HG21	1.97	0.47
18:CR:24:ALA:C	18:CR:26:LEU:H	2.23	0.47
19:CS:36:ARG:HD2	19:CS:52:TYR:O	2.15	0.47
26:DA:83:G:OP2	45:DY:95:LYS:NZ	2.45	0.47
26:DA:853:G:H2'	26:DA:854:G:H8	1.79	0.47
26:DA:1910:G:C6	26:DA:1911:U:C4	3.02	0.47
26:DA:2398:U:H2'	26:DA:2399:G:C8	2.50	0.47
26:DA:2485:G:C2	26:DA:2486:G:C8	3.03	0.47
26:DA:2500:U:H2'	26:DA:2504:U:C5	2.50	0.47
27:DB:78:A:C2	27:DB:100:A:C4	3.03	0.47
31:DG:48:GLU:O	31:DG:51:ARG:HG3	2.15	0.47
45:DY:12:THR:O	45:DY:75:ILE:N	2.41	0.47
1:AA:406:G:OP1	4:AD:5:ILE:HD11	2.14	0.47
1:AA:765:G:H5"	1:AA:766:A:OP1	2.15	0.47
1:AA:1286:A:H2'	1:AA:1287:A:H4'	1.95	0.47
26:BA:37:C:H2'	26:BA:38:A:C8	2.49	0.47
26:BA:328:U:H4'	45:BY:68:HIS:CG	2.50	0.47
26:BA:1029:A:OP1	37:BQ:128:LYS:NZ	2.45	0.47
26:BA:2507:C:H2'	26:BA:2508:G:O4'	2.14	0.47
26:BA:2543:G:H2'	26:BA:2544:G:C8	2.50	0.47
48:B1:23:LYS:HB3	48:B1:29:GLY:HA3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:B6:13:CYS:SG	53:B6:47:THR:HG21	2.54	0.47
1:CA:163:C:H2'	1:CA:164:U:O4'	2.14	0.47
1:CA:493:G:H2'	1:CA:494:U:C5	2.50	0.47
1:CA:857:C:H2'	1:CA:858:G:O4'	2.15	0.47
1:CA:1266:G:N1	1:CA:1269:A:OP2	2.47	0.47
1:CA:1271:G:H5'	1:CA:1314:C:H5"	1.95	0.47
1:CA:1398:A:OP1	1:CA:1401:G:OP1	2.33	0.47
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.97	0.47
3:CC:54:ARG:HB2	3:CC:69:HIS:HB2	1.95	0.47
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.50	0.47
24:CX:41:C:H2'	24:CX:42:G:C8	2.49	0.47
26:DA:593:G:C6	26:DA:594:U:C4	3.03	0.47
26:DA:2199:A:H3'	26:DA:2200:C:H6	1.80	0.47
26:DA:2467:C:OP1	56:D9:6:SER:OG	2.29	0.47
27:DB:8:U:O2'	39:DS:40:ILE:HD13	2.14	0.47
30:DF:39:TRP:CD1	30:DF:101:LEU:HB2	2.49	0.47
32:DH:41:MET:HE1	32:DH:65:HIS:HA	1.96	0.47
1:AA:190:U:H2'	1:AA:191:G:C8	2.50	0.47
1:AA:243:A:H4'	1:AA:244:U:H5"	1.97	0.47
1:AA:913:A:OP1	12:AL:46:LYS:NZ	2.33	0.47
1:AA:985:C:H2'	1:AA:986:A:C8	2.50	0.47
1:AA:1276:G:H2'	1:AA:1277:C:C6	2.50	0.47
7:AG:136:LYS:O	7:AG:140:ASP:HB2	2.15	0.47
8:AH:11:THR:HG23	8:AH:14:ARG:HH12	1.79	0.47
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.44	0.47
26:BA:222:A:H5"	26:BA:421:U:OP1	2.14	0.47
26:BA:281:G:H1'	26:BA:360:G:N2	2.29	0.47
26:BA:869:G:H2'	26:BA:870:A:O4'	2.15	0.47
26:BA:2238:G:H2'	26:BA:2238:G:N3	2.30	0.47
26:BA:2724:C:OP1	29:BE:118:LYS:NZ	2.45	0.47
38:BR:97:VAL:HG22	38:BR:114:VAL:HG22	1.97	0.47
1:CA:736:C:H2'	1:CA:737:A:C8	2.50	0.47
1:CA:786:G:C2	1:CA:797:C:C2	3.03	0.47
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.38	0.47
1:CA:1358:U:H5"	14:CN:33:VAL:O	2.15	0.47
11:CK:62:GLN:HB2	11:CK:93:GLN:HG3	1.95	0.47
26:DA:1187:G:H5'	42:DV:81:TYR:CE1	2.50	0.47
26:DA:2335:A:C8	26:DA:2337:G:C5	3.03	0.47
26:DA:2477:C:N4	56:D9:10:ILE:HG23	2.30	0.47
26:DA:2722:G:H5"	26:DA:2820:A:N7	2.30	0.47
27:DB:87:G:N2	27:DB:90:A:OP2	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DG:41:GLN:NE2	31:DG:153:ARG:HB3	2.17	0.47
33:DI:127:VAL:HG22	33:DI:139:GLN:OE1	2.15	0.47
40:DT:77:PRO:HB2	40:DT:80:SER:HB2	1.97	0.47
1:AA:134:A:H61	16:AP:25:ARG:NH1	2.13	0.46
1:AA:520:A:N1	1:AA:536:C:H1'	2.30	0.46
1:AA:841:U:H5	1:AA:848:C:H1'	1.77	0.46
1:AA:934:C:H5	1:AA:1344:C:H2'	1.79	0.46
1:AA:1014:A:H4'	19:AS:14:HIS:CE1	2.49	0.46
1:AA:1036:G:N2	1:AA:1037:C:H1'	2.30	0.46
1:AA:1095:U:OP2	1:AA:1108:G:N1	2.43	0.46
15:AO:24:SER:OG	15:AO:25:THR:N	2.49	0.46
24:AX:19:G:H4'	24:AX:20:U:OP2	2.15	0.46
26:BA:119:A:H4'	26:BA:120:U:OP1	2.16	0.46
26:BA:330:A:H2	26:BA:1210:A:O2'	1.96	0.46
26:BA:998:C:OP1	61:BA:4488:HOH:O	2.21	0.46
26:BA:1358:G:O2'	26:BA:1359:A:H5"	2.15	0.46
26:BA:2120:G:H2'	26:BA:2121:G:H5'	1.97	0.46
26:BA:2356:C:OP1	47:B0:24:LYS:NZ	2.39	0.46
26:BA:2564:A:OP1	26:BA:2648:C:H4'	2.16	0.46
28:BD:232:PRO:HB3	28:BD:244:ARG:CZ	2.45	0.46
28:BD:275:LYS:HB3	28:BD:276:LYS:H	1.47	0.46
45:BY:6:HIS:HE1	45:BY:72:VAL:O	1.98	0.46
1:CA:750:G:N2	15:CO:23:GLY:O	2.42	0.46
1:CA:1010:G:H2'	1:CA:1011:G:C8	2.49	0.46
2:CB:170:GLU:O	2:CB:174:VAL:HG23	2.15	0.46
4:CD:23:GLY:O	4:CD:26:CYS:HB2	2.14	0.46
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.50	0.46
18:CR:45:SER:OG	18:CR:47:THR:HG22	2.16	0.46
26:DA:601:C:O2'	26:DA:605:C:OP1	2.32	0.46
26:DA:1935:G:H1'	26:DA:1964:G:N2	2.31	0.46
26:DA:2126:A:H2	26:DA:2127:G:N3	2.12	0.46
26:DA:2172:U:O2'	26:DA:2173:A:OP1	2.30	0.46
27:DB:42:C:O2	31:DG:93:THR:N	2.38	0.46
40:DT:23:ARG:HG3	40:DT:120:ARG:NH1	2.30	0.46
45:DY:5:MET:HE2	45:DY:5:MET:HB2	1.75	0.46
1:AA:358:U:H2'	1:AA:359:U:H6	1.80	0.46
1:AA:966:G:H21	9:AI:127:LYS:NZ	2.07	0.46
1:AA:967:C:H3'	1:AA:968:A:H2'	1.97	0.46
4:AD:20:TYR:HA	4:AD:26:CYS:SG	2.56	0.46
11:AK:78:GLN:O	11:AK:103:LEU:HD22	2.15	0.46
19:AS:66:MET:HA	51:B4:58:ARG:NH1	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.16	0.46
26:BA:27:G:N2	26:BA:512:G:H1'	2.30	0.46
26:BA:280:C:H2'	26:BA:281:G:O4'	2.15	0.46
26:BA:744:G:H5"	26:BA:1658:C:H5"	1.97	0.46
26:BA:832:G:N3	36:BP:53:GLY:HA3	2.30	0.46
26:BA:2392:A:O3'	55:B8:27:THR:HB	2.15	0.46
26:BA:2398:U:H2'	26:BA:2399:G:C8	2.51	0.46
26:BA:2845:G:H2'	26:BA:2846:G:C8	2.50	0.46
38:BR:38:VAL:HG22	38:BR:112:ALA:HB2	1.97	0.46
1:CA:313:A:H2'	1:CA:314:C:C6	2.49	0.46
1:CA:1153:C:N4	1:CA:1154:G:H21	2.10	0.46
1:CA:1166:G:H8	1:CA:1166:G:O5'	1.98	0.46
1:CA:1356:G:H8	1:CA:1356:G:O5'	1.98	0.46
2:CB:97:TRP:CZ2	2:CB:102:LEU:HD13	2.50	0.46
14:CN:26:ARG:HD3	14:CN:43:CYS:SG	2.54	0.46
14:CN:48:ALA:HB2	14:CN:53:LEU:HD12	1.97	0.46
26:DA:96:G:H4'	49:D2:48:HIS:CD2	2.50	0.46
26:DA:1021:A:C8	26:DA:1021:A:H3'	2.50	0.46
26:DA:2753:A:N3	56:D9:15:LYS:NZ	2.55	0.46
26:DA:2845:G:H5"	40:DT:54:ARG:O	2.15	0.46
26:DA:2886:G:H2'	26:DA:2887:U:H6	1.79	0.46
27:DB:37:C:C5	27:DB:38:C:C4	3.04	0.46
30:DF:154:VAL:HG22	30:DF:191:ARG:HB2	1.98	0.46
33:DI:52:ARG:HH11	33:DI:52:ARG:HG3	1.79	0.46
1:AA:107:G:H2'	1:AA:108:G:O4'	2.15	0.46
1:AA:606:G:H1'	1:AA:632:A:H61	1.80	0.46
1:AA:826:C:H2'	1:AA:827:U:C6	2.50	0.46
1:AA:1092:A:H5'	1:AA:1092:A:H8	1.80	0.46
1:AA:1165:C:N3	1:AA:1171:G:O6	2.49	0.46
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.36	0.46
1:AA:1404:C:H2'	1:AA:1405:G:C8	2.49	0.46
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.97	0.46
9:AI:47:LEU:O	9:AI:50:LEU:HG	2.15	0.46
24:AX:61:C:H2'	24:AX:62:C:C6	2.50	0.46
26:BA:271(R):G:C2'	26:BA:271(S):G:H5"	2.42	0.46
26:BA:754:C:H2'	26:BA:755:C:C6	2.49	0.46
26:BA:1171:G:H3'	26:BA:1173:G:H5'	1.98	0.46
26:BA:1412:A:H2'	26:BA:1413:G:C8	2.50	0.46
26:BA:1459:G:H5"	26:BA:1460:A:OP2	2.16	0.46
26:BA:2207:G:H2'	26:BA:2208:A:C2	2.49	0.46
26:BA:2335:A:C8	26:BA:2337:G:C5	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2801(A):A:N3	26:BA:2895:U:H1'	2.30	0.46
27:BB:48:A:H2'	27:BB:49:C:C6	2.50	0.46
28:BD:97:TYR:HE1	28:BD:103:ARG:HG3	1.80	0.46
35:BO:98:VAL:HG22	35:BO:118:ALA:HA	1.97	0.46
1:CA:77:G:C5	1:CA:93:G:C2	3.04	0.46
1:CA:335:C:H2'	1:CA:336:C:C6	2.50	0.46
1:CA:765:G:N1	1:CA:812:C:O2'	2.40	0.46
2:CB:16:HIS:O	2:CB:18:GLY:N	2.48	0.46
2:CB:223:ILE:HA	2:CB:226:ARG:HG2	1.97	0.46
4:CD:108:LEU:HD12	4:CD:108:LEU:HA	1.68	0.46
13:CM:17:VAL:O	13:CM:20:THR:OG1	2.30	0.46
17:CQ:64:PRO:HB3	17:CQ:70:ARG:NH1	2.30	0.46
26:DA:320:A:H4'	26:DA:322:A:N7	2.30	0.46
26:DA:471:A:H2'	26:DA:472:A:O4'	2.15	0.46
26:DA:577:G:O2'	26:DA:1254:A:OP1	2.34	0.46
26:DA:666:G:H4'	36:DP:49:ARG:NH2	2.30	0.46
26:DA:725:G:C6	26:DA:726:G:N1	2.83	0.46
26:DA:1394:U:C4	26:DA:1395:A:C5	3.03	0.46
26:DA:1486:A:H2'	26:DA:1487:G:H8	1.81	0.46
26:DA:1547:C:O2'	26:DA:1548:C:H5'	2.15	0.46
26:DA:1820:U:C4	28:DD:202:LYS:HD3	2.50	0.46
26:DA:2406:U:H2'	26:DA:2406:U:OP2	2.15	0.46
26:DA:2591:C:H2'	26:DA:2592:G:C8	2.51	0.46
36:DP:21:ARG:HD3	36:DP:21:ARG:HA	1.70	0.46
1:AA:598:U:H2'	1:AA:599:C:C6	2.50	0.46
1:AA:672:U:O2'	1:AA:673:G:O5'	2.32	0.46
4:AD:33:MET:HB2	58:AD:302:SF4:S2	2.55	0.46
25:AY:75:C:H5"	25:AY:76:A:OP1	2.14	0.46
26:BA:64:A:C5	44:BX:66:LEU:HD12	2.50	0.46
26:BA:196:A:O2'	26:BA:805:G:O6	2.26	0.46
26:BA:569:U:O2'	26:BA:983:A:N1	2.41	0.46
26:BA:666:G:C2'	26:BA:667:U:H5'	2.45	0.46
26:BA:826:U:C4'	36:BP:55:ARG:HB2	2.45	0.46
26:BA:1341:U:O2	44:BX:80:ILE:HD12	2.15	0.46
26:BA:2127:G:O2'	26:BA:2128:C:O4'	2.34	0.46
26:BA:2162:G:C5'	26:BA:2172:U:H2'	2.46	0.46
26:BA:2345:G:N3	26:BA:2381:C:H2'	2.30	0.46
26:BA:2695:C:H2'	26:BA:2696:U:C6	2.51	0.46
1:CA:18:C:H5'	1:CA:1079:G:H1'	1.95	0.46
1:CA:229:U:H2'	1:CA:230:G:C8	2.51	0.46
1:CA:1055:A:H5'	1:CA:1055:A:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.61	0.46
1:CA:1295:G:O2'	13:CM:14:ARG:NH1	2.48	0.46
1:CA:1402:C:H2'	1:CA:1403:C:O4'	2.15	0.46
3:CC:124:ILE:HD11	3:CC:189:ALA:HB1	1.98	0.46
20:CT:40:ALA:HB2	20:CT:55:ILE:HG22	1.97	0.46
24:CX:19:G:H1	24:CX:56:C:N4	2.09	0.46
26:DA:58:G:O2'	26:DA:73:A:N1	2.43	0.46
26:DA:1399:C:OP1	44:DX:25:LYS:NZ	2.48	0.46
26:DA:2017:U:O2	52:D5:10:LYS:HB2	2.15	0.46
26:DA:2148:G:H2'	26:DA:2149:G:H8	1.80	0.46
26:DA:2823:A:OP1	29:DE:113:PHE:HB2	2.15	0.46
27:DB:32:C:N3	27:DB:33:G:C5	2.84	0.46
28:DD:276:LYS:HD3	28:DD:276:LYS:H	1.81	0.46
29:DE:72:VAL:HG22	29:DE:73:GLU:HB3	1.96	0.46
36:DP:47:ASP:OD2	36:DP:50:ARG:NH2	2.49	0.46
46:DZ:119:GLU:H	46:DZ:119:GLU:HG2	1.49	0.46
1:AA:49:U:O2'	1:AA:50:A:H2'	2.14	0.46
1:AA:975:A:N6	1:AA:1367:C:O4'	2.48	0.46
6:AF:21:LEU:O	6:AF:25:ILE:HG12	2.15	0.46
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.15	0.46
26:BA:34:C:H41	26:BA:447:A:N6	2.14	0.46
26:BA:385:C:O2	36:BP:71:VAL:HG21	2.15	0.46
26:BA:768:G:O2'	26:BA:1379:A:N1	2.41	0.46
26:BA:969:U:H2'	26:BA:970:C:C6	2.51	0.46
26:BA:1430:C:H2'	26:BA:1431:U:C6	2.49	0.46
26:BA:1783:A:H5'	26:BA:2608:G:H4'	1.97	0.46
26:BA:2094:G:OP1	33:BI:22:LYS:HD2	2.14	0.46
26:BA:2461:C:H2'	26:BA:2462:U:C6	2.51	0.46
26:BA:2512:C:H2'	26:BA:2513:G:O4'	2.15	0.46
42:BV:23:GLU:OE1	42:BV:89:GLN:NE2	2.47	0.46
51:B4:54:GLY:HA2	51:B4:55:ARG:HA	1.48	0.46
1:CA:130:A:N3	1:CA:263:A:O2'	2.37	0.46
1:CA:342:C:C2'	1:CA:343:U:H5'	2.46	0.46
1:CA:448:A:P	1:CA:485:G:H22	2.38	0.46
1:CA:1038:C:H2'	1:CA:1039:C:C6	2.51	0.46
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.98	0.46
4:CD:155:LEU:HD23	4:CD:156:GLU:H	1.81	0.46
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.16	0.46
24:CX:49:G:N1	24:CX:65:C:C4	2.71	0.46
26:DA:1359:A:N6	26:DA:1372:U:C4	2.83	0.46
26:DA:1578:U:C2'	26:DA:1579:A:H5'	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2199:A:H3'	26:DA:2200:C:C6	2.51	0.46
26:DA:2712:U:O2'	26:DA:2713:A:H5'	2.16	0.46
27:DB:31:C:C5	27:DB:32:C:H5	2.33	0.46
27:DB:43:C:H2'	27:DB:44:G:H5"	1.98	0.46
35:DO:1:MET:HG3	35:DO:67:LYS:HG2	1.97	0.46
1:AA:674:G:H2'	1:AA:675:A:C8	2.50	0.46
1:AA:1025:U:O2	1:AA:1036:G:O6	2.34	0.46
1:AA:1493:A:H2'	26:BA:1913:A:N1	2.30	0.46
2:AB:21:ARG:H	2:AB:21:ARG:HD2	1.80	0.46
3:AC:85:ARG:O	3:AC:89:GLU:N	2.47	0.46
4:AD:81:GLU:OE1	4:AD:139:ARG:NH1	2.36	0.46
4:AD:103:ASN:O	4:AD:107:ARG:HG2	2.15	0.46
26:BA:674:G:H1'	30:BF:74:ARG:HD3	1.97	0.46
26:BA:1794:U:H2'	26:BA:1795:C:H6	1.80	0.46
26:BA:1814:G:H4'	28:BD:51:VAL:HG21	1.98	0.46
33:BI:85:GLU:O	33:BI:123:LEU:HD12	2.15	0.46
1:CA:344:A:H4'	1:CA:345:C:OP2	2.16	0.46
1:CA:512:U:O4'	4:CD:43:HIS:HE1	1.98	0.46
1:CA:1456:G:O6	20:CT:54:LYS:HE3	2.15	0.46
6:CF:75:LEU:O	6:CF:79:LEU:HG	2.15	0.46
7:CG:29:LYS:HG3	7:CG:101:LEU:HB3	1.97	0.46
9:CI:73:GLN:HA	9:CI:76:ALA:HB3	1.98	0.46
10:CJ:44:VAL:HG13	10:CJ:66:ARG:HG2	1.97	0.46
26:DA:898:C:H2'	26:DA:899:A:O4'	2.16	0.46
26:DA:1353:A:H2'	26:DA:1354:A:C8	2.51	0.46
26:DA:1654:A:C1'	26:DA:2823:A:H5'	2.46	0.46
26:DA:2370:G:C6	26:DA:2371:G:C6	3.03	0.46
26:DA:2808:U:H2'	26:DA:2891:G:N1	2.30	0.46
28:DD:3:VAL:HG13	28:DD:17:THR:HB	1.96	0.46
29:DE:116:VAL:HG11	29:DE:138:PRO:HB3	1.98	0.46
30:DF:129:PHE:CE2	30:DF:163:VAL:HG11	2.51	0.46
31:DG:68:PRO:HG2	31:DG:90:LEU:HD22	1.97	0.46
32:DH:7:LEU:O	32:DH:69:ARG:NH1	2.47	0.46
35:DO:52:VAL:HG12	35:DO:94:ARG:NH2	2.31	0.46
41:DU:58:ARG:HA	41:DU:61:TRP:CE3	2.51	0.46
1:AA:56:U:H2'	1:AA:57:G:H8	1.76	0.46
1:AA:189(C):C:H2'	1:AA:189(D):C:O4'	2.16	0.46
1:AA:951:G:C2'	1:AA:952:U:H5'	2.46	0.46
1:AA:976:G:C8	1:AA:1362:C:N4	2.83	0.46
2:AB:223:ILE:HA	2:AB:226:ARG:HG2	1.97	0.46
9:AI:77:ILE:O	9:AI:81:ILE:HG22	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:59:TYR:O	13:AM:63:THR:OG1	2.25	0.46
26:BA:2610:C:O2	61:BA:4295:HOH:O	2.20	0.46
26:BA:2646:C:OP2	26:BA:2732:G:O2'	2.34	0.46
26:BA:2693:A:H2'	26:BA:2694:G:H8	1.80	0.46
27:BB:87:G:N2	27:BB:90:A:OP2	2.44	0.46
30:BF:8:GLN:HE22	30:BF:21:ALA:HB2	1.81	0.46
40:BT:53:ARG:HB3	40:BT:53:ARG:CZ	2.46	0.46
1:CA:90:U:O2'	1:CA:91:C:H5'	2.15	0.46
1:CA:269:C:H2'	1:CA:270:A:C8	2.51	0.46
1:CA:419:C:H5"	1:CA:513:C:H1'	1.98	0.46
1:CA:967:C:H2'	1:CA:968:A:C8	2.51	0.46
1:CA:994:A:C5	1:CA:1216:G:H4'	2.50	0.46
1:CA:1025:U:N3	1:CA:1036:G:N1	2.64	0.46
1:CA:1127:G:H5'	1:CA:1281:U:O2	2.16	0.46
1:CA:1316:G:N2	1:CA:1318:A:H3'	2.31	0.46
2:CB:19:HIS:CD2	2:CB:20:GLU:H	2.34	0.46
2:CB:82:ARG:HG2	2:CB:83:MET:N	2.31	0.46
2:CB:204:ASN:O	2:CB:210:SER:OG	2.24	0.46
13:CM:68:GLY:HA3	31:DG:116:ASP:CG	2.39	0.46
26:DA:994:C:H1'	42:DV:10:LYS:HE3	1.97	0.46
26:DA:1230:C:H2'	26:DA:1231:G:C8	2.48	0.46
26:DA:2815:C:H2'	26:DA:2816:C:C6	2.51	0.46
28:DD:183:ARG:HG3	28:DD:270:ILE:HG12	1.97	0.46
41:DU:28:ARG:NH1	41:DU:38:THR:OG1	2.43	0.46
46:DZ:5:LEU:HG	46:DZ:47:VAL:HG21	1.98	0.46
50:D3:8:LEU:O	50:D3:32:GLN:N	2.36	0.46
1:AA:309:G:H2'	1:AA:310:G:H8	1.81	0.46
1:AA:539:A:H2'	1:AA:540:G:C8	2.50	0.46
1:AA:737:A:O5'	6:AF:92:LYS:NZ	2.46	0.46
1:AA:814:A:H2'	1:AA:816:A:H5"	1.98	0.46
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.41	0.46
1:AA:1273:G:H3'	1:AA:1274:G:C8	2.51	0.46
1:AA:1346:A:N1	1:AA:1374:A:H5"	2.30	0.46
1:AA:1366:C:HO2'	10:AJ:60:ARG:HH22	1.62	0.46
1:AA:1414:U:H3	1:AA:1486:G:H1	1.63	0.46
1:AA:1492:A:H2'	1:AA:1493:A:C8	2.51	0.46
5:AE:103:GLY:O	5:AE:106:PRO:HD2	2.16	0.46
8:AH:33:GLU:HG2	8:AH:48:TYR:CE2	2.50	0.46
11:AK:29:ILE:HG23	11:AK:44:SER:HB3	1.98	0.46
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.81	0.46
26:BA:252:G:OP1	36:BP:50:ARG:NH1	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:631:A:H2'	26:BA:632:A:O4'	2.14	0.46
26:BA:911:A:H2'	37:BQ:9:TYR:OH	2.16	0.46
26:BA:1359:A:C6	26:BA:1372:U:N3	2.82	0.46
26:BA:2162:G:N1	26:BA:2163:C:C4	2.84	0.46
26:BA:2179:C:H2'	26:BA:2180:U:C6	2.50	0.46
26:BA:2478:A:OP2	56:B9:2:LYS:NZ	2.41	0.46
26:BA:2723:C:H4'	38:BR:1:MET:HG3	1.98	0.46
61:BA:4873:HOH:O	29:BE:162:ALA:HB3	2.16	0.46
28:BD:79:VAL:HG12	28:BD:113:VAL:HA	1.97	0.46
41:BU:28:ARG:NH1	41:BU:38:THR:OG1	2.43	0.46
46:BZ:150:LEU:O	46:BZ:171:ILE:HG13	2.15	0.46
1:CA:838:G:C6	1:CA:848:C:N4	2.82	0.46
1:CA:958:A:N3	1:CA:985:C:O2'	2.46	0.46
2:CB:97:TRP:CH2	2:CB:101:MET:HB2	2.51	0.46
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.98	0.46
9:CI:86:VAL:HA	9:CI:89:ASN:O	2.16	0.46
26:DA:30:G:H2'	26:DA:31:C:H6	1.79	0.46
26:DA:195:A:H61	26:DA:198:C:H3'	1.81	0.46
26:DA:652:C:C2'	26:DA:652(A):A:H5'	2.46	0.46
26:DA:754:C:H2'	26:DA:755:C:C6	2.51	0.46
26:DA:910:A:N1	26:DA:2277:G:H1'	2.31	0.46
26:DA:1429:G:H2'	26:DA:1430:C:C6	2.51	0.46
26:DA:1474:C:H2'	26:DA:1475:G:C8	2.51	0.46
26:DA:1851:U:C4	26:DA:1852:C:C4	3.04	0.46
26:DA:1853:A:N3	26:DA:2233:U:O2'	2.38	0.46
26:DA:2242:G:H2'	26:DA:2243:U:O4'	2.16	0.46
26:DA:2741:A:OP1	56:D9:22:ARG:NH2	2.45	0.46
26:DA:2785:C:HO2'	29:DE:66:HIS:CE1	2.32	0.46
26:DA:2881:C:H2'	26:DA:2882:A:O4'	2.16	0.46
32:DH:70:THR:HG22	32:DH:74:ASN:ND2	2.31	0.46
37:DQ:26:TYR:CD1	37:DQ:28:ALA:HB2	2.51	0.46
43:DW:46:PHE:O	43:DW:50:VAL:HG23	2.16	0.46
1:AA:43:C:H2'	1:AA:44:G:O4'	2.15	0.46
1:AA:533:A:O2'	1:AA:535:A:OP2	2.24	0.46
1:AA:600:C:H5'	8:AH:129:VAL:HA	1.98	0.46
1:AA:762:C:H2'	1:AA:763:G:H8	1.80	0.46
1:AA:927:G:H1	1:AA:1390:U:H3	1.63	0.46
1:AA:1065:U:H4'	1:AA:1066:C:O5'	2.15	0.46
1:AA:1165:C:N4	1:AA:1166:G:C6	2.84	0.46
4:AD:172:PRO:HB2	4:AD:187:ARG:NH2	2.31	0.46
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2282:G:OP1	26:BA:2283:C:H1'	2.16	0.46
26:BA:2328:A:H2'	26:BA:2329:G:C8	2.50	0.46
32:BH:4:ILE:O	32:BH:69:ARG:HG2	2.16	0.46
40:BT:60:THR:HG22	40:BT:77:PRO:HA	1.97	0.46
51:B4:61:ARG:HG3	51:B4:62:ARG:H	1.81	0.46
1:CA:262:A:C6	1:CA:263:A:C6	3.04	0.46
1:CA:973:G:H3'	1:CA:974:A:H5"	1.97	0.46
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.51	0.46
3:CC:191:THR:HG21	3:CC:193:TYR:CZ	2.51	0.46
7:CG:75:VAL:HG13	7:CG:145:ALA:HA	1.98	0.46
11:CK:77:MET:HE2	11:CK:77:MET:HB2	1.78	0.46
24:CX:29:G:C6	24:CX:30:G:C5	3.04	0.46
26:DA:320:A:H4'	26:DA:322:A:C8	2.51	0.46
26:DA:566:U:H2'	26:DA:567:A:O4'	2.16	0.46
26:DA:773:U:H2'	26:DA:774:A:H5'	1.98	0.46
26:DA:1184:G:OP1	50:D3:30:ARG:HD2	2.16	0.46
26:DA:1243:G:H2'	26:DA:1244:G:O4'	2.15	0.46
26:DA:1375:C:H2'	26:DA:1376:C:C6	2.51	0.46
26:DA:1913:A:H4'	26:DA:1914:C:C5'	2.46	0.46
26:DA:2153:G:H3'	26:DA:2154:G:C8	2.50	0.46
26:DA:2200:C:O2	26:DA:2226:C:N4	2.49	0.46
28:DD:73:VAL:HG13	28:DD:120:GLY:HA3	1.98	0.46
30:DF:24:LEU:HD21	30:DF:114:VAL:HG12	1.97	0.46
42:DV:21:ARG:HG2	42:DV:91:TYR:CD2	2.51	0.46
1:AA:189(C):C:N4	1:AA:189(H):G:H1	2.14	0.46
1:AA:600:C:O2'	1:AA:601:C:H5'	2.16	0.46
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.51	0.46
22:AV:13:A:H4'	22:AV:14:A:OP2	2.16	0.46
26:BA:931:G:O2'	50:B3:24:LYS:HD3	2.16	0.46
26:BA:1045:A:OP1	26:BA:1047:G:H5"	2.16	0.46
26:BA:2032:G:H1'	29:BE:145:LYS:HD3	1.98	0.46
34:BN:12:ARG:NH1	34:BN:38:HIS:HE2	2.14	0.46
35:BO:4:PRO:O	35:BO:5:GLN:HB2	2.16	0.46
41:BU:108:GLU:O	41:BU:112:ARG:HG2	2.15	0.46
51:B4:68:ARG:HD2	51:B4:69:LYS:N	2.29	0.46
1:CA:98:G:C6	1:CA:99:U:C4	3.03	0.46
1:CA:262:A:H2'	1:CA:263:A:C8	2.51	0.46
1:CA:634:C:H2'	1:CA:635:G:H8	1.81	0.46
1:CA:685:G:C2	1:CA:686:U:C4	3.04	0.46
1:CA:741:G:H5"	15:CO:59:MET:HE1	1.97	0.46
1:CA:748:C:H4'	1:CA:749:C:O5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CH:34:GLU:OE1	8:CH:37:ARG:NH1	2.49	0.46
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.15	0.46
24:CX:22:G:H2'	24:CX:23:C:C6	2.51	0.46
26:DA:576:U:H2'	26:DA:577:G:C8	2.51	0.46
26:DA:717:G:H2'	26:DA:718:A:O4'	2.17	0.46
26:DA:784:A:C6	28:DD:229:VAL:HG21	2.51	0.46
26:DA:1021:A:H3'	26:DA:1021:A:H8	1.80	0.46
26:DA:2419:U:H2'	26:DA:2420:C:C6	2.51	0.46
26:DA:2493:U:H2'	26:DA:2494:G:O4'	2.16	0.46
27:DB:63:G:H2'	27:DB:64:C:C6	2.50	0.46
27:DB:80:U:H2'	27:DB:81:G:C8	2.50	0.46
33:DI:88:ILE:HG21	33:DI:144:VAL:CG1	2.46	0.46
34:DN:115:ARG:HA	34:DN:118:LYS:HE3	1.98	0.46
51:D4:59:PHE:HA	51:D4:60:GLN:C	2.40	0.46
1:AA:102:G:O2'	1:AA:151:A:N3	2.31	0.45
1:AA:143:A:H2'	1:AA:143:A:N3	2.31	0.45
1:AA:348:G:C2'	1:AA:349:A:H5'	2.46	0.45
1:AA:779:C:H2'	1:AA:780:A:O4'	2.16	0.45
1:AA:1216:G:H5"	14:AN:5:ALA:CB	2.46	0.45
2:AB:35:GLU:OE1	2:AB:38:GLY:HA2	2.17	0.45
24:AX:50:U:O5'	24:AX:50:U:H6	1.99	0.45
26:BA:144:C:H5'	44:BX:2:LYS:HE2	1.98	0.45
26:BA:722:A:H2'	26:BA:723:G:C8	2.51	0.45
26:BA:1654:A:C1'	26:BA:2823:A:H5'	2.46	0.45
26:BA:1697:G:OP2	26:BA:1698:A:O2'	2.18	0.45
26:BA:2139:C:C2	26:BA:2153:G:C2	3.05	0.45
26:BA:2685:G:H5'	35:BO:68:GLU:CD	2.41	0.45
30:BF:178:PRO:HB2	30:BF:201:VAL:CG2	2.47	0.45
33:BI:43:ASN:HD22	33:BI:43:ASN:C	2.24	0.45
38:BR:44:LEU:HD22	38:BR:48:VAL:HG23	1.99	0.45
42:BV:55:ALA:HB2	42:BV:101:GLY:HA2	1.98	0.45
1:CA:375:U:O3'	16:CP:6:LEU:HB2	2.17	0.45
1:CA:407:G:N1	1:CA:436:C:C2	2.83	0.45
1:CA:779:C:H2'	1:CA:780:A:O4'	2.16	0.45
4:CD:112:VAL:HG22	4:CD:116:GLN:OE1	2.16	0.45
15:CO:5:LYS:O	15:CO:9:GLN:HG2	2.17	0.45
24:CX:19:G:H4'	24:CX:20:U:OP2	2.15	0.45
24:CX:60:U:H3'	24:CX:61:C:H6	1.81	0.45
26:DA:448:U:C4	26:DA:583:G:H1'	2.51	0.45
26:DA:1220:A:OP2	41:DU:19:LYS:NZ	2.46	0.45
26:DA:1932:A:H2'	26:DA:1933:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2082:A:H3'	26:DA:2083:G:H8	1.81	0.45
26:DA:2133:G:O2'	26:DA:2157:G:N2	2.31	0.45
26:DA:2137:C:N4	26:DA:2154:G:N1	2.29	0.45
26:DA:2820:A:OP2	38:DR:2:ARG:NH2	2.49	0.45
61:DA:4083:HOH:O	36:DP:16:ARG:HG3	2.15	0.45
27:DB:1:U:H2'	27:DB:2:C:C6	2.51	0.45
27:DB:16:G:H2'	27:DB:17:C:C6	2.51	0.45
34:DN:104:LYS:HA	34:DN:107:LEU:HD12	1.98	0.45
36:DP:6:LEU:HD23	36:DP:6:LEU:HA	1.79	0.45
1:AA:93:G:H2'	1:AA:96:U:O4'	2.16	0.45
1:AA:892:A:O2'	1:AA:1415:G:H4'	2.16	0.45
1:AA:1252:A:H61	1:AA:1285:A:N6	2.05	0.45
5:AE:144:THR:OG1	5:AE:147:ASP:OD2	2.32	0.45
11:AK:45:GLY:O	11:AK:50:TYR:HB2	2.17	0.45
26:BA:1530:C:H42	26:BA:1539:G:H1	1.65	0.45
26:BA:1721:G:H5'	26:BA:1722:A:OP2	2.17	0.45
26:BA:1916:A:H2'	26:BA:1917:U:O4'	2.16	0.45
26:BA:2065:C:H2'	26:BA:2066:C:C6	2.51	0.45
26:BA:2127:G:C2	26:BA:2128:C:C2	3.04	0.45
46:BZ:107:THR:HA	46:BZ:108:PRO:HD3	1.73	0.45
55:B8:23:VAL:CG1	55:B8:47:LYS:HD3	2.46	0.45
1:CA:90:U:C2'	1:CA:91:C:H5'	2.46	0.45
1:CA:728:A:OP1	1:CA:742:G:O2'	2.34	0.45
1:CA:758:G:H5'	1:CA:880:C:H1'	1.98	0.45
1:CA:978:A:O2'	1:CA:1321:C:N4	2.48	0.45
1:CA:1202:G:H2'	1:CA:1203:C:O4'	2.16	0.45
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.17	0.45
1:CA:1371:G:C6	1:CA:1372:U:C4	3.04	0.45
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.84	0.45
3:CC:33:LEU:HD21	14:CN:53:LEU:HD22	1.97	0.45
7:CG:51:GLN:HE21	7:CG:51:GLN:HB3	1.64	0.45
9:CI:72:GLY:O	9:CI:76:ALA:N	2.43	0.45
24:CX:38:A:H8	24:CX:38:A:O5'	1.99	0.45
26:DA:184:C:H2'	26:DA:185:U:H6	1.80	0.45
26:DA:2124:G:H3'	26:DA:2125:G:H5"	1.96	0.45
26:DA:2203:U:H2'	26:DA:2205:C:H6	1.78	0.45
34:DN:4:TYR:CE2	41:DU:100:VAL:HG11	2.51	0.45
43:DW:79:GLY:HA3	43:DW:100:THR:HG22	1.97	0.45
51:D4:34:GLU:H	51:D4:34:GLU:CD	2.24	0.45
1:AA:22:G:H4'	1:AA:885:G:C8	2.51	0.45
1:AA:66:G:H2'	1:AA:67:C:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:625:G:H4'	16:AP:16:HIS:HB3	1.97	0.45
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.82	0.45
1:AA:1152:A:OP1	10:AJ:70:ARG:NH2	2.50	0.45
1:AA:1152:A:H5'	10:AJ:13:HIS:CG	2.52	0.45
12:AL:97:ARG:HB2	12:AL:98:TYR:CE2	2.51	0.45
26:BA:904:C:H2'	26:BA:905:U:C6	2.52	0.45
26:BA:1171:G:H5'	26:BA:1173:G:OP2	2.16	0.45
26:BA:1639:U:O2'	26:BA:1640:C:H5'	2.17	0.45
26:BA:2075:U:OP2	26:BA:2238:G:O2'	2.28	0.45
33:BI:106:GLY:HA2	33:BI:107:VAL:CG2	2.44	0.45
46:BZ:110:GLY:N	46:BZ:144:LEU:O	2.43	0.45
49:B2:35:LEU:HB3	49:B2:50:ILE:HG12	1.99	0.45
52:B5:40:LYS:NZ	52:B5:44:THR:O	2.49	0.45
1:CA:72:C:N3	1:CA:97:G:C2	2.83	0.45
1:CA:131:C:H2'	1:CA:132:C:C6	2.51	0.45
1:CA:162:A:N3	1:CA:348:G:H4'	2.31	0.45
1:CA:1464:G:OP1	40:DT:108:ARG:HD3	2.16	0.45
11:CK:34:ASP:OD2	11:CK:38:ASN:HB2	2.17	0.45
23:CW:76:PPU:N	24:CX:76:31H:N3'	2.61	0.45
24:CX:7:G:H5"	24:CX:8:4SU:H5	1.98	0.45
26:DA:330:A:C2	26:DA:1210:A:H2'	2.51	0.45
26:DA:608:A:OP1	30:DF:100:THR:OG1	2.25	0.45
26:DA:628:G:O2'	26:DA:651:G:O2'	2.35	0.45
26:DA:629:G:H5"	26:DA:650:C:O2'	2.16	0.45
26:DA:947:G:N2	26:DA:971:C:C2	2.84	0.45
26:DA:1037:G:H2'	26:DA:1038:C:O4'	2.17	0.45
26:DA:1250:G:N7	36:DP:18:ARG:NH2	2.64	0.45
26:DA:1265:A:H8	26:DA:1265:A:OP1	2.00	0.45
26:DA:2016:U:H2'	26:DA:2017:U:C6	2.52	0.45
26:DA:2704:C:H2'	26:DA:2705:A:O4'	2.16	0.45
26:DA:2773:C:O2'	26:DA:2774:C:H5'	2.16	0.45
28:DD:121:PRO:HB3	28:DD:135:PHE:CE2	2.51	0.45
30:DF:116:ASP:OD2	36:DP:1:MET:N	2.46	0.45
30:DF:156:LEU:HD21	30:DF:163:VAL:HG12	1.98	0.45
37:DQ:18:LYS:O	37:DQ:98:LYS:NZ	2.45	0.45
38:DR:36:THR:HG22	38:DR:37:THR:H	1.81	0.45
39:DS:110:LEU:HD12	39:DS:110:LEU:HA	1.80	0.45
42:DV:60:GLU:N	42:DV:95:LEU:O	2.38	0.45
45:DY:6:HIS:H	45:DY:6:HIS:CD2	2.34	0.45
55:D8:9:GLY:O	55:D8:13:ARG:HG2	2.16	0.45
1:AA:1030:C:N3	1:AA:1031:G:N2	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1225:A:H2'	1:AA:1226:C:C5	2.51	0.45
2:AB:146:GLN:O	2:AB:150:SER:HB3	2.16	0.45
6:AF:12:PRO:HG3	6:AF:57:GLN:O	2.16	0.45
17:AQ:76:LEU:HD12	17:AQ:77:VAL:H	1.82	0.45
26:BA:795:C:H2'	26:BA:796:C:C6	2.52	0.45
26:BA:874:G:C2'	26:BA:875:G:H5'	2.46	0.45
26:BA:1045:A:OP1	26:BA:1046:A:H3'	2.16	0.45
26:BA:1415:U:O2'	26:BA:1417:C:OP1	2.29	0.45
26:BA:2439:A:H5'	26:BA:2439:A:C8	2.52	0.45
51:B4:59:PHE:HB2	51:B4:62:ARG:CZ	2.46	0.45
1:CA:5:U:H6	1:CA:5:U:H2'	1.53	0.45
1:CA:509:A:H2'	1:CA:510:A:C8	2.50	0.45
1:CA:1080:A:H5"	1:CA:1081:G:OP2	2.17	0.45
1:CA:1176:A:H2'	1:CA:1177:G:O4'	2.16	0.45
1:CA:1255:G:P	10:CJ:45:ARG:HH22	2.40	0.45
3:CC:35:GLU:HG3	3:CC:36:ASP:N	2.31	0.45
12:CL:33:ARG:O	12:CL:85:ILE:HG12	2.16	0.45
13:CM:3:ARG:HB3	13:CM:8:GLU:HA	1.99	0.45
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.29	0.45
19:CS:40:ILE:HD12	19:CS:69:HIS:O	2.16	0.45
26:DA:196:A:C4	26:DA:805:G:C6	3.04	0.45
26:DA:250:G:C6	26:DA:251:A:C6	3.04	0.45
26:DA:507:A:H5"	26:DA:508:G:H3'	1.98	0.45
26:DA:719:C:H2'	26:DA:720:C:C6	2.51	0.45
26:DA:815:C:H2'	26:DA:816:C:C6	2.52	0.45
26:DA:828:U:C5	26:DA:2247:A:H4'	2.52	0.45
26:DA:1011:G:H1'	26:DA:1013:C:O4'	2.16	0.45
26:DA:1242:A:N1	36:DP:4:SER:OG	2.45	0.45
26:DA:1613:G:C2	26:DA:1619:G:C5	3.05	0.45
26:DA:2016:U:O2'	52:D5:7:PRO:O	2.33	0.45
33:DI:110:ASP:HA	33:DI:111:PRO:HD3	1.80	0.45
35:DO:98:VAL:HG22	35:DO:118:ALA:HA	1.99	0.45
49:D2:28:LYS:HB3	49:D2:57:ILE:HG12	1.97	0.45
1:AA:429:U:H4'	1:AA:430:A:O5'	2.16	0.45
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.49	0.45
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.52	0.45
2:AB:80:ILE:HD12	2:AB:211:ILE:HG22	1.98	0.45
2:AB:82:ARG:NH1	2:AB:86:GLU:OE2	2.50	0.45
7:AG:140:ASP:OD1	7:AG:143:ARG:NH2	2.42	0.45
10:AJ:64:GLU:HG2	14:AN:59:ALA:HB2	1.99	0.45
13:AM:19:LEU:HD12	13:AM:19:LEU:HA	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:82:ILE:O	15:AO:86:GLY:N	2.50	0.45
16:AP:6:LEU:HB3	16:AP:17:TYR:CD1	2.51	0.45
26:BA:145:G:H2'	26:BA:146:G:C8	2.51	0.45
26:BA:588:U:H2'	26:BA:589:C:C6	2.51	0.45
26:BA:957:A:N1	26:BA:2458:G:H4'	2.32	0.45
26:BA:2167:U:H5'	26:BA:2168:G:OP2	2.17	0.45
26:BA:2478:A:H2'	26:BA:2479:G:O4'	2.16	0.45
26:BA:2691:C:O3'	26:BA:2871:C:H4'	2.17	0.45
26:BA:2820:A:P	38:BR:2:ARG:HH22	2.39	0.45
61:BA:4902:HOH:O	55:B8:42:ARG:HD2	2.15	0.45
29:BE:73:GLU:H	29:BE:73:GLU:HG3	1.60	0.45
31:BG:56:ALA:HA	31:BG:153:ARG:NH2	2.31	0.45
44:BX:5:TYR:CZ	49:B2:30:ARG:HB2	2.52	0.45
46:BZ:154:ASP:OD1	46:BZ:155:LEU:HD13	2.17	0.45
1:CA:189(A):C:C2'	1:CA:189(B):C:H5'	2.46	0.45
1:CA:509:A:H5'	4:CD:54:TYR:HD1	1.81	0.45
1:CA:624:C:O2'	1:CA:625:G:H5'	2.17	0.45
1:CA:709:G:H2'	1:CA:710:G:H5'	1.98	0.45
1:CA:950:U:H2'	1:CA:951:G:H8	1.81	0.45
1:CA:976:G:OP1	14:CN:32:SER:N	2.38	0.45
1:CA:1002:G:N3	1:CA:1003:G:C8	2.85	0.45
1:CA:1515:C:H2'	1:CA:1516:G:C8	2.52	0.45
4:CD:78:LEU:HD22	4:CD:96:LEU:HB3	1.99	0.45
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.43	0.45
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.50	0.45
26:DA:71:A:H5"	26:DA:73:A:N9	2.32	0.45
26:DA:222:A:H3'	26:DA:421:U:H5'	1.97	0.45
26:DA:754:C:H2'	26:DA:755:C:H6	1.82	0.45
26:DA:2139:C:H3'	26:DA:2140:C:H6	1.80	0.45
26:DA:2567:G:H2'	26:DA:2568:C:C6	2.51	0.45
26:DA:2679:A:H4'	29:DE:165:VAL:HG11	1.98	0.45
26:DA:2833:G:H4'	26:DA:2834:G:OP2	2.17	0.45
26:DA:2854:G:H2'	26:DA:2855:C:C6	2.50	0.45
26:DA:2886:G:H2'	26:DA:2887:U:C6	2.51	0.45
28:DD:132:PRO:HD3	28:DD:190:TYR:CZ	2.51	0.45
32:DH:28:GLY:HA3	32:DH:79:VAL:HB	1.98	0.45
1:AA:79:G:C6	1:AA:90:U:N3	2.84	0.45
1:AA:160:A:H2'	1:AA:161:A:C8	2.52	0.45
1:AA:280:C:N3	17:AQ:39:SER:N	2.65	0.45
1:AA:375:U:OP1	16:AP:69:THR:HG21	2.16	0.45
1:AA:688:G:H2'	1:AA:689:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1173:G:N1	1:AA:1174:G:C5	2.85	0.45
1:AA:1298:C:H2'	7:AG:114:ARG:NH1	2.31	0.45
16:AP:59:TRP:HA	16:AP:62:VAL:HG12	1.99	0.45
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.40	0.45
21:AU:15:ARG:HB2	21:AU:15:ARG:HH11	1.81	0.45
24:AX:13:C:O2'	26:BA:1924:C:H4'	2.15	0.45
26:BA:142(A):C:H2'	26:BA:143:G:O4'	2.16	0.45
26:BA:1453:U:H1'	38:BR:60:LEU:HD21	1.98	0.45
26:BA:1864:U:OP1	26:BA:2410:G:O2'	2.25	0.45
26:BA:2134:A:N1	26:BA:2158:A:C8	2.85	0.45
26:BA:2336:A:H61	47:B0:43:THR:CG2	2.27	0.45
28:BD:152:GLY:O	28:BD:154:LYS:HG2	2.17	0.45
41:BU:110:VAL:HG12	41:BU:114:LYS:HE2	1.98	0.45
46:BZ:104:PHE:HB3	46:BZ:141:VAL:HG21	1.99	0.45
54:B7:1:MET:HE2	54:B7:1:MET:HB3	1.77	0.45
1:CA:34:C:H2'	1:CA:35:G:C8	2.51	0.45
1:CA:293:G:H5'	1:CA:610:G:C2	2.52	0.45
1:CA:339:C:H2'	1:CA:340:U:C6	2.52	0.45
1:CA:762:C:H2'	1:CA:763:G:C8	2.51	0.45
1:CA:1400:C:C5	24:CX:35:A:C4	3.05	0.45
4:CD:173:TRP:CH2	4:CD:194:LEU:HD23	2.52	0.45
6:CF:6:VAL:HG13	6:CF:90:VAL:HG22	1.98	0.45
6:CF:89:MET:HE1	18:CR:72:ARG:HB3	1.99	0.45
26:DA:118:A:N3	26:DA:178:G:H1'	2.32	0.45
26:DA:823:G:H2'	26:DA:824:A:C8	2.52	0.45
26:DA:2152:G:H5'	26:DA:2153:G:OP2	2.17	0.45
26:DA:2427:C:OP1	61:DA:4236:HOH:O	2.21	0.45
26:DA:2701:C:H2'	26:DA:2702:U:H2'	1.99	0.45
31:DG:15:VAL:HG22	31:DG:175:LEU:HB3	1.98	0.45
40:DT:29:ARG:HB3	40:DT:87:ASP:HB2	1.99	0.45
1:AA:192:U:H2'	1:AA:193:C:C6	2.52	0.45
1:AA:370:C:H2'	1:AA:371:G:C8	2.52	0.45
1:AA:1044:A:C5	1:AA:1045:C:H1'	2.52	0.45
1:AA:1095:U:P	1:AA:1108:G:H1	2.39	0.45
1:AA:1310:G:H1	1:AA:1327:C:H42	1.63	0.45
1:AA:1431:C:H2'	1:AA:1432:G:O4'	2.16	0.45
2:AB:207:ALA:O	2:AB:210:SER:HB3	2.16	0.45
26:BA:656:G:H2'	26:BA:657:U:O4'	2.16	0.45
26:BA:1798:U:H5'	28:BD:259:THR:CG2	2.45	0.45
26:BA:2319:G:H22	39:BS:3:ARG:NE	2.15	0.45
26:BA:2319:G:C2	39:BS:3:ARG:HA	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2785:C:H2'	26:BA:2786:U:O4'	2.17	0.45
28:BD:145:VAL:HG13	28:BD:191:ALA:HB2	1.99	0.45
30:BF:56:GLU:OE2	30:BF:93:LYS:NZ	2.46	0.45
32:BH:23:ARG:HD2	32:BH:34:GLU:OE1	2.16	0.45
32:BH:150:ALA:HA	32:BH:153:LYS:HG3	1.98	0.45
35:BO:63:VAL:HB	35:BO:102:VAL:HG12	1.99	0.45
36:BP:63:PRO:HB2	55:B8:30:ARG:NH2	2.32	0.45
43:BW:18:ARG:HG3	43:BW:76:VAL:HB	1.99	0.45
47:B0:43:THR:HG23	47:B0:43:THR:O	2.16	0.45
1:CA:791:G:N2	1:CA:1497:G:O3'	2.49	0.45
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.52	0.45
1:CA:1292:U:OP2	7:CG:41:ARG:NH2	2.50	0.45
1:CA:1327:C:H5"	21:CU:20:LYS:HB3	1.99	0.45
4:CD:70:ILE:HD11	4:CD:74:GLN:HB3	1.99	0.45
5:CE:92:LYS:HB3	5:CE:119:LEU:HB2	1.98	0.45
24:CX:65:C:N4	24:CX:66:C:C4	2.85	0.45
26:DA:17:G:H4'	41:DU:25:TRP:NE1	2.31	0.45
26:DA:724:U:H2'	26:DA:725:G:O4'	2.16	0.45
26:DA:856:C:HO2'	26:DA:857:C:P	2.38	0.45
26:DA:858:U:O2	26:DA:2268:A:H2'	2.17	0.45
26:DA:1817:G:H2'	26:DA:1818:U:H5'	1.98	0.45
26:DA:2114:A:H2'	26:DA:2114:A:N3	2.32	0.45
26:DA:2129:C:O2'	26:DA:2130:U:H5'	2.16	0.45
26:DA:2312:U:H2'	26:DA:2313:C:C6	2.52	0.45
26:DA:2572:A:OP1	26:DA:2574:G:O2'	2.35	0.45
26:DA:2697:G:H2'	26:DA:2698:U:O4'	2.17	0.45
32:DH:43:VAL:HG13	32:DH:52:VAL:HG22	1.99	0.45
37:DQ:62:GLY:HA2	46:DZ:116:VAL:HG21	1.99	0.45
50:D3:18:ASP:OD1	50:D3:18:ASP:N	2.50	0.45
50:D3:46:ASN:O	50:D3:50:VAL:HG22	2.17	0.45
1:AA:178:C:H2'	1:AA:179:A:C8	2.52	0.45
1:AA:397:A:H3'	1:AA:397:A:N3	2.32	0.45
1:AA:581:G:OP1	15:AO:61:GLY:HA3	2.17	0.45
3:AC:21:ARG:NH1	3:AC:56:ASP:OD2	2.50	0.45
4:AD:18:LYS:HE3	4:AD:20:TYR:OH	2.17	0.45
4:AD:128:VAL:HG12	4:AD:129:ASN:ND2	2.31	0.45
19:AS:65:ASN:ND2	19:AS:66:MET:HG2	2.32	0.45
26:BA:228:A:H3'	26:BA:229:A:C5'	2.47	0.45
26:BA:573:G:O2'	26:BA:574:C:H3'	2.16	0.45
26:BA:639:U:H2'	26:BA:640:C:C6	2.52	0.45
26:BA:1932:A:H2'	26:BA:1933:G:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2277:G:P	47:B0:10:THR:HG21	2.57	0.45
30:BF:18:ARG:HG2	30:BF:19:GLU:H	1.81	0.45
31:BG:61:ALA:O	31:BG:65:GLY:N	2.39	0.45
31:BG:108:ASN:HD22	51:B4:22:ILE:HG21	1.82	0.45
33:BI:122:GLU:HB2	33:BI:126:TYR:OH	2.17	0.45
36:BP:65:ARG:HG3	55:B8:25:MET:CG	2.47	0.45
42:BV:14:VAL:HB	42:BV:96:ILE:HG13	1.97	0.45
1:CA:193:C:H2'	1:CA:194:C:H6	1.82	0.45
1:CA:737:A:O2'	1:CA:738:C:H5'	2.16	0.45
1:CA:936:C:H1'	1:CA:1382:C:H42	1.80	0.45
1:CA:1118:C:C2	1:CA:1119:C:C5	3.05	0.45
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.17	0.45
19:CS:14:HIS:O	19:CS:18:LYS:HG3	2.16	0.45
20:CT:57:ARG:HH12	20:CT:100:ILE:HD12	1.82	0.45
24:CX:41:C:C2	24:CX:42:G:C8	3.04	0.45
26:DA:79:G:O2'	26:DA:346:A:N3	2.35	0.45
26:DA:192:C:O2'	26:DA:802:A:N3	2.50	0.45
26:DA:455:C:N3	26:DA:472:A:H2'	2.31	0.45
26:DA:940:G:O2'	61:DA:3711:HOH:O	2.18	0.45
26:DA:1394:U:H4'	26:DA:1603:A:H4'	1.99	0.45
26:DA:1721:G:H5'	26:DA:1722:A:H5"	1.99	0.45
26:DA:2114:A:C8	26:DA:2168:G:H1'	2.51	0.45
26:DA:2302:G:C2	26:DA:2315:G:C2	3.05	0.45
26:DA:2416:C:O2'	26:DA:2417:C:H5'	2.17	0.45
36:DP:38:GLN:O	36:DP:39:LYS:HB3	2.16	0.45
36:DP:65:ARG:HG3	55:D8:25:MET:CG	2.47	0.45
1:AA:67:C:H2'	1:AA:68:G:H8	1.79	0.45
1:AA:922:G:H2'	1:AA:923:A:C8	2.52	0.45
1:AA:1133:G:H2'	1:AA:1134:G:H8	1.81	0.45
1:AA:1136:U:H5"	1:AA:1137:C:C2	2.52	0.45
1:AA:1291:G:H4'	9:AI:39:GLY:HA3	1.99	0.45
5:AE:143:ARG:NH1	8:AH:77:GLU:OE2	2.49	0.45
10:AJ:5:ARG:NH2	10:AJ:71:LEU:HD21	2.32	0.45
13:AM:51:ALA:HA	13:AM:54:VAL:HG22	1.98	0.45
26:BA:242:G:C8	55:B8:5:LYS:HG2	2.51	0.45
26:BA:340:A:H2'	26:BA:341:G:O4'	2.17	0.45
26:BA:1113:U:H2'	26:BA:1114:G:C8	2.52	0.45
26:BA:1557:C:H5"	26:BA:1558:A:OP2	2.17	0.45
29:BE:31:CYS:HB3	29:BE:49:LEU:HG	1.99	0.45
31:BG:124:SER:HB2	31:BG:131:TYR:CE1	2.52	0.45
40:BT:127:ALA:O	40:BT:128:GLU:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:BX:65:ARG:HB2	44:BX:70:LEU:HD23	1.99	0.45
1:CA:296:U:O2'	1:CA:556:C:O2	2.30	0.45
1:CA:982:U:H4'	1:CA:983:A:O5'	2.16	0.45
1:CA:1053:G:H4'	1:CA:1054:C:H5'	1.99	0.45
1:CA:1099:G:C2	1:CA:1100:C:O2	2.70	0.45
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	1.99	0.45
6:CF:2:ARG:CZ	6:CF:69:GLU:HG2	2.46	0.45
6:CF:50:TYR:OH	18:CR:74:ARG:O	2.24	0.45
7:CG:42:ILE:HG22	7:CG:120:ILE:HD12	1.98	0.45
13:CM:82:MET:O	13:CM:93:ARG:NH2	2.48	0.45
24:CX:15:G:C4	24:CX:59:A:N6	2.85	0.45
26:DA:191:A:H2'	26:DA:192:C:C6	2.52	0.45
26:DA:265:A:C8	26:DA:266:G:H1'	2.52	0.45
26:DA:893:C:H5'	26:DA:894:C:OP2	2.17	0.45
26:DA:1473:G:H2'	26:DA:1474:C:O4'	2.16	0.45
26:DA:1557:C:H5"	26:DA:1558:A:OP2	2.17	0.45
26:DA:2315:G:C6	26:DA:2316:C:N4	2.85	0.45
28:DD:77:ALA:HB2	28:DD:97:TYR:CD2	2.52	0.45
29:DE:101:ARG:CZ	29:DE:171:GLU:HB2	2.47	0.45
43:DW:72:LYS:N	43:DW:106:ILE:O	2.48	0.45
54:D7:13:ALA:HB2	54:D7:46:VAL:HG21	1.99	0.45
6:AF:89:MET:HG2	6:AF:91:VAL:HG23	1.99	0.45
10:AJ:5:ARG:HE	10:AJ:5:ARG:HB3	1.48	0.45
10:AJ:57:LYS:HD2	10:AJ:60:ARG:HH21	1.81	0.45
26:BA:466:A:O3'	54:B7:33:ARG:NH1	2.48	0.45
26:BA:1842:G:O2'	28:BD:253:GLN:NE2	2.38	0.45
26:BA:2161:C:O2'	26:BA:2173:A:H4'	2.17	0.45
27:BB:96:U:OP1	46:BZ:14:LYS:NZ	2.49	0.45
28:BD:101:GLU:HG2	28:BD:103:ARG:HD3	1.98	0.45
1:CA:192:U:O2'	20:CT:60:GLU:OE2	2.22	0.45
1:CA:266:G:O3'	17:CQ:67:LYS:HB2	2.16	0.45
1:CA:624:C:O2'	16:CP:10:GLY:HA2	2.16	0.45
1:CA:779:C:O2'	11:CK:120:ARG:HD3	2.17	0.45
1:CA:1064:G:H1'	1:CA:1065:U:OP2	2.16	0.45
1:CA:1124:G:O2'	1:CA:1145:C:C4	2.70	0.45
1:CA:1280:A:H2'	1:CA:1281:U:N3	2.31	0.45
1:CA:1405:G:H2'	1:CA:1406:U:C6	2.51	0.45
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.98	0.45
8:CH:9:MET:HG3	8:CH:26:VAL:HG21	1.99	0.45
8:CH:81:HIS:N	8:CH:138:TRP:O	2.50	0.45
24:CX:30:G:C6	24:CX:31:G:N7	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1359:A:N1	26:DA:1372:U:O4	2.50	0.45
26:DA:1660:C:H2'	26:DA:1661:G:H8	1.82	0.45
26:DA:1826:G:H2'	26:DA:1827:C:C6	2.51	0.45
26:DA:1903:G:OP1	28:DD:241:PRO:HB2	2.16	0.45
26:DA:2153:G:C6	26:DA:2154:G:C6	3.05	0.45
26:DA:2675:A:H5'	35:DO:29:ASN:O	2.17	0.45
31:DG:61:ALA:O	31:DG:65:GLY:N	2.44	0.45
31:DG:111:LEU:O	31:DG:114:ILE:HB	2.17	0.45
33:DI:14:ASP:N	33:DI:17:GLN:OE1	2.43	0.45
39:DS:38:GLN:HA	39:DS:50:SER:HA	1.99	0.45
51:D4:15:ILE:N	51:D4:31:ILE:O	2.32	0.45
1:AA:708:C:H2'	1:AA:709:G:H8	1.82	0.44
1:AA:937:A:H2'	1:AA:938:A:H5'	1.99	0.44
1:AA:1052:U:H5"	1:AA:1053:G:OP2	2.17	0.44
1:AA:1124:G:H5"	10:AJ:35:SER:OG	2.17	0.44
1:AA:1187:G:H2'	1:AA:1188:A:C8	2.52	0.44
1:AA:1227:A:OP1	19:AS:80:TYR:OH	2.32	0.44
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.22	0.44
26:BA:271(F):C:H2'	26:BA:271(G):C:C6	2.52	0.44
26:BA:288:C:H2'	26:BA:289:A:H8	1.82	0.44
26:BA:1186:G:H2'	26:BA:1187:G:O4'	2.17	0.44
26:BA:1447:G:N2	26:BA:1464:C:O2	2.25	0.44
26:BA:1963:U:H4'	26:BA:1964:G:OP1	2.17	0.44
26:BA:2118:U:H4'	26:BA:2119:A:OP1	2.16	0.44
26:BA:2467:C:H4'	37:BQ:123:HIS:CG	2.52	0.44
31:BG:148:MET:HB2	31:BG:148:MET:HE3	1.60	0.44
36:BP:98:GLU:O	36:BP:101:VAL:HB	2.16	0.44
41:BU:50:ARG:HG2	41:BU:53:ARG:NH2	2.32	0.44
1:CA:630:G:H2'	1:CA:631:G:C8	2.52	0.44
1:CA:690:G:O5'	1:CA:690:G:H8	1.99	0.44
1:CA:707:C:H5"	11:CK:85:ARG:NH1	2.32	0.44
1:CA:922:G:H2'	1:CA:923:A:C8	2.52	0.44
1:CA:1171:G:O2'	1:CA:1172:C:H5'	2.16	0.44
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.82	0.44
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.98	0.44
2:CB:207:ALA:O	2:CB:211:ILE:HG13	2.17	0.44
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.57	0.44
11:CK:92:GLU:OE2	11:CK:96:ARG:NH1	2.50	0.44
20:CT:62:LEU:HD23	20:CT:62:LEU:HA	1.82	0.44
24:CX:19:G:P	24:CX:60:U:H3	2.40	0.44
26:DA:182:A:H2	26:DA:433:C:O2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:466:A:O3'	54:D7:33:ARG:NH1	2.50	0.44
26:DA:539:G:H2'	26:DA:540:C:H6	1.82	0.44
26:DA:601:C:O2'	26:DA:605:C:H5"	2.18	0.44
26:DA:884:C:H2'	26:DA:885:C:O4'	2.17	0.44
26:DA:1183:G:H4'	50:D3:29:ARG:HH22	1.82	0.44
26:DA:1287:A:C5	26:DA:1288:U:C4	3.05	0.44
26:DA:1864:U:OP1	26:DA:2410:G:O2'	2.30	0.44
26:DA:2127:G:C6	26:DA:2161:C:N3	2.84	0.44
26:DA:2273:A:O2'	26:DA:2274:A:H5'	2.17	0.44
26:DA:2416:C:C2'	26:DA:2417:C:H5'	2.47	0.44
26:DA:2564:A:OP1	26:DA:2648:C:O2'	2.28	0.44
30:DF:164:ARG:O	30:DF:168:ARG:HB2	2.16	0.44
32:DH:144:VAL:O	32:DH:148:ILE:HG12	2.17	0.44
36:DP:84:ASN:CG	36:DP:117:GLU:HB2	2.42	0.44
37:DQ:38:GLU:HB2	37:DQ:127:ILE:HG22	1.99	0.44
42:DV:85:LYS:HE3	42:DV:85:LYS:HB2	1.72	0.44
42:DV:89:GLN:HA	42:DV:90:PRO:HD3	1.88	0.44
1:AA:573:A:N3	1:AA:883:C:O2'	2.41	0.44
1:AA:1278:U:H5'	1:AA:1279:A:O4'	2.17	0.44
3:AC:181:ASN:C	3:AC:181:ASN:HD22	2.26	0.44
24:AX:9:G:N3	24:AX:45:G:H2'	2.31	0.44
26:BA:307:G:H21	26:BA:330:A:H62	1.66	0.44
26:BA:1175:U:HO2'	26:BA:1176:G:C5'	2.26	0.44
45:BY:54:LYS:HA	45:BY:56:PRO:HD3	2.00	0.44
53:B6:11:LEU:HB3	53:B6:49:HIS:HB3	1.99	0.44
1:CA:73:G:C6	1:CA:76:C:C5	3.05	0.44
1:CA:164:U:H2'	1:CA:165:C:C6	2.52	0.44
1:CA:937:A:H2'	1:CA:938:A:H5'	1.99	0.44
1:CA:1417:G:H22	1:CA:1482:G:H2'	1.81	0.44
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.17	0.44
7:CG:22:LEU:HD13	7:CG:97:GLN:CD	2.42	0.44
14:CN:3:ARG:HD2	14:CN:4:LYS:N	2.32	0.44
17:CQ:45:HIS:HD2	17:CQ:65:ILE:HG12	1.82	0.44
24:CX:29:G:N1	24:CX:30:G:C4	2.85	0.44
26:DA:210:C:H2'	26:DA:211:A:C8	2.52	0.44
26:DA:339:U:O5'	26:DA:339:U:H6	2.00	0.44
26:DA:444:C:H4'	30:DF:49:ALA:HB2	1.99	0.44
26:DA:864:G:N7	37:DQ:22:LYS:NZ	2.50	0.44
26:DA:1223:G:N2	26:DA:1227:G:C4	2.85	0.44
26:DA:1676:A:H2'	26:DA:1677:A:O4'	2.18	0.44
26:DA:2063:C:C4	26:DA:2064:C:C4	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2552:U:C2	26:DA:2554:U:H5"	2.51	0.44
27:DB:114:C:H2'	27:DB:115:G:O4'	2.17	0.44
45:DY:9:LYS:HA	45:DY:10:GLY:HA2	1.56	0.44
51:D4:26:SER:OG	51:D4:27:THR:N	2.48	0.44
1:AA:920:U:H2'	1:AA:921:U:C6	2.52	0.44
1:AA:1107:C:C4	1:AA:1108:G:C8	3.05	0.44
1:AA:1262:C:N3	1:AA:1273:G:C6	2.85	0.44
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.53	0.44
10:AJ:47:PHE:CZ	14:AN:37:PHE:HE1	2.36	0.44
26:BA:292:C:H2'	26:BA:293:U:C6	2.52	0.44
26:BA:571:A:N6	26:BA:2499:C:O3'	2.47	0.44
26:BA:1750:G:O2'	26:BA:2860:A:N1	2.45	0.44
26:BA:2181:G:HO2'	26:BA:2182:G:P	2.41	0.44
26:BA:2728:U:H2'	26:BA:2729:G:C8	2.53	0.44
30:BF:129:PHE:HA	30:BF:142:TRP:NE1	2.31	0.44
31:BG:15:VAL:HG21	31:BG:176:LEU:HD23	2.00	0.44
1:CA:19:C:H4'	1:CA:864:A:O4'	2.17	0.44
1:CA:892:A:HO2'	1:CA:1415:G:H4'	1.83	0.44
1:CA:936:C:H2'	1:CA:937:A:O4'	2.18	0.44
1:CA:1159:U:O4'	1:CA:1182:G:N2	2.50	0.44
1:CA:1216:G:OP1	14:CN:2:ALA:HA	2.18	0.44
1:CA:1261:A:C6	1:CA:1262:C:C2	3.05	0.44
1:CA:1405:G:O4'	1:CA:1519:A:H4'	2.17	0.44
2:CB:224:GLN:HA	2:CB:228:GLY:O	2.18	0.44
6:CF:24:GLU:HG3	6:CF:28:ARG:HD3	1.99	0.44
6:CF:46:ARG:HB3	6:CF:60:PHE:CE1	2.51	0.44
26:DA:248:G:O5'	26:DA:249:C:H5"	2.17	0.44
26:DA:854:G:H2'	26:DA:855:G:H8	1.82	0.44
26:DA:1608:A:H1'	26:DA:1610:A:OP2	2.17	0.44
26:DA:1826:G:H4'	28:DD:242:ARG:CZ	2.47	0.44
26:DA:1826:G:H4'	28:DD:242:ARG:NH1	2.32	0.44
26:DA:1978:A:H2'	26:DA:1979:C:O4'	2.17	0.44
26:DA:2101:G:H2'	26:DA:2102:U:O4'	2.17	0.44
26:DA:2131:G:C8	26:DA:2133:G:N1	2.86	0.44
26:DA:2187:G:C2	26:DA:2188:C:C2	3.05	0.44
61:DA:3809:HOH:O	30:DF:68:LYS:HE2	2.17	0.44
38:DR:72:ASP:OD2	38:DR:75:LEU:HB2	2.18	0.44
53:D6:14:THR:O	53:D6:17:LYS:NZ	2.47	0.44
1:AA:499:A:H4'	1:AA:500:G:H5'	1.99	0.44
1:AA:715:A:H2'	1:AA:716:A:C8	2.53	0.44
1:AA:985:C:H2'	1:AA:986:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:986:A:H2'	1:AA:987:G:C8	2.53	0.44
1:AA:1008:C:H2'	1:AA:1009:G:O4'	2.16	0.44
1:AA:1173:G:C6	1:AA:1174:G:C5	3.06	0.44
11:AK:41:THR:OG1	11:AK:42:TRP:N	2.51	0.44
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.99	0.44
15:AO:17:ARG:HD3	15:AO:26:GLU:CD	2.41	0.44
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.18	0.44
24:AX:16:C:H5"	24:AX:17:C:C5	2.53	0.44
26:BA:123:G:H2'	26:BA:124:G:O4'	2.18	0.44
26:BA:286:C:H2'	26:BA:287:C:C6	2.53	0.44
26:BA:811:U:P	36:BP:29:LYS:H	2.40	0.44
26:BA:871:U:OP1	37:BQ:5:ARG:HD3	2.17	0.44
26:BA:1501:C:H2'	26:BA:1502:C:C6	2.52	0.44
26:BA:1793:C:H2'	26:BA:1794:U:C6	2.53	0.44
26:BA:2163:C:C4	26:BA:2164:C:O2	2.71	0.44
31:BG:7:LEU:HD23	31:BG:7:LEU:HA	1.85	0.44
31:BG:41:GLN:HB3	31:BG:43:LEU:HD13	1.99	0.44
1:CA:66:G:H2'	1:CA:67:C:H5'	1.98	0.44
1:CA:1112:C:C2	3:CC:178:LEU:HB2	2.52	0.44
1:CA:1400:C:N4	24:CX:34:C:H2'	2.26	0.44
2:CB:103:THR:HA	2:CB:180:LEU:HD11	1.99	0.44
5:CE:41:VAL:O	5:CE:67:VAL:HG13	2.17	0.44
26:DA:1359:A:C6	26:DA:1372:U:O4	2.69	0.44
26:DA:1370:C:N4	26:DA:1371:G:C6	2.86	0.44
26:DA:2031:A:C6	26:DA:2498:C:H1'	2.53	0.44
26:DA:2140:C:C2	26:DA:2152:G:C2	3.05	0.44
26:DA:2151:G:H2'	26:DA:2152:G:C8	2.41	0.44
29:DE:36:ARG:NH2	29:DE:86:PRO:O	2.47	0.44
32:DH:26:VAL:HB	32:DH:33:LEU:HD12	1.99	0.44
32:DH:76:VAL:O	32:DH:80:SER:OG	2.26	0.44
42:DV:29:PRO:HA	42:DV:61:VAL:HG22	1.99	0.44
44:DX:12:VAL:HG21	44:DX:27:THR:HG22	1.99	0.44
1:AA:110:C:O2'	16:AP:25:ARG:O	2.30	0.44
1:AA:222:U:H2'	1:AA:223:U:C6	2.52	0.44
1:AA:420:U:O2'	1:AA:423:G:O6	2.28	0.44
1:AA:1442(A):G:C8	40:BT:118:ARG:HG2	2.53	0.44
3:AC:180:ALA:O	3:AC:182:ILE:N	2.51	0.44
13:AM:14:ARG:HB2	13:AM:16:ASP:OD1	2.16	0.44
24:AX:16:C:H5"	24:AX:17:C:H5	1.83	0.44
26:BA:189:G:O6	26:BA:205:G:O2'	2.29	0.44
26:BA:554:U:C4	26:BA:555:U:C4	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1155:A:OP1	41:BU:55:ARG:HD3	2.17	0.44
26:BA:1182:A:H2'	26:BA:1183:G:C8	2.53	0.44
27:BB:6:C:H2'	27:BB:7:G:H5"	2.00	0.44
28:BD:38:LYS:HA	28:BD:38:LYS:HD2	1.87	0.44
32:BH:54:ARG:HD3	32:BH:65:HIS:ND1	2.32	0.44
32:BH:61:HIS:O	32:BH:65:HIS:HB2	2.18	0.44
35:BO:122:LEU:HD13	40:BT:72:VAL:HG11	1.98	0.44
36:BP:27:HIS:O	36:BP:31:ALA:HA	2.16	0.44
37:BQ:7:MET:HE1	37:BQ:93:TYR:OH	2.18	0.44
41:BU:86:ALA:HB2	41:BU:116:ALA:HB2	1.98	0.44
44:BX:50:LYS:HB3	44:BX:87:GLN:HE22	1.82	0.44
51:B4:59:PHE:O	51:B4:62:ARG:NE	2.47	0.44
1:CA:156:G:N1	1:CA:165:C:N3	2.39	0.44
1:CA:560:U:O2'	1:CA:561:U:OP2	2.32	0.44
1:CA:765:G:H5"	1:CA:766:A:OP1	2.18	0.44
1:CA:775:G:N2	1:CA:804:U:O4	2.51	0.44
1:CA:1118:C:OP1	9:CI:9:ARG:HD2	2.17	0.44
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.80	0.44
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.21	0.44
10:CJ:55:LYS:HG3	10:CJ:56:HIS:N	2.31	0.44
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.53	0.44
26:DA:340:A:H2'	26:DA:341:G:O4'	2.17	0.44
26:DA:469:G:O6	54:D7:37:LYS:HE2	2.17	0.44
26:DA:483:A:O4'	45:DY:48:ALA:HB1	2.17	0.44
26:DA:1224:C:O2'	42:DV:85:LYS:HA	2.18	0.44
26:DA:1333:C:H2'	26:DA:1334:G:H8	1.83	0.44
26:DA:1422:G:H1'	26:DA:1496:A:N1	2.33	0.44
26:DA:1857:G:C6	26:DA:1858:G:N1	2.86	0.44
26:DA:1963:U:H4'	26:DA:1964:G:OP1	2.17	0.44
26:DA:2137:C:C4	26:DA:2138:C:N4	2.85	0.44
26:DA:2328:A:H2'	26:DA:2329:G:C8	2.53	0.44
26:DA:2357:U:OP1	47:D0:20:ARG:HD3	2.18	0.44
26:DA:2489:G:C6	26:DA:2490:G:C6	3.06	0.44
46:DZ:70:LEU:HD11	46:DZ:98:MET:HE3	1.99	0.44
46:DZ:92:SER:O	46:DZ:130:PRO:HG2	2.17	0.44
1:AA:164:U:H2'	1:AA:165:C:C6	2.52	0.44
1:AA:509:A:H5'	4:AD:54:TYR:HD2	1.82	0.44
1:AA:828:A:N6	1:AA:858:G:O2'	2.51	0.44
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.99	0.44
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	1.98	0.44
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:79:GLU:HG3	5:AE:93:PRO:HD2	2.00	0.44
8:AH:25:ASP:OD1	8:AH:60:ARG:HG3	2.17	0.44
11:AK:99:GLN:HE21	11:AK:108:ILE:HD11	1.82	0.44
13:AM:84:ILE:HD12	19:AS:74:PHE:CE2	2.52	0.44
26:BA:247:G:H4'	26:BA:386:G:C5	2.52	0.44
26:BA:363(C):G:H2'	26:BA:363(D):G:C8	2.53	0.44
26:BA:573:G:OP2	42:BV:78:LYS:NZ	2.48	0.44
26:BA:1529:G:C6	26:BA:1530:C:N4	2.86	0.44
26:BA:2038:G:H2'	26:BA:2039:C:O4'	2.18	0.44
26:BA:2384:G:P	47:B0:55:ARG:HH12	2.40	0.44
30:BF:74:ARG:H	30:BF:74:ARG:HG3	1.50	0.44
31:BG:16:ARG:HH21	31:BG:31:VAL:HG11	1.81	0.44
40:BT:37:GLY:HA2	40:BT:38:ASN:HA	1.69	0.44
44:BX:35:THR:HG22	44:BX:38:GLU:HB2	2.00	0.44
1:CA:598:U:H4'	8:CH:94:TYR:CD2	2.52	0.44
1:CA:616:G:C2	1:CA:617:G:C8	3.06	0.44
1:CA:1010:G:H2'	1:CA:1011:G:H8	1.83	0.44
2:CB:210:SER:O	2:CB:214:ILE:HG12	2.18	0.44
3:CC:36:ASP:O	3:CC:39:ILE:HB	2.18	0.44
5:CE:68:GLU:OE1	5:CE:70:PRO:HG3	2.17	0.44
12:CL:34:ARG:HE	12:CL:34:ARG:HB3	1.47	0.44
12:CL:97:ARG:HB2	12:CL:98:TYR:CE2	2.52	0.44
24:CX:13:C:O2'	26:DA:1924:C:H4'	2.18	0.44
24:CX:30:G:C4	24:CX:31:G:C8	3.05	0.44
26:DA:815:C:H2'	26:DA:816:C:H6	1.81	0.44
26:DA:1126:A:H4'	26:DA:1127:A:O5'	2.18	0.44
26:DA:2024:G:N7	61:DA:3704:HOH:O	2.36	0.44
26:DA:2248:C:OP2	61:DA:3945:HOH:O	2.21	0.44
26:DA:2442:C:H2'	26:DA:2443:C:H6	1.83	0.44
31:DG:125:PHE:CZ	31:DG:170:ARG:HA	2.53	0.44
32:DH:95:ARG:HG2	32:DH:96:ALA:N	2.32	0.44
40:DT:2:ASN:O	40:DT:6:LEU:HD22	2.18	0.44
1:AA:53:A:H61	1:AA:358:U:H3	1.65	0.44
1:AA:614:A:C2'	1:AA:615:C:H5'	2.48	0.44
1:AA:938:A:C6	1:AA:939:G:C5	3.06	0.44
1:AA:1250:A:H4'	9:AI:68:GLY:N	2.33	0.44
1:AA:1252:A:N6	1:AA:1285:A:H61	2.06	0.44
1:AA:1330:U:H4'	13:AM:23:TYR:CZ	2.53	0.44
1:AA:1503:A:N3	22:AV:13:A:C6	2.85	0.44
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	1.99	0.44
3:AC:27:LYS:HA	3:AC:27:LYS:NZ	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:63:LYS:HG3	4:AD:198:VAL:HG22	2.00	0.44
4:AD:118:ARG:HG3	4:AD:136:PRO:HB3	2.00	0.44
5:AE:31:LEU:HD11	5:AE:129:ILE:HA	2.00	0.44
5:AE:102:ALA:HB2	5:AE:120:THR:HG21	2.00	0.44
11:AK:69:ALA:O	11:AK:73:MET:HG3	2.18	0.44
26:BA:1459:G:C3'	26:BA:1460:A:H5"	2.47	0.44
26:BA:2625:G:H2'	26:BA:2626:C:H6	1.83	0.44
29:BE:51:PHE:O	29:BE:77:ILE:HD12	2.18	0.44
30:BF:184:TYR:O	30:BF:188:ARG:HG3	2.18	0.44
34:BN:4:TYR:CE2	41:BU:100:VAL:HG11	2.52	0.44
46:BZ:117:LEU:HD23	46:BZ:119:GLU:OE1	2.18	0.44
1:CA:337:C:H2'	1:CA:338:A:H8	1.83	0.44
1:CA:976:G:O2'	1:CA:1362:C:N4	2.50	0.44
1:CA:982:U:H5	14:CN:31:ARG:HH22	1.62	0.44
1:CA:1038:C:O2'	1:CA:1039:C:H5'	2.17	0.44
2:CB:162:ILE:O	2:CB:162:ILE:HG13	2.17	0.44
5:CE:72:GLN:O	5:CE:75:THR:HG22	2.18	0.44
8:CH:14:ARG:O	8:CH:18:ARG:HD3	2.18	0.44
19:CS:9:VAL:HB	51:D4:67:TYR:CD2	2.47	0.44
24:CX:30:G:H2'	24:CX:31:G:O4'	2.17	0.44
26:DA:265:A:H1'	26:DA:266:G:O4'	2.18	0.44
26:DA:375:C:H2'	26:DA:376:C:H6	1.82	0.44
26:DA:483:A:O2'	45:DY:49:VAL:O	2.25	0.44
26:DA:1232:G:C2	26:DA:1233:C:C2	3.05	0.44
26:DA:1321:A:H2'	26:DA:1322:A:O4'	2.17	0.44
26:DA:1470:G:H5"	26:DA:1471:A:OP1	2.17	0.44
26:DA:2138:C:N3	26:DA:2153:G:N2	2.59	0.44
26:DA:2166:G:H5'	26:DA:2167:U:O5'	2.18	0.44
26:DA:2389:G:H5"	26:DA:2390:U:O4'	2.18	0.44
46:DZ:69:THR:HG22	46:DZ:90:VAL:HG13	2.00	0.44
54:D7:12:ARG:NH2	54:D7:44:PRO:HB3	2.32	0.44
1:AA:90:U:O2'	1:AA:91:C:H5'	2.18	0.44
1:AA:605:U:C2'	1:AA:606:G:H5'	2.47	0.44
1:AA:1010:G:N2	1:AA:1020:U:H1'	2.33	0.44
1:AA:1165:C:H2'	1:AA:1166:G:O4'	2.17	0.44
2:AB:20:GLU:O	2:AB:40:HIS:HB2	2.18	0.44
2:AB:92:TYR:HE2	2:AB:94:ASN:HB2	1.83	0.44
3:AC:39:ILE:O	3:AC:43:LEU:HG	2.17	0.44
3:AC:118:GLN:H	3:AC:118:GLN:HG2	1.51	0.44
19:AS:22:LEU:HB3	19:AS:27:GLU:HG3	2.00	0.44
26:BA:468:G:N7	54:B7:39:ARG:NH2	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:629:G:N3	26:BA:639:U:O2'	2.49	0.44
26:BA:818:G:H4'	26:BA:838:C:O3'	2.17	0.44
26:BA:2165:G:H1	26:BA:2172:U:H5	1.62	0.44
36:BP:19:VAL:HG12	36:BP:27:HIS:HB3	2.00	0.44
42:BV:5:VAL:HG21	42:BV:35:LEU:HD23	1.99	0.44
43:BW:86:LEU:HD12	43:BW:87:PRO:HD2	2.00	0.44
46:BZ:111:VAL:O	46:BZ:112:ARG:HB2	2.17	0.44
48:B1:52:ARG:HH12	48:B1:57:GLU:HB2	1.83	0.44
1:CA:683:G:H2'	1:CA:684:A:C8	2.52	0.44
1:CA:1095:U:H5"	1:CA:1109:C:O2	2.17	0.44
1:CA:1121:U:C2'	1:CA:1122:U:H5'	2.47	0.44
1:CA:1350:A:C5	1:CA:1351:U:C4	3.05	0.44
2:CB:76:GLN:HB2	2:CB:208:ILE:HG12	1.99	0.44
3:CC:33:LEU:HD21	14:CN:53:LEU:CD2	2.47	0.44
3:CC:105:GLU:H	3:CC:105:GLU:HG3	1.54	0.44
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	2.00	0.44
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.18	0.44
26:DA:1614:A:C2	43:DW:93:ALA:HB2	2.52	0.44
26:DA:2773:C:OP1	29:DE:164:ARG:NE	2.41	0.44
27:DB:13:A:N3	27:DB:16:G:H1'	2.33	0.44
31:DG:138:GLN:NE2	31:DG:153:ARG:HB2	2.33	0.44
1:AA:69:G:H2'	1:AA:70:G:H8	1.83	0.44
1:AA:418:C:H1'	1:AA:540:G:O2'	2.16	0.44
1:AA:547:A:H4'	1:AA:548:G:O5'	2.18	0.44
1:AA:679:C:C2'	1:AA:680:C:H5'	2.47	0.44
3:AC:13:GLY:HA3	14:AN:57:ARG:NH2	2.33	0.44
3:AC:22:TRP:CE2	14:AN:54:PRO:HG3	2.52	0.44
5:AE:36:ASP:OD2	5:AE:40:ARG:HB2	2.18	0.44
9:AI:21:PRO:HA	9:AI:59:PHE:HA	2.00	0.44
19:AS:37:ARG:H	19:AS:37:ARG:HG3	1.38	0.44
26:BA:172:C:H2'	26:BA:173:G:O4'	2.18	0.44
26:BA:709:U:H2'	26:BA:710:G:C8	2.53	0.44
26:BA:1996:C:H4'	26:BA:1997:G:OP1	2.16	0.44
26:BA:2133:G:N2	26:BA:2158:A:C2	2.86	0.44
26:BA:2134:A:N3	26:BA:2134:A:C2'	2.80	0.44
37:BQ:56:ARG:HH11	37:BQ:56:ARG:HG2	1.83	0.44
43:BW:20:VAL:HG11	43:BW:44:ALA:HA	2.00	0.44
1:CA:486:U:H2'	1:CA:487:A:H8	1.82	0.44
1:CA:958:A:N6	19:CS:77:THR:HG23	2.32	0.44
1:CA:1046:A:H61	1:CA:1213:A:H61	1.64	0.44
1:CA:1076:C:OP1	2:CB:175:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:96:LEU:HD23	9:CI:96:LEU:HA	1.84	0.44
16:CP:21:VAL:HG11	16:CP:59:TRP:NE1	2.33	0.44
26:DA:1007:C:C2	26:DA:1008:C:C5	3.06	0.44
26:DA:1420:U:HO2'	26:DA:1421:G:P	2.41	0.44
26:DA:1742:G:O5'	26:DA:1742:G:H8	2.00	0.44
26:DA:2302:G:C2	26:DA:2303:G:C8	3.05	0.44
26:DA:2686:G:C2	26:DA:2724:C:O2	2.71	0.44
27:DB:28:C:H5"	39:DS:31:SER:HB3	1.99	0.44
33:DI:82:ARG:C	33:DI:89:TYR:HB2	2.43	0.44
35:DO:63:VAL:HG12	35:DO:106:LEU:HD11	1.99	0.44
42:DV:40:LEU:HB2	42:DV:46:VAL:HG13	1.99	0.44
47:D0:82:ARG:HA	47:D0:83:PRO:HD3	1.79	0.44
1:AA:38:G:H22	1:AA:397:A:H5"	1.83	0.43
1:AA:189(A):C:C2'	1:AA:189(B):C:H5'	2.48	0.43
1:AA:288:A:H2'	1:AA:289:G:H4'	1.99	0.43
1:AA:421:U:O2	1:AA:421:U:H2'	2.16	0.43
1:AA:738:C:H2'	1:AA:739:C:C6	2.53	0.43
1:AA:993:G:N3	1:AA:993:G:H2'	2.33	0.43
1:AA:1134:G:C2	1:AA:1141:C:C2	3.06	0.43
1:AA:1503:A:N3	22:AV:13:A:N6	2.65	0.43
4:AD:85:LYS:HG3	4:AD:86:LYS:HG2	1.99	0.43
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.54	0.43
26:BA:2134:A:C2	26:BA:2159:G:H1'	2.52	0.43
26:BA:2285:C:N4	53:B6:24:GLU:OE1	2.50	0.43
27:BB:66:A:H61	27:BB:108:U:H2'	1.83	0.43
28:BD:134:ARG:HG3	28:BD:135:PHE:CE2	2.53	0.43
32:BH:13:LYS:HA	32:BH:14:GLY:HA2	1.58	0.43
39:BS:105:ALA:O	39:BS:110:LEU:HB2	2.18	0.43
44:BX:32:PRO:HA	44:BX:77:LYS:HB2	1.99	0.43
45:BY:9:LYS:HA	45:BY:10:GLY:HA2	1.69	0.43
1:CA:66:G:C2'	1:CA:67:C:H5'	2.48	0.43
1:CA:164:U:H2'	1:CA:165:C:H6	1.83	0.43
1:CA:321:A:C2	1:CA:333:G:C2	3.06	0.43
1:CA:344:A:H5"	1:CA:345:C:H5	1.81	0.43
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.51	0.43
1:CA:763:G:H2'	1:CA:764:C:H5'	1.99	0.43
1:CA:881:G:P	12:CL:12:ARG:HH22	2.40	0.43
1:CA:991:U:H3'	1:CA:1212:U:H3	1.82	0.43
1:CA:1001(A):G:H3'	1:CA:1002:G:O4'	2.17	0.43
1:CA:1100:C:H5	2:CB:96:ARG:HH22	1.66	0.43
1:CA:1125:U:C3'	1:CA:1126:U:H5"	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.33	0.43
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.80	0.43
3:CC:126:ARG:HB2	3:CC:128:PHE:CE1	2.53	0.43
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	2.00	0.43
20:CT:24:LEU:HD12	20:CT:24:LEU:HA	1.76	0.43
26:DA:200:U:O2	26:DA:386:G:N2	2.51	0.43
26:DA:839:U:H1'	26:DA:1191:G:H1'	2.00	0.43
26:DA:1165:U:H2'	26:DA:1166:C:C6	2.53	0.43
26:DA:1264:G:O5'	26:DA:1264:G:H8	2.01	0.43
26:DA:1411:C:H2'	26:DA:1412:A:H8	1.82	0.43
26:DA:1421:G:C2	26:DA:1422:G:C8	3.06	0.43
26:DA:1484:G:O6	26:DA:1505:C:N4	2.47	0.43
26:DA:1593:G:H2'	26:DA:1594:G:C8	2.53	0.43
26:DA:1849:G:H2'	26:DA:1850:G:H8	1.82	0.43
26:DA:1952:A:OP1	35:DO:42:SER:OG	2.34	0.43
27:DB:104:U:O3'	46:DZ:72:ARG:HD2	2.17	0.43
32:DH:12:PRO:O	32:DH:15:VAL:HG13	2.18	0.43
33:DI:87:LYS:CA	33:DI:122:GLU:HA	2.47	0.43
36:DP:59:LEU:HD23	55:D8:58:ILE:HD13	2.00	0.43
37:DQ:86:GLY:HA3	47:D0:10:THR:CG2	2.48	0.43
39:DS:95:HIS:CG	39:DS:96:GLY:N	2.86	0.43
42:DV:37:VAL:O	42:DV:51:VAL:HG23	2.18	0.43
46:DZ:53:ILE:HG22	46:DZ:71:VAL:O	2.18	0.43
48:D1:83:GLU:HA	48:D1:84:GLY:HA2	1.62	0.43
56:D9:29:ASN:HB3	56:D9:32:HIS:ND1	2.33	0.43
1:AA:453:A:C5	1:AA:454:C:C4	3.06	0.43
1:AA:1168:A:C6	1:AA:1169:A:C6	3.07	0.43
1:AA:1397:C:H4'	22:AV:23:A:C2	2.53	0.43
2:AB:24:TRP:CZ3	2:AB:26:PRO:HA	2.53	0.43
5:AE:52:PRO:HG2	5:AE:53:LEU:HD12	1.99	0.43
9:AI:3:GLN:HG3	9:AI:20:ARG:HE	1.83	0.43
11:AK:50:TYR:HE1	11:AK:54:ARG:HE	1.64	0.43
26:BA:700:G:O2'	26:BA:1632:A:N3	2.42	0.43
26:BA:1111:A:N3	26:BA:1112:G:H1'	2.33	0.43
26:BA:1582:C:O2'	26:BA:1586:A:N3	2.51	0.43
26:BA:2188:C:H2'	26:BA:2189:U:O4'	2.18	0.43
26:BA:2543:G:H21	26:BA:2646:C:H5"	1.82	0.43
27:BB:83:G:H4'	50:B3:52:HIS:CG	2.53	0.43
28:BD:145:VAL:HG11	28:BD:175:LEU:HD11	1.99	0.43
46:BZ:92:SER:O	46:BZ:130:PRO:HG2	2.17	0.43
1:CA:73:G:N1	1:CA:76:C:C5	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:110:C:O2'	16:CP:25:ARG:O	2.31	0.43
1:CA:731:G:H5'	1:CA:766:A:H4'	2.00	0.43
1:CA:1361:G:H8	1:CA:1361:G:O5'	2.01	0.43
2:CB:125:PRO:O	2:CB:127:ILE:N	2.51	0.43
4:CD:11:LEU:O	4:CD:15:GLU:HB2	2.18	0.43
6:CF:95:GLU:HA	6:CF:96:PRO:HD3	1.90	0.43
16:CP:43:LYS:HG2	16:CP:48:TRP:CD2	2.53	0.43
24:CX:54:5MU:O4	24:CX:58:A:N7	2.51	0.43
26:DA:854:G:H2'	26:DA:855:G:C8	2.53	0.43
26:DA:1263:U:C4	26:DA:1264:G:C6	3.06	0.43
26:DA:1860:G:H1	26:DA:1882:C:N4	2.16	0.43
26:DA:1959:G:C6	26:DA:1960:A:C5	3.06	0.43
26:DA:2469:A:H5"	26:DA:2470:G:OP2	2.18	0.43
26:DA:2785:C:OP1	29:DE:41:LYS:NZ	2.45	0.43
27:DB:42:C:N3	31:DG:93:THR:HB	2.33	0.43
45:DY:20:TYR:CE1	45:DY:43:ASN:HA	2.52	0.43
1:AA:235:C:H1'	17:AQ:61:GLU:CD	2.42	0.43
1:AA:748:C:H4'	1:AA:749:C:O5'	2.19	0.43
2:AB:139:LYS:O	2:AB:143:GLU:HG3	2.18	0.43
6:AF:17:SER:O	6:AF:21:LEU:HG	2.18	0.43
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.19	0.43
7:AG:76:ARG:NH2	7:AG:156:TRP:HZ2	2.16	0.43
8:AH:103:VAL:HG21	8:AH:110:ALA:HB2	2.00	0.43
20:AT:36:LEU:HD22	20:AT:55:ILE:HG23	2.00	0.43
26:BA:579:G:H2'	26:BA:580:C:C6	2.53	0.43
26:BA:2817:G:OP1	38:BR:42:LYS:NZ	2.45	0.43
39:BS:59:LYS:HE3	39:BS:60:GLY:H	1.82	0.43
42:BV:21:ARG:HG2	42:BV:91:TYR:CD1	2.53	0.43
42:BV:29:PRO:HA	42:BV:61:VAL:HG22	2.00	0.43
46:BZ:124:ILE:HG23	46:BZ:126:VAL:HG23	2.00	0.43
1:CA:340:U:H2'	1:CA:341:C:C6	2.54	0.43
1:CA:392:G:H2'	1:CA:393:A:H8	1.82	0.43
1:CA:419:C:H5"	1:CA:513:C:C1'	2.49	0.43
1:CA:619:U:O2	4:CD:133:VAL:HA	2.18	0.43
1:CA:635:G:H2'	1:CA:636:U:O4'	2.18	0.43
1:CA:829:G:H1	1:CA:857:C:H42	1.65	0.43
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.32	0.43
2:CB:166:ASP:O	2:CB:170:GLU:N	2.44	0.43
9:CI:23:ASN:HD22	9:CI:25:LYS:H	1.67	0.43
26:DA:185:U:H2'	26:DA:186:G:C8	2.53	0.43
26:DA:211:A:H2'	26:DA:212:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:271(Q):G:H2'	26:DA:271(R):G:H8	1.82	0.43
26:DA:619:G:O5'	26:DA:620:G:N2	2.51	0.43
26:DA:863:A:H2'	26:DA:864:G:C8	2.53	0.43
26:DA:900:A:O2'	26:DA:901:A:OP1	2.34	0.43
26:DA:923:C:H2'	26:DA:924:C:H6	1.83	0.43
26:DA:938:G:OP1	55:D8:52:LYS:HD2	2.18	0.43
26:DA:1028:A:H61	26:DA:1125:G:H2'	1.82	0.43
26:DA:1513:C:H2'	26:DA:1514:U:C6	2.54	0.43
26:DA:1826:G:H2'	26:DA:1827:C:H6	1.82	0.43
26:DA:2347:C:O2'	53:D6:21:TYR:OH	2.11	0.43
26:DA:2483:C:N3	37:DQ:124:LYS:NZ	2.59	0.43
26:DA:2893:G:H4'	26:DA:2894:G:O5'	2.18	0.43
33:DI:75:LEU:HD11	33:DI:105:HIS:CD2	2.53	0.43
43:DW:84:ARG:HG3	43:DW:98:LYS:HD2	2.00	0.43
46:DZ:157:LEU:C	46:DZ:161:VAL:HG11	2.43	0.43
49:D2:1:MET:HE2	49:D2:6:VAL:HG22	2.00	0.43
1:AA:105:G:H2'	1:AA:106:C:C6	2.54	0.43
1:AA:271:C:H2'	1:AA:272:C:C6	2.53	0.43
1:AA:310:G:H5'	16:AP:31:LYS:HB2	1.99	0.43
1:AA:321:A:N7	1:AA:328:C:O2'	2.37	0.43
1:AA:593:G:C2	1:AA:594:G:C4	3.06	0.43
1:AA:1304:G:C5	1:AA:1305:G:C6	3.06	0.43
1:AA:1469:G:H2'	1:AA:1470:G:C8	2.53	0.43
1:AA:1525:G:OP2	11:AK:120:ARG:NH2	2.52	0.43
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.36	0.43
3:AC:16:ARG:HH22	3:AC:183:ASP:HA	1.82	0.43
19:AS:53:ASN:OD1	19:AS:56:GLN:N	2.37	0.43
21:AU:15:ARG:HB2	21:AU:15:ARG:NH1	2.33	0.43
24:AX:7:G:O2'	24:AX:49:G:H5'	2.18	0.43
26:BA:330:A:C2	26:BA:1210:A:H2'	2.52	0.43
26:BA:493:G:H2'	26:BA:494:G:O4'	2.17	0.43
26:BA:535:C:O3'	41:BU:53:ARG:NH1	2.51	0.43
26:BA:1364:G:OP2	48:B1:3:LYS:HG3	2.18	0.43
26:BA:2256:G:H2'	26:BA:2257:U:O4'	2.19	0.43
26:BA:2287:A:C4	26:BA:2289:G:C8	3.07	0.43
26:BA:2791:C:H5'	26:BA:2893:G:N2	2.32	0.43
28:BD:72:LYS:HE3	28:BD:72:LYS:HB3	1.82	0.43
29:BE:96:PHE:O	29:BE:175:VAL:HG11	2.18	0.43
31:BG:66:GLN:HG2	51:B4:1:MET:HE1	2.01	0.43
40:BT:8:LYS:HD3	40:BT:8:LYS:HA	1.79	0.43
45:BY:13:VAL:HG12	45:BY:74:PRO:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BZ:93:ASP:HB2	46:BZ:131:ARG:NH2	2.33	0.43
1:CA:399:G:H2'	1:CA:400:C:C6	2.54	0.43
1:CA:1055:A:H62	1:CA:1200:C:N4	2.16	0.43
1:CA:1104:G:C2'	1:CA:1105:A:H5'	2.48	0.43
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.18	0.43
1:CA:1235:U:H2'	1:CA:1236:A:O4'	2.18	0.43
24:CX:19:G:C4	24:CX:57:A:C2	3.06	0.43
26:DA:7:G:H5"	34:DN:130:HIS:CE1	2.53	0.43
26:DA:51:G:H1'	26:DA:119:A:N1	2.33	0.43
26:DA:330:A:H2	26:DA:1210:A:C2'	2.32	0.43
26:DA:523:C:H4'	26:DA:540:C:O2	2.19	0.43
26:DA:873:G:H1	26:DA:904:C:H42	1.66	0.43
26:DA:1493:C:H41	26:DA:2206:G:C2'	2.31	0.43
26:DA:1570:A:C6	26:DA:1571:A:C6	3.05	0.43
26:DA:2489:G:C6	26:DA:2490:G:N1	2.87	0.43
26:DA:2492:U:H2'	26:DA:2493:U:C6	2.54	0.43
26:DA:2651:C:C2'	26:DA:2652:C:H5'	2.48	0.43
26:DA:2846:G:H2'	26:DA:2847:U:O4'	2.18	0.43
28:DD:132:PRO:HG2	28:DD:135:PHE:HD2	1.81	0.43
28:DD:223:GLY:HA3	28:DD:231:HIS:CE1	2.54	0.43
30:DF:184:TYR:O	30:DF:188:ARG:HG3	2.18	0.43
31:DG:18:GLU:OE2	31:DG:21:ARG:NH2	2.51	0.43
35:DO:23:ARG:HG3	35:DO:24:VAL:N	2.32	0.43
46:DZ:149:SER:HB2	46:DZ:172:ALA:O	2.18	0.43
46:DZ:157:LEU:HB3	46:DZ:161:VAL:HG13	2.00	0.43
1:AA:22:G:C6	1:AA:23:C:C4	3.06	0.43
1:AA:182:U:H5'	1:AA:182:U:H6	1.83	0.43
1:AA:542:G:OP1	4:AD:10:ARG:NH2	2.50	0.43
1:AA:600:C:N3	1:AA:639:G:C2	2.87	0.43
1:AA:1003:G:N1	1:AA:1004:A:N3	2.66	0.43
1:AA:1017:G:H2'	1:AA:1018:C:O4'	2.19	0.43
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	2.01	0.43
7:AG:28:ASN:HA	7:AG:31:MET:HE2	2.00	0.43
14:AN:15:LYS:HE2	14:AN:16:PHE:CE1	2.53	0.43
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.33	0.43
23:AW:76:PPU:HD1	26:BA:2506:U:O4'	2.19	0.43
26:BA:444:C:H4'	30:BF:49:ALA:HB2	2.00	0.43
26:BA:459:U:H5"	54:B7:40:TRP:CD2	2.53	0.43
26:BA:2801(A):A:H1'	26:BA:2895:U:H1'	2.00	0.43
32:BH:56:SER:OG	32:BH:57:ASP:N	2.49	0.43
36:BP:6:LEU:HA	36:BP:6:LEU:HD23	1.75	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BS:49:VAL:HG22	39:BS:73:LEU:HD12	2.00	0.43
43:BW:51:LEU:HD23	43:BW:105:VAL:HG11	1.99	0.43
48:B1:6:GLU:CD	48:B1:61:ARG:H	2.27	0.43
1:CA:77:G:C6	1:CA:93:G:C6	3.06	0.43
1:CA:667:G:O2'	15:CO:49:ASP:OD1	2.20	0.43
1:CA:828:A:C2	1:CA:829:G:H1'	2.53	0.43
1:CA:1144:G:C6	1:CA:1145:C:N4	2.86	0.43
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.53	0.43
1:CA:1400:C:N3	24:CX:34:C:C2	2.87	0.43
1:CA:1432:G:OP1	40:DT:108:ARG:HB2	2.17	0.43
1:CA:1507:A:H2'	1:CA:1508:G:O4'	2.19	0.43
3:CC:131:ARG:NH1	5:CE:50:GLU:HG3	2.34	0.43
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.50	0.43
26:DA:271(F):C:H2'	26:DA:271(G):C:C6	2.53	0.43
26:DA:379:G:O2'	26:DA:2232:U:OP1	2.35	0.43
26:DA:753:C:H2'	26:DA:754:C:H6	1.83	0.43
26:DA:1159:U:H2'	26:DA:1160:G:H8	1.84	0.43
26:DA:1334:G:C6	26:DA:1335:U:C4	3.06	0.43
26:DA:1652:A:H2'	26:DA:1653:G:H5'	2.01	0.43
26:DA:1693:U:O2'	28:DD:14:ARG:NH2	2.51	0.43
26:DA:1827:C:OP2	28:DD:222:ARG:HD2	2.18	0.43
26:DA:2094:G:P	33:DI:22:LYS:HD2	2.58	0.43
26:DA:2341:G:H2'	26:DA:2342:C:O4'	2.17	0.43
26:DA:2695:C:H2'	26:DA:2696:U:H6	1.81	0.43
26:DA:2748:A:H5'	32:DH:4:ILE:HD12	2.00	0.43
26:DA:2831:G:O2'	26:DA:2883:A:H2'	2.18	0.43
32:DH:38:SER:OG	32:DH:40:GLU:HG3	2.19	0.43
33:DI:8:PRO:HB3	33:DI:14:ASP:OD1	2.19	0.43
35:DO:10:VAL:HG13	35:DO:17:ARG:C	2.44	0.43
35:DO:73:ASP:HB2	40:DT:82:LEU:HD13	2.00	0.43
36:DP:121:LYS:O	36:DP:123:LEU:N	2.48	0.43
45:DY:56:PRO:C	45:DY:58:GLY:H	2.27	0.43
1:AA:99:U:H2'	1:AA:100:C:C6	2.53	0.43
1:AA:262:A:H2'	1:AA:263:A:C8	2.53	0.43
1:AA:575:G:O2'	1:AA:821:G:H5'	2.18	0.43
1:AA:991:U:O2'	1:AA:992:U:OP2	2.26	0.43
8:AH:69:ARG:HE	8:AH:69:ARG:HB2	1.52	0.43
19:AS:12:ASP:C	19:AS:14:HIS:H	2.25	0.43
26:BA:1121:C:H2'	26:BA:1122:G:O4'	2.18	0.43
26:BA:1142(A):A:C4	26:BA:1144:G:C8	3.07	0.43
26:BA:1257:C:H4'	30:BF:83:PHE:CE1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1858:G:N2	26:BA:1883:G:H2'	2.34	0.43
26:BA:2357:U:OP1	47:B0:20:ARG:NH1	2.51	0.43
27:BB:105:A:H2'	27:BB:106:G:O4'	2.18	0.43
28:BD:223:GLY:HA3	28:BD:231:HIS:CE1	2.53	0.43
30:BF:132:VAL:HA	30:BF:138:GLU:HB3	2.00	0.43
32:BH:154:PRO:HB3	32:BH:163:TYR:CZ	2.53	0.43
34:BN:4:TYR:HE2	34:BN:41:ASP:HB2	1.83	0.43
37:BQ:21:THR:HG21	37:BQ:101:ARG:HD3	2.00	0.43
1:CA:265:G:H5'	17:CQ:64:PRO:O	2.17	0.43
1:CA:515:G:C5	1:CA:516:U:C4	3.06	0.43
1:CA:647:C:H2'	1:CA:648:A:H8	1.84	0.43
1:CA:971:G:O6	1:CA:1364:U:O2'	2.32	0.43
1:CA:1148:U:O2'	9:CI:66:ARG:NH1	2.51	0.43
1:CA:1272:G:C2'	1:CA:1273:G:H5'	2.48	0.43
1:CA:1277:C:O2'	1:CA:1279:A:C8	2.71	0.43
3:CC:34:LEU:HD22	14:CN:25:VAL:HG11	2.00	0.43
3:CC:54:ARG:HB3	3:CC:54:ARG:HH11	1.83	0.43
4:CD:103:ASN:O	4:CD:107:ARG:HG2	2.19	0.43
18:CR:32:ARG:HA	18:CR:69:THR:HG21	2.01	0.43
19:CS:11:VAL:HG13	19:CS:38:SER:HB3	2.01	0.43
26:DA:1359:A:N6	26:DA:1372:U:N3	2.67	0.43
26:DA:2110:G:OP1	26:DA:2118:U:N3	2.51	0.43
26:DA:2378:A:H4'	39:DS:23:ARG:HD2	2.00	0.43
30:DF:93:LYS:HD3	30:DF:93:LYS:HA	1.91	0.43
31:DG:11:TYR:HA	31:DG:15:VAL:HB	2.00	0.43
36:DP:38:GLN:HG2	36:DP:45:LEU:N	2.33	0.43
51:D4:40:HIS:HA	51:D4:41:PRO:HD2	1.76	0.43
54:D7:34:ARG:NH1	54:D7:41:ARG:O	2.52	0.43
1:AA:401:C:H2'	1:AA:402:G:H8	1.83	0.43
1:AA:792:A:H4'	1:AA:793:U:C5'	2.48	0.43
1:AA:1173:G:C6	1:AA:1174:G:N7	2.86	0.43
1:AA:1179:A:H4'	9:AI:103:THR:HA	2.00	0.43
13:AM:13:LYS:HA	13:AM:44:ARG:HH11	1.84	0.43
26:BA:185:U:H4'	26:BA:218:A:H4'	2.01	0.43
26:BA:1857:G:C6	26:BA:1858:G:C6	3.07	0.43
26:BA:2099:U:H2'	26:BA:2100:G:C8	2.54	0.43
26:BA:2490:G:H8	26:BA:2490:G:OP2	2.01	0.43
30:BF:32:LEU:HB3	30:BF:112:MET:HE1	1.99	0.43
31:BG:16:ARG:HE	31:BG:31:VAL:HG11	1.84	0.43
33:BI:92:VAL:HG11	33:BI:144:VAL:HG11	2.01	0.43
36:BP:50:ARG:HG2	55:B8:61:LEU:HD11	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:B0:17:GLN:O	47:B0:19:LYS:NZ	2.50	0.43
1:CA:96:U:O2'	1:CA:97:G:C8	2.65	0.43
1:CA:189:G:H2'	1:CA:189(A):C:C6	2.54	0.43
1:CA:243:A:H4'	1:CA:244:U:H5"	2.00	0.43
1:CA:766:A:H2'	1:CA:767:A:O4'	2.18	0.43
1:CA:1122:U:H2'	1:CA:1123:A:C8	2.54	0.43
1:CA:1222:G:H5'	19:CS:77:THR:HG21	2.00	0.43
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.53	0.43
2:CB:84:GLU:HB3	2:CB:219:VAL:HG21	2.00	0.43
3:CC:6:HIS:HA	3:CC:7:PRO:HD3	1.80	0.43
4:CD:108:LEU:HB3	4:CD:110:PHE:CE1	2.54	0.43
4:CD:133:VAL:HG11	4:CD:138:TYR:CD2	2.54	0.43
6:CF:8:ILE:HG22	6:CF:10:LEU:HD13	2.00	0.43
12:CL:84:LEU:HB2	12:CL:105:TYR:CE2	2.54	0.43
14:CN:4:LYS:HA	14:CN:7:ILE:HG12	2.01	0.43
15:CO:58:MET:O	15:CO:62:GLN:N	2.40	0.43
19:CS:56:GLN:HE21	19:CS:56:GLN:HB3	1.59	0.43
26:DA:466:A:N3	26:DA:683:C:H1'	2.34	0.43
26:DA:614(B):G:H1'	30:DF:44:ARG:HB2	2.00	0.43
26:DA:851:U:O2'	50:D3:42:ALA:O	2.29	0.43
26:DA:1364:G:OP2	48:D1:3:LYS:HG3	2.19	0.43
26:DA:1709:U:H2'	26:DA:1710:C:C6	2.54	0.43
26:DA:2274:A:C5	26:DA:2276:G:C8	3.06	0.43
26:DA:2526:G:H5'	26:DA:2742:C:O2'	2.18	0.43
26:DA:2848:G:C8	40:DT:97:ALA:HB2	2.53	0.43
34:DN:23:LEU:HD12	34:DN:99:LEU:HD23	2.00	0.43
36:DP:58:THR:O	36:DP:62:LEU:HG	2.18	0.43
48:D1:72:GLU:HG2	48:D1:76:ARG:HD3	2.00	0.43
1:AA:309:G:H1'	1:AA:608:A:C2	2.54	0.43
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.54	0.43
1:AA:1316:G:H4'	14:AN:18:VAL:HG13	2.01	0.43
7:AG:23:VAL:O	7:AG:27:ILE:HG12	2.18	0.43
13:AM:91:ARG:NE	13:AM:97:PRO:O	2.51	0.43
26:BA:262:A:H2'	26:BA:263:C:O4'	2.18	0.43
26:BA:272:G:N7	26:BA:421:U:H2'	2.34	0.43
26:BA:746:A:H2'	26:BA:2612:C:H5"	1.99	0.43
26:BA:2175:C:C2'	26:BA:2176:A:H5'	2.48	0.43
26:BA:2544:G:H2'	26:BA:2545:G:O4'	2.18	0.43
26:BA:2657:A:H1'	26:BA:2665:A:N6	2.34	0.43
33:BI:72:LEU:O	33:BI:74:ASN:N	2.48	0.43
1:CA:35:G:C4	1:CA:550:G:N2	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:189(K):U:H2'	1:CA:189(L):G:C8	2.53	0.43
1:CA:626:U:H2'	1:CA:627:G:O4'	2.19	0.43
1:CA:792:A:O2'	1:CA:794:A:N7	2.40	0.43
1:CA:860:A:OP2	61:CA:4111:HOH:O	2.21	0.43
1:CA:944:G:N1	1:CA:1338:G:OP2	2.41	0.43
1:CA:1005:A:H3'	1:CA:1006:C:O4'	2.19	0.43
1:CA:1007:C:O5'	1:CA:1007:C:H6	2.02	0.43
1:CA:1073:U:H2'	1:CA:1074:G:H8	1.84	0.43
1:CA:1095:U:C4	1:CA:1096:C:C4	3.07	0.43
1:CA:1277:C:O2'	1:CA:1279:A:H8	2.01	0.43
1:CA:1320:C:O4'	19:CS:73:GLU:HG3	2.19	0.43
1:CA:1343:G:H2'	1:CA:1344:C:H6	1.80	0.43
1:CA:1352:C:N3	1:CA:1371:G:C6	2.87	0.43
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.53	0.43
24:CX:19:G:N1	24:CX:56:C:N4	2.56	0.43
26:DA:279:C:H2'	26:DA:280:C:C6	2.54	0.43
26:DA:557:U:H2'	26:DA:558:G:C8	2.54	0.43
26:DA:573:G:H1	26:DA:2031:A:P	2.41	0.43
26:DA:602:G:O2'	26:DA:655:A:N6	2.51	0.43
26:DA:616:G:H5'	30:DF:205:ARG:HD2	2.01	0.43
26:DA:797:C:H2'	26:DA:798:G:O4'	2.19	0.43
26:DA:1269:A:O2'	26:DA:1325:G:O6	2.32	0.43
26:DA:1688:U:O2	26:DA:1700:A:H8	2.02	0.43
26:DA:1778:U:H2'	26:DA:1784:A:N6	2.34	0.43
26:DA:1782:C:O2'	26:DA:2609:U:H5"	2.19	0.43
26:DA:1918:A:HO2'	26:DA:1920:C:N4	2.13	0.43
26:DA:2108:C:H2'	26:DA:2109:U:H6	1.83	0.43
26:DA:2224:G:H4'	26:DA:2226:C:C2	2.53	0.43
26:DA:2807:G:N1	26:DA:2808:U:N3	2.67	0.43
31:DG:10:LYS:HG3	31:DG:14:GLU:OE1	2.19	0.43
1:AA:173:U:C5	1:AA:198:G:H8	2.37	0.43
1:AA:255:G:H1'	17:AQ:16:GLN:NE2	2.34	0.43
1:AA:1112:C:C4	3:AC:178:LEU:HD23	2.54	0.43
3:AC:138:VAL:HG23	3:AC:151:VAL:HG23	2.01	0.43
26:BA:755:C:H2'	26:BA:756:C:H6	1.84	0.43
26:BA:844:C:C2'	26:BA:845:G:H5'	2.49	0.43
26:BA:848:G:N9	26:BA:933:A:H8	2.17	0.43
26:BA:1127:A:N3	26:BA:2518:A:H5"	2.34	0.43
26:BA:1364:G:OP1	48:B1:2:SER:HA	2.19	0.43
26:BA:2591:C:H2'	26:BA:2592:G:C8	2.54	0.43
27:BB:78:A:H2'	27:BB:79:C:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BE:167:VAL:HG12	29:BE:189:PRO:HD3	2.01	0.43
32:BH:18:GLU:HB3	32:BH:25:LYS:HB2	2.00	0.43
32:BH:35:VAL:HA	32:BH:36:PRO:HD2	1.92	0.43
35:BO:20:MET:HE3	35:BO:44:LYS:HE3	2.00	0.43
41:BU:66:ASN:O	41:BU:70:ARG:HG3	2.18	0.43
1:CA:255:G:C6	1:CA:256:U:C4	3.07	0.43
1:CA:664:G:P	18:CR:64:ARG:HH21	2.42	0.43
1:CA:1208:C:H2'	1:CA:1209:C:O4'	2.19	0.43
1:CA:1392:G:O2'	1:CA:1393:U:H5'	2.19	0.43
4:CD:120:LEU:HD23	4:CD:120:LEU:HA	1.88	0.43
26:DA:27:G:O2'	26:DA:28:A:OP2	2.32	0.43
26:DA:422:A:H2'	26:DA:423:A:C8	2.54	0.43
26:DA:557:U:H2'	26:DA:558:G:H8	1.84	0.43
26:DA:1153:C:OP1	41:DU:92:ARG:NH1	2.50	0.43
26:DA:1288:U:C2	26:DA:1327:C:C2	3.07	0.43
26:DA:1359:A:N1	26:DA:1372:U:C4	2.86	0.43
26:DA:1394:U:OP1	61:DA:3949:HOH:O	2.20	0.43
26:DA:1486:A:H2'	26:DA:1487:G:C8	2.54	0.43
26:DA:1641:A:H2'	26:DA:1642:G:O4'	2.18	0.43
26:DA:2153:G:H2'	26:DA:2153:G:N3	2.33	0.43
26:DA:2336:A:H61	47:D0:43:THR:HG22	1.84	0.43
26:DA:2352:A:N6	26:DA:2365:G:O2'	2.51	0.43
35:DO:78:ARG:HH22	40:DT:75:ILE:HD11	1.84	0.43
43:DW:13:SER:HA	43:DW:14:PRO:HD3	1.89	0.43
44:DX:1:MET:HE3	44:DX:3:THR:HG22	2.01	0.43
53:D6:6:ARG:HH11	53:D6:26:ASN:HB2	1.84	0.43
1:AA:408:A:H2'	1:AA:409:G:O4'	2.18	0.43
1:AA:683:G:H2'	1:AA:684:A:H8	1.84	0.43
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.19	0.43
15:AO:3:ILE:O	15:AO:3:ILE:HG12	2.19	0.43
26:BA:236:C:H2'	26:BA:237:C:C6	2.53	0.43
26:BA:445:C:O2'	26:BA:446:G:H5'	2.19	0.43
26:BA:1309:G:H4'	54:B7:7:PRO:HB2	2.01	0.43
26:BA:2125:G:H1	26:BA:2172:U:P	2.40	0.43
35:BO:120:GLU:OE1	40:BT:67:SER:OG	2.29	0.43
1:CA:358:U:H2'	1:CA:359:U:C6	2.54	0.43
1:CA:417:C:O5'	1:CA:417:C:H6	2.02	0.43
1:CA:585:G:N3	1:CA:879:C:H4'	2.34	0.43
1:CA:950:U:H2'	1:CA:951:G:C8	2.53	0.43
1:CA:1064:G:OP1	1:CA:1386:G:H4'	2.19	0.43
1:CA:1109:C:H2'	1:CA:1110:A:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1137:C:O5'	1:CA:1137:C:H6	2.02	0.43
1:CA:1237:C:O2	1:CA:1334:G:O2'	2.34	0.43
3:CC:22:TRP:CD1	3:CC:57:ILE:HG22	2.54	0.43
4:CD:8:VAL:O	4:CD:11:LEU:HB2	2.19	0.43
7:CG:28:ASN:HA	7:CG:31:MET:HE2	2.01	0.43
8:CH:44:PHE:HE2	8:CH:109:ILE:HG12	1.84	0.43
26:DA:171:G:H2'	26:DA:172:C:H6	1.83	0.43
26:DA:355:G:H2'	26:DA:356:G:C8	2.54	0.43
26:DA:414:C:H2'	26:DA:415:A:C8	2.54	0.43
26:DA:1449:A:OP2	26:DA:1449:A:H8	2.02	0.43
26:DA:2109:U:N3	26:DA:2110:G:N7	2.66	0.43
26:DA:2136:C:HO2'	26:DA:2137:C:H6	1.67	0.43
26:DA:2706:G:O2'	38:DR:64:ARG:HD3	2.19	0.43
29:DE:37:ARG:NH1	29:DE:42:ASP:OD1	2.49	0.43
40:DT:59:THR:HG23	40:DT:78:LEU:CB	2.46	0.43
1:AA:201:C:N4	1:AA:216:G:H22	2.17	0.42
1:AA:300:A:H1'	1:AA:565:U:O2	2.19	0.42
1:AA:686:U:O4	1:AA:703:G:O2'	2.25	0.42
1:AA:718:G:C8	11:AK:116:HIS:HB3	2.53	0.42
1:AA:864:A:H2'	1:AA:865:A:C8	2.53	0.42
4:AD:138:TYR:CD1	4:AD:138:TYR:C	2.97	0.42
7:AG:144:MET:HE2	7:AG:144:MET:HB3	1.73	0.42
13:AM:4:ILE:HA	13:AM:5:ALA:HA	1.81	0.42
20:AT:29:LYS:HB2	20:AT:71:THR:HG21	2.01	0.42
26:BA:250:G:OP2	55:B8:13:ARG:NH2	2.52	0.42
26:BA:303:U:H2'	26:BA:304:G:H8	1.84	0.42
26:BA:828:U:H2'	26:BA:829:A:C8	2.54	0.42
26:BA:947:G:OP2	61:BA:4650:HOH:O	2.22	0.42
26:BA:962:G:H4'	26:BA:2496:C:O2'	2.19	0.42
26:BA:1317:A:H2'	26:BA:1318:C:C6	2.53	0.42
26:BA:1654:A:H2'	26:BA:1655:A:H8	1.83	0.42
26:BA:1934:C:H4'	26:BA:1974:C:O3'	2.19	0.42
26:BA:2554:U:H2'	26:BA:2555:U:C6	2.53	0.42
26:BA:2557:G:H2'	26:BA:2558:C:C6	2.53	0.42
26:BA:2636:U:H1'	26:BA:2783:G:N2	2.35	0.42
26:BA:2712:U:OP1	26:BA:2714:G:H4'	2.19	0.42
26:BA:2821:A:H2'	26:BA:2822:G:O4'	2.18	0.42
26:BA:2836:U:C4	26:BA:2883:A:N6	2.87	0.42
30:BF:106:ARG:H	30:BF:106:ARG:HG2	1.49	0.42
41:BU:10:ARG:NH2	61:BU:301:HOH:O	2.52	0.42
1:CA:679:C:C2'	1:CA:680:C:H5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1013:G:N2	1:CA:1015:A:H3'	2.34	0.42
1:CA:1090:U:H2'	1:CA:1091:U:C6	2.53	0.42
1:CA:1101:A:N6	2:CB:176:GLU:OE2	2.51	0.42
1:CA:1227:A:OP2	13:CM:111:LYS:HE3	2.18	0.42
1:CA:1512:U:H2'	1:CA:1513:A:C8	2.53	0.42
4:CD:12:CYS:SG	4:CD:19:LEU:HB2	2.58	0.42
5:CE:93:PRO:HG2	8:CH:105:ARG:CZ	2.49	0.42
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.18	0.42
13:CM:50:GLU:HG3	13:CM:54:VAL:HG13	2.00	0.42
23:CW:76:PPU:H102	26:DA:2584:U:H4'	2.01	0.42
26:DA:872:A:H2'	26:DA:873:G:O4'	2.19	0.42
26:DA:2052:G:H4'	29:DE:143:ASN:O	2.19	0.42
26:DA:2070:G:C2	26:DA:2442:C:C2	3.07	0.42
27:DB:43:C:C4	27:DB:45:A:C6	3.07	0.42
27:DB:68:C:H2'	27:DB:69:G:O4'	2.18	0.42
28:DD:38:LYS:HA	28:DD:38:LYS:HD2	1.83	0.42
31:DG:143:GLU:H	31:DG:143:GLU:HG2	1.32	0.42
32:DH:58:GLU:O	32:DH:62:LYS:HG3	2.19	0.42
35:DO:4:PRO:O	35:DO:5:GLN:HB2	2.19	0.42
36:DP:46:LYS:HB3	36:DP:46:LYS:HE3	1.80	0.42
42:DV:57:VAL:HG12	42:DV:99:ILE:HG12	2.00	0.42
46:DZ:91:LEU:HD23	46:DZ:130:PRO:HB3	2.01	0.42
51:D4:40:HIS:ND1	51:D4:43:TYR:HD2	2.17	0.42
52:D5:49:CYS:SG	52:D5:51:TYR:HB2	2.58	0.42
1:AA:266:G:H5"	1:AA:268:C:H41	1.84	0.42
1:AA:630:G:H2'	1:AA:631:G:H8	1.84	0.42
1:AA:762:C:H2'	1:AA:763:G:C8	2.55	0.42
1:AA:952:U:H2'	1:AA:953:G:C8	2.54	0.42
1:AA:1151:A:HO2'	1:AA:1152:A:H8	1.67	0.42
1:AA:1322:C:H4'	1:AA:1323:G:OP1	2.20	0.42
1:AA:1355:G:H2'	1:AA:1356:G:H8	1.84	0.42
1:AA:1417:G:C6	1:AA:1482:G:C6	3.08	0.42
13:AM:88:ARG:HG3	13:AM:98:VAL:HG12	2.01	0.42
24:AX:5:G:N2	24:AX:68:C:N3	2.58	0.42
26:BA:670:A:H4'	26:BA:671:C:O5'	2.20	0.42
26:BA:812:C:H5"	26:BA:1250:G:O2'	2.19	0.42
26:BA:919:G:N2	26:BA:2269:A:OP2	2.52	0.42
26:BA:1790:C:H2'	26:BA:1791:A:C5	2.54	0.42
26:BA:1820:U:C4	28:BD:160:GLY:HA3	2.54	0.42
26:BA:1828:G:H4'	26:BA:1829:A:OP1	2.18	0.42
26:BA:2315:G:H2'	26:BA:2316:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2607:G:H2'	26:BA:2608:G:O4'	2.19	0.42
26:BA:2822:G:O2'	26:BA:2824:C:OP2	2.28	0.42
33:BI:140:LEU:HD23	33:BI:140:LEU:HA	1.86	0.42
35:BO:92:GLU:HG3	35:BO:93:PRO:HD2	2.00	0.42
37:BQ:34:LEU:HD11	37:BQ:129:THR:HB	2.00	0.42
38:BR:31:HIS:C	38:BR:33:ARG:H	2.27	0.42
46:BZ:48:PHE:CE1	46:BZ:71:VAL:HG11	2.55	0.42
46:BZ:98:MET:O	46:BZ:125:LEU:HA	2.20	0.42
51:B4:41:PRO:HG3	51:B4:49:PHE:CE2	2.54	0.42
1:CA:49:U:H3	1:CA:362:G:H1'	1.84	0.42
1:CA:524:G:H2'	1:CA:525:C:C6	2.54	0.42
1:CA:598:U:H2'	1:CA:599:C:H6	1.83	0.42
1:CA:630:G:H2'	1:CA:631:G:H8	1.84	0.42
1:CA:892:A:C6	1:CA:893:C:C4	3.08	0.42
1:CA:1007:C:O2	1:CA:1022:G:N1	2.31	0.42
1:CA:1400:C:O4'	22:CV:18:G:H1'	2.19	0.42
2:CB:16:HIS:HD2	2:CB:204:ASN:N	2.17	0.42
2:CB:55:PHE:O	2:CB:59:GLU:N	2.32	0.42
4:CD:50:ARG:HA	4:CD:51:PRO:HD3	1.85	0.42
18:CR:53:ARG:HA	18:CR:56:THR:OG1	2.18	0.42
18:CR:76:LEU:HD12	18:CR:76:LEU:HA	1.76	0.42
21:CU:9:ARG:O	21:CU:13:ILE:HG13	2.19	0.42
24:CX:42:G:H2'	24:CX:43:A:C8	2.51	0.42
26:DA:83:G:N2	26:DA:102:G:H1'	2.34	0.42
26:DA:226:G:H21	26:DA:228:A:H62	1.68	0.42
26:DA:506:G:O3'	26:DA:507:A:H8	2.02	0.42
26:DA:819:A:H5'	26:DA:973:A:N1	2.34	0.42
26:DA:1439:A:H2'	26:DA:1440:G:O4'	2.19	0.42
26:DA:1530:C:O2'	26:DA:1531:C:P	2.77	0.42
26:DA:2110:G:C2	26:DA:2120:G:H1'	2.53	0.42
26:DA:2139:C:N4	26:DA:2153:G:C2	2.87	0.42
26:DA:2303:G:H2'	26:DA:2304:G:O4'	2.19	0.42
26:DA:2395:C:O2'	48:D1:30:VAL:HG22	2.19	0.42
26:DA:2494:G:O2'	37:DQ:80:GLU:HA	2.19	0.42
30:DF:149:ASP:OD1	30:DF:149:ASP:N	2.47	0.42
31:DG:144:ILE:HA	31:DG:148:MET:HE1	2.01	0.42
36:DP:44:GLY:HA3	36:DP:45:LEU:HB2	2.01	0.42
37:DQ:118:LEU:HB2	37:DQ:131:ILE:HD13	2.02	0.42
40:DT:92:GLY:O	40:DT:120:ARG:NH2	2.51	0.42
43:DW:69:LEU:HD22	43:DW:107:LEU:HB3	2.00	0.42
46:DZ:141:VAL:HG12	46:DZ:144:LEU:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DZ:158:PRO:HA	46:DZ:159:PRO:HD3	1.90	0.42
55:D8:10:ALA:HB3	55:D8:62:LEU:HD21	2.01	0.42
55:D8:30:ARG:HD3	55:D8:30:ARG:HA	1.57	0.42
1:AA:503:C:H2'	1:AA:504:C:C6	2.54	0.42
1:AA:1130:A:H5'	9:AI:18:PHE:CE2	2.54	0.42
1:AA:1202:G:O2'	14:AN:29:ARG:HG3	2.19	0.42
1:AA:1445:C:C2	1:AA:1458:G:C2	3.07	0.42
1:AA:1456:G:H1	20:AT:51:GLU:CD	2.27	0.42
2:AB:170:GLU:O	2:AB:174:VAL:HG23	2.20	0.42
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.19	0.42
4:AD:108:LEU:HD12	4:AD:108:LEU:HA	1.83	0.42
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.84	0.42
7:AG:55:GLY:O	7:AG:56:GLN:HG3	2.19	0.42
20:AT:10:LEU:HD23	20:AT:11:SER:H	1.83	0.42
26:BA:18:C:O2'	26:BA:554:U:OP1	2.36	0.42
26:BA:135:G:C6	26:BA:145:G:C6	3.07	0.42
26:BA:744:G:OP1	29:BE:132:HIS:ND1	2.50	0.42
26:BA:1131:G:O6	26:BA:2040:C:H1'	2.20	0.42
26:BA:1423:G:H2'	26:BA:1424:G:H8	1.84	0.42
26:BA:1477:A:H2'	26:BA:1478:G:O4'	2.19	0.42
26:BA:1665:A:H2'	26:BA:1666:G:O4'	2.18	0.42
26:BA:1992:G:H4'	26:BA:1993:U:H5	1.84	0.42
26:BA:2821:A:O2'	26:BA:2826:A:N1	2.44	0.42
30:BF:150:GLY:HA2	30:BF:172:TRP:CD2	2.55	0.42
34:BN:112:LEU:O	34:BN:116:LEU:HG	2.19	0.42
36:BP:3:LEU:HD12	36:BP:3:LEU:HA	1.84	0.42
36:BP:138:LEU:HD23	36:BP:145:PRO:HG3	2.01	0.42
48:B1:7:ILE:HG23	48:B1:98:LEU:HD11	2.01	0.42
1:CA:435:C:O5'	1:CA:435:C:H6	2.01	0.42
1:CA:831:U:C2'	1:CA:832:C:H5'	2.50	0.42
1:CA:1400:C:H4'	22:CV:18:G:O2'	2.19	0.42
3:CC:114:PRO:HA	3:CC:185:GLY:HA3	2.00	0.42
3:CC:115:LEU:HD12	3:CC:115:LEU:HA	1.82	0.42
12:CL:33:ARG:HG2	12:CL:60:LEU:HD12	2.02	0.42
13:CM:60:VAL:HG23	13:CM:64:TRP:CZ3	2.53	0.42
19:CS:23:ASN:HA	19:CS:27:GLU:CD	2.45	0.42
19:CS:27:GLU:HG2	19:CS:47:HIS:CD2	2.54	0.42
24:CX:61:C:H2'	24:CX:62:C:C6	2.54	0.42
26:DA:67:U:H2'	26:DA:68:G:O4'	2.19	0.42
26:DA:676:A:H1'	26:DA:2443:C:H1'	2.00	0.42
26:DA:876:C:H2'	26:DA:877:U:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1721:G:H2'	26:DA:1740:G:O6	2.19	0.42
27:DB:30:C:O2	27:DB:31:C:C6	2.72	0.42
29:DE:176:ILE:HG22	29:DE:178:GLU:HG2	2.01	0.42
1:AA:384:G:H2'	1:AA:385:C:C6	2.53	0.42
1:AA:730:G:C5	1:AA:731:G:H1'	2.55	0.42
1:AA:991:U:H6	1:AA:991:U:H2'	1.65	0.42
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.07	0.42
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	2.02	0.42
8:AH:23:SER:HB3	8:AH:62:TYR:CD2	2.54	0.42
8:AH:86:ILE:HG12	8:AH:135:CYS:HA	2.01	0.42
9:AI:5:TYR:HH	9:AI:7:THR:HG1	1.59	0.42
11:AK:73:MET:HG2	11:AK:103:LEU:HD21	2.00	0.42
26:BA:38:A:H2'	26:BA:39:C:C6	2.55	0.42
26:BA:536:A:H2'	26:BA:537:C:C6	2.55	0.42
26:BA:774:A:H2'	26:BA:774:A:N3	2.35	0.42
26:BA:776:G:N7	26:BA:793:A:O2'	2.50	0.42
26:BA:1047:G:HO2'	26:BA:1048:A:P	2.41	0.42
26:BA:2108:C:H2'	26:BA:2109:U:O4'	2.19	0.42
26:BA:2742:C:OP1	56:B9:35:ARG:HD3	2.19	0.42
35:BO:15:GLY:O	35:BO:47:ILE:HG12	2.19	0.42
40:BT:22:PHE:HA	40:BT:91:ARG:HH12	1.84	0.42
1:CA:38:G:H1	1:CA:397:A:H5"	1.84	0.42
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.55	0.42
3:CC:115:LEU:O	3:CC:118:GLN:HG2	2.19	0.42
4:CD:175:SER:HB3	4:CD:186:LEU:HD21	2.01	0.42
7:CG:46:ALA:HA	7:CG:49:ILE:HD12	2.02	0.42
8:CH:94:TYR:HD1	8:CH:132:GLU:HA	1.84	0.42
8:CH:97:VAL:HA	8:CH:100:ILE:HG13	2.01	0.42
11:CK:38:ASN:HA	11:CK:39:PRO:HD3	1.94	0.42
11:CK:120:ARG:HA	11:CK:121:PRO:HD3	1.82	0.42
26:DA:108:U:C2	26:DA:109:G:C8	3.07	0.42
26:DA:208:C:H2'	26:DA:209:C:H6	1.82	0.42
26:DA:911:A:H2'	37:DQ:9:TYR:OH	2.19	0.42
26:DA:1191:G:H2'	26:DA:1192:G:H8	1.84	0.42
26:DA:1384:A:N3	26:DA:1405:U:H1'	2.33	0.42
26:DA:2316:C:O2'	26:DA:2317:C:H5'	2.19	0.42
27:DB:6:C:H2'	27:DB:7:G:H5"	2.00	0.42
28:DD:134:ARG:O	28:DD:168:ARG:NH2	2.52	0.42
29:DE:72:VAL:HG13	29:DE:73:GLU:O	2.19	0.42
30:DF:53:THR:HG23	30:DF:55:GLY:N	2.31	0.42
32:DH:10:PRO:O	32:DH:76:VAL:HG21	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DI:88:ILE:HG23	33:DI:123:LEU:HA	2.00	0.42
33:DI:125:GLU:HA	33:DI:142:VAL:O	2.20	0.42
36:DP:39:LYS:CB	36:DP:45:LEU:HG	2.48	0.42
38:DR:38:VAL:HB	38:DR:39:PRO:HD3	2.00	0.42
1:AA:192:U:H4'	20:AT:57:ARG:HD3	2.00	0.42
1:AA:1509:C:H2'	1:AA:1510:U:O4'	2.20	0.42
2:AB:61:LEU:HD12	2:AB:61:LEU:HA	1.85	0.42
7:AG:126:ASP:O	7:AG:131:LYS:N	2.50	0.42
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.35	0.42
16:AP:2:VAL:HG22	16:AP:64:ALA:HA	2.01	0.42
26:BA:286:C:H2'	26:BA:287:C:H6	1.85	0.42
26:BA:786:C:H5"	26:BA:1780:A:C8	2.55	0.42
26:BA:1015:G:N2	26:BA:1147:C:O2	2.47	0.42
26:BA:2040:C:H2'	26:BA:2041:U:O4'	2.20	0.42
45:BY:86:ARG:HD2	45:BY:100:ALA:HA	2.01	0.42
51:B4:16:CYS:SG	51:B4:17:GLY:N	2.92	0.42
53:B6:8:LYS:HG2	55:B8:34:TRP:CD1	2.55	0.42
1:CA:71:C:H42	1:CA:98:G:H1	1.66	0.42
1:CA:153:C:H2'	1:CA:154:C:C6	2.55	0.42
1:CA:189:G:H2'	1:CA:189(A):C:O4'	2.20	0.42
1:CA:333:G:H4'	20:CT:16:HIS:CE1	2.54	0.42
1:CA:581:G:O2'	1:CA:582:U:H5'	2.19	0.42
1:CA:625:G:H4'	16:CP:16:HIS:HB3	2.02	0.42
1:CA:838:G:C2	1:CA:849:C:C2	3.07	0.42
1:CA:1089:G:C2	1:CA:1097:C:C2	3.07	0.42
1:CA:1120:G:C5	1:CA:1121:U:C5	3.07	0.42
1:CA:1513:A:C6	1:CA:1514:C:N4	2.88	0.42
2:CB:96:ARG:NE	2:CB:98:LEU:HD13	2.34	0.42
3:CC:124:ILE:HD11	3:CC:189:ALA:CB	2.49	0.42
7:CG:27:ILE:O	7:CG:31:MET:N	2.53	0.42
7:CG:113:GLU:CG	7:CG:119:ARG:HG2	2.49	0.42
13:CM:57:ARG:NE	51:D4:34:GLU:HB3	2.34	0.42
15:CO:31:LEU:HD23	15:CO:31:LEU:HA	1.87	0.42
24:CX:31:G:C5	24:CX:32:5MC:C4	3.07	0.42
26:DA:272(G):C:N4	26:DA:363(C):G:H1	2.11	0.42
26:DA:329:G:H8	26:DA:329:G:OP1	2.02	0.42
26:DA:362:U:OP1	26:DA:362:U:H3'	2.20	0.42
26:DA:1674:G:N2	26:DA:1677:A:N1	2.53	0.42
26:DA:1913:A:H4'	26:DA:1914:C:O5'	2.19	0.42
26:DA:2151:G:C4	26:DA:2152:G:C8	3.07	0.42
26:DA:2630:G:H2'	26:DA:2631:G:H8	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2758:A:C4	32:DH:67:LEU:HD21	2.55	0.42
33:DI:62:LYS:HE2	33:DI:133:HIS:NE2	2.34	0.42
37:DQ:29:PHE:HB2	37:DQ:105:GLU:OE2	2.19	0.42
40:DT:11:GLU:OE1	40:DT:57:PHE:HB3	2.19	0.42
1:AA:194:C:O3'	20:AT:68:LYS:HD2	2.19	0.42
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	2.01	0.42
1:AA:399:G:H2'	1:AA:400:C:C6	2.54	0.42
1:AA:1053:G:H4'	1:AA:1054:C:H5'	2.01	0.42
1:AA:1366:C:H2'	1:AA:1367:C:H6	1.85	0.42
6:AF:11:ASN:HB3	6:AF:14:LEU:HG	2.00	0.42
7:AG:29:LYS:HD3	7:AG:29:LYS:HA	1.94	0.42
8:AH:4:ASP:CG	8:AH:85:ARG:HH11	2.28	0.42
8:AH:11:THR:HG23	8:AH:14:ARG:NH1	2.34	0.42
9:AI:26:VAL:HG22	9:AI:61:ALA:HB3	2.01	0.42
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	2.01	0.42
13:AM:3:ARG:O	13:AM:57:ARG:NH2	2.48	0.42
26:BA:478:A:C6	26:BA:480:A:C6	3.07	0.42
26:BA:910:A:H62	37:BQ:12:GLN:HA	1.85	0.42
26:BA:1208:C:C4	26:BA:1209:G:N7	2.88	0.42
26:BA:1285:G:N2	26:BA:1328:G:H5"	2.35	0.42
26:BA:2096:U:O4	26:BA:2193:G:O6	2.36	0.42
26:BA:2236:C:H2'	26:BA:2237:G:O4'	2.20	0.42
26:BA:2544:G:H1'	26:BA:2646:C:H4'	2.01	0.42
43:BW:24:ILE:HA	43:BW:27:LYS:HG3	2.01	0.42
46:BZ:68:PRO:O	46:BZ:91:LEU:HB2	2.19	0.42
51:B4:40:HIS:O	51:B4:43:TYR:N	2.53	0.42
1:CA:33:A:N3	12:CL:32:PHE:HE2	2.17	0.42
1:CA:76:C:N4	1:CA:96:U:C2	2.88	0.42
1:CA:374:A:C6	1:CA:375:U:C4	3.07	0.42
1:CA:582:U:C2	1:CA:760:G:C6	3.07	0.42
1:CA:918:A:H2'	1:CA:919:A:C8	2.53	0.42
1:CA:1055:A:C8	1:CA:1206:G:C2	3.07	0.42
1:CA:1075:C:C2'	1:CA:1076:C:H5'	2.50	0.42
1:CA:1272:G:H2'	1:CA:1273:G:H5'	2.01	0.42
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.27	0.42
1:CA:1342:C:O2'	9:CI:124:GLN:HG3	2.19	0.42
1:CA:1400:C:C6	22:CV:18:G:C2	3.08	0.42
4:CD:125:HIS:O	4:CD:149:ALA:N	2.42	0.42
13:CM:44:ARG:HB2	13:CM:47:ASP:OD1	2.19	0.42
20:CT:56:MET:HE1	20:CT:85:MET:HG2	2.02	0.42
26:DA:925:C:H2'	26:DA:926:A:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1009:A:O5'	26:DA:1009:A:H8	2.02	0.42
26:DA:1026:U:H4'	26:DA:1027:A:OP1	2.19	0.42
26:DA:1034:G:H8	26:DA:1034:G:OP1	2.02	0.42
26:DA:1836:C:H2'	26:DA:1837:C:H6	1.84	0.42
26:DA:2176:A:H2'	26:DA:2177:C:C6	2.55	0.42
26:DA:2243:U:H2'	26:DA:2244:U:C6	2.54	0.42
26:DA:2400:G:H2'	26:DA:2401:U:H6	1.83	0.42
26:DA:2662:A:H2'	26:DA:2663:G:O4'	2.19	0.42
27:DB:4:C:H42	27:DB:117:G:H1	1.67	0.42
27:DB:30:C:OP2	39:DS:32:LEU:HD11	2.20	0.42
29:DE:170:LEU:HB3	29:DE:184:VAL:CG2	2.50	0.42
31:DG:27:ASN:HB3	31:DG:30:GLU:HB2	2.02	0.42
32:DH:126:PRO:HG2	32:DH:130:ARG:HD2	2.00	0.42
34:DN:36:GLY:HA3	34:DN:49:GLY:HA2	2.02	0.42
35:DO:47:ILE:HB	35:DO:48:PRO:HD2	2.02	0.42
36:DP:1:MET:HE2	36:DP:5:ASP:HB3	2.02	0.42
51:D4:16:CYS:SG	51:D4:17:GLY:N	2.93	0.42
1:AA:112:G:OP2	16:AP:27:LYS:HD2	2.18	0.42
1:AA:486:U:H2'	1:AA:487:A:H8	1.84	0.42
1:AA:736:C:H2'	1:AA:737:A:C8	2.55	0.42
1:AA:899:C:O5'	1:AA:899:C:H6	2.02	0.42
3:AC:35:GLU:CD	3:AC:59:ARG:HH22	2.26	0.42
3:AC:131:ARG:HH12	5:AE:50:GLU:HG3	1.84	0.42
16:AP:28:ARG:NH1	16:AP:29:ASP:OD2	2.45	0.42
17:AQ:64:PRO:HB3	17:AQ:70:ARG:NH1	2.34	0.42
26:BA:151:C:H2'	26:BA:152:G:H8	1.85	0.42
26:BA:272:G:O2'	26:BA:421:U:OP2	2.27	0.42
26:BA:954:G:H5"	37:BQ:13:GLN:HB3	2.01	0.42
26:BA:1424:G:H2'	26:BA:1425:G:O4'	2.19	0.42
26:BA:1525:G:H2'	26:BA:1526:G:O4'	2.20	0.42
26:BA:1902:C:H5'	28:BD:246:PRO:HD3	2.01	0.42
26:BA:2139:C:H5'	26:BA:2140:C:OP2	2.19	0.42
26:BA:2259:G:C2	26:BA:2282:G:N1	2.88	0.42
26:BA:2537:U:H2'	26:BA:2538:C:C6	2.54	0.42
26:BA:2567:G:H2'	26:BA:2568:C:C6	2.55	0.42
26:BA:2784:C:O2'	29:BE:42:ASP:OD1	2.21	0.42
26:BA:2818:G:OP1	26:BA:2837:G:O2'	2.35	0.42
29:BE:49:LEU:HA	29:BE:49:LEU:HD12	1.77	0.42
30:BF:167:ALA:O	30:BF:170:LEU:HB2	2.20	0.42
31:BG:128:ARG:HE	31:BG:128:ARG:HB2	1.38	0.42
31:BG:179:PRO:HG3	51:B4:43:TYR:OH	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BP:52:GLU:HB3	36:BP:55:ARG:NH1	2.35	0.42
39:BS:3:ARG:HE	39:BS:4:LEU:N	2.18	0.42
40:BT:94:ALA:HB1	40:BT:99:LEU:HD21	2.01	0.42
46:BZ:150:LEU:HG	46:BZ:151:HIS:H	1.84	0.42
53:B6:6:ARG:HH12	53:B6:26:ASN:HB2	1.83	0.42
1:CA:514:C:N4	1:CA:515:G:O6	2.52	0.42
1:CA:1087:G:C4	1:CA:1099:G:N2	2.87	0.42
1:CA:1095:U:H2'	1:CA:1096:C:O4'	2.20	0.42
1:CA:1132:C:H42	1:CA:1142:G:H1	1.67	0.42
1:CA:1227:A:H3'	1:CA:1227:A:C8	2.54	0.42
1:CA:1250:A:O3'	9:CI:67:GLY:HA2	2.20	0.42
1:CA:1442(A):G:O2'	40:DT:118:ARG:HG2	2.20	0.42
18:CR:74:ARG:HB3	18:CR:81:PHE:CZ	2.55	0.42
26:DA:253:C:H2'	26:DA:254:G:O4'	2.20	0.42
26:DA:271(F):C:H2'	26:DA:271(G):C:O4'	2.20	0.42
26:DA:448:U:O4	26:DA:583:G:H1'	2.20	0.42
26:DA:634:C:H2'	26:DA:635:C:C6	2.54	0.42
26:DA:801:G:OP2	30:DF:55:GLY:HA2	2.20	0.42
26:DA:866:A:H2'	26:DA:866:A:N3	2.35	0.42
26:DA:928:G:H8	26:DA:928:G:O5'	2.02	0.42
26:DA:2099:U:H3	26:DA:2190:G:H1	1.66	0.42
26:DA:2106:G:H2'	26:DA:2107:C:O4'	2.20	0.42
26:DA:2164:C:H5"	26:DA:2165:G:C8	2.54	0.42
26:DA:2220:G:H2'	26:DA:2221:G:C8	2.55	0.42
26:DA:2611:U:C4	52:D5:3:LYS:HG2	2.54	0.42
26:DA:2722:G:H2'	26:DA:2723:C:C6	2.54	0.42
26:DA:2787:C:H2'	26:DA:2788:C:C6	2.55	0.42
26:DA:2848:G:H1'	26:DA:2867:G:N2	2.33	0.42
33:DI:80:PRO:HA	33:DI:145:VAL:O	2.20	0.42
39:DS:80:LEU:HD12	39:DS:80:LEU:HA	1.82	0.42
41:DU:69:CYS:HB3	41:DU:74:LEU:HD13	2.01	0.42
46:DZ:53:ILE:H	46:DZ:53:ILE:HG13	1.70	0.42
51:D4:62:ARG:HB2	51:D4:63:TYR:CD1	2.54	0.42
51:D4:64:GLY:C	51:D4:66:SER:N	2.76	0.42
53:D6:23:THR:OG1	53:D6:24:GLU:N	2.53	0.42
54:D7:8:ASN:HB3	54:D7:11:LYS:HB3	2.01	0.42
1:AA:495:A:H4'	1:AA:496:A:OP1	2.18	0.42
1:AA:681:C:C2	1:AA:710:G:C2	3.07	0.42
1:AA:758:G:H5'	1:AA:880:C:H1'	2.01	0.42
1:AA:840:C:H4'	1:AA:841:U:OP1	2.20	0.42
1:AA:1203:C:C2'	1:AA:1204:A:H5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1239:A:C4	1:AA:1298:C:N4	2.87	0.42
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.20	0.42
2:AB:12:GLU:HG3	2:AB:13:ALA:N	2.35	0.42
3:AC:22:TRP:CD1	3:AC:59:ARG:HD2	2.55	0.42
4:AD:15:GLU:CG	4:AD:63:LYS:HB3	2.49	0.42
26:BA:141:A:H8	26:BA:1408:C:HO2'	1.60	0.42
26:BA:297:C:OP1	45:BY:87:LYS:NZ	2.42	0.42
26:BA:336:C:O2'	45:BY:35:TYR:OH	2.30	0.42
26:BA:1022:G:C5	26:BA:1140:C:C4	3.07	0.42
26:BA:1107:G:O2'	26:BA:1108:U:H5'	2.20	0.42
26:BA:1316:U:H2'	26:BA:1317:A:C8	2.55	0.42
26:BA:1540:U:H2'	26:BA:1541:G:O4'	2.20	0.42
26:BA:2124:G:N2	26:BA:2174:C:N3	2.58	0.42
26:BA:2141:G:C6	26:BA:2142:C:C2	3.07	0.42
26:BA:2471:C:H2'	26:BA:2472:G:O4'	2.20	0.42
27:BB:30:C:H2'	27:BB:31:C:C5'	2.49	0.42
29:BE:9:VAL:HG22	29:BE:25:VAL:HB	2.01	0.42
30:BF:64:ILE:HD12	30:BF:65:TRP:CZ3	2.55	0.42
31:BG:56:ALA:HA	31:BG:153:ARG:HH21	1.85	0.42
42:BV:89:GLN:HA	42:BV:90:PRO:HD3	1.97	0.42
43:BW:13:SER:HA	43:BW:14:PRO:HD3	1.84	0.42
44:BX:24:GLY:O	44:BX:83:VAL:HG22	2.20	0.42
1:CA:124:G:P	1:CA:310:G:H21	2.42	0.42
1:CA:288:A:H2'	1:CA:289:G:H4'	2.01	0.42
1:CA:486:U:H2'	1:CA:487:A:C8	2.55	0.42
1:CA:593:G:C6	1:CA:647:C:N3	2.88	0.42
1:CA:656:C:H2'	1:CA:657:G:O4'	2.20	0.42
1:CA:737:A:H2'	1:CA:738:C:C6	2.54	0.42
1:CA:1128:C:C2	1:CA:1147:C:N4	2.87	0.42
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.55	0.42
1:CA:1252:A:H61	1:CA:1285:A:H61	1.65	0.42
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.40	0.42
1:CA:1525:G:H2'	1:CA:1526:G:O4'	2.20	0.42
4:CD:88:VAL:O	4:CD:92:VAL:HG23	2.20	0.42
4:CD:102:ASP:OD1	4:CD:103:ASN:N	2.53	0.42
7:CG:22:LEU:HG	7:CG:62:PHE:CZ	2.55	0.42
8:CH:31:PHE:O	8:CH:35:ILE:HG13	2.20	0.42
9:CI:8:GLY:HA2	9:CI:79:LEU:HB3	2.01	0.42
26:DA:321:G:C5	26:DA:341:G:H4'	2.54	0.42
26:DA:859:G:N2	26:DA:917:A:OP2	2.53	0.42
26:DA:1156:A:H8	26:DA:1156:A:OP1	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1166:C:H2'	26:DA:1167:U:H6	1.84	0.42
26:DA:1227:G:OP1	41:DU:13:LYS:HG2	2.20	0.42
26:DA:1598:C:O3'	44:DX:35:THR:OG1	2.37	0.42
26:DA:1637:A:H4'	26:DA:2711:A:O2'	2.20	0.42
26:DA:2078:C:C4	26:DA:2079:U:C4	3.07	0.42
26:DA:2135:A:H61	26:DA:2157:G:N2	2.18	0.42
26:DA:2153:G:H3'	26:DA:2154:G:H8	1.84	0.42
26:DA:2162:G:O3'	26:DA:2172:U:H6	2.03	0.42
26:DA:2359:C:H2'	26:DA:2360:A:O4'	2.19	0.42
26:DA:2467:C:C4	26:DA:2468:G:C6	3.07	0.42
26:DA:2498:C:O2'	26:DA:2499:C:H5'	2.20	0.42
26:DA:2584:U:O2'	61:DA:3701:HOH:O	2.17	0.42
26:DA:2721:A:H2'	26:DA:2722:G:O4'	2.19	0.42
27:DB:33:G:C5	27:DB:34:U:C4	3.07	0.42
29:DE:170:LEU:HB3	29:DE:184:VAL:HG22	2.01	0.42
31:DG:33:ARG:NH1	31:DG:33:ARG:HB2	2.34	0.42
32:DH:71:LEU:O	32:DH:75:ALA:N	2.53	0.42
40:DT:73:GLU:OE1	40:DT:103:ARG:NE	2.53	0.42
1:AA:262:A:C6	1:AA:263:A:C6	3.08	0.42
1:AA:375:U:O2'	16:AP:6:LEU:O	2.36	0.42
1:AA:979:C:O2	14:AN:19:ARG:HG2	2.20	0.42
1:AA:1358:U:H2'	1:AA:1359:C:O4'	2.20	0.42
3:AC:35:GLU:O	3:AC:39:ILE:HG13	2.20	0.42
20:AT:56:MET:HE2	20:AT:85:MET:HA	2.02	0.42
24:AX:53:G:H3'	24:AX:54:5MU:H73	2.02	0.42
26:BA:1311:G:N7	54:B7:9:ARG:NH2	2.67	0.42
26:BA:1566:A:OP1	28:BD:211:ARG:NH1	2.53	0.42
26:BA:1800:C:H3'	28:BD:147:LEU:HD23	2.02	0.42
26:BA:1889:A:N1	26:BA:2234:G:H1'	2.34	0.42
26:BA:2141:G:N7	26:BA:2151:G:C2	2.88	0.42
26:BA:2492:U:H2'	26:BA:2493:U:H6	1.85	0.42
27:BB:55:U:H2'	27:BB:56:G:O4'	2.20	0.42
29:BE:144:ARG:HB3	29:BE:145:LYS:H	1.52	0.42
31:BG:138:GLN:HB3	31:BG:153:ARG:O	2.19	0.42
33:BI:72:LEU:C	33:BI:74:ASN:N	2.76	0.42
37:BQ:21:THR:HG21	37:BQ:101:ARG:HB2	2.02	0.42
54:B7:24:THR:HA	54:B7:25:PRO:HD3	1.96	0.42
1:CA:362:G:N1	1:CA:365:U:OP2	2.50	0.42
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.35	0.42
1:CA:1004:A:H62	1:CA:1037:C:H2'	1.85	0.42
5:CE:90:VAL:O	5:CE:120:THR:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CJ:65:LEU:HB2	14:CN:56:VAL:HG22	2.01	0.42
26:DA:846:C:H4'	26:DA:847:U:O4'	2.19	0.42
26:DA:864:G:OP2	37:DQ:22:LYS:HE2	2.20	0.42
26:DA:918:A:C5	26:DA:919:G:H1'	2.55	0.42
26:DA:1248:G:C2	41:DU:3:ARG:HD2	2.55	0.42
26:DA:1313:U:H2'	26:DA:1610:A:C2	2.55	0.42
26:DA:1351:C:C2	26:DA:1381:G:C2	3.08	0.42
26:DA:1496:A:H2'	26:DA:1498:C:C5	2.55	0.42
26:DA:1636:C:H2'	26:DA:1637:A:H8	1.85	0.42
26:DA:2120:G:C2	26:DA:2121:G:C8	3.07	0.42
26:DA:2187:G:C5	26:DA:2188:C:C4	3.08	0.42
26:DA:2784:C:O2'	29:DE:42:ASP:OD1	2.27	0.42
26:DA:2870:C:H2'	26:DA:2871:C:O4'	2.20	0.42
27:DB:71:C:H1'	27:DB:107:G:N2	2.34	0.42
28:DD:158:ALA:O	28:DD:161:THR:OG1	2.30	0.42
29:DE:174:ASP:OD1	29:DE:175:VAL:N	2.53	0.42
39:DS:11:LYS:O	39:DS:15:ARG:HG3	2.20	0.42
44:DX:54:VAL:HG22	44:DX:81:VAL:HG12	2.01	0.42
46:DZ:10:ARG:HG3	46:DZ:36:LYS:HB3	2.01	0.42
1:AA:430:A:OP2	4:AD:8:VAL:HG12	2.19	0.42
1:AA:692:U:H2'	1:AA:694:A:OP2	2.20	0.42
1:AA:841:U:P	1:AA:841:U:O4'	2.78	0.42
1:AA:1517:G:H1'	26:BA:1919:A:O3'	2.18	0.42
4:AD:120:LEU:HD23	4:AD:120:LEU:HA	1.77	0.42
13:AM:3:ARG:HH22	13:AM:11:ARG:HE	1.68	0.42
14:AN:48:ALA:HB2	14:AN:53:LEU:HD12	2.02	0.42
26:BA:330:A:O2'	26:BA:331:A:H8	2.02	0.42
26:BA:479:A:N3	26:BA:481:G:H5"	2.34	0.42
26:BA:1655:A:H4'	29:BE:115:GLY:N	2.35	0.42
26:BA:1983:C:H4'	26:BA:2606:C:H4'	2.01	0.42
27:BB:4:C:H2'	27:BB:5:C:O4'	2.19	0.42
27:BB:103:G:O2'	46:BZ:73:GLN:NE2	2.53	0.42
28:BD:264:LYS:HA	28:BD:265:PRO:HD3	1.91	0.42
30:BF:178:PRO:HB2	30:BF:201:VAL:HG21	2.02	0.42
33:BI:10:GLU:H	33:BI:10:GLU:HG3	1.35	0.42
33:BI:83:ALA:HB2	33:BI:88:ILE:HA	2.01	0.42
39:BS:83:LYS:HB2	39:BS:83:LYS:HE2	1.92	0.42
50:B3:8:LEU:O	50:B3:32:GLN:N	2.40	0.42
1:CA:193:C:H2'	1:CA:194:C:C6	2.55	0.42
1:CA:382:A:H2'	1:CA:383:A:H8	1.82	0.42
1:CA:608:A:H2'	1:CA:609:A:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:885:G:O2'	1:CA:886:G:H5'	2.20	0.42
1:CA:1026:G:H3'	1:CA:1026:G:N3	2.35	0.42
1:CA:1060:C:C5	3:CC:2:GLY:HA2	2.55	0.42
1:CA:1134:G:N3	1:CA:1134:G:H2'	2.35	0.42
4:CD:134:ASP:O	4:CD:136:PRO:HD3	2.20	0.42
5:CE:57:LYS:HG2	5:CE:61:TYR:HE2	1.85	0.42
6:CF:14:LEU:HD22	6:CF:18:GLN:HB3	2.02	0.42
7:CG:50:ILE:HD11	7:CG:58:PRO:HB3	2.01	0.42
7:CG:111:ARG:HB2	7:CG:119:ARG:HD2	2.01	0.42
10:CJ:40:LEU:HD12	10:CJ:69:ASN:HB3	2.02	0.42
23:CW:76:PPU:H8	23:CW:76:PPU:C5'	2.36	0.42
23:CW:76:PPU:HD2	26:DA:2451:A:C4	2.54	0.42
24:CX:72:A:H5"	24:CX:73:A:OP2	2.20	0.42
26:DA:39:C:H2'	26:DA:40:C:H6	1.85	0.42
26:DA:357:A:H2'	26:DA:358:U:C6	2.55	0.42
26:DA:407:G:H2'	26:DA:408:G:C8	2.55	0.42
26:DA:522:G:C6	26:DA:523:C:C4	3.08	0.42
26:DA:528:A:O2'	26:DA:529:A:H5'	2.19	0.42
26:DA:1363:C:H2'	26:DA:1364:G:H8	1.85	0.42
26:DA:1475:G:C2	26:DA:1517:G:C2	3.08	0.42
26:DA:1894:C:H2'	26:DA:1895:C:H6	1.85	0.42
26:DA:1973:G:H2'	26:DA:1974:C:C6	2.55	0.42
26:DA:2001:A:H2'	26:DA:2002:G:H8	1.80	0.42
26:DA:2105:C:H2'	26:DA:2106:G:C8	2.54	0.42
26:DA:2129:C:H2'	26:DA:2130:U:C6	2.55	0.42
26:DA:2376:A:H2'	26:DA:2377:A:O4'	2.20	0.42
26:DA:2784:C:H1'	29:DE:37:ARG:HH12	1.84	0.42
27:DB:24:G:H5'	27:DB:25:A:N6	2.32	0.42
28:DD:12:SER:HB3	28:DD:208:LYS:HB3	2.02	0.42
29:DE:11:MET:HG2	29:DE:24:THR:HB	2.01	0.42
31:DG:31:VAL:HA	31:DG:32:PRO:HD2	1.68	0.42
33:DI:52:ARG:HH11	33:DI:52:ARG:CG	2.33	0.42
35:DO:24:VAL:HG12	35:DO:39:ILE:HG22	2.02	0.42
50:D3:4:LEU:O	50:D3:36:VAL:HA	2.20	0.42
1:AA:283:C:C2'	1:AA:284:G:H5'	2.51	0.41
1:AA:831:U:C2'	1:AA:832:C:H5'	2.50	0.41
1:AA:1001:A:N1	1:AA:1040:U:O4	2.53	0.41
3:AC:77:ILE:HG13	3:AC:78:GLY:N	2.35	0.41
16:AP:14:ASN:N	16:AP:15:PRO:HD3	2.35	0.41
20:AT:53:LEU:HD13	20:AT:100:ILE:O	2.20	0.41
20:AT:55:ILE:HD13	20:AT:55:ILE:HA	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:272(J):C:H2'	26:BA:274:G:C8	2.55	0.41
26:BA:322:A:H3'	30:BF:169:ASN:ND2	2.35	0.41
26:BA:596:G:H2'	26:BA:597:U:O4'	2.20	0.41
26:BA:662:G:H5"	36:BP:16:ARG:HG2	2.02	0.41
26:BA:1445:A:H1'	26:BA:1460:A:C2	2.55	0.41
26:BA:1448:G:H5"	26:BA:1542:A:OP2	2.20	0.41
26:BA:1608:A:H1'	26:BA:1610:A:OP2	2.20	0.41
26:BA:1748:G:H2'	26:BA:1749:A:O4'	2.20	0.41
26:BA:2142:C:N3	26:BA:2149:G:C6	2.88	0.41
26:BA:2144:U:O2'	26:BA:2145:C:H2'	2.20	0.41
26:BA:2153:G:C2	26:BA:2154:G:C8	3.07	0.41
26:BA:2506:U:C2	26:BA:2585:U:O4	2.73	0.41
26:BA:2812:G:H2'	26:BA:2813:A:O4'	2.20	0.41
29:BE:182:LEU:HD21	29:BE:198:VAL:HG11	2.02	0.41
30:BF:196:LEU:HD23	30:BF:196:LEU:HA	1.81	0.41
34:BN:48:MET:H	34:BN:48:MET:HG3	1.77	0.41
41:BU:69:CYS:HB3	41:BU:74:LEU:HD13	2.02	0.41
44:BX:31:HIS:CD2	44:BX:33:LYS:HB2	2.55	0.41
44:BX:88:LYS:HE3	44:BX:88:LYS:HB2	1.84	0.41
1:CA:427:U:H3'	1:CA:428:G:H2'	2.01	0.41
1:CA:683:G:C6	1:CA:684:A:C6	3.08	0.41
1:CA:712:A:N6	1:CA:713:G:C6	2.88	0.41
1:CA:894:G:C6	1:CA:895:G:C5	3.08	0.41
1:CA:926:G:H5"	1:CA:927:G:O5'	2.20	0.41
1:CA:999:C:C2	1:CA:1042:G:N2	2.81	0.41
1:CA:1002:G:C4	1:CA:1003:G:C8	3.08	0.41
1:CA:1126:U:C2	1:CA:1281:U:O4	2.73	0.41
1:CA:1127:G:N2	1:CA:1147:C:H41	2.18	0.41
1:CA:1134:G:H2'	1:CA:1135:U:H5'	2.02	0.41
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.84	0.41
3:CC:125:GLU:HG3	3:CC:190:ARG:HG2	2.02	0.41
8:CH:30:ARG:O	8:CH:34:GLU:HG2	2.19	0.41
12:CL:103:GLY:N	12:CL:107:ALA:O	2.48	0.41
26:DA:64:A:O3'	44:DX:71:GLY:HA3	2.20	0.41
26:DA:106:C:H2'	26:DA:107:C:H6	1.84	0.41
26:DA:780:G:H8	26:DA:780:G:O5'	2.02	0.41
26:DA:870:A:OP1	37:DQ:6:ARG:NE	2.49	0.41
26:DA:1364:G:P	48:D1:3:LYS:HG3	2.59	0.41
26:DA:1721:G:H8	26:DA:1741:A:H62	1.67	0.41
26:DA:2120:G:N2	26:DA:2179:C:C2	2.88	0.41
26:DA:2153:G:C2	26:DA:2154:G:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DD:276:LYS:H	28:DD:276:LYS:CD	2.32	0.41
36:DP:96:THR:HA	36:DP:126:VAL:HB	2.01	0.41
36:DP:101:VAL:HG23	36:DP:106:LEU:HD13	2.02	0.41
39:DS:37:ALA:N	39:DS:51:ALA:O	2.52	0.41
40:DT:108:ARG:HA	40:DT:111:ARG:NH1	2.35	0.41
43:DW:66:GLU:HA	43:DW:69:LEU:HD12	2.02	0.41
1:AA:58:C:H6	1:AA:58:C:O5'	2.02	0.41
1:AA:228:A:H2'	1:AA:229:U:O4'	2.20	0.41
1:AA:411:A:O2'	1:AA:413:G:H5'	2.20	0.41
1:AA:626:U:H2'	1:AA:627:G:O4'	2.20	0.41
1:AA:875:C:H1'	8:AH:15:ASN:OD1	2.20	0.41
1:AA:1007:C:N3	1:AA:1022:G:O6	2.52	0.41
1:AA:1071:C:H42	1:AA:1104:G:H1	1.68	0.41
1:AA:1304:G:C6	1:AA:1305:G:N1	2.88	0.41
2:AB:71:VAL:HG12	2:AB:170:GLU:HG3	2.02	0.41
5:AE:33:VAL:HG21	5:AE:109:ILE:HG12	2.02	0.41
11:AK:120:ARG:HA	11:AK:121:PRO:HD3	1.86	0.41
13:AM:70:LEU:O	13:AM:74:VAL:HG23	2.20	0.41
15:AO:62:GLN:HA	15:AO:65:ARG:NH1	2.34	0.41
26:BA:109:G:H2'	26:BA:110:G:O4'	2.20	0.41
26:BA:171:G:C2'	26:BA:172:C:H5'	2.50	0.41
26:BA:288:C:H2'	26:BA:289:A:C8	2.56	0.41
26:BA:795:C:H2'	26:BA:796:C:H6	1.85	0.41
26:BA:817:C:H4'	26:BA:932:G:C5	2.55	0.41
26:BA:1021:A:C8	26:BA:1021:A:C3'	3.00	0.41
26:BA:1111:A:H4'	26:BA:1112:G:OP1	2.21	0.41
26:BA:2014:A:H2'	26:BA:2015:A:C8	2.55	0.41
26:BA:2364:C:O2	47:B0:36:ILE:HD11	2.20	0.41
26:BA:2390:U:P	55:B8:35:GLN:HE22	2.44	0.41
26:BA:2391:G:O6	26:BA:2425:A:H8	2.03	0.41
37:BQ:57:HIS:CD2	37:BQ:117:ALA:HB2	2.55	0.41
39:BS:59:LYS:CE	39:BS:60:GLY:H	2.34	0.41
41:BU:104:GLN:CD	41:BU:104:GLN:H	2.29	0.41
55:B8:60:LEU:HD23	55:B8:60:LEU:HA	1.91	0.41
1:CA:8:A:N7	4:CD:209:ARG:HA	2.35	0.41
1:CA:185:A:H8	1:CA:185:A:O5'	2.03	0.41
1:CA:265:G:N2	1:CA:267:C:H5'	2.35	0.41
1:CA:321:A:N7	1:CA:328:C:O2'	2.31	0.41
1:CA:348:G:O2'	1:CA:349:A:H5'	2.19	0.41
1:CA:507:C:OP2	1:CA:508:C:O2'	2.35	0.41
1:CA:690:G:C6	1:CA:691:G:C6	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:746:A:H4'	1:CA:837:G:O2'	2.20	0.41
1:CA:909:A:H2'	1:CA:910:C:O4'	2.20	0.41
1:CA:967:C:H2'	1:CA:968:A:N7	2.34	0.41
1:CA:1014:A:P	1:CA:1014:A:H8	2.43	0.41
1:CA:1118:C:H2'	1:CA:1119:C:H6	1.85	0.41
1:CA:1245:A:N1	1:CA:1292:U:O2	2.53	0.41
1:CA:1330:U:H4'	13:CM:23:TYR:CZ	2.55	0.41
1:CA:1493:A:H2'	26:DA:1913:A:N6	2.34	0.41
3:CC:131:ARG:O	3:CC:135:LYS:HB2	2.21	0.41
3:CC:159:GLY:HA2	3:CC:193:TYR:CE1	2.56	0.41
17:CQ:95:TYR:O	17:CQ:98:LEU:HB2	2.20	0.41
20:CT:30:LYS:O	20:CT:34:LYS:HG3	2.20	0.41
26:DA:271(Q):G:C2	26:DA:271(R):G:C5	3.08	0.41
26:DA:729:G:H5'	26:DA:730:C:C5'	2.50	0.41
26:DA:1012:U:C5	34:DN:28:THR:HG21	2.55	0.41
26:DA:1015:G:O2'	26:DA:1016:G:H5'	2.19	0.41
26:DA:1354:A:H2'	26:DA:1355:G:O4'	2.19	0.41
26:DA:1372:U:O4	26:DA:1373:A:C5	2.74	0.41
26:DA:1422:G:C4	26:DA:1423:G:C8	3.08	0.41
26:DA:1489:U:O2'	26:DA:1490:A:H8	2.03	0.41
26:DA:1507:A:HO2'	26:DA:1508:A:P	2.43	0.41
26:DA:1832:C:N4	26:DA:1833:U:C4	2.88	0.41
26:DA:1897:G:C6	26:DA:1898:U:C4	3.08	0.41
26:DA:2269:A:OP1	61:DA:4046:HOH:O	2.22	0.41
34:DN:138:LEU:HD23	34:DN:138:LEU:HA	1.84	0.41
37:DQ:52:VAL:HA	37:DQ:55:VAL:HG12	2.03	0.41
45:DY:19:LYS:HB3	45:DY:19:LYS:HE2	1.70	0.41
50:D3:41:PRO:HA	50:D3:44:ARG:HB3	2.01	0.41
55:D8:63:PRO:HG2	55:D8:64:TYR:CE2	2.55	0.41
1:AA:19:C:O2'	1:AA:572:A:N1	2.50	0.41
1:AA:489:C:OP1	4:AD:132:ARG:NH2	2.53	0.41
1:AA:636:U:H5'	17:AQ:2:PRO:HG3	2.03	0.41
1:AA:981:U:O5'	1:AA:981:U:H6	2.03	0.41
1:AA:1172:C:C5	1:AA:1173:G:N7	2.88	0.41
1:AA:1409:C:H2'	1:AA:1410:G:H8	1.85	0.41
5:AE:84:PHE:CE2	5:AE:133:TYR:HD2	2.38	0.41
15:AO:3:ILE:H	15:AO:3:ILE:HD13	1.84	0.41
26:BA:307:G:N2	26:BA:309:G:H3'	2.35	0.41
26:BA:814:C:H4'	26:BA:1224:C:O2	2.20	0.41
26:BA:1930:G:N2	26:BA:1968:G:H2'	2.35	0.41
26:BA:2786:U:H2'	26:BA:2787:C:C6	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2789:C:O4'	26:BA:2892:A:H2	2.04	0.41
28:BD:142:VAL:HG13	28:BD:191:ALA:HB1	2.02	0.41
28:BD:215:LEU:HD13	28:BD:217:ARG:NH2	2.35	0.41
30:BF:31:HIS:NE2	30:BF:35:GLU:OE2	2.53	0.41
39:BS:87:PHE:HB2	39:BS:112:PHE:CE2	2.55	0.41
40:BT:35:LYS:HB2	40:BT:35:LYS:HE3	1.72	0.41
1:CA:44:G:H1	1:CA:398:C:N4	2.10	0.41
1:CA:304:U:H2'	1:CA:305:G:C8	2.56	0.41
1:CA:503:C:OP2	12:CL:116:SER:HB3	2.20	0.41
1:CA:515:G:C6	1:CA:516:U:C4	3.09	0.41
1:CA:829:G:O6	61:CA:4089:HOH:O	2.19	0.41
1:CA:939:G:P	7:CG:95:ARG:HH12	2.43	0.41
1:CA:1119:C:O2'	1:CA:1120:G:O4'	2.21	0.41
1:CA:1132:C:C4	1:CA:1133:G:N7	2.88	0.41
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.20	0.41
8:CH:58:TYR:O	8:CH:59:LEU:HD23	2.19	0.41
9:CI:23:ASN:HD22	9:CI:25:LYS:HG2	1.86	0.41
13:CM:65:LYS:CB	51:D4:50:VAL:HG11	2.47	0.41
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.55	0.41
26:DA:347:A:H2'	26:DA:348:G:H8	1.85	0.41
26:DA:565:C:H2'	26:DA:566:U:O4'	2.20	0.41
26:DA:1359:A:N1	26:DA:1360:A:C5	2.88	0.41
26:DA:1529:G:O2'	26:DA:1530:C:H5'	2.20	0.41
26:DA:1688:U:H3	26:DA:1700:A:C5'	2.33	0.41
26:DA:2145:C:H6	26:DA:2145:C:H2'	1.65	0.41
26:DA:2232:U:P	48:D1:40:ARG:HH12	2.43	0.41
26:DA:2506:U:C2	26:DA:2585:U:O4	2.73	0.41
26:DA:2588:G:H2'	26:DA:2589:A:O4'	2.19	0.41
27:DB:42:C:O2'	31:DG:66:GLN:HG2	2.19	0.41
29:DE:122:PHE:HZ	29:DE:155:LYS:HB2	1.84	0.41
29:DE:176:ILE:HB	29:DE:181:LEU:HB2	2.02	0.41
31:DG:97:ASP:O	31:DG:101:ILE:HG13	2.21	0.41
33:DI:87:LYS:CB	33:DI:122:GLU:HA	2.49	0.41
44:DX:59:VAL:HG21	44:DX:78:LYS:HE3	2.02	0.41
46:DZ:76:LEU:HD12	46:DZ:76:LEU:HA	1.85	0.41
1:AA:35:G:H2'	1:AA:36:C:C6	2.55	0.41
1:AA:110:C:H2'	1:AA:111:G:O4'	2.19	0.41
1:AA:328:C:H4'	1:AA:329:A:H5'	2.02	0.41
1:AA:830:G:H2'	1:AA:831:U:O4'	2.21	0.41
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.20	0.41
1:AA:1047:G:O2'	1:AA:1215:G:O2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1112:C:H6	1:AA:1112:C:O5'	2.03	0.41
1:AA:1125:U:H4'	10:AJ:5:ARG:NH2	2.31	0.41
4:AD:196:LEU:C	4:AD:198:VAL:N	2.79	0.41
5:AE:77:PRO:HG2	5:AE:142:LEU:HD22	2.03	0.41
8:AH:82:HIS:NE2	8:AH:84:ARG:HG2	2.35	0.41
9:AI:4:TYR:CE1	9:AI:88:TYR:HD1	2.38	0.41
15:AO:70:LEU:HD11	15:AO:77:ARG:HB2	2.03	0.41
19:AS:3:ARG:HH11	19:AS:10:PHE:HB2	1.86	0.41
26:BA:324:A:H2'	26:BA:325:G:O4'	2.20	0.41
26:BA:1045:A:OP1	26:BA:1045:A:H4'	2.20	0.41
26:BA:1297:C:O2'	26:BA:1302:A:N1	2.53	0.41
26:BA:2277:G:OP2	47:B0:12:ASN:HB2	2.20	0.41
28:BD:5:LYS:HB3	28:BD:5:LYS:HE3	1.55	0.41
28:BD:166:GLN:HB2	28:BD:174:ILE:HG22	2.02	0.41
29:BE:19:ARG:CZ	35:BO:72:PRO:HB3	2.50	0.41
29:BE:93:VAL:HG13	61:BE:3106:HOH:O	2.20	0.41
31:BG:16:ARG:HB2	31:BG:17:PRO:HD3	2.02	0.41
37:BQ:70:PRO:HA	37:BQ:94:VAL:O	2.20	0.41
53:B6:6:ARG:NE	53:B6:24:GLU:OE1	2.38	0.41
1:CA:114:U:H2'	1:CA:115:G:C8	2.55	0.41
1:CA:408:A:C2	1:CA:435:C:O2	2.74	0.41
1:CA:615:C:H2'	1:CA:616:G:H8	1.85	0.41
1:CA:789:U:H2'	1:CA:791:G:OP2	2.21	0.41
1:CA:942:G:H21	9:CI:124:GLN:NE2	2.19	0.41
1:CA:951:G:C6	1:CA:952:U:C4	3.09	0.41
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.56	0.41
1:CA:1153:C:N4	1:CA:1154:G:N2	2.68	0.41
1:CA:1157:A:H5'	1:CA:1158:C:N1	2.35	0.41
1:CA:1295:G:O3'	13:CM:14:ARG:NH1	2.53	0.41
1:CA:1367:C:OP1	9:CI:114:TYR:HA	2.20	0.41
1:CA:1494:G:H5'	26:DA:1913:A:C5	2.56	0.41
5:CE:59:GLY:O	5:CE:62:ALA:HB3	2.20	0.41
5:CE:76:ILE:HB	5:CE:77:PRO:HD2	2.03	0.41
13:CM:20:THR:HA	13:CM:25:ILE:HG22	2.01	0.41
18:CR:61:LYS:HA	18:CR:64:ARG:NH1	2.36	0.41
20:CT:54:LYS:N	20:CT:100:ILE:HD11	2.34	0.41
26:DA:45:C:H2'	26:DA:47:C:C6	2.56	0.41
26:DA:468:G:OP2	54:D7:37:LYS:NZ	2.47	0.41
26:DA:701:G:O2'	26:DA:1631(A):A:N1	2.53	0.41
26:DA:853:G:H2'	26:DA:854:G:C8	2.55	0.41
26:DA:874:G:H5'	26:DA:874:G:C8	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:910:A:C6	26:DA:911:A:C6	3.08	0.41
26:DA:1303:G:C6	26:DA:1304:C:C4	3.07	0.41
26:DA:1377:G:OP2	61:DA:4242:HOH:O	2.21	0.41
26:DA:1445(A):C:H2'	26:DA:1446:C:C6	2.54	0.41
26:DA:1614:A:P	26:DA:1614:A:H8	2.43	0.41
26:DA:1654:A:H1'	26:DA:2823:A:H5'	2.03	0.41
26:DA:1816:G:H3'	28:DD:62:TYR:CE1	2.56	0.41
26:DA:2101:G:C6	26:DA:2102:U:N3	2.89	0.41
26:DA:2168:G:H5'	26:DA:2169:A:OP2	2.19	0.41
26:DA:2292:C:H2'	26:DA:2293:C:C6	2.55	0.41
26:DA:2302:G:N3	26:DA:2315:G:N2	2.68	0.41
32:DH:3:ARG:HB3	32:DH:3:ARG:HH11	1.85	0.41
32:DH:45:VAL:HA	32:DH:50:VAL:HG22	2.01	0.41
36:DP:81:GLN:HB3	36:DP:106:LEU:HD23	2.02	0.41
46:DZ:156:LYS:HE3	46:DZ:156:LYS:HB3	1.55	0.41
53:D6:6:ARG:NH1	53:D6:26:ASN:HB2	2.35	0.41
1:AA:345:C:H4'	1:AA:346:G:N3	2.35	0.41
1:AA:688:G:H2'	1:AA:689:C:H6	1.86	0.41
1:AA:922:G:N3	1:AA:1398:A:H2	2.19	0.41
1:AA:967:C:H4'	9:AI:125:TYR:HE1	1.85	0.41
1:AA:1379:G:N7	7:AG:2:ALA:HB3	2.35	0.41
2:AB:41:ILE:HD13	2:AB:41:ILE:HA	1.95	0.41
2:AB:86:GLU:C	2:AB:89:GLY:H	2.29	0.41
6:AF:97:PHE:HB3	18:AR:32:ARG:HD3	2.03	0.41
9:AI:50:LEU:HD23	9:AI:81:ILE:CD1	2.50	0.41
14:AN:37:PHE:CE2	14:AN:53:LEU:HD13	2.55	0.41
26:BA:338:G:C2'	26:BA:339:U:H5'	2.51	0.41
26:BA:857:C:OP1	47:B0:77:ARG:NH2	2.52	0.41
26:BA:858:U:O2	26:BA:2268:A:H2'	2.21	0.41
26:BA:1017:G:N2	26:BA:1145:C:O2	2.38	0.41
26:BA:1614:A:P	26:BA:1614:A:H8	2.43	0.41
26:BA:1682:G:C4	26:BA:1757:U:C2	3.08	0.41
26:BA:2776:A:C6	26:BA:2778:A:C6	3.09	0.41
26:BA:2849:U:OP2	40:BT:95:ARG:NH1	2.53	0.41
27:BB:24:G:O2'	27:BB:56:G:N7	2.48	0.41
29:BE:119:ARG:CG	29:BE:160:TYR:HB2	2.51	0.41
30:BF:172:TRP:CD1	30:BF:172:TRP:H	2.39	0.41
31:BG:66:GLN:HE21	31:BG:66:GLN:HB3	1.59	0.41
39:BS:110:LEU:HD12	39:BS:110:LEU:HA	1.80	0.41
49:B2:32:LEU:HD13	49:B2:36:ARG:NH1	2.35	0.41
1:CA:203:U:H2'	1:CA:203:U:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:229:U:H5”	16:CP:33:ILE:HD12	2.01	0.41
1:CA:580:U:H2’	1:CA:581:G:O4’	2.20	0.41
1:CA:638:G:H2’	1:CA:639:G:O4’	2.20	0.41
1:CA:986:A:C6	1:CA:1220:G:C2	3.09	0.41
1:CA:1120:G:N1	1:CA:1154:G:C2	2.88	0.41
1:CA:1255:G:O3’	1:CA:1258:G:H1’	2.20	0.41
1:CA:1276:G:H2’	1:CA:1277:C:H6	1.85	0.41
1:CA:1327:C:H2’	1:CA:1328:C:C6	2.55	0.41
2:CB:122:PHE:HD1	2:CB:123:ALA:H	1.67	0.41
20:CT:56:MET:HG3	20:CT:57:ARG:N	2.36	0.41
26:DA:16:G:H2’	26:DA:17:G:H8	1.85	0.41
26:DA:271(H):G:O2’	26:DA:271(I):G:OP2	2.38	0.41
26:DA:363(C):G:H8	26:DA:363(C):G:O5’	2.03	0.41
26:DA:606:U:H4’	26:DA:658:C:H4’	2.01	0.41
26:DA:966:G:C6	26:DA:967:C:N4	2.89	0.41
26:DA:1114:G:H2’	26:DA:1115:G:O4’	2.20	0.41
26:DA:1248:G:C5	41:DU:3:ARG:HB2	2.55	0.41
26:DA:1580:A:OP2	26:DA:1580:A:H8	2.04	0.41
26:DA:2155:G:O6	26:DA:2156:G:C2	2.74	0.41
26:DA:2467:C:OP1	56:D9:8:LYS:NZ	2.41	0.41
26:DA:2492:U:H2’	26:DA:2493:U:H6	1.84	0.41
26:DA:2515:C:H2’	26:DA:2516:G:C8	2.54	0.41
27:DB:63:G:H2’	27:DB:64:C:H6	1.85	0.41
31:DG:165:THR:OG1	31:DG:168:GLU:HG3	2.21	0.41
32:DH:24:VAL:HG13	32:DH:37:VAL:HG21	2.01	0.41
34:DN:34:LEU:O	34:DN:49:GLY:HA3	2.21	0.41
35:DO:104:ARG:NH2	35:DO:121:VAL:O	2.53	0.41
36:DP:100:LEU:HD23	36:DP:100:LEU:HA	1.82	0.41
46:DZ:44:PHE:CZ	46:DZ:86:VAL:HG11	2.56	0.41
48:D1:75:GLU:HA	48:D1:78:LYS:HE3	2.02	0.41
51:D4:54:GLY:HA2	51:D4:55:ARG:HA	1.53	0.41
1:AA:782:A:H4’	1:AA:1514:C:O2’	2.21	0.41
1:AA:909:A:H2’	1:AA:910:C:O4’	2.20	0.41
1:AA:952:U:H2’	1:AA:953:G:H8	1.86	0.41
1:AA:1005:A:H1’	1:AA:1036:G:N2	2.36	0.41
1:AA:1027:C:H2’	1:AA:1028:C:C5	2.55	0.41
1:AA:1164:G:C5	1:AA:1173:G:C2	3.09	0.41
4:AD:28:SER:O	4:AD:31:CYS:HB3	2.21	0.41
7:AG:21:VAL:O	7:AG:24:THR:OG1	2.34	0.41
7:AG:88:PRO:HB3	7:AG:145:ALA:O	2.20	0.41
7:AG:109:ASN:HA	7:AG:119:ARG:HE	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AS:45:VAL:HA	19:AS:62:ILE:HG22	2.02	0.41
26:BA:1328:G:O2'	26:BA:1329:U:H2'	2.20	0.41
26:BA:2443:C:OP1	30:BF:68:LYS:HD3	2.20	0.41
31:BG:17:PRO:HA	31:BG:20:ILE:HD12	2.03	0.41
37:BQ:115:MET:SD	37:BQ:131:ILE:HG21	2.61	0.41
40:BT:24:PRO:HD3	40:BT:52:ILE:HD12	2.01	0.41
41:BU:61:TRP:CH2	41:BU:93:LYS:HB2	2.56	0.41
1:CA:861:G:HO2'	1:CA:874:G:HO2'	1.68	0.41
1:CA:866:C:C4	1:CA:867:G:H1'	2.55	0.41
1:CA:1162:C:C2	1:CA:1175:G:C2	3.09	0.41
1:CA:1368:G:C2'	1:CA:1369:C:H5'	2.50	0.41
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	2.03	0.41
9:CI:47:LEU:O	9:CI:50:LEU:HG	2.21	0.41
10:CJ:59:SER:O	10:CJ:60:ARG:HD3	2.21	0.41
11:CK:92:GLU:HB3	11:CK:96:ARG:NH1	2.35	0.41
12:CL:34:ARG:HG2	12:CL:35:GLY:N	2.35	0.41
26:DA:493:G:H2'	26:DA:494:G:O4'	2.20	0.41
26:DA:1152:C:H2'	26:DA:1153:C:H6	1.85	0.41
26:DA:1359:A:N6	26:DA:1360:A:C2	2.89	0.41
26:DA:1449:A:HO2'	26:DA:1529:G:N2	2.15	0.41
26:DA:1600:C:O2'	26:DA:1601:G:H5'	2.21	0.41
26:DA:2416:C:H2'	26:DA:2417:C:H6	1.86	0.41
26:DA:2542:A:H4'	26:DA:2543:G:C8	2.56	0.41
26:DA:2653:U:H5"	26:DA:2654:A:OP2	2.21	0.41
33:DI:93:THR:HG22	33:DI:116:LEU:HD22	2.02	0.41
44:DX:4:ALA:HB1	44:DX:42:ALA:HA	2.03	0.41
45:DY:65:ALA:HA	45:DY:66:PRO:HD3	1.93	0.41
1:AA:167:G:H2'	1:AA:168:G:C8	2.54	0.41
1:AA:203:U:H2'	1:AA:203:U:OP2	2.20	0.41
1:AA:890:G:N2	1:AA:906:G:H2'	2.36	0.41
2:AB:187:LEU:HD23	2:AB:201:ILE:HB	2.02	0.41
26:BA:22:C:H2'	26:BA:23:G:O4'	2.20	0.41
26:BA:64:A:O3'	44:BX:71:GLY:HA3	2.20	0.41
26:BA:419:C:H2'	26:BA:420:C:O4'	2.20	0.41
26:BA:1113:U:H2'	26:BA:1114:G:H8	1.85	0.41
26:BA:1448:G:H1'	26:BA:1528:A:N1	2.35	0.41
26:BA:1636:C:H2'	26:BA:1637:A:C8	2.55	0.41
26:BA:1796:U:H2'	26:BA:1797:C:H6	1.84	0.41
26:BA:1853:A:H2'	26:BA:1854:A:C8	2.56	0.41
26:BA:2011:U:H2'	26:BA:2012:G:O4'	2.20	0.41
26:BA:2634:G:C2	26:BA:2635:C:C2	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2774:C:H2'	26:BA:2775:A:O4'	2.21	0.41
26:BA:2845:G:H2'	26:BA:2846:G:H8	1.84	0.41
31:BG:122:PRO:HD3	31:BG:181:ARG:HG2	2.02	0.41
34:BN:62:VAL:CG1	34:BN:66:LYS:HB2	2.51	0.41
34:BN:108:PRO:O	34:BN:113:GLY:HA3	2.20	0.41
35:BO:98:VAL:HG13	35:BO:117:LEU:HB3	2.03	0.41
37:BQ:54:MET:HG3	37:BQ:121:ALA:HB2	2.01	0.41
44:BX:31:HIS:HA	44:BX:32:PRO:HD3	1.91	0.41
1:CA:583:A:O2'	17:CQ:91:ARG:NE	2.54	0.41
1:CA:950:U:OP2	13:CM:102:ARG:HD3	2.20	0.41
1:CA:1010:G:C4	1:CA:1011:G:C8	3.08	0.41
1:CA:1047:G:H8	1:CA:1047:G:O5'	2.04	0.41
1:CA:1067:A:H8	1:CA:1067:A:O5'	2.04	0.41
1:CA:1120:G:C6	1:CA:1154:G:C2	3.09	0.41
1:CA:1158:C:O3'	2:CB:133:LYS:NZ	2.54	0.41
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	2.03	0.41
3:CC:130:VAL:O	3:CC:134:ILE:HD13	2.21	0.41
3:CC:154:SER:O	3:CC:197:GLY:N	2.49	0.41
4:CD:13:ARG:NH1	4:CD:38:TYR:O	2.52	0.41
6:CF:34:GLY:O	6:CF:67:MET:HA	2.21	0.41
11:CK:81:ASP:OD1	11:CK:106:LYS:HE2	2.20	0.41
12:CL:56:ALA:HB3	12:CL:100:ILE:HD11	2.03	0.41
16:CP:33:ILE:HG12	16:CP:33:ILE:H	1.73	0.41
26:DA:118:A:H1'	26:DA:178:G:O4'	2.21	0.41
26:DA:247:G:H4'	26:DA:386:G:C5	2.56	0.41
26:DA:270:A:C2	26:DA:366:C:H4'	2.56	0.41
26:DA:649:G:H2'	26:DA:650:C:O4'	2.20	0.41
26:DA:993:G:C6	26:DA:994:C:C4	3.08	0.41
26:DA:1190:G:H5"	36:DP:32:THR:HA	2.02	0.41
26:DA:1408:C:H2'	26:DA:1409:C:C6	2.56	0.41
26:DA:1647:G:P	26:DA:1647:G:H3'	2.60	0.41
26:DA:1745(A):C:H5'	26:DA:1746:G:OP2	2.20	0.41
26:DA:1850:G:H2'	26:DA:1851:U:O4'	2.20	0.41
26:DA:2711:A:OP1	26:DA:2712:U:H3'	2.20	0.41
26:DA:2787:C:H2'	26:DA:2788:C:H6	1.86	0.41
27:DB:20:C:N4	27:DB:21:G:C6	2.88	0.41
29:DE:37:ARG:HB2	29:DE:46:ALA:H	1.85	0.41
30:DF:129:PHE:CD2	30:DF:163:VAL:HG21	2.56	0.41
30:DF:179:GLU:H	30:DF:179:GLU:CD	2.29	0.41
33:DI:40:THR:HG23	33:DI:43:ASN:ND2	2.32	0.41
35:DO:68:GLU:H	35:DO:68:GLU:CD	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DO:77:ILE:HA	40:DT:73:GLU:O	2.21	0.41
36:DP:138:LEU:HD23	36:DP:145:PRO:HG3	2.03	0.41
42:DV:8:GLY:O	42:DV:10:LYS:NZ	2.54	0.41
48:D1:52:ARG:NH1	48:D1:57:GLU:OE2	2.53	0.41
51:D4:57:GLU:HA	51:D4:58:ARG:HA	1.67	0.41
1:AA:189(B):C:H2'	1:AA:189(C):C:C6	2.56	0.41
1:AA:451:A:H61	1:AA:480:U:H2'	1.85	0.41
1:AA:942:G:C2	1:AA:1342:C:C2	3.09	0.41
1:AA:1173:G:C2	1:AA:1174:G:C4	3.08	0.41
1:AA:1250:A:C2	1:AA:1370:G:H1'	2.55	0.41
1:AA:1298:C:H4'	1:AA:1299:A:C4	2.55	0.41
4:AD:173:TRP:CD1	4:AD:173:TRP:H	2.38	0.41
7:AG:74:GLU:HG2	7:AG:91:VAL:HG22	2.03	0.41
8:AH:4:ASP:OD2	8:AH:85:ARG:NH1	2.54	0.41
16:AP:74:LEU:HG	16:AP:79:VAL:HG21	2.03	0.41
26:BA:123:G:O3'	26:BA:1376:C:H4'	2.20	0.41
26:BA:271(S):G:H2'	26:BA:271(T):C:O4'	2.21	0.41
26:BA:324:A:N6	26:BA:338:G:O2'	2.49	0.41
26:BA:471:A:H2'	26:BA:472:A:O4'	2.20	0.41
26:BA:973:A:C8	26:BA:1188:U:C2	3.08	0.41
26:BA:1230:C:H2'	26:BA:1231:G:C8	2.55	0.41
26:BA:1359:A:C2	26:BA:1372:U:C4	3.08	0.41
26:BA:1496:A:N3	26:BA:1577:C:O2'	2.46	0.41
26:BA:1805:U:O2	28:BD:50:THR:HB	2.21	0.41
26:BA:2162:G:H5'	26:BA:2172:U:H2'	2.02	0.41
30:BF:33:LEU:HD12	30:BF:33:LEU:HA	1.92	0.41
32:BH:3:ARG:NE	32:BH:3:ARG:HA	2.34	0.41
34:BN:23:LEU:HD12	34:BN:99:LEU:HD23	2.03	0.41
36:BP:58:THR:O	36:BP:62:LEU:HG	2.21	0.41
38:BR:74:LYS:HG2	38:BR:77:ARG:HH21	1.86	0.41
41:BU:86:ALA:O	42:BV:49:THR:HG23	2.21	0.41
44:BX:5:TYR:CE1	49:B2:30:ARG:HB2	2.55	0.41
45:BY:87:LYS:HB3	45:BY:95:LYS:HD3	2.03	0.41
51:B4:6:HIS:HA	51:B4:7:PRO:HD3	1.95	0.41
51:B4:28:LYS:HD3	51:B4:31:ILE:HD11	2.02	0.41
1:CA:527:G:O6	12:CL:49:ASN:ND2	2.53	0.41
1:CA:552:U:O2	12:CL:31:PRO:HB3	2.21	0.41
1:CA:1056:U:H4'	3:CC:163:ALA:HB2	2.02	0.41
1:CA:1068:G:N3	1:CA:1191:A:C2	2.89	0.41
1:CA:1262:C:C2'	1:CA:1263:C:H5'	2.51	0.41
1:CA:1352:C:N4	1:CA:1370:G:H1	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1410:G:H2'	1:CA:1411:C:C6	2.56	0.41
2:CB:158:LEU:HD12	2:CB:158:LEU:H	1.84	0.41
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.56	0.41
6:CF:76:ALA:O	6:CF:80:ARG:HG3	2.21	0.41
7:CG:18:TYR:CG	7:CG:59:LEU:HD13	2.56	0.41
9:CI:32:ASP:HB3	9:CI:35:GLU:HG3	2.02	0.41
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	2.03	0.41
26:DA:152:G:H2'	26:DA:153:C:C6	2.56	0.41
26:DA:328:U:H4'	45:DY:68:HIS:CG	2.56	0.41
26:DA:370:G:OP1	26:DA:403:U:N3	2.42	0.41
26:DA:503:A:C5	26:DA:506:G:C6	3.08	0.41
26:DA:974:G:C6	26:DA:1186:G:C6	3.09	0.41
26:DA:1124:C:H1'	56:D9:36:GLN:NE2	2.36	0.41
26:DA:1279:G:H2'	26:DA:1280:G:O4'	2.21	0.41
26:DA:1341:U:O2	44:DX:80:ILE:HD12	2.21	0.41
26:DA:1495:A:H2'	26:DA:1496:A:C8	2.55	0.41
26:DA:1819:A:H5"	28:DD:161:THR:HG21	2.03	0.41
27:DB:90:A:C5	27:DB:91:C:H1'	2.56	0.41
34:DN:62:VAL:CG1	34:DN:66:LYS:HB2	2.50	0.41
38:DR:24:GLN:HE22	38:DR:36:THR:HG21	1.86	0.41
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.35	0.41
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.69	0.41
1:AA:265:G:H5'	17:AQ:64:PRO:O	2.21	0.41
1:AA:350:G:O2'	1:AA:351:G:H5'	2.21	0.41
1:AA:407:G:N2	1:AA:436:C:C2	2.89	0.41
1:AA:472:A:H5"	16:AP:80:PHE:HB3	2.02	0.41
1:AA:691:G:P	11:AK:26:ASN:HD22	2.44	0.41
1:AA:738:C:H2'	1:AA:739:C:H6	1.86	0.41
1:AA:748:C:H1'	1:AA:749:C:OP2	2.20	0.41
1:AA:995:C:O2	14:AN:4:LYS:NZ	2.50	0.41
1:AA:1003:G:N3	1:AA:1004:A:H1'	2.36	0.41
1:AA:1164:G:C2'	1:AA:1165:C:H5'	2.51	0.41
1:AA:1216:G:H5"	14:AN:5:ALA:HB2	2.03	0.41
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.56	0.41
1:AA:1263:C:H2'	1:AA:1264:C:C6	2.56	0.41
2:AB:101:MET:HA	2:AB:108:ILE:HD12	2.02	0.41
2:AB:105:PHE:CZ	2:AB:155:LEU:HD12	2.55	0.41
2:AB:211:ILE:H	2:AB:211:ILE:HG13	1.66	0.41
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.85	0.41
3:AC:87:LEU:O	3:AC:91:LEU:N	2.30	0.41
4:AD:155:LEU:HD23	4:AD:156:GLU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:60:TYR:C	5:AE:60:TYR:CD1	2.99	0.41
8:AH:21:LYS:HD2	8:AH:21:LYS:HA	1.85	0.41
8:AH:104:ARG:HG3	8:AH:138:TRP:CD2	2.56	0.41
9:AI:4:TYR:CE2	9:AI:88:TYR:HA	2.56	0.41
11:AK:20:TYR:O	11:AK:30:VAL:HA	2.21	0.41
16:AP:8:ARG:NH2	16:AP:15:PRO:HG3	2.35	0.41
17:AQ:10:VAL:HG13	17:AQ:19:VAL:HB	2.02	0.41
19:AS:36:ARG:HD2	19:AS:52:TYR:O	2.21	0.41
26:BA:245:G:O5'	36:BP:73:GLY:HA2	2.20	0.41
26:BA:1395:A:C6	26:BA:1398:C:C2	3.09	0.41
26:BA:1527:G:H5"	26:BA:1528:A:OP1	2.20	0.41
26:BA:1692:U:O2'	26:BA:1693:U:H2'	2.20	0.41
26:BA:2080:G:OP1	48:B1:35:THR:HG21	2.20	0.41
26:BA:2168:G:O6	26:BA:2171:A:H8	2.03	0.41
26:BA:2284:C:OP1	53:B6:3:SER:OG	2.32	0.41
26:BA:2347:C:H2'	26:BA:2348:U:C6	2.55	0.41
26:BA:2516:G:C6	26:BA:2517:C:C4	3.09	0.41
26:BA:2516:G:C5	26:BA:2517:C:C4	3.09	0.41
26:BA:2760:C:H2'	26:BA:2761:G:H5"	2.02	0.41
26:BA:2820:A:C6	38:BR:4:LEU:HD11	2.56	0.41
27:BB:14:U:OP2	27:BB:70:C:O2'	2.35	0.41
29:BE:170:LEU:HB3	29:BE:184:VAL:HG22	2.02	0.41
30:BF:60:SER:OG	30:BF:61:GLY:N	2.53	0.41
31:BG:14:GLU:O	31:BG:17:PRO:HD2	2.21	0.41
31:BG:41:GLN:NE2	31:BG:153:ARG:HB3	2.34	0.41
33:BI:12:LEU:HA	33:BI:12:LEU:HD23	1.79	0.41
38:BR:38:VAL:HB	38:BR:39:PRO:HD3	2.02	0.41
39:BS:20:ARG:NH2	47:B0:48:GLY:O	2.54	0.41
40:BT:95:ARG:HH11	40:BT:95:ARG:CG	2.34	0.41
42:BV:65:GLY:HA3	42:BV:91:TYR:CZ	2.56	0.41
45:BY:54:LYS:HA	45:BY:55:TYR:HA	1.89	0.41
48:B1:95:LEU:HD12	48:B1:95:LEU:HA	1.87	0.41
48:B1:97:LEU:HD23	48:B1:97:LEU:HA	1.86	0.41
55:B8:4:MET:HE3	55:B8:63:PRO:CG	2.50	0.41
1:CA:60:A:N3	1:CA:61:G:H1'	2.36	0.41
1:CA:266:G:H8	1:CA:266:G:H2'	1.62	0.41
1:CA:475:G:H2'	1:CA:476:G:C8	2.56	0.41
1:CA:502:G:H2'	1:CA:503:C:O4'	2.21	0.41
1:CA:522:C:H5"	12:CL:120:TYR:OH	2.21	0.41
1:CA:764:C:H4'	15:CO:50:HIS:HB3	2.03	0.41
1:CA:945:G:C2	1:CA:946:A:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:949:A:C6	1:CA:950:U:C4	3.09	0.41
1:CA:968:A:H8	1:CA:968:A:O5'	2.03	0.41
1:CA:1005:A:N3	1:CA:1005:A:H2'	2.35	0.41
1:CA:1022:G:H2'	1:CA:1023:G:H8	1.86	0.41
1:CA:1079:G:O3'	5:CE:14:ARG:NH2	2.54	0.41
1:CA:1155:G:N7	1:CA:1156:G:C5	2.89	0.41
1:CA:1194:U:H4'	5:CE:22:GLY:O	2.21	0.41
1:CA:1249:C:O2'	9:CI:73:GLN:NE2	2.54	0.41
1:CA:1291:G:C6	1:CA:1292:U:C4	3.08	0.41
1:CA:1325:C:O2'	1:CA:1326:C:H5'	2.20	0.41
1:CA:1381:U:H2'	1:CA:1382:C:H5'	2.03	0.41
2:CB:91:PRO:HG3	2:CB:154:LEU:HD12	2.03	0.41
3:CC:24:ALA:HB1	3:CC:28:GLN:O	2.20	0.41
4:CD:112:VAL:HG13	4:CD:161:ASN:OD1	2.21	0.41
5:CE:93:PRO:HA	5:CE:118:ILE:HD12	2.02	0.41
5:CE:106:PRO:HB3	5:CE:135:THR:OG1	2.20	0.41
5:CE:135:THR:O	5:CE:139:LEU:HG	2.21	0.41
9:CI:100:GLY:O	9:CI:103:THR:HG22	2.21	0.41
10:CJ:11:PHE:HE1	10:CJ:67:THR:HB	1.85	0.41
13:CM:50:GLU:O	13:CM:54:VAL:HG13	2.21	0.41
18:CR:51:LEU:HA	18:CR:52:PRO:HD3	1.90	0.41
26:DA:45:C:H2'	26:DA:47:C:H6	1.86	0.41
26:DA:82:G:O6	61:DA:4071:HOH:O	2.21	0.41
26:DA:460:A:C2	26:DA:470:A:C4	3.09	0.41
26:DA:573:G:O2'	26:DA:574:C:H3'	2.20	0.41
26:DA:735:A:N7	26:DA:761:A:H2	2.18	0.41
26:DA:1140:C:O3'	34:DN:25:ARG:NH1	2.53	0.41
26:DA:1667:G:O2'	26:DA:1991:U:O4	2.37	0.41
26:DA:1820:U:C2	28:DD:202:LYS:HB3	2.55	0.41
26:DA:1906:G:C8	26:DA:1929:G:H2'	2.55	0.41
26:DA:2126:A:C5	26:DA:2163:C:H1'	2.56	0.41
26:DA:2142:C:H2'	26:DA:2143:C:H6	1.83	0.41
26:DA:2563:U:H4'	35:DO:28:SER:HA	2.02	0.41
26:DA:2646:C:O5'	26:DA:2646:C:H6	2.04	0.41
26:DA:2693:A:C2	26:DA:2694:G:C8	3.09	0.41
26:DA:2884:U:C4	26:DA:2885:C:C2	3.09	0.41
29:DE:141:ILE:O	29:DE:154:LYS:HE2	2.21	0.41
30:DF:31:HIS:HB2	36:DP:9:ASN:OD1	2.21	0.41
30:DF:39:TRP:CG	30:DF:101:LEU:HB2	2.56	0.41
31:DG:181:ARG:HE	31:DG:181:ARG:HB3	1.78	0.41
32:DH:70:THR:HG22	32:DH:74:ASN:HD21	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DI:72:LEU:HD12	33:DI:138:ILE:HG22	2.03	0.41
33:DI:114:LEU:HD11	33:DI:128:LEU:HD13	2.02	0.41
38:DR:100:LEU:HD13	38:DR:100:LEU:HA	1.86	0.41
40:DT:56:GLY:O	40:DT:59:THR:HG22	2.21	0.41
51:D4:34:GLU:OE2	51:D4:35:VAL:HG12	2.20	0.41
51:D4:61:ARG:NE	51:D4:61:ARG:O	2.53	0.41
54:D7:9:ARG:HE	54:D7:47:ARG:HG3	1.86	0.41
54:D7:22:MET:HA	54:D7:28:ARG:HG2	2.03	0.41
1:AA:1019:C:H5"	1:AA:1019:C:H6	1.86	0.41
1:AA:1024:G:H2'	1:AA:1025:U:H5'	2.02	0.41
1:AA:1409:C:H2'	1:AA:1410:G:C8	2.56	0.41
2:AB:60:ASP:OD1	2:AB:64:ARG:NE	2.48	0.41
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.46	0.41
7:AG:73:MET:HE2	7:AG:73:MET:HB2	1.86	0.41
13:AM:3:ARG:HG3	13:AM:4:ILE:N	2.36	0.41
13:AM:91:ARG:HD2	13:AM:91:ARG:HA	1.86	0.41
15:AO:74:ASP:HA	15:AO:75:PRO:HD2	1.94	0.41
24:AX:12:G:H4'	26:BA:1908:C:O2	2.21	0.41
26:BA:223:A:N1	26:BA:407:G:O2'	2.37	0.41
26:BA:809:G:C5	26:BA:810:U:C4	3.09	0.41
26:BA:874:G:H2'	26:BA:875:G:H5'	2.02	0.41
26:BA:952:G:OP1	37:BQ:16:ARG:NH2	2.54	0.41
26:BA:1175:U:HO2'	26:BA:1176:G:P	2.39	0.41
26:BA:1649:G:C6	26:BA:2009:G:C6	3.10	0.41
26:BA:1653:G:H4'	26:BA:1654:A:O5'	2.21	0.41
26:BA:1935:G:H1'	26:BA:1964:G:N2	2.35	0.41
26:BA:2135:A:H8	26:BA:2135:A:O5'	2.04	0.41
26:BA:2144:U:H2'	26:BA:2146:C:C5	2.56	0.41
26:BA:2162:G:C6	26:BA:2163:C:N4	2.89	0.41
26:BA:2480:C:N4	26:BA:2481:G:C6	2.89	0.41
40:BT:91:ARG:HH11	40:BT:120:ARG:NH1	2.19	0.41
1:CA:77:G:C6	1:CA:78:G:C6	3.09	0.41
1:CA:698:G:C6	1:CA:699:C:C4	3.09	0.41
1:CA:728:A:O4'	15:CO:54:ARG:NH2	2.54	0.41
1:CA:751:U:O4'	15:CO:24:SER:HA	2.20	0.41
1:CA:1221:G:H4'	19:CS:77:THR:OG1	2.21	0.41
4:CD:92:VAL:O	4:CD:96:LEU:HD22	2.21	0.41
6:CF:2:ARG:NE	6:CF:69:GLU:HG2	2.36	0.41
26:DA:535:C:H2'	26:DA:536:A:O4'	2.21	0.41
26:DA:565:C:C5	42:DV:78:LYS:HE3	2.56	0.41
26:DA:848:G:C2	26:DA:933:A:H1'	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1232:G:H2'	26:DA:1233:C:C6	2.56	0.41
26:DA:1363:C:O2'	26:DA:1809:A:N3	2.47	0.41
26:DA:2514:U:H2'	26:DA:2515:C:C6	2.56	0.41
27:DB:59:A:H2'	27:DB:60:C:O4'	2.22	0.41
34:DN:30:ILE:O	34:DN:34:LEU:HD22	2.21	0.41
35:DO:7:TYR:HE1	35:DO:20:MET:HE3	1.86	0.41
46:DZ:54:HIS:CG	46:DZ:101:PRO:HG3	2.56	0.41
46:DZ:98:MET:HE2	46:DZ:98:MET:HB2	1.96	0.41
51:D4:46:GLN:C	51:D4:48:ARG:N	2.80	0.41
1:AA:26:A:N6	1:AA:558:G:O2'	2.52	0.40
1:AA:78:G:C6	1:AA:91:C:N4	2.81	0.40
1:AA:300:A:O2'	1:AA:564:C:O2	2.37	0.40
1:AA:1009:G:N2	1:AA:1020:U:O2	2.44	0.40
1:AA:1226:C:P	13:AM:91:ARG:HH12	2.44	0.40
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.87	0.40
2:AB:231:GLU:HB2	2:AB:232:PRO:CD	2.50	0.40
8:AH:14:ARG:O	8:AH:18:ARG:HD3	2.21	0.40
8:AH:51:VAL:HG12	8:AH:52:ASP:N	2.37	0.40
26:BA:686:G:N2	26:BA:788:A:H61	2.19	0.40
26:BA:848:G:N3	26:BA:933:A:H1'	2.36	0.40
26:BA:1530:C:O2'	26:BA:1531:C:P	2.79	0.40
26:BA:1530:C:HO2'	26:BA:1531:C:P	2.40	0.40
26:BA:2019:A:H5"	41:BU:27:LEU:HD12	2.02	0.40
26:BA:2116:G:N2	26:BA:2162:G:OP1	2.54	0.40
26:BA:2533:A:H2'	26:BA:2534:A:O4'	2.20	0.40
28:BD:134:ARG:HG3	28:BD:135:PHE:CD2	2.56	0.40
39:BS:87:PHE:HB2	39:BS:112:PHE:CD2	2.56	0.40
1:CA:92:C:N4	1:CA:93:G:N7	2.68	0.40
1:CA:221:C:H2'	1:CA:222:U:H6	1.87	0.40
1:CA:355:C:H2'	1:CA:356:A:O4'	2.21	0.40
1:CA:512:U:OP1	4:CD:46:LYS:HE2	2.21	0.40
1:CA:1005:A:OP2	1:CA:1024:G:N1	2.54	0.40
1:CA:1064:G:N2	1:CA:1190:G:H2'	2.36	0.40
1:CA:1304:G:C6	1:CA:1305:G:C6	3.09	0.40
1:CA:1368:G:OP2	9:CI:112:LYS:HG3	2.21	0.40
1:CA:1524:C:H2'	1:CA:1525:G:O4'	2.21	0.40
5:CE:41:VAL:HG22	5:CE:69:VAL:HG11	2.03	0.40
16:CP:20:VAL:HG21	16:CP:32:TYR:CD2	2.56	0.40
24:CX:60:U:H3'	24:CX:61:C:C6	2.56	0.40
26:DA:141:A:H8	26:DA:1408:C:HO2'	1.59	0.40
26:DA:565:C:H4'	26:DA:1253:A:C6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1007:C:OP2	61:DA:4086:HOH:O	2.21	0.40
26:DA:1914:C:H2'	26:DA:1915:U:H6	1.85	0.40
26:DA:2283:C:C2	26:DA:2389:G:C2	3.08	0.40
26:DA:2793:G:H2'	26:DA:2794:C:O4'	2.21	0.40
26:DA:2808:U:O2'	26:DA:2809:A:H5'	2.20	0.40
26:DA:2882:A:OP1	38:DR:96:ARG:NE	2.48	0.40
27:DB:73:A:C4	27:DB:105:A:C2	3.09	0.40
35:DO:60:ALA:HB1	35:DO:84:ALA:HB1	2.04	0.40
43:DW:86:LEU:HA	43:DW:87:PRO:HD3	1.94	0.40
54:D7:26:GLY:O	54:D7:30:VAL:HG23	2.22	0.40
1:AA:937:A:C2'	1:AA:938:A:H5'	2.51	0.40
2:AB:18:GLY:HA3	2:AB:41:ILE:HD13	2.03	0.40
2:AB:90:MET:HA	2:AB:91:PRO:HD3	1.92	0.40
12:AL:42:THR:HA	12:AL:53:ARG:O	2.22	0.40
26:BA:69:C:O2	26:BA:73:A:O2'	2.31	0.40
26:BA:732:C:H2'	26:BA:733:G:O4'	2.20	0.40
26:BA:1512:U:H2'	26:BA:1513:C:C6	2.56	0.40
26:BA:2129:C:N3	26:BA:2160:G:C2	2.89	0.40
29:BE:1:MET:HE2	29:BE:202:LYS:HE3	2.02	0.40
33:BI:93:THR:H	33:BI:96:ASP:CG	2.29	0.40
38:BR:29:LEU:HD12	38:BR:29:LEU:HA	1.82	0.40
38:BR:109:ALA:HA	38:BR:110:PRO:HD2	1.92	0.40
44:BX:92:LEU:C	44:BX:94:GLY:H	2.28	0.40
51:B4:61:ARG:O	51:B4:62:ARG:C	2.64	0.40
55:B8:7:HIS:HB3	55:B8:61:LEU:HB3	2.03	0.40
1:CA:42:G:O2'	1:CA:622:A:N1	2.49	0.40
1:CA:97:G:N1	1:CA:98:G:C5	2.89	0.40
1:CA:636:U:H2'	1:CA:637:G:C8	2.55	0.40
1:CA:718:G:H5'	11:CK:117:ASN:ND2	2.36	0.40
1:CA:977:A:O3'	1:CA:980:C:N4	2.48	0.40
1:CA:1107:C:C4	1:CA:1108:G:C8	3.09	0.40
1:CA:1120:G:C6	1:CA:1121:U:C4	3.08	0.40
1:CA:1342:C:H4'	9:CI:125:TYR:O	2.21	0.40
1:CA:1471:G:C2'	1:CA:1472:U:H5'	2.51	0.40
1:CA:1517:G:H1'	26:DA:1919:A:O3'	2.21	0.40
4:CD:175:SER:OG	4:CD:184:LYS:HB2	2.21	0.40
6:CF:2:ARG:NH2	15:CO:2:PRO:HD2	2.34	0.40
8:CH:44:PHE:CE2	8:CH:109:ILE:HG12	2.55	0.40
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	2.03	0.40
9:CI:33:PHE:HZ	9:CI:46:ALA:HB3	1.86	0.40
11:CK:48:ILE:O	11:CK:50:TYR:N	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:60:LEU:HD23	12:CL:66:VAL:HG22	2.02	0.40
15:CO:50:HIS:O	15:CO:53:HIS:HB3	2.21	0.40
26:DA:6:A:C2'	26:DA:7:G:H5'	2.50	0.40
26:DA:271(H):G:O6	26:DA:271(Q):G:C6	2.74	0.40
26:DA:311:A:C6	26:DA:328:U:C4	3.10	0.40
26:DA:979:G:H5"	26:DA:980:A:H5"	2.03	0.40
26:DA:1188:U:C4'	42:DV:79:VAL:HG22	2.51	0.40
26:DA:1354:A:H5"	28:DD:38:LYS:HD3	2.02	0.40
26:DA:1533:G:C6	26:DA:1537:G:C6	3.09	0.40
26:DA:2125:G:N2	26:DA:2173:A:C8	2.86	0.40
26:DA:2830:G:O2'	26:DA:2883:A:N1	2.41	0.40
31:DG:60:LEU:HD13	31:DG:60:LEU:HA	1.89	0.40
1:AA:347:G:C6	1:AA:348:G:C5	3.09	0.40
1:AA:582:U:H2'	1:AA:583:A:C8	2.57	0.40
1:AA:1368:G:C2'	1:AA:1369:C:H5'	2.51	0.40
2:AB:126:GLU:HB3	2:AB:127:ILE:H	1.67	0.40
2:AB:155:LEU:HD11	2:AB:159:PRO:HD3	2.03	0.40
4:AD:88:VAL:HG22	5:AE:97:GLY:HA2	2.04	0.40
17:AQ:32:TYR:O	17:AQ:34:LYS:N	2.54	0.40
19:AS:69:HIS:N	51:B4:58:ARG:NH2	2.70	0.40
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	2.03	0.40
24:AX:43:A:H2'	24:AX:44:A:C8	2.57	0.40
26:BA:250:G:P	55:B8:13:ARG:NH2	2.95	0.40
26:BA:435:C:H2'	26:BA:436:C:H5'	2.03	0.40
26:BA:467:G:O2'	26:BA:796:C:O2'	2.32	0.40
26:BA:755:C:H2'	26:BA:756:C:C6	2.56	0.40
26:BA:868:U:C4	26:BA:869:G:N7	2.90	0.40
26:BA:1194:A:H2'	26:BA:1195:G:O4'	2.22	0.40
26:BA:1231:G:H2'	26:BA:1232:G:C8	2.56	0.40
26:BA:1569:A:H2'	26:BA:1570:A:O4'	2.21	0.40
26:BA:1791:A:C8	26:BA:1792:G:C8	3.09	0.40
26:BA:1791:A:OP2	26:BA:1791:A:H8	2.05	0.40
26:BA:1815:A:H8	26:BA:1815:A:OP1	2.05	0.40
26:BA:2141:G:N1	26:BA:2142:C:O2	2.54	0.40
26:BA:2699:C:H2'	26:BA:2700:C:O4'	2.21	0.40
29:BE:181:LEU:HA	29:BE:181:LEU:HD12	1.83	0.40
31:BG:10:LYS:HG3	31:BG:14:GLU:OE1	2.22	0.40
32:BH:41:MET:HE2	32:BH:65:HIS:HA	2.04	0.40
47:B0:50:ASN:HB3	47:B0:63:VAL:HG22	2.03	0.40
48:B1:17:SER:HB2	48:B1:40:ARG:HG2	2.02	0.40
53:B6:10:LEU:HG	53:B6:54:ILE:HG13	2.01	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:17:U:H2'	1:CA:18:C:H6	1.86	0.40
1:CA:120:A:C6	1:CA:122:G:C2	3.09	0.40
1:CA:444:C:H2'	1:CA:445:G:C8	2.57	0.40
1:CA:636:U:O2'	1:CA:637:G:H5'	2.22	0.40
1:CA:830:G:H2'	1:CA:831:U:O4'	2.21	0.40
1:CA:949:A:C5	1:CA:950:U:C4	3.10	0.40
3:CC:112:SER:O	3:CC:116:VAL:HG23	2.21	0.40
8:CH:20:TYR:HA	8:CH:65:TYR:OH	2.21	0.40
10:CJ:43:ARG:HB2	10:CJ:67:THR:HG23	2.04	0.40
24:CX:6:G:C2	24:CX:68:C:C2	3.10	0.40
26:DA:360:G:H2'	26:DA:361:G:H8	1.85	0.40
26:DA:422:A:C6	26:DA:423:A:C6	3.10	0.40
26:DA:453:C:H5"	61:DA:4438:HOH:O	2.20	0.40
26:DA:638:G:H2'	26:DA:639:U:O4'	2.21	0.40
26:DA:975(A):G:H1'	26:DA:990:A:C2	2.57	0.40
26:DA:1152:C:H2'	26:DA:1153:C:C6	2.57	0.40
26:DA:1182:A:H2'	26:DA:1183:G:C8	2.56	0.40
26:DA:1448:G:H5"	26:DA:1449:A:OP1	2.21	0.40
26:DA:2099:U:H2'	26:DA:2100:G:H8	1.86	0.40
26:DA:2154:G:C2	26:DA:2155:G:N7	2.89	0.40
26:DA:2200:C:O2'	26:DA:2227:A:N1	2.51	0.40
26:DA:2263:C:H41	47:D0:15:ASP:HA	1.87	0.40
26:DA:2849:U:H4'	26:DA:2868:A:C2	2.57	0.40
29:DE:120:TRP:CD1	29:DE:155:LYS:HB3	2.57	0.40
30:DF:32:LEU:HB3	30:DF:112:MET:HE1	2.03	0.40
30:DF:37:VAL:O	30:DF:41:LEU:HG	2.21	0.40
31:DG:73:ALA:O	31:DG:84:LYS:HG3	2.21	0.40
31:DG:97:ASP:HA	31:DG:100:TRP:HD1	1.87	0.40
32:DH:42:ARG:HD3	32:DH:44:VAL:HG23	2.04	0.40
32:DH:127:GLU:C	32:DH:129:THR:H	2.29	0.40
39:DS:43:GLU:OE1	47:D0:49:LYS:NZ	2.31	0.40
1:AA:265:G:N2	1:AA:267:C:H5'	2.37	0.40
1:AA:428:G:H4'	1:AA:429:U:O5'	2.21	0.40
1:AA:875:C:C4	1:AA:876:G:N7	2.90	0.40
1:AA:1174:G:H5"	1:AA:1174:G:H8	1.87	0.40
7:AG:26:PHE:CE2	7:AG:30:ILE:HD11	2.57	0.40
10:AJ:81:THR:HA	10:AJ:84:GLN:HB3	2.03	0.40
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.21	0.40
26:BA:128:C:H2'	26:BA:129:C:O4'	2.22	0.40
26:BA:196:A:N3	26:BA:196:A:H2'	2.36	0.40
26:BA:255:A:H1'	26:BA:384:U:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:469:G:O6	54:B7:37:LYS:HE2	2.21	0.40
26:BA:528:A:C2	26:BA:2043:C:H5'	2.56	0.40
26:BA:531:C:H4'	26:BA:532:A:H5"	2.03	0.40
26:BA:642:G:O2'	26:BA:644:A:N7	2.51	0.40
26:BA:1052:C:O5'	26:BA:1052:C:H6	2.04	0.40
26:BA:1210:A:H4'	26:BA:1211:U:O5'	2.21	0.40
26:BA:1446:C:O2'	26:BA:1545:A:O2'	2.33	0.40
26:BA:2051:A:H4'	29:BE:141:ILE:HG12	2.03	0.40
26:BA:2127:G:H1'	26:BA:2173:A:C2	2.56	0.40
26:BA:2223:G:OP1	28:BD:172:TYR:OH	2.36	0.40
26:BA:2245:U:O2'	26:BA:2436:G:OP2	2.37	0.40
26:BA:2317:C:H2'	26:BA:2318:G:O4'	2.21	0.40
26:BA:2393:A:O2'	36:BP:60:MET:O	2.32	0.40
27:BB:96:U:H2'	27:BB:97:G:C8	2.56	0.40
31:BG:126:ASP:HB2	31:BG:130:ASN:HB2	2.04	0.40
32:BH:11:VAL:HG21	32:BH:50:VAL:HG23	2.03	0.40
43:BW:33:ARG:NE	43:BW:52:GLU:OE1	2.50	0.40
49:B2:29:LYS:HG2	49:B2:57:ILE:HD13	2.02	0.40
51:B4:48:ARG:HA	51:B4:48:ARG:CZ	2.52	0.40
51:B4:57:GLU:OE2	51:B4:58:ARG:HG3	2.21	0.40
1:CA:1106:G:C6	1:CA:1107:C:C4	3.09	0.40
1:CA:1409:C:H2'	1:CA:1410:G:H8	1.85	0.40
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.87	0.40
4:CD:168:ARG:H	4:CD:168:ARG:HG2	1.65	0.40
7:CG:52:GLU:H	7:CG:52:GLU:HG2	1.69	0.40
13:CM:33:ALA:HA	13:CM:59:TYR:CE2	2.56	0.40
14:CN:6:LEU:HD12	14:CN:6:LEU:HA	1.95	0.40
15:CO:48:LYS:HA	15:CO:48:LYS:HD3	1.83	0.40
24:CX:22:G:H2'	24:CX:23:C:H6	1.86	0.40
26:DA:183:C:C2'	26:DA:184:C:H5'	2.51	0.40
26:DA:260:G:C6	26:DA:261:G:C8	3.09	0.40
26:DA:466:A:H1'	26:DA:683:C:O4'	2.20	0.40
26:DA:660:G:C6	26:DA:661:C:C4	3.10	0.40
26:DA:786:C:H5"	26:DA:1780:A:N7	2.36	0.40
26:DA:873:G:H1	26:DA:904:C:N4	2.19	0.40
26:DA:1203:G:H2'	26:DA:1241:A:N6	2.37	0.40
26:DA:1790:C:H2'	26:DA:1791:A:C5	2.56	0.40
26:DA:2093:G:C6	26:DA:2225:A:C8	3.10	0.40
26:DA:2104:G:O2'	26:DA:2105:C:O4'	2.36	0.40
26:DA:2141:G:H2'	26:DA:2142:C:O4'	2.21	0.40
26:DA:2151:G:N3	26:DA:2152:G:C8	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2286:A:N3	26:DA:2286:A:H2'	2.36	0.40
27:DB:16:G:O6	27:DB:66:A:H2	2.04	0.40
29:DE:119:ARG:HH11	29:DE:119:ARG:HD3	1.77	0.40
30:DF:34:TRP:CZ2	36:DP:8:PRO:HG3	2.57	0.40
31:DG:107:LEU:HD21	31:DG:178:PHE:CE1	2.56	0.40
37:DQ:17:LEU:HD21	37:DQ:96:VAL:HG13	2.03	0.40
38:DR:70:LEU:HD13	38:DR:75:LEU:HD13	2.03	0.40
39:DS:11:LYS:HD2	39:DS:15:ARG:NH1	2.37	0.40
39:DS:35:ILE:HG22	39:DS:53:SER:HB3	2.04	0.40
40:DT:99:LEU:O	40:DT:100:TYR:C	2.65	0.40
50:D3:19:GLN:O	50:D3:23:LEU:HD22	2.22	0.40
1:AA:146:G:C2	1:AA:147:G:C4	3.10	0.40
1:AA:715:A:H1'	1:AA:777:A:N1	2.35	0.40
1:AA:1060:C:P	14:AN:45:ARG:HH22	2.44	0.40
1:AA:1531:A:H2'	1:AA:1532:U:C4	2.56	0.40
3:AC:115:LEU:HA	3:AC:115:LEU:HD12	1.88	0.40
4:AD:86:LYS:H	4:AD:86:LYS:HG2	1.61	0.40
9:AI:97:LYS:HB3	9:AI:98:PRO:HD3	2.04	0.40
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.52	0.40
13:AM:11:ARG:C	13:AM:13:LYS:H	2.29	0.40
16:AP:60:LEU:HD13	16:AP:60:LEU:HA	1.83	0.40
18:AR:24:ALA:C	18:AR:26:LEU:H	2.30	0.40
20:AT:36:LEU:HD23	20:AT:36:LEU:HA	1.84	0.40
26:BA:26:G:H1'	26:BA:515:A:H61	1.86	0.40
26:BA:117:G:OP2	26:BA:119:A:O2'	2.33	0.40
26:BA:201:C:O2'	26:BA:251:A:N1	2.51	0.40
26:BA:438:G:H2'	26:BA:440:G:C8	2.56	0.40
26:BA:780:G:H1'	26:BA:785:G:C2	2.56	0.40
26:BA:1168:G:O2'	26:BA:1169:G:H5'	2.22	0.40
26:BA:1674:G:H1'	26:BA:1676:A:N6	2.35	0.40
26:BA:2001:A:H2'	26:BA:2002:G:C8	2.56	0.40
26:BA:2651:C:H2'	26:BA:2652:C:H6	1.85	0.40
29:BE:35:GLN:OE1	29:BE:66:HIS:HE1	2.05	0.40
30:BF:183:VAL:O	30:BF:187:VAL:HG23	2.21	0.40
32:BH:117:PRO:HG3	32:BH:123:PHE:CD2	2.56	0.40
35:BO:101:PRO:HG3	40:BT:67:SER:OG	2.22	0.40
37:BQ:12:GLN:HG2	37:BQ:73:PRO:HD2	2.03	0.40
37:BQ:37:LEU:HD21	37:BQ:130:LYS:HE2	2.04	0.40
37:BQ:104:PHE:HE2	37:BQ:125:LEU:HD11	1.87	0.40
38:BR:87:TYR:OH	38:BR:116:LEU:HB3	2.21	0.40
39:BS:41:ASP:HB2	39:BS:48:LEU:HD21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:B2:48:HIS:CE1	49:B2:49:LYS:HG3	2.57	0.40
50:B3:10:LYS:HB3	50:B3:53:LEU:HA	2.04	0.40
55:B8:39:LYS:HA	55:B8:42:ARG:NH1	2.37	0.40
1:CA:485:G:O2'	1:CA:486:U:OP2	2.39	0.40
1:CA:538:G:H5"	12:CL:114:LYS:HB2	2.03	0.40
1:CA:1025:U:C4	1:CA:1036:G:O6	2.75	0.40
1:CA:1125:U:O2'	1:CA:1126:U:C2'	2.68	0.40
1:CA:1392:G:N2	1:CA:1502:A:H8	2.18	0.40
4:CD:46:LYS:O	4:CD:47:ARG:HB3	2.22	0.40
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.21	0.40
26:DA:300:A:OP1	45:DY:86:ARG:NH2	2.52	0.40
26:DA:452:G:C4	26:DA:458:G:C6	3.09	0.40
26:DA:729:G:H2'	26:DA:1775:U:O2	2.20	0.40
26:DA:959:A:N3	26:DA:2457:U:O2'	2.47	0.40
26:DA:996:A:N6	26:DA:1160:G:C6	2.89	0.40
26:DA:1002:G:H2'	26:DA:1003:G:O4'	2.21	0.40
26:DA:1598:C:H2'	26:DA:1599:C:C6	2.57	0.40
26:DA:2298:A:H2	26:DA:2321:G:C5	2.39	0.40
26:DA:2623:G:H4'	26:DA:2825:C:O2	2.22	0.40
27:DB:108:U:H5'	27:DB:109:C:OP2	2.22	0.40
32:DH:150:ALA:HA	32:DH:153:LYS:HG3	2.02	0.40
33:DI:44:LEU:HD13	33:DI:44:LEU:HA	1.92	0.40
34:DN:75:TYR:CE2	34:DN:77:GLY:HA2	2.56	0.40
35:DO:63:VAL:HB	35:DO:102:VAL:HG12	2.03	0.40
36:DP:127:ALA:C	36:DP:148:LEU:HD23	2.47	0.40
37:DQ:76:LYS:HB3	37:DQ:91:GLU:HG3	2.03	0.40
43:DW:86:LEU:HD22	43:DW:96:ILE:HD11	2.04	0.40
44:DX:12:VAL:HG22	44:DX:29:TRP:CE2	2.57	0.40
47:D0:27:GLU:HG3	47:D0:68:GLU:HA	2.04	0.40
51:D4:18:CYS:HB3	51:D4:39:CYS:HB3	2.04	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1043:C:O2'	26:DA:2137:C:O2'[2_655]	2.08	0.12
33:BI:89:TYR:O	1:CA:357:G:O2'[3_654]	2.10	0.10
38:BR:33:ARG:NH2	42:BV:53:GLU:OE2[4_445]	2.19	0.01

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	AB	229/256 (90%)	204 (89%)	21 (9%)	4 (2%)	7 25
2	CB	229/256 (90%)	204 (89%)	14 (6%)	11 (5%)	2 6
3	AC	204/239 (85%)	189 (93%)	13 (6%)	2 (1%)	12 38
3	CC	204/239 (85%)	188 (92%)	15 (7%)	1 (0%)	24 55
4	AD	206/209 (99%)	198 (96%)	7 (3%)	1 (0%)	24 55
4	CD	206/209 (99%)	196 (95%)	7 (3%)	3 (2%)	8 28
5	AE	146/162 (90%)	136 (93%)	9 (6%)	1 (1%)	18 47
5	CE	146/162 (90%)	135 (92%)	10 (7%)	1 (1%)	18 47
6	AF	98/101 (97%)	96 (98%)	2 (2%)	0	100 100
6	CF	98/101 (97%)	97 (99%)	1 (1%)	0	100 100
7	AG	153/156 (98%)	143 (94%)	7 (5%)	3 (2%)	6 21
7	CG	153/156 (98%)	143 (94%)	9 (6%)	1 (1%)	18 47
8	AH	135/138 (98%)	133 (98%)	2 (2%)	0	100 100
8	CH	135/138 (98%)	130 (96%)	4 (3%)	1 (1%)	18 47
9	AI	125/128 (98%)	118 (94%)	7 (6%)	0	100 100
9	CI	125/128 (98%)	118 (94%)	6 (5%)	1 (1%)	16 44
10	AJ	95/105 (90%)	83 (87%)	5 (5%)	7 (7%)	1 2
10	CJ	94/105 (90%)	83 (88%)	6 (6%)	5 (5%)	1 5
11	AK	112/129 (87%)	106 (95%)	5 (4%)	1 (1%)	14 41
11	CK	112/129 (87%)	105 (94%)	6 (5%)	1 (1%)	14 41
12	AL	120/132 (91%)	116 (97%)	4 (3%)	0	100 100
12	CL	120/132 (91%)	113 (94%)	7 (6%)	0	100 100
13	AM	121/126 (96%)	113 (93%)	6 (5%)	2 (2%)	7 25
13	CM	120/126 (95%)	110 (92%)	9 (8%)	1 (1%)	16 44
14	AN	58/61 (95%)	57 (98%)	1 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	CN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
15	AO	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
15	CO	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	AP	80/88 (91%)	75 (94%)	5 (6%)	0	100	100
16	CP	80/88 (91%)	76 (95%)	4 (5%)	0	100	100
17	AQ	97/105 (92%)	90 (93%)	7 (7%)	0	100	100
17	CQ	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
18	AR	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
18	CR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
19	AS	81/93 (87%)	70 (86%)	11 (14%)	0	100	100
19	CS	81/93 (87%)	71 (88%)	8 (10%)	2 (2%)	4	16
20	AT	94/106 (89%)	85 (90%)	3 (3%)	6 (6%)	1	3
20	CT	94/106 (89%)	84 (89%)	6 (6%)	4 (4%)	2	7
21	AU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
21	CU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
28	BD	273/276 (99%)	263 (96%)	9 (3%)	1 (0%)	30	60
28	DD	273/276 (99%)	261 (96%)	10 (4%)	2 (1%)	18	47
29	BE	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	24	55
29	DE	202/206 (98%)	193 (96%)	7 (4%)	2 (1%)	12	38
30	BF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	24	55
30	DF	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	12	38
31	BG	179/182 (98%)	166 (93%)	9 (5%)	4 (2%)	5	19
31	DG	179/182 (98%)	166 (93%)	9 (5%)	4 (2%)	5	19
32	BH	172/180 (96%)	161 (94%)	9 (5%)	2 (1%)	10	34
32	DH	172/180 (96%)	163 (95%)	7 (4%)	2 (1%)	10	34
33	BI	144/148 (97%)	132 (92%)	9 (6%)	3 (2%)	5	20
33	DI	144/148 (97%)	130 (90%)	12 (8%)	2 (1%)	9	30
34	BN	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
34	DN	138/140 (99%)	132 (96%)	5 (4%)	1 (1%)	18	47
35	BO	120/122 (98%)	114 (95%)	5 (4%)	1 (1%)	16	44
35	DO	120/122 (98%)	115 (96%)	4 (3%)	1 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
36	BP	147/150 (98%)	138 (94%)	8 (5%)	1 (1%)	18 47
36	DP	147/150 (98%)	133 (90%)	13 (9%)	1 (1%)	18 47
37	BQ	139/141 (99%)	133 (96%)	6 (4%)	0	100 100
37	DQ	139/141 (99%)	134 (96%)	5 (4%)	0	100 100
38	BR	116/118 (98%)	111 (96%)	5 (4%)	0	100 100
38	DR	116/118 (98%)	111 (96%)	5 (4%)	0	100 100
39	BS	108/112 (96%)	104 (96%)	4 (4%)	0	100 100
39	DS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	14 41
40	BT	129/146 (88%)	121 (94%)	8 (6%)	0	100 100
40	DT	129/146 (88%)	125 (97%)	3 (2%)	1 (1%)	16 44
41	BU	114/118 (97%)	114 (100%)	0	0	100 100
41	DU	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
42	BV	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	12 38
42	DV	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12 38
43	BW	110/113 (97%)	109 (99%)	1 (1%)	0	100 100
43	DW	110/113 (97%)	109 (99%)	1 (1%)	0	100 100
44	BX	93/96 (97%)	91 (98%)	2 (2%)	0	100 100
44	DX	93/96 (97%)	91 (98%)	2 (2%)	0	100 100
45	BY	105/110 (96%)	95 (90%)	10 (10%)	0	100 100
45	DY	105/110 (96%)	99 (94%)	6 (6%)	0	100 100
46	BZ	169/206 (82%)	148 (88%)	19 (11%)	2 (1%)	10 34
46	DZ	172/206 (84%)	156 (91%)	14 (8%)	2 (1%)	10 34
47	B0	81/85 (95%)	78 (96%)	3 (4%)	0	100 100
47	D0	81/85 (95%)	77 (95%)	4 (5%)	0	100 100
48	B1	95/98 (97%)	94 (99%)	0	1 (1%)	11 36
48	D1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11 36
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%)	55 (96%)	2 (4%)	0	100 100
50	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
51	B4	67/71 (94%)	54 (81%)	8 (12%)	5 (8%)	1 2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
51	D4	67/71 (94%)	53 (79%)	10 (15%)	4 (6%)	1 3
52	B5	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
52	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
53	B6	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
53	D6	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
54	B7	46/49 (94%)	46 (100%)	0	0	100 100
54	D7	46/49 (94%)	45 (98%)	0	1 (2%)	5 19
55	B8	62/65 (95%)	61 (98%)	1 (2%)	0	100 100
55	D8	62/65 (95%)	61 (98%)	1 (2%)	0	100 100
56	B9	35/37 (95%)	35 (100%)	0	0	100 100
56	D9	35/37 (95%)	35 (100%)	0	0	100 100
All	All	11409/12128 (94%)	10783 (94%)	516 (4%)	110 (1%)	12 38

All (110) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	231	GLU
4	AD	166	LYS
7	AG	80	VAL
10	AJ	55	LYS
20	AT	10	LEU
28	BD	275	LYS
30	BF	130	ALA
31	BG	49	ASP
31	BG	51	ARG
32	BH	92	ILE
46	BZ	152	ALA
51	B4	62	ARG
2	CB	8	LYS
2	CB	16	HIS
2	CB	20	GLU
2	CB	126	GLU
9	CI	54	ASP
13	CM	85	GLY
20	CT	99	LEU
30	DF	21	ALA
30	DF	130	ALA
31	DG	81	LYS

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Mol	Chain	Res	Type
33	DI	10	GLU
36	DP	29	LYS
48	D1	3	LYS
51	D4	39	CYS
51	D4	62	ARG
54	D7	46	VAL
10	AJ	31	GLY
10	AJ	56	HIS
10	AJ	77	PRO
11	AK	49	GLY
20	AT	47	GLY
20	AT	68	LYS
20	AT	96	GLY
48	B1	3	LYS
51	B4	45	GLY
51	B4	65	ASP
2	CB	17	PHE
2	CB	121	LEU
2	CB	128	GLU
4	CD	47	ARG
4	CD	167	GLY
7	CG	7	ALA
10	CJ	79	ARG
20	CT	47	GLY
31	DG	43	LEU
32	DH	47	GLU
33	DI	81	VAL
40	DT	100	TYR
51	D4	45	GLY
10	AJ	79	ARG
10	AJ	91	PRO
29	BE	52	LEU
31	BG	43	LEU
46	BZ	114	GLY
2	CB	122	PHE
10	CJ	77	PRO
10	CJ	78	ASN
19	CS	12	ASP
19	CS	65	ASN
20	CT	102	GLY
28	DD	239	ARG
29	DE	52	LEU

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Mol	Chain	Res	Type
29	DE	73	GLU
31	DG	32	PRO
46	DZ	101	PRO
5	AE	85	GLY
7	AG	6	ARG
7	AG	81	GLY
13	AM	67	GLU
20	AT	102	GLY
31	BG	32	PRO
35	BO	5	GLN
36	BP	29	LYS
51	B4	58	ARG
2	CB	10	LEU
2	CB	78	GLN
20	CT	95	ALA
28	DD	3	VAL
31	DG	51	ARG
32	DH	126	PRO
34	DN	2	LYS
35	DO	5	GLN
39	DS	84	GLN
51	D4	38	LYS
3	AC	181	ASN
20	AT	100	ILE
32	BH	47	GLU
33	BI	107	VAL
51	B4	57	GLU
2	CB	231	GLU
4	CD	46	LYS
5	CE	69	VAL
2	AB	78	GLN
13	AM	4	ILE
33	BI	73	GLU
8	CH	73	ASP
3	AC	66	VAL
10	AJ	75	ILE
42	BV	79	VAL
10	CJ	75	ILE
42	DV	79	VAL
33	BI	119	PRO
3	CC	108	ASN
10	CJ	91	PRO

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Mol	Chain	Res	Type
2	AB	124	SER
2	AB	125	PRO
11	CK	49	GLY
46	DZ	114	GLY

5.3.2 Protein sidechains (i)

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%)	156 (81%)	36 (19%)	1 5
2	CB	187/220 (85%)	158 (84%)	29 (16%)	2 9
3	AC	143/188 (76%)	125 (87%)	18 (13%)	4 15
3	CC	140/188 (74%)	122 (87%)	18 (13%)	4 14
4	AD	170/181 (94%)	153 (90%)	17 (10%)	7 24
4	CD	173/181 (96%)	154 (89%)	19 (11%)	6 20
5	AE	113/123 (92%)	105 (93%)	8 (7%)	13 39
5	CE	114/123 (93%)	106 (93%)	8 (7%)	14 40
6	AF	83/90 (92%)	76 (92%)	7 (8%)	10 32
6	CF	85/90 (94%)	77 (91%)	8 (9%)	8 27
7	AG	119/127 (94%)	103 (87%)	16 (13%)	4 13
7	CG	120/127 (94%)	107 (89%)	13 (11%)	6 21
8	AH	114/119 (96%)	107 (94%)	7 (6%)	17 46
8	CH	114/119 (96%)	101 (89%)	13 (11%)	5 19
9	AI	90/99 (91%)	73 (81%)	17 (19%)	1 5
9	CI	89/99 (90%)	76 (85%)	13 (15%)	3 11
10	AJ	66/92 (72%)	59 (89%)	7 (11%)	6 22
10	CJ	69/92 (75%)	62 (90%)	7 (10%)	7 23
11	AK	82/99 (83%)	76 (93%)	6 (7%)	13 38
11	CK	83/99 (84%)	80 (96%)	3 (4%)	31 66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
12	AL	97/109 (89%)	87 (90%)	10 (10%)	7 23
12	CL	97/109 (89%)	91 (94%)	6 (6%)	16 45
13	AM	93/101 (92%)	80 (86%)	13 (14%)	3 12
13	CM	92/101 (91%)	79 (86%)	13 (14%)	3 12
14	AN	49/50 (98%)	43 (88%)	6 (12%)	5 16
14	CN	49/50 (98%)	43 (88%)	6 (12%)	5 16
15	AO	78/80 (98%)	67 (86%)	11 (14%)	3 12
15	CO	78/80 (98%)	68 (87%)	10 (13%)	4 15
16	AP	69/74 (93%)	57 (83%)	12 (17%)	2 7
16	CP	68/74 (92%)	58 (85%)	10 (15%)	3 10
17	AQ	94/97 (97%)	90 (96%)	4 (4%)	26 60
17	CQ	94/97 (97%)	86 (92%)	8 (8%)	10 31
18	AR	59/77 (77%)	51 (86%)	8 (14%)	3 13
18	CR	59/77 (77%)	51 (86%)	8 (14%)	3 13
19	AS	69/80 (86%)	62 (90%)	7 (10%)	7 23
19	CS	67/80 (84%)	60 (90%)	7 (10%)	7 22
20	AT	70/82 (85%)	60 (86%)	10 (14%)	3 11
20	CT	70/82 (85%)	60 (86%)	10 (14%)	3 11
21	AU	18/22 (82%)	15 (83%)	3 (17%)	2 8
21	CU	18/22 (82%)	16 (89%)	2 (11%)	6 20
28	BD	215/218 (99%)	200 (93%)	15 (7%)	14 40
28	DD	215/218 (99%)	194 (90%)	21 (10%)	7 25
29	BE	164/166 (99%)	140 (85%)	24 (15%)	3 11
29	DE	164/166 (99%)	140 (85%)	24 (15%)	3 11
30	BF	160/166 (96%)	140 (88%)	20 (12%)	4 15
30	DF	159/166 (96%)	143 (90%)	16 (10%)	7 23
31	BG	143/156 (92%)	127 (89%)	16 (11%)	6 19
31	DG	142/156 (91%)	121 (85%)	21 (15%)	3 10
32	BH	144/148 (97%)	133 (92%)	11 (8%)	12 36
32	DH	144/148 (97%)	132 (92%)	12 (8%)	10 32
33	BI	110/124 (89%)	90 (82%)	20 (18%)	2 6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
33	DI	104/124 (84%)	88 (85%)	16 (15%)	2 10
34	BN	118/119 (99%)	98 (83%)	20 (17%)	2 7
34	DN	118/119 (99%)	104 (88%)	14 (12%)	5 17
35	BO	100/100 (100%)	92 (92%)	8 (8%)	11 34
35	DO	100/100 (100%)	95 (95%)	5 (5%)	22 54
36	BP	115/116 (99%)	102 (89%)	13 (11%)	5 19
36	DP	115/116 (99%)	99 (86%)	16 (14%)	3 12
37	BQ	111/111 (100%)	101 (91%)	10 (9%)	9 28
37	DQ	111/111 (100%)	101 (91%)	10 (9%)	9 28
38	BR	101/101 (100%)	82 (81%)	19 (19%)	1 5
38	DR	101/101 (100%)	83 (82%)	18 (18%)	2 6
39	BS	87/88 (99%)	75 (86%)	12 (14%)	3 12
39	DS	85/88 (97%)	70 (82%)	15 (18%)	2 7
40	BT	115/127 (91%)	104 (90%)	11 (10%)	8 26
40	DT	113/127 (89%)	101 (89%)	12 (11%)	6 22
41	BU	93/94 (99%)	84 (90%)	9 (10%)	8 25
41	DU	93/94 (99%)	87 (94%)	6 (6%)	15 43
42	BV	80/82 (98%)	65 (81%)	15 (19%)	1 5
42	DV	80/82 (98%)	67 (84%)	13 (16%)	2 8
43	BW	90/92 (98%)	81 (90%)	9 (10%)	7 24
43	DW	90/92 (98%)	81 (90%)	9 (10%)	7 24
44	BX	77/78 (99%)	72 (94%)	5 (6%)	15 43
44	DX	77/78 (99%)	69 (90%)	8 (10%)	7 22
45	BY	85/91 (93%)	74 (87%)	11 (13%)	4 14
45	DY	85/91 (93%)	79 (93%)	6 (7%)	13 39
46	BZ	145/179 (81%)	128 (88%)	17 (12%)	5 18
46	DZ	145/179 (81%)	122 (84%)	23 (16%)	2 9
47	B0	65/67 (97%)	59 (91%)	6 (9%)	8 27
47	D0	65/67 (97%)	59 (91%)	6 (9%)	8 27
48	B1	80/83 (96%)	73 (91%)	7 (9%)	9 29
48	D1	80/83 (96%)	73 (91%)	7 (9%)	9 29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
49	B2	65/67 (97%)	57 (88%)	8 (12%)	4 16
49	D2	65/67 (97%)	59 (91%)	6 (9%)	8 27
50	B3	51/52 (98%)	44 (86%)	7 (14%)	3 13
50	D3	50/52 (96%)	45 (90%)	5 (10%)	7 24
51	B4	59/63 (94%)	46 (78%)	13 (22%)	1 3
51	D4	53/63 (84%)	46 (87%)	7 (13%)	4 14
52	B5	50/52 (96%)	47 (94%)	3 (6%)	17 47
52	D5	50/52 (96%)	47 (94%)	3 (6%)	17 47
53	B6	51/52 (98%)	44 (86%)	7 (14%)	3 13
53	D6	50/52 (96%)	47 (94%)	3 (6%)	17 47
54	B7	41/42 (98%)	39 (95%)	2 (5%)	22 55
54	D7	41/42 (98%)	39 (95%)	2 (5%)	22 55
55	B8	53/55 (96%)	48 (91%)	5 (9%)	8 27
55	D8	54/55 (98%)	50 (93%)	4 (7%)	13 37
56	B9	34/34 (100%)	31 (91%)	3 (9%)	9 29
56	D9	34/34 (100%)	33 (97%)	1 (3%)	37 73
All	All	9319/10066 (93%)	8250 (88%)	1069 (12%)	5 18

All (1069) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	7	VAL
2	AB	8	LYS
2	AB	10	LEU
2	AB	11	LEU
2	AB	15	VAL
2	AB	17	PHE
2	AB	20	GLU
2	AB	21	ARG
2	AB	39	ILE
2	AB	50	GLU
2	AB	67	THR
2	AB	80	ILE
2	AB	81	VAL
2	AB	90	MET
2	AB	96	ARG

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Mol	Chain	Res	Type
2	AB	108	ILE
2	AB	114	ARG
2	AB	124	SER
2	AB	127	ILE
2	AB	142	LEU
2	AB	145	LEU
2	AB	155	LEU
2	AB	156	LYS
2	AB	157	ARG
2	AB	169	LYS
2	AB	170	GLU
2	AB	185	ILE
2	AB	187	LEU
2	AB	189	ASP
2	AB	200	ILE
2	AB	205	ASP
2	AB	213	LEU
2	AB	221	LEU
2	AB	223	ILE
2	AB	224	GLN
2	AB	233	SER
3	AC	3	ASN
3	AC	15	THR
3	AC	17	ASP
3	AC	27	LYS
3	AC	28	GLN
3	AC	44	GLU
3	AC	47	LEU
3	AC	54	ARG
3	AC	104	GLN
3	AC	115	LEU
3	AC	118	GLN
3	AC	131	ARG
3	AC	138	VAL
3	AC	150	LYS
3	AC	196	LEU
3	AC	198	VAL
3	AC	204	LEU
3	AC	207	VAL
4	AD	5	ILE
4	AD	31	CYS
4	AD	49	ARG

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Mol	Chain	Res	Type
4	AD	58	LEU
4	AD	85	LYS
4	AD	86	LYS
4	AD	91	SER
4	AD	108	LEU
4	AD	118	ARG
4	AD	127	THR
4	AD	135	LEU
4	AD	150	GLU
4	AD	157	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	170	VAL
4	AD	182	LYS
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	57	LYS
5	AE	67	VAL
5	AE	71	LEU
5	AE	91	LEU
5	AE	120	THR
6	AF	17	SER
6	AF	40	VAL
6	AF	69	GLU
6	AF	70	ASP
6	AF	75	LEU
6	AF	81	ILE
6	AF	82	ARG
7	AG	8	GLU
7	AG	9	VAL
7	AG	10	ARG
7	AG	13	GLN
7	AG	27	ILE
7	AG	32	ARG
7	AG	52	GLU
7	AG	53	LYS
7	AG	75	VAL
7	AG	76	ARG
7	AG	79	ARG
7	AG	104	LEU
7	AG	113	GLU

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Mol	Chain	Res	Type
7	AG	114	ARG
7	AG	137	LYS
7	AG	138	LYS
8	AH	26	VAL
8	AH	91	ARG
8	AH	112	LEU
8	AH	115	SER
8	AH	127	LEU
8	AH	133	LEU
8	AH	137	VAL
9	AI	3	GLN
9	AI	11	LYS
9	AI	17	VAL
9	AI	23	ASN
9	AI	42	ARG
9	AI	50	LEU
9	AI	53	VAL
9	AI	63	ILE
9	AI	64	THR
9	AI	81	ILE
9	AI	89	ASN
9	AI	92	TYR
9	AI	103	THR
9	AI	105	ASP
9	AI	108	VAL
9	AI	127	LYS
9	AI	128	ARG
10	AJ	5	ARG
10	AJ	7	LYS
10	AJ	38	ILE
10	AJ	49	VAL
10	AJ	67	THR
10	AJ	81	THR
10	AJ	98	ILE
11	AK	14	VAL
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	96	ARG
11	AK	104	GLN
12	AL	33	ARG
12	AL	40	VAL

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Mol	Chain	Res	Type
12	AL	52	LEU
12	AL	53	ARG
12	AL	57	LYS
12	AL	60	LEU
12	AL	70	ILE
12	AL	83	VAL
12	AL	84	LEU
12	AL	116	SER
13	AM	3	ARG
13	AM	4	ILE
13	AM	19	LEU
13	AM	43	THR
13	AM	47	ASP
13	AM	49	THR
13	AM	70	LEU
13	AM	73	GLU
13	AM	78	ILE
13	AM	84	ILE
13	AM	98	VAL
13	AM	102	ARG
13	AM	110	ARG
14	AN	3	ARG
14	AN	7	ILE
14	AN	18	VAL
14	AN	22	THR
14	AN	23	ARG
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	24	SER
15	AO	26	GLU
15	AO	39	LEU
15	AO	41	GLU
15	AO	47	LYS
15	AO	64	ARG
15	AO	66	LEU
15	AO	71	GLN
15	AO	83	GLU
16	AP	2	VAL
16	AP	11	SER
16	AP	12	LYS
16	AP	19	ILE

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Mol	Chain	Res	Type
16	AP	21	VAL
16	AP	27	LYS
16	AP	33	ILE
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	67	THR
16	AP	69	THR
17	AQ	6	LEU
17	AQ	9	VAL
17	AQ	24	GLU
17	AQ	74	LEU
18	AR	28	GLU
18	AR	31	LEU
18	AR	32	ARG
18	AR	35	ARG
18	AR	37	VAL
18	AR	38	GLU
18	AR	58	LEU
18	AR	76	LEU
19	AS	9	VAL
19	AS	12	ASP
19	AS	28	LYS
19	AS	37	ARG
19	AS	41	VAL
19	AS	65	ASN
19	AS	66	MET
20	AT	9	ASN
20	AT	10	LEU
20	AT	24	LEU
20	AT	45	GLN
20	AT	51	GLU
20	AT	54	LYS
20	AT	62	LEU
20	AT	71	THR
20	AT	74	LYS
20	AT	90	GLN
21	AU	7	ARG
21	AU	9	ARG
21	AU	10	ARG
28	BD	61	LEU
28	BD	94	LEU

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Mol	Chain	Res	Type
28	BD	99	ASP
28	BD	103	ARG
28	BD	113	VAL
28	BD	126	GLN
28	BD	138	VAL
28	BD	142	VAL
28	BD	193	VAL
28	BD	211	ARG
28	BD	221	VAL
28	BD	229	VAL
28	BD	257	LEU
28	BD	260	ARG
28	BD	275	LYS
29	BE	7	VAL
29	BE	9	VAL
29	BE	12	THR
29	BE	21	VAL
29	BE	24	THR
29	BE	33	VAL
29	BE	34	VAL
29	BE	45	THR
29	BE	47	VAL
29	BE	49	LEU
29	BE	73	GLU
29	BE	75	VAL
29	BE	77	ILE
29	BE	78	LEU
29	BE	82	ARG
29	BE	111	ARG
29	BE	116	VAL
29	BE	119	ARG
29	BE	144	ARG
29	BE	154	LYS
29	BE	163	GLU
29	BE	175	VAL
29	BE	178	GLU
29	BE	181	LEU
30	BF	19	GLU
30	BF	20	LEU
30	BF	24	LEU
30	BF	33	LEU
30	BF	38	ARG

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Mol	Chain	Res	Type
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	170	LEU
30	BF	183	VAL
30	BF	192	LEU
30	BF	197	ASP
30	BF	201	VAL
31	BG	3	LEU
31	BG	5	VAL
31	BG	7	LEU
31	BG	21	ARG
31	BG	43	LEU
31	BG	45	GLU
31	BG	60	LEU
31	BG	70	VAL
31	BG	81	LYS
31	BG	82	LEU
31	BG	128	ARG
31	BG	133	LEU
31	BG	136	ARG
31	BG	140	ILE
31	BG	143	GLU
31	BG	148	MET
32	BH	2	SER
32	BH	6	ARG
32	BH	15	VAL
32	BH	41	MET
32	BH	49	VAL
32	BH	69	ARG
32	BH	71	LEU
32	BH	84	SER
32	BH	95	ARG
32	BH	98	LEU
32	BH	101	ARG

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Mol	Chain	Res	Type
33	BI	5	LEU
33	BI	9	LEU
33	BI	10	GLU
33	BI	12	LEU
33	BI	20	ASP
33	BI	38	LEU
33	BI	40	THR
33	BI	43	ASN
33	BI	47	LEU
33	BI	48	GLU
33	BI	50	ARG
33	BI	57	ARG
33	BI	61	ARG
33	BI	66	GLU
33	BI	92	VAL
33	BI	96	ASP
33	BI	101	LEU
33	BI	109	ILE
33	BI	140	LEU
33	BI	142	VAL
34	BN	1	MET
34	BN	10	GLU
34	BN	28	THR
34	BN	33	LEU
34	BN	34	LEU
34	BN	46	VAL
34	BN	48	MET
34	BN	61	ARG
34	BN	62	VAL
34	BN	67	LEU
34	BN	68	GLU
34	BN	83	LYS
34	BN	85	ILE
34	BN	87	LEU
34	BN	97	ARG
34	BN	99	LEU
34	BN	104	LYS
34	BN	120	LEU
34	BN	133	GLN
34	BN	138	LEU
35	BO	8	LEU
35	BO	10	VAL

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Mol	Chain	Res	Type
35	BO	23	ARG
35	BO	24	VAL
35	BO	92	GLU
35	BO	94	ARG
35	BO	97	ARG
35	BO	98	VAL
36	BP	42	SER
36	BP	55	ARG
36	BP	65	ARG
36	BP	68	GLN
36	BP	70	GLN
36	BP	76	LYS
36	BP	95	VAL
36	BP	106	LEU
36	BP	112	LEU
36	BP	119	GLU
36	BP	125	VAL
36	BP	148	LEU
36	BP	149	GLU
37	BQ	21	THR
37	BQ	35	VAL
37	BQ	45	GLN
37	BQ	55	VAL
37	BQ	56	ARG
37	BQ	59	ARG
37	BQ	60	ARG
37	BQ	75	THR
37	BQ	109	VAL
37	BQ	110	THR
38	BR	1	MET
38	BR	6	SER
38	BR	15	SER
38	BR	18	LEU
38	BR	24	GLN
38	BR	28	LEU
38	BR	29	LEU
38	BR	30	THR
38	BR	33	ARG
38	BR	36	THR
38	BR	44	LEU
38	BR	54	LEU
38	BR	60	LEU

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Mol	Chain	Res	Type
38	BR	65	LEU
38	BR	67	LEU
38	BR	75	LEU
38	BR	79	LEU
38	BR	100	LEU
38	BR	111	LEU
39	BS	14	VAL
39	BS	20	ARG
39	BS	33	LYS
39	BS	48	LEU
39	BS	49	VAL
39	BS	52	SER
39	BS	57	LYS
39	BS	59	LYS
39	BS	61	ASN
39	BS	78	LEU
39	BS	83	LYS
39	BS	110	LEU
40	BT	6	LEU
40	BT	16	ARG
40	BT	23	ARG
40	BT	28	VAL
40	BT	49	VAL
40	BT	64	ARG
40	BT	65	LYS
40	BT	89	VAL
40	BT	96	ARG
40	BT	113	LYS
40	BT	118	ARG
41	BU	5	LYS
41	BU	8	VAL
41	BU	36	ARG
41	BU	74	LEU
41	BU	83	LEU
41	BU	92	ARG
41	BU	93	LYS
41	BU	95	LEU
41	BU	104	GLN
42	BV	6	LYS
42	BV	18	LEU
42	BV	21	ARG
42	BV	28	GLU

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Mol	Chain	Res	Type
42	BV	43	GLU
42	BV	46	VAL
42	BV	51	VAL
42	BV	52	VAL
42	BV	61	VAL
42	BV	72	VAL
42	BV	73	SER
42	BV	78	LYS
42	BV	79	VAL
42	BV	95	LEU
42	BV	100	ARG
43	BW	4	LYS
43	BW	11	ARG
43	BW	17	VAL
43	BW	19	LEU
43	BW	23	LEU
43	BW	51	LEU
43	BW	60	ASN
43	BW	100	THR
43	BW	107	LEU
44	BX	57	LEU
44	BX	65	ARG
44	BX	72	LYS
44	BX	76	ARG
44	BX	88	LYS
45	BY	1	MET
45	BY	7	VAL
45	BY	11	ASP
45	BY	19	LYS
45	BY	23	ARG
45	BY	31	LEU
45	BY	61	ILE
45	BY	72	VAL
45	BY	85	VAL
45	BY	90	LEU
45	BY	91	GLU
46	BZ	5	LEU
46	BZ	6	LYS
46	BZ	19	ARG
46	BZ	58	VAL
46	BZ	61	LEU
46	BZ	72	ARG

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Mol	Chain	Res	Type
46	BZ	76	LEU
46	BZ	91	LEU
46	BZ	96	VAL
46	BZ	107	THR
46	BZ	120	ILE
46	BZ	136	PHE
46	BZ	142	SER
46	BZ	144	LEU
46	BZ	154	ASP
46	BZ	155	LEU
46	BZ	162	GLU
47	B0	7	LEU
47	B0	20	ARG
47	B0	30	VAL
47	B0	49	LYS
47	B0	55	ARG
47	B0	67	VAL
48	B1	21	ARG
48	B1	35	THR
48	B1	40	ARG
48	B1	75	GLU
48	B1	78	LYS
48	B1	89	GLU
48	B1	95	LEU
49	B2	3	LEU
49	B2	28	LYS
49	B2	30	ARG
49	B2	32	LEU
49	B2	52	ASP
49	B2	55	ARG
49	B2	64	LEU
49	B2	70	GLN
50	B3	8	LEU
50	B3	23	LEU
50	B3	31	LEU
50	B3	32	GLN
50	B3	40	THR
50	B3	54	VAL
50	B3	60	GLU
51	B4	3	GLU
51	B4	28	LYS
51	B4	34	GLU

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Mol	Chain	Res	Type
51	B4	46	GLN
51	B4	49	PHE
51	B4	50	VAL
51	B4	56	VAL
51	B4	59	PHE
51	B4	60	GLN
51	B4	61	ARG
51	B4	67	TYR
51	B4	68	ARG
51	B4	69	LYS
52	B5	6	VAL
52	B5	29	THR
52	B5	40	LYS
53	B6	4	GLU
53	B6	6	ARG
53	B6	14	THR
53	B6	28	ARG
53	B6	38	LYS
53	B6	48	VAL
53	B6	52	VAL
54	B7	1	MET
54	B7	24	THR
55	B8	13	ARG
55	B8	14	VAL
55	B8	23	VAL
55	B8	32	LEU
55	B8	41	ILE
56	B9	4	ARG
56	B9	22	ARG
56	B9	27	CYS
2	CB	7	VAL
2	CB	10	LEU
2	CB	17	PHE
2	CB	35	GLU
2	CB	50	GLU
2	CB	63	MET
2	CB	80	ILE
2	CB	81	VAL
2	CB	82	ARG
2	CB	90	MET
2	CB	96	ARG
2	CB	98	LEU

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Mol	Chain	Res	Type
2	CB	115	LEU
2	CB	117	GLU
2	CB	119	GLU
2	CB	128	GLU
2	CB	142	LEU
2	CB	154	LEU
2	CB	155	LEU
2	CB	185	ILE
2	CB	187	LEU
2	CB	189	ASP
2	CB	200	ILE
2	CB	213	LEU
2	CB	217	ARG
2	CB	221	LEU
2	CB	222	ILE
2	CB	230	VAL
2	CB	233	SER
3	CC	3	ASN
3	CC	15	THR
3	CC	20	SER
3	CC	21	ARG
3	CC	28	GLN
3	CC	32	LEU
3	CC	47	LEU
3	CC	52	LEU
3	CC	105	GLU
3	CC	115	LEU
3	CC	118	GLN
3	CC	125	GLU
3	CC	126	ARG
3	CC	131	ARG
3	CC	138	VAL
3	CC	152	ILE
3	CC	198	VAL
3	CC	207	VAL
4	CD	5	ILE
4	CD	13	ARG
4	CD	31	CYS
4	CD	34	GLU
4	CD	47	ARG
4	CD	58	LEU
4	CD	74	GLN

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Mol	Chain	Res	Type
4	CD	85	LYS
4	CD	96	LEU
4	CD	108	LEU
4	CD	115	ARG
4	CD	135	LEU
4	CD	138	TYR
4	CD	155	LEU
4	CD	157	LEU
4	CD	158	ILE
4	CD	169	LYS
4	CD	170	VAL
4	CD	194	LEU
5	CE	12	LEU
5	CE	24	ARG
5	CE	41	VAL
5	CE	47	LYS
5	CE	63	ARG
5	CE	67	VAL
5	CE	91	LEU
5	CE	120	THR
6	CF	10	LEU
6	CF	28	ARG
6	CF	40	VAL
6	CF	41	GLU
6	CF	72	VAL
6	CF	75	LEU
6	CF	81	ILE
6	CF	94	GLN
7	CG	9	VAL
7	CG	13	GLN
7	CG	27	ILE
7	CG	32	ARG
7	CG	33	ASP
7	CG	51	GLN
7	CG	73	MET
7	CG	75	VAL
7	CG	76	ARG
7	CG	104	LEU
7	CG	113	GLU
7	CG	144	MET
7	CG	155	ARG
8	CH	21	LYS

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Mol	Chain	Res	Type
8	CH	26	VAL
8	CH	38	ILE
8	CH	78	GLN
8	CH	84	ARG
8	CH	91	ARG
8	CH	99	GLU
8	CH	109	ILE
8	CH	112	LEU
8	CH	115	SER
8	CH	133	LEU
8	CH	135	CYS
8	CH	137	VAL
9	CI	3	GLN
9	CI	7	THR
9	CI	14	VAL
9	CI	17	VAL
9	CI	23	ASN
9	CI	53	VAL
9	CI	56	LEU
9	CI	64	THR
9	CI	81	ILE
9	CI	86	VAL
9	CI	102	LEU
9	CI	108	VAL
9	CI	128	ARG
10	CJ	6	ILE
10	CJ	29	ARG
10	CJ	59	SER
10	CJ	67	THR
10	CJ	81	THR
10	CJ	98	ILE
10	CJ	100	THR
11	CK	14	VAL
11	CK	96	ARG
11	CK	114	VAL
12	CL	33	ARG
12	CL	34	ARG
12	CL	40	VAL
12	CL	83	VAL
12	CL	84	LEU
12	CL	124	LYS
13	CM	4	ILE

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Mol	Chain	Res	Type
13	CM	15	VAL
13	CM	19	LEU
13	CM	25	ILE
13	CM	27	LYS
13	CM	49	THR
13	CM	56	LEU
13	CM	70	LEU
13	CM	78	ILE
13	CM	84	ILE
13	CM	98	VAL
13	CM	110	ARG
13	CM	121	LYS
14	CN	3	ARG
14	CN	12	ARG
14	CN	18	VAL
14	CN	22	THR
14	CN	23	ARG
14	CN	33	VAL
15	CO	3	ILE
15	CO	5	LYS
15	CO	10	LYS
15	CO	24	SER
15	CO	26	GLU
15	CO	38	ARG
15	CO	39	LEU
15	CO	41	GLU
15	CO	83	GLU
15	CO	87	ILE
16	CP	2	VAL
16	CP	11	SER
16	CP	20	VAL
16	CP	21	VAL
16	CP	28	ARG
16	CP	32	TYR
16	CP	33	ILE
16	CP	60	LEU
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	14	LYS
17	CQ	36	ILE
17	CQ	49	GLU

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Mol	Chain	Res	Type
17	CQ	60	ILE
17	CQ	74	LEU
17	CQ	96	GLU
17	CQ	99	SER
18	CR	25	THR
18	CR	26	LEU
18	CR	32	ARG
18	CR	35	ARG
18	CR	41	LYS
18	CR	58	LEU
18	CR	69	THR
18	CR	76	LEU
19	CS	22	LEU
19	CS	28	LYS
19	CS	41	VAL
19	CS	56	GLN
19	CS	65	ASN
19	CS	66	MET
19	CS	77	THR
20	CT	10	LEU
20	CT	24	LEU
20	CT	36	LEU
20	CT	41	ILE
20	CT	45	GLN
20	CT	51	GLU
20	CT	56	MET
20	CT	71	THR
20	CT	80	ARG
20	CT	90	GLN
21	CU	7	ARG
21	CU	10	ARG
28	DD	3	VAL
28	DD	13	ARG
28	DD	61	LEU
28	DD	94	LEU
28	DD	99	ASP
28	DD	103	ARG
28	DD	106	ILE
28	DD	113	VAL
28	DD	126	GLN
28	DD	134	ARG
28	DD	138	VAL

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Mol	Chain	Res	Type
28	DD	142	VAL
28	DD	169	GLU
28	DD	193	VAL
28	DD	211	ARG
28	DD	221	VAL
28	DD	229	VAL
28	DD	242	ARG
28	DD	257	LEU
28	DD	260	ARG
28	DD	276	LYS
29	DE	7	VAL
29	DE	9	VAL
29	DE	21	VAL
29	DE	24	THR
29	DE	33	VAL
29	DE	34	VAL
29	DE	45	THR
29	DE	52	LEU
29	DE	72	VAL
29	DE	73	GLU
29	DE	75	VAL
29	DE	78	LEU
29	DE	82	ARG
29	DE	104	VAL
29	DE	111	ARG
29	DE	116	VAL
29	DE	119	ARG
29	DE	134	ILE
29	DE	144	ARG
29	DE	154	LYS
29	DE	163	GLU
29	DE	175	VAL
29	DE	178	GLU
29	DE	181	LEU
30	DF	20	LEU
30	DF	24	LEU
30	DF	33	LEU
30	DF	57	VAL
30	DF	74	ARG
30	DF	88	VAL
30	DF	106	ARG
30	DF	110	LEU

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Mol	Chain	Res	Type
30	DF	132	VAL
30	DF	135	LYS
30	DF	140	LEU
30	DF	162	LEU
30	DF	170	LEU
30	DF	183	VAL
30	DF	192	LEU
30	DF	201	VAL
31	DG	3	LEU
31	DG	5	VAL
31	DG	7	LEU
31	DG	9	ARG
31	DG	16	ARG
31	DG	35	GLU
31	DG	36	LYS
31	DG	43	LEU
31	DG	45	GLU
31	DG	47	LYS
31	DG	60	LEU
31	DG	70	VAL
31	DG	98	ARG
31	DG	128	ARG
31	DG	133	LEU
31	DG	136	ARG
31	DG	140	ILE
31	DG	143	GLU
31	DG	148	MET
31	DG	164	GLU
31	DG	170	ARG
32	DH	2	SER
32	DH	3	ARG
32	DH	15	VAL
32	DH	33	LEU
32	DH	34	GLU
32	DH	43	VAL
32	DH	49	VAL
32	DH	69	ARG
32	DH	76	VAL
32	DH	81	GLU
32	DH	95	ARG
32	DH	171	LEU
33	DI	5	LEU

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Mol	Chain	Res	Type
33	DI	9	LEU
33	DI	12	LEU
33	DI	20	ASP
33	DI	40	THR
33	DI	43	ASN
33	DI	44	LEU
33	DI	50	ARG
33	DI	52	ARG
33	DI	68	LEU
33	DI	75	LEU
33	DI	77	LEU
33	DI	87	LYS
33	DI	92	VAL
33	DI	93	THR
33	DI	101	LEU
34	DN	1	MET
34	DN	28	THR
34	DN	33	LEU
34	DN	34	LEU
34	DN	46	VAL
34	DN	48	MET
34	DN	62	VAL
34	DN	67	LEU
34	DN	85	ILE
34	DN	87	LEU
34	DN	97	ARG
34	DN	99	LEU
34	DN	120	LEU
34	DN	138	LEU
35	DO	8	LEU
35	DO	10	VAL
35	DO	23	ARG
35	DO	69	ILE
35	DO	98	VAL
36	DP	1	MET
36	DP	3	LEU
36	DP	45	LEU
36	DP	55	ARG
36	DP	59	LEU
36	DP	65	ARG
36	DP	68	GLN
36	DP	70	GLN

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Mol	Chain	Res	Type
36	DP	83	VAL
36	DP	95	VAL
36	DP	99	LEU
36	DP	106	LEU
36	DP	112	LEU
36	DP	119	GLU
36	DP	125	VAL
36	DP	148	LEU
37	DQ	1	MET
37	DQ	21	THR
37	DQ	45	GLN
37	DQ	54	MET
37	DQ	55	VAL
37	DQ	56	ARG
37	DQ	60	ARG
37	DQ	75	THR
37	DQ	109	VAL
37	DQ	131	ILE
38	DR	1	MET
38	DR	6	SER
38	DR	15	SER
38	DR	24	GLN
38	DR	28	LEU
38	DR	29	LEU
38	DR	30	THR
38	DR	36	THR
38	DR	44	LEU
38	DR	54	LEU
38	DR	60	LEU
38	DR	63	ARG
38	DR	65	LEU
38	DR	67	LEU
38	DR	75	LEU
38	DR	79	LEU
38	DR	100	LEU
38	DR	111	LEU
39	DS	14	VAL
39	DS	33	LYS
39	DS	35	ILE
39	DS	36	TYR
39	DS	44	LYS
39	DS	48	LEU

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Mol	Chain	Res	Type
39	DS	52	SER
39	DS	57	LYS
39	DS	67	ARG
39	DS	68	GLN
39	DS	69	VAL
39	DS	71	ARG
39	DS	75	GLU
39	DS	80	LEU
39	DS	110	LEU
40	DT	6	LEU
40	DT	16	ARG
40	DT	17	THR
40	DT	23	ARG
40	DT	28	VAL
40	DT	49	VAL
40	DT	64	ARG
40	DT	89	VAL
40	DT	96	ARG
40	DT	108	ARG
40	DT	113	LYS
40	DT	118	ARG
41	DU	36	ARG
41	DU	74	LEU
41	DU	89	GLU
41	DU	92	ARG
41	DU	93	LYS
41	DU	104	GLN
42	DV	6	LYS
42	DV	15	GLU
42	DV	21	ARG
42	DV	38	LEU
42	DV	46	VAL
42	DV	52	VAL
42	DV	57	VAL
42	DV	61	VAL
42	DV	62	LEU
42	DV	72	VAL
42	DV	73	SER
42	DV	78	LYS
42	DV	79	VAL
43	DW	4	LYS
43	DW	11	ARG

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Mol	Chain	Res	Type
43	DW	17	VAL
43	DW	19	LEU
43	DW	23	LEU
43	DW	51	LEU
43	DW	63	ASP
43	DW	100	THR
43	DW	107	LEU
44	DX	1	MET
44	DX	57	LEU
44	DX	72	LYS
44	DX	76	ARG
44	DX	81	VAL
44	DX	88	LYS
44	DX	90	GLU
44	DX	92	LEU
45	DY	7	VAL
45	DY	11	ASP
45	DY	19	LYS
45	DY	72	VAL
45	DY	85	VAL
45	DY	90	LEU
46	DZ	5	LEU
46	DZ	11	GLU
46	DZ	18	LEU
46	DZ	19	ARG
46	DZ	50	GLN
46	DZ	61	LEU
46	DZ	72	ARG
46	DZ	74	VAL
46	DZ	76	LEU
46	DZ	86	VAL
46	DZ	91	LEU
46	DZ	96	VAL
46	DZ	107	THR
46	DZ	119	GLU
46	DZ	120	ILE
46	DZ	136	PHE
46	DZ	144	LEU
46	DZ	154	ASP
46	DZ	155	LEU
46	DZ	156	LYS
46	DZ	162	GLU

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Mol	Chain	Res	Type
46	DZ	170	THR
46	DZ	174	VAL
47	D0	19	LYS
47	D0	20	ARG
47	D0	24	LYS
47	D0	30	VAL
47	D0	49	LYS
47	D0	67	VAL
48	D1	4	VAL
48	D1	21	ARG
48	D1	35	THR
48	D1	40	ARG
48	D1	59	THR
48	D1	78	LYS
48	D1	95	LEU
49	D2	28	LYS
49	D2	30	ARG
49	D2	32	LEU
49	D2	45	SER
49	D2	55	ARG
49	D2	70	GLN
50	D3	8	LEU
50	D3	23	LEU
50	D3	31	LEU
50	D3	40	THR
50	D3	54	VAL
51	D4	3	GLU
51	D4	34	GLU
51	D4	50	VAL
51	D4	52	THR
51	D4	56	VAL
51	D4	68	ARG
51	D4	69	LYS
52	D5	6	VAL
52	D5	29	THR
52	D5	40	LYS
53	D6	30	THR
53	D6	38	LYS
53	D6	48	VAL
54	D7	1	MET
54	D7	14	LYS
55	D8	14	VAL

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Mol	Chain	Res	Type
55	D8	26	LYS
55	D8	32	LEU
55	D8	41	ILE
56	D9	4	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (176) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	94	ASN
3	AC	6	HIS
3	AC	37	GLN
3	AC	102	ASN
3	AC	104	GLN
3	AC	123	GLN
3	AC	136	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	45	GLN
4	AD	77	ASN
4	AD	123	HIS
4	AD	129	ASN
4	AD	161	ASN
4	AD	199	ASN
4	AD	201	GLN
5	AE	20	GLN
5	AE	38	GLN
5	AE	65	ASN
6	AF	94	GLN
6	AF	100	ASN
7	AG	13	GLN
7	AG	28	ASN
8	AH	78	GLN
9	AI	23	ASN
9	AI	31	GLN
9	AI	73	GLN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	93	GLN
11	AK	99	GLN
11	AK	104	GLN
12	AL	78	GLN
15	AO	28	GLN

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Mol	Chain	Res	Type
15	AO	50	HIS
15	AO	62	GLN
17	AQ	94	ASN
19	AS	56	GLN
19	AS	57	HIS
19	AS	65	ASN
19	AS	83	HIS
20	AT	9	ASN
20	AT	45	GLN
20	AT	73	HIS
20	AT	90	GLN
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
31	BG	132	ASN
33	BI	43	ASN
33	BI	54	GLN
33	BI	105	HIS
34	BN	69	GLN
36	BP	38	GLN
36	BP	70	GLN
37	BQ	45	GLN
37	BQ	57	HIS
37	BQ	141	GLN
38	BR	50	HIS
38	BR	71	GLN
39	BS	68	GLN
39	BS	95	HIS
40	BT	43	GLN
40	BT	123	GLN
41	BU	81	HIS
41	BU	94	ASN
41	BU	117	GLN
43	BW	40	ASN
43	BW	60	ASN
44	BX	31	HIS
44	BX	82	GLN

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Mol	Chain	Res	Type
45	BY	6	HIS
45	BY	43	ASN
46	BZ	73	GLN
46	BZ	132	ASN
49	B2	48	HIS
49	B2	70	GLN
51	B4	46	GLN
52	B5	23	HIS
53	B6	20	ASN
56	B9	36	GLN
2	CB	16	HIS
2	CB	19	HIS
2	CB	40	HIS
2	CB	146	GLN
2	CB	212	GLN
2	CB	224	GLN
3	CC	6	HIS
3	CC	28	GLN
3	CC	102	ASN
3	CC	118	GLN
3	CC	123	GLN
3	CC	181	ASN
4	CD	45	GLN
4	CD	77	ASN
4	CD	123	HIS
4	CD	129	ASN
4	CD	160	GLN
5	CE	141	GLN
6	CF	64	GLN
6	CF	100	ASN
7	CG	28	ASN
7	CG	51	GLN
7	CG	56	GLN
7	CG	86	GLN
7	CG	109	ASN
9	CI	23	ASN
9	CI	58	HIS
9	CI	73	GLN
9	CI	124	GLN
10	CJ	13	HIS
10	CJ	21	GLN
10	CJ	62	HIS

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Mol	Chain	Res	Type
11	CK	22	HIS
11	CK	93	GLN
12	CL	78	GLN
15	CO	9	GLN
15	CO	28	GLN
15	CO	62	GLN
17	CQ	16	GLN
17	CQ	94	ASN
19	CS	23	ASN
19	CS	56	GLN
19	CS	65	ASN
19	CS	83	HIS
20	CT	16	HIS
20	CT	45	GLN
20	CT	73	HIS
20	CT	75	ASN
28	DD	164	GLN
28	DD	166	GLN
28	DD	253	GLN
29	DE	143	ASN
30	DF	69	HIS
30	DF	160	ASN
30	DF	169	ASN
30	DF	203	GLN
31	DG	40	ASN
31	DG	41	GLN
31	DG	79	ASN
32	DH	74	ASN
33	DI	43	ASN
33	DI	54	GLN
33	DI	133	HIS
34	DN	101	HIS
36	DP	38	GLN
36	DP	70	GLN
37	DQ	45	GLN
38	DR	13	HIS
38	DR	24	GLN
40	DT	43	GLN
40	DT	58	ASN
40	DT	79	HIS
41	DU	72	HIS
41	DU	94	ASN

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Mol	Chain	Res	Type
43	DW	60	ASN
43	DW	111	HIS
44	DX	31	HIS
44	DX	82	GLN
45	DY	43	ASN
46	DZ	55	HIS
46	DZ	132	ASN
46	DZ	151	HIS
47	D0	70	GLN
48	D1	19	GLN
49	D2	46	GLN
51	D4	60	GLN
52	D5	23	HIS
53	D6	20	ASN
54	D7	36	GLN
56	D9	36	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1521 (98%)	407 (27%)	26 (1%)
1	CA	1501/1521 (98%)	413 (27%)	28 (1%)
22	AV	12/24 (50%)	7 (58%)	0
22	CV	5/24 (20%)	4 (80%)	0
23	AW	1/3 (33%)	0	0
23	CW	1/3 (33%)	0	0
24	AX	74/77 (96%)	26 (35%)	2 (2%)
24	CX	74/77 (96%)	31 (41%)	4 (5%)
25	AY	4/76 (5%)	1 (25%)	0
25	CY	4/76 (5%)	1 (25%)	0
26	BA	2811/2915 (96%)	531 (18%)	30 (1%)
26	DA	2791/2915 (95%)	598 (21%)	30 (1%)
27	BB	120/121 (99%)	16 (13%)	2 (1%)
27	DB	119/121 (98%)	31 (26%)	0
All	All	9012/9474 (95%)	2066 (22%)	122 (1%)

All (2066) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	7	G

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Mol	Chain	Res	Type
1	AA	9	G
1	AA	15	G
1	AA	22	G
1	AA	29	G
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	50	A
1	AA	51	A
1	AA	55	A
1	AA	61	G
1	AA	68	G
1	AA	69	G
1	AA	73	G
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	96	U
1	AA	100	C
1	AA	101	A
1	AA	111	G
1	AA	112	G
1	AA	115	G
1	AA	116	A
1	AA	121	C
1	AA	129(A)	G
1	AA	131	C
1	AA	144	G
1	AA	146	G
1	AA	155	C
1	AA	163	C
1	AA	170	U
1	AA	171	A
1	AA	173	U
1	AA	174	C
1	AA	178	C
1	AA	180	U
1	AA	182	U
1	AA	189(A)	C
1	AA	189(B)	C
1	AA	189(D)	C

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Mol	Chain	Res	Type
1	AA	189(H)	G
1	AA	189(J)	G
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	221	C
1	AA	230	G
1	AA	247	G
1	AA	248	C
1	AA	251	G
1	AA	258	G
1	AA	259	G
1	AA	266	G
1	AA	267	C
1	AA	274	A
1	AA	280	C
1	AA	283	C
1	AA	289	G
1	AA	301	G
1	AA	318	G
1	AA	320	C
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	332	G
1	AA	343	U
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	374	A

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Mol	Chain	Res	Type
1	AA	383	A
1	AA	384	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	414	A
1	AA	421	U
1	AA	422	C
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	432	A
1	AA	439	A
1	AA	442	C
1	AA	445	G
1	AA	452	A
1	AA	457	C
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	484	G
1	AA	485	G
1	AA	495	A
1	AA	496	A
1	AA	498	U
1	AA	504	C
1	AA	505	G
1	AA	508	C
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	519	C
1	AA	521	G
1	AA	524	G
1	AA	527	G
1	AA	528	C
1	AA	531	U

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Mol	Chain	Res	Type
1	AA	532	A
1	AA	533	A
1	AA	544	G
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	562	C
1	AA	571	U
1	AA	572	A
1	AA	573	A
1	AA	575	G
1	AA	576	G
1	AA	577	G
1	AA	581	G
1	AA	592	G
1	AA	593	G
1	AA	596	C
1	AA	604	G
1	AA	606	G
1	AA	611	A
1	AA	615	C
1	AA	622	A
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	645	C
1	AA	646	U
1	AA	647	C
1	AA	648	A
1	AA	649	G
1	AA	653	A
1	AA	660	G
1	AA	665	A
1	AA	671	G
1	AA	673	G
1	AA	677	U
1	AA	680	C
1	AA	684	A
1	AA	687	A
1	AA	688	G
1	AA	693	G

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Mol	Chain	Res	Type
1	AA	701	C
1	AA	710	G
1	AA	711	G
1	AA	717	C
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	733	A
1	AA	748	C
1	AA	749	C
1	AA	752	G
1	AA	755	G
1	AA	759	A
1	AA	764	C
1	AA	766	A
1	AA	777	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	798	G
1	AA	802	A
1	AA	806	C
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	821	G
1	AA	828	A
1	AA	832	C
1	AA	833	U
1	AA	835	U
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	849	C
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	860	A
1	AA	868	C
1	AA	869	G
1	AA	874	G

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Mol	Chain	Res	Type
1	AA	885	G
1	AA	886	G
1	AA	902	G
1	AA	913	A
1	AA	914	A
1	AA	922	G
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	936	C
1	AA	938	A
1	AA	942	G
1	AA	945	G
1	AA	952	U
1	AA	954	G
1	AA	960	U
1	AA	961	U
1	AA	965	A
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	982	U
1	AA	983	A
1	AA	992	U
1	AA	993	G
1	AA	999	C
1	AA	1000	U
1	AA	1001(A)	G
1	AA	1002	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1011	G
1	AA	1017	G
1	AA	1019	C

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Mol	Chain	Res	Type
1	AA	1020	U
1	AA	1021	G
1	AA	1022	G
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1036	G
1	AA	1037	C
1	AA	1039	C
1	AA	1043	C
1	AA	1045	C
1	AA	1052	U
1	AA	1054	C
1	AA	1055	A
1	AA	1056	U
1	AA	1057	G
1	AA	1063	C
1	AA	1064	G
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1092	A
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1122	U
1	AA	1124	G
1	AA	1125	U
1	AA	1126	U
1	AA	1128	C
1	AA	1130	A

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Mol	Chain	Res	Type
1	AA	1132	C
1	AA	1134	G
1	AA	1135	U
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1145	C
1	AA	1146	A
1	AA	1152	A
1	AA	1157	A
1	AA	1158	C
1	AA	1159	U
1	AA	1160	G
1	AA	1164	G
1	AA	1165	C
1	AA	1169	A
1	AA	1174	G
1	AA	1176	A
1	AA	1181	G
1	AA	1183	A
1	AA	1184	G
1	AA	1185	G
1	AA	1196	U
1	AA	1197	G
1	AA	1199	U
1	AA	1200	C
1	AA	1202	G
1	AA	1204	A
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1218	C
1	AA	1227	A
1	AA	1228	C
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1244	C
1	AA	1256	A
1	AA	1257	U

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Mol	Chain	Res	Type
1	AA	1258	G
1	AA	1260	C
1	AA	1262	C
1	AA	1264	C
1	AA	1265	G
1	AA	1270	C
1	AA	1273	G
1	AA	1274	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1286	A
1	AA	1287	A
1	AA	1296	C
1	AA	1297	C
1	AA	1298	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1317	C
1	AA	1320	C
1	AA	1321	C
1	AA	1322	C
1	AA	1326	C
1	AA	1338	G
1	AA	1340	A
1	AA	1342	C
1	AA	1347	G
1	AA	1360	A
1	AA	1363	C
1	AA	1365	G
1	AA	1370	G
1	AA	1371	G
1	AA	1376	U
1	AA	1377	A
1	AA	1379	G
1	AA	1383	C
1	AA	1396	A
1	AA	1397	C
1	AA	1398	A
1	AA	1402	C
1	AA	1419	G

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Mol	Chain	Res	Type
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1457	G
1	AA	1458	G
1	AA	1472	U
1	AA	1475	G
1	AA	1487	G
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1507	A
1	AA	1517	G
1	AA	1520	G
1	AA	1525	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	13	A
22	AV	15	A
22	AV	18	G
22	AV	19	U
22	AV	20	U
22	AV	23	A
22	AV	24	A
24	AX	9	G
24	AX	13	C
24	AX	16	C
24	AX	17	C
24	AX	17(A)	U
24	AX	18	G
24	AX	19	G
24	AX	20	U

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Mol	Chain	Res	Type
24	AX	21	A
24	AX	25	C
24	AX	27	U
24	AX	31	G
24	AX	41	C
24	AX	45	G
24	AX	47	U
24	AX	48	C
24	AX	52	G
24	AX	56	C
24	AX	59	A
24	AX	61	C
24	AX	62	C
24	AX	66	C
24	AX	67	C
24	AX	68	C
24	AX	70	G
24	AX	72	A
25	AY	75	C
26	BA	7	G
26	BA	10	G
26	BA	12	U
26	BA	13	A
26	BA	27	G
26	BA	34	C
26	BA	45	C
26	BA	61	G
26	BA	71	A
26	BA	72	U
26	BA	74	A
26	BA	75	G
26	BA	84	A
26	BA	95	G
26	BA	102	G
26	BA	118	A
26	BA	119	A
26	BA	120	U
26	BA	122	G
26	BA	125	G
26	BA	140	G
26	BA	172	C
26	BA	177	G

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Mol	Chain	Res	Type
26	BA	182	A
26	BA	188	G
26	BA	196	A
26	BA	199	A
26	BA	205	G
26	BA	215	G
26	BA	216	A
26	BA	221	A
26	BA	222	A
26	BA	225	A
26	BA	229	A
26	BA	233	A
26	BA	243	U
26	BA	244	A
26	BA	248	G
26	BA	267	C
26	BA	271(I)	G
26	BA	271(K)	U
26	BA	271(L)	U
26	BA	271(M)	G
26	BA	271(N)	U
26	BA	271(S)	G
26	BA	272(A)	U
26	BA	272(B)	G
26	BA	272(G)	C
26	BA	272(H)	C
26	BA	279	C
26	BA	282	A
26	BA	311	A
26	BA	329	G
26	BA	330	A
26	BA	339	U
26	BA	345	A
26	BA	352	G
26	BA	356	G
26	BA	357	A
26	BA	359	A
26	BA	363	G
26	BA	380	U
26	BA	386	G
26	BA	396	G
26	BA	405	U

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Mol	Chain	Res	Type
26	BA	407	G
26	BA	411	G
26	BA	412	A
26	BA	421	U
26	BA	428	A
26	BA	436	C
26	BA	442	G
26	BA	443	A
26	BA	444	C
26	BA	448	U
26	BA	451	C
26	BA	454	A
26	BA	456	C
26	BA	457	A
26	BA	481	G
26	BA	494	G
26	BA	504	U
26	BA	505	A
26	BA	508	G
26	BA	509	C
26	BA	512	G
26	BA	528	A
26	BA	530	G
26	BA	531	C
26	BA	532	A
26	BA	533	G
26	BA	545	G
26	BA	549	G
26	BA	563	G
26	BA	568	U
26	BA	573	G
26	BA	574	C
26	BA	575	A
26	BA	593	G
26	BA	603	A
26	BA	604	G
26	BA	607	U
26	BA	610	G
26	BA	614(B)	G
26	BA	615	G
26	BA	619	G
26	BA	627	A

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Mol	Chain	Res	Type
26	BA	637	A
26	BA	645	C
26	BA	646	A
26	BA	647	G
26	BA	652(D)	C
26	BA	652(E)	G
26	BA	652(F)	G
26	BA	652(T)	C
26	BA	652(U)	G
26	BA	667	U
26	BA	669	G
26	BA	676	A
26	BA	677	A
26	BA	686	G
26	BA	714	U
26	BA	717	G
26	BA	726	G
26	BA	730	C
26	BA	764	A
26	BA	771	G
26	BA	775	G
26	BA	776	G
26	BA	782	A
26	BA	784	A
26	BA	785	G
26	BA	789	A
26	BA	792	G
26	BA	793	A
26	BA	805	G
26	BA	812	C
26	BA	819	A
26	BA	827	U
26	BA	828	U
26	BA	830	G
26	BA	859	G
26	BA	866	A
26	BA	875	G
26	BA	879	G
26	BA	880	G
26	BA	881	G
26	BA	884	C
26	BA	885	C

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Mol	Chain	Res	Type
26	BA	886	C
26	BA	887	A
26	BA	888	C
26	BA	889	C
26	BA	890	A
26	BA	892	G
26	BA	895	U
26	BA	896	A
26	BA	897	C
26	BA	907	U
26	BA	910	A
26	BA	914	C
26	BA	931	G
26	BA	932	G
26	BA	941	A
26	BA	945	A
26	BA	946	G
26	BA	953	A
26	BA	958	U
26	BA	959	A
26	BA	961	C
26	BA	974	G
26	BA	975	C
26	BA	975(A)	G
26	BA	983	A
26	BA	996	A
26	BA	1012	U
26	BA	1013	C
26	BA	1022	G
26	BA	1026	U
26	BA	1033	U
26	BA	1038	C
26	BA	1039	G
26	BA	1040	C
26	BA	1042	G
26	BA	1045	A
26	BA	1046	A
26	BA	1107	G
26	BA	1108	U
26	BA	1109	C
26	BA	1110	G
26	BA	1111	A

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Mol	Chain	Res	Type
26	BA	1112	G
26	BA	1128	A
26	BA	1129	A
26	BA	1130	U
26	BA	1135	C
26	BA	1136	G
26	BA	1139	G
26	BA	1141	U
26	BA	1149	G
26	BA	1155	A
26	BA	1171	G
26	BA	1173	G
26	BA	1174	A
26	BA	1175	U
26	BA	1176	G
26	BA	1177	A
26	BA	1178	C
26	BA	1210	A
26	BA	1211	U
26	BA	1218	C
26	BA	1220	A
26	BA	1244	G
26	BA	1250	G
26	BA	1253	A
26	BA	1256	G
26	BA	1271	G
26	BA	1272	A
26	BA	1273	U
26	BA	1300	U
26	BA	1301	A
26	BA	1303	G
26	BA	1308	A
26	BA	1314	C
26	BA	1319	G
26	BA	1320	C
26	BA	1321	A
26	BA	1335	U
26	BA	1352	U
26	BA	1359	A
26	BA	1365	A
26	BA	1369	G
26	BA	1370	C

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Mol	Chain	Res	Type
26	BA	1380	G
26	BA	1384	A
26	BA	1385	G
26	BA	1386	C
26	BA	1395	A
26	BA	1416	G
26	BA	1417	C
26	BA	1420	U
26	BA	1421	G
26	BA	1428	C
26	BA	1437	C
26	BA	1445	A
26	BA	1449	A
26	BA	1450	G
26	BA	1455	G
26	BA	1458	C
26	BA	1459	G
26	BA	1460	A
26	BA	1467	C
26	BA	1471	A
26	BA	1478	G
26	BA	1482	G
26	BA	1490	A
26	BA	1491	G
26	BA	1492	G
26	BA	1493	C
26	BA	1496	A
26	BA	1505	C
26	BA	1507	A
26	BA	1508	A
26	BA	1509	C
26	BA	1509(A)	A
26	BA	1513	C
26	BA	1525	G
26	BA	1531	C
26	BA	1532	C
26	BA	1541	G
26	BA	1543	C
26	BA	1547	C
26	BA	1554	A
26	BA	1555	G
26	BA	1558	A

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Mol	Chain	Res	Type
26	BA	1566	A
26	BA	1569	A
26	BA	1578	U
26	BA	1581	G
26	BA	1584	C
26	BA	1586	A
26	BA	1608	A
26	BA	1610	A
26	BA	1644	C
26	BA	1647	G
26	BA	1648	C
26	BA	1654	A
26	BA	1664	A
26	BA	1667	G
26	BA	1674	G
26	BA	1691	C
26	BA	1696	G
26	BA	1700	A
26	BA	1701	A
26	BA	1703	G
26	BA	1721	G
26	BA	1722	A
26	BA	1746	G
26	BA	1747(A)	G
26	BA	1748	G
26	BA	1756	G
26	BA	1762	A
26	BA	1763	G
26	BA	1764	G
26	BA	1773	A
26	BA	1777	U
26	BA	1779	U
26	BA	1780	A
26	BA	1782	C
26	BA	1786	A
26	BA	1791	A
26	BA	1800	C
26	BA	1801	G
26	BA	1816	G
26	BA	1827	C
26	BA	1829	A
26	BA	1847	A

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Mol	Chain	Res	Type
26	BA	1877	A
26	BA	1878	G
26	BA	1889	A
26	BA	1900	A
26	BA	1906	G
26	BA	1912	A
26	BA	1913	A
26	BA	1915	U
26	BA	1919	A
26	BA	1924	C
26	BA	1927	A
26	BA	1929	G
26	BA	1930	G
26	BA	1936	A
26	BA	1937	A
26	BA	1938	A
26	BA	1940	U
26	BA	1941	C
26	BA	1955	U
26	BA	1963	U
26	BA	1964	G
26	BA	1967	C
26	BA	1969	A
26	BA	1970	A
26	BA	1971	A
26	BA	1972	A
26	BA	1984	G
26	BA	1991	U
26	BA	1992	G
26	BA	1993	U
26	BA	1996	C
26	BA	1997	G
26	BA	2023	G
26	BA	2027	G
26	BA	2031	A
26	BA	2032	G
26	BA	2033	A
26	BA	2035	G
26	BA	2043	C
26	BA	2051	A
26	BA	2055	C
26	BA	2056	G

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Mol	Chain	Res	Type
26	BA	2060	A
26	BA	2061	G
26	BA	2062	A
26	BA	2069	G
26	BA	2093	G
26	BA	2096	U
26	BA	2097	C
26	BA	2100	G
26	BA	2101	G
26	BA	2102	U
26	BA	2106	G
26	BA	2117	A
26	BA	2118	U
26	BA	2119	A
26	BA	2121	G
26	BA	2123	G
26	BA	2125	G
26	BA	2126	A
26	BA	2127	G
26	BA	2128	C
26	BA	2129	C
26	BA	2130	U
26	BA	2131	G
26	BA	2132	U
26	BA	2134	A
26	BA	2135	A
26	BA	2136	C
26	BA	2140	C
26	BA	2141	G
26	BA	2142	C
26	BA	2145	C
26	BA	2147	G
26	BA	2148	G
26	BA	2157	G
26	BA	2158	A
26	BA	2159	G
26	BA	2160	G
26	BA	2164	C
26	BA	2166	G
26	BA	2167	U
26	BA	2168	G
26	BA	2169	A

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Mol	Chain	Res	Type
26	BA	2170	A
26	BA	2171	A
26	BA	2172	U
26	BA	2173	A
26	BA	2175	C
26	BA	2176	A
26	BA	2178	C
26	BA	2181	G
26	BA	2182	G
26	BA	2184	G
26	BA	2188	C
26	BA	2189	U
26	BA	2190	G
26	BA	2192	G
26	BA	2198	A
26	BA	2199	A
26	BA	2206	G
26	BA	2207	G
26	BA	2208	A
26	BA	2218	U
26	BA	2219	G
26	BA	2225	A
26	BA	2238	G
26	BA	2239	G
26	BA	2268	A
26	BA	2269	A
26	BA	2279	G
26	BA	2283	C
26	BA	2287	A
26	BA	2305	A
26	BA	2308	G
26	BA	2316	C
26	BA	2320	A
26	BA	2325	G
26	BA	2326	C
26	BA	2334	G
26	BA	2335	A
26	BA	2336	A
26	BA	2343	C
26	BA	2347	C
26	BA	2350	C
26	BA	2361	A

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Mol	Chain	Res	Type
26	BA	2372	G
26	BA	2383	G
26	BA	2385	C
26	BA	2389	G
26	BA	2396	G
26	BA	2406	U
26	BA	2407	G
26	BA	2410	G
26	BA	2424	C
26	BA	2425	A
26	BA	2429	G
26	BA	2430	A
26	BA	2432	A
26	BA	2434	A
26	BA	2435	A
26	BA	2439	A
26	BA	2440	C
26	BA	2441	C
26	BA	2445	G
26	BA	2448	A
26	BA	2469	A
26	BA	2474	C
26	BA	2476	A
26	BA	2484	G
26	BA	2487	G
26	BA	2490	G
26	BA	2491	U
26	BA	2494	G
26	BA	2502	G
26	BA	2505	G
26	BA	2518	A
26	BA	2525	G
26	BA	2529	G
26	BA	2531	A
26	BA	2536	G
26	BA	2538	C
26	BA	2554	U
26	BA	2566	A
26	BA	2567	G
26	BA	2573	C
26	BA	2579	C
26	BA	2582	G

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Mol	Chain	Res	Type
26	BA	2585	U
26	BA	2602	A
26	BA	2609	U
26	BA	2610	C
26	BA	2611	U
26	BA	2612	C
26	BA	2629	A
26	BA	2630	G
26	BA	2646	C
26	BA	2654	A
26	BA	2669	G
26	BA	2689	U
26	BA	2690	C
26	BA	2702	U
26	BA	2703	C
26	BA	2712(A)	A
26	BA	2713	A
26	BA	2714	G
26	BA	2726	U
26	BA	2733	A
26	BA	2755	C
26	BA	2757	A
26	BA	2758	A
26	BA	2761	G
26	BA	2764	A
26	BA	2765	A
26	BA	2766	G
26	BA	2778	A
26	BA	2790	A
26	BA	2791	C
26	BA	2792	G
26	BA	2793	G
26	BA	2802	G
26	BA	2807	G
26	BA	2818	G
26	BA	2820	A
26	BA	2821	A
26	BA	2835	A
26	BA	2872	G
26	BA	2873	A
26	BA	2876	G
26	BA	2880	C

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Mol	Chain	Res	Type
26	BA	2884	U
26	BA	2892	A
26	BA	2893	G
26	BA	2894	G
27	BB	2	C
27	BB	7	G
27	BB	13	A
27	BB	24	G
27	BB	32	C
27	BB	51	G
27	BB	52	A
27	BB	53	A
27	BB	56	G
27	BB	63	G
27	BB	73	A
27	BB	75	G
27	BB	85	G
27	BB	93	G
27	BB	106	G
27	BB	110	G
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	15	G
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	50	A
1	CA	51	A
1	CA	55	A
1	CA	58	C
1	CA	61	G
1	CA	66	G
1	CA	68	G
1	CA	69	G
1	CA	72	C
1	CA	73	G
1	CA	79	G

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Mol	Chain	Res	Type
1	CA	88	A
1	CA	91	C
1	CA	96	U
1	CA	97	G
1	CA	100	C
1	CA	101	A
1	CA	105	G
1	CA	111	G
1	CA	112	G
1	CA	115	G
1	CA	116	A
1	CA	121	C
1	CA	129(A)	G
1	CA	131	C
1	CA	139	G
1	CA	144	G
1	CA	146	G
1	CA	155	C
1	CA	156	G
1	CA	163	C
1	CA	170	U
1	CA	171	A
1	CA	173	U
1	CA	174	C
1	CA	178	C
1	CA	180	U
1	CA	182	U
1	CA	189(A)	C
1	CA	189(B)	C
1	CA	189(D)	C
1	CA	189(H)	G
1	CA	190	U
1	CA	195	A
1	CA	197	A
1	CA	200	G
1	CA	201	C
1	CA	202	U
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	221	C
1	CA	226	G

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Mol	Chain	Res	Type
1	CA	230	G
1	CA	247	G
1	CA	248	C
1	CA	251	G
1	CA	258	G
1	CA	259	G
1	CA	266	G
1	CA	267	C
1	CA	274	A
1	CA	280	C
1	CA	283	C
1	CA	289	G
1	CA	301	G
1	CA	318	G
1	CA	320	C
1	CA	321	A
1	CA	328	C
1	CA	329	A
1	CA	332	G
1	CA	343	U
1	CA	344	A
1	CA	346	G
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	374	A
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	409	G
1	CA	412	A
1	CA	413	G
1	CA	414	A
1	CA	421	U
1	CA	422	C
1	CA	424	G
1	CA	429	U

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Mol	Chain	Res	Type
1	CA	430	A
1	CA	432	A
1	CA	434	U
1	CA	439	A
1	CA	442	C
1	CA	452	A
1	CA	456	C
1	CA	461	A
1	CA	470	C
1	CA	471	G
1	CA	484	G
1	CA	485	G
1	CA	495	A
1	CA	496	A
1	CA	498	U
1	CA	504	C
1	CA	505	G
1	CA	508	C
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	519	C
1	CA	521	G
1	CA	527	G
1	CA	528	C
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	544	G
1	CA	547	A
1	CA	559	A
1	CA	560	U
1	CA	561	U
1	CA	562	C
1	CA	571	U
1	CA	572	A
1	CA	573	A
1	CA	575	G
1	CA	576	G
1	CA	577	G

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Mol	Chain	Res	Type
1	CA	581	G
1	CA	592	G
1	CA	593	G
1	CA	596	C
1	CA	604	G
1	CA	606	G
1	CA	611	A
1	CA	612	C
1	CA	615	C
1	CA	622	A
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	645	C
1	CA	646	U
1	CA	647	C
1	CA	649	G
1	CA	653	A
1	CA	660	G
1	CA	665	A
1	CA	671	G
1	CA	673	G
1	CA	677	U
1	CA	680	C
1	CA	684	A
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	701	C
1	CA	710	G
1	CA	711	G
1	CA	717	C
1	CA	721	G
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	733	A
1	CA	748	C
1	CA	749	C
1	CA	752	G
1	CA	755	G
1	CA	759	A

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Mol	Chain	Res	Type
1	CA	764	C
1	CA	766	A
1	CA	777	A
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	798	G
1	CA	802	A
1	CA	806	C
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	821	G
1	CA	826	C
1	CA	828	A
1	CA	832	C
1	CA	833	U
1	CA	835	U
1	CA	838	G
1	CA	840	C
1	CA	841	U
1	CA	848	C
1	CA	849	C
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	860	A
1	CA	868	C
1	CA	869	G
1	CA	874	G
1	CA	885	G
1	CA	886	G
1	CA	887	G
1	CA	902	G
1	CA	913	A
1	CA	914	A
1	CA	922	G
1	CA	926	G
1	CA	927	G
1	CA	934	C
1	CA	936	C
1	CA	938	A

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Mol	Chain	Res	Type
1	CA	942	G
1	CA	945	G
1	CA	952	U
1	CA	954	G
1	CA	960	U
1	CA	961	U
1	CA	965	A
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
1	CA	977	A
1	CA	979	C
1	CA	981	U
1	CA	982	U
1	CA	983	A
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	1002	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1011	G
1	CA	1017	G
1	CA	1018	C
1	CA	1020	U
1	CA	1022	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1030(D)	A
1	CA	1036	G
1	CA	1037	C
1	CA	1038	C

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Mol	Chain	Res	Type
1	CA	1039	C
1	CA	1041	A
1	CA	1043	C
1	CA	1045	C
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1056	U
1	CA	1057	G
1	CA	1063	C
1	CA	1064	G
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1086	U
1	CA	1092	A
1	CA	1093	A
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1117	G
1	CA	1122	U
1	CA	1124	G
1	CA	1125	U
1	CA	1126	U
1	CA	1128	C
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1145	C
1	CA	1146	A

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Mol	Chain	Res	Type
1	CA	1147	C
1	CA	1152	A
1	CA	1157	A
1	CA	1158	C
1	CA	1159	U
1	CA	1160	G
1	CA	1165	C
1	CA	1170	A
1	CA	1174	G
1	CA	1176	A
1	CA	1181	G
1	CA	1183	A
1	CA	1184	G
1	CA	1185	G
1	CA	1196	U
1	CA	1197	G
1	CA	1199	U
1	CA	1200	C
1	CA	1202	G
1	CA	1204	A
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1214	C
1	CA	1218	C
1	CA	1227	A
1	CA	1228	C
1	CA	1236	A
1	CA	1240	U
1	CA	1244	C
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1264	C
1	CA	1265	G
1	CA	1270	C
1	CA	1274	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1284	C

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Mol	Chain	Res	Type
1	CA	1287	A
1	CA	1296	C
1	CA	1297	C
1	CA	1298	C
1	CA	1300	G
1	CA	1316	G
1	CA	1317	C
1	CA	1321	C
1	CA	1322	C
1	CA	1326	C
1	CA	1338	G
1	CA	1340	A
1	CA	1342	C
1	CA	1347	G
1	CA	1360	A
1	CA	1363	C
1	CA	1365	G
1	CA	1370	G
1	CA	1376	U
1	CA	1377	A
1	CA	1379	G
1	CA	1383	C
1	CA	1396	A
1	CA	1397	C
1	CA	1398	A
1	CA	1400	C
1	CA	1402	C
1	CA	1419	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1446	U
1	CA	1447	A
1	CA	1452	C
1	CA	1457	G
1	CA	1458	G
1	CA	1472	U
1	CA	1475	G
1	CA	1487	G
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G

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Mol	Chain	Res	Type
1	CA	1497	G
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1507	A
1	CA	1517	G
1	CA	1520	G
1	CA	1525	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	15	A
22	CV	16	A
22	CV	18	G
22	CV	19	U
24	CX	4	G
24	CX	8	4SU
24	CX	9	G
24	CX	13	C
24	CX	16	C
24	CX	17	C
24	CX	17(A)	U
24	CX	18	G
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	25	C
24	CX	27	U
24	CX	31	G
24	CX	41	C
24	CX	42	G
24	CX	45	G
24	CX	47	U
24	CX	48	C
24	CX	52	G
24	CX	56	C
24	CX	59	A
24	CX	60	U
24	CX	61	C
24	CX	62	C

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Mol	Chain	Res	Type
24	CX	65	C
24	CX	66	C
24	CX	67	C
24	CX	68	C
24	CX	70	G
24	CX	72	A
25	CY	76	A
26	DA	7	G
26	DA	9	U
26	DA	10	G
26	DA	11	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	50	U
26	DA	61	G
26	DA	63	U
26	DA	68	G
26	DA	71	A
26	DA	74	A
26	DA	75	G
26	DA	78	A
26	DA	84	A
26	DA	95	G
26	DA	102	G
26	DA	118	A
26	DA	119	A
26	DA	120	U
26	DA	122	G
26	DA	131	G
26	DA	139	G
26	DA	141	A
26	DA	154(A)	C
26	DA	157	U
26	DA	181	A
26	DA	182	A
26	DA	184	C
26	DA	196	A
26	DA	199	A

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Mol	Chain	Res	Type
26	DA	205	G
26	DA	213	A
26	DA	214	G
26	DA	216	A
26	DA	221	A
26	DA	222	A
26	DA	224	G
26	DA	225	A
26	DA	229	A
26	DA	233	A
26	DA	245	G
26	DA	248	G
26	DA	250	G
26	DA	260	G
26	DA	261	G
26	DA	264	C
26	DA	265	A
26	DA	266	G
26	DA	271(D)	G
26	DA	271(I)	G
26	DA	271(K)	U
26	DA	271(L)	U
26	DA	271(M)	G
26	DA	271(N)	U
26	DA	271(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	285	C
26	DA	292	C
26	DA	302	C
26	DA	311	A
26	DA	317	G
26	DA	324	A
26	DA	327	G
26	DA	329	G
26	DA	330	A
26	DA	345	A
26	DA	352	G
26	DA	363	G

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Mol	Chain	Res	Type
26	DA	363(B)	G
26	DA	363(E)	U
26	DA	363(F)	A
26	DA	372	G
26	DA	386	G
26	DA	391	G
26	DA	396	G
26	DA	405	U
26	DA	411	G
26	DA	412	A
26	DA	415	A
26	DA	416	C
26	DA	421	U
26	DA	422	A
26	DA	428	A
26	DA	442	G
26	DA	443	A
26	DA	444	C
26	DA	446	G
26	DA	455	C
26	DA	456	C
26	DA	457	A
26	DA	470	A
26	DA	474	G
26	DA	481	G
26	DA	482	A
26	DA	487	C
26	DA	496	G
26	DA	504	U
26	DA	505	A
26	DA	508	G
26	DA	509	C
26	DA	519	U
26	DA	530	G
26	DA	531	C
26	DA	532	A
26	DA	533	G
26	DA	536	A
26	DA	545	G
26	DA	556	G
26	DA	563	G
26	DA	573	G

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Mol	Chain	Res	Type
26	DA	575	A
26	DA	586	A
26	DA	595	C
26	DA	603	A
26	DA	604	G
26	DA	607	U
26	DA	614(B)	G
26	DA	615	G
26	DA	627	A
26	DA	637	A
26	DA	640	C
26	DA	645	C
26	DA	646	A
26	DA	647	G
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	653	A
26	DA	669	G
26	DA	670	A
26	DA	677	A
26	DA	686	G
26	DA	708	C
26	DA	709	U
26	DA	717	G
26	DA	729	G
26	DA	730	C
26	DA	740	U
26	DA	753	C
26	DA	759	G
26	DA	765	G
26	DA	771	G
26	DA	775	G
26	DA	776	G
26	DA	782	A
26	DA	783	A
26	DA	784	A
26	DA	785	G
26	DA	790	C
26	DA	792	G

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Mol	Chain	Res	Type
26	DA	805	G
26	DA	812	C
26	DA	819	A
26	DA	821	A
26	DA	827	U
26	DA	828	U
26	DA	847	U
26	DA	857	C
26	DA	859	G
26	DA	866	A
26	DA	869	G
26	DA	874	G
26	DA	875	G
26	DA	879	G
26	DA	880	G
26	DA	882	G
26	DA	884	C
26	DA	886	C
26	DA	887	A
26	DA	888	C
26	DA	889	C
26	DA	890	A
26	DA	894	C
26	DA	896	A
26	DA	900	A
26	DA	901	A
26	DA	910	A
26	DA	912	C
26	DA	915	C
26	DA	917	A
26	DA	921	G
26	DA	932	G
26	DA	933	A
26	DA	941	A
26	DA	945	A
26	DA	946	G
26	DA	953	A
26	DA	961	C
26	DA	974	G
26	DA	975	C
26	DA	979	G
26	DA	980	A

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Mol	Chain	Res	Type
26	DA	983	A
26	DA	996	A
26	DA	1012	U
26	DA	1013	C
26	DA	1017	G
26	DA	1020	A
26	DA	1022	G
26	DA	1025	G
26	DA	1026	U
26	DA	1027	A
26	DA	1033	U
26	DA	1038	C
26	DA	1039	G
26	DA	1042	G
26	DA	1043	C
26	DA	1114	G
26	DA	1116	C
26	DA	1127	A
26	DA	1128	A
26	DA	1129	A
26	DA	1130	U
26	DA	1135	C
26	DA	1136	G
26	DA	1139	G
26	DA	1142(A)	A
26	DA	1166	C
26	DA	1170	G
26	DA	1171	G
26	DA	1206	G
26	DA	1210	A
26	DA	1211	U
26	DA	1212	G
26	DA	1220	A
26	DA	1229	G
26	DA	1244	G
26	DA	1249	U
26	DA	1253	A
26	DA	1256	G
26	DA	1271	G
26	DA	1272	A
26	DA	1273	U
26	DA	1296	G

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Mol	Chain	Res	Type
26	DA	1300	U
26	DA	1301	A
26	DA	1303	G
26	DA	1308	A
26	DA	1314	C
26	DA	1320	C
26	DA	1341	U
26	DA	1342	A
26	DA	1352	U
26	DA	1357	U
26	DA	1358	G
26	DA	1359	A
26	DA	1365	A
26	DA	1370	C
26	DA	1379	A
26	DA	1380	G
26	DA	1384	A
26	DA	1385	G
26	DA	1386	C
26	DA	1392	A
26	DA	1395	A
26	DA	1412	A
26	DA	1416	G
26	DA	1417	C
26	DA	1419	A
26	DA	1420	U
26	DA	1421	G
26	DA	1427	A
26	DA	1428	C
26	DA	1437	C
26	DA	1445	A
26	DA	1449	A
26	DA	1450	G
26	DA	1451	C
26	DA	1455	G
26	DA	1459	G
26	DA	1467	C
26	DA	1471	A
26	DA	1482	G
26	DA	1488	G
26	DA	1493	C
26	DA	1494	A

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Mol	Chain	Res	Type
26	DA	1497	U
26	DA	1504	C
26	DA	1508	A
26	DA	1509	C
26	DA	1509(A)	A
26	DA	1509(B)	A
26	DA	1512	U
26	DA	1520	G
26	DA	1523	U
26	DA	1525	G
26	DA	1530	C
26	DA	1531	C
26	DA	1532	C
26	DA	1542	A
26	DA	1545	A
26	DA	1547	C
26	DA	1548	C
26	DA	1558	A
26	DA	1559	G
26	DA	1569	A
26	DA	1578	U
26	DA	1579	A
26	DA	1583	A
26	DA	1586	A
26	DA	1592	C
26	DA	1597	A
26	DA	1598	C
26	DA	1608	A
26	DA	1610	A
26	DA	1631	C
26	DA	1636	C
26	DA	1640	C
26	DA	1645	G
26	DA	1647	G
26	DA	1648	C
26	DA	1653	G
26	DA	1654	A
26	DA	1674	G
26	DA	1684	C
26	DA	1696	G
26	DA	1700	A
26	DA	1701	A

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Mol	Chain	Res	Type
26	DA	1703	G
26	DA	1721	G
26	DA	1722	A
26	DA	1740	G
26	DA	1742	G
26	DA	1743	C
26	DA	1744	C
26	DA	1745(A)	C
26	DA	1746	G
26	DA	1750	G
26	DA	1756	G
26	DA	1762	A
26	DA	1763	G
26	DA	1764	G
26	DA	1773	A
26	DA	1780	A
26	DA	1791	A
26	DA	1800	C
26	DA	1801	G
26	DA	1812	A
26	DA	1816	G
26	DA	1829	A
26	DA	1831	G
26	DA	1835	G
26	DA	1839	G
26	DA	1840	G
26	DA	1847	A
26	DA	1848	A
26	DA	1859	A
26	DA	1862	G
26	DA	1866	C
26	DA	1877	A
26	DA	1878	G
26	DA	1882	C
26	DA	1889	A
26	DA	1896	G
26	DA	1900	A
26	DA	1906	G
26	DA	1913	A
26	DA	1914	C
26	DA	1915	U
26	DA	1929	G

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Mol	Chain	Res	Type
26	DA	1930	G
26	DA	1936	A
26	DA	1937	A
26	DA	1938	A
26	DA	1940	U
26	DA	1955	U
26	DA	1960	A
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	2024	G
26	DA	2031	A
26	DA	2033	A
26	DA	2043	C
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	2093	G
26	DA	2097	C
26	DA	2104	G
26	DA	2105	C
26	DA	2106	G
26	DA	2111	C
26	DA	2113	U
26	DA	2114	A
26	DA	2115	G
26	DA	2119	A
26	DA	2120	G
26	DA	2122	U
26	DA	2123	G
26	DA	2125	G
26	DA	2126	A

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Mol	Chain	Res	Type
26	DA	2127	G
26	DA	2128	C
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	2140	C
26	DA	2141	G
26	DA	2143	C
26	DA	2144	U
26	DA	2146	C
26	DA	2150	U
26	DA	2151	G
26	DA	2153	G
26	DA	2154	G
26	DA	2157	G
26	DA	2158	A
26	DA	2159	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	2172	U
26	DA	2173	A
26	DA	2174	C
26	DA	2175	C
26	DA	2178	C
26	DA	2181	G
26	DA	2184	G
26	DA	2185	C
26	DA	2189	U
26	DA	2192	G

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Mol	Chain	Res	Type
26	DA	2193	G
26	DA	2198	A
26	DA	2200	C
26	DA	2206	G
26	DA	2207	G
26	DA	2208	A
26	DA	2218	U
26	DA	2219	G
26	DA	2225	A
26	DA	2238	G
26	DA	2239	G
26	DA	2274	A
26	DA	2275	C
26	DA	2279	G
26	DA	2282	G
26	DA	2283	C
26	DA	2287	A
26	DA	2288	A
26	DA	2291	U
26	DA	2303	G
26	DA	2305	A
26	DA	2308	G
26	DA	2318	G
26	DA	2319	G
26	DA	2320	A
26	DA	2325	G
26	DA	2333	A
26	DA	2334	G
26	DA	2336	A
26	DA	2337	G
26	DA	2342	C
26	DA	2343	C
26	DA	2347	C
26	DA	2349	G
26	DA	2354	G
26	DA	2377	A
26	DA	2379	G
26	DA	2383	G
26	DA	2385	C
26	DA	2388	A
26	DA	2402	C
26	DA	2406	U

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Mol	Chain	Res	Type
26	DA	2410	G
26	DA	2417	C
26	DA	2418	A
26	DA	2422	A
26	DA	2423	U
26	DA	2425	A
26	DA	2427	C
26	DA	2429	G
26	DA	2430	A
26	DA	2435	A
26	DA	2439	A
26	DA	2440	C
26	DA	2441	C
26	DA	2448	A
26	DA	2453	A
26	DA	2459	A
26	DA	2460	U
26	DA	2465	C
26	DA	2469	A
26	DA	2476	A
26	DA	2477	C
26	DA	2480	C
26	DA	2484	G
26	DA	2487	G
26	DA	2490	G
26	DA	2502	G
26	DA	2505	G
26	DA	2518	A
26	DA	2529	G
26	DA	2532	G
26	DA	2535	G
26	DA	2536	G
26	DA	2542	A
26	DA	2549	G
26	DA	2554	U
26	DA	2562	U
26	DA	2566	A
26	DA	2567	G
26	DA	2569	G
26	DA	2602	A
26	DA	2603	G
26	DA	2609	U

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Mol	Chain	Res	Type
26	DA	2610	C
26	DA	2611	U
26	DA	2612	C
26	DA	2615	U
26	DA	2627	G
26	DA	2629	A
26	DA	2630	G
26	DA	2632	A
26	DA	2634	G
26	DA	2641	G
26	DA	2652	C
26	DA	2654	A
26	DA	2660	A
26	DA	2661	G
26	DA	2663	G
26	DA	2669	G
26	DA	2689	U
26	DA	2690	C
26	DA	2702	U
26	DA	2703	C
26	DA	2706	G
26	DA	2707	G
26	DA	2712(A)	A
26	DA	2713	A
26	DA	2714	G
26	DA	2721	A
26	DA	2726	U
26	DA	2733	A
26	DA	2746	U
26	DA	2751	G
26	DA	2757	A
26	DA	2758	A
26	DA	2759	G
26	DA	2764	A
26	DA	2765	A
26	DA	2766	G
26	DA	2774	C
26	DA	2775	A
26	DA	2778	A
26	DA	2780	G
26	DA	2789	C
26	DA	2794	C

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Mol	Chain	Res	Type
26	DA	2802	G
26	DA	2803	C
26	DA	2809	A
26	DA	2810	A
26	DA	2818	G
26	DA	2820	A
26	DA	2821	A
26	DA	2834	G
26	DA	2835	A
26	DA	2861	G
26	DA	2872	G
26	DA	2879	C
26	DA	2880	C
26	DA	2892	A
26	DA	2894	G
26	DA	2895	U
26	DA	2897	U
27	DB	2	C
27	DB	3	C
27	DB	7	G
27	DB	8	U
27	DB	9	G
27	DB	11	C
27	DB	12	C
27	DB	13	A
27	DB	15	A
27	DB	25	A
27	DB	30	C
27	DB	31	C
27	DB	33	G
27	DB	39	A
27	DB	41	U
27	DB	42	C
27	DB	44	G
27	DB	54	G
27	DB	56	G
27	DB	59	A
27	DB	67	G
27	DB	73	A
27	DB	75	G
27	DB	85	G
27	DB	91	C

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Mol	Chain	Res	Type
27	DB	93	G
27	DB	101	G
27	DB	108	U
27	DB	110	G
27	DB	111	G
27	DB	115	G

All (122) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	250	A
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1027	C
1	AA	1054	C
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1201	A
1	AA	1212	U
1	AA	1256	A
1	AA	1285	A
1	AA	1299	A
1	AA	1442	G
1	AA	1447	A
1	AA	1492	A
24	AX	16	C
24	AX	47	U
26	BA	71	A
26	BA	271(J)	C
26	BA	271(K)	U
26	BA	271(M)	G

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Mol	Chain	Res	Type
26	BA	278	A
26	BA	827	U
26	BA	958	U
26	BA	1174	A
26	BA	1175	U
26	BA	1176	G
26	BA	1210	A
26	BA	1300	U
26	BA	1301	A
26	BA	1379	A
26	BA	1530	C
26	BA	1653	G
26	BA	1828	G
26	BA	1992	G
26	BA	2126	A
26	BA	2127	G
26	BA	2158	A
26	BA	2170	A
26	BA	2181	G
26	BA	2183	C
26	BA	2187	G
26	BA	2406	U
26	BA	2439	A
26	BA	2689	U
26	BA	2756	U
26	BA	2893	G
27	BB	1	U
27	BB	52	A
1	CA	60	A
1	CA	65	U
1	CA	88	A
1	CA	96	U
1	CA	115	G
1	CA	250	A
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	687	A
1	CA	748	C
1	CA	913	A

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Mol	Chain	Res	Type
1	CA	991	U
1	CA	992	U
1	CA	1054	C
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1183	A
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1442	G
1	CA	1447	A
1	CA	1492	A
24	CX	16	C
24	CX	18	G
24	CX	41	C
24	CX	46	G
26	DA	271(K)	U
26	DA	271(M)	G
26	DA	277	C
26	DA	362	U
26	DA	669	G
26	DA	752	A
26	DA	774	A
26	DA	856	C
26	DA	900	A
26	DA	1026	U
26	DA	1210	A
26	DA	1395	A
26	DA	1420	U
26	DA	1427	A
26	DA	1493	C
26	DA	1530	C
26	DA	1558	A
26	DA	1653	G
26	DA	1913	A
26	DA	1992	G
26	DA	2104	G
26	DA	2110	G
26	DA	2282	G
26	DA	2406	U

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Mol	Chain	Res	Type
26	DA	2422	A
26	DA	2428	G
26	DA	2439	A
26	DA	2602	A
26	DA	2689	U
26	DA	2756	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
24	31H	AX	76	24,57	29,32,35	1.32	4 (13%)	34,45,50	2.54	12 (35%)
24	PSU	AX	55	24	18,21,22	1.37	2 (11%)	21,30,33	2.06	3 (14%)
24	5MU	AX	54	24	19,22,23	1.38	5 (26%)	27,32,35	2.21	6 (22%)
24	31H	CX	76	24,57,60	31,34,35	1.34	4 (12%)	35,47,50	2.46	13 (37%)
24	4SU	AX	8	24	18,21,22	2.24	5 (27%)	25,30,33	1.70	4 (16%)
24	5MC	AX	32	24	19,22,23	1.61	3 (15%)	26,32,35	1.27	3 (11%)
24	PSU	CX	55	24	18,21,22	1.33	2 (11%)	21,30,33	1.95	4 (19%)
23	PPU	AW	76	23,26	37,40,41	1.35	3 (8%)	47,57,60	2.10	14 (29%)
24	4SU	CX	8	24	18,21,22	1.99	5 (27%)	25,30,33	1.65	5 (20%)
24	5MC	CX	32	24	19,22,23	1.63	2 (10%)	26,32,35	1.06	2 (7%)
24	5MU	CX	54	24	19,22,23	1.35	5 (26%)	27,32,35	2.24	6 (22%)
23	PPU	CW	76	23,26	37,40,41	1.27	3 (8%)	47,57,60	2.27	15 (31%)

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
24	31H	AX	76	24,57	-	7/19/37/41	0/3/3/3
24	PSU	AX	55	24	-	0/7/25/26	0/2/2/2
24	5MU	AX	54	24	-	0/7/25/26	0/2/2/2
24	31H	CX	76	24,57,60	-	9/22/40/41	0/3/3/3
24	4SU	AX	8	24	-	0/7/25/26	0/2/2/2
24	5MC	AX	32	24	-	0/7/25/26	0/2/2/2
24	PSU	CX	55	24	-	0/7/25/26	0/2/2/2
23	PPU	AW	76	23,26	-	3/25/43/44	0/4/4/4
24	4SU	CX	8	24	-	0/7/25/26	0/2/2/2
24	5MC	CX	32	24	-	0/7/25/26	0/2/2/2
24	5MU	CX	54	24	-	0/7/25/26	0/2/2/2
23	PPU	CW	76	23,26	-	6/25/43/44	0/4/4/4

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CX	32	5MC	C5-C4	5.90	1.48	1.44
24	AX	32	5MC	C5-C4	5.59	1.48	1.44
23	AW	76	PPU	C5-C4	5.20	1.48	1.39
24	AX	8	4SU	C4-N3	-5.14	1.32	1.37
23	CW	76	PPU	C5-C4	4.93	1.47	1.39
24	CX	8	4SU	C4-S4	-4.90	1.60	1.68
24	AX	8	4SU	C4-S4	-4.85	1.60	1.68
24	CX	76	31H	C5-N7	-4.02	1.31	1.39
24	CX	8	4SU	C4-N3	-3.99	1.33	1.37
24	AX	8	4SU	C5-C4	-3.89	1.37	1.42
24	AX	55	PSU	C6-C5	3.72	1.39	1.35
24	CX	55	PSU	C6-C5	3.58	1.39	1.35
24	AX	8	4SU	C2-N3	-3.43	1.32	1.38
24	CX	8	4SU	C5-C4	-3.38	1.38	1.42
24	AX	76	31H	C5-C6	-3.30	1.31	1.41
24	CX	76	31H	C5-C4	-3.24	1.33	1.39
23	AW	76	PPU	C5-C6	3.00	1.49	1.41
24	AX	76	31H	C5-C4	-2.94	1.33	1.39
24	CX	32	5MC	C6-C5	2.91	1.39	1.34
24	CX	54	5MU	C6-C5	2.81	1.39	1.34
24	AX	54	5MU	C4-N3	-2.80	1.33	1.38
24	AX	76	31H	C5-N7	-2.80	1.34	1.39
23	CW	76	PPU	C5-C6	2.78	1.48	1.41
24	AX	32	5MC	C6-C5	2.74	1.39	1.34
24	AX	54	5MU	C6-C5	2.73	1.39	1.34
24	CX	76	31H	C5-C6	-2.73	1.33	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AX	32	5MC	C6-N1	-2.71	1.33	1.38
23	CW	76	PPU	C5-N7	-2.64	1.34	1.39
24	CX	76	31H	C3'-N3'	2.59	1.49	1.45
23	AW	76	PPU	C5-N7	-2.56	1.34	1.39
24	CX	54	5MU	C4-N3	-2.49	1.34	1.38
24	AX	55	PSU	C4-N3	-2.48	1.34	1.38
24	CX	8	4SU	O2-C2	2.44	1.27	1.23
24	AX	8	4SU	O2-C2	2.43	1.27	1.23
24	CX	55	PSU	C4-N3	-2.35	1.34	1.38
24	AX	54	5MU	C4-C5	2.25	1.48	1.44
24	CX	54	5MU	C2-N3	-2.24	1.34	1.38
24	CX	54	5MU	C4-C5	2.24	1.48	1.44
24	AX	54	5MU	C6-N1	-2.21	1.34	1.38
24	CX	54	5MU	C6-N1	-2.19	1.34	1.38
24	AX	76	31H	C3'-N3'	2.19	1.49	1.45
24	AX	54	5MU	C2-N3	-2.17	1.34	1.38
24	CX	8	4SU	C2-N1	2.12	1.41	1.38

All (87) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	CX	76	31H	O4'-C1'-N9	7.99	123.44	108.09
23	CW	76	PPU	C5-C4-N3	-6.74	117.43	126.72
24	AX	76	31H	C5-C4-N3	-6.60	117.63	126.72
24	AX	55	PSU	N1-C2-N3	6.34	121.86	115.17
23	AW	76	PPU	C5-C4-N3	-6.33	118.00	126.72
24	CX	55	PSU	N1-C2-N3	5.98	121.48	115.17
24	AX	76	31H	N1-C2-N3	-5.89	119.67	128.58
24	CX	76	31H	N1-C2-N3	-5.80	119.81	128.58
24	AX	54	5MU	N3-C2-N1	5.61	122.20	114.89
24	AX	54	5MU	C4-N3-C2	-5.42	120.23	127.34
24	CX	54	5MU	C4-N3-C2	-5.32	120.37	127.34
23	CW	76	PPU	N3-C4-N9	5.21	136.02	127.17
24	CX	54	5MU	N3-C2-N1	5.05	121.47	114.89
24	CX	76	31H	C5-C4-N3	-5.03	119.79	126.72
24	CX	8	4SU	C5-C4-N3	4.99	119.39	114.75
24	AX	76	31H	C5-C4-N9	4.83	111.07	105.81
23	AW	76	PPU	N3-C4-N9	4.79	135.31	127.17
23	CW	76	PPU	N1-C6-N6	4.73	122.61	116.86
24	AX	76	31H	O4'-C1'-N9	4.70	117.12	108.09
24	CX	54	5MU	O4-C4-C5	-4.58	119.68	124.92
24	CX	54	5MU	C5-C4-N3	4.45	119.19	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	AX	76	31H	C6-C5-C4	4.41	123.20	117.18
24	AX	8	4SU	C6-C5-C4	-4.37	116.17	119.95
24	AX	54	5MU	C5-C4-N3	4.30	119.06	115.32
24	CX	54	5MU	C5-C6-N1	-4.22	118.73	123.31
23	CW	76	PPU	C9-N6-C6	-4.16	109.94	120.52
23	AW	76	PPU	C10-N6-C6	-4.16	109.95	120.52
24	AX	55	PSU	C4-N3-C2	-4.10	120.72	126.37
23	AW	76	PPU	C2-N1-C6	4.05	121.73	111.83
24	AX	54	5MU	O4-C4-C5	-4.03	120.31	124.92
24	CX	55	PSU	C4-N3-C2	-4.01	120.84	126.37
24	AX	32	5MC	C5-C6-N1	-3.96	119.01	123.31
23	AW	76	PPU	C4-C5-N7	-3.89	106.14	110.58
24	AX	55	PSU	O2-C2-N1	-3.89	118.78	122.79
24	CX	54	5MU	O2-C2-N1	-3.86	117.78	122.80
24	AX	76	31H	C4-C5-N7	-3.79	106.25	110.58
23	CW	76	PPU	C2-N1-C6	3.77	121.05	111.83
24	AX	76	31H	C2-N3-C4	3.77	121.04	111.83
23	CW	76	PPU	C2-N3-C4	3.77	121.04	111.83
24	AX	54	5MU	C5-C6-N1	-3.72	119.27	123.31
24	AX	8	4SU	C5-C4-N3	3.57	118.07	114.75
24	AX	8	4SU	O2-C2-N1	3.51	127.37	122.80
24	AX	54	5MU	O2-C2-N1	-3.49	118.26	122.80
23	CW	76	PPU	C10-N6-C9	-3.47	105.02	116.18
24	CX	76	31H	N9-C8-N7	-3.45	109.05	113.94
24	CX	76	31H	C2-N3-C4	3.40	120.14	111.83
23	CW	76	PPU	C4-C5-N7	-3.34	106.76	110.58
23	AW	76	PPU	C2-N3-C4	3.33	119.97	111.83
24	AX	76	31H	N9-C8-N7	-3.32	109.22	113.94
24	CX	76	31H	O4'-C4'-C3'	3.29	108.91	104.13
23	AW	76	PPU	N1-C6-N6	3.26	120.83	116.86
24	CX	8	4SU	C4-N3-C2	-3.20	124.25	127.31
24	AX	8	4SU	C1'-N1-C2	3.18	123.31	117.59
23	CW	76	PPU	C5-C6-N6	-3.17	120.31	125.33
24	CX	8	4SU	C5-C4-S4	-3.13	120.73	124.31
23	CW	76	PPU	C10-N6-C6	-3.11	112.62	120.52
24	CX	76	31H	C5-N7-C8	3.03	108.21	103.45
24	CX	55	PSU	O2-C2-N1	-3.02	119.68	122.79
24	AX	76	31H	C5-N7-C8	2.99	108.14	103.45
24	CX	8	4SU	C1'-N1-C2	2.97	122.92	117.59
24	AX	32	5MC	C5-C4-N3	-2.93	118.75	121.75
24	CX	32	5MC	C5-C6-N1	-2.93	120.13	123.31
23	CW	76	PPU	C4-C5-C6	2.86	118.87	115.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CW	76	PPU	CA-C-N3'	2.85	120.07	116.21
23	AW	76	PPU	C3'-N3'-C	-2.82	118.91	123.20
23	AW	76	PPU	C4-C5-C6	2.76	118.76	115.91
24	CX	76	31H	C5-C4-N9	2.69	108.74	105.81
24	AX	76	31H	C4'-O4'-C1'	-2.68	103.54	109.47
23	CW	76	PPU	N3-C2-N1	-2.66	124.56	128.58
23	AW	76	PPU	O4'-C4'-C3'	2.64	107.96	104.13
24	CX	32	5MC	C5-C4-N3	-2.62	119.07	121.75
23	AW	76	PPU	C9-N6-C6	-2.57	114.00	120.52
24	CX	76	31H	N3-C4-N9	2.53	131.47	127.17
23	AW	76	PPU	C5-N7-C8	2.49	107.36	103.45
24	CX	76	31H	CA-N-CN	-2.45	119.06	122.82
24	AX	76	31H	N3-C4-N9	2.43	131.29	127.17
23	AW	76	PPU	C10-N6-C9	-2.39	108.50	116.18
24	CX	55	PSU	C5-C6-N1	-2.39	118.83	122.14
23	AW	76	PPU	N3-C2-N1	-2.32	125.06	128.58
24	CX	8	4SU	C6-C5-C4	-2.28	117.97	119.95
24	AX	32	5MC	O2-C2-N3	-2.21	118.84	122.33
23	CW	76	PPU	C5-N7-C8	2.20	106.91	103.45
24	CX	76	31H	C4-C5-N7	-2.19	108.08	110.58
24	CX	76	31H	C6-C5-C4	2.18	120.15	117.18
24	AX	76	31H	O4'-C1'-C2'	-2.17	101.97	106.62
23	CW	76	PPU	C3'-N3'-C	-2.12	119.97	123.20
24	CX	76	31H	OCN-CN-N	-2.02	120.11	125.32

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	CX	76	31H	C3'-C4'-C5'-O5'
24	CX	76	31H	C-CA-CB-CG
24	CX	76	31H	N-CA-CB-CG
24	CX	76	31H	OCN-CN-N-CA
23	AW	76	PPU	CE2-CZ-OC-CM
23	AW	76	PPU	CE1-CZ-OC-CM
24	AX	76	31H	C3'-C4'-C5'-O5'
24	CX	76	31H	O4'-C4'-C5'-O5'
24	AX	76	31H	C4'-C5'-O5'-P
24	AX	76	31H	O4'-C4'-C5'-O5'
24	AX	76	31H	C-CA-CB-CG
24	CX	76	31H	O-C-CA-N
24	CX	76	31H	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
24	CX	76	31H	N3'-C-CA-N
23	AW	76	PPU	C5-C6-N6-C9
23	CW	76	PPU	C5-C6-N6-C9
23	CW	76	PPU	C5-C6-N6-C10
24	AX	76	31H	N-CA-CB-CG
23	CW	76	PPU	N-CA-CB-CG
24	AX	76	31H	N3'-C-CA-N
24	AX	76	31H	N3'-C-CA-CB
24	CX	76	31H	O-C-CA-CB
23	CW	76	PPU	CE1-CZ-OC-CM
23	CW	76	PPU	N1-C6-N6-C9
23	CW	76	PPU	N1-C6-N6-C10

There are no ring outliers.

10 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	AX	55	PSU	1	0
24	AX	54	5MU	1	0
24	CX	76	31H	4	0
24	AX	8	4SU	2	0
24	CX	55	PSU	1	0
23	AW	76	PPU	5	0
24	CX	8	4SU	2	0
24	CX	32	5MC	2	0
24	CX	54	5MU	1	0
23	CW	76	PPU	11	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1916 ligands modelled in this entry, 1914 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	302	4	0,12,12	-	-	-		
58	SF4	CD	501	4	0,12,12	-	-	-		

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	302	4	-	-	0/6/5/5
58	SF4	CD	501	4	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	AD	302	SF4	1	0
58	CD	501	SF4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AA	1498/1521 (98%)	0.93	99 (6%) 24 18	39, 73, 93, 105	0
1	CA	1503/1521 (98%)	1.22	236 (15%) 5 4	41, 75, 94, 106	0
2	AB	231/256 (90%)	1.54	50 (21%) 2 2	69, 82, 91, 101	0
2	CB	231/256 (90%)	1.90	99 (42%) 0 0	71, 84, 93, 101	0
3	AC	206/239 (86%)	1.47	46 (22%) 2 1	67, 79, 89, 95	0
3	CC	206/239 (86%)	1.83	75 (36%) 1 0	70, 81, 91, 95	0
4	AD	208/209 (99%)	1.52	57 (27%) 1 1	57, 74, 85, 91	0
4	CD	208/209 (99%)	1.98	97 (46%) 0 0	57, 75, 85, 92	0
5	AE	148/162 (91%)	1.25	26 (17%) 4 3	59, 71, 82, 90	0
5	CE	148/162 (91%)	1.60	42 (28%) 1 1	59, 73, 84, 91	0
6	AF	100/101 (99%)	1.03	10 (10%) 12 9	54, 69, 78, 83	0
6	CF	100/101 (99%)	1.20	15 (15%) 5 4	56, 71, 80, 83	0
7	AG	155/156 (99%)	1.29	30 (19%) 3 2	64, 76, 86, 92	0
7	CG	155/156 (99%)	1.68	44 (28%) 1 1	67, 78, 88, 92	0
8	AH	137/138 (99%)	1.37	27 (19%) 3 2	60, 72, 80, 85	0
8	CH	137/138 (99%)	1.49	28 (20%) 3 2	62, 74, 82, 85	0
9	AI	127/128 (99%)	1.80	47 (37%) 1 0	64, 83, 91, 96	0
9	CI	127/128 (99%)	2.85	96 (75%) 0 0	69, 84, 91, 98	0
10	AJ	97/105 (92%)	2.08	47 (48%) 0 0	66, 83, 92, 94	0
10	CJ	96/105 (91%)	2.32	56 (58%) 0 0	69, 85, 93, 94	0
11	AK	114/129 (88%)	1.12	17 (14%) 5 4	46, 70, 81, 85	0
11	CK	114/129 (88%)	1.42	24 (21%) 2 2	50, 71, 82, 85	0
12	AL	122/132 (92%)	0.90	11 (9%) 15 11	50, 64, 73, 81	0
12	CL	122/132 (92%)	1.22	16 (13%) 7 6	52, 65, 75, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	AM	123/126 (97%)	1.44	28 (22%) 2 1	58, 72, 83, 90	0
13	CM	122/126 (96%)	2.43	81 (66%) 0 0	72, 85, 93, 100	0
14	AN	60/61 (98%)	1.88	24 (40%) 1 0	65, 75, 81, 82	0
14	CN	60/61 (98%)	2.73	44 (73%) 0 0	69, 78, 83, 86	0
15	AO	88/89 (98%)	1.20	13 (14%) 5 4	54, 69, 81, 85	0
15	CO	88/89 (98%)	1.31	16 (18%) 3 2	53, 71, 82, 87	0
16	AP	82/88 (93%)	2.00	34 (41%) 0 0	59, 72, 82, 85	0
16	CP	82/88 (93%)	1.73	30 (36%) 1 0	57, 71, 81, 85	0
17	AQ	99/105 (94%)	1.17	12 (12%) 8 6	58, 71, 80, 83	0
17	CQ	99/105 (94%)	1.28	17 (17%) 4 3	56, 72, 81, 83	0
18	AR	68/88 (77%)	0.89	3 (4%) 39 31	59, 70, 80, 84	0
18	CR	68/88 (77%)	1.38	16 (23%) 2 1	60, 71, 82, 85	0
19	AS	83/93 (89%)	1.32	10 (12%) 9 6	72, 82, 89, 93	0
19	CS	83/93 (89%)	2.14	45 (54%) 0 0	73, 84, 91, 95	0
20	AT	96/106 (90%)	1.36	20 (20%) 2 2	60, 71, 83, 85	0
20	CT	96/106 (90%)	1.24	16 (16%) 4 3	56, 71, 83, 85	0
21	AU	23/27 (85%)	2.09	14 (60%) 0 0	69, 74, 79, 85	0
21	CU	23/27 (85%)	2.77	15 (65%) 0 0	71, 76, 84, 86	0
22	AV	13/24 (54%)	2.20	7 (53%) 0 0	56, 88, 93, 97	0
22	CV	6/24 (25%)	3.09	4 (66%) 0 0	59, 76, 95, 96	0
23	AW	2/3 (66%)	0.01	0 100 100	30, 30, 30, 37	0
23	CW	2/3 (66%)	1.48	0 100 100	50, 50, 50, 57	0
24	AX	71/77 (92%)	0.94	3 (4%) 40 32	27, 70, 84, 92	0
24	CX	71/77 (92%)	1.34	13 (18%) 3 2	30, 75, 86, 93	0
25	AY	5/76 (6%)	1.51	2 (40%) 1 0	51, 76, 87, 94	0
25	CY	5/76 (6%)	1.38	0 100 100	60, 79, 90, 91	0
26	BA	2819/2915 (96%)	0.08	107 (3%) 44 35	20, 42, 89, 107	0
26	DA	2800/2915 (96%)	0.18	117 (4%) 40 32	22, 46, 90, 107	0
27	BB	120/121 (99%)	0.63	3 (2%) 58 48	37, 63, 77, 88	0
27	DB	120/121 (99%)	1.27	24 (20%) 3 2	42, 68, 80, 91	0
28	BD	275/276 (99%)	0.44	7 (2%) 58 48	21, 41, 58, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	DD	275/276 (99%)	0.47	7 (2%) 58 48	23, 43, 61, 80	0
29	BE	204/206 (99%)	0.46	4 (1%) 65 56	21, 46, 65, 82	0
29	DE	204/206 (99%)	0.42	4 (1%) 65 56	23, 48, 67, 84	0
30	BF	203/210 (96%)	0.53	5 (2%) 58 48	22, 51, 73, 87	0
30	DF	203/210 (96%)	0.48	3 (1%) 72 63	24, 54, 74, 86	0
31	BG	181/182 (99%)	1.37	37 (20%) 3 2	55, 70, 82, 93	0
31	DG	181/182 (99%)	2.03	86 (47%) 0 0	59, 74, 85, 93	0
32	BH	174/180 (96%)	1.34	31 (17%) 4 3	49, 65, 77, 81	0
32	DH	174/180 (96%)	1.32	33 (18%) 3 2	52, 70, 80, 84	0
33	BI	146/148 (98%)	1.50	32 (21%) 2 2	47, 81, 90, 95	0
33	DI	146/148 (98%)	3.16	100 (68%) 0 0	46, 84, 94, 99	0
34	BN	140/140 (100%)	0.70	10 (7%) 22 16	29, 49, 72, 82	0
34	DN	140/140 (100%)	0.71	2 (1%) 73 64	33, 53, 74, 83	0
35	BO	122/122 (100%)	0.24	4 (3%) 49 39	26, 42, 61, 65	0
35	DO	122/122 (100%)	0.72	4 (3%) 49 39	36, 57, 70, 79	0
36	BP	149/150 (99%)	0.65	6 (4%) 42 33	25, 52, 76, 85	0
36	DP	149/150 (99%)	0.79	7 (4%) 36 29	28, 54, 78, 86	0
37	BQ	141/141 (100%)	0.75	9 (6%) 25 18	29, 51, 65, 78	0
37	DQ	141/141 (100%)	0.95	15 (10%) 11 8	31, 55, 69, 79	0
38	BR	118/118 (100%)	0.02	0 100 100	23, 37, 56, 63	0
38	DR	118/118 (100%)	0.41	0 100 100	31, 50, 64, 71	0
39	BS	110/112 (98%)	0.43	4 (3%) 46 37	33, 51, 63, 76	0
39	DS	110/112 (98%)	1.78	39 (35%) 1 0	55, 76, 86, 89	0
40	BT	131/146 (89%)	0.38	7 (5%) 32 24	27, 44, 73, 86	0
40	DT	131/146 (89%)	0.95	10 (7%) 20 14	42, 59, 78, 86	0
41	BU	116/118 (98%)	-0.13	1 (0%) 81 74	18, 32, 52, 73	0
41	DU	116/118 (98%)	0.59	2 (1%) 69 60	37, 58, 75, 80	0
42	BV	101/101 (100%)	0.12	1 (0%) 79 72	20, 42, 61, 76	0
42	DV	101/101 (100%)	0.75	6 (5%) 28 21	36, 67, 81, 87	0
43	BW	112/113 (99%)	-0.17	0 100 100	20, 33, 51, 84	0
43	DW	112/113 (99%)	0.38	2 (1%) 67 58	32, 47, 65, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	BX	95/96 (98%)	0.02	1 (1%) 78 70	22, 37, 57, 82	0
44	DX	95/96 (98%)	0.79	9 (9%) 14 10	39, 59, 73, 82	0
45	BY	107/110 (97%)	0.52	2 (1%) 66 57	32, 48, 70, 81	0
45	DY	107/110 (97%)	1.14	12 (11%) 10 7	48, 68, 78, 89	0
46	BZ	171/206 (83%)	0.92	17 (9%) 13 9	40, 63, 83, 88	0
46	DZ	174/206 (84%)	1.75	62 (35%) 1 0	64, 82, 94, 97	0
47	B0	83/85 (97%)	0.13	1 (1%) 76 68	23, 38, 52, 66	0
47	D0	83/85 (97%)	1.17	13 (15%) 5 4	36, 61, 72, 81	0
48	B1	97/98 (98%)	0.34	4 (4%) 41 33	21, 42, 65, 74	0
48	D1	97/98 (98%)	0.83	9 (9%) 14 10	30, 54, 76, 82	0
49	B2	70/72 (97%)	0.36	2 (2%) 53 43	32, 48, 63, 87	0
49	D2	70/72 (97%)	0.76	3 (4%) 40 31	50, 67, 78, 83	0
50	B3	59/60 (98%)	0.06	1 (1%) 69 60	21, 37, 62, 81	0
50	D3	59/60 (98%)	0.72	3 (5%) 33 25	44, 60, 77, 87	0
51	B4	69/71 (97%)	1.29	17 (24%) 2 1	54, 76, 90, 98	0
51	D4	69/71 (97%)	1.97	26 (37%) 1 0	80, 90, 95, 99	0
52	B5	59/60 (98%)	-0.17	1 (1%) 69 60	19, 33, 53, 65	0
52	D5	59/60 (98%)	0.40	0 100 100	28, 48, 69, 72	0
53	B6	53/54 (98%)	-0.15	0 100 100	28, 40, 60, 64	0
53	D6	53/54 (98%)	0.90	3 (5%) 29 22	43, 59, 72, 82	0
54	B7	48/49 (97%)	-0.10	1 (2%) 63 54	18, 25, 54, 63	0
54	D7	48/49 (97%)	0.24	2 (4%) 40 32	29, 39, 63, 81	0
55	B8	64/65 (98%)	0.05	1 (1%) 70 61	23, 32, 46, 61	0
55	D8	64/65 (98%)	0.69	1 (1%) 70 61	37, 55, 66, 70	0
56	B9	37/37 (100%)	0.83	3 (8%) 18 13	27, 49, 67, 71	0
56	D9	37/37 (100%)	1.20	5 (13%) 7 5	46, 54, 67, 74	0
All	All	20640/21602 (95%)	0.84	2690 (13%) 7 6	18, 63, 89, 107	0

All (2690) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
33	DI	65	ALA	8.9
9	CI	126	SER	8.6

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Mol	Chain	Res	Type	RSRZ
33	DI	111	PRO	8.3
7	AG	79	ARG	8.1
33	DI	96	ASP	8.0
33	DI	119	PRO	7.9
33	DI	145	VAL	7.9
33	DI	114	LEU	7.5
33	DI	100	ALA	7.1
31	DG	28	VAL	7.1
9	CI	64	THR	6.6
13	AM	124	PRO	6.5
9	CI	9	ARG	6.4
33	DI	120	ILE	6.3
19	CS	71	LEU	6.3
33	DI	93	THR	6.2
33	DI	128	LEU	6.1
9	CI	102	LEU	6.1
13	CM	123	ALA	6.1
26	BA	2120	G	6.0
13	CM	124	PRO	6.0
5	CE	85	GLY	5.9
1	AA	1532	U	5.9
26	BA	2804	C	5.8
1	CA	1532	U	5.8
39	DS	33	LYS	5.8
33	DI	88	ILE	5.8
33	DI	97	ILE	5.7
33	DI	116	LEU	5.6
33	DI	130	TYR	5.6
33	DI	58	LEU	5.6
33	DI	83	ALA	5.5
9	CI	10	ARG	5.5
1	CA	1030(B)	C	5.5
33	DI	144	VAL	5.5
33	DI	124	GLY	5.5
26	BA	2145	C	5.5
8	AH	3	THR	5.4
33	DI	89	TYR	5.4
14	AN	2	ALA	5.4
2	AB	133	LYS	5.4
10	AJ	34	VAL	5.3
7	CG	80	VAL	5.3
5	CE	94	ALA	5.3

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Mol	Chain	Res	Type	RSRZ
51	D4	56	VAL	5.2
33	DI	98	ALA	5.2
26	DA	2138	C	5.2
21	CU	6	ARG	5.1
26	DA	2156	G	5.1
26	DA	2155	G	5.1
3	CC	14	ILE	5.1
13	CM	75	ALA	5.1
10	AJ	75	ILE	5.0
28	BD	2	ALA	5.0
9	CI	56	LEU	5.0
33	DI	118	LYS	5.0
26	DA	2116	G	5.0
33	DI	109	ILE	4.9
13	CM	102	ARG	4.9
33	DI	101	LEU	4.9
11	AK	13	GLN	4.9
4	CD	154	ASN	4.9
22	CV	18	G	4.9
19	CS	13	ASP	4.9
14	CN	25	VAL	4.9
16	AP	82	GLN	4.9
2	AB	129	GLU	4.9
33	DI	127	VAL	4.9
21	CU	5	ASP	4.9
29	BE	89	ASP	4.9
33	DI	146	ALA	4.8
9	CI	19	LEU	4.8
33	DI	72	LEU	4.8
31	BG	49	ASP	4.8
33	DI	85	GLU	4.8
32	BH	2	SER	4.8
46	DZ	150	LEU	4.8
14	CN	5	ALA	4.8
10	AJ	76	ASN	4.8
51	B4	49	PHE	4.8
3	AC	87	LEU	4.8
22	CV	14	A	4.8
33	DI	113	ARG	4.8
13	CM	66	LEU	4.7
39	DS	3	ARG	4.7
33	DI	94	ALA	4.7

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Mol	Chain	Res	Type	RSRZ
33	DI	123	LEU	4.7
16	AP	68	ASP	4.7
19	CS	2	PRO	4.7
33	DI	110	ASP	4.7
1	CA	1115	C	4.7
2	AB	188	ALA	4.7
2	AB	237	ALA	4.7
2	CB	11	LEU	4.7
33	DI	99	GLU	4.7
1	AA	1024	G	4.7
10	CJ	59	SER	4.6
37	BQ	60	ARG	4.6
1	CA	1531	A	4.6
27	DB	118	G	4.6
1	CA	1119	C	4.6
22	AV	24	A	4.6
44	DX	92	LEU	4.6
45	BY	91	GLU	4.6
51	B4	50	VAL	4.6
9	CI	7	THR	4.6
28	DD	262	ARG	4.6
4	AD	167	GLY	4.6
7	CG	83	ALA	4.6
9	CI	46	ALA	4.6
21	CU	14	TRP	4.5
33	DI	68	LEU	4.5
31	DG	2	PRO	4.5
26	BA	2111	C	4.5
9	CI	43	ALA	4.5
22	CV	19	U	4.5
39	DS	7	TYR	4.5
13	AM	123	ALA	4.5
9	CI	30	GLY	4.5
51	D4	49	PHE	4.5
4	CD	158	ILE	4.5
9	CI	13	ALA	4.5
10	CJ	40	LEU	4.5
1	CA	80	G	4.4
6	AF	55	ASP	4.4
14	CN	44	LEU	4.4
28	DD	2	ALA	4.4
33	DI	59	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
2	CB	129	GLU	4.4
1	CA	1030(A)	G	4.4
51	B4	46	GLN	4.4
33	DI	112	LYS	4.4
16	CP	68	ASP	4.4
2	AB	7	VAL	4.3
11	CK	117	ASN	4.3
13	CM	105	THR	4.3
33	DI	108	THR	4.3
3	CC	87	LEU	4.3
4	CD	162	LEU	4.3
51	D4	9	LEU	4.3
14	CN	33	VAL	4.3
7	AG	80	VAL	4.3
14	CN	20	ALA	4.3
30	DF	21	ALA	4.3
33	DI	92	VAL	4.3
45	DY	90	LEU	4.3
33	DI	126	TYR	4.3
9	AI	14	VAL	4.3
9	CI	123	PRO	4.3
54	D7	48	LYS	4.3
56	D9	12	ASP	4.3
1	AA	1001	A	4.2
2	CB	200	ILE	4.2
46	DZ	172	ALA	4.2
33	DI	122	GLU	4.2
33	DI	86	THR	4.2
2	CB	163	PHE	4.2
9	CI	47	LEU	4.2
33	DI	55	ALA	4.2
1	AA	1257	U	4.2
13	CM	100	GLY	4.2
26	DA	2157	G	4.2
33	DI	79	ILE	4.2
45	DY	1	MET	4.2
2	CB	97	TRP	4.2
31	DG	29	TRP	4.2
1	AA	1447	A	4.2
9	CI	65	VAL	4.2
33	DI	142	VAL	4.2
9	CI	45	ALA	4.2

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Mol	Chain	Res	Type	RSRZ
11	CK	49	GLY	4.2
51	D4	57	GLU	4.2
47	D0	69	PHE	4.2
1	CA	1002	G	4.1
13	AM	122	LYS	4.1
16	AP	25	ARG	4.1
14	CN	53	LEU	4.1
3	CC	189	ALA	4.1
3	AC	2	GLY	4.1
8	CH	80	ILE	4.1
3	CC	207	VAL	4.1
26	DA	2133	G	4.1
26	DA	2149	G	4.1
31	BG	119	GLY	4.1
33	DI	140	LEU	4.1
13	CM	98	VAL	4.1
2	CB	237	ALA	4.1
8	AH	94	TYR	4.1
26	BA	2174	C	4.1
26	DA	2139	C	4.1
33	BI	84	GLY	4.1
48	D1	2	SER	4.1
26	DA	2112	G	4.1
14	AN	37	PHE	4.1
32	BH	55	PRO	4.1
33	DI	134	PRO	4.1
2	AB	134	GLU	4.1
26	DA	1026	U	4.1
26	DA	2894	G	4.1
14	CN	22	THR	4.0
42	DV	20	LEU	4.0
1	CA	88	A	4.0
2	CB	165	VAL	4.0
31	DG	17	PRO	4.0
14	CN	2	ALA	4.0
21	CU	16	GLY	4.0
1	CA	1400	C	4.0
14	CN	18	VAL	4.0
21	CU	23	PRO	4.0
46	DZ	171	ILE	4.0
3	CC	201	TYR	4.0
33	BI	89	TYR	4.0

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Mol	Chain	Res	Type	RSRZ
32	BH	59	ARG	4.0
2	CB	177	ALA	4.0
4	AD	155	LEU	4.0
4	CD	194	LEU	4.0
33	DI	136	VAL	4.0
51	D4	44	THR	4.0
9	AI	13	ALA	4.0
10	AJ	69	ASN	4.0
26	DA	2173	A	4.0
19	CS	35	SER	4.0
26	DA	2131	G	4.0
19	AS	84	GLY	3.9
33	DI	84	GLY	3.9
32	BH	58	GLU	3.9
8	AH	2	LEU	3.9
9	CI	36	TYR	3.9
31	DG	109	VAL	3.9
50	D3	2	PRO	3.9
7	CG	81	GLY	3.9
14	CN	61	TRP	3.9
9	CI	124	GLN	3.9
51	D4	50	VAL	3.9
33	DI	137	PRO	3.9
9	AI	7	THR	3.9
10	CJ	48	THR	3.9
31	DG	73	ALA	3.9
20	CT	13	LEU	3.9
10	CJ	94	VAL	3.9
49	B2	70	GLN	3.9
19	CS	69	HIS	3.9
5	AE	124	GLY	3.9
9	AI	56	LEU	3.9
20	AT	13	LEU	3.9
20	AT	74	LYS	3.9
5	CE	100	VAL	3.9
10	AJ	72	VAL	3.9
39	DS	36	TYR	3.9
56	B9	17	ILE	3.9
4	CD	137	SER	3.9
26	DA	2142	C	3.9
2	CB	99	GLY	3.8
9	AI	127	LYS	3.8

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Mol	Chain	Res	Type	RSRZ
8	AH	4	ASP	3.8
9	CI	17	VAL	3.8
7	CG	84	ASN	3.8
11	AK	25	TYR	3.8
21	AU	9	ARG	3.8
26	DA	2137	C	3.8
31	DG	23	PHE	3.8
1	CA	950	U	3.8
13	CM	101	GLN	3.8
4	CD	29	PRO	3.8
31	BG	75	LYS	3.8
10	CJ	93	GLY	3.8
13	CM	68	GLY	3.8
14	CN	60	SER	3.8
9	AI	87	GLN	3.8
3	CC	187	ALA	3.8
7	AG	55	GLY	3.8
10	CJ	42	THR	3.8
39	DS	96	GLY	3.8
1	CA	1034	G	3.8
26	BA	2110	G	3.8
26	DA	2154	G	3.8
14	CN	15	LYS	3.8
26	DA	2789	C	3.8
14	CN	30	ALA	3.8
16	AP	7	ALA	3.8
19	CS	52	TYR	3.8
4	CD	155	LEU	3.8
31	DG	53	LEU	3.8
33	DI	77	LEU	3.8
36	DP	108	LYS	3.7
8	CH	72	PRO	3.7
9	CI	52	ALA	3.7
9	CI	50	LEU	3.7
26	BA	1026	U	3.7
1	AA	630	G	3.7
19	CS	46	GLY	3.7
9	CI	66	ARG	3.7
4	CD	152	SER	3.7
9	CI	26	VAL	3.7
33	DI	138	ILE	3.7
33	DI	143	SER	3.7

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Mol	Chain	Res	Type	RSRZ
32	DH	88	LEU	3.7
9	CI	12	GLU	3.7
26	BA	2181	G	3.7
26	BA	2793	G	3.7
1	CA	949	A	3.7
17	CQ	100	LYS	3.7
26	BA	2135	A	3.7
4	AD	176	LEU	3.7
4	CD	32	ALA	3.7
8	AH	119	LEU	3.7
10	CJ	65	LEU	3.7
4	AD	110	PHE	3.7
1	CA	84	U	3.7
2	CB	21	ARG	3.7
21	CU	17	THR	3.7
7	CG	21	VAL	3.7
56	D9	17	ILE	3.7
1	AA	1001(A)	G	3.7
1	AA	1030(A)	G	3.7
9	AI	126	SER	3.7
26	BA	2115	G	3.7
26	BA	2157	G	3.7
26	BA	2162	G	3.7
26	BA	2805	G	3.7
7	AG	83	ALA	3.7
33	DI	56	LYS	3.7
13	CM	67	GLU	3.7
2	CB	127	ILE	3.7
33	DI	78	THR	3.7
47	D0	3	HIS	3.6
26	DA	2169	A	3.6
1	CA	951	G	3.6
2	AB	66	GLY	3.6
7	CG	5	ARG	3.6
9	CI	83	ARG	3.6
15	AO	89	GLY	3.6
16	AP	81	ARG	3.6
5	CE	13	ILE	3.6
17	CQ	39	SER	3.6
16	CP	5	ARG	3.6
20	CT	74	LYS	3.6
3	CC	13	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
4	CD	134	ASP	3.6
51	D4	45	GLY	3.6
4	CD	88	VAL	3.6
11	CK	30	VAL	3.6
11	CK	31	THR	3.6
10	AJ	71	LEU	3.6
26	DA	362	U	3.6
27	DB	55	U	3.6
16	AP	1	MET	3.6
36	BP	105	LEU	3.6
39	DS	34	HIS	3.6
4	CD	45	GLN	3.6
16	CP	12	LYS	3.6
28	BD	38	LYS	3.6
31	DG	136	ARG	3.6
40	BT	37	GLY	3.6
1	AA	1030(B)	C	3.6
1	CA	1492	A	3.6
10	AJ	64	GLU	3.6
2	CB	236	TYR	3.6
33	DI	129	THR	3.6
32	BH	67	LEU	3.6
1	CA	973	G	3.6
26	BA	2121	G	3.6
2	CB	161	ALA	3.6
9	CI	11	LYS	3.6
28	DD	38	LYS	3.6
7	CG	4	ARG	3.6
13	CM	94	ARG	3.6
4	CD	208	SER	3.6
32	DH	44	VAL	3.6
33	BI	10	GLU	3.6
13	CM	23	TYR	3.6
7	CG	16	LEU	3.6
8	CH	9	MET	3.6
26	DA	2114	A	3.6
10	CJ	37	PRO	3.6
33	DI	69	LYS	3.5
1	CA	1001(A)	G	3.5
10	CJ	54	PHE	3.5
11	CK	118	GLY	3.5
2	AB	165	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
12	AL	18	VAL	3.5
3	AC	62	ASP	3.5
9	CI	79	LEU	3.5
16	AP	38	TYR	3.5
1	CA	948	C	3.5
10	CJ	46	ARG	3.5
2	AB	135	GLN	3.5
26	BA	12	U	3.5
26	BA	2113	U	3.5
9	CI	59	PHE	3.5
46	DZ	104	PHE	3.5
3	CC	2	GLY	3.5
2	AB	12	GLU	3.5
2	CB	93	VAL	3.5
2	CB	230	VAL	3.5
13	CM	60	VAL	3.5
1	CA	1033	G	3.5
8	AH	89	PRO	3.5
13	CM	87	TYR	3.5
44	DX	69	TYR	3.5
22	AV	23	A	3.5
26	BA	2146	C	3.5
3	CC	5	ILE	3.5
10	CJ	47	PHE	3.5
7	AG	82	GLY	3.5
11	AK	14	VAL	3.5
45	DY	51	VAL	3.5
9	CI	2	GLU	3.5
5	AE	92	LYS	3.5
13	CM	31	LYS	3.5
33	DI	87	LYS	3.5
9	CI	21	PRO	3.5
9	AI	125	TYR	3.5
14	CN	21	TYR	3.5
16	CP	69	THR	3.5
26	DA	2168	G	3.5
13	CM	78	ILE	3.5
26	DA	2117	A	3.5
3	CC	195	VAL	3.5
9	CI	14	VAL	3.5
3	CC	188	LEU	3.5
4	CD	34	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
13	CM	48	LEU	3.5
13	CM	121	LYS	3.5
31	DG	76	SER	3.5
13	CM	113	PRO	3.5
21	CU	9	ARG	3.5
51	B4	48	ARG	3.5
13	CM	106	ASN	3.5
20	CT	9	ASN	3.5
33	DI	63	ALA	3.5
33	DI	51	ILE	3.4
26	DA	2125	G	3.4
3	AC	13	GLY	3.4
9	CI	68	GLY	3.4
46	DZ	114	GLY	3.4
9	AI	19	LEU	3.4
33	DI	62	LYS	3.4
9	CI	20	ARG	3.4
10	CJ	43	ARG	3.4
14	CN	3	ARG	3.4
2	CB	205	ASP	3.4
9	CI	27	THR	3.4
39	DS	39	ILE	3.4
13	CM	122	LYS	3.4
21	AU	2	GLY	3.4
39	DS	56	LEU	3.4
47	D0	84	LEU	3.4
1	CA	1365	G	3.4
26	DA	2166	G	3.4
26	BA	889	C	3.4
13	CM	92	HIS	3.4
31	DG	169	ALA	3.4
31	BG	146	TYR	3.4
9	AI	85	LEU	3.4
33	DI	15	VAL	3.4
1	AA	1033	G	3.4
1	CA	1202	G	3.4
16	CP	48	TRP	3.4
9	CI	63	ILE	3.4
1	CA	1322	C	3.4
8	AH	32	LYS	3.4
8	CH	2	LEU	3.4
39	DS	48	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
5	AE	21	ALA	3.4
9	CI	15	ALA	3.4
1	CA	1126	U	3.4
4	CD	70	ILE	3.4
4	CD	169	LYS	3.4
31	DG	20	ILE	3.4
1	CA	968	A	3.4
4	CD	20	TYR	3.4
11	AK	125	PHE	3.4
19	CS	22	LEU	3.3
22	AV	13	A	3.4
22	CV	15	A	3.4
26	DA	2135	A	3.4
1	CA	1154	G	3.3
6	AF	88	VAL	3.3
26	BA	614(B)	G	3.3
26	DA	1171	G	3.3
33	DI	81	VAL	3.3
1	CA	980	C	3.3
20	CT	80	ARG	3.3
15	AO	19	PRO	3.3
3	AC	182	ILE	3.3
10	CJ	74	ILE	3.3
3	AC	15	THR	3.3
11	AK	36	ASP	3.3
16	AP	2	VAL	3.3
1	CA	1151	A	3.3
26	BA	2173	A	3.3
1	CA	1030	C	3.3
26	BA	2178	C	3.3
26	BA	1176	G	3.3
26	DA	2115	G	3.3
13	AM	121	LYS	3.3
9	CI	82	ALA	3.3
10	AJ	20	ALA	3.3
10	CJ	38	ILE	3.3
2	CB	122	PHE	3.3
26	DA	2109	U	3.3
33	DI	107	VAL	3.3
4	CD	102	ASP	3.3
33	DI	121	LYS	3.3
18	CR	60	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	CA	971	G	3.3
1	CA	1127	G	3.3
27	DB	23	G	3.3
3	CC	12	LEU	3.3
13	CM	90	LEU	3.3
14	CN	39	LEU	3.3
45	DY	57	GLN	3.3
13	CM	45	VAL	3.3
33	DI	76	THR	3.3
13	AM	6	GLY	3.3
17	CQ	97	SER	3.3
20	AT	103	GLY	3.3
33	BI	124	GLY	3.3
3	CC	48	TYR	3.3
14	CN	34	TYR	3.3
26	BA	2167	U	3.3
9	CI	29	ASN	3.3
33	DI	60	GLU	3.3
39	DS	57	LYS	3.3
10	CJ	6	ILE	3.3
17	CQ	44	ALA	3.3
2	CB	145	LEU	3.3
1	AA	1027	C	3.3
9	AI	59	PHE	3.3
14	CN	23	ARG	3.3
5	CE	20	GLN	3.3
1	CA	1220	G	3.3
4	CD	173	TRP	3.3
5	AE	88	LYS	3.2
11	CK	75	TYR	3.2
2	CB	134	GLU	3.2
8	AH	5	PRO	3.2
2	AB	63	MET	3.2
14	CN	42	ILE	3.2
39	DS	35	ILE	3.2
2	CB	154	LEU	3.2
1	AA	1286	A	3.2
1	CA	1275	A	3.2
9	CI	44	VAL	3.2
14	AN	18	VAL	3.2
1	CA	1214	C	3.2
13	CM	103	THR	3.2

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Mol	Chain	Res	Type	RSRZ
26	BA	888	C	3.2
26	BA	2179	C	3.2
11	CK	25	TYR	3.2
6	CF	83	ASP	3.2
10	AJ	73	ASP	3.2
1	CA	1121	U	3.2
1	CA	1219	U	3.2
10	CJ	77	PRO	3.2
2	CB	102	LEU	3.2
5	CE	119	LEU	3.2
14	AN	5	ALA	3.2
46	DZ	41	LEU	3.2
8	CH	53	VAL	3.2
31	DG	31	VAL	3.2
1	CA	1035	A	3.2
2	CB	22	LYS	3.2
26	BA	2114	A	3.2
26	BA	2119	A	3.2
3	CC	185	GLY	3.2
16	AP	22	THR	3.2
17	CQ	80	GLY	3.2
19	CS	79	THR	3.2
21	CU	2	GLY	3.2
28	BD	41	GLY	3.2
33	DI	90	GLY	3.2
2	CB	201	ILE	3.2
9	AI	81	ILE	3.2
10	AJ	96	ILE	3.2
10	CJ	75	ILE	3.2
32	BH	148	ILE	3.2
26	DA	2132	U	3.2
2	CB	187	LEU	3.2
3	CC	190	ARG	3.2
5	AE	102	ALA	3.2
24	CX	31	G	3.2
26	BA	2116	G	3.2
26	DA	2153	G	3.2
27	DB	56	G	3.2
46	DZ	88	PHE	3.2
10	CJ	49	VAL	3.2
2	CB	133	LYS	3.2
4	CD	90	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	AA	1531	A	3.2
21	AU	23	PRO	3.2
7	CG	33	ASP	3.2
1	CA	1028	C	3.2
7	CG	37	ASN	3.2
13	CM	77	ASN	3.2
26	DA	2161	C	3.2
26	DA	2804	C	3.2
3	CC	71	ALA	3.2
13	CM	107	ALA	3.2
15	CO	68	ARG	3.2
33	DI	53	ALA	3.2
49	B2	69	ARG	3.2
10	CJ	34	VAL	3.2
10	CJ	44	VAL	3.2
13	CM	117	VAL	3.2
31	BG	182	LYS	3.2
1	AA	951	G	3.2
1	AA	1224	G	3.2
1	CA	1117	G	3.2
1	CA	1530	G	3.2
4	CD	167	GLY	3.2
26	DA	171	G	3.2
26	DA	271(M)	G	3.2
31	DG	71	THR	3.2
32	BH	116	GLU	3.2
3	CC	7	PRO	3.2
10	AJ	4	ILE	3.2
4	AD	152	SER	3.1
6	CF	79	LEU	3.1
7	CG	78	ARG	3.1
10	AJ	46	ARG	3.1
21	AU	24	ARG	3.1
21	CU	10	ARG	3.1
31	DG	3	LEU	3.1
10	CJ	32	ALA	3.1
13	AM	2	ALA	3.1
14	AN	59	ALA	3.1
31	BG	79	ASN	3.1
13	CM	27	LYS	3.1
1	AA	1029	C	3.1
1	CA	1364	U	3.1

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Mol	Chain	Res	Type	RSRZ
14	CN	37	PHE	3.1
16	AP	80	PHE	3.1
4	AD	170	VAL	3.1
43	DW	85	VAL	3.1
51	B4	56	VAL	3.1
46	DZ	118	GLN	3.1
5	AE	23	GLY	3.1
9	CI	39	GLY	3.1
3	AC	95	THR	3.1
11	AK	31	THR	3.1
31	BG	35	GLU	3.1
10	AJ	98	ILE	3.1
13	CM	4	ILE	3.1
1	CA	1178	G	3.1
1	CA	1190	G	3.1
26	BA	2141	G	3.1
26	DA	2805	G	3.1
39	BS	3	ARG	3.1
10	CJ	56	HIS	3.1
24	CX	59	A	3.1
26	BA	2144	U	3.1
1	CA	1038	C	3.1
1	CA	1397	C	3.1
2	CB	14	GLY	3.1
14	CN	51	GLY	3.1
26	BA	1914	C	3.1
32	BH	14	GLY	3.1
13	CM	69	GLU	3.1
31	BG	48	GLU	3.1
2	CB	234	PRO	3.1
33	DI	80	PRO	3.1
7	CG	79	ARG	3.1
13	CM	88	ARG	3.1
32	BH	64	LEU	3.1
3	CC	22	TRP	3.1
9	CI	5	TYR	3.1
1	AA	220	G	3.1
1	AA	1002	G	3.1
1	CA	1032	G	3.1
6	CF	40	VAL	3.1
14	CN	43	CYS	3.1
26	BA	2125	G	3.1

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Mol	Chain	Res	Type	RSRZ
26	DA	2147	G	3.1
1	CA	1363(A)	A	3.1
27	DB	25	A	3.1
4	CD	160	GLN	3.1
11	AK	118	GLY	3.1
19	CS	49	ILE	3.1
1	CA	1363	C	3.1
5	CE	24	ARG	3.1
13	AM	102	ARG	3.1
17	AQ	68	ARG	3.1
19	AS	29	ARG	3.1
21	CU	15	ARG	3.1
32	DH	98	LEU	3.1
51	B4	52	THR	3.1
39	DS	62	LYS	3.1
9	AI	106	ALA	3.1
8	CH	82	HIS	3.1
14	AN	16	PHE	3.1
14	AN	36	PHE	3.1
32	DH	2	SER	3.1
3	CC	170	GLN	3.1
51	B4	54	GLY	3.1
1	AA	532	A	3.1
1	CA	506	G	3.1
1	CA	941	G	3.1
1	CA	1156	G	3.1
24	CX	46	G	3.1
26	BA	2117	A	3.1
4	AD	145	GLU	3.1
4	CD	159	ARG	3.1
10	CJ	5	ARG	3.1
33	DI	50	ARG	3.1
7	CG	88	PRO	3.1
31	BG	120	LEU	3.1
33	DI	125	GLU	3.1
26	DA	2316	C	3.1
3	CC	128	PHE	3.0
14	CN	36	PHE	3.0
9	CI	125	TYR	3.0
21	AU	21	TYR	3.0
10	AJ	86	MET	3.0
18	CR	45	SER	3.0

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Mol	Chain	Res	Type	RSRZ
46	BZ	154	ASP	3.0
3	CC	9	GLY	3.0
31	DG	24	GLY	3.0
33	DI	106	GLY	3.0
19	CS	36	ARG	3.0
19	CS	62	ILE	3.0
2	AB	215	LEU	3.0
7	AG	16	LEU	3.0
8	CH	99	GLU	3.0
9	CI	98	PRO	3.0
14	CN	8	GLU	3.0
14	CN	46	GLU	3.0
31	BG	30	GLU	3.0
48	B1	98	LEU	3.0
1	CA	963	G	3.0
1	CA	1003	G	3.0
9	CI	18	PHE	3.0
16	AP	48	TRP	3.0
46	DZ	1	MET	3.0
1	CA	979	C	3.0
26	DA	34	C	3.0
26	DA	2140	C	3.0
4	AD	102	ASP	3.0
4	CD	141	ARG	3.0
28	BD	276	LYS	3.0
33	BI	112	LYS	3.0
33	DI	141	LYS	3.0
2	CB	121	LEU	3.0
14	CN	6	LEU	3.0
12	AL	5	PRO	3.0
13	CM	41	PRO	3.0
29	DE	163	GLU	3.0
31	DG	59	GLU	3.0
33	BI	111	PRO	3.0
1	AA	1005	A	3.0
1	CA	414	A	3.0
13	CM	118	ALA	3.0
26	DA	652(B)	A	3.0
5	CE	90	VAL	3.0
32	DH	115	VAL	3.0
34	DN	9	VAL	3.0
46	BZ	105	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	CA	9	G	3.0
1	CA	1224	G	3.0
7	AG	85	TYR	3.0
16	AP	39	TYR	3.0
19	CS	80	TYR	3.0
1	AA	163	C	3.0
1	CA	1113	C	3.0
4	CD	87	GLY	3.0
9	CI	70	LYS	3.0
33	BI	88	ILE	3.0
37	DQ	60	ARG	3.0
4	AD	83	SER	3.0
45	BY	107	ASP	3.0
46	DZ	155	LEU	3.0
4	CD	163	GLU	3.0
48	D1	75	GLU	3.0
50	D3	60	GLU	3.0
26	DA	2118	U	3.0
7	CG	17	VAL	3.0
10	AJ	47	PHE	3.0
51	D4	40	HIS	3.0
1	CA	1236	A	3.0
19	CS	70	LYS	3.0
21	CU	24	ARG	3.0
31	DG	146	TYR	3.0
33	DI	52	ARG	3.0
3	AC	80	GLY	3.0
5	CE	22	GLY	3.0
9	CI	96	LEU	3.0
10	CJ	71	LEU	3.0
16	AP	6	LEU	3.0
1	AA	380	G	3.0
1	AA	1026	G	3.0
26	BA	2112	G	3.0
26	BA	2147	G	3.0
26	DA	10	G	3.0
26	DA	2162	G	3.0
27	DB	119	G	3.0
31	DG	4	ASP	3.0
31	DG	126	ASP	3.0
1	CA	1029	C	3.0
19	CS	33	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	AA	1446	U	3.0
4	AD	182	LYS	2.9
3	CC	131	ARG	2.9
3	CC	167	TRP	2.9
8	AH	92	ARG	2.9
14	CN	31	ARG	2.9
31	DG	140	ILE	2.9
2	AB	221	LEU	2.9
3	AC	175	LEU	2.9
8	CH	66	GLY	2.9
12	CL	29	GLY	2.9
32	BH	71	LEU	2.9
37	BQ	12	GLN	2.9
37	BQ	61	GLY	2.9
2	CB	231	GLU	2.9
11	CK	36	ASP	2.9
46	DZ	130	PRO	2.9
51	D4	29	PRO	2.9
32	BH	56	SER	2.9
33	DI	91	SER	2.9
1	AA	1030(C)	G	2.9
26	BA	2168	G	2.9
26	BA	2792	G	2.9
26	DA	2299	G	2.9
1	CA	1116	C	2.9
1	CA	1218	C	2.9
3	CC	117	ALA	2.9
9	AI	45	ALA	2.9
13	AM	107	ALA	2.9
24	CX	34	C	2.9
26	BA	2803	C	2.9
10	CJ	87	THR	2.9
39	DS	29	PHE	2.9
3	AC	14	ILE	2.9
8	CH	100	ILE	2.9
9	CI	74	ILE	2.9
2	AB	33	TYR	2.9
9	CI	6	GLY	2.9
51	D4	63	TYR	2.9
8	CH	27	PRO	2.9
32	DH	55	PRO	2.9
10	CJ	76	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
31	DG	147	ASP	2.9
40	DT	1	MET	2.9
2	CB	13	ALA	2.9
31	DG	171	ALA	2.9
7	AG	4	ARG	2.9
9	CI	107	ARG	2.9
26	DA	2108	C	2.9
31	BG	16	ARG	2.9
31	DG	115	ARG	2.9
26	DA	2206	G	2.9
26	DA	2893	G	2.9
10	CJ	23	ILE	2.9
32	DH	9	ILE	2.9
13	CM	34	LEU	2.9
18	CR	76	LEU	2.9
46	DZ	125	LEU	2.9
9	CI	69	GLY	2.9
9	CI	115	GLY	2.9
2	AB	126	GLU	2.9
3	AC	35	GLU	2.9
29	BE	73	GLU	2.9
31	DG	54	GLU	2.9
4	CD	28	SER	2.9
9	CI	106	ALA	2.9
14	CN	11	LYS	2.9
14	CN	50	LYS	2.9
32	DH	50	VAL	2.9
45	DY	72	VAL	2.9
2	CB	181	PHE	2.9
4	CD	209	ARG	2.9
5	AE	120	THR	2.9
10	CJ	60	ARG	2.9
18	AR	42	ARG	2.9
47	D0	44	ARG	2.9
3	CC	152	ILE	2.9
39	DS	54	LEU	2.9
48	B1	97	LEU	2.9
26	BA	2108	C	2.9
1	AA	102	G	2.9
2	CB	91	PRO	2.9
26	DA	2151	G	2.9
31	DG	12	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
5	CE	122	GLU	2.9
9	CI	35	GLU	2.9
46	DZ	168	GLU	2.9
14	AN	15	LYS	2.9
34	BN	84	LYS	2.9
3	AC	65	ALA	2.9
3	CC	133	ALA	2.9
8	CH	19	VAL	2.9
8	CH	97	VAL	2.9
7	AG	115	ARG	2.9
13	CM	99	ARG	2.9
16	CP	26	ARG	2.9
17	AQ	99	SER	2.9
46	BZ	52	SER	2.9
27	DB	29	A	2.9
39	DS	58	LEU	2.9
44	BX	95	LEU	2.9
46	DZ	124	ILE	2.9
14	AN	14	PRO	2.8
31	DG	32	PRO	2.8
31	DG	41	GLN	2.8
31	DG	142	PRO	2.8
1	CA	1129	C	2.8
3	CC	161	GLU	2.8
5	CE	81	GLU	2.8
10	CJ	64	GLU	2.8
33	BI	121	LYS	2.8
49	D2	66	GLU	2.8
1	CA	630	G	2.8
1	CA	1017	G	2.8
2	CB	81	VAL	2.8
3	AC	66	VAL	2.8
3	CC	168	ALA	2.8
4	CD	170	VAL	2.8
2	CB	57	PHE	2.8
4	AD	209	ARG	2.8
7	CG	7	ALA	2.8
15	AO	27	VAL	2.8
26	DA	2160	G	2.8
39	DS	98	VAL	2.8
51	D4	10	VAL	2.8
9	AI	18	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
9	CI	104	ARG	2.8
46	BZ	136	PHE	2.8
10	CJ	17	ASP	2.8
31	DG	97	ASP	2.8
33	DI	133	HIS	2.8
5	AE	119	LEU	2.8
18	CR	47	THR	2.8
26	DA	2119	A	2.8
26	DA	2134	A	2.8
4	AD	23	GLY	2.8
20	CT	103	GLY	2.8
37	DQ	61	GLY	2.8
9	CI	49	PRO	2.8
10	AJ	37	PRO	2.8
13	CM	120	LYS	2.8
15	CO	76	GLU	2.8
26	BA	271(K)	U	2.8
26	DA	2144	U	2.8
51	D4	25	TYR	2.8
1	CA	1118	C	2.8
5	CE	86	ALA	2.8
7	AG	78	ARG	2.8
15	CO	79	ARG	2.8
19	CS	75	ALA	2.8
26	BA	154(A)	C	2.8
26	BA	2142	C	2.8
26	DA	1043	C	2.8
37	DQ	106	VAL	2.8
40	BT	131	ALA	2.8
46	BZ	112	ARG	2.8
31	DG	132	ASN	2.8
16	AP	19	ILE	2.8
19	CS	16	LEU	2.8
1	AA	79	G	2.8
1	CA	1331	G	2.8
13	CM	109	THR	2.8
26	DA	2318	G	2.8
26	DA	2802	G	2.8
31	DG	93	THR	2.8
1	CA	250	A	2.8
1	CA	1493	A	2.8
4	CD	2	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
26	BA	2170	A	2.8
27	DB	120	A	2.8
33	DI	132	PRO	2.8
19	CS	73	GLU	2.8
3	CC	138	VAL	2.8
5	CE	105	VAL	2.8
8	AH	85	ARG	2.8
11	CK	80	VAL	2.8
13	AM	108	ARG	2.8
14	CN	12	ARG	2.8
18	AR	60	ALA	2.8
22	AV	20	U	2.8
31	BG	109	VAL	2.8
40	DT	131	ALA	2.8
4	CD	176	LEU	2.8
4	CD	202	LEU	2.8
5	CE	89	ILE	2.8
9	CI	99	LEU	2.8
13	CM	25	ILE	2.8
39	DS	4	LEU	2.8
1	AA	1363	C	2.8
26	BA	2143	C	2.8
26	DA	1536	C	2.8
26	DA	2174	C	2.8
6	AF	17	SER	2.8
7	AG	77	SER	2.8
9	CI	71	SER	2.8
51	D4	52	THR	2.8
5	CE	10	MET	2.8
2	CB	75	LYS	2.8
39	DS	11	LYS	2.8
9	CI	67	GLY	2.8
1	CA	1222	G	2.8
10	AJ	77	PRO	2.8
26	DA	2120	G	2.8
33	DI	54	GLN	2.8
1	CA	1250	A	2.8
4	AD	150	GLU	2.8
10	CJ	83	GLU	2.8
55	B8	65	GLU	2.8
9	CI	121	ARG	2.8
13	CM	64	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
21	AU	14	TRP	2.8
33	DI	67	ARG	2.8
40	DT	125	ARG	2.8
9	AI	41	VAL	2.8
46	DZ	174	VAL	2.8
2	AB	13	ALA	2.8
12	CL	69	TYR	2.8
31	DG	6	ALA	2.8
40	BT	130	ALA	2.8
46	DZ	17	ALA	2.8
1	AA	1040	U	2.8
8	CH	39	LEU	2.8
14	CN	7	ILE	2.8
15	CO	3	ILE	2.8
19	CS	5	LEU	2.8
27	DB	1	U	2.8
4	CD	165	MET	2.8
13	CM	43	THR	2.8
32	BH	140	LYS	2.8
20	AT	70	SER	2.8
26	DA	2136	C	2.8
4	AD	2	GLY	2.8
4	AD	87	GLY	2.8
4	CD	180	GLY	2.8
6	CF	44	GLY	2.8
9	CI	24	GLY	2.8
9	CI	100	GLY	2.8
13	CM	119	GLY	2.8
41	BU	117	GLN	2.7
2	CB	178	ARG	2.7
17	CQ	24	GLU	2.7
31	BG	137	GLU	2.7
8	AH	26	VAL	2.7
9	CI	41	VAL	2.7
10	CJ	72	VAL	2.7
11	CK	84	VAL	2.7
46	DZ	161	VAL	2.7
1	AA	1023	G	2.7
1	CA	11	G	2.7
1	CA	853	G	2.7
1	CA	1024	G	2.7
1	CA	1447	A	2.7

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Mol	Chain	Res	Type	RSRZ
2	AB	123	ALA	2.7
3	CC	163	ALA	2.7
7	AG	26	PHE	2.7
18	AR	76	LEU	2.7
26	BA	11	G	2.7
26	BA	548	A	2.7
31	DG	102	PHE	2.7
2	CB	196	LEU	2.7
5	CE	151	LEU	2.7
9	CI	4	TYR	2.7
31	DG	25	TYR	2.7
22	AV	19	U	2.7
2	CB	90	MET	2.7
10	CJ	14	LYS	2.7
51	D4	28	LYS	2.7
31	DG	156	ASP	2.7
7	CG	77	SER	2.7
32	DH	39	PRO	2.7
1	CA	1114	C	2.7
1	CA	1234	C	2.7
24	AX	67	C	2.7
26	BA	2107	C	2.7
31	BG	26	GLN	2.7
10	CJ	61	GLU	2.7
31	DG	35	GLU	2.7
33	DI	10	GLU	2.7
33	DI	48	GLU	2.7
2	AB	15	VAL	2.7
3	CC	186	PHE	2.7
4	AD	5	ILE	2.7
4	AD	120	LEU	2.7
4	CD	146	ILE	2.7
8	CH	31	PHE	2.7
9	CI	61	ALA	2.7
15	AO	3	ILE	2.7
37	DQ	104	PHE	2.7
2	CB	40	HIS	2.7
3	CC	23	TYR	2.7
9	CI	62	TYR	2.7
16	AP	13	HIS	2.7
34	BN	72	TYR	2.7
1	AA	143	A	2.7

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Mol	Chain	Res	Type	RSRZ
9	CI	118	LYS	2.7
24	CX	35	A	2.7
24	CX	43	A	2.7
26	DA	2170	A	2.7
27	DB	26	A	2.7
1	AA	68	G	2.7
1	CA	942	G	2.7
1	CA	1120	G	2.7
1	CA	1138	G	2.7
1	CA	1343	G	2.7
24	CX	42	G	2.7
26	DA	2110	G	2.7
27	DB	61	G	2.7
10	AJ	78	ASN	2.7
3	CC	192	THR	2.7
3	CC	17	ASP	2.7
4	AD	124	GLY	2.7
4	CD	23	GLY	2.7
14	CN	29	ARG	2.7
31	DG	87	PRO	2.7
2	AB	109	SER	2.7
7	CG	74	GLU	2.7
13	AM	50	GLU	2.7
34	BN	68	GLU	2.7
35	DO	68	GLU	2.7
2	CB	7	VAL	2.7
9	CI	86	VAL	2.7
1	CA	970	C	2.7
3	CC	129	ALA	2.7
6	CF	45	LEU	2.7
8	AH	80	ILE	2.7
9	AI	43	ALA	2.7
9	CI	33	PHE	2.7
26	BA	2175	C	2.7
27	DB	6	C	2.7
27	DB	30	C	2.7
31	DG	172	LEU	2.7
33	BI	109	ILE	2.7
33	BI	146	ALA	2.7
36	BP	12	ALA	2.7
39	DS	12	PHE	2.7
3	AC	167	TRP	2.7

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Mol	Chain	Res	Type	RSRZ
4	CD	9	CYS	2.7
17	AQ	14	LYS	2.7
17	AQ	100	LYS	2.7
3	AC	29	TYR	2.7
7	CG	18	TYR	2.7
21	AU	18	TYR	2.7
26	DA	6	A	2.7
19	CS	63	THR	2.7
26	BA	2118	U	2.7
3	CC	156	ARG	2.7
13	AM	104	ARG	2.7
13	AM	114	ARG	2.7
13	CM	71	ARG	2.7
31	DG	127	GLY	2.7
9	CI	32	ASP	2.7
42	DV	26	ASP	2.7
1	AA	1530	G	2.7
26	BA	2155	G	2.7
26	BA	2166	G	2.7
26	DA	2159	G	2.7
27	DB	54	G	2.7
46	DZ	142	SER	2.7
9	AI	17	VAL	2.7
2	CB	41	ILE	2.7
4	CD	164	ALA	2.7
5	CE	84	PHE	2.7
7	AG	2	ALA	2.7
31	DG	125	PHE	2.7
31	DG	141	PHE	2.7
51	B4	59	PHE	2.7
4	AD	173	TRP	2.7
7	AG	156	TRP	2.7
10	CJ	62	HIS	2.7
2	CB	31	TYR	2.7
7	CG	85	TYR	2.7
26	DA	2143	C	2.7
4	CD	73	ARG	2.7
13	CM	80	ARG	2.7
31	DG	16	ARG	2.7
46	BZ	80	ARG	2.7
4	CD	183	GLY	2.7
8	CH	130	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
9	AI	98	PRO	2.7
9	AI	115	GLY	2.7
16	AP	44	THR	2.7
21	AU	4	GLY	2.7
32	DH	100	GLY	2.7
33	BI	86	THR	2.7
36	BP	66	GLY	2.7
47	D0	76	GLY	2.7
1	AA	222	U	2.7
22	AV	12	A	2.7
9	CI	75	ASP	2.7
9	CI	105	ASP	2.7
10	AJ	17	ASP	2.7
19	AS	13	ASP	2.7
31	DG	116	ASP	2.7
9	AI	2	GLU	2.7
9	CI	87	GLN	2.7
10	AJ	33	GLN	2.7
2	CB	136	VAL	2.7
17	AQ	19	VAL	2.7
18	CR	83	GLU	2.7
31	DG	37	VAL	2.7
39	DS	69	VAL	2.7
2	AB	11	LEU	2.7
2	CB	44	LEU	2.7
2	CB	222	ILE	2.6
3	CC	124	ILE	2.6
31	DG	139	LEU	2.7
39	DS	52	SER	2.7
3	AC	10	PHE	2.6
20	AT	21	LYS	2.6
32	BH	13	LYS	2.6
5	CE	138	ALA	2.6
45	DY	16	ALA	2.6
46	DZ	136	PHE	2.6
1	CA	1361	G	2.6
26	BA	1117	G	2.6
14	CN	40	CYS	2.6
3	CC	155	GLY	2.6
4	CD	51	PRO	2.6
5	CE	97	GLY	2.6
9	AI	67	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
15	CO	89	GLY	2.6
16	AP	15	PRO	2.6
1	CA	90	U	2.6
1	CA	1212	U	2.6
2	CB	98	LEU	2.6
4	AD	157	LEU	2.6
4	CD	150	GLU	2.6
6	CF	75	LEU	2.6
7	CG	12	LEU	2.6
10	AJ	8	LEU	2.6
11	AK	92	GLU	2.6
13	CM	73	GLU	2.6
16	CP	62	VAL	2.6
26	BA	2122	U	2.6
14	AN	7	ILE	2.6
18	CR	84	LYS	2.6
33	BI	131	LYS	2.6
39	DS	32	LEU	2.6
51	D4	65	ASP	2.6
19	CS	31	ILE	2.6
25	AY	73	A	2.6
39	DS	55	ALA	2.6
2	AB	97	TRP	2.6
2	CB	199	TYR	2.6
16	CP	8	ARG	2.6
2	AB	202	PRO	2.6
2	CB	227	GLY	2.6
2	CB	232	PRO	2.6
8	AH	90	GLY	2.6
8	CH	71	GLY	2.6
10	AJ	36	GLY	2.6
10	AJ	93	GLY	2.6
20	CT	69	GLY	2.6
46	BZ	106	GLY	2.6
21	CU	8	THR	2.6
1	CA	76	C	2.6
1	CA	1217	C	2.6
1	CA	1321	C	2.6
2	CB	118	LEU	2.6
6	AF	48	LEU	2.6
13	AM	106	ASN	2.6
19	CS	60	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
26	BA	885	C	2.6
26	BA	2188	C	2.6
3	CC	134	ILE	2.6
4	AD	156	GLU	2.6
5	AE	80	ILE	2.6
5	CE	79	GLU	2.6
7	CG	11	GLN	2.6
7	CG	129	GLU	2.6
13	CM	22	ILE	2.6
31	BG	164	GLU	2.6
31	DG	157	ILE	2.6
4	CD	193	ASP	2.6
6	AF	70	ASP	2.6
16	CP	47	ASP	2.6
3	CC	113	ALA	2.6
3	CC	149	ALA	2.6
14	CN	16	PHE	2.6
31	DG	117	PHE	2.6
33	DI	115	ALA	2.6
37	DQ	136	ALA	2.6
1	CA	1014	A	2.6
1	CA	1251	A	2.6
46	DZ	149	SER	2.6
4	CD	47	ARG	2.6
36	DP	15	ARG	2.6
19	CS	34	TRP	2.6
4	CD	4	TYR	2.6
3	CC	80	GLY	2.6
4	CD	6	GLY	2.6
13	CM	89	GLY	2.6
3	AC	26	LYS	2.6
10	AJ	7	LYS	2.6
13	AM	31	LYS	2.6
13	AM	115	LYS	2.6
1	CA	1355	G	2.6
1	CA	1373	G	2.6
1	CA	1401	G	2.6
2	AB	136	VAL	2.6
2	AB	187	LEU	2.6
4	CD	5	ILE	2.6
7	CG	61	VAL	2.6
20	CT	10	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
16	CP	4	ILE	2.6
26	DA	2148	G	2.6
31	BG	160	VAL	2.6
32	DH	67	LEU	2.6
32	DH	76	VAL	2.6
34	BN	53	VAL	2.6
46	DZ	157	LEU	2.6
8	CH	38	ILE	2.6
2	CB	37	ASN	2.6
4	AD	154	ASN	2.6
9	CI	38	GLN	2.6
39	DS	61	ASN	2.6
51	D4	30	GLU	2.6
2	CB	77	ALA	2.6
9	AI	46	ALA	2.6
18	CR	43	PHE	2.6
19	CS	24	ALA	2.6
33	DI	14	ASP	2.6
40	DT	130	ALA	2.6
1	CA	1112	C	2.6
1	CA	1149	C	2.6
10	CJ	13	HIS	2.6
14	AN	60	SER	2.6
19	AS	35	SER	2.6
37	DQ	59	ARG	2.6
1	AA	149	A	2.6
1	CA	1030(D)	A	2.6
1	CA	1213	A	2.6
26	DA	896	A	2.6
4	AD	38	TYR	2.6
4	CD	69	GLY	2.6
8	CH	74	PRO	2.6
9	AI	5	TYR	2.6
11	AK	123	LYS	2.6
12	CL	126	LYS	2.6
13	CM	21	TYR	2.6
20	AT	96	GLY	2.6
44	DX	86	GLY	2.6
56	D9	30	PRO	2.6
4	AD	204	ILE	2.6
16	CP	53	VAL	2.6
32	DH	107	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
47	D0	43	THR	2.6
4	AD	179	GLU	2.6
18	CR	46	GLU	2.6
2	CB	173	ALA	2.6
7	AG	84	ASN	2.6
10	AJ	11	PHE	2.6
53	D6	22	ALA	2.6
1	AA	1036	G	2.5
1	CA	407	G	2.5
13	CM	47	ASP	2.6
1	CA	1025	U	2.5
7	AG	153	HIS	2.5
9	AI	9	ARG	2.5
10	AJ	60	ARG	2.5
16	CP	71	ARG	2.5
19	AS	78	ARG	2.5
21	AU	15	ARG	2.5
32	DH	97	ARG	2.5
1	AA	76	C	2.5
1	AA	454	C	2.5
1	AA	1007	C	2.5
26	BA	271(J)	C	2.5
26	DA	652(T)	C	2.5
32	DH	134	SER	2.5
2	CB	27	LYS	2.5
9	AI	95	LYS	2.5
2	CB	202	PRO	2.5
26	BA	887	A	2.5
27	DB	58	A	2.5
3	AC	204	LEU	2.5
4	CD	96	LEU	2.5
14	AN	6	LEU	2.5
21	AU	11	GLY	2.5
4	AD	88	VAL	2.5
11	CK	21	ILE	2.5
18	CR	37	VAL	2.5
32	BH	44	VAL	2.5
40	DT	121	ILE	2.5
3	CC	162	GLN	2.5
4	CD	80	GLU	2.5
12	CL	37	CYS	2.5
9	CI	122	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
31	BG	50	ALA	2.5
4	CD	3	ARG	2.5
16	CP	25	ARG	2.5
21	AU	10	ARG	2.5
32	DH	60	ARG	2.5
37	BQ	10	ARG	2.5
1	CA	204	U	2.5
14	AN	32	SER	2.5
1	AA	77	G	2.5
1	AA	1003	G	2.5
1	CA	79	G	2.5
1	CA	413	G	2.5
26	DA	352	G	2.5
27	BB	85	G	2.5
1	AA	63	C	2.5
1	AA	1030	C	2.5
1	CA	508	C	2.5
1	CA	1354	C	2.5
26	DA	645	C	2.5
27	BB	11	C	2.5
3	CC	33	LEU	2.5
15	CO	75	PRO	2.5
16	CP	46	PRO	2.5
4	AD	16	GLY	2.5
2	AB	48	MET	2.5
7	CG	49	ILE	2.5
11	CK	14	VAL	2.5
14	AN	56	VAL	2.5
15	CO	78	TYR	2.5
34	BN	140	VAL	2.5
46	DZ	38	TYR	2.5
2	AB	9	GLU	2.5
2	CB	86	GLU	2.5
4	AD	192	GLU	2.5
37	BQ	104	PHE	2.5
5	AE	138	ALA	2.5
9	AI	52	ALA	2.5
30	BF	21	ALA	2.5
31	DG	46	ALA	2.5
32	BH	75	ALA	2.5
5	AE	18	ARG	2.5
14	AN	43	CYS	2.5

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Mol	Chain	Res	Type	RSRZ
33	DI	82	ARG	2.5
41	DU	94	ASN	2.5
2	AB	19	HIS	2.5
14	CN	4	LYS	2.5
46	DZ	40	ASP	2.5
47	D0	5	LYS	2.5
51	D4	51	ASP	2.5
1	CA	982	U	2.5
2	AB	158	LEU	2.5
4	CD	136	PRO	2.5
20	AT	10	LEU	2.5
31	DG	19	LEU	2.5
33	DI	44	LEU	2.5
2	AB	127	ILE	2.5
46	DZ	146	ILE	2.5
13	CM	74	VAL	2.5
1	CA	1018	C	2.5
16	AP	17	TYR	2.5
17	CQ	32	TYR	2.5
26	DA	2146	C	2.5
1	AA	631	G	2.5
1	CA	933	G	2.5
1	CA	1104	G	2.5
1	CA	1310	G	2.5
26	BA	652(C)	G	2.5
26	BA	2319	G	2.5
3	AC	206	GLU	2.5
4	CD	24	GLU	2.5
7	CG	26	PHE	2.5
3	CC	137	ALA	2.5
9	CI	103	THR	2.5
16	AP	69	THR	2.5
16	CP	7	ALA	2.5
18	CR	20	ALA	2.5
20	AT	12	ALA	2.5
21	AU	8	THR	2.5
31	DG	161	THR	2.5
48	D1	60	PHE	2.5
9	CI	119	ALA	2.5
10	AJ	26	ALA	2.5
32	DH	150	ALA	2.5
33	DI	46	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
44	DX	91	ALA	2.5
46	DZ	164	ALA	2.5
7	AG	5	ARG	2.5
12	CL	19	ARG	2.5
14	CN	41	ARG	2.5
19	AS	3	ARG	2.5
37	DQ	6	ARG	2.5
4	CD	43	HIS	2.5
5	CE	130	ASN	2.5
2	AB	10	LEU	2.5
2	CB	213	LEU	2.5
5	CE	123	LEU	2.5
12	CL	27	LEU	2.5
46	BZ	150	LEU	2.5
2	CB	235	SER	2.5
13	CM	97	PRO	2.5
1	CA	1232	U	2.5
4	CD	124	GLY	2.5
11	CK	83	ILE	2.5
13	CM	112	GLY	2.5
20	CT	11	SER	2.5
31	DG	119	GLY	2.5
46	DZ	106	GLY	2.5
46	DZ	166	SER	2.5
3	AC	55	VAL	2.5
8	AH	95	VAL	2.5
11	CK	105	VAL	2.5
3	CC	10	PHE	2.5
14	AN	34	TYR	2.5
15	CO	15	PHE	2.5
15	CO	18	PHE	2.5
31	DG	168	GLU	2.5
51	D4	43	TYR	2.5
2	CB	53	ARG	2.5
3	AC	38	ARG	2.5
10	AJ	29	ARG	2.5
1	AA	1452	C	2.5
2	CB	103	THR	2.5
9	AI	27	THR	2.5
9	AI	64	THR	2.5
33	BI	100	ALA	2.5
42	DV	92	THR	2.5

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Mol	Chain	Res	Type	RSRZ
9	AI	11	LYS	2.5
1	AA	933	G	2.5
1	AA	1190	G	2.5
1	AA	1386	G	2.5
1	CA	1050	G	2.5
1	CA	1061	G	2.5
26	BA	10	G	2.5
26	DA	652(E)	G	2.5
26	DA	2182	G	2.5
1	CA	1503	A	2.5
9	CI	117	HIS	2.5
26	DA	229	A	2.5
32	DH	111	HIS	2.5
2	CB	166	ASP	2.4
7	CG	38	LEU	2.4
7	CG	104	LEU	2.4
9	AI	102	LEU	2.4
20	CT	36	LEU	2.4
31	DG	43	LEU	2.4
46	DZ	18	LEU	2.4
46	DZ	140	ASP	2.4
3	CC	8	ILE	2.4
8	CH	83	ILE	2.4
9	CI	90	PRO	2.4
10	AJ	74	ILE	2.4
29	DE	74	PRO	2.4
5	CE	67	VAL	2.4
14	AN	51	GLY	2.4
33	BI	145	VAL	2.4
36	DP	34	GLY	2.4
37	DQ	62	GLY	2.4
8	AH	115	SER	2.4
11	CK	24	SER	2.4
1	CA	1281	U	2.4
26	DA	2172	U	2.4
9	AI	12	GLU	2.4
33	DI	73	GLU	2.4
3	CC	199	LYS	2.4
4	CD	74	GLN	2.4
5	CE	88	LYS	2.4
11	CK	13	GLN	2.4
31	DG	50	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
10	AJ	100	THR	2.4
1	CA	89	C	2.4
24	CX	28	C	2.4
26	BA	652(S)	C	2.4
13	AM	40	ASN	2.4
5	CE	31	LEU	2.4
6	CF	21	LEU	2.4
10	CJ	8	LEU	2.4
18	CR	78	LEU	2.4
31	BG	3	LEU	2.4
1	AA	1030(D)	A	2.4
1	CA	1280	A	2.4
1	CA	1286	A	2.4
26	BA	899	A	2.4
26	DA	2176	A	2.4
1	CA	73	G	2.4
1	CA	966	G	2.4
1	CA	1491	G	2.4
3	AC	124	ILE	2.4
5	AE	5	ASP	2.4
5	CE	96	PRO	2.4
7	AG	50	ILE	2.4
10	AJ	38	ILE	2.4
24	AX	70	G	2.4
26	BA	2206	G	2.4
26	BA	2802	G	2.4
26	DA	2304	G	2.4
33	BI	97	ILE	2.4
13	AM	45	VAL	2.4
13	CM	95	GLY	2.4
30	BF	208	GLY	2.4
9	CI	16	ARG	2.4
28	DD	217	ARG	2.4
2	CB	70	PHE	2.4
7	AG	43	PHE	2.4
10	CJ	55	LYS	2.4
16	AP	27	LYS	2.4
16	AP	31	LYS	2.4
16	AP	35	LYS	2.4
31	BG	84	LYS	2.4
33	BI	45	LYS	2.4
4	CD	62	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
5	AE	61	TYR	2.4
7	AG	154	TYR	2.4
9	AI	114	TYR	2.4
46	DZ	50	GLN	2.4
32	BH	70	THR	2.4
2	CB	19	HIS	2.4
15	AO	87	ILE	2.4
31	DG	39	ILE	2.4
46	BZ	171	ILE	2.4
1	CA	1019	C	2.4
1	CA	1054	C	2.4
1	CA	1282	C	2.4
11	CK	119	CYS	2.4
2	AB	230	VAL	2.4
2	CB	38	GLY	2.4
3	CC	75	VAL	2.4
4	CD	140	VAL	2.4
7	AG	33	ASP	2.4
9	AI	30	GLY	2.4
9	CI	28	VAL	2.4
9	CI	53	VAL	2.4
10	CJ	36	GLY	2.4
20	AT	102	GLY	2.4
46	DZ	42	VAL	2.4
1	AA	1256	A	2.4
1	AA	1492	A	2.4
1	CA	532	A	2.4
26	BA	2134	A	2.4
26	DA	278	A	2.4
4	AD	191	ARG	2.4
31	BG	51	ARG	2.4
44	DX	88	LYS	2.4
48	D1	81	LYS	2.4
1	AA	181	G	2.4
1	AA	1031	G	2.4
1	CA	1368	G	2.4
2	CB	17	PHE	2.4
9	CI	37	PHE	2.4
26	BA	2151	G	2.4
26	DA	2121	G	2.4
27	DB	117	G	2.4
37	DQ	65	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
46	DZ	162	GLU	2.4
13	CM	72	ALA	2.4
20	AT	95	ALA	2.4
26	BA	2189	U	2.4
3	CC	178	LEU	2.4
4	AD	11	LEU	2.4
16	AP	49	LEU	2.4
31	BG	53	LEU	2.4
31	DG	34	LEU	2.4
5	AE	129	ILE	2.4
13	CM	39	ILE	2.4
29	BE	77	ILE	2.4
31	DG	88	ILE	2.4
13	AM	41	PRO	2.4
33	DI	8	PRO	2.4
5	AE	32	VAL	2.4
19	CS	19	VAL	2.4
19	CS	58	VAL	2.4
32	DH	11	VAL	2.4
2	AB	106	LYS	2.4
4	AD	115	ARG	2.4
9	CI	127	LYS	2.4
20	AT	25	ARG	2.4
40	BT	108	ARG	2.4
1	CA	1277	C	2.4
1	CA	1362	C	2.4
1	CA	964	A	2.4
1	CA	974	A	2.4
6	CF	60	PHE	2.4
37	BQ	69	PHE	2.4
33	DI	135	GLU	2.4
37	DQ	139	GLU	2.4
4	AD	111	ALA	2.4
20	CT	66	ALA	2.4
29	DE	204	ALA	2.4
4	AD	160	GLN	2.4
4	CD	99	SER	2.4
6	AF	57	GLN	2.4
53	D6	42	TRP	2.4
1	CA	952	U	2.4
1	CA	1079	G	2.4
1	CA	1356	G	2.4

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Mol	Chain	Res	Type	RSRZ
1	CA	1371	G	2.4
9	CI	92	TYR	2.4
13	CM	63	THR	2.4
26	BA	1173	G	2.4
26	BA	2182	G	2.4
26	DA	2127	G	2.4
26	DA	2150	U	2.4
31	DG	145	THR	2.4
46	DZ	99	TYR	2.4
51	B4	63	TYR	2.4
2	AB	118	LEU	2.4
10	AJ	40	LEU	2.4
31	DG	144	ILE	2.4
5	AE	15	ARG	2.3
5	CE	82	VAL	2.3
5	CE	107	ARG	2.3
6	AF	71	ARG	2.3
13	CM	13	LYS	2.3
20	CT	75	ASN	2.3
33	BI	103	ARG	2.3
40	BT	115	ARG	2.3
46	DZ	4	ARG	2.3
50	D3	58	VAL	2.3
2	CB	18	GLY	2.3
48	D1	28	GLY	2.3
4	CD	177	ASP	2.3
9	CI	101	PHE	2.3
40	BT	107	ASP	2.3
47	D0	71	ASP	2.3
4	CD	205	GLU	2.3
10	AJ	32	ALA	2.3
19	CS	64	GLU	2.3
51	B4	57	GLU	2.3
54	D7	45	ALA	2.3
1	CA	840	C	2.3
1	CA	1223	C	2.3
7	CG	106	GLN	2.3
25	AY	72	C	2.3
26	BA	2164	C	2.3
26	BA	2326	C	2.3
26	DA	1509	C	2.3
27	BB	12	C	2.3

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Mol	Chain	Res	Type	RSRZ
36	BP	70	GLN	2.3
44	DX	87	GLN	2.3
1	CA	1248	A	2.3
1	CA	1349	A	2.3
3	AC	49	SER	2.3
26	DA	2801(A)	A	2.3
33	DI	102	SER	2.3
2	CB	69	LEU	2.3
6	CF	61	LEU	2.3
7	CG	151	TYR	2.3
9	CI	40	LEU	2.3
9	CI	88	TYR	2.3
10	CJ	88	LEU	2.3
11	AK	57	THR	2.3
15	CO	22	THR	2.3
16	CP	16	HIS	2.3
17	AQ	18	THR	2.3
19	CS	48	THR	2.3
30	DF	12	LEU	2.3
39	DS	5	THR	2.3
39	DS	26	LEU	2.3
46	DZ	5	LEU	2.3
1	CA	960	U	2.3
8	CH	86	ILE	2.3
11	AK	21	ILE	2.3
3	AC	27	LYS	2.3
10	CJ	39	PRO	2.3
28	DD	276	LYS	2.3
46	DZ	68	PRO	2.3
48	D1	48	LYS	2.3
1	AA	104	G	2.3
1	AA	148	G	2.3
1	CA	976	G	2.3
1	CA	1276	G	2.3
2	AB	144	ARG	2.3
3	CC	11	ARG	2.3
4	CD	36	ARG	2.3
13	CM	104	ARG	2.3
19	CS	45	VAL	2.3
26	DA	2141	G	2.3
46	DZ	105	VAL	2.3
2	CB	100	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
51	D4	54	GLY	2.3
32	DH	123	PHE	2.3
4	CD	190	ASP	2.3
2	AB	186	ALA	2.3
7	CG	57	GLU	2.3
51	B4	51	ASP	2.3
56	B9	12	ASP	2.3
7	CG	147	ALA	2.3
12	CL	68	ALA	2.3
31	DG	110	ALA	2.3
6	CF	16	GLN	2.3
33	DI	17	GLN	2.3
11	AK	53	SER	2.3
11	CK	103	LEU	2.3
17	CQ	22	LEU	2.3
31	DG	62	LEU	2.3
33	DI	35	LEU	2.3
46	DZ	129	SER	2.3
1	AA	48	C	2.3
1	AA	174	C	2.3
2	AB	40	HIS	2.3
1	CA	969	A	2.3
2	CB	148	TYR	2.3
26	BA	886	C	2.3
6	CF	81	ILE	2.3
26	DA	2298	A	2.3
31	BG	140	ILE	2.3
14	CN	9	LYS	2.3
19	CS	18	LYS	2.3
28	BD	261	LYS	2.3
1	CA	1150	U	2.3
2	CB	167	PRO	2.3
14	CN	45	ARG	2.3
19	AS	59	PRO	2.3
32	DH	42	ARG	2.3
33	BI	80	PRO	2.3
3	CC	130	VAL	2.3
7	CG	69	VAL	2.3
16	CP	20	VAL	2.3
28	BD	229	VAL	2.3
33	BI	81	VAL	2.3
34	BN	9	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
39	DS	46	VAL	2.3
4	CD	130	GLY	2.3
7	CG	34	GLY	2.3
9	AI	6	GLY	2.3
43	DW	112	GLY	2.3
5	AE	45	PHE	2.3
10	CJ	63	PHE	2.3
51	D4	42	PHE	2.3
1	AA	1337	G	2.3
1	CA	70	G	2.3
1	CA	1077	G	2.3
1	CA	1300	G	2.3
10	AJ	25	GLU	2.3
10	CJ	27	ALA	2.3
15	AO	14	GLU	2.3
18	CR	73	ALA	2.3
20	AT	66	ALA	2.3
26	BA	1537	G	2.3
26	DA	2106	G	2.3
26	DA	2303	G	2.3
26	DA	2793	G	2.3
32	BH	47	GLU	2.3
4	CD	181	MET	2.3
12	CL	92	ASP	2.3
3	AC	28	GLN	2.3
3	AC	107	GLN	2.3
3	CC	37	GLN	2.3
31	BG	111	LEU	2.3
32	BH	88	LEU	2.3
32	BH	98	LEU	2.3
33	BI	44	LEU	2.3
56	B9	27	CYS	2.3
9	CI	116	LYS	2.3
12	AL	91	LYS	2.3
13	AM	39	ILE	2.3
18	CR	65	ILE	2.3
28	BD	275	LYS	2.3
28	DD	275	LYS	2.3
46	DZ	120	ILE	2.3
16	CP	22	THR	2.3
40	BT	17	THR	2.3
4	AD	168	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
11	AK	75	TYR	2.3
12	CL	64	TYR	2.3
13	CM	108	ARG	2.3
31	DG	9	ARG	2.3
32	DH	157	TYR	2.3
48	B1	26	ARG	2.3
1	AA	137	C	2.3
1	AA	1008	C	2.3
1	CA	1285	A	2.3
1	CA	1336	C	2.3
2	CB	174	VAL	2.3
7	CG	58	PRO	2.3
9	AI	44	VAL	2.3
13	AM	117	VAL	2.3
19	CS	11	VAL	2.3
39	DS	91	PRO	2.3
26	BA	2161	C	2.3
26	BA	2790	A	2.3
26	DA	2107	C	2.3
26	DA	2896	C	2.3
47	D0	38	VAL	2.3
26	DA	2113	U	2.3
3	AC	9	GLY	2.3
7	CG	82	GLY	2.3
4	CD	110	PHE	2.3
2	CB	20	GLU	2.3
4	CD	145	GLU	2.3
13	AM	42	ALA	2.3
13	CM	28	ALA	2.3
19	CS	66	MET	2.3
33	DI	7	GLU	2.3
46	DZ	152	ALA	2.3
48	B1	75	GLU	2.3
53	D6	2	ALA	2.3
3	AC	91	LEU	2.3
16	CP	6	LEU	2.3
18	CR	85	LEU	2.3
19	AS	5	LEU	2.3
19	CS	20	LEU	2.3
31	DG	138	GLN	2.3
33	DI	38	LEU	2.3
39	DS	73	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
46	DZ	24	LEU	2.3
19	AS	18	LYS	2.3
31	BG	74	LYS	2.3
1	CA	888	G	2.3
1	CA	1036	G	2.3
1	CA	1231	G	2.3
1	CA	1347	G	2.3
4	CD	126	ILE	2.3
4	CD	204	ILE	2.3
9	CI	81	ILE	2.3
10	CJ	82	ILE	2.3
17	AQ	65	ILE	2.3
26	BA	2833	G	2.3
3	AC	79	ARG	2.3
3	CC	177	THR	2.3
9	AI	104	ARG	2.3
10	AJ	79	ARG	2.3
10	CJ	100	THR	2.3
14	CN	32	SER	2.3
20	AT	71	THR	2.3
32	BH	63	SER	2.3
2	AB	93	VAL	2.3
2	CB	15	VAL	2.3
3	AC	86	VAL	2.3
3	CC	109	PRO	2.3
10	CJ	53	PRO	2.3
32	BH	157	TYR	2.3
45	DY	55	TYR	2.3
16	AP	53	VAL	2.3
17	CQ	77	VAL	2.3
19	CS	67	VAL	2.3
32	DH	99	VAL	2.3
39	BS	46	VAL	2.3
46	DZ	159	PRO	2.3
13	CM	38	GLY	2.3
16	AP	63	GLY	2.3
21	CU	4	GLY	2.3
30	BF	131	GLY	2.3
39	DS	45	GLY	2.3
1	AA	90	U	2.3
1	AA	343	U	2.3
1	AA	1000	U	2.3

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Mol	Chain	Res	Type	RSRZ
1	CA	1247	U	2.3
26	BA	272(A)	U	2.3
1	AA	134	A	2.2
1	AA	1493	A	2.2
1	CA	482	A	2.2
1	CA	848	C	2.2
1	CA	1039	C	2.2
1	CA	1180	A	2.2
7	AG	62	PHE	2.2
16	CP	9	PHE	2.2
26	BA	1045	A	2.2
26	DA	2128	C	2.2
27	DB	59	A	2.2
27	DB	88	C	2.2
31	BG	80	PHE	2.2
32	BH	123	PHE	2.2
2	AB	37	ASN	2.2
3	AC	92	ALA	2.2
3	AC	181	ASN	2.2
5	AE	83	GLU	2.2
9	CI	55	ALA	2.2
9	CI	94	ALA	2.2
10	CJ	69	ASN	2.2
11	CK	38	ASN	2.2
13	CM	30	ALA	2.2
29	DE	121	ASN	2.2
31	DG	30	GLU	2.2
32	DH	58	GLU	2.2
33	DI	43	ASN	2.2
33	DI	64	GLU	2.2
47	D0	68	GLU	2.2
2	CB	215	LEU	2.2
4	CD	157	LEU	2.2
10	AJ	65	LEU	2.2
36	DP	45	LEU	2.2
13	AM	27	LYS	2.2
13	CM	46	LYS	2.2
44	DX	33	LYS	2.2
10	CJ	12	ASP	2.2
5	CE	80	ILE	2.2
8	AH	45	ILE	2.2
10	AJ	6	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
8	AH	84	ARG	2.2
9	AI	121	ARG	2.2
12	AL	89	ARG	2.2
21	CU	22	ARG	2.2
10	AJ	42	THR	2.2
13	AM	49	THR	2.2
4	CD	92	VAL	2.2
4	CD	178	VAL	2.2
8	AH	137	VAL	2.2
13	AM	113	PRO	2.2
19	CS	4	SER	2.2
31	BG	31	VAL	2.2
39	DS	27	SER	2.2
39	DS	49	VAL	2.2
1	AA	627	G	2.2
1	AA	1032	G	2.2
1	CA	97	G	2.2
1	CA	438	G	2.2
1	CA	644	G	2.2
1	CA	657	G	2.2
1	CA	851	G	2.2
1	CA	1193	G	2.2
1	CA	1221	G	2.2
1	CA	1370	G	2.2
1	CA	1392	G	2.2
26	BA	2133	G	2.2
26	DA	883	G	2.2
26	DA	1533	G	2.2
26	DA	2123	G	2.2
15	AO	20	GLY	2.2
39	DS	60	GLY	2.2
36	DP	1	MET	2.2
39	DS	87	PHE	2.2
3	AC	61	ALA	2.2
4	CD	111	ALA	2.2
10	AJ	18	ALA	2.2
31	DG	13	GLU	2.2
31	DG	107	LEU	2.2
32	BH	124	GLU	2.2
37	DQ	28	ALA	2.2
1	AA	221	C	2.2
1	CA	972	C	2.2

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Mol	Chain	Res	Type	RSRZ
1	CA	1105	A	2.2
1	CA	1179	A	2.2
1	CA	1287	A	2.2
6	CF	43	LEU	2.2
13	CM	96	LEU	2.2
33	BI	123	LEU	2.2
39	BS	48	LEU	2.2
46	DZ	84	GLU	2.2
46	DZ	138	GLU	2.2
7	AG	35	LYS	2.2
8	AH	88	LYS	2.2
9	CI	95	LYS	2.2
10	CJ	78	ASN	2.2
12	CL	47	LYS	2.2
13	AM	120	LYS	2.2
26	BA	652(T)	C	2.2
26	BA	2136	C	2.2
26	BA	2140	C	2.2
26	BA	2158	A	2.2
26	DA	277	C	2.2
26	DA	1913	A	2.2
27	DB	60	C	2.2
33	DI	131	LYS	2.2
28	DD	112	GLN	2.2
4	AD	132	ARG	2.2
33	DI	105	HIS	2.2
48	D1	61	ARG	2.2
3	CC	86	VAL	2.2
4	AD	12	CYS	2.2
4	AD	140	VAL	2.2
9	AI	65	VAL	2.2
9	CI	108	VAL	2.2
10	CJ	41	PRO	2.2
11	CK	113	PRO	2.2
31	BG	28	VAL	2.2
32	BH	52	VAL	2.2
32	DH	37	VAL	2.2
33	DI	3	VAL	2.2
34	BN	73	THR	2.2
42	DV	5	VAL	2.2
47	D0	81	VAL	2.2
54	B7	46	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
4	AD	137	SER	2.2
8	CH	113	SER	2.2
10	CJ	19	SER	2.2
13	CM	59	TYR	2.2
16	CP	39	TYR	2.2
51	D4	26	SER	2.2
11	CK	86	GLY	2.2
16	CP	78	GLY	2.2
31	DG	148	MET	2.2
35	DO	1	MET	2.2
46	BZ	1	MET	2.2
49	D2	1	MET	2.2
19	CS	10	PHE	2.2
31	BG	178	PHE	2.2
4	AD	149	ALA	2.2
4	AD	169	LYS	2.2
4	CD	82	ALA	2.2
5	CE	17	ALA	2.2
6	AF	49	ALA	2.2
7	CG	2	ALA	2.2
8	CH	116	LYS	2.2
9	CI	113	LYS	2.2
11	CK	71	LYS	2.2
22	AV	18	G	2.2
24	CX	30	G	2.2
26	BA	1106	G	2.2
31	BG	73	ALA	2.2
33	BI	2	LYS	2.2
33	BI	94	ALA	2.2
51	D4	8	LYS	2.2
1	CA	1353	G	2.2
6	CF	95	GLU	2.2
50	B3	60	GLU	2.2
1	CA	17	U	2.2
24	CX	47	U	2.2
26	DA	2897	U	2.2
11	AK	27	ASN	2.2
2	AB	53	ARG	2.2
2	CB	42	ILE	2.2
4	CD	49	ARG	2.2
7	CG	32	ARG	2.2
13	AM	4	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
15	CO	88	ARG	2.2
20	AT	23	ARG	2.2
21	AU	13	ILE	2.2
31	BG	88	ILE	2.2
34	BN	115	ARG	2.2
40	DT	53	ARG	2.2
46	BZ	133	ILE	2.2
1	AA	161	A	2.2
1	AA	1183	A	2.2
1	CA	1004	A	2.2
1	CA	1016	A	2.2
1	CA	1252	A	2.2
19	CS	83	HIS	2.2
26	DA	2158	A	2.2
26	BA	2794	C	2.2
47	B0	3	HIS	2.2
35	BO	81	ASP	2.2
2	CB	131	PRO	2.2
4	AD	148	VAL	2.2
9	AI	109	VAL	2.2
14	CN	14	PRO	2.2
16	CP	2	VAL	2.2
30	BF	89	VAL	2.2
46	DZ	165	VAL	2.2
2	CB	24	TRP	2.2
16	CP	67	THR	2.2
3	CC	142	MET	2.2
56	D9	11	CYS	2.2
5	CE	124	GLY	2.2
7	AG	81	GLY	2.2
15	AO	69	TYR	2.2
42	DV	42	GLY	2.2
4	CD	185	PHE	2.2
17	CQ	87	LYS	2.2
19	CS	25	LYS	2.2
31	DG	180	PHE	2.2
33	BI	62	LYS	2.2
49	D2	54	LYS	2.2
4	AD	135	LEU	2.2
8	AH	127	LEU	2.2
15	AO	57	LEU	2.2
30	DF	162	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
31	DG	90	LEU	2.2
31	DG	103	LEU	2.2
31	DG	135	LEU	2.2
37	BQ	2	LEU	2.2
39	BS	24	LEU	2.2
10	AJ	95	GLU	2.2
17	AQ	24	GLU	2.2
29	BE	204	ALA	2.2
31	DG	56	ALA	2.2
37	BQ	139	GLU	2.2
40	DT	5	ALA	2.2
51	B4	53	GLU	2.2
5	CE	76	ILE	2.2
8	AH	100	ILE	2.2
31	DG	77	ILE	2.2
1	CA	841	U	2.2
10	AJ	84	GLN	2.2
1	AA	945	G	2.2
1	AA	1154	G	2.2
1	AA	1258	G	2.2
1	AA	1387	G	2.2
1	CA	953	G	2.2
1	CA	993	G	2.2
1	CA	1026	G	2.2
1	CA	1181	G	2.2
1	CA	1266	G	2.2
1	CA	1273	G	2.2
10	AJ	68	HIS	2.2
20	CT	73	HIS	2.2
24	CX	29	G	2.2
26	DA	2315	G	2.2
46	DZ	121	HIS	2.2
1	AA	152	A	2.2
1	CA	1080	A	2.2
1	CA	1152	A	2.2
1	CA	1333	A	2.2
4	CD	112	VAL	2.2
12	CL	40	VAL	2.2
15	CO	19	PRO	2.2
26	DA	887	A	2.2
32	DH	21	PRO	2.2
33	BI	144	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
45	DY	107	ASP	2.2
46	BZ	165	VAL	2.2
1	AA	175	C	2.2
1	AA	1051	C	2.2
1	CA	1007	C	2.2
1	CA	1027	C	2.2
1	CA	1382	C	2.2
26	DA	886	C	2.2
26	DA	2803	C	2.2
5	AE	98	THR	2.2
12	AL	67	THR	2.2
3	CC	4	LYS	2.2
4	AD	69	GLY	2.2
5	AE	44	GLY	2.2
5	CE	92	LYS	2.2
19	CS	72	GLY	2.2
51	B4	17	GLY	2.2
46	DZ	8	TYR	2.2
2	CB	10	LEU	2.2
3	CC	91	LEU	2.2
4	CD	108	LEU	2.2
8	CH	63	LEU	2.2
16	AP	60	LEU	2.2
19	CS	30	LEU	2.2
2	CB	49	GLU	2.2
3	CC	146	ALA	2.2
4	CD	156	GLU	2.2
7	CG	117	ALA	2.2
20	CT	12	ALA	2.2
2	CB	30	ARG	2.1
5	AE	25	ARG	2.1
5	CE	18	ARG	2.1
6	CF	3	ARG	2.1
10	CJ	50	ILE	2.1
11	AK	126	ARG	2.1
12	AL	19	ARG	2.1
13	CM	110	ARG	2.1
16	CP	72	ARG	2.1
21	AU	6	ARG	2.1
31	BG	113	ARG	2.1
51	B4	55	ARG	2.1
16	AP	76	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
3	AC	3	ASN	2.1
3	CC	31	HIS	2.1
8	CH	81	HIS	2.1
11	AK	117	ASN	2.1
36	DP	84	ASN	2.1
39	DS	16	ASN	2.1
2	AB	131	PRO	2.1
11	CK	47	VAL	2.1
15	AO	2	PRO	2.1
16	CP	21	VAL	2.1
32	DH	45	VAL	2.1
46	DZ	58	VAL	2.1
46	DZ	111	VAL	2.1
46	DZ	128	VAL	2.1
2	CB	101	MET	2.1
12	AL	92	ASP	2.1
1	AA	347	G	2.1
1	AA	1178	G	2.1
1	CA	838	G	2.1
1	CA	1011	G	2.1
1	CA	1047	G	2.1
5	CE	47	LYS	2.1
8	AH	98	LYS	2.1
1	CA	1102	A	2.1
1	CA	1146	A	2.1
3	CC	194	GLY	2.1
13	CM	20	THR	2.1
18	CR	61	LYS	2.1
26	BA	880	G	2.1
26	BA	2101	G	2.1
26	BA	2148	G	2.1
26	BA	2165	G	2.1
27	DB	57	A	2.1
1	AA	754	C	2.1
1	AA	1006	C	2.1
1	AA	1066	C	2.1
1	AA	1119	C	2.1
1	AA	1400	C	2.1
1	CA	984	C	2.1
3	AC	188	LEU	2.1
6	AF	21	LEU	2.1
16	AP	74	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
24	CX	48	C	2.1
26	BA	1509	C	2.1
31	DG	106	LEU	2.1
32	BH	171	LEU	2.1
46	BZ	117	LEU	2.1
46	BZ	144	LEU	2.1
4	CD	38	TYR	2.1
2	CB	188	ALA	2.1
3	CC	53	ALA	2.1
3	CC	121	ALA	2.1
11	CK	89	ALA	2.1
12	CL	118	SER	2.1
14	AN	30	ALA	2.1
15	AO	24	SER	2.1
35	DO	51	ALA	2.1
2	AB	175	ARG	2.1
3	AC	16	ARG	2.1
4	CD	153	ARG	2.1
4	CD	168	ARG	2.1
13	CM	29	ARG	2.1
14	AN	35	ARG	2.1
3	CC	182	ILE	2.1
8	AH	134	ILE	2.1
17	CQ	65	ILE	2.1
4	CD	201	GLN	2.1
16	CP	82	GLN	2.1
9	AI	117	HIS	2.1
46	DZ	55	HIS	2.1
4	CD	161	ASN	2.1
20	AT	26	ASN	2.1
1	AA	1235	U	2.1
3	CC	174	PRO	2.1
19	CS	76	PRO	2.1
31	DG	122	PRO	2.1
44	DX	52	VAL	2.1
46	DZ	25	PRO	2.1
6	AF	54	LYS	2.1
17	AQ	37	LYS	2.1
20	CT	34	LYS	2.1
31	DG	182	LYS	2.1
32	DH	138	LYS	2.1
3	AC	67	THR	2.1

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Mol	Chain	Res	Type	RSRZ
35	BO	110	GLY	2.1
2	CB	61	LEU	2.1
13	CM	70	LEU	2.1
15	CO	81	LEU	2.1
16	CP	73	LEU	2.1
33	DI	47	LEU	2.1
1	AA	101	A	2.1
1	CA	431	A	2.1
2	CB	92	TYR	2.1
2	CB	123	ALA	2.1
2	CB	209	ARG	2.1
4	AD	48	ALA	2.1
9	AI	94	ALA	2.1
11	AK	89	ALA	2.1
12	CL	89	ARG	2.1
14	AN	19	ARG	2.1
14	AN	31	ARG	2.1
24	CX	44	A	2.1
31	DG	33	ARG	2.1
35	BO	17	ARG	2.1
36	DP	141	ALA	2.1
51	B4	62	ARG	2.1
1	AA	66	G	2.1
1	AA	1050	G	2.1
1	CA	725	G	2.1
2	AB	214	ILE	2.1
2	CB	126	GLU	2.1
2	CB	162	ILE	2.1
3	CC	57	ILE	2.1
4	CD	192	GLU	2.1
1	AA	1028	C	2.1
1	AA	1069	C	2.1
1	CA	121	C	2.1
1	CA	924	C	2.1
1	CA	1037	C	2.1
8	CH	115	SER	2.1
15	AO	73	GLU	2.1
24	AX	31	G	2.1
26	BA	1107	G	2.1
26	BA	2127	G	2.1
26	BA	2131	G	2.1
26	BA	2156	G	2.1

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Mol	Chain	Res	Type	RSRZ
26	BA	2159	G	2.1
26	DA	614(B)	G	2.1
26	DA	1030	G	2.1
27	DB	18	G	2.1
27	DB	24	G	2.1
33	BI	7	GLU	2.1
46	DZ	57	ILE	2.1
26	DA	897	C	2.1
26	DA	2111	C	2.1
5	AE	20	GLN	2.1
51	B4	47	GLN	2.1
10	AJ	56	HIS	2.1
10	CJ	68	HIS	2.1
14	CN	49	HIS	2.1
2	CB	71	VAL	2.1
2	CB	83	MET	2.1
3	CC	64	VAL	2.1
4	AD	29	PRO	2.1
4	AD	151	LYS	2.1
4	CD	166	LYS	2.1
5	AE	10	MET	2.1
9	AI	53	VAL	2.1
13	CM	54	VAL	2.1
17	AQ	5	VAL	2.1
16	AP	46	PRO	2.1
20	AT	9	ASN	2.1
20	AT	54	LYS	2.1
32	DH	114	VAL	2.1
4	CD	172	PRO	2.1
7	AG	112	PRO	2.1
45	DY	92	ASN	2.1
46	BZ	108	PRO	2.1
46	DZ	23	LYS	2.1
1	AA	223	U	2.1
26	DA	895	U	2.1
27	DB	22	U	2.1
4	AD	180	GLY	2.1
4	CD	16	GLY	2.1
5	CE	23	GLY	2.1
5	CE	39	GLY	2.1
7	CG	59	LEU	2.1
13	CM	16	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
13	CM	81	LEU	2.1
15	CO	20	GLY	2.1
16	AP	47	ASP	2.1
20	AT	72	LEU	2.1
32	BH	166	GLY	2.1
33	BI	38	LEU	2.1
55	D8	45	GLY	2.1
2	AB	70	PHE	2.1
4	AD	75	PHE	2.1
5	AE	135	THR	2.1
2	CB	144	ARG	2.1
14	AN	26	ARG	2.1
16	CP	59	TRP	2.1
20	CT	8	ARG	2.1
30	BF	172	TRP	2.1
32	BH	3	ARG	2.1
33	BI	82	ARG	2.1
37	DQ	16	ARG	2.1
51	D4	48	ARG	2.1
8	AH	20	TYR	2.1
9	AI	63	ILE	2.1
9	CI	114	TYR	2.1
12	AL	7	ILE	2.1
31	BG	158	ALA	2.1
32	BH	102	ALA	2.1
39	DS	79	ALA	2.1
32	DH	124	GLU	2.1
37	DQ	32	TYR	2.1
39	DS	92	TYR	2.1
51	D4	53	GLU	2.1
1	CA	10	A	2.1
1	CA	415	A	2.1
1	CA	1183	A	2.1
4	AD	91	SER	2.1
8	AH	29	SER	2.1
10	AJ	35	SER	2.1
10	CJ	30	SER	2.1
26	BA	229	A	2.1
26	BA	1913	A	2.1
26	BA	2062	A	2.1
26	BA	2126	A	2.1
3	CC	136	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	AA	594	G	2.1
1	AA	1034	G	2.1
1	AA	1039	C	2.1
1	AA	1353	G	2.1
1	CA	77	G	2.1
1	CA	138	G	2.1
1	CA	201	C	2.1
1	CA	530	G	2.1
1	CA	931	C	2.1
1	CA	1021	G	2.1
1	CA	1210	C	2.1
1	CA	1216	G	2.1
1	CA	1230	C	2.1
1	CA	1320	C	2.1
1	CA	1344	C	2.1
3	CC	45	LYS	2.1
16	AP	3	LYS	2.1
17	CQ	29	HIS	2.1
20	AT	73	HIS	2.1
20	CT	48	LYS	2.1
26	BA	2123	G	2.1
26	DA	271(J)	C	2.1
32	DH	61	HIS	2.1
33	BI	118	LYS	2.1
46	DZ	151	HIS	2.1
7	AG	17	VAL	2.1
26	DA	2807	G	2.1
46	BZ	161	VAL	2.1
46	DZ	37	VAL	2.1
46	DZ	126	VAL	2.1
4	AD	37	PRO	2.1
33	BI	119	PRO	2.1
16	AP	14	ASN	2.1
2	CB	149	LEU	2.1
7	AG	12	LEU	2.1
10	CJ	85	LEU	2.1
31	DG	7	LEU	2.1
32	BH	105	LEU	2.1
36	BP	88	LEU	2.1
3	AC	74	GLY	2.1
26	BA	2150	U	2.1
31	BG	129	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
48	D1	22	GLY	2.1
3	AC	21	ARG	2.1
3	CC	172	ARG	2.1
4	AD	153	ARG	2.1
4	CD	118	ARG	2.1
4	CD	122	ARG	2.1
5	CE	98	THR	2.1
8	AH	102	ARG	2.1
8	CH	125	ARG	2.1
9	CI	60	ASP	2.1
10	AJ	87	THR	2.1
13	AM	105	THR	2.1
13	CM	3	ARG	2.1
16	AP	5	ARG	2.1
31	BG	147	ASP	2.1
44	DX	68	ARG	2.1
47	D0	74	ARG	2.1
51	B4	24	THR	2.1
51	D4	55	ARG	2.1
2	AB	200	ILE	2.1
2	AB	223	ILE	2.1
2	CB	211	ILE	2.1
4	AD	195	ALA	2.1
4	CD	55	ALA	2.1
17	CQ	36	ILE	2.1
19	CS	40	ILE	2.1
31	BG	46	ALA	2.1
41	DU	21	ALA	2.1
46	DZ	133	ILE	2.1
7	AG	8	GLU	2.1
7	CG	90	GLU	2.1
13	CM	32	GLU	2.1
19	AS	27	GLU	2.1
31	BG	167	GLU	2.1
31	DG	48	GLU	2.1
46	BZ	119	GLU	2.1
46	DZ	60	GLU	2.1
3	AC	23	TYR	2.1
4	AD	4	TYR	2.1
5	CE	60	TYR	2.1
17	CQ	51	TYR	2.1
31	BG	12	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
4	AD	86	LYS	2.0
4	CD	63	LYS	2.0
12	CL	23	LYS	2.0
12	CL	91	LYS	2.0
16	CP	76	GLN	2.0
42	DV	1	MET	2.0
51	D4	2	LYS	2.0
1	AA	151	A	2.0
1	CA	1041	A	2.0
10	AJ	24	VAL	2.0
14	CN	56	VAL	2.0
26	BA	1174	A	2.0
26	DA	2629	A	2.0
32	BH	76	VAL	2.0
34	DN	5	VAL	2.0
46	DZ	83	PRO	2.0
1	CA	525	C	2.0
1	CA	934	C	2.0
1	CA	1006	C	2.0
1	CA	1059	C	2.0
1	CA	1246	C	2.0
2	CB	158	LEU	2.0
3	CC	108	ASN	2.0
8	AH	63	LEU	2.0
13	AM	34	LEU	2.0
36	BP	3	LEU	2.0
1	CA	391	G	2.0
1	CA	410	G	2.0
1	CA	1023	G	2.0
1	CA	1155	G	2.0
1	CA	1215	G	2.0
2	CB	111	ARG	2.0
3	CC	83	ARG	2.0
7	AG	34	GLY	2.0
14	AN	23	ARG	2.0
26	BA	2190	G	2.0
26	DA	275	G	2.0
27	DB	19	G	2.0
32	DH	22	GLY	2.0
35	DO	27	GLY	2.0
37	DQ	33	GLY	2.0
37	DQ	56	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
45	DY	60	PHE	2.0
46	DZ	160	GLY	2.0
47	D0	82	ARG	2.0
56	D9	21	GLY	2.0
5	CE	120	THR	2.0
8	CH	17	THR	2.0
14	CN	13	THR	2.0
34	BN	43	THR	2.0
3	AC	100	ALA	2.0
3	CC	169	ALA	2.0
5	AE	94	ALA	2.0
9	AI	91	ASP	2.0
39	DS	6	ALA	2.0
8	CH	138	TRP	2.0
33	BI	122	GLU	2.0
52	B5	59	GLU	2.0
2	AB	236	TYR	2.0
3	CC	150	LYS	2.0
6	CF	54	LYS	2.0
12	AL	23	LYS	2.0
13	CM	36	LYS	2.0
21	CU	18	TYR	2.0
40	DT	14	TYR	2.0
45	DY	21	LYS	2.0
45	DY	94	LYS	2.0
17	AQ	15	MET	2.0
17	CQ	15	MET	2.0
2	AB	174	VAL	2.0
2	CB	112	VAL	2.0
3	AC	138	VAL	2.0
4	CD	17	VAL	2.0
7	CG	141	VAL	2.0
10	CJ	33	GLN	2.0
14	AN	33	VAL	2.0
15	CO	71	GLN	2.0
19	CS	47	HIS	2.0
32	BH	133	VAL	2.0
33	BI	42	SER	2.0
1	AA	1299	A	2.0
1	CA	171	A	2.0
1	CA	1111	A	2.0
2	AB	61	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
4	AD	186	LEU	2.0
14	CN	47	LEU	2.0
26	DA	2310	A	2.0
40	DT	6	LEU	2.0
3	AC	190	ARG	2.0
4	CD	199	ASN	2.0
7	AG	41	ARG	2.0
7	CG	149	ARG	2.0
9	AI	83	ARG	2.0
31	DG	128	ARG	2.0
32	DH	130	ARG	2.0
35	BO	49	ARG	2.0
39	DS	15	ARG	2.0
9	AI	100	GLY	2.0
19	CS	84	GLY	2.0
42	BV	42	GLY	2.0
1	AA	1054	C	2.0
1	CA	400	C	2.0
1	CA	1325	C	2.0
2	CB	80	ILE	2.0
7	CG	30	ILE	2.0
10	AJ	23	ILE	2.0
13	CM	9	ILE	2.0
20	AT	55	ILE	2.0
26	BA	2139	C	2.0
26	DA	2317	C	2.0
31	DG	52	ILE	2.0
2	CB	207	ALA	2.0
4	AD	32	ALA	2.0
5	CE	134	ALA	2.0
12	AL	6	THR	2.0
12	AL	107	ALA	2.0
13	CM	49	THR	2.0
15	AO	30	ALA	2.0
31	DG	69	ALA	2.0
31	DG	158	ALA	2.0
37	BQ	28	ALA	2.0
46	DZ	173	ALA	2.0
1	CA	961	U	2.0
1	AA	346	G	2.0
1	CA	78	G	2.0
1	CA	331	G	2.0

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Mol	Chain	Res	Type	RSRZ
1	CA	550	G	2.0
1	CA	988	G	2.0
1	CA	1094	G	2.0
1	CA	1124	G	2.0
1	CA	1187	G	2.0
1	CA	1523	G	2.0
2	AB	49	GLU	2.0
2	AB	191	ASP	2.0
3	AC	17	ASP	2.0
2	CB	139	LYS	2.0
4	CD	81	GLU	2.0
4	CD	86	LYS	2.0
5	AE	145	LYS	2.0
5	CE	83	GLU	2.0
13	CM	52	GLU	2.0
13	CM	58	GLU	2.0
26	BA	2102	U	2.0
26	DA	2167	U	2.0
31	DG	14	GLU	2.0
31	DG	49	ASP	2.0
26	BA	652(U)	G	2.0
26	DA	2124	G	2.0
26	DA	2165	G	2.0
26	DA	2319	G	2.0
33	DI	70	GLU	2.0
34	BN	83	LYS	2.0
48	D1	83	GLU	2.0
3	AC	18	TRP	2.0
3	AC	22	TRP	2.0
4	AD	20	TYR	2.0
4	CD	68	TYR	2.0
40	DT	100	TYR	2.0
7	CG	23	VAL	2.0
12	CL	96	VAL	2.0
13	CM	17	VAL	2.0
15	CO	60	VAL	2.0
16	AP	62	VAL	2.0
17	AQ	23	VAL	2.0
17	CQ	23	VAL	2.0
17	CQ	35	VAL	2.0
18	CR	86	VAL	2.0
19	CS	9	VAL	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
24	5MC	CX	32	21/22	0.79	0.18	68,80,88,99	0
24	4SU	CX	8	20/21	0.84	0.14	61,80,93,118	0
24	5MU	CX	54	21/22	0.85	0.14	71,79,92,107	0
24	PSU	CX	55	20/21	0.85	0.12	61,72,81,89	0
24	PSU	AX	55	20/21	0.87	0.14	58,70,77,82	0
24	5MU	AX	54	21/22	0.89	0.14	57,67,82,96	0
24	31H	CX	76	32/33	0.92	0.15	23,42,61,84	10
24	4SU	AX	8	20/21	0.93	0.11	47,59,67,84	0
24	5MC	AX	32	21/22	0.94	0.12	46,55,75,77	0
24	31H	AX	76	30/33	0.95	0.14	14,31,55,77	8
23	PPU	CW	76	37/38	0.96	0.10	27,41,53,63	0
23	PPU	AW	76	37/38	0.97	0.09	12,29,37,42	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3553	1/1	0.17	0.34	75,75,75,75	0
57	MG	CA	3148	1/1	0.26	0.29	81,81,81,81	0
57	MG	BA	3502	1/1	0.45	0.23	57,57,57,57	0
57	MG	BA	3175	1/1	0.49	0.24	55,55,55,55	0
57	MG	CA	3023	1/1	0.53	0.26	88,88,88,88	0
57	MG	CA	3129	1/1	0.54	0.35	83,83,83,83	0
57	MG	CA	3062	1/1	0.55	0.43	73,73,73,73	0
57	MG	AA	3166	1/1	0.55	0.21	70,70,70,70	0
57	MG	DA	3555	1/1	0.59	0.28	70,70,70,70	0
57	MG	CA	3116	1/1	0.60	0.21	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3160	1/1	0.60	0.24	65,65,65,65	0
57	MG	CA	3060	1/1	0.61	0.30	78,78,78,78	0
57	MG	CA	3107	1/1	0.61	0.36	89,89,89,89	0
57	MG	CA	3106	1/1	0.62	0.21	65,65,65,65	0
57	MG	CA	3094	1/1	0.63	0.34	80,80,80,80	0
57	MG	AA	3080	1/1	0.63	0.35	82,82,82,82	0
57	MG	CA	3085	1/1	0.63	0.38	71,71,71,71	0
57	MG	DA	3491	1/1	0.64	0.21	43,43,43,43	0
57	MG	AA	3109	1/1	0.64	0.30	75,75,75,75	0
57	MG	CA	3082	1/1	0.64	0.27	71,71,71,71	0
57	MG	BA	3651	1/1	0.65	0.28	62,62,62,62	0
57	MG	CA	3158	1/1	0.65	0.28	66,66,66,66	0
57	MG	AA	3063	1/1	0.66	0.22	89,89,89,89	0
57	MG	CA	3120	1/1	0.66	0.35	72,72,72,72	0
57	MG	BA	3487	1/1	0.66	0.27	70,70,70,70	0
57	MG	DA	3595	1/1	0.66	0.15	65,65,65,65	0
57	MG	BA	3113	1/1	0.68	0.17	57,57,57,57	0
57	MG	CA	3139	1/1	0.68	0.20	82,82,82,82	0
57	MG	CA	3126	1/1	0.68	0.28	73,73,73,73	0
57	MG	AA	3014	1/1	0.69	0.23	73,73,73,73	0
57	MG	AX	3011	1/1	0.69	0.39	73,73,73,73	0
57	MG	DA	3565	1/1	0.69	0.23	49,49,49,49	0
57	MG	AA	3146	1/1	0.69	0.19	81,81,81,81	0
57	MG	BA	3091	1/1	0.70	0.17	56,56,56,56	0
57	MG	CA	3030	1/1	0.70	0.30	75,75,75,75	0
57	MG	DA	3609	1/1	0.70	0.24	55,55,55,55	0
57	MG	AA	3198	1/1	0.71	0.15	66,66,66,66	0
57	MG	AA	3069	1/1	0.71	0.29	75,75,75,75	0
57	MG	AA	3145	1/1	0.71	0.40	71,71,71,71	0
57	MG	DA	3374	1/1	0.71	0.15	42,42,42,42	0
57	MG	CA	3119	1/1	0.71	0.18	74,74,74,74	0
57	MG	DA	3533	1/1	0.72	0.30	47,47,47,47	0
57	MG	DA	3547	1/1	0.72	0.28	68,68,68,68	0
57	MG	DA	3548	1/1	0.72	0.14	58,58,58,58	0
57	MG	BA	3674	1/1	0.72	0.19	59,59,59,59	0
57	MG	CA	3004	1/1	0.72	0.16	70,70,70,70	0
57	MG	DA	3303	1/1	0.72	0.20	57,57,57,57	0
57	MG	AA	3056	1/1	0.72	0.26	66,66,66,66	0
57	MG	CA	3152	1/1	0.72	0.21	66,66,66,66	0
57	MG	DB	3002	1/1	0.72	0.25	75,75,75,75	0
57	MG	DA	3162	1/1	0.74	0.27	58,58,58,58	0
57	MG	AA	3018	1/1	0.74	0.19	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3001	1/1	0.74	0.22	45,45,45,45	0
57	MG	DA	3550	1/1	0.74	0.26	63,63,63,63	0
57	MG	CA	3154	1/1	0.74	0.32	68,68,68,68	0
57	MG	DR	3001	1/1	0.74	0.52	66,66,66,66	0
57	MG	AA	3064	1/1	0.75	0.23	65,65,65,65	0
57	MG	BA	3610	1/1	0.75	0.27	60,60,60,60	0
57	MG	CA	3113	1/1	0.75	0.23	75,75,75,75	0
57	MG	AA	3046	1/1	0.75	0.33	72,72,72,72	0
57	MG	DB	3008	1/1	0.75	0.15	59,59,59,59	0
57	MG	AA	3132	1/1	0.75	0.26	67,67,67,67	0
57	MG	DV	202	1/1	0.75	0.26	75,75,75,75	0
57	MG	D8	101	1/1	0.75	0.31	60,60,60,60	0
57	MG	BA	3625	1/1	0.76	0.16	46,46,46,46	0
57	MG	CA	3059	1/1	0.76	0.26	60,60,60,60	0
57	MG	AA	3123	1/1	0.76	0.27	59,59,59,59	0
57	MG	DA	3304	1/1	0.76	0.16	44,44,44,44	0
57	MG	DA	3608	1/1	0.76	0.18	61,61,61,61	0
57	MG	AA	3054	1/1	0.76	0.30	62,62,62,62	0
57	MG	BA	3519	1/1	0.76	0.15	26,26,26,26	0
57	MG	CA	3017	1/1	0.76	0.31	69,69,69,69	0
57	MG	BA	3470	1/1	0.76	0.16	69,69,69,69	0
57	MG	DA	3134	1/1	0.76	0.28	59,59,59,59	0
57	MG	DA	3135	1/1	0.76	0.26	61,61,61,61	0
57	MG	DA	3158	1/1	0.77	0.11	52,52,52,52	0
57	MG	BA	3577	1/1	0.77	0.24	35,35,35,35	0
57	MG	BA	3587	1/1	0.77	0.21	51,51,51,51	0
57	MG	CA	3098	1/1	0.77	0.16	76,76,76,76	0
57	MG	CA	3155	1/1	0.77	0.25	66,66,66,66	0
57	MG	DA	3342	1/1	0.77	0.16	49,49,49,49	0
57	MG	CA	3020	1/1	0.77	0.11	51,51,51,51	0
57	MG	DA	3390	1/1	0.77	0.21	54,54,54,54	0
57	MG	AA	3160	1/1	0.77	0.21	58,58,58,58	0
57	MG	DA	3003	1/1	0.77	0.12	56,56,56,56	0
57	MG	CA	3134	1/1	0.77	0.14	72,72,72,72	0
57	MG	CA	3027	1/1	0.77	0.24	62,62,62,62	0
57	MG	BG	3002	1/1	0.78	0.14	65,65,65,65	0
57	MG	CA	3042	1/1	0.78	0.29	68,68,68,68	0
57	MG	BA	3595	1/1	0.78	0.26	52,52,52,52	0
57	MG	DA	3610	1/1	0.78	0.18	42,42,42,42	0
57	MG	CX	3002	1/1	0.78	0.37	75,75,75,75	0
57	MG	BA	3416	1/1	0.78	0.15	73,73,73,73	0
57	MG	BA	3425	1/1	0.78	0.15	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	3127	1/1	0.78	0.25	73,73,73,73	0
57	MG	BA	3413	1/1	0.78	0.13	50,50,50,50	0
57	MG	DA	3417	1/1	0.79	0.20	46,46,46,46	0
57	MG	DA	3426	1/1	0.79	0.28	38,38,38,38	0
57	MG	DA	3439	1/1	0.79	0.12	44,44,44,44	0
57	MG	DA	3458	1/1	0.79	0.11	44,44,44,44	0
57	MG	BA	3630	1/1	0.79	0.29	72,72,72,72	0
57	MG	CA	3117	1/1	0.79	0.17	100,100,100,100	0
57	MG	BA	3412	1/1	0.79	0.27	44,44,44,44	0
57	MG	AA	3193	1/1	0.79	0.40	77,77,77,77	0
57	MG	BA	3533	1/1	0.79	0.23	45,45,45,45	0
57	MG	DA	3142	1/1	0.79	0.23	50,50,50,50	0
57	MG	BZ	3001	1/1	0.79	0.15	56,56,56,56	0
57	MG	CA	3084	1/1	0.79	0.27	58,58,58,58	0
57	MG	AA	3041	1/1	0.79	0.26	62,62,62,62	0
57	MG	DA	3601	1/1	0.79	0.16	43,43,43,43	0
57	MG	DA	3276	1/1	0.79	0.12	56,56,56,56	0
57	MG	DA	3291	1/1	0.79	0.18	56,56,56,56	0
57	MG	DA	3297	1/1	0.79	0.17	48,48,48,48	0
57	MG	BA	3579	1/1	0.79	0.16	44,44,44,44	0
57	MG	AA	3001	1/1	0.79	0.24	72,72,72,72	0
57	MG	BA	3235	1/1	0.79	0.15	52,52,52,52	0
57	MG	BA	3482	1/1	0.79	0.13	56,56,56,56	0
57	MG	BA	3281	1/1	0.79	0.14	46,46,46,46	0
57	MG	CA	3135	1/1	0.80	0.26	85,85,85,85	0
57	MG	DA	3461	1/1	0.80	0.20	55,55,55,55	0
57	MG	BA	3467	1/1	0.80	0.22	51,51,51,51	0
57	MG	DA	3509	1/1	0.80	0.23	42,42,42,42	0
57	MG	CA	3035	1/1	0.80	0.26	63,63,63,63	0
57	MG	DA	3193	1/1	0.80	0.16	43,43,43,43	0
57	MG	DA	3204	1/1	0.80	0.17	39,39,39,39	0
57	MG	DA	3223	1/1	0.80	0.24	56,56,56,56	0
57	MG	BF	309	1/1	0.80	0.15	61,61,61,61	0
57	MG	DA	3280	1/1	0.80	0.21	49,49,49,49	0
57	MG	BA	3604	1/1	0.80	0.17	62,62,62,62	0
57	MG	DA	3569	1/1	0.80	0.13	42,42,42,42	0
57	MG	BA	3207	1/1	0.80	0.17	55,55,55,55	0
57	MG	AA	3068	1/1	0.80	0.18	64,64,64,64	0
57	MG	CA	3081	1/1	0.80	0.16	67,67,67,67	0
57	MG	DA	3328	1/1	0.80	0.16	66,66,66,66	0
57	MG	AA	3125	1/1	0.80	0.21	60,60,60,60	0
57	MG	DA	3615	1/1	0.80	0.12	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3625	1/1	0.80	0.20	57,57,57,57	0
57	MG	BA	3631	1/1	0.80	0.15	53,53,53,53	0
57	MG	DA	3125	1/1	0.80	0.15	48,48,48,48	0
57	MG	CA	3127	1/1	0.80	0.33	76,76,76,76	0
57	MG	BA	3374	1/1	0.80	0.16	48,48,48,48	0
57	MG	BA	3656	1/1	0.80	0.20	57,57,57,57	0
57	MG	DA	3208	1/1	0.81	0.16	50,50,50,50	0
57	MG	BA	3598	1/1	0.81	0.18	54,54,54,54	0
57	MG	AX	3003	1/1	0.81	0.30	66,66,66,66	0
57	MG	BA	3530	1/1	0.81	0.18	20,20,20,20	0
57	MG	AA	3113	1/1	0.81	0.32	54,54,54,54	0
57	MG	CA	3008	1/1	0.81	0.41	67,67,67,67	0
57	MG	BA	3535	1/1	0.81	0.16	29,29,29,29	0
57	MG	DA	3064	1/1	0.81	0.16	52,52,52,52	0
57	MG	DA	3308	1/1	0.81	0.15	52,52,52,52	0
57	MG	DA	3314	1/1	0.81	0.17	56,56,56,56	0
57	MG	DA	3596	1/1	0.81	0.21	71,71,71,71	0
57	MG	DA	3087	1/1	0.81	0.23	65,65,65,65	0
57	MG	CA	3019	1/1	0.81	0.17	57,57,57,57	0
57	MG	AA	3180	1/1	0.81	0.10	61,61,61,61	0
57	MG	CA	3133	1/1	0.81	0.27	69,69,69,69	0
57	MG	DA	3409	1/1	0.81	0.18	70,70,70,70	0
57	MG	CA	3091	1/1	0.81	0.26	75,75,75,75	0
57	MG	AA	3150	1/1	0.81	0.20	65,65,65,65	0
57	MG	AA	3090	1/1	0.81	0.22	70,70,70,70	0
57	MG	CA	3146	1/1	0.81	0.22	74,74,74,74	0
57	MG	AF	3001	1/1	0.81	0.14	58,58,58,58	0
57	MG	BA	3700	1/1	0.81	0.41	69,69,69,69	0
57	MG	AX	3002	1/1	0.82	0.20	67,67,67,67	0
57	MG	DA	3447	1/1	0.82	0.16	48,48,48,48	0
57	MG	CA	3051	1/1	0.82	0.25	57,57,57,57	0
57	MG	CA	3053	1/1	0.82	0.26	59,59,59,59	0
57	MG	DA	3182	1/1	0.82	0.43	52,52,52,52	0
57	MG	BA	3263	1/1	0.82	0.28	50,50,50,50	0
57	MG	AA	3122	1/1	0.82	0.22	52,52,52,52	0
57	MG	DA	3543	1/1	0.82	0.22	61,61,61,61	0
57	MG	BA	3350	1/1	0.82	0.11	43,43,43,43	0
57	MG	CA	3078	1/1	0.82	0.21	63,63,63,63	0
57	MG	DA	3252	1/1	0.82	0.12	63,63,63,63	0
57	MG	BB	3020	1/1	0.82	0.14	55,55,55,55	0
57	MG	BA	3351	1/1	0.82	0.12	62,62,62,62	0
57	MG	BA	3372	1/1	0.82	0.16	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	3134	1/1	0.82	0.15	59,59,59,59	0
57	MG	AA	3151	1/1	0.82	0.21	72,72,72,72	0
57	MG	BA	3105	1/1	0.82	0.17	45,45,45,45	0
57	MG	AA	3085	1/1	0.82	0.31	69,69,69,69	0
57	MG	DA	3602	1/1	0.82	0.20	50,50,50,50	0
57	MG	AA	3163	1/1	0.82	0.19	70,70,70,70	0
57	MG	BA	3204	1/1	0.82	0.24	61,61,61,61	0
57	MG	AN	502	1/1	0.82	0.16	61,61,61,61	0
57	MG	CA	3115	1/1	0.82	0.15	59,59,59,59	0
57	MG	DA	3624	1/1	0.82	0.21	66,66,66,66	0
57	MG	DA	3380	1/1	0.82	0.21	65,65,65,65	0
57	MG	BA	3216	1/1	0.82	0.13	35,35,35,35	0
57	MG	BA	3220	1/1	0.82	0.35	54,54,54,54	0
57	MG	DA	3412	1/1	0.82	0.15	60,60,60,60	0
57	MG	BA	3636	1/1	0.82	0.24	45,45,45,45	0
57	MG	DW	201	1/1	0.82	0.22	70,70,70,70	0
57	MG	CA	3038	1/1	0.82	0.12	68,68,68,68	0
57	MG	BA	3303	1/1	0.83	0.15	39,39,39,39	0
57	MG	DA	3499	1/1	0.83	0.10	47,47,47,47	0
57	MG	CA	3006	1/1	0.83	0.10	43,43,43,43	0
57	MG	CA	3140	1/1	0.83	0.15	48,48,48,48	0
57	MG	BA	3611	1/1	0.83	0.21	61,61,61,61	0
57	MG	DA	3544	1/1	0.83	0.15	59,59,59,59	0
57	MG	BA	3136	1/1	0.83	0.14	56,56,56,56	0
57	MG	BA	3514	1/1	0.83	0.24	36,36,36,36	0
57	MG	BA	3003	1/1	0.83	0.09	44,44,44,44	0
57	MG	BA	3634	1/1	0.83	0.18	58,58,58,58	0
57	MG	DA	3554	1/1	0.83	0.10	46,46,46,46	0
57	MG	CA	3105	1/1	0.83	0.27	76,76,76,76	0
57	MG	BA	3178	1/1	0.83	0.23	52,52,52,52	0
57	MG	BA	3639	1/1	0.83	0.12	46,46,46,46	0
57	MG	DA	3576	1/1	0.83	0.22	46,46,46,46	0
57	MG	BA	3011	1/1	0.83	0.13	32,32,32,32	0
57	MG	DA	3017	1/1	0.83	0.29	58,58,58,58	0
57	MG	DA	3059	1/1	0.83	0.12	60,60,60,60	0
57	MG	BA	3064	1/1	0.83	0.14	38,38,38,38	0
57	MG	DA	3356	1/1	0.83	0.15	53,53,53,53	0
57	MG	BA	3066	1/1	0.83	0.29	53,53,53,53	0
57	MG	DA	3112	1/1	0.83	0.23	63,63,63,63	0
57	MG	CA	3043	1/1	0.83	0.30	68,68,68,68	0
57	MG	CA	3044	1/1	0.83	0.11	59,59,59,59	0
57	MG	BA	3688	1/1	0.83	0.20	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	3061	1/1	0.83	0.20	65,65,65,65	0
57	MG	BA	3221	1/1	0.83	0.34	59,59,59,59	0
57	MG	DO	5001	1/1	0.83	0.19	53,53,53,53	0
57	MG	AA	3066	1/1	0.83	0.14	66,66,66,66	0
57	MG	BA	3109	1/1	0.83	0.15	53,53,53,53	0
57	MG	AA	3006	1/1	0.83	0.12	62,62,62,62	0
57	MG	DA	3189	1/1	0.83	0.15	57,57,57,57	0
57	MG	AA	3011	1/1	0.84	0.12	67,67,67,67	0
57	MG	DA	3437	1/1	0.84	0.18	48,48,48,48	0
57	MG	CA	3005	1/1	0.84	0.24	81,81,81,81	0
57	MG	AA	3196	1/1	0.84	0.17	60,60,60,60	0
57	MG	BA	3266	1/1	0.84	0.24	53,53,53,53	0
57	MG	AA	3171	1/1	0.84	0.17	45,45,45,45	0
57	MG	CA	3110	1/1	0.84	0.18	56,56,56,56	0
57	MG	DA	3493	1/1	0.84	0.17	53,53,53,53	0
57	MG	AA	3199	1/1	0.84	0.17	58,58,58,58	0
57	MG	CA	3114	1/1	0.84	0.22	96,96,96,96	0
57	MG	DA	3526	1/1	0.84	0.11	41,41,41,41	0
57	MG	BA	3323	1/1	0.84	0.16	59,59,59,59	0
57	MG	BA	3347	1/1	0.84	0.19	32,32,32,32	0
57	MG	AA	3205	1/1	0.84	0.18	48,48,48,48	0
57	MG	BA	3032	1/1	0.84	0.17	30,30,30,30	0
57	MG	BA	3644	1/1	0.84	0.25	48,48,48,48	0
57	MG	CA	3125	1/1	0.84	0.14	64,64,64,64	0
57	MG	BA	3649	1/1	0.84	0.18	65,65,65,65	0
57	MG	BA	3359	1/1	0.84	0.14	56,56,56,56	0
57	MG	BA	3060	1/1	0.84	0.22	59,59,59,59	0
57	MG	BA	3671	1/1	0.84	0.21	55,55,55,55	0
57	MG	DA	3277	1/1	0.84	0.32	50,50,50,50	0
57	MG	AE	3001	1/1	0.84	0.12	85,85,85,85	0
57	MG	AA	3175	1/1	0.84	0.35	61,61,61,61	0
57	MG	CA	3055	1/1	0.84	0.20	66,66,66,66	0
57	MG	CA	3058	1/1	0.84	0.44	70,70,70,70	0
57	MG	BA	3585	1/1	0.84	0.12	45,45,45,45	0
57	MG	BB	3019	1/1	0.84	0.21	62,62,62,62	0
57	MG	CA	3061	1/1	0.84	0.16	87,87,87,87	0
57	MG	BA	3088	1/1	0.84	0.30	59,59,59,59	0
57	MG	DA	3337	1/1	0.84	0.15	46,46,46,46	0
57	MG	DA	3619	1/1	0.84	0.23	63,63,63,63	0
57	MG	BA	3590	1/1	0.84	0.30	62,62,62,62	0
57	MG	AA	3043	1/1	0.84	0.28	59,59,59,59	0
57	MG	DA	3628	1/1	0.84	0.26	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CK	3001	1/1	0.84	0.20	57,57,57,57	0
57	MG	BN	3002	1/1	0.84	0.12	46,46,46,46	0
57	MG	DD	307	1/1	0.84	0.11	50,50,50,50	0
57	MG	BW	202	1/1	0.84	0.43	41,41,41,41	0
57	MG	BA	3419	1/1	0.84	0.29	58,58,58,58	0
57	MG	CA	3090	1/1	0.84	0.35	64,64,64,64	0
57	MG	CA	3003	1/1	0.84	0.17	74,74,74,74	0
57	MG	DA	3419	1/1	0.84	0.15	37,37,37,37	0
57	MG	BA	3222	1/1	0.85	0.14	52,52,52,52	0
57	MG	CA	3014	1/1	0.85	0.19	58,58,58,58	0
57	MG	DA	3381	1/1	0.85	0.24	55,55,55,55	0
57	MG	CA	3015	1/1	0.85	0.21	61,61,61,61	0
57	MG	DA	3069	1/1	0.85	0.35	59,59,59,59	0
57	MG	DA	3411	1/1	0.85	0.14	51,51,51,51	0
57	MG	DA	3074	1/1	0.85	0.18	38,38,38,38	0
57	MG	DA	3076	1/1	0.85	0.20	53,53,53,53	0
57	MG	AA	3114	1/1	0.85	0.31	57,57,57,57	0
57	MG	DA	3425	1/1	0.85	0.14	40,40,40,40	0
57	MG	DA	3111	1/1	0.85	0.15	54,54,54,54	0
57	MG	BA	3380	1/1	0.85	0.14	55,55,55,55	0
57	MG	DA	3117	1/1	0.85	0.10	40,40,40,40	0
57	MG	DA	3446	1/1	0.85	0.17	37,37,37,37	0
57	MG	BA	3540	1/1	0.85	0.13	24,24,24,24	0
57	MG	DA	3455	1/1	0.85	0.16	34,34,34,34	0
57	MG	BA	3543	1/1	0.85	0.14	69,69,69,69	0
57	MG	BA	3567	1/1	0.85	0.16	55,55,55,55	0
57	MG	BA	3241	1/1	0.85	0.30	53,53,53,53	0
57	MG	DA	3144	1/1	0.85	0.09	48,48,48,48	0
57	MG	AA	3093	1/1	0.85	0.29	56,56,56,56	0
57	MG	BA	3672	1/1	0.85	0.13	28,28,28,28	0
57	MG	CA	3041	1/1	0.85	0.23	62,62,62,62	0
57	MG	DA	3527	1/1	0.85	0.14	52,52,52,52	0
57	MG	DA	3168	1/1	0.85	0.29	50,50,50,50	0
57	MG	BA	3584	1/1	0.85	0.15	59,59,59,59	0
57	MG	DA	3187	1/1	0.85	0.12	39,39,39,39	0
57	MG	BA	3683	1/1	0.85	0.17	44,44,44,44	0
57	MG	DA	3191	1/1	0.85	0.12	54,54,54,54	0
57	MG	BA	3155	1/1	0.85	0.20	44,44,44,44	0
57	MG	BA	3692	1/1	0.85	0.31	64,64,64,64	0
57	MG	AA	3133	1/1	0.85	0.20	59,59,59,59	0
57	MG	DA	3217	1/1	0.85	0.27	50,50,50,50	0
57	MG	BB	3008	1/1	0.85	0.15	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3248	1/1	0.85	0.09	59,59,59,59	0
57	MG	AA	3189	1/1	0.85	0.17	69,69,69,69	0
57	MG	DA	3256	1/1	0.85	0.18	52,52,52,52	0
57	MG	DA	3259	1/1	0.85	0.09	39,39,39,39	0
57	MG	AA	3155	1/1	0.85	0.18	65,65,65,65	0
57	MG	BA	3328	1/1	0.85	0.13	55,55,55,55	0
57	MG	BA	3602	1/1	0.85	0.36	65,65,65,65	0
57	MG	DA	3283	1/1	0.85	0.12	40,40,40,40	0
57	MG	BA	3474	1/1	0.85	0.16	64,64,64,64	0
57	MG	CA	3071	1/1	0.85	0.30	49,49,49,49	0
57	MG	CA	3075	1/1	0.85	0.14	48,48,48,48	0
57	MG	BA	3337	1/1	0.85	0.17	51,51,51,51	0
57	MG	DA	3307	1/1	0.85	0.21	51,51,51,51	0
57	MG	AA	3004	1/1	0.85	0.38	61,61,61,61	0
57	MG	DA	3312	1/1	0.85	0.17	30,30,30,30	0
57	MG	DB	3005	1/1	0.85	0.24	54,54,54,54	0
57	MG	BA	3615	1/1	0.85	0.13	60,60,60,60	0
57	MG	DA	3319	1/1	0.85	0.26	45,45,45,45	0
57	MG	AX	3008	1/1	0.85	0.09	58,58,58,58	0
57	MG	AA	3137	1/1	0.85	0.46	66,66,66,66	0
57	MG	AA	3065	1/1	0.85	0.13	48,48,48,48	0
57	MG	DA	3353	1/1	0.85	0.14	42,42,42,42	0
57	MG	CA	3007	1/1	0.85	0.19	55,55,55,55	0
57	MG	DA	3457	1/1	0.86	0.14	45,45,45,45	0
57	MG	DA	3271	1/1	0.86	0.20	47,47,47,47	0
57	MG	AA	3142	1/1	0.86	0.27	53,53,53,53	0
57	MG	DA	3472	1/1	0.86	0.11	24,24,24,24	0
57	MG	DA	3481	1/1	0.86	0.17	69,69,69,69	0
57	MG	BA	3492	1/1	0.86	0.10	30,30,30,30	0
57	MG	DA	3066	1/1	0.86	0.09	55,55,55,55	0
57	MG	BA	3415	1/1	0.86	0.16	61,61,61,61	0
57	MG	AA	3170	1/1	0.86	0.15	70,70,70,70	0
57	MG	DA	3520	1/1	0.86	0.13	51,51,51,51	0
57	MG	BA	3107	1/1	0.86	0.25	49,49,49,49	0
57	MG	BA	3597	1/1	0.86	0.26	56,56,56,56	0
57	MG	BA	3525	1/1	0.86	0.15	49,49,49,49	0
57	MG	BA	3666	1/1	0.86	0.16	79,79,79,79	0
57	MG	BA	3600	1/1	0.86	0.25	59,59,59,59	0
57	MG	AA	3126	1/1	0.86	0.15	52,52,52,52	0
57	MG	BA	3603	1/1	0.86	0.15	42,42,42,42	0
57	MG	BA	3679	1/1	0.86	0.10	38,38,38,38	0
57	MG	DA	3322	1/1	0.86	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3426	1/1	0.86	0.14	30,30,30,30	0
57	MG	BA	3429	1/1	0.86	0.12	37,37,37,37	0
57	MG	DA	3561	1/1	0.86	0.14	51,51,51,51	0
57	MG	DA	3148	1/1	0.86	0.16	45,45,45,45	0
57	MG	DA	3346	1/1	0.86	0.11	39,39,39,39	0
57	MG	DA	3571	1/1	0.86	0.12	54,54,54,54	0
57	MG	BA	3451	1/1	0.86	0.16	59,59,59,59	0
57	MG	DA	3592	1/1	0.86	0.16	62,62,62,62	0
57	MG	CA	3025	1/1	0.86	0.17	66,66,66,66	0
57	MG	DA	3366	1/1	0.86	0.14	40,40,40,40	0
57	MG	DA	3370	1/1	0.86	0.24	72,72,72,72	0
57	MG	BA	3613	1/1	0.86	0.19	74,74,74,74	0
57	MG	CA	3147	1/1	0.86	0.14	56,56,56,56	0
57	MG	CA	3029	1/1	0.86	0.11	48,48,48,48	0
57	MG	AA	3047	1/1	0.86	0.14	59,59,59,59	0
57	MG	AA	3178	1/1	0.86	0.23	67,67,67,67	0
57	MG	DA	3410	1/1	0.86	0.13	37,37,37,37	0
57	MG	CA	3099	1/1	0.86	0.17	50,50,50,50	0
57	MG	CA	3102	1/1	0.86	0.14	56,56,56,56	0
57	MG	CJ	5001	1/1	0.86	0.07	51,51,51,51	0
57	MG	BA	3628	1/1	0.86	0.18	60,60,60,60	0
57	MG	BD	311	1/1	0.86	0.14	60,60,60,60	0
57	MG	DA	3220	1/1	0.86	0.19	54,54,54,54	0
57	MG	AA	3201	1/1	0.86	0.26	68,68,68,68	0
57	MG	DG	3001	1/1	0.86	0.08	49,49,49,49	0
57	MG	AA	3106	1/1	0.86	0.25	53,53,53,53	0
57	MG	DA	3443	1/1	0.86	0.13	27,27,27,27	0
57	MG	CA	3111	1/1	0.86	0.18	65,65,65,65	0
57	MG	DA	3043	1/1	0.86	0.14	44,44,44,44	0
57	MG	DA	3051	1/1	0.86	0.11	54,54,54,54	0
57	MG	BA	3052	1/1	0.87	0.23	44,44,44,44	0
57	MG	CA	3066	1/1	0.87	0.30	69,69,69,69	0
57	MG	DA	3444	1/1	0.87	0.15	37,37,37,37	0
57	MG	CA	3067	1/1	0.87	0.17	45,45,45,45	0
57	MG	CA	3068	1/1	0.87	0.22	53,53,53,53	0
57	MG	DA	3453	1/1	0.87	0.13	44,44,44,44	0
57	MG	AA	3124	1/1	0.87	0.34	58,58,58,58	0
57	MG	DA	3456	1/1	0.87	0.30	59,59,59,59	0
57	MG	DA	3219	1/1	0.87	0.12	54,54,54,54	0
57	MG	BA	3549	1/1	0.87	0.22	55,55,55,55	0
57	MG	CA	3153	1/1	0.87	0.33	57,57,57,57	0
57	MG	DA	3226	1/1	0.87	0.26	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3565	1/1	0.87	0.12	50,50,50,50	0
57	MG	BA	3316	1/1	0.87	0.21	49,49,49,49	0
57	MG	CA	3012	1/1	0.87	0.27	45,45,45,45	0
57	MG	DA	3495	1/1	0.87	0.10	48,48,48,48	0
57	MG	CE	3001	1/1	0.87	0.14	80,80,80,80	0
57	MG	DA	3260	1/1	0.87	0.11	43,43,43,43	0
57	MG	DA	3519	1/1	0.87	0.18	60,60,60,60	0
57	MG	BA	3061	1/1	0.87	0.17	58,58,58,58	0
57	MG	DA	3521	1/1	0.87	0.12	57,57,57,57	0
57	MG	BA	3199	1/1	0.87	0.27	60,60,60,60	0
57	MG	BA	3652	1/1	0.87	0.18	65,65,65,65	0
57	MG	AA	3188	1/1	0.87	0.12	62,62,62,62	0
57	MG	DA	3537	1/1	0.87	0.12	45,45,45,45	0
57	MG	DA	3539	1/1	0.87	0.21	52,52,52,52	0
57	MG	CA	3092	1/1	0.87	0.17	76,76,76,76	0
57	MG	BA	3454	1/1	0.87	0.10	45,45,45,45	0
57	MG	DA	3027	1/1	0.87	0.09	42,42,42,42	0
57	MG	DA	3038	1/1	0.87	0.12	39,39,39,39	0
57	MG	CA	3021	1/1	0.87	0.11	46,46,46,46	0
57	MG	CA	3022	1/1	0.87	0.27	55,55,55,55	0
57	MG	BA	3465	1/1	0.87	0.17	44,44,44,44	0
57	MG	BA	3344	1/1	0.87	0.19	48,48,48,48	0
57	MG	CA	3026	1/1	0.87	0.17	59,59,59,59	0
57	MG	AA	3008	1/1	0.87	0.19	65,65,65,65	0
57	MG	CA	3028	1/1	0.87	0.26	57,57,57,57	0
57	MG	BA	3349	1/1	0.87	0.13	55,55,55,55	0
57	MG	BA	3480	1/1	0.87	0.22	50,50,50,50	0
57	MG	DA	3584	1/1	0.87	0.17	63,63,63,63	0
57	MG	DA	3591	1/1	0.87	0.12	69,69,69,69	0
57	MG	DA	3090	1/1	0.87	0.12	52,52,52,52	0
57	MG	AA	3156	1/1	0.87	0.24	86,86,86,86	0
57	MG	BA	3002	1/1	0.87	0.18	45,45,45,45	0
57	MG	AA	3075	1/1	0.87	0.13	57,57,57,57	0
57	MG	AA	3040	1/1	0.87	0.29	67,67,67,67	0
57	MG	DA	3606	1/1	0.87	0.25	54,54,54,54	0
57	MG	DA	3607	1/1	0.87	0.21	73,73,73,73	0
57	MG	DA	3130	1/1	0.87	0.16	55,55,55,55	0
57	MG	BA	3609	1/1	0.87	0.21	47,47,47,47	0
57	MG	BA	3224	1/1	0.87	0.25	48,48,48,48	0
57	MG	CA	3121	1/1	0.87	0.24	51,51,51,51	0
57	MG	BA	3515	1/1	0.87	0.14	44,44,44,44	0
57	MG	DA	3397	1/1	0.87	0.15	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3024	1/1	0.87	0.11	42,42,42,42	0
57	MG	BA	3385	1/1	0.87	0.20	34,34,34,34	0
57	MG	BA	3621	1/1	0.87	0.11	18,18,18,18	0
57	MG	DB	3003	1/1	0.87	0.18	76,76,76,76	0
57	MG	CA	3131	1/1	0.87	0.15	57,57,57,57	0
57	MG	DA	3415	1/1	0.87	0.25	55,55,55,55	0
57	MG	DA	3165	1/1	0.87	0.21	54,54,54,54	0
57	MG	BA	3111	1/1	0.87	0.22	51,51,51,51	0
57	MG	AS	101	1/1	0.87	0.15	55,55,55,55	0
57	MG	BA	3050	1/1	0.87	0.11	44,44,44,44	0
57	MG	DA	3429	1/1	0.87	0.15	38,38,38,38	0
57	MG	DA	3430	1/1	0.87	0.13	26,26,26,26	0
57	MG	CA	3138	1/1	0.87	0.32	66,66,66,66	0
57	MG	DA	3228	1/1	0.88	0.19	49,49,49,49	0
57	MG	CW	101	1/1	0.88	0.12	43,43,43,43	0
57	MG	BB	3009	1/1	0.88	0.21	63,63,63,63	0
57	MG	DA	3254	1/1	0.88	0.27	42,42,42,42	0
57	MG	CA	3032	1/1	0.88	0.29	58,58,58,58	0
57	MG	DA	3002	1/1	0.88	0.23	44,44,44,44	0
57	MG	CA	3103	1/1	0.88	0.24	71,71,71,71	0
57	MG	CA	3104	1/1	0.88	0.16	37,37,37,37	0
57	MG	CA	3034	1/1	0.88	0.15	49,49,49,49	0
57	MG	BA	3614	1/1	0.88	0.18	64,64,64,64	0
57	MG	BA	3320	1/1	0.88	0.12	56,56,56,56	0
57	MG	CA	3109	1/1	0.88	0.21	61,61,61,61	0
57	MG	DA	3511	1/1	0.88	0.09	40,40,40,40	0
57	MG	DA	3284	1/1	0.88	0.17	51,51,51,51	0
57	MG	DA	3053	1/1	0.88	0.29	50,50,50,50	0
57	MG	BA	3322	1/1	0.88	0.15	40,40,40,40	0
57	MG	BA	3548	1/1	0.88	0.21	54,54,54,54	0
57	MG	BA	3188	1/1	0.88	0.22	48,48,48,48	0
57	MG	AA	3077	1/1	0.88	0.23	52,52,52,52	0
57	MG	DA	3072	1/1	0.88	0.22	46,46,46,46	0
57	MG	BQ	3003	1/1	0.88	0.15	68,68,68,68	0
57	MG	CA	3052	1/1	0.88	0.14	61,61,61,61	0
57	MG	AA	3108	1/1	0.88	0.18	54,54,54,54	0
57	MG	DA	3545	1/1	0.88	0.11	70,70,70,70	0
57	MG	CA	3054	1/1	0.88	0.27	53,53,53,53	0
57	MG	DA	3102	1/1	0.88	0.23	64,64,64,64	0
57	MG	DA	3331	1/1	0.88	0.25	54,54,54,54	0
57	MG	BA	3633	1/1	0.88	0.23	54,54,54,54	0
57	MG	CA	3056	1/1	0.88	0.15	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3205	1/1	0.88	0.24	52,52,52,52	0
57	MG	DA	3351	1/1	0.88	0.24	45,45,45,45	0
57	MG	AA	3173	1/1	0.88	0.10	53,53,53,53	0
57	MG	DA	3355	1/1	0.88	0.12	48,48,48,48	0
57	MG	BA	3090	1/1	0.88	0.26	50,50,50,50	0
57	MG	DA	3362	1/1	0.88	0.24	48,48,48,48	0
57	MG	AA	3049	1/1	0.88	0.18	43,43,43,43	0
57	MG	DA	3586	1/1	0.88	0.12	21,21,21,21	0
57	MG	CA	3130	1/1	0.88	0.14	88,88,88,88	0
57	MG	AD	303	1/1	0.88	0.29	60,60,60,60	0
57	MG	BA	3017	1/1	0.88	0.19	48,48,48,48	0
57	MG	AA	3042	1/1	0.88	0.26	52,52,52,52	0
57	MG	BA	3031	1/1	0.88	0.21	51,51,51,51	0
57	MG	CA	3136	1/1	0.88	0.25	68,68,68,68	0
57	MG	DA	3605	1/1	0.88	0.11	64,64,64,64	0
57	MG	DA	3406	1/1	0.88	0.13	62,62,62,62	0
57	MG	DA	3408	1/1	0.88	0.09	44,44,44,44	0
57	MG	BA	3238	1/1	0.88	0.17	26,26,26,26	0
57	MG	BA	3599	1/1	0.88	0.14	43,43,43,43	0
57	MG	AA	3032	1/1	0.88	0.34	80,80,80,80	0
57	MG	DA	3170	1/1	0.88	0.34	47,47,47,47	0
57	MG	CA	3144	1/1	0.88	0.22	58,58,58,58	0
57	MG	BA	3409	1/1	0.88	0.18	27,27,27,27	0
57	MG	DA	3188	1/1	0.88	0.26	48,48,48,48	0
57	MG	BA	3116	1/1	0.88	0.35	54,54,54,54	0
57	MG	CA	3083	1/1	0.88	0.38	71,71,71,71	0
57	MG	DA	3428	1/1	0.88	0.15	46,46,46,46	0
57	MG	AA	3117	1/1	0.88	0.22	55,55,55,55	0
57	MG	AA	3121	1/1	0.88	0.18	66,66,66,66	0
57	MG	DD	306	1/1	0.88	0.20	44,44,44,44	0
57	MG	BA	3691	1/1	0.88	0.23	54,54,54,54	0
57	MG	DA	3209	1/1	0.88	0.20	53,53,53,53	0
57	MG	BA	3532	1/1	0.88	0.16	39,39,39,39	0
57	MG	AA	3059	1/1	0.88	0.29	61,61,61,61	0
57	MG	BB	3001	1/1	0.88	0.16	44,44,44,44	0
57	MG	CA	3096	1/1	0.88	0.13	51,51,51,51	0
57	MG	AA	3097	1/1	0.88	0.11	45,45,45,45	0
59	ZN	D4	501	1/1	0.88	0.10	154,154,154,154	0
57	MG	BA	3560	1/1	0.89	0.17	54,54,54,54	0
57	MG	DA	3435	1/1	0.89	0.12	59,59,59,59	0
57	MG	DA	3185	1/1	0.89	0.36	57,57,57,57	0
57	MG	BA	3673	1/1	0.89	0.12	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3223	1/1	0.89	0.08	38,38,38,38	0
57	MG	BA	3678	1/1	0.89	0.13	49,49,49,49	0
57	MG	AA	3031	1/1	0.89	0.07	41,41,41,41	0
57	MG	BA	3680	1/1	0.89	0.11	46,46,46,46	0
57	MG	DA	3449	1/1	0.89	0.12	52,52,52,52	0
57	MG	BA	3682	1/1	0.89	0.11	30,30,30,30	0
57	MG	AA	3120	1/1	0.89	0.15	53,53,53,53	0
57	MG	AA	3206	1/1	0.89	0.14	62,62,62,62	0
57	MG	DA	3210	1/1	0.89	0.34	57,57,57,57	0
57	MG	AA	3098	1/1	0.89	0.10	42,42,42,42	0
57	MG	BA	3261	1/1	0.89	0.16	52,52,52,52	0
57	MG	BA	3422	1/1	0.89	0.13	39,39,39,39	0
57	MG	BA	3135	1/1	0.89	0.13	48,48,48,48	0
57	MG	DA	3225	1/1	0.89	0.14	42,42,42,42	0
57	MG	BA	3264	1/1	0.89	0.13	47,47,47,47	0
57	MG	AA	3099	1/1	0.89	0.14	59,59,59,59	0
57	MG	DA	3496	1/1	0.89	0.20	63,63,63,63	0
57	MG	DA	3498	1/1	0.89	0.09	66,66,66,66	0
57	MG	DA	3245	1/1	0.89	0.13	46,46,46,46	0
57	MG	DA	3503	1/1	0.89	0.08	51,51,51,51	0
57	MG	DA	3506	1/1	0.89	0.27	38,38,38,38	0
57	MG	BA	3434	1/1	0.89	0.13	27,27,27,27	0
57	MG	CA	3064	1/1	0.89	0.27	64,64,64,64	0
57	MG	DA	3513	1/1	0.89	0.12	49,49,49,49	0
57	MG	DA	3514	1/1	0.89	0.14	34,34,34,34	0
57	MG	DA	3515	1/1	0.89	0.16	53,53,53,53	0
57	MG	BA	3442	1/1	0.89	0.15	51,51,51,51	0
57	MG	BA	3138	1/1	0.89	0.28	57,57,57,57	0
57	MG	BF	305	1/1	0.89	0.08	33,33,33,33	0
57	MG	AA	3100	1/1	0.89	0.26	69,69,69,69	0
57	MG	BA	3460	1/1	0.89	0.09	43,43,43,43	0
57	MG	DA	3529	1/1	0.89	0.12	43,43,43,43	0
57	MG	DA	3273	1/1	0.89	0.15	41,41,41,41	0
57	MG	BA	3304	1/1	0.89	0.21	49,49,49,49	0
57	MG	BA	3605	1/1	0.89	0.22	44,44,44,44	0
57	MG	CX	3003	1/1	0.89	0.10	53,53,53,53	0
57	MG	BA	3162	1/1	0.89	0.13	39,39,39,39	0
57	MG	BA	3317	1/1	0.89	0.16	49,49,49,49	0
57	MG	B7	102	1/1	0.89	0.12	53,53,53,53	0
57	MG	DA	3013	1/1	0.89	0.12	43,43,43,43	0
57	MG	BA	3166	1/1	0.89	0.23	45,45,45,45	0
57	MG	CA	3086	1/1	0.89	0.20	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3034	1/1	0.89	0.32	46,46,46,46	0
57	MG	DA	3036	1/1	0.89	0.11	48,48,48,48	0
57	MG	CA	3088	1/1	0.89	0.20	61,61,61,61	0
57	MG	CA	3089	1/1	0.89	0.22	65,65,65,65	0
57	MG	DA	3315	1/1	0.89	0.23	57,57,57,57	0
57	MG	DA	3045	1/1	0.89	0.15	39,39,39,39	0
57	MG	DA	3572	1/1	0.89	0.13	46,46,46,46	0
57	MG	DA	3575	1/1	0.89	0.11	19,19,19,19	0
57	MG	AA	3104	1/1	0.89	0.12	47,47,47,47	0
57	MG	BA	3177	1/1	0.89	0.11	39,39,39,39	0
57	MG	BA	3324	1/1	0.89	0.18	61,61,61,61	0
57	MG	AA	3186	1/1	0.89	0.11	43,43,43,43	0
57	MG	BA	3623	1/1	0.89	0.09	42,42,42,42	0
57	MG	DA	3593	1/1	0.89	0.21	49,49,49,49	0
57	MG	CA	3010	1/1	0.89	0.27	56,56,56,56	0
57	MG	BA	3179	1/1	0.89	0.24	49,49,49,49	0
57	MG	DA	3600	1/1	0.89	0.16	45,45,45,45	0
57	MG	BA	3507	1/1	0.89	0.13	48,48,48,48	0
57	MG	AA	3003	1/1	0.89	0.20	53,53,53,53	0
57	MG	BA	3198	1/1	0.89	0.23	45,45,45,45	0
57	MG	AA	3062	1/1	0.89	0.27	57,57,57,57	0
57	MG	DA	3093	1/1	0.89	0.12	45,45,45,45	0
57	MG	DA	3097	1/1	0.89	0.13	50,50,50,50	0
57	MG	DA	3372	1/1	0.89	0.10	49,49,49,49	0
57	MG	BA	3068	1/1	0.89	0.23	46,46,46,46	0
57	MG	BA	3635	1/1	0.89	0.11	59,59,59,59	0
57	MG	BA	3526	1/1	0.89	0.16	48,48,48,48	0
57	MG	BA	3074	1/1	0.89	0.15	43,43,43,43	0
57	MG	DA	3396	1/1	0.89	0.14	43,43,43,43	0
57	MG	AA	3086	1/1	0.89	0.08	45,45,45,45	0
57	MG	BA	3370	1/1	0.89	0.12	32,32,32,32	0
57	MG	AA	3131	1/1	0.89	0.15	56,56,56,56	0
57	MG	AA	3039	1/1	0.89	0.40	62,62,62,62	0
57	MG	DA	3139	1/1	0.89	0.22	49,49,49,49	0
57	MG	AA	3057	1/1	0.89	0.09	38,38,38,38	0
57	MG	BA	3660	1/1	0.89	0.15	62,62,62,62	0
57	MG	BA	3665	1/1	0.89	0.11	50,50,50,50	0
57	MG	CA	3033	1/1	0.89	0.21	67,67,67,67	0
57	MG	AA	3200	1/1	0.89	0.14	58,58,58,58	0
57	MG	CA	3122	1/1	0.89	0.12	50,50,50,50	0
57	MG	BA	3404	1/1	0.89	0.16	30,30,30,30	0
57	MG	CA	3036	1/1	0.89	0.18	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CA	3037	1/1	0.89	0.25	60,60,60,60	0
57	MG	DA	3448	1/1	0.90	0.16	36,36,36,36	0
57	MG	BA	3293	1/1	0.90	0.15	43,43,43,43	0
57	MG	BA	3302	1/1	0.90	0.12	50,50,50,50	0
57	MG	AA	3195	1/1	0.90	0.13	58,58,58,58	0
57	MG	BA	3558	1/1	0.90	0.19	63,63,63,63	0
57	MG	DA	3246	1/1	0.90	0.32	57,57,57,57	0
57	MG	BA	3559	1/1	0.90	0.12	36,36,36,36	0
57	MG	DA	3460	1/1	0.90	0.10	57,57,57,57	0
57	MG	BA	3196	1/1	0.90	0.28	51,51,51,51	0
57	MG	DA	3468	1/1	0.90	0.26	64,64,64,64	0
57	MG	DA	3469	1/1	0.90	0.19	41,41,41,41	0
57	MG	BA	3306	1/1	0.90	0.11	32,32,32,32	0
57	MG	DA	3479	1/1	0.90	0.20	45,45,45,45	0
57	MG	DA	3039	1/1	0.90	0.20	48,48,48,48	0
57	MG	BA	3428	1/1	0.90	0.19	54,54,54,54	0
57	MG	BA	3569	1/1	0.90	0.18	46,46,46,46	0
57	MG	DA	3262	1/1	0.90	0.11	39,39,39,39	0
57	MG	DA	3266	1/1	0.90	0.10	45,45,45,45	0
57	MG	DA	3497	1/1	0.90	0.15	61,61,61,61	0
57	MG	DA	3269	1/1	0.90	0.13	40,40,40,40	0
57	MG	BA	3197	1/1	0.90	0.12	32,32,32,32	0
57	MG	BA	3108	1/1	0.90	0.13	36,36,36,36	0
57	MG	DA	3056	1/1	0.90	0.07	35,35,35,35	0
57	MG	BA	3437	1/1	0.90	0.20	52,52,52,52	0
57	MG	AA	3115	1/1	0.90	0.25	38,38,38,38	0
57	MG	BA	3443	1/1	0.90	0.16	38,38,38,38	0
57	MG	BA	3445	1/1	0.90	0.15	35,35,35,35	0
57	MG	DA	3286	1/1	0.90	0.19	45,45,45,45	0
57	MG	DA	3287	1/1	0.90	0.12	58,58,58,58	0
57	MG	DA	3288	1/1	0.90	0.14	32,32,32,32	0
57	MG	DA	3289	1/1	0.90	0.28	50,50,50,50	0
57	MG	BA	3446	1/1	0.90	0.11	49,49,49,49	0
57	MG	BA	3689	1/1	0.90	0.10	46,46,46,46	0
57	MG	AA	3017	1/1	0.90	0.07	63,63,63,63	0
57	MG	DA	3081	1/1	0.90	0.15	45,45,45,45	0
57	MG	DA	3082	1/1	0.90	0.15	47,47,47,47	0
57	MG	BA	3112	1/1	0.90	0.32	58,58,58,58	0
57	MG	BA	3696	1/1	0.90	0.11	41,41,41,41	0
57	MG	AA	3007	1/1	0.90	0.13	47,47,47,47	0
57	MG	AA	3140	1/1	0.90	0.18	56,56,56,56	0
57	MG	BA	3333	1/1	0.90	0.09	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3110	1/1	0.90	0.09	60,60,60,60	0
57	MG	AA	3158	1/1	0.90	0.10	72,72,72,72	0
57	MG	BB	3018	1/1	0.90	0.07	43,43,43,43	0
57	MG	AA	3203	1/1	0.90	0.11	42,42,42,42	0
57	MG	DA	3118	1/1	0.90	0.08	46,46,46,46	0
57	MG	DA	3343	1/1	0.90	0.13	37,37,37,37	0
57	MG	DA	3122	1/1	0.90	0.14	58,58,58,58	0
57	MG	DA	3568	1/1	0.90	0.10	45,45,45,45	0
57	MG	AA	3141	1/1	0.90	0.09	54,54,54,54	0
57	MG	AA	3111	1/1	0.90	0.15	70,70,70,70	0
57	MG	CA	3132	1/1	0.90	0.12	51,51,51,51	0
57	MG	BE	3002	1/1	0.90	0.21	50,50,50,50	0
57	MG	DA	3136	1/1	0.90	0.30	62,62,62,62	0
57	MG	DA	3579	1/1	0.90	0.15	58,58,58,58	0
57	MG	DA	3581	1/1	0.90	0.12	53,53,53,53	0
57	MG	BA	3082	1/1	0.90	0.10	57,57,57,57	0
57	MG	DA	3369	1/1	0.90	0.14	36,36,36,36	0
57	MG	DA	3141	1/1	0.90	0.18	37,37,37,37	0
57	MG	BA	3229	1/1	0.90	0.37	52,52,52,52	0
57	MG	BA	3494	1/1	0.90	0.12	30,30,30,30	0
57	MG	DA	3376	1/1	0.90	0.18	40,40,40,40	0
57	MG	DA	3146	1/1	0.90	0.09	44,44,44,44	0
57	MG	BA	3499	1/1	0.90	0.31	51,51,51,51	0
57	MG	BA	3164	1/1	0.90	0.15	44,44,44,44	0
57	MG	DA	3394	1/1	0.90	0.11	48,48,48,48	0
57	MG	BU	201	1/1	0.90	0.09	36,36,36,36	0
57	MG	BU	202	1/1	0.90	0.10	45,45,45,45	0
57	MG	BA	3360	1/1	0.90	0.16	60,60,60,60	0
57	MG	BW	203	1/1	0.90	0.13	39,39,39,39	0
57	MG	AA	3021	1/1	0.90	0.24	58,58,58,58	0
57	MG	CA	3150	1/1	0.90	0.20	66,66,66,66	0
57	MG	DA	3184	1/1	0.90	0.09	44,44,44,44	0
57	MG	AA	3190	1/1	0.90	0.12	75,75,75,75	0
57	MG	BA	3247	1/1	0.90	0.13	37,37,37,37	0
57	MG	BA	3629	1/1	0.90	0.18	37,37,37,37	0
57	MG	BA	3520	1/1	0.90	0.17	46,46,46,46	0
57	MG	BA	3257	1/1	0.90	0.14	40,40,40,40	0
57	MG	BA	3029	1/1	0.90	0.24	53,53,53,53	0
57	MG	BA	3100	1/1	0.90	0.14	40,40,40,40	0
57	MG	DA	3207	1/1	0.90	0.20	39,39,39,39	0
57	MG	DB	3009	1/1	0.90	0.27	55,55,55,55	0
57	MG	CA	3087	1/1	0.90	0.21	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CT	3001	1/1	0.90	0.14	59,59,59,59	0
57	MG	DE	303	1/1	0.90	0.20	49,49,49,49	0
57	MG	AA	3089	1/1	0.90	0.24	61,61,61,61	0
57	MG	BA	3180	1/1	0.90	0.11	32,32,32,32	0
57	MG	DA	3442	1/1	0.90	0.17	34,34,34,34	0
57	MG	DU	3001	1/1	0.90	0.32	56,56,56,56	0
57	MG	BA	3271	1/1	0.90	0.26	45,45,45,45	0
57	MG	BA	3537	1/1	0.90	0.08	35,35,35,35	0
57	MG	BA	3183	1/1	0.90	0.15	50,50,50,50	0
57	MG	DA	3224	1/1	0.90	0.29	60,60,60,60	0
57	MG	DA	3475	1/1	0.91	0.13	35,35,35,35	0
57	MG	DA	3105	1/1	0.91	0.13	37,37,37,37	0
57	MG	DA	3106	1/1	0.91	0.14	52,52,52,52	0
57	MG	BP	3001	1/1	0.91	0.26	49,49,49,49	0
57	MG	BA	3574	1/1	0.91	0.10	41,41,41,41	0
57	MG	BA	3575	1/1	0.91	0.12	30,30,30,30	0
57	MG	DA	3301	1/1	0.91	0.21	54,54,54,54	0
57	MG	BA	3369	1/1	0.91	0.15	57,57,57,57	0
57	MG	AA	3058	1/1	0.91	0.16	48,48,48,48	0
57	MG	DA	3120	1/1	0.91	0.17	55,55,55,55	0
57	MG	DA	3502	1/1	0.91	0.11	51,51,51,51	0
57	MG	AA	3053	1/1	0.91	0.12	54,54,54,54	0
57	MG	DA	3504	1/1	0.91	0.09	46,46,46,46	0
57	MG	DA	3310	1/1	0.91	0.10	43,43,43,43	0
57	MG	BA	3284	1/1	0.91	0.10	41,41,41,41	0
57	MG	DA	3313	1/1	0.91	0.11	51,51,51,51	0
57	MG	B0	102	1/1	0.91	0.11	53,53,53,53	0
57	MG	DA	3132	1/1	0.91	0.12	53,53,53,53	0
57	MG	B1	101	1/1	0.91	0.22	37,37,37,37	0
57	MG	BA	3378	1/1	0.91	0.17	45,45,45,45	0
57	MG	CA	3145	1/1	0.91	0.10	49,49,49,49	0
57	MG	CA	3069	1/1	0.91	0.33	56,56,56,56	0
57	MG	DA	3335	1/1	0.91	0.09	48,48,48,48	0
57	MG	B7	103	1/1	0.91	0.13	51,51,51,51	0
57	MG	DA	3528	1/1	0.91	0.11	60,60,60,60	0
57	MG	CA	3073	1/1	0.91	0.13	57,57,57,57	0
57	MG	CA	3074	1/1	0.91	0.26	51,51,51,51	0
57	MG	CA	3001	1/1	0.91	0.10	53,53,53,53	0
57	MG	AA	3016	1/1	0.91	0.12	52,52,52,52	0
57	MG	DA	3542	1/1	0.91	0.11	44,44,44,44	0
57	MG	BA	3297	1/1	0.91	0.11	36,36,36,36	0
57	MG	BA	3669	1/1	0.91	0.11	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3301	1/1	0.91	0.19	43,43,43,43	0
57	MG	DA	3358	1/1	0.91	0.26	45,45,45,45	0
57	MG	BA	3072	1/1	0.91	0.10	32,32,32,32	0
57	MG	AA	3191	1/1	0.91	0.19	56,56,56,56	0
57	MG	DA	3551	1/1	0.91	0.13	57,57,57,57	0
57	MG	BA	3020	1/1	0.91	0.25	55,55,55,55	0
57	MG	BA	3677	1/1	0.91	0.14	30,30,30,30	0
57	MG	BA	3144	1/1	0.91	0.15	42,42,42,42	0
57	MG	BA	3148	1/1	0.91	0.22	44,44,44,44	0
57	MG	DA	3564	1/1	0.91	0.11	48,48,48,48	0
57	MG	BA	3084	1/1	0.91	0.13	37,37,37,37	0
57	MG	DA	3566	1/1	0.91	0.09	40,40,40,40	0
57	MG	AA	3084	1/1	0.91	0.10	43,43,43,43	0
57	MG	AA	3172	1/1	0.91	0.25	54,54,54,54	0
57	MG	BA	3684	1/1	0.91	0.10	47,47,47,47	0
57	MG	DA	3007	1/1	0.91	0.10	48,48,48,48	0
57	MG	DA	3010	1/1	0.91	0.13	51,51,51,51	0
57	MG	DA	3011	1/1	0.91	0.10	36,36,36,36	0
57	MG	AA	3154	1/1	0.91	0.13	46,46,46,46	0
57	MG	BA	3233	1/1	0.91	0.20	55,55,55,55	0
57	MG	BA	3094	1/1	0.91	0.08	46,46,46,46	0
57	MG	BA	3099	1/1	0.91	0.14	36,36,36,36	0
57	MG	DA	3587	1/1	0.91	0.10	35,35,35,35	0
57	MG	DA	3589	1/1	0.91	0.11	52,52,52,52	0
57	MG	AA	3197	1/1	0.91	0.09	50,50,50,50	0
57	MG	BA	3618	1/1	0.91	0.13	64,64,64,64	0
57	MG	BA	3707	1/1	0.91	0.28	34,34,34,34	0
57	MG	BA	3717	1/1	0.91	0.36	40,40,40,40	0
57	MG	CA	3031	1/1	0.91	0.13	55,55,55,55	0
57	MG	BA	3619	1/1	0.91	0.19	54,54,54,54	0
57	MG	DA	3227	1/1	0.91	0.14	57,57,57,57	0
57	MG	BB	3005	1/1	0.91	0.16	42,42,42,42	0
57	MG	DA	3234	1/1	0.91	0.16	34,34,34,34	0
57	MG	DA	3239	1/1	0.91	0.25	51,51,51,51	0
57	MG	DA	3432	1/1	0.91	0.08	33,33,33,33	0
57	MG	BA	3338	1/1	0.91	0.08	50,50,50,50	0
57	MG	BA	3244	1/1	0.91	0.26	29,29,29,29	0
57	MG	DA	3062	1/1	0.91	0.11	49,49,49,49	0
57	MG	DA	3611	1/1	0.91	0.18	58,58,58,58	0
57	MG	DA	3612	1/1	0.91	0.16	64,64,64,64	0
57	MG	DA	3441	1/1	0.91	0.21	43,43,43,43	0
57	MG	BA	3104	1/1	0.91	0.14	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3033	1/1	0.91	0.10	39,39,39,39	0
57	MG	DA	3255	1/1	0.91	0.22	34,34,34,34	0
57	MG	DA	3445	1/1	0.91	0.12	59,59,59,59	0
57	MG	DA	3068	1/1	0.91	0.12	48,48,48,48	0
57	MG	AA	3036	1/1	0.91	0.11	51,51,51,51	0
57	MG	BD	302	1/1	0.91	0.14	38,38,38,38	0
57	MG	BD	308	1/1	0.91	0.19	41,41,41,41	0
57	MG	AA	3051	1/1	0.91	0.27	51,51,51,51	0
57	MG	BE	3001	1/1	0.91	0.23	48,48,48,48	0
57	MG	CA	3045	1/1	0.91	0.15	53,53,53,53	0
57	MG	DE	301	1/1	0.91	0.16	52,52,52,52	0
57	MG	AA	3073	1/1	0.91	0.30	59,59,59,59	0
57	MG	AA	3105	1/1	0.91	0.12	59,59,59,59	0
57	MG	DA	3091	1/1	0.91	0.12	37,37,37,37	0
57	MG	DP	201	1/1	0.91	0.15	61,61,61,61	0
57	MG	DQ	3001	1/1	0.91	0.14	58,58,58,58	0
57	MG	BA	3466	1/1	0.91	0.16	57,57,57,57	0
57	MG	DR	3002	1/1	0.91	0.13	51,51,51,51	0
57	MG	DA	3462	1/1	0.91	0.25	35,35,35,35	0
57	MG	BA	3366	1/1	0.91	0.11	38,38,38,38	0
57	MG	BA	3571	1/1	0.91	0.11	24,24,24,24	0
57	MG	DA	3104	1/1	0.91	0.16	47,47,47,47	0
57	MG	DA	3473	1/1	0.91	0.11	32,32,32,32	0
57	MG	CA	3143	1/1	0.92	0.11	59,59,59,59	0
57	MG	AA	3079	1/1	0.92	0.15	62,62,62,62	0
57	MG	AV	3001	1/1	0.92	0.25	59,59,59,59	0
57	MG	BA	3570	1/1	0.92	0.09	48,48,48,48	0
57	MG	BA	3318	1/1	0.92	0.13	39,39,39,39	0
57	MG	DA	3190	1/1	0.92	0.22	52,52,52,52	0
57	MG	BA	3127	1/1	0.92	0.19	41,41,41,41	0
57	MG	BA	3685	1/1	0.92	0.18	40,40,40,40	0
57	MG	DA	3201	1/1	0.92	0.14	42,42,42,42	0
57	MG	BA	3132	1/1	0.92	0.15	52,52,52,52	0
57	MG	BA	3576	1/1	0.92	0.13	29,29,29,29	0
57	MG	DA	3450	1/1	0.92	0.12	34,34,34,34	0
57	MG	AA	3152	1/1	0.92	0.12	64,64,64,64	0
57	MG	AA	3139	1/1	0.92	0.11	51,51,51,51	0
57	MG	CA	3157	1/1	0.92	0.22	61,61,61,61	0
57	MG	DA	3212	1/1	0.92	0.07	47,47,47,47	0
57	MG	BA	3583	1/1	0.92	0.09	54,54,54,54	0
57	MG	BA	3073	1/1	0.92	0.16	39,39,39,39	0
57	MG	CF	3001	1/1	0.92	0.13	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	3174	1/1	0.92	0.13	64,64,64,64	0
57	MG	BA	3712	1/1	0.92	0.08	30,30,30,30	0
57	MG	BA	3334	1/1	0.92	0.11	37,37,37,37	0
57	MG	BA	3335	1/1	0.92	0.08	26,26,26,26	0
57	MG	BB	3002	1/1	0.92	0.17	44,44,44,44	0
57	MG	BA	3462	1/1	0.92	0.18	51,51,51,51	0
57	MG	DA	3476	1/1	0.92	0.12	49,49,49,49	0
57	MG	AA	3119	1/1	0.92	0.22	50,50,50,50	0
57	MG	BA	3230	1/1	0.92	0.21	45,45,45,45	0
57	MG	DA	3485	1/1	0.92	0.07	41,41,41,41	0
57	MG	DA	3488	1/1	0.92	0.12	47,47,47,47	0
57	MG	DA	3242	1/1	0.92	0.12	48,48,48,48	0
57	MG	DA	3492	1/1	0.92	0.08	45,45,45,45	0
57	MG	BB	3015	1/1	0.92	0.10	42,42,42,42	0
57	MG	DA	3494	1/1	0.92	0.17	56,56,56,56	0
57	MG	BA	3340	1/1	0.92	0.12	59,59,59,59	0
57	MG	BA	3468	1/1	0.92	0.08	42,42,42,42	0
57	MG	DA	3250	1/1	0.92	0.16	41,41,41,41	0
57	MG	BA	3601	1/1	0.92	0.17	69,69,69,69	0
57	MG	BA	3153	1/1	0.92	0.10	53,53,53,53	0
57	MG	AA	3035	1/1	0.92	0.30	52,52,52,52	0
57	MG	AA	3179	1/1	0.92	0.11	56,56,56,56	0
57	MG	DA	3028	1/1	0.92	0.20	52,52,52,52	0
57	MG	AA	3101	1/1	0.92	0.24	53,53,53,53	0
57	MG	DA	3035	1/1	0.92	0.12	45,45,45,45	0
57	MG	DA	3510	1/1	0.92	0.19	52,52,52,52	0
57	MG	DA	3263	1/1	0.92	0.17	47,47,47,47	0
57	MG	DA	3265	1/1	0.92	0.08	33,33,33,33	0
57	MG	AA	3202	1/1	0.92	0.19	60,60,60,60	0
57	MG	DA	3268	1/1	0.92	0.09	35,35,35,35	0
57	MG	CA	3076	1/1	0.92	0.27	59,59,59,59	0
57	MG	BA	3353	1/1	0.92	0.07	46,46,46,46	0
57	MG	DA	3042	1/1	0.92	0.23	37,37,37,37	0
57	MG	DA	3274	1/1	0.92	0.14	45,45,45,45	0
57	MG	BF	306	1/1	0.92	0.08	43,43,43,43	0
57	MG	BF	308	1/1	0.92	0.14	46,46,46,46	0
57	MG	DA	3046	1/1	0.92	0.22	50,50,50,50	0
57	MG	DA	3048	1/1	0.92	0.16	53,53,53,53	0
57	MG	DA	3534	1/1	0.92	0.08	30,30,30,30	0
57	MG	BA	3172	1/1	0.92	0.09	27,27,27,27	0
57	MG	DA	3538	1/1	0.92	0.12	77,77,77,77	0
57	MG	BG	3001	1/1	0.92	0.23	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3612	1/1	0.92	0.17	58,58,58,58	0
57	MG	BA	3497	1/1	0.92	0.15	41,41,41,41	0
57	MG	AA	3183	1/1	0.92	0.12	43,43,43,43	0
57	MG	BA	3097	1/1	0.92	0.13	44,44,44,44	0
57	MG	DA	3296	1/1	0.92	0.13	46,46,46,46	0
57	MG	AA	3204	1/1	0.92	0.21	64,64,64,64	0
57	MG	DA	3300	1/1	0.92	0.11	38,38,38,38	0
57	MG	BA	3509	1/1	0.92	0.23	34,34,34,34	0
57	MG	BA	3511	1/1	0.92	0.13	41,41,41,41	0
57	MG	BA	3622	1/1	0.92	0.07	24,24,24,24	0
57	MG	CA	3093	1/1	0.92	0.18	69,69,69,69	0
57	MG	AA	3143	1/1	0.92	0.09	32,32,32,32	0
57	MG	DA	3078	1/1	0.92	0.15	49,49,49,49	0
57	MG	DA	3080	1/1	0.92	0.19	64,64,64,64	0
57	MG	BA	3102	1/1	0.92	0.19	43,43,43,43	0
57	MG	CA	3097	1/1	0.92	0.11	43,43,43,43	0
57	MG	B0	103	1/1	0.92	0.10	38,38,38,38	0
57	MG	B0	104	1/1	0.92	0.12	49,49,49,49	0
57	MG	BA	3516	1/1	0.92	0.12	32,32,32,32	0
57	MG	DA	3574	1/1	0.92	0.08	59,59,59,59	0
57	MG	DA	3327	1/1	0.92	0.08	49,49,49,49	0
57	MG	AA	3162	1/1	0.92	0.10	40,40,40,40	0
57	MG	DA	3578	1/1	0.92	0.14	63,63,63,63	0
57	MG	BA	3375	1/1	0.92	0.15	46,46,46,46	0
57	MG	DA	3332	1/1	0.92	0.14	52,52,52,52	0
57	MG	BA	3521	1/1	0.92	0.19	32,32,32,32	0
57	MG	CA	3002	1/1	0.92	0.10	66,66,66,66	0
57	MG	BA	3632	1/1	0.92	0.10	43,43,43,43	0
57	MG	BA	3523	1/1	0.92	0.09	31,31,31,31	0
57	MG	BA	3185	1/1	0.92	0.41	34,34,34,34	0
57	MG	AA	3207	1/1	0.92	0.18	57,57,57,57	0
57	MG	BA	3381	1/1	0.92	0.11	30,30,30,30	0
57	MG	BA	3638	1/1	0.92	0.08	41,41,41,41	0
57	MG	BA	3287	1/1	0.92	0.23	42,42,42,42	0
57	MG	AA	3013	1/1	0.92	0.17	53,53,53,53	0
57	MG	BA	3648	1/1	0.92	0.12	50,50,50,50	0
57	MG	BA	3534	1/1	0.92	0.20	23,23,23,23	0
57	MG	DA	3604	1/1	0.92	0.21	61,61,61,61	0
57	MG	DA	3367	1/1	0.92	0.09	24,24,24,24	0
57	MG	CA	3016	1/1	0.92	0.13	52,52,52,52	0
57	MG	BA	3408	1/1	0.92	0.13	42,42,42,42	0
57	MG	AA	3027	1/1	0.92	0.11	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3298	1/1	0.92	0.19	50,50,50,50	0
57	MG	BA	3659	1/1	0.92	0.13	47,47,47,47	0
57	MG	DA	3138	1/1	0.92	0.12	39,39,39,39	0
57	MG	AA	3034	1/1	0.92	0.21	47,47,47,47	0
57	MG	DA	3613	1/1	0.92	0.17	45,45,45,45	0
57	MG	DA	3614	1/1	0.92	0.39	56,56,56,56	0
57	MG	DA	3383	1/1	0.92	0.07	45,45,45,45	0
57	MG	DA	3617	1/1	0.92	0.12	40,40,40,40	0
57	MG	BA	3664	1/1	0.92	0.13	66,66,66,66	0
57	MG	DA	3621	1/1	0.92	0.15	61,61,61,61	0
57	MG	BA	3544	1/1	0.92	0.11	52,52,52,52	0
57	MG	BA	3545	1/1	0.92	0.12	34,34,34,34	0
57	MG	DA	3626	1/1	0.92	0.14	38,38,38,38	0
57	MG	DA	3627	1/1	0.92	0.12	56,56,56,56	0
57	MG	BA	3547	1/1	0.92	0.09	33,33,33,33	0
57	MG	DA	3404	1/1	0.92	0.11	48,48,48,48	0
57	MG	AJ	201	1/1	0.92	0.36	67,67,67,67	0
57	MG	DA	3407	1/1	0.92	0.12	67,67,67,67	0
57	MG	DB	3006	1/1	0.92	0.12	44,44,44,44	0
57	MG	DA	3149	1/1	0.92	0.13	42,42,42,42	0
57	MG	DA	3152	1/1	0.92	0.16	38,38,38,38	0
57	MG	DD	305	1/1	0.92	0.15	48,48,48,48	0
57	MG	BA	3200	1/1	0.92	0.22	39,39,39,39	0
57	MG	DA	3159	1/1	0.92	0.16	32,32,32,32	0
57	MG	BA	3203	1/1	0.92	0.25	56,56,56,56	0
57	MG	AA	3192	1/1	0.92	0.15	72,72,72,72	0
57	MG	DF	3003	1/1	0.92	0.13	36,36,36,36	0
57	MG	DF	3004	1/1	0.92	0.15	56,56,56,56	0
57	MG	DA	3164	1/1	0.92	0.14	44,44,44,44	0
57	MG	CA	3137	1/1	0.92	0.11	81,81,81,81	0
57	MG	DA	3420	1/1	0.92	0.10	41,41,41,41	0
57	MG	BA	3675	1/1	0.92	0.12	41,41,41,41	0
57	MG	BA	3310	1/1	0.92	0.24	43,43,43,43	0
57	MG	DA	3171	1/1	0.92	0.17	38,38,38,38	0
57	MG	DA	3177	1/1	0.92	0.26	29,29,29,29	0
57	MG	DU	3002	1/1	0.92	0.14	67,67,67,67	0
57	MG	DA	3178	1/1	0.92	0.17	39,39,39,39	0
57	MG	DA	3181	1/1	0.92	0.17	36,36,36,36	0
57	MG	DA	3434	1/1	0.92	0.08	48,48,48,48	0
57	MG	BA	3313	1/1	0.92	0.12	30,30,30,30	0
57	MG	BA	3464	1/1	0.93	0.10	26,26,26,26	0
57	MG	BB	3012	1/1	0.93	0.11	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3019	1/1	0.93	0.18	54,54,54,54	0
57	MG	DA	3021	1/1	0.93	0.11	50,50,50,50	0
57	MG	DA	3230	1/1	0.93	0.25	46,46,46,46	0
57	MG	DA	3232	1/1	0.93	0.08	48,48,48,48	0
57	MG	BA	3062	1/1	0.93	0.20	52,52,52,52	0
57	MG	DA	3235	1/1	0.93	0.29	48,48,48,48	0
57	MG	DA	3236	1/1	0.93	0.07	45,45,45,45	0
57	MG	DA	3238	1/1	0.93	0.32	31,31,31,31	0
57	MG	CA	3070	1/1	0.93	0.23	42,42,42,42	0
57	MG	DA	3241	1/1	0.93	0.13	40,40,40,40	0
57	MG	AA	3144	1/1	0.93	0.20	44,44,44,44	0
57	MG	BA	3336	1/1	0.93	0.12	47,47,47,47	0
57	MG	AA	3038	1/1	0.93	0.24	58,58,58,58	0
57	MG	DA	3477	1/1	0.93	0.08	37,37,37,37	0
57	MG	DA	3478	1/1	0.93	0.16	57,57,57,57	0
57	MG	DA	3037	1/1	0.93	0.10	41,41,41,41	0
57	MG	BA	3225	1/1	0.93	0.07	45,45,45,45	0
57	MG	DA	3484	1/1	0.93	0.07	41,41,41,41	0
57	MG	BA	3339	1/1	0.93	0.23	52,52,52,52	0
57	MG	DA	3487	1/1	0.93	0.13	44,44,44,44	0
57	MG	CA	3077	1/1	0.93	0.21	63,63,63,63	0
57	MG	BA	3606	1/1	0.93	0.15	39,39,39,39	0
57	MG	CA	3079	1/1	0.93	0.13	42,42,42,42	0
57	MG	AA	3020	1/1	0.93	0.16	62,62,62,62	0
57	MG	DA	3047	1/1	0.93	0.19	44,44,44,44	0
57	MG	BA	3069	1/1	0.93	0.26	48,48,48,48	0
57	MG	BF	302	1/1	0.93	0.10	59,59,59,59	0
57	MG	BA	3486	1/1	0.93	0.08	32,32,32,32	0
57	MG	DA	3054	1/1	0.93	0.10	40,40,40,40	0
57	MG	BA	3143	1/1	0.93	0.18	41,41,41,41	0
57	MG	BA	3070	1/1	0.93	0.10	44,44,44,44	0
57	MG	DA	3270	1/1	0.93	0.24	57,57,57,57	0
57	MG	AA	3129	1/1	0.93	0.13	37,37,37,37	0
57	MG	BA	3151	1/1	0.93	0.12	42,42,42,42	0
57	MG	DA	3508	1/1	0.93	0.11	58,58,58,58	0
57	MG	BA	3152	1/1	0.93	0.13	45,45,45,45	0
57	MG	BA	3357	1/1	0.93	0.10	31,31,31,31	0
57	MG	BO	5001	1/1	0.93	0.09	49,49,49,49	0
57	MG	BA	3620	1/1	0.93	0.09	35,35,35,35	0
57	MG	AA	3067	1/1	0.93	0.09	47,47,47,47	0
57	MG	AA	3048	1/1	0.93	0.13	42,42,42,42	0
57	MG	DA	3077	1/1	0.93	0.35	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3075	1/1	0.93	0.36	45,45,45,45	0
57	MG	DA	3079	1/1	0.93	0.11	41,41,41,41	0
57	MG	DA	3524	1/1	0.93	0.11	40,40,40,40	0
57	MG	BA	3079	1/1	0.93	0.27	55,55,55,55	0
57	MG	DA	3290	1/1	0.93	0.13	43,43,43,43	0
57	MG	BA	3626	1/1	0.93	0.16	48,48,48,48	0
57	MG	BA	3627	1/1	0.93	0.07	28,28,28,28	0
57	MG	AA	3176	1/1	0.93	0.07	43,43,43,43	0
57	MG	BA	3171	1/1	0.93	0.17	44,44,44,44	0
57	MG	AA	3177	1/1	0.93	0.23	66,66,66,66	0
57	MG	BA	3277	1/1	0.93	0.20	34,34,34,34	0
57	MG	DA	3095	1/1	0.93	0.12	45,45,45,45	0
57	MG	BA	3279	1/1	0.93	0.24	48,48,48,48	0
57	MG	BA	3005	1/1	0.93	0.11	44,44,44,44	0
57	MG	AA	3153	1/1	0.93	0.09	46,46,46,46	0
57	MG	AA	3118	1/1	0.93	0.19	50,50,50,50	0
57	MG	DA	3546	1/1	0.93	0.09	41,41,41,41	0
57	MG	BA	3386	1/1	0.93	0.17	30,30,30,30	0
57	MG	DA	3107	1/1	0.93	0.14	39,39,39,39	0
57	MG	DA	3109	1/1	0.93	0.10	45,45,45,45	0
57	MG	DA	3317	1/1	0.93	0.17	42,42,42,42	0
57	MG	DA	3318	1/1	0.93	0.09	39,39,39,39	0
57	MG	BA	3531	1/1	0.93	0.17	20,20,20,20	0
57	MG	DA	3320	1/1	0.93	0.06	19,19,19,19	0
57	MG	DA	3558	1/1	0.93	0.07	45,45,45,45	0
57	MG	DA	3559	1/1	0.93	0.13	31,31,31,31	0
57	MG	DA	3321	1/1	0.93	0.11	40,40,40,40	0
57	MG	BA	3387	1/1	0.93	0.09	29,29,29,29	0
57	MG	DA	3324	1/1	0.93	0.12	42,42,42,42	0
57	MG	DA	3326	1/1	0.93	0.08	40,40,40,40	0
57	MG	DA	3567	1/1	0.93	0.08	49,49,49,49	0
57	MG	BA	3642	1/1	0.93	0.12	50,50,50,50	0
57	MG	DA	3114	1/1	0.93	0.08	51,51,51,51	0
57	MG	DA	3329	1/1	0.93	0.24	54,54,54,54	0
57	MG	DA	3330	1/1	0.93	0.16	49,49,49,49	0
57	MG	BA	3388	1/1	0.93	0.09	31,31,31,31	0
57	MG	BA	3397	1/1	0.93	0.09	33,33,33,33	0
57	MG	DA	3119	1/1	0.93	0.13	52,52,52,52	0
57	MG	CA	3118	1/1	0.93	0.08	69,69,69,69	0
57	MG	BA	3398	1/1	0.93	0.20	36,36,36,36	0
57	MG	CA	3011	1/1	0.93	0.27	39,39,39,39	0
57	MG	DA	3128	1/1	0.93	0.23	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3019	1/1	0.93	0.08	30,30,30,30	0
57	MG	CA	3013	1/1	0.93	0.22	45,45,45,45	0
57	MG	BA	3406	1/1	0.93	0.12	24,24,24,24	0
57	MG	DA	3590	1/1	0.93	0.12	58,58,58,58	0
57	MG	BA	3407	1/1	0.93	0.13	29,29,29,29	0
57	MG	AA	3005	1/1	0.93	0.10	66,66,66,66	0
57	MG	CA	3128	1/1	0.93	0.14	43,43,43,43	0
57	MG	DA	3594	1/1	0.93	0.17	51,51,51,51	0
57	MG	DA	3365	1/1	0.93	0.15	54,54,54,54	0
57	MG	BA	3098	1/1	0.93	0.38	50,50,50,50	0
57	MG	BA	3299	1/1	0.93	0.12	27,27,27,27	0
57	MG	BA	3300	1/1	0.93	0.10	55,55,55,55	0
57	MG	BA	3021	1/1	0.93	0.11	35,35,35,35	0
57	MG	DA	3603	1/1	0.93	0.12	40,40,40,40	0
57	MG	BA	3555	1/1	0.93	0.12	62,62,62,62	0
57	MG	AA	3024	1/1	0.93	0.20	49,49,49,49	0
57	MG	DA	3375	1/1	0.93	0.12	30,30,30,30	0
57	MG	BA	3417	1/1	0.93	0.12	49,49,49,49	0
57	MG	BA	3027	1/1	0.93	0.51	36,36,36,36	0
57	MG	DA	3157	1/1	0.93	0.19	44,44,44,44	0
57	MG	BA	3103	1/1	0.93	0.38	62,62,62,62	0
57	MG	DA	3385	1/1	0.93	0.07	47,47,47,47	0
57	MG	BA	3566	1/1	0.93	0.14	31,31,31,31	0
57	MG	DA	3391	1/1	0.93	0.10	39,39,39,39	0
57	MG	AA	3184	1/1	0.93	0.18	56,56,56,56	0
57	MG	BA	3307	1/1	0.93	0.20	31,31,31,31	0
57	MG	AA	3107	1/1	0.93	0.18	50,50,50,50	0
57	MG	DA	3618	1/1	0.93	0.09	46,46,46,46	0
57	MG	AD	301	1/1	0.93	0.11	47,47,47,47	0
57	MG	BA	3681	1/1	0.93	0.17	42,42,42,42	0
57	MG	DA	3622	1/1	0.93	0.43	58,58,58,58	0
57	MG	BA	3573	1/1	0.93	0.12	29,29,29,29	0
57	MG	BA	3430	1/1	0.93	0.10	54,54,54,54	0
57	MG	DA	3173	1/1	0.93	0.18	42,42,42,42	0
57	MG	BA	3433	1/1	0.93	0.08	32,32,32,32	0
57	MG	BA	3201	1/1	0.93	0.10	44,44,44,44	0
57	MG	AA	3019	1/1	0.93	0.25	52,52,52,52	0
57	MG	BA	3035	1/1	0.93	0.08	28,28,28,28	0
57	MG	BA	3581	1/1	0.93	0.09	55,55,55,55	0
57	MG	AA	3029	1/1	0.93	0.08	42,42,42,42	0
57	MG	AA	3110	1/1	0.93	0.29	52,52,52,52	0
57	MG	BA	3698	1/1	0.93	0.18	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CA	3159	1/1	0.93	0.13	46,46,46,46	0
57	MG	CA	3046	1/1	0.93	0.17	53,53,53,53	0
57	MG	BA	3214	1/1	0.93	0.20	48,48,48,48	0
57	MG	BA	3702	1/1	0.93	0.07	41,41,41,41	0
57	MG	DE	302	1/1	0.93	0.27	51,51,51,51	0
57	MG	DA	3195	1/1	0.93	0.16	42,42,42,42	0
57	MG	DF	3001	1/1	0.93	0.07	36,36,36,36	0
57	MG	DA	3196	1/1	0.93	0.12	46,46,46,46	0
57	MG	BA	3448	1/1	0.93	0.07	42,42,42,42	0
57	MG	DA	3436	1/1	0.93	0.08	61,61,61,61	0
57	MG	BA	3709	1/1	0.93	0.23	45,45,45,45	0
57	MG	BA	3589	1/1	0.93	0.10	35,35,35,35	0
57	MG	DP	202	1/1	0.93	0.12	48,48,48,48	0
57	MG	BA	3713	1/1	0.93	0.19	63,63,63,63	0
57	MG	BA	3715	1/1	0.93	0.10	33,33,33,33	0
57	MG	AA	3164	1/1	0.93	0.17	54,54,54,54	0
57	MG	BA	3325	1/1	0.93	0.07	38,38,38,38	0
57	MG	BA	3596	1/1	0.93	0.06	56,56,56,56	0
57	MG	DA	3006	1/1	0.93	0.17	40,40,40,40	0
57	MG	BB	3004	1/1	0.93	0.06	43,43,43,43	0
57	MG	DY	502	1/1	0.93	0.15	56,56,56,56	0
57	MG	AA	3055	1/1	0.93	0.28	53,53,53,53	0
59	ZN	B9	501	1/1	0.93	0.09	59,59,59,59	0
57	MG	BA	3126	1/1	0.93	0.17	34,34,34,34	0
57	MG	BU	208	1/1	0.94	0.30	39,39,39,39	0
57	MG	BA	3217	1/1	0.94	0.41	57,57,57,57	0
57	MG	BA	3018	1/1	0.94	0.17	58,58,58,58	0
57	MG	BW	205	1/1	0.94	0.09	30,30,30,30	0
57	MG	AA	3187	1/1	0.94	0.15	47,47,47,47	0
57	MG	BA	3312	1/1	0.94	0.15	44,44,44,44	0
57	MG	DA	3483	1/1	0.94	0.23	41,41,41,41	0
57	MG	AA	3023	1/1	0.94	0.07	60,60,60,60	0
57	MG	DA	3084	1/1	0.94	0.17	42,42,42,42	0
57	MG	DA	3486	1/1	0.94	0.14	37,37,37,37	0
57	MG	DA	3086	1/1	0.94	0.08	41,41,41,41	0
57	MG	BA	3156	1/1	0.94	0.08	43,43,43,43	0
57	MG	DA	3490	1/1	0.94	0.11	62,62,62,62	0
57	MG	DA	3088	1/1	0.94	0.14	41,41,41,41	0
57	MG	DA	3278	1/1	0.94	0.06	38,38,38,38	0
57	MG	BA	3643	1/1	0.94	0.15	47,47,47,47	0
57	MG	BA	3161	1/1	0.94	0.14	54,54,54,54	0
57	MG	BA	3542	1/1	0.94	0.10	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	3168	1/1	0.94	0.07	56,56,56,56	0
57	MG	AX	3005	1/1	0.94	0.32	57,57,57,57	0
57	MG	DA	3098	1/1	0.94	0.11	32,32,32,32	0
57	MG	CA	3112	1/1	0.94	0.07	31,31,31,31	0
57	MG	DA	3500	1/1	0.94	0.08	32,32,32,32	0
57	MG	DA	3501	1/1	0.94	0.09	47,47,47,47	0
57	MG	AX	3006	1/1	0.94	0.26	59,59,59,59	0
57	MG	BA	3654	1/1	0.94	0.16	42,42,42,42	0
57	MG	DA	3293	1/1	0.94	0.11	41,41,41,41	0
57	MG	BA	3421	1/1	0.94	0.14	29,29,29,29	0
57	MG	BA	3657	1/1	0.94	0.14	55,55,55,55	0
57	MG	BA	3028	1/1	0.94	0.14	31,31,31,31	0
57	MG	AA	3026	1/1	0.94	0.09	61,61,61,61	0
57	MG	BA	3550	1/1	0.94	0.16	60,60,60,60	0
57	MG	BA	3174	1/1	0.94	0.14	44,44,44,44	0
57	MG	DA	3113	1/1	0.94	0.12	42,42,42,42	0
57	MG	BA	3556	1/1	0.94	0.13	52,52,52,52	0
57	MG	DA	3115	1/1	0.94	0.11	58,58,58,58	0
57	MG	AX	3009	1/1	0.94	0.11	50,50,50,50	0
57	MG	BA	3331	1/1	0.94	0.14	39,39,39,39	0
57	MG	DA	3522	1/1	0.94	0.09	41,41,41,41	0
57	MG	BA	3243	1/1	0.94	0.18	46,46,46,46	0
57	MG	BA	3431	1/1	0.94	0.12	25,25,25,25	0
57	MG	DA	3121	1/1	0.94	0.07	39,39,39,39	0
57	MG	AA	3094	1/1	0.94	0.15	54,54,54,54	0
57	MG	CA	3018	1/1	0.94	0.10	47,47,47,47	0
57	MG	DA	3530	1/1	0.94	0.07	43,43,43,43	0
57	MG	DA	3531	1/1	0.94	0.09	40,40,40,40	0
57	MG	DA	3532	1/1	0.94	0.09	43,43,43,43	0
57	MG	BA	3245	1/1	0.94	0.28	37,37,37,37	0
57	MG	DA	3129	1/1	0.94	0.13	41,41,41,41	0
57	MG	DA	3536	1/1	0.94	0.10	48,48,48,48	0
57	MG	BA	3435	1/1	0.94	0.11	31,31,31,31	0
57	MG	BA	3076	1/1	0.94	0.17	34,34,34,34	0
57	MG	BA	3441	1/1	0.94	0.15	56,56,56,56	0
57	MG	BA	3114	1/1	0.94	0.17	41,41,41,41	0
57	MG	BA	3258	1/1	0.94	0.07	35,35,35,35	0
57	MG	DA	3137	1/1	0.94	0.17	48,48,48,48	0
57	MG	BA	3259	1/1	0.94	0.20	40,40,40,40	0
57	MG	BA	3260	1/1	0.94	0.14	45,45,45,45	0
57	MG	BA	3447	1/1	0.94	0.10	44,44,44,44	0
57	MG	BA	3342	1/1	0.94	0.15	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3450	1/1	0.94	0.06	45,45,45,45	0
57	MG	BA	3115	1/1	0.94	0.33	49,49,49,49	0
57	MG	DA	3552	1/1	0.94	0.08	43,43,43,43	0
57	MG	BA	3690	1/1	0.94	0.14	49,49,49,49	0
57	MG	AA	3044	1/1	0.94	0.14	46,46,46,46	0
57	MG	DA	3347	1/1	0.94	0.10	32,32,32,32	0
57	MG	BA	3457	1/1	0.94	0.07	41,41,41,41	0
57	MG	DA	3155	1/1	0.94	0.11	34,34,34,34	0
57	MG	BA	3693	1/1	0.94	0.09	48,48,48,48	0
57	MG	DA	3563	1/1	0.94	0.16	55,55,55,55	0
57	MG	BA	3119	1/1	0.94	0.14	41,41,41,41	0
57	MG	BA	3123	1/1	0.94	0.10	56,56,56,56	0
57	MG	DA	3360	1/1	0.94	0.09	54,54,54,54	0
57	MG	BA	3463	1/1	0.94	0.09	43,43,43,43	0
57	MG	DA	3364	1/1	0.94	0.09	49,49,49,49	0
57	MG	BA	3267	1/1	0.94	0.25	33,33,33,33	0
57	MG	DA	3163	1/1	0.94	0.18	43,43,43,43	0
57	MG	BA	3703	1/1	0.94	0.13	47,47,47,47	0
57	MG	DA	3573	1/1	0.94	0.08	49,49,49,49	0
57	MG	DA	3368	1/1	0.94	0.07	58,58,58,58	0
57	MG	BA	3189	1/1	0.94	0.17	33,33,33,33	0
57	MG	BA	3356	1/1	0.94	0.08	36,36,36,36	0
57	MG	BA	3710	1/1	0.94	0.08	21,21,21,21	0
57	MG	BA	3711	1/1	0.94	0.24	46,46,46,46	0
57	MG	CA	3160	1/1	0.94	0.27	49,49,49,49	0
57	MG	DA	3582	1/1	0.94	0.08	24,24,24,24	0
57	MG	CA	3048	1/1	0.94	0.18	48,48,48,48	0
57	MG	DA	3585	1/1	0.94	0.15	45,45,45,45	0
57	MG	DA	3379	1/1	0.94	0.09	37,37,37,37	0
57	MG	CA	3050	1/1	0.94	0.18	56,56,56,56	0
57	MG	BA	3272	1/1	0.94	0.25	38,38,38,38	0
57	MG	BA	3358	1/1	0.94	0.07	35,35,35,35	0
57	MG	BA	3080	1/1	0.94	0.29	51,51,51,51	0
57	MG	DA	3389	1/1	0.94	0.07	31,31,31,31	0
57	MG	BA	3471	1/1	0.94	0.05	42,42,42,42	0
57	MG	DA	3186	1/1	0.94	0.07	33,33,33,33	0
57	MG	DA	3392	1/1	0.94	0.16	40,40,40,40	0
57	MG	DA	3393	1/1	0.94	0.14	41,41,41,41	0
57	MG	BA	3720	1/1	0.94	0.14	48,48,48,48	0
57	MG	BA	3278	1/1	0.94	0.08	38,38,38,38	0
57	MG	BA	3364	1/1	0.94	0.10	37,37,37,37	0
57	MG	DA	3398	1/1	0.94	0.09	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3402	1/1	0.94	0.10	47,47,47,47	0
57	MG	AA	3078	1/1	0.94	0.07	66,66,66,66	0
57	MG	BA	3280	1/1	0.94	0.21	46,46,46,46	0
57	MG	BA	3130	1/1	0.94	0.22	39,39,39,39	0
57	MG	BA	3042	1/1	0.94	0.15	34,34,34,34	0
57	MG	CA	3063	1/1	0.94	0.23	59,59,59,59	0
57	MG	BA	3286	1/1	0.94	0.12	33,33,33,33	0
57	MG	DA	3203	1/1	0.94	0.10	46,46,46,46	0
57	MG	CA	3065	1/1	0.94	0.15	60,60,60,60	0
57	MG	DA	3205	1/1	0.94	0.10	52,52,52,52	0
57	MG	BA	3134	1/1	0.94	0.14	43,43,43,43	0
57	MG	DA	3418	1/1	0.94	0.10	41,41,41,41	0
57	MG	BA	3377	1/1	0.94	0.19	58,58,58,58	0
57	MG	BA	3500	1/1	0.94	0.07	54,54,54,54	0
57	MG	DA	3422	1/1	0.94	0.15	40,40,40,40	0
57	MG	BA	3043	1/1	0.94	0.09	44,44,44,44	0
57	MG	BA	3504	1/1	0.94	0.16	33,33,33,33	0
57	MG	DA	3623	1/1	0.94	0.06	31,31,31,31	0
57	MG	DA	3032	1/1	0.94	0.07	34,34,34,34	0
57	MG	BA	3616	1/1	0.94	0.08	32,32,32,32	0
57	MG	BA	3617	1/1	0.94	0.09	59,59,59,59	0
57	MG	DA	3431	1/1	0.94	0.13	56,56,56,56	0
57	MG	BA	3379	1/1	0.94	0.19	69,69,69,69	0
57	MG	BA	3295	1/1	0.94	0.11	56,56,56,56	0
57	MG	BE	3006	1/1	0.94	0.12	72,72,72,72	0
57	MG	DB	3004	1/1	0.94	0.06	38,38,38,38	0
57	MG	BA	3510	1/1	0.94	0.11	20,20,20,20	0
57	MG	BA	3047	1/1	0.94	0.08	44,44,44,44	0
57	MG	BA	3513	1/1	0.94	0.11	55,55,55,55	0
57	MG	DA	3440	1/1	0.94	0.16	44,44,44,44	0
57	MG	DD	304	1/1	0.94	0.08	40,40,40,40	0
57	MG	CA	3080	1/1	0.94	0.21	61,61,61,61	0
57	MG	BF	307	1/1	0.94	0.18	25,25,25,25	0
57	MG	AA	3087	1/1	0.94	0.10	57,57,57,57	0
57	MG	BA	3007	1/1	0.94	0.14	39,39,39,39	0
57	MG	BA	3055	1/1	0.94	0.12	43,43,43,43	0
57	MG	BA	3213	1/1	0.94	0.10	48,48,48,48	0
57	MG	DE	304	1/1	0.94	0.14	47,47,47,47	0
57	MG	BN	3001	1/1	0.94	0.26	46,46,46,46	0
57	MG	DA	3055	1/1	0.94	0.09	35,35,35,35	0
57	MG	BA	3389	1/1	0.94	0.09	57,57,57,57	0
57	MG	DA	3244	1/1	0.94	0.11	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DN	5001	1/1	0.94	0.08	53,53,53,53	0
57	MG	BN	3004	1/1	0.94	0.33	49,49,49,49	0
57	MG	DA	3454	1/1	0.94	0.10	28,28,28,28	0
57	MG	DA	3060	1/1	0.94	0.16	50,50,50,50	0
57	MG	DA	3061	1/1	0.94	0.17	36,36,36,36	0
57	MG	AN	503	1/1	0.94	0.23	61,61,61,61	0
57	MG	DA	3251	1/1	0.94	0.25	34,34,34,34	0
57	MG	BA	3215	1/1	0.94	0.14	53,53,53,53	0
57	MG	BA	3401	1/1	0.94	0.20	31,31,31,31	0
57	MG	DU	3004	1/1	0.94	0.16	69,69,69,69	0
57	MG	BR	203	1/1	0.94	0.17	31,31,31,31	0
57	MG	DA	3467	1/1	0.94	0.07	28,28,28,28	0
57	MG	BA	3402	1/1	0.94	0.14	39,39,39,39	0
57	MG	D3	3001	1/1	0.94	0.09	54,54,54,54	0
57	MG	AA	3030	1/1	0.94	0.15	41,41,41,41	0
57	MG	CA	3095	1/1	0.94	0.16	52,52,52,52	0
57	MG	DA	3075	1/1	0.94	0.07	40,40,40,40	0
60	K	AX	3001	1/1	0.94	0.09	39,39,39,39	0
57	MG	BA	3015	1/1	0.95	0.11	50,50,50,50	0
57	MG	BA	3373	1/1	0.95	0.23	46,46,46,46	0
57	MG	BA	3483	1/1	0.95	0.09	36,36,36,36	0
57	MG	DA	3471	1/1	0.95	0.12	23,23,23,23	0
57	MG	BA	3191	1/1	0.95	0.04	22,22,22,22	0
57	MG	DA	3249	1/1	0.95	0.19	48,48,48,48	0
57	MG	BB	3011	1/1	0.95	0.06	40,40,40,40	0
57	MG	BA	3607	1/1	0.95	0.09	41,41,41,41	0
57	MG	BA	3608	1/1	0.95	0.08	50,50,50,50	0
57	MG	DA	3253	1/1	0.95	0.16	34,34,34,34	0
57	MG	DA	3058	1/1	0.95	0.08	47,47,47,47	0
57	MG	BB	3016	1/1	0.95	0.06	39,39,39,39	0
57	MG	BA	3193	1/1	0.95	0.18	30,30,30,30	0
57	MG	BA	3282	1/1	0.95	0.12	44,44,44,44	0
57	MG	BA	3195	1/1	0.95	0.11	46,46,46,46	0
57	MG	DA	3261	1/1	0.95	0.14	38,38,38,38	0
57	MG	DA	3063	1/1	0.95	0.09	40,40,40,40	0
57	MG	BA	3495	1/1	0.95	0.25	47,47,47,47	0
57	MG	BD	306	1/1	0.95	0.13	30,30,30,30	0
57	MG	DA	3067	1/1	0.95	0.16	54,54,54,54	0
57	MG	DA	3267	1/1	0.95	0.18	45,45,45,45	0
57	MG	BA	3496	1/1	0.95	0.19	33,33,33,33	0
57	MG	BD	310	1/1	0.95	0.20	34,34,34,34	0
57	MG	DA	3070	1/1	0.95	0.10	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3118	1/1	0.95	0.21	28,28,28,28	0
57	MG	AE	3002	1/1	0.95	0.14	61,61,61,61	0
57	MG	BA	3120	1/1	0.95	0.26	52,52,52,52	0
57	MG	BA	3501	1/1	0.95	0.06	67,67,67,67	0
57	MG	BA	3383	1/1	0.95	0.09	37,37,37,37	0
57	MG	BF	304	1/1	0.95	0.13	35,35,35,35	0
57	MG	DA	3279	1/1	0.95	0.18	50,50,50,50	0
57	MG	BA	3294	1/1	0.95	0.18	37,37,37,37	0
57	MG	BA	3506	1/1	0.95	0.07	39,39,39,39	0
57	MG	DA	3505	1/1	0.95	0.09	41,41,41,41	0
57	MG	AA	3015	1/1	0.95	0.08	28,28,28,28	0
57	MG	DA	3285	1/1	0.95	0.10	50,50,50,50	0
57	MG	BA	3508	1/1	0.95	0.15	52,52,52,52	0
57	MG	BA	3125	1/1	0.95	0.22	30,30,30,30	0
57	MG	BF	310	1/1	0.95	0.07	51,51,51,51	0
57	MG	AA	3194	1/1	0.95	0.18	41,41,41,41	0
57	MG	AA	3028	1/1	0.95	0.12	58,58,58,58	0
57	MG	DA	3089	1/1	0.95	0.14	36,36,36,36	0
57	MG	DA	3517	1/1	0.95	0.10	36,36,36,36	0
57	MG	DA	3518	1/1	0.95	0.06	42,42,42,42	0
57	MG	DA	3292	1/1	0.95	0.07	29,29,29,29	0
57	MG	BA	3391	1/1	0.95	0.18	30,30,30,30	0
57	MG	BA	3392	1/1	0.95	0.12	27,27,27,27	0
57	MG	BN	3003	1/1	0.95	0.10	61,61,61,61	0
57	MG	BA	3129	1/1	0.95	0.05	30,30,30,30	0
57	MG	BN	3006	1/1	0.95	0.32	47,47,47,47	0
57	MG	CA	3100	1/1	0.95	0.08	48,48,48,48	0
57	MG	AA	3002	1/1	0.95	0.07	58,58,58,58	0
57	MG	DA	3103	1/1	0.95	0.16	55,55,55,55	0
57	MG	BA	3517	1/1	0.95	0.07	20,20,20,20	0
57	MG	DA	3309	1/1	0.95	0.08	34,34,34,34	0
57	MG	BA	3399	1/1	0.95	0.08	26,26,26,26	0
57	MG	BR	201	1/1	0.95	0.20	30,30,30,30	0
57	MG	BA	3131	1/1	0.95	0.26	31,31,31,31	0
57	MG	DA	3535	1/1	0.95	0.09	21,21,21,21	0
57	MG	BA	3210	1/1	0.95	0.08	42,42,42,42	0
57	MG	BA	3211	1/1	0.95	0.19	50,50,50,50	0
57	MG	DA	3316	1/1	0.95	0.11	39,39,39,39	0
57	MG	BU	206	1/1	0.95	0.12	39,39,39,39	0
57	MG	AA	3012	1/1	0.95	0.28	61,61,61,61	0
57	MG	BW	201	1/1	0.95	0.17	48,48,48,48	0
57	MG	AA	3009	1/1	0.95	0.12	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3529	1/1	0.95	0.22	29,29,29,29	0
57	MG	BA	3640	1/1	0.95	0.09	53,53,53,53	0
57	MG	BA	3641	1/1	0.95	0.09	33,33,33,33	0
57	MG	BA	3308	1/1	0.95	0.08	14,14,14,14	0
57	MG	DA	3549	1/1	0.95	0.16	47,47,47,47	0
57	MG	BA	3078	1/1	0.95	0.17	55,55,55,55	0
57	MG	BA	3410	1/1	0.95	0.10	40,40,40,40	0
57	MG	BA	3645	1/1	0.95	0.10	43,43,43,43	0
57	MG	DA	3123	1/1	0.95	0.17	45,45,45,45	0
57	MG	B3	3001	1/1	0.95	0.10	43,43,43,43	0
57	MG	DA	3126	1/1	0.95	0.13	39,39,39,39	0
57	MG	DA	3334	1/1	0.95	0.06	31,31,31,31	0
57	MG	B3	3002	1/1	0.95	0.09	58,58,58,58	0
57	MG	DA	3560	1/1	0.95	0.18	48,48,48,48	0
57	MG	DA	3336	1/1	0.95	0.15	38,38,38,38	0
57	MG	DA	3562	1/1	0.95	0.07	58,58,58,58	0
57	MG	CA	3123	1/1	0.95	0.14	53,53,53,53	0
57	MG	CA	3124	1/1	0.95	0.16	57,57,57,57	0
57	MG	B5	101	1/1	0.95	0.09	30,30,30,30	0
57	MG	DA	3345	1/1	0.95	0.08	28,28,28,28	0
57	MG	DA	3133	1/1	0.95	0.11	52,52,52,52	0
57	MG	BA	3411	1/1	0.95	0.10	24,24,24,24	0
57	MG	AA	3157	1/1	0.95	0.09	38,38,38,38	0
57	MG	AA	3088	1/1	0.95	0.16	40,40,40,40	0
57	MG	BA	3536	1/1	0.95	0.09	42,42,42,42	0
57	MG	BA	3315	1/1	0.95	0.09	42,42,42,42	0
57	MG	DA	3357	1/1	0.95	0.07	29,29,29,29	0
57	MG	BA	3655	1/1	0.95	0.16	68,68,68,68	0
57	MG	BA	3219	1/1	0.95	0.27	42,42,42,42	0
57	MG	DA	3577	1/1	0.95	0.09	25,25,25,25	0
57	MG	BA	3541	1/1	0.95	0.11	43,43,43,43	0
57	MG	BA	3139	1/1	0.95	0.19	45,45,45,45	0
57	MG	AA	3071	1/1	0.95	0.25	41,41,41,41	0
57	MG	CA	3009	1/1	0.95	0.07	44,44,44,44	0
57	MG	DA	3583	1/1	0.95	0.10	44,44,44,44	0
57	MG	BA	3661	1/1	0.95	0.19	56,56,56,56	0
57	MG	DA	3151	1/1	0.95	0.22	48,48,48,48	0
57	MG	BA	3662	1/1	0.95	0.27	62,62,62,62	0
57	MG	AA	3060	1/1	0.95	0.26	49,49,49,49	0
57	MG	DA	3156	1/1	0.95	0.16	46,46,46,46	0
57	MG	AX	3007	1/1	0.95	0.22	54,54,54,54	0
57	MG	CA	3141	1/1	0.95	0.20	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3424	1/1	0.95	0.13	29,29,29,29	0
57	MG	DA	3378	1/1	0.95	0.11	33,33,33,33	0
57	MG	BA	3668	1/1	0.95	0.17	39,39,39,39	0
57	MG	BA	3149	1/1	0.95	0.07	40,40,40,40	0
57	MG	AA	3050	1/1	0.95	0.20	49,49,49,49	0
57	MG	BA	3228	1/1	0.95	0.15	33,33,33,33	0
57	MG	DA	3384	1/1	0.95	0.09	41,41,41,41	0
57	MG	BA	3038	1/1	0.95	0.06	38,38,38,38	0
57	MG	DA	3388	1/1	0.95	0.08	33,33,33,33	0
57	MG	DA	3166	1/1	0.95	0.19	47,47,47,47	0
57	MG	CA	3149	1/1	0.95	0.08	49,49,49,49	0
57	MG	DA	3169	1/1	0.95	0.12	45,45,45,45	0
57	MG	BA	3329	1/1	0.95	0.05	21,21,21,21	0
57	MG	BA	3093	1/1	0.95	0.10	23,23,23,23	0
57	MG	DA	3172	1/1	0.95	0.05	32,32,32,32	0
57	MG	AA	3076	1/1	0.95	0.31	62,62,62,62	0
57	MG	DA	3174	1/1	0.95	0.16	38,38,38,38	0
57	MG	AX	3010	1/1	0.95	0.08	61,61,61,61	0
57	MG	BA	3561	1/1	0.95	0.13	37,37,37,37	0
57	MG	BA	3564	1/1	0.95	0.17	44,44,44,44	0
57	MG	BA	3158	1/1	0.95	0.15	48,48,48,48	0
57	MG	BA	3240	1/1	0.95	0.27	52,52,52,52	0
57	MG	BA	3045	1/1	0.95	0.19	33,33,33,33	0
57	MG	AA	3165	1/1	0.95	0.13	47,47,47,47	0
57	MG	BA	3048	1/1	0.95	0.08	44,44,44,44	0
57	MG	BA	3686	1/1	0.95	0.20	36,36,36,36	0
57	MG	BA	3165	1/1	0.95	0.18	34,34,34,34	0
57	MG	DA	3413	1/1	0.95	0.18	30,30,30,30	0
57	MG	BA	3049	1/1	0.95	0.19	53,53,53,53	0
57	MG	AX	3012	1/1	0.95	0.08	15,15,15,15	0
57	MG	AA	3025	1/1	0.95	0.19	46,46,46,46	0
57	MG	BA	3173	1/1	0.95	0.19	28,28,28,28	0
57	MG	DA	3629	1/1	0.95	0.10	40,40,40,40	0
57	MG	DB	3001	1/1	0.95	0.08	50,50,50,50	0
57	MG	BA	3054	1/1	0.95	0.21	44,44,44,44	0
57	MG	DA	3198	1/1	0.95	0.10	41,41,41,41	0
57	MG	DA	3424	1/1	0.95	0.09	56,56,56,56	0
57	MG	CA	3039	1/1	0.95	0.09	52,52,52,52	0
57	MG	DA	3202	1/1	0.95	0.31	41,41,41,41	0
57	MG	DB	3007	1/1	0.95	0.07	55,55,55,55	0
57	MG	DA	3427	1/1	0.95	0.07	26,26,26,26	0
57	MG	BA	3694	1/1	0.95	0.12	11,11,11,11	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DB	3010	1/1	0.95	0.17	55,55,55,55	0
57	MG	DD	301	1/1	0.95	0.08	31,31,31,31	0
57	MG	DD	302	1/1	0.95	0.12	50,50,50,50	0
57	MG	DA	3005	1/1	0.95	0.15	29,29,29,29	0
57	MG	BA	3452	1/1	0.95	0.07	15,15,15,15	0
57	MG	AA	3033	1/1	0.95	0.19	43,43,43,43	0
57	MG	BA	3455	1/1	0.95	0.10	44,44,44,44	0
57	MG	BA	3262	1/1	0.95	0.14	38,38,38,38	0
57	MG	BA	3059	1/1	0.95	0.27	50,50,50,50	0
57	MG	BA	3704	1/1	0.95	0.09	31,31,31,31	0
57	MG	DA	3213	1/1	0.95	0.09	51,51,51,51	0
57	MG	BA	3705	1/1	0.95	0.15	32,32,32,32	0
57	MG	AA	3148	1/1	0.95	0.10	61,61,61,61	0
57	MG	DA	3022	1/1	0.95	0.06	27,27,27,27	0
57	MG	DA	3026	1/1	0.95	0.16	41,41,41,41	0
57	MG	BA	3006	1/1	0.95	0.09	38,38,38,38	0
57	MG	AA	3130	1/1	0.95	0.17	52,52,52,52	0
57	MG	BA	3181	1/1	0.95	0.09	49,49,49,49	0
57	MG	BA	3063	1/1	0.95	0.08	39,39,39,39	0
57	MG	BA	3273	1/1	0.95	0.12	30,30,30,30	0
57	MG	DQ	3002	1/1	0.95	0.10	45,45,45,45	0
57	MG	DQ	3003	1/1	0.95	0.22	59,59,59,59	0
57	MG	DA	3229	1/1	0.95	0.18	39,39,39,39	0
57	MG	CA	3057	1/1	0.95	0.09	48,48,48,48	0
57	MG	BA	3714	1/1	0.95	0.07	42,42,42,42	0
57	MG	DA	3452	1/1	0.95	0.07	40,40,40,40	0
57	MG	DU	3003	1/1	0.95	0.13	60,60,60,60	0
57	MG	DA	3233	1/1	0.95	0.18	41,41,41,41	0
57	MG	BA	3368	1/1	0.95	0.20	26,26,26,26	0
57	MG	AA	3010	1/1	0.95	0.10	54,54,54,54	0
57	MG	DA	3040	1/1	0.95	0.17	48,48,48,48	0
57	MG	DA	3237	1/1	0.95	0.24	41,41,41,41	0
57	MG	BA	3719	1/1	0.95	0.11	53,53,53,53	0
57	MG	D8	102	1/1	0.95	0.24	63,63,63,63	0
57	MG	BA	3012	1/1	0.95	0.10	38,38,38,38	0
59	ZN	CN	501	1/1	0.95	0.06	101,101,101,101	0
57	MG	BA	3472	1/1	0.95	0.07	39,39,39,39	0
57	MG	BA	3371	1/1	0.95	0.12	53,53,53,53	0
60	K	CX	3001	1/1	0.95	0.07	54,54,54,54	0
57	MG	DA	3023	1/1	0.96	0.09	35,35,35,35	0
57	MG	BA	3321	1/1	0.96	0.09	31,31,31,31	0
57	MG	BA	3122	1/1	0.96	0.12	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	3072	1/1	0.96	0.27	65,65,65,65	0
57	MG	DA	3031	1/1	0.96	0.05	36,36,36,36	0
57	MG	BQ	3001	1/1	0.96	0.22	51,51,51,51	0
57	MG	BQ	3002	1/1	0.96	0.25	39,39,39,39	0
57	MG	DA	3338	1/1	0.96	0.07	36,36,36,36	0
57	MG	BA	3390	1/1	0.96	0.06	31,31,31,31	0
57	MG	DA	3179	1/1	0.96	0.27	50,50,50,50	0
57	MG	DA	3180	1/1	0.96	0.30	41,41,41,41	0
57	MG	BQ	3004	1/1	0.96	0.13	35,35,35,35	0
57	MG	BQ	3005	1/1	0.96	0.11	39,39,39,39	0
57	MG	DA	3350	1/1	0.96	0.25	44,44,44,44	0
57	MG	BA	3667	1/1	0.96	0.11	31,31,31,31	0
57	MG	BR	202	1/1	0.96	0.16	49,49,49,49	0
57	MG	BA	3206	1/1	0.96	0.05	37,37,37,37	0
57	MG	BA	3092	1/1	0.96	0.06	32,32,32,32	0
57	MG	BA	3476	1/1	0.96	0.07	37,37,37,37	0
57	MG	BA	3394	1/1	0.96	0.09	22,22,22,22	0
57	MG	BA	3578	1/1	0.96	0.06	43,43,43,43	0
57	MG	BV	202	1/1	0.96	0.13	29,29,29,29	0
57	MG	DA	3192	1/1	0.96	0.13	31,31,31,31	0
57	MG	BV	203	1/1	0.96	0.06	31,31,31,31	0
57	MG	DA	3540	1/1	0.96	0.05	43,43,43,43	0
57	MG	DA	3194	1/1	0.96	0.10	43,43,43,43	0
57	MG	DA	3049	1/1	0.96	0.19	46,46,46,46	0
57	MG	DA	3050	1/1	0.96	0.16	48,48,48,48	0
57	MG	DA	3197	1/1	0.96	0.10	35,35,35,35	0
57	MG	BA	3396	1/1	0.96	0.15	20,20,20,20	0
57	MG	DA	3371	1/1	0.96	0.11	47,47,47,47	0
57	MG	DA	3200	1/1	0.96	0.08	38,38,38,38	0
57	MG	BA	3167	1/1	0.96	0.25	51,51,51,51	0
57	MG	BA	3676	1/1	0.96	0.17	44,44,44,44	0
57	MG	BW	204	1/1	0.96	0.12	27,27,27,27	0
57	MG	BA	3582	1/1	0.96	0.09	23,23,23,23	0
57	MG	BX	101	1/1	0.96	0.11	36,36,36,36	0
57	MG	DA	3206	1/1	0.96	0.14	37,37,37,37	0
57	MG	BA	3484	1/1	0.96	0.09	50,50,50,50	0
57	MG	B0	101	1/1	0.96	0.07	33,33,33,33	0
57	MG	BA	3169	1/1	0.96	0.12	40,40,40,40	0
57	MG	BA	3212	1/1	0.96	0.18	24,24,24,24	0
57	MG	DA	3387	1/1	0.96	0.07	29,29,29,29	0
57	MG	BA	3489	1/1	0.96	0.14	36,36,36,36	0
57	MG	BA	3170	1/1	0.96	0.10	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3214	1/1	0.96	0.07	43,43,43,43	0
57	MG	DA	3215	1/1	0.96	0.06	35,35,35,35	0
57	MG	DA	3065	1/1	0.96	0.10	38,38,38,38	0
57	MG	DA	3218	1/1	0.96	0.05	36,36,36,36	0
57	MG	BA	3010	1/1	0.96	0.17	45,45,45,45	0
57	MG	BA	3403	1/1	0.96	0.08	22,22,22,22	0
57	MG	BA	3036	1/1	0.96	0.35	42,42,42,42	0
57	MG	BA	3275	1/1	0.96	0.10	38,38,38,38	0
57	MG	BA	3498	1/1	0.96	0.14	45,45,45,45	0
57	MG	DA	3071	1/1	0.96	0.09	42,42,42,42	0
57	MG	DA	3405	1/1	0.96	0.12	45,45,45,45	0
57	MG	B8	101	1/1	0.96	0.11	34,34,34,34	0
57	MG	DA	3073	1/1	0.96	0.23	49,49,49,49	0
57	MG	B9	502	1/1	0.96	0.07	31,31,31,31	0
57	MG	AA	3135	1/1	0.96	0.10	52,52,52,52	0
57	MG	DA	3231	1/1	0.96	0.12	33,33,33,33	0
57	MG	AA	3136	1/1	0.96	0.08	43,43,43,43	0
57	MG	BA	3218	1/1	0.96	0.34	52,52,52,52	0
57	MG	AA	3037	1/1	0.96	0.07	48,48,48,48	0
57	MG	BA	3176	1/1	0.96	0.10	35,35,35,35	0
57	MG	BA	3044	1/1	0.96	0.06	40,40,40,40	0
57	MG	BA	3345	1/1	0.96	0.09	36,36,36,36	0
57	MG	BA	3414	1/1	0.96	0.17	59,59,59,59	0
57	MG	BA	3071	1/1	0.96	0.19	48,48,48,48	0
57	MG	DA	3421	1/1	0.96	0.07	31,31,31,31	0
57	MG	BA	3348	1/1	0.96	0.05	17,17,17,17	0
57	MG	AA	3096	1/1	0.96	0.11	57,57,57,57	0
57	MG	DA	3243	1/1	0.96	0.26	41,41,41,41	0
57	MG	AA	3074	1/1	0.96	0.16	38,38,38,38	0
57	MG	BA	3289	1/1	0.96	0.12	41,41,41,41	0
57	MG	DA	3597	1/1	0.96	0.06	42,42,42,42	0
57	MG	DA	3598	1/1	0.96	0.12	48,48,48,48	0
57	MG	BA	3352	1/1	0.96	0.11	29,29,29,29	0
57	MG	BA	3290	1/1	0.96	0.06	43,43,43,43	0
57	MG	DA	3092	1/1	0.96	0.05	29,29,29,29	0
57	MG	BA	3354	1/1	0.96	0.06	31,31,31,31	0
57	MG	BA	3518	1/1	0.96	0.12	48,48,48,48	0
57	MG	DA	3096	1/1	0.96	0.11	52,52,52,52	0
57	MG	BA	3355	1/1	0.96	0.06	30,30,30,30	0
57	MG	AA	3185	1/1	0.96	0.07	50,50,50,50	0
57	MG	DA	3100	1/1	0.96	0.21	38,38,38,38	0
57	MG	BA	3106	1/1	0.96	0.16	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3142	1/1	0.96	0.11	35,35,35,35	0
57	MG	BA	3524	1/1	0.96	0.09	39,39,39,39	0
57	MG	AA	3128	1/1	0.96	0.23	53,53,53,53	0
57	MG	BA	3432	1/1	0.96	0.15	35,35,35,35	0
57	MG	AA	3022	1/1	0.96	0.09	57,57,57,57	0
57	MG	DA	3108	1/1	0.96	0.10	50,50,50,50	0
57	MG	DA	3616	1/1	0.96	0.06	28,28,28,28	0
57	MG	AK	3001	1/1	0.96	0.12	55,55,55,55	0
57	MG	BB	3003	1/1	0.96	0.16	40,40,40,40	0
57	MG	BA	3365	1/1	0.96	0.09	40,40,40,40	0
57	MG	BA	3436	1/1	0.96	0.09	21,21,21,21	0
57	MG	BB	3006	1/1	0.96	0.15	42,42,42,42	0
57	MG	BA	3236	1/1	0.96	0.10	39,39,39,39	0
57	MG	BA	3439	1/1	0.96	0.07	12,12,12,12	0
57	MG	CA	3142	1/1	0.96	0.16	55,55,55,55	0
57	MG	BA	3440	1/1	0.96	0.13	40,40,40,40	0
57	MG	BA	3367	1/1	0.96	0.06	42,42,42,42	0
57	MG	BB	3013	1/1	0.96	0.16	43,43,43,43	0
57	MG	BA	3237	1/1	0.96	0.10	36,36,36,36	0
57	MG	DA	3459	1/1	0.96	0.31	40,40,40,40	0
57	MG	BA	3001	1/1	0.96	0.33	48,48,48,48	0
57	MG	DA	3281	1/1	0.96	0.07	37,37,37,37	0
57	MG	BA	3239	1/1	0.96	0.08	42,42,42,42	0
57	MG	DA	3463	1/1	0.96	0.07	54,54,54,54	0
57	MG	DA	3465	1/1	0.96	0.13	45,45,45,45	0
57	MG	DA	3124	1/1	0.96	0.12	30,30,30,30	0
57	MG	CA	3040	1/1	0.96	0.24	67,67,67,67	0
57	MG	BA	3194	1/1	0.96	0.21	42,42,42,42	0
57	MG	CA	3151	1/1	0.96	0.07	58,58,58,58	0
57	MG	AA	3083	1/1	0.96	0.26	38,38,38,38	0
57	MG	BA	3242	1/1	0.96	0.17	45,45,45,45	0
57	MG	DD	303	1/1	0.96	0.14	42,42,42,42	0
57	MG	DA	3474	1/1	0.96	0.13	52,52,52,52	0
57	MG	BA	3449	1/1	0.96	0.06	31,31,31,31	0
57	MG	BA	3546	1/1	0.96	0.09	27,27,27,27	0
57	MG	BD	309	1/1	0.96	0.15	33,33,33,33	0
57	MG	CA	3047	1/1	0.96	0.14	50,50,50,50	0
57	MG	BA	3058	1/1	0.96	0.11	24,24,24,24	0
57	MG	CA	3049	1/1	0.96	0.09	42,42,42,42	0
57	MG	BA	3083	1/1	0.96	0.15	33,33,33,33	0
57	MG	BA	3376	1/1	0.96	0.11	21,21,21,21	0
57	MG	DF	3002	1/1	0.96	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3453	1/1	0.96	0.09	47,47,47,47	0
57	MG	BE	3003	1/1	0.96	0.09	25,25,25,25	0
57	MG	DA	3305	1/1	0.96	0.07	48,48,48,48	0
57	MG	BE	3004	1/1	0.96	0.07	49,49,49,49	0
57	MG	DA	3489	1/1	0.96	0.07	38,38,38,38	0
57	MG	BA	3552	1/1	0.96	0.10	59,59,59,59	0
57	MG	DA	3147	1/1	0.96	0.06	42,42,42,42	0
57	MG	BF	301	1/1	0.96	0.05	30,30,30,30	0
57	MG	DA	3311	1/1	0.96	0.08	42,42,42,42	0
57	MG	BA	3647	1/1	0.96	0.09	41,41,41,41	0
57	MG	AA	3045	1/1	0.96	0.08	44,44,44,44	0
57	MG	BA	3246	1/1	0.96	0.11	46,46,46,46	0
57	MG	BA	3650	1/1	0.96	0.06	49,49,49,49	0
57	MG	BA	3314	1/1	0.96	0.22	42,42,42,42	0
57	MG	BA	3458	1/1	0.96	0.06	40,40,40,40	0
57	MG	BA	3087	1/1	0.96	0.17	44,44,44,44	0
57	MG	DV	201	1/1	0.96	0.10	49,49,49,49	0
57	MG	BA	3254	1/1	0.96	0.14	30,30,30,30	0
57	MG	BA	3382	1/1	0.96	0.09	31,31,31,31	0
57	MG	DW	202	1/1	0.96	0.07	43,43,43,43	0
57	MG	DA	3161	1/1	0.96	0.09	35,35,35,35	0
57	MG	AA	3092	1/1	0.96	0.11	36,36,36,36	0
57	MG	DA	3323	1/1	0.96	0.06	39,39,39,39	0
57	MG	BA	3658	1/1	0.96	0.06	16,16,16,16	0
57	MG	DA	3018	1/1	0.96	0.32	51,51,51,51	0
57	MG	BA	3089	1/1	0.96	0.11	30,30,30,30	0
57	MG	AA	3102	1/1	0.96	0.21	52,52,52,52	0
57	MG	BA	3568	1/1	0.96	0.16	43,43,43,43	0
57	MG	DA	3512	1/1	0.96	0.05	24,24,24,24	0
57	MG	DA	3052	1/1	0.97	0.07	33,33,33,33	0
57	MG	BA	3327	1/1	0.97	0.09	32,32,32,32	0
57	MG	BA	3594	1/1	0.97	0.11	34,34,34,34	0
57	MG	BA	3256	1/1	0.97	0.09	36,36,36,36	0
57	MG	BA	3146	1/1	0.97	0.12	47,47,47,47	0
57	MG	DA	3344	1/1	0.97	0.05	42,42,42,42	0
57	MG	BA	3147	1/1	0.97	0.09	34,34,34,34	0
57	MG	AA	3082	1/1	0.97	0.08	55,55,55,55	0
57	MG	CA	3101	1/1	0.97	0.13	41,41,41,41	0
57	MG	DA	3349	1/1	0.97	0.11	35,35,35,35	0
57	MG	AA	3116	1/1	0.97	0.13	41,41,41,41	0
57	MG	BA	3150	1/1	0.97	0.17	40,40,40,40	0
57	MG	DA	3352	1/1	0.97	0.12	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3110	1/1	0.97	0.12	40,40,40,40	0
57	MG	DA	3354	1/1	0.97	0.13	25,25,25,25	0
57	MG	DA	3199	1/1	0.97	0.05	41,41,41,41	0
57	MG	B5	103	1/1	0.97	0.06	50,50,50,50	0
57	MG	BA	3202	1/1	0.97	0.19	42,42,42,42	0
57	MG	AM	201	1/1	0.97	0.04	43,43,43,43	0
57	MG	DA	3359	1/1	0.97	0.09	42,42,42,42	0
57	MG	BA	3701	1/1	0.97	0.12	17,17,17,17	0
57	MG	AA	3103	1/1	0.97	0.15	42,42,42,42	0
57	MG	AA	3070	1/1	0.97	0.22	43,43,43,43	0
57	MG	BA	3268	1/1	0.97	0.07	45,45,45,45	0
57	MG	BA	3269	1/1	0.97	0.09	30,30,30,30	0
57	MG	BA	3418	1/1	0.97	0.11	26,26,26,26	0
57	MG	BA	3270	1/1	0.97	0.23	47,47,47,47	0
57	MG	BA	3022	1/1	0.97	0.20	47,47,47,47	0
57	MG	DA	3211	1/1	0.97	0.05	43,43,43,43	0
57	MG	BA	3023	1/1	0.97	0.07	25,25,25,25	0
57	MG	BA	3423	1/1	0.97	0.10	26,26,26,26	0
57	MG	DA	3373	1/1	0.97	0.12	43,43,43,43	0
57	MG	BA	3208	1/1	0.97	0.04	33,33,33,33	0
57	MG	BA	3274	1/1	0.97	0.17	44,44,44,44	0
57	MG	DA	3216	1/1	0.97	0.17	43,43,43,43	0
57	MG	DA	3377	1/1	0.97	0.07	31,31,31,31	0
57	MG	BA	3209	1/1	0.97	0.16	32,32,32,32	0
57	MG	BA	3716	1/1	0.97	0.10	53,53,53,53	0
57	MG	BA	3159	1/1	0.97	0.10	43,43,43,43	0
57	MG	AA	3167	1/1	0.97	0.05	65,65,65,65	0
57	MG	DA	3382	1/1	0.97	0.09	20,20,20,20	0
57	MG	DA	3221	1/1	0.97	0.09	49,49,49,49	0
57	MG	DA	3556	1/1	0.97	0.08	49,49,49,49	0
57	MG	DA	3222	1/1	0.97	0.09	38,38,38,38	0
57	MG	DA	3083	1/1	0.97	0.07	30,30,30,30	0
57	MG	DA	3386	1/1	0.97	0.12	39,39,39,39	0
57	MG	BA	3117	1/1	0.97	0.11	24,24,24,24	0
57	MG	DA	3085	1/1	0.97	0.05	27,27,27,27	0
57	MG	BA	3163	1/1	0.97	0.16	43,43,43,43	0
57	MG	BA	3522	1/1	0.97	0.06	34,34,34,34	0
57	MG	BA	3025	1/1	0.97	0.09	12,12,12,12	0
57	MG	BA	3056	1/1	0.97	0.10	21,21,21,21	0
57	MG	BA	3026	1/1	0.97	0.18	36,36,36,36	0
57	MG	BA	3624	1/1	0.97	0.09	26,26,26,26	0
57	MG	BB	3007	1/1	0.97	0.05	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3285	1/1	0.97	0.10	21,21,21,21	0
57	MG	CA	3024	1/1	0.97	0.09	58,58,58,58	0
57	MG	BA	3527	1/1	0.97	0.14	37,37,37,37	0
57	MG	BA	3121	1/1	0.97	0.16	48,48,48,48	0
57	MG	BA	3361	1/1	0.97	0.08	38,38,38,38	0
57	MG	BA	3438	1/1	0.97	0.09	19,19,19,19	0
57	MG	DA	3101	1/1	0.97	0.16	45,45,45,45	0
57	MG	DA	3240	1/1	0.97	0.18	36,36,36,36	0
57	MG	BA	3362	1/1	0.97	0.06	43,43,43,43	0
57	MG	DA	3580	1/1	0.97	0.05	47,47,47,47	0
57	MG	BA	3168	1/1	0.97	0.04	32,32,32,32	0
57	MG	BB	3017	1/1	0.97	0.05	28,28,28,28	0
57	MG	BA	3288	1/1	0.97	0.05	37,37,37,37	0
57	MG	AA	3081	1/1	0.97	0.10	44,44,44,44	0
57	MG	DA	3414	1/1	0.97	0.08	37,37,37,37	0
57	MG	AW	101	1/1	0.97	0.12	24,24,24,24	0
57	MG	DA	3416	1/1	0.97	0.08	46,46,46,46	0
57	MG	DA	3247	1/1	0.97	0.08	43,43,43,43	0
57	MG	BD	301	1/1	0.97	0.20	37,37,37,37	0
57	MG	BA	3291	1/1	0.97	0.16	44,44,44,44	0
57	MG	BD	303	1/1	0.97	0.26	42,42,42,42	0
57	MG	BD	304	1/1	0.97	0.07	36,36,36,36	0
57	MG	BD	305	1/1	0.97	0.11	41,41,41,41	0
57	MG	DA	3423	1/1	0.97	0.15	33,33,33,33	0
57	MG	BA	3538	1/1	0.97	0.07	25,25,25,25	0
57	MG	BA	3539	1/1	0.97	0.11	18,18,18,18	0
57	MG	BA	3292	1/1	0.97	0.10	26,26,26,26	0
57	MG	DA	3116	1/1	0.97	0.05	36,36,36,36	0
57	MG	DA	3257	1/1	0.97	0.25	46,46,46,46	0
57	MG	DA	3258	1/1	0.97	0.16	32,32,32,32	0
57	MG	BA	3124	1/1	0.97	0.06	31,31,31,31	0
57	MG	AA	3169	1/1	0.97	0.16	48,48,48,48	0
57	MG	BA	3030	1/1	0.97	0.07	44,44,44,44	0
57	MG	DA	3433	1/1	0.97	0.11	27,27,27,27	0
57	MG	BA	3296	1/1	0.97	0.11	31,31,31,31	0
57	MG	AA	3112	1/1	0.97	0.09	44,44,44,44	0
57	MG	BA	3095	1/1	0.97	0.13	29,29,29,29	0
57	MG	BA	3008	1/1	0.97	0.06	22,22,22,22	0
57	MG	DA	3438	1/1	0.97	0.12	42,42,42,42	0
57	MG	AA	3095	1/1	0.97	0.14	44,44,44,44	0
57	MG	BA	3067	1/1	0.97	0.21	26,26,26,26	0
57	MG	BF	303	1/1	0.97	0.09	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3456	1/1	0.97	0.13	44,44,44,44	0
57	MG	BA	3551	1/1	0.97	0.10	17,17,17,17	0
57	MG	BA	3232	1/1	0.97	0.09	31,31,31,31	0
57	MG	BA	3653	1/1	0.97	0.12	51,51,51,51	0
57	MG	BA	3553	1/1	0.97	0.10	41,41,41,41	0
57	MG	BA	3133	1/1	0.97	0.19	29,29,29,29	0
57	MG	BA	3459	1/1	0.97	0.20	44,44,44,44	0
57	MG	BA	3234	1/1	0.97	0.22	39,39,39,39	0
57	MG	BA	3461	1/1	0.97	0.12	32,32,32,32	0
57	MG	BA	3034	1/1	0.97	0.06	21,21,21,21	0
57	MG	DA	3282	1/1	0.97	0.11	36,36,36,36	0
57	MG	BA	3101	1/1	0.97	0.12	29,29,29,29	0
57	MG	DA	3140	1/1	0.97	0.09	38,38,38,38	0
57	MG	DA	3008	1/1	0.97	0.07	26,26,26,26	0
57	MG	BA	3562	1/1	0.97	0.14	47,47,47,47	0
57	MG	DA	3143	1/1	0.97	0.13	47,47,47,47	0
57	MG	BA	3384	1/1	0.97	0.15	19,19,19,19	0
57	MG	DA	3145	1/1	0.97	0.13	38,38,38,38	0
57	MG	BN	3005	1/1	0.97	0.06	31,31,31,31	0
57	MG	DA	3014	1/1	0.97	0.07	45,45,45,45	0
57	MG	DA	3016	1/1	0.97	0.07	34,34,34,34	0
57	MG	DA	3464	1/1	0.97	0.07	51,51,51,51	0
57	MG	BA	3663	1/1	0.97	0.08	36,36,36,36	0
57	MG	DA	3466	1/1	0.97	0.12	41,41,41,41	0
57	MG	DA	3294	1/1	0.97	0.11	18,18,18,18	0
57	MG	BA	3182	1/1	0.97	0.14	36,36,36,36	0
57	MG	AA	3147	1/1	0.97	0.06	51,51,51,51	0
57	MG	DA	3470	1/1	0.97	0.06	34,34,34,34	0
57	MG	DA	3298	1/1	0.97	0.09	35,35,35,35	0
57	MG	DA	3299	1/1	0.97	0.05	32,32,32,32	0
57	MG	DA	3153	1/1	0.97	0.10	34,34,34,34	0
57	MG	DA	3154	1/1	0.97	0.11	40,40,40,40	0
57	MG	DA	3020	1/1	0.97	0.09	32,32,32,32	0
57	MG	BP	3003	1/1	0.97	0.08	42,42,42,42	0
57	MG	BA	3184	1/1	0.97	0.10	42,42,42,42	0
57	MG	BA	3137	1/1	0.97	0.06	57,57,57,57	0
57	MG	DA	3024	1/1	0.97	0.10	29,29,29,29	0
57	MG	DA	3480	1/1	0.97	0.06	28,28,28,28	0
57	MG	BA	3469	1/1	0.97	0.13	42,42,42,42	0
57	MG	DA	3482	1/1	0.97	0.14	31,31,31,31	0
57	MG	AA	3138	1/1	0.97	0.13	40,40,40,40	0
57	MG	BA	3670	1/1	0.97	0.07	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3029	1/1	0.97	0.08	44,44,44,44	0
57	MG	BA	3013	1/1	0.97	0.09	36,36,36,36	0
57	MG	BA	3190	1/1	0.97	0.15	24,24,24,24	0
57	MG	BA	3141	1/1	0.97	0.09	38,38,38,38	0
57	MG	BA	3192	1/1	0.97	0.04	35,35,35,35	0
57	MG	BA	3395	1/1	0.97	0.11	19,19,19,19	0
57	MG	BU	204	1/1	0.97	0.15	38,38,38,38	0
57	MG	BU	205	1/1	0.97	0.07	32,32,32,32	0
57	MG	BA	3481	1/1	0.97	0.16	35,35,35,35	0
57	MG	BA	3040	1/1	0.97	0.13	28,28,28,28	0
57	MG	DA	3041	1/1	0.97	0.06	36,36,36,36	0
57	MG	DA	3176	1/1	0.97	0.12	42,42,42,42	0
57	MG	AA	3091	1/1	0.97	0.15	35,35,35,35	0
57	MG	DA	3325	1/1	0.97	0.07	43,43,43,43	0
57	MG	BA	3249	1/1	0.97	0.19	44,44,44,44	0
57	MG	DA	3044	1/1	0.97	0.09	38,38,38,38	0
57	MG	BA	3485	1/1	0.97	0.08	40,40,40,40	0
57	MG	BA	3251	1/1	0.97	0.26	48,48,48,48	0
57	MG	BA	3016	1/1	0.97	0.07	35,35,35,35	0
58	SF4	AD	302	8/8	0.97	0.06	59,71,78,78	0
58	SF4	CD	501	8/8	0.97	0.05	59,71,83,91	0
57	MG	BA	3255	1/1	0.97	0.05	37,37,37,37	0
57	MG	BA	3490	1/1	0.97	0.12	17,17,17,17	0
57	MG	DA	3333	1/1	0.97	0.09	41,41,41,41	0
59	ZN	D9	501	1/1	0.97	0.05	75,75,75,75	0
57	MG	BA	3491	1/1	0.97	0.08	33,33,33,33	0
57	MG	BY	201	1/1	0.97	0.08	51,51,51,51	0
57	MG	BA	3563	1/1	0.98	0.04	38,38,38,38	0
57	MG	BA	3248	1/1	0.98	0.15	32,32,32,32	0
57	MG	BA	3157	1/1	0.98	0.04	42,42,42,42	0
57	MG	BA	3250	1/1	0.98	0.06	47,47,47,47	0
57	MG	BA	3473	1/1	0.98	0.07	31,31,31,31	0
57	MG	DA	3150	1/1	0.98	0.27	41,41,41,41	0
57	MG	AX	3004	1/1	0.98	0.07	45,45,45,45	0
57	MG	BU	203	1/1	0.98	0.13	35,35,35,35	0
57	MG	BA	3393	1/1	0.98	0.07	30,30,30,30	0
57	MG	DA	3599	1/1	0.98	0.13	36,36,36,36	0
57	MG	BB	3010	1/1	0.98	0.09	28,28,28,28	0
57	MG	BA	3479	1/1	0.98	0.07	22,22,22,22	0
57	MG	DA	3004	1/1	0.98	0.16	32,32,32,32	0
57	MG	BU	207	1/1	0.98	0.07	23,23,23,23	0
57	MG	DA	3507	1/1	0.98	0.05	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3283	1/1	0.98	0.18	22,22,22,22	0
57	MG	BV	201	1/1	0.98	0.10	33,33,33,33	0
57	MG	BA	3252	1/1	0.98	0.19	30,30,30,30	0
57	MG	BA	3528	1/1	0.98	0.10	37,37,37,37	0
57	MG	BV	204	1/1	0.98	0.04	36,36,36,36	0
57	MG	DA	3012	1/1	0.98	0.06	42,42,42,42	0
57	MG	BA	3253	1/1	0.98	0.21	28,28,28,28	0
57	MG	BA	3057	1/1	0.98	0.10	21,21,21,21	0
57	MG	DA	3015	1/1	0.98	0.24	41,41,41,41	0
57	MG	DA	3167	1/1	0.98	0.08	26,26,26,26	0
57	MG	BA	3226	1/1	0.98	0.24	36,36,36,36	0
57	MG	BA	3227	1/1	0.98	0.16	39,39,39,39	0
57	MG	BA	3160	1/1	0.98	0.10	23,23,23,23	0
57	MG	BA	3580	1/1	0.98	0.17	13,13,13,13	0
57	MG	DA	3523	1/1	0.98	0.07	45,45,45,45	0
57	MG	DA	3620	1/1	0.98	0.13	47,47,47,47	0
57	MG	DA	3341	1/1	0.98	0.06	32,32,32,32	0
57	MG	DA	3525	1/1	0.98	0.04	40,40,40,40	0
57	MG	AA	3052	1/1	0.98	0.12	53,53,53,53	0
57	MG	DA	3094	1/1	0.98	0.13	38,38,38,38	0
57	MG	BA	3326	1/1	0.98	0.06	40,40,40,40	0
57	MG	BA	3046	1/1	0.98	0.05	30,30,30,30	0
57	MG	BA	3405	1/1	0.98	0.09	31,31,31,31	0
57	MG	BA	3687	1/1	0.98	0.11	30,30,30,30	0
57	MG	DA	3348	1/1	0.98	0.08	33,33,33,33	0
57	MG	DA	3099	1/1	0.98	0.06	40,40,40,40	0
57	MG	DA	3025	1/1	0.98	0.15	35,35,35,35	0
57	MG	BD	307	1/1	0.98	0.10	40,40,40,40	0
57	MG	BA	3231	1/1	0.98	0.19	42,42,42,42	0
57	MG	DA	3183	1/1	0.98	0.10	31,31,31,31	0
57	MG	DA	3264	1/1	0.98	0.04	33,33,33,33	0
57	MG	B2	3001	1/1	0.98	0.06	43,43,43,43	0
57	MG	BA	3586	1/1	0.98	0.04	33,33,33,33	0
57	MG	DA	3541	1/1	0.98	0.07	40,40,40,40	0
57	MG	DA	3030	1/1	0.98	0.18	32,32,32,32	0
57	MG	BA	3037	1/1	0.98	0.08	38,38,38,38	0
57	MG	DA	3451	1/1	0.98	0.14	39,39,39,39	0
57	MG	BA	3330	1/1	0.98	0.08	14,14,14,14	0
57	MG	DA	3033	1/1	0.98	0.11	46,46,46,46	0
57	MG	AA	3181	1/1	0.98	0.07	82,82,82,82	0
57	MG	BA	3591	1/1	0.98	0.04	42,42,42,42	0
57	MG	BA	3593	1/1	0.98	0.07	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3275	1/1	0.98	0.10	36,36,36,36	0
57	MG	BA	3695	1/1	0.98	0.10	19,19,19,19	0
57	MG	BA	3187	1/1	0.98	0.06	35,35,35,35	0
57	MG	BE	3007	1/1	0.98	0.09	31,31,31,31	0
57	MG	BA	3039	1/1	0.98	0.04	27,27,27,27	0
57	MG	BA	3699	1/1	0.98	0.04	33,33,33,33	0
57	MG	BA	3646	1/1	0.98	0.06	43,43,43,43	0
57	MG	DA	3557	1/1	0.98	0.07	54,54,54,54	0
57	MG	BA	3145	1/1	0.98	0.14	41,41,41,41	0
57	MG	BA	3014	1/1	0.98	0.15	46,46,46,46	0
57	MG	CA	3072	1/1	0.98	0.31	38,38,38,38	0
57	MG	BA	3128	1/1	0.98	0.07	33,33,33,33	0
57	MG	BA	3096	1/1	0.98	0.11	39,39,39,39	0
57	MG	BA	3051	1/1	0.98	0.10	36,36,36,36	0
57	MG	BA	3706	1/1	0.98	0.19	27,27,27,27	0
57	MG	BA	3065	1/1	0.98	0.18	43,43,43,43	0
57	MG	BA	3708	1/1	0.98	0.13	38,38,38,38	0
57	MG	DA	3127	1/1	0.98	0.22	40,40,40,40	0
57	MG	BA	3341	1/1	0.98	0.04	52,52,52,52	0
57	MG	BA	3041	1/1	0.98	0.10	39,39,39,39	0
57	MG	BA	3053	1/1	0.98	0.06	33,33,33,33	0
57	MG	DA	3131	1/1	0.98	0.12	34,34,34,34	0
57	MG	BA	3305	1/1	0.98	0.10	45,45,45,45	0
57	MG	BA	3554	1/1	0.98	0.05	44,44,44,44	0
57	MG	DA	3057	1/1	0.98	0.13	22,22,22,22	0
57	MG	BA	3346	1/1	0.98	0.12	29,29,29,29	0
57	MG	AA	3149	1/1	0.98	0.08	48,48,48,48	0
57	MG	DA	3302	1/1	0.98	0.11	30,30,30,30	0
57	MG	D5	101	1/1	0.98	0.09	42,42,42,42	0
57	MG	BA	3557	1/1	0.98	0.10	35,35,35,35	0
57	MG	BA	3154	1/1	0.98	0.12	36,36,36,36	0
57	MG	DA	3395	1/1	0.98	0.03	31,31,31,31	0
57	MG	BP	3002	1/1	0.98	0.16	32,32,32,32	0
59	ZN	AN	501	1/1	0.98	0.05	71,71,71,71	0
59	ZN	B4	501	1/1	0.98	0.04	94,94,94,94	0
57	MG	BA	3718	1/1	0.98	0.05	36,36,36,36	0
57	MG	BA	3276	1/1	0.98	0.13	19,19,19,19	0
57	MG	BA	3427	1/1	0.98	0.08	23,23,23,23	0
57	MG	DA	3403	1/1	0.98	0.09	31,31,31,31	0
57	MG	BA	3085	1/1	0.98	0.07	18,18,18,18	0
57	MG	BA	3004	1/1	0.98	0.06	26,26,26,26	0
57	MG	BA	3475	1/1	0.99	0.04	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3175	1/1	0.99	0.08	42,42,42,42	0
57	MG	BA	3572	1/1	0.99	0.09	27,27,27,27	0
57	MG	BA	3319	1/1	0.99	0.06	37,37,37,37	0
57	MG	BA	3477	1/1	0.99	0.04	19,19,19,19	0
57	MG	BA	3332	1/1	0.99	0.08	29,29,29,29	0
57	MG	BA	3081	1/1	0.99	0.07	26,26,26,26	0
57	MG	BA	3503	1/1	0.99	0.05	50,50,50,50	0
57	MG	BA	3186	1/1	0.99	0.14	42,42,42,42	0
57	MG	CA	3108	1/1	0.99	0.06	51,51,51,51	0
57	MG	BA	3505	1/1	0.99	0.09	16,16,16,16	0
57	MG	DA	3009	1/1	0.99	0.06	39,39,39,39	0
57	MG	DA	3295	1/1	0.99	0.05	58,58,58,58	0
57	MG	BA	3363	1/1	0.99	0.05	31,31,31,31	0
57	MG	BA	3444	1/1	0.99	0.09	32,32,32,32	0
57	MG	AA	3182	1/1	0.99	0.04	40,40,40,40	0
57	MG	DA	3516	1/1	0.99	0.03	43,43,43,43	0
57	MG	BA	3311	1/1	0.99	0.05	42,42,42,42	0
57	MG	DA	3339	1/1	0.99	0.05	23,23,23,23	0
57	MG	BA	3637	1/1	0.99	0.07	40,40,40,40	0
57	MG	BA	3077	1/1	0.99	0.09	33,33,33,33	0
57	MG	BA	3140	1/1	0.99	0.16	26,26,26,26	0
57	MG	BP	3004	1/1	0.99	0.06	41,41,41,41	0
57	MG	BA	3488	1/1	0.99	0.03	34,34,34,34	0
57	MG	BA	3009	1/1	0.99	0.03	34,34,34,34	0
57	MG	DA	3306	1/1	0.99	0.06	31,31,31,31	0
57	MG	BA	3588	1/1	0.99	0.06	19,19,19,19	0
57	MG	BA	3697	1/1	0.99	0.06	23,23,23,23	0
57	MG	AA	3159	1/1	0.99	0.04	31,31,31,31	0
57	MG	CA	3156	1/1	0.99	0.06	57,57,57,57	0
57	MG	DA	3272	1/1	0.99	0.04	29,29,29,29	0
57	MG	BE	3005	1/1	0.99	0.06	15,15,15,15	0
57	MG	BA	3400	1/1	0.99	0.09	33,33,33,33	0
57	MG	B7	101	1/1	0.99	0.07	48,48,48,48	0
57	MG	BA	3086	1/1	0.99	0.08	15,15,15,15	0
57	MG	DA	3399	1/1	0.99	0.06	26,26,26,26	0
57	MG	DA	3400	1/1	0.99	0.03	33,33,33,33	0
57	MG	DA	3401	1/1	0.99	0.03	36,36,36,36	0
57	MG	BA	3493	1/1	0.99	0.07	39,39,39,39	0
57	MG	BA	3265	1/1	0.99	0.05	30,30,30,30	0
59	ZN	BY	202	1/1	0.99	0.04	70,70,70,70	0
57	MG	BA	3343	1/1	0.99	0.07	18,18,18,18	0
59	ZN	B5	102	1/1	0.99	0.03	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
59	ZN	B6	501	1/1	0.99	0.03	43,43,43,43	0
57	MG	DA	3588	1/1	0.99	0.04	21,21,21,21	0
57	MG	BA	3420	1/1	0.99	0.04	23,23,23,23	0
59	ZN	DY	501	1/1	0.99	0.04	88,88,88,88	0
57	MG	DA	3361	1/1	0.99	0.06	32,32,32,32	0
59	ZN	D5	102	1/1	0.99	0.06	58,58,58,58	0
59	ZN	D6	501	1/1	0.99	0.06	64,64,64,64	0
57	MG	AA	3161	1/1	0.99	0.07	28,28,28,28	0
57	MG	DA	3363	1/1	0.99	0.10	35,35,35,35	0
57	MG	BB	3014	1/1	0.99	0.02	41,41,41,41	0
57	MG	BA	3512	1/1	1.00	0.04	32,32,32,32	0
57	MG	BA	3478	1/1	1.00	0.05	22,22,22,22	0
57	MG	DA	3570	1/1	1.00	0.04	28,28,28,28	0
57	MG	DA	3340	1/1	1.00	0.07	38,38,38,38	0
57	MG	BA	3592	1/1	1.00	0.05	14,14,14,14	0
57	MG	BA	3309	1/1	1.00	0.05	31,31,31,31	0

6.5 Other polymers (i)

There are no such residues in this entry.