Full wwPDB X-ray Structure Validation Report (i)

Mar 5, 2026 – 12:25 PM UTC

PDB ID	:	1VY6 / pdb_00001vy6
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in the pre-attack state of peptide bond formation containing short substrate-mimic Cytidine-Puromycin in the A site and acylated tRNA in the P site.
Authors	:	Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on	:	2014-05-13
Resolution	:	2.90 Å(reported)

This is a Full wwPDB 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 (i) 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 (i)) were used in the production of this report:

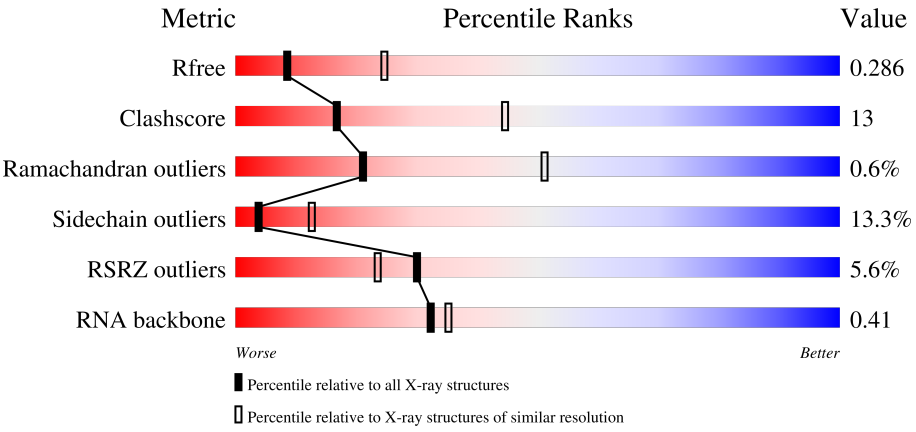
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 2.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)
RNA backbone	3983	1120 (3.10-2.70)

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	3% 42% 42% 14% ·
1	CA	1521	6% 40% 45% 14% ·
2	AB	256	11% 39% 39% 10% · 10%
2	CB	256	20% 35% 45% 10% · 10%

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Mol	Chain	Length	Quality of chain
3	AC	239	8% 49% 34% 14%
3	CC	239	13% 49% 31% 7% 14%
4	AD	209	11% 63% 29% 7%
4	CD	209	11% 57% 35% 7%
5	AE	162	7% 57% 29% 6% 9%
5	CE	162	8% 47% 37% 7% 9%
6	AF	101	6% 59% 38%
6	CF	101	2% 61% 33% 5%
7	AG	156	10% 66% 28% 5%
7	CG	156	13% 64% 31%
8	AH	138	2% 64% 30% 6%
8	CH	138	7% 60% 35%
9	AI	128	19% 51% 41% 7%
9	CI	128	50% 44% 47% 9%
10	AJ	105	14% 54% 35% 8%
10	CJ	105	47% 50% 37% 5% 9%
11	AK	129	5% 59% 26% 12%
11	CK	129	2% 57% 29% 12%
12	AL	132	5% 63% 23% 6% 8%
12	CL	132	4% 61% 29% 8%
13	AM	126	18% 52% 37% 6%
13	CM	126	28% 50% 37% 10%
14	AN	61	18% 51% 41% 7%
14	CN	61	46% 41% 41% 16%
15	AO	89	8% 60% 36%

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Mol	Chain	Length	Quality of chain
15	CO	89	7% 54% 42%
16	AP	88	18% 52% 28% 13% 7%
16	CP	88	18% 49% 36% 8% 7%
17	AQ	105	7% 68% 22% 5% 6%
17	CQ	105	2% 59% 33% 6%
18	AR	88	5% 49% 25% 23%
18	CR	88	44% 31% 23%
19	AS	93	11% 53% 30% 5% 11%
19	CS	93	23% 30% 53% 5% 11%
20	AT	106	14% 53% 30% 8% 9%
20	CT	106	8% 54% 30% 6% 9%
21	AU	27	19% 44% 37% 15%
21	CU	27	26% 37% 44% 15%
22	AV	24	25% 17% 33% 46%
22	CV	24	29% 21% 25% 50%
23	AW	2	50% 50%
23	CW	2	50% 50%
24	AX	77	3% 38% 35% 26%
24	CX	77	36% 38% 25%
25	BA	2915	3% 54% 34% 9%
25	DA	2915	2% 44% 41% 11%
26	BB	121	60% 32% 7%
26	DB	121	4% 29% 48% 22%
27	BD	276	2% 72% 22% 5%
27	DD	276	62% 34%

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Mol	Chain	Length	Quality of chain
28	BE	206	64% 29% 6%
28	DE	206	63% 27% 8%
29	BF	210	68% 25%
29	DF	210	53% 38% 5%
30	BG	182	14% 64% 25% 9%
30	DG	182	20% 46% 42% 10%
31	BH	180	3% 66% 28%
31	DH	180	4% 58% 32% 6%
32	BI	148	2% 61% 28% 10%
32	DI	148	17% 61% 28% 9%
33	BN	140	3% 69% 26% 5%
33	DN	140	60% 34% 6%
34	BO	122	64% 34%
34	DO	122	62% 34%
35	BP	150	67% 26% 6%
35	DP	150	56% 35% 7%
36	BQ	141	63% 35%
36	DQ	141	2% 57% 35% 8%
37	BR	118	2% 61% 30% 9%
37	DR	118	64% 30% 6%
38	BS	112	66% 28%
38	DS	112	13% 47% 42% 9%
39	BT	146	56% 30% 10%
39	DT	146	55% 26% 8% 10%
40	BU	118	76% 19%

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Mol	Chain	Length	Quality of chain
40	DU	118	3% 62% 31% 5%
41	BV	101	71% 21% 8%
41	DV	101	61% 33% 6%
42	BW	113	77% 18%
42	DW	113	69% 26%
43	BX	96	72% 26%
43	DX	96	5% 71% 27%
44	BY	110	58% 36%
44	DY	110	7% 65% 29%
45	BZ	206	56% 23% 17%
45	DZ	206	5% 41% 38% 5% 16%
46	B0	85	65% 27% 6%
46	D0	85	9% 61% 28% 8%
47	B1	98	3% 81% 14%
47	D1	98	60% 34% 5%
48	B2	72	64% 32%
48	D2	72	58% 33% 6%
49	B3	60	65% 28% 5%
49	D3	60	3% 60% 37%
50	B4	71	11% 48% 30% 18%
50	D4	71	25% 39% 44% 14%
51	B5	60	65% 30%
51	D5	60	77% 22%
52	B6	54	69% 24% 6%
52	D6	54	69% 24% 6%

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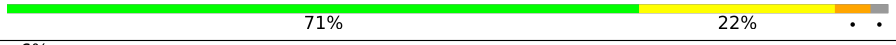
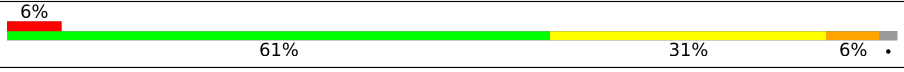
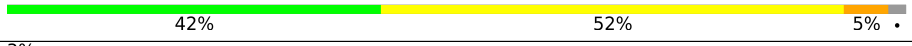
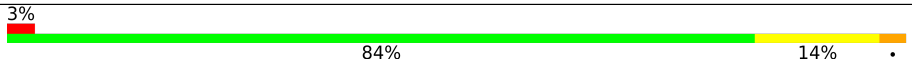
Mol	Chain	Length	Quality of chain
53	B7	49	
53	D7	49	
54	B8	65	
54	D8	65	
55	B9	37	
55	D9	37	

2 Entry composition (i)

There are 60 unique types of molecules in this entry. The entry contains 289646 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
			1670	1047	332	284	7			

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

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

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

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

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

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

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

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

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

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

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

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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	CJ	96	Total	C	N	O	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	12	Total	C	N	O	P	0	0	0
			252	115	46	80	11			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2819	Total	C	N	O	P	0	0	0
			60729	27026	11370	19515	2818			
25	DA	2800	Total	C	N	O	P	0	0	0
			60311	26840	11284	19388	2799			

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 39 is a protein called 50S ribosomal protein L19.

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

- Molecule 40 is a protein called 50S ribosomal protein L20.

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

- Molecule 41 is a protein called 50S ribosomal protein L21.

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B4	69	Total	C	N	O	S	0	0	0
			552	349	99	99	5			
50	D4	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 51 is a protein called 50S ribosomal protein L32.

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

- Molecule 52 is a protein called 50S ribosomal protein L33.

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

- Molecule 53 is a protein called 50S ribosomal protein L34.

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

- Molecule 54 is a protein called 50S ribosomal protein L35.

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

- Molecule 55 is a protein called 50S ribosomal protein L36.

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

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AA	187	Total	Mg	0	0
			187	187		
56	AD	1	Total	Mg	0	0
			1	1		
56	AE	2	Total	Mg	0	0
			2	2		
56	AF	1	Total	Mg	0	0
			1	1		
56	AK	1	Total	Mg	0	0
			1	1		
56	AL	1	Total	Mg	0	0
			1	1		
56	AM	1	Total	Mg	0	0
			1	1		
56	AN	1	Total	Mg	0	0
			1	1		
56	AX	7	Total	Mg	0	0
			7	7		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	BA	675	Total Mg 675 675	0	0
56	BB	18	Total Mg 18 18	0	0
56	BD	8	Total Mg 8 8	0	0
56	BE	6	Total Mg 6 6	0	0
56	BF	5	Total Mg 5 5	0	0
56	BG	3	Total Mg 3 3	0	0
56	BH	1	Total Mg 1 1	0	0
56	BN	2	Total Mg 2 2	0	0
56	BO	1	Total Mg 1 1	0	0
56	BP	4	Total Mg 4 4	0	0
56	BQ	3	Total Mg 3 3	0	0
56	BR	3	Total Mg 3 3	0	0
56	BU	5	Total Mg 5 5	0	0
56	BV	3	Total Mg 3 3	0	0
56	BW	4	Total Mg 4 4	0	0
56	BX	3	Total Mg 3 3	0	0
56	BY	2	Total Mg 2 2	0	0
56	BZ	1	Total Mg 1 1	0	0
56	B0	5	Total Mg 5 5	0	0
56	B3	2	Total Mg 2 2	0	0
56	B4	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	B5	2	Total Mg 2 2	0	0
56	B7	4	Total Mg 4 4	0	0
56	B8	1	Total Mg 1 1	0	0
56	B9	1	Total Mg 1 1	0	0
56	CA	154	Total Mg 154 154	0	0
56	CE	2	Total Mg 2 2	0	0
56	CF	1	Total Mg 1 1	0	0
56	CJ	1	Total Mg 1 1	0	0
56	CK	1	Total Mg 1 1	0	0
56	CT	1	Total Mg 1 1	0	0
56	CX	1	Total Mg 1 1	0	0
56	DA	595	Total Mg 595 595	0	0
56	DB	12	Total Mg 12 12	0	0
56	DD	2	Total Mg 2 2	0	0
56	DE	5	Total Mg 5 5	0	0
56	DF	3	Total Mg 3 3	0	0
56	DG	1	Total Mg 1 1	0	0
56	DN	1	Total Mg 1 1	0	0
56	DP	1	Total Mg 1 1	0	0
56	DQ	3	Total Mg 3 3	0	0
56	DR	2	Total Mg 2 2	0	0

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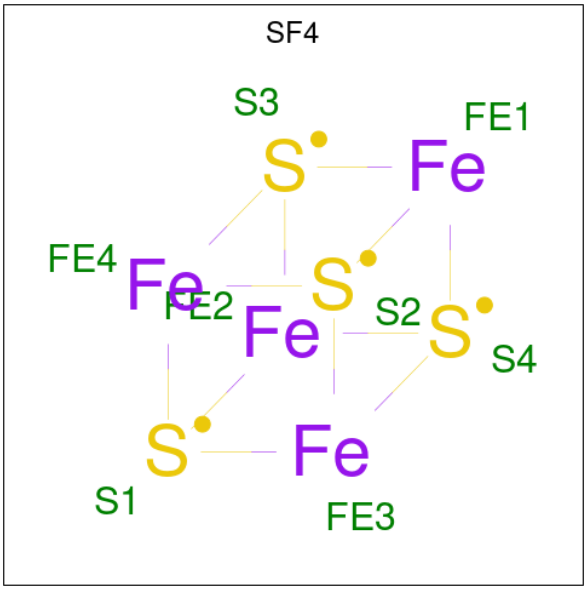
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	DT	1	Total Mg 1 1	0	0
56	DU	1	Total Mg 1 1	0	0
56	DV	2	Total Mg 2 2	0	0
56	DW	2	Total Mg 2 2	0	0
56	DY	1	Total Mg 1 1	0	0
56	D0	1	Total Mg 1 1	0	0
56	D3	1	Total Mg 1 1	0	0
56	D5	1	Total Mg 1 1	0	0
56	D7	1	Total Mg 1 1	0	0
56	D8	2	Total Mg 2 2	0	0

- Molecule 57 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



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

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

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 59 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 60 is water.

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

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

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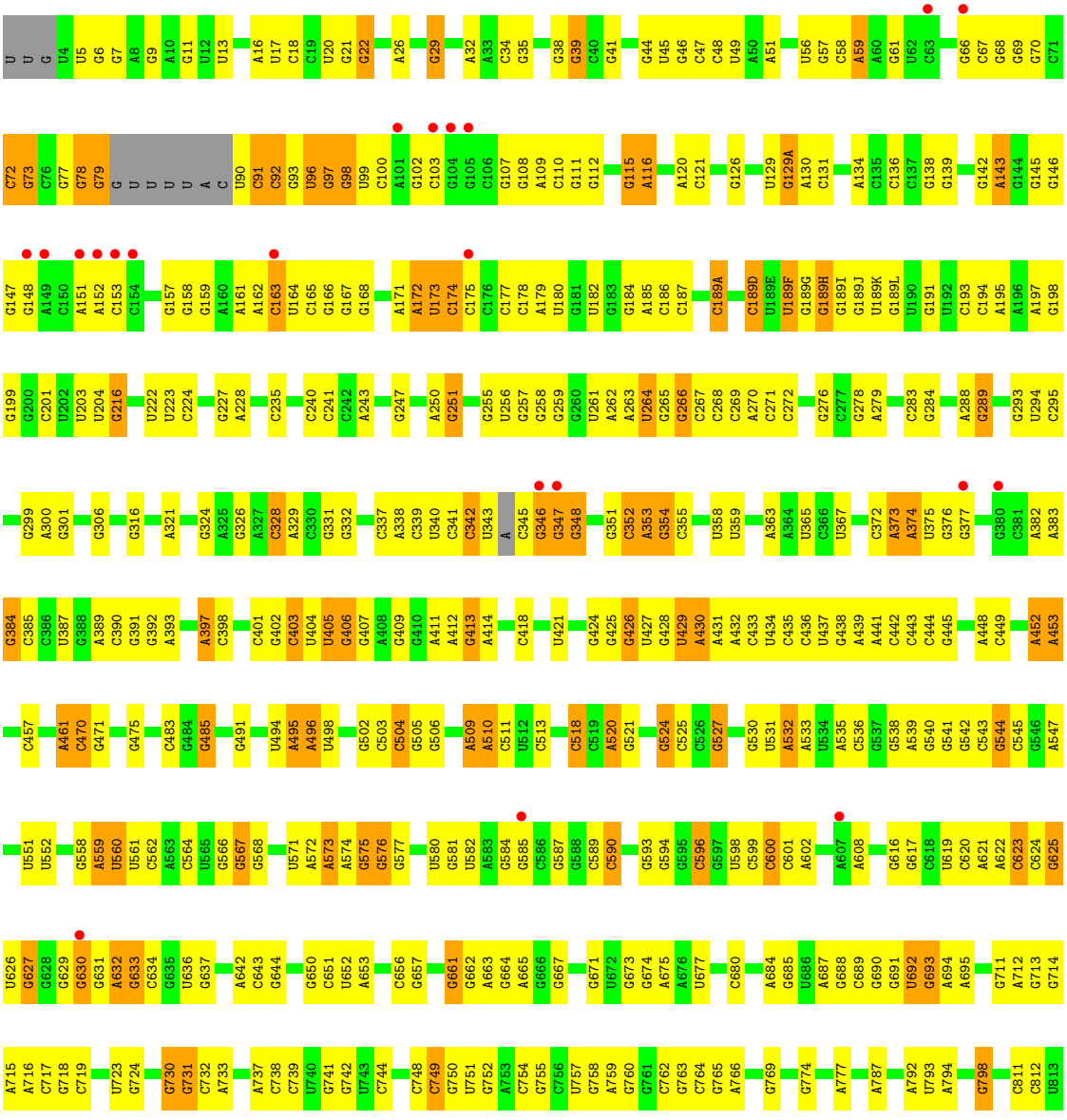
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	DF	6	Total O 6 6	0	0
60	DO	1	Total O 1 1	0	0
60	DP	6	Total O 6 6	0	0
60	DU	3	Total O 3 3	0	0
60	DV	1	Total O 1 1	0	0
60	DW	1	Total O 1 1	0	0
60	DX	3	Total O 3 3	0	0
60	D0	5	Total O 5 5	0	0
60	D1	1	Total O 1 1	0	0
60	D3	1	Total O 1 1	0	0
60	D8	3	Total O 3 3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

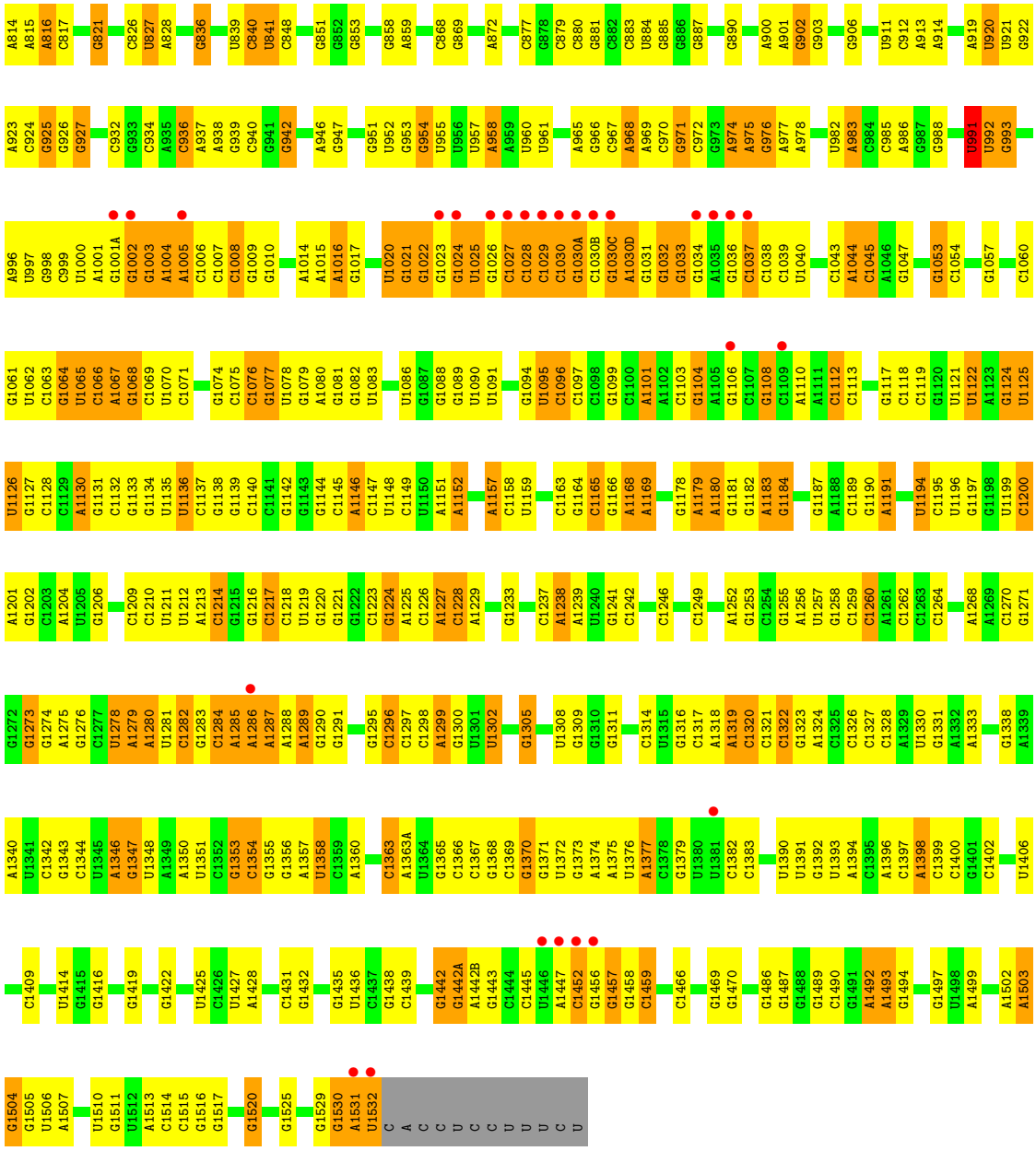
3 Residue-property plots (i)

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

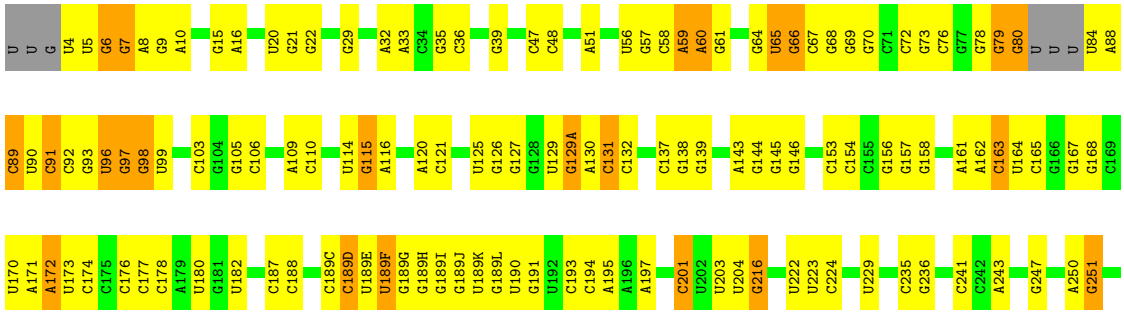
Chain AA:

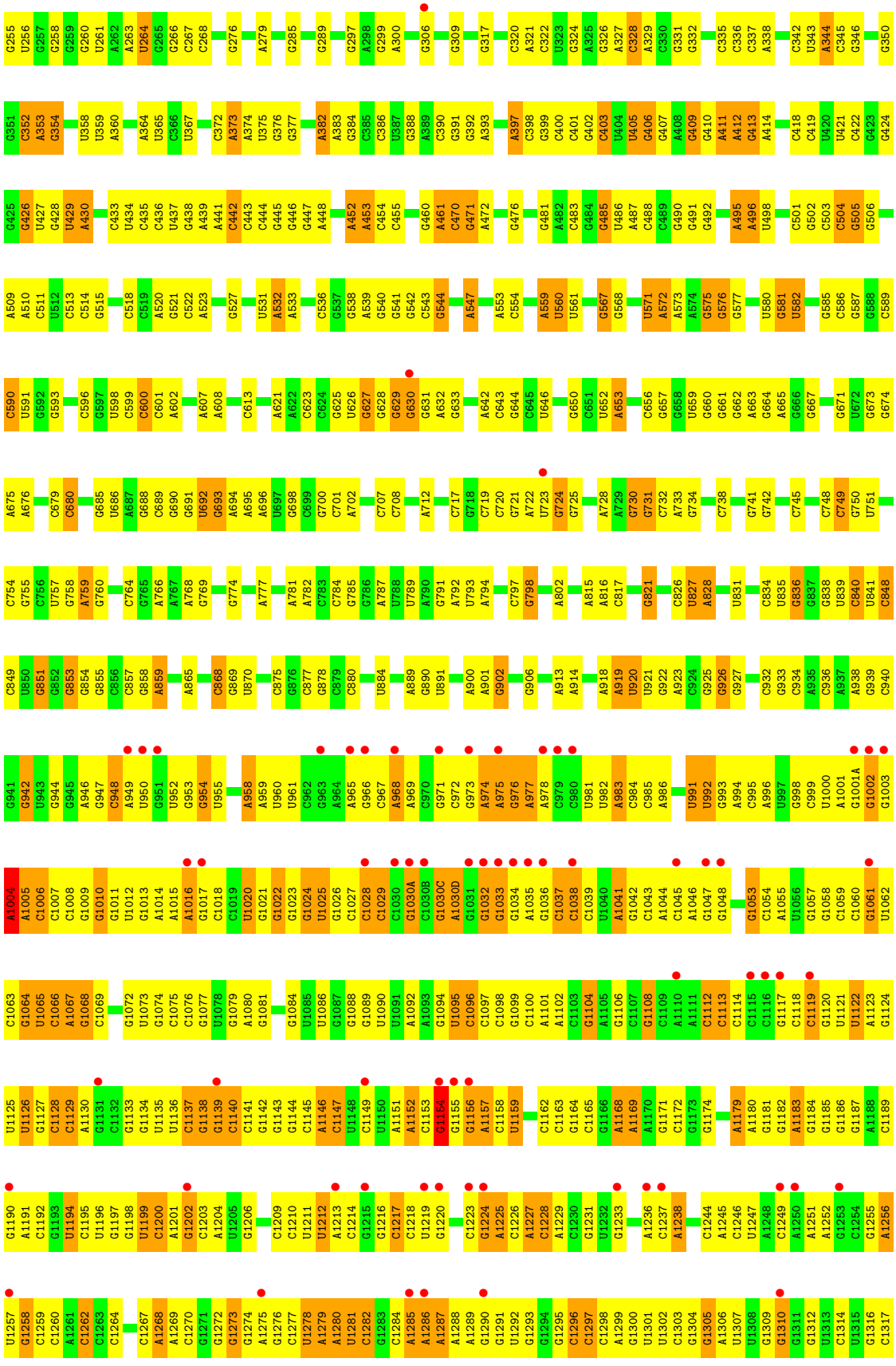


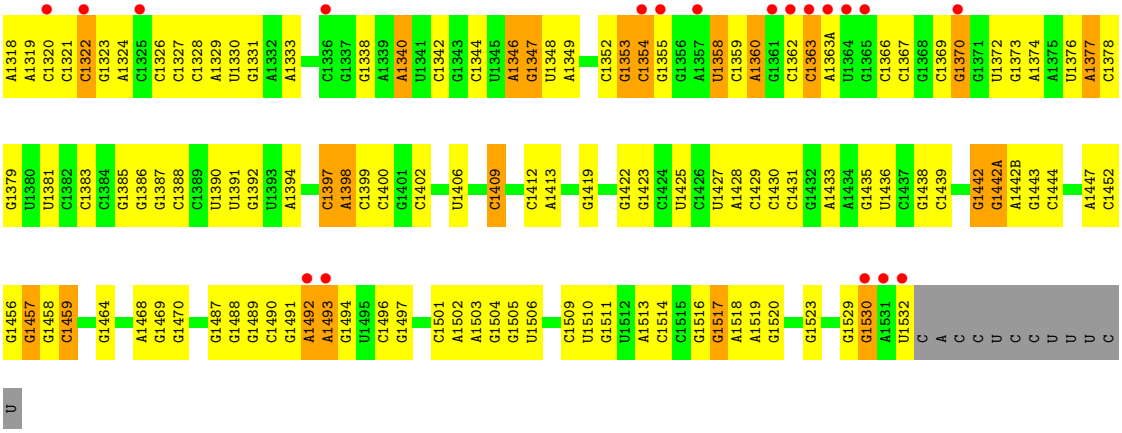


• Molecule 1: 16S Ribosomal RNA

Chain CA:

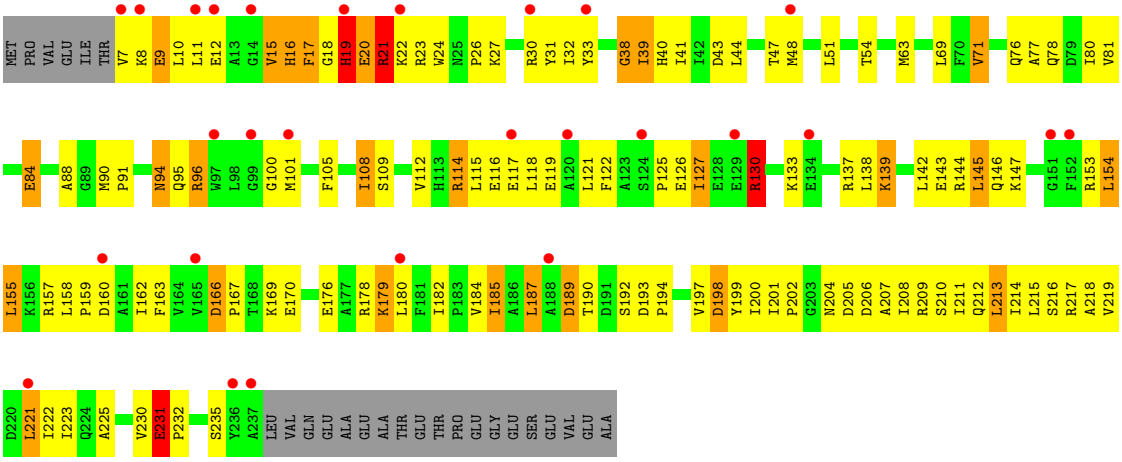






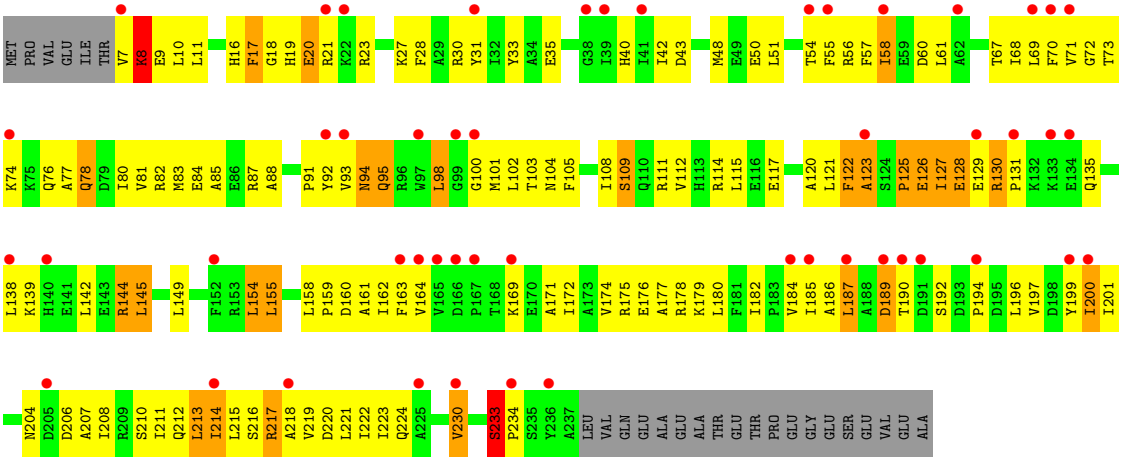
• Molecule 2: 30S ribosomal protein S2

Chain AB:



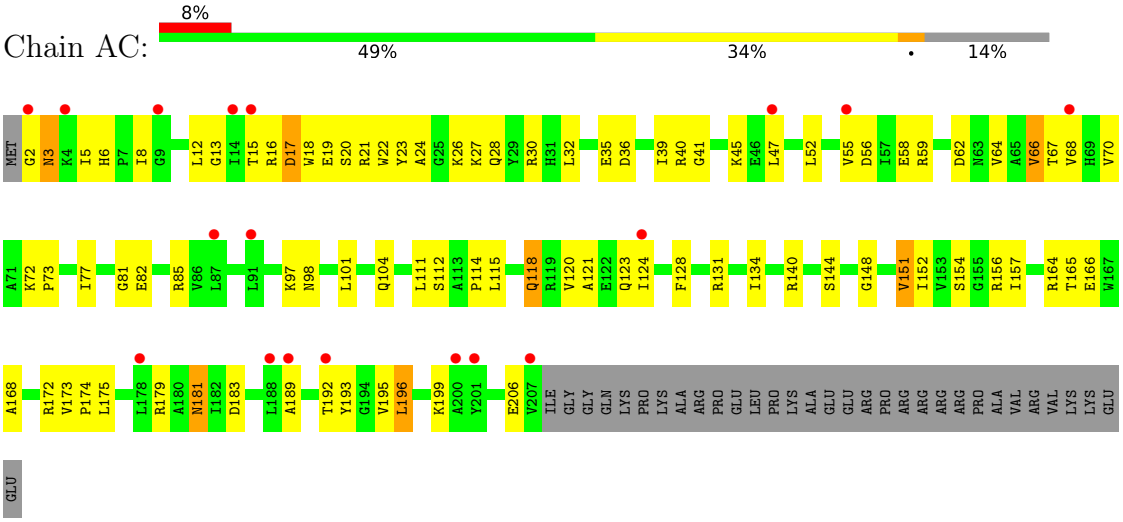
• Molecule 2: 30S ribosomal protein S2

Chain CB:



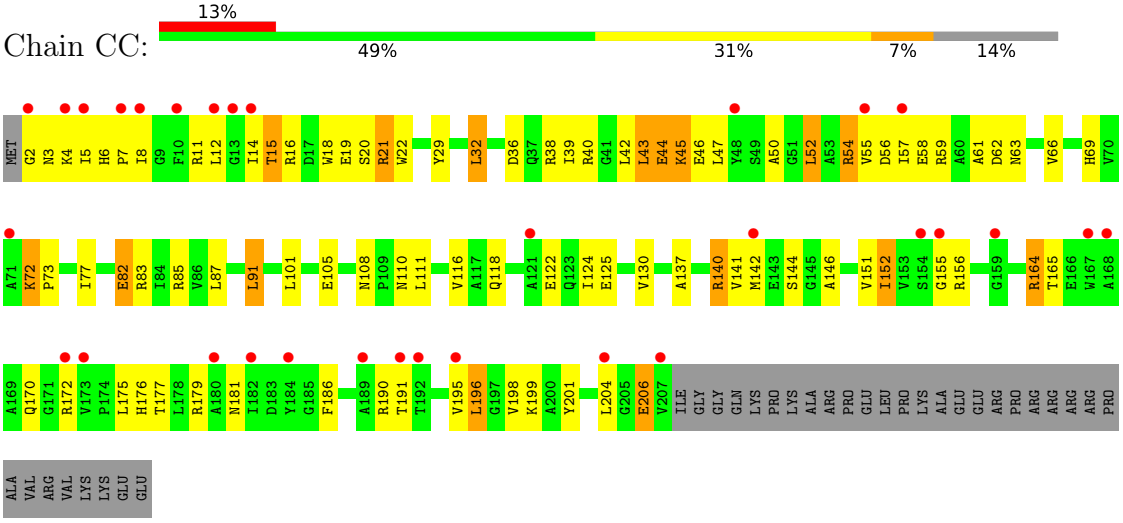
• Molecule 3: 30S ribosomal protein S3

Chain AC:



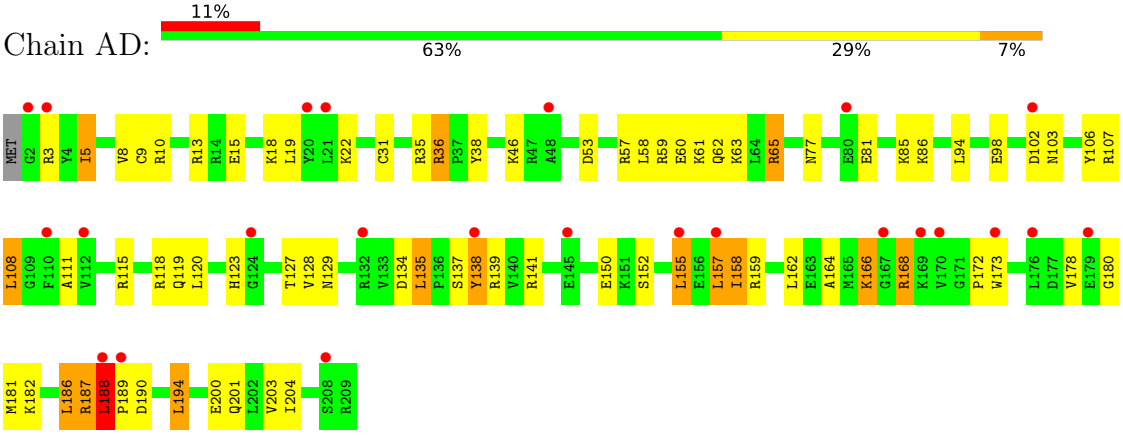
• Molecule 3: 30S ribosomal protein S3

Chain CC:



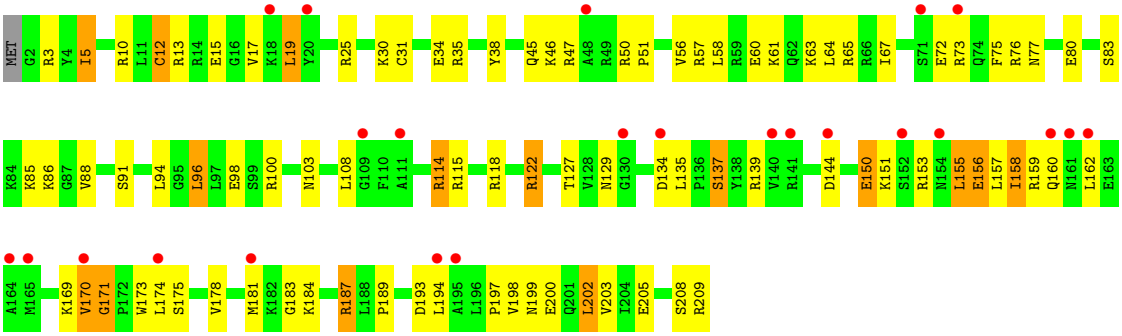
• Molecule 4: 30S ribosomal protein S4

Chain AD:

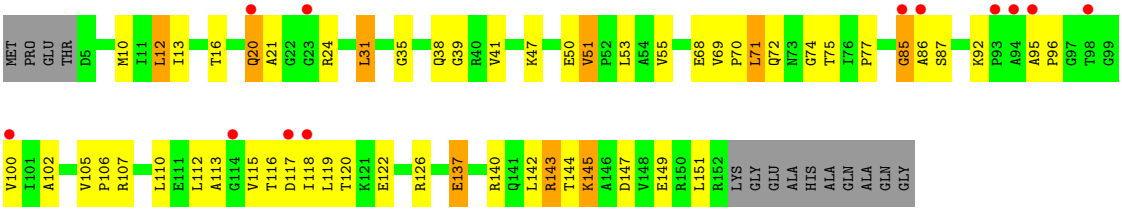


• Molecule 4: 30S ribosomal protein S4

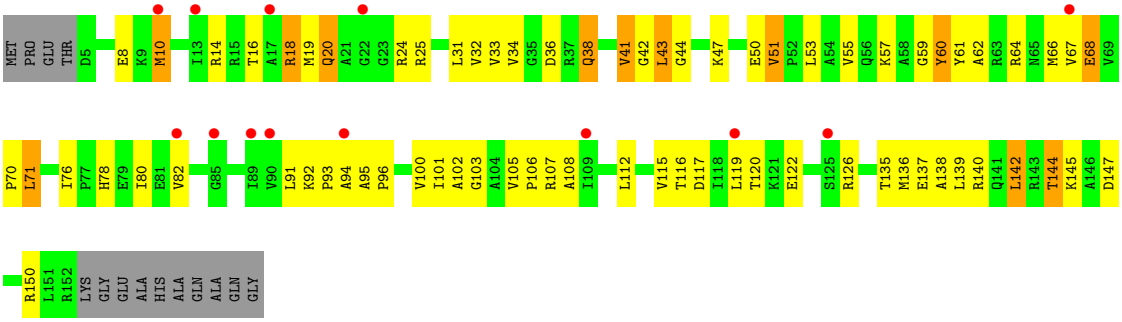
Chain CD:



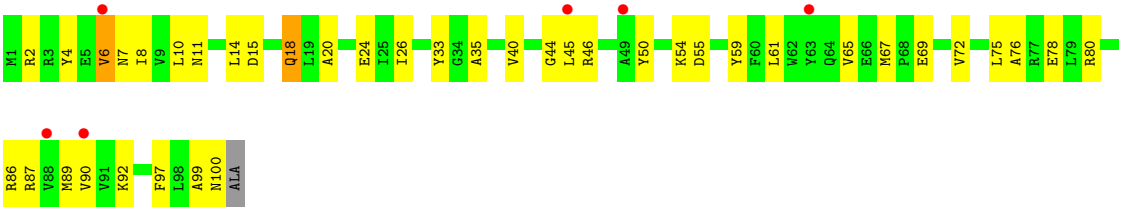
• Molecule 5: 30S ribosomal protein S5



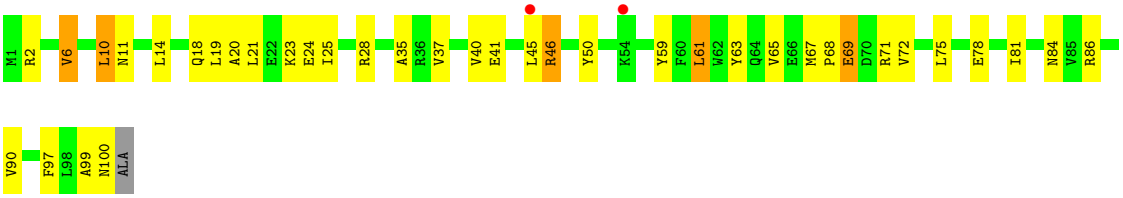
• Molecule 5: 30S ribosomal protein S5



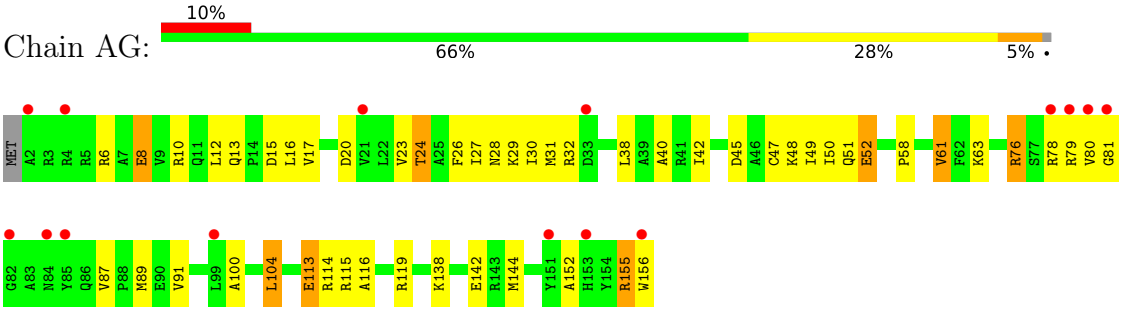
• Molecule 6: 30S ribosomal protein S6



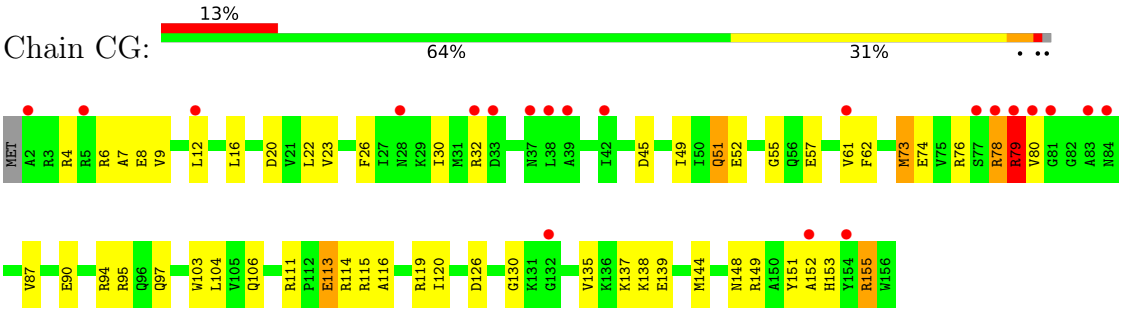
• Molecule 6: 30S ribosomal protein S6



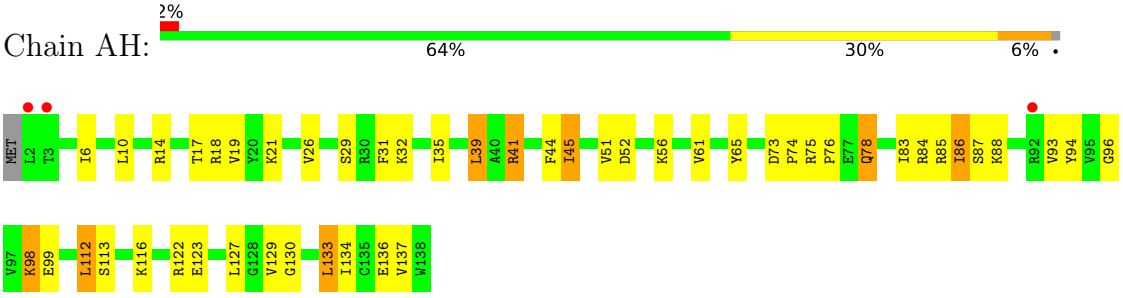
• Molecule 7: 30S ribosomal protein S7



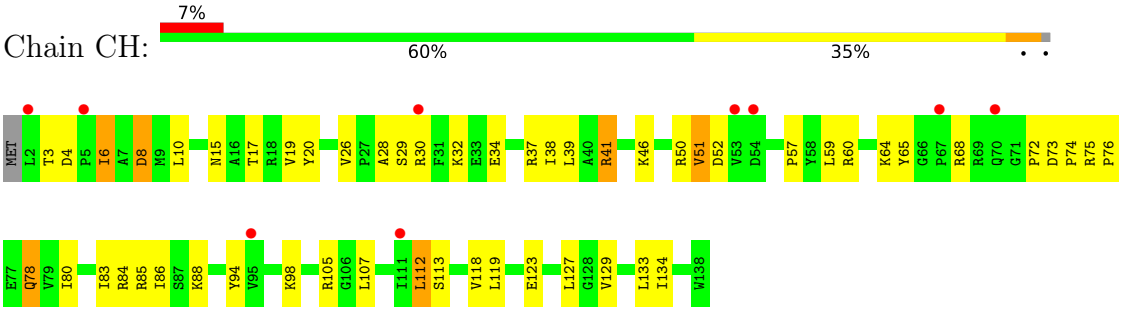
• Molecule 7: 30S ribosomal protein S7



• Molecule 8: 30S ribosomal protein S8

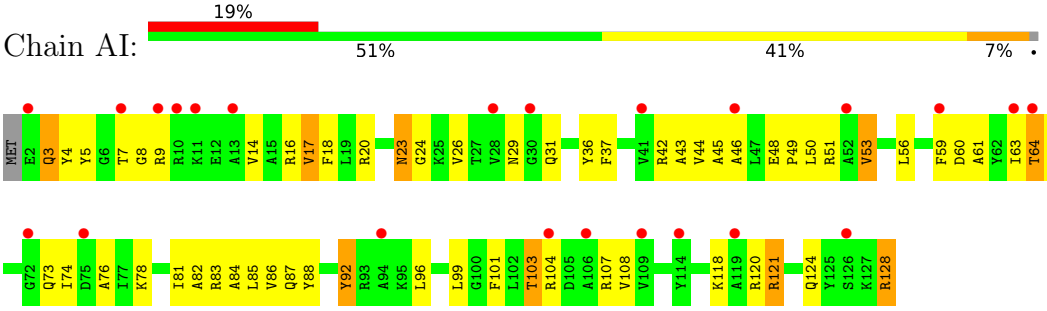


• Molecule 8: 30S ribosomal protein S8



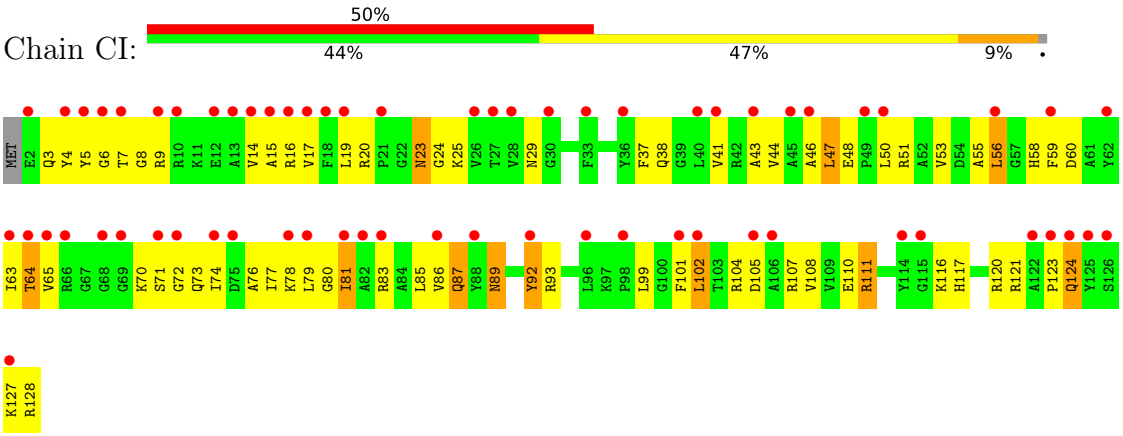
• Molecule 9: 30S ribosomal protein S9

Chain AI:



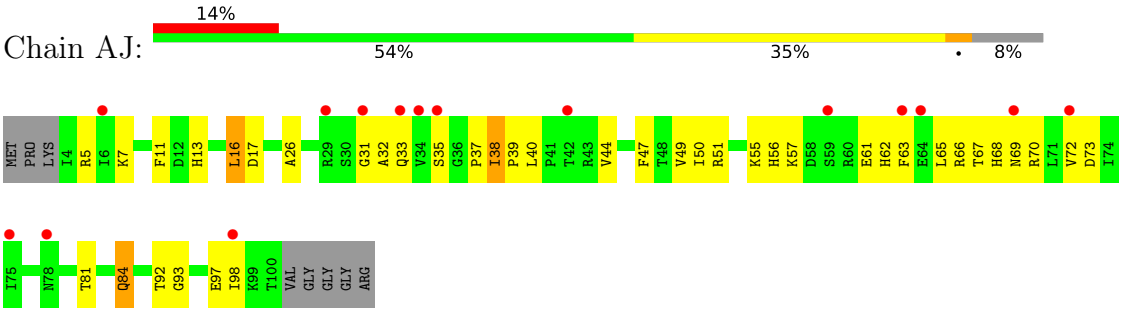
• Molecule 9: 30S ribosomal protein S9

Chain CI:



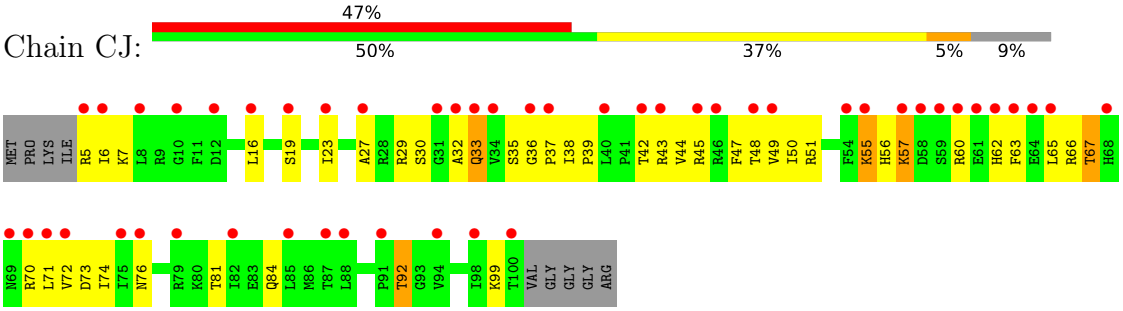
• Molecule 10: 30S ribosomal protein S10

Chain AJ:



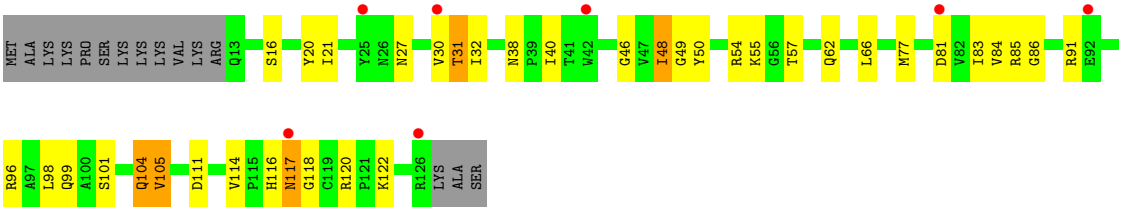
• Molecule 10: 30S ribosomal protein S10

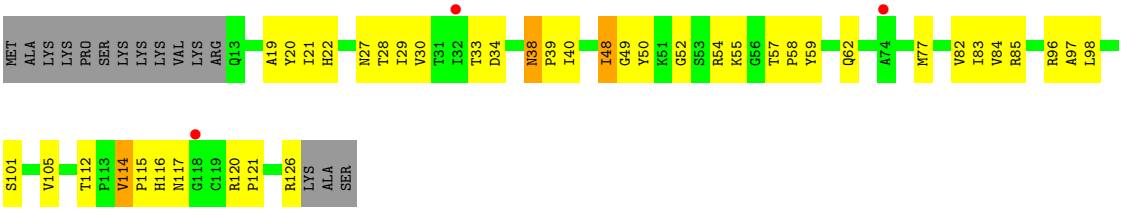
Chain CJ:



• Molecule 11: 30S ribosomal protein S11

Chain AK:



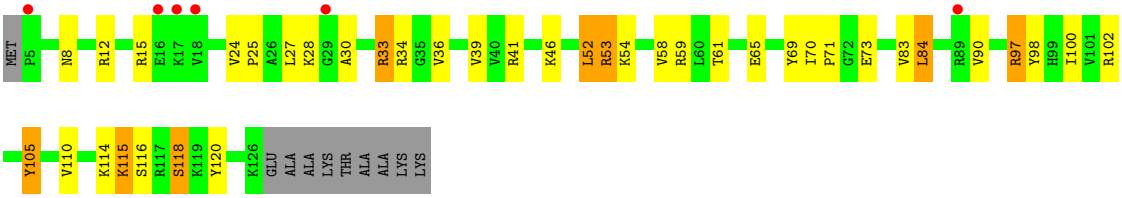


• Molecule 11: 30S ribosomal protein S11

Chain CK:

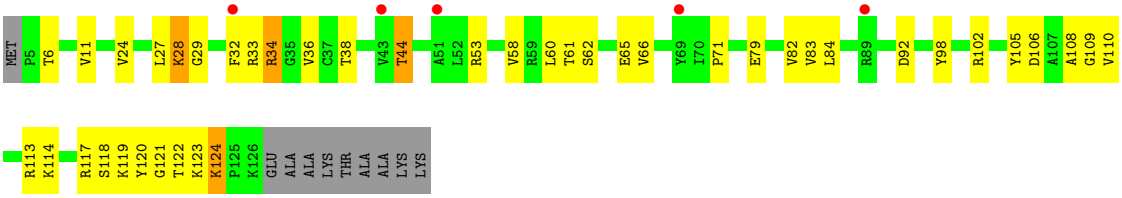
• Molecule 12: 30S ribosomal protein S12

Chain AL:



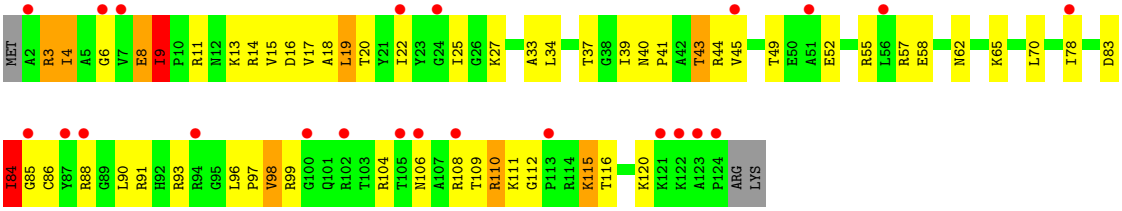
• Molecule 12: 30S ribosomal protein S12

Chain CL:



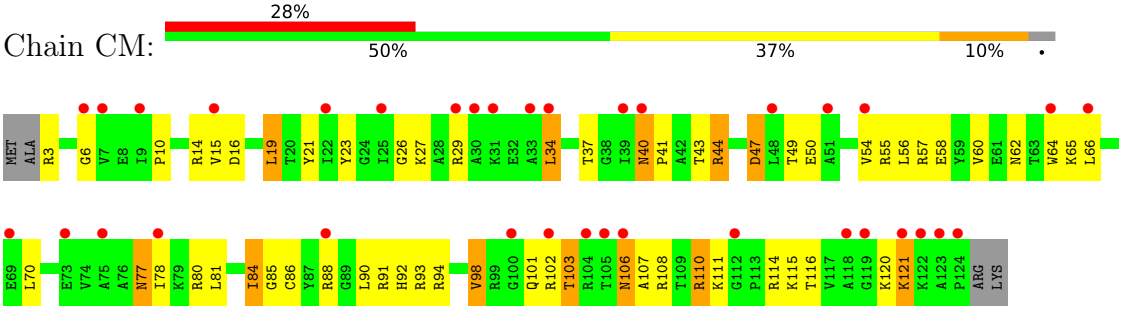
• Molecule 13: 30S ribosomal protein S13

Chain AM:



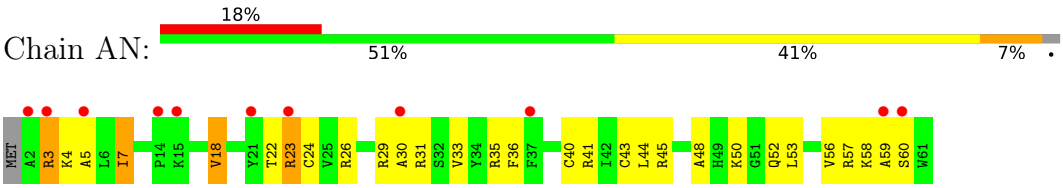
• Molecule 13: 30S ribosomal protein S13

Chain CM:



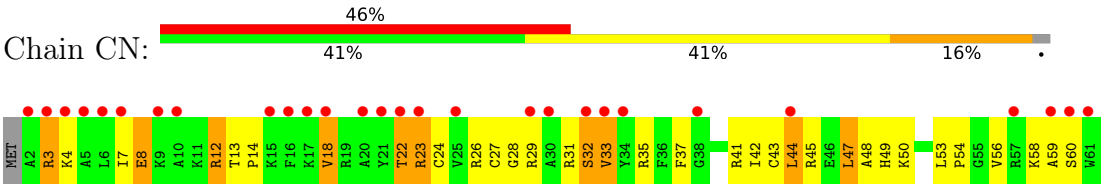
• Molecule 14: 30S ribosomal protein S14 type Z

Chain AN:



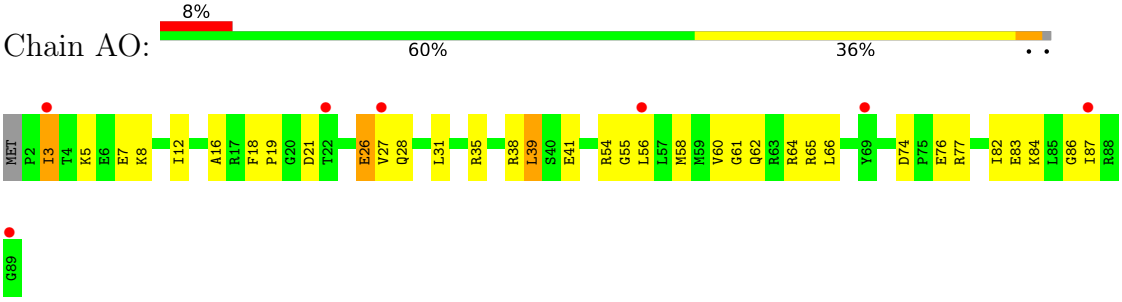
• Molecule 14: 30S ribosomal protein S14 type Z

Chain CN:



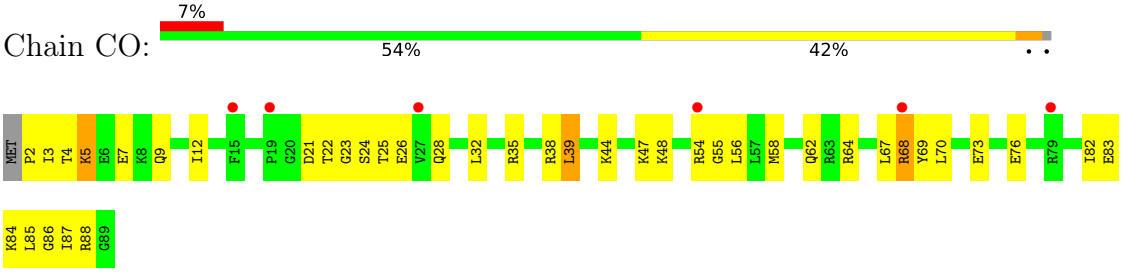
• Molecule 15: 30S ribosomal protein S15

Chain AO:



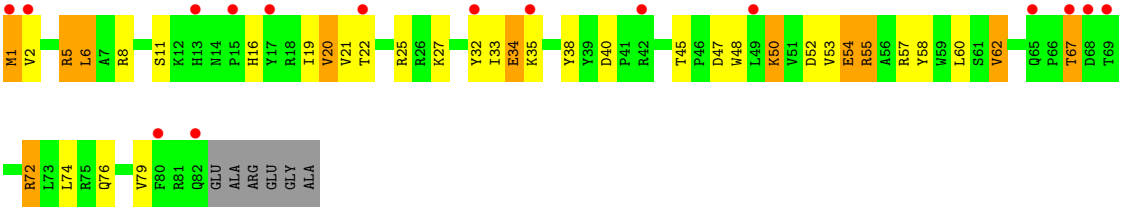
• Molecule 15: 30S ribosomal protein S15

Chain CO:

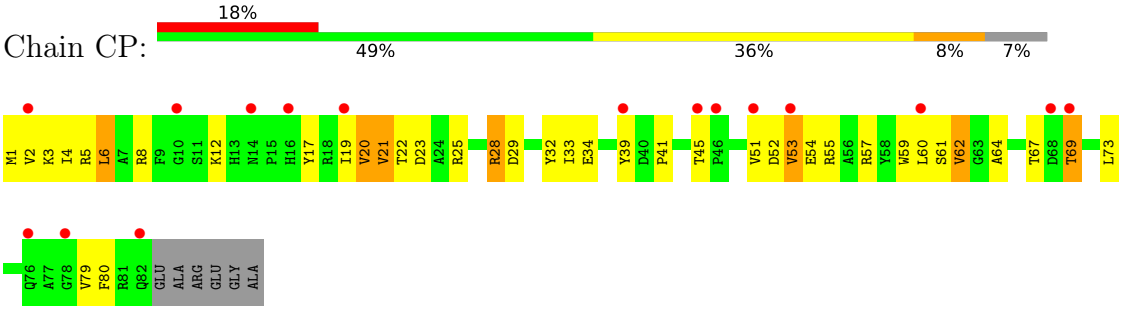


• Molecule 16: 30S ribosomal protein S16

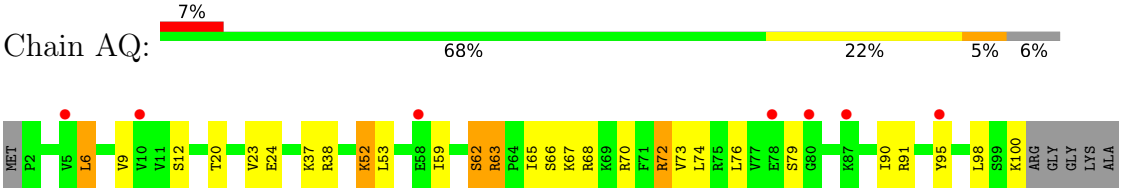
Chain AP:



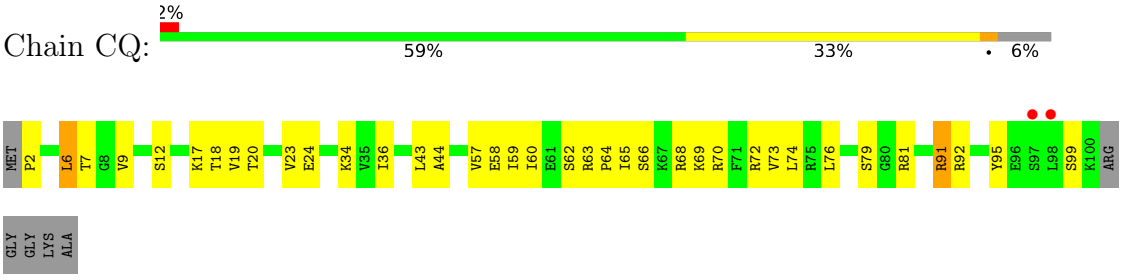
• Molecule 16: 30S ribosomal protein S16



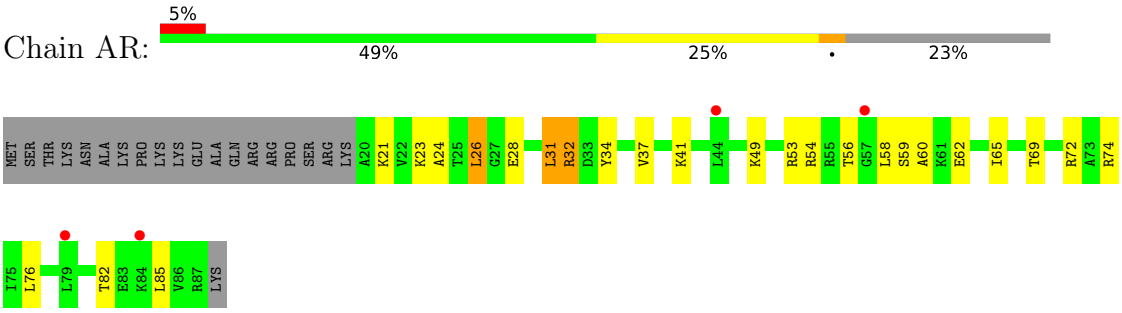
• Molecule 17: 30S ribosomal protein S17



• Molecule 17: 30S ribosomal protein S17



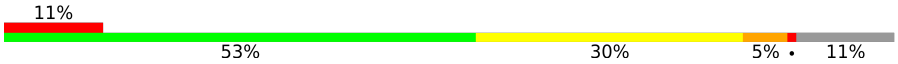
• Molecule 18: 30S ribosomal protein S18

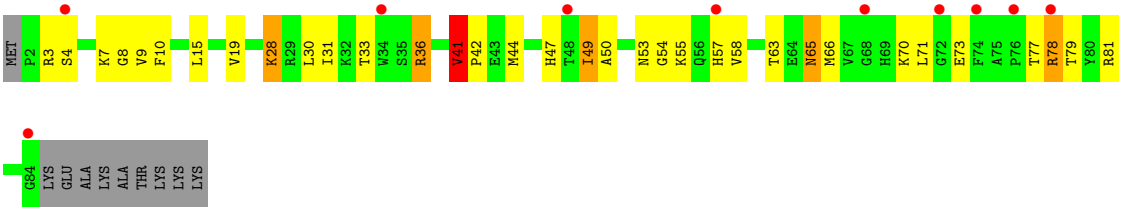


• Molecule 18: 30S ribosomal protein S18

• Molecule 19: 30S ribosomal protein S19

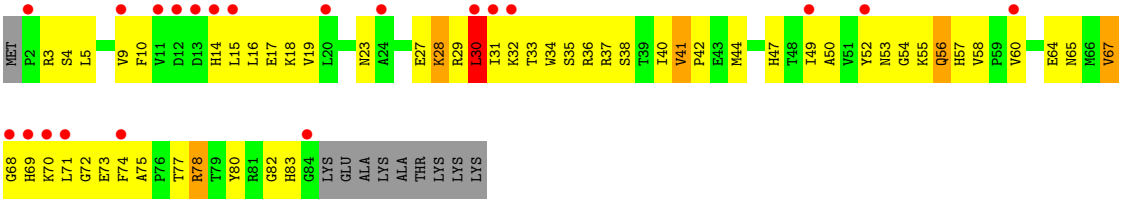
Chain AS:





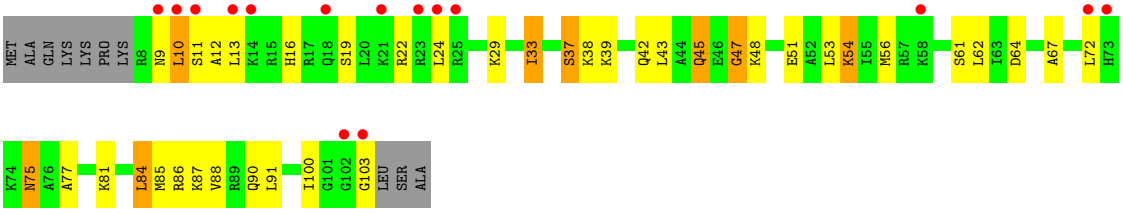
• Molecule 19: 30S ribosomal protein S19

Chain CS:



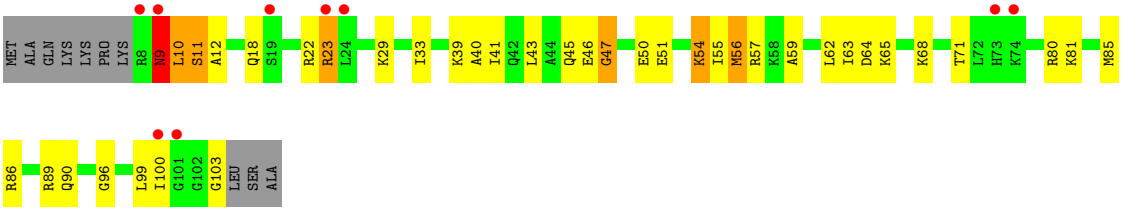
• Molecule 20: 30S ribosomal protein S20

Chain AT:



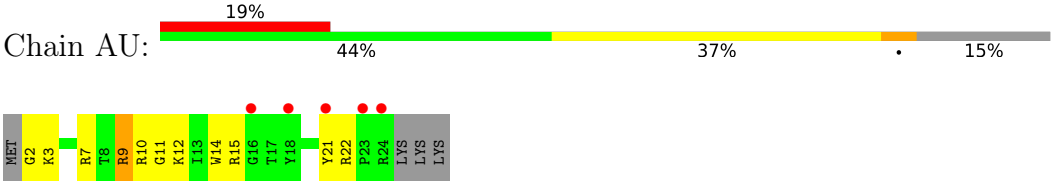
• Molecule 20: 30S ribosomal protein S20

Chain CT:



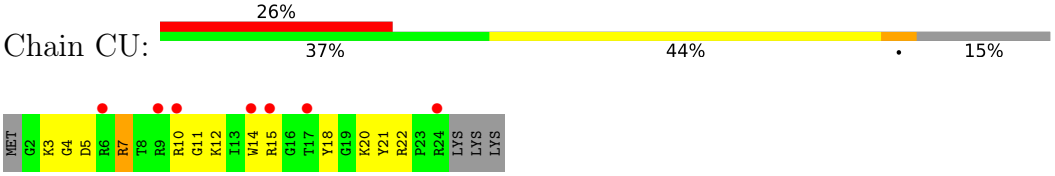
• Molecule 21: 30S ribosomal protein Thx

Chain AU:



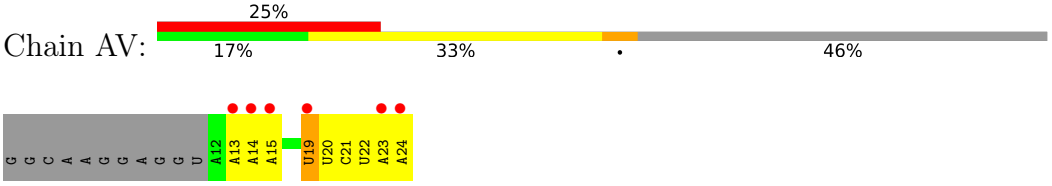
• Molecule 21: 30S ribosomal protein Thx

Chain CU:



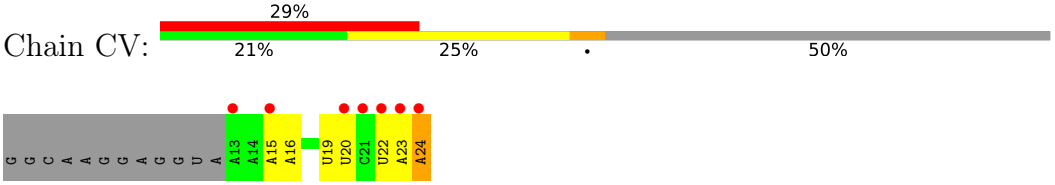
• Molecule 22: mRNA

Chain AV:



• Molecule 22: mRNA

Chain CV:



• Molecule 23: Cytidine-Puromycin

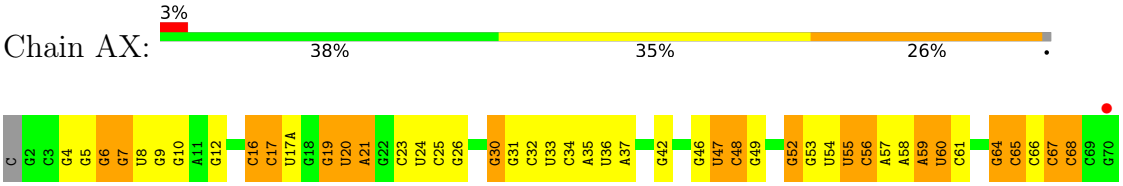
Chain AW:

• Molecule 23: Cytidine-Puromycin

Chain CW:

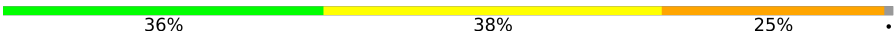
• Molecule 24: P-site tRNA

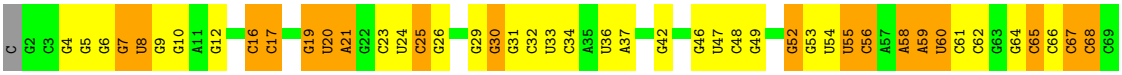
Chain AX:



• Molecule 24: P-site tRNA

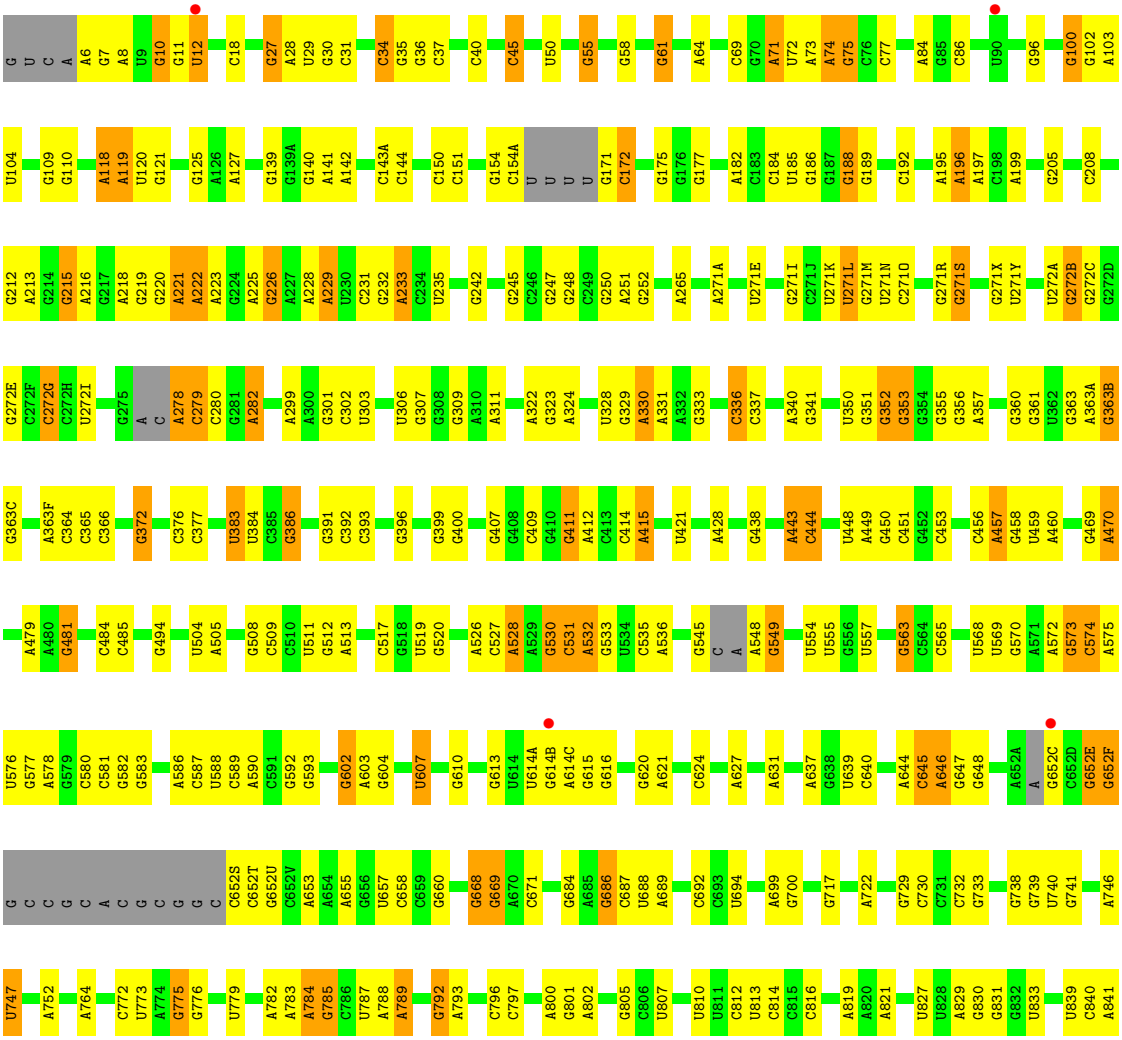
Chain CX:

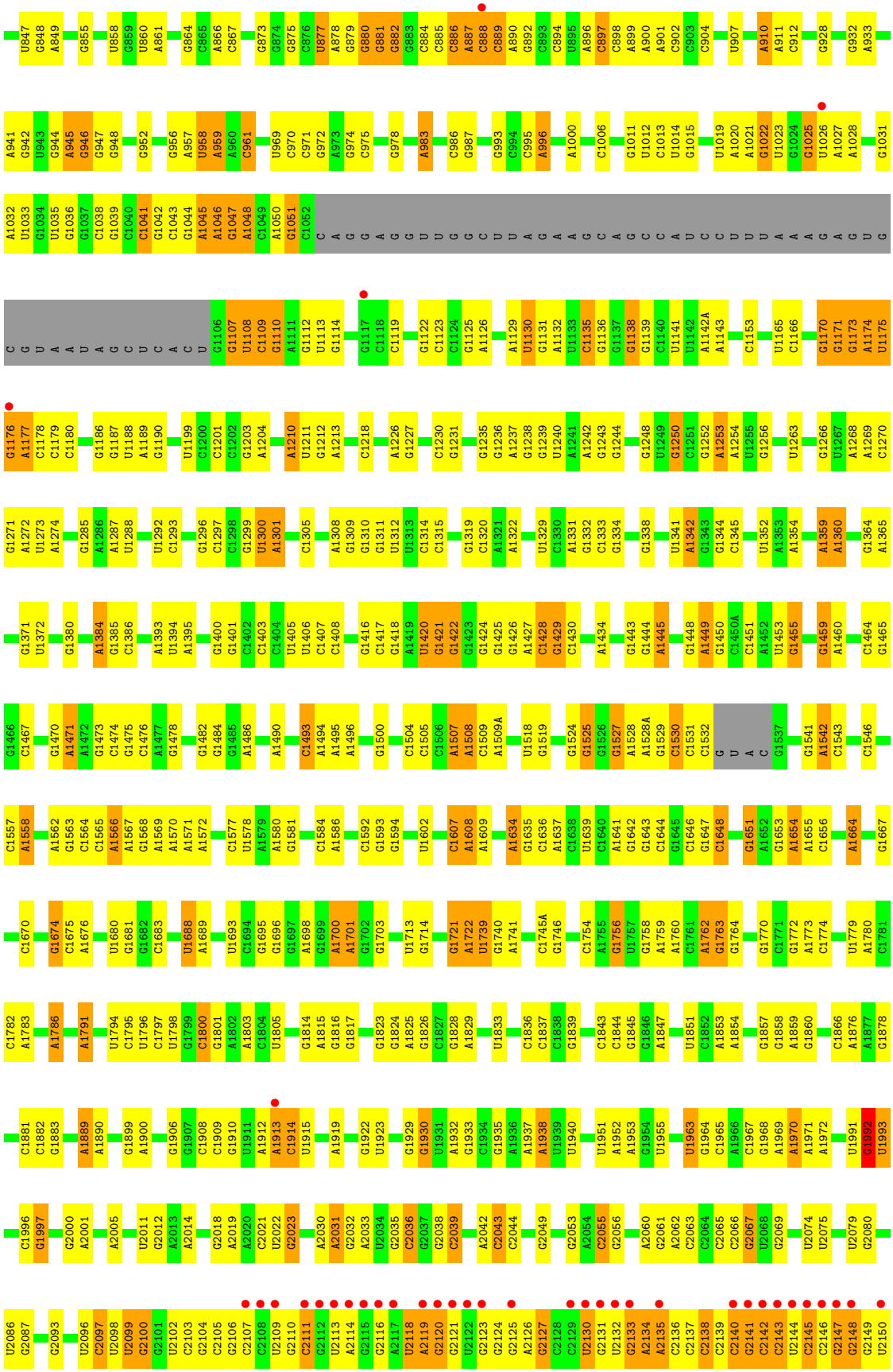


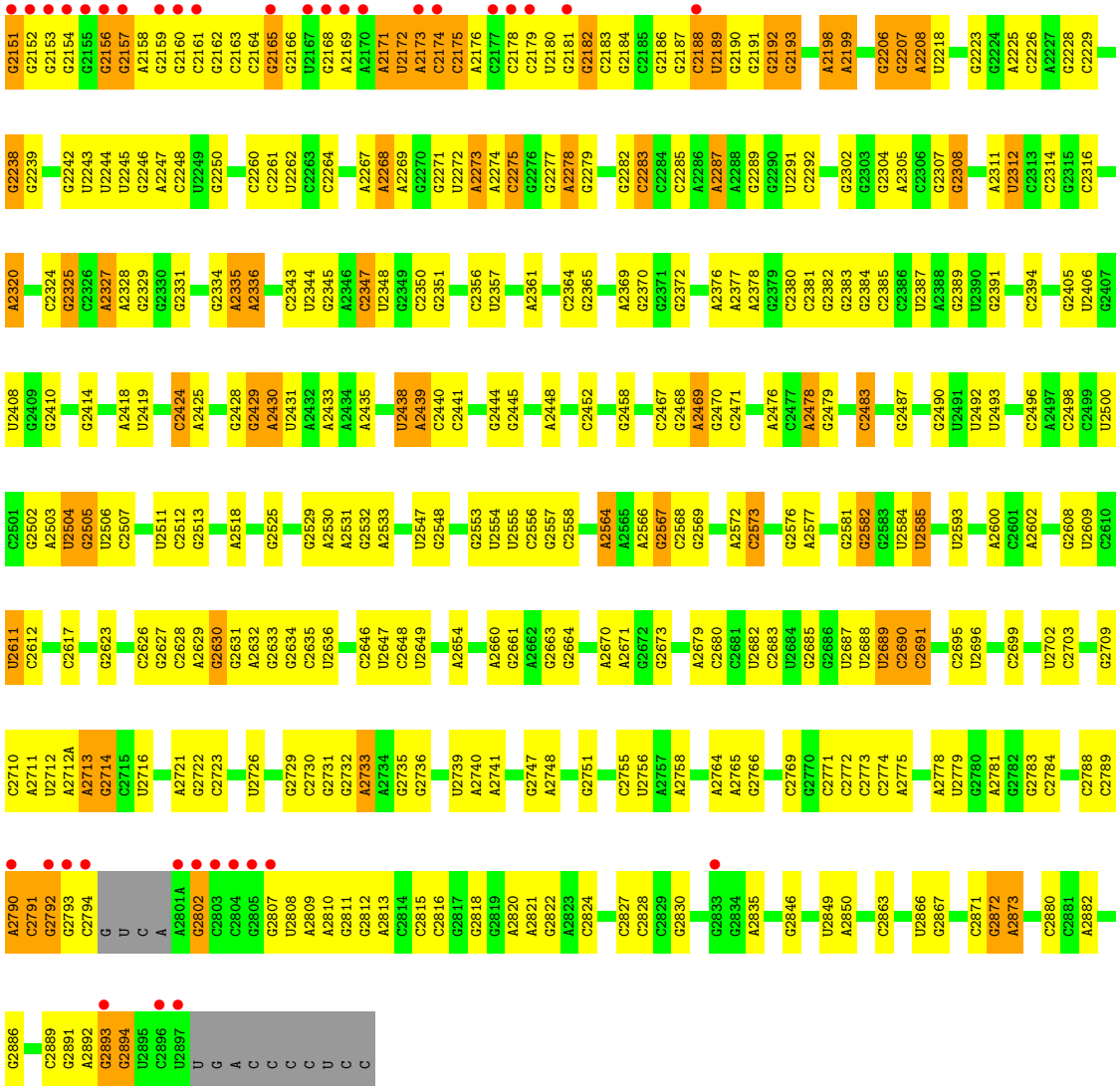


• Molecule 25: 23S Ribosomal RNA

Chain BA:

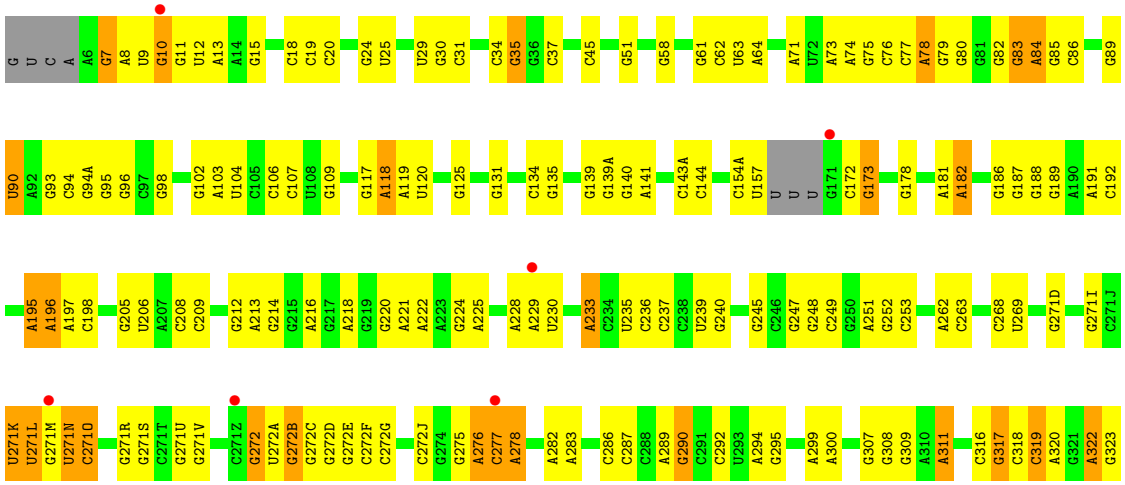


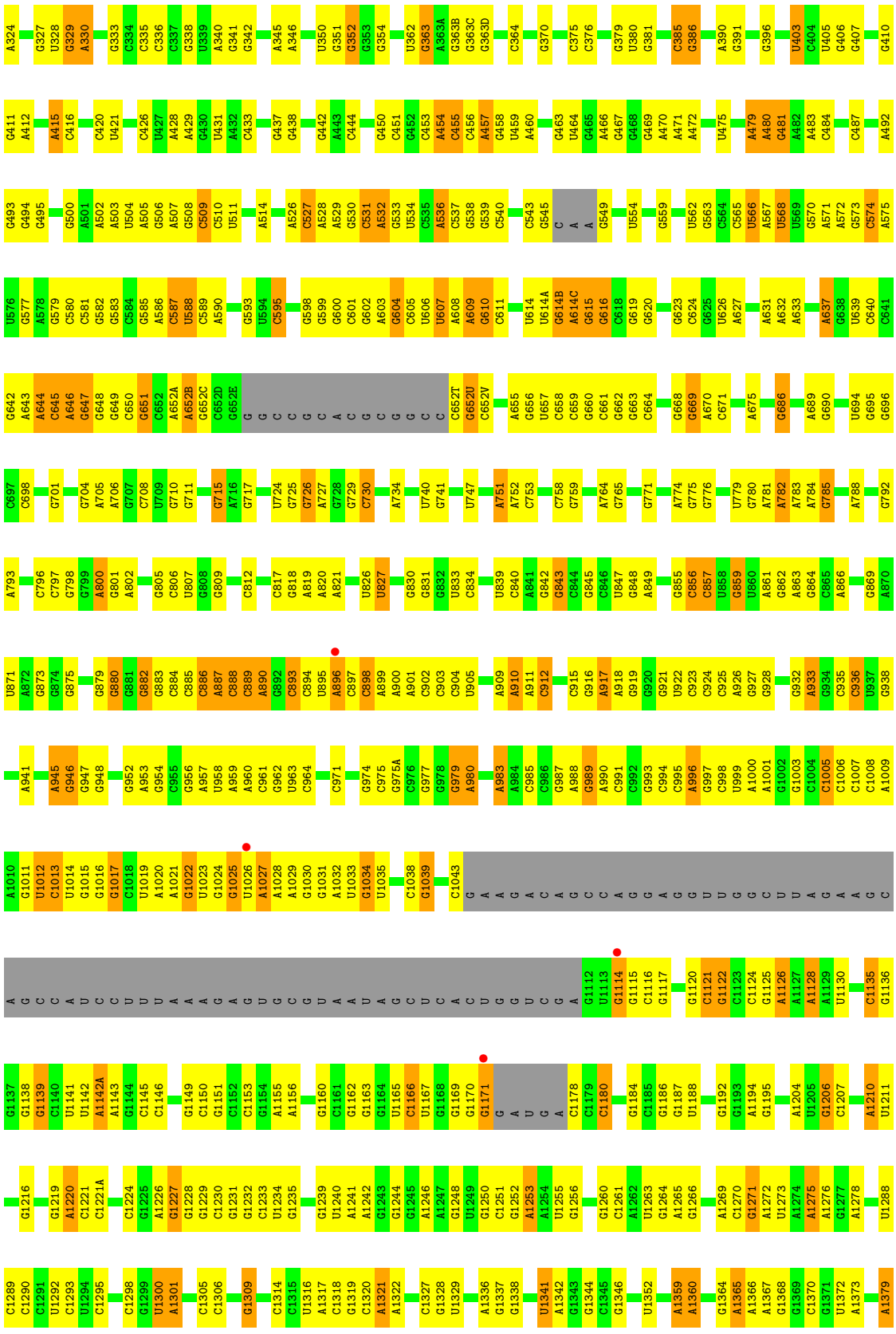




• Molecule 25: 23S Ribosomal RNA

Chain DA:

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G411 A412 A415 C416 C420 U421 C426 U427 A428 A429 G430 U431 A432 C433 G437 G438 G442 A443 C444 G450 C451 G452 C453 A454 C455 C456 A457 G458 U459 A460 G463 U464 G465 A466 G467 G468 G469 A470 A471 A472 U475 A479 A480 G481 A482 A483 C484 C487 A492
G493 G494 G495 G500 A501 A502 A503 U504 A505 G506 A507 G508 C509 C510 U511 A514 A526 C527 A528 G529 G530 C531 A532 G533 U534 C535 A536 C537 G538 G539 C540 C543 G545 C A A G549 U554 G559 U562 G563 C564 C565 U566 A567 U568 U569 G570 A571 A572 G573 C574 A575
U576 G577 A578 G579 C580 C581 G582 G583 C584 G585 A586 C587 U588 C589 A590 G593 U594 C595 G598 G599 G600 C601 G602 A603 G604 C605 U606 U607 A608 A609 G610 C611 U614 U614A G614B A614C G615 G616 C618 G619 G620 G623 C624 G625 U626 A627 A631 A632 A633 A637 G638 U639 C640 C641
G642 A643 A644 C645 A646 G647 G648 G649 C650 G651 C652 A652A A652B G652C C652D G652E G C C C G C A C G C G C C652T G652U C652V A655 G656 U657 C658 C659 G660 C661 G662 G663 C664 G668 G669 A670 C671 A675 G686 A689 G690 U694 G695 G696
C697 C698 G701 G704 A705 A706 G707 C708 U709 G710 G711 G715 A716 G717 U724 G725 G726 A727 G728 G729 C730 A734 U740 G741 U747 A751 A752 C753 C758 G759 A764 G765 G771 A774 G775 G776 U779 G780 A781 A782 A783 A784 G785 A788 G792
A793 C796 C797 G798 G799 A800 G801 A802 G805 C806 U807 G808 G809 C812 C817 G818 A819 A820 A821 U826 U827 G830 G831 G832 U833 C834 U839 C840 A841 G842 G843 C844 G845 C846 U847 G848 A849 G855 C856 C857 U858 G859 U860 A861 G862 A863 G864 C865 A866 G869 A870
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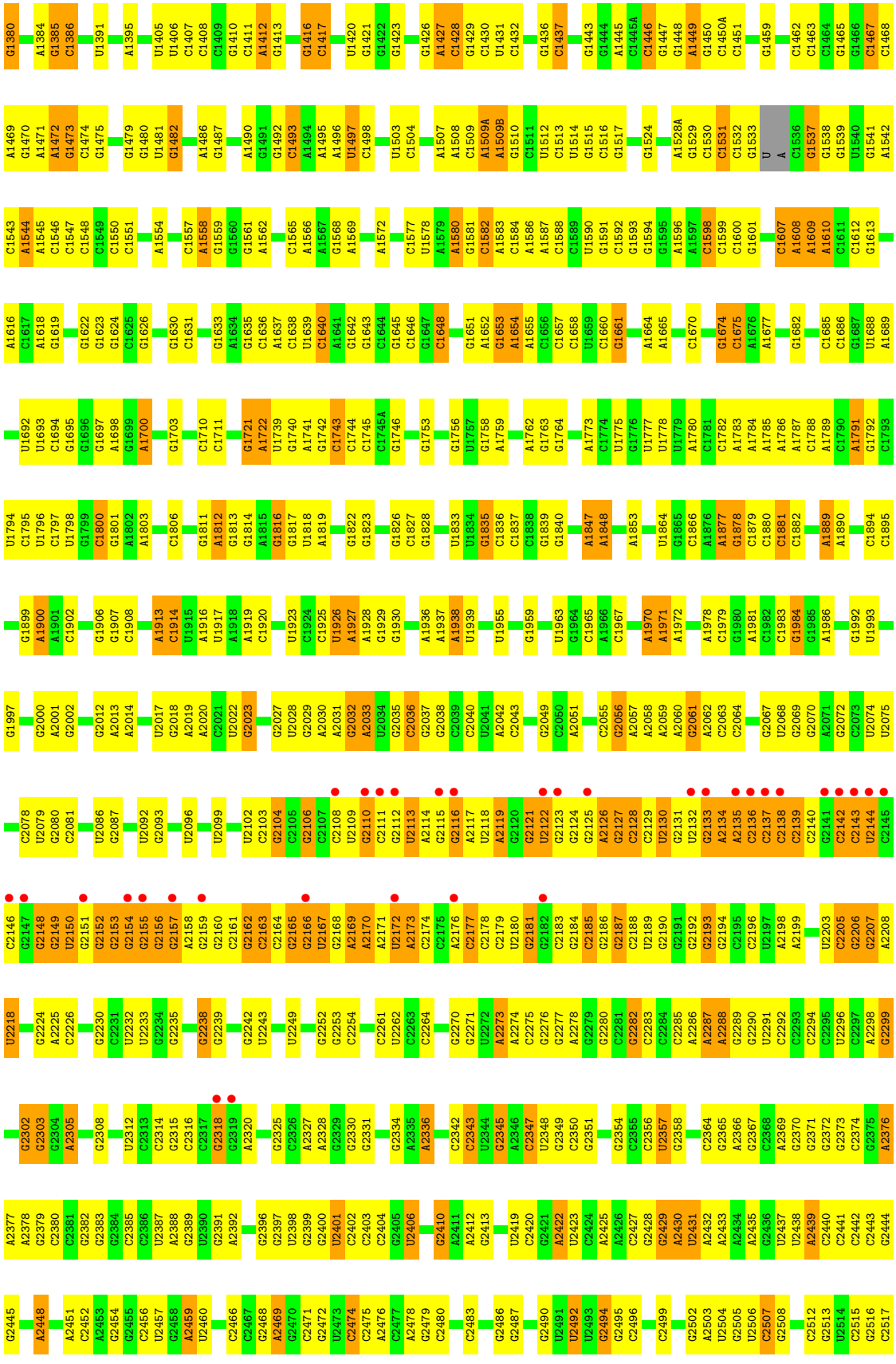
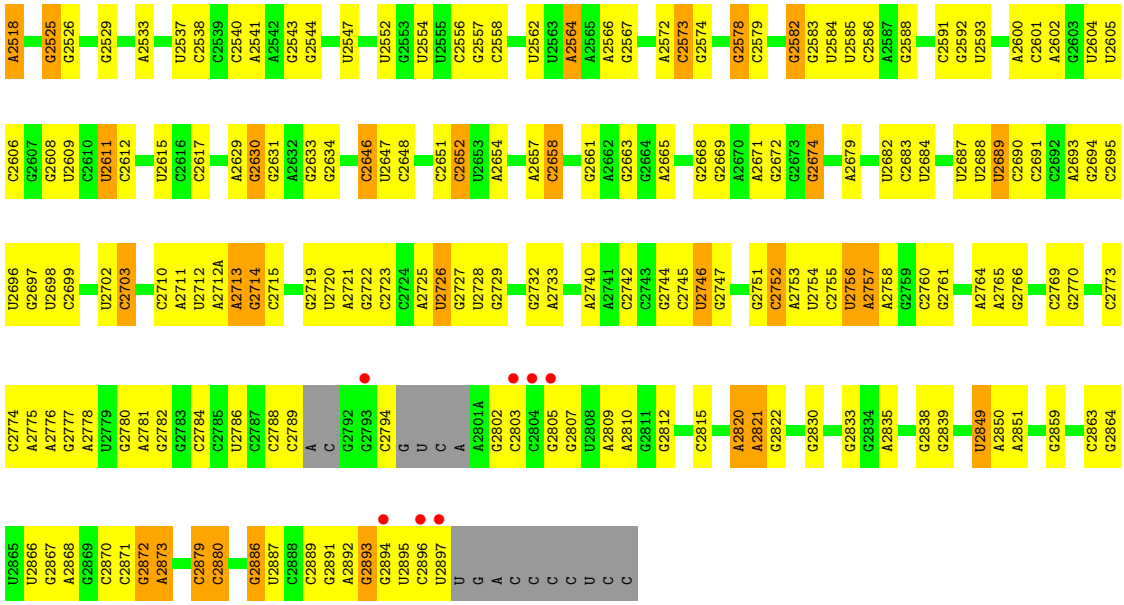


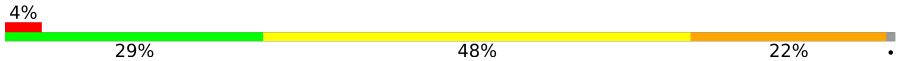


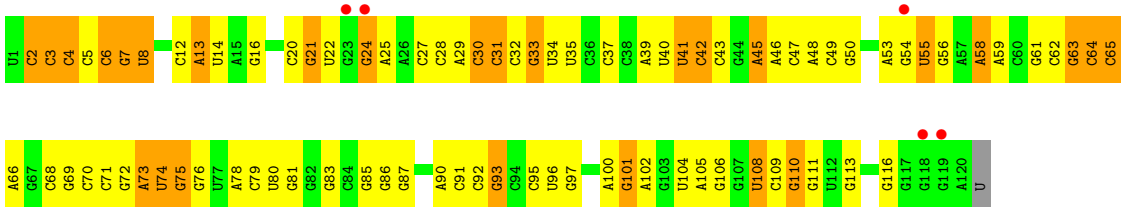
• Molecule 26: 5S Ribosomal RNA

Chain BB:

• Molecule 26: 5S Ribosomal RNA

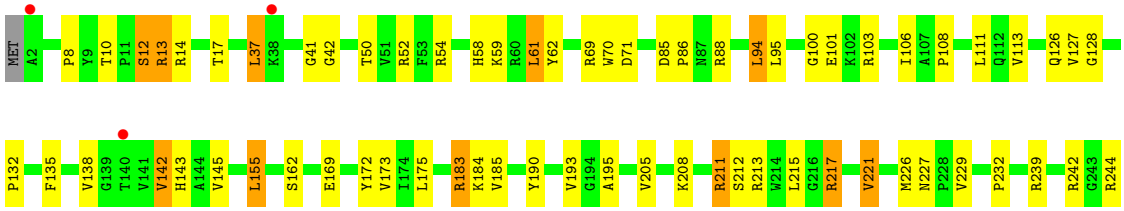
Chain DB:

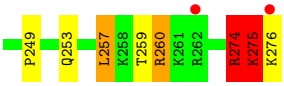




• Molecule 27: 50S ribosomal protein L2

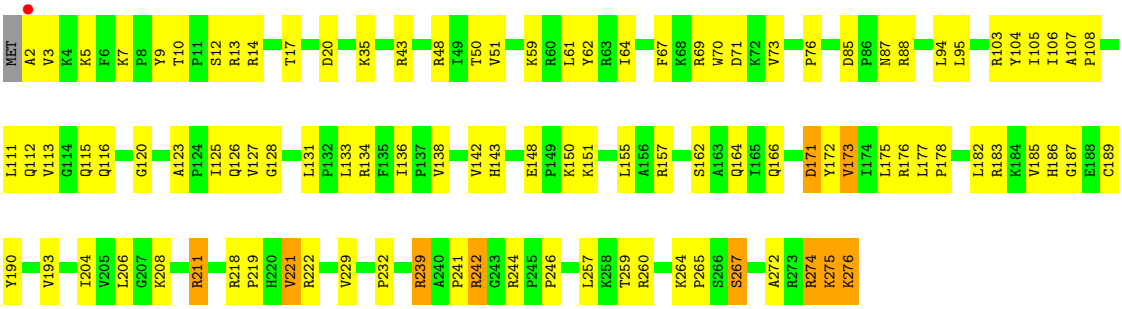
Chain BD:





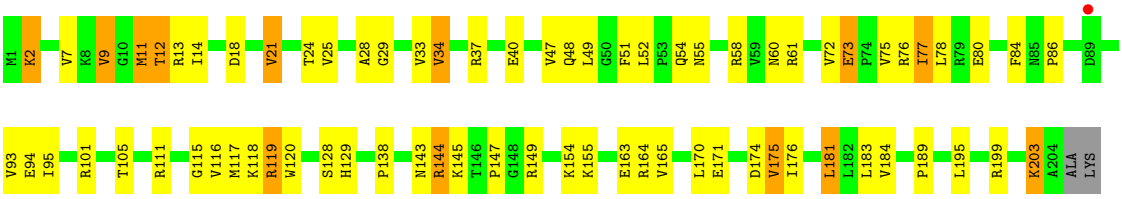
• Molecule 27: 50S ribosomal protein L2

Chain DD:



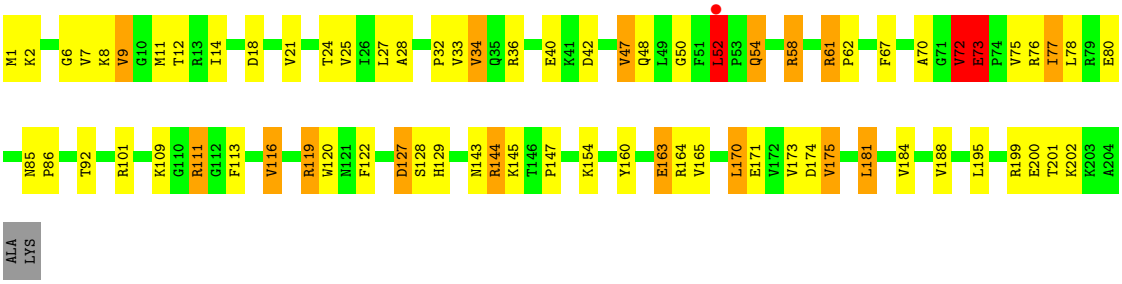
• Molecule 28: 50S ribosomal protein L3

Chain BE:



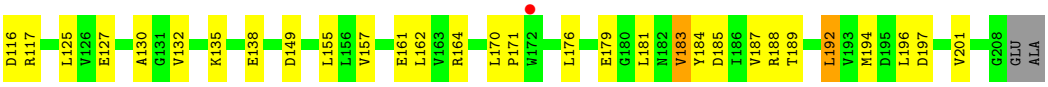
• Molecule 28: 50S ribosomal protein L3

Chain DE:



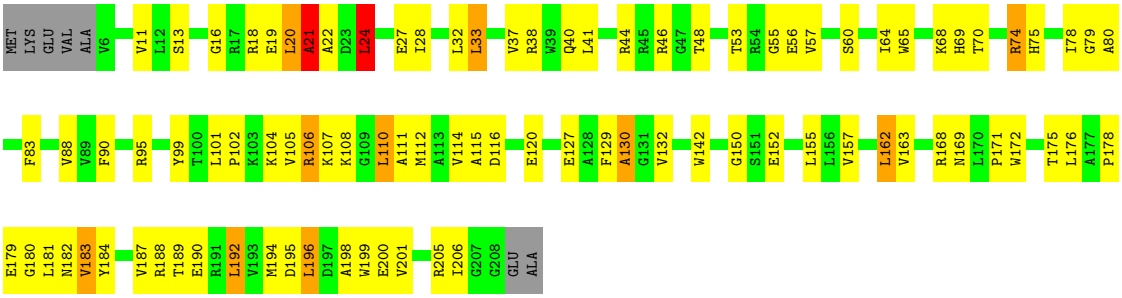
• Molecule 29: 50S ribosomal protein L4

Chain BF:



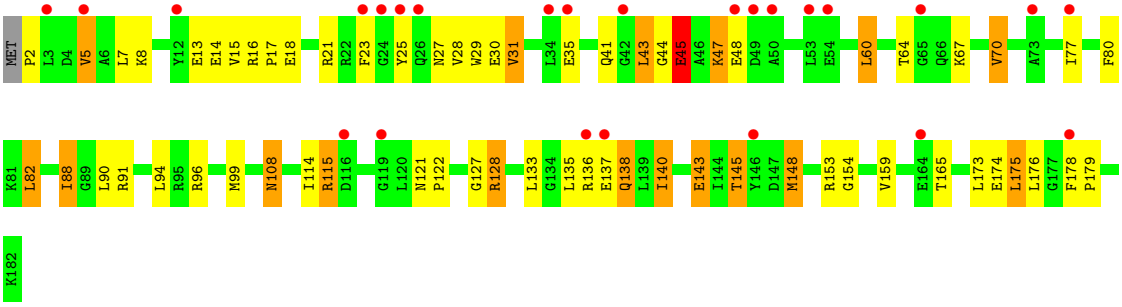
• Molecule 29: 50S ribosomal protein L4

Chain DF:



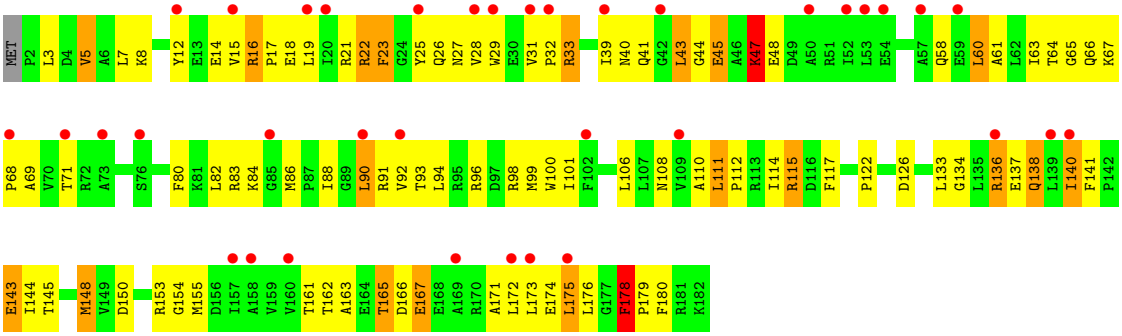
• Molecule 30: 50S ribosomal protein L5

Chain BG:



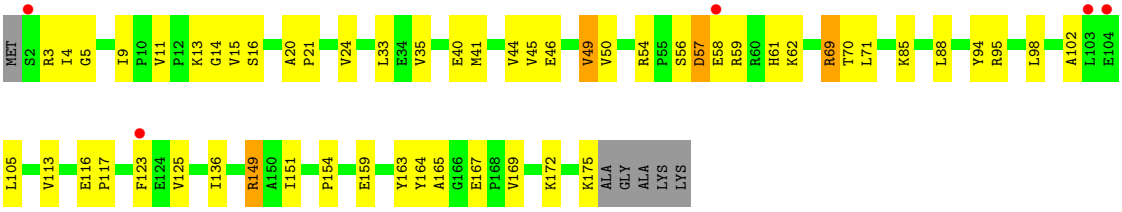
• Molecule 30: 50S ribosomal protein L5

Chain DG:



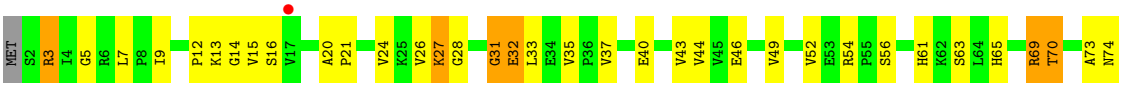
• Molecule 31: 50S ribosomal protein L6

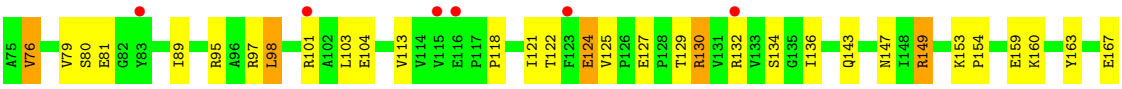
Chain BH:

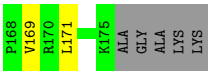


• Molecule 31: 50S ribosomal protein L6

Chain DH:

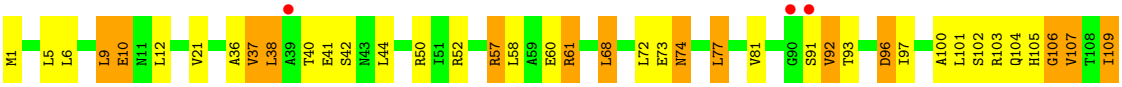


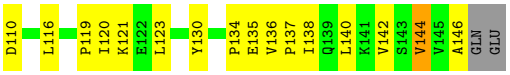




• Molecule 32: 50S ribosomal protein L9

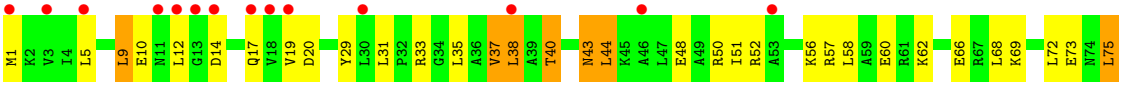
Chain BI:

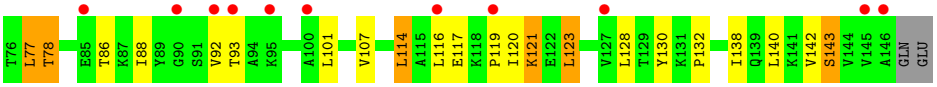




• Molecule 32: 50S ribosomal protein L9

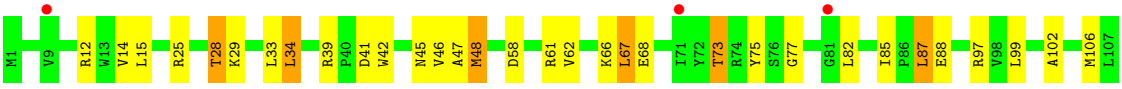
Chain DI:





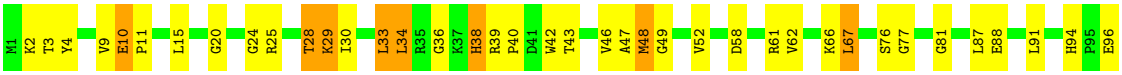
• Molecule 33: 50S ribosomal protein L13

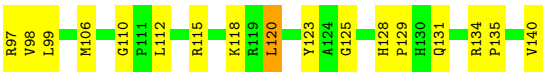
Chain BN:



• Molecule 33: 50S ribosomal protein L13

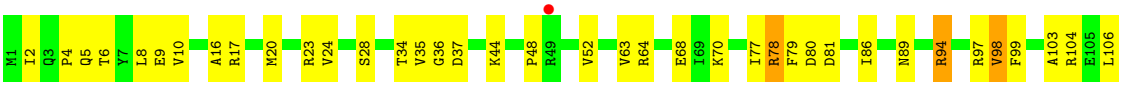
Chain DN:

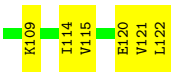




• Molecule 34: 50S ribosomal protein L14

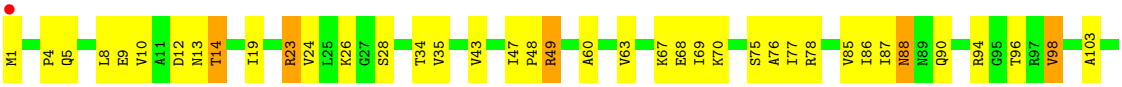
Chain BO:





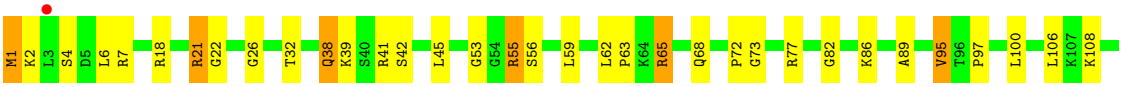
• Molecule 34: 50S ribosomal protein L14

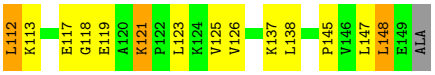
Chain DO:



• Molecule 35: 50S ribosomal protein L15

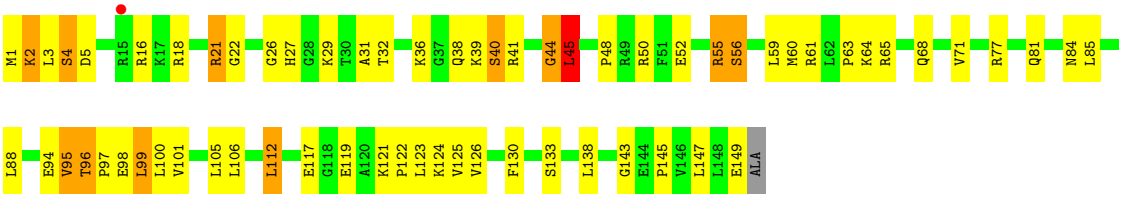
Chain BP:



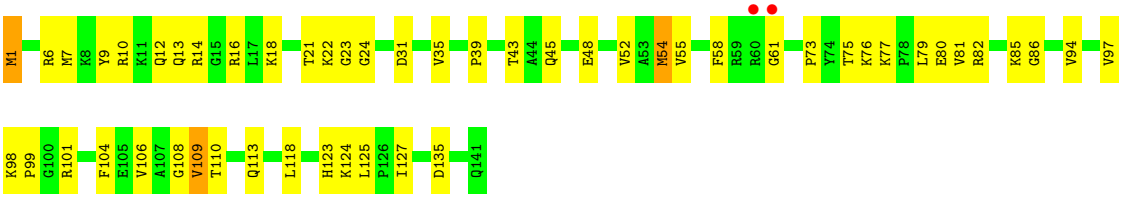


• Molecule 35: 50S ribosomal protein L15

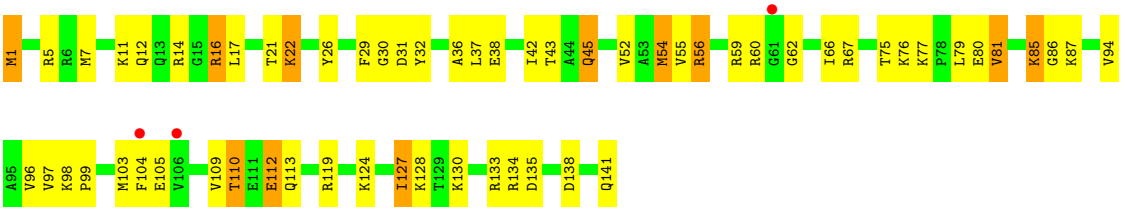
Chain DP:



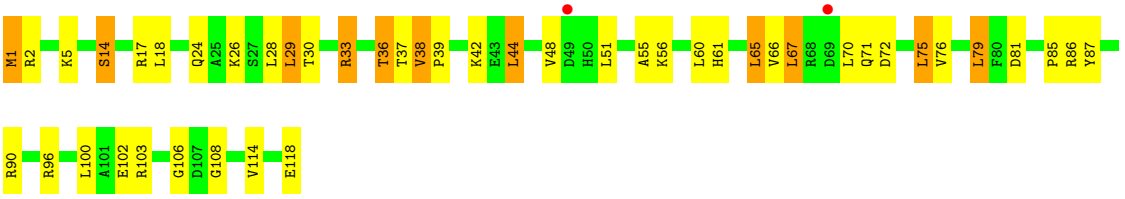
• Molecule 36: 50S ribosomal protein L16



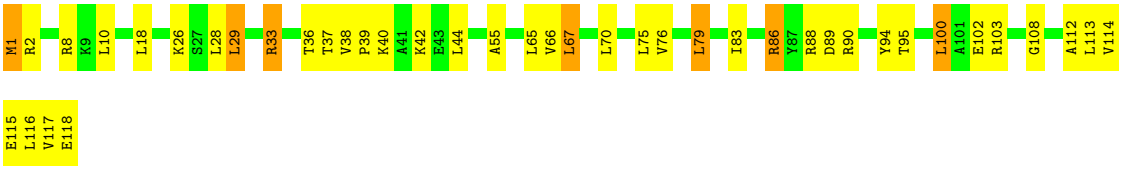
• Molecule 36: 50S ribosomal protein L16



• Molecule 37: 50S ribosomal protein L17

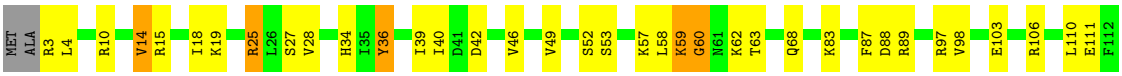


• Molecule 37: 50S ribosomal protein L17



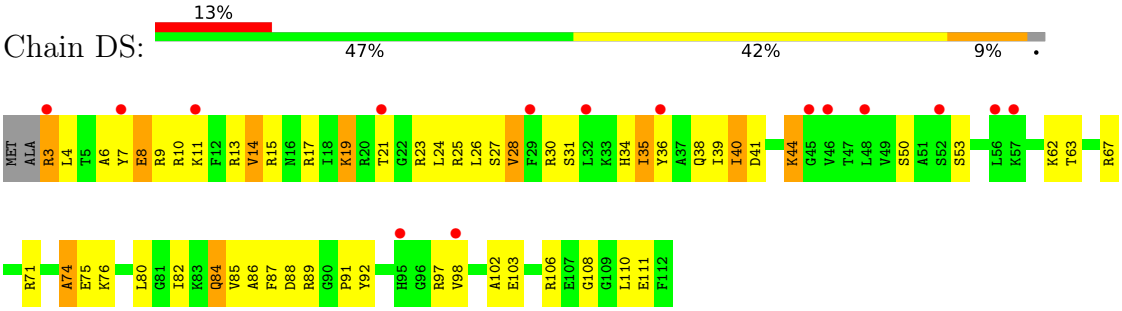
• Molecule 38: 50S ribosomal protein L18

Chain BS:



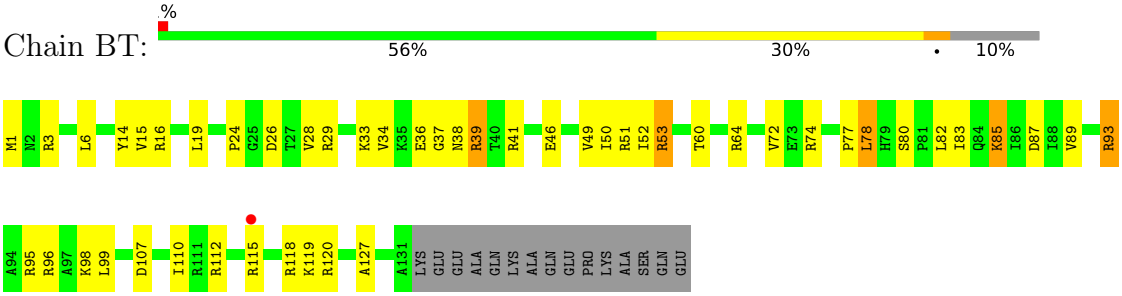
• Molecule 38: 50S ribosomal protein L18

Chain DS:



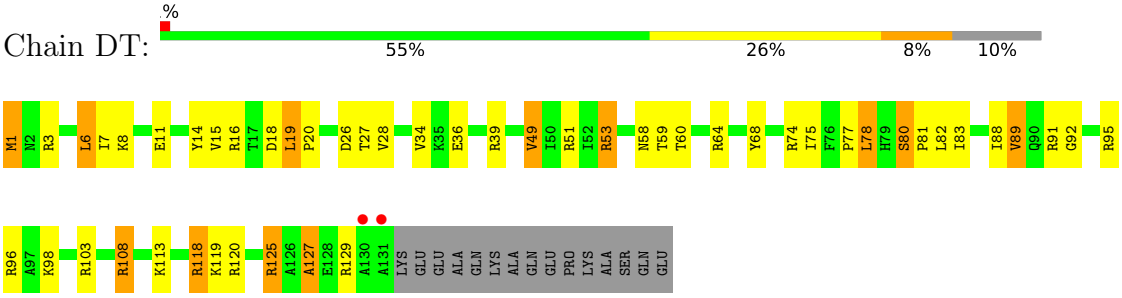
• Molecule 39: 50S ribosomal protein L19

Chain BT:



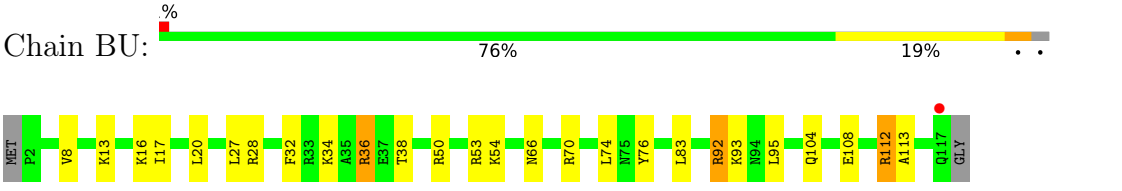
• Molecule 39: 50S ribosomal protein L19

Chain DT:



• Molecule 40: 50S ribosomal protein L20

Chain BU:



• Molecule 40: 50S ribosomal protein L20

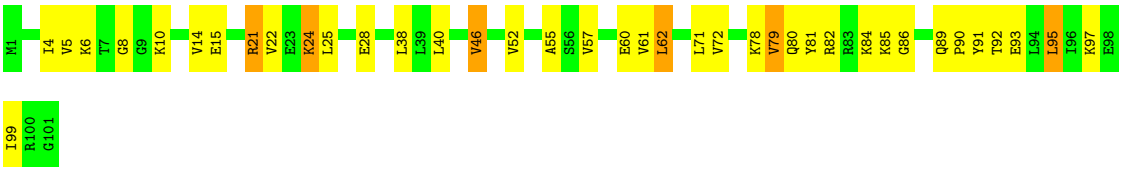
Chain DU:

• Molecule 41: 50S ribosomal protein L21

Chain BV:

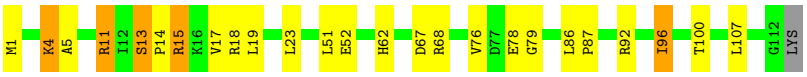
• Molecule 41: 50S ribosomal protein L21

Chain DV:



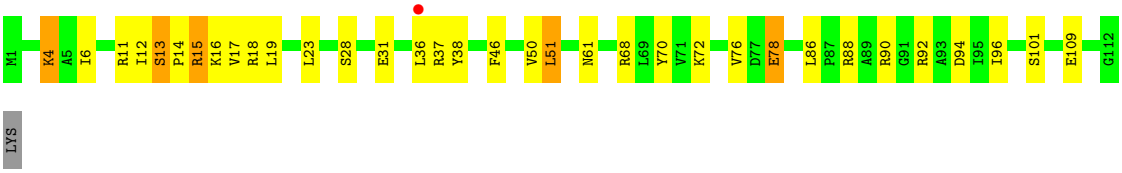
• Molecule 42: 50S ribosomal protein L22

Chain BW:



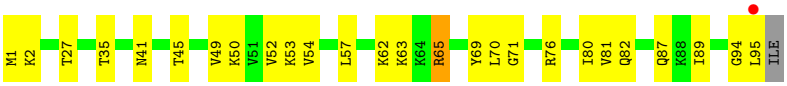
• Molecule 42: 50S ribosomal protein L22

Chain DW:



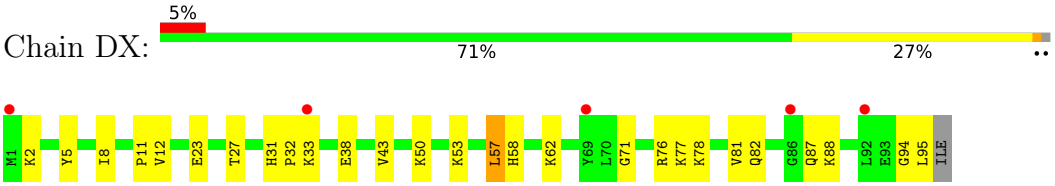
• Molecule 43: 50S ribosomal protein L23

Chain BX:



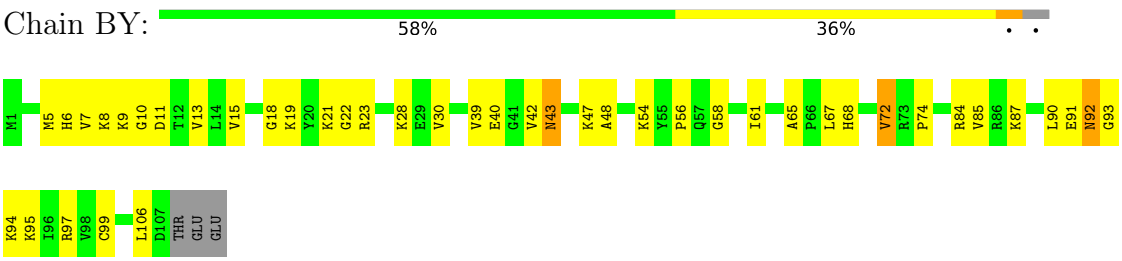
• Molecule 43: 50S ribosomal protein L23

Chain DX:



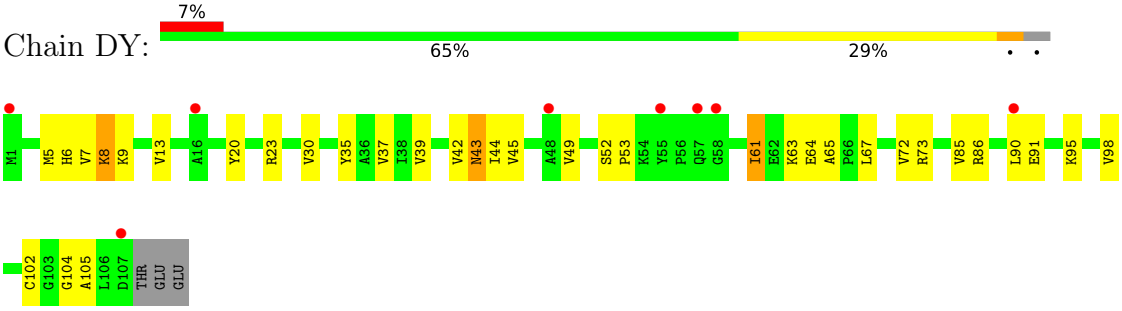
• Molecule 44: 50S ribosomal protein L24

Chain BY:



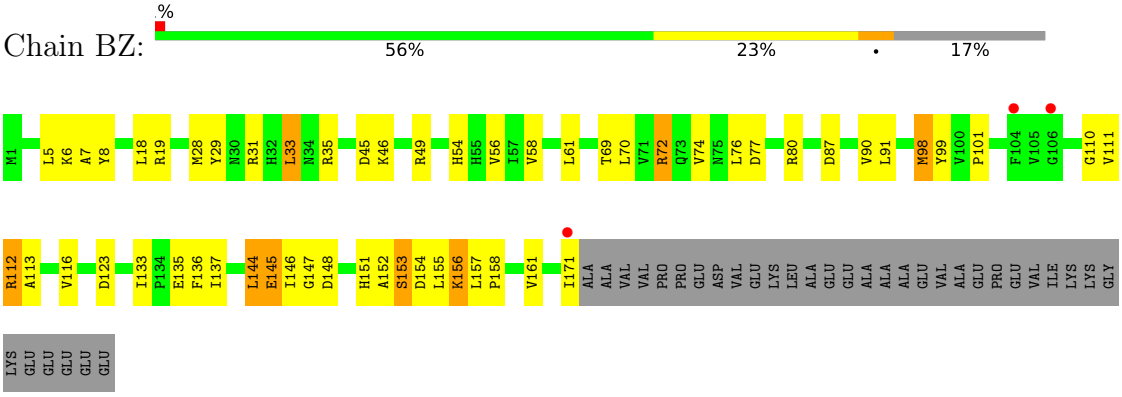
• Molecule 44: 50S ribosomal protein L24

Chain DY:



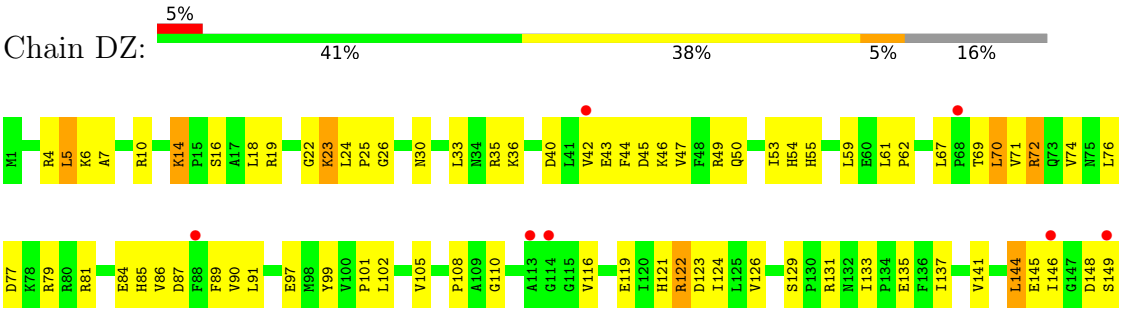
• Molecule 45: 50S ribosomal protein L25

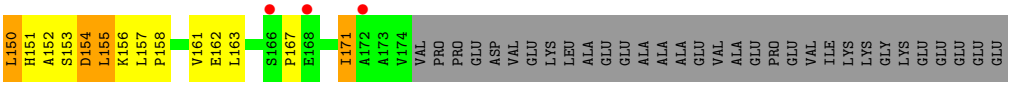
Chain BZ:



• Molecule 45: 50S ribosomal protein L25

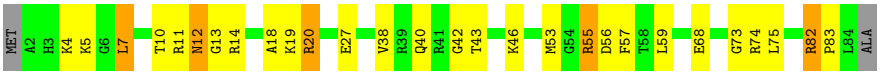
Chain DZ:





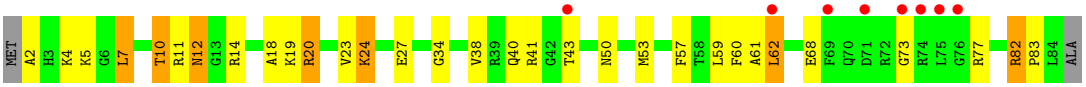
• Molecule 46: 50S ribosomal protein L27

Chain B0:



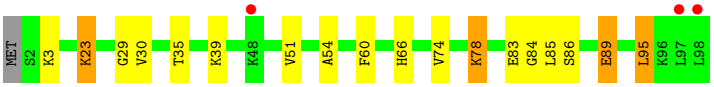
• Molecule 46: 50S ribosomal protein L27

Chain D0:



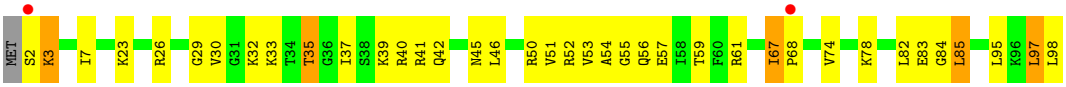
• Molecule 47: 50S ribosomal protein L28

Chain B1:



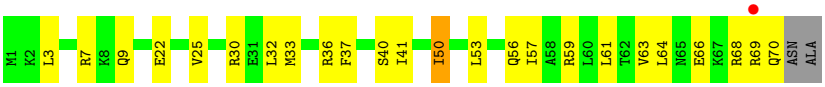
• Molecule 47: 50S ribosomal protein L28

Chain D1:



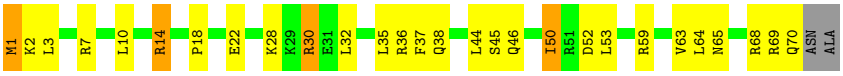
• Molecule 48: 50S ribosomal protein L29

Chain B2:



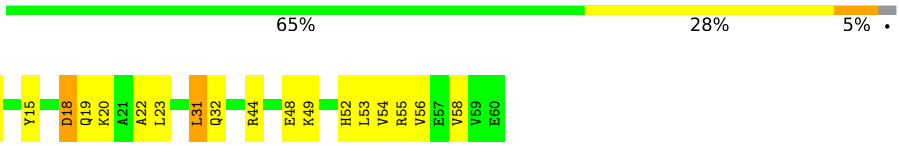
• Molecule 48: 50S ribosomal protein L29

Chain D2:



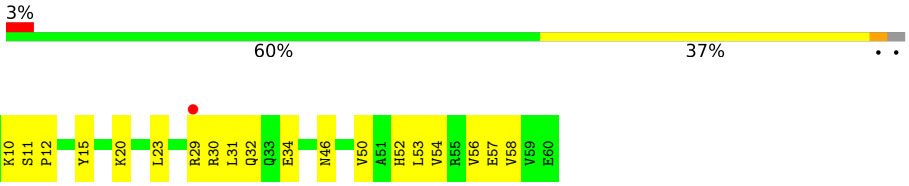
• Molecule 49: 50S ribosomal protein L30

Chain B3:



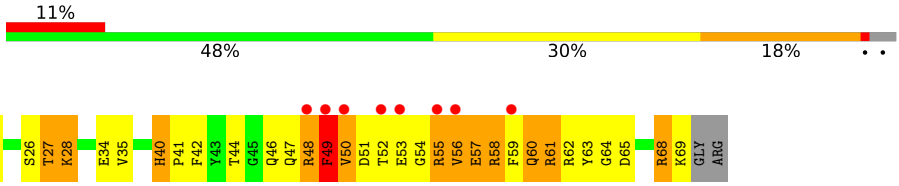
• Molecule 49: 50S ribosomal protein L30

Chain D3:



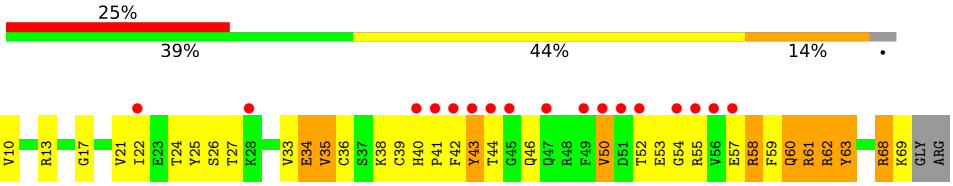
• Molecule 50: 50S ribosomal protein L31

Chain B4:



• Molecule 50: 50S ribosomal protein L31

Chain D4:

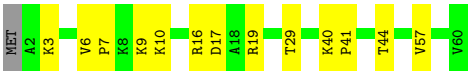


• Molecule 51: 50S ribosomal protein L32

Chain B5:

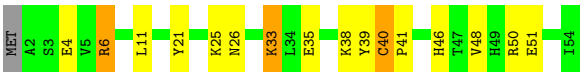
• Molecule 51: 50S ribosomal protein L32

Chain D5:



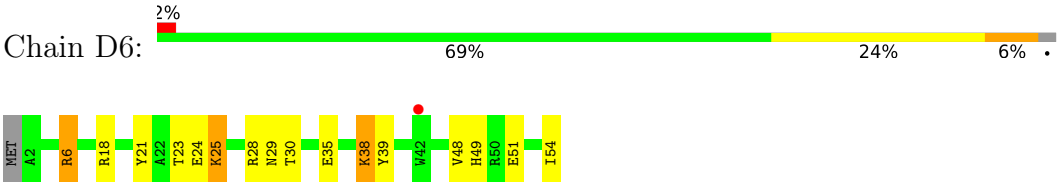
• Molecule 52: 50S ribosomal protein L33

Chain B6:



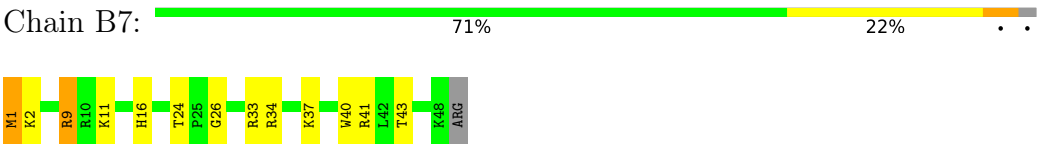
• Molecule 52: 50S ribosomal protein L33

Chain D6:



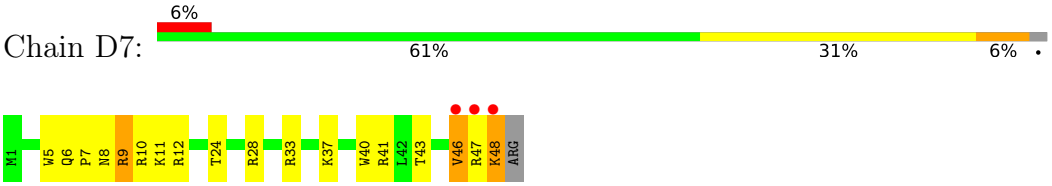
• Molecule 53: 50S ribosomal protein L34

Chain B7:



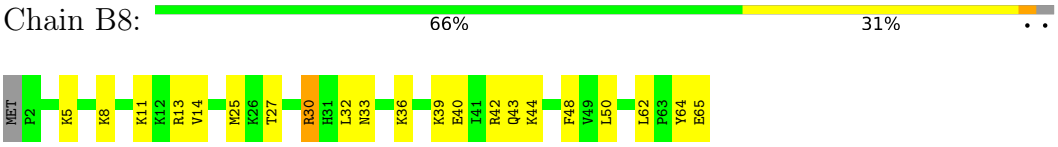
• Molecule 53: 50S ribosomal protein L34

Chain D7:



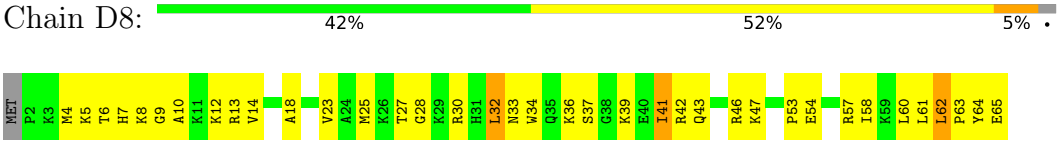
• Molecule 54: 50S ribosomal protein L35

Chain B8:



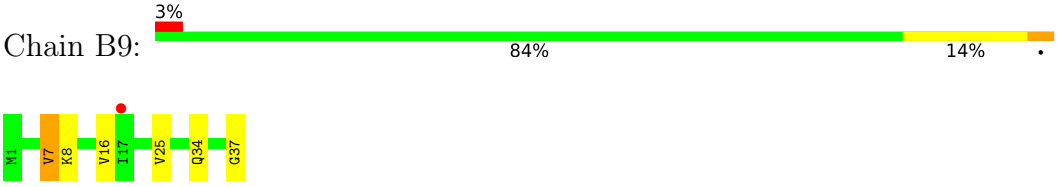
• Molecule 54: 50S ribosomal protein L35

Chain D8:



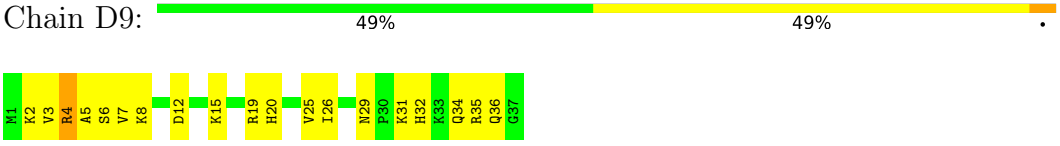
• Molecule 55: 50S ribosomal protein L36

Chain B9:



• Molecule 55: 50S ribosomal protein L36

Chain D9:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.25Å 448.46Å 618.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	362.98 – 2.90 362.98 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.9 (362.98-2.90) 96.9 (362.98-2.90)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.31 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.231 , 0.286 0.232 , 0.286	Depositor DCC
R_{free} test set	61606 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å^2)	54.8	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 74.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.37$, $< L^2 > = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	289646	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

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

[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: 5MC, 5MU, SF4, ZN, 31H, PPU, PSU, MG, 4SU, K

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	0.22	0/36049	0.44	2/56261 (0.0%)
1	CA	0.23	0/36170	0.46	5/56452 (0.0%)
2	AB	0.43	0/1881	1.04	14/2542 (0.6%)
2	CB	0.44	0/1860	1.04	12/2518 (0.5%)
3	AC	0.42	0/1576	0.85	0/2130
3	CC	0.42	0/1566	0.96	2/2119 (0.1%)
4	AD	0.41	0/1689	0.96	4/2267 (0.2%)
4	CD	0.40	0/1700	0.91	2/2280 (0.1%)
5	AE	0.41	0/1145	0.88	0/1543
5	CE	0.41	0/1149	0.97	5/1548 (0.3%)
6	AF	0.41	0/819	0.84	0/1111
6	CF	0.37	0/829	0.75	0/1123
7	AG	0.37	0/1250	0.88	2/1679 (0.1%)
7	CG	0.40	0/1254	0.99	6/1683 (0.4%)
8	AH	0.37	0/1108	0.90	2/1494 (0.1%)
8	CH	0.36	0/1108	0.88	1/1494 (0.1%)
9	AI	0.41	0/1002	0.96	2/1346 (0.1%)
9	CI	0.44	0/997	0.95	2/1343 (0.1%)
10	AJ	0.39	0/722	0.91	2/982 (0.2%)
10	CJ	0.45	0/727	0.96	0/988
11	AK	0.38	0/844	0.88	2/1145 (0.2%)
11	CK	0.39	0/848	0.89	2/1149 (0.2%)
12	AL	0.39	0/946	0.82	1/1274 (0.1%)
12	CL	0.39	0/946	0.94	5/1274 (0.4%)
13	AM	0.40	0/969	1.04	3/1302 (0.2%)
13	CM	0.45	0/961	0.96	3/1291 (0.2%)
14	AN	0.39	0/501	0.83	0/664
14	CN	0.40	0/501	0.90	0/664
15	AO	0.39	0/739	0.89	1/985 (0.1%)
15	CO	0.38	0/739	0.84	0/985
16	AP	0.39	0/697	0.86	0/939
16	CP	0.37	0/693	0.87	2/935 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	AQ	0.37	0/836	0.80	0/1117
17	CQ	0.34	0/836	0.84	0/1117
18	AR	0.36	0/560	0.85	0/746
18	CR	0.39	0/560	0.86	0/746
19	AS	0.37	0/667	0.94	3/900 (0.3%)
19	CS	0.46	0/661	1.09	5/893 (0.6%)
20	AT	0.40	0/730	0.96	0/965
20	CT	0.42	0/729	0.98	1/965 (0.1%)
21	AU	0.36	0/203	0.87	0/266
21	CU	0.38	0/203	0.92	0/266
22	AV	0.24	0/310	0.39	0/480
22	CV	0.25	0/282	0.43	0/437
23	AW	0.20	0/18	0.39	0/26
23	CW	0.15	0/18	0.34	0/26
24	AX	0.29	0/1700	0.48	0/2650
24	CX	0.30	0/1700	0.49	0/2650
25	BA	0.26	0/68013	0.44	1/106165 (0.0%)
25	DA	0.23	0/67542	0.44	0/105428
26	BB	0.24	0/2878	0.48	0/4490
26	DB	0.24	0/2878	0.44	0/4490
27	BD	0.48	0/2186	0.90	4/2944 (0.1%)
27	DD	0.43	0/2186	0.93	5/2944 (0.2%)
28	BE	0.44	0/1592	0.89	2/2149 (0.1%)
28	DE	0.44	0/1592	0.94	5/2149 (0.2%)
29	BF	0.47	0/1619	0.85	0/2193
29	DF	0.41	0/1615	0.94	5/2188 (0.2%)
30	BG	0.40	0/1450	0.96	5/1959 (0.3%)
30	DG	0.45	0/1449	1.10	11/1958 (0.6%)
31	BH	0.44	0/1356	0.91	1/1834 (0.1%)
31	DH	0.39	0/1356	0.96	3/1834 (0.2%)
32	BI	0.40	0/1100	0.93	2/1501 (0.1%)
32	DI	0.39	0/1076	0.91	0/1471
33	BN	0.44	0/1144	0.89	6/1543 (0.4%)
33	DN	0.42	0/1144	1.01	9/1543 (0.6%)
34	BO	0.47	0/943	0.85	0/1269
34	DO	0.44	0/943	0.85	0/1269
35	BP	0.44	0/1152	0.89	3/1533 (0.2%)
35	DP	0.39	0/1152	0.94	6/1533 (0.4%)
36	BQ	0.47	0/1143	0.82	1/1527 (0.1%)
36	DQ	0.42	0/1143	0.89	0/1527
37	BR	0.45	0/982	0.82	1/1312 (0.1%)
37	DR	0.41	0/982	0.78	0/1312
38	BS	0.43	0/887	0.87	1/1180 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	DS	0.40	0/880	0.96	2/1172 (0.2%)
39	BT	0.41	0/1105	0.85	0/1477
39	DT	0.38	0/1097	0.84	2/1468 (0.1%)
40	BU	0.47	0/977	0.84	0/1301
40	DU	0.42	0/977	0.84	0/1301
41	BV	0.45	0/782	0.83	0/1049
41	DV	0.40	0/782	0.90	1/1049 (0.1%)
42	BW	0.49	0/897	0.86	2/1205 (0.2%)
42	DW	0.43	0/897	0.85	2/1205 (0.2%)
43	BX	0.48	0/764	0.84	1/1025 (0.1%)
43	DX	0.41	0/764	0.85	0/1025
44	BY	0.46	0/819	0.91	1/1095 (0.1%)
44	DY	0.40	0/819	0.94	1/1095 (0.1%)
45	BZ	0.43	0/1379	0.98	7/1873 (0.4%)
45	DZ	0.39	0/1390	1.00	8/1890 (0.4%)
46	B0	0.42	0/662	0.90	2/881 (0.2%)
46	D0	0.38	0/662	0.91	3/881 (0.3%)
47	B1	0.44	0/762	0.88	1/1014 (0.1%)
47	D1	0.40	0/762	0.85	1/1014 (0.1%)
48	B2	0.44	0/590	0.88	1/781 (0.1%)
48	D2	0.39	0/590	0.82	0/781
49	B3	0.45	0/474	0.90	0/635
49	D3	0.37	0/469	0.88	0/630
50	B4	0.50	0/565	1.23	10/761 (1.3%)
50	D4	0.49	0/545	1.13	2/737 (0.3%)
51	B5	0.48	0/469	0.80	1/635 (0.2%)
51	D5	0.44	0/469	0.81	0/635
52	B6	0.46	0/460	0.82	2/613 (0.3%)
52	D6	0.37	0/456	0.81	0/608
53	B7	0.48	0/426	0.80	0/561
53	D7	0.46	0/426	0.83	2/561 (0.4%)
54	B8	0.49	0/519	0.88	0/684
54	D8	0.38	0/525	0.89	2/691 (0.3%)
55	B9	0.42	0/310	0.78	0/407
55	D9	0.38	0/310	0.84	0/407
All	All	0.31	0/310281	0.61	216/464152 (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	2
7	AG	0	1
20	CT	0	1
27	BD	0	1
38	BS	0	1
All	All	0	6

There are no bond length outliers.

All (216) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	AM	84	ILE	N-CA-C	10.82	122.79	111.00
30	DG	178	PHE	CA-C-N	9.77	130.16	119.90
30	DG	178	PHE	C-N-CA	9.77	130.16	119.90
7	CG	79	ARG	N-CA-C	9.07	122.09	108.31
33	DN	10	GLU	CA-C-N	8.92	129.00	119.90
33	DN	10	GLU	C-N-CA	8.92	129.00	119.90
46	B0	13	GLY	N-CA-C	8.89	124.27	114.40
50	B4	60	GLN	N-CA-C	-8.70	101.98	112.59
7	CG	79	ARG	CB-CA-C	-8.65	106.59	116.54
45	DZ	158	PRO	CA-C-N	8.48	128.99	119.92
45	DZ	158	PRO	C-N-CA	8.48	128.99	119.92
2	CB	122	PHE	N-CA-C	-8.45	96.68	109.94
45	BZ	153	SER	N-CA-C	-8.02	102.49	111.07
4	AD	188	LEU	CA-C-N	7.94	128.43	119.93
4	AD	188	LEU	C-N-CA	7.94	128.43	119.93
28	DE	73	GLU	CA-C-N	7.91	127.97	119.90
28	DE	73	GLU	C-N-CA	7.91	127.97	119.90
44	DY	91	GLU	N-CA-C	-7.86	103.48	113.23
46	D0	82	ARG	CA-C-N	7.75	128.22	119.92
46	D0	82	ARG	C-N-CA	7.75	128.22	119.92
32	BI	110	ASP	CA-C-N	7.65	127.20	119.24
32	BI	110	ASP	C-N-CA	7.65	127.20	119.24
35	BP	22	GLY	CA-C-N	7.64	126.92	118.97
35	BP	22	GLY	C-N-CA	7.64	126.92	118.97
29	DF	24	LEU	CA-C-N	7.60	127.65	119.90
29	DF	24	LEU	C-N-CA	7.60	127.65	119.90
28	DE	72	VAL	CA-C-N	7.53	135.25	121.70
28	DE	72	VAL	C-N-CA	7.53	135.25	121.70
36	BQ	24	GLY	N-CA-C	-7.21	104.65	115.32
30	DG	166	ASP	N-CA-C	7.15	119.15	111.36
46	B0	12	ASN	N-CA-C	7.12	121.68	112.92
45	BZ	158	PRO	CA-C-N	7.11	128.73	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	BZ	158	PRO	C-N-CA	7.11	128.73	119.84
50	B4	40	HIS	CA-C-N	7.02	128.61	119.84
50	B4	40	HIS	C-N-CA	7.02	128.61	119.84
19	CS	67	VAL	N-CA-C	7.02	117.16	110.42
2	AB	9	GLU	N-CA-C	7.01	119.97	109.25
1	CA	1154	G	N1-C2-N2	-6.98	95.25	116.20
15	AO	87	ILE	N-CA-C	6.90	118.22	111.67
4	CD	171	GLY	CA-C-N	6.89	127.47	119.47
4	CD	171	GLY	C-N-CA	6.89	127.47	119.47
12	CL	44	THR	CA-C-N	6.89	127.34	120.52
12	CL	44	THR	C-N-CA	6.89	127.34	120.52
35	DP	44	GLY	CA-C-N	6.86	134.04	121.70
35	DP	44	GLY	C-N-CA	6.86	134.04	121.70
4	AD	135	LEU	CA-C-N	6.77	126.47	119.56
4	AD	135	LEU	C-N-CA	6.77	126.47	119.56
16	CP	45	THR	CA-C-N	6.74	128.27	119.84
16	CP	45	THR	C-N-CA	6.74	128.27	119.84
19	AS	36	ARG	N-CA-C	-6.71	105.12	113.38
50	D4	46	GLN	CB-CA-C	-6.67	108.89	116.63
30	DG	141	PHE	CA-C-N	6.62	125.85	118.97
30	DG	141	PHE	C-N-CA	6.62	125.85	118.97
7	CG	8	GLU	N-CA-C	6.55	119.48	110.24
54	D8	62	LEU	CA-C-N	6.47	126.18	119.64
54	D8	62	LEU	C-N-CA	6.47	126.18	119.64
30	BG	45	GLU	N-CA-C	-6.47	104.65	112.54
35	DP	22	GLY	CA-C-N	6.46	125.69	118.97
35	DP	22	GLY	C-N-CA	6.46	125.69	118.97
2	CB	9	GLU	N-CA-C	6.31	124.24	110.80
50	B4	52	THR	N-CA-C	-6.30	105.53	112.72
2	CB	130	ARG	N-CA-C	6.29	117.99	110.07
42	BW	13	SER	CA-C-N	6.28	125.77	119.24
42	BW	13	SER	C-N-CA	6.28	125.77	119.24
3	CC	91	LEU	N-CA-C	6.25	117.90	111.14
30	DG	174	GLU	N-CA-C	-6.24	105.98	113.97
19	CS	41	VAL	CA-C-N	6.23	127.63	119.84
19	CS	41	VAL	C-N-CA	6.23	127.63	119.84
50	B4	68	ARG	N-CA-C	6.20	118.98	110.24
47	B1	84	GLY	N-CA-C	-6.20	106.86	114.92
2	AB	23	ARG	N-CA-C	-6.18	106.01	112.93
5	CE	68	GLU	N-CA-C	6.17	118.80	111.33
27	BD	274	ARG	N-CA-C	6.17	119.21	109.96
45	DZ	129	SER	CA-C-N	6.09	125.58	119.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	DZ	129	SER	C-N-CA	6.09	125.58	119.24
33	DN	94	HIS	CA-C-N	6.08	125.70	119.56
33	DN	94	HIS	C-N-CA	6.08	125.70	119.56
10	AJ	33	GLN	N-CA-C	6.06	118.32	108.26
9	CI	44	VAL	N-CA-C	-6.03	107.38	113.47
9	CI	59	PHE	N-CA-C	6.02	118.71	108.90
53	D7	6	GLN	CA-C-N	6.01	126.03	119.90
53	D7	6	GLN	C-N-CA	6.01	126.03	119.90
29	DF	79	GLY	N-CA-C	-5.99	107.47	115.32
38	DS	74	ALA	N-CA-C	5.99	117.89	111.36
2	AB	127	ILE	N-CA-C	5.98	116.97	108.42
1	CA	1154	G	N3-C2-N2	5.97	137.82	119.90
1	CA	1119	C	N1-C2-O2	5.97	136.81	118.90
33	DN	77	GLY	N-CA-C	-5.94	107.62	114.69
13	CM	40	ASN	CA-C-N	5.92	126.34	119.47
13	CM	40	ASN	C-N-CA	5.92	126.34	119.47
25	BA	1992	G	C2'-C3'-O3'	5.92	118.39	109.50
30	DG	26	GLN	N-CA-C	-5.89	106.09	113.28
1	AA	991	U	P-O3'-C3'	5.88	129.02	120.20
52	B6	40	CYS	CA-C-N	5.88	125.42	119.19
52	B6	40	CYS	C-N-CA	5.88	125.42	119.19
27	BD	41	GLY	N-CA-C	-5.88	107.54	115.36
7	CG	57	GLU	CA-C-N	5.87	126.01	119.32
7	CG	57	GLU	C-N-CA	5.87	126.01	119.32
2	AB	21	ARG	N-CA-C	5.86	118.31	107.99
45	DZ	133	ILE	CA-C-N	5.84	126.03	120.31
45	DZ	133	ILE	C-N-CA	5.84	126.03	120.31
33	DN	110	GLY	CA-C-N	5.83	125.04	118.97
33	DN	110	GLY	C-N-CA	5.83	125.04	118.97
13	CM	106	ASN	N-CA-C	5.82	117.70	108.67
8	AH	56	LYS	CA-C-N	5.78	127.34	120.23
8	AH	56	LYS	C-N-CA	5.78	127.34	120.23
33	BN	110	GLY	CA-C-N	5.78	124.98	118.97
33	BN	110	GLY	C-N-CA	5.78	124.98	118.97
13	AM	9	ILE	CA-C-N	5.78	126.07	119.83
13	AM	9	ILE	C-N-CA	5.78	126.07	119.83
12	CL	28	LYS	N-CA-C	5.77	119.20	111.24
38	DS	82	ILE	N-CA-C	5.75	116.49	109.30
1	CA	1004	A	O4'-C1'-N9	5.75	117.13	108.50
41	DV	14	VAL	N-CA-C	5.75	117.96	108.99
39	DT	80	SER	CA-C-N	5.73	125.43	119.82
39	DT	80	SER	C-N-CA	5.73	125.43	119.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
19	CS	10	PHE	N-CA-C	5.71	118.03	108.96
35	DP	40	SER	N-CA-C	-5.71	105.04	112.23
2	AB	38	GLY	N-CA-C	-5.70	106.12	114.90
30	BG	127	GLY	N-CA-C	-5.70	107.12	113.79
27	DD	275	LYS	N-CA-C	-5.69	100.51	109.50
11	AK	38	ASN	CA-C-N	5.68	126.01	119.93
11	AK	38	ASN	C-N-CA	5.68	126.01	119.93
29	DF	21	ALA	CA-C-N	5.67	131.91	121.70
29	DF	21	ALA	C-N-CA	5.67	131.91	121.70
2	CB	95	GLN	N-CA-C	5.66	116.66	108.34
30	BG	31	VAL	CA-C-N	5.65	125.66	119.90
30	BG	31	VAL	C-N-CA	5.65	125.66	119.90
2	CB	129	GLU	N-CA-C	-5.64	105.90	112.89
35	DP	26	GLY	N-CA-C	-5.62	107.48	115.30
20	CT	11	SER	N-CA-C	-5.58	106.14	113.17
12	CL	119	LYS	N-CA-C	-5.57	102.65	110.50
8	CH	6	ILE	N-CA-C	5.56	115.65	110.42
50	D4	52	THR	N-CA-C	-5.56	106.34	113.23
2	AB	130	ARG	N-CA-C	-5.56	103.04	109.93
33	BN	125	GLY	CA-C-N	5.55	126.03	120.04
33	BN	125	GLY	C-N-CA	5.55	126.03	120.04
7	AG	116	ALA	N-CA-C	5.53	117.30	111.28
45	BZ	157	LEU	CA-C-N	5.50	126.04	120.38
45	BZ	157	LEU	C-N-CA	5.50	126.04	120.38
45	DZ	14	LYS	CA-C-N	5.49	125.84	119.47
45	DZ	14	LYS	C-N-CA	5.49	125.84	119.47
5	CE	145	LYS	N-CA-C	-5.49	105.30	111.28
31	DH	31	GLY	N-CA-C	5.48	117.39	110.38
45	BZ	133	ILE	CA-C-N	5.47	125.67	120.31
45	BZ	133	ILE	C-N-CA	5.47	125.67	120.31
19	CS	30	LEU	N-CA-C	5.47	118.16	110.23
27	BD	275	LYS	N-CA-C	5.45	122.40	110.80
30	BG	174	GLU	N-CA-C	-5.45	106.76	113.41
3	CC	130	VAL	N-CA-C	5.45	115.65	110.53
35	BP	38	GLN	N-CA-C	5.44	117.21	111.28
43	BX	69	TYR	N-CA-C	5.43	117.61	107.99
1	AA	991	U	C2'-C3'-O3'	5.42	117.64	109.50
9	AI	63	ILE	N-CA-C	5.42	115.80	107.77
27	BD	42	GLY	N-CA-C	-5.42	107.72	115.64
51	B5	41	PRO	O-C-N	5.41	123.69	121.15
1	CA	1154	G	C5-C6-O6	5.41	144.82	128.60
9	AI	44	VAL	N-CA-C	-5.40	107.86	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	DG	65	GLY	N-CA-C	-5.39	107.81	115.30
10	AJ	32	ALA	N-CA-C	5.39	119.02	112.23
30	DG	22	ARG	N-CA-C	5.39	117.85	111.33
48	B2	69	ARG	N-CA-C	5.38	116.95	111.14
30	DG	48	GLU	N-CA-C	-5.36	106.75	113.72
50	B4	28	LYS	CA-C-N	5.35	124.68	118.85
50	B4	28	LYS	C-N-CA	5.35	124.68	118.85
33	DN	125	GLY	CA-C-N	5.34	125.04	119.64
33	DN	125	GLY	C-N-CA	5.34	125.04	119.64
2	CB	130	ARG	CA-C-N	5.34	125.28	119.78
2	CB	130	ARG	C-N-CA	5.34	125.28	119.78
27	DD	136	ILE	CA-C-N	5.31	125.61	119.93
27	DD	136	ILE	C-N-CA	5.31	125.61	119.93
44	BY	92	ASN	N-CA-C	5.30	117.06	111.28
11	CK	38	ASN	CA-C-N	5.29	125.59	119.93
11	CK	38	ASN	C-N-CA	5.29	125.59	119.93
50	B4	65	ASP	N-CA-C	-5.28	106.68	113.02
27	DD	107	ALA	CA-C-N	5.27	125.47	120.31
27	DD	107	ALA	C-N-CA	5.27	125.47	120.31
28	DE	127	ASP	N-CA-C	-5.26	106.72	112.72
2	AB	90	MET	CA-C-N	5.26	125.17	119.76
2	AB	90	MET	C-N-CA	5.26	125.17	119.76
28	BE	21	VAL	CA-C-N	5.26	125.42	119.90
28	BE	21	VAL	C-N-CA	5.26	125.42	119.90
46	D0	12	ASN	CB-CA-C	-5.25	109.51	117.07
7	CG	78	ARG	N-CA-C	5.21	116.67	107.61
2	AB	10	LEU	N-CA-C	5.20	121.88	110.80
2	AB	166	ASP	CA-C-N	5.18	124.97	119.28
2	AB	166	ASP	C-N-CA	5.18	124.97	119.28
38	BS	40	ILE	N-CA-C	5.16	116.02	108.53
2	AB	193	ASP	CA-C-N	5.13	124.31	118.97
2	AB	193	ASP	C-N-CA	5.13	124.31	118.97
2	CB	233	SER	N-CA-C	5.13	116.46	110.31
31	DH	153	LYS	CA-C-N	5.13	125.42	119.93
31	DH	153	LYS	C-N-CA	5.13	125.42	119.93
37	BR	38	VAL	CB-CA-C	-5.12	108.83	113.70
2	CB	123	ALA	CB-CA-C	-5.12	110.69	116.63
7	AG	17	VAL	N-CA-C	5.12	115.23	110.42
2	AB	84	GLU	N-CA-C	5.11	116.86	111.28
2	CB	112	VAL	N-CA-C	-5.11	105.14	112.35
30	DG	23	PHE	N-CA-C	-5.11	106.45	113.30
47	D1	67	ILE	CB-CA-C	-5.10	108.86	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
19	AS	41	VAL	CA-C-N	5.09	126.20	119.84
19	AS	41	VAL	C-N-CA	5.09	126.20	119.84
5	CE	105	VAL	CA-C-N	-5.09	113.47	119.84
5	CE	105	VAL	C-N-CA	-5.09	113.47	119.84
31	BH	9	ILE	N-CA-C	5.09	112.58	107.55
33	BN	128	HIS	CA-C-N	5.08	125.76	120.12
33	BN	128	HIS	C-N-CA	5.08	125.76	120.12
50	B4	51	ASP	N-CA-C	5.06	117.50	107.98
12	AL	105	TYR	CB-CA-C	-5.05	110.77	116.63
42	DW	13	SER	CA-C-N	5.04	124.48	119.24
42	DW	13	SER	C-N-CA	5.04	124.48	119.24
2	CB	95	GLN	CB-CA-C	-5.03	109.19	116.54
12	CL	105	TYR	CB-CA-C	-5.03	110.80	116.63
2	CB	214	ILE	N-CA-C	5.03	115.25	110.53
5	CE	103	GLY	N-CA-C	-5.02	106.11	112.54
50	B4	49	PHE	CB-CA-C	-5.01	110.77	116.54

There are no chirality outliers.

All (6) planarity outliers are listed below:

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

5.2 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	16254	643	0
1	CA	32312	0	16307	730	0
2	AB	1846	0	1867	87	0
2	CB	1825	0	1828	99	0
3	AC	1552	0	1546	69	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	CC	1542	0	1517	72	0
4	AD	1659	0	1676	66	0
4	CD	1670	0	1703	68	0
5	AE	1129	0	1185	31	0
5	CE	1133	0	1191	55	0
6	AF	806	0	793	32	0
6	CF	816	0	808	25	0
7	AG	1231	0	1238	30	0
7	CG	1235	0	1249	31	0
8	AH	1088	0	1126	26	0
8	CH	1088	0	1126	38	0
9	AI	983	0	986	52	0
9	CI	978	0	966	56	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	35	0
11	AK	829	0	825	18	0
11	CK	833	0	836	24	0
12	AL	930	0	979	32	0
12	CL	930	0	980	34	0
13	AM	958	0	1002	40	0
13	CM	950	0	988	56	0
14	AN	492	0	529	25	0
14	CN	492	0	529	36	0
15	AO	728	0	760	22	0
15	CO	728	0	760	31	0
16	AP	681	0	697	30	0
16	CP	677	0	686	28	0
17	AQ	823	0	891	23	0
17	CQ	823	0	891	22	0
18	AR	555	0	618	16	0
18	CR	555	0	618	22	0
19	AS	652	0	662	28	0
19	CS	646	0	644	53	0
20	AT	728	0	798	29	0
20	CT	727	0	796	29	0
21	AU	199	0	208	8	0
21	CU	199	0	208	12	0
22	AV	277	0	140	6	0
22	CV	252	0	130	8	0
23	AW	54	0	40	5	0
23	CW	54	0	40	7	0
24	AX	1635	0	838	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	CX	1635	0	838	39	0
25	BA	60729	0	30621	828	0
25	DA	60311	0	30408	1074	0
26	BB	2573	0	1306	30	0
26	DB	2573	0	1306	90	0
27	BD	2136	0	2218	60	0
27	DD	2136	0	2217	68	0
28	BE	1559	0	1618	55	0
28	DE	1559	0	1618	59	0
29	BF	1584	0	1625	39	0
29	DF	1580	0	1619	71	0
30	BG	1425	0	1443	45	0
30	DG	1424	0	1434	79	0
31	BH	1330	0	1407	29	0
31	DH	1330	0	1407	43	0
32	BI	1085	0	1114	40	0
32	DI	1061	0	1080	34	0
33	BN	1117	0	1184	26	0
33	DN	1117	0	1184	35	0
34	BO	933	0	996	27	0
34	DO	933	0	996	36	0
35	BP	1135	0	1212	36	0
35	DP	1135	0	1211	54	0
36	BQ	1122	0	1179	35	0
36	DQ	1122	0	1179	48	0
37	BR	968	0	1033	28	0
37	DR	968	0	1033	30	0
38	BS	877	0	938	23	0
38	DS	870	0	923	52	0
39	BT	1091	0	1151	32	0
39	DT	1083	0	1136	39	0
40	BU	959	0	1019	19	0
40	DU	959	0	1019	32	0
41	BV	771	0	830	16	0
41	DV	771	0	830	24	0
42	BW	886	0	940	11	0
42	DW	886	0	940	18	0
43	BX	750	0	814	14	0
43	DX	750	0	814	17	0
44	BY	806	0	881	31	0
44	DY	806	0	881	25	0
45	BZ	1349	0	1355	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	DZ	1360	0	1363	64	0
46	B0	653	0	674	29	0
46	D0	653	0	674	25	0
47	B1	755	0	826	12	0
47	D1	755	0	826	26	0
48	B2	588	0	643	13	0
48	D2	588	0	643	18	0
49	B3	469	0	518	9	0
49	D3	464	0	514	16	0
50	B4	552	0	533	27	0
50	D4	532	0	503	31	0
51	B5	455	0	465	12	0
51	D5	455	0	465	13	0
52	B6	453	0	473	9	0
52	D6	449	0	469	14	0
53	B7	418	0	467	13	0
53	D7	418	0	467	13	0
54	B8	511	0	571	18	0
54	D8	517	0	582	34	0
55	B9	307	0	335	4	0
55	D9	307	0	335	13	0
56	AA	187	0	0	0	0
56	AD	1	0	0	0	0
56	AE	2	0	0	0	0
56	AF	1	0	0	0	0
56	AK	1	0	0	0	0
56	AL	1	0	0	0	0
56	AM	1	0	0	0	0
56	AN	1	0	0	0	0
56	AX	7	0	0	0	0
56	B0	5	0	0	0	0
56	B3	2	0	0	0	0
56	B4	1	0	0	0	0
56	B5	2	0	0	0	0
56	B7	4	0	0	0	0
56	B8	1	0	0	0	0
56	B9	1	0	0	0	0
56	BA	675	0	0	0	0
56	BB	18	0	0	0	0
56	BD	8	0	0	0	0
56	BE	6	0	0	0	0
56	BF	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	BG	3	0	0	0	0
56	BH	1	0	0	0	0
56	BN	2	0	0	0	0
56	BO	1	0	0	0	0
56	BP	4	0	0	0	0
56	BQ	3	0	0	0	0
56	BR	3	0	0	0	0
56	BU	5	0	0	0	0
56	BV	3	0	0	0	0
56	BW	4	0	0	0	0
56	BX	3	0	0	0	0
56	BY	2	0	0	0	0
56	BZ	1	0	0	0	0
56	CA	154	0	0	0	0
56	CE	2	0	0	0	0
56	CF	1	0	0	0	0
56	CJ	1	0	0	0	0
56	CK	1	0	0	0	0
56	CT	1	0	0	0	0
56	CX	1	0	0	0	0
56	D0	1	0	0	0	0
56	D3	1	0	0	0	0
56	D5	1	0	0	0	0
56	D7	1	0	0	0	0
56	D8	2	0	0	0	0
56	DA	595	0	0	0	0
56	DB	12	0	0	0	0
56	DD	2	0	0	0	0
56	DE	5	0	0	0	0
56	DF	3	0	0	0	0
56	DG	1	0	0	0	0
56	DN	1	0	0	0	0
56	DP	1	0	0	0	0
56	DQ	3	0	0	0	0
56	DR	2	0	0	0	0
56	DT	1	0	0	0	0
56	DU	1	0	0	0	0
56	DV	2	0	0	0	0
56	DW	2	0	0	0	0
56	DY	1	0	0	0	0
57	AD	8	0	0	0	0
57	CD	8	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	AN	1	0	0	0	0
58	B4	1	0	0	0	0
58	B5	1	0	0	0	0
58	B6	1	0	0	0	0
58	B9	1	0	0	0	0
58	BY	1	0	0	0	0
58	CN	1	0	0	0	0
58	D4	1	0	0	0	0
58	D5	1	0	0	0	0
58	D6	1	0	0	0	0
58	D9	1	0	0	0	0
58	DY	1	0	0	0	0
59	AX	1	0	0	0	0
59	DA	1	0	0	0	0
60	AA	165	0	0	12	0
60	AJ	1	0	0	0	0
60	AL	3	0	0	2	0
60	AP	1	0	0	0	0
60	AU	1	0	0	0	0
60	AV	2	0	0	0	0
60	AW	3	0	0	0	0
60	B0	4	0	0	0	0
60	B1	2	0	0	0	0
60	B2	1	0	0	0	0
60	B3	1	0	0	0	0
60	B5	2	0	0	0	0
60	B7	2	0	0	1	0
60	B8	8	0	0	2	0
60	BA	924	0	0	62	0
60	BB	27	0	0	0	0
60	BD	6	0	0	2	0
60	BE	8	0	0	0	0
60	BF	6	0	0	1	0
60	BG	1	0	0	0	0
60	BH	1	0	0	1	0
60	BN	3	0	0	0	0
60	BO	1	0	0	0	0
60	BP	14	0	0	2	0
60	BQ	2	0	0	0	0
60	BS	1	0	0	0	0
60	BT	4	0	0	1	0
60	BU	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	BV	5	0	0	0	0
60	BW	1	0	0	0	0
60	BX	2	0	0	0	0
60	BZ	1	0	0	0	0
60	CA	113	0	0	5	0
60	CE	2	0	0	0	0
60	CJ	2	0	0	1	0
60	CL	1	0	0	1	0
60	CO	1	0	0	0	0
60	CW	1	0	0	1	0
60	CX	1	0	0	1	0
60	D0	5	0	0	0	0
60	D1	1	0	0	0	0
60	D3	1	0	0	2	0
60	D8	3	0	0	0	0
60	DA	689	0	0	58	0
60	DB	9	0	0	0	0
60	DD	11	0	0	2	0
60	DE	5	0	0	1	0
60	DF	6	0	0	0	0
60	DO	1	0	0	0	0
60	DP	6	0	0	0	0
60	DU	3	0	0	0	0
60	DV	1	0	0	0	0
60	DW	1	0	0	0	0
60	DX	3	0	0	0	0
All	All	289646	0	193084	5817	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (5817) 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)
25:DA:2121:G:H1	25:DA:2177:C:N4	1.35	1.23
19:CS:42:PRO:HG3	50:D4:61:ARG:HG2	1.39	1.04
1:AA:1028:C:N4	1:AA:1033:G:H1	1.56	1.01
25:DA:2128:C:H42	25:DA:2160:G:H1	1.08	1.00
25:DA:2137:C:H42	25:DA:2154:G:H1	1.05	0.99
1:CA:1164:G:H1	1:CA:1172:C:N4	1.58	0.98
1:CA:76:C:H42	1:CA:93:G:H1	1.08	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1028:C:H42	1:AA:1033:G:H1	0.99	0.97
25:BA:2124:G:H1	25:BA:2174:C:N4	1.62	0.97
1:CA:1114:C:H42	1:CA:1186:G:H1	0.99	0.96
1:AA:1502:A:H2	1:AA:1505:G:H1	1.14	0.95
25:DA:1169:G:H1	25:DA:1180:C:H42	1.11	0.95
1:CA:70:G:H1	1:CA:99:U:H3	1.12	0.94
16:AP:57:ARG:NH2	16:AP:79:VAL:O	2.00	0.93
30:BG:138:GLN:HE21	30:BG:138:GLN:H	1.13	0.93
1:AA:1246:C:H42	1:AA:1291:G:H1	1.15	0.92
1:AA:997:U:H3	1:AA:1044:A:H61	1.12	0.92
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.35	0.92
3:AC:118:GLN:HE21	3:AC:118:GLN:H	1.14	0.91
45:DZ:126:VAL:HG11	45:DZ:161:VAL:HG22	1.53	0.90
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.51	0.89
1:CA:1114:C:N4	1:CA:1186:G:H1	1.68	0.89
25:DA:2121:G:N2	25:DA:2177:C:N3	2.19	0.89
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.06	0.89
25:BA:2124:G:H1	25:BA:2174:C:H42	1.01	0.89
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.06	0.89
1:AA:1008:C:H42	1:AA:1021:G:H1	1.12	0.88
28:DE:54:GLN:HG2	28:DE:76:ARG:HG2	1.53	0.87
2:AB:155:LEU:HD11	2:AB:159:PRO:HD3	1.55	0.87
25:BA:2683:C:O2	34:BO:70:LYS:NZ	2.07	0.87
43:BX:53:LYS:HB3	43:BX:82:GLN:HB3	1.57	0.87
4:AD:166:LYS:HA	4:AD:178:VAL:HG21	1.57	0.86
50:B4:57:GLU:HB3	50:B4:58:ARG:HA	1.57	0.86
25:DA:1607:C:N4	25:DA:1622:G:OP2	2.08	0.86
25:BA:250:G:OP2	54:B8:13:ARG:NH2	2.07	0.86
1:AA:538:G:H5"	12:AL:114:LYS:HB2	1.57	0.86
25:BA:847:U:O4	25:BA:933:A:N6	2.08	0.86
43:DX:53:LYS:HB3	43:DX:82:GLN:HB3	1.57	0.86
1:AA:991:U:O2'	1:AA:992:U:OP2	1.94	0.86
25:BA:2124:G:N2	25:BA:2174:C:N3	2.24	0.85
1:AA:1311:G:H1	1:AA:1326:C:H42	1.21	0.85
41:DV:60:GLU:OE2	41:DV:97:LYS:NZ	2.10	0.85
25:BA:2243:U:OP1	60:BA:3807:HOH:O	1.94	0.84
25:DA:740:U:OP2	60:DA:4407:HOH:O	1.95	0.84
25:DA:272(G):C:H42	25:DA:363(C):G:H1	1.22	0.84
1:AA:201:C:H42	1:AA:216:G:H22	1.25	0.84
25:BA:993:G:OP1	40:BU:50:ARG:NH2	2.08	0.84
1:CA:400:C:H5"	4:CD:73:ARG:HH22	1.42	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1332:G:OP1	60:BA:4290:HOH:O	1.95	0.84
25:BA:1176:G:H1'	25:BA:1177:A:H5'	1.57	0.84
1:AA:1320:C:H5'	19:AS:70:LYS:HG3	1.58	0.84
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.11	0.84
45:DZ:121:HIS:HB2	45:DZ:171:ILE:HG22	1.60	0.84
25:DA:2807:G:N1	25:DA:2893:G:O6	2.11	0.83
25:DA:994:C:OP1	40:DU:53:ARG:NH2	2.11	0.83
1:CA:1075:C:OP1	2:CB:179:LYS:NZ	2.12	0.83
1:AA:1028:C:N3	1:AA:1033:G:N2	2.27	0.83
25:BA:2140:C:O2	25:BA:2151:G:N1	2.10	0.83
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.60	0.83
39:DT:19:LEU:HD23	39:DT:20:PRO:HD2	1.60	0.83
3:AC:172:ARG:NH2	3:AC:206:GLU:OE1	2.12	0.83
25:BA:279:C:H42	25:BA:361:G:H1	1.24	0.83
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.11	0.83
29:DF:53:THR:HG23	29:DF:55:GLY:H	1.44	0.83
25:BA:2140:C:N3	25:BA:2151:G:O6	2.12	0.83
25:BA:880:G:N2	25:BA:898:C:O2	2.12	0.83
25:BA:2139:C:N4	25:BA:2152:G:N1	2.27	0.83
25:DA:2683:C:O2	34:DO:70:LYS:NZ	2.10	0.82
50:B4:59:PHE:HD2	50:B4:62:ARG:HH22	1.26	0.82
25:DA:2867:G:OP2	39:DT:119:LYS:NZ	2.11	0.82
1:AA:975:A:H4'	1:AA:976:G:H5"	1.61	0.82
25:DA:299:A:H5"	44:DY:86:ARG:HH21	1.44	0.82
25:BA:2689:U:H4'	25:BA:2690:C:H5'	1.62	0.82
2:CB:80:ILE:HD13	2:CB:211:ILE:HB	1.61	0.82
3:AC:111:LEU:HD21	3:AC:144:SER:HB3	1.61	0.82
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.13	0.82
27:DD:85:ASP:OD2	27:DD:88:ARG:NH1	2.13	0.82
28:DE:27:LEU:HD22	39:DT:1:MET:HE3	1.60	0.82
1:AA:1008:C:N4	1:AA:1021:G:H1	1.77	0.81
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.13	0.81
2:CB:84:GLU:HB3	2:CB:219:VAL:HG21	1.61	0.81
24:CX:21:A:H61	24:CX:46:G:H2'	1.44	0.81
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.62	0.81
25:DA:2166:G:H3'	25:DA:2167:U:H5"	1.60	0.81
46:D0:11:ARG:O	46:D0:14:ARG:NH2	2.14	0.81
35:DP:56:SER:HB2	35:DP:61:ARG:HD2	1.61	0.81
19:AS:65:ASN:HA	50:B4:58:ARG:HG3	1.63	0.81
25:BA:1689:A:H62	25:BA:1698:A:H2	1.24	0.81
1:AA:1008:C:N3	1:AA:1021:G:N2	2.29	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:78:G:N2	1:AA:91:C:N3	2.28	0.81
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.43	0.81
1:CA:1262:C:N3	1:CA:1273:G:N2	2.29	0.81
25:BA:2142:C:N3	25:BA:2149:G:O6	2.14	0.81
1:CA:995:C:O2	14:CN:4:LYS:NZ	2.15	0.80
3:AC:82:GLU:HG2	3:AC:85:ARG:HH21	1.47	0.80
1:CA:1262:C:N4	1:CA:1273:G:N1	2.29	0.80
1:CA:1409:C:O2	1:CA:1491:G:N2	2.13	0.80
8:CH:41:ARG:NH2	8:CH:123:GLU:OE2	2.15	0.80
25:DA:1022:G:H22	25:DA:1142(A):A:H2	1.28	0.80
34:DO:35:VAL:HG11	34:DO:103:ALA:HB3	1.61	0.80
25:DA:245:G:O6	54:D8:8:LYS:NZ	2.15	0.80
25:DA:1693:U:O2'	27:DD:14:ARG:NH2	2.14	0.80
25:BA:631:A:OP1	35:BP:65:ARG:NH1	2.15	0.80
1:CA:76:C:N4	1:CA:93:G:H1	1.78	0.80
25:DA:2127:G:O6	25:DA:2161:C:N3	2.14	0.80
39:DT:16:ARG:NH2	39:DT:83:ILE:O	2.15	0.80
1:AA:664:G:H22	1:AA:741:G:H1	1.30	0.80
25:BA:2150:U:H2'	25:BA:2151:G:C8	2.17	0.80
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.64	0.80
25:DA:1039:G:O6	25:DA:1116:C:N4	2.15	0.80
32:DI:77:LEU:HB3	32:DI:142:VAL:HG12	1.62	0.80
3:CC:40:ARG:NH2	3:CC:55:VAL:O	2.15	0.80
1:AA:407:G:H5"	4:AD:115:ARG:HG2	1.64	0.80
23:CW:76:PPU:OP1	60:CW:101:HOH:O	1.99	0.80
32:BI:130:TYR:HB3	32:BI:138:ILE:HB	1.64	0.79
1:CA:1436:U:OP1	20:CT:23:ARG:NH2	2.14	0.79
25:DA:1019:U:H3	25:DA:1142(A):A:H62	1.28	0.79
15:CO:4:THR:OG1	15:CO:7:GLU:OE1	2.00	0.79
1:AA:1030:C:N3	1:AA:1031:G:N2	2.30	0.79
25:DA:2137:C:N4	25:DA:2154:G:H1	1.79	0.79
45:DZ:72:ARG:NH2	45:DZ:97:GLU:O	2.15	0.79
1:CA:201:C:H42	1:CA:216:G:H1	1.29	0.79
1:CA:950:U:H3	1:CA:1231:G:H1	1.29	0.79
15:CO:54:ARG:HG2	15:CO:58:MET:HE2	1.64	0.79
1:AA:1025:U:O2	1:AA:1036:G:O6	2.01	0.79
25:BA:100:G:O2'	48:B2:7:ARG:NH2	2.15	0.79
54:B8:62:LEU:HB3	54:B8:65:GLU:HG3	1.64	0.79
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.64	0.79
1:AA:1228:C:OP1	13:AM:115:LYS:N	2.15	0.79
25:BA:1310:G:OP2	53:B7:9:ARG:NH1	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2287:A:H62	25:BA:2344:U:H3	1.29	0.79
29:BF:18:ARG:NH2	29:BF:127:GLU:OE1	2.15	0.79
46:B0:11:ARG:O	46:B0:14:ARG:NH2	2.16	0.79
28:DE:72:VAL:HG22	28:DE:73:GLU:HG3	1.64	0.79
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.15	0.79
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.15	0.78
25:BA:400:G:N7	60:BA:4516:HOH:O	2.16	0.78
35:BP:42:SER:O	60:BP:304:HOH:O	2.00	0.78
35:BP:89:ALA:O	35:BP:121:LYS:NZ	2.15	0.78
1:CA:613:C:N4	1:CA:627:G:O6	2.16	0.78
25:DA:2128:C:N4	25:DA:2160:G:H1	1.81	0.78
25:BA:2533:A:OP2	60:BA:3962:HOH:O	2.00	0.78
30:DG:114:ILE:HG23	30:DG:136:ARG:HH22	1.48	0.78
43:DX:8:ILE:O	48:D2:36:ARG:NH2	2.15	0.78
1:AA:78:G:N1	1:AA:91:C:N4	2.31	0.78
25:BA:2646:C:OP2	25:BA:2732:G:O2'	1.99	0.78
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.66	0.78
1:CA:1164:G:N2	1:CA:1172:C:N3	2.31	0.78
25:DA:2805:G:H2'	25:DA:2807:G:C8	2.18	0.78
1:AA:1246:C:N4	1:AA:1291:G:H1	1.82	0.78
1:AA:642:A:N3	8:AH:113:SER:OG	2.16	0.78
25:BA:1315:C:OP2	60:BA:4290:HOH:O	2.01	0.78
25:DA:1309:G:H4'	53:D7:7:PRO:HB2	1.65	0.78
4:CD:103:ASN:OD1	4:CD:114:ARG:NH2	2.16	0.77
49:D3:5:LYS:NZ	49:D3:34:GLU:OE2	2.16	0.77
2:AB:15:VAL:O	2:AB:16:HIS:ND1	2.13	0.77
13:AM:58:GLU:O	13:AM:62:ASN:ND2	2.17	0.77
1:CA:1204:A:OP1	14:CN:3:ARG:NH1	2.17	0.77
27:BD:71:ASP:HB2	27:BD:103:ARG:HH22	1.48	0.77
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.66	0.77
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.02	0.77
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.17	0.77
25:DA:11:G:N7	60:DA:4445:HOH:O	2.17	0.77
27:DD:276:LYS:HD3	27:DD:276:LYS:H	1.49	0.77
1:CA:158:G:N2	1:CA:163:C:O2	2.16	0.77
25:DA:2357:U:OP1	46:D0:20:ARG:NH1	2.17	0.77
25:BA:2711:A:OP1	60:BA:4079:HOH:O	2.03	0.77
34:BO:35:VAL:HG11	34:BO:103:ALA:HB3	1.67	0.77
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.18	0.77
1:CA:542:G:OP1	4:CD:10:ARG:NH1	2.16	0.77
3:CC:5:ILE:HD11	14:CN:58:LYS:HE3	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:13:ARG:NH1	4:CD:38:TYR:O	2.18	0.77
22:CV:16:A:H61	24:CX:36:U:H3	1.33	0.77
25:BA:2285:C:OP2	52:B6:6:ARG:NH1	2.17	0.76
13:AM:39:ILE:HD12	13:AM:52:GLU:HG3	1.67	0.76
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.18	0.76
30:DG:176:LEU:HB2	30:DG:178:PHE:HE1	1.46	0.76
25:DA:2127:G:N1	25:DA:2161:C:O2	2.18	0.76
1:AA:997:U:H3	1:AA:1044:A:N6	1.83	0.76
1:CA:1310:G:OP1	13:CM:77:ASN:ND2	2.18	0.76
24:CX:19:G:H1	24:CX:56:C:H42	1.34	0.76
30:DG:176:LEU:HB2	30:DG:178:PHE:CE1	2.19	0.76
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.50	0.76
25:BA:1470:G:N7	60:BA:3868:HOH:O	2.17	0.76
1:CA:1392:G:H21	1:CA:1502:A:H8	1.31	0.76
25:DA:2657:A:O3'	31:DH:160:LYS:NZ	2.18	0.76
35:BP:26:GLY:O	60:BP:305:HOH:O	2.03	0.76
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.18	0.76
5:CE:50:GLU:HB2	5:CE:53:LEU:HD12	1.67	0.76
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.51	0.76
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.67	0.76
32:BI:77:LEU:HB3	32:BI:142:VAL:HG12	1.68	0.76
26:DB:22:U:H3	26:DB:61:G:H1	1.32	0.76
1:AA:1030:C:N4	1:AA:1031:G:N1	2.34	0.76
26:DB:5:C:OP1	26:DB:61:G:O2'	2.03	0.76
47:B1:23:LYS:HB3	47:B1:29:GLY:HA3	1.67	0.75
1:CA:575:G:N2	1:CA:880:C:O2	2.17	0.75
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.18	0.75
4:AD:173:TRP:HA	4:AD:187:ARG:CZ	2.16	0.75
25:DA:785:G:OP2	60:DA:4120:HOH:O	2.02	0.75
25:DA:1689:A:H62	25:DA:1698:A:H2	1.32	0.75
38:DS:41:ASP:O	38:DS:44:LYS:NZ	2.20	0.75
1:CA:975:A:H4'	1:CA:976:G:H5"	1.67	0.75
14:CN:37:PHE:HZ	14:CN:56:VAL:HG21	1.49	0.75
25:BA:2139:C:N4	25:BA:2152:G:C6	2.54	0.75
25:BA:2721:A:N7	60:BA:3890:HOH:O	2.19	0.75
27:BD:108:PRO:HB3	27:BD:143:HIS:CE1	2.21	0.75
30:BG:143:GLU:O	50:B4:28:LYS:NZ	2.19	0.75
27:DD:71:ASP:HB2	27:DD:103:ARG:HH22	1.50	0.75
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.04	0.75
25:BA:2713:A:OP1	37:BR:14:SER:OG	2.05	0.75
34:BO:86:ILE:HG22	34:BO:94:ARG:HG3	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CS:36:ARG:NH2	19:CS:75:ALA:O	2.19	0.75
1:AA:1125:U:O2'	1:AA:1127:G:N7	2.16	0.75
45:BZ:69:THR:HG22	45:BZ:90:VAL:HA	1.68	0.75
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.68	0.75
25:DA:2121:G:H1	25:DA:2177:C:H42	0.76	0.75
25:BA:1695:G:N7	27:BD:14:ARG:NH2	2.34	0.75
41:DV:52:VAL:HG21	41:DV:55:ALA:HB3	1.68	0.75
25:BA:956:G:O6	60:BA:3746:HOH:O	2.05	0.75
25:BA:2867:G:OP2	39:BT:119:LYS:NZ	2.19	0.75
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.20	0.75
13:AM:3:ARG:HG2	13:AM:8:GLU:HG3	1.69	0.74
49:B3:18:ASP:OD1	49:B3:18:ASP:N	2.20	0.74
1:CA:1353:G:OP1	21:CU:10:ARG:NH1	2.19	0.74
6:CF:11:ASN:HB3	6:CF:14:LEU:HG	1.67	0.74
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.69	0.74
1:CA:986:A:N3	19:CS:52:TYR:OH	2.20	0.74
38:DS:34:HIS:ND1	38:DS:53:SER:OG	2.19	0.74
13:AM:86:CYS:HB2	19:AS:73:GLU:HB3	1.68	0.74
26:BB:87:G:N2	26:BB:90:A:OP2	2.18	0.74
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.69	0.74
25:DA:2137:C:N3	25:DA:2154:G:N2	2.35	0.74
26:DB:87:G:N2	26:DB:90:A:OP2	2.21	0.74
25:DA:330:A:H2	25:DA:1210:A:H2'	1.52	0.74
25:DA:1828:G:OP1	60:DA:4417:HOH:O	2.06	0.74
25:DA:2114:A:N6	25:DA:2119:A:N7	2.36	0.74
25:BA:2114:A:N6	25:BA:2119:A:N7	2.35	0.74
25:BA:2142:C:O2	25:BA:2149:G:N1	2.15	0.74
25:DA:2122:U:O4	25:DA:2176:A:N1	2.21	0.74
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.69	0.74
25:BA:671:C:N4	60:BA:4439:HOH:O	2.20	0.74
1:CA:1029:C:N4	1:CA:1032:G:H1	1.84	0.74
2:CB:102:LEU:HD23	2:CB:182:ILE:HD13	1.70	0.74
13:CM:84:ILE:O	13:CM:86:CYS:N	2.16	0.74
25:DA:1143:A:OP1	33:DN:25:ARG:NH2	2.21	0.74
25:BA:2308:G:O6	25:BA:2311:A:N6	2.16	0.73
48:B2:22:GLU:OE2	48:B2:68:ARG:NH2	2.21	0.73
1:AA:153:C:H42	1:AA:168:G:H1	1.34	0.73
25:BA:245:G:O6	54:B8:8:LYS:NZ	2.21	0.73
25:BA:2141:G:O6	25:BA:2150:U:O2	2.06	0.73
4:CD:108:LEU:HD21	4:CD:183:GLY:HA3	1.70	0.73
25:DA:1890:A:OP2	60:DA:4558:HOH:O	2.06	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.52	0.73
25:DA:2518:A:OP2	60:DA:4240:HOH:O	2.06	0.73
16:AP:34:GLU:OE2	16:AP:55:ARG:NH2	2.20	0.73
1:CA:831:U:H3	1:CA:855:G:H1	1.35	0.73
25:DA:2629:A:O2'	25:DA:2630:G:OP2	2.04	0.73
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.52	0.73
4:AD:186:LEU:HB2	4:AD:187:ARG:HH21	1.54	0.73
1:CA:455:C:H42	1:CA:476:G:H1	1.37	0.73
1:CA:352:C:OP2	60:CA:4035:HOH:O	2.06	0.73
1:CA:1120:G:C6	1:CA:1154:G:N2	2.57	0.73
25:DA:782:A:OP2	60:DA:4013:HOH:O	2.07	0.73
47:D1:52:ARG:HH21	47:D1:57:GLU:HB2	1.54	0.73
25:BA:2096:U:H3	25:BA:2193:G:H1	1.35	0.73
25:DA:2119:A:H2	25:DA:2171:A:H5'	1.54	0.73
25:DA:2171:A:N3	25:DA:2172:U:N3	2.36	0.73
25:BA:2107:C:H42	25:BA:2182:G:H1	1.36	0.73
35:BP:126:VAL:HG12	35:BP:148:LEU:HD23	1.70	0.73
6:CF:35:ALA:HB2	6:CF:67:MET:HE2	1.71	0.73
1:AA:662:G:H2'	1:AA:663:A:C8	2.24	0.72
25:DA:2753:A:N3	55:D9:15:LYS:NZ	2.36	0.72
10:AJ:31:GLY:HA3	10:AJ:81:THR:HG21	1.71	0.72
24:AX:49:G:H1	24:AX:65:C:H42	1.37	0.72
25:BA:2139:C:N3	25:BA:2152:G:N2	2.37	0.72
1:CA:875:C:H1'	8:CH:15:ASN:HD21	1.53	0.72
25:DA:918:A:O2'	26:DB:97:G:N2	2.20	0.72
25:DA:2064:C:OP2	60:DA:4454:HOH:O	2.05	0.72
25:DA:601:C:OP1	29:DF:108:LYS:NZ	2.21	0.72
25:BA:1693:U:O2'	27:BD:14:ARG:NH2	2.22	0.72
25:DA:2805:G:H2'	25:DA:2807:G:H8	1.51	0.72
1:AA:1183:A:H3'	1:AA:1184:G:H5"	1.72	0.72
25:BA:1019:U:H3	25:BA:1142(A):A:H62	1.35	0.72
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.22	0.72
25:DA:82:G:N1	25:DA:103:A:OP2	2.19	0.72
3:CC:111:LEU:HD22	3:CC:146:ALA:HB2	1.71	0.72
25:BA:517:C:OP1	51:B5:16:ARG:NH2	2.20	0.72
19:CS:15:LEU:HA	19:CS:18:LYS:HD2	1.70	0.72
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.56	0.72
29:BF:61:GLY:O	60:BF:406:HOH:O	2.06	0.72
30:BG:138:GLN:HE21	30:BG:138:GLN:N	1.87	0.72
37:BR:103:ARG:NH1	37:BR:108:GLY:O	2.22	0.72
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:D0:27:GLU:HG3	46:D0:68:GLU:HA	1.72	0.72
9:AI:17:VAL:HG11	9:AI:81:ILE:HA	1.70	0.72
15:AO:39:LEU:HD12	15:AO:56:LEU:HB2	1.71	0.72
25:BA:2005:A:OP1	60:BA:4104:HOH:O	2.06	0.72
26:DB:50:G:OP1	38:DS:63:THR:N	2.22	0.72
1:AA:339:C:OP2	34:BO:97:ARG:NH1	2.21	0.72
1:AA:953:G:N7	13:AM:104:ARG:NH2	2.36	0.72
1:AA:1036:G:H3'	1:AA:1037:C:H6	1.53	0.72
24:AX:76:31H:OP1	25:BA:2439:A:N6	2.23	0.72
25:BA:1670:C:OP1	60:BA:3797:HOH:O	2.07	0.72
1:CA:1035:A:H2'	1:CA:1036:G:H8	1.53	0.71
31:DH:3:ARG:HB3	31:DH:3:ARG:HH11	1.54	0.71
1:AA:574:A:OP2	60:AA:4009:HOH:O	2.08	0.71
1:AA:674:G:H2'	1:AA:675:A:H8	1.54	0.71
25:BA:1199:U:OP1	60:BA:4387:HOH:O	2.08	0.71
1:CA:1029:C:N3	1:CA:1032:G:N2	2.38	0.71
1:CA:1244:C:H42	1:CA:1293:G:H1	1.36	0.71
4:CD:98:GLU:HG2	4:CD:189:PRO:HG2	1.72	0.71
25:DA:2183:C:H2'	25:DA:2184:G:H8	1.55	0.71
37:DR:33:ARG:NH1	37:DR:115:GLU:OE2	2.23	0.71
7:CG:79:ARG:HE	7:CG:80:VAL:HG23	1.54	0.71
16:CP:57:ARG:NH2	16:CP:79:VAL:O	2.23	0.71
25:BA:1798:U:H5'	27:BD:259:THR:HG22	1.72	0.71
1:AA:936:C:O2	1:AA:1382:C:N4	2.21	0.71
3:AC:70:VAL:HG22	3:AC:72:LYS:H	1.55	0.71
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.70	0.71
45:BZ:45:ASP:OD2	45:BZ:49:ARG:NH1	2.23	0.71
1:CA:1006:C:OP1	1:CA:1037:C:O2'	2.08	0.71
25:DA:2302:G:N2	30:DG:126:ASP:OD1	2.21	0.71
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.71	0.71
15:AO:54:ARG:HG2	15:AO:58:MET:HE2	1.73	0.71
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.24	0.71
25:BA:2500:U:O2'	25:BA:2504:U:OP1	2.09	0.71
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.24	0.71
25:DA:997:G:OP1	40:DU:92:ARG:NE	2.24	0.71
25:DA:2238:G:N7	60:DA:4590:HOH:O	2.23	0.71
35:DP:95:VAL:HA	35:DP:99:LEU:HD21	1.73	0.71
30:BG:5:VAL:HG22	30:BG:8:LYS:H	1.56	0.71
5:CE:43:LEU:HD22	5:CE:136:MET:HG3	1.72	0.71
12:CL:71:PRO:O	12:CL:102:ARG:NH1	2.22	0.71
36:DQ:43:THR:HA	36:DQ:94:VAL:HG12	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:DW:14:PRO:HG2	42:DW:78:GLU:HG2	1.71	0.71
49:D3:29:ARG:HB3	49:D3:30:ARG:HH11	1.56	0.71
6:AF:18:GLN:N	6:AF:18:GLN:OE1	2.23	0.71
25:BA:1342:A:O2'	25:BA:1344:G:OP2	2.07	0.71
25:DA:568:U:O4	60:DA:4115:HOH:O	2.06	0.71
4:AD:13:ARG:NH1	4:AD:38:TYR:O	2.24	0.70
25:DA:2830:G:OP1	28:DE:76:ARG:NH2	2.24	0.70
25:DA:500:G:N1	25:DA:503:A:OP2	2.22	0.70
25:DA:2186:G:H2'	25:DA:2187:G:H5"	1.71	0.70
20:AT:33:ILE:HD12	20:AT:62:LEU:HB3	1.73	0.70
25:DA:1939:U:OP1	25:DA:2604:U:O2'	2.08	0.70
25:BA:31:C:OP1	60:BA:4386:HOH:O	2.09	0.70
25:BA:687:C:H5"	53:B7:2:LYS:HE2	1.73	0.70
25:BA:816:C:OP2	60:BA:4006:HOH:O	2.09	0.70
25:BA:1189:A:OP2	60:BA:4298:HOH:O	2.10	0.70
2:CB:174:VAL:HG11	2:CB:196:LEU:HG	1.74	0.70
13:CM:65:LYS:HA	50:D4:50:VAL:HG11	1.73	0.70
45:DZ:119:GLU:HB2	45:DZ:122:ARG:HH11	1.56	0.70
48:D2:38:GLN:HB3	48:D2:44:LEU:HB2	1.73	0.70
1:AA:96:U:O2'	1:AA:97:G:H5'	1.92	0.70
1:AA:1069:C:OP2	60:AA:4012:HOH:O	2.09	0.70
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.07	0.70
25:BA:1828:G:OP1	60:BA:4340:HOH:O	2.09	0.70
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.72	0.70
3:CC:11:ARG:NH2	3:CC:177:THR:O	2.24	0.70
5:CE:144:THR:H	5:CE:147:ASP:HB2	1.57	0.70
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.09	0.70
13:AM:34:LEU:HD13	13:AM:41:PRO:HA	1.73	0.70
25:DA:993:G:OP1	40:DU:50:ARG:NH2	2.25	0.70
25:DA:1204:A:H2	25:DA:1241:A:H62	1.39	0.70
25:DA:2552:U:OP2	60:DA:4610:HOH:O	2.10	0.70
36:DQ:29:PHE:O	45:DZ:122:ARG:NH2	2.23	0.70
8:AH:73:ASP:OD1	8:AH:75:ARG:NH1	2.25	0.70
1:CA:1002:G:H1	1:CA:1038:C:N4	1.90	0.70
25:DA:2674:G:H5"	34:DO:26:LYS:HE3	1.72	0.70
42:DW:18:ARG:HG3	42:DW:76:VAL:HB	1.73	0.70
45:DZ:23:LYS:HG3	45:DZ:40:ASP:HA	1.74	0.70
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.26	0.70
1:CA:986:A:O2'	19:CS:55:LYS:O	2.08	0.70
1:CA:1228:C:OP1	13:CM:115:LYS:N	2.25	0.70
24:CX:23:C:H2'	24:CX:24:U:H6	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:14:LEU:HB3	6:AF:18:GLN:NE2	2.06	0.70
24:AX:59:A:H2'	24:AX:60:U:H5'	1.74	0.70
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	1.92	0.70
32:DI:37:VAL:HG12	32:DI:38:LEU:HD12	1.73	0.70
29:BF:53:THR:HG23	29:BF:55:GLY:H	1.57	0.70
25:DA:643:A:N1	25:DA:2369:A:O2'	2.24	0.70
25:DA:2113:U:O2	25:DA:2169:A:N6	2.24	0.70
27:DD:242:ARG:O	60:DD:407:HOH:O	2.10	0.70
1:AA:545:C:OP2	4:AD:65:ARG:NH2	2.25	0.69
1:AA:1279:A:O2'	1:AA:1282:C:N4	2.25	0.69
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.73	0.69
1:CA:1164:G:N1	1:CA:1172:C:N4	2.38	0.69
2:CB:163:PHE:HD1	2:CB:185:ILE:HG13	1.57	0.69
2:CB:178:ARG:HH22	8:CH:68:ARG:HH22	1.38	0.69
1:AA:1311:G:H1	1:AA:1326:C:N4	1.90	0.69
1:CA:1262:C:N4	1:CA:1273:G:H1	1.90	0.69
25:BA:18:C:O2'	25:BA:554:U:OP1	2.10	0.69
34:BO:37:ASP:OD1	34:BO:109:LYS:NZ	2.25	0.69
37:BR:56:LYS:NZ	37:BR:87:TYR:O	2.25	0.69
25:DA:2646:C:OP2	25:DA:2732:G:O2'	2.08	0.69
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.09	0.69
1:AA:1259:C:H42	1:AA:1276:G:H1	1.36	0.69
53:B7:33:ARG:NH2	60:B7:3102:HOH:O	2.25	0.69
25:BA:1786:A:H1'	25:BA:1938:A:N6	2.06	0.69
27:BD:37:LEU:HD12	27:BD:62:TYR:HB2	1.73	0.69
25:DA:1783:A:H5'	25:DA:2608:G:H4'	1.75	0.69
26:DB:75:G:N2	45:DZ:87:ASP:OD1	2.25	0.69
30:DG:41:GLN:HE21	30:DG:155:MET:HB3	1.56	0.69
1:CA:991:U:O2'	1:CA:992:U:O5'	2.11	0.69
25:BA:1434:A:H61	25:BA:1558:A:H62	1.38	0.69
47:B1:86:SER:OG	47:B1:89:GLU:OE1	2.10	0.69
3:CC:82:GLU:HG2	3:CC:85:ARG:HH21	1.58	0.69
27:DD:221:VAL:O	60:DD:411:HOH:O	2.09	0.69
1:AA:13:U:OP1	60:AA:4118:HOH:O	2.10	0.69
1:AA:1007:C:N3	1:AA:1022:G:O6	2.25	0.69
27:BD:108:PRO:HB3	27:BD:143:HIS:HE1	1.58	0.69
25:DA:2347:C:HO2'	52:D6:21:TYR:HH	1.40	0.69
28:DE:128:SER:OG	28:DE:129:HIS:N	2.21	0.69
30:DG:150:ASP:OD1	30:DG:153:ARG:NH1	2.22	0.69
34:DO:115:VAL:HG13	34:DO:121:VAL:HG21	1.75	0.69
25:BA:739:G:OP1	60:BA:4315:HOH:O	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2144:U:H1'	25:BA:2148:G:H22	1.57	0.69
25:BA:2811:G:H5'	28:BE:60:ASN:HD22	1.58	0.69
33:DN:20:GLY:HA2	33:DN:61:ARG:HE	1.58	0.69
1:AA:405:U:OP2	4:AD:3:ARG:NH2	2.25	0.69
1:AA:418:C:H42	1:AA:425:G:H1	1.41	0.69
10:AJ:13:HIS:HA	10:AJ:16:LEU:HB3	1.75	0.69
25:BA:1648:C:OP1	60:BA:4313:HOH:O	2.11	0.69
1:CA:446:G:H1	1:CA:488:C:H42	1.41	0.69
1:AA:78:G:C2	1:AA:91:C:N3	2.61	0.68
1:AA:328:C:H4'	1:AA:329:A:H5'	1.75	0.68
1:AA:509:A:N1	60:AA:4114:HOH:O	2.24	0.68
1:AA:903:G:OP1	60:AA:4036:HOH:O	2.10	0.68
2:AB:18:GLY:HA3	2:AB:41:ILE:HD13	1.73	0.68
44:BY:43:ASN:HB3	44:BY:65:ALA:HB3	1.76	0.68
25:DA:1269:A:N7	60:DA:4606:HOH:O	2.25	0.68
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.93	0.68
25:DA:2336:A:H61	46:D0:43:THR:HG22	1.57	0.68
29:DF:155:LEU:HD11	29:DF:176:LEU:HD12	1.74	0.68
1:AA:972:C:OP1	60:AA:4142:HOH:O	2.10	0.68
1:CA:985:C:H42	1:CA:1220:G:H1	1.40	0.68
25:DA:880:G:N2	25:DA:898:C:O2	2.26	0.68
24:AX:21:A:H61	24:AX:46:G:H2'	1.58	0.68
25:BA:801:G:O6	29:BF:53:THR:OG1	2.10	0.68
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	1.75	0.68
9:CI:116:LYS:HA	9:CI:123:PRO:HD3	1.73	0.68
25:DA:2130:U:H4'	25:DA:2133:G:H4'	1.74	0.68
30:DG:43:LEU:HD12	30:DG:45:GLU:HG3	1.75	0.68
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.75	0.68
25:BA:1970:A:OP2	60:BA:4046:HOH:O	2.12	0.68
1:CA:1464:G:OP1	39:DT:108:ARG:NH1	2.27	0.68
25:DA:2099:U:H3	25:DA:2190:G:H1	1.42	0.68
27:DD:76:PRO:HB2	27:DD:116:GLN:HE21	1.58	0.68
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.75	0.68
25:BA:2372:G:O6	60:BA:4144:HOH:O	2.10	0.68
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.75	0.68
10:CJ:30:SER:OG	10:CJ:84:GLN:OE1	2.12	0.68
25:DA:1902:C:OP1	60:DA:4018:HOH:O	2.11	0.68
1:AA:1502:A:H2	1:AA:1505:G:N1	1.91	0.68
2:CB:103:THR:HA	2:CB:180:LEU:HD11	1.76	0.68
25:DA:1800:C:OP2	27:DD:183:ARG:NH2	2.26	0.68
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BD:85:ASP:OD2	27:BD:88:ARG:NH1	2.26	0.68
1:CA:403:C:OP1	4:CD:137:SER:OG	2.12	0.68
4:CD:122:ARG:NH1	4:CD:134:ASP:O	2.27	0.68
1:AA:1316:G:H22	1:AA:1319:A:H5"	1.58	0.68
2:AB:187:LEU:HD13	2:AB:205:ASP:HB3	1.75	0.68
25:BA:1338:G:N7	43:BX:62:LYS:NZ	2.41	0.68
1:CA:539:A:H2'	1:CA:540:G:C8	2.28	0.68
5:CE:18:ARG:HG2	5:CE:25:ARG:HB2	1.76	0.68
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	1.76	0.68
25:DA:31:C:OP1	60:DA:4439:HOH:O	2.10	0.68
41:DV:6:LYS:HB2	41:DV:38:LEU:HD21	1.76	0.68
29:BF:101:LEU:O	29:BF:106:ARG:NH1	2.26	0.68
1:CA:1029:C:N4	1:CA:1032:G:N1	2.42	0.68
26:DB:76:G:N2	26:DB:101:G:O6	2.26	0.68
30:DG:114:ILE:HG23	30:DG:136:ARG:NH2	2.09	0.68
25:BA:1300:U:H4'	25:BA:1301:A:H5"	1.75	0.67
25:DA:370:G:OP2	60:DA:4069:HOH:O	2.12	0.67
25:DA:2128:C:N3	25:DA:2160:G:N2	2.43	0.67
25:BA:1507:A:O2'	25:BA:1508:A:O4'	2.12	0.67
25:BA:2748:A:H5'	31:BH:4:ILE:HD12	1.75	0.67
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.41	0.67
25:DA:509:C:OP1	60:DA:4471:HOH:O	2.11	0.67
1:AA:103:C:O2'	1:AA:172:A:N1	2.26	0.67
1:AA:145:G:H1	1:AA:177:C:H42	1.42	0.67
3:AC:121:ALA:HB1	3:AC:189:ALA:HB2	1.75	0.67
16:AP:1:MET:SD	16:AP:1:MET:N	2.64	0.67
25:BA:535:C:O3'	40:BU:53:ARG:NH1	2.26	0.67
25:BA:1798:U:H5"	27:BD:260:ARG:HB3	1.76	0.67
36:BQ:135:ASP:OD2	45:BZ:49:ARG:NH2	2.25	0.67
39:BT:16:ARG:NH2	39:BT:83:ILE:O	2.27	0.67
44:BY:54:LYS:HA	44:BY:56:PRO:HD3	1.74	0.67
1:AA:976:G:H5'	1:AA:1358:U:O2'	1.94	0.67
25:BA:2445:G:OP1	29:BF:74:ARG:NH2	2.26	0.67
30:BG:138:GLN:HE22	30:BG:153:ARG:H	1.43	0.67
26:DB:48:A:OP2	38:DS:30:ARG:NH2	2.27	0.67
37:DR:79:LEU:HA	37:DR:83:ILE:HD12	1.77	0.67
35:BP:138:LEU:HD23	35:BP:145:PRO:HG3	1.76	0.67
19:CS:9:VAL:HG21	50:D4:61:ARG:HH22	1.59	0.67
25:DA:631:A:OP1	35:DP:65:ARG:NH1	2.24	0.67
25:DA:827:U:OP1	60:DA:4458:HOH:O	2.12	0.67
25:DA:2136:C:H41	25:DA:2156:G:H21	1.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:99:TYR:HB3	45:DZ:123:ASP:HB2	1.76	0.67
1:AA:911:U:OP2	12:AL:97:ARG:NH1	2.28	0.67
42:BW:18:ARG:HG3	42:BW:76:VAL:HB	1.76	0.67
1:CA:1162:C:H42	1:CA:1174:G:H1	1.43	0.67
25:DA:2404:C:O3'	35:DP:77:ARG:NH2	2.27	0.67
37:DR:33:ARG:NH2	51:D5:57:VAL:O	2.28	0.67
25:BA:1636:C:H2'	25:BA:1637:A:C8	2.30	0.67
25:DA:320:A:O2'	25:DA:322:A:OP2	2.12	0.67
25:DA:1986:A:OP1	60:DA:4251:HOH:O	2.12	0.67
25:DA:807:U:OP2	35:DP:41:ARG:NH2	2.27	0.67
39:DT:16:ARG:HD3	39:DT:19:LEU:HD12	1.77	0.67
39:DT:125:ARG:O	39:DT:129:ARG:NH1	2.27	0.67
44:DY:39:VAL:HB	44:DY:42:VAL:HB	1.75	0.67
25:BA:1176:G:H1'	25:BA:1177:A:C5'	2.25	0.67
6:CF:81:ILE:HD11	27:DD:125:ILE:HB	1.76	0.67
8:CH:10:LEU:HD22	8:CH:83:ILE:HD11	1.77	0.67
25:DA:458:G:O2'	25:DA:469:G:O6	2.11	0.67
1:AA:1279:A:O2'	1:AA:1281:U:OP2	2.13	0.67
25:BA:1299:G:OP1	60:BA:4327:HOH:O	2.11	0.67
25:BA:1713:U:H2'	25:BA:1714:G:H8	1.60	0.67
1:CA:402:G:H2'	1:CA:403:C:H5'	1.75	0.67
26:DB:29:A:O2'	26:DB:58:A:N1	2.27	0.67
34:DO:13:ASN:ND2	34:DO:96:THR:OG1	2.26	0.67
25:BA:2408:U:OP2	60:BA:3989:HOH:O	2.13	0.66
1:CA:1277:C:O2'	1:CA:1279:A:N7	2.28	0.66
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.24	0.66
1:AA:630:G:H2'	1:AA:631:G:H8	1.60	0.66
20:AT:75:ASN:OD1	20:AT:75:ASN:N	2.28	0.66
25:BA:587:C:OP2	35:BP:21:ARG:NH2	2.29	0.66
1:CA:8:A:C6	4:CD:209:ARG:HB2	2.30	0.66
25:DA:1592:C:H2'	25:DA:1593:G:H8	1.60	0.66
29:DF:18:ARG:NH2	29:DF:127:GLU:OE1	2.27	0.66
30:DG:41:GLN:NE2	30:DG:154:GLY:O	2.28	0.66
36:DQ:135:ASP:OD2	45:DZ:49:ARG:NH2	2.26	0.66
45:DZ:119:GLU:O	45:DZ:122:ARG:NH1	2.29	0.66
48:D2:22:GLU:OE2	48:D2:68:ARG:NH2	2.28	0.66
1:AA:158:G:N2	1:AA:163:C:O2	2.28	0.66
3:AC:30:ARG:NH1	14:AN:35:ARG:O	2.29	0.66
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.26	0.66
25:BA:957:A:N1	25:BA:2458:G:H4'	2.09	0.66
1:CA:1210:C:H2'	1:CA:1211:U:H5"	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:81:VAL:O	2:CB:85:ALA:N	2.29	0.66
25:DA:83:G:O2'	25:DA:102:G:N2	2.29	0.66
36:DQ:141:GLN:HE22	45:DZ:74:VAL:HG13	1.60	0.66
47:D1:3:LYS:HB2	47:D1:61:ARG:NH1	2.11	0.66
49:D3:11:SER:O	60:D3:4001:HOH:O	2.14	0.66
25:BA:1125:G:H5'	55:B9:37:GLY:HA2	1.78	0.66
25:BA:2103:C:H42	25:BA:2186:G:H1	1.42	0.66
25:BA:2125:G:H22	25:BA:2172:U:P	2.18	0.66
27:BD:227:ASN:OD1	60:BD:405:HOH:O	2.13	0.66
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.77	0.66
2:AB:84:GLU:HB3	2:AB:219:VAL:HG21	1.76	0.66
25:BA:1022:G:H22	25:BA:1142(A):A:H2	1.41	0.66
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.28	0.66
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.59	0.66
25:BA:2151:G:H2'	25:BA:2152:G:C8	2.31	0.66
1:CA:1114:C:N3	1:CA:1186:G:N2	2.39	0.66
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.28	0.66
48:D2:14:ARG:HA	48:D2:63:VAL:HG11	1.77	0.66
1:AA:998:G:H1	1:AA:1043:C:H42	1.44	0.66
2:AB:231:GLU:HB2	2:AB:232:PRO:HD3	1.77	0.66
25:BA:1815:A:OP2	27:BD:54:ARG:NH2	2.29	0.66
25:BA:2327:A:H2'	25:BA:2328:A:C8	2.31	0.66
26:BB:7:G:H1	26:BB:114:C:H42	1.42	0.66
1:CA:953:G:H5'	1:CA:965:A:N6	2.10	0.66
25:DA:948:G:N2	25:DA:985:C:OP2	2.28	0.66
25:DA:2079:U:O3'	47:D1:35:THR:OG1	2.14	0.66
42:DW:4:LYS:HE2	42:DW:6:ILE:HD11	1.75	0.66
1:AA:957:U:H5"	19:AS:81:ARG:HH12	1.61	0.66
25:BA:1794:U:H2'	25:BA:1795:C:H6	1.61	0.66
25:BA:2138:C:H42	25:BA:2153:G:H1	1.44	0.66
38:BS:28:VAL:HG11	38:BS:98:VAL:HG13	1.78	0.66
25:BA:2430:A:H2'	25:BA:2430:A:N3	2.10	0.66
25:BA:2687:U:OP2	60:BA:4420:HOH:O	2.14	0.66
24:CX:52:G:H1	24:CX:62:C:H42	1.44	0.66
25:DA:135:G:N2	25:DA:144:C:N3	2.34	0.66
7:AG:15:ASP:HB3	7:AG:24:THR:HG23	1.77	0.65
1:CA:923:A:O2'	1:CA:1399:C:OP2	2.13	0.65
25:DA:543:C:N4	25:DA:549:G:O6	2.18	0.65
25:DA:2572:A:OP1	25:DA:2574:G:O2'	2.14	0.65
33:DN:29:LYS:NZ	33:DN:140:VAL:O	2.28	0.65
1:CA:1164:G:N2	1:CA:1172:C:C2	2.63	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.62	0.65
3:AC:20:SER:HG	3:AC:40:ARG:HH12	1.44	0.65
1:CA:560:U:OP2	60:CA:4097:HOH:O	2.12	0.65
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.29	0.65
25:DA:1645:G:H5"	25:DA:1646:C:H5'	1.79	0.65
29:DF:130:ALA:H	29:DF:142:TRP:CD1	2.14	0.65
31:DH:12:PRO:HD2	31:DH:76:VAL:HG21	1.77	0.65
1:AA:596:C:OP2	60:AA:4064:HOH:O	2.13	0.65
1:AA:1273:G:H3'	1:AA:1274:G:H8	1.60	0.65
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.78	0.65
25:DA:863:A:OP2	36:DQ:22:LYS:HD3	1.97	0.65
25:DA:1269:A:OP2	60:DA:4607:HOH:O	2.13	0.65
25:DA:2689:U:OP2	25:DA:2719:G:N2	2.23	0.65
26:DB:55:U:H1'	30:DG:29:TRP:CD1	2.32	0.65
35:DP:96:THR:HG23	35:DP:99:LEU:HD23	1.78	0.65
44:BY:92:ASN:N	44:BY:93:GLY:HA2	2.11	0.65
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.31	0.65
1:CA:1165:C:H42	1:CA:1171:G:H1	1.44	0.65
2:CB:204:ASN:O	2:CB:210:SER:OG	2.09	0.65
1:AA:1298:C:OP2	7:AG:114:ARG:NH2	2.30	0.65
25:BA:2483:C:N3	36:BQ:124:LYS:NZ	2.44	0.65
26:BB:33:G:H5'	30:BG:2:PRO:HD3	1.79	0.65
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.78	0.65
1:CA:1153:C:H42	1:CA:1154:G:H21	1.44	0.65
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.79	0.65
25:DA:528:A:C2	25:DA:2042:A:H2'	2.32	0.65
25:DA:1537:G:H2'	25:DA:1538:G:H8	1.62	0.65
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.25	0.65
8:AH:116:LYS:HD2	8:AH:129:VAL:HG11	1.77	0.65
9:AI:5:TYR:HE1	9:AI:16:ARG:HB2	1.62	0.65
31:BH:46:GLU:HB2	31:BH:49:VAL:HG12	1.79	0.65
3:CC:40:ARG:HA	3:CC:43:LEU:HD22	1.79	0.65
24:CX:59:A:H2'	24:CX:60:U:H5'	1.79	0.65
25:DA:1025:G:C4	25:DA:1135:C:H1'	2.31	0.65
1:AA:1210:C:H2'	1:AA:1211:U:H5"	1.79	0.65
25:BA:2014:A:N1	60:BA:3705:HOH:O	2.29	0.65
1:CA:576:G:OP1	60:CA:4013:HOH:O	2.15	0.65
25:DA:559:G:H22	40:DU:49:HIS:CE1	2.14	0.65
25:DA:1171:G:H1	25:DA:1178:C:H42	1.44	0.65
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.78	0.65
25:BA:1048:A:OP2	25:BA:1109:C:N4	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1654:A:OP2	60:BA:3948:HOH:O	2.14	0.65
38:BS:27:SER:HA	38:BS:88:ASP:HB3	1.78	0.65
44:BY:92:ASN:HB2	44:BY:94:LYS:HG2	1.79	0.65
2:CB:111:ARG:HH21	2:CB:114:ARG:HB2	1.61	0.65
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.79	0.65
15:AO:8:LYS:HG2	15:AO:12:ILE:HD11	1.79	0.65
30:BG:41:GLN:HB3	30:BG:43:LEU:HD13	1.79	0.65
50:B4:26:SER:OG	50:B4:27:THR:N	2.29	0.65
1:CA:297:G:O2'	1:CA:299:G:N7	2.26	0.65
1:CA:1035:A:H2'	1:CA:1036:G:C8	2.31	0.65
25:DA:2104:G:H1	25:DA:2185:C:H42	1.43	0.65
35:DP:48:PRO:O	54:D8:57:ARG:NH2	2.29	0.65
46:D0:10:THR:HG22	46:D0:12:ASN:H	1.61	0.65
1:AA:21:G:OP1	60:AA:4101:HOH:O	2.15	0.64
1:AA:1086:U:H3	1:AA:1099:G:H22	1.45	0.64
3:AC:52:LEU:HD21	3:AC:55:VAL:HG23	1.79	0.64
23:AW:76:PPU:N	24:AX:76:31H:O2'	2.30	0.64
25:BA:1274:A:N3	25:BA:1297:C:H1'	2.12	0.64
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.15	0.64
3:CC:42:LEU:O	3:CC:45:LYS:NZ	2.23	0.64
37:DR:67:LEU:HD13	37:DR:76:VAL:HG21	1.77	0.64
1:AA:1443:G:N2	1:AA:1459:C:O2	2.29	0.64
2:AB:76:GLN:HB2	2:AB:208:ILE:HG12	1.80	0.64
9:CI:23:ASN:ND2	9:CI:60:ASP:OD1	2.31	0.64
25:DA:182:A:N3	25:DA:433:C:O2'	2.24	0.64
37:DR:103:ARG:NH1	37:DR:108:GLY:O	2.29	0.64
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.30	0.64
25:BA:789:A:N1	60:BA:4021:HOH:O	2.30	0.64
25:BA:2503:A:OP1	60:BA:4285:HOH:O	2.15	0.64
16:CP:59:TRP:HA	16:CP:62:VAL:HG12	1.79	0.64
25:BA:1800:C:OP2	27:BD:183:ARG:NH2	2.31	0.64
25:BA:2581:G:O6	60:BA:4149:HOH:O	2.08	0.64
1:CA:1320:C:C2	19:CS:72:GLY:HA3	2.33	0.64
25:DA:2376:A:N3	38:DS:106:ARG:NH2	2.46	0.64
34:DO:48:PRO:HB2	34:DO:49:ARG:HD3	1.78	0.64
1:AA:139:G:N2	1:AA:224:C:O2	2.30	0.64
39:BT:107:ASP:HA	39:BT:110:ILE:HD12	1.79	0.64
1:CA:405:U:OP2	4:CD:3:ARG:NH2	2.30	0.64
1:CA:1318:A:H5"	19:CS:3:ARG:HH22	1.63	0.64
25:DA:2744:G:N2	31:DH:143:GLN:OE1	2.30	0.64
20:AT:33:ILE:O	20:AT:37:SER:OG	2.14	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:741:G:OP2	60:BA:4321:HOH:O	2.15	0.64
1:CA:954:G:H21	1:CA:1227:A:H62	1.46	0.64
24:CX:21:A:N6	24:CX:46:G:H2'	2.10	0.64
24:CX:76:31H:OP1	25:DA:2439:A:N6	2.31	0.64
25:DA:589:C:H2'	25:DA:590:A:C8	2.33	0.64
25:DA:648:G:O2'	25:DA:2351:G:OP1	2.09	0.64
25:DA:1840:G:OP2	60:DA:4543:HOH:O	2.15	0.64
38:DS:27:SER:HA	38:DS:88:ASP:HB3	1.79	0.64
1:AA:363:A:OP2	12:AL:34:ARG:NH1	2.31	0.64
25:BA:1602:U:O4	60:BA:3971:HOH:O	2.09	0.64
45:BZ:77:ASP:OD2	45:BZ:80:ARG:NH1	2.30	0.64
1:CA:1086:U:H3	1:CA:1099:G:H22	1.46	0.64
25:DA:2291:U:H5"	25:DA:2380:C:H1'	1.79	0.64
25:DA:2815:C:H5'	51:D5:29:THR:HG21	1.79	0.64
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.31	0.64
38:BS:59:LYS:HE2	38:BS:60:GLY:H	1.61	0.64
25:DA:1803:A:O2'	27:DD:259:THR:HG21	1.97	0.64
25:DA:2356:C:OP1	46:D0:24:LYS:NZ	2.24	0.64
25:BA:860:U:OP2	60:BA:4251:HOH:O	2.15	0.64
1:CA:56:U:H2'	1:CA:57:G:C8	2.32	0.64
1:CA:955:U:H3	1:CA:1225:A:H2	1.46	0.64
2:CB:155:LEU:HD11	2:CB:159:PRO:HG3	1.80	0.64
24:CX:67:C:H2'	24:CX:68:C:H5'	1.79	0.64
25:DA:1220:A:OP2	40:DU:19:LYS:NZ	2.31	0.64
1:AA:1030:C:H42	1:AA:1031:G:H1	1.43	0.64
1:AA:1110:A:OP2	60:AA:4137:HOH:O	2.16	0.64
1:AA:1125:U:H5'	10:AJ:5:ARG:HH22	1.62	0.64
9:AI:50:LEU:HD13	9:AI:56:LEU:HA	1.78	0.64
25:BA:831:G:O2'	35:BP:38:GLN:NE2	2.31	0.64
25:BA:1384:A:N7	60:BA:3821:HOH:O	2.30	0.64
25:BA:1449:A:O2'	25:BA:1529:G:N2	2.22	0.64
25:DA:1192:G:N7	60:DA:4648:HOH:O	2.29	0.64
29:DF:24:LEU:HD21	29:DF:114:VAL:HG12	1.79	0.64
1:AA:1187:G:N3	14:AN:60:SER:OG	2.31	0.63
1:AA:1327:C:OP2	21:AU:12:LYS:NZ	2.31	0.63
25:BA:184:C:H2'	25:BA:185:U:C6	2.33	0.63
25:BA:414:C:H2'	25:BA:415:A:C8	2.33	0.63
38:BS:14:VAL:O	38:BS:18:ILE:HG12	1.98	0.63
1:CA:1120:G:O6	1:CA:1154:G:N2	2.28	0.63
1:CA:1397:C:OP2	22:CV:23:A:O2'	2.14	0.63
25:DA:729:G:C6	27:DD:208:LYS:HB2	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2345:G:OP2	52:D6:38:LYS:HD3	1.99	0.63
25:DA:2682:U:OP2	60:DA:4106:HOH:O	2.15	0.63
1:AA:1416:G:N7	60:AA:4089:HOH:O	2.31	0.63
5:AE:144:THR:H	5:AE:147:ASP:HB2	1.62	0.63
16:AP:50:LYS:HA	16:AP:50:LYS:HZ3	1.62	0.63
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.79	0.63
25:DA:918:A:N3	26:DB:80:U:O2'	2.26	0.63
25:DA:2000:G:N7	60:DA:4310:HOH:O	2.30	0.63
25:DA:2445:G:OP1	29:DF:74:ARG:NH2	2.31	0.63
1:AA:11:G:O2'	1:AA:506:G:N2	2.30	0.63
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.31	0.63
25:BA:910:A:OP2	60:BA:4252:HOH:O	2.15	0.63
25:BA:2105:C:H2'	25:BA:2106:G:C8	2.33	0.63
38:BS:59:LYS:NZ	38:BS:68:GLN:OE1	2.30	0.63
12:CL:28:LYS:HD2	12:CL:62:SER:HB2	1.79	0.63
25:DA:442:G:H21	29:DF:48:THR:HB	1.63	0.63
25:DA:1449:A:O2'	25:DA:1529:G:N2	2.23	0.63
26:DB:20:C:H2'	26:DB:21:G:H5'	1.78	0.63
28:DE:9:VAL:HG22	28:DE:25:VAL:HB	1.78	0.63
38:DS:15:ARG:O	38:DS:19:LYS:NZ	2.31	0.63
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.80	0.63
25:BA:2773:C:OP1	28:BE:164:ARG:NE	2.22	0.63
25:DA:2169:A:O2'	25:DA:2170:A:O5'	2.16	0.63
26:DB:33:G:O6	26:DB:49:C:N4	2.29	0.63
29:DF:11:VAL:HB	29:DF:18:ARG:HB3	1.81	0.63
25:BA:1823:G:OP1	27:BD:54:ARG:NH1	2.29	0.63
25:DA:135:G:H1	25:DA:144:C:H42	1.43	0.63
25:DA:637:A:OP1	35:DP:133:SER:OG	2.14	0.63
45:DZ:5:LEU:HG	45:DZ:47:VAL:HG21	1.81	0.63
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.31	0.63
3:AC:5:ILE:HG12	3:AC:6:HIS:H	1.64	0.63
25:BA:279:C:N4	25:BA:361:G:H1	1.93	0.63
1:CA:78:G:H2'	1:CA:79:G:H5"	1.80	0.63
20:CT:10:LEU:HD23	20:CT:11:SER:H	1.63	0.63
35:DP:39:LYS:HB2	35:DP:45:LEU:HD23	1.79	0.63
1:AA:403:C:OP1	4:AD:137:SER:OG	2.16	0.63
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.11	0.63
15:CO:87:ILE:HG22	15:CO:88:ARG:H	1.63	0.63
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.14	0.63
24:CX:52:G:H2'	24:CX:53:G:H8	1.64	0.63
25:DA:2137:C:H2'	25:DA:2138:C:C6	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2630:G:H2'	25:DA:2631:G:H8	1.64	0.63
33:DN:58:ASP:OD1	33:DN:58:ASP:N	2.32	0.63
29:BF:185:ASP:HA	29:BF:188:ARG:HD3	1.80	0.63
35:BP:63:PRO:HD3	54:B8:27:THR:HG22	1.81	0.63
48:B2:22:GLU:HG3	48:B2:64:LEU:HD11	1.81	0.63
13:CM:29:ARG:HB3	13:CM:64:TRP:CZ3	2.34	0.63
25:DA:857:C:H4'	46:D0:23:VAL:HG21	1.80	0.63
30:DG:44:GLY:N	30:DG:88:ILE:O	2.31	0.63
50:D4:59:PHE:O	50:D4:62:ARG:NH2	2.26	0.63
1:AA:1097:C:O2'	1:AA:1169:A:N3	2.28	0.63
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.62	0.63
25:BA:1047:G:HO2'	25:BA:1048:A:H8	1.47	0.63
49:B3:6:VAL:HG13	49:B3:56:VAL:HG22	1.79	0.63
5:CE:8:GLU:HG3	5:CE:34:VAL:HG23	1.81	0.63
25:DA:1012:U:H5	33:DN:28:THR:HG21	1.63	0.63
25:DA:2327:A:H2'	25:DA:2328:A:C8	2.34	0.63
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.16	0.62
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.45	0.62
30:BG:15:VAL:HG21	30:BG:176:LEU:HD23	1.81	0.62
30:BG:138:GLN:H	30:BG:138:GLN:NE2	1.93	0.62
1:CA:110:C:O2'	16:CP:25:ARG:O	2.17	0.62
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.31	0.62
25:DA:2291:U:H2'	25:DA:2292:C:C6	2.34	0.62
25:DA:2747:G:N2	25:DA:2756:U:OP1	2.32	0.62
27:DD:171:ASP:OD1	27:DD:171:ASP:N	2.31	0.62
47:D1:3:LYS:HB2	47:D1:61:ARG:HH12	1.64	0.62
1:AA:97:G:O2'	1:AA:98:G:H5"	1.99	0.62
1:AA:198:G:H2'	1:AA:199:G:H8	1.64	0.62
25:BA:303:U:O4	60:BA:4299:HOH:O	2.13	0.62
25:BA:1113:U:H2'	25:BA:1114:G:C8	2.33	0.62
15:CO:44:LYS:O	15:CO:47:LYS:NZ	2.32	0.62
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.31	0.62
31:DH:43:VAL:HG12	31:DH:52:VAL:HG22	1.81	0.62
1:AA:402:G:H2'	1:AA:403:C:H5'	1.79	0.62
1:AA:624:C:H2'	1:AA:625:G:H8	1.64	0.62
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.31	0.62
25:BA:2130:U:H4'	25:BA:2133:G:H4'	1.80	0.62
28:BE:105:THR:OG1	28:BE:199:ARG:NH2	2.32	0.62
15:CO:2:PRO:O	15:CO:38:ARG:NH2	2.28	0.62
25:DA:1864:U:OP1	25:DA:2410:G:O2'	2.11	0.62
53:D7:5:TRP:NE1	53:D7:7:PRO:HG3	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1503:A:N3	22:AV:13:A:N6	2.47	0.62
3:AC:118:GLN:H	3:AC:118:GLN:NE2	1.93	0.62
1:CA:642:A:N3	8:CH:113:SER:OG	2.32	0.62
1:CA:1516:G:N2	1:CA:1519:A:OP2	2.32	0.62
2:CB:69:LEU:HB2	2:CB:159:PRO:HG2	1.82	0.62
45:DZ:102:LEU:HD23	45:DZ:137:ILE:HB	1.81	0.62
1:AA:674:G:H2'	1:AA:675:A:C8	2.33	0.62
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.81	0.62
25:BA:1041:C:H42	25:BA:1114:G:H1	1.46	0.62
25:BA:1567:A:H2'	27:BD:86:PRO:HG3	1.81	0.62
25:BA:2316:C:O2'	30:BG:128:ARG:NH1	2.32	0.62
30:BG:13:GLU:HG3	30:BG:14:GLU:HG3	1.80	0.62
1:CA:1055:A:H2'	3:CC:156:ARG:HD2	1.82	0.62
15:CO:64:ARG:NH2	25:DA:715:G:OP1	2.32	0.62
25:DA:831:G:O2'	35:DP:38:GLN:NE2	2.32	0.62
34:DO:88:ASN:ND2	34:DO:90:GLN:OE1	2.27	0.62
1:AA:262:A:H2'	1:AA:263:A:C8	2.34	0.62
25:BA:69:C:O2	25:BA:73:A:O2'	2.17	0.62
25:BA:652(E):G:H2'	25:BA:652(F):G:H5"	1.82	0.62
28:BE:9:VAL:HG22	28:BE:25:VAL:HB	1.82	0.62
25:DA:1530:C:O2'	25:DA:1531:C:O5'	2.12	0.62
1:AA:1469:G:H2'	1:AA:1470:G:C8	2.35	0.62
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.32	0.62
25:BA:1269:A:N7	60:BA:4105:HOH:O	2.31	0.62
38:BS:25:ARG:NH1	38:BS:42:ASP:OD1	2.32	0.62
1:CA:397:A:N7	1:CA:547:A:O2'	2.33	0.62
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.80	0.62
45:DZ:110:GLY:HA2	45:DZ:146:ILE:HG13	1.81	0.62
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.00	0.62
25:BA:323:G:C8	29:BF:171:PRO:HG3	2.35	0.62
25:BA:729:G:C6	27:BD:208:LYS:HB2	2.34	0.62
32:BI:68:LEU:HD11	32:BI:109:ILE:HD11	1.82	0.62
25:DA:649:G:H4'	54:D8:46:ARG:HH22	1.65	0.62
25:DA:2001:A:H2'	25:DA:2002:G:C8	2.35	0.62
25:DA:2540:C:O2'	25:DA:2740:A:N3	2.32	0.62
28:DE:174:ASP:OD1	28:DE:175:VAL:N	2.32	0.62
32:DI:9:LEU:HD21	32:DI:35:LEU:HD22	1.80	0.62
25:BA:271(R):G:H2'	25:BA:271(S):G:H5"	1.81	0.62
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.14	0.62
25:DA:1692:U:H2'	25:DA:1694:C:C5	2.34	0.62
28:DE:9:VAL:HB	39:DT:3:ARG:HG2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:153:C:N4	1:AA:168:G:H1	1.98	0.62
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.34	0.62
25:BA:271(L):U:H5'	32:BI:50:ARG:HH12	1.63	0.62
25:BA:821:A:O2'	25:BA:946:G:OP2	2.13	0.62
25:BA:2791:C:H5'	25:BA:2893:G:N2	2.15	0.62
32:BI:106:GLY:HA2	32:BI:107:VAL:HB	1.82	0.62
1:CA:137:C:H2'	1:CA:138:G:H8	1.63	0.62
1:CA:392:G:H2'	1:CA:393:A:C8	2.34	0.62
2:CB:91:PRO:HG2	2:CB:155:LEU:HD13	1.82	0.62
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.00	0.61
3:AC:118:GLN:HE21	3:AC:118:GLN:N	1.94	0.61
39:BT:29:ARG:HG3	39:BT:46:GLU:HB2	1.80	0.61
1:CA:392:G:H2'	1:CA:393:A:H8	1.64	0.61
1:CA:948:C:H42	1:CA:1233:G:H1	1.48	0.61
25:DA:1593:G:H2'	25:DA:1594:G:C8	2.35	0.61
1:AA:67:C:O2'	1:AA:171:A:N3	2.31	0.61
1:AA:584:G:H5'	17:AQ:91:ARG:HH22	1.65	0.61
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.33	0.61
2:AB:115:LEU:O	2:AB:119:GLU:N	2.33	0.61
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.82	0.61
25:BA:2133:G:O2'	25:BA:2157:G:N2	2.29	0.61
31:BH:24:VAL:HG22	31:BH:35:VAL:HB	1.81	0.61
1:CA:662:G:H2'	1:CA:663:A:H8	1.65	0.61
25:DA:2029:G:N1	25:DA:2033:A:OP2	2.24	0.61
36:DQ:81:VAL:HG12	46:D0:5:LYS:HD3	1.80	0.61
43:DX:32:PRO:O	43:DX:77:LYS:NZ	2.30	0.61
45:DZ:23:LYS:HE2	45:DZ:40:ASP:CG	2.25	0.61
45:DZ:154:ASP:OD2	45:DZ:154:ASP:N	2.33	0.61
1:AA:26:A:N6	1:AA:558:G:O2'	2.32	0.61
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.29	0.61
1:CA:662:G:H2'	1:CA:663:A:C8	2.35	0.61
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.82	0.61
25:DA:2723:C:H5"	37:DR:1:MET:HE2	1.83	0.61
29:DF:40:GLN:HE22	29:DF:184:TYR:H	1.46	0.61
30:DG:179:PRO:HB2	50:D4:42:PHE:HE1	1.64	0.61
1:AA:601:C:H2'	1:AA:602:A:H8	1.65	0.61
24:AX:64:G:O2'	36:BQ:10:ARG:NH2	2.30	0.61
25:BA:2110:G:O2'	25:BA:2120:G:OP2	2.19	0.61
1:CA:447:G:O6	1:CA:485:G:O2'	2.18	0.61
2:CB:189:ASP:OD1	2:CB:189:ASP:N	2.31	0.61
3:CC:20:SER:HB2	3:CC:40:ARG:HH12	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CT:57:ARG:HH12	20:CT:100:ILE:HD12	1.66	0.61
25:DA:526:A:OP1	60:DA:4386:HOH:O	2.15	0.61
30:DG:44:GLY:O	30:DG:47:LYS:HB2	2.00	0.61
38:DS:24:LEU:O	38:DS:86:ALA:N	2.29	0.61
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.83	0.61
25:BA:2328:A:H2'	25:BA:2329:G:C8	2.35	0.61
27:BD:253:GLN:HB2	27:BD:257:LEU:HD12	1.82	0.61
29:BF:155:LEU:HB3	29:BF:192:LEU:HD23	1.81	0.61
29:BF:157:VAL:HB	29:BF:194:MET:HG2	1.82	0.61
32:BI:92:VAL:HG13	32:BI:120:ILE:HB	1.82	0.61
1:CA:1297:C:OP1	13:CM:44:ARG:NH2	2.34	0.61
45:DZ:10:ARG:NH2	45:DZ:26:GLY:O	2.32	0.61
1:AA:1259:C:O2'	1:AA:1283:G:N2	2.29	0.61
25:BA:1448:G:O2'	25:BA:1528(A):A:N1	2.32	0.61
25:BA:2125:G:O2'	25:BA:2173:A:N6	2.34	0.61
25:BA:2139:C:N3	25:BA:2152:G:C2	2.69	0.61
1:CA:853:G:H2'	1:CA:854:G:H8	1.65	0.61
5:CE:144:THR:HB	5:CE:147:ASP:H	1.64	0.61
25:DA:1019:U:OP1	25:DA:1035:U:O2'	2.18	0.61
32:BI:72:LEU:HD21	32:BI:107:VAL:HG11	1.82	0.61
10:CJ:27:ALA:HA	10:CJ:81:THR:HG21	1.82	0.61
25:DA:7:G:H1	25:DA:2896:C:H42	1.47	0.61
25:DA:1300:U:H4'	25:DA:1301:A:H5"	1.81	0.61
1:AA:953:G:H5'	1:AA:965:A:H61	1.66	0.61
1:AA:1422:G:H5"	34:BO:48:PRO:HB3	1.83	0.61
25:BA:2141:G:C5	25:BA:2142:C:H1'	2.35	0.61
37:BR:33:ARG:NH2	51:B5:57:VAL:O	2.28	0.61
26:DB:49:C:H2'	26:DB:50:G:C8	2.36	0.61
31:DH:24:VAL:HG13	31:DH:37:VAL:HG21	1.81	0.61
1:AA:1117:G:H5"	9:AI:104:ARG:NH2	2.14	0.61
1:CA:974:A:OP2	14:CN:29:ARG:NH2	2.33	0.61
1:CA:1062:U:O4	3:CC:2:GLY:N	2.33	0.61
25:DA:1630:G:N2	25:DA:1636:C:O2	2.34	0.61
29:DF:155:LEU:HB2	29:DF:189:THR:HG21	1.82	0.61
9:AI:7:THR:O	9:AI:83:ARG:NH1	2.31	0.61
9:AI:16:ARG:HG3	9:AI:64:THR:HB	1.82	0.61
25:BA:2756:U:O2'	60:BA:3904:HOH:O	2.16	0.61
1:CA:317:G:N2	1:CA:336:C:O2	2.34	0.61
1:CA:580:U:H5"	15:CO:58:MET:HG2	1.81	0.61
1:CA:977:A:H2'	1:CA:977:A:N3	2.15	0.61
1:CA:1048:G:H1	1:CA:1209:C:H42	1.49	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:45:LYS:NZ	3:CC:46:GLU:HG2	2.15	0.61
4:CD:57:ARG:NH2	4:CD:205:GLU:OE2	2.34	0.61
9:CI:16:ARG:HB2	9:CI:64:THR:HB	1.82	0.61
20:CT:23:ARG:HH11	20:CT:23:ARG:CG	2.14	0.61
25:DA:1270:C:H5"	25:DA:1271:G:H5'	1.83	0.61
1:AA:167:G:H2'	1:AA:168:G:H8	1.66	0.60
1:AA:201:C:N4	1:AA:216:G:H22	1.96	0.60
1:AA:691:G:H2'	1:AA:692:U:C6	2.36	0.60
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.18	0.60
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.83	0.60
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.34	0.60
5:AE:77:PRO:HD2	5:AE:142:LEU:HD13	1.83	0.60
25:BA:2139:C:C4	25:BA:2152:G:N1	2.69	0.60
30:BG:16:ARG:HH21	30:BG:31:VAL:HG11	1.66	0.60
39:BT:26:ASP:OD1	39:BT:120:ARG:NH2	2.32	0.60
1:CA:97:G:O2'	1:CA:98:G:H5"	2.01	0.60
10:CJ:44:VAL:HG22	10:CJ:66:ARG:HG2	1.83	0.60
25:DA:89:G:H3'	25:DA:90:U:H5"	1.81	0.60
25:DA:1338:G:N7	43:DX:62:LYS:NZ	2.48	0.60
25:DA:2291:U:OP1	25:DA:2380:C:O2'	2.19	0.60
1:AA:673:G:H2'	1:AA:674:G:C8	2.36	0.60
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	1.83	0.60
15:AO:55:GLY:HA2	15:AO:58:MET:HE3	1.83	0.60
25:BA:1292:U:H2'	25:BA:1293:C:C6	2.36	0.60
1:CA:64:G:H4'	1:CA:65:U:H3'	1.83	0.60
1:CA:1069:C:O2'	1:CA:1192:C:O2	2.18	0.60
20:CT:56:MET:HE1	20:CT:85:MET:HG2	1.82	0.60
25:DA:565:C:OP1	41:DV:82:ARG:NH2	2.33	0.60
30:DG:18:GLU:HG2	30:DG:175:LEU:HD21	1.83	0.60
49:D3:15:TYR:O	49:D3:20:LYS:NZ	2.34	0.60
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.83	0.60
8:AH:112:LEU:HA	8:AH:134:ILE:HG12	1.83	0.60
25:BA:196:A:H62	35:BP:38:GLN:HE22	1.49	0.60
34:BO:98:VAL:HG11	34:BO:114:ILE:HG23	1.83	0.60
1:CA:1058:G:H1	1:CA:1199:U:H3	1.49	0.60
25:DA:500:G:N2	25:DA:502:A:H3'	2.17	0.60
38:DS:67:ARG:O	38:DS:71:ARG:HG3	2.01	0.60
25:BA:1300:U:H4'	25:BA:1301:A:C5'	2.32	0.60
25:BA:1714:G:H1	25:BA:1745(A):C:H42	1.49	0.60
1:CA:1002:G:H1	1:CA:1038:C:H42	1.47	0.60
8:CH:34:GLU:OE1	8:CH:37:ARG:NH1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:483:A:O2'	44:DY:49:VAL:O	2.13	0.60
25:DA:956:G:H5"	36:DQ:77:LYS:HD2	1.82	0.60
25:DA:1271:G:OP2	60:DA:4401:HOH:O	2.16	0.60
25:DA:2121:G:N1	25:DA:2177:C:N4	2.16	0.60
30:DG:15:VAL:HG21	30:DG:176:LEU:HD23	1.82	0.60
1:AA:976:G:N2	1:AA:1363:C:OP2	2.35	0.60
1:AA:1469:G:H2'	1:AA:1470:G:H8	1.66	0.60
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.83	0.60
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.35	0.60
9:AI:31:GLN:HE21	9:AI:36:TYR:HD1	1.49	0.60
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.82	0.60
25:BA:639:U:H2'	25:BA:640:C:C6	2.36	0.60
6:CF:46:ARG:HH21	18:CR:37:VAL:HG11	1.66	0.60
25:DA:2118:U:C4	25:DA:2149:G:H1'	2.36	0.60
5:AE:100:VAL:HG22	5:AE:118:ILE:HG22	1.83	0.60
7:AG:78:ARG:HE	7:AG:156:TRP:HB3	1.67	0.60
15:AO:26:GLU:OE2	15:AO:77:ARG:NH2	2.23	0.60
25:BA:1108:U:O2'	25:BA:1109:C:O4'	2.20	0.60
25:BA:2165:G:H1	25:BA:2172:U:H5	1.50	0.60
25:BA:2377:A:H2'	25:BA:2378:A:C8	2.37	0.60
32:BI:100:ALA:HA	32:BI:103:ARG:HD2	1.82	0.60
38:BS:34:HIS:ND1	38:BS:53:SER:OG	2.32	0.60
5:CE:92:LYS:HB3	5:CE:119:LEU:HB2	1.83	0.60
7:CG:78:ARG:HG2	7:CG:79:ARG:HB2	1.83	0.60
25:DA:2492:U:OP1	60:DA:4358:HOH:O	2.16	0.60
32:DI:92:VAL:HG13	32:DI:120:ILE:HB	1.84	0.60
18:AR:31:LEU:HD23	18:AR:31:LEU:H	1.67	0.60
25:BA:528:A:N1	25:BA:2042:A:H2'	2.16	0.60
1:CA:127:G:HO2'	17:CQ:2:PRO:N	2.00	0.60
1:CA:222:U:H2'	1:CA:223:U:C6	2.37	0.60
1:CA:738:C:OP1	6:CF:2:ARG:NH1	2.35	0.60
1:CA:1047:G:H5"	14:CN:4:LYS:HE3	1.83	0.60
9:CI:20:ARG:O	9:CI:60:ASP:N	2.34	0.60
1:AA:67:C:H2'	1:AA:68:G:C8	2.36	0.60
2:AB:69:LEU:HB2	2:AB:159:PRO:HG2	1.83	0.60
25:BA:1174:A:H4'	25:BA:1175:U:OP1	2.01	0.60
25:BA:1568:G:H5"	27:BD:61:LEU:HD13	1.84	0.60
1:CA:975:A:N1	10:CJ:48:THR:HB	2.16	0.60
2:CB:84:GLU:OE1	2:CB:87:ARG:NH2	2.34	0.60
25:DA:1278:A:OP1	37:DR:36:THR:HG23	2.02	0.60
26:DB:55:U:O3'	30:DG:27:ASN:ND2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BB:45:A:OP2	30:BG:96:ARG:NH2	2.32	0.60
1:CA:35:G:O2'	12:CL:118:SER:O	2.15	0.60
1:CA:1004:A:H5"	1:CA:1025:U:C5	2.36	0.60
1:CA:1327:C:OP2	21:CU:12:LYS:NZ	2.26	0.60
2:CB:76:GLN:HE21	2:CB:208:ILE:HG12	1.66	0.60
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.84	0.60
25:DA:1798:U:OP2	27:DD:274:ARG:NH2	2.35	0.60
31:DH:40:GLU:OE1	31:DH:61:HIS:NE2	2.34	0.60
49:D3:10:LYS:HB3	49:D3:53:LEU:HA	1.83	0.60
25:BA:752:A:H3'	53:B7:1:MET:HE1	1.83	0.60
37:BR:67:LEU:HD13	37:BR:76:VAL:HG21	1.84	0.60
1:CA:58:C:O2'	1:CA:388:G:N7	2.32	0.60
1:CA:953:G:H5'	1:CA:965:A:H61	1.66	0.60
1:CA:1189:C:H5"	3:CC:5:ILE:HD12	1.83	0.60
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.12	0.60
1:CA:1321:C:H5"	1:CA:1322:C:H2'	1.84	0.60
4:CD:158:ILE:HG23	4:CD:162:LEU:HD12	1.83	0.60
25:DA:833:U:H2'	25:DA:834:C:C6	2.37	0.60
25:DA:2115:G:H4'	25:DA:2167:U:C4	2.37	0.60
25:DA:2135:A:H61	25:DA:2157:G:H21	1.49	0.60
25:DA:2537:U:H2'	25:DA:2538:C:C6	2.36	0.60
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.24	0.59
1:AA:1278:U:H5'	1:AA:1279:A:H5'	1.84	0.59
2:AB:91:PRO:HG3	2:AB:154:LEU:HB3	1.83	0.59
25:BA:2065:C:H2'	25:BA:2066:C:H6	1.66	0.59
25:BA:2168:G:C6	25:BA:2171:A:H8	2.20	0.59
49:B3:10:LYS:HB3	49:B3:53:LEU:HA	1.84	0.59
50:B4:53:GLU:C	50:B4:55:ARG:H	2.10	0.59
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HG2	1.83	0.59
25:DA:2203:U:H2'	25:DA:2205:C:C6	2.37	0.59
29:DF:21:ALA:HB3	29:DF:22:ALA:HA	1.83	0.59
1:AA:193:C:H2'	1:AA:194:C:H6	1.67	0.59
10:AJ:81:THR:HA	10:AJ:84:GLN:HB3	1.82	0.59
23:AW:76:PPU:H103	25:BA:2584:U:H5'	1.84	0.59
25:BA:1025:G:C4	25:BA:1135:C:H1'	2.37	0.59
1:CA:437:U:H5'	4:CD:155:LEU:HD21	1.84	0.59
2:CB:8:LYS:HZ3	2:CB:51:LEU:HB2	1.68	0.59
25:DA:106:C:O2	25:DA:294:A:O2'	2.20	0.59
25:DA:987:G:O2'	25:DA:1000:A:N3	2.27	0.59
25:DA:1030:G:OP2	36:DQ:128:LYS:NZ	2.33	0.59
35:DP:52:GLU:HB3	35:DP:55:ARG:HH11	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:DW:68:ARG:HB3	42:DW:109:GLU:HG2	1.84	0.59
45:DZ:19:ARG:NH1	45:DZ:84:GLU:O	2.35	0.59
45:DZ:45:ASP:OD2	45:DZ:49:ARG:NH1	2.35	0.59
1:CA:328:C:H4'	1:CA:329:A:H5'	1.85	0.59
1:CA:1028:C:N3	1:CA:1033:G:C6	2.71	0.59
25:DA:2693:A:H2'	25:DA:2694:G:H8	1.66	0.59
30:DG:64:THR:HB	30:DG:94:LEU:HD21	1.83	0.59
1:AA:429:U:O2'	4:AD:22:LYS:NZ	2.34	0.59
1:AA:1226:C:OP1	13:AM:91:ARG:NH1	2.34	0.59
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.02	0.59
25:BA:652(F):G:H22	25:BA:652(S):C:H2'	1.68	0.59
27:BD:69:ARG:NH2	27:BD:128:GLY:O	2.35	0.59
27:BD:242:ARG:O	60:BD:403:HOH:O	2.17	0.59
1:CA:309:G:O2'	1:CA:607:A:N1	2.36	0.59
1:CA:1318:A:OP1	19:CS:3:ARG:NH1	2.36	0.59
20:CT:43:LEU:O	20:CT:47:GLY:N	2.35	0.59
25:DA:614(A):U:H4'	25:DA:614(B):G:H5'	1.84	0.59
25:DA:632:A:H2'	25:DA:633:A:C8	2.37	0.59
26:DB:95:C:H2'	26:DB:96:U:C6	2.36	0.59
1:AA:376:G:H4'	16:AP:5:ARG:HE	1.67	0.59
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.37	0.59
1:AA:1273:G:H3'	1:AA:1274:G:C8	2.36	0.59
3:AC:179:ARG:NH1	3:AC:206:GLU:OE2	2.35	0.59
6:AF:35:ALA:HB2	6:AF:67:MET:HE2	1.83	0.59
25:BA:692:C:HO2'	25:BA:1354:A:HO2'	1.51	0.59
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.65	0.59
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.84	0.59
3:CC:164:ARG:HD2	3:CC:165:THR:H	1.66	0.59
9:CI:7:THR:OG1	9:CI:83:ARG:NH1	2.36	0.59
9:CI:50:LEU:HD21	9:CI:81:ILE:HD11	1.83	0.59
28:DE:14:ILE:HD11	28:DE:173:VAL:HG11	1.84	0.59
36:DQ:79:LEU:HB3	36:DQ:80:GLU:HG3	1.84	0.59
1:AA:201:C:H42	1:AA:216:G:N2	2.00	0.59
25:BA:1794:U:H2'	25:BA:1795:C:C6	2.37	0.59
25:BA:2118:U:O4	25:BA:2149:G:H1'	2.03	0.59
25:DA:694:U:OP1	27:DD:59:LYS:NZ	2.34	0.59
1:AA:316:G:OP2	1:AA:351:G:O2'	2.20	0.59
1:AA:413:G:N2	1:AA:428:G:H1'	2.18	0.59
25:BA:197:A:N6	25:BA:2430:A:O2'	2.35	0.59
25:BA:576:U:OP1	60:BA:4285:HOH:O	2.17	0.59
25:BA:800:A:H8	25:BA:800:A:OP1	1.86	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BB:91:C:OP2	36:BQ:16:ARG:NH1	2.35	0.59
27:BD:169:GLU:OE1	27:BD:184:LYS:NZ	2.35	0.59
25:DA:2879:C:OP2	60:DA:4350:HOH:O	2.17	0.59
25:BA:1866:C:H2'	25:BA:1876:A:O4'	2.03	0.59
25:DA:1590:U:H2'	25:DA:1591:G:H8	1.68	0.59
42:DW:18:ARG:NH1	42:DW:76:VAL:O	2.36	0.59
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.85	0.59
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.34	0.59
25:BA:144:C:H5'	43:BX:2:LYS:HD2	1.84	0.59
1:CA:1189:C:OP1	10:CJ:51:ARG:NH2	2.35	0.59
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.85	0.59
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.85	0.59
11:CK:33:THR:HA	11:CK:39:PRO:HA	1.83	0.59
13:CM:6:GLY:O	30:DG:115:ARG:NH2	2.35	0.59
25:DA:2206:G:H3'	25:DA:2207:G:C8	2.38	0.59
25:DA:2276:G:H5'	36:DQ:86:GLY:HA2	1.83	0.59
25:DA:2515:C:H2'	25:DA:2516:G:H8	1.68	0.59
25:DA:2788:C:OP1	28:DE:61:ARG:NH2	2.36	0.59
8:AH:29:SER:HB2	8:AH:32:LYS:HG3	1.85	0.59
25:BA:568:U:H5'	25:BA:945:A:N1	2.18	0.59
25:BA:1171:G:H3'	25:BA:1173:G:H5'	1.84	0.59
34:BO:63:VAL:HG12	34:BO:106:LEU:HD11	1.85	0.59
48:B2:25:VAL:HG13	48:B2:57:ILE:HG23	1.84	0.59
52:B6:11:LEU:HB2	52:B6:21:TYR:HB2	1.85	0.59
25:DA:706:A:OP1	27:DD:7:LYS:NZ	2.23	0.59
25:DA:2398:U:H2'	25:DA:2399:G:C8	2.37	0.59
34:DO:60:ALA:HA	34:DO:87:ILE:HG12	1.85	0.59
1:AA:974:A:OP2	14:AN:29:ARG:NH2	2.35	0.58
1:AA:993:G:O6	1:AA:1045:C:N4	2.35	0.58
1:AA:1289:A:OP1	21:AU:9:ARG:NH2	2.36	0.58
25:BA:1403:C:H5"	25:BA:1471:A:H1'	1.84	0.58
27:BD:132:PRO:HG2	27:BD:135:PHE:CD2	2.38	0.58
32:BI:102:SER:O	32:BI:106:GLY:HA3	2.02	0.58
44:BY:92:ASN:HB2	44:BY:94:LYS:H	1.66	0.58
1:CA:1397:C:H4'	22:CV:23:A:C6	2.37	0.58
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.36	0.58
25:DA:1017:G:N7	60:DA:4475:HOH:O	2.31	0.58
25:DA:1265:A:OP2	60:DA:4244:HOH:O	2.16	0.58
25:DA:1721:G:H8	25:DA:1741:A:H62	1.49	0.58
25:DA:2126:A:N6	25:DA:2162:G:O2'	2.36	0.58
27:DD:206:LEU:HD22	27:DD:211:ARG:HG2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DS:26:LEU:HA	38:DS:39:ILE:HG12	1.85	0.58
1:AA:78:G:C6	1:AA:91:C:N4	2.69	0.58
1:AA:376:G:H5"	16:AP:5:ARG:HB2	1.85	0.58
1:AA:1286:A:C8	1:AA:1287:A:H4'	2.38	0.58
25:BA:729:G:OP1	27:BD:10:THR:OG1	2.15	0.58
25:BA:2188:C:H2'	25:BA:2189:U:O4'	2.04	0.58
1:CA:572:A:OP1	60:CA:4030:HOH:O	2.17	0.58
1:CA:1153:C:H42	1:CA:1154:G:N2	2.01	0.58
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.33	0.58
8:CH:37:ARG:NH2	8:CH:118:VAL:O	2.36	0.58
9:CI:53:VAL:O	9:CI:55:ALA:N	2.33	0.58
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.38	0.58
25:DA:131:G:OP1	60:DA:4073:HOH:O	2.17	0.58
25:DA:1665:A:H4'	34:DO:67:LYS:HB2	1.84	0.58
25:DA:2125:G:H22	25:DA:2172:U:H5'	1.68	0.58
34:DO:19:ILE:HG22	34:DO:43:VAL:HA	1.86	0.58
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.18	0.58
25:BA:858:U:O2	25:BA:2268:A:H2'	2.04	0.58
25:BA:2572:A:N7	28:BE:144:ARG:HD2	2.17	0.58
50:B4:63:TYR:N	50:B4:64:GLY:HA2	2.18	0.58
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.84	0.58
10:CJ:5:ARG:N	10:CJ:99:LYS:O	2.37	0.58
11:CK:22:HIS:HD2	11:CK:29:ILE:HD12	1.68	0.58
25:DA:958:U:OP2	36:DQ:14:ARG:NH1	2.37	0.58
30:DG:144:ILE:HG23	30:DG:148:MET:HE1	1.84	0.58
1:AA:159:G:N2	1:AA:162:A:OP2	2.35	0.58
27:BD:145:VAL:HB	27:BD:155:LEU:HB2	1.84	0.58
1:CA:400:C:H5"	4:CD:73:ARG:NH2	2.15	0.58
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.38	0.58
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.38	0.58
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.84	0.58
25:DA:1592:C:H2'	25:DA:1593:G:C8	2.38	0.58
25:DA:2126:A:N3	25:DA:2127:G:H1'	2.19	0.58
25:DA:2611:U:C4	51:D5:3:LYS:HG2	2.38	0.58
28:DE:199:ARG:HH12	28:DE:202:LYS:HE2	1.68	0.58
30:DG:33:ARG:HE	30:DG:162:THR:HG21	1.66	0.58
41:DV:62:LEU:HD11	41:DV:95:LEU:HB2	1.86	0.58
44:DY:37:VAL:N	44:DY:67:LEU:O	2.32	0.58
1:AA:1241:G:H1	1:AA:1296:C:H42	1.49	0.58
1:CA:1032:G:H2'	1:CA:1033:G:C8	2.38	0.58
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DQ:26:TYR:O	36:DQ:67:ARG:NH1	2.37	0.58
50:D4:40:HIS:HD2	50:D4:41:PRO:HD2	1.68	0.58
1:AA:93:G:H2'	1:AA:96:U:O4'	2.03	0.58
1:AA:401:C:H2'	1:AA:402:G:C8	2.37	0.58
10:AJ:47:PHE:N	10:AJ:63:PHE:O	2.37	0.58
1:CA:1123:A:H4'	10:CJ:36:GLY:HA3	1.86	0.58
1:CA:1164:G:H1	1:CA:1172:C:H42	1.49	0.58
18:CR:56:THR:HB	18:CR:58:LEU:HD23	1.85	0.58
25:DA:616:G:H5'	29:DF:205:ARG:HD2	1.85	0.58
27:DD:108:PRO:HG2	27:DD:111:LEU:HB2	1.85	0.58
8:AH:21:LYS:O	8:AH:65:TYR:OH	2.17	0.58
25:BA:668:G:H5'	25:BA:669:G:OP2	2.03	0.58
25:BA:1153:C:OP1	40:BU:92:ARG:NH1	2.36	0.58
1:CA:1378:C:H5"	7:CG:6:ARG:HH21	1.68	0.58
15:CO:55:GLY:HA2	15:CO:58:MET:HE3	1.85	0.58
25:DA:140:G:H22	25:DA:1596:A:H4'	1.69	0.58
25:DA:644:A:H4'	25:DA:645:C:C5	2.39	0.58
25:DA:1226:A:OP1	41:DV:84:LYS:NZ	2.21	0.58
25:DA:1674:G:N2	25:DA:1677:A:N1	2.51	0.58
25:DA:2273:A:H2'	25:DA:2274:A:C8	2.38	0.58
28:DE:18:ASP:HB3	39:DT:82:LEU:HD21	1.85	0.58
35:DP:63:PRO:HD3	54:D8:27:THR:HG22	1.86	0.58
35:DP:81:GLN:NE2	35:DP:105:LEU:O	2.37	0.58
25:BA:2431:U:OP1	60:BA:3998:HOH:O	2.16	0.58
28:BE:47:VAL:HG21	28:BE:86:PRO:HD2	1.84	0.58
33:BN:12:ARG:HH21	33:BN:138:LEU:HD11	1.67	0.58
47:B1:54:ALA:HB1	47:B1:83:GLU:HG3	1.86	0.58
1:CA:977:A:H1'	1:CA:982:U:O4	2.04	0.58
1:CA:1002:G:N2	1:CA:1038:C:N3	2.51	0.58
25:DA:453:C:O2	25:DA:457:A:O2'	2.22	0.58
25:DA:1410:G:H2'	25:DA:1411:C:C6	2.38	0.58
1:AA:1008:C:N4	1:AA:1021:G:N1	2.33	0.58
25:BA:271(L):U:H5'	32:BI:50:ARG:NH1	2.18	0.58
25:BA:1031:G:H5"	55:B9:8:LYS:HE3	1.86	0.58
1:CA:664:G:OP1	18:CR:64:ARG:NH1	2.35	0.58
1:CA:1002:G:N3	1:CA:1003:G:H8	2.01	0.58
1:CA:1423:G:H5'	34:DO:49:ARG:HH12	1.68	0.58
2:CB:33:TYR:HB2	2:CB:43:ASP:HA	1.84	0.58
2:CB:122:PHE:HD1	2:CB:123:ALA:H	1.50	0.58
13:CM:120:LYS:HA	13:CM:121:LYS:NZ	2.18	0.58
25:DA:1266:G:O2'	25:DA:2012:G:O6	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:988:G:H1	1:AA:1217:C:H42	1.51	0.58
4:AD:85:LYS:HG3	4:AD:86:LYS:H	1.67	0.58
5:AE:68:GLU:HG3	5:AE:70:PRO:HD3	1.86	0.58
25:BA:118:A:H5'	25:BA:119:A:H8	1.68	0.58
31:BH:40:GLU:OE1	31:BH:61:HIS:NE2	2.37	0.58
32:BI:93:THR:H	32:BI:96:ASP:CG	2.12	0.58
1:CA:427:U:O2'	1:CA:541:G:OP1	2.18	0.58
1:CA:985:C:H2'	1:CA:986:A:C8	2.39	0.58
3:CC:43:LEU:HD23	3:CC:44:GLU:N	2.19	0.58
22:CV:16:A:N6	24:CX:36:U:H3	2.01	0.58
25:DA:84:A:H5"	44:DY:8:LYS:HE3	1.86	0.58
25:DA:375:C:H2'	25:DA:376:C:C6	2.39	0.58
25:DA:1688:U:O2	25:DA:1700:A:H5'	2.03	0.58
39:DT:60:THR:HG22	39:DT:77:PRO:HA	1.86	0.58
25:BA:2065:C:H2'	25:BA:2066:C:C6	2.38	0.57
44:BY:99:CYS:HB2	44:BY:106:LEU:HD21	1.86	0.57
1:CA:401:C:OP2	4:CD:73:ARG:NH1	2.37	0.57
1:CA:1309:G:H5'	13:CM:78:ILE:HD11	1.86	0.57
25:DA:1827:C:OP2	27:DD:222:ARG:NH1	2.37	0.57
25:DA:2143:C:H2'	25:DA:2144:U:O4'	2.04	0.57
25:DA:2343:C:O2'	25:DA:2373:G:O2'	2.13	0.57
33:DN:15:LEU:HB2	33:DN:135:PRO:HB2	1.86	0.57
1:AA:353:A:H8	1:AA:353:A:H5'	1.69	0.57
1:AA:427:U:O2'	1:AA:541:G:OP1	2.21	0.57
28:BE:12:THR:HG22	28:BE:13:ARG:H	1.68	0.57
30:BG:64:THR:HB	30:BG:94:LEU:HD21	1.84	0.57
40:BU:66:ASN:O	40:BU:70:ARG:HG3	2.03	0.57
1:CA:59:A:H5"	1:CA:60:A:H5"	1.84	0.57
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.40	0.57
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.68	0.57
13:CM:65:LYS:NZ	50:D4:53:GLU:OE1	2.33	0.57
16:CP:19:ILE:HD11	16:CP:39:TYR:HB2	1.85	0.57
26:DB:7:G:N3	38:DS:38:GLN:NE2	2.43	0.57
26:DB:20:C:H42	26:DB:63:G:H1	1.50	0.57
38:DS:28:VAL:HG13	38:DS:35:ILE:HD11	1.86	0.57
38:DS:89:ARG:HG2	38:DS:92:TYR:O	2.04	0.57
1:AA:158:G:H21	1:AA:162:A:H62	1.50	0.57
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.86	0.57
1:AA:881:G:P	12:AL:12:ARG:HH22	2.26	0.57
3:AC:124:ILE:HD12	3:AC:196:LEU:HD12	1.86	0.57
41:BV:14:VAL:HB	41:BV:96:ILE:HG13	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:153:ARG:O	4:CD:159:ARG:NH2	2.37	0.57
25:DA:2291:U:O2'	25:DA:2374:C:O2	2.19	0.57
39:DT:88:ILE:HG21	39:DT:91:ARG:HD3	1.86	0.57
1:AA:539:A:OP2	12:AL:115:LYS:HD2	2.05	0.57
1:AA:1259:C:N4	1:AA:1276:G:H1	2.02	0.57
25:BA:1178:C:H2'	25:BA:1179:C:C6	2.40	0.57
25:BA:2123:G:H1	25:BA:2175:C:H42	1.53	0.57
32:BI:104:GLN:C	32:BI:106:GLY:H	2.11	0.57
1:CA:745:C:OP1	1:CA:851:G:O2'	2.19	0.57
2:CB:87:ARG:NE	2:CB:233:SER:HB3	2.19	0.57
5:CE:19:MET:SD	5:CE:24:ARG:HG2	2.44	0.57
17:CQ:57:VAL:HG12	17:CQ:76:LEU:HA	1.86	0.57
20:CT:64:ASP:OD2	20:CT:81:LYS:NZ	2.36	0.57
25:DA:833:U:O2	35:DP:55:ARG:NH2	2.37	0.57
2:AB:163:PHE:HA	2:AB:185:ILE:HG12	1.84	0.57
25:BA:956:G:OP2	36:BQ:14:ARG:NH2	2.38	0.57
25:BA:1859:A:N6	25:BA:1883:G:O2'	2.36	0.57
25:BA:2143:C:H2'	25:BA:2144:U:O4'	2.04	0.57
1:CA:103:C:O2'	1:CA:172:A:N1	2.37	0.57
1:CA:1326:C:H5"	21:CU:18:TYR:O	2.03	0.57
1:CA:1349:A:H5"	9:CI:121:ARG:HB2	1.85	0.57
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.86	0.57
25:DA:668:G:H5'	25:DA:669:G:OP2	2.04	0.57
25:DA:821:A:H2'	25:DA:946:G:H5"	1.84	0.57
26:DB:66:A:H61	26:DB:108:U:H3'	1.70	0.57
30:DG:178:PHE:N	30:DG:178:PHE:CD1	2.71	0.57
1:AA:509:A:N3	1:AA:543:C:O2'	2.33	0.57
1:AA:559:A:H4'	1:AA:560:U:H3'	1.86	0.57
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.19	0.57
10:AJ:7:LYS:HB3	10:AJ:97:GLU:HB2	1.86	0.57
1:CA:190:U:H2'	1:CA:191:G:C8	2.40	0.57
1:CA:1067:A:O2'	1:CA:1068:G:OP2	2.19	0.57
2:CB:83:MET:HB3	2:CB:234:PRO:HB2	1.87	0.57
19:CS:9:VAL:HG21	50:D4:61:ARG:NH2	2.20	0.57
25:DA:2150:U:H2'	25:DA:2151:G:C8	2.40	0.57
27:DD:112:GLN:H	27:DD:115:GLN:NE2	2.02	0.57
1:AA:624:C:H2'	1:AA:625:G:C8	2.39	0.57
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.37	0.57
24:AX:55:PSU:O2'	24:AX:57:A:N7	2.34	0.57
25:BA:1770:G:OP1	60:BA:4522:HOH:O	2.17	0.57
1:CA:1134:G:H2'	1:CA:1134:G:N3	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:45:LYS:HZ1	3:CC:46:GLU:HG2	1.70	0.57
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.45	0.57
25:DA:656:G:H2'	25:DA:657:U:O4'	2.04	0.57
25:DA:1565:C:H42	25:DA:1568:G:H1	1.52	0.57
25:DA:2454:G:O6	60:DA:4290:HOH:O	2.16	0.57
1:AA:21:G:H2'	1:AA:22:G:C8	2.40	0.57
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.17	0.57
3:AC:164:ARG:HG2	3:AC:165:THR:H	1.69	0.57
6:AF:97:PHE:HB2	18:AR:32:ARG:HE	1.68	0.57
25:BA:602:G:O2'	25:BA:655:A:N6	2.37	0.57
25:BA:875:G:H1	25:BA:902:C:H42	1.51	0.57
25:BA:1860:G:N2	25:BA:1883:G:H1'	2.20	0.57
25:BA:1963:U:H4'	25:BA:1964:G:OP1	2.03	0.57
25:BA:2577:A:H5'	51:B5:3:LYS:HD2	1.87	0.57
25:BA:2810:A:N6	25:BA:2891:G:O2'	2.34	0.57
2:CB:122:PHE:HA	2:CB:127:ILE:HD12	1.87	0.57
5:CE:10:MET:SD	5:CE:10:MET:N	2.77	0.57
17:CQ:12:SER:HB3	17:CQ:20:THR:HB	1.85	0.57
25:DA:2104:G:H1	25:DA:2185:C:N4	2.02	0.57
25:DA:2630:G:H2'	25:DA:2631:G:C8	2.40	0.57
29:DF:184:TYR:CE2	29:DF:188:ARG:HD2	2.40	0.57
1:AA:17:U:H2'	1:AA:18:C:C6	2.40	0.57
1:AA:1194:U:H2'	1:AA:1195:C:C6	2.40	0.57
1:AA:1288:A:N1	1:AA:1371:G:H1'	2.20	0.57
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.87	0.57
7:CG:116:ALA:O	7:CG:120:ILE:HG12	2.04	0.57
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.85	0.57
25:DA:689:A:N3	25:DA:779:U:O2'	2.36	0.57
25:DA:1710:C:H2'	25:DA:1711:C:H6	1.70	0.57
27:BD:17:THR:O	27:BD:211:ARG:NH2	2.38	0.57
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.40	0.57
2:CB:187:LEU:HB2	2:CB:201:ILE:HB	1.87	0.57
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.87	0.57
25:DA:883:G:O6	25:DA:893:C:N4	2.29	0.57
25:DA:2331:G:O2'	25:DA:2336:A:N1	2.31	0.57
25:DA:2679:A:H4'	28:DE:165:VAL:HG11	1.87	0.57
1:AA:56:U:H2'	1:AA:57:G:C8	2.40	0.56
1:AA:346:G:H2'	1:AA:347:G:H4'	1.87	0.56
20:AT:43:LEU:O	20:AT:47:GLY:N	2.38	0.56
25:BA:61:G:H5'	48:B2:50:ILE:HG21	1.86	0.56
25:BA:996:A:OP2	40:BU:93:LYS:NZ	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2012:G:OP1	42:BW:11:ARG:NH2	2.36	0.56
25:BA:2564:A:C2	25:BA:2647:U:H4'	2.40	0.56
32:BI:96:ASP:OD1	32:BI:96:ASP:N	2.38	0.56
1:CA:36:C:OP1	12:CL:123:LYS:HE3	2.04	0.56
1:CA:486:U:H2'	1:CA:487:A:H8	1.70	0.56
1:CA:1137:C:H5"	1:CA:1138:G:OP1	2.04	0.56
10:CJ:30:SER:O	10:CJ:81:THR:OG1	2.23	0.56
11:CK:48:ILE:O	11:CK:50:TYR:N	2.38	0.56
25:DA:1916:A:H2'	25:DA:1917:U:O4'	2.05	0.56
25:DA:1971:A:OP2	27:DD:242:ARG:NH2	2.38	0.56
26:DB:24:G:H21	26:DB:27:C:H42	1.53	0.56
39:DT:53:ARG:HB3	39:DT:53:ARG:NH1	2.20	0.56
44:DY:61:ILE:HD11	44:DY:63:LYS:HE3	1.85	0.56
1:AA:198:G:H2'	1:AA:199:G:C8	2.40	0.56
1:AA:1015:A:N3	1:AA:1218:C:O2'	2.35	0.56
3:AC:26:LYS:HA	14:AN:36:PHE:HE1	1.70	0.56
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.37	0.56
25:BA:2146:C:H4'	25:BA:2147:G:C4	2.40	0.56
30:BG:138:GLN:NE2	30:BG:153:ARG:H	2.02	0.56
48:B2:63:VAL:HA	48:B2:66:GLU:HB2	1.86	0.56
1:CA:538:G:H5"	12:CL:114:LYS:HB2	1.87	0.56
1:CA:921:U:O2	5:CE:19:MET:HB2	2.06	0.56
25:DA:300:A:H1'	25:DA:319:C:H1'	1.87	0.56
25:DA:1165:U:H2'	25:DA:1166:C:C6	2.41	0.56
25:DA:2185:C:H2'	25:DA:2186:G:H8	1.71	0.56
31:DH:70:THR:HA	31:DH:73:ALA:HB3	1.86	0.56
50:D4:38:LYS:O	50:D4:40:HIS:N	2.27	0.56
51:D5:16:ARG:NH1	51:D5:17:ASP:OD1	2.38	0.56
25:BA:2127:G:H21	25:BA:2173:A:H1'	1.70	0.56
25:BA:2243:U:H2'	25:BA:2244:U:C6	2.40	0.56
49:B3:44:ARG:O	49:B3:48:GLU:HG3	2.05	0.56
1:CA:1329:A:H5"	13:CM:26:GLY:N	2.20	0.56
25:DA:751:A:H5'	42:DW:90:ARG:HA	1.87	0.56
25:DA:989:G:H4'	25:DA:990:A:OP1	2.05	0.56
25:DA:2249:U:N3	25:DA:2253:G:OP2	2.36	0.56
25:DA:2507:C:H5"	25:DA:2573:C:N4	2.19	0.56
25:DA:2562:U:H1'	34:DO:23:ARG:HH11	1.70	0.56
28:DE:47:VAL:HG11	28:DE:86:PRO:HD2	1.87	0.56
29:DF:64:ILE:HD11	29:DF:75:HIS:HB2	1.87	0.56
30:DG:173:LEU:HD22	30:DG:178:PHE:CZ	2.40	0.56
36:DQ:109:VAL:HG13	36:DQ:113:GLN:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DR:55:ALA:HB2	37:DR:79:LEU:HD13	1.86	0.56
38:DS:10:ARG:HA	38:DS:13:ARG:HE	1.70	0.56
1:AA:1028:C:C4	1:AA:1029:C:H1'	2.40	0.56
1:AA:1330:U:O4	1:AA:1331:G:N1	2.39	0.56
25:BA:1188:U:H4'	41:BV:79:VAL:HG22	1.86	0.56
34:BO:2:ILE:HD12	34:BO:6:THR:HG21	1.85	0.56
47:B1:51:VAL:HG11	47:B1:74:VAL:HG21	1.86	0.56
1:CA:630:G:H2'	1:CA:631:G:H8	1.70	0.56
1:CA:693:G:H2'	1:CA:694:A:C8	2.40	0.56
7:CG:49:ILE:HA	7:CG:52:GLU:HG2	1.87	0.56
29:DF:33:LEU:HD13	29:DF:112:MET:HE2	1.88	0.56
33:DN:4:TYR:CE2	40:DU:100:VAL:HG11	2.40	0.56
43:DX:50:LYS:HB3	43:DX:87:GLN:HE22	1.71	0.56
45:DZ:145:GLU:HG3	45:DZ:146:ILE:H	1.70	0.56
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.06	0.56
25:BA:911:A:H2'	36:BQ:9:TYR:OH	2.05	0.56
29:BF:183:VAL:O	29:BF:187:VAL:HG23	2.06	0.56
31:BH:11:VAL:HG21	31:BH:50:VAL:HG23	1.88	0.56
1:CA:958:A:N6	19:CS:77:THR:O	2.38	0.56
1:CA:1121:U:O4	1:CA:1152:A:N1	2.38	0.56
18:CR:47:THR:HG21	18:CR:49:LYS:HE2	1.88	0.56
20:CT:59:ALA:O	20:CT:63:ILE:HG13	2.05	0.56
25:DA:511:U:H4'	25:DA:1235:G:H4'	1.86	0.56
25:DA:1792:G:N2	25:DA:1827:C:O2	2.36	0.56
25:DA:1794:U:H2'	25:DA:1795:C:C6	2.40	0.56
25:DA:2788:C:H5"	28:DE:61:ARG:HH21	1.69	0.56
1:AA:711:G:OP1	6:AF:54:LYS:NZ	2.39	0.56
31:BH:33:LEU:HD21	31:BH:136:ILE:HG13	1.87	0.56
31:BH:56:SER:OG	31:BH:57:ASP:N	2.38	0.56
33:BN:108:PRO:O	33:BN:113:GLY:HA3	2.05	0.56
1:CA:1154:G:N7	1:CA:1155:G:C8	2.74	0.56
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.40	0.56
3:CC:5:ILE:HG12	3:CC:6:HIS:H	1.71	0.56
46:D0:40:GLN:HE21	46:D0:57:PHE:HB3	1.71	0.56
7:AG:20:ASP:OD2	7:AG:63:LYS:NZ	2.37	0.56
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.21	0.56
35:BP:95:VAL:HG13	35:BP:125:VAL:HG12	1.88	0.56
1:CA:1074:G:OP1	5:CE:64:ARG:NH2	2.38	0.56
1:CA:1104:G:H4'	2:CB:111:ARG:HH11	1.71	0.56
3:CC:36:ASP:OD1	3:CC:57:ILE:HG21	2.06	0.56
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CR:25:THR:O	18:CR:25:THR:OG1	2.24	0.56
27:DD:127:VAL:HA	27:DD:193:VAL:HG23	1.87	0.56
27:DD:175:LEU:HD12	27:DD:185:VAL:HG21	1.87	0.56
42:DW:12:ILE:O	42:DW:101:SER:OG	2.23	0.56
1:AA:1309:G:OP2	13:AM:99:ARG:NH2	2.39	0.56
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.06	0.56
4:AD:81:GLU:OE1	4:AD:139:ARG:NH2	2.38	0.56
1:CA:977:A:O2'	1:CA:981:U:N3	2.32	0.56
8:CH:30:ARG:O	8:CH:34:GLU:HG2	2.06	0.56
13:CM:3:ARG:HA	50:D4:34:GLU:HG2	1.87	0.56
25:DA:271(U):G:H2'	25:DA:271(V):G:H8	1.70	0.56
25:DA:652(B):A:N1	25:DA:655:A:H1'	2.20	0.56
25:DA:1166:C:H2'	25:DA:1167:U:C6	2.40	0.56
25:DA:2059:A:O2'	29:DF:69:HIS:HD2	1.89	0.56
25:DA:2183:C:H2'	25:DA:2184:G:C8	2.39	0.56
28:DE:116:VAL:HG13	28:DE:122:PHE:HB2	1.87	0.56
33:DN:43:THR:N	33:DN:48:MET:SD	2.77	0.56
1:AA:185:A:H2'	1:AA:186:C:C6	2.41	0.56
1:AA:1399:C:C2	1:AA:1502:A:N6	2.73	0.56
24:AX:67:C:H2'	24:AX:68:C:H5'	1.87	0.56
25:BA:686:G:OP1	53:B7:11:LYS:NZ	2.38	0.56
25:BA:1634:A:OP2	60:BA:3951:HOH:O	2.18	0.56
46:B0:27:GLU:HG3	46:B0:68:GLU:HA	1.88	0.56
1:CA:1014:A:H4'	19:CS:14:HIS:CE1	2.41	0.56
25:DA:1443:G:H1	25:DA:1548:C:H42	1.53	0.56
25:DA:2379:G:H4'	38:DS:21:THR:HG21	1.88	0.56
25:DA:2727:G:O2'	34:DO:70:LYS:NZ	2.39	0.56
32:DI:31:LEU:HD21	32:DI:38:LEU:HG	1.88	0.56
1:AA:1030:C:N4	1:AA:1031:G:H1	2.02	0.56
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.86	0.56
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.41	0.56
2:AB:114:ARG:NH2	2:AB:117:GLU:OE2	2.39	0.56
25:BA:221:A:N1	25:BA:265:A:O2'	2.37	0.56
1:CA:1438:G:H2'	1:CA:1439:C:C6	2.41	0.56
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.71	0.56
9:CI:23:ASN:HD22	9:CI:24:GLY:N	2.03	0.56
25:DA:1786:A:OP1	60:DA:4235:HOH:O	2.18	0.56
30:DG:5:VAL:HG22	30:DG:8:LYS:H	1.70	0.56
30:DG:41:GLN:HG3	30:DG:60:LEU:HD21	1.87	0.56
50:D4:59:PHE:HA	50:D4:61:ARG:N	2.21	0.56
1:AA:448:A:P	1:AA:485:G:H22	2.29	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1492:A:N3	22:AV:20:U:O2'	2.39	0.55
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.88	0.55
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.39	0.55
25:BA:1721:G:H8	25:BA:1741:A:H62	1.52	0.55
25:BA:1796:U:H2'	25:BA:1797:C:C6	2.41	0.55
25:BA:2789:C:H1'	25:BA:2894:G:H22	1.70	0.55
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.21	0.55
1:CA:1162:C:N4	1:CA:1174:G:H1	2.04	0.55
7:CG:148:ASN:HD22	7:CG:151:TYR:HD2	1.55	0.55
20:CT:54:LYS:HB2	20:CT:100:ILE:HD11	1.87	0.55
24:CX:75:C:OP1	60:CX:201:HOH:O	2.18	0.55
25:DA:61:G:H1	25:DA:94:C:H42	1.54	0.55
25:DA:1270:C:O2'	25:DA:1648:C:OP2	2.14	0.55
25:DA:2364:C:H2'	25:DA:2365:G:O4'	2.07	0.55
26:DB:55:U:O2'	30:DG:27:ASN:OD1	2.24	0.55
27:DD:17:THR:O	27:DD:211:ARG:NH2	2.39	0.55
36:DQ:62:GLY:HA2	45:DZ:116:VAL:HG21	1.88	0.55
1:AA:1279:A:H4'	1:AA:1281:U:H5	1.71	0.55
7:AG:47:CYS:HA	7:AG:50:ILE:HG12	1.89	0.55
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.70	0.55
25:BA:802:A:OP1	60:BA:4135:HOH:O	2.18	0.55
25:BA:2099:U:H3	25:BA:2190:G:H1	1.54	0.55
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.41	0.55
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.06	0.55
25:DA:186:G:H2'	25:DA:187:G:H8	1.71	0.55
25:DA:492:A:H2'	25:DA:493:G:O4'	2.07	0.55
25:DA:657:U:H2'	25:DA:658:C:C6	2.41	0.55
25:DA:2019:A:H4'	40:DU:34:LYS:HD2	1.88	0.55
45:DZ:152:ALA:HA	45:DZ:155:LEU:HD13	1.86	0.55
1:AA:1189:C:H5"	3:AC:5:ILE:HD12	1.89	0.55
2:AB:198:ASP:OD2	2:AB:198:ASP:N	2.39	0.55
14:AN:3:ARG:O	14:AN:7:ILE:N	2.38	0.55
25:BA:2731:G:H5"	28:BE:203:LYS:HE3	1.87	0.55
5:CE:93:PRO:O	8:CH:105:ARG:NH2	2.40	0.55
25:DA:527:C:OP1	60:DA:4386:HOH:O	2.18	0.55
25:DA:2117:A:H61	25:DA:2171:A:H61	1.54	0.55
25:DA:2163:C:H5"	25:DA:2172:U:H5'	1.87	0.55
27:DD:12:SER:HB3	27:DD:208:LYS:HB3	1.88	0.55
30:DG:63:ILE:HA	30:DG:143:GLU:HG3	1.88	0.55
33:DN:33:LEU:HB3	33:DN:52:VAL:HG21	1.88	0.55
52:D6:21:TYR:CE2	52:D6:38:LYS:HG3	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:300:A:O2'	1:AA:564:C:N3	2.33	0.55
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.07	0.55
25:BA:582:G:H2'	25:BA:583:G:C8	2.41	0.55
35:BP:86:LYS:HB3	35:BP:118:GLY:HA3	1.87	0.55
44:BY:13:VAL:HG12	44:BY:74:PRO:HA	1.88	0.55
7:CG:16:LEU:HD13	9:CI:41:VAL:HG12	1.88	0.55
25:DA:918:A:C5	25:DA:919:G:H1'	2.42	0.55
25:DA:1149:G:H2'	25:DA:1150:C:C6	2.41	0.55
28:DE:163:GLU:HG2	28:DE:164:ARG:N	2.20	0.55
49:D3:6:VAL:HG22	49:D3:56:VAL:HG13	1.88	0.55
1:AA:1003:G:C2	1:AA:1004:A:N3	2.74	0.55
13:AM:49:THR:HB	13:AM:52:GLU:H	1.72	0.55
25:BA:1023:U:OP2	60:BA:4468:HOH:O	2.18	0.55
25:BA:1107:G:H2'	25:BA:1107:G:N3	2.22	0.55
44:BY:92:ASN:CB	44:BY:94:LYS:HG2	2.37	0.55
45:BZ:99:TYR:HB3	45:BZ:123:ASP:HB2	1.87	0.55
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.06	0.55
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.75	0.55
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.40	0.55
22:CV:22:U:H2'	22:CV:23:A:C8	2.41	0.55
25:DA:587:C:OP1	35:DP:21:ARG:NH2	2.40	0.55
25:DA:848:G:H2'	25:DA:849:A:C8	2.41	0.55
25:DA:926:A:H2'	25:DA:927:G:H8	1.71	0.55
25:DA:2074:U:H2'	25:DA:2075:U:C6	2.41	0.55
32:DI:62:LYS:O	32:DI:66:GLU:HG2	2.06	0.55
33:DN:38:HIS:CE1	33:DN:39:ARG:HG3	2.41	0.55
45:DZ:55:HIS:HE1	45:DZ:135:GLU:HG3	1.71	0.55
4:AD:111:ALA:HB2	4:AD:120:LEU:HD12	1.88	0.55
6:AF:14:LEU:HB3	6:AF:18:GLN:HE22	1.71	0.55
26:BB:75:G:H5"	26:BB:75:G:H8	1.71	0.55
41:BV:65:GLY:HA3	41:BV:91:TYR:CZ	2.42	0.55
43:BX:41:ASN:O	43:BX:45:THR:HG22	2.06	0.55
8:CH:112:LEU:HA	8:CH:134:ILE:HG12	1.88	0.55
16:CP:28:ARG:NH1	16:CP:29:ASP:OD2	2.40	0.55
25:DA:83:G:OP2	44:DY:95:LYS:NZ	2.39	0.55
25:DA:1532:C:N4	25:DA:1537:G:O6	2.38	0.55
25:DA:2755:C:H3'	55:D9:19:ARG:HH21	1.72	0.55
26:DB:8:U:H3	26:DB:113:G:H1	1.54	0.55
45:DZ:145:GLU:H	45:DZ:148:ASP:HB2	1.72	0.55
1:AA:428:G:OP2	4:AD:10:ARG:NH1	2.36	0.55
1:AA:1095:U:OP1	1:AA:1108:G:N2	2.31	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BR:90:ARG:NH2	37:BR:118:GLU:OXT	2.40	0.55
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.89	0.55
6:CF:50:TYR:OH	18:CR:74:ARG:O	2.23	0.55
17:CQ:18:THR:HG23	17:CQ:69:LYS:HD3	1.88	0.55
9:AI:23:ASN:HD22	9:AI:23:ASN:H	1.55	0.55
25:BA:1174:A:H1'	25:BA:1175:U:H5"	1.89	0.55
25:BA:2791:C:H2'	25:BA:2792:G:C8	2.42	0.55
1:CA:297:G:N2	1:CA:300:A:OP2	2.39	0.55
1:CA:1127:G:N2	1:CA:1147:C:H41	2.05	0.55
2:CB:120:ALA:C	2:CB:122:PHE:H	2.13	0.55
4:CD:96:LEU:HD12	4:CD:139:ARG:HH21	1.71	0.55
24:CX:19:G:H4'	24:CX:20:U:OP2	2.06	0.55
25:DA:2821:A:H2'	25:DA:2822:G:C8	2.42	0.55
26:DB:13:A:C2	26:DB:16:G:H1'	2.42	0.55
30:DG:112:PRO:HB3	50:D4:35:VAL:HG22	1.87	0.55
1:AA:186:C:H2'	1:AA:187:C:C6	2.41	0.55
1:AA:942:G:H21	9:AI:124:GLN:NE2	2.04	0.55
4:AD:98:GLU:OE1	4:AD:107:ARG:NH1	2.40	0.55
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.07	0.55
10:AJ:16:LEU:HD22	10:AJ:68:HIS:HB2	1.89	0.55
13:AM:3:ARG:HD2	13:AM:9:ILE:HG13	1.88	0.55
15:AO:74:ASP:HB3	15:AO:77:ARG:HB2	1.87	0.55
25:BA:607:U:OP1	29:BF:102:PRO:HA	2.06	0.55
25:BA:657:U:H2'	25:BA:658:C:C6	2.42	0.55
25:BA:1636:C:O2'	25:BA:1760:A:N3	2.37	0.55
1:CA:1028:C:N3	1:CA:1033:G:O6	2.40	0.55
25:DA:2135:A:H2'	25:DA:2136:C:C6	2.41	0.55
25:DA:2406:U:OP1	60:DA:4156:HOH:O	2.18	0.55
25:DA:2526:G:H5'	25:DA:2742:C:O2'	2.07	0.55
26:DB:66:A:N6	26:DB:108:U:H3'	2.22	0.55
55:D9:25:VAL:HB	55:D9:34:GLN:HB2	1.88	0.55
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.36	0.55
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.42	0.55
16:AP:22:THR:HA	16:AP:33:ILE:HG12	1.89	0.55
25:BA:2849:U:OP2	39:BT:95:ARG:NH1	2.40	0.55
26:BB:105:A:P	45:BZ:72:ARG:HH12	2.29	0.55
27:BD:12:SER:HB3	27:BD:208:LYS:HB3	1.88	0.55
52:B6:6:ARG:NH1	52:B6:26:ASN:HB2	2.22	0.55
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.22	0.55
1:CA:1025:U:N3	1:CA:1036:G:N1	2.55	0.55
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.89	0.55
3:CC:43:LEU:HD21	3:CC:55:VAL:HG21	1.87	0.55
3:CC:156:ARG:H	3:CC:196:LEU:HD22	1.72	0.55
25:DA:391:G:O2'	25:DA:410:G:OP1	2.16	0.55
25:DA:979:G:H5"	25:DA:980:A:H5"	1.88	0.55
25:DA:1227:G:H2'	25:DA:1228:G:O4'	2.07	0.55
25:DA:1250:G:OP2	35:DP:21:ARG:NH1	2.40	0.55
30:DG:83:ARG:N	30:DG:86:MET:SD	2.70	0.55
32:DI:130:TYR:CE2	32:DI:132:PRO:HB3	2.42	0.55
34:DO:63:VAL:HG11	34:DO:85:VAL:HG23	1.87	0.55
45:DZ:6:LYS:HE3	45:DZ:43:GLU:OE1	2.07	0.55
1:AA:954:G:H21	1:AA:1227:A:H62	1.55	0.54
1:AA:1095:U:P	1:AA:1108:G:H1	2.30	0.54
2:AB:21:ARG:HB3	2:AB:38:GLY:O	2.07	0.54
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.88	0.54
12:AL:34:ARG:NH2	60:AL:301:HOH:O	2.39	0.54
24:AX:7:G:O2'	24:AX:49:G:H5'	2.07	0.54
25:BA:1045:A:OP1	25:BA:1046:A:H3'	2.06	0.54
25:BA:1107:G:N2	25:BA:1108:U:O4	2.40	0.54
31:BH:159:GLU:HG2	31:BH:169:VAL:HG11	1.89	0.54
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.88	0.54
25:DA:286:C:H2'	25:DA:287:C:C6	2.41	0.54
25:DA:1561:G:H2'	25:DA:1562:A:C8	2.41	0.54
25:DA:2115:G:H1'	25:DA:2117:A:H62	1.71	0.54
1:AA:270:A:H2'	1:AA:271:C:C6	2.41	0.54
1:AA:1346:A:N1	1:AA:1374:A:H5"	2.22	0.54
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.90	0.54
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.89	0.54
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.27	0.54
1:CA:1288:A:N3	1:CA:1352:C:O2'	2.39	0.54
4:CD:61:LYS:NZ	4:CD:72:GLU:OE1	2.39	0.54
25:DA:1019:U:H3	25:DA:1142(A):A:N6	2.03	0.54
25:DA:2150:U:H2'	25:DA:2151:G:H8	1.73	0.54
26:DB:42:C:O2	30:DG:93:THR:N	2.34	0.54
26:DB:42:C:O2'	30:DG:67:LYS:O	2.19	0.54
30:DG:68:PRO:HG2	30:DG:90:LEU:HD22	1.89	0.54
35:DP:121:LYS:HG2	35:DP:122:PRO:HD2	1.89	0.54
38:DS:8:GLU:H	38:DS:8:GLU:CD	2.15	0.54
1:AA:1112:C:O2	3:AC:179:ARG:HG3	2.06	0.54
24:AX:59:A:C2'	24:AX:60:U:H5'	2.38	0.54
25:BA:10:G:N2	25:BA:2802:G:OP1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:784:A:H5'	25:BA:785:G:OP1	2.08	0.54
25:BA:1380:G:N2	25:BA:1570:A:N1	2.54	0.54
36:BQ:18:LYS:O	36:BQ:98:LYS:NZ	2.21	0.54
47:B1:85:LEU:HB3	47:B1:89:GLU:HG3	1.88	0.54
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.23	0.54
1:CA:1442(A):G:C8	39:DT:118:ARG:HG2	2.42	0.54
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.05	0.54
4:CD:162:LEU:HD22	4:CD:178:VAL:HG13	1.87	0.54
23:CW:76:PPU:H92	25:DA:2584:U:H4'	1.90	0.54
25:DA:861:A:N3	26:DB:79:C:O2'	2.35	0.54
1:AA:347:G:H2'	1:AA:348:G:C8	2.42	0.54
1:AA:677:U:H3	1:AA:713:G:H22	1.56	0.54
1:AA:1296:C:OP1	13:AM:44:ARG:NH2	2.40	0.54
13:AM:9:ILE:HB	13:AM:18:ALA:HB1	1.89	0.54
24:AX:19:G:H4'	24:AX:20:U:OP2	2.07	0.54
25:BA:55:G:O2'	25:BA:127:A:N1	2.38	0.54
25:BA:586:A:H5'	29:BF:89:VAL:HG21	1.87	0.54
25:BA:880:G:H2'	25:BA:881:G:C8	2.42	0.54
25:BA:2110:G:OP2	25:BA:2118:U:N3	2.41	0.54
25:BA:2248:C:OP2	60:BA:4101:HOH:O	2.18	0.54
1:CA:982:U:H4'	1:CA:983:A:O5'	2.08	0.54
12:CL:60:LEU:HD21	12:CL:66:VAL:HG22	1.89	0.54
25:DA:2136:C:O2'	25:DA:2137:C:O5'	2.21	0.54
25:DA:2139:C:H42	25:DA:2152:G:H1	1.56	0.54
26:DB:32:C:H42	26:DB:50:G:H1	1.55	0.54
30:DG:111:LEU:HA	30:DG:114:ILE:HG13	1.88	0.54
32:DI:40:THR:HG23	32:DI:43:ASN:ND2	2.22	0.54
44:DY:37:VAL:O	44:DY:67:LEU:N	2.40	0.54
50:D4:33:VAL:HG12	50:D4:35:VAL:H	1.71	0.54
1:AA:518:C:O2'	1:AA:1492:A:N6	2.37	0.54
1:AA:877:C:H5"	8:AH:88:LYS:HD3	1.89	0.54
1:AA:1039:C:H2'	1:AA:1040:U:O4'	2.06	0.54
2:AB:95:GLN:HG3	2:AB:147:LYS:HG2	1.88	0.54
5:AE:92:LYS:HD3	5:AE:119:LEU:HD12	1.90	0.54
25:BA:226:G:H21	25:BA:228:A:H62	1.54	0.54
25:BA:456:C:H4'	60:BA:3733:HOH:O	2.08	0.54
25:BA:2690:C:OP1	37:BR:17:ARG:NH1	2.27	0.54
1:CA:981:U:O5'	1:CA:981:U:H6	1.90	0.54
1:CA:1275:A:H2'	1:CA:1276:G:O4'	2.08	0.54
1:CA:1330:U:H4'	13:CM:23:TYR:CZ	2.42	0.54
3:CC:181:ASN:HD21	3:CC:204:LEU:HD12	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:218:A:C2	25:DA:235:U:H4'	2.43	0.54
25:DA:463:G:N2	25:DA:466:A:OP2	2.29	0.54
25:DA:1446:C:H42	25:DA:1465:G:H1	1.56	0.54
25:DA:2314:C:H2'	25:DA:2315:G:C8	2.43	0.54
25:DA:2726:U:H4'	34:DO:1:MET:HE1	1.89	0.54
36:DQ:32:TYR:CE1	36:DQ:133:ARG:HG3	2.42	0.54
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.72	0.54
8:AH:83:ILE:HG13	8:AH:137:VAL:HG22	1.88	0.54
29:BF:149:ASP:OD1	29:BF:149:ASP:N	2.38	0.54
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.42	0.54
25:DA:134:C:H2'	25:DA:135:G:C8	2.42	0.54
25:DA:352:G:N2	25:DA:429:A:H5"	2.23	0.54
25:DA:1031:G:H5"	55:D9:8:LYS:HE3	1.89	0.54
25:DA:2391:G:O2'	25:DA:2422:A:N7	2.41	0.54
27:DD:10:THR:OG1	27:DD:13:ARG:HG2	2.07	0.54
32:DI:38:LEU:HB2	32:DI:40:THR:HG22	1.90	0.54
1:AA:159:G:H2'	1:AA:161:A:OP2	2.08	0.54
25:BA:887:A:O2'	25:BA:888:C:OP2	2.24	0.54
25:BA:1237:A:OP1	60:BA:4542:HOH:O	2.19	0.54
25:BA:2312:U:H5'	30:BG:88:ILE:HD11	1.89	0.54
38:BS:83:LYS:HG2	38:BS:111:GLU:HG3	1.88	0.54
1:CA:1298:C:OP2	7:CG:114:ARG:NH2	2.41	0.54
1:CA:1318:A:H5"	19:CS:3:ARG:NH2	2.22	0.54
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.43	0.54
5:CE:57:LYS:HG2	5:CE:61:TYR:HE2	1.73	0.54
25:DA:885:C:H3'	25:DA:886:C:H5"	1.90	0.54
25:DA:1609:A:OP2	60:DA:4280:HOH:O	2.18	0.54
28:DE:36:ARG:NH1	28:DE:85:ASN:OD1	2.41	0.54
31:DH:28:GLY:N	31:DH:31:GLY:O	2.41	0.54
37:DR:38:VAL:HG12	37:DR:42:LYS:HE3	1.89	0.54
38:DS:67:ARG:HG3	38:DS:71:ARG:HD2	1.90	0.54
41:DV:21:ARG:HG2	41:DV:91:TYR:CD2	2.43	0.54
1:AA:147:G:H2'	1:AA:148:G:H8	1.71	0.54
1:AA:890:G:O2'	1:AA:906:G:O6	2.23	0.54
1:AA:1106:G:H5"	3:AC:172:ARG:HG2	1.90	0.54
12:AL:54:LYS:N	12:AL:54:LYS:HD2	2.23	0.54
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.90	0.54
25:BA:1593:G:H2'	25:BA:1594:G:C8	2.43	0.54
26:BB:12:C:H2'	46:B0:73:GLY:HA3	1.90	0.54
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.89	0.54
1:CA:1392:G:N2	1:CA:1502:A:H8	2.04	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:217:ARG:HA	2:CB:220:ASP:HB2	1.90	0.54
7:CG:51:GLN:HA	7:CG:55:GLY:HA2	1.90	0.54
25:DA:459:U:H5"	53:D7:40:TRP:CD2	2.43	0.54
28:DE:72:VAL:HG13	28:DE:73:GLU:O	2.08	0.54
31:DH:69:ARG:HG3	31:DH:70:THR:N	2.23	0.54
32:DI:1:MET:N	32:DI:20:ASP:OD1	2.26	0.54
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.90	0.54
13:AM:65:LYS:O	13:AM:70:LEU:HD12	2.08	0.54
21:AU:12:LYS:HB3	21:AU:22:ARG:HD2	1.90	0.54
25:BA:692:C:O2'	25:BA:1354:A:O2'	2.24	0.54
25:BA:848:G:H2'	25:BA:849:A:C8	2.42	0.54
25:BA:2168:G:C6	25:BA:2171:A:C8	2.95	0.54
27:BD:71:ASP:CB	27:BD:103:ARG:HH22	2.19	0.54
28:BE:174:ASP:OD1	28:BE:175:VAL:N	2.41	0.54
1:CA:156:G:N2	1:CA:165:C:O2	2.40	0.54
1:CA:1376:U:H3'	7:CG:94:ARG:HH21	1.72	0.54
2:CB:91:PRO:HG3	2:CB:154:LEU:HB3	1.89	0.54
25:DA:1023:U:OP2	60:DA:4482:HOH:O	2.18	0.54
25:DA:2042:A:OP1	60:DA:4137:HOH:O	2.19	0.54
25:DA:2173:A:H3'	25:DA:2173:A:OP2	2.08	0.54
27:DD:182:LEU:HB2	27:DD:272:ALA:HB3	1.89	0.54
24:AX:33:U:O2'	24:AX:35:A:N7	2.37	0.54
25:BA:36:G:N3	25:BA:450:G:O2'	2.40	0.54
25:BA:1421:G:O2'	25:BA:1494:A:N6	2.41	0.54
25:BA:2031:A:C6	25:BA:2498:C:H1'	2.43	0.54
26:BB:50:G:OP1	38:BS:63:THR:OG1	2.26	0.54
34:BO:80:ASP:OD2	39:BT:64:ARG:NH2	2.41	0.54
1:CA:598:U:H2'	1:CA:599:C:C6	2.43	0.54
25:DA:1169:G:H1	25:DA:1180:C:N4	1.92	0.54
25:DA:1509(B):A:H2'	25:DA:1510:G:C8	2.42	0.54
25:DA:1894:C:H2'	25:DA:1895:C:H6	1.72	0.54
25:DA:2086:U:H2'	25:DA:2087:G:C8	2.42	0.54
31:DH:97:ARG:HE	31:DH:104:GLU:CD	2.16	0.54
1:AA:164:U:H2'	1:AA:165:C:C6	2.42	0.53
1:AA:299:G:H2'	1:AA:300:A:C8	2.43	0.53
1:AA:662:G:O2'	1:AA:836:G:OP1	2.26	0.53
1:AA:1099:G:OP2	2:AB:144:ARG:NH2	2.40	0.53
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.44	0.53
41:BV:98:GLU:OE1	41:BV:100:ARG:NH1	2.37	0.53
45:BZ:7:ALA:HB3	45:BZ:61:LEU:HD12	1.90	0.53
45:BZ:111:VAL:C	45:BZ:113:ALA:H	2.15	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1120:G:C6	1:CA:1121:U:C4	2.96	0.53
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.07	0.53
4:CD:88:VAL:HG22	5:CE:96:PRO:HB2	1.90	0.53
15:CO:87:ILE:HG22	15:CO:88:ARG:N	2.23	0.53
25:DA:871:U:OP1	36:DQ:5:ARG:HG2	2.08	0.53
25:DA:1031:G:H21	55:D9:36:GLN:HE22	1.56	0.53
25:DA:1114:G:H2'	25:DA:1115:G:C8	2.42	0.53
25:DA:2588:G:OP1	60:DA:4367:HOH:O	2.18	0.53
27:DD:69:ARG:NH2	27:DD:128:GLY:O	2.42	0.53
30:DG:115:ARG:HG3	30:DG:136:ARG:HH21	1.73	0.53
40:DU:83:LEU:HD12	40:DU:88:ILE:HB	1.90	0.53
49:D3:6:VAL:HG13	49:D3:56:VAL:HG22	1.90	0.53
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.33	0.53
25:BA:528:A:C2	25:BA:2043:C:H4'	2.43	0.53
25:BA:548:A:O2'	25:BA:549:G:OP1	2.23	0.53
25:BA:647:G:H8	25:BA:647:G:O5'	1.91	0.53
25:BA:1371:G:H2'	25:BA:1372:U:H5	1.73	0.53
25:BA:2893:G:H4'	25:BA:2894:G:O5'	2.08	0.53
33:BN:58:ASP:N	33:BN:58:ASP:OD1	2.41	0.53
1:CA:977:A:N1	1:CA:1224:G:N7	2.55	0.53
1:CA:1014:A:H5'	19:CS:18:LYS:HZ2	1.73	0.53
1:CA:1080:A:H5'	5:CE:14:ARG:HH21	1.73	0.53
1:CA:1244:C:N4	1:CA:1293:G:H1	2.04	0.53
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.42	0.53
10:CJ:43:ARG:HB2	10:CJ:67:THR:HG23	1.90	0.53
12:CL:113:ARG:NH2	60:CL:201:HOH:O	2.41	0.53
16:CP:21:VAL:HG22	16:CP:33:ILE:HB	1.89	0.53
24:CX:19:G:H1	24:CX:56:C:N4	2.03	0.53
25:DA:7:G:H2'	25:DA:8:A:H8	1.73	0.53
25:DA:1427:A:H4'	25:DA:1428:C:O5'	2.08	0.53
1:AA:184:G:H2'	1:AA:185:A:H8	1.72	0.53
9:AI:20:ARG:O	9:AI:60:ASP:N	2.42	0.53
25:BA:278:A:O2'	25:BA:279:C:OP1	2.24	0.53
25:BA:1405:U:H2'	25:BA:1406:U:C6	2.44	0.53
1:CA:412:A:O4'	4:CD:35:ARG:NH2	2.41	0.53
1:CA:920:U:H2'	1:CA:921:U:C6	2.43	0.53
2:CB:178:ARG:NH1	2:CB:196:LEU:O	2.41	0.53
4:CD:175:SER:OG	4:CD:184:LYS:HB2	2.07	0.53
9:CI:99:LEU:HB3	9:CI:101:PHE:HE1	1.73	0.53
25:DA:7:G:H1	25:DA:2896:C:N4	2.06	0.53
25:DA:797:C:H2'	25:DA:798:G:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1653:G:H3'	37:DR:2:ARG:HD3	1.89	0.53
25:DA:2156:G:H5"	25:DA:2157:G:OP2	2.08	0.53
32:DI:56:LYS:O	32:DI:60:GLU:N	2.40	0.53
48:D2:1:MET:HB2	48:D2:52:ASP:OD1	2.09	0.53
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.89	0.53
1:AA:1253:G:H1	1:AA:1284:C:H42	1.55	0.53
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.91	0.53
9:AI:86:VAL:HG13	9:AI:96:LEU:HD12	1.91	0.53
25:BA:910:A:H62	36:BQ:12:GLN:HA	1.73	0.53
25:BA:2635:C:O2'	28:BE:80:GLU:OE1	2.23	0.53
28:BE:47:VAL:HG12	28:BE:49:LEU:HD12	1.89	0.53
1:CA:1013:G:N2	1:CA:1015:A:H3'	2.23	0.53
2:CB:216:SER:O	2:CB:220:ASP:N	2.42	0.53
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.90	0.53
13:CM:19:LEU:HD21	13:CM:56:LEU:HD21	1.90	0.53
24:CX:16:C:H3'	24:CX:17:C:O2	2.08	0.53
25:DA:212:G:H2'	25:DA:213:A:O4'	2.07	0.53
25:DA:903:C:H2'	25:DA:904:C:C6	2.43	0.53
25:DA:2698:U:H2'	25:DA:2699:C:C6	2.44	0.53
26:DB:90:A:C5	26:DB:91:C:H1'	2.43	0.53
41:DV:8:GLY:O	41:DV:10:LYS:NZ	2.41	0.53
1:AA:167:G:H2'	1:AA:168:G:C8	2.43	0.53
25:BA:1322:A:N1	25:BA:1333:C:O2'	2.38	0.53
25:BA:2111:C:N3	25:BA:2145:C:O2'	2.38	0.53
25:BA:2627:G:O2'	25:BA:2781:A:N1	2.30	0.53
31:BH:117:PRO:HG3	31:BH:123:PHE:CD2	2.44	0.53
39:BT:85:LYS:NZ	39:BT:87:ASP:OD2	2.26	0.53
43:BX:50:LYS:N	43:BX:87:GLN:OE1	2.41	0.53
46:B0:40:GLN:HE21	46:B0:57:PHE:HB3	1.74	0.53
1:CA:337:C:H2'	1:CA:338:A:C8	2.44	0.53
1:CA:406:G:H2'	1:CA:407:G:H8	1.73	0.53
1:CA:977:A:HO2'	1:CA:981:U:H3	1.55	0.53
1:CA:1000:U:H3	1:CA:1041:A:H61	1.55	0.53
1:CA:1023:G:H3'	1:CA:1024:G:H8	1.73	0.53
5:CE:33:VAL:HA	5:CE:43:LEU:HA	1.90	0.53
25:DA:1120:G:H2'	25:DA:1121:C:O4'	2.09	0.53
25:DA:2312:U:H5'	30:DG:88:ILE:HD11	1.91	0.53
26:DB:24:G:H5'	26:DB:25:A:N7	2.24	0.53
27:DD:242:ARG:N	27:DD:242:ARG:HD3	2.23	0.53
42:DW:88:ARG:NH1	42:DW:94:ASP:OD2	2.38	0.53
44:DY:23:ARG:HG2	44:DY:42:VAL:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.41	0.53
24:AX:66:C:H2'	24:AX:67:C:O4'	2.07	0.53
25:BA:578:A:OP2	60:BA:3879:HOH:O	2.19	0.53
25:BA:2418:A:H2'	25:BA:2419:U:C6	2.43	0.53
28:BE:2:LYS:NZ	28:BE:95:ILE:O	2.40	0.53
31:BH:102:ALA:HA	31:BH:117:PRO:HD3	1.91	0.53
34:BO:79:PHE:CD1	39:BT:72:VAL:HG22	2.44	0.53
44:BY:7:VAL:HG21	44:BY:72:VAL:HG12	1.89	0.53
54:B8:39:LYS:O	54:B8:43:GLN:HG3	2.09	0.53
1:CA:67:C:H2'	1:CA:68:G:C8	2.44	0.53
1:CA:1023:G:C4	1:CA:1024:G:C8	2.97	0.53
6:CF:14:LEU:HD22	6:CF:18:GLN:HB2	1.91	0.53
9:CI:99:LEU:HB3	9:CI:101:PHE:CE1	2.44	0.53
11:CK:58:PRO:O	11:CK:62:GLN:N	2.41	0.53
14:CN:48:ALA:HB2	14:CN:53:LEU:HD12	1.90	0.53
25:DA:10:G:H2'	25:DA:11:G:C8	2.44	0.53
25:DA:197:A:N6	25:DA:2430:A:O2'	2.41	0.53
25:DA:996:A:OP2	40:DU:93:LYS:NZ	2.26	0.53
25:DA:2218:U:N3	47:D1:55:GLY:O	2.42	0.53
29:DF:157:VAL:HB	29:DF:194:MET:HG2	1.90	0.53
30:DG:136:ARG:HD2	30:DG:137:GLU:N	2.23	0.53
1:AA:1027:C:N3	1:AA:1034:G:C6	2.76	0.53
1:AA:1168:A:H2'	1:AA:1169:A:C8	2.43	0.53
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.90	0.53
6:AF:20:ALA:O	6:AF:24:GLU:N	2.39	0.53
25:BA:189:G:OP2	47:B1:39:LYS:NZ	2.42	0.53
1:CA:975:A:N6	1:CA:1367:C:O4'	2.42	0.53
21:CU:12:LYS:HB3	21:CU:22:ARG:HD2	1.91	0.53
25:DA:806:C:O2	25:DA:2444:G:O2'	2.27	0.53
25:DA:2136:C:O2'	25:DA:2137:C:H6	1.91	0.53
25:DA:2302:G:H2'	25:DA:2303:G:H5'	1.90	0.53
26:DB:70:C:H2'	26:DB:71:C:H6	1.73	0.53
26:DB:95:C:H2'	26:DB:96:U:H6	1.73	0.53
53:D7:12:ARG:HD3	53:D7:46:VAL:HB	1.91	0.53
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	1.91	0.53
2:AB:119:GLU:OE2	2:AB:153:ARG:NH2	2.38	0.53
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.09	0.53
25:BA:1713:U:H2'	25:BA:1714:G:C8	2.42	0.53
40:BU:50:ARG:HG2	40:BU:53:ARG:NH2	2.23	0.53
51:B5:16:ARG:HG3	51:B5:17:ASP:N	2.23	0.53
1:CA:411:A:OP1	4:CD:30:LYS:NZ	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:199:ASN:HB3	4:CD:202:LEU:HG	1.91	0.53
7:CG:138:LYS:HD3	7:CG:139:GLU:HG3	1.91	0.53
25:DA:220:G:O2'	25:DA:233:A:N3	2.37	0.53
25:DA:495:G:N3	42:DW:61:ASN:ND2	2.56	0.53
25:DA:642:G:H21	25:DA:646:A:H2	1.56	0.53
25:DA:2163:C:OP1	25:DA:2165:G:N2	2.42	0.53
25:DA:2547:U:O2	34:DO:23:ARG:NH2	2.41	0.53
26:DB:2:C:H2'	26:DB:3:C:C6	2.44	0.53
28:DE:52:LEU:HD22	28:DE:77:ILE:HD11	1.90	0.53
45:DZ:102:LEU:HD11	45:DZ:124:ILE:HB	1.91	0.53
51:D5:41:PRO:O	51:D5:44:THR:OG1	2.25	0.53
1:AA:599:C:HO2'	8:AH:130:GLY:H	1.57	0.53
1:AA:826:C:H2'	1:AA:827:U:C6	2.44	0.53
11:AK:62:GLN:O	11:AK:66:LEU:HG	2.09	0.53
24:AX:4:G:H2'	24:AX:5:G:C8	2.44	0.53
25:BA:873:G:H1	25:BA:904:C:H42	1.57	0.53
25:BA:2271:G:C5'	46:B0:20:ARG:HE	2.22	0.53
28:BE:9:VAL:HB	39:BT:3:ARG:HG2	1.91	0.53
32:BI:72:LEU:C	32:BI:74:ASN:H	2.17	0.53
33:BN:34:LEU:HD21	33:BN:120:LEU:HB2	1.91	0.53
36:BQ:109:VAL:HG22	36:BQ:113:GLN:OE1	2.09	0.53
45:BZ:151:HIS:O	45:BZ:153:SER:N	2.42	0.53
1:CA:600:C:H5"	8:CH:129:VAL:HA	1.89	0.53
1:CA:1004:A:H5'	1:CA:1024:G:H22	1.73	0.53
1:CA:1219:U:O2'	19:CS:34:TRP:O	2.25	0.53
1:CA:1268:A:H2'	1:CA:1269:A:C8	2.44	0.53
2:CB:208:ILE:O	2:CB:212:GLN:HB2	2.09	0.53
5:CE:34:VAL:N	5:CE:42:GLY:O	2.27	0.53
23:CW:76:PPU:O2'	25:DA:2585:U:O4	2.18	0.53
25:DA:963:U:OP1	60:DA:4035:HOH:O	2.19	0.53
25:DA:2103:C:C2'	25:DA:2104:G:H5'	2.39	0.53
25:DA:2695:C:H2'	25:DA:2696:U:C6	2.44	0.53
25:DA:2886:G:H2'	25:DA:2887:U:H6	1.74	0.53
26:DB:68:C:H2'	26:DB:69:G:H8	1.73	0.53
37:DR:29:LEU:HD23	37:DR:70:LEU:HD11	1.89	0.53
52:D6:25:LYS:NZ	52:D6:51:GLU:OE2	2.39	0.53
1:AA:661:G:H1	1:AA:744:C:H42	1.55	0.53
1:AA:714:G:H2'	1:AA:715:A:C8	2.44	0.53
1:AA:1216:G:H5"	14:AN:5:ALA:HB2	1.90	0.53
25:BA:2102:U:H3	25:BA:2187:G:H1	1.56	0.53
25:BA:2788:C:OP1	28:BE:61:ARG:NH2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BG:41:GLN:HG3	30:BG:60:LEU:HD21	1.91	0.53
36:BQ:82:ARG:CZ	46:B0:4:LYS:HE3	2.39	0.53
45:BZ:29:TYR:HA	45:BZ:33:LEU:HD12	1.90	0.53
1:CA:589:C:C2'	1:CA:590:C:H5'	2.39	0.53
1:CA:985:C:H2'	1:CA:986:A:H8	1.73	0.53
10:CJ:51:ARG:HD3	14:CN:45:ARG:NH2	2.23	0.53
24:CX:10:G:O6	24:CX:25:C:N3	2.42	0.53
25:DA:140:G:N2	25:DA:1596:A:H4'	2.24	0.53
25:DA:1447:G:O2'	25:DA:1544:A:N3	2.37	0.53
25:DA:2032:G:H1'	28:DE:145:LYS:HD3	1.91	0.53
25:DA:2116:G:N7	25:DA:2166:G:N2	2.44	0.53
25:DA:2725:A:H1'	25:DA:2726:U:H2'	1.90	0.53
1:AA:765:G:N1	1:AA:812:C:O2'	2.40	0.52
6:AF:18:GLN:N	6:AF:18:GLN:CD	2.66	0.52
12:AL:25:PRO:HG2	12:AL:97:ARG:HH21	1.74	0.52
13:AM:88:ARG:HG3	13:AM:98:VAL:HG11	1.91	0.52
25:BA:573:G:O2'	25:BA:574:C:H3'	2.09	0.52
25:BA:2648:C:H2'	25:BA:2649:U:C6	2.44	0.52
28:BE:28:ALA:HB3	28:BE:93:VAL:HG12	1.89	0.52
43:BX:27:THR:HG23	43:BX:80:ILE:HG13	1.90	0.52
54:B8:40:GLU:HG2	54:B8:44:LYS:HE2	1.90	0.52
13:CM:50:GLU:HG2	13:CM:54:VAL:HG13	1.91	0.52
13:CM:65:LYS:HB2	50:D4:50:VAL:HG21	1.91	0.52
19:CS:28:LYS:HB2	19:CS:29:ARG:CB	2.39	0.52
25:DA:538:G:H2'	25:DA:539:G:H8	1.73	0.52
25:DA:2203:U:H2'	25:DA:2205:C:H6	1.73	0.52
25:DA:2378:A:H4'	38:DS:23:ARG:HD2	1.90	0.52
36:DQ:37:LEU:HD21	36:DQ:130:LYS:HE2	1.91	0.52
41:DV:40:LEU:HB2	41:DV:46:VAL:HG13	1.90	0.52
45:DZ:7:ALA:HB3	45:DZ:61:LEU:HD12	1.91	0.52
1:AA:57:G:H2'	1:AA:58:C:C6	2.45	0.52
1:AA:619:U:N3	4:AD:134:ASP:OD1	2.37	0.52
1:AA:673:G:H1	1:AA:717:C:H42	1.56	0.52
2:AB:7:VAL:HG11	2:AB:221:LEU:HD22	1.91	0.52
10:AJ:65:LEU:HD13	14:AN:56:VAL:HG22	1.91	0.52
25:BA:861:A:OP2	60:BA:4253:HOH:O	2.19	0.52
25:BA:2074:U:OP1	60:BA:4051:HOH:O	2.18	0.52
34:BO:115:VAL:HG13	34:BO:121:VAL:HG21	1.90	0.52
1:CA:626:U:H2'	1:CA:627:G:H5"	1.92	0.52
16:CP:52:ASP:O	16:CP:54:GLU:N	2.37	0.52
25:DA:1359:A:H2'	25:DA:1360:A:H5'	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1913:A:H4'	25:DA:1914:C:C5'	2.39	0.52
26:DB:101:G:H2'	26:DB:102:A:O4'	2.09	0.52
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.92	0.52
1:AA:922:G:N3	1:AA:1398:A:H2	2.06	0.52
8:AH:84:ARG:NH1	8:AH:136:GLU:OE2	2.42	0.52
9:AI:85:LEU:HB3	9:AI:92:TYR:CD2	2.45	0.52
1:CA:955:U:O4	1:CA:1225:A:N1	2.42	0.52
1:CA:1024:G:H2'	1:CA:1025:U:H5"	1.90	0.52
1:CA:1053:G:N7	1:CA:1200:C:H5"	2.24	0.52
1:CA:1328:C:O2'	13:CM:29:ARG:NH2	2.42	0.52
1:CA:1342:C:H1'	9:CI:124:GLN:NE2	2.23	0.52
4:CD:3:ARG:HD3	4:CD:118:ARG:HD3	1.91	0.52
25:DA:1186:G:C2	25:DA:1187:G:H1'	2.44	0.52
25:DA:2376:A:H3'	25:DA:2377:A:H8	1.74	0.52
25:DA:2784:C:O2'	28:DE:42:ASP:OD1	2.15	0.52
30:DG:122:PRO:HG3	30:DG:180:PHE:HB3	1.91	0.52
2:AB:212:GLN:O	2:AB:216:SER:OG	2.17	0.52
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.44	0.52
8:AH:45:ILE:HG21	8:AH:61:VAL:HG13	1.91	0.52
25:BA:2023:G:H5'	25:BA:2617:C:H4'	1.92	0.52
25:BA:2142:C:H2'	25:BA:2143:C:C6	2.44	0.52
1:CA:76:C:N3	1:CA:93:G:N2	2.47	0.52
1:CA:258:G:H1	1:CA:268:C:H42	1.58	0.52
1:CA:1002:G:C2	1:CA:1003:G:H8	2.27	0.52
1:CA:1004:A:H62	1:CA:1037:C:H3'	1.75	0.52
3:CC:8:ILE:HG23	3:CC:16:ARG:HG2	1.90	0.52
9:CI:47:LEU:HB3	9:CI:50:LEU:HD12	1.91	0.52
13:CM:23:TYR:HE1	13:CM:70:LEU:HD22	1.73	0.52
24:CX:52:G:H2'	24:CX:53:G:C8	2.42	0.52
25:DA:2172:U:O2'	25:DA:2173:A:O5'	2.26	0.52
25:DA:2261:C:H1'	25:DA:2388:A:N3	2.23	0.52
25:DA:2345:G:H5'	25:DA:2347:C:O4'	2.09	0.52
26:DB:92:C:H5"	45:DZ:79:ARG:HH22	1.73	0.52
27:DD:264:LYS:O	27:DD:267:SER:OG	2.27	0.52
30:DG:32:PRO:HB2	30:DG:172:LEU:HD22	1.92	0.52
1:AA:1260:C:O5'	1:AA:1284:C:H4'	2.10	0.52
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.91	0.52
25:BA:330:A:H2	25:BA:1210:A:HO2'	1.57	0.52
25:BA:1464:C:H2'	25:BA:1465:G:C8	2.45	0.52
25:BA:2127:G:N2	25:BA:2173:A:H1'	2.25	0.52
1:CA:187:C:O2'	20:CT:89:ARG:NH2	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:352:C:O2'	1:CA:354:G:OP1	2.26	0.52
1:CA:835:U:H3	1:CA:851:G:H1	1.56	0.52
1:CA:1118:C:N3	1:CA:1156:G:N2	2.57	0.52
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.45	0.52
5:CE:93:PRO:HG2	8:CH:105:ARG:NE	2.25	0.52
13:CM:23:TYR:CE1	13:CM:70:LEU:HD22	2.43	0.52
24:CX:23:C:H2'	24:CX:24:U:C6	2.40	0.52
25:DA:2556:C:H2'	25:DA:2557:G:O4'	2.09	0.52
35:DP:97:PRO:HD3	35:DP:126:VAL:O	2.10	0.52
45:DZ:45:ASP:O	45:DZ:49:ARG:HG3	2.10	0.52
50:D4:1:MET:HE2	50:D4:6:HIS:CE1	2.44	0.52
1:AA:269:C:H2'	1:AA:270:A:C8	2.44	0.52
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.44	0.52
1:AA:1239:A:O2'	7:AG:114:ARG:O	2.24	0.52
4:AD:178:VAL:C	4:AD:180:GLY:H	2.18	0.52
25:BA:2086:U:H2'	25:BA:2087:G:C8	2.45	0.52
30:BG:108:ASN:OD1	30:BG:108:ASN:N	2.41	0.52
1:CA:757:U:H2'	1:CA:758:G:O4'	2.09	0.52
1:CA:922:G:N3	1:CA:1398:A:H2	2.08	0.52
1:CA:985:C:N4	1:CA:1220:G:H1	2.06	0.52
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.10	0.52
1:CA:1226:C:OP2	13:CM:91:ARG:NH2	2.43	0.52
4:CD:31:CYS:O	4:CD:35:ARG:HG3	2.10	0.52
9:CI:23:ASN:ND2	9:CI:25:LYS:H	2.08	0.52
14:CN:47:LEU:HD12	14:CN:53:LEU:HD21	1.92	0.52
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.22	0.52
24:CX:7:G:O2'	24:CX:49:G:H5'	2.09	0.52
25:DA:224:G:N7	25:DA:420:C:H4'	2.24	0.52
25:DA:236:C:H2'	25:DA:237:C:C6	2.45	0.52
25:DA:514:A:N3	25:DA:581:C:O2'	2.40	0.52
25:DA:857:C:OP2	46:D0:77:ARG:NH2	2.41	0.52
25:DA:1496:A:N3	25:DA:1577:C:O2'	2.41	0.52
28:DE:72:VAL:HG13	28:DE:73:GLU:C	2.34	0.52
29:DF:110:LEU:HD21	29:DF:181:LEU:HG	1.92	0.52
31:DH:103:LEU:HD13	31:DH:125:VAL:HG21	1.92	0.52
35:DP:1:MET:HG2	35:DP:5:ASP:HB2	1.91	0.52
1:AA:630:G:H2'	1:AA:631:G:C8	2.43	0.52
2:AB:118:LEU:HD21	2:AB:138:LEU:HD22	1.92	0.52
4:AD:3:ARG:HD3	4:AD:118:ARG:HD2	1.92	0.52
5:AE:145:LYS:O	5:AE:149:GLU:HG2	2.09	0.52
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AX:49:G:H1	24:AX:65:C:N4	2.04	0.52
25:BA:882:G:H1	25:BA:894:C:H42	1.55	0.52
25:BA:952:G:OP1	36:BQ:16:ARG:NH2	2.43	0.52
25:BA:2492:U:H2'	25:BA:2493:U:H6	1.74	0.52
26:BB:12:C:O2'	46:B0:74:ARG:HG2	2.09	0.52
32:BI:60:GLU:HG3	32:BI:61:ARG:HH12	1.75	0.52
35:BP:97:PRO:HD3	35:BP:126:VAL:O	2.10	0.52
46:B0:46:LYS:NZ	46:B0:75:LEU:O	2.42	0.52
1:CA:593:G:H1	1:CA:646:U:H3	1.58	0.52
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.25	0.52
2:CB:207:ALA:O	2:CB:210:SER:HB3	2.09	0.52
4:CD:63:LYS:O	4:CD:67:ILE:HG13	2.10	0.52
25:DA:574:C:N3	28:DE:145:LYS:NZ	2.52	0.52
25:DA:1639:U:OP1	60:DA:4253:HOH:O	2.19	0.52
25:DA:2518:A:OP2	60:DA:4239:HOH:O	2.19	0.52
27:DD:148:GLU:HB2	27:DD:151:LYS:HD2	1.92	0.52
28:DE:67:PHE:HB3	28:DE:72:VAL:HG12	1.91	0.52
29:DF:130:ALA:H	29:DF:142:TRP:HD1	1.57	0.52
39:DT:53:ARG:HB3	39:DT:53:ARG:HH11	1.75	0.52
1:AA:737:A:H5"	6:AF:92:LYS:HG3	1.91	0.52
1:AA:1346:A:O2'	7:AG:10:ARG:NH2	2.43	0.52
50:B4:44:THR:OG1	50:B4:47:GLN:OE1	2.28	0.52
1:CA:946:A:O2'	1:CA:1333:A:N3	2.31	0.52
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.44	0.52
1:CA:1329:A:H5'	13:CM:29:ARG:HG3	1.91	0.52
25:DA:1264:G:H2'	25:DA:2014:A:N6	2.24	0.52
25:DA:2142:C:H2'	25:DA:2143:C:O4'	2.09	0.52
26:DB:37:C:N3	26:DB:48:A:O2'	2.42	0.52
34:DO:76:ALA:HB3	39:DT:75:ILE:HB	1.92	0.52
1:AA:158:G:H21	1:AA:162:A:N6	2.08	0.52
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.10	0.52
4:AD:188:LEU:H	4:AD:188:LEU:CD2	2.23	0.52
25:BA:1309:G:P	53:B7:9:ARG:HD3	2.50	0.52
25:BA:1935:G:H1'	25:BA:1964:G:N2	2.25	0.52
27:BD:132:PRO:HD3	27:BD:190:TYR:CZ	2.45	0.52
29:BF:155:LEU:HB2	29:BF:189:THR:HG21	1.92	0.52
1:CA:409:G:H1	1:CA:433:C:H42	1.58	0.52
1:CA:972:C:OP2	10:CJ:57:LYS:HE2	2.10	0.52
1:CA:975:A:N6	10:CJ:60:ARG:HH12	2.08	0.52
19:CS:27:GLU:HG2	19:CS:47:HIS:CE1	2.44	0.52
21:CU:3:LYS:HD3	21:CU:14:TRP:CD1	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:479:A:H4'	25:DA:480:A:OP1	2.09	0.52
25:DA:1742:G:H2'	25:DA:1743:C:C6	2.45	0.52
25:DA:2166:G:H2'	25:DA:2167:U:C2	2.44	0.52
25:DA:2400:G:O3'	52:D6:18:ARG:NH1	2.43	0.52
25:DA:2752:C:H3'	25:DA:2753:A:H8	1.75	0.52
30:DG:167:GLU:OE1	30:DG:167:GLU:N	2.39	0.52
36:DQ:36:ALA:HB2	36:DQ:103:MET:SD	2.50	0.52
38:DS:44:LYS:HZ2	38:DS:44:LYS:H	1.58	0.52
39:DT:77:PRO:HB2	39:DT:80:SER:HB2	1.90	0.52
1:AA:693:G:H2'	1:AA:694:A:C8	2.45	0.52
1:AA:1445:C:H42	1:AA:1457:G:H1	1.56	0.52
3:AC:36:ASP:OD1	3:AC:59:ARG:NH2	2.34	0.52
17:AQ:59:ILE:HG22	17:AQ:73:VAL:HA	1.91	0.52
25:BA:1250:G:N7	35:BP:18:ARG:NH2	2.58	0.52
25:BA:2198:A:H4'	25:BA:2199:A:OP1	2.10	0.52
26:BB:1:U:O2'	26:BB:2:C:OP1	2.27	0.52
1:CA:998:G:H1	1:CA:1043:C:H42	1.58	0.52
3:CC:66:VAL:HG21	3:CC:91:LEU:HD21	1.92	0.52
13:CM:10:PRO:HG2	13:CM:21:TYR:CD2	2.44	0.52
25:DA:817:C:H2'	25:DA:818:G:O4'	2.10	0.52
25:DA:1753:G:OP1	39:DT:95:ARG:HD3	2.09	0.52
1:AA:631:G:H2'	1:AA:632:A:C8	2.45	0.51
1:AA:730:G:H5"	1:AA:731:G:OP2	2.09	0.51
1:AA:1457:G:H2'	1:AA:1458:G:C8	2.45	0.51
1:AA:1503:A:H1'	22:AV:13:A:H61	1.75	0.51
25:BA:242:G:C8	54:B8:5:LYS:HG2	2.44	0.51
25:BA:689:A:N3	25:BA:779:U:O2'	2.39	0.51
25:BA:796:C:H2'	25:BA:797:C:C6	2.45	0.51
25:BA:942:G:OP2	35:BP:39:LYS:NZ	2.31	0.51
25:BA:2123:G:H1	25:BA:2175:C:N4	2.07	0.51
25:BA:2569:G:O6	60:BA:4451:HOH:O	2.19	0.51
25:BA:2830:G:OP1	28:BE:76:ARG:NH2	2.43	0.51
43:BX:49:VAL:HG11	43:BX:89:ILE:HG12	1.92	0.51
1:CA:838:G:H1	1:CA:848:C:N4	2.08	0.51
1:CA:959:A:O2'	1:CA:984:C:O2'	2.20	0.51
1:CA:1316:G:H4'	14:CN:18:VAL:HG13	1.92	0.51
1:CA:1346:A:N1	1:CA:1374:A:H5"	2.26	0.51
25:DA:18:C:H2'	25:DA:19:C:C6	2.46	0.51
25:DA:455:C:N3	25:DA:472:A:H2'	2.25	0.51
25:DA:658:C:H2'	25:DA:659:C:C6	2.44	0.51
25:DA:1024:G:C8	25:DA:1025:G:H2'	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1248:G:C5	40:DU:3:ARG:HB2	2.45	0.51
25:DA:1796:U:H2'	25:DA:1797:C:C6	2.45	0.51
29:DF:150:GLY:HA2	29:DF:172:TRP:CD2	2.45	0.51
31:DH:159:GLU:HG2	31:DH:169:VAL:HG11	1.92	0.51
39:DT:59:THR:HG23	39:DT:78:LEU:HB3	1.92	0.51
1:AA:193:C:H2'	1:AA:194:C:C6	2.45	0.51
1:AA:689:C:OP1	11:AK:27:ASN:ND2	2.38	0.51
24:AX:6:G:H1	24:AX:67:C:H42	1.58	0.51
25:BA:1688:U:O2	25:BA:1700:A:H5'	2.10	0.51
25:BA:1993:U:H4'	28:BE:128:SER:HB3	1.92	0.51
25:BA:2567:G:H2'	25:BA:2568:C:C6	2.45	0.51
25:BA:2735:G:H2'	25:BA:2736:G:C8	2.45	0.51
28:BE:143:ASN:HD22	28:BE:147:PRO:HD2	1.75	0.51
41:BV:76:LYS:HB2	41:BV:81:TYR:HB3	1.90	0.51
50:B4:48:ARG:NH1	50:B4:48:ARG:HA	2.24	0.51
1:CA:344:A:H4'	1:CA:345:C:OP2	2.10	0.51
1:CA:540:G:H2'	1:CA:541:G:C8	2.45	0.51
3:CC:50:ALA:HB1	3:CC:72:LYS:O	2.10	0.51
14:CN:12:ARG:HG2	14:CN:13:THR:N	2.26	0.51
25:DA:686:G:OP1	53:D7:11:LYS:NZ	2.43	0.51
25:DA:2206:G:H5"	25:DA:2207:G:N7	2.25	0.51
27:DD:164:GLN:NE2	27:DD:166:GLN:OE1	2.41	0.51
1:AA:324:G:OP1	20:AT:22:ARG:NE	2.38	0.51
1:AA:1130:A:H5'	9:AI:18:PHE:CE2	2.46	0.51
2:AB:142:LEU:O	2:AB:146:GLN:N	2.31	0.51
8:AH:112:LEU:HB3	8:AH:133:LEU:HA	1.91	0.51
12:AL:53:ARG:HG2	12:AL:69:TYR:CE1	2.45	0.51
13:AM:6:GLY:O	30:BG:115:ARG:NH2	2.42	0.51
20:AT:47:GLY:HA2	20:AT:48:LYS:HB2	1.91	0.51
25:BA:29:U:H2'	25:BA:30:G:C8	2.46	0.51
25:BA:139:G:N3	43:BX:41:ASN:ND2	2.53	0.51
25:BA:251:A:C5	25:BA:252:G:H1'	2.45	0.51
25:BA:1266:G:O5'	42:BW:15:ARG:NH2	2.43	0.51
25:BA:2161:C:O2'	25:BA:2173:A:H4'	2.09	0.51
25:BA:2272:U:H5"	25:BA:2273:A:OP1	2.10	0.51
29:BF:31:HIS:NE2	29:BF:35:GLU:OE2	2.43	0.51
32:BI:91:SER:HB3	32:BI:119:PRO:HB2	1.93	0.51
1:CA:336:C:H2'	1:CA:337:C:C6	2.46	0.51
1:CA:601:C:H2'	1:CA:602:A:H8	1.76	0.51
1:CA:1010:G:H2'	1:CA:1011:G:H8	1.74	0.51
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:17:VAL:HG11	9:CI:80:GLY:C	2.35	0.51
12:CL:53:ARG:NH1	12:CL:92:ASP:OD2	2.37	0.51
25:DA:262:A:H2'	25:DA:263:C:O4'	2.10	0.51
25:DA:370:G:OP1	25:DA:403:U:N3	2.26	0.51
25:DA:839:U:H2'	25:DA:840:C:C6	2.46	0.51
25:DA:1226:A:H5"	40:DU:16:LYS:NZ	2.24	0.51
25:DA:1710:C:H2'	25:DA:1711:C:C6	2.45	0.51
25:DA:2430:A:N3	25:DA:2430:A:H2'	2.25	0.51
25:DA:2722:G:H2'	25:DA:2723:C:C6	2.45	0.51
30:DG:23:PHE:HB2	30:DG:25:TYR:CZ	2.45	0.51
43:DX:11:PRO:HG3	48:D2:37:PHE:CD2	2.46	0.51
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.75	0.51
2:AB:121:LEU:HD13	2:AB:126:GLU:HG2	1.92	0.51
11:AK:98:LEU:O	11:AK:101:SER:OG	2.23	0.51
25:BA:880:G:H2'	25:BA:881:G:H8	1.75	0.51
25:BA:958:U:OP2	36:BQ:14:ARG:NH1	2.44	0.51
25:BA:1359:A:H2'	25:BA:1360:A:H5'	1.92	0.51
44:BY:11:ASP:OD1	44:BY:97:ARG:NH2	2.41	0.51
46:B0:40:GLN:HE22	46:B0:43:THR:HA	1.75	0.51
1:CA:1122:U:O4	1:CA:1123:A:N6	2.43	0.51
10:CJ:38:ILE:HG12	10:CJ:71:LEU:O	2.11	0.51
12:CL:102:ARG:HB3	12:CL:108:ALA:O	2.10	0.51
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.10	0.51
25:DA:651:G:H4'	54:D8:18:ALA:HB3	1.92	0.51
25:DA:2742:C:OP1	55:D9:35:ARG:HD3	2.10	0.51
29:DF:20:LEU:HD22	29:DF:21:ALA:H	1.76	0.51
1:AA:166:G:H2'	1:AA:167:G:C8	2.45	0.51
1:AA:342:C:H2'	1:AA:343:U:H5"	1.93	0.51
1:AA:1427:U:H2'	1:AA:1428:A:C8	2.45	0.51
1:AA:1525:G:OP2	11:AK:120:ARG:NH2	2.43	0.51
4:AD:166:LYS:HB2	4:AD:168:ARG:NH1	2.25	0.51
7:AG:113:GLU:HG2	7:AG:119:ARG:HG2	1.91	0.51
17:AQ:52:LYS:HG2	17:AQ:53:LEU:N	2.25	0.51
25:BA:1210:A:H5"	25:BA:1212:G:O4'	2.10	0.51
25:BA:1338:G:O2'	25:BA:1393:A:N1	2.37	0.51
25:BA:1527:G:H5"	25:BA:1528:A:OP1	2.10	0.51
25:BA:1833:U:O2'	25:BA:1969:A:N1	2.36	0.51
25:BA:2134:A:OP2	25:BA:2157:G:N2	2.43	0.51
33:BN:42:TRP:CD1	33:BN:48:MET:HE1	2.46	0.51
44:BY:87:LYS:HD2	44:BY:95:LYS:HD3	1.92	0.51
1:CA:460:G:N2	1:CA:471:G:OP2	2.37	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:976:G:OP2	1:CA:1358:U:O2'	2.23	0.51
1:CA:986:A:H1'	19:CS:54:GLY:O	2.11	0.51
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.46	0.51
1:CA:1249:C:H5'	9:CI:70:LYS:HE2	1.92	0.51
4:CD:150:GLU:HA	4:CD:153:ARG:HG3	1.93	0.51
19:CS:40:ILE:HB	19:CS:67:VAL:O	2.11	0.51
25:DA:2113:U:H3	25:DA:2170:A:H61	1.58	0.51
25:DA:2151:G:H2'	25:DA:2152:G:H8	1.76	0.51
25:DA:2347:C:H2'	25:DA:2348:U:C6	2.46	0.51
1:AA:1149:C:O2'	1:AA:1280:A:N1	2.43	0.51
14:AN:29:ARG:HH21	14:AN:31:ARG:HB2	1.75	0.51
23:AW:76:PPU:HM2	25:BA:2452:C:N3	2.26	0.51
25:BA:350:U:H2'	25:BA:351:G:O4'	2.10	0.51
1:CA:542:G:P	4:CD:10:ARG:HH12	2.33	0.51
2:CB:19:HIS:CD2	2:CB:20:GLU:H	2.29	0.51
13:CM:92:HIS:CE1	13:CM:98:VAL:HG21	2.46	0.51
23:CW:76:PPU:N	24:CX:76:31H:O2'	2.44	0.51
25:DA:172:C:H2'	25:DA:173:G:C8	2.46	0.51
25:DA:323:G:H5'	29:DF:169:ASN:HD21	1.76	0.51
25:DA:370:G:N7	60:DA:4068:HOH:O	2.34	0.51
25:DA:442:G:N2	29:DF:48:THR:HB	2.26	0.51
25:DA:601:C:O2	25:DA:605:C:H4'	2.11	0.51
25:DA:1364:G:OP2	47:D1:3:LYS:HG3	2.10	0.51
25:DA:1593:G:H2'	25:DA:1594:G:H8	1.76	0.51
25:DA:1791:A:H3'	25:DA:1792:G:C8	2.46	0.51
26:DB:80:U:H2'	26:DB:81:G:C8	2.45	0.51
30:DG:165:THR:HB	30:DG:167:GLU:OE1	2.10	0.51
1:AA:240:C:H2'	1:AA:241:C:C6	2.45	0.51
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.46	0.51
3:AC:22:TRP:CH2	3:AC:32:LEU:HB3	2.46	0.51
6:AF:14:LEU:HD22	6:AF:18:GLN:HE21	1.76	0.51
12:AL:84:LEU:HB2	12:AL:105:TYR:CE2	2.46	0.51
25:BA:453:C:O2	25:BA:457:A:O2'	2.29	0.51
25:BA:1518:U:H2'	25:BA:1519:G:O4'	2.10	0.51
25:BA:2336:A:H61	46:B0:43:THR:CG2	2.23	0.51
25:BA:2387:U:OP1	46:B0:55:ARG:NH2	2.43	0.51
25:BA:2687:U:H2'	25:BA:2688:U:O4'	2.09	0.51
32:BI:92:VAL:HG11	32:BI:144:VAL:HG11	1.93	0.51
38:BS:39:ILE:HB	38:BS:49:VAL:HG12	1.93	0.51
55:B9:16:VAL:HG22	55:B9:25:VAL:HG22	1.92	0.51
1:CA:505:G:H2'	1:CA:506:G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1307:U:OP1	13:CM:101:GLN:NE2	2.43	0.51
8:CH:4:ASP:O	8:CH:8:ASP:HB3	2.11	0.51
25:DA:859:G:N2	25:DA:917:A:OP2	2.39	0.51
26:DB:27:C:C4	26:DB:28:C:C4	2.99	0.51
28:DE:36:ARG:HG2	28:DE:47:VAL:HG12	1.92	0.51
28:DE:54:GLN:HE22	28:DE:58:ARG:HG2	1.75	0.51
1:AA:1003:G:N2	1:AA:1038:C:N3	2.59	0.51
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.11	0.51
1:AA:1531:A:H2'	1:AA:1532:U:C4	2.46	0.51
3:AC:172:ARG:HB3	3:AC:174:PRO:HD3	1.92	0.51
8:AH:86:ILE:HG21	8:AH:133:LEU:HD13	1.91	0.51
14:AN:24:CYS:HB2	14:AN:40:CYS:HB3	1.92	0.51
19:AS:9:VAL:HG21	50:B4:61:ARG:HH12	1.74	0.51
25:BA:1021:A:O2'	25:BA:1123:C:OP1	2.22	0.51
25:BA:1881:C:H2'	25:BA:1882:C:C6	2.46	0.51
25:BA:2139:C:C2	25:BA:2152:G:N2	2.79	0.51
32:BI:68:LEU:HD22	32:BI:72:LEU:HG	1.92	0.51
40:BU:17:ILE:HG13	40:BU:32:PHE:HE1	1.76	0.51
1:CA:959:A:HO2'	1:CA:984:C:HO2'	1.52	0.51
2:CB:71:VAL:HB	2:CB:164:VAL:HA	1.92	0.51
14:CN:37:PHE:HE2	14:CN:53:LEU:HD13	1.74	0.51
25:DA:1379:A:H4'	25:DA:1380:G:OP2	2.11	0.51
25:DA:2296:U:OP2	38:DS:9:ARG:NH2	2.43	0.51
30:DG:64:THR:HG21	30:DG:92:VAL:HG11	1.91	0.51
31:DH:122:THR:O	31:DH:134:SER:OG	2.29	0.51
44:DY:44:ILE:HD13	44:DY:64:GLU:HG3	1.93	0.51
1:AA:1179:A:H4'	9:AI:103:THR:HA	1.92	0.51
7:AG:138:LYS:NZ	7:AG:142:GLU:OE2	2.43	0.51
15:AO:82:ILE:O	15:AO:86:GLY:N	2.44	0.51
19:AS:19:VAL:HG11	19:AS:44:MET:HA	1.92	0.51
25:BA:957:A:H5'	36:BQ:76:LYS:HG3	1.92	0.51
25:BA:1045:A:OP1	25:BA:1045:A:H4'	2.11	0.51
26:BB:7:G:H1	26:BB:114:C:N4	2.08	0.51
26:BB:66:A:H61	26:BB:108:U:H2'	1.76	0.51
30:BG:47:LYS:HG3	30:BG:48:GLU:H	1.76	0.51
53:B7:34:ARG:NH1	53:B7:41:ARG:O	2.44	0.51
1:CA:505:G:H2'	1:CA:506:G:H8	1.75	0.51
1:CA:522:C:H2'	1:CA:523:A:O4'	2.11	0.51
1:CA:994:A:C5	1:CA:1216:G:H4'	2.46	0.51
2:CB:177:ALA:HB1	2:CB:182:ILE:HB	1.92	0.51
2:CB:220:ASP:O	2:CB:223:ILE:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:73:PRO:O	3:CC:77:ILE:HG12	2.11	0.51
16:CP:17:TYR:HE1	16:CP:41:PRO:HG3	1.76	0.51
25:DA:30:G:H2'	25:DA:31:C:C6	2.45	0.51
25:DA:172:C:H2'	25:DA:173:G:H8	1.74	0.51
25:DA:2172:U:H1'	25:DA:2173:A:OP1	2.11	0.51
28:DE:111:ARG:HG3	28:DE:160:TYR:CD2	2.46	0.51
35:DP:138:LEU:HD23	35:DP:145:PRO:HG3	1.93	0.51
1:AA:692:U:O2'	1:AA:694:A:N7	2.34	0.51
1:AA:1047:G:H5"	14:AN:4:LYS:HD2	1.93	0.51
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.93	0.51
9:AI:9:ARG:HG2	9:AI:14:VAL:HG12	1.93	0.51
15:AO:62:GLN:HA	15:AO:65:ARG:NH1	2.25	0.51
25:BA:536:A:H5'	40:BU:53:ARG:HD3	1.92	0.51
25:BA:1226:A:OP1	41:BV:84:LYS:HE2	2.10	0.51
25:BA:2600:A:N6	60:BA:4071:HOH:O	2.37	0.51
38:BS:3:ARG:HE	38:BS:4:LEU:H	1.59	0.51
43:BX:65:ARG:NH1	43:BX:70:LEU:HD21	2.26	0.51
1:CA:1097:C:H2'	1:CA:1098:C:H6	1.74	0.51
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.46	0.51
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	1.93	0.51
25:DA:780:G:O2'	25:DA:783:A:N6	2.44	0.51
25:DA:797:C:OP1	29:DF:60:SER:OG	2.18	0.51
25:DA:1021:A:H62	25:DA:1141:U:H3	1.58	0.51
25:DA:1239:G:H2'	25:DA:1240:U:O4'	2.09	0.51
25:DA:2591:C:OP1	27:DD:239:ARG:HD2	2.11	0.51
46:D0:53:MET:HG3	46:D0:59:LEU:HD23	1.92	0.51
52:D6:25:LYS:HE2	52:D6:30:THR:O	2.11	0.51
2:AB:12:GLU:HA	2:AB:213:LEU:HD11	1.93	0.50
24:AX:23:C:H2'	24:AX:24:U:H6	1.75	0.50
25:BA:877:U:H3	25:BA:899:A:H2	1.59	0.50
25:BA:2000:G:OP1	37:BR:5:LYS:NZ	2.44	0.50
25:BA:2100:G:H1	25:BA:2189:U:H3	1.58	0.50
25:BA:2439:A:H5'	25:BA:2439:A:H8	1.76	0.50
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.76	0.50
24:CX:52:G:H1	24:CX:62:C:N4	2.08	0.50
24:CX:55:PSU:N3	24:CX:58:A:OP2	2.31	0.50
25:DA:362:U:O2'	25:DA:363:G:H5'	2.11	0.50
25:DA:1819:A:H2	27:DD:274:ARG:HD3	1.77	0.50
25:DA:2180:U:H2'	25:DA:2181:G:O4'	2.11	0.50
25:DA:2483:C:N3	36:DQ:124:LYS:NZ	2.53	0.50
30:DG:80:PHE:C	30:DG:82:LEU:H	2.18	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DH:104:GLU:HA	31:DH:113:VAL:O	2.11	0.50
45:DZ:22:GLY:O	45:DZ:23:LYS:HE3	2.10	0.50
1:AA:376:G:H1	1:AA:387:U:H3	1.59	0.50
1:AA:982:U:H4'	1:AA:983:A:O5'	2.11	0.50
1:AA:1038:C:H2'	1:AA:1039:C:C6	2.47	0.50
1:AA:1278:U:H5'	1:AA:1279:A:C5'	2.40	0.50
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.46	0.50
6:AF:2:ARG:HB2	6:AF:4:TYR:CZ	2.45	0.50
11:AK:32:ILE:O	11:AK:40:ILE:N	2.30	0.50
25:BA:411:G:C5	35:BP:72:PRO:HB3	2.47	0.50
25:BA:592:G:HO2'	54:B8:64:TYR:HH	1.59	0.50
25:BA:2022:U:O2'	25:BA:2617:C:H5'	2.11	0.50
25:BA:2107:C:N4	25:BA:2182:G:H1	2.04	0.50
50:B4:41:PRO:HG3	50:B4:49:PHE:CE1	2.46	0.50
1:CA:901:A:H5"	1:CA:902:G:OP2	2.10	0.50
1:CA:1186:G:H4'	9:CI:110:GLU:CD	2.36	0.50
25:DA:724:U:H2'	25:DA:725:G:O4'	2.10	0.50
25:DA:2687:U:H2'	25:DA:2688:U:O4'	2.11	0.50
30:DG:101:ILE:HD13	50:D4:25:TYR:HB2	1.92	0.50
33:DN:30:ILE:O	33:DN:34:LEU:HD22	2.11	0.50
41:DV:57:VAL:HG12	41:DV:99:ILE:HG23	1.93	0.50
43:DX:5:TYR:CE1	48:D2:30:ARG:HB2	2.46	0.50
1:AA:444:C:H2'	1:AA:445:G:C8	2.46	0.50
1:AA:573:A:N3	1:AA:883:C:O2'	2.44	0.50
1:AA:900:A:H2'	1:AA:901:A:C8	2.46	0.50
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.11	0.50
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.74	0.50
25:BA:7:G:H2'	25:BA:8:A:O4'	2.10	0.50
25:BA:1143:A:OP1	33:BN:25:ARG:NH2	2.44	0.50
27:BD:132:PRO:HG2	27:BD:135:PHE:HD2	1.76	0.50
28:BE:101:ARG:CZ	28:BE:171:GLU:HB2	2.42	0.50
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.10	0.50
1:CA:1034:G:H5"	1:CA:1035:A:OP2	2.11	0.50
1:CA:1517:G:H1'	25:DA:1919:A:O3'	2.10	0.50
11:CK:62:GLN:HG3	11:CK:97:ALA:HB2	1.94	0.50
25:DA:1450(A):C:N4	25:DA:1451:C:H41	2.09	0.50
25:DA:2747:G:H1	25:DA:2754:U:H2'	1.76	0.50
30:DG:106:LEU:O	30:DG:111:LEU:HD22	2.10	0.50
32:DI:14:ASP:N	32:DI:17:GLN:OE1	2.41	0.50
37:DR:36:THR:HG22	37:DR:37:THR:H	1.76	0.50
37:DR:83:ILE:O	37:DR:86:ARG:HG2	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:105:VAL:O	45:DZ:141:VAL:HG22	2.12	0.50
54:D8:6:THR:HG23	54:D8:64:TYR:HD2	1.77	0.50
1:AA:1179:A:O3'	9:AI:103:THR:HB	2.12	0.50
2:AB:78:GLN:NE2	2:AB:94:ASN:O	2.44	0.50
3:AC:157:ILE:HD12	3:AC:164:ARG:HB3	1.91	0.50
4:AD:107:ARG:NH2	4:AD:194:LEU:HD21	2.26	0.50
6:AF:50:TYR:OH	18:AR:74:ARG:O	2.26	0.50
10:AJ:44:VAL:HG22	10:AJ:66:ARG:HE	1.75	0.50
12:AL:8:ASN:O	12:AL:12:ARG:HG3	2.12	0.50
16:AP:48:TRP:HH2	16:AP:76:GLN:HE22	1.57	0.50
25:BA:2553:G:H1'	25:BA:2582:G:H21	1.77	0.50
27:BD:175:LEU:HD12	27:BD:185:VAL:HG21	1.93	0.50
1:CA:448:A:P	1:CA:485:G:H22	2.34	0.50
1:CA:693:G:H2'	1:CA:694:A:H8	1.75	0.50
1:CA:768:A:H4'	1:CA:1523:G:N2	2.26	0.50
1:CA:1010:G:H22	1:CA:1020:U:H1'	1.76	0.50
2:CB:71:VAL:HA	2:CB:93:VAL:HG23	1.93	0.50
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.11	0.50
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.93	0.50
25:DA:83:G:HO2'	25:DA:84:A:H8	1.59	0.50
25:DA:450:G:OP1	25:DA:1248:G:N2	2.43	0.50
25:DA:1784:A:N7	60:DA:4017:HOH:O	2.35	0.50
25:DA:2286:A:P	52:D6:29:ASN:HD22	2.34	0.50
25:DA:2370:G:C6	25:DA:2371:G:C6	3.00	0.50
26:DB:20:C:C2'	26:DB:21:G:H5'	2.42	0.50
1:AA:1089:G:H1	1:AA:1096:C:H42	1.60	0.50
2:AB:143:GLU:HA	2:AB:146:GLN:HB3	1.93	0.50
16:AP:38:TYR:OH	16:AP:47:ASP:OD2	2.20	0.50
25:BA:228:A:H8	25:BA:229:A:H5'	1.76	0.50
25:BA:1426:G:O2'	25:BA:1572:A:N6	2.45	0.50
25:BA:2712:U:OP1	25:BA:2714:G:H4'	2.11	0.50
1:CA:343:U:H2'	1:CA:345:C:C5	2.46	0.50
24:CX:67:C:C2'	24:CX:68:C:H5'	2.41	0.50
25:DA:536:A:H2'	25:DA:537:C:C6	2.47	0.50
25:DA:2119:A:C2	25:DA:2171:A:H5'	2.42	0.50
26:DB:33:G:C6	26:DB:34:U:N3	2.80	0.50
26:DB:40:U:O2'	26:DB:42:C:H5'	2.11	0.50
31:DH:118:PRO:HD2	31:DH:121:ILE:HG21	1.94	0.50
39:DT:26:ASP:O	39:DT:49:VAL:HG12	2.11	0.50
1:AA:601:C:H2'	1:AA:602:A:C8	2.46	0.50
1:AA:1264:C:H42	1:AA:1271:G:H1	1.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.29	0.50
9:AI:4:TYR:CD1	9:AI:88:TYR:HA	2.47	0.50
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.45	0.50
25:BA:855:G:O2'	46:B0:27:GLU:OE2	2.25	0.50
25:BA:2670:A:H2'	25:BA:2671:A:O4'	2.11	0.50
1:CA:1015:A:H1'	1:CA:1219:U:H5'	1.94	0.50
1:CA:1065:U:H6	1:CA:1190:G:H21	1.57	0.50
1:CA:1224:G:N1	1:CA:1322:C:O4'	2.45	0.50
24:CX:59:A:C2'	24:CX:60:U:H5'	2.40	0.50
25:DA:859:G:O2'	25:DA:916:G:O6	2.27	0.50
25:DA:1011:G:OP2	40:DU:66:ASN:ND2	2.42	0.50
25:DA:2815:C:C5'	51:D5:29:THR:HG21	2.41	0.50
26:DB:5:C:H42	26:DB:116:G:H1	1.59	0.50
31:DH:3:ARG:HB3	31:DH:3:ARG:NH1	2.24	0.50
38:DS:15:ARG:HD3	38:DS:25:ARG:HH21	1.76	0.50
1:AA:261:U:O2'	1:AA:263:A:N7	2.42	0.50
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.47	0.50
25:BA:2206:G:H5'	25:BA:2207:G:N7	2.27	0.50
26:BB:31:C:H4'	30:BG:29:TRP:CH2	2.47	0.50
27:BD:142:VAL:HG22	27:BD:193:VAL:HA	1.94	0.50
30:BG:67:LYS:HE2	50:B4:5:ILE:HD12	1.94	0.50
2:CB:78:GLN:NE2	2:CB:95:GLN:HE22	2.09	0.50
2:CB:144:ARG:HB3	2:CB:144:ARG:HH11	1.76	0.50
4:CD:85:LYS:HG3	4:CD:86:LYS:H	1.75	0.50
15:CO:82:ILE:O	15:CO:86:GLY:N	2.45	0.50
25:DA:272(E):G:C2	25:DA:364:C:C2	3.00	0.50
25:DA:459:U:H2'	25:DA:460:A:H8	1.77	0.50
25:DA:1289:C:H2'	25:DA:1290:C:H6	1.77	0.50
25:DA:1412:A:H2'	25:DA:1413:G:C8	2.46	0.50
25:DA:1639:U:H2'	25:DA:1640:C:H5"	1.92	0.50
25:DA:2646:C:H2'	25:DA:2647:U:O4'	2.11	0.50
26:DB:16:G:H1	26:DB:68:C:H42	1.59	0.50
28:DE:101:ARG:HB2	28:DE:201:THR:HG21	1.94	0.50
30:DG:61:ALA:HA	30:DG:66:GLN:O	2.12	0.50
31:DH:70:THR:O	31:DH:74:ASN:N	2.39	0.50
32:DI:72:LEU:HD21	32:DI:107:VAL:HG11	1.93	0.50
34:DO:68:GLU:HB3	34:DO:78:ARG:HB2	1.94	0.50
1:AA:69:G:H2'	1:AA:70:G:C8	2.47	0.50
1:AA:532:A:N6	3:AC:156:ARG:HH12	2.10	0.50
1:AA:718:G:O6	18:AR:74:ARG:NH1	2.45	0.50
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:71:VAL:HG12	2:AB:170:GLU:HG3	1.94	0.50
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.76	0.50
24:AX:21:A:N6	24:AX:46:G:H2'	2.26	0.50
25:BA:1173:G:N1	25:BA:1176:G:OP2	2.44	0.50
25:BA:1187:G:H5"	41:BV:81:TYR:CE1	2.47	0.50
25:BA:2036:C:N4	60:BA:4309:HOH:O	2.45	0.50
25:BA:2038:G:H2'	25:BA:2039:C:O4'	2.12	0.50
25:BA:2364:C:H2'	25:BA:2365:G:O4'	2.12	0.50
30:BG:173:LEU:O	30:BG:178:PHE:HB2	2.11	0.50
36:BQ:85:LYS:HG2	46:B0:7:LEU:HB3	1.92	0.50
52:B6:33:LYS:HA	52:B6:33:LYS:HE3	1.92	0.50
1:CA:571:U:O2	1:CA:918:A:H5'	2.12	0.50
1:CA:973:G:OP1	10:CJ:57:LYS:HD3	2.12	0.50
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.47	0.50
1:CA:1154:G:N7	1:CA:1155:G:C4	2.79	0.50
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.26	0.50
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.94	0.50
11:CK:98:LEU:O	11:CK:101:SER:OG	2.20	0.50
25:DA:235:U:H2'	25:DA:236:C:C6	2.47	0.50
25:DA:1557:C:OP2	25:DA:1558:A:O2'	2.24	0.50
25:DA:1853:A:N3	25:DA:2233:U:O2'	2.42	0.50
25:DA:2136:C:N4	25:DA:2156:G:H21	2.10	0.50
29:DF:102:PRO:HB2	29:DF:105:VAL:HG23	1.93	0.50
42:DW:70:TYR:OH	42:DW:72:LYS:HG3	2.12	0.50
1:AA:45:U:H2'	1:AA:46:G:C8	2.47	0.50
1:AA:972:C:O3'	10:AJ:57:LYS:HD3	2.12	0.50
1:AA:1067:A:O2'	1:AA:1068:G:OP2	2.25	0.50
13:AM:96:LEU:HB3	13:AM:97:PRO:HD2	1.93	0.50
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.76	0.50
25:BA:1930:G:O2'	25:BA:1968:G:O6	2.22	0.50
25:BA:1992:G:N7	60:BA:4121:HOH:O	2.34	0.50
47:B1:60:PHE:HE2	47:B1:95:LEU:HD11	1.76	0.50
50:B4:61:ARG:HG3	50:B4:62:ARG:H	1.77	0.50
1:CA:36:C:H5"	12:CL:123:LYS:HD3	1.94	0.50
3:CC:6:HIS:CE1	14:CN:50:LYS:HG3	2.46	0.50
14:CN:47:LEU:HB2	14:CN:53:LEU:HG	1.93	0.50
19:CS:68:GLY:H	50:D4:58:ARG:NH1	2.08	0.50
24:CX:36:U:H2'	24:CX:37:A:C8	2.46	0.50
25:DA:195:A:H2'	25:DA:198:C:N4	2.27	0.50
25:DA:249:C:O2	54:D8:12:LYS:NZ	2.43	0.50
25:DA:459:U:H2'	25:DA:460:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1250:G:N7	35:DP:18:ARG:NH2	2.60	0.50
25:DA:2299:G:N1	25:DA:2318:G:N7	2.59	0.50
25:DA:2540:C:H2'	25:DA:2541:A:O4'	2.11	0.50
27:DD:133:LEU:HB3	27:DD:173:VAL:HG11	1.94	0.50
31:DH:20:ALA:HB1	31:DH:21:PRO:HD2	1.94	0.50
35:DP:85:LEU:HA	35:DP:88:LEU:HD12	1.94	0.50
1:AA:166:G:H2'	1:AA:167:G:H8	1.76	0.49
1:AA:373:A:H2'	1:AA:374:A:H8	1.75	0.49
1:AA:503:C:C2'	1:AA:504:C:H5'	2.42	0.49
1:AA:584:G:H5'	17:AQ:91:ARG:NH2	2.27	0.49
1:AA:584:G:H2'	1:AA:585:G:C8	2.47	0.49
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.26	0.49
1:AA:1125:U:H1'	1:AA:1126:U:H2'	1.94	0.49
2:AB:115:LEU:HD13	2:AB:145:LEU:HG	1.94	0.49
12:AL:53:ARG:HG2	12:AL:69:TYR:HE1	1.76	0.49
25:BA:272(G):C:H42	25:BA:363(C):G:H1	1.60	0.49
25:BA:1213:A:H1'	25:BA:1238:G:N3	2.28	0.49
25:BA:1664:A:H1'	25:BA:2685:G:O2'	2.12	0.49
25:BA:2382:G:H21	54:B8:42:ARG:NH2	2.10	0.49
28:BE:7:VAL:HG23	28:BE:51:PHE:HE2	1.77	0.49
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.47	0.49
1:CA:674:G:H2'	1:CA:675:A:H8	1.76	0.49
1:CA:701:C:OP1	1:CA:702:A:O2'	2.15	0.49
1:CA:1002:G:N2	1:CA:1039:C:C4	2.80	0.49
1:CA:1002:G:C2	1:CA:1003:G:C8	3.00	0.49
1:CA:1376:U:O5'	7:CG:94:ARG:NH2	2.45	0.49
1:CA:1412:C:H42	1:CA:1488:G:H1	1.59	0.49
1:CA:1458:G:C2'	1:CA:1459:C:H5'	2.42	0.49
3:CC:39:ILE:HG22	3:CC:43:LEU:HD13	1.93	0.49
9:CI:65:VAL:HG21	9:CI:73:GLN:HB3	1.92	0.49
12:CL:110:VAL:HG23	12:CL:120:TYR:HB3	1.93	0.49
25:DA:957:A:H5'	36:DQ:76:LYS:HG3	1.93	0.49
29:DF:13:SER:OG	29:DF:16:GLY:O	2.22	0.49
29:DF:184:TYR:O	29:DF:188:ARG:HG3	2.12	0.49
1:AA:757:U:O2'	1:AA:879:C:O2	2.29	0.49
1:AA:1036:G:H5'	1:AA:1037:C:OP2	2.12	0.49
1:AA:1125:U:O2	1:AA:1126:U:O2'	2.23	0.49
3:AC:22:TRP:HA	10:AJ:93:GLY:HA2	1.94	0.49
25:BA:1113:U:H2'	25:BA:1114:G:H8	1.77	0.49
25:BA:2369:A:H2'	25:BA:2370:G:H8	1.76	0.49
29:BF:102:PRO:HB2	29:BF:105:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BO:64:ARG:NH1	34:BO:81:ASP:OD1	2.45	0.49
39:BT:24:PRO:HD3	39:BT:52:ILE:HD12	1.94	0.49
1:CA:826:C:H2'	1:CA:827:U:C6	2.46	0.49
1:CA:1279:A:OP1	10:CJ:7:LYS:NZ	2.45	0.49
1:CA:1318:A:H1'	19:CS:37:ARG:HD3	1.94	0.49
2:CB:121:LEU:O	2:CB:127:ILE:HB	2.12	0.49
3:CC:54:ARG:HG3	3:CC:69:HIS:HB2	1.94	0.49
3:CC:83:ARG:O	3:CC:87:LEU:N	2.42	0.49
6:CF:37:VAL:HA	6:CF:65:VAL:HG12	1.92	0.49
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.39	0.49
15:CO:64:ARG:O	15:CO:68:ARG:N	2.45	0.49
18:CR:29:PHE:HE1	18:CR:31:LEU:HD13	1.77	0.49
25:DA:479:A:N3	25:DA:481:G:H5"	2.27	0.49
25:DA:652(A):A:N3	25:DA:652(A):A:H2'	2.26	0.49
25:DA:1016:G:H2'	25:DA:1017:G:O4'	2.12	0.49
25:DA:1028:A:N3	25:DA:2486:G:O2'	2.45	0.49
25:DA:2123:G:H2'	25:DA:2124:G:C8	2.46	0.49
26:DB:6:C:C2	26:DB:116:G:N2	2.80	0.49
31:DH:27:LYS:HA	31:DH:32:GLU:HA	1.94	0.49
34:DO:119:PRO:HB2	39:DT:68:TYR:CE2	2.48	0.49
38:DS:44:LYS:NZ	38:DS:44:LYS:H	2.10	0.49
39:DT:51:ARG:HG3	39:DT:98:LYS:HD2	1.95	0.49
40:DU:109:LEU:HA	40:DU:112:ARG:HG3	1.93	0.49
1:AA:111:G:H5"	16:AP:27:LYS:HG2	1.94	0.49
1:AA:510:A:N3	1:AA:543:C:H1'	2.27	0.49
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.27	0.49
6:AF:65:VAL:HG21	6:AF:67:MET:HE3	1.94	0.49
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.94	0.49
12:AL:28:LYS:HB2	12:AL:33:ARG:HH12	1.77	0.49
25:BA:792:G:O2'	25:BA:2440:C:N3	2.39	0.49
25:BA:1342:A:OP2	60:BA:3971:HOH:O	2.20	0.49
25:BA:2118:U:OP1	25:BA:2148:G:H4'	2.12	0.49
25:BA:2138:C:N4	25:BA:2153:G:H1	2.09	0.49
27:BD:127:VAL:HA	27:BD:193:VAL:HG23	1.94	0.49
32:BI:104:GLN:O	32:BI:106:GLY:N	2.40	0.49
33:BN:47:ALA:HB2	33:BN:112:LEU:HD11	1.94	0.49
41:BV:55:ALA:HB2	41:BV:101:GLY:HA2	1.95	0.49
1:CA:691:G:O6	11:CK:52:GLY:HA2	2.12	0.49
1:CA:1190:G:H5'	3:CC:176:HIS:CE1	2.48	0.49
1:CA:1227:A:C2	19:CS:83:HIS:HB3	2.48	0.49
3:CC:181:ASN:ND2	3:CC:204:LEU:HD12	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:855:G:H2'	25:DA:856:C:C6	2.47	0.49
25:DA:1023:U:O2'	25:DA:1122:G:H5'	2.11	0.49
28:DE:34:VAL:HG22	28:DE:48:GLN:HB3	1.95	0.49
38:DS:50:SER:O	38:DS:76:LYS:NZ	2.34	0.49
45:DZ:157:LEU:HD11	45:DZ:163:LEU:HB2	1.94	0.49
54:D8:33:ASN:HA	54:D8:36:LYS:HD2	1.93	0.49
1:AA:560:U:H5'	1:AA:566:G:N2	2.27	0.49
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.47	0.49
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.94	0.49
3:AC:17:ASP:HB3	3:AC:21:ARG:HH21	1.77	0.49
10:AJ:26:ALA:HB1	10:AJ:84:GLN:NE2	2.28	0.49
25:BA:897:C:H2'	25:BA:898:C:C6	2.47	0.49
25:BA:1204:A:N6	25:BA:1240:U:H2'	2.27	0.49
25:BA:1688:U:H1'	25:BA:1701:A:C6	2.47	0.49
25:BA:1881:C:H2'	25:BA:1882:C:H6	1.77	0.49
25:BA:2097:C:H2'	25:BA:2098:U:O4'	2.13	0.49
25:BA:2493:U:OP1	60:BA:4231:HOH:O	2.20	0.49
32:BI:93:THR:HG22	32:BI:119:PRO:HB3	1.94	0.49
35:BP:62:LEU:O	54:B8:13:ARG:HD3	2.12	0.49
39:BT:60:THR:HG22	39:BT:77:PRO:HA	1.92	0.49
44:BY:6:HIS:H	44:BY:6:HIS:CD2	2.31	0.49
1:CA:353:A:H5'	1:CA:353:A:H8	1.77	0.49
1:CA:418:C:H2'	1:CA:419:C:C6	2.46	0.49
1:CA:495:A:H4'	1:CA:496:A:OP1	2.13	0.49
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.46	0.49
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	1.94	0.49
4:CD:65:ARG:HG2	4:CD:75:PHE:CD1	2.46	0.49
25:DA:62:C:H42	25:DA:93:G:H1	1.60	0.49
25:DA:275:G:H2'	25:DA:276:A:O4'	2.12	0.49
25:DA:340:A:H2'	25:DA:341:G:O4'	2.12	0.49
25:DA:579:G:H2'	25:DA:580:C:C6	2.48	0.49
25:DA:896:A:N6	45:DZ:146:ILE:HD13	2.27	0.49
25:DA:1022:G:N2	25:DA:1142(A):A:H2	2.05	0.49
25:DA:1316:U:H2'	25:DA:1317:A:H8	1.77	0.49
25:DA:2022:U:O2'	25:DA:2617:C:H5'	2.12	0.49
25:DA:2471:C:H2'	25:DA:2472:G:O4'	2.12	0.49
46:D0:38:VAL:HG12	46:D0:40:GLN:HG2	1.95	0.49
48:D2:65:ASN:OD1	48:D2:69:ARG:NH1	2.46	0.49
1:AA:524:G:H2'	1:AA:525:C:C6	2.48	0.49
1:AA:1328:C:OP1	21:AU:21:TYR:OH	2.30	0.49
2:AB:112:VAL:O	2:AB:116:GLU:N	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:309:G:H4'	44:BY:18:GLY:HA2	1.95	0.49
25:BA:687:C:H2'	25:BA:688:U:O4'	2.12	0.49
25:BA:1035:U:H2'	25:BA:1036:G:C8	2.47	0.49
25:BA:1186:G:H2'	25:BA:1187:G:O4'	2.13	0.49
25:BA:1651:G:H5'	37:BR:39:PRO:HG2	1.94	0.49
25:BA:2207:G:O2'	25:BA:2208:A:OP1	2.27	0.49
28:BE:18:ASP:OD2	39:BT:33:LYS:NZ	2.36	0.49
31:BH:56:SER:HB3	31:BH:61:HIS:ND1	2.28	0.49
34:BO:97:ARG:NH2	34:BO:99:PHE:HE1	2.10	0.49
37:BR:51:LEU:HD22	37:BR:66:VAL:HG13	1.94	0.49
1:CA:364:A:H2'	1:CA:365:U:C6	2.48	0.49
1:CA:1106:G:H5"	3:CC:172:ARG:HG2	1.95	0.49
4:CD:17:VAL:HG13	4:CD:19:LEU:HD22	1.94	0.49
19:CS:40:ILE:HD11	19:CS:74:PHE:CE2	2.47	0.49
25:DA:1462:C:H4'	25:DA:2703:C:H5'	1.95	0.49
25:DA:1674:G:H21	25:DA:1677:A:H61	1.58	0.49
25:DA:1813:G:H1'	27:DD:50:THR:OG1	2.12	0.49
25:DA:2176:A:H2'	25:DA:2177:C:C5	2.48	0.49
25:DA:2351:G:O5'	25:DA:2351:G:H8	1.95	0.49
28:DE:54:GLN:HE22	28:DE:58:ARG:HB3	1.77	0.49
30:DG:114:ILE:HA	30:DG:140:ILE:HD11	1.94	0.49
1:AA:558:G:OP1	60:AA:4061:HOH:O	2.20	0.49
1:AA:589:C:C2'	1:AA:590:C:H5'	2.43	0.49
1:AA:749:C:H2'	1:AA:750:G:H8	1.77	0.49
1:AA:1226:C:O2'	13:AM:111:LYS:NZ	2.45	0.49
1:AA:1366:C:H2'	1:AA:1367:C:H6	1.78	0.49
4:AD:188:LEU:H	4:AD:188:LEU:HD23	1.77	0.49
10:AJ:69:ASN:O	10:AJ:70:ARG:HD3	2.12	0.49
15:AO:16:ALA:HB1	15:AO:21:ASP:HB3	1.95	0.49
25:BA:184:C:H2'	25:BA:185:U:H6	1.75	0.49
25:BA:340:A:H2'	25:BA:341:G:O4'	2.13	0.49
25:BA:459:U:H2'	25:BA:460:A:H8	1.77	0.49
25:BA:1266:G:O6	42:BW:13:SER:OG	2.23	0.49
25:BA:2735:G:H2'	25:BA:2736:G:H8	1.78	0.49
25:BA:2791:C:O2	25:BA:2807:G:N1	2.45	0.49
25:BA:2863:C:OP1	39:BT:93:ARG:NH2	2.45	0.49
54:B8:42:ARG:NH1	60:B8:5105:HOH:O	2.25	0.49
1:CA:96:U:O2'	1:CA:97:G:H5'	2.12	0.49
1:CA:406:G:H2'	1:CA:407:G:C8	2.48	0.49
1:CA:690:G:O5'	1:CA:690:G:H8	1.96	0.49
1:CA:1151:A:N3	10:CJ:39:PRO:HG3	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.21	0.49
1:CA:1390:U:H2'	1:CA:1391:U:C6	2.47	0.49
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.94	0.49
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.93	0.49
9:CI:85:LEU:HB3	9:CI:92:TYR:CD2	2.48	0.49
25:DA:614:U:H2'	25:DA:614(A):U:O4'	2.12	0.49
25:DA:895:U:H3	25:DA:897:C:N4	2.10	0.49
25:DA:935:C:H2'	25:DA:936:C:C6	2.48	0.49
25:DA:1005:C:H2'	25:DA:1006:C:H6	1.78	0.49
25:DA:1204:A:H2	25:DA:1241:A:N6	2.09	0.49
25:DA:1503:U:H2'	25:DA:1504:C:C6	2.48	0.49
25:DA:1623:G:H2'	25:DA:1624:G:H8	1.77	0.49
25:DA:2134:A:N3	25:DA:2159:G:O2'	2.40	0.49
25:DA:2683:C:OP1	39:DT:53:ARG:NH2	2.46	0.49
38:DS:10:ARG:O	38:DS:14:VAL:HG12	2.12	0.49
1:AA:69:G:H2'	1:AA:70:G:H8	1.78	0.49
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.28	0.49
1:AA:1131:G:H8	1:AA:1131:G:O5'	1.95	0.49
1:AA:1295:G:C2'	1:AA:1296:C:H5'	2.42	0.49
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.94	0.49
3:AC:73:PRO:O	3:AC:77:ILE:HG12	2.12	0.49
3:AC:193:TYR:HE2	3:AC:196:LEU:HD11	1.78	0.49
20:AT:43:LEU:HD13	20:AT:51:GLU:HB3	1.94	0.49
21:AU:3:LYS:HD3	21:AU:14:TRP:CD1	2.47	0.49
25:BA:1021:A:H62	25:BA:1141:U:H3	1.59	0.49
25:BA:2223:G:OP1	27:BD:172:TYR:OH	2.29	0.49
37:BR:36:THR:HG22	37:BR:37:THR:H	1.77	0.49
55:B9:7:VAL:HG12	55:B9:34:GLN:HB3	1.95	0.49
1:CA:967:C:H3'	1:CA:968:A:H2'	1.93	0.49
1:CA:1014:A:O5'	1:CA:1014:A:H8	1.95	0.49
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.47	0.49
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.12	0.49
1:CA:1366:C:H2'	1:CA:1367:C:H6	1.78	0.49
2:CB:7:VAL:HG12	2:CB:8:LYS:H	1.77	0.49
11:CK:21:ILE:HB	11:CK:84:VAL:HG22	1.95	0.49
25:DA:1359:A:N6	25:DA:1372:U:H3	2.11	0.49
25:DA:2106:G:O6	25:DA:2183:C:N3	2.45	0.49
25:DA:2657:A:H3'	25:DA:2658:C:H6	1.78	0.49
29:DF:101:LEU:HD12	29:DF:102:PRO:HD2	1.95	0.49
30:DG:15:VAL:HG22	30:DG:175:LEU:HB3	1.95	0.49
34:DO:76:ALA:O	39:DT:74:ARG:HD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:D1:54:ALA:HB1	47:D1:83:GLU:HG3	1.95	0.49
1:AA:346:G:OP1	39:BT:41:ARG:NH1	2.46	0.49
1:AA:520:A:O2'	12:AL:73:GLU:OE1	2.24	0.49
5:AE:77:PRO:HG2	5:AE:142:LEU:HD22	1.95	0.49
12:AL:69:TYR:CD1	12:AL:90:VAL:HG21	2.48	0.49
25:BA:250:G:P	54:B8:13:ARG:HH22	2.34	0.49
25:BA:301:G:OP2	44:BY:84:ARG:NH2	2.45	0.49
25:BA:330:A:H2	25:BA:1210:A:O2'	1.96	0.49
25:BA:613:G:O2'	25:BA:614(C):A:N1	2.36	0.49
25:BA:1268:A:H2'	25:BA:1269:A:O4'	2.11	0.49
25:BA:1899:G:H2'	25:BA:1899:G:N3	2.27	0.49
29:BF:33:LEU:HB3	35:BP:6:LEU:HD21	1.94	0.49
4:CD:64:LEU:HB2	4:CD:198:VAL:HG21	1.95	0.49
4:CD:76:ARG:NE	4:CD:80:GLU:OE1	2.41	0.49
7:CG:153:HIS:CE1	11:CK:58:PRO:HD2	2.48	0.49
14:CN:45:ARG:O	14:CN:49:HIS:HD2	1.96	0.49
24:CX:29:G:C2'	24:CX:30:G:H5'	2.42	0.49
24:CX:36:U:H2'	24:CX:37:A:H8	1.78	0.49
25:DA:35:G:H1'	25:DA:454:A:C4	2.47	0.49
25:DA:247:G:H4'	25:DA:386:G:C5	2.48	0.49
25:DA:888:C:H2'	25:DA:889:C:C4	2.48	0.49
25:DA:1028:A:N6	25:DA:1125:G:H2'	2.28	0.49
25:DA:1336:A:H2'	25:DA:1337:G:C8	2.47	0.49
25:DA:1514:U:H2'	25:DA:1515:G:C8	2.48	0.49
25:DA:1721:G:H5'	25:DA:1722:A:H5"	1.95	0.49
25:DA:1971:A:OP1	60:DA:4205:HOH:O	2.19	0.49
26:DB:14:U:O3'	26:DB:108:U:O2'	2.30	0.49
35:DP:52:GLU:HB3	35:DP:55:ARG:NH1	2.27	0.49
36:DQ:52:VAL:O	36:DQ:56:ARG:HB2	2.12	0.49
45:DZ:30:ASN:ND2	45:DZ:90:VAL:O	2.38	0.49
25:BA:142:A:HO2'	25:BA:1407:C:HO2'	1.56	0.49
25:BA:831:G:N2	35:BP:53:GLY:O	2.46	0.49
30:BG:43:LEU:C	30:BG:45:GLU:H	2.20	0.49
31:BH:113:VAL:HG11	31:BH:151:ILE:HD13	1.94	0.49
39:BT:53:ARG:HB3	39:BT:53:ARG:CZ	2.42	0.49
40:BU:76:TYR:OH	40:BU:92:ARG:NH1	2.39	0.49
1:CA:20:U:H2'	1:CA:21:G:O4'	2.12	0.49
1:CA:1127:G:H21	1:CA:1147:C:H41	1.61	0.49
5:CE:80:ILE:HG22	5:CE:91:LEU:HB2	1.94	0.49
25:DA:7:G:H2'	25:DA:8:A:C8	2.47	0.49
37:DR:88:ARG:NH2	37:DR:89:ASP:OD2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DX:12:VAL:HG21	43:DX:27:THR:HG22	1.95	0.49
48:D2:10:LEU:O	48:D2:14:ARG:HB2	2.12	0.49
1:AA:425:G:C2'	1:AA:426:G:H5'	2.43	0.49
1:AA:737:A:OP2	6:AF:92:LYS:NZ	2.40	0.49
1:AA:998:G:H1	1:AA:1043:C:N4	2.10	0.49
4:AD:138:TYR:HD1	4:AD:139:ARG:N	2.11	0.49
20:AT:10:LEU:HD23	20:AT:11:SER:H	1.76	0.49
20:AT:53:LEU:HD13	20:AT:100:ILE:O	2.13	0.49
25:BA:470:A:OP1	29:BF:59:TYR:HE1	1.95	0.49
31:BH:5:GLY:HA2	31:BH:69:ARG:HB3	1.95	0.49
45:BZ:151:HIS:C	45:BZ:153:SER:H	2.21	0.49
49:B3:8:LEU:O	49:B3:32:GLN:N	2.34	0.49
51:B5:16:ARG:O	51:B5:20:ARG:HG3	2.13	0.49
1:CA:390:C:H2'	1:CA:391:G:C8	2.48	0.49
1:CA:1004:A:C8	1:CA:1005:A:H4'	2.45	0.49
2:CB:212:GLN:O	2:CB:216:SER:OG	2.21	0.49
14:CN:24:CYS:O	14:CN:28:GLY:N	2.37	0.49
19:CS:53:ASN:HB2	19:CS:77:THR:HA	1.94	0.49
25:DA:86:C:H4'	25:DA:104:U:H1'	1.95	0.49
25:DA:566:U:P	41:DV:80:GLN:HE21	2.34	0.49
25:DA:570:G:H2'	25:DA:2030:A:C5	2.48	0.49
25:DA:1495:A:H2'	25:DA:1496:A:C8	2.48	0.49
25:DA:1675:C:O5'	25:DA:1675:C:H6	1.96	0.49
25:DA:1798:U:H5'	27:DD:259:THR:HG22	1.95	0.49
25:DA:2123:G:H2'	25:DA:2124:G:H8	1.78	0.49
25:DA:2230:G:H1'	47:D1:45:ASN:CG	2.38	0.49
28:DE:127:ASP:OD2	60:DE:3105:HOH:O	2.19	0.49
32:DI:123:LEU:HD23	32:DI:123:LEU:H	1.77	0.49
33:DN:47:ALA:HB2	33:DN:112:LEU:HD11	1.95	0.49
1:AA:376:G:OP2	16:AP:67:THR:HG21	2.13	0.48
1:AA:593:G:H2'	1:AA:594:G:O4'	2.13	0.48
1:AA:1149:C:OP2	9:AI:9:ARG:NH2	2.38	0.48
2:AB:27:LYS:O	2:AB:30:ARG:NH1	2.46	0.48
3:AC:8:ILE:HG23	3:AC:16:ARG:HG2	1.95	0.48
9:AI:85:LEU:HB3	9:AI:92:TYR:HD2	1.76	0.48
25:BA:813:U:H2'	25:BA:814:C:C6	2.48	0.48
25:BA:875:G:H1	25:BA:902:C:N4	2.11	0.48
25:BA:987:G:O2'	25:BA:1000:A:N3	2.43	0.48
25:BA:2356:C:H2'	25:BA:2357:U:O4'	2.13	0.48
25:BA:2506:U:OP1	28:BE:144:ARG:NH2	2.46	0.48
1:CA:399:G:H2'	1:CA:400:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:405:U:P	4:CD:3:ARG:HH21	2.35	0.48
1:CA:1114:C:H1'	14:CN:60:SER:HB3	1.94	0.48
1:CA:1353:G:H2'	1:CA:1354:C:C6	2.48	0.48
4:CD:129:ASN:HD21	4:CD:144:ASP:HA	1.77	0.48
10:CJ:5:ARG:N	60:CJ:5101:HOH:O	2.46	0.48
12:CL:27:LEU:O	12:CL:33:ARG:NE	2.32	0.48
13:CM:107:ALA:O	13:CM:111:LYS:HB2	2.13	0.48
23:CW:76:PPU:HD2	25:DA:2451:A:C4	2.48	0.48
25:DA:1365:A:O4'	47:D1:41:ARG:NH2	2.46	0.48
25:DA:2070:G:C2	25:DA:2442:C:C2	3.01	0.48
25:DA:2345:G:OP1	52:D6:38:LYS:NZ	2.45	0.48
26:DB:55:U:H1'	30:DG:29:TRP:HD1	1.78	0.48
30:DG:108:ASN:O	50:D4:36:CYS:HA	2.13	0.48
31:DH:28:GLY:HA3	31:DH:79:VAL:HB	1.94	0.48
45:DZ:150:LEU:HA	45:DZ:150:LEU:HD13	1.65	0.48
1:AA:946:A:H2'	1:AA:947:G:C8	2.49	0.48
1:AA:1121:U:C2'	1:AA:1122:U:H5'	2.43	0.48
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	1.94	0.48
6:AF:10:LEU:HB2	6:AF:59:TYR:HB3	1.95	0.48
25:BA:458:G:C8	53:B7:37:LYS:HG2	2.49	0.48
25:BA:587:C:C6	25:BA:671:C:H1'	2.49	0.48
25:BA:1019:U:O2'	25:BA:1021:A:H2	1.96	0.48
25:BA:1786:A:H1'	25:BA:1938:A:H61	1.78	0.48
25:BA:2273:A:H2'	25:BA:2274:A:C8	2.48	0.48
27:BD:8:PRO:HB3	27:BD:14:ARG:HG3	1.95	0.48
31:BH:56:SER:OG	31:BH:58:GLU:HG2	2.13	0.48
38:BS:10:ARG:O	38:BS:14:VAL:HG13	2.12	0.48
1:CA:413:G:H21	1:CA:428:G:H1'	1.78	0.48
1:CA:502:G:OP1	12:CL:118:SER:OG	2.30	0.48
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.13	0.48
1:CA:1258:G:H2'	1:CA:1259:C:C6	2.48	0.48
1:CA:1492:A:H2'	1:CA:1493:A:C8	2.48	0.48
19:CS:38:SER:O	19:CS:71:LEU:HB2	2.13	0.48
25:DA:964:C:O2'	25:DA:2273:A:N3	2.40	0.48
25:DA:1541:G:OP2	25:DA:1542:A:O2'	2.30	0.48
25:DA:1607:C:H4'	25:DA:1608:A:O5'	2.12	0.48
25:DA:1899:G:N3	25:DA:1899:G:H2'	2.27	0.48
25:DA:2128:C:N4	25:DA:2160:G:N1	2.43	0.48
25:DA:2562:U:H1'	34:DO:23:ARG:NH1	2.28	0.48
25:DA:2693:A:H2'	25:DA:2694:G:C8	2.46	0.48
25:DA:2756:U:H3'	55:D9:20:HIS:CD2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DE:72:VAL:HA	28:DE:73:GLU:CG	2.43	0.48
34:DO:34:THR:OG1	34:DO:35:VAL:N	2.46	0.48
35:DP:50:ARG:HG2	54:D8:61:LEU:HD11	1.96	0.48
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.93	0.48
1:AA:1014:A:H2'	1:AA:1015:A:C8	2.48	0.48
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.13	0.48
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.48	0.48
28:BE:128:SER:OG	28:BE:129:HIS:N	2.45	0.48
48:B2:9:GLN:HE22	48:B2:56:GLN:HG2	1.78	0.48
1:CA:139:G:N2	1:CA:224:C:O2	2.43	0.48
1:CA:359:U:H2'	1:CA:360:A:C8	2.47	0.48
1:CA:375:U:H5"	16:CP:6:LEU:HD23	1.96	0.48
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.13	0.48
10:CJ:45:ARG:O	10:CJ:65:LEU:N	2.42	0.48
25:DA:921:G:H2'	25:DA:922:U:C6	2.48	0.48
25:DA:2151:G:H2'	25:DA:2152:G:C8	2.48	0.48
25:DA:2285:C:OP2	52:D6:6:ARG:NH1	2.45	0.48
25:DA:2287:A:O2'	25:DA:2288:A:H5"	2.13	0.48
26:DB:24:G:H21	26:DB:27:C:N4	2.11	0.48
28:DE:34:VAL:HG21	28:DE:78:LEU:HD11	1.95	0.48
30:DG:3:LEU:HD11	30:DG:5:VAL:HG12	1.95	0.48
35:DP:2:LYS:HZ3	35:DP:4:SER:HG	1.56	0.48
35:DP:64:LYS:HA	54:D8:13:ARG:HB3	1.94	0.48
37:DR:66:VAL:HG11	37:DR:79:LEU:HD12	1.96	0.48
1:AA:667:G:OP1	1:AA:732:C:O2'	2.20	0.48
1:AA:1151:A:O2'	1:AA:1152:A:O5'	2.26	0.48
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.93	0.48
4:AD:186:LEU:HB2	4:AD:187:ARG:NH2	2.25	0.48
8:AH:14:ARG:O	8:AH:18:ARG:HD3	2.12	0.48
25:BA:1011:G:OP2	40:BU:70:ARG:NH2	2.45	0.48
26:BB:8:U:O3'	38:BS:25:ARG:NH2	2.45	0.48
1:CA:559:A:H4'	1:CA:560:U:H3'	1.93	0.48
1:CA:1227:A:N3	19:CS:83:HIS:HB3	2.27	0.48
1:CA:1422:G:H5"	34:DO:48:PRO:HB3	1.94	0.48
2:CB:82:ARG:HG3	2:CB:92:TYR:OH	2.14	0.48
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.13	0.48
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.14	0.48
25:DA:80:G:H1	25:DA:106:C:H42	1.60	0.48
25:DA:117:G:OP2	25:DA:119:A:O2'	2.26	0.48
25:DA:583:G:OP2	40:DU:10:ARG:NH1	2.47	0.48
25:DA:615:G:OP1	29:DF:40:GLN:HG2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:729:G:C5	27:DD:208:LYS:HB2	2.49	0.48
25:DA:975(A):G:O2'	25:DA:1156:A:N1	2.45	0.48
25:DA:2849:U:H4'	25:DA:2868:A:C2	2.48	0.48
45:DZ:7:ALA:O	45:DZ:62:PRO:HD3	2.13	0.48
1:AA:165:C:H2'	1:AA:166:G:C8	2.49	0.48
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	1.96	0.48
3:AC:62:ASP:O	3:AC:97:LYS:HB3	2.14	0.48
25:BA:875:G:O3'	45:BZ:151:HIS:HE1	1.96	0.48
25:BA:1028:A:N6	25:BA:1125:G:H2'	2.29	0.48
25:BA:1524:G:H2'	25:BA:1525:G:O4'	2.14	0.48
25:BA:1826:G:H4'	27:BD:242:ARG:CZ	2.43	0.48
25:BA:2809:A:H62	25:BA:2891:G:H2'	1.78	0.48
32:BI:40:THR:O	32:BI:44:LEU:N	2.43	0.48
37:BR:55:ALA:HB2	37:BR:79:LEU:HD13	1.94	0.48
1:CA:674:G:H2'	1:CA:675:A:C8	2.49	0.48
1:CA:1023:G:H3'	1:CA:1024:G:C8	2.48	0.48
1:CA:1120:G:C6	1:CA:1154:G:C2	3.01	0.48
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.49	0.48
10:CJ:45:ARG:HB3	10:CJ:65:LEU:HB3	1.94	0.48
12:CL:82:VAL:O	12:CL:106:ASP:HB2	2.13	0.48
13:CM:16:ASP:OD1	13:CM:16:ASP:N	2.46	0.48
14:CN:29:ARG:HG2	14:CN:31:ARG:H	1.79	0.48
25:DA:639:U:H2'	25:DA:640:C:C6	2.49	0.48
25:DA:2392:A:O3'	54:D8:27:THR:HB	2.13	0.48
26:DB:42:C:C4	26:DB:43:C:C4	3.02	0.48
29:DF:80:ALA:HB3	29:DF:83:PHE:HD1	1.78	0.48
35:DP:21:ARG:HD3	35:DP:21:ARG:HA	1.51	0.48
36:DQ:30:GLY:O	36:DQ:134:ARG:HD3	2.14	0.48
45:DZ:69:THR:HG22	45:DZ:90:VAL:HG22	1.95	0.48
1:AA:352:C:O2'	1:AA:354:G:OP1	2.24	0.48
5:AE:137:GLU:HG2	5:AE:140:ARG:NH1	2.28	0.48
7:AG:89:MET:SD	7:AG:155:ARG:HB2	2.53	0.48
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.95	0.48
25:BA:363(A):A:H2'	25:BA:363(B):G:C8	2.49	0.48
25:BA:1798:U:H5'	27:BD:259:THR:CG2	2.42	0.48
25:BA:2080:G:OP1	47:B1:35:THR:HG21	2.13	0.48
25:BA:2250:G:O2'	25:BA:2496:C:OP1	2.24	0.48
1:CA:1151:A:O2'	1:CA:1152:A:O5'	2.32	0.48
1:CA:1295:G:C2'	1:CA:1296:C:H5'	2.42	0.48
1:CA:1328:C:O3'	13:CM:29:ARG:HG3	2.13	0.48
1:CA:1516:G:H2'	1:CA:1518:A:OP2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:80:ILE:HD12	2:CB:208:ILE:HG23	1.95	0.48
2:CB:142:LEU:HA	2:CB:145:LEU:HD22	1.96	0.48
13:CM:65:LYS:O	13:CM:70:LEU:HD12	2.14	0.48
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.43	0.48
25:DA:271(U):G:H2'	25:DA:271(V):G:C8	2.48	0.48
25:DA:272(B):G:H2'	25:DA:272(C):G:H8	1.79	0.48
25:DA:619:G:H3'	25:DA:620:G:H21	1.78	0.48
25:DA:820:A:H2'	25:DA:821:A:O4'	2.14	0.48
25:DA:1328:G:O2'	25:DA:1329:U:H2'	2.13	0.48
25:DA:1467:C:C5	25:DA:1546:C:H2'	2.48	0.48
25:DA:1486:A:O2'	25:DA:1487:G:H5'	2.14	0.48
25:DA:1509(A):A:N3	25:DA:1509(A):A:H5"	2.29	0.48
29:DF:111:ALA:HB2	29:DF:206:ILE:HG21	1.96	0.48
36:DQ:54:MET:HE1	36:DQ:104:PHE:HB3	1.96	0.48
39:DT:92:GLY:O	39:DT:120:ARG:NH2	2.46	0.48
47:D1:50:ARG:HG2	47:D1:59:THR:HG22	1.95	0.48
1:AA:448:A:O5'	1:AA:485:G:N2	2.42	0.48
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.78	0.48
2:AB:32:ILE:HD13	2:AB:40:HIS:CD2	2.48	0.48
22:AV:22:U:H2'	22:AV:23:A:C8	2.48	0.48
25:BA:646:A:H2'	25:BA:647:G:O4'	2.14	0.48
26:BB:14:U:OP2	26:BB:70:C:O2'	2.16	0.48
34:BO:34:THR:OG1	34:BO:35:VAL:N	2.45	0.48
35:BP:65:ARG:HG3	54:B8:25:MET:HG3	1.96	0.48
1:CA:407:G:H5"	4:CD:115:ARG:HB3	1.96	0.48
3:CC:61:ALA:C	3:CC:63:ASN:H	2.22	0.48
8:CH:73:ASP:OD1	8:CH:75:ARG:NH1	2.46	0.48
10:CJ:37:PRO:HA	10:CJ:72:VAL:HG12	1.96	0.48
17:CQ:43:LEU:HD12	17:CQ:68:ARG:HB3	1.95	0.48
19:CS:30:LEU:HD11	19:CS:32:LYS:HG3	1.95	0.48
25:DA:475:U:H4'	25:DA:510:C:H5'	1.96	0.48
25:DA:1139:G:O3'	33:DN:24:GLY:HA3	2.14	0.48
25:DA:1155:A:H5"	40:DU:55:ARG:HD3	1.95	0.48
28:DE:2:LYS:HG3	28:DE:200:GLU:HB2	1.94	0.48
34:DO:120:GLU:HB2	39:DT:68:TYR:HE2	1.79	0.48
41:DV:25:LEU:H	41:DV:92:THR:HG1	1.61	0.48
46:D0:34:GLY:N	46:D0:61:ALA:O	2.37	0.48
50:D4:58:ARG:HG2	50:D4:59:PHE:HD1	1.79	0.48
53:D7:24:THR:O	53:D7:28:ARG:HG3	2.13	0.48
1:AA:625:G:H4'	16:AP:16:HIS:CG	2.49	0.48
1:AA:1229:A:O3'	24:AX:30:G:H5"	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2291:U:OP1	25:BA:2380:C:O2'	2.31	0.48
25:BA:2311:A:N1	30:BG:47:LYS:NZ	2.61	0.48
1:CA:8:A:N6	4:CD:209:ARG:HB2	2.28	0.48
1:CA:66:G:H8	1:CA:66:G:OP1	1.95	0.48
1:CA:442:C:H42	1:CA:492:G:H1	1.61	0.48
1:CA:696:A:H8	1:CA:696:A:O5'	1.97	0.48
1:CA:1456:G:O6	20:CT:54:LYS:HE3	2.13	0.48
2:CB:158:LEU:HD12	2:CB:158:LEU:H	1.78	0.48
25:DA:1416:G:O2'	25:DA:1417:C:OP2	2.21	0.48
25:DA:1665:A:OP2	60:DA:4604:HOH:O	2.20	0.48
25:DA:1927:A:H2'	25:DA:1928:A:C8	2.49	0.48
25:DA:2469:A:O2'	36:DQ:56:ARG:HD2	2.13	0.48
25:DA:2515:C:H2'	25:DA:2516:G:C8	2.48	0.48
25:DA:2786:U:O2'	28:DE:62:PRO:O	2.24	0.48
26:DB:3:C:H2'	26:DB:4:C:C6	2.48	0.48
26:DB:46:A:H2'	26:DB:47:C:C6	2.49	0.48
31:DH:76:VAL:HA	31:DH:79:VAL:HG22	1.96	0.48
38:DS:23:ARG:NH2	38:DS:84:GLN:HG2	2.29	0.48
40:DU:20:LEU:HB3	40:DU:39:LEU:HD11	1.96	0.48
1:AA:405:U:OP2	4:AD:3:ARG:CZ	2.61	0.48
12:AL:27:LEU:HD23	12:AL:30:ALA:O	2.14	0.48
16:AP:54:GLU:O	16:AP:57:ARG:HB3	2.13	0.48
17:AQ:6:LEU:HG	17:AQ:23:VAL:HG11	1.93	0.48
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.95	0.48
25:BA:27:G:N2	25:BA:512:G:H1'	2.29	0.48
25:BA:247:G:H4'	25:BA:386:G:C5	2.49	0.48
25:BA:2632:A:O2'	25:BA:2811:G:O2'	2.20	0.48
26:BB:75:G:N2	45:BZ:87:ASP:OD1	2.44	0.48
44:BY:92:ASN:HD22	44:BY:92:ASN:H	1.61	0.48
1:CA:1004:A:H5'	1:CA:1024:G:N2	2.29	0.48
1:CA:1246:C:H2'	1:CA:1247:U:H6	1.79	0.48
1:CA:1353:G:H2'	1:CA:1354:C:H6	1.79	0.48
10:CJ:47:PHE:HB2	10:CJ:63:PHE:HB2	1.94	0.48
25:DA:271(K):U:H4'	25:DA:271(L):U:OP2	2.13	0.48
25:DA:1260:G:C6	25:DA:1261:C:C4	3.01	0.48
25:DA:2348:U:O4	25:DA:2382:G:N1	2.46	0.48
25:DA:2533:A:OP1	25:DA:2665:A:O2'	2.31	0.48
30:DG:171:ALA:O	30:DG:175:LEU:N	2.45	0.48
35:DP:63:PRO:HG2	54:D8:25:MET:HB2	1.96	0.48
36:DQ:97:VAL:HG21	36:DQ:103:MET:HE3	1.95	0.48
1:AA:551:U:H2'	1:AA:552:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1252:A:H61	1:AA:1285:A:H61	1.61	0.48
1:AA:1320:C:N4	19:AS:36:ARG:HB2	2.29	0.48
2:AB:187:LEU:HD23	2:AB:201:ILE:O	2.13	0.48
3:AC:35:GLU:CD	3:AC:59:ARG:HH12	2.20	0.48
25:BA:648:G:O2'	25:BA:2351:G:OP1	2.27	0.48
25:BA:772:C:H2'	25:BA:773:U:H6	1.79	0.48
25:BA:1639:U:H4'	25:BA:2699:C:H4'	1.95	0.48
25:BA:2116:G:N2	25:BA:2162:G:OP1	2.34	0.48
25:BA:2492:U:H2'	25:BA:2493:U:C6	2.48	0.48
1:CA:6:G:O2'	1:CA:7:G:H5'	2.14	0.48
1:CA:105:G:H2'	1:CA:106:C:C6	2.49	0.48
1:CA:131:C:H2'	1:CA:132:C:C6	2.49	0.48
1:CA:382:A:H2'	1:CA:383:A:H8	1.79	0.48
1:CA:447:G:O6	60:CA:4099:HOH:O	2.17	0.48
2:CB:213:LEU:HD13	2:CB:214:ILE:HD13	1.95	0.48
5:CE:36:ASP:C	5:CE:38:GLN:H	2.22	0.48
8:CH:37:ARG:HH21	8:CH:38:ILE:HD11	1.78	0.48
12:CL:11:VAL:HG11	17:CQ:36:ILE:HG21	1.96	0.48
25:DA:595:C:H42	25:DA:662:G:H1	1.60	0.48
25:DA:1791:A:H3'	25:DA:1792:G:H8	1.79	0.48
25:DA:1803:A:H4'	27:DD:259:THR:HG23	1.96	0.48
35:DP:44:GLY:CA	35:DP:45:LEU:HB2	2.43	0.48
1:AA:662:G:H2'	1:AA:663:A:H8	1.75	0.47
1:AA:1200:C:OP1	60:AA:4099:HOH:O	2.20	0.47
3:AC:81:GLY:O	3:AC:85:ARG:HG3	2.14	0.47
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.47	0.47
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.13	0.47
25:BA:103:A:H8	25:BA:103:A:O5'	1.97	0.47
25:BA:569:U:O2'	25:BA:983:A:N1	2.33	0.47
25:BA:1045:A:H1'	25:BA:1047:G:N3	2.29	0.47
25:BA:1796:U:H2'	25:BA:1797:C:H6	1.77	0.47
25:BA:1817:G:OP1	27:BD:88:ARG:NH2	2.47	0.47
25:BA:1825:A:OP1	27:BD:249:PRO:HD3	2.14	0.47
25:BA:2103:C:C2	25:BA:2187:G:C2	3.02	0.47
25:BA:2424:C:O2	25:BA:2429:G:O2'	2.18	0.47
34:BO:36:GLY:HA2	34:BO:106:LEU:HD23	1.96	0.47
1:CA:193:C:H2'	1:CA:194:C:H6	1.78	0.47
1:CA:397:A:H3'	1:CA:397:A:N3	2.29	0.47
1:CA:1323:G:H4'	1:CA:1363:C:C2	2.49	0.47
5:CE:34:VAL:O	5:CE:42:GLY:N	2.45	0.47
11:CK:33:THR:C	11:CK:40:ILE:HG12	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:10:PRO:HG2	13:CM:21:TYR:HD2	1.79	0.47
15:CO:9:GLN:HA	15:CO:12:ILE:HD12	1.95	0.47
25:DA:289:A:H2'	25:DA:290:G:O4'	2.14	0.47
25:DA:317:G:H2'	25:DA:318:C:O4'	2.14	0.47
25:DA:390:A:H4'	25:DA:391:G:H5'	1.96	0.47
25:DA:686:G:N2	25:DA:788:A:H61	2.12	0.47
25:DA:1012:U:C5	33:DN:28:THR:HG21	2.47	0.47
25:DA:1638:C:H5"	25:DA:2710:C:O2'	2.14	0.47
30:DG:179:PRO:HB2	50:D4:42:PHE:CE1	2.48	0.47
36:DQ:138:ASP:OD2	45:DZ:81:ARG:NH1	2.47	0.47
46:D0:19:LYS:HE2	46:D0:19:LYS:HB2	1.65	0.47
1:AA:35:G:O2'	12:AL:118:SER:O	2.24	0.47
1:AA:339:C:H2'	1:AA:340:U:C6	2.50	0.47
1:AA:429:U:H3'	4:AD:9:CYS:SG	2.54	0.47
1:AA:651:C:N4	1:AA:752:G:O2'	2.47	0.47
1:AA:690:G:C6	1:AA:691:G:C6	3.02	0.47
1:AA:1431:C:H2'	1:AA:1432:G:O4'	2.14	0.47
1:AA:1456:G:O6	20:AT:54:LYS:NZ	2.46	0.47
2:AB:207:ALA:O	2:AB:211:ILE:HG13	2.14	0.47
11:AK:48:ILE:O	11:AK:50:TYR:N	2.47	0.47
26:BB:43:C:OP1	50:B4:6:HIS:NE2	2.40	0.47
1:CA:114:U:H2'	1:CA:115:G:C8	2.49	0.47
1:CA:926:G:H22	22:CV:16:A:P	2.36	0.47
1:CA:1304:G:C6	1:CA:1305:G:N1	2.82	0.47
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.13	0.47
14:CN:3:ARG:O	14:CN:7:ILE:HG23	2.14	0.47
20:CT:50:GLU:HG3	20:CT:100:ILE:HG23	1.96	0.47
25:DA:1188:U:C4'	41:DV:79:VAL:HG22	2.43	0.47
25:DA:1481:U:H3	25:DA:1510:G:H1	1.61	0.47
25:DA:1670:C:O2	28:DE:129:HIS:NE2	2.40	0.47
25:DA:1959:G:OP2	60:DA:4575:HOH:O	2.20	0.47
25:DA:2296:U:OP2	38:DS:6:ALA:HB2	2.14	0.47
25:DA:2468:G:OP1	36:DQ:119:ARG:NH2	2.45	0.47
25:DA:2572:A:N7	28:DE:144:ARG:HD2	2.28	0.47
25:DA:2710:C:H2'	25:DA:2711:A:C8	2.50	0.47
26:DB:24:G:N2	26:DB:27:C:H42	2.11	0.47
29:DF:183:VAL:O	29:DF:187:VAL:HG23	2.14	0.47
46:D0:82:ARG:HA	46:D0:83:PRO:HD3	1.71	0.47
55:D9:4:ARG:HD3	55:D9:6:SER:O	2.14	0.47
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.13	0.47
4:AD:107:ARG:HH22	4:AD:194:LEU:HD21	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:173:TRP:HA	4:AD:187:ARG:NH2	2.28	0.47
7:AG:16:LEU:HD11	9:AI:45:ALA:HB2	1.96	0.47
25:BA:1047:G:H2'	25:BA:1110:G:H1	1.79	0.47
25:BA:1400:G:H2'	25:BA:1401:G:C8	2.49	0.47
34:BO:77:ILE:HD12	39:BT:74:ARG:HD3	1.97	0.47
45:BZ:137:ILE:HA	45:BZ:156:LYS:NZ	2.28	0.47
52:B6:35:GLU:CD	52:B6:50:ARG:HH11	2.22	0.47
1:CA:643:C:H2'	1:CA:644:G:H8	1.78	0.47
1:CA:1057:G:H2'	1:CA:1058:G:O4'	2.13	0.47
1:CA:1427:U:H2'	1:CA:1428:A:C8	2.48	0.47
6:CF:97:PHE:HD2	18:CR:31:LEU:HD23	1.79	0.47
8:CH:28:ALA:HB3	8:CH:57:PRO:HB2	1.96	0.47
25:DA:1224:C:O2'	41:DV:86:GLY:N	2.42	0.47
25:DA:1292:U:H2'	25:DA:1293:C:C6	2.49	0.47
25:DA:2137:C:C2	25:DA:2155:G:C6	3.02	0.47
29:DF:24:LEU:HD23	29:DF:115:ALA:HA	1.95	0.47
30:DG:12:TYR:HA	30:DG:16:ARG:HG3	1.96	0.47
50:D4:57:GLU:HA	50:D4:58:ARG:HA	1.70	0.47
1:AA:129(A):G:O2'	1:AA:189(F):U:OP1	2.24	0.47
1:AA:130:A:C8	17:AQ:63:ARG:HB2	2.49	0.47
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.46	0.47
2:AB:184:VAL:HG12	2:AB:197:VAL:HG13	1.96	0.47
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.31	0.47
5:AE:113:ALA:HB3	5:AE:115:VAL:HG23	1.96	0.47
6:AF:2:ARG:NE	6:AF:69:GLU:HG2	2.29	0.47
6:AF:7:ASN:HD21	18:AR:34:TYR:HE1	1.62	0.47
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.47	0.47
25:BA:278:A:H2'	25:BA:279:C:C5	2.49	0.47
25:BA:971:C:H2'	25:BA:972:G:O4'	2.14	0.47
25:BA:1178:C:H2'	25:BA:1179:C:H6	1.79	0.47
25:BA:1403:C:C5'	25:BA:1471:A:H1'	2.44	0.47
25:BA:2144:U:H2'	25:BA:2146:C:C5	2.49	0.47
25:BA:2287:A:N6	25:BA:2344:U:H3	2.04	0.47
33:BN:15:LEU:HD12	33:BN:137:LYS:HG2	1.97	0.47
36:BQ:12:GLN:HG2	36:BQ:73:PRO:HD2	1.95	0.47
1:CA:56:U:H2'	1:CA:57:G:H8	1.80	0.47
1:CA:1004:A:C6	1:CA:1037:C:C2	3.02	0.47
1:CA:1329:A:OP2	21:CU:7:ARG:NH2	2.47	0.47
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.29	0.47
2:CB:172:ILE:HG22	2:CB:176:GLU:HG3	1.96	0.47
6:CF:14:LEU:HD13	6:CF:19:LEU:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.49	0.47
25:DA:192:C:O2'	25:DA:802:A:N3	2.40	0.47
25:DA:235:U:H2'	25:DA:236:C:H6	1.79	0.47
25:DA:585:G:H2'	25:DA:1251:C:H42	1.79	0.47
25:DA:1300:U:H4'	25:DA:1301:A:C5'	2.43	0.47
25:DA:1613:G:C2	25:DA:1619:G:C5	3.02	0.47
25:DA:2171:A:H1'	25:DA:2172:U:C2	2.49	0.47
25:DA:2371:G:C2	25:DA:2372:G:C8	3.03	0.47
29:DF:53:THR:HG22	29:DF:56:GLU:HG3	1.95	0.47
30:DG:14:GLU:C	30:DG:17:PRO:HD2	2.38	0.47
33:DN:36:GLY:HA2	33:DN:38:HIS:CE1	2.49	0.47
35:DP:121:LYS:HB3	35:DP:123:LEU:HG	1.96	0.47
36:DQ:29:PHE:HB2	36:DQ:105:GLU:OE2	2.14	0.47
38:DS:74:ALA:HB3	38:DS:108:GLY:HA3	1.95	0.47
4:AD:201:GLN:HE22	4:AD:204:ILE:HD12	1.79	0.47
15:AO:84:LYS:O	15:AO:84:LYS:HD3	2.14	0.47
25:BA:694:U:OP1	27:BD:59:LYS:NZ	2.42	0.47
25:BA:747:U:O2	25:BA:2014:A:H1'	2.14	0.47
25:BA:900:A:H2'	25:BA:901:A:O4'	2.14	0.47
25:BA:1050:A:H2'	25:BA:1051:G:C8	2.49	0.47
25:BA:1173:G:HO2'	25:BA:1174:A:C5'	2.27	0.47
25:BA:1913:A:H4'	25:BA:1914:C:C5'	2.45	0.47
25:BA:2324:C:H5"	25:BA:2325:G:H5'	1.96	0.47
25:BA:2660:A:H2'	25:BA:2661:G:O4'	2.14	0.47
25:BA:2815:C:H2'	25:BA:2816:C:C6	2.49	0.47
26:BB:24:G:N7	26:BB:56:G:H2'	2.29	0.47
30:BG:18:GLU:HG2	30:BG:175:LEU:HD21	1.96	0.47
31:BH:98:LEU:HD13	31:BH:125:VAL:HG23	1.97	0.47
36:BQ:31:ASP:N	36:BQ:106:VAL:O	2.40	0.47
1:CA:143:A:H5"	1:CA:144:G:H5'	1.95	0.47
1:CA:576:G:O6	1:CA:880:C:O2'	2.23	0.47
1:CA:878:G:OP1	8:CH:88:LYS:HB3	2.14	0.47
2:CB:73:THR:OG1	2:CB:95:GLN:O	2.12	0.47
2:CB:98:LEU:HB2	2:CB:101:MET:HE3	1.95	0.47
3:CC:20:SER:HB2	3:CC:40:ARG:NH1	2.28	0.47
6:CF:97:PHE:CZ	18:CR:61:LYS:HE3	2.49	0.47
13:CM:14:ARG:HG3	13:CM:44:ARG:NH1	2.29	0.47
13:CM:81:LEU:HD21	13:CM:88:ARG:NH2	2.29	0.47
14:CN:22:THR:HB	14:CN:33:VAL:HG21	1.96	0.47
19:CS:40:ILE:HA	19:CS:44:MET:SD	2.54	0.47
25:DA:208:C:H2'	25:DA:209:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:311:A:C6	25:DA:328:U:C4	3.02	0.47
25:DA:652(T):C:H2'	25:DA:652(U):G:C8	2.50	0.47
25:DA:1160:G:N2	41:DV:10:LYS:HZ2	2.13	0.47
25:DA:2154:G:H2'	25:DA:2154:G:N3	2.29	0.47
25:DA:2156:G:N7	25:DA:2157:G:N1	2.62	0.47
26:DB:29:A:P	38:DS:31:SER:HB2	2.54	0.47
28:DE:170:LEU:HB3	28:DE:184:VAL:CG2	2.45	0.47
40:DU:82:GLY:O	40:DU:86:ALA:N	2.42	0.47
45:DZ:24:LEU:HD12	45:DZ:25:PRO:HD2	1.96	0.47
55:D9:3:VAL:HA	55:D9:35:ARG:O	2.15	0.47
1:AA:189(D):C:O2	1:AA:189(H):G:N1	2.48	0.47
1:AA:376:G:O2'	16:AP:5:ARG:NH2	2.47	0.47
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.35	0.47
3:AC:123:GLN:HB3	3:AC:128:PHE:HD2	1.80	0.47
7:AG:15:ASP:OD1	7:AG:20:ASP:N	2.46	0.47
8:AH:87:SER:HA	8:AH:93:VAL:HG23	1.95	0.47
25:BA:279:C:H2'	25:BA:280:C:H5'	1.97	0.47
25:BA:652(C):G:N2	25:BA:653:A:H1'	2.29	0.47
25:BA:2439:A:H5'	25:BA:2439:A:C8	2.49	0.47
25:BA:2882:A:OP1	37:BR:96:ARG:NE	2.40	0.47
27:BD:13:ARG:HD2	27:BD:13:ARG:HA	1.67	0.47
27:BD:162:SER:HB3	27:BD:195:ALA:HB2	1.96	0.47
41:BV:72:VAL:HG13	41:BV:85:LYS:HB3	1.97	0.47
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.80	0.47
25:DA:582:G:H2'	25:DA:583:G:C8	2.50	0.47
25:DA:971:C:OP1	25:DA:989:G:N1	2.33	0.47
25:DA:2103:C:H2'	25:DA:2104:G:H5'	1.97	0.47
25:DA:2615:U:C2	51:D5:7:PRO:HA	2.49	0.47
29:DF:40:GLN:NE2	29:DF:184:TYR:H	2.12	0.47
54:D8:54:GLU:O	54:D8:58:ILE:HG13	2.15	0.47
1:AA:38:G:O2'	1:AA:39:G:H5"	2.15	0.47
1:AA:78:G:N2	1:AA:91:C:C2	2.83	0.47
1:AA:134:A:H61	16:AP:25:ARG:NH1	2.13	0.47
1:AA:171:A:H2'	1:AA:172:A:C8	2.49	0.47
1:AA:266:G:H5"	1:AA:268:C:H41	1.79	0.47
1:AA:542:G:P	4:AD:10:ARG:HH22	2.38	0.47
1:AA:975:A:N6	1:AA:1367:C:O4'	2.48	0.47
1:AA:1103:C:H2'	1:AA:1104:G:O4'	2.14	0.47
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.30	0.47
2:AB:211:ILE:O	2:AB:215:LEU:HB2	2.14	0.47
3:AC:47:LEU:HD13	3:AC:68:VAL:HG11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:49:PRO:HG2	9:AI:81:ILE:HG23	1.96	0.47
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.50	0.47
9:AI:118:LYS:HG3	9:AI:121:ARG:HB3	1.97	0.47
20:AT:56:MET:HE1	20:AT:85:MET:HA	1.97	0.47
25:BA:7:G:H5"	33:BN:121:LYS:NZ	2.28	0.47
25:BA:192:C:O2'	25:BA:802:A:N3	2.47	0.47
25:BA:444:C:H4'	29:BF:49:ALA:HB2	1.96	0.47
25:BA:589:C:H2'	25:BA:590:A:C8	2.50	0.47
25:BA:2066:C:C2'	25:BA:2067:G:H5'	2.45	0.47
25:BA:2162:G:H5"	25:BA:2172:U:H2'	1.96	0.47
25:BA:2531:A:N7	31:BH:175:LYS:HD2	2.30	0.47
28:BE:25:VAL:HG22	28:BE:183:LEU:HD11	1.96	0.47
30:BG:145:THR:HB	30:BG:148:MET:HG3	1.97	0.47
31:BH:3:ARG:HD3	31:BH:54:ARG:HH12	1.79	0.47
32:BI:123:LEU:HA	32:BI:144:VAL:HG23	1.97	0.47
36:BQ:21:THR:OG1	36:BQ:99:PRO:O	2.32	0.47
44:BY:92:ASN:HB2	44:BY:94:LYS:N	2.28	0.47
45:BZ:72:ARG:HG2	45:BZ:72:ARG:HH11	1.80	0.47
48:B2:33:MET:HE3	48:B2:37:PHE:CZ	2.50	0.47
1:CA:176:C:H2'	1:CA:177:C:H6	1.79	0.47
1:CA:438:G:N1	1:CA:495:A:OP2	2.36	0.47
1:CA:503:C:C2'	1:CA:504:C:H5'	2.44	0.47
1:CA:1264:C:O2	1:CA:1272:G:N2	2.48	0.47
3:CC:32:LEU:O	3:CC:36:ASP:HB2	2.13	0.47
3:CC:179:ARG:O	3:CC:206:GLU:HB3	2.15	0.47
4:CD:19:LEU:HD13	4:CD:19:LEU:HA	1.72	0.47
5:CE:82:VAL:HG21	5:CE:138:ALA:HA	1.96	0.47
5:CE:139:LEU:HA	5:CE:142:LEU:HD12	1.97	0.47
17:CQ:59:ILE:HG22	17:CQ:73:VAL:HA	1.96	0.47
19:CS:37:ARG:O	19:CS:70:LYS:NZ	2.44	0.47
24:CX:10:G:N2	24:CX:26:G:H1'	2.30	0.47
25:DA:442:G:H4'	29:DF:46:ARG:HG3	1.96	0.47
25:DA:450:G:P	25:DA:1248:G:H22	2.38	0.47
25:DA:1188:U:H4'	41:DV:79:VAL:HG22	1.96	0.47
25:DA:1446:C:O2	25:DA:1545:A:O2'	2.32	0.47
25:DA:1448:G:O2'	25:DA:1528(A):A:N1	2.43	0.47
25:DA:2850:A:N7	25:DA:2868:A:O2'	2.37	0.47
26:DB:2:C:O2'	26:DB:3:C:H5'	2.14	0.47
26:DB:110:G:H2'	26:DB:111:G:H8	1.80	0.47
27:DD:111:LEU:HD22	27:DD:115:GLN:NE2	2.30	0.47
28:DE:143:ASN:HD22	28:DE:147:PRO:HD3	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DE:181:LEU:HD11	39:DT:6:LEU:HG	1.97	0.47
29:DF:116:ASP:O	29:DF:120:GLU:HG2	2.15	0.47
30:DG:138:GLN:HB3	30:DG:153:ARG:O	2.15	0.47
32:DI:66:GLU:OE2	32:DI:69:LYS:HD3	2.13	0.47
33:DN:67:LEU:O	33:DN:88:GLU:HG3	2.15	0.47
36:DQ:85:LYS:HG2	46:D0:7:LEU:HB3	1.96	0.47
54:D8:10:ALA:HB3	54:D8:62:LEU:HD21	1.97	0.47
1:AA:96:U:H2'	1:AA:97:G:C8	2.50	0.47
1:AA:431:A:H2'	1:AA:432:A:O4'	2.15	0.47
2:AB:180:LEU:C	2:AB:182:ILE:H	2.21	0.47
2:AB:210:SER:O	2:AB:214:ILE:HG12	2.15	0.47
4:AD:155:LEU:CD2	4:AD:157:LEU:H	2.28	0.47
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.15	0.47
14:AN:4:LYS:HA	14:AN:7:ILE:HG22	1.97	0.47
16:AP:52:ASP:CG	16:AP:55:ARG:HB2	2.40	0.47
25:BA:526:A:N3	25:BA:2044:C:H1'	2.30	0.47
25:BA:657:U:H2'	25:BA:658:C:H6	1.80	0.47
25:BA:1032:A:H2	25:BA:1122:G:H22	1.63	0.47
25:BA:1475:G:H2'	25:BA:1476:C:C6	2.50	0.47
25:BA:2729:G:H2'	25:BA:2730:C:O4'	2.14	0.47
36:BQ:23:GLY:O	36:BQ:101:ARG:NH1	2.48	0.47
50:B4:40:HIS:CE1	50:B4:42:PHE:HB3	2.50	0.47
52:B6:40:CYS:HA	52:B6:41:PRO:HD3	1.72	0.47
1:CA:444:C:H2'	1:CA:445:G:C8	2.50	0.47
1:CA:728:A:OP1	15:CO:54:ARG:NH1	2.48	0.47
1:CA:1028:C:O2	1:CA:1033:G:N1	2.48	0.47
1:CA:1187:G:H4'	9:CI:111:ARG:HH11	1.80	0.47
1:CA:1330:U:H2'	1:CA:1331:G:H5'	1.97	0.47
7:CG:144:MET:HE2	7:CG:144:MET:HA	1.96	0.47
15:CO:5:LYS:O	15:CO:9:GLN:HG2	2.15	0.47
25:DA:1027:A:N6	25:DA:1126:A:C4	2.83	0.47
25:DA:1608:A:H1'	25:DA:1610:A:OP2	2.14	0.47
25:DA:1688:U:H2'	25:DA:1698:A:N6	2.30	0.47
25:DA:2820:A:O2'	25:DA:2821:A:OP1	2.30	0.47
32:DI:72:LEU:HA	32:DI:75:LEU:HD23	1.97	0.47
47:D1:23:LYS:HB3	47:D1:29:GLY:HA3	1.97	0.47
47:D1:83:GLU:HA	47:D1:84:GLY:HA2	1.65	0.47
1:AA:539:A:H2'	1:AA:540:G:C8	2.50	0.47
1:AA:636:U:H2'	1:AA:637:G:C8	2.50	0.47
1:AA:1025:U:C2	1:AA:1036:G:O6	2.68	0.47
25:BA:570:G:H2'	25:BA:2030:A:C5	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:576:U:O5'	25:BA:576:U:H6	1.98	0.47
25:BA:829:A:N7	25:BA:2248:C:H5'	2.30	0.47
25:BA:889:C:H2'	25:BA:889:C:OP2	2.15	0.47
28:BE:34:VAL:HG21	28:BE:78:LEU:HD11	1.96	0.47
44:BY:5:MET:HG2	44:BY:30:VAL:HG11	1.97	0.47
1:CA:1252:A:H61	1:CA:1285:A:H61	1.61	0.47
2:CB:19:HIS:CE1	2:CB:206:ASP:HB2	2.50	0.47
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.47	0.47
25:DA:385:C:O2	35:DP:71:VAL:HG21	2.14	0.47
25:DA:1512:U:H2'	25:DA:1513:C:C6	2.50	0.47
25:DA:1537:G:H2'	25:DA:1538:G:C8	2.47	0.47
25:DA:2057:A:H2'	25:DA:2058:A:C8	2.50	0.47
25:DA:2156:G:H8	25:DA:2156:G:O5'	1.98	0.47
32:DI:12:LEU:HD22	32:DI:19:VAL:HG21	1.97	0.47
1:AA:580:U:H5"	15:AO:58:MET:HG2	1.96	0.47
1:AA:868:C:H2'	1:AA:869:G:O4'	2.14	0.47
1:AA:1005:A:N3	1:AA:1036:G:N2	2.62	0.47
2:AB:231:GLU:HB2	2:AB:232:PRO:CD	2.38	0.47
19:AS:19:VAL:HG21	19:AS:44:MET:HG2	1.96	0.47
25:BA:218:A:C2	25:BA:235:U:H4'	2.50	0.47
25:BA:1607:C:H5"	25:BA:1608:A:H5'	1.97	0.47
25:BA:1643:G:H2'	25:BA:1644:C:O4'	2.14	0.47
25:BA:2291:U:H2'	25:BA:2292:C:C6	2.50	0.47
25:BA:2740:A:H2'	25:BA:2741:A:C8	2.50	0.47
34:BO:4:PRO:O	34:BO:5:GLN:HB2	2.15	0.47
49:B3:19:GLN:OE1	49:B3:52:HIS:NE2	2.39	0.47
52:B6:39:TYR:HA	52:B6:46:HIS:HA	1.97	0.47
3:CC:82:GLU:HG2	3:CC:85:ARG:NH2	2.28	0.47
5:CE:94:ALA:HB2	5:CE:119:LEU:HG	1.98	0.47
25:DA:335:C:H4'	44:DY:73:ARG:HD3	1.97	0.47
25:DA:571:A:N6	25:DA:2499:C:O3'	2.48	0.47
25:DA:1983:C:H2'	25:DA:1984:G:H5"	1.96	0.47
25:DA:2138:C:H42	25:DA:2153:G:H1	1.62	0.47
30:DG:82:LEU:HA	30:DG:86:MET:SD	2.55	0.47
33:DN:91:LEU:HG	33:DN:98:VAL:HG21	1.97	0.47
45:DZ:54:HIS:HB3	45:DZ:101:PRO:HD3	1.97	0.47
1:AA:438:G:N1	1:AA:495:A:OP2	2.27	0.46
1:AA:798:G:OP1	11:AK:122:LYS:NZ	2.46	0.46
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.50	0.46
13:AM:83:ASP:HA	25:BA:888:C:O2	2.15	0.46
25:BA:271(L):U:OP1	32:BI:50:ARG:NH1	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1429:G:H2'	25:BA:1430:C:C6	2.51	0.46
25:BA:1641:A:H2'	25:BA:1642:G:O4'	2.16	0.46
25:BA:2850:A:OP2	25:BA:2866:U:H5	1.98	0.46
28:BE:144:ARG:HB3	28:BE:145:LYS:H	1.50	0.46
31:BH:149:ARG:NH1	31:BH:167:GLU:OE2	2.42	0.46
48:B2:36:ARG:O	48:B2:40:SER:N	2.40	0.46
1:CA:472:A:H5"	16:CP:80:PHE:HB3	1.97	0.46
1:CA:952:U:H2'	1:CA:953:G:C8	2.50	0.46
1:CA:1028:C:C2	1:CA:1033:G:N1	2.83	0.46
1:CA:1122:U:C4	1:CA:1123:A:N7	2.84	0.46
1:CA:1144:G:N2	1:CA:1146:A:H62	2.13	0.46
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.15	0.46
2:CB:207:ALA:HB3	2:CB:210:SER:HB2	1.97	0.46
4:CD:150:GLU:OE2	4:CD:151:LYS:N	2.49	0.46
13:CM:16:ASP:HB3	13:CM:34:LEU:HD11	1.96	0.46
13:CM:90:LEU:HA	13:CM:93:ARG:HG3	1.98	0.46
21:CU:7:ARG:NH1	21:CU:21:TYR:OH	2.48	0.46
25:DA:479:A:H1'	25:DA:481:G:H5"	1.96	0.46
25:DA:839:U:H2'	25:DA:840:C:H6	1.80	0.46
25:DA:1493:C:C5	25:DA:2206:G:H2'	2.50	0.46
25:DA:2206:G:H3'	25:DA:2207:G:H8	1.78	0.46
25:DA:2302:G:C2'	25:DA:2303:G:H5'	2.44	0.46
25:DA:2769:C:H2'	25:DA:2770:G:O4'	2.15	0.46
25:DA:2838:G:C6	25:DA:2839:G:C5	3.03	0.46
26:DB:50:G:OP2	38:DS:62:LYS:HB2	2.14	0.46
29:DF:37:VAL:O	29:DF:41:LEU:HG	2.15	0.46
32:DI:40:THR:HG23	32:DI:43:ASN:HD21	1.79	0.46
45:DZ:121:HIS:HB3	45:DZ:123:ASP:O	2.15	0.46
1:AA:643:C:H2'	1:AA:644:G:H8	1.79	0.46
1:AA:1097:C:O2	1:AA:1169:A:H2	1.98	0.46
2:AB:101:MET:HA	2:AB:108:ILE:HD12	1.95	0.46
4:AD:102:ASP:OD1	4:AD:103:ASN:N	2.48	0.46
20:AT:64:ASP:OD2	20:AT:81:LYS:NZ	2.43	0.46
25:BA:2179:C:H2'	25:BA:2180:U:C6	2.49	0.46
25:BA:2335:A:O2'	25:BA:2336:A:OP2	2.26	0.46
25:BA:2431:U:O2'	25:BA:2433:A:N7	2.46	0.46
25:BA:2467:C:H4'	36:BQ:123:HIS:CD2	2.51	0.46
27:BD:221:VAL:HG22	27:BD:226:MET:HE2	1.97	0.46
31:BH:69:ARG:HG3	31:BH:70:THR:N	2.30	0.46
39:BT:33:LYS:HB3	39:BT:82:LEU:HD23	1.96	0.46
39:BT:53:ARG:NH1	39:BT:60:THR:OG1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BT:112:ARG:HG3	39:BT:115:ARG:HH21	1.80	0.46
45:BZ:145:GLU:O	45:BZ:148:ASP:N	2.48	0.46
1:CA:598:U:H4'	8:CH:94:TYR:CD2	2.50	0.46
1:CA:664:G:H22	1:CA:741:G:H1	1.62	0.46
1:CA:877:C:O2	8:CH:3:THR:OG1	2.32	0.46
1:CA:1344:C:H5'	9:CI:121:ARG:HA	1.98	0.46
1:CA:1431:C:H42	1:CA:1469:G:H1	1.63	0.46
5:CE:71:LEU:HD11	5:CE:115:VAL:HG22	1.96	0.46
11:CK:85:ARG:HG2	11:CK:112:THR:HA	1.97	0.46
25:DA:817:C:O2'	25:DA:839:U:H5"	2.14	0.46
25:DA:902:C:H2'	25:DA:903:C:C6	2.50	0.46
25:DA:995:C:O2	33:DN:3:THR:OG1	2.24	0.46
25:DA:1938:A:N3	25:DA:2605:U:O2'	2.44	0.46
27:DD:2:ALA:HB3	27:DD:20:ASP:HB3	1.97	0.46
38:DS:7:TYR:CE2	38:DS:11:LYS:HE2	2.51	0.46
44:DY:102:CYS:SG	44:DY:104:GLY:N	2.78	0.46
45:DZ:108:PRO:HB3	45:DZ:144:LEU:HD12	1.97	0.46
50:D4:26:SER:OG	50:D4:27:THR:N	2.46	0.46
1:AA:107:G:H2'	1:AA:108:G:O4'	2.15	0.46
1:AA:278:G:C2	17:AQ:95:TYR:HD2	2.33	0.46
1:AA:429:U:H1'	1:AA:430:A:H5"	1.97	0.46
1:AA:430:A:OP2	4:AD:8:VAL:HG12	2.15	0.46
1:AA:1060:C:N4	3:AC:2:GLY:HA3	2.30	0.46
3:AC:114:PRO:HD3	3:AC:183:ASP:OD1	2.16	0.46
25:BA:969:U:H2'	25:BA:970:C:C6	2.50	0.46
33:BN:42:TRP:HD1	33:BN:48:MET:HE1	1.80	0.46
36:BQ:54:MET:HE2	36:BQ:54:MET:HB2	1.83	0.46
38:BS:15:ARG:O	38:BS:19:LYS:HG2	2.15	0.46
1:CA:193:C:H2'	1:CA:194:C:C6	2.51	0.46
1:CA:601:C:H2'	1:CA:602:A:C8	2.50	0.46
1:CA:673:G:H2'	1:CA:674:G:C8	2.49	0.46
1:CA:689:C:H42	1:CA:698:G:H1	1.62	0.46
1:CA:1185:G:C2	1:CA:1186:G:H1'	2.50	0.46
1:CA:1530:G:OP1	1:CA:1530:G:H4'	2.14	0.46
2:CB:8:LYS:HE2	2:CB:51:LEU:HD13	1.96	0.46
3:CC:45:LYS:H	3:CC:45:LYS:HE3	1.79	0.46
9:CI:23:ASN:HD22	9:CI:25:LYS:H	1.61	0.46
25:DA:415:A:H2'	25:DA:416:C:H6	1.80	0.46
25:DA:467:G:OP1	53:D7:33:ARG:NH1	2.48	0.46
25:DA:664:C:OP2	60:DA:4171:HOH:O	2.20	0.46
26:DB:90:A:N7	26:DB:91:C:H1'	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DS:28:VAL:HG11	38:DS:98:VAL:HG13	1.98	0.46
1:AA:222:U:H2'	1:AA:223:U:C6	2.50	0.46
1:AA:384:G:H2'	1:AA:385:C:C6	2.50	0.46
1:AA:958:A:C6	19:AS:55:LYS:HB2	2.51	0.46
1:AA:1414:U:H3	1:AA:1486:G:H1	1.64	0.46
20:AT:45:GLN:HE21	20:AT:45:GLN:HB3	1.54	0.46
25:BA:459:U:H5"	53:B7:40:TRP:CD2	2.50	0.46
25:BA:1675:C:N3	28:BE:128:SER:OG	2.49	0.46
38:BS:62:LYS:HB3	38:BS:97:ARG:NE	2.31	0.46
43:BX:65:ARG:HH11	43:BX:70:LEU:HD21	1.79	0.46
45:BZ:28:MET:HE1	45:BZ:61:LEU:HD21	1.98	0.46
1:CA:176:C:H2'	1:CA:177:C:C6	2.50	0.46
1:CA:922:G:H2'	1:CA:923:A:C8	2.50	0.46
1:CA:1469:G:H2'	1:CA:1470:G:C8	2.50	0.46
1:CA:1502:A:H2	1:CA:1505:G:H1	1.63	0.46
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.51	0.46
4:CD:61:LYS:HZ1	4:CD:72:GLU:CD	2.22	0.46
9:CI:37:PHE:HB3	9:CI:43:ALA:CB	2.45	0.46
9:CI:70:LYS:O	9:CI:74:ILE:HG13	2.16	0.46
25:DA:528:A:H2	25:DA:2042:A:H2'	1.79	0.46
25:DA:1336:A:H2'	25:DA:1337:G:H8	1.81	0.46
25:DA:2392:A:N3	35:DP:61:ARG:HG2	2.31	0.46
25:DA:2630:G:H1	25:DA:2788:C:H42	1.63	0.46
33:DN:123:TYR:CE2	33:DN:129:PRO:HD2	2.51	0.46
34:DO:1:MET:HG3	34:DO:67:LYS:HG2	1.96	0.46
36:DQ:22:LYS:N	36:DQ:22:LYS:HE2	2.31	0.46
38:DS:15:ARG:HE	38:DS:88:ASP:CG	2.23	0.46
47:D1:53:VAL:HG22	47:D1:74:VAL:HG13	1.97	0.46
49:D3:5:LYS:HE3	49:D3:57:GLU:CD	2.39	0.46
2:AB:24:TRP:CZ3	2:AB:26:PRO:HA	2.50	0.46
3:AC:64:VAL:HG22	3:AC:66:VAL:HG23	1.96	0.46
12:AL:52:LEU:O	12:AL:54:LYS:NZ	2.47	0.46
12:AL:116:SER:OG	60:AL:303:HOH:O	2.21	0.46
25:BA:1204:A:H61	25:BA:1240:U:H2'	1.80	0.46
25:BA:1448:G:H1'	25:BA:1528:A:N1	2.31	0.46
25:BA:2438:U:O2'	25:BA:2440:C:OP1	2.29	0.46
26:BB:13:A:N1	26:BB:69:G:O2'	2.45	0.46
43:BX:54:VAL:HG22	43:BX:81:VAL:HG12	1.96	0.46
54:B8:33:ASN:HA	54:B8:36:LYS:HD2	1.97	0.46
1:CA:540:G:H2'	1:CA:541:G:H8	1.80	0.46
1:CA:659:U:H2'	1:CA:660:G:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1227:A:H8	1:CA:1227:A:H3'	1.80	0.46
1:CA:1247:U:H1'	1:CA:1291:G:N2	2.30	0.46
1:CA:1298:C:H4'	1:CA:1299:A:C4	2.50	0.46
3:CC:116:VAL:HG22	3:CC:140:ARG:HH22	1.81	0.46
11:CK:20:TYR:CZ	11:CK:83:ILE:HD12	2.51	0.46
12:CL:109:GLY:HA3	12:CL:121:GLY:O	2.15	0.46
19:CS:50:ALA:HA	19:CS:58:VAL:O	2.15	0.46
25:DA:1230:C:H2'	25:DA:1231:G:H8	1.80	0.46
25:DA:2809:A:H2'	25:DA:2810:A:C8	2.51	0.46
27:DD:164:GLN:NE2	27:DD:176:ARG:HH12	2.14	0.46
42:DW:86:LEU:HD22	42:DW:96:ILE:HD11	1.98	0.46
45:DZ:69:THR:HG22	45:DZ:90:VAL:HA	1.98	0.46
52:D6:35:GLU:HA	52:D6:49:HIS:O	2.16	0.46
1:AA:98:G:H2'	1:AA:99:U:O4'	2.16	0.46
1:AA:189(A):C:N4	1:AA:189(J):G:H1	2.14	0.46
1:AA:858:G:O6	1:AA:869:G:H3'	2.16	0.46
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.04	0.46
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.50	0.46
1:AA:1318:A:OP1	19:AS:7:LYS:NZ	2.29	0.46
1:AA:1452:C:O2'	1:AA:1456:G:H5"	2.16	0.46
6:AF:11:ASN:HB3	6:AF:14:LEU:HG	1.98	0.46
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.16	0.46
25:BA:143(A):C:H2'	25:BA:144:C:H6	1.80	0.46
25:BA:2633:G:H2'	25:BA:2634:G:O4'	2.16	0.46
27:BD:275:LYS:HB3	27:BD:276:LYS:H	1.37	0.46
28:BE:105:THR:HG21	28:BE:164:ARG:CZ	2.45	0.46
44:BY:9:LYS:HA	44:BY:10:GLY:HA2	1.60	0.46
45:BZ:161:VAL:HG13	45:BZ:161:VAL:O	2.16	0.46
8:CH:29:SER:HB3	8:CH:32:LYS:HG3	1.96	0.46
14:CN:26:ARG:HB3	14:CN:43:CYS:SG	2.55	0.46
25:DA:1811:G:H2'	25:DA:1812:A:O4'	2.16	0.46
25:DA:2312:U:H4'	30:DG:71:THR:HB	1.96	0.46
25:DA:2382:G:H21	54:D8:42:ARG:NH2	2.13	0.46
25:DA:2682:U:H5'	28:DE:11:MET:O	2.16	0.46
25:DA:2712:U:H2'	25:DA:2714:G:H5"	1.97	0.46
25:DA:2850:A:H2'	25:DA:2851:A:C8	2.50	0.46
27:DD:133:LEU:HD12	27:DD:189:CYS:HB2	1.98	0.46
50:D4:53:GLU:HG2	50:D4:54:GLY:N	2.31	0.46
1:AA:255:G:C6	1:AA:256:U:C4	3.03	0.46
5:AE:51:VAL:O	5:AE:55:VAL:HG23	2.16	0.46
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:19:LEU:HA	13:AM:22:ILE:HD12	1.98	0.46
25:BA:84:A:P	44:BY:8:LYS:HD2	2.55	0.46
25:BA:222:A:H5"	25:BA:421:U:OP1	2.16	0.46
25:BA:848:G:O6	25:BA:928:G:H2'	2.16	0.46
25:BA:2376:A:N3	38:BS:106:ARG:NH2	2.61	0.46
32:BI:1:MET:N	32:BI:21:VAL:O	2.33	0.46
1:CA:707:C:H2'	1:CA:708:C:C6	2.50	0.46
1:CA:1003:G:H2'	1:CA:1004:A:H1'	1.97	0.46
2:CB:16:HIS:O	2:CB:17:PHE:HD1	1.98	0.46
2:CB:54:THR:O	2:CB:57:PHE:HB3	2.15	0.46
4:CD:173:TRP:HB3	4:CD:187:ARG:HE	1.81	0.46
8:CH:46:LYS:HG2	8:CH:64:LYS:HE2	1.97	0.46
9:CI:78:LYS:HE2	9:CI:101:PHE:CD2	2.51	0.46
9:CI:89:ASN:O	9:CI:92:TYR:HB2	2.16	0.46
15:CO:69:TYR:CZ	15:CO:73:GLU:HG3	2.51	0.46
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.97	0.46
25:DA:952:G:P	36:DQ:16:ARG:HH22	2.38	0.46
25:DA:991:C:H42	25:DA:1163:G:H1	1.63	0.46
25:DA:1301:A:H2	25:DA:1626:G:N3	2.13	0.46
25:DA:1472:A:H2'	25:DA:1473:G:O4'	2.16	0.46
25:DA:1619:G:N7	60:DA:4281:HOH:O	2.36	0.46
25:DA:1697:G:OP2	25:DA:1698:A:O2'	2.28	0.46
25:DA:2126:A:H4'	25:DA:2127:G:OP1	2.15	0.46
30:DG:96:ARG:O	30:DG:99:MET:HB3	2.15	0.46
49:D3:10:LYS:HG2	60:D3:4001:HOH:O	2.15	0.46
1:AA:347:G:O2'	1:AA:348:G:OP1	2.33	0.46
1:AA:1296:C:H5"	13:AM:14:ARG:HD2	1.96	0.46
25:BA:1170:G:C2	25:BA:1171:G:H1'	2.50	0.46
25:BA:1270:C:O2'	25:BA:1648:C:OP2	2.30	0.46
25:BA:1774:C:O5'	25:BA:1774:C:H6	1.99	0.46
25:BA:2103:C:N4	25:BA:2186:G:H1	2.10	0.46
1:CA:405:U:P	4:CD:3:ARG:NH2	2.89	0.46
1:CA:720:C:H2'	1:CA:721:G:C8	2.51	0.46
1:CA:1126:U:H4'	1:CA:1281:U:H1'	1.97	0.46
1:CA:1352:C:OP1	21:CU:3:LYS:NZ	2.39	0.46
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.51	0.46
1:CA:1496:C:H4'	25:DA:1920:C:O2'	2.16	0.46
2:CB:125:PRO:HB2	2:CB:126:GLU:H	1.56	0.46
8:CH:78:GLN:HG2	8:CH:80:ILE:O	2.16	0.46
25:DA:78:A:H2'	25:DA:79:G:H8	1.80	0.46
25:DA:431:U:H6	25:DA:431:U:O5'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:875:G:O2'	45:DZ:151:HIS:HE1	1.99	0.46
25:DA:1269:A:H2'	25:DA:1270:C:C6	2.51	0.46
25:DA:1344:G:O2'	25:DA:1385:G:H2'	2.16	0.46
26:DB:73:A:C4	26:DB:105:A:C2	3.04	0.46
31:DH:89:ILE:O	31:DH:129:THR:HG23	2.16	0.46
37:DR:95:THR:HG22	37:DR:116:LEU:HD23	1.98	0.46
45:DZ:119:GLU:HB2	45:DZ:122:ARG:NH1	2.29	0.46
1:AA:358:U:H2'	1:AA:359:U:H6	1.81	0.46
1:AA:626:U:H2'	1:AA:627:G:C8	2.51	0.46
1:AA:924:C:H2'	1:AA:925:G:H8	1.81	0.46
1:AA:946:A:O2'	1:AA:1333:A:N3	2.40	0.46
1:AA:1006:C:H42	1:AA:1023:G:H1	1.64	0.46
1:AA:1089:G:H1	1:AA:1096:C:N4	2.14	0.46
3:AC:156:ARG:H	3:AC:196:LEU:HD22	1.81	0.46
13:AM:16:ASP:N	13:AM:16:ASP:OD1	2.49	0.46
25:BA:185:U:H4'	25:BA:218:A:H4'	1.97	0.46
25:BA:1496:A:N3	25:BA:1577:C:O2'	2.35	0.46
25:BA:1882:C:H2'	25:BA:1883:G:O4'	2.15	0.46
25:BA:2055:C:O2	60:BA:4028:HOH:O	2.21	0.46
37:BR:44:LEU:HD22	37:BR:48:VAL:HG23	1.98	0.46
44:BY:43:ASN:HD22	44:BY:43:ASN:HA	1.55	0.46
44:BY:56:PRO:C	44:BY:58:GLY:H	2.24	0.46
50:B4:49:PHE:HB3	50:B4:50:VAL:H	1.53	0.46
54:B8:62:LEU:HB3	54:B8:65:GLU:CG	2.41	0.46
1:CA:581:G:N2	1:CA:759:A:OP2	2.41	0.46
1:CA:608:A:H4'	16:CP:32:TYR:OH	2.15	0.46
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.49	0.46
1:CA:1095:U:C4	1:CA:1096:C:C4	3.04	0.46
1:CA:1119:C:N3	1:CA:1154:G:O6	2.48	0.46
1:CA:1237:C:H5"	1:CA:1238:A:O4'	2.16	0.46
1:CA:1367:C:O2'	10:CJ:48:THR:OG1	2.34	0.46
7:CG:153:HIS:HE1	11:CK:57:THR:HG22	1.81	0.46
9:CI:15:ALA:HB2	9:CI:65:VAL:HG23	1.97	0.46
10:CJ:16:LEU:HD13	10:CJ:70:ARG:HG2	1.97	0.46
25:DA:796:C:H2'	25:DA:797:C:C6	2.51	0.46
25:DA:924:C:H2'	25:DA:925:C:C6	2.51	0.46
25:DA:1803:A:N1	25:DA:1822:G:O2'	2.47	0.46
25:DA:2037:G:O2'	25:DA:2038:G:H5'	2.16	0.46
25:DA:2165:G:H2'	25:DA:2166:G:C8	2.51	0.46
25:DA:2330:G:H2'	25:DA:2331:G:O4'	2.16	0.46
25:DA:2412:A:H2'	25:DA:2413:G:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2747:G:H1'	25:DA:2757:A:H61	1.81	0.46
25:DA:2773:C:H2'	25:DA:2774:C:H6	1.81	0.46
25:DA:2889:C:H3'	25:DA:2891:G:C8	2.51	0.46
32:DI:114:LEU:HD11	32:DI:128:LEU:HB3	1.98	0.46
33:DN:10:GLU:HA	33:DN:11:PRO:HD2	1.70	0.46
46:D0:24:LYS:HE2	46:D0:24:LYS:HA	1.97	0.46
1:AA:126:G:H4'	1:AA:634:C:O2	2.16	0.46
1:AA:266:G:O3'	17:AQ:67:LYS:HB2	2.16	0.46
1:AA:826:C:H2'	1:AA:827:U:H6	1.81	0.46
1:AA:999:C:H2'	1:AA:1000:U:O4'	2.15	0.46
1:AA:1445:C:N4	1:AA:1457:G:H1	2.14	0.46
1:AA:1515:C:H2'	1:AA:1516:G:C8	2.51	0.46
25:BA:848:G:C4	25:BA:933:A:H8	2.34	0.46
25:BA:1227:G:OP1	40:BU:13:LYS:HE3	2.16	0.46
25:BA:1359:A:N3	25:BA:1359:A:H5'	2.31	0.46
25:BA:1759:A:H1'	25:BA:2711:A:C2	2.51	0.46
25:BA:2238:G:H2'	25:BA:2238:G:N3	2.31	0.46
30:BG:179:PRO:HB2	50:B4:42:PHE:HE1	1.80	0.46
37:BR:26:LYS:HE2	37:BR:70:LEU:O	2.16	0.46
51:B5:11:THR:HG23	51:B5:15:ARG:HB3	1.96	0.46
1:CA:145:G:H1	1:CA:177:C:H42	1.63	0.46
1:CA:926:G:N2	22:CV:16:A:OP1	2.48	0.46
1:CA:1203:C:H2'	1:CA:1204:A:O4'	2.15	0.46
2:CB:120:ALA:C	2:CB:122:PHE:N	2.73	0.46
3:CC:38:ARG:O	3:CC:42:LEU:N	2.39	0.46
5:CE:68:GLU:HG3	5:CE:70:PRO:HD3	1.98	0.46
6:CF:67:MET:HE1	6:CF:75:LEU:HG	1.97	0.46
16:CP:4:ILE:HG13	16:CP:64:ALA:HB1	1.97	0.46
19:CS:32:LYS:HE2	19:CS:57:HIS:CD2	2.51	0.46
25:DA:251:A:C5	25:DA:252:G:H1'	2.51	0.46
25:DA:1319:G:C6	25:DA:1320:C:N4	2.84	0.46
25:DA:1587:A:H2'	25:DA:1588:C:C6	2.51	0.46
25:DA:1630:G:H2'	25:DA:1631:C:C6	2.51	0.46
25:DA:2349:G:OP1	60:DA:4065:HOH:O	2.21	0.46
25:DA:2615:U:N1	51:D5:7:PRO:HA	2.31	0.46
26:DB:27:C:O3'	38:DS:36:TYR:OH	2.33	0.46
28:DE:6:GLY:HA2	28:DE:28:ALA:HA	1.98	0.46
31:DH:46:GLU:HB2	31:DH:49:VAL:HG12	1.97	0.46
36:DQ:75:THR:HG21	36:DQ:87:LYS:NZ	2.31	0.46
54:D8:32:LEU:O	54:D8:36:LYS:HE3	2.16	0.46
1:AA:283:C:H2'	1:AA:284:G:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:757:U:H2'	1:AA:758:G:O4'	2.15	0.45
1:AA:978:A:O2'	1:AA:1322:C:N3	2.49	0.45
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.16	0.45
1:AA:1216:G:H5"	14:AN:5:ALA:CB	2.46	0.45
4:AD:164:ALA:O	4:AD:168:ARG:NH1	2.46	0.45
7:AG:26:PHE:CE2	7:AG:30:ILE:HD11	2.51	0.45
16:AP:38:TYR:CZ	16:AP:50:LYS:HB2	2.52	0.45
20:AT:16:HIS:O	20:AT:19:SER:OG	2.32	0.45
25:BA:271(A):A:H61	25:BA:271(X):G:H1'	1.81	0.45
25:BA:1203:G:O2'	25:BA:1242:A:N6	2.44	0.45
25:BA:1287:A:N1	25:BA:1648:C:O2'	2.47	0.45
25:BA:1680:U:H2'	25:BA:1681:G:O4'	2.16	0.45
25:BA:2275:C:O2	36:BQ:85:LYS:HG3	2.17	0.45
28:BE:115:GLY:O	28:BE:119:ARG:HB2	2.17	0.45
30:BG:27:ASN:HB3	30:BG:30:GLU:HB2	1.98	0.45
36:BQ:43:THR:HG22	36:BQ:94:VAL:HG12	1.99	0.45
39:BT:19:LEU:HD12	39:BT:78:LEU:HD13	1.97	0.45
50:B4:59:PHE:HB2	50:B4:62:ARG:HH12	1.82	0.45
1:CA:109:A:H2'	1:CA:326:G:N2	2.31	0.45
1:CA:407:G:OP1	4:CD:115:ARG:NH2	2.49	0.45
1:CA:1024:G:C2'	1:CA:1025:U:H5"	2.45	0.45
1:CA:1100:C:H2'	1:CA:1102:A:O5'	2.16	0.45
3:CC:47:LEU:CB	3:CC:52:LEU:HB2	2.46	0.45
25:DA:506:G:O3'	25:DA:507:A:H8	1.99	0.45
25:DA:637:A:H2'	35:DP:117:GLU:OE2	2.16	0.45
25:DA:2134:A:H3'	25:DA:2135:A:C8	2.51	0.45
25:DA:2206:G:OP2	25:DA:2206:G:H4'	2.16	0.45
25:DA:2774:C:H2'	25:DA:2775:A:O4'	2.16	0.45
25:DA:2776:A:H4'	25:DA:2777:G:H5"	1.97	0.45
25:DA:2849:U:P	39:DT:95:ARG:HH12	2.39	0.45
25:DA:2886:G:H2'	25:DA:2887:U:C6	2.51	0.45
34:DO:75:SER:OG	39:DT:74:ARG:NH1	2.49	0.45
35:DP:52:GLU:HG2	54:D8:57:ARG:HH12	1.81	0.45
45:DZ:99:TYR:HA	45:DZ:124:ILE:O	2.16	0.45
54:D8:6:THR:HG22	54:D8:63:PRO:HD2	1.97	0.45
1:AA:147:G:C4	1:AA:148:G:C8	3.04	0.45
1:AA:651:C:N4	1:AA:652:U:O4	2.49	0.45
1:AA:920:U:H2'	1:AA:921:U:C6	2.50	0.45
1:AA:1151:A:N3	10:AJ:39:PRO:HG3	2.31	0.45
1:AA:1241:G:H1	1:AA:1296:C:N4	2.14	0.45
1:AA:1295:G:H2'	1:AA:1296:C:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:173:TRP:CD1	4:AD:173:TRP:H	2.33	0.45
6:AF:100:ASN:HB2	18:AR:28:GLU:HA	1.98	0.45
22:AV:19:U:H2'	22:AV:20:U:C6	2.51	0.45
25:BA:278:A:H2'	25:BA:279:C:C6	2.51	0.45
25:BA:848:G:N3	25:BA:933:A:H1'	2.31	0.45
25:BA:2695:C:H2'	25:BA:2696:U:H6	1.81	0.45
25:BA:2712:U:H2'	25:BA:2714:G:H5"	1.99	0.45
25:BA:2771:C:H2'	25:BA:2772:C:C6	2.51	0.45
35:BP:100:LEU:HD12	35:BP:112:LEU:HD11	1.98	0.45
37:BR:38:VAL:HG12	37:BR:42:LYS:HE3	1.98	0.45
39:BT:37:GLY:HA2	39:BT:38:ASN:HA	1.72	0.45
46:B0:38:VAL:HG12	46:B0:40:GLN:HG2	1.99	0.45
51:B5:9:LYS:HD3	51:B5:9:LYS:HA	1.70	0.45
1:CA:144:G:H1	1:CA:178:C:H42	1.64	0.45
1:CA:1154:G:N7	1:CA:1155:G:C5	2.84	0.45
3:CC:110:ASN:O	3:CC:141:VAL:HG22	2.16	0.45
14:CN:32:SER:O	14:CN:32:SER:OG	2.24	0.45
25:DA:695:G:H2'	25:DA:696:G:O4'	2.17	0.45
25:DA:1151:G:O2'	40:DU:77:SER:O	2.34	0.45
25:DA:1263:U:H1'	51:D5:10:LYS:HG3	1.99	0.45
25:DA:2017:U:O2	51:D5:10:LYS:HB2	2.15	0.45
25:DA:2023:G:H1	25:DA:2040:C:H42	1.64	0.45
25:DA:2137:C:N4	25:DA:2154:G:N1	2.47	0.45
29:DF:18:ARG:HG2	29:DF:19:GLU:H	1.81	0.45
30:DG:161:THR:HG22	30:DG:163:ALA:H	1.81	0.45
35:DP:38:GLN:O	35:DP:39:LYS:HB3	2.16	0.45
36:DQ:85:LYS:HD3	36:DQ:85:LYS:N	2.31	0.45
44:DY:5:MET:HE2	44:DY:5:MET:HB2	1.70	0.45
45:DZ:59:LEU:HD12	45:DZ:69:THR:HG21	1.97	0.45
53:D7:8:ASN:OD1	53:D7:11:LYS:N	2.26	0.45
55:D9:29:ASN:HB3	55:D9:32:HIS:ND1	2.30	0.45
1:AA:1024:G:H2'	1:AA:1025:U:H5'	1.98	0.45
4:AD:128:VAL:HG11	4:AD:138:TYR:CE2	2.51	0.45
13:AM:11:ARG:HA	13:AM:45:VAL:HB	1.98	0.45
24:AX:76:31H:H5"	60:BA:3701:HOH:O	2.17	0.45
25:BA:11:G:H2'	25:BA:12:U:H5'	1.97	0.45
25:BA:336:C:H2'	25:BA:337:C:H6	1.81	0.45
25:BA:910:A:N3	25:BA:2264:C:O2'	2.41	0.45
25:BA:1341:U:OP2	25:BA:1394:U:O2'	2.27	0.45
25:BA:1507:A:O2'	25:BA:1508:A:O5'	2.33	0.45
25:BA:1557:C:OP2	25:BA:1558:A:O2'	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2053:G:OP1	28:BE:144:ARG:HG2	2.17	0.45
25:BA:2626:C:H2'	25:BA:2627:G:O4'	2.16	0.45
25:BA:2774:C:H2'	25:BA:2775:A:O4'	2.15	0.45
42:BW:1:MET:HE2	42:BW:62:HIS:HB3	1.98	0.45
45:BZ:98:MET:HE2	45:BZ:98:MET:HB2	1.71	0.45
1:CA:1030(C):G:H2'	1:CA:1030(D):A:C8	2.51	0.45
1:CA:1095:U:P	1:CA:1108:G:H1	2.38	0.45
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	1.97	0.45
1:CA:1394:A:N6	1:CA:1501:C:H5'	2.31	0.45
4:CD:170:VAL:HG22	4:CD:171:GLY:H	1.82	0.45
25:DA:589:C:H2'	25:DA:590:A:H8	1.79	0.45
25:DA:607:U:OP1	29:DF:102:PRO:HA	2.16	0.45
25:DA:1925:C:H2'	25:DA:1926:U:H5"	1.98	0.45
25:DA:1978:A:H2'	25:DA:1979:C:H6	1.81	0.45
25:DA:2166:G:H3'	25:DA:2167:U:C5'	2.40	0.45
26:DB:30:C:H2'	26:DB:31:C:H5'	1.97	0.45
26:DB:43:C:C4	26:DB:45:A:N6	2.84	0.45
28:DE:144:ARG:HB3	28:DE:145:LYS:H	1.46	0.45
29:DF:192:LEU:HD13	29:DF:194:MET:HE2	1.98	0.45
32:DI:48:GLU:HG3	32:DI:52:ARG:NH1	2.32	0.45
32:DI:77:LEU:HG	32:DI:101:LEU:HD12	1.99	0.45
43:DX:43:VAL:HG21	43:DX:81:VAL:HG11	1.97	0.45
45:DZ:77:ASP:HA	45:DZ:84:GLU:OE2	2.16	0.45
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.52	0.45
1:AA:988:G:H1	1:AA:1217:C:N4	2.13	0.45
1:AA:1321:C:O2'	19:AS:78:ARG:NH1	2.49	0.45
4:AD:201:GLN:NE2	4:AD:204:ILE:HD12	2.31	0.45
25:BA:580:C:H2'	25:BA:581:C:C6	2.51	0.45
25:BA:2347:C:H2'	25:BA:2348:U:C6	2.52	0.45
25:BA:2747:G:O6	25:BA:2755:C:H5"	2.16	0.45
27:BD:215:LEU:HB2	27:BD:217:ARG:HG3	1.98	0.45
43:BX:94:GLY:N	43:BX:95:LEU:HA	2.31	0.45
52:B6:35:GLU:HG2	52:B6:50:ARG:HD3	1.99	0.45
1:CA:189(C):C:H2'	1:CA:189(D):C:O4'	2.16	0.45
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.82	0.45
1:CA:608:A:H4'	16:CP:32:TYR:HH	1.81	0.45
1:CA:827:U:H5"	1:CA:828:A:OP2	2.16	0.45
1:CA:1011:G:C6	1:CA:1012:U:C2	3.05	0.45
6:CF:100:ASN:ND2	18:CR:23:LYS:HE2	2.31	0.45
8:CH:119:LEU:HB3	8:CH:123:GLU:HB2	1.99	0.45
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:774:A:N3	25:DA:774:A:H2'	2.31	0.45
25:DA:855:G:C6	25:DA:856:C:N4	2.84	0.45
25:DA:1405:U:H2'	25:DA:1406:U:C6	2.51	0.45
25:DA:1877:A:H5'	25:DA:1878:G:OP2	2.17	0.45
28:DE:48:GLN:HG3	28:DE:80:GLU:HG2	1.98	0.45
29:DF:101:LEU:O	29:DF:106:ARG:NH1	2.45	0.45
30:DG:106:LEU:HA	30:DG:110:ALA:HB3	1.99	0.45
31:DH:124:GLU:OE1	31:DH:132:ARG:HB3	2.16	0.45
45:DZ:10:ARG:HG3	45:DZ:36:LYS:HB3	1.97	0.45
1:AA:347:G:O2'	1:AA:348:G:P	2.74	0.45
1:AA:955:U:OP1	13:AM:120:LYS:HD2	2.17	0.45
1:AA:1124:G:N7	1:AA:1145:C:O2'	2.47	0.45
1:AA:1246:C:N3	1:AA:1291:G:N2	2.51	0.45
3:AC:181:ASN:C	3:AC:181:ASN:HD22	2.24	0.45
4:AD:158:ILE:HG12	4:AD:159:ARG:N	2.31	0.45
4:AD:173:TRP:HA	4:AD:187:ARG:NE	2.31	0.45
5:AE:24:ARG:HE	5:AE:24:ARG:HB3	1.65	0.45
7:AG:45:ASP:O	7:AG:49:ILE:HG13	2.15	0.45
10:AJ:38:ILE:H	10:AJ:38:ILE:HG13	1.54	0.45
25:BA:11:G:H2'	25:BA:12:U:C5'	2.46	0.45
25:BA:299:A:N1	25:BA:322:A:O2'	2.32	0.45
25:BA:621:A:OP2	35:BP:108:LYS:NZ	2.45	0.45
25:BA:1364:G:N7	47:B1:3:LYS:HE2	2.31	0.45
25:BA:2140:C:N3	25:BA:2151:G:C6	2.84	0.45
25:BA:2691:C:O3'	25:BA:2871:C:H4'	2.17	0.45
25:BA:2791:C:H2'	25:BA:2792:G:H8	1.81	0.45
30:BG:23:PHE:HB2	30:BG:25:TYR:CE1	2.51	0.45
31:BH:116:GLU:HG3	31:BH:117:PRO:HD2	1.97	0.45
32:BI:135:GLU:C	32:BI:137:PRO:HD3	2.40	0.45
44:BY:92:ASN:H	44:BY:92:ASN:ND2	2.14	0.45
52:B6:25:LYS:NZ	52:B6:51:GLU:OE2	2.42	0.45
1:CA:279:A:OP2	17:CQ:95:TYR:OH	2.32	0.45
1:CA:444:C:O2	1:CA:490:G:N1	2.49	0.45
3:CC:137:ALA:HA	3:CC:140:ARG:HH11	1.82	0.45
3:CC:140:ARG:CZ	3:CC:140:ARG:HB2	2.46	0.45
5:CE:43:LEU:HB3	5:CE:136:MET:SD	2.57	0.45
5:CE:76:ILE:O	5:CE:93:PRO:HB3	2.17	0.45
6:CF:61:LEU:HG	6:CF:63:TYR:CE1	2.51	0.45
9:CI:51:ARG:NH1	9:CI:56:LEU:HD21	2.32	0.45
15:CO:85:LEU:HB3	15:CO:87:ILE:HG13	1.97	0.45
25:DA:572:A:N7	60:DA:4291:HOH:O	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2051:A:H5'	25:DA:2578:G:O4'	2.16	0.45
25:DA:2130:U:H3	25:DA:2159:G:N2	2.15	0.45
27:DD:43:ARG:HA	27:DD:48:ARG:O	2.16	0.45
1:AA:189(A):C:H42	1:AA:189(J):G:H1	1.64	0.45
1:AA:193:C:H4'	20:AT:61:SER:HB2	1.99	0.45
1:AA:258:G:H2'	1:AA:259:G:H8	1.81	0.45
1:AA:461:A:O2'	1:AA:470:C:H5'	2.16	0.45
1:AA:952:U:H2'	1:AA:953:G:C8	2.52	0.45
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.17	0.45
2:AB:215:LEU:O	2:AB:219:VAL:HG23	2.17	0.45
25:BA:27:G:O2'	25:BA:28:A:OP2	2.31	0.45
25:BA:45:C:OP2	25:BA:215:G:H5'	2.17	0.45
25:BA:307:G:H21	25:BA:330:A:H62	1.65	0.45
25:BA:784:A:C8	25:BA:792:G:C5	3.05	0.45
25:BA:2369:A:H2'	25:BA:2370:G:C8	2.51	0.45
33:BN:112:LEU:O	33:BN:116:LEU:HG	2.16	0.45
44:BY:47:LYS:NZ	44:BY:48:ALA:O	2.48	0.45
45:BZ:146:ILE:HA	45:BZ:147:GLY:HA2	1.75	0.45
49:B3:22:ALA:HB2	49:B3:49:LYS:HD3	1.99	0.45
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.50	0.45
7:CG:152:ALA:O	7:CG:155:ARG:HB3	2.16	0.45
9:CI:71:SER:HA	9:CI:74:ILE:HD12	1.99	0.45
11:CK:34:ASP:OD1	11:CK:38:ASN:N	2.46	0.45
17:CQ:62:SER:OG	17:CQ:72:ARG:HD3	2.16	0.45
17:CQ:92:ARG:NH1	17:CQ:95:TYR:OH	2.50	0.45
25:DA:29:U:H2'	25:DA:30:G:C8	2.51	0.45
25:DA:329:G:H8	25:DA:329:G:OP1	1.99	0.45
25:DA:586:A:N1	25:DA:809:G:O2'	2.39	0.45
25:DA:2173:A:C2	25:DA:2174:C:H1'	2.52	0.45
25:DA:2443:C:OP1	29:DF:68:LYS:HD3	2.17	0.45
27:DD:108:PRO:HB3	27:DD:143:HIS:CE1	2.52	0.45
32:DI:48:GLU:HG3	32:DI:52:ARG:HH11	1.81	0.45
40:DU:112:ARG:H	40:DU:112:ARG:HG2	1.52	0.45
44:DY:43:ASN:OD1	44:DY:65:ALA:HB3	2.16	0.45
1:AA:300:A:H2'	1:AA:301:G:O4'	2.17	0.45
1:AA:840:C:H4'	1:AA:841:U:OP1	2.14	0.45
1:AA:1003:G:N2	1:AA:1038:C:C4	2.85	0.45
1:AA:1144:G:N2	1:AA:1146:A:H62	2.15	0.45
1:AA:1149:C:OP1	9:AI:14:VAL:HG11	2.17	0.45
2:AB:19:HIS:HA	2:AB:39:ILE:HG23	1.98	0.45
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:31:PHE:O	8:AH:35:ILE:HG12	2.17	0.45
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.99	0.45
13:AM:108:ARG:O	13:AM:112:GLY:N	2.44	0.45
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.17	0.45
25:BA:1022:G:N7	33:BN:66:LYS:HE2	2.32	0.45
25:BA:1754:C:N3	25:BA:2716:U:O2'	2.45	0.45
25:BA:2124:G:N1	25:BA:2174:C:N4	2.30	0.45
28:BE:29:GLY:H	28:BE:93:VAL:HG13	1.80	0.45
29:BF:20:LEU:HD22	29:BF:21:ALA:H	1.82	0.45
32:BI:57:ARG:HD3	32:BI:58:LEU:N	2.31	0.45
37:BR:67:LEU:O	37:BR:71:GLN:N	2.48	0.45
1:CA:858:G:N1	1:CA:870:U:OP2	2.37	0.45
1:CA:1154:G:O6	1:CA:1155:G:C6	2.70	0.45
13:CM:57:ARG:NH1	50:D4:17:GLY:HA3	2.31	0.45
25:DA:531:C:H4'	25:DA:532:A:H5"	1.97	0.45
25:DA:675:A:N3	25:DA:2443:C:O2'	2.45	0.45
25:DA:977:G:N3	25:DA:1001:A:H2	2.15	0.45
25:DA:1288:U:C2	25:DA:1327:C:O2	2.70	0.45
25:DA:1449:A:OP2	25:DA:1449:A:H8	1.99	0.45
25:DA:2262:U:H4'	25:DA:2328:A:C2	2.51	0.45
25:DA:2713:A:OP2	25:DA:2713:A:H4'	2.16	0.45
31:DH:127:GLU:HB2	31:DH:130:ARG:HB2	1.98	0.45
35:DP:97:PRO:O	35:DP:101:VAL:HG23	2.16	0.45
38:DS:3:ARG:O	38:DS:4:LEU:HD23	2.17	0.45
47:D1:67:ILE:N	47:D1:68:PRO:HD2	2.32	0.45
48:D2:18:PRO:HB3	48:D2:68:ARG:NH1	2.32	0.45
1:AA:227:G:H2'	1:AA:228:A:O4'	2.17	0.45
1:AA:1028:C:C5	1:AA:1029:C:H1'	2.52	0.45
1:AA:1216:G:H2'	1:AA:1217:C:H5"	1.98	0.45
1:AA:1298:C:H4'	1:AA:1299:A:O4'	2.16	0.45
3:AC:120:VAL:O	3:AC:124:ILE:HG23	2.16	0.45
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.99	0.45
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.78	0.45
19:AS:63:THR:HG1	19:AS:66:MET:HE3	1.80	0.45
25:BA:2391:G:O2'	25:BA:2424:C:N4	2.38	0.45
25:BA:2530:A:N7	31:BH:172:LYS:NZ	2.62	0.45
25:BA:2679:A:H4'	28:BE:165:VAL:HG11	1.99	0.45
49:B3:31:LEU:HD23	49:B3:31:LEU:HA	1.77	0.45
1:CA:69:G:H2'	1:CA:70:G:H8	1.82	0.45
1:CA:322:C:O2'	20:CT:23:ARG:HD2	2.16	0.45
1:CA:628:G:C2'	1:CA:629:G:H5'	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1277:C:O2'	1:CA:1279:A:C8	2.69	0.45
24:CX:65:C:H2'	24:CX:66:C:O4'	2.17	0.45
25:DA:18:C:H2'	25:DA:19:C:H6	1.82	0.45
25:DA:375:C:H2'	25:DA:376:C:H6	1.79	0.45
25:DA:565:C:H2'	25:DA:566:U:O4'	2.17	0.45
25:DA:589:C:P	35:DP:16:ARG:HH12	2.40	0.45
25:DA:1013:C:H2'	25:DA:1014:U:C6	2.52	0.45
25:DA:1878:G:H2'	25:DA:1879:C:C6	2.51	0.45
32:DI:9:LEU:HD13	32:DI:9:LEU:HA	1.79	0.45
40:DU:49:HIS:HA	40:DU:52:ARG:HB3	1.98	0.45
1:AA:266:G:O2'	17:AQ:67:LYS:HD3	2.17	0.45
1:AA:762:C:H2'	1:AA:763:G:C8	2.52	0.45
1:AA:953:G:H5'	1:AA:965:A:N6	2.32	0.45
2:AB:30:ARG:HH22	2:AB:194:PRO:HB2	1.81	0.45
24:AX:10:G:N2	24:AX:26:G:H1'	2.32	0.45
25:BA:511:U:O4	25:BA:512:G:N1	2.50	0.45
25:BA:527:C:C5	25:BA:2779:U:H2'	2.52	0.45
25:BA:2512:C:H2'	25:BA:2513:G:O4'	2.17	0.45
29:BF:161:GLU:HG2	29:BF:164:ARG:NH2	2.32	0.45
1:CA:1097:C:H2'	1:CA:1098:C:C6	2.52	0.45
6:CF:68:PRO:HG2	6:CF:71:ARG:NH1	2.32	0.45
25:DA:186:G:H2'	25:DA:187:G:C8	2.52	0.45
25:DA:272(B):G:H2'	25:DA:272(C):G:C8	2.51	0.45
29:DF:157:VAL:HG12	29:DF:198:ALA:HB1	1.98	0.45
36:DQ:38:GLU:HB2	36:DQ:127:ILE:HG22	1.99	0.45
38:DS:84:GLN:HG3	38:DS:111:GLU:OE2	2.17	0.45
39:DT:64:ARG:NH1	39:DT:103:ARG:HA	2.31	0.45
1:AA:112:G:H4'	1:AA:389:A:H4'	1.98	0.45
1:AA:675:A:H1'	11:AK:116:HIS:CD2	2.52	0.45
6:AF:6:VAL:HG13	6:AF:90:VAL:HG22	1.99	0.45
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	1.99	0.45
10:AJ:67:THR:O	10:AJ:67:THR:OG1	2.35	0.45
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.47	0.45
25:BA:272(B):G:H2'	25:BA:272(C):G:O4'	2.16	0.45
25:BA:330:A:HO2'	25:BA:331:A:H8	1.61	0.45
25:BA:1296:G:OP1	25:BA:2709:G:O2'	2.30	0.45
25:BA:1853:A:H2'	25:BA:1854:A:C8	2.52	0.45
29:BF:53:THR:HG22	29:BF:56:GLU:HG3	1.98	0.45
29:BF:155:LEU:HD11	29:BF:176:LEU:HD12	1.99	0.45
34:BO:104:ARG:HE	39:BT:36:GLU:HG2	1.82	0.45
37:BR:29:LEU:HD12	37:BR:29:LEU:HA	1.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:223:U:H2'	1:CA:224:C:H6	1.82	0.45
1:CA:543:C:C2'	1:CA:544:G:H5'	2.47	0.45
1:CA:838:G:N2	1:CA:848:C:N3	2.66	0.45
1:CA:984:C:O5'	1:CA:984:C:H6	2.00	0.45
2:CB:87:ARG:NH1	2:CB:230:VAL:HG11	2.33	0.45
5:CE:57:LYS:HG2	5:CE:61:TYR:CE2	2.52	0.45
13:CM:108:ARG:CZ	13:CM:114:ARG:HG2	2.47	0.45
16:CP:53:VAL:HG13	16:CP:79:VAL:HG22	1.98	0.45
25:DA:251:A:P	54:D8:7:HIS:HE2	2.39	0.45
25:DA:277:C:O2'	25:DA:278:A:OP1	2.30	0.45
25:DA:670:A:H4'	25:DA:671:C:O5'	2.17	0.45
25:DA:863:A:H2'	25:DA:864:G:C8	2.52	0.45
25:DA:983:A:OP1	60:DA:4292:HOH:O	2.21	0.45
25:DA:1359:A:N1	25:DA:1372:U:O4	2.50	0.45
25:DA:1474:C:H2'	25:DA:1475:G:H8	1.82	0.45
25:DA:1637:A:H4'	25:DA:2711:A:O2'	2.17	0.45
25:DA:1839:G:C8	25:DA:1927:A:H1'	2.52	0.45
27:DD:62:TYR:HA	27:DD:87:ASN:OD1	2.17	0.45
29:DF:41:LEU:O	29:DF:44:ARG:HG2	2.16	0.45
30:DG:66:GLN:OE1	30:DG:98:ARG:NE	2.47	0.45
40:DU:17:ILE:HG13	40:DU:32:PHE:CE1	2.52	0.45
1:AA:92:C:H2'	1:AA:93:G:O4'	2.17	0.44
1:AA:881:G:OP2	12:AL:12:ARG:NH2	2.50	0.44
1:AA:1223:C:H5"	1:AA:1224:G:H5'	1.97	0.44
2:AB:130:ARG:HH11	2:AB:130:ARG:HG3	1.82	0.44
4:AD:128:VAL:HG12	4:AD:129:ASN:HD22	1.82	0.44
17:AQ:67:LYS:HA	17:AQ:70:ARG:HH12	1.81	0.44
18:AR:56:THR:HB	18:AR:58:LEU:HD23	1.99	0.44
25:BA:878:A:C6	25:BA:900:A:C5	3.05	0.44
25:BA:2690:C:H5"	25:BA:2872:G:H21	1.82	0.44
27:BD:70:TRP:HB3	27:BD:190:TYR:CE1	2.52	0.44
29:BF:116:ASP:OD2	35:BP:1:MET:N	2.35	0.44
33:BN:75:TYR:CE2	33:BN:77:GLY:HA2	2.52	0.44
36:BQ:108:GLY:HA3	45:BZ:116:VAL:HG13	1.99	0.44
1:CA:486:U:H2'	1:CA:487:A:C8	2.51	0.44
1:CA:868:C:H2'	1:CA:869:G:O4'	2.17	0.44
1:CA:1022:G:H2'	1:CA:1023:G:H8	1.82	0.44
1:CA:1063:C:H3'	1:CA:1064:G:H2'	1.99	0.44
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.33	0.44
3:CC:186:PHE:HA	3:CC:198:VAL:O	2.17	0.44
5:CE:135:THR:O	5:CE:138:ALA:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:37:PHE:HB3	9:CI:43:ALA:HB1	1.98	0.44
17:CQ:7:THR:O	17:CQ:23:VAL:HG13	2.17	0.44
25:DA:272(D):G:H1	25:DA:364:C:H42	1.65	0.44
25:DA:887:A:H4'	25:DA:888:C:H5	1.82	0.44
25:DA:2134:A:H1'	25:DA:2159:G:H21	1.82	0.44
25:DA:2292:C:OP1	38:DS:17:ARG:NH1	2.42	0.44
25:DA:2365:G:H4'	46:D0:60:PHE:CZ	2.52	0.44
40:DU:8:VAL:HG12	40:DU:11:ARG:NH2	2.32	0.44
45:DZ:70:LEU:O	45:DZ:89:PHE:N	2.42	0.44
49:D3:7:LYS:HE3	49:D3:32:GLN:HG3	1.99	0.44
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.45	0.44
1:AA:1147:C:O2'	9:AI:16:ARG:HD3	2.17	0.44
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.52	0.44
4:AD:106:TYR:HD1	4:AD:107:ARG:HD2	1.83	0.44
25:BA:77:C:OP1	48:B2:59:ARG:HD3	2.17	0.44
25:BA:150:C:H2'	25:BA:151:C:C6	2.52	0.44
25:BA:220:G:O2'	25:BA:233:A:N3	2.41	0.44
25:BA:978:G:C2	25:BA:986:C:C2	3.05	0.44
27:BD:17:THR:OG1	27:BD:205:VAL:N	2.32	0.44
31:BH:164:TYR:HB2	31:BH:167:GLU:HB2	1.99	0.44
32:BI:81:VAL:O	32:BI:146:ALA:HA	2.18	0.44
45:BZ:56:VAL:HA	45:BZ:70:LEU:HD23	2.00	0.44
1:CA:10:A:OP2	5:CE:126:ARG:HD2	2.17	0.44
1:CA:256:U:OP1	17:CQ:17:LYS:NZ	2.37	0.44
1:CA:393:A:OP2	16:CP:12:LYS:HD2	2.17	0.44
1:CA:429:U:H1'	1:CA:430:A:H5"	1.98	0.44
1:CA:939:G:C6	1:CA:940:C:N4	2.85	0.44
1:CA:1328:C:O2'	13:CM:29:ARG:NE	2.51	0.44
2:CB:207:ALA:O	2:CB:211:ILE:HG13	2.17	0.44
3:CC:144:SER:O	3:CC:144:SER:OG	2.36	0.44
9:CI:23:ASN:HD22	9:CI:24:GLY:H	1.66	0.44
16:CP:69:THR:O	16:CP:73:LEU:HG	2.17	0.44
24:CX:12:G:H4'	25:DA:1908:C:O2	2.17	0.44
25:DA:64:A:O3'	43:DX:71:GLY:HA3	2.17	0.44
25:DA:84:A:N1	25:DA:98:G:O2'	2.44	0.44
25:DA:606:U:H4'	25:DA:658:C:H4'	1.98	0.44
25:DA:856:C:O2'	25:DA:857:C:OP1	2.31	0.44
25:DA:1011:G:C2	25:DA:1151:G:C2	3.06	0.44
25:DA:1264:G:OP1	51:D5:19:ARG:NH2	2.40	0.44
25:DA:1359:A:N3	25:DA:1359:A:H5'	2.32	0.44
25:DA:1847:A:H4'	25:DA:1848:A:OP2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2184:G:H2'	25:DA:2185:C:C6	2.52	0.44
31:DH:13:LYS:HA	31:DH:14:GLY:HA2	1.60	0.44
39:DT:16:ARG:HG2	39:DT:18:ASP:OD1	2.17	0.44
50:D4:40:HIS:HB3	50:D4:43:TYR:HB2	1.97	0.44
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.63	0.44
1:AA:346:G:C4	1:AA:347:G:H1'	2.52	0.44
1:AA:530:G:O6	22:AV:21:C:H1'	2.17	0.44
1:AA:1090:U:H2'	1:AA:1091:U:C6	2.52	0.44
1:AA:1133:G:C6	1:AA:1142:G:C6	3.06	0.44
1:AA:1241:G:H2'	1:AA:1242:C:H6	1.82	0.44
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.53	0.44
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	2.00	0.44
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.66	0.44
23:AW:76:PPU:H92	25:BA:2584:U:H4'	1.98	0.44
25:BA:652(F):G:N2	25:BA:652(S):C:H2'	2.31	0.44
25:BA:897:C:H2'	25:BA:898:C:H6	1.80	0.44
25:BA:1453:U:O2'	25:BA:1455:G:N7	2.47	0.44
25:BA:1783:A:H5'	25:BA:2608:G:H4'	1.99	0.44
29:BF:117:ARG:NH2	35:BP:1:MET:O	2.51	0.44
46:B0:10:THR:HB	46:B0:12:ASN:H	1.82	0.44
1:CA:229:U:O2'	16:CP:23:ASP:OD2	2.31	0.44
1:CA:255:G:OP1	17:CQ:69:LYS:NZ	2.38	0.44
1:CA:522:C:H41	12:CL:53:ARG:NH2	2.11	0.44
1:CA:826:C:H2'	1:CA:827:U:H6	1.83	0.44
1:CA:978:A:O2'	1:CA:1321:C:N4	2.49	0.44
1:CA:991:U:HO2'	1:CA:992:U:P	2.40	0.44
1:CA:1156:G:H5'	1:CA:1157:A:OP2	2.18	0.44
1:CA:1262:C:N4	1:CA:1273:G:C6	2.78	0.44
3:CC:19:GLU:O	3:CC:56:ASP:HA	2.17	0.44
17:CQ:92:ARG:O	17:CQ:95:TYR:HB2	2.18	0.44
25:DA:95:G:H4'	48:D2:46:GLN:HA	1.98	0.44
25:DA:953:A:OP2	36:DQ:16:ARG:NH2	2.41	0.44
25:DA:2113:U:C2	25:DA:2169:A:N6	2.85	0.44
25:DA:2176:A:H2'	25:DA:2177:C:C6	2.53	0.44
25:DA:2419:U:OP1	54:D8:41:ILE:HD12	2.18	0.44
25:DA:2419:U:O2'	52:D6:54:ILE:HD11	2.17	0.44
43:DX:31:HIS:CD2	43:DX:33:LYS:H	2.35	0.44
52:D6:38:LYS:HE3	52:D6:39:TYR:H	1.83	0.44
1:AA:112:G:H5'	1:AA:389:A:O2'	2.18	0.44
1:AA:185:A:H2'	1:AA:186:C:H6	1.80	0.44
1:AA:1007:C:N3	1:AA:1022:G:C6	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1125:U:C5'	10:AJ:5:ARG:HH22	2.28	0.44
6:AF:89:MET:HE1	18:AR:72:ARG:HB3	2.00	0.44
25:BA:484:C:H2'	25:BA:485:C:C6	2.53	0.44
25:BA:829:A:N7	25:BA:2247:A:O2'	2.46	0.44
25:BA:1213:A:N3	25:BA:1238:G:O2'	2.44	0.44
25:BA:1297:C:OP1	25:BA:2710:C:H4'	2.18	0.44
25:BA:2153:G:H2'	25:BA:2154:G:H8	1.83	0.44
26:BB:114:C:O2'	38:BS:46:VAL:HG13	2.17	0.44
30:BG:148:MET:HE3	30:BG:148:MET:HB2	1.66	0.44
31:BH:85:LYS:NZ	60:BH:4001:HOH:O	2.51	0.44
45:BZ:35:ARG:HD2	45:BZ:35:ARG:HA	1.69	0.44
45:BZ:155:LEU:HD12	45:BZ:155:LEU:HA	1.76	0.44
1:CA:375:U:H4'	16:CP:17:TYR:HE2	1.81	0.44
1:CA:413:G:N2	1:CA:428:G:H1'	2.33	0.44
1:CA:567:G:H2'	1:CA:568:G:O4'	2.18	0.44
1:CA:922:G:C6	1:CA:923:A:C6	3.04	0.44
1:CA:1042:G:C2	1:CA:1043:C:C2	3.05	0.44
1:CA:1118:C:H2'	1:CA:1119:C:H6	1.82	0.44
1:CA:1295:G:H2'	1:CA:1296:C:H5'	1.98	0.44
5:CE:136:MET:O	5:CE:140:ARG:N	2.46	0.44
14:CN:37:PHE:CE2	14:CN:44:LEU:HD13	2.52	0.44
15:CO:87:ILE:CG2	15:CO:88:ARG:H	2.29	0.44
25:DA:78:A:H2'	25:DA:79:G:C8	2.53	0.44
25:DA:272(D):G:C2	25:DA:272(E):G:C8	3.05	0.44
25:DA:272(G):C:N4	25:DA:363(C):G:H1	2.02	0.44
25:DA:320:A:H4'	25:DA:322:A:C8	2.53	0.44
25:DA:793:A:OP2	25:DA:2072:G:H5'	2.16	0.44
25:DA:889:C:O2'	25:DA:890:A:O5'	2.33	0.44
25:DA:1411:C:H2'	25:DA:1412:A:C8	2.53	0.44
25:DA:1657:C:H2'	25:DA:1658:C:C6	2.53	0.44
25:DA:2270:G:H2'	25:DA:2271:G:O4'	2.16	0.44
25:DA:2788:C:O2'	25:DA:2809:A:N3	2.46	0.44
26:DB:16:G:H1	26:DB:68:C:N4	2.16	0.44
26:DB:42:C:O2'	30:DG:66:GLN:HG2	2.17	0.44
38:DS:75:GLU:OE2	38:DS:75:GLU:N	2.29	0.44
1:AA:405:U:OP2	4:AD:3:ARG:NH1	2.51	0.44
1:AA:452:A:O2'	1:AA:453:A:H5"	2.18	0.44
1:AA:599:C:C2'	1:AA:600:C:H5'	2.47	0.44
3:AC:41:GLY:O	3:AC:45:LYS:HG2	2.18	0.44
25:BA:1165:U:H2'	25:BA:1166:C:C6	2.53	0.44
25:BA:1406:U:H2'	25:BA:1407:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1889:A:H2'	25:BA:1890:A:C8	2.53	0.44
25:BA:2279:G:O6	46:B0:14:ARG:HD2	2.18	0.44
25:BA:2722:G:H2'	25:BA:2723:C:C6	2.53	0.44
31:BH:88:LEU:HD23	31:BH:165:ALA:HA	1.98	0.44
32:BI:93:THR:O	32:BI:97:ILE:HG13	2.18	0.44
50:B4:53:GLU:HG3	50:B4:54:GLY:N	2.32	0.44
1:CA:90:U:C2'	1:CA:91:C:H5'	2.47	0.44
1:CA:453:A:C6	1:CA:454:C:C4	3.06	0.44
1:CA:688:G:C6	1:CA:700:G:C2	3.06	0.44
1:CA:784:C:H4'	25:DA:1837:C:OP1	2.17	0.44
1:CA:1005:A:H1'	1:CA:1025:U:C2	2.53	0.44
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.53	0.44
13:CM:14:ARG:HA	13:CM:43:THR:O	2.18	0.44
16:CP:1:MET:HE2	16:CP:1:MET:HB3	1.90	0.44
19:CS:19:VAL:O	19:CS:23:ASN:ND2	2.51	0.44
20:CT:56:MET:HG3	20:CT:57:ARG:N	2.33	0.44
25:DA:336:C:HO2'	44:DY:35:TYR:HH	1.61	0.44
25:DA:1028:A:OP2	25:DA:1126:A:N6	2.50	0.44
25:DA:1654:A:OP1	37:DR:1:MET:HA	2.18	0.44
25:DA:2318:G:H21	38:DS:3:ARG:CZ	2.30	0.44
25:DA:2472:G:H2'	25:DA:2475:C:H42	1.82	0.44
26:DB:41:U:C6	30:DG:69:ALA:HB1	2.53	0.44
47:D1:40:ARG:NH2	47:D1:42:GLN:HG2	2.33	0.44
1:AA:430:A:P	4:AD:8:VAL:H	2.41	0.44
2:AB:114:ARG:O	2:AB:118:LEU:HB2	2.17	0.44
3:AC:32:LEU:HD22	3:AC:59:ARG:HD3	1.99	0.44
8:AH:75:ARG:HA	8:AH:76:PRO:HD2	1.91	0.44
18:AR:24:ALA:C	18:AR:26:LEU:H	2.25	0.44
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.32	0.44
25:BA:376:C:H2'	25:BA:377:C:C6	2.53	0.44
25:BA:956:G:N2	25:BA:959:A:H3'	2.33	0.44
25:BA:1179:C:H2'	25:BA:1180:C:H6	1.83	0.44
25:BA:1421:G:C2	25:BA:1422:G:C8	3.06	0.44
25:BA:2018:G:H21	40:BU:34:LYS:NZ	2.16	0.44
29:BF:179:GLU:CD	29:BF:179:GLU:H	2.26	0.44
33:BN:67:LEU:HD12	33:BN:67:LEU:HA	1.67	0.44
42:BW:14:PRO:HG2	42:BW:78:GLU:HG2	1.99	0.44
50:B4:63:TYR:N	50:B4:63:TYR:CD1	2.85	0.44
53:B7:24:THR:HG22	53:B7:26:GLY:H	1.82	0.44
1:CA:59:A:H3'	1:CA:331:G:H22	1.82	0.44
1:CA:90:U:O2'	1:CA:91:C:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:130:A:N3	1:CA:263:A:O2'	2.46	0.44
1:CA:167:G:H2'	1:CA:168:G:H8	1.82	0.44
1:CA:377:G:H1	1:CA:386:C:H42	1.65	0.44
1:CA:839:U:O2'	1:CA:840:C:OP1	2.33	0.44
1:CA:1014:A:C2	1:CA:1219:U:H1'	2.52	0.44
1:CA:1469:G:H2'	1:CA:1470:G:H8	1.82	0.44
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.99	0.44
24:CX:19:G:N2	24:CX:56:C:N3	2.53	0.44
25:DA:379:G:O2'	25:DA:2232:U:OP1	2.35	0.44
25:DA:783:A:N3	25:DA:783:A:H2'	2.31	0.44
25:DA:1468:C:H42	25:DA:1524:G:H1	1.66	0.44
25:DA:1674:G:H21	25:DA:1677:A:N6	2.16	0.44
25:DA:1900:A:OP2	60:DA:4200:HOH:O	2.21	0.44
25:DA:2315:G:H2'	25:DA:2316:C:C6	2.53	0.44
25:DA:2552:U:O5'	25:DA:2552:U:H6	2.00	0.44
25:DA:2872:G:C2	25:DA:2873:A:N6	2.86	0.44
27:DD:123:ALA:O	27:DD:131:LEU:HD21	2.17	0.44
31:DH:80:SER:OG	31:DH:81:GLU:OE1	2.26	0.44
35:DP:94:GLU:HG3	35:DP:124:LYS:HD3	2.00	0.44
1:AA:1030:C:N4	1:AA:1031:G:C6	2.79	0.44
18:AR:65:ILE:O	18:AR:69:THR:HG23	2.18	0.44
24:AX:23:C:H2'	24:AX:24:U:C6	2.52	0.44
25:BA:141:A:H8	25:BA:1408:C:HO2'	1.54	0.44
25:BA:572:A:H2'	25:BA:573:G:O4'	2.18	0.44
25:BA:660:G:O3'	29:BF:38:ARG:NH2	2.50	0.44
25:BA:1434:A:N6	25:BA:1558:A:H62	2.10	0.44
25:BA:2304:G:H22	25:BA:2312:U:H3	1.64	0.44
32:BI:130:TYR:HD2	32:BI:138:ILE:HD12	1.83	0.44
1:CA:260:G:C6	1:CA:261:U:C4	3.06	0.44
1:CA:410:G:H5"	4:CD:30:LYS:NZ	2.33	0.44
1:CA:730:G:H5"	1:CA:731:G:OP2	2.18	0.44
1:CA:1079:G:H2'	1:CA:1080:A:C8	2.53	0.44
2:CB:35:GLU:HB2	2:CB:40:HIS:HD2	1.83	0.44
5:CE:41:VAL:O	5:CE:66:MET:HA	2.18	0.44
15:CO:32:LEU:HD23	15:CO:32:LEU:HA	1.87	0.44
25:DA:614(C):A:C4	29:DF:180:GLY:HA2	2.52	0.44
25:DA:705:A:H1'	27:DD:9:TYR:CE2	2.52	0.44
28:DE:8:LYS:NZ	28:DE:188:VAL:O	2.48	0.44
31:DH:143:GLN:HE21	31:DH:147:ASN:HD21	1.65	0.44
44:DY:52:SER:HB2	44:DY:53:PRO:HD2	1.98	0.44
48:D2:3:LEU:O	48:D2:7:ARG:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:D3:12:PRO:HB2	49:D3:20:LYS:HG2	1.99	0.44
1:AA:1060:C:C4	3:AC:2:GLY:HA3	2.52	0.44
1:AA:1157:A:N7	1:AA:1180:A:N6	2.65	0.44
1:AA:1499:A:H1'	1:AA:1520:G:H5'	2.00	0.44
2:AB:20:GLU:HA	2:AB:21:ARG:NH2	2.32	0.44
3:AC:21:ARG:HG3	3:AC:58:GLU:HG2	2.00	0.44
17:AQ:38:ARG:HD3	17:AQ:38:ARG:HA	1.83	0.44
25:BA:479:A:N3	25:BA:481:G:H5"	2.32	0.44
25:BA:684:G:OP1	53:B7:16:HIS:ND1	2.50	0.44
25:BA:1227:G:OP2	40:BU:16:LYS:NZ	2.34	0.44
25:BA:1243:G:O2'	35:BP:4:SER:O	2.32	0.44
25:BA:1674:G:H1'	25:BA:1676:A:N6	2.32	0.44
25:BA:1991:U:H2'	25:BA:1992:G:H5"	2.00	0.44
25:BA:2690:C:H5"	25:BA:2872:G:N2	2.33	0.44
25:BA:2811:G:H5'	28:BE:60:ASN:ND2	2.29	0.44
34:BO:16:ALA:HB2	34:BO:52:VAL:HG21	1.98	0.44
36:BQ:54:MET:SD	36:BQ:118:LEU:HD23	2.57	0.44
39:BT:50:ILE:HA	39:BT:99:LEU:HD12	2.00	0.44
48:B2:61:LEU:HD23	48:B2:61:LEU:HA	1.74	0.44
1:CA:358:U:H2'	1:CA:359:U:C6	2.53	0.44
1:CA:1014:A:H5'	19:CS:18:LYS:NZ	2.32	0.44
1:CA:1064:G:H1'	1:CA:1065:U:OP2	2.18	0.44
1:CA:1429:C:H2'	1:CA:1430:C:H6	1.83	0.44
2:CB:87:ARG:HH11	2:CB:230:VAL:HG11	1.83	0.44
4:CD:63:LYS:HD2	4:CD:197:PRO:O	2.17	0.44
25:DA:271(N):U:O2'	25:DA:271(O):C:H5'	2.18	0.44
25:DA:698:C:O2'	25:DA:734:A:N6	2.51	0.44
25:DA:1550:C:H2'	25:DA:1551:C:H6	1.82	0.44
25:DA:1777:U:H2'	25:DA:1778:U:C6	2.53	0.44
25:DA:2129:C:H2'	25:DA:2130:U:C4	2.52	0.44
25:DA:2138:C:N4	25:DA:2153:G:H1	2.16	0.44
25:DA:2474:C:H5"	25:DA:2475:C:OP2	2.17	0.44
25:DA:2657:A:H3'	25:DA:2658:C:C6	2.53	0.44
26:DB:50:G:OP2	38:DS:62:LYS:HD2	2.17	0.44
29:DF:129:PHE:CE2	29:DF:163:VAL:HG11	2.53	0.44
29:DF:187:VAL:HG12	35:DP:3:LEU:HD12	1.99	0.44
30:DG:5:VAL:HG13	30:DG:8:LYS:HG3	2.00	0.44
34:DO:4:PRO:O	34:DO:5:GLN:HB2	2.17	0.44
40:DU:92:ARG:HA	40:DU:95:LEU:HB2	1.98	0.44
41:DV:89:GLN:HA	41:DV:90:PRO:HD3	1.84	0.44
42:DW:16:LYS:O	42:DW:19:LEU:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:D5:9:LYS:HD3	51:D5:9:LYS:HA	1.77	0.44
1:AA:77:G:C2'	1:AA:78:G:H5'	2.48	0.44
1:AA:288:A:H2'	1:AA:289:G:H4'	2.00	0.44
1:AA:502:G:OP1	12:AL:118:SER:HB3	2.18	0.44
2:AB:30:ARG:NH2	2:AB:194:PRO:HB2	2.33	0.44
2:AB:166:ASP:HA	2:AB:167:PRO:HD3	1.85	0.44
4:AD:61:LYS:HA	4:AD:203:VAL:HG22	1.99	0.44
4:AD:138:TYR:CD1	4:AD:138:TYR:C	2.96	0.44
25:BA:141:A:C8	25:BA:1408:C:O2'	2.68	0.44
25:BA:1021:A:H8	25:BA:1021:A:H3'	1.83	0.44
25:BA:1131:G:H21	33:BN:73:THR:HG21	1.83	0.44
25:BA:2206:G:H3'	25:BA:2207:G:C8	2.53	0.44
25:BA:2556:C:H2'	25:BA:2557:G:O4'	2.18	0.44
28:BE:120:TRP:CE3	28:BE:155:LYS:HD3	2.53	0.44
29:BF:74:ARG:H	29:BF:74:ARG:HG3	1.44	0.44
32:BI:37:VAL:HG12	32:BI:38:LEU:HD12	1.99	0.44
40:BU:28:ARG:HD3	40:BU:38:THR:OG1	2.18	0.44
1:CA:4:U:C4	8:CH:105:ARG:HD3	2.53	0.44
1:CA:401:C:H2'	1:CA:402:G:C8	2.53	0.44
1:CA:675:A:O2'	11:CK:114:VAL:O	2.35	0.44
1:CA:685:G:C2	1:CA:686:U:C4	3.06	0.44
1:CA:797:C:O2'	1:CA:798:G:H5'	2.18	0.44
1:CA:828:A:OP1	1:CA:828:A:H4'	2.17	0.44
1:CA:1202:G:C6	14:CN:42:ILE:HG21	2.52	0.44
1:CA:1429:C:H2'	1:CA:1430:C:C6	2.53	0.44
1:CA:1493:A:C8	25:DA:1913:A:N1	2.86	0.44
2:CB:218:ALA:O	2:CB:222:ILE:HG23	2.18	0.44
5:CE:60:TYR:CD1	5:CE:60:TYR:C	2.96	0.44
25:DA:380:U:H2'	25:DA:381:G:H8	1.83	0.44
25:DA:649:G:H2'	25:DA:650:C:O4'	2.18	0.44
25:DA:910:A:H62	36:DQ:12:GLN:HA	1.83	0.44
25:DA:1826:G:H4'	27:DD:242:ARG:CZ	2.47	0.44
25:DA:2135:A:H61	25:DA:2157:G:N2	2.15	0.44
25:DA:2193:G:C4	25:DA:2194:G:C8	3.06	0.44
25:DA:2651:C:O2'	25:DA:2652:C:H5'	2.17	0.44
25:DA:2695:C:H2'	25:DA:2696:U:H6	1.83	0.44
26:DB:54:G:H21	30:DG:29:TRP:HZ2	1.64	0.44
28:DE:14:ILE:HB	39:DT:14:TYR:CE2	2.52	0.44
28:DE:32:PRO:HD2	28:DE:50:GLY:O	2.18	0.44
28:DE:72:VAL:HA	28:DE:73:GLU:HG3	2.00	0.44
28:DE:101:ARG:CZ	28:DE:171:GLU:HB3	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DF:107:LYS:HG2	29:DF:206:ILE:HA	2.00	0.44
30:DG:7:LEU:HD23	30:DG:100:TRP:HE3	1.81	0.44
33:DN:128:HIS:HA	33:DN:129:PRO:HD3	1.84	0.44
39:DT:36:GLU:O	39:DT:39:ARG:HG3	2.18	0.44
44:DY:67:LEU:HD23	44:DY:67:LEU:HA	1.85	0.44
45:DZ:19:ARG:HG3	45:DZ:25:PRO:HD3	1.99	0.44
47:D1:51:VAL:HG12	47:D1:53:VAL:HG23	1.99	0.44
47:D1:52:ARG:HA	47:D1:56:GLN:O	2.17	0.44
1:AA:293:G:C6	1:AA:294:U:C4	3.05	0.43
1:AA:544:G:OP1	4:AD:59:ARG:NH2	2.33	0.43
1:AA:738:C:H2'	1:AA:739:C:C6	2.53	0.43
1:AA:1082:G:H2'	1:AA:1083:U:O4'	2.18	0.43
1:AA:1369:C:H2'	1:AA:1370:G:C8	2.53	0.43
25:BA:64:A:O3'	43:BX:71:GLY:HA3	2.18	0.43
25:BA:833:U:O2	35:BP:55:ARG:NH2	2.51	0.43
25:BA:947:G:H2'	25:BA:948:G:C8	2.53	0.43
25:BA:1042:G:H2'	25:BA:1043:C:C6	2.53	0.43
25:BA:1243:G:O3'	35:BP:7:ARG:NH2	2.50	0.43
25:BA:2302:G:H1	25:BA:2314:C:H42	1.65	0.43
33:BN:73:THR:HG23	33:BN:82:LEU:HD11	2.00	0.43
1:CA:36:C:O2'	12:CL:117:ARG:NH2	2.50	0.43
1:CA:410:G:P	4:CD:30:LYS:HZ3	2.38	0.43
1:CA:589:C:H2'	1:CA:590:C:H5'	2.00	0.43
1:CA:679:C:H2'	1:CA:680:C:C6	2.53	0.43
1:CA:991:U:H3'	1:CA:1212:U:N3	2.33	0.43
1:CA:1042:G:C6	1:CA:1043:C:C4	3.06	0.43
1:CA:1066:C:H2'	1:CA:1067:A:C8	2.52	0.43
4:CD:12:CYS:SG	4:CD:19:LEU:N	2.87	0.43
13:CM:65:LYS:O	13:CM:66:LEU:HD23	2.17	0.43
19:CS:69:HIS:HB3	19:CS:73:GLU:HG3	2.00	0.43
19:CS:77:THR:HG23	19:CS:78:ARG:HG2	2.00	0.43
20:CT:9:ASN:ND2	20:CT:10:LEU:HA	2.33	0.43
25:DA:18:C:O2'	25:DA:554:U:OP1	2.36	0.43
25:DA:910:A:N3	25:DA:2264:C:O2'	2.39	0.43
25:DA:1410:G:H2'	25:DA:1411:C:H6	1.81	0.43
25:DA:1600:C:OP1	43:DX:58:HIS:NE2	2.29	0.43
25:DA:2137:C:O2'	25:DA:2138:C:H5'	2.18	0.43
25:DA:2781:A:H5"	25:DA:2782:G:H5'	2.00	0.43
29:DF:40:GLN:NE2	29:DF:182:ASN:HB2	2.32	0.43
29:DF:152:GLU:HA	29:DF:190:GLU:OE2	2.18	0.43
34:DO:77:ILE:HD12	39:DT:74:ARG:HD3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DQ:110:THR:HG23	36:DQ:113:GLN:OE1	2.18	0.43
47:D1:82:LEU:O	47:D1:85:LEU:HD23	2.18	0.43
54:D8:39:LYS:HA	54:D8:42:ARG:NH1	2.33	0.43
1:AA:457:C:N4	1:AA:475:G:O6	2.51	0.43
1:AA:576:G:O6	1:AA:880:C:O2'	2.28	0.43
1:AA:942:G:C2	1:AA:1342:C:C2	3.06	0.43
5:AE:116:THR:HG23	5:AE:117:ASP:OD2	2.19	0.43
8:AH:6:ILE:HB	8:AH:85:ARG:NH1	2.33	0.43
12:AL:33:ARG:HD2	12:AL:33:ARG:HA	1.80	0.43
12:AL:58:VAL:O	12:AL:65:GLU:HA	2.18	0.43
14:AN:50:LYS:HE2	14:AN:52:GLN:NE2	2.33	0.43
25:BA:459:U:H2'	25:BA:460:A:C8	2.52	0.43
25:BA:557:U:O2	33:BN:45:ASN:HB2	2.18	0.43
25:BA:699:A:H2'	25:BA:700:G:O4'	2.18	0.43
25:BA:1027:A:C6	25:BA:1126:A:C4	3.06	0.43
25:BA:1449:A:HO2'	25:BA:1529:G:H21	1.58	0.43
25:BA:1951:U:H2'	25:BA:1953:A:OP2	2.17	0.43
25:BA:2267:A:H5"	25:BA:2268:A:H5'	1.99	0.43
25:BA:2789:C:O2	25:BA:2894:G:N1	2.50	0.43
26:BB:29:A:H2'	26:BB:30:C:O4'	2.18	0.43
28:BE:54:GLN:OE1	28:BE:55:ASN:N	2.42	0.43
31:BH:154:PRO:HB3	31:BH:163:TYR:CZ	2.52	0.43
34:BO:17:ARG:HD3	34:BO:17:ARG:HA	1.87	0.43
1:CA:324:G:N1	1:CA:327:A:OP2	2.51	0.43
1:CA:377:G:OP1	16:CP:3:LYS:HD2	2.18	0.43
1:CA:948:C:N4	1:CA:1233:G:H1	2.14	0.43
1:CA:958:A:H5"	1:CA:959:A:OP2	2.17	0.43
1:CA:995:C:N3	1:CA:1046:A:O2'	2.46	0.43
1:CA:1058:G:H2'	1:CA:1059:C:O4'	2.18	0.43
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.54	0.43
4:CD:98:GLU:O	4:CD:103:ASN:ND2	2.51	0.43
6:CF:23:LYS:HE2	6:CF:23:LYS:HB3	1.75	0.43
9:CI:72:GLY:O	9:CI:76:ALA:N	2.47	0.43
12:CL:113:ARG:HB3	12:CL:122:THR:HG21	2.00	0.43
17:CQ:19:VAL:HG23	17:CQ:44:ALA:HB3	2.00	0.43
19:CS:30:LEU:HD12	19:CS:31:ILE:N	2.33	0.43
25:DA:78:A:N6	25:DA:109:G:O6	2.50	0.43
25:DA:85:G:OP2	44:DY:9:LYS:HB3	2.18	0.43
25:DA:144:C:H5'	43:DX:2:LYS:HG2	2.00	0.43
25:DA:833:U:H2'	25:DA:834:C:H6	1.79	0.43
25:DA:1230:C:H2'	25:DA:1231:G:C8	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1275:A:N1	25:DA:1295:C:O2'	2.46	0.43
25:DA:1443:G:H1	25:DA:1548:C:N4	2.15	0.43
25:DA:1660:C:H2'	25:DA:1661:G:H8	1.82	0.43
25:DA:2056:G:OP1	60:DA:4373:HOH:O	2.21	0.43
25:DA:2342:C:O2'	25:DA:2374:C:H5"	2.18	0.43
26:DB:48:A:P	38:DS:30:ARG:HH12	2.40	0.43
29:DF:33:LEU:HD12	29:DF:33:LEU:HA	1.80	0.43
29:DF:108:LYS:O	29:DF:112:MET:HG3	2.18	0.43
29:DF:116:ASP:OD2	35:DP:1:MET:N	2.50	0.43
34:DO:14:THR:HG21	34:DO:86:ILE:HB	2.00	0.43
35:DP:100:LEU:HD12	35:DP:112:LEU:HD11	1.99	0.43
38:DS:91:PRO:HD2	38:DS:92:TYR:CE2	2.53	0.43
42:DW:28:SER:OG	42:DW:31:GLU:HG3	2.17	0.43
46:D0:68:GLU:HB2	46:D0:82:ARG:NH1	2.32	0.43
47:D1:51:VAL:HG11	47:D1:74:VAL:HG21	2.00	0.43
1:AA:109:A:C6	1:AA:326:G:C6	3.06	0.43
1:AA:262:A:C6	1:AA:263:A:C6	3.06	0.43
1:AA:452:A:H4'	16:AP:72:ARG:HH12	1.83	0.43
1:AA:1125:U:H4'	1:AA:1126:U:OP1	2.19	0.43
25:BA:732:C:H2'	25:BA:733:G:O4'	2.19	0.43
25:BA:864:G:OP2	36:BQ:22:LYS:HE2	2.19	0.43
36:BQ:48:GLU:O	36:BQ:52:VAL:HG23	2.19	0.43
37:BR:72:ASP:O	37:BR:76:VAL:HG23	2.18	0.43
1:CA:461:A:O2'	1:CA:470:C:H5'	2.17	0.43
1:CA:721:G:H4'	1:CA:722:A:O4'	2.17	0.43
1:CA:890:G:O2'	1:CA:906:G:O6	2.18	0.43
1:CA:999:C:H42	1:CA:1042:G:H1	1.66	0.43
1:CA:1225:A:OP1	13:CM:103:THR:OG1	2.35	0.43
1:CA:1493:A:H8	25:DA:1913:A:N1	2.16	0.43
2:CB:184:VAL:HG12	2:CB:197:VAL:HG13	2.00	0.43
7:CG:103:TRP:HA	7:CG:106:GLN:HB2	2.00	0.43
13:CM:44:ARG:HB2	13:CM:47:ASP:OD1	2.19	0.43
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.18	0.43
25:DA:182:A:H2	25:DA:433:C:O2	2.01	0.43
25:DA:1788:C:H2'	25:DA:1789:A:H8	1.83	0.43
25:DA:1835:G:H5"	25:DA:1836:C:OP2	2.18	0.43
28:DE:70:ALA:C	28:DE:72:VAL:H	2.27	0.43
33:DN:48:MET:HE3	33:DN:48:MET:HB2	1.70	0.43
37:DR:118:GLU:H	37:DR:118:GLU:CD	2.26	0.43
45:DZ:55:HIS:CE1	45:DZ:135:GLU:HG3	2.51	0.43
1:AA:608:A:H4'	16:AP:32:TYR:OH	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1027:C:O2	1:AA:1034:G:N1	2.52	0.43
2:AB:185:ILE:HA	2:AB:199:TYR:O	2.18	0.43
6:AF:44:GLY:HA2	6:AF:59:TYR:CE2	2.53	0.43
7:AG:113:GLU:CD	7:AG:113:GLU:H	2.20	0.43
8:AH:39:LEU:HD12	8:AH:44:PHE:HB2	2.01	0.43
9:AI:37:PHE:HB3	9:AI:43:ALA:CB	2.48	0.43
10:AJ:5:ARG:O	10:AJ:98:ILE:HA	2.19	0.43
14:AN:48:ALA:HB2	14:AN:53:LEU:HD12	2.01	0.43
16:AP:21:VAL:HG13	16:AP:33:ILE:HB	1.99	0.43
20:AT:56:MET:HE3	20:AT:88:VAL:HG21	1.99	0.43
25:BA:71:A:OP2	25:BA:71:A:H3'	2.19	0.43
25:BA:84:A:H5"	44:BY:8:LYS:HG3	2.00	0.43
25:BA:1047:G:H2'	25:BA:1110:G:N1	2.33	0.43
28:BE:176:ILE:HB	28:BE:181:LEU:HB2	1.99	0.43
45:BZ:137:ILE:HA	45:BZ:156:LYS:HZ1	1.83	0.43
47:B1:78:LYS:HE3	47:B1:78:LYS:HB2	1.68	0.43
1:CA:335:C:O2'	1:CA:1433:A:N3	2.43	0.43
1:CA:1112:C:H42	3:CC:177:THR:HA	1.81	0.43
1:CA:1155:G:C6	1:CA:1156:G:C4	3.06	0.43
2:CB:100:GLY:O	2:CB:104:ASN:N	2.50	0.43
3:CC:47:LEU:HB3	3:CC:52:LEU:HB2	2.00	0.43
3:CC:124:ILE:HD12	3:CC:191:THR:HG23	2.01	0.43
5:CE:108:ALA:O	5:CE:112:LEU:HG	2.18	0.43
18:CR:58:LEU:HB3	18:CR:62:GLU:HG3	2.01	0.43
19:CS:14:HIS:CE1	19:CS:15:LEU:HD13	2.53	0.43
25:DA:534:U:H5'	40:DU:42:ALA:HB1	2.00	0.43
25:DA:590:A:OP1	29:DF:95:ARG:NH1	2.51	0.43
25:DA:1266:G:O5'	42:DW:15:ARG:NH2	2.51	0.43
25:DA:1581:G:H2'	25:DA:1582:C:O4'	2.17	0.43
25:DA:1637:A:OP2	60:DA:4628:HOH:O	2.21	0.43
25:DA:1788:C:H2'	25:DA:1789:A:C8	2.53	0.43
25:DA:1894:C:H2'	25:DA:1895:C:C6	2.52	0.43
25:DA:2037:G:H2'	25:DA:2038:G:C8	2.54	0.43
25:DA:2148:G:H2'	25:DA:2149:G:C8	2.53	0.43
25:DA:2466:C:H5'	55:D9:5:ALA:HB3	2.00	0.43
29:DF:162:LEU:H	29:DF:162:LEU:HD22	1.83	0.43
30:DG:43:LEU:C	30:DG:45:GLU:H	2.25	0.43
34:DO:120:GLU:HG2	34:DO:122:LEU:HG	2.00	0.43
42:DW:13:SER:HA	42:DW:14:PRO:HD3	1.88	0.43
1:AA:90:U:C2'	1:AA:91:C:H5'	2.49	0.43
1:AA:345:C:H4'	1:AA:346:G:C4	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:540:G:H2'	1:AA:541:G:C8	2.54	0.43
1:AA:600:C:H2'	1:AA:601:C:C6	2.54	0.43
1:AA:1077:G:H5"	1:AA:1078:U:OP2	2.18	0.43
4:AD:31:CYS:O	4:AD:35:ARG:HG3	2.17	0.43
6:AF:18:GLN:CD	6:AF:18:GLN:H	2.19	0.43
8:AH:17:THR:HB	8:AH:78:GLN:OE1	2.19	0.43
9:AI:4:TYR:CE1	9:AI:88:TYR:HA	2.53	0.43
14:AN:3:ARG:HB3	14:AN:3:ARG:HH21	1.83	0.43
17:AQ:12:SER:HB3	17:AQ:20:THR:HB	2.01	0.43
25:BA:2376:A:N6	38:BS:89:ARG:HD3	2.33	0.43
25:BA:2663:G:C6	25:BA:2664:G:C4	3.06	0.43
25:BA:2812:G:H2'	25:BA:2813:A:C8	2.53	0.43
26:BB:7:G:H8	26:BB:7:G:H5"	1.84	0.43
27:BD:132:PRO:HG2	27:BD:135:PHE:CE2	2.53	0.43
32:BI:60:GLU:HG3	32:BI:61:ARG:NH1	2.33	0.43
42:BW:4:LYS:HG2	42:BW:5:ALA:N	2.33	0.43
50:B4:55:ARG:N	50:B4:56:VAL:HA	2.32	0.43
1:CA:382:A:H2'	1:CA:383:A:C8	2.53	0.43
1:CA:452:A:O2'	1:CA:453:A:H5"	2.19	0.43
1:CA:750:G:N2	15:CO:23:GLY:O	2.43	0.43
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.88	0.43
4:CD:158:ILE:HD13	4:CD:158:ILE:HA	1.91	0.43
5:CE:116:THR:HG23	5:CE:117:ASP:OD2	2.19	0.43
10:CJ:33:GLN:H	10:CJ:76:ASN:H	1.66	0.43
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.33	0.43
16:CP:6:LEU:HB3	16:CP:17:TYR:HD2	1.82	0.43
25:DA:935:C:H2'	25:DA:936:C:H6	1.82	0.43
25:DA:1721:G:N1	25:DA:1739:U:OP2	2.51	0.43
27:DD:108:PRO:HB3	27:DD:143:HIS:HE1	1.84	0.43
31:DH:9:ILE:HG12	31:DH:69:ARG:HD2	1.99	0.43
31:DH:97:ARG:O	31:DH:103:LEU:HD12	2.19	0.43
31:DH:149:ARG:NH1	31:DH:167:GLU:OE2	2.50	0.43
32:DI:73:GLU:HG3	32:DI:138:ILE:HG23	1.99	0.43
34:DO:106:LEU:HD23	34:DO:106:LEU:HA	1.87	0.43
35:DP:121:LYS:O	35:DP:123:LEU:N	2.49	0.43
41:DV:24:LYS:HA	41:DV:92:THR:OG1	2.19	0.43
41:DV:52:VAL:CG2	41:DV:55:ALA:HB3	2.44	0.43
45:DZ:156:LYS:HE2	45:DZ:156:LYS:HB3	1.79	0.43
1:AA:589:C:H42	1:AA:650:G:H1	1.66	0.43
1:AA:1118:C:O5'	1:AA:1118:C:H6	2.00	0.43
4:AD:36:ARG:HB2	4:AD:38:TYR:CZ	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:69:VAL:HG22	5:AE:71:LEU:HD23	2.01	0.43
7:AG:144:MET:HE2	7:AG:144:MET:HB3	1.73	0.43
24:AX:16:C:O2'	24:AX:17:C:H5'	2.18	0.43
25:BA:1653:G:H3'	37:BR:2:ARG:HB2	2.00	0.43
25:BA:1805:U:O2	27:BD:50:THR:HB	2.19	0.43
25:BA:1814:G:H2'	25:BA:1815:A:C8	2.54	0.43
25:BA:2712:U:O2'	25:BA:2713:A:H5'	2.18	0.43
25:BA:2830:G:H5"	28:BE:58:ARG:CZ	2.49	0.43
30:BG:43:LEU:HB3	30:BG:44:GLY:H	1.59	0.43
1:CA:191:G:N2	20:CT:103:GLY:HA2	2.33	0.43
1:CA:1165:C:N4	1:CA:1171:G:H1	2.13	0.43
1:CA:1227:A:H3'	1:CA:1227:A:C8	2.53	0.43
1:CA:1328:C:H2'	1:CA:1329:A:O4'	2.19	0.43
3:CC:7:PRO:HG3	3:CC:175:LEU:HD23	2.00	0.43
3:CC:199:LYS:HB3	3:CC:201:TYR:HE1	1.83	0.43
10:CJ:42:THR:HG21	10:CJ:66:ARG:HB3	2.00	0.43
25:DA:898:C:H2'	25:DA:899:A:O4'	2.18	0.43
25:DA:910:A:C6	25:DA:911:A:C6	3.07	0.43
25:DA:1785:A:H2'	25:DA:1787:A:N7	2.34	0.43
25:DA:2298:A:H2'	25:DA:2299:G:O4'	2.18	0.43
26:DB:50:G:OP1	38:DS:63:THR:OG1	2.28	0.43
26:DB:83:G:H4'	49:D3:52:HIS:CG	2.53	0.43
26:DB:110:G:H2'	26:DB:111:G:C8	2.54	0.43
28:DE:1:MET:HE3	28:DE:199:ARG:HB3	2.00	0.43
42:DW:46:PHE:O	42:DW:50:VAL:HG23	2.19	0.43
1:AA:404:U:H3'	4:AD:3:ARG:NH2	2.33	0.43
1:AA:542:G:OP1	4:AD:10:ARG:NH2	2.47	0.43
1:AA:1068:G:N2	1:AA:1191:A:N3	2.62	0.43
1:AA:1164:G:H2'	1:AA:1165:C:C6	2.54	0.43
1:AA:1347:G:C8	9:AI:107:ARG:HB2	2.54	0.43
1:AA:1356:G:H2'	1:AA:1357:A:H8	1.78	0.43
5:AE:72:GLN:O	5:AE:75:THR:HG22	2.19	0.43
8:AH:96:GLY:N	8:AH:99:GLU:OE2	2.24	0.43
16:AP:74:LEU:HG	16:AP:79:VAL:HG21	2.00	0.43
25:BA:528:A:C2	25:BA:2042:A:H2'	2.53	0.43
25:BA:1021:A:H61	25:BA:1142(A):A:H61	1.66	0.43
25:BA:1045:A:O2'	25:BA:1047:G:C4	2.67	0.43
25:BA:2141:G:C5	25:BA:2151:G:C2	3.07	0.43
25:BA:2153:G:H2'	25:BA:2154:G:C8	2.54	0.43
25:BA:2260:C:H2'	25:BA:2261:C:H6	1.84	0.43
28:BE:181:LEU:HD11	39:BT:6:LEU:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BN:138:LEU:HA	33:BN:138:LEU:HD23	1.73	0.43
37:BR:2:ARG:NH1	37:BR:5:LYS:O	2.51	0.43
37:BR:36:THR:HG22	37:BR:37:THR:N	2.34	0.43
38:BS:15:ARG:NE	38:BS:88:ASP:OD2	2.29	0.43
39:BT:50:ILE:HB	39:BT:99:LEU:HB2	2.00	0.43
1:CA:153:C:H2'	1:CA:154:C:C6	2.53	0.43
1:CA:161:A:H2'	1:CA:162:A:C8	2.53	0.43
1:CA:375:U:H4'	16:CP:17:TYR:CE2	2.54	0.43
1:CA:599:C:C2'	1:CA:600:C:H5'	2.49	0.43
1:CA:933:G:C6	1:CA:1385:G:C6	3.06	0.43
1:CA:1057:G:H5'	3:CC:155:GLY:HA2	2.00	0.43
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.54	0.43
1:CA:1159:U:O4'	1:CA:1182:G:N2	2.52	0.43
1:CA:1328:C:OP2	21:CU:7:ARG:NH1	2.51	0.43
1:CA:1347:G:H5"	9:CI:107:ARG:HB3	1.99	0.43
1:CA:1369:C:H2'	1:CA:1370:G:O4'	2.19	0.43
8:CH:50:ARG:HA	8:CH:59:LEU:HD23	2.00	0.43
9:CI:9:ARG:HB2	9:CI:104:ARG:HD2	2.00	0.43
15:CO:58:MET:O	15:CO:62:GLN:N	2.49	0.43
25:DA:458:G:C8	53:D7:37:LYS:HG2	2.54	0.43
25:DA:856:C:H2'	25:DA:857:C:C6	2.53	0.43
25:DA:903:C:H2'	25:DA:904:C:H6	1.80	0.43
25:DA:1003:G:N2	25:DA:1153:C:C2	2.86	0.43
25:DA:1221:C:H2'	25:DA:1221(A):C:C6	2.53	0.43
25:DA:1907:G:C6	25:DA:1908:C:C4	3.06	0.43
25:DA:2397:G:N2	25:DA:2420:C:H1'	2.33	0.43
26:DB:42:C:H2'	30:DG:66:GLN:HE21	1.83	0.43
26:DB:43:C:OP1	50:D4:6:HIS:NE2	2.50	0.43
30:DG:96:ARG:N	30:DG:99:MET:HE2	2.34	0.43
37:DR:26:LYS:HE2	37:DR:70:LEU:O	2.19	0.43
37:DR:38:VAL:HB	37:DR:39:PRO:HD3	2.01	0.43
45:DZ:14:LYS:HE2	45:DZ:16:SER:OG	2.18	0.43
52:D6:23:THR:OG1	52:D6:24:GLU:N	2.45	0.43
54:D8:39:LYS:O	54:D8:43:GLN:HG3	2.19	0.43
1:AA:543:C:C2'	1:AA:544:G:H5'	2.49	0.43
1:AA:575:G:O2'	1:AA:821:G:H5'	2.19	0.43
11:AK:104:GLN:HE21	11:AK:104:GLN:HB3	1.62	0.43
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.18	0.43
19:AS:36:ARG:NH1	19:AS:53:ASN:HA	2.34	0.43
24:AX:47:U:H5"	24:AX:48:C:OP1	2.19	0.43
25:BA:574:C:N3	28:BE:145:LYS:NZ	2.64	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1021:A:H3'	25:BA:1021:A:C8	2.53	0.43
25:BA:1292:U:H2'	25:BA:1293:C:H6	1.84	0.43
25:BA:2278:A:OP2	46:B0:12:ASN:ND2	2.48	0.43
25:BA:2320:A:N3	25:BA:2320:A:H2'	2.34	0.43
25:BA:2507:C:H4'	25:BA:2573:C:N4	2.33	0.43
25:BA:2635:C:H4'	28:BE:48:GLN:HE21	1.84	0.43
25:BA:2732:G:H3'	25:BA:2733:A:O4'	2.18	0.43
29:BF:33:LEU:HD12	29:BF:33:LEU:HA	1.82	0.43
35:BP:86:LYS:HE3	35:BP:117:GLU:HB3	2.01	0.43
44:BY:28:LYS:HD2	44:BY:40:GLU:HG3	2.01	0.43
1:CA:1312:G:H5'	19:CS:5:LEU:HD21	2.01	0.43
4:CD:91:SER:HA	4:CD:94:LEU:HD12	2.01	0.43
5:CE:60:TYR:C	5:CE:60:TYR:HD1	2.27	0.43
5:CE:93:PRO:HG2	8:CH:105:ARG:CZ	2.48	0.43
8:CH:17:THR:HB	8:CH:78:GLN:OE1	2.18	0.43
13:CM:93:ARG:NH1	25:DA:888:C:OP1	2.48	0.43
15:CO:54:ARG:O	15:CO:58:MET:HG3	2.18	0.43
25:DA:10:G:H2'	25:DA:11:G:H8	1.83	0.43
25:DA:307:G:H2'	25:DA:309:G:OP2	2.19	0.43
25:DA:459:U:OP2	25:DA:469:G:N1	2.34	0.43
25:DA:1216:G:N2	25:DA:1234:U:H1'	2.33	0.43
25:DA:1516:C:H2'	25:DA:1517:G:C8	2.54	0.43
25:DA:1971:A:C4	27:DD:241:PRO:HD3	2.53	0.43
25:DA:2207:G:H8	25:DA:2207:G:OP1	2.01	0.43
28:DE:181:LEU:HD12	28:DE:181:LEU:HA	1.82	0.43
29:DF:179:GLU:CD	29:DF:179:GLU:H	2.26	0.43
32:DI:66:GLU:HA	32:DI:69:LYS:HB3	2.00	0.43
36:DQ:7:MET:HE2	36:DQ:7:MET:HB3	1.86	0.43
39:DT:127:ALA:C	39:DT:129:ARG:H	2.27	0.43
45:DZ:35:ARG:HA	45:DZ:35:ARG:HD2	1.74	0.43
1:AA:56:U:H2'	1:AA:57:G:H8	1.83	0.43
1:AA:673:G:H1	1:AA:717:C:N4	2.17	0.43
1:AA:814:A:N7	1:AA:816:A:C4	2.87	0.43
1:AA:923:A:O2'	1:AA:1399:C:OP2	2.29	0.43
1:AA:1128:C:H4'	1:AA:1148:U:O2	2.19	0.43
1:AA:1134:G:H2'	1:AA:1134:G:N3	2.32	0.43
1:AA:1285:A:H1'	1:AA:1286:A:OP2	2.19	0.43
4:AD:108:LEU:HD12	4:AD:108:LEU:HA	1.91	0.43
7:AG:76:ARG:N	7:AG:87:VAL:O	2.44	0.43
14:AN:3:ARG:HA	14:AN:3:ARG:HD2	1.61	0.43
15:AO:8:LYS:HE3	15:AO:31:LEU:HD22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:12:ILE:HG23	15:AO:27:VAL:HG11	2.01	0.43
16:AP:58:TYR:O	16:AP:62:VAL:HG23	2.18	0.43
18:AR:21:LYS:HE2	18:AR:54:ARG:O	2.19	0.43
25:BA:581:C:H2'	25:BA:582:G:H8	1.84	0.43
25:BA:588:U:H2'	25:BA:589:C:C6	2.54	0.43
25:BA:1285:G:C5	25:BA:1329:U:C4	3.07	0.43
25:BA:1445:A:H8	25:BA:1460:A:C5	2.37	0.43
25:BA:1798:U:OP2	27:BD:274:ARG:NH2	2.52	0.43
25:BA:2331:G:O2'	25:BA:2336:A:N1	2.45	0.43
30:BG:138:GLN:HE22	30:BG:153:ARG:N	2.11	0.43
35:BP:121:LYS:HB3	35:BP:123:LEU:HG	2.00	0.43
1:CA:129(A):G:O2'	1:CA:189(F):U:OP1	2.25	0.43
1:CA:241:C:H42	1:CA:285:G:H1	1.65	0.43
1:CA:944:G:C2	1:CA:1340:A:C6	3.06	0.43
1:CA:1030(A):G:N3	1:CA:1030(C):G:C8	2.87	0.43
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.54	0.43
1:CA:1386:G:C2	1:CA:1387:G:C8	3.06	0.43
2:CB:27:LYS:O	2:CB:30:ARG:NH1	2.51	0.43
2:CB:70:PHE:HB3	2:CB:81:VAL:HG11	2.00	0.43
8:CH:34:GLU:HB3	8:CH:118:VAL:HG21	1.99	0.43
9:CI:16:ARG:O	9:CI:64:THR:N	2.50	0.43
20:CT:40:ALA:HB2	20:CT:55:ILE:HG22	2.01	0.43
25:DA:195:A:H2'	25:DA:198:C:H41	1.83	0.43
25:DA:330:A:H2	25:DA:1210:A:C2'	2.27	0.43
25:DA:602:G:H4'	25:DA:604:G:H4'	1.99	0.43
25:DA:1028:A:H2'	25:DA:1029:A:C8	2.54	0.43
25:DA:1366:A:H2'	25:DA:1367:A:O4'	2.19	0.43
25:DA:1880:C:C2'	25:DA:1881:C:H5'	2.49	0.43
25:DA:2369:A:H2'	25:DA:2370:G:H8	1.84	0.43
25:DA:2633:G:H5"	25:DA:2812:G:H5'	2.00	0.43
27:DD:218:ARG:HB3	27:DD:219:PRO:HD2	2.01	0.43
33:DN:42:TRP:HA	33:DN:48:MET:HE1	2.01	0.43
33:DN:115:ARG:HA	33:DN:118:LYS:HE3	2.01	0.43
38:DS:26:LEU:HD22	38:DS:87:PHE:CE1	2.53	0.43
40:DU:76:TYR:CE1	40:DU:80:ILE:HG13	2.54	0.43
1:AA:72:C:H2'	1:AA:73:G:O4'	2.19	0.43
1:AA:520:A:N1	1:AA:536:C:H1'	2.34	0.43
1:AA:616:G:C2	1:AA:617:G:C8	3.07	0.43
1:AA:1030:C:N3	1:AA:1031:G:C2	2.87	0.43
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.18	0.43
1:AA:1237:C:H5"	1:AA:1238:A:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:19:HIS:CD2	2:AB:206:ASP:HB2	2.54	0.43
2:AB:218:ALA:O	2:AB:222:ILE:HG13	2.19	0.43
4:AD:172:PRO:O	4:AD:187:ARG:NH2	2.51	0.43
12:AL:34:ARG:HH11	12:AL:61:THR:HG21	1.84	0.43
21:AU:3:LYS:HA	21:AU:11:GLY:HA2	2.01	0.43
24:AX:19:G:C4	24:AX:57:A:C2	3.06	0.43
24:AX:36:U:H2'	24:AX:37:A:C8	2.54	0.43
25:BA:1331:A:H2'	25:BA:1333:C:C5	2.54	0.43
25:BA:1541:G:H3'	25:BA:1542:A:H2'	2.01	0.43
25:BA:1562:A:H2'	25:BA:1563:G:C8	2.53	0.43
34:BO:120:GLU:HG2	34:BO:122:LEU:HG	2.01	0.43
44:BY:39:VAL:HB	44:BY:42:VAL:HB	2.01	0.43
47:B1:86:SER:O	47:B1:89:GLU:HG2	2.19	0.43
1:CA:80:G:N2	1:CA:90:U:H1'	2.34	0.43
1:CA:375:U:C2	1:CA:376:G:C8	3.07	0.43
1:CA:691:G:H2'	1:CA:692:U:C6	2.54	0.43
1:CA:724:G:C2	1:CA:725:G:C8	3.06	0.43
1:CA:827:U:O2'	8:CH:19:VAL:HG11	2.19	0.43
1:CA:857:C:H2'	1:CA:858:G:O4'	2.19	0.43
1:CA:1362:C:H2'	1:CA:1363:C:H5"	2.01	0.43
2:CB:28:PHE:CE1	2:CB:31:TYR:HB2	2.54	0.43
2:CB:160:ASP:N	2:CB:160:ASP:OD1	2.52	0.43
7:CG:115:ARG:O	7:CG:119:ARG:HG3	2.19	0.43
10:CJ:55:LYS:O	10:CJ:57:LYS:N	2.52	0.43
11:CK:19:ALA:HB3	11:CK:82:VAL:HG22	1.99	0.43
11:CK:120:ARG:HA	11:CK:121:PRO:HD3	1.85	0.43
20:CT:43:LEU:HD13	20:CT:51:GLU:HB3	2.01	0.43
25:DA:268:C:H2'	25:DA:269:U:O4'	2.18	0.43
25:DA:493:G:H2'	25:DA:494:G:O4'	2.18	0.43
25:DA:764:A:N1	25:DA:1789:A:O2'	2.43	0.43
25:DA:1221:C:H2'	25:DA:1221(A):C:H6	1.83	0.43
25:DA:1232:G:C6	25:DA:1233:C:C4	3.07	0.43
25:DA:1265:A:H61	25:DA:2013:A:H5"	1.84	0.43
25:DA:1652:A:OP1	37:DR:8:ARG:NH1	2.51	0.43
25:DA:2380:C:H6	25:DA:2380:C:O5'	2.02	0.43
27:DD:13:ARG:HA	27:DD:13:ARG:HD2	1.85	0.43
29:DF:64:ILE:HG13	29:DF:65:TRP:N	2.34	0.43
29:DF:64:ILE:HG21	29:DF:78:ILE:HG23	2.01	0.43
36:DQ:1:MET:HE3	36:DQ:45:GLN:HE22	1.84	0.43
37:DR:10:LEU:HD23	37:DR:10:LEU:HA	1.85	0.43
1:AA:426:G:H2'	1:AA:427:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.53	0.42
1:AA:1157:A:H61	1:AA:1178:G:H21	1.67	0.42
4:AD:60:GLU:OE2	4:AD:63:LYS:NZ	2.51	0.42
4:AD:94:LEU:O	4:AD:98:GLU:N	2.52	0.42
4:AD:166:LYS:HB2	4:AD:168:ARG:HH12	1.84	0.42
15:AO:3:ILE:H	15:AO:3:ILE:HD13	1.84	0.42
20:AT:48:LYS:HA	20:AT:48:LYS:HD3	1.90	0.42
25:BA:911:A:N1	25:BA:2277:G:O2'	2.46	0.42
25:BA:1141:U:OP1	33:BN:25:ARG:NH1	2.52	0.42
25:BA:1791:A:H8	25:BA:1791:A:OP2	2.02	0.42
25:BA:2364:C:H4'	46:B0:56:ASP:OD1	2.19	0.42
27:BD:17:THR:HG1	27:BD:205:VAL:H	1.61	0.42
29:BF:24:LEU:HD21	29:BF:114:VAL:HG12	2.00	0.42
36:BQ:1:MET:SD	36:BQ:1:MET:N	2.83	0.42
42:BW:86:LEU:HD12	42:BW:87:PRO:HD2	2.01	0.42
45:BZ:110:GLY:CA	45:BZ:145:GLU:HA	2.49	0.42
45:BZ:110:GLY:N	45:BZ:144:LEU:O	2.48	0.42
1:CA:1008:C:C2	1:CA:1022:G:C2	3.07	0.42
2:CB:145:LEU:O	2:CB:149:LEU:HB2	2.20	0.42
3:CC:18:TRP:HE3	3:CC:18:TRP:H	1.67	0.42
5:CE:51:VAL:O	5:CE:55:VAL:HG23	2.19	0.42
6:CF:99:ALA:HB1	18:CR:23:LYS:HE3	2.01	0.42
9:CI:127:LYS:O	9:CI:128:ARG:HB3	2.18	0.42
13:CM:40:ASN:HA	13:CM:41:PRO:HD3	1.92	0.42
13:CM:80:ARG:HH21	19:CS:69:HIS:HE1	1.68	0.42
13:CM:94:ARG:NH1	19:CS:80:TYR:HD2	2.17	0.42
19:CS:56:GLN:HE21	19:CS:56:GLN:HB3	1.52	0.42
20:CT:23:ARG:HH11	20:CT:23:ARG:HG3	1.84	0.42
25:DA:271(R):G:H5"	47:D1:97:LEU:HD21	2.00	0.42
25:DA:539:G:H2'	25:DA:540:C:C6	2.54	0.42
25:DA:646:A:H2'	25:DA:647:G:O4'	2.19	0.42
25:DA:909:A:N6	25:DA:912:C:O2	2.52	0.42
25:DA:1462:C:H2'	25:DA:1463:C:O4'	2.20	0.42
25:DA:1685:C:H2'	25:DA:1686:C:H6	1.83	0.42
25:DA:1983:C:H4'	25:DA:2606:C:O3'	2.18	0.42
25:DA:2305:A:H5"	30:DG:134:GLY:HA3	2.00	0.42
25:DA:2507:C:H2'	25:DA:2508:G:O4'	2.19	0.42
26:DB:53:A:H2'	26:DB:53:A:N3	2.34	0.42
29:DF:168:ARG:HB2	29:DF:175:THR:HG21	2.01	0.42
39:DT:80:SER:HA	39:DT:81:PRO:HD2	1.90	0.42
44:DY:45:VAL:N	44:DY:63:LYS:O	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:D8:62:LEU:HB3	54:D8:65:GLU:HG3	2.01	0.42
1:AA:376:G:H2'	1:AA:377:G:H8	1.84	0.42
1:AA:518:C:O2'	1:AA:530:G:N2	2.52	0.42
1:AA:927:G:H1	1:AA:1390:U:H3	1.67	0.42
1:AA:1038:C:H2'	1:AA:1039:C:H6	1.82	0.42
1:AA:1220:G:N2	19:AS:54:GLY:O	2.48	0.42
1:AA:1343:G:O2'	9:AI:121:ARG:HD3	2.19	0.42
1:AA:1392:G:N2	1:AA:1502:A:H8	2.17	0.42
1:AA:1393:U:O2'	1:AA:1394:A:H2'	2.20	0.42
1:AA:1438:G:H2'	1:AA:1439:C:C6	2.54	0.42
1:AA:1503:A:H5'	1:AA:1532:U:OP2	2.19	0.42
2:AB:32:ILE:HD13	2:AB:40:HIS:HD2	1.84	0.42
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.52	0.42
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	2.01	0.42
7:AG:38:LEU:O	7:AG:42:ILE:HG13	2.19	0.42
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.19	0.42
25:BA:531:C:H4'	25:BA:532:A:H5"	1.99	0.42
25:BA:961:C:N4	60:BA:3765:HOH:O	2.36	0.42
25:BA:1451:C:H42	25:BA:1459:G:H1	1.68	0.42
25:BA:1495:A:H2'	25:BA:1496:A:C8	2.53	0.42
25:BA:1721:G:N1	25:BA:1739:U:OP2	2.52	0.42
25:BA:2074:U:H2'	25:BA:2075:U:C6	2.53	0.42
25:BA:2228:G:C5	25:BA:2229:C:C4	3.06	0.42
34:BO:20:MET:HE3	34:BO:44:LYS:HE3	2.02	0.42
35:BP:2:LYS:HE3	35:BP:4:SER:OG	2.19	0.42
51:B5:41:PRO:HA	51:B5:42:PRO:HD3	1.89	0.42
1:CA:553:A:C6	1:CA:554:C:C4	3.07	0.42
1:CA:938:A:C2	1:CA:1376:U:H1'	2.54	0.42
1:CA:1144:G:H21	1:CA:1146:A:H62	1.66	0.42
1:CA:1191:A:OP2	3:CC:3:ASN:ND2	2.52	0.42
2:CB:28:PHE:CD1	2:CB:190:THR:HA	2.54	0.42
2:CB:163:PHE:CD1	2:CB:185:ILE:HG13	2.46	0.42
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.67	0.42
5:CE:78:HIS:HB3	8:CH:107:LEU:HD12	2.00	0.42
6:CF:24:GLU:HG3	6:CF:28:ARG:HD2	2.01	0.42
9:CI:17:VAL:HG11	9:CI:81:ILE:N	2.34	0.42
12:CL:124:LYS:HB2	12:CL:124:LYS:NZ	2.35	0.42
24:CX:24:U:O2'	25:DA:1923:U:OP1	2.33	0.42
25:DA:686:G:C4	53:D7:11:LYS:HG2	2.54	0.42
25:DA:873:G:N2	25:DA:905:U:O2	2.51	0.42
25:DA:1128:A:O2'	25:DA:2490:G:OP1	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1653:G:H4'	25:DA:1654:A:O5'	2.19	0.42
25:DA:1816:G:O6	27:DD:35:LYS:NZ	2.49	0.42
25:DA:1817:G:C6	25:DA:1818:U:C4	3.06	0.42
25:DA:2400:G:H2'	25:DA:2401:U:H6	1.84	0.42
25:DA:2564:A:C2	25:DA:2647:U:H4'	2.53	0.42
26:DB:64:C:H2'	26:DB:65:C:C6	2.55	0.42
26:DB:75:G:H21	45:DZ:85:HIS:CE1	2.37	0.42
29:DF:20:LEU:HD23	29:DF:20:LEU:HA	1.80	0.42
35:DP:27:HIS:O	35:DP:31:ALA:HA	2.18	0.42
37:DR:67:LEU:HD13	37:DR:67:LEU:HA	1.81	0.42
39:DT:27:THR:HB	39:DT:89:VAL:HG23	2.00	0.42
45:DZ:44:PHE:CZ	45:DZ:86:VAL:HG11	2.55	0.42
49:D3:46:ASN:O	49:D3:50:VAL:HG22	2.20	0.42
55:D9:2:LYS:HE2	55:D9:31:LYS:O	2.20	0.42
1:AA:99:U:H2'	1:AA:100:C:C6	2.54	0.42
1:AA:142:G:H2'	1:AA:143:A:H8	1.85	0.42
1:AA:257:G:C6	1:AA:258:G:C5	3.07	0.42
1:AA:620:C:H2'	1:AA:621:A:O4'	2.19	0.42
1:AA:1346:A:OP1	9:AI:120:ARG:NH1	2.37	0.42
2:AB:122:PHE:CE2	2:AB:139:LYS:HE2	2.54	0.42
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	2.01	0.42
5:AE:102:ALA:O	5:AE:107:ARG:NH1	2.52	0.42
25:BA:519:U:H2'	25:BA:520:G:C8	2.54	0.42
25:BA:807:U:OP2	35:BP:41:ARG:NH2	2.52	0.42
25:BA:1173:G:O2'	25:BA:1174:A:O5'	2.33	0.42
25:BA:1420:U:O2'	25:BA:1421:G:OP1	2.31	0.42
25:BA:1427:A:H4'	25:BA:1428:C:O4'	2.19	0.42
25:BA:2191:G:H5'	25:BA:2192:G:OP2	2.19	0.42
25:BA:2633:G:H5'	25:BA:2811:G:O2'	2.19	0.42
33:BN:39:ARG:NH2	33:BN:41:ASP:OD2	2.52	0.42
34:BO:78:ARG:HD2	60:BT:202:HOH:O	2.18	0.42
41:BV:40:LEU:HB2	41:BV:46:VAL:HG13	2.01	0.42
42:BW:14:PRO:HG2	42:BW:78:GLU:CD	2.45	0.42
1:CA:93:G:C6	1:CA:96:U:C4	3.07	0.42
1:CA:129(A):G:N3	1:CA:189(F):U:H5"	2.35	0.42
1:CA:187:C:H2'	1:CA:188:C:H6	1.83	0.42
1:CA:191:G:C2	20:CT:103:GLY:HA2	2.54	0.42
1:CA:582:U:O4	1:CA:758:G:H2'	2.19	0.42
1:CA:939:G:H2'	1:CA:940:C:C6	2.54	0.42
1:CA:1080:A:H5'	5:CE:14:ARG:NH2	2.34	0.42
1:CA:1118:C:C6	1:CA:1119:C:H5	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:92:HIS:HA	13:CM:110:ARG:HH12	1.84	0.42
18:CR:59:SER:OG	18:CR:62:GLU:HG2	2.19	0.42
25:DA:350:U:H2'	25:DA:351:G:O4'	2.19	0.42
25:DA:577:G:H8	25:DA:577:G:O5'	2.03	0.42
25:DA:623:G:H2'	25:DA:624:C:C6	2.54	0.42
25:DA:660:G:H5'	29:DF:99:TYR:CE2	2.54	0.42
25:DA:1246:A:OP1	29:DF:38:ARG:NH1	2.52	0.42
25:DA:1385:G:H4'	25:DA:1386:C:OP1	2.19	0.42
25:DA:1970:A:OP2	60:DA:4202:HOH:O	2.22	0.42
25:DA:2400:G:H2'	25:DA:2401:U:C6	2.54	0.42
25:DA:2745:C:C4	25:DA:2746:U:C4	3.07	0.42
26:DB:62:C:H2'	26:DB:63:G:C8	2.54	0.42
27:DD:171:ASP:O	27:DD:187:GLY:N	2.46	0.42
31:DH:81:GLU:OE1	31:DH:81:GLU:N	2.46	0.42
32:DI:88:ILE:O	32:DI:121:LYS:NZ	2.44	0.42
33:DN:39:ARG:HA	33:DN:40:PRO:HD3	1.85	0.42
36:DQ:85:LYS:NZ	46:D0:7:LEU:HG	2.34	0.42
38:DS:38:GLN:HG3	38:DS:40:ILE:HD11	2.00	0.42
54:D8:60:LEU:HD23	54:D8:60:LEU:HA	1.84	0.42
1:AA:1053:G:N7	1:AA:1200:C:H5"	2.34	0.42
1:AA:1316:G:O3'	14:AN:18:VAL:HG22	2.19	0.42
7:AG:58:PRO:O	7:AG:61:VAL:HG12	2.19	0.42
9:AI:99:LEU:HB3	9:AI:101:PHE:HE1	1.84	0.42
17:AQ:37:LYS:O	17:AQ:38:ARG:HD3	2.20	0.42
19:AS:15:LEU:HD13	19:AS:33:THR:HB	2.00	0.42
25:BA:686:G:N2	25:BA:788:A:H61	2.17	0.42
25:BA:1252:G:OP1	40:BU:36:ARG:NH2	2.52	0.42
25:BA:1996:C:H4'	25:BA:1997:G:OP1	2.19	0.42
25:BA:2135:A:N6	25:BA:2156:G:O2'	2.47	0.42
25:BA:2166:G:N7	25:BA:2168:G:N2	2.61	0.42
25:BA:2271:G:OP1	46:B0:18:ALA:HB1	2.20	0.42
25:BA:2271:G:H5"	46:B0:20:ARG:HE	1.85	0.42
25:BA:2336:A:H61	46:B0:43:THR:HG22	1.84	0.42
25:BA:2511:U:O2'	28:BE:138:PRO:O	2.24	0.42
25:BA:2791:C:H6	25:BA:2791:C:OP2	2.02	0.42
27:BD:101:GLU:OE1	27:BD:103:ARG:HD3	2.19	0.42
29:BF:7:TYR:O	29:BF:21:ALA:HA	2.18	0.42
29:BF:93:LYS:HD3	29:BF:93:LYS:HA	1.88	0.42
30:BG:121:ASN:HA	30:BG:122:PRO:HD2	1.88	0.42
41:BV:62:LEU:HD13	41:BV:95:LEU:HB2	2.01	0.42
1:CA:97:G:C4	1:CA:98:G:C8	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:722:A:N6	1:CA:724:G:C2	2.88	0.42
1:CA:784:C:H2'	1:CA:785:G:O4'	2.19	0.42
1:CA:975:A:H8	1:CA:975:A:H5'	1.83	0.42
1:CA:1014:A:H2'	1:CA:1015:A:C8	2.55	0.42
1:CA:1142:G:C2	1:CA:1143:G:H1'	2.54	0.42
6:CF:6:VAL:HG13	6:CF:90:VAL:HG22	2.02	0.42
8:CH:75:ARG:HA	8:CH:76:PRO:HD2	1.83	0.42
11:CK:48:ILE:H	11:CK:48:ILE:HG12	1.54	0.42
25:DA:76:C:O3'	48:D2:59:ARG:HG3	2.20	0.42
25:DA:380:U:H2'	25:DA:381:G:C8	2.54	0.42
25:DA:588:U:H1'	29:DF:90:PHE:HB3	2.01	0.42
25:DA:690:G:H5'	60:DA:4052:HOH:O	2.19	0.42
25:DA:1005:C:H4'	25:DA:1012:U:C6	2.54	0.42
25:DA:1337:G:H2'	25:DA:1338:G:O4'	2.19	0.42
25:DA:1514:U:H2'	25:DA:1515:G:H8	1.84	0.42
25:DA:1593:G:C2	25:DA:1594:G:C4	3.07	0.42
25:DA:1692:U:O2'	25:DA:1693:U:H2'	2.19	0.42
25:DA:2106:G:C6	25:DA:2184:G:C6	3.07	0.42
25:DA:2110:G:O6	25:DA:2179:C:N3	2.51	0.42
25:DA:2512:C:H2'	25:DA:2513:G:O4'	2.19	0.42
25:DA:2880:C:O3'	37:DR:90:ARG:NH1	2.52	0.42
27:DD:64:ILE:O	27:DD:104:TYR:HB2	2.19	0.42
27:DD:70:TRP:HB3	27:DD:190:TYR:CE1	2.54	0.42
28:DE:111:ARG:HD3	37:DR:1:MET:HE1	2.00	0.42
32:DI:78:THR:HG23	32:DI:143:SER:OG	2.20	0.42
1:AA:102:G:O2'	1:AA:151:A:N3	2.34	0.42
1:AA:345:C:H5	39:BT:39:ARG:HH22	1.68	0.42
1:AA:1194:U:H2'	1:AA:1195:C:H6	1.84	0.42
5:AE:35:GLY:HA3	5:AE:112:LEU:HB3	2.01	0.42
6:AF:8:ILE:HD13	6:AF:26:ILE:HD13	2.00	0.42
9:AI:49:PRO:HB3	9:AI:82:ALA:HB2	2.01	0.42
20:AT:38:LYS:O	20:AT:42:GLN:N	2.44	0.42
25:BA:28:A:H1'	25:BA:513:A:C2	2.55	0.42
25:BA:74:A:H5'	25:BA:75:G:O4'	2.20	0.42
25:BA:383:U:H5"	25:BA:384:U:OP2	2.19	0.42
25:BA:458:G:C5	53:B7:37:LYS:HE2	2.53	0.42
25:BA:565:C:H4'	25:BA:1253:A:C6	2.55	0.42
25:BA:1263:U:H1'	51:B5:10:LYS:HG3	2.01	0.42
25:BA:1675:C:O2	28:BE:128:SER:OG	2.37	0.42
25:BA:2394:C:OP1	54:B8:30:ARG:NH1	2.52	0.42
25:BA:2732:G:OP1	28:BE:203:LYS:HE2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BQ:86:GLY:HA3	46:B0:10:THR:HG23	2.01	0.42
40:BU:112:ARG:H	40:BU:112:ARG:HG2	1.42	0.42
46:B0:40:GLN:NE2	46:B0:43:THR:HA	2.35	0.42
1:CA:170:U:O2'	1:CA:171:A:H5'	2.20	0.42
1:CA:1048:G:OP2	14:CN:3:ARG:NH2	2.53	0.42
1:CA:1224:G:C6	1:CA:1322:C:O4'	2.72	0.42
1:CA:1306:A:C6	1:CA:1307:U:C4	3.06	0.42
12:CL:34:ARG:O	12:CL:61:THR:HG23	2.19	0.42
18:CR:73:ALA:HB3	18:CR:79:LEU:HD12	2.01	0.42
20:CT:65:LYS:HA	20:CT:68:LYS:HD3	2.01	0.42
25:DA:143(A):C:H4'	43:DX:38:GLU:OE1	2.19	0.42
25:DA:1426:G:O2'	25:DA:1572:A:N6	2.46	0.42
25:DA:2870:C:H2'	25:DA:2871:C:O4'	2.19	0.42
27:DD:232:PRO:HB3	27:DD:244:ARG:CZ	2.50	0.42
28:DE:119:ARG:HB3	28:DE:120:TRP:CD1	2.55	0.42
30:DG:16:ARG:HB2	30:DG:17:PRO:HD3	2.01	0.42
32:DI:116:LEU:HD21	32:DI:119:PRO:HA	2.01	0.42
36:DQ:22:LYS:H	36:DQ:22:LYS:HG2	1.60	0.42
44:DY:20:TYR:CE1	44:DY:43:ASN:HA	2.54	0.42
1:AA:924:C:H2'	1:AA:925:G:C8	2.54	0.42
1:AA:951:G:N3	1:AA:970:C:O2'	2.49	0.42
3:AC:5:ILE:HG12	3:AC:6:HIS:N	2.32	0.42
3:AC:123:GLN:HB3	3:AC:128:PHE:CD2	2.55	0.42
3:AC:131:ARG:HE	3:AC:166:GLU:CD	2.27	0.42
13:AM:34:LEU:CD1	13:AM:41:PRO:HA	2.47	0.42
16:AP:48:TRP:HH2	16:AP:76:GLN:NE2	2.16	0.42
25:BA:328:U:H4'	44:BY:68:HIS:CG	2.54	0.42
25:BA:576:U:H2'	25:BA:577:G:C8	2.54	0.42
25:BA:956:G:H5"	36:BQ:77:LYS:HD2	2.02	0.42
25:BA:1239:G:H2'	25:BA:1240:U:O4'	2.20	0.42
25:BA:1756:G:O2'	25:BA:1758:G:H5"	2.20	0.42
25:BA:1762:A:H2'	60:BA:4156:HOH:O	2.17	0.42
25:BA:2791:C:OP2	25:BA:2791:C:C6	2.73	0.42
26:BB:11:C:H3'	26:BB:12:C:C6	2.55	0.42
26:BB:41:U:O4	30:BG:70:VAL:HB	2.18	0.42
29:BF:135:LYS:HB2	29:BF:138:GLU:CD	2.45	0.42
29:BF:196:LEU:HD23	29:BF:196:LEU:HA	1.86	0.42
36:BQ:39:PRO:HA	36:BQ:97:VAL:O	2.19	0.42
44:BY:15:VAL:O	44:BY:22:GLY:N	2.47	0.42
1:CA:84:U:H4'	1:CA:89:C:N4	2.35	0.42
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.55	0.42

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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	0.42
2:CB:171:ALA:O	2:CB:175:ARG:HG3	2.20	0.42
4:CD:156:GLU:O	4:CD:160:GLN:HG3	2.20	0.42
6:CF:10:LEU:HB2	6:CF:59:TYR:HB3	2.01	0.42
9:CI:128:ARG:OXT	9:CI:128:ARG:HG2	2.20	0.42
20:CT:39:LYS:HB2	20:CT:39:LYS:HE3	1.84	0.42
25:DA:31:C:H5"	25:DA:1239:G:OP1	2.20	0.42
25:DA:253:C:OP2	54:D8:5:LYS:NZ	2.33	0.42
25:DA:747:U:O2	25:DA:2014:A:H1'	2.20	0.42
25:DA:1642:G:H2'	25:DA:1643:G:C8	2.55	0.42
25:DA:2018:G:H2'	25:DA:2019:A:O4'	2.18	0.42
25:DA:2130:U:H3	25:DA:2159:G:H22	1.66	0.42
25:DA:2697:G:H2'	25:DA:2698:U:O4'	2.20	0.42
25:DA:2728:U:H2'	25:DA:2729:G:C8	2.54	0.42
35:DP:31:ALA:O	35:DP:32:THR:OG1	2.30	0.42
1:AA:178:C:H2'	1:AA:179:A:H8	1.84	0.42
1:AA:901:A:H5"	1:AA:902:G:OP2	2.19	0.42
1:AA:985:C:H2'	1:AA:986:A:C8	2.54	0.42
1:AA:1132:C:H2'	1:AA:1133:G:H8	1.82	0.42
1:AA:1280:A:H8	10:AJ:40:LEU:HD22	1.85	0.42
2:AB:18:GLY:O	2:AB:19:HIS:HB3	2.19	0.42
3:AC:35:GLU:O	3:AC:39:ILE:HG13	2.19	0.42
3:AC:156:ARG:N	3:AC:196:LEU:HD22	2.35	0.42
17:AQ:6:LEU:HD12	17:AQ:6:LEU:HA	1.83	0.42
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	2.01	0.42
25:BA:443:A:H1'	25:BA:1201:C:O4'	2.19	0.42
25:BA:2011:U:H2'	25:BA:2012:G:O4'	2.18	0.42
25:BA:2125:G:N2	25:BA:2172:U:OP1	2.45	0.42
25:BA:2149:G:H3'	25:BA:2150:U:C6	2.54	0.42
27:BD:94:LEU:HD22	27:BD:95:LEU:N	2.34	0.42
30:BG:41:GLN:NE2	30:BG:154:GLY:O	2.52	0.42
37:BR:72:ASP:OD2	37:BR:75:LEU:HB2	2.20	0.42
44:BY:67:LEU:HD23	44:BY:67:LEU:HA	1.92	0.42
48:B2:3:LEU:HD22	48:B2:7:ARG:HE	1.83	0.42
50:B4:62:ARG:HA	50:B4:62:ARG:HD3	1.86	0.42
1:CA:125:U:H2'	1:CA:126:G:C8	2.55	0.42
1:CA:585:G:O3'	17:CQ:34:LYS:NZ	2.53	0.42
1:CA:652:U:O2'	1:CA:653:A:OP2	2.33	0.42
1:CA:789:U:H2'	1:CA:791:G:OP2	2.19	0.42
1:CA:827:U:H2'	1:CA:859:A:H61	1.85	0.42
1:CA:848:C:O2'	1:CA:849:C:H5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.85	0.42
1:CA:1140:C:H2'	1:CA:1141:C:C6	2.54	0.42
1:CA:1157:A:H5'	1:CA:1158:C:N1	2.34	0.42
1:CA:1327:C:H5"	21:CU:20:LYS:HB3	2.02	0.42
2:CB:135:GLN:O	2:CB:139:LYS:HB2	2.20	0.42
6:CF:21:LEU:O	6:CF:25:ILE:HG13	2.20	0.42
15:CO:22:THR:OG1	15:CO:23:GLY:N	2.53	0.42
17:CQ:81:ARG:HD2	17:CQ:81:ARG:HA	1.83	0.42
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.20	0.42
25:DA:78:A:C6	25:DA:109:G:C6	3.07	0.42
25:DA:191:A:H2'	25:DA:192:C:C6	2.54	0.42
25:DA:464:U:H4'	53:D7:5:TRP:CZ3	2.54	0.42
25:DA:608:A:C6	25:DA:609:A:C6	3.07	0.42
25:DA:1009:A:N3	25:DA:1153:C:O2'	2.50	0.42
25:DA:2061:G:H5"	25:DA:2503:A:C2	2.54	0.42
25:DA:2127:G:C6	25:DA:2161:C:N3	2.86	0.42
25:DA:2282:G:H4'	25:DA:2389:G:O2'	2.18	0.42
25:DA:2529:G:O6	55:D9:31:LYS:NZ	2.52	0.42
27:DD:95:LEU:HD11	27:DD:105:ILE:HD13	2.00	0.42
35:DP:143:GLY:O	35:DP:145:PRO:HD3	2.19	0.42
38:DS:4:LEU:HD22	38:DS:8:GLU:OE1	2.20	0.42
44:DY:6:HIS:H	44:DY:6:HIS:CD2	2.38	0.42
45:DZ:67:LEU:HD23	45:DZ:67:LEU:HA	1.86	0.42
50:D4:68:ARG:HB3	50:D4:69:LYS:H	1.60	0.42
1:AA:1037:C:O2	1:AA:1037:C:H2'	2.18	0.42
1:AA:1063:C:H3'	1:AA:1064:G:H2'	2.01	0.42
1:AA:1311:G:N2	1:AA:1326:C:N3	2.56	0.42
4:AD:59:ARG:NH2	4:AD:62:GLN:HG3	2.34	0.42
9:AI:84:ALA:O	9:AI:88:TYR:N	2.47	0.42
11:AK:54:ARG:O	11:AK:57:THR:OG1	2.37	0.42
24:AX:17:C:OP2	24:AX:17(A):U:O2'	2.30	0.42
25:BA:171:G:O2'	25:BA:172:C:H5'	2.19	0.42
25:BA:563:G:H22	25:BA:578:A:H2	1.66	0.42
25:BA:839:U:H2'	25:BA:840:C:C6	2.53	0.42
25:BA:944:G:H5"	25:BA:945:A:O5'	2.20	0.42
25:BA:1179:C:H2'	25:BA:1180:C:C6	2.54	0.42
25:BA:2282:G:OP1	25:BA:2283:C:H1'	2.20	0.42
32:BI:50:ARG:HD2	32:BI:50:ARG:HA	1.90	0.42
36:BQ:79:LEU:HD23	36:BQ:79:LEU:HA	1.91	0.42
50:B4:53:GLU:C	50:B4:55:ARG:N	2.78	0.42
1:CA:190:U:H2'	1:CA:191:G:H8	1.80	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:320:C:O2'	1:CA:1435:G:H1'	2.20	0.42
1:CA:995:C:H4'	14:CN:8:GLU:OE2	2.20	0.42
1:CA:1220:G:H5'	19:CS:35:SER:HA	2.01	0.42
1:CA:1303:C:C4	1:CA:1304:G:C5	3.08	0.42
15:CO:21:ASP:OD2	15:CO:24:SER:HB3	2.19	0.42
25:DA:79:G:H1	25:DA:107:C:H42	1.67	0.42
25:DA:704:G:O2'	25:DA:726:G:N2	2.41	0.42
25:DA:1022:G:N7	33:DN:66:LYS:HE2	2.35	0.42
25:DA:1839:G:N7	25:DA:1927:A:H1'	2.35	0.42
25:DA:2155:G:H2'	25:DA:2156:G:H5'	2.01	0.42
25:DA:2186:G:C2'	25:DA:2187:G:H5"	2.44	0.42
25:DA:2224:G:H4'	25:DA:2226:C:C2	2.55	0.42
29:DF:178:PRO:HB3	29:DF:198:ALA:CB	2.50	0.42
30:DG:21:ARG:HG3	30:DG:22:ARG:N	2.34	0.42
30:DG:61:ALA:HB1	50:D4:7:PRO:HG2	2.01	0.42
33:DN:120:LEU:HD23	33:DN:120:LEU:HA	1.92	0.42
34:DO:12:ASP:OD1	34:DO:14:THR:OG1	2.31	0.42
49:D3:8:LEU:O	49:D3:32:GLN:N	2.43	0.42
1:AA:44:G:C2	1:AA:45:U:H1'	2.55	0.42
1:AA:240:C:H2'	1:AA:241:C:H6	1.82	0.42
1:AA:337:C:H2'	1:AA:338:A:C8	2.54	0.42
1:AA:390:C:H2'	1:AA:391:G:C8	2.54	0.42
1:AA:925:G:H1'	1:AA:1502:A:C4	2.55	0.42
1:AA:1458:G:C2'	1:AA:1459:C:H5'	2.50	0.42
2:AB:24:TRP:CD1	2:AB:24:TRP:H	2.38	0.42
6:AF:86:ARG:O	6:AF:87:ARG:HG2	2.20	0.42
7:AG:48:LYS:O	7:AG:52:GLU:HG2	2.20	0.42
10:AJ:50:ILE:HD11	10:AJ:57:LYS:HD2	2.01	0.42
18:AR:59:SER:OG	18:AR:60:ALA:N	2.53	0.42
25:BA:30:G:H2'	25:BA:31:C:C6	2.55	0.42
25:BA:245:G:O5'	35:BP:73:GLY:HA2	2.20	0.42
25:BA:392:C:H2'	25:BA:393:C:C6	2.54	0.42
25:BA:1568:G:H1'	27:BD:58:HIS:HE1	1.85	0.42
25:BA:1570:A:H2'	25:BA:1571:A:C8	2.55	0.42
25:BA:2140:C:C2	25:BA:2151:G:N1	2.73	0.42
25:BA:2593:U:O4	60:BA:4071:HOH:O	2.18	0.42
25:BA:2784:C:H1'	28:BE:37:ARG:NH1	2.35	0.42
30:BG:96:ARG:O	30:BG:99:MET:HB3	2.19	0.42
32:BI:134:PRO:C	32:BI:136:VAL:H	2.28	0.42
33:BN:14:VAL:HG13	33:BN:138:LEU:HB2	2.02	0.42
35:BP:82:GLY:HA2	35:BP:113:LYS:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BR:81:ASP:O	37:BR:85:PRO:HG2	2.20	0.42
46:B0:40:GLN:NE2	46:B0:42:GLY:O	2.53	0.42
1:CA:373:A:H1'	1:CA:481:G:N3	2.35	0.42
1:CA:501:C:H2'	1:CA:502:G:H8	1.85	0.42
1:CA:947:G:H2'	1:CA:948:C:O4'	2.20	0.42
1:CA:1118:C:C2	1:CA:1119:C:C5	3.08	0.42
7:CG:135:VAL:HA	7:CG:138:LYS:HB3	2.02	0.42
19:CS:49:ILE:O	19:CS:60:VAL:N	2.48	0.42
25:DA:19:C:H2'	25:DA:20:C:H6	1.83	0.42
25:DA:727:A:OP1	25:DA:1431:U:O2'	2.36	0.42
25:DA:729:G:H5'	25:DA:730:C:H5"	2.02	0.42
25:DA:1341:U:H5'	43:DX:57:LEU:HB3	2.01	0.42
25:DA:1902:C:H5'	27:DD:246:PRO:HD3	2.02	0.42
25:DA:1978:A:H2'	25:DA:1979:C:C6	2.55	0.42
25:DA:2035:G:P	25:DA:2036:C:H41	2.42	0.42
25:DA:2169:A:H2'	25:DA:2170:A:C8	2.55	0.42
25:DA:2170:A:H8	25:DA:2170:A:OP2	2.02	0.42
25:DA:2378:A:H8	25:DA:2378:A:O5'	2.03	0.42
25:DA:2600:A:H2'	25:DA:2601:C:C6	2.55	0.42
27:DD:172:TYR:CD1	27:DD:186:HIS:HA	2.55	0.42
30:DG:5:VAL:O	30:DG:8:LYS:HB2	2.20	0.42
31:DH:3:ARG:HH12	31:DH:5:GLY:N	2.16	0.42
32:DI:57:ARG:HG3	32:DI:58:LEU:N	2.33	0.42
33:DN:134:ARG:N	33:DN:135:PRO:HD3	2.35	0.42
34:DO:98:VAL:HG13	34:DO:117:LEU:HB2	2.02	0.42
35:DP:59:LEU:HD23	54:D8:58:ILE:HD13	2.01	0.42
39:DT:7:ILE:O	39:DT:11:GLU:HG3	2.20	0.42
42:DW:37:ARG:HD2	42:DW:38:TYR:CE2	2.55	0.42
54:D8:23:VAL:HG22	54:D8:47:LYS:HB3	2.02	0.42
1:AA:110:C:H2'	1:AA:111:G:O4'	2.20	0.42
1:AA:418:C:N4	1:AA:425:G:H1	2.12	0.42
1:AA:585:G:OP1	17:AQ:37:LYS:HD2	2.19	0.42
1:AA:1136:U:H6	1:AA:1136:U:H3'	1.85	0.42
1:AA:1320:C:C4	19:AS:36:ARG:HB2	2.55	0.42
1:AA:1374:A:O2'	7:AG:28:ASN:HB3	2.20	0.42
4:AD:162:LEU:HD13	4:AD:181:MET:HG2	2.02	0.42
11:AK:99:GLN:HG3	11:AK:105:VAL:HG11	2.01	0.42
13:AM:40:ASN:HB3	13:AM:43:THR:OG1	2.20	0.42
13:AM:40:ASN:HA	13:AM:41:PRO:HD2	1.86	0.42
19:AS:41:VAL:O	19:AS:44:MET:N	2.45	0.42
25:BA:772:C:H2'	25:BA:773:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1188:U:C4'	41:BV:79:VAL:HG22	2.50	0.42
25:BA:1287:A:N7	37:BR:106:GLY:HA3	2.35	0.42
25:BA:1418:G:H8	25:BA:1418:G:O5'	2.02	0.42
25:BA:1824:G:OP1	27:BD:52:ARG:HD3	2.20	0.42
25:BA:1857:G:C6	25:BA:1858:G:C6	3.07	0.42
25:BA:2134:A:OP2	25:BA:2134:A:H8	2.02	0.42
25:BA:2135:A:H61	25:BA:2156:G:C2'	2.33	0.42
25:BA:2469:A:C2	25:BA:2470:G:H1'	2.55	0.42
25:BA:2872:G:O2'	25:BA:2873:A:H5'	2.19	0.42
28:BE:51:PHE:HB3	28:BE:77:ILE:HD12	2.02	0.42
40:BU:83:LEU:HD12	40:BU:113:ALA:HB2	2.02	0.42
1:CA:33:A:N3	12:CL:32:PHE:HE2	2.18	0.42
1:CA:586:C:O2'	1:CA:878:G:H4'	2.19	0.42
1:CA:664:G:H22	1:CA:741:G:H22	1.68	0.42
1:CA:675:A:H2'	1:CA:676:A:C8	2.55	0.42
1:CA:707:C:H2'	1:CA:708:C:H6	1.84	0.42
1:CA:834:C:H2'	1:CA:835:U:C6	2.55	0.42
1:CA:900:A:H2'	1:CA:901:A:C8	2.55	0.42
1:CA:1154:G:N7	1:CA:1155:G:N9	2.68	0.42
1:CA:1223:C:H5"	1:CA:1224:G:H5'	2.01	0.42
1:CA:1258:G:H2'	1:CA:1259:C:H6	1.84	0.42
4:CD:155:LEU:HD22	4:CD:157:LEU:H	1.85	0.42
7:CG:149:ARG:HG2	11:CK:59:TYR:CE1	2.55	0.42
8:CH:68:ARG:NH1	8:CH:74:PRO:HB3	2.35	0.42
15:CO:5:LYS:NZ	15:CO:5:LYS:HB2	2.35	0.42
18:CR:69:THR:HA	18:CR:72:ARG:HD2	2.02	0.42
25:DA:77:C:H2'	25:DA:78:A:H8	1.85	0.42
25:DA:196:A:H2'	25:DA:196:A:N3	2.35	0.42
25:DA:272:G:C2	25:DA:421:U:C4	3.07	0.42
25:DA:947:G:N2	25:DA:971:C:C2	2.88	0.42
25:DA:1580:A:H3'	25:DA:1581:G:C8	2.55	0.42
27:DD:67:PHE:CE1	27:DD:157:ARG:HD2	2.55	0.42
29:DF:196:LEU:O	29:DF:199:TRP:HB3	2.20	0.42
30:DG:3:LEU:CD1	30:DG:5:VAL:HG12	2.49	0.42
38:DS:39:ILE:HD13	38:DS:85:VAL:HG21	2.01	0.42
1:AA:375:U:O3'	16:AP:6:LEU:HB2	2.20	0.41
1:AA:405:U:H4'	1:AA:496:A:O2'	2.20	0.41
1:AA:922:G:H2'	1:AA:923:A:C8	2.55	0.41
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.55	0.41
1:AA:1308:U:OP2	13:AM:99:ARG:HD2	2.20	0.41
1:AA:1530:G:OP1	1:AA:1530:G:H4'	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:23:TYR:CG	3:AC:24:ALA:N	2.86	0.41
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.53	0.41
9:AI:86:VAL:HA	9:AI:92:TYR:HB2	2.02	0.41
11:AK:21:ILE:HB	11:AK:84:VAL:HG22	2.02	0.41
13:AM:90:LEU:HA	13:AM:93:ARG:HG3	2.01	0.41
25:BA:109:G:H2'	25:BA:110:G:O4'	2.20	0.41
25:BA:185:U:H2'	25:BA:186:G:H8	1.85	0.41
25:BA:212:G:H2'	25:BA:213:A:O4'	2.20	0.41
25:BA:336:C:H2'	25:BA:337:C:C6	2.55	0.41
25:BA:686:G:C4	53:B7:11:LYS:HG2	2.55	0.41
25:BA:1006:C:C2	25:BA:1138:G:N2	2.88	0.41
25:BA:1190:G:H5"	35:BP:32:THR:HA	2.01	0.41
25:BA:1405:U:H2'	25:BA:1406:U:H6	1.85	0.41
25:BA:1803:A:O2'	27:BD:259:THR:HG21	2.20	0.41
25:BA:1828:G:H4'	25:BA:1829:A:OP1	2.19	0.41
25:BA:1922:G:H2'	25:BA:1923:U:O4'	2.20	0.41
25:BA:2163:C:OP1	25:BA:2165:G:N1	2.53	0.41
26:BB:34:U:O2'	26:BB:44:G:N7	2.50	0.41
28:BE:183:LEU:HD12	28:BE:183:LEU:HA	1.87	0.41
35:BP:118:GLY:O	35:BP:137:LYS:NZ	2.50	0.41
36:BQ:58:PHE:HB3	36:BQ:61:GLY:O	2.20	0.41
1:CA:401:C:O2'	1:CA:621:A:N3	2.47	0.41
1:CA:532:A:N6	3:CC:156:ARG:HH22	2.17	0.41
1:CA:657:G:N2	1:CA:749:C:O2	2.44	0.41
1:CA:918:A:H2'	1:CA:919:A:O4'	2.20	0.41
1:CA:922:G:N3	1:CA:1398:A:C2	2.88	0.41
1:CA:1006:C:H2'	1:CA:1007:C:O4'	2.20	0.41
1:CA:1276:G:O2'	1:CA:1277:C:H5'	2.20	0.41
1:CA:1292:U:H5'	9:CI:38:GLN:NE2	2.35	0.41
1:CA:1399:C:C2	1:CA:1502:A:N6	2.88	0.41
2:CB:16:HIS:HB3	2:CB:210:SER:CB	2.50	0.41
2:CB:27:LYS:O	2:CB:194:PRO:HG2	2.20	0.41
4:CD:100:ARG:NH1	4:CD:137:SER:HB3	2.35	0.41
20:CT:54:LYS:HA	20:CT:57:ARG:NH1	2.35	0.41
25:DA:37:C:H4'	25:DA:451:C:OP1	2.20	0.41
25:DA:598:G:H2'	25:DA:599:G:O4'	2.20	0.41
25:DA:1145:C:H2'	25:DA:1146:C:C6	2.55	0.41
25:DA:1598:C:H2'	25:DA:1599:C:C6	2.55	0.41
32:DI:44:LEU:HD13	32:DI:44:LEU:HA	1.86	0.41
36:DQ:112:GLU:HG2	36:DQ:113:GLN:N	2.32	0.41
36:DQ:133:ARG:HG2	36:DQ:134:ARG:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DS:84:GLN:H	38:DS:111:GLU:HB2	1.84	0.41
40:DU:28:ARG:HD3	40:DU:38:THR:OG1	2.20	0.41
46:D0:50:ASN:HA	46:D0:62:LEU:HD11	2.02	0.41
50:D4:9:LEU:HD23	50:D4:9:LEU:HA	1.90	0.41
1:AA:59:A:N6	1:AA:331:G:H1'	2.35	0.41
1:AA:540:G:H2'	1:AA:541:G:O4'	2.21	0.41
1:AA:971:G:N1	1:AA:1363(A):A:OP2	2.44	0.41
1:AA:1117:G:H5"	9:AI:104:ARG:CZ	2.50	0.41
1:AA:1319:A:OP2	19:AS:3:ARG:HG3	2.20	0.41
9:AI:26:VAL:HG22	9:AI:61:ALA:HB3	2.02	0.41
11:AK:85:ARG:HG2	11:AK:111:ASP:O	2.19	0.41
12:AL:97:ARG:HG3	12:AL:98:TYR:CE1	2.55	0.41
17:AQ:76:LEU:HD21	17:AQ:79:SER:OG	2.21	0.41
25:BA:143(A):C:H2'	25:BA:144:C:C6	2.55	0.41
25:BA:185:U:H2'	25:BA:186:G:C8	2.55	0.41
25:BA:392:C:H5"	25:BA:409:C:H5"	2.02	0.41
25:BA:1130:U:O2	28:BE:149:ARG:NH2	2.45	0.41
25:BA:2584:U:O2	25:BA:2585:U:C4	2.73	0.41
26:BB:114:C:HO2'	38:BS:46:VAL:HG13	1.86	0.41
29:BF:110:LEU:HD21	29:BF:181:LEU:HG	2.02	0.41
32:BI:9:LEU:HD22	32:BI:9:LEU:HA	1.83	0.41
46:B0:82:ARG:HA	46:B0:83:PRO:HD3	1.87	0.41
1:CA:109:A:C6	1:CA:326:G:C6	3.08	0.41
1:CA:255:G:C6	1:CA:256:U:C4	3.08	0.41
1:CA:667:G:OP1	1:CA:732:C:O2'	2.22	0.41
1:CA:1005:A:H5"	1:CA:1006:C:C5	2.55	0.41
1:CA:1092:A:H5"	7:CG:4:ARG:CZ	2.50	0.41
1:CA:1443:G:H2'	1:CA:1444:C:C6	2.55	0.41
5:CE:32:VAL:O	5:CE:44:GLY:N	2.36	0.41
8:CH:112:LEU:HB3	8:CH:133:LEU:HA	2.02	0.41
9:CI:19:LEU:C	9:CI:20:ARG:HD2	2.45	0.41
9:CI:102:LEU:H	9:CI:102:LEU:HG	1.57	0.41
24:CX:76:31H:H61	46:D0:2:ALA:HB3	1.85	0.41
25:DA:84:A:H5'	44:DY:8:LYS:HB3	2.03	0.41
25:DA:538:G:H2'	25:DA:539:G:C8	2.53	0.41
25:DA:729:G:H2'	25:DA:1775:U:H1'	2.03	0.41
25:DA:1124:C:H2'	25:DA:1125:G:O4'	2.20	0.41
25:DA:1316:U:H2'	25:DA:1317:A:C8	2.55	0.41
25:DA:1429:G:H2'	25:DA:1430:C:C6	2.55	0.41
25:DA:1436:G:C2	25:DA:1437:C:C2	3.08	0.41
25:DA:1497:U:H5"	25:DA:1498:C:C5	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1652:A:N7	25:DA:1653:G:C6	2.88	0.41
25:DA:1660:C:O2'	25:DA:1661:G:H5'	2.20	0.41
25:DA:2432:A:C6	25:DA:2433:A:C6	3.09	0.41
25:DA:2454:G:N7	60:DA:4288:HOH:O	2.37	0.41
25:DA:2671:A:H2'	25:DA:2672:G:O4'	2.20	0.41
30:DG:19:LEU:HD11	30:DG:172:LEU:HB2	2.02	0.41
31:DH:26:VAL:O	31:DH:33:LEU:N	2.36	0.41
31:DH:35:VAL:O	31:DH:37:VAL:HG23	2.19	0.41
35:DP:45:LEU:HD22	35:DP:45:LEU:HA	1.79	0.41
41:DV:22:VAL:O	41:DV:92:THR:N	2.24	0.41
1:AA:392:G:H2'	1:AA:393:A:H8	1.85	0.41
1:AA:432:A:H3'	1:AA:433:C:H6	1.85	0.41
1:AA:567:G:H2'	1:AA:568:G:O4'	2.20	0.41
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.55	0.41
9:AI:48:GLU:HA	9:AI:51:ARG:HG3	2.03	0.41
12:AL:39:VAL:HG12	12:AL:41:ARG:HG2	2.03	0.41
13:AM:17:VAL:O	13:AM:20:THR:OG1	2.28	0.41
13:AM:96:LEU:C	13:AM:110:ARG:HG2	2.46	0.41
16:AP:20:VAL:HG23	16:AP:35:LYS:HA	2.02	0.41
25:BA:272(E):G:C2	25:BA:364:C:C2	3.08	0.41
25:BA:458:G:O2'	25:BA:469:G:O6	2.28	0.41
25:BA:1312:U:OP2	43:BX:63:LYS:NZ	2.45	0.41
25:BA:2630:G:H2'	25:BA:2631:G:C8	2.56	0.41
25:BA:2680:C:H5'	28:BE:189:PRO:HA	2.01	0.41
33:BN:67:LEU:O	33:BN:88:GLU:HG3	2.20	0.41
37:BR:1:MET:HE2	37:BR:1:MET:HB3	1.94	0.41
42:BW:86:LEU:HD22	42:BW:96:ILE:HD11	2.02	0.41
1:CA:835:U:C2	1:CA:836:G:C8	3.08	0.41
1:CA:1030(A):G:OP1	1:CA:1030(A):G:H4'	2.21	0.41
1:CA:1113:C:O2'	3:CC:14:ILE:HD11	2.20	0.41
1:CA:1145:C:H4'	1:CA:1146:A:C5'	2.51	0.41
5:CE:80:ILE:CG2	5:CE:91:LEU:HB2	2.50	0.41
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.56	0.41
11:CK:52:GLY:H	11:CK:55:LYS:HE2	1.84	0.41
13:CM:120:LYS:HA	13:CM:121:LYS:HZ3	1.84	0.41
25:DA:58:G:O2'	25:DA:73:A:N1	2.45	0.41
25:DA:98:G:OP1	48:D2:2:LYS:HA	2.21	0.41
25:DA:554:U:O4	60:DA:4015:HOH:O	2.19	0.41
25:DA:567:A:OP2	35:DP:29:LYS:NZ	2.42	0.41
25:DA:581:C:H2'	25:DA:582:G:C8	2.54	0.41
25:DA:1580:A:H3'	25:DA:1581:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2379:G:H4'	38:DS:21:THR:CG2	2.51	0.41
35:DP:38:GLN:C	35:DP:40:SER:H	2.28	0.41
1:AA:153:C:N3	1:AA:168:G:N2	2.48	0.41
1:AA:174:C:H2'	1:AA:175:C:C6	2.55	0.41
1:AA:1327:C:H2'	1:AA:1328:C:C6	2.55	0.41
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	2.02	0.41
3:AC:32:LEU:HD23	3:AC:32:LEU:HA	1.81	0.41
5:AE:85:GLY:C	5:AE:87:SER:H	2.29	0.41
7:AG:100:ALA:O	7:AG:104:LEU:HB2	2.20	0.41
16:AP:40:ASP:HB3	16:AP:48:TRP:HB2	2.02	0.41
25:BA:84:A:H3'	44:BY:8:LYS:HG2	2.02	0.41
25:BA:301:G:H1'	25:BA:302:C:C6	2.54	0.41
25:BA:330:A:H2	25:BA:1210:A:C2'	2.32	0.41
25:BA:1655:A:H3'	25:BA:1656:C:C6	2.55	0.41
25:BA:2532:G:C6	25:BA:2533:A:C6	3.08	0.41
25:BA:2611:U:C4	51:B5:3:LYS:HG2	2.55	0.41
25:BA:2685:G:H5'	34:BO:68:GLU:OE1	2.19	0.41
25:BA:2790:A:N3	25:BA:2790:A:H2'	2.35	0.41
28:BE:14:ILE:HB	39:BT:14:TYR:CE2	2.55	0.41
30:BG:136:ARG:HG3	30:BG:137:GLU:HG3	2.03	0.41
31:BH:71:LEU:HD12	31:BH:71:LEU:HA	1.86	0.41
36:BQ:79:LEU:HB3	36:BQ:80:GLU:HG3	2.00	0.41
41:BV:98:GLU:CD	41:BV:100:ARG:HH11	2.28	0.41
42:BW:79:GLY:HA3	42:BW:100:THR:HG22	2.02	0.41
50:B4:57:GLU:N	50:B4:60:GLN:HG3	2.36	0.41
54:B8:48:PHE:CE2	54:B8:50:LEU:HD23	2.56	0.41
1:CA:664:G:OP1	18:CR:64:ARG:NH2	2.51	0.41
1:CA:942:G:C2	1:CA:1342:C:C2	3.08	0.41
1:CA:1048:G:H1	1:CA:1209:C:N4	2.15	0.41
1:CA:1057:G:C5	1:CA:1204:A:C2	3.09	0.41
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.36	0.41
1:CA:1492:A:H2'	1:CA:1493:A:C4	2.56	0.41
3:CC:122:GLU:HA	3:CC:125:GLU:OE2	2.19	0.41
7:CG:20:ASP:OD2	7:CG:23:VAL:HG23	2.20	0.41
8:CH:4:ASP:OD1	8:CH:6:ILE:N	2.53	0.41
11:CK:116:HIS:O	11:CK:117:ASN:HB2	2.20	0.41
19:CS:36:ARG:NE	19:CS:72:GLY:HA2	2.34	0.41
20:CT:23:ARG:CG	20:CT:23:ARG:NH1	2.82	0.41
25:DA:76:C:O2'	48:D2:59:ARG:HA	2.20	0.41
25:DA:80:G:H5'	25:DA:346:A:H1'	2.01	0.41
25:DA:118:A:N3	25:DA:178:G:H1'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:800:A:H8	25:DA:800:A:OP1	2.04	0.41
25:DA:962:G:H4'	25:DA:2496:C:O2'	2.21	0.41
25:DA:998:C:H2'	25:DA:999:U:O4'	2.20	0.41
25:DA:1005:C:H2'	25:DA:1006:C:C6	2.55	0.41
25:DA:1184:G:OP1	49:D3:30:ARG:HD2	2.21	0.41
25:DA:1651:G:OP1	37:DR:40:LYS:HE3	2.20	0.41
25:DA:1651:G:H2'	25:DA:1652:A:O4'	2.20	0.41
25:DA:2578:G:H2'	25:DA:2579:C:C6	2.55	0.41
25:DA:2723:C:OP2	28:DE:109:LYS:NZ	2.53	0.41
26:DB:29:A:C2	26:DB:30:C:C2	3.09	0.41
32:DI:130:TYR:HD2	32:DI:138:ILE:HD12	1.85	0.41
33:DN:33:LEU:HD13	33:DN:33:LEU:HA	1.94	0.41
35:DP:60:MET:HA	54:D8:13:ARG:NH1	2.36	0.41
36:DQ:42:ILE:HD13	36:DQ:97:VAL:HB	2.02	0.41
37:DR:94:TYR:C	37:DR:117:VAL:HG23	2.45	0.41
41:DV:62:LEU:HD23	41:DV:93:GLU:HG2	2.01	0.41
45:DZ:42:VAL:HG13	45:DZ:43:GLU:HG3	2.02	0.41
47:D1:82:LEU:C	47:D1:85:LEU:HD23	2.45	0.41
1:AA:341:C:O2'	1:AA:342:C:H5'	2.21	0.41
1:AA:1147:C:H6	1:AA:1147:C:O5'	2.03	0.41
1:AA:1169:A:O5'	1:AA:1169:A:H8	2.03	0.41
9:AI:65:VAL:HG21	9:AI:73:GLN:HB3	2.02	0.41
11:AK:86:GLY:O	11:AK:91:ARG:HD3	2.21	0.41
14:AN:26:ARG:HD3	14:AN:43:CYS:HB3	2.02	0.41
19:AS:31:ILE:HB	19:AS:49:ILE:HG13	2.02	0.41
25:BA:34:C:H5"	25:BA:35:G:OP2	2.21	0.41
25:BA:530:G:C5	25:BA:2022:U:H5"	2.55	0.41
25:BA:2086:U:H2'	25:BA:2087:G:H8	1.86	0.41
25:BA:2242:G:O6	60:BA:3937:HOH:O	2.21	0.41
25:BA:2262:U:OP2	46:B0:19:LYS:NZ	2.47	0.41
32:BI:12:LEU:HD23	32:BI:12:LEU:HA	1.85	0.41
45:BZ:110:GLY:N	45:BZ:145:GLU:HA	2.36	0.41
54:B8:42:ARG:HD2	60:B8:5105:HOH:O	2.21	0.41
1:CA:15:G:C4	1:CA:16:A:C8	3.09	0.41
1:CA:514:C:H2'	1:CA:515:G:C8	2.55	0.41
1:CA:781:A:C8	1:CA:782:A:C8	3.09	0.41
1:CA:1121:U:C4	1:CA:1122:U:C4	3.08	0.41
2:CB:72:GLY:O	2:CB:94:ASN:HA	2.21	0.41
4:CD:50:ARG:HA	4:CD:51:PRO:HD3	1.94	0.41
25:DA:928:G:H8	25:DA:928:G:O5'	2.03	0.41
25:DA:1882:C:H5'	47:D1:26:ARG:HH22	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1889:A:H1'	25:DA:2087:G:O4'	2.20	0.41
25:DA:2125:G:H22	25:DA:2172:U:C5'	2.31	0.41
25:DA:2287:A:C5	25:DA:2289:G:C5	3.09	0.41
25:DA:2387:U:H1'	46:D0:41:ARG:HE	1.85	0.41
25:DA:2437:U:H2'	25:DA:2438:U:C6	2.56	0.41
25:DA:2525:G:H1	25:DA:2538:C:H42	1.69	0.41
30:DG:39:ILE:O	30:DG:91:ARG:HA	2.20	0.41
37:DR:36:THR:HG22	37:DR:37:THR:N	2.35	0.41
45:DZ:153:SER:HB3	45:DZ:167:PRO:HB3	2.03	0.41
1:AA:57:G:H2'	1:AA:58:C:H6	1.85	0.41
1:AA:527:G:O2'	1:AA:535:A:N1	2.37	0.41
1:AA:730:G:C5	1:AA:731:G:H1'	2.55	0.41
1:AA:762:C:H2'	1:AA:763:G:H8	1.86	0.41
1:AA:936:C:H2'	1:AA:937:A:O4'	2.21	0.41
1:AA:1493:A:H2'	25:BA:1913:A:N1	2.35	0.41
17:AQ:52:LYS:HG2	17:AQ:53:LEU:H	1.83	0.41
19:AS:50:ALA:HA	19:AS:58:VAL:O	2.20	0.41
25:BA:352:G:O2'	25:BA:353:G:H5'	2.20	0.41
25:BA:573:G:OP2	41:BV:78:LYS:NZ	2.42	0.41
25:BA:840:C:H2'	25:BA:841:A:C8	2.55	0.41
25:BA:1680:U:O2	25:BA:1763:G:H3'	2.21	0.41
25:BA:2345:G:N3	25:BA:2381:C:H2'	2.36	0.41
25:BA:2444:G:P	29:BF:68:LYS:HD2	2.60	0.41
25:BA:2827:C:H2'	25:BA:2828:C:C6	2.56	0.41
27:BD:162:SER:HB3	27:BD:195:ALA:CB	2.51	0.41
29:BF:184:TYR:CE2	29:BF:188:ARG:HD2	2.55	0.41
1:CA:250:A:H4'	1:CA:251:G:O5'	2.19	0.41
1:CA:264:U:O2	17:CQ:64:PRO:HG2	2.20	0.41
1:CA:853:G:H2'	1:CA:854:G:C8	2.51	0.41
1:CA:1034:G:C6	1:CA:1035:A:C2	3.09	0.41
1:CA:1097:C:O2	1:CA:1169:A:H2	2.03	0.41
2:CB:105:PHE:O	2:CB:109:SER:HB2	2.20	0.41
2:CB:180:LEU:HB2	2:CB:182:ILE:HD12	2.01	0.41
6:CF:20:ALA:O	6:CF:24:GLU:N	2.49	0.41
6:CF:99:ALA:HB2	18:CR:31:LEU:HD21	2.02	0.41
9:CI:5:TYR:H	9:CI:87:GLN:HE22	1.69	0.41
9:CI:8:GLY:HA3	9:CI:76:ALA:O	2.21	0.41
14:CN:47:LEU:HD12	14:CN:53:LEU:CD2	2.50	0.41
16:CP:55:ARG:HA	16:CP:55:ARG:HD2	1.80	0.41
18:CR:40:LEU:HD13	18:CR:79:LEU:HD11	2.03	0.41
25:DA:272(F):C:H42	25:DA:363(D):G:H1	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:608:A:H2'	25:DA:609:A:C8	2.56	0.41
25:DA:842:G:H2'	25:DA:843:G:O4'	2.20	0.41
25:DA:994:C:H1'	41:DV:10:LYS:HE3	2.01	0.41
25:DA:1138:G:N3	33:DN:106:MET:HE2	2.35	0.41
25:DA:1206:G:H2'	25:DA:1207:C:C6	2.54	0.41
25:DA:1423:G:C4'	25:DA:1492:G:H21	2.33	0.41
25:DA:1474:C:H2'	25:DA:1475:G:C8	2.54	0.41
25:DA:2078:C:H2'	25:DA:2079:U:C6	2.55	0.41
25:DA:2494:G:C6	25:DA:2495:G:C5	3.07	0.41
26:DB:2:C:H2'	26:DB:3:C:H6	1.86	0.41
26:DB:5:C:O2'	26:DB:27:C:O2	2.38	0.41
26:DB:83:G:H4'	49:D3:52:HIS:ND1	2.35	0.41
27:DD:264:LYS:HA	27:DD:265:PRO:HD3	1.94	0.41
31:DH:101:ARG:NH2	31:DH:122:THR:HA	2.35	0.41
33:DN:76:SER:OG	33:DN:81:GLY:HA3	2.20	0.41
33:DN:96:GLU:H	33:DN:96:GLU:CD	2.29	0.41
34:DO:88:ASN:CG	34:DO:90:GLN:H	2.28	0.41
38:DS:87:PHE:CZ	38:DS:102:ALA:HB2	2.56	0.41
1:AA:16:A:O2'	5:AE:16:THR:HB	2.21	0.41
1:AA:49:U:O4	1:AA:365:U:H5	2.04	0.41
1:AA:264:U:H2'	1:AA:265:G:O4'	2.21	0.41
1:AA:1025:U:O2	1:AA:1036:G:C6	2.73	0.41
1:AA:1347:G:H5"	9:AI:107:ARG:HB3	2.01	0.41
7:AG:20:ASP:HB3	7:AG:23:VAL:HG23	2.01	0.41
10:AJ:7:LYS:N	10:AJ:97:GLU:O	2.38	0.41
11:AK:116:HIS:O	11:AK:117:ASN:HB2	2.20	0.41
13:AM:33:ALA:O	13:AM:37:THR:OG1	2.23	0.41
20:AT:33:ILE:CD1	20:AT:62:LEU:HB3	2.47	0.41
25:BA:86:C:H4'	25:BA:104:U:H1'	2.02	0.41
25:BA:620:G:N3	25:BA:620:G:H5'	2.35	0.41
25:BA:995:C:OP2	40:BU:54:LYS:NZ	2.49	0.41
25:BA:1287:A:C5	25:BA:1288:U:C4	3.08	0.41
25:BA:1371:G:H2'	25:BA:1372:U:C5	2.54	0.41
25:BA:1473:G:H2'	25:BA:1474:C:O4'	2.21	0.41
25:BA:1932:A:H2'	25:BA:1933:G:O4'	2.19	0.41
26:BB:5:C:O2'	26:BB:27:C:O2	2.38	0.41
26:BB:110:G:H2'	26:BB:111:G:C8	2.56	0.41
32:BI:72:LEU:O	32:BI:74:ASN:N	2.54	0.41
34:BO:79:PHE:HD1	39:BT:72:VAL:HG22	1.85	0.41
41:BV:51:VAL:HG23	41:BV:52:VAL:O	2.21	0.41
48:B2:37:PHE:O	48:B2:41:ILE:HG12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:B5:48:GLU:O	51:B5:60:VAL:HG11	2.21	0.41
1:CA:405:U:H5"	1:CA:406:G:O5'	2.21	0.41
1:CA:976:G:N2	1:CA:1363:C:OP2	2.53	0.41
1:CA:1502:A:H2	1:CA:1505:G:N1	2.18	0.41
2:CB:221:LEU:HD23	2:CB:221:LEU:HA	1.87	0.41
5:CE:139:LEU:HA	5:CE:142:LEU:CD1	2.51	0.41
7:CG:73:MET:HG3	7:CG:90:GLU:HA	2.02	0.41
9:CI:23:ASN:ND2	9:CI:23:ASN:H	2.19	0.41
13:CM:91:ARG:HA	13:CM:91:ARG:HD2	1.81	0.41
14:CN:23:ARG:NH1	14:CN:28:GLY:O	2.53	0.41
23:CW:76:PPU:N	24:CX:76:31H:N3'	2.66	0.41
25:DA:565:C:H4'	25:DA:1253:A:C6	2.55	0.41
25:DA:610:G:H2'	25:DA:611:C:C6	2.56	0.41
25:DA:740:U:H2'	25:DA:741:G:C8	2.56	0.41
25:DA:1364:G:OP1	47:D1:2:SER:HA	2.20	0.41
25:DA:1777:U:H2'	25:DA:1778:U:H6	1.85	0.41
25:DA:2242:G:H2'	25:DA:2243:U:O4'	2.20	0.41
25:DA:2252:G:H2'	25:DA:2253:G:O4'	2.20	0.41
25:DA:2459:A:H5"	25:DA:2460:U:OP2	2.20	0.41
25:DA:2557:G:H2'	25:DA:2558:C:C6	2.55	0.41
25:DA:2683:C:H2'	25:DA:2684:U:H6	1.85	0.41
25:DA:2863:C:H2'	25:DA:2864:G:H8	1.86	0.41
26:DB:33:G:C2	26:DB:50:G:C2	3.09	0.41
31:DH:98:LEU:HD22	31:DH:125:VAL:HG23	2.02	0.41
31:DH:154:PRO:HB3	31:DH:163:TYR:CZ	2.56	0.41
33:DN:34:LEU:O	33:DN:49:GLY:HA3	2.20	0.41
50:D4:60:GLN:O	50:D4:63:TYR:HE2	2.04	0.41
1:AA:79:G:C2	1:AA:90:U:O2	2.74	0.41
1:AA:163:C:H2'	1:AA:164:U:C6	2.56	0.41
1:AA:623:C:H2'	1:AA:624:C:O4'	2.20	0.41
1:AA:1435:G:N2	1:AA:1466:C:O2	2.44	0.41
2:AB:114:ARG:HG2	2:AB:145:LEU:HD21	2.03	0.41
2:AB:162:ILE:HD11	2:AB:184:VAL:HG22	2.02	0.41
2:AB:166:ASP:HB3	2:AB:169:LYS:HB2	2.03	0.41
2:AB:215:LEU:HA	2:AB:215:LEU:HD23	1.85	0.41
4:AD:158:ILE:HD13	4:AD:158:ILE:H	1.86	0.41
6:AF:45:LEU:O	6:AF:46:ARG:HG3	2.20	0.41
7:AG:28:ASN:HD22	7:AG:31:MET:CE	2.34	0.41
9:AI:16:ARG:CZ	9:AI:64:THR:HG21	2.51	0.41
15:AO:62:GLN:O	15:AO:66:LEU:HD13	2.21	0.41
25:BA:247:G:H4'	25:BA:386:G:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:355:G:H2'	25:BA:356:G:O4'	2.20	0.41
25:BA:1230:C:H2'	25:BA:1231:G:C8	2.55	0.41
25:BA:1443:G:H2'	25:BA:1444:G:C8	2.56	0.41
25:BA:1493:C:C5	25:BA:2206:G:H1'	2.55	0.41
25:BA:1500:G:O2'	27:BD:100:GLY:O	2.38	0.41
25:BA:1779:U:H2'	60:BA:4539:HOH:O	2.20	0.41
25:BA:1844:C:H2'	25:BA:1845:G:H8	1.86	0.41
25:BA:2130:U:O2'	25:BA:2131:G:N2	2.31	0.41
25:BA:2282:G:H4'	25:BA:2389:G:O2'	2.21	0.41
26:BB:57:A:N3	30:BG:29:TRP:HB3	2.36	0.41
29:BF:184:TYR:O	29:BF:188:ARG:HG3	2.21	0.41
31:BH:94:TYR:N	31:BH:94:TYR:CD1	2.89	0.41
33:BN:28:THR:HG22	33:BN:29:LYS:N	2.33	0.41
37:BR:24:GLN:HE21	37:BR:44:LEU:HG	1.85	0.41
45:BZ:54:HIS:ND1	45:BZ:101:PRO:HG3	2.36	0.41
1:CA:91:C:H2'	1:CA:92:C:C6	2.55	0.41
3:CC:66:VAL:O	3:CC:101:LEU:HA	2.20	0.41
3:CC:186:PHE:HD1	3:CC:198:VAL:O	2.03	0.41
4:CD:51:PRO:HB2	4:CD:56:VAL:HG23	2.03	0.41
9:CI:53:VAL:HG21	9:CI:92:TYR:CE1	2.55	0.41
12:CL:117:ARG:NH2	12:CL:124:LYS:HB3	2.35	0.41
17:CQ:43:LEU:HG	17:CQ:68:ARG:HG2	2.03	0.41
25:DA:324:A:N6	25:DA:338:G:O2'	2.54	0.41
25:DA:598:G:C6	25:DA:599:G:C5	3.09	0.41
25:DA:663:G:C6	25:DA:664:C:C4	3.09	0.41
25:DA:827:U:O2'	25:DA:2068:U:C2	2.60	0.41
25:DA:923:C:H2'	25:DA:924:C:C6	2.55	0.41
25:DA:953:A:H2'	25:DA:954:G:H8	1.85	0.41
25:DA:1014:U:H2'	25:DA:1015:G:H8	1.85	0.41
25:DA:1142:U:H5"	25:DA:1142(A):A:H5'	2.03	0.41
25:DA:1429:G:H1'	25:DA:1568:G:H1'	2.03	0.41
25:DA:1655:A:H1'	28:DE:113:PHE:CE1	2.56	0.41
25:DA:1744:C:H2'	25:DA:1745:C:C6	2.55	0.41
25:DA:2113:U:H3	25:DA:2170:A:N6	2.19	0.41
25:DA:2456:C:C4	25:DA:2457:U:C4	3.09	0.41
26:DB:12:C:H2'	46:D0:73:GLY:HA3	2.03	0.41
31:DH:7:LEU:HD23	31:DH:69:ARG:CZ	2.50	0.41
40:DU:49:HIS:O	40:DU:53:ARG:N	2.53	0.41
47:D1:7:ILE:HG23	47:D1:98:LEU:HD11	2.03	0.41
54:D8:9:GLY:O	54:D8:13:ARG:HG2	2.20	0.41
1:AA:66:G:O4'	1:AA:173:U:C4	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:115:G:H4'	1:AA:116:A:O5'	2.20	0.41
1:AA:250:A:H4'	1:AA:251:G:O5'	2.21	0.41
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.61	0.41
1:AA:448:A:H2'	1:AA:449:C:C6	2.56	0.41
1:AA:621:A:H2'	1:AA:622:A:C8	2.55	0.41
1:AA:811:C:O2'	1:AA:901:A:N1	2.46	0.41
1:AA:869:G:O5'	1:AA:869:G:H8	2.04	0.41
1:AA:985:C:H2'	1:AA:986:A:H8	1.86	0.41
1:AA:1027:C:O2'	1:AA:1028:C:O5'	2.39	0.41
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.50	0.41
1:AA:1305:G:OP1	21:AU:2:GLY:HA3	2.21	0.41
1:AA:1350:A:H2'	1:AA:1351:U:O4'	2.21	0.41
2:AB:130:ARG:HG3	2:AB:130:ARG:NH1	2.35	0.41
4:AD:53:ASP:O	4:AD:57:ARG:HD2	2.21	0.41
4:AD:120:LEU:HD23	4:AD:120:LEU:HA	1.84	0.41
6:AF:15:ASP:O	6:AF:18:GLN:NE2	2.49	0.41
8:AH:98:LYS:H	8:AH:98:LYS:HD2	1.85	0.41
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	2.02	0.41
12:AL:110:VAL:HG23	12:AL:120:TYR:HB3	2.02	0.41
17:AQ:52:LYS:NZ	17:AQ:52:LYS:HB3	2.35	0.41
19:AS:28:LYS:HE3	19:AS:28:LYS:HB3	1.87	0.41
20:AT:29:LYS:O	20:AT:33:ILE:HG12	2.21	0.41
20:AT:56:MET:HE2	20:AT:84:LEU:HD13	2.02	0.41
20:AT:72:LEU:HD23	20:AT:72:LEU:HA	1.95	0.41
23:AW:76:PPU:HD1	25:BA:2506:U:H1'	2.02	0.41
24:AX:4:G:H2'	24:AX:5:G:H8	1.84	0.41
24:AX:12:G:H4'	25:BA:1908:C:O2	2.21	0.41
25:BA:231:C:H2'	25:BA:232:G:O4'	2.20	0.41
25:BA:306:U:H2'	25:BA:307:G:O4'	2.20	0.41
25:BA:372:G:H5'	47:B1:66:HIS:NE2	2.36	0.41
25:BA:1014:U:H2'	25:BA:1015:G:C8	2.55	0.41
25:BA:1424:G:H2'	25:BA:1425:G:O4'	2.21	0.41
25:BA:1434:A:H61	25:BA:1558:A:N6	2.12	0.41
25:BA:1566:A:OP1	27:BD:211:ARG:NH1	2.53	0.41
25:BA:1689:A:N6	25:BA:1698:A:H2	2.05	0.41
25:BA:1721:G:H5'	25:BA:1722:A:OP2	2.20	0.41
25:BA:2019:A:H5"	40:BU:27:LEU:HD12	2.03	0.41
25:BA:2103:C:H2'	25:BA:2104:G:C8	2.56	0.41
25:BA:2505:G:O6	25:BA:2576:G:H2'	2.21	0.41
28:BE:9:VAL:CG2	28:BE:25:VAL:HB	2.50	0.41
30:BG:77:ILE:HG21	30:BG:80:PHE:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BG:77:ILE:HD13	30:BG:82:LEU:HD12	2.02	0.41
30:BG:143:GLU:H	30:BG:143:GLU:HG2	1.46	0.41
32:BI:6:LEU:HG	32:BI:36:ALA:HA	2.01	0.41
33:BN:87:LEU:HD23	33:BN:87:LEU:HA	1.90	0.41
38:BS:36:TYR:CD1	38:BS:36:TYR:N	2.88	0.41
38:BS:87:PHE:HZ	38:BS:98:VAL:HG12	1.86	0.41
39:BT:53:ARG:HB3	39:BT:53:ARG:NH1	2.36	0.41
41:BV:35:LEU:HA	41:BV:36:PRO:HD3	1.92	0.41
45:BZ:111:VAL:C	45:BZ:113:ALA:N	2.79	0.41
45:BZ:111:VAL:HG12	45:BZ:112:ARG:H	1.86	0.41
46:B0:53:MET:HE2	46:B0:53:MET:HB3	1.86	0.41
50:B4:61:ARG:O	50:B4:62:ARG:C	2.64	0.41
1:CA:187:C:H5"	20:CT:86:ARG:HG3	2.02	0.41
1:CA:235:C:H2'	1:CA:236:G:H8	1.85	0.41
1:CA:685:G:N1	1:CA:686:U:O4	2.54	0.41
1:CA:848:C:O5'	1:CA:848:C:H6	2.04	0.41
1:CA:865:A:H8	1:CA:865:A:O5'	2.04	0.41
1:CA:954:G:H5'	13:CM:120:LYS:HD3	2.03	0.41
1:CA:1003:G:C6	1:CA:1004:A:C2	3.09	0.41
1:CA:1041:A:N6	1:CA:1042:G:C6	2.89	0.41
1:CA:1067:A:N3	1:CA:1068:G:H1'	2.36	0.41
1:CA:1229:A:O3'	24:CX:30:G:H5"	2.20	0.41
1:CA:1273:G:H5'	1:CA:1274:G:OP2	2.21	0.41
2:CB:186:ALA:O	2:CB:200:ILE:HA	2.21	0.41
3:CC:12:LEU:HD23	3:CC:12:LEU:HA	1.94	0.41
3:CC:20:SER:OG	3:CC:22:TRP:NE1	2.52	0.41
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.27	0.41
4:CD:15:GLU:HG2	4:CD:63:LYS:HG3	2.03	0.41
12:CL:66:VAL:HG21	12:CL:98:TYR:CE2	2.56	0.41
13:CM:86:CYS:HB2	19:CS:73:GLU:HB3	2.03	0.41
14:CN:13:THR:HA	14:CN:14:PRO:HD3	1.85	0.41
18:CR:74:ARG:HG3	18:CR:79:LEU:HB2	2.03	0.41
25:DA:24:G:H2'	25:DA:25:U:O4'	2.21	0.41
25:DA:271(R):G:C2	25:DA:271(S):G:C5	3.08	0.41
25:DA:330:A:C2	25:DA:1210:A:H2'	2.42	0.41
25:DA:437:G:H2'	25:DA:438:G:O4'	2.21	0.41
25:DA:600:G:H5'	29:DF:32:LEU:HD12	2.02	0.41
25:DA:826:U:H5"	25:DA:2429:G:P	2.61	0.41
25:DA:910:A:N6	25:DA:2277:G:O2'	2.40	0.41
25:DA:917:A:N3	25:DA:917:A:H2'	2.36	0.41
25:DA:1007:C:C4	25:DA:1008:C:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1032:A:H2	25:DA:1122:G:H22	1.69	0.41
25:DA:1372:U:O5'	25:DA:1372:U:H6	2.04	0.41
25:DA:1479:G:C6	25:DA:1480:G:C5	3.09	0.41
25:DA:1633:G:N2	25:DA:1635:G:H1'	2.35	0.41
25:DA:2369:A:H2'	25:DA:2370:G:C8	2.56	0.41
25:DA:2516:G:C6	25:DA:2517:C:C4	3.09	0.41
25:DA:2537:U:H2'	25:DA:2538:C:H6	1.81	0.41
26:DB:78:A:C2	26:DB:100:A:C4	3.09	0.41
27:DD:70:TRP:CE2	27:DD:150:LYS:HD3	2.56	0.41
31:DH:98:LEU:HD13	31:DH:98:LEU:HA	1.93	0.41
32:DI:29:TYR:O	32:DI:33:ARG:HG3	2.21	0.41
33:DN:34:LEU:HD21	33:DN:120:LEU:HG	2.03	0.41
36:DQ:66:ILE:HG12	36:DQ:104:PHE:CE1	2.55	0.41
36:DQ:75:THR:HG21	36:DQ:87:LYS:HZ3	1.86	0.41
38:DS:74:ALA:CB	38:DS:108:GLY:HA3	2.51	0.41
40:DU:97:ASP:OD2	40:DU:101:ARG:HD2	2.20	0.41
1:AA:29:G:O2'	1:AA:295:C:H4'	2.21	0.41
1:AA:271:C:H2'	1:AA:272:C:H6	1.85	0.41
1:AA:438:G:O2'	1:AA:494:U:O4	2.38	0.41
1:AA:1057:G:C4	1:AA:1204:A:C2	3.09	0.41
1:AA:1233:G:O2'	1:AA:1365:G:OP1	2.38	0.41
1:AA:1353:G:O2'	1:AA:1354:C:H5'	2.21	0.41
1:AA:1371:G:O3'	9:AI:69:GLY:HA3	2.20	0.41
7:AG:52:GLU:HG2	7:AG:52:GLU:H	1.59	0.41
24:AX:56:C:O5'	24:AX:56:C:H6	2.04	0.41
25:BA:1529:G:C6	25:BA:1530:C:N4	2.89	0.41
25:BA:1564:C:H2'	25:BA:1565:C:C6	2.56	0.41
25:BA:1843:C:H2'	25:BA:1844:C:C6	2.55	0.41
25:BA:2125:G:N1	25:BA:2172:U:OP1	2.52	0.41
25:BA:2547:U:H2'	25:BA:2548:G:C8	2.55	0.41
32:BI:9:LEU:HD13	32:BI:10:GLU:HG3	2.02	0.41
33:BN:102:ALA:O	33:BN:106:MET:HG3	2.21	0.41
36:BQ:104:PHE:HE2	36:BQ:125:LEU:HD11	1.86	0.41
37:BR:61:HIS:O	37:BR:65:LEU:HD22	2.21	0.41
45:BZ:6:LYS:HD3	45:BZ:8:TYR:OH	2.21	0.41
46:B0:53:MET:HG3	46:B0:59:LEU:HD23	2.03	0.41
1:CA:163:C:H2'	1:CA:164:U:O4'	2.21	0.41
1:CA:299:G:H2'	1:CA:300:A:C8	2.56	0.41
1:CA:750:G:N3	15:CO:23:GLY:HA3	2.35	0.41
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.21	0.41
1:CA:1226:C:OP1	13:CM:91:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:137:ALA:HA	3:CC:140:ARG:HD3	2.02	0.41
4:CD:173:TRP:NE1	4:CD:189:PRO:HG3	2.35	0.41
5:CE:95:ALA:HB1	5:CE:96:PRO:HD2	2.03	0.41
12:CL:58:VAL:O	12:CL:65:GLU:HA	2.21	0.41
24:CX:10:G:C2	24:CX:26:G:H1'	2.56	0.41
25:DA:710:G:H2'	25:DA:711:G:C8	2.55	0.41
25:DA:848:G:C2	25:DA:933:A:H1'	2.56	0.41
25:DA:2160:G:H2'	25:DA:2161:C:O4'	2.21	0.41
25:DA:2290:G:C6	25:DA:2291:U:C4	3.09	0.41
26:DB:73:A:C6	26:DB:74:U:C2	3.09	0.41
32:DI:114:LEU:HD22	32:DI:130:TYR:HA	2.03	0.41
35:DP:138:LEU:HD12	35:DP:138:LEU:HA	1.93	0.41
37:DR:100:LEU:HD11	37:DR:113:LEU:HD23	2.02	0.41
43:DX:94:GLY:N	43:DX:95:LEU:HA	2.36	0.41
44:DY:7:VAL:HG11	44:DY:13:VAL:HG11	2.02	0.41
45:DZ:53:ILE:HG22	45:DZ:71:VAL:O	2.20	0.41
53:D7:9:ARG:NH2	53:D7:47:ARG:HD2	2.36	0.41
54:D8:28:GLY:O	54:D8:36:LYS:NZ	2.47	0.41
1:AA:20:U:H2'	1:AA:21:G:O4'	2.21	0.40
1:AA:136:C:H42	1:AA:227:G:H1	1.70	0.40
1:AA:689:C:P	11:AK:46:GLY:HA3	2.61	0.40
1:AA:716:A:N3	11:AK:118:GLY:HA2	2.36	0.40
1:AA:719:C:H1'	18:AR:49:LYS:HB3	2.03	0.40
1:AA:938:A:C6	1:AA:939:G:C5	3.09	0.40
1:AA:1027:C:O2'	1:AA:1028:C:C6	2.69	0.40
1:AA:1209:C:O2'	1:AA:1214:C:N4	2.52	0.40
1:AA:1275:A:H2'	1:AA:1276:G:C8	2.55	0.40
1:AA:1375:A:H4'	7:AG:29:LYS:HE2	2.03	0.40
2:AB:105:PHE:HB2	2:AB:158:LEU:HD11	2.02	0.40
3:AC:173:VAL:O	3:AC:175:LEU:HD12	2.21	0.40
5:AE:39:GLY:HA2	5:AE:71:LEU:HD21	2.02	0.40
13:AM:3:ARG:HD2	13:AM:9:ILE:CG1	2.50	0.40
25:BA:40:C:H42	25:BA:438:G:H1	1.69	0.40
25:BA:219:G:H2'	25:BA:220:G:C8	2.56	0.40
25:BA:365:C:H2'	25:BA:366:C:O4'	2.20	0.40
25:BA:624:C:O2'	25:BA:657:U:OP1	2.31	0.40
25:BA:738:G:C6	25:BA:739:G:C2	3.09	0.40
25:BA:1047:G:H2'	25:BA:1110:G:H22	1.86	0.40
25:BA:1655:A:H3'	25:BA:1656:C:H6	1.86	0.40
25:BA:2141:G:C4	25:BA:2142:C:H1'	2.55	0.40
25:BA:2161:C:N4	25:BA:2162:G:O6	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2822:G:O2'	25:BA:2824:C:OP2	2.33	0.40
28:BE:72:VAL:HG12	28:BE:73:GLU:O	2.22	0.40
30:BG:16:ARG:HB2	30:BG:17:PRO:HD3	2.03	0.40
30:BG:44:GLY:N	30:BG:88:ILE:O	2.54	0.40
31:BH:13:LYS:HA	31:BH:14:GLY:HA2	1.61	0.40
31:BH:20:ALA:HB1	31:BH:21:PRO:HD2	2.03	0.40
35:BP:21:ARG:HD3	35:BP:21:ARG:HA	1.90	0.40
38:BS:3:ARG:HE	38:BS:4:LEU:N	2.18	0.40
49:B3:15:TYR:O	49:B3:20:LYS:NZ	2.52	0.40
50:B4:61:ARG:HG3	50:B4:62:ARG:N	2.36	0.40
1:CA:600:C:H2'	1:CA:601:C:C6	2.57	0.40
1:CA:717:C:H2'	1:CA:734:G:OP2	2.21	0.40
1:CA:889:A:OP1	1:CA:891:U:H1'	2.21	0.40
1:CA:967:C:H5"	1:CA:968:A:OP2	2.21	0.40
1:CA:1120:G:N1	1:CA:1154:G:N3	2.69	0.40
1:CA:1216:G:H2'	1:CA:1217:C:H5"	2.01	0.40
1:CA:1493:A:C8	25:DA:1913:A:N6	2.86	0.40
2:CB:87:ARG:HE	2:CB:233:SER:HB3	1.87	0.40
3:CC:108:ASN:OD1	3:CC:110:ASN:HB2	2.21	0.40
3:CC:199:LYS:HB3	3:CC:201:TYR:CE1	2.56	0.40
7:CG:45:ASP:O	7:CG:49:ILE:HG12	2.21	0.40
10:CJ:50:ILE:HB	14:CN:41:ARG:NE	2.35	0.40
14:CN:53:LEU:HA	14:CN:54:PRO:HD2	1.89	0.40
15:CO:67:LEU:HA	15:CO:67:LEU:HD23	1.88	0.40
19:CS:36:ARG:CZ	19:CS:72:GLY:HA2	2.51	0.40
25:DA:593:G:H4'	54:D8:4:MET:HE2	2.03	0.40
25:DA:602:G:O2'	25:DA:655:A:N6	2.54	0.40
25:DA:605:C:OP1	29:DF:104:LYS:NZ	2.54	0.40
25:DA:856:C:HO2'	25:DA:857:C:P	2.44	0.40
25:DA:1321:A:H2'	25:DA:1322:A:O4'	2.21	0.40
25:DA:1407:C:H2'	25:DA:1408:C:C6	2.56	0.40
25:DA:1482:G:C6	25:DA:1507:A:C6	3.09	0.40
25:DA:1819:A:H2'	27:DD:178:PRO:HB2	2.03	0.40
25:DA:2351:G:O6	54:D8:39:LYS:HG3	2.21	0.40
26:DB:16:G:C6	26:DB:69:G:C2	3.09	0.40
26:DB:92:C:H2'	26:DB:93:G:H8	1.87	0.40
29:DF:112:MET:HE3	29:DF:112:MET:HB3	1.88	0.40
31:DH:56:SER:HB2	31:DH:61:HIS:ND1	2.36	0.40
34:DO:47:ILE:HB	34:DO:48:PRO:HD2	2.03	0.40
35:DP:125:VAL:HG23	35:DP:130:PHE:HZ	1.86	0.40
36:DQ:17:LEU:HD21	36:DQ:96:VAL:HG13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:DU:8:VAL:O	40:DU:12:ARG:HG3	2.21	0.40
45:DZ:161:VAL:O	45:DZ:161:VAL:HG13	2.20	0.40
54:D8:8:LYS:O	54:D8:12:LYS:HG3	2.21	0.40
1:AA:397:A:N3	1:AA:397:A:H3'	2.36	0.40
1:AA:633:G:H2'	1:AA:634:C:C6	2.56	0.40
1:AA:967:C:H5"	1:AA:968:A:OP2	2.21	0.40
1:AA:1079:G:C6	1:AA:1080:A:N6	2.89	0.40
1:AA:1157:A:H61	1:AA:1178:G:N2	2.19	0.40
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.50	0.40
20:AT:67:ALA:HB2	20:AT:77:ALA:HB2	2.02	0.40
24:AX:52:G:H2'	24:AX:53:G:H8	1.86	0.40
25:BA:188:G:H1	25:BA:208:C:H42	1.67	0.40
25:BA:775:G:O6	25:BA:787:U:H2'	2.21	0.40
25:BA:867:C:N3	25:BA:912:C:O2'	2.43	0.40
25:BA:910:A:C5	36:BQ:13:GLN:HG3	2.56	0.40
25:BA:2163:C:H2'	25:BA:2164:C:O4'	2.21	0.40
34:BO:70:LYS:HE2	34:BO:70:LYS:HB3	1.82	0.40
1:CA:575:G:C6	1:CA:821:G:N7	2.89	0.40
1:CA:1003:G:C6	1:CA:1004:A:H2	2.39	0.40
1:CA:1155:G:C6	1:CA:1156:G:C5	3.09	0.40
1:CA:1353:G:O2'	1:CA:1354:C:H5'	2.21	0.40
1:CA:1358:U:H2'	1:CA:1359:C:O4'	2.21	0.40
1:CA:1423:G:OP1	34:DO:49:ARG:NH2	2.54	0.40
5:CE:135:THR:O	5:CE:139:LEU:N	2.52	0.40
7:CG:74:GLU:OE1	7:CG:95:ARG:NE	2.44	0.40
7:CG:126:ASP:O	7:CG:130:GLY:N	2.54	0.40
8:CH:41:ARG:HB3	8:CH:41:ARG:CZ	2.52	0.40
15:CO:25:THR:HG21	15:CO:70:LEU:HB2	2.03	0.40
16:CP:20:VAL:HG22	16:CP:34:GLU:O	2.22	0.40
20:CT:29:LYS:O	20:CT:33:ILE:HG13	2.21	0.40
25:DA:125:G:H1'	53:D7:48:LYS:HE2	2.03	0.40
25:DA:880:G:C2	25:DA:898:C:O2	2.74	0.40
25:DA:945:A:C4	25:DA:2448:A:C2	3.09	0.40
25:DA:1412:A:N1	25:DA:1591:G:C6	2.89	0.40
25:DA:1759:A:H4'	25:DA:2715:C:O4'	2.20	0.40
25:DA:2153:G:H5"	25:DA:2154:G:OP2	2.21	0.40
25:DA:2271:G:OP1	46:D0:18:ALA:HB1	2.20	0.40
25:DA:2291:U:O2'	25:DA:2374:C:H1'	2.20	0.40
25:DA:2431:U:O2'	25:DA:2433:A:N7	2.42	0.40
25:DA:2582:G:N2	25:DA:2583:G:H1'	2.36	0.40
30:DG:114:ILE:HG22	30:DG:117:PHE:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DH:54:ARG:HD3	31:DH:65:HIS:ND1	2.36	0.40
33:DN:67:LEU:HD12	33:DN:67:LEU:HA	1.81	0.40
43:DX:57:LEU:HD13	43:DX:78:LYS:HB3	2.02	0.40
44:DY:98:VAL:HA	44:DY:105:ALA:HA	2.03	0.40
48:D2:35:LEU:HD23	48:D2:35:LEU:HA	1.86	0.40
52:D6:38:LYS:CE	52:D6:39:TYR:H	2.34	0.40
54:D8:53:PRO:O	54:D8:57:ARG:HG3	2.22	0.40
1:AA:34:C:H2'	1:AA:35:G:C8	2.57	0.40
1:AA:954:G:C6	1:AA:955:U:C4	3.09	0.40
1:AA:1002:G:C2	1:AA:1003:G:H1'	2.56	0.40
1:AA:1259:C:O2	1:AA:1283:G:H1'	2.21	0.40
1:AA:1457:G:H2'	1:AA:1458:G:H8	1.82	0.40
1:AA:1531:A:H3'	1:AA:1532:U:C6	2.56	0.40
2:AB:30:ARG:HG3	2:AB:31:TYR:CD1	2.56	0.40
3:AC:134:ILE:HG22	3:AC:168:ALA:HB3	2.02	0.40
9:AI:128:ARG:NH1	24:AX:35:A:OP2	2.54	0.40
19:AS:71:LEU:HD23	19:AS:71:LEU:HA	1.89	0.40
25:BA:577:G:O2'	25:BA:1254:A:OP1	2.36	0.40
25:BA:644:A:H4'	25:BA:645:C:C5	2.56	0.40
25:BA:810:U:O5'	25:BA:810:U:H6	2.04	0.40
25:BA:886:C:OP1	25:BA:886:C:H4'	2.19	0.40
25:BA:1177:A:N3	25:BA:1177:A:H2'	2.35	0.40
25:BA:1443:G:H2'	25:BA:1444:G:H8	1.86	0.40
25:BA:2478:A:H2'	25:BA:2479:G:O4'	2.22	0.40
25:BA:2584:U:O2	25:BA:2585:U:N3	2.54	0.40
27:BD:108:PRO:HG2	27:BD:111:LEU:HB2	2.03	0.40
28:BE:47:VAL:HG23	28:BE:84:PHE:O	2.21	0.40
30:BG:114:ILE:HA	30:BG:140:ILE:HD11	2.04	0.40
45:BZ:33:LEU:H	45:BZ:33:LEU:HG	1.82	0.40
51:B5:49:CYS:SG	51:B5:51:TYR:HB2	2.62	0.40
1:CA:1023:G:C5	1:CA:1024:G:C8	3.09	0.40
1:CA:1122:U:C4	1:CA:1123:A:C5	3.10	0.40
1:CA:1281:U:P	1:CA:1282:C:H41	2.44	0.40
2:CB:50:GLU:OE1	2:CB:200:ILE:HG12	2.21	0.40
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.56	0.40
10:CJ:19:SER:O	10:CJ:23:ILE:HG12	2.19	0.40
12:CL:34:ARG:HE	12:CL:34:ARG:HB3	1.45	0.40
25:DA:239:U:H2'	25:DA:240:G:O4'	2.21	0.40
25:DA:323:G:C8	29:DF:171:PRO:HG3	2.56	0.40
25:DA:619:G:H3'	25:DA:620:G:N2	2.35	0.40
25:DA:661:C:H2'	25:DA:662:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:862:G:H2'	25:DA:863:A:O4'	2.21	0.40
25:DA:1034:G:C6	25:DA:1035:U:C4	3.09	0.40
25:DA:1162:G:H2'	25:DA:1163:G:H8	1.85	0.40
25:DA:1187:G:H5'	41:DV:81:TYR:CE1	2.57	0.40
25:DA:1252:G:C2	25:DA:1253:A:C2	3.09	0.40
25:DA:1346:G:C6	25:DA:1601:G:C6	3.09	0.40
25:DA:1469:A:H2'	25:DA:1470:G:O4'	2.22	0.40
25:DA:2591:C:H2'	25:DA:2592:G:C8	2.56	0.40
25:DA:2647:U:H2'	25:DA:2648:C:C6	2.57	0.40
26:DB:8:U:O2'	38:DS:40:ILE:HD13	2.21	0.40
26:DB:104:U:O3'	45:DZ:72:ARG:HD2	2.21	0.40
27:DD:177:LEU:HB3	27:DD:178:PRO:HD2	2.04	0.40
36:DQ:21:THR:OG1	36:DQ:99:PRO:O	2.37	0.40
38:DS:35:ILE:HB	38:DS:97:ARG:HH21	1.85	0.40
40:DU:27:LEU:HA	40:DU:30:LYS:HB2	2.04	0.40
45:DZ:53:ILE:HG22	45:DZ:71:VAL:HB	2.02	0.40
1:AA:191:G:N3	20:AT:103:GLY:HA2	2.37	0.40
1:AA:657:G:H4'	15:AO:28:GLN:HG2	2.04	0.40
1:AA:664:G:N2	1:AA:741:G:H1	2.09	0.40
1:AA:684:A:H2'	1:AA:685:G:O4'	2.21	0.40
1:AA:939:G:N3	1:AA:1375:A:H2	2.19	0.40
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.86	0.40
2:AB:22:LYS:C	2:AB:24:TRP:H	2.29	0.40
3:AC:131:ARG:NH2	3:AC:166:GLU:OE2	2.52	0.40
13:AM:91:ARG:HA	13:AM:91:ARG:HD2	1.85	0.40
16:AP:40:ASP:N	16:AP:48:TRP:O	2.45	0.40
17:AQ:62:SER:OG	17:AQ:72:ARG:HG2	2.21	0.40
19:AS:42:PRO:HD3	50:B4:61:ARG:HD3	2.03	0.40
25:BA:58:G:O2'	25:BA:73:A:N1	2.48	0.40
25:BA:282:A:N3	25:BA:282:A:H2'	2.37	0.40
25:BA:1484:G:H1	25:BA:1505:C:N4	2.20	0.40
25:BA:1930:G:N2	25:BA:1968:G:H2'	2.37	0.40
25:BA:2277:G:P	46:B0:10:THR:HG21	2.61	0.40
25:BA:2557:G:H2'	25:BA:2558:C:C6	2.56	0.40
25:BA:2682:U:H5'	28:BE:11:MET:O	2.21	0.40
27:BD:213:ARG:HD2	27:BD:217:ARG:O	2.22	0.40
39:BT:51:ARG:HG3	39:BT:98:LYS:HD2	2.03	0.40
1:CA:797:C:C2'	1:CA:798:G:H5'	2.51	0.40
1:CA:949:A:C6	1:CA:950:U:C4	3.09	0.40
1:CA:1168:A:H2'	1:CA:1169:A:C8	2.55	0.40
1:CA:1194:U:H2'	1:CA:1195:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1226:C:P	13:CM:91:ARG:HH12	2.45	0.40
6:CF:84:ASN:O	6:CF:86:ARG:HG3	2.22	0.40
7:CG:87:VAL:HG11	7:CG:155:ARG:HA	2.03	0.40
9:CI:16:ARG:O	9:CI:63:ILE:HA	2.21	0.40
24:CX:4:G:H2'	24:CX:5:G:C8	2.57	0.40
25:DA:626:U:O2	35:DP:105:LEU:HD22	2.22	0.40
25:DA:882:G:N2	25:DA:894:C:N3	2.69	0.40
25:DA:1364:G:P	47:D1:3:LYS:HG3	2.62	0.40
25:DA:1411:C:H2'	25:DA:1412:A:H8	1.87	0.40
25:DA:1431:U:H2'	25:DA:1432:C:C6	2.56	0.40
25:DA:1814:G:H4'	27:DD:51:VAL:HG21	2.04	0.40
25:DA:2027:G:H2'	25:DA:2028:U:O4'	2.22	0.40
25:DA:2126:A:N1	25:DA:2173:A:C8	2.90	0.40
25:DA:2187:G:H8	25:DA:2187:G:C5'	2.35	0.40
25:DA:2503:A:H4'	25:DA:2504:U:OP1	2.22	0.40
25:DA:2543:G:H2'	25:DA:2544:G:C8	2.56	0.40
26:DB:24:G:H4'	26:DB:25:A:C8	2.56	0.40
28:DE:12:THR:HG22	39:DT:58:ASN:OD1	2.21	0.40
30:DG:173:LEU:O	30:DG:178:PHE:HB2	2.22	0.40
32:DI:40:THR:O	32:DI:44:LEU:HB2	2.21	0.40
35:DP:84:ASN:CG	35:DP:117:GLU:HB2	2.46	0.40
51:D5:19:ARG:HH11	51:D5:19:ARG:HD2	1.73	0.40
1:AA:885:G:H1	1:AA:912:C:H42	1.70	0.40
1:AA:1396:A:O4'	1:AA:1398:A:H1'	2.22	0.40
9:AI:8:GLY:HA3	9:AI:76:ALA:O	2.22	0.40
18:AR:53:ARG:HG2	18:AR:58:LEU:O	2.21	0.40
25:BA:6:A:H2	33:BN:133:GLN:HE22	1.68	0.40
25:BA:271(X):G:C2	25:BA:271(Y):U:O4	2.74	0.40
25:BA:511:U:H4'	25:BA:1235:G:H4'	2.02	0.40
25:BA:2079:U:H2'	25:BA:2080:G:O4'	2.20	0.40
25:BA:2165:G:O6	25:BA:2171:A:O2'	2.36	0.40
25:BA:2245:U:H5"	25:BA:2246:G:H5'	2.04	0.40
25:BA:2636:U:H1'	25:BA:2783:G:N2	2.36	0.40
27:BD:232:PRO:HB3	27:BD:244:ARG:NH2	2.36	0.40
28:BE:117:MET:HE2	28:BE:117:MET:HB3	1.95	0.40
28:BE:164:ARG:HH11	28:BE:164:ARG:HD2	1.77	0.40
32:BI:52:ARG:HB2	32:BI:52:ARG:NH2	2.37	0.40
32:BI:57:ARG:HD3	32:BI:58:LEU:H	1.86	0.40
39:BT:77:PRO:HB2	39:BT:80:SER:HB2	2.04	0.40
44:BY:90:LEU:HD13	44:BY:90:LEU:HA	1.93	0.40
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1017:G:H2'	1:CA:1018:C:O4'	2.22	0.40
1:CA:1089:G:C6	1:CA:1090:U:C4	3.10	0.40
5:CE:24:ARG:NH1	22:CV:24:A:OP2	2.54	0.40
5:CE:59:GLY:O	5:CE:62:ALA:HB3	2.21	0.40
11:CK:115:PRO:C	11:CK:117:ASN:H	2.29	0.40
13:CM:65:LYS:N	50:D4:50:VAL:HG21	2.36	0.40
17:CQ:91:ARG:HG2	17:CQ:95:TYR:HE1	1.85	0.40
23:CW:76:PPU:HM2	25:DA:2452:C:N3	2.37	0.40
25:DA:30:G:C5	25:DA:31:C:C4	3.10	0.40
25:DA:61:G:H5'	48:D2:50:ILE:HG21	2.03	0.40
25:DA:189:G:OP2	47:D1:39:LYS:NZ	2.54	0.40
25:DA:335:C:H4'	44:DY:73:ARG:CD	2.51	0.40
25:DA:534:U:H6	25:DA:534:U:O5'	2.04	0.40
25:DA:987:G:H2'	25:DA:988:A:O4'	2.22	0.40
25:DA:2080:G:H2'	25:DA:2081:C:H6	1.87	0.40
25:DA:2153:G:H3'	25:DA:2154:G:H8	1.86	0.40
25:DA:2516:G:C6	25:DA:2517:C:N4	2.89	0.40
25:DA:2592:G:C6	25:DA:2593:U:C4	3.10	0.40
25:DA:2773:C:H2'	25:DA:2774:C:C6	2.57	0.40
26:DB:54:G:H8	26:DB:54:G:O5'	2.04	0.40
27:DD:71:ASP:CB	27:DD:103:ARG:HH22	2.27	0.40
27:DD:73:VAL:HG13	27:DD:120:GLY:HA3	2.02	0.40
28:DE:7:VAL:CG1	28:DE:27:LEU:HB3	2.51	0.40
37:DR:100:LEU:HD22	37:DR:112:ALA:HA	2.02	0.40
39:DT:59:THR:HG23	39:DT:78:LEU:CB	2.52	0.40
40:DU:90:VAL:HG13	41:DV:4:ILE:HG21	2.04	0.40
40:DU:108:GLU:O	40:DU:112:ARG:HG2	2.22	0.40
42:DW:36:LEU:HD12	42:DW:51:LEU:HD12	2.04	0.40
48:D2:1:MET:HB2	48:D2:52:ASP:CG	2.45	0.40

There are no symmetry-related clashes.

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%)	208 (91%)	18 (8%)	3 (1%)	9 32
2	CB	229/256 (90%)	206 (90%)	17 (7%)	6 (3%)	4 17
3	AC	204/239 (85%)	193 (95%)	10 (5%)	1 (0%)	24 54
3	CC	204/239 (85%)	187 (92%)	15 (7%)	2 (1%)	12 39
4	AD	206/209 (99%)	195 (95%)	9 (4%)	2 (1%)	12 39
4	CD	206/209 (99%)	194 (94%)	11 (5%)	1 (0%)	24 54
5	AE	146/162 (90%)	140 (96%)	4 (3%)	2 (1%)	9 30
5	CE	146/162 (90%)	142 (97%)	4 (3%)	0	100 100
6	AF	98/101 (97%)	96 (98%)	2 (2%)	0	100 100
6	CF	98/101 (97%)	96 (98%)	2 (2%)	0	100 100
7	AG	153/156 (98%)	148 (97%)	2 (1%)	3 (2%)	6 22
7	CG	153/156 (98%)	151 (99%)	1 (1%)	1 (1%)	18 48
8	AH	135/138 (98%)	133 (98%)	2 (2%)	0	100 100
8	CH	135/138 (98%)	132 (98%)	3 (2%)	0	100 100
9	AI	125/128 (98%)	118 (94%)	7 (6%)	0	100 100
9	CI	125/128 (98%)	120 (96%)	5 (4%)	0	100 100
10	AJ	95/105 (90%)	87 (92%)	7 (7%)	1 (1%)	11 36
10	CJ	94/105 (90%)	87 (93%)	5 (5%)	2 (2%)	5 21
11	AK	112/129 (87%)	104 (93%)	5 (4%)	3 (3%)	4 16
11	CK	112/129 (87%)	103 (92%)	7 (6%)	2 (2%)	6 25
12	AL	120/132 (91%)	115 (96%)	5 (4%)	0	100 100
12	CL	120/132 (91%)	113 (94%)	7 (6%)	0	100 100
13	AM	121/126 (96%)	113 (93%)	8 (7%)	0	100 100
13	CM	120/126 (95%)	114 (95%)	5 (4%)	1 (1%)	16 44
14	AN	58/61 (95%)	55 (95%)	3 (5%)	0	100 100
14	CN	58/61 (95%)	55 (95%)	3 (5%)	0	100 100
15	AO	86/89 (97%)	83 (96%)	3 (4%)	0	100 100
15	CO	86/89 (97%)	81 (94%)	5 (6%)	0	100 100
16	AP	80/88 (91%)	77 (96%)	3 (4%)	0	100 100
16	CP	80/88 (91%)	77 (96%)	2 (2%)	1 (1%)	9 32
17	AQ	97/105 (92%)	92 (95%)	4 (4%)	1 (1%)	12 39
17	CQ	97/105 (92%)	94 (97%)	3 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	AR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
18	CR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
19	AS	81/93 (87%)	76 (94%)	5 (6%)	0	100	100
19	CS	81/93 (87%)	75 (93%)	6 (7%)	0	100	100
20	AT	94/106 (89%)	87 (93%)	6 (6%)	1 (1%)	11	36
20	CT	94/106 (89%)	86 (92%)	5 (5%)	3 (3%)	3	13
21	AU	21/27 (78%)	21 (100%)	0	0	100	100
21	CU	21/27 (78%)	21 (100%)	0	0	100	100
27	BD	273/276 (99%)	263 (96%)	9 (3%)	1 (0%)	30	59
27	DD	273/276 (99%)	262 (96%)	9 (3%)	2 (1%)	18	48
28	BE	202/206 (98%)	195 (96%)	6 (3%)	1 (0%)	24	54
28	DE	202/206 (98%)	193 (96%)	7 (4%)	2 (1%)	12	39
29	BF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	24	54
29	DF	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	12	39
30	BG	179/182 (98%)	171 (96%)	7 (4%)	1 (1%)	21	51
30	DG	179/182 (98%)	167 (93%)	11 (6%)	1 (1%)	21	51
31	BH	172/180 (96%)	169 (98%)	3 (2%)	0	100	100
31	DH	172/180 (96%)	168 (98%)	4 (2%)	0	100	100
32	BI	144/148 (97%)	130 (90%)	10 (7%)	4 (3%)	4	15
32	DI	144/148 (97%)	137 (95%)	6 (4%)	1 (1%)	18	48
33	BN	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
33	DN	138/140 (99%)	135 (98%)	2 (1%)	1 (1%)	18	48
34	BO	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
34	DO	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
35	BP	147/150 (98%)	141 (96%)	6 (4%)	0	100	100
35	DP	147/150 (98%)	140 (95%)	5 (3%)	2 (1%)	9	30
36	BQ	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
36	DQ	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
37	BR	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
37	DR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
38	BS	108/112 (96%)	103 (95%)	4 (4%)	1 (1%)	14	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
38	DS	108/112 (96%)	105 (97%)	2 (2%)	1 (1%)	14 41
39	BT	129/146 (88%)	123 (95%)	4 (3%)	2 (2%)	7 27
39	DT	129/146 (88%)	125 (97%)	3 (2%)	1 (1%)	16 44
40	BU	114/118 (97%)	114 (100%)	0	0	100 100
40	DU	114/118 (97%)	114 (100%)	0	0	100 100
41	BV	99/101 (98%)	93 (94%)	6 (6%)	0	100 100
41	DV	99/101 (98%)	95 (96%)	4 (4%)	0	100 100
42	BW	110/113 (97%)	110 (100%)	0	0	100 100
42	DW	110/113 (97%)	110 (100%)	0	0	100 100
43	BX	93/96 (97%)	89 (96%)	4 (4%)	0	100 100
43	DX	93/96 (97%)	90 (97%)	3 (3%)	0	100 100
44	BY	105/110 (96%)	99 (94%)	6 (6%)	0	100 100
44	DY	105/110 (96%)	102 (97%)	3 (3%)	0	100 100
45	BZ	169/206 (82%)	152 (90%)	16 (10%)	1 (1%)	21 51
45	DZ	172/206 (84%)	158 (92%)	14 (8%)	0	100 100
46	B0	81/85 (95%)	81 (100%)	0	0	100 100
46	D0	81/85 (95%)	79 (98%)	1 (1%)	1 (1%)	10 34
47	B1	95/98 (97%)	94 (99%)	1 (1%)	0	100 100
47	D1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11 36
48	B2	68/72 (94%)	67 (98%)	1 (2%)	0	100 100
48	D2	68/72 (94%)	67 (98%)	1 (2%)	0	100 100
49	B3	57/60 (95%)	57 (100%)	0	0	100 100
49	D3	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
50	B4	67/71 (94%)	56 (84%)	9 (13%)	2 (3%)	3 14
50	D4	67/71 (94%)	54 (81%)	8 (12%)	5 (8%)	1 2
51	B5	57/60 (95%)	57 (100%)	0	0	100 100
51	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
52	B6	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
52	D6	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
53	B7	46/49 (94%)	46 (100%)	0	0	100 100
53	D7	46/49 (94%)	45 (98%)	0	1 (2%)	5 20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	B8	62/65 (95%)	62 (100%)	0	0	100	100
54	D8	62/65 (95%)	62 (100%)	0	0	100	100
55	B9	35/37 (95%)	35 (100%)	0	0	100	100
55	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11409/12128 (94%)	10906 (96%)	432 (4%)	71 (1%)	21	51

All (71) Ramachandran outliers are listed below:

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

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

5.3.2 Protein sidechains (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%)	150 (78%)	42 (22%)	1 3
2	CB	187/220 (85%)	153 (82%)	34 (18%)	2 6
3	AC	143/188 (76%)	126 (88%)	17 (12%)	5 16
3	CC	140/188 (74%)	119 (85%)	21 (15%)	3 10
4	AD	170/181 (94%)	144 (85%)	26 (15%)	3 9
4	CD	172/181 (95%)	144 (84%)	28 (16%)	2 8
5	AE	113/123 (92%)	98 (87%)	15 (13%)	4 12
5	CE	114/123 (93%)	96 (84%)	18 (16%)	2 8
6	AF	83/90 (92%)	77 (93%)	6 (7%)	13 39
6	CF	85/90 (94%)	76 (89%)	9 (11%)	6 22
7	AG	119/127 (94%)	104 (87%)	15 (13%)	4 14
7	CG	120/127 (94%)	107 (89%)	13 (11%)	6 21
8	AH	114/119 (96%)	100 (88%)	14 (12%)	4 15
8	CH	114/119 (96%)	101 (89%)	13 (11%)	5 18
9	AI	90/99 (91%)	75 (83%)	15 (17%)	2 7
9	CI	89/99 (90%)	70 (79%)	19 (21%)	1 4
10	AJ	66/92 (72%)	63 (96%)	3 (4%)	24 58
10	CJ	69/92 (75%)	62 (90%)	7 (10%)	7 24
11	AK	82/99 (83%)	71 (87%)	11 (13%)	4 12
11	CK	83/99 (84%)	76 (92%)	7 (8%)	10 31
12	AL	97/109 (89%)	86 (89%)	11 (11%)	5 19
12	CL	97/109 (89%)	88 (91%)	9 (9%)	8 27
13	AM	93/101 (92%)	74 (80%)	19 (20%)	1 4
13	CM	92/101 (91%)	75 (82%)	17 (18%)	1 5
14	AN	49/50 (98%)	42 (86%)	7 (14%)	3 11
14	CN	49/50 (98%)	39 (80%)	10 (20%)	1 4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
15	AO	78/80 (98%)	68 (87%)	10 (13%)	4 14
15	CO	78/80 (98%)	69 (88%)	9 (12%)	5 18
16	AP	69/74 (93%)	52 (75%)	17 (25%)	1 2
16	CP	68/74 (92%)	56 (82%)	12 (18%)	2 6
17	AQ	94/97 (97%)	83 (88%)	11 (12%)	5 17
17	CQ	94/97 (97%)	84 (89%)	10 (11%)	6 22
18	AR	59/77 (77%)	51 (86%)	8 (14%)	3 12
18	CR	59/77 (77%)	51 (86%)	8 (14%)	3 12
19	AS	69/80 (86%)	60 (87%)	9 (13%)	4 13
19	CS	67/80 (84%)	57 (85%)	10 (15%)	3 10
20	AT	70/82 (85%)	60 (86%)	10 (14%)	3 11
20	CT	70/82 (85%)	58 (83%)	12 (17%)	2 7
21	AU	18/22 (82%)	15 (83%)	3 (17%)	2 7
21	CU	18/22 (82%)	16 (89%)	2 (11%)	6 20
27	BD	215/218 (99%)	194 (90%)	21 (10%)	7 25
27	DD	215/218 (99%)	191 (89%)	24 (11%)	6 19
28	BE	164/166 (99%)	138 (84%)	26 (16%)	2 8
28	DE	164/166 (99%)	138 (84%)	26 (16%)	2 8
29	BF	160/166 (96%)	141 (88%)	19 (12%)	5 16
29	DF	159/166 (96%)	140 (88%)	19 (12%)	5 16
30	BG	143/156 (92%)	117 (82%)	26 (18%)	2 6
30	DG	142/156 (91%)	116 (82%)	26 (18%)	2 6
31	BH	144/148 (97%)	131 (91%)	13 (9%)	9 28
31	DH	144/148 (97%)	127 (88%)	17 (12%)	5 17
32	BI	110/124 (89%)	90 (82%)	20 (18%)	2 6
32	DI	104/124 (84%)	83 (80%)	21 (20%)	1 4
33	BN	118/119 (99%)	103 (87%)	15 (13%)	4 14
33	DN	118/119 (99%)	103 (87%)	15 (13%)	4 14
34	BO	100/100 (100%)	90 (90%)	10 (10%)	7 24
34	DO	100/100 (100%)	88 (88%)	12 (12%)	5 16
35	BP	115/116 (99%)	99 (86%)	16 (14%)	3 11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
35	DP	115/116 (99%)	99 (86%)	16 (14%)	3 11
36	BQ	111/111 (100%)	99 (89%)	12 (11%)	6 21
36	DQ	111/111 (100%)	94 (85%)	17 (15%)	3 9
37	BR	101/101 (100%)	83 (82%)	18 (18%)	2 6
37	DR	101/101 (100%)	87 (86%)	14 (14%)	3 11
38	BS	87/88 (99%)	79 (91%)	8 (9%)	8 27
38	DS	85/88 (97%)	74 (87%)	11 (13%)	4 13
39	BT	115/127 (91%)	103 (90%)	12 (10%)	7 23
39	DT	113/127 (89%)	97 (86%)	16 (14%)	3 11
40	BU	93/94 (99%)	84 (90%)	9 (10%)	8 25
40	DU	93/94 (99%)	84 (90%)	9 (10%)	8 25
41	BV	80/82 (98%)	66 (82%)	14 (18%)	2 6
41	DV	80/82 (98%)	66 (82%)	14 (18%)	2 6
42	BW	90/92 (98%)	77 (86%)	13 (14%)	3 11
42	DW	90/92 (98%)	82 (91%)	8 (9%)	9 28
43	BX	77/78 (99%)	71 (92%)	6 (8%)	11 35
43	DX	77/78 (99%)	73 (95%)	4 (5%)	21 52
44	BY	85/91 (93%)	77 (91%)	8 (9%)	8 26
44	DY	85/91 (93%)	78 (92%)	7 (8%)	10 32
45	BZ	145/179 (81%)	125 (86%)	20 (14%)	3 12
45	DZ	145/179 (81%)	125 (86%)	20 (14%)	3 12
46	B0	65/67 (97%)	60 (92%)	5 (8%)	12 35
46	D0	65/67 (97%)	60 (92%)	5 (8%)	12 35
47	B1	80/83 (96%)	75 (94%)	5 (6%)	16 45
47	D1	80/83 (96%)	70 (88%)	10 (12%)	4 15
48	B2	65/67 (97%)	60 (92%)	5 (8%)	12 35
48	D2	65/67 (97%)	55 (85%)	10 (15%)	2 9
49	B3	51/52 (98%)	44 (86%)	7 (14%)	3 12
49	D3	50/52 (96%)	45 (90%)	5 (10%)	7 24
50	B4	59/63 (94%)	44 (75%)	15 (25%)	0 2
50	D4	53/63 (84%)	38 (72%)	15 (28%)	0 1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
51	B5	50/52 (96%)	44 (88%)	6 (12%)	5 16
51	D5	50/52 (96%)	48 (96%)	2 (4%)	28 62
52	B6	51/52 (98%)	46 (90%)	5 (10%)	7 25
52	D6	50/52 (96%)	45 (90%)	5 (10%)	7 24
53	B7	41/42 (98%)	38 (93%)	3 (7%)	13 38
53	D7	41/42 (98%)	36 (88%)	5 (12%)	5 16
54	B8	53/55 (96%)	49 (92%)	4 (8%)	12 37
54	D8	54/55 (98%)	48 (89%)	6 (11%)	6 20
55	B9	34/34 (100%)	33 (97%)	1 (3%)	37 71
55	D9	34/34 (100%)	30 (88%)	4 (12%)	5 17
All	All	9318/10066 (93%)	8076 (87%)	1242 (13%)	4 12

All (1242) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	8	LYS
2	AB	11	LEU
2	AB	15	VAL
2	AB	16	HIS
2	AB	17	PHE
2	AB	19	HIS
2	AB	20	GLU
2	AB	21	ARG
2	AB	39	ILE
2	AB	48	MET
2	AB	71	VAL
2	AB	81	VAL
2	AB	94	ASN
2	AB	96	ARG
2	AB	108	ILE
2	AB	114	ARG
2	AB	127	ILE
2	AB	130	ARG
2	AB	133	LYS
2	AB	137	ARG
2	AB	139	LYS
2	AB	145	LEU
2	AB	154	LEU

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Mol	Chain	Res	Type
2	AB	155	LEU
2	AB	157	ARG
2	AB	160	ASP
2	AB	179	LYS
2	AB	185	ILE
2	AB	187	LEU
2	AB	189	ASP
2	AB	190	THR
2	AB	192	SER
2	AB	198	ASP
2	AB	200	ILE
2	AB	209	ARG
2	AB	213	LEU
2	AB	217	ARG
2	AB	221	LEU
2	AB	223	ILE
2	AB	230	VAL
2	AB	231	GLU
2	AB	235	SER
3	AC	3	ASN
3	AC	17	ASP
3	AC	27	LYS
3	AC	28	GLN
3	AC	98	ASN
3	AC	101	LEU
3	AC	104	GLN
3	AC	112	SER
3	AC	115	LEU
3	AC	118	GLN
3	AC	140	ARG
3	AC	151	VAL
3	AC	154	SER
3	AC	181	ASN
3	AC	192	THR
3	AC	195	VAL
3	AC	196	LEU
4	AD	5	ILE
4	AD	18	LYS
4	AD	19	LEU
4	AD	36	ARG
4	AD	46	LYS
4	AD	58	LEU

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Mol	Chain	Res	Type
4	AD	65	ARG
4	AD	77	ASN
4	AD	108	LEU
4	AD	127	THR
4	AD	135	LEU
4	AD	138	TYR
4	AD	141	ARG
4	AD	150	GLU
4	AD	152	SER
4	AD	155	LEU
4	AD	157	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	182	LYS
4	AD	186	LEU
4	AD	187	ARG
4	AD	188	LEU
4	AD	190	ASP
4	AD	194	LEU
4	AD	200	GLU
5	AE	10	MET
5	AE	12	LEU
5	AE	13	ILE
5	AE	20	GLN
5	AE	31	LEU
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	51	VAL
5	AE	71	LEU
5	AE	120	THR
5	AE	137	GLU
5	AE	143	ARG
5	AE	145	LYS
5	AE	151	LEU
6	AF	6	VAL
6	AF	18	GLN
6	AF	40	VAL
6	AF	55	ASP
6	AF	61	LEU
6	AF	78	GLU
7	AG	6	ARG

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Mol	Chain	Res	Type
7	AG	8	GLU
7	AG	12	LEU
7	AG	13	GLN
7	AG	24	THR
7	AG	32	ARG
7	AG	51	GLN
7	AG	52	GLU
7	AG	61	VAL
7	AG	76	ARG
7	AG	91	VAL
7	AG	104	LEU
7	AG	113	GLU
7	AG	115	ARG
7	AG	155	ARG
8	AH	19	VAL
8	AH	26	VAL
8	AH	39	LEU
8	AH	41	ARG
8	AH	45	ILE
8	AH	51	VAL
8	AH	52	ASP
8	AH	78	GLN
8	AH	86	ILE
8	AH	98	LYS
8	AH	112	LEU
8	AH	122	ARG
8	AH	127	LEU
8	AH	133	LEU
9	AI	3	GLN
9	AI	17	VAL
9	AI	23	ASN
9	AI	29	ASN
9	AI	42	ARG
9	AI	53	VAL
9	AI	64	THR
9	AI	66	ARG
9	AI	78	LYS
9	AI	87	GLN
9	AI	92	TYR
9	AI	103	THR
9	AI	108	VAL
9	AI	121	ARG

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Mol	Chain	Res	Type
9	AI	128	ARG
10	AJ	16	LEU
10	AJ	38	ILE
10	AJ	84	GLN
11	AK	16	SER
11	AK	30	VAL
11	AK	31	THR
11	AK	48	ILE
11	AK	55	LYS
11	AK	77	MET
11	AK	81	ASP
11	AK	83	ILE
11	AK	96	ARG
11	AK	104	GLN
11	AK	114	VAL
12	AL	33	ARG
12	AL	36	VAL
12	AL	46	LYS
12	AL	52	LEU
12	AL	53	ARG
12	AL	59	ARG
12	AL	83	VAL
12	AL	84	LEU
12	AL	97	ARG
12	AL	115	LYS
12	AL	118	SER
13	AM	3	ARG
13	AM	4	ILE
13	AM	8	GLU
13	AM	9	ILE
13	AM	15	VAL
13	AM	19	LEU
13	AM	25	ILE
13	AM	27	LYS
13	AM	43	THR
13	AM	55	ARG
13	AM	57	ARG
13	AM	78	ILE
13	AM	84	ILE
13	AM	98	VAL
13	AM	106	ASN
13	AM	109	THR

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Mol	Chain	Res	Type
13	AM	110	ARG
13	AM	115	LYS
13	AM	116	THR
14	AN	3	ARG
14	AN	7	ILE
14	AN	18	VAL
14	AN	22	THR
14	AN	23	ARG
14	AN	33	VAL
14	AN	44	LEU
15	AO	3	ILE
15	AO	5	LYS
15	AO	7	GLU
15	AO	26	GLU
15	AO	38	ARG
15	AO	39	LEU
15	AO	41	GLU
15	AO	64	ARG
15	AO	76	GLU
15	AO	83	GLU
16	AP	1	MET
16	AP	2	VAL
16	AP	5	ARG
16	AP	6	LEU
16	AP	8	ARG
16	AP	11	SER
16	AP	19	ILE
16	AP	20	VAL
16	AP	34	GLU
16	AP	45	THR
16	AP	50	LYS
16	AP	54	GLU
16	AP	55	ARG
16	AP	60	LEU
16	AP	62	VAL
16	AP	67	THR
16	AP	72	ARG
17	AQ	6	LEU
17	AQ	9	VAL
17	AQ	24	GLU
17	AQ	52	LYS
17	AQ	62	SER

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Mol	Chain	Res	Type
17	AQ	63	ARG
17	AQ	65	ILE
17	AQ	72	ARG
17	AQ	74	LEU
17	AQ	90	ILE
17	AQ	100	LYS
18	AR	26	LEU
18	AR	31	LEU
18	AR	32	ARG
18	AR	37	VAL
18	AR	41	LYS
18	AR	76	LEU
18	AR	82	THR
18	AR	85	LEU
19	AS	28	LYS
19	AS	30	LEU
19	AS	41	VAL
19	AS	47	HIS
19	AS	49	ILE
19	AS	65	ASN
19	AS	77	THR
19	AS	78	ARG
19	AS	79	THR
20	AT	9	ASN
20	AT	10	LEU
20	AT	13	LEU
20	AT	24	LEU
20	AT	33	ILE
20	AT	37	SER
20	AT	45	GLN
20	AT	54	LYS
20	AT	75	ASN
20	AT	84	LEU
21	AU	7	ARG
21	AU	9	ARG
21	AU	15	ARG
27	BD	12	SER
27	BD	13	ARG
27	BD	37	LEU
27	BD	61	LEU
27	BD	94	LEU
27	BD	106	ILE

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Mol	Chain	Res	Type
27	BD	113	VAL
27	BD	126	GLN
27	BD	138	VAL
27	BD	142	VAL
27	BD	155	LEU
27	BD	173	VAL
27	BD	183	ARG
27	BD	211	ARG
27	BD	212	SER
27	BD	217	ARG
27	BD	221	VAL
27	BD	229	VAL
27	BD	239	ARG
27	BD	257	LEU
27	BD	260	ARG
28	BE	2	LYS
28	BE	9	VAL
28	BE	11	MET
28	BE	12	THR
28	BE	21	VAL
28	BE	24	THR
28	BE	33	VAL
28	BE	34	VAL
28	BE	40	GLU
28	BE	73	GLU
28	BE	75	VAL
28	BE	77	ILE
28	BE	94	GLU
28	BE	111	ARG
28	BE	116	VAL
28	BE	118	LYS
28	BE	119	ARG
28	BE	144	ARG
28	BE	154	LYS
28	BE	163	GLU
28	BE	170	LEU
28	BE	175	VAL
28	BE	181	LEU
28	BE	184	VAL
28	BE	195	LEU
28	BE	203	LYS
29	BF	20	LEU

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Mol	Chain	Res	Type
29	BF	24	LEU
29	BF	28	ILE
29	BF	33	LEU
29	BF	57	VAL
29	BF	70	THR
29	BF	72	ARG
29	BF	74	ARG
29	BF	88	VAL
29	BF	106	ARG
29	BF	110	LEU
29	BF	125	LEU
29	BF	132	VAL
29	BF	162	LEU
29	BF	170	LEU
29	BF	183	VAL
29	BF	192	LEU
29	BF	197	ASP
29	BF	201	VAL
30	BG	5	VAL
30	BG	7	LEU
30	BG	21	ARG
30	BG	28	VAL
30	BG	35	GLU
30	BG	43	LEU
30	BG	45	GLU
30	BG	60	LEU
30	BG	70	VAL
30	BG	82	LEU
30	BG	88	ILE
30	BG	90	LEU
30	BG	91	ARG
30	BG	108	ASN
30	BG	115	ARG
30	BG	128	ARG
30	BG	133	LEU
30	BG	135	LEU
30	BG	138	GLN
30	BG	140	ILE
30	BG	143	GLU
30	BG	145	THR
30	BG	148	MET
30	BG	159	VAL

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Mol	Chain	Res	Type
30	BG	165	THR
30	BG	175	LEU
31	BH	15	VAL
31	BH	16	SER
31	BH	41	MET
31	BH	44	VAL
31	BH	45	VAL
31	BH	49	VAL
31	BH	57	ASP
31	BH	59	ARG
31	BH	62	LYS
31	BH	69	ARG
31	BH	95	ARG
31	BH	105	LEU
31	BH	149	ARG
32	BI	5	LEU
32	BI	9	LEU
32	BI	10	GLU
32	BI	37	VAL
32	BI	38	LEU
32	BI	41	GLU
32	BI	42	SER
32	BI	57	ARG
32	BI	61	ARG
32	BI	68	LEU
32	BI	74	ASN
32	BI	77	LEU
32	BI	92	VAL
32	BI	96	ASP
32	BI	101	LEU
32	BI	109	ILE
32	BI	116	LEU
32	BI	121	LYS
32	BI	140	LEU
32	BI	144	VAL
33	BN	28	THR
33	BN	33	LEU
33	BN	34	LEU
33	BN	46	VAL
33	BN	48	MET
33	BN	61	ARG
33	BN	62	VAL

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Mol	Chain	Res	Type
33	BN	67	LEU
33	BN	68	GLU
33	BN	73	THR
33	BN	85	ILE
33	BN	87	LEU
33	BN	97	ARG
33	BN	99	LEU
33	BN	120	LEU
34	BO	8	LEU
34	BO	9	GLU
34	BO	10	VAL
34	BO	23	ARG
34	BO	24	VAL
34	BO	28	SER
34	BO	78	ARG
34	BO	89	ASN
34	BO	94	ARG
34	BO	98	VAL
35	BP	1	MET
35	BP	21	ARG
35	BP	45	LEU
35	BP	55	ARG
35	BP	56	SER
35	BP	59	LEU
35	BP	65	ARG
35	BP	68	GLN
35	BP	77	ARG
35	BP	95	VAL
35	BP	106	LEU
35	BP	112	LEU
35	BP	119	GLU
35	BP	121	LYS
35	BP	147	LEU
35	BP	148	LEU
36	BQ	1	MET
36	BQ	6	ARG
36	BQ	7	MET
36	BQ	35	VAL
36	BQ	45	GLN
36	BQ	54	MET
36	BQ	55	VAL
36	BQ	75	THR

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Mol	Chain	Res	Type
36	BQ	81	VAL
36	BQ	109	VAL
36	BQ	110	THR
36	BQ	127	ILE
37	BR	1	MET
37	BR	14	SER
37	BR	18	LEU
37	BR	28	LEU
37	BR	29	LEU
37	BR	30	THR
37	BR	33	ARG
37	BR	36	THR
37	BR	44	LEU
37	BR	60	LEU
37	BR	65	LEU
37	BR	67	LEU
37	BR	75	LEU
37	BR	79	LEU
37	BR	86	ARG
37	BR	100	LEU
37	BR	102	GLU
37	BR	114	VAL
38	BS	14	VAL
38	BS	25	ARG
38	BS	36	TYR
38	BS	52	SER
38	BS	57	LYS
38	BS	59	LYS
38	BS	103	GLU
38	BS	110	LEU
39	BT	1	MET
39	BT	15	VAL
39	BT	28	VAL
39	BT	34	VAL
39	BT	49	VAL
39	BT	53	ARG
39	BT	78	LEU
39	BT	85	LYS
39	BT	89	VAL
39	BT	93	ARG
39	BT	96	ARG
39	BT	118	ARG

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Mol	Chain	Res	Type
40	BU	8	VAL
40	BU	20	LEU
40	BU	36	ARG
40	BU	74	LEU
40	BU	92	ARG
40	BU	95	LEU
40	BU	104	GLN
40	BU	108	GLU
40	BU	112	ARG
41	BV	18	LEU
41	BV	21	ARG
41	BV	43	GLU
41	BV	46	VAL
41	BV	51	VAL
41	BV	52	VAL
41	BV	61	VAL
41	BV	71	LEU
41	BV	72	VAL
41	BV	73	SER
41	BV	78	LYS
41	BV	79	VAL
41	BV	85	LYS
41	BV	95	LEU
42	BW	4	LYS
42	BW	11	ARG
42	BW	15	ARG
42	BW	17	VAL
42	BW	19	LEU
42	BW	23	LEU
42	BW	51	LEU
42	BW	52	GLU
42	BW	67	ASP
42	BW	68	ARG
42	BW	92	ARG
42	BW	96	ILE
42	BW	107	LEU
43	BX	1	MET
43	BX	35	THR
43	BX	52	VAL
43	BX	57	LEU
43	BX	65	ARG
43	BX	76	ARG

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Mol	Chain	Res	Type
44	BY	19	LYS
44	BY	21	LYS
44	BY	23	ARG
44	BY	43	ASN
44	BY	61	ILE
44	BY	72	VAL
44	BY	85	VAL
44	BY	91	GLU
45	BZ	5	LEU
45	BZ	18	LEU
45	BZ	19	ARG
45	BZ	31	ARG
45	BZ	33	LEU
45	BZ	46	LYS
45	BZ	58	VAL
45	BZ	72	ARG
45	BZ	74	VAL
45	BZ	76	LEU
45	BZ	91	LEU
45	BZ	98	MET
45	BZ	112	ARG
45	BZ	135	GLU
45	BZ	136	PHE
45	BZ	144	LEU
45	BZ	145	GLU
45	BZ	154	ASP
45	BZ	156	LYS
45	BZ	171	ILE
46	B0	5	LYS
46	B0	7	LEU
46	B0	20	ARG
46	B0	55	ARG
46	B0	82	ARG
47	B1	23	LYS
47	B1	30	VAL
47	B1	78	LYS
47	B1	89	GLU
47	B1	95	LEU
48	B2	30	ARG
48	B2	32	LEU
48	B2	50	ILE
48	B2	53	LEU

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Mol	Chain	Res	Type
48	B2	70	GLN
49	B3	8	LEU
49	B3	18	ASP
49	B3	23	LEU
49	B3	31	LEU
49	B3	54	VAL
49	B3	55	ARG
49	B3	58	VAL
50	B4	3	GLU
50	B4	5	ILE
50	B4	10	VAL
50	B4	27	THR
50	B4	34	GLU
50	B4	35	VAL
50	B4	46	GLN
50	B4	48	ARG
50	B4	49	PHE
50	B4	50	VAL
50	B4	56	VAL
50	B4	58	ARG
50	B4	61	ARG
50	B4	68	ARG
50	B4	69	LYS
51	B5	6	VAL
51	B5	16	ARG
51	B5	29	THR
51	B5	40	LYS
51	B5	58	LEU
51	B5	59	GLU
52	B6	4	GLU
52	B6	6	ARG
52	B6	33	LYS
52	B6	38	LYS
52	B6	48	VAL
53	B7	1	MET
53	B7	9	ARG
53	B7	43	THR
54	B8	11	LYS
54	B8	14	VAL
54	B8	30	ARG
54	B8	32	LEU
55	B9	7	VAL

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Mol	Chain	Res	Type
2	CB	8	LYS
2	CB	11	LEU
2	CB	17	PHE
2	CB	23	ARG
2	CB	48	MET
2	CB	56	ARG
2	CB	58	ILE
2	CB	60	ASP
2	CB	61	LEU
2	CB	67	THR
2	CB	94	ASN
2	CB	98	LEU
2	CB	108	ILE
2	CB	109	SER
2	CB	115	LEU
2	CB	117	GLU
2	CB	126	GLU
2	CB	127	ILE
2	CB	128	GLU
2	CB	138	LEU
2	CB	144	ARG
2	CB	145	LEU
2	CB	154	LEU
2	CB	155	LEU
2	CB	169	LYS
2	CB	187	LEU
2	CB	189	ASP
2	CB	192	SER
2	CB	200	ILE
2	CB	213	LEU
2	CB	217	ARG
2	CB	224	GLN
2	CB	230	VAL
2	CB	233	SER
3	CC	15	THR
3	CC	21	ARG
3	CC	32	LEU
3	CC	43	LEU
3	CC	44	GLU
3	CC	45	LYS
3	CC	52	LEU
3	CC	54	ARG

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Mol	Chain	Res	Type
3	CC	59	ARG
3	CC	72	LYS
3	CC	82	GLU
3	CC	105	GLU
3	CC	118	GLN
3	CC	140	ARG
3	CC	151	VAL
3	CC	152	ILE
3	CC	164	ARG
3	CC	190	ARG
3	CC	195	VAL
3	CC	196	LEU
3	CC	206	GLU
4	CD	5	ILE
4	CD	12	CYS
4	CD	19	LEU
4	CD	34	GLU
4	CD	45	GLN
4	CD	46	LYS
4	CD	47	ARG
4	CD	58	LEU
4	CD	77	ASN
4	CD	83	SER
4	CD	96	LEU
4	CD	114	ARG
4	CD	122	ARG
4	CD	127	THR
4	CD	135	LEU
4	CD	137	SER
4	CD	150	GLU
4	CD	155	LEU
4	CD	156	GLU
4	CD	158	ILE
4	CD	169	LYS
4	CD	170	VAL
4	CD	181	MET
4	CD	187	ARG
4	CD	194	LEU
4	CD	200	GLU
4	CD	202	LEU
4	CD	203	VAL
5	CE	10	MET

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Mol	Chain	Res	Type
5	CE	16	THR
5	CE	18	ARG
5	CE	20	GLN
5	CE	31	LEU
5	CE	38	GLN
5	CE	41	VAL
5	CE	43	LEU
5	CE	47	LYS
5	CE	51	VAL
5	CE	60	TYR
5	CE	67	VAL
5	CE	71	LEU
5	CE	120	THR
5	CE	137	GLU
5	CE	142	LEU
5	CE	144	THR
5	CE	150	ARG
6	CF	6	VAL
6	CF	10	LEU
6	CF	40	VAL
6	CF	41	GLU
6	CF	45	LEU
6	CF	46	ARG
6	CF	61	LEU
6	CF	69	GLU
6	CF	78	GLU
7	CG	9	VAL
7	CG	12	LEU
7	CG	32	ARG
7	CG	51	GLN
7	CG	61	VAL
7	CG	73	MET
7	CG	76	ARG
7	CG	79	ARG
7	CG	97	GLN
7	CG	104	LEU
7	CG	113	GLU
7	CG	137	LYS
7	CG	155	ARG
8	CH	8	ASP
8	CH	26	VAL
8	CH	39	LEU

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Mol	Chain	Res	Type
8	CH	41	ARG
8	CH	51	VAL
8	CH	52	ASP
8	CH	78	GLN
8	CH	84	ARG
8	CH	85	ARG
8	CH	86	ILE
8	CH	98	LYS
8	CH	112	LEU
8	CH	127	LEU
9	CI	3	GLN
9	CI	23	ASN
9	CI	29	ASN
9	CI	47	LEU
9	CI	48	GLU
9	CI	56	LEU
9	CI	64	THR
9	CI	81	ILE
9	CI	86	VAL
9	CI	87	GLN
9	CI	89	ASN
9	CI	92	TYR
9	CI	93	ARG
9	CI	102	LEU
9	CI	105	ASP
9	CI	108	VAL
9	CI	111	ARG
9	CI	117	HIS
9	CI	124	GLN
10	CJ	6	ILE
10	CJ	29	ARG
10	CJ	33	GLN
10	CJ	57	LYS
10	CJ	67	THR
10	CJ	74	ILE
10	CJ	92	THR
11	CK	30	VAL
11	CK	48	ILE
11	CK	54	ARG
11	CK	77	MET
11	CK	96	ARG
11	CK	114	VAL

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Mol	Chain	Res	Type
11	CK	126	ARG
12	CL	6	THR
12	CL	34	ARG
12	CL	36	VAL
12	CL	38	THR
12	CL	44	THR
12	CL	79	GLU
12	CL	83	VAL
12	CL	84	LEU
12	CL	124	LYS
13	CM	15	VAL
13	CM	19	LEU
13	CM	27	LYS
13	CM	34	LEU
13	CM	44	ARG
13	CM	47	ASP
13	CM	49	THR
13	CM	60	VAL
13	CM	77	ASN
13	CM	84	ILE
13	CM	98	VAL
13	CM	102	ARG
13	CM	103	THR
13	CM	106	ASN
13	CM	110	ARG
13	CM	116	THR
13	CM	121	LYS
14	CN	3	ARG
14	CN	8	GLU
14	CN	12	ARG
14	CN	18	VAL
14	CN	22	THR
14	CN	23	ARG
14	CN	32	SER
14	CN	33	VAL
14	CN	44	LEU
14	CN	47	LEU
15	CO	3	ILE
15	CO	5	LYS
15	CO	26	GLU
15	CO	39	LEU
15	CO	48	LYS

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Mol	Chain	Res	Type
15	CO	68	ARG
15	CO	76	GLU
15	CO	83	GLU
15	CO	84	LYS
16	CP	2	VAL
16	CP	5	ARG
16	CP	6	LEU
16	CP	8	ARG
16	CP	20	VAL
16	CP	21	VAL
16	CP	28	ARG
16	CP	60	LEU
16	CP	61	SER
16	CP	62	VAL
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	9	VAL
17	CQ	24	GLU
17	CQ	60	ILE
17	CQ	63	ARG
17	CQ	65	ILE
17	CQ	74	LEU
17	CQ	79	SER
17	CQ	91	ARG
17	CQ	99	SER
18	CR	25	THR
18	CR	26	LEU
18	CR	31	LEU
18	CR	32	ARG
18	CR	35	ARG
18	CR	41	LYS
18	CR	76	LEU
18	CR	85	LEU
19	CS	16	LEU
19	CS	17	GLU
19	CS	28	LYS
19	CS	30	LEU
19	CS	33	THR
19	CS	41	VAL
19	CS	56	GLN
19	CS	64	GLU

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Mol	Chain	Res	Type
19	CS	65	ASN
19	CS	78	ARG
20	CT	9	ASN
20	CT	10	LEU
20	CT	23	ARG
20	CT	41	ILE
20	CT	45	GLN
20	CT	46	GLU
20	CT	54	LYS
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	90	GLN
21	CU	7	ARG
21	CU	15	ARG
27	DD	5	LYS
27	DD	61	LEU
27	DD	94	LEU
27	DD	106	ILE
27	DD	113	VAL
27	DD	126	GLN
27	DD	134	ARG
27	DD	138	VAL
27	DD	142	VAL
27	DD	155	LEU
27	DD	162	SER
27	DD	171	ASP
27	DD	173	VAL
27	DD	204	ILE
27	DD	211	ARG
27	DD	221	VAL
27	DD	229	VAL
27	DD	242	ARG
27	DD	257	LEU
27	DD	260	ARG
27	DD	267	SER
27	DD	274	ARG
27	DD	275	LYS
27	DD	276	LYS
28	DE	9	VAL
28	DE	21	VAL

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Mol	Chain	Res	Type
28	DE	24	THR
28	DE	33	VAL
28	DE	34	VAL
28	DE	40	GLU
28	DE	47	VAL
28	DE	52	LEU
28	DE	54	GLN
28	DE	58	ARG
28	DE	61	ARG
28	DE	72	VAL
28	DE	73	GLU
28	DE	75	VAL
28	DE	77	ILE
28	DE	92	THR
28	DE	111	ARG
28	DE	116	VAL
28	DE	119	ARG
28	DE	144	ARG
28	DE	154	LYS
28	DE	163	GLU
28	DE	170	LEU
28	DE	175	VAL
28	DE	181	LEU
28	DE	195	LEU
29	DF	20	LEU
29	DF	24	LEU
29	DF	27	GLU
29	DF	28	ILE
29	DF	33	LEU
29	DF	57	VAL
29	DF	70	THR
29	DF	74	ARG
29	DF	88	VAL
29	DF	106	ARG
29	DF	110	LEU
29	DF	132	VAL
29	DF	162	LEU
29	DF	183	VAL
29	DF	192	LEU
29	DF	195	ASP
29	DF	196	LEU
29	DF	200	GLU

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Mol	Chain	Res	Type
29	DF	201	VAL
30	DG	5	VAL
30	DG	16	ARG
30	DG	28	VAL
30	DG	31	VAL
30	DG	33	ARG
30	DG	40	ASN
30	DG	43	LEU
30	DG	45	GLU
30	DG	47	LYS
30	DG	58	GLN
30	DG	60	LEU
30	DG	84	LYS
30	DG	90	LEU
30	DG	111	LEU
30	DG	115	ARG
30	DG	133	LEU
30	DG	136	ARG
30	DG	138	GLN
30	DG	140	ILE
30	DG	143	GLU
30	DG	145	THR
30	DG	148	MET
30	DG	165	THR
30	DG	167	GLU
30	DG	175	LEU
30	DG	178	PHE
31	DH	3	ARG
31	DH	15	VAL
31	DH	16	SER
31	DH	27	LYS
31	DH	32	GLU
31	DH	44	VAL
31	DH	63	SER
31	DH	69	ARG
31	DH	70	THR
31	DH	76	VAL
31	DH	95	ARG
31	DH	98	LEU
31	DH	124	GLU
31	DH	130	ARG
31	DH	136	ILE

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Mol	Chain	Res	Type
31	DH	149	ARG
31	DH	171	LEU
32	DI	5	LEU
32	DI	9	LEU
32	DI	37	VAL
32	DI	38	LEU
32	DI	40	THR
32	DI	43	ASN
32	DI	44	LEU
32	DI	50	ARG
32	DI	51	ILE
32	DI	68	LEU
32	DI	75	LEU
32	DI	77	LEU
32	DI	78	THR
32	DI	86	THR
32	DI	93	THR
32	DI	114	LEU
32	DI	117	GLU
32	DI	121	LYS
32	DI	123	LEU
32	DI	140	LEU
32	DI	143	SER
33	DN	9	VAL
33	DN	28	THR
33	DN	29	LYS
33	DN	33	LEU
33	DN	34	LEU
33	DN	38	HIS
33	DN	46	VAL
33	DN	48	MET
33	DN	62	VAL
33	DN	67	LEU
33	DN	87	LEU
33	DN	97	ARG
33	DN	99	LEU
33	DN	120	LEU
33	DN	131	GLN
34	DO	8	LEU
34	DO	9	GLU
34	DO	10	VAL
34	DO	14	THR

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Mol	Chain	Res	Type
34	DO	23	ARG
34	DO	24	VAL
34	DO	28	SER
34	DO	49	ARG
34	DO	69	ILE
34	DO	88	ASN
34	DO	94	ARG
34	DO	98	VAL
35	DP	2	LYS
35	DP	4	SER
35	DP	21	ARG
35	DP	45	LEU
35	DP	55	ARG
35	DP	56	SER
35	DP	68	GLN
35	DP	95	VAL
35	DP	96	THR
35	DP	98	GLU
35	DP	99	LEU
35	DP	106	LEU
35	DP	112	LEU
35	DP	119	GLU
35	DP	147	LEU
35	DP	149	GLU
36	DQ	1	MET
36	DQ	11	LYS
36	DQ	16	ARG
36	DQ	22	LYS
36	DQ	31	ASP
36	DQ	45	GLN
36	DQ	54	MET
36	DQ	55	VAL
36	DQ	56	ARG
36	DQ	59	ARG
36	DQ	60	ARG
36	DQ	81	VAL
36	DQ	85	LYS
36	DQ	98	LYS
36	DQ	110	THR
36	DQ	112	GLU
36	DQ	127	ILE
37	DR	1	MET

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Mol	Chain	Res	Type
37	DR	18	LEU
37	DR	28	LEU
37	DR	29	LEU
37	DR	33	ARG
37	DR	44	LEU
37	DR	65	LEU
37	DR	67	LEU
37	DR	75	LEU
37	DR	79	LEU
37	DR	86	ARG
37	DR	100	LEU
37	DR	102	GLU
37	DR	114	VAL
38	DS	3	ARG
38	DS	8	GLU
38	DS	14	VAL
38	DS	19	LYS
38	DS	28	VAL
38	DS	35	ILE
38	DS	40	ILE
38	DS	44	LYS
38	DS	80	LEU
38	DS	103	GLU
38	DS	110	LEU
39	DT	1	MET
39	DT	6	LEU
39	DT	8	LYS
39	DT	15	VAL
39	DT	19	LEU
39	DT	28	VAL
39	DT	34	VAL
39	DT	49	VAL
39	DT	53	ARG
39	DT	78	LEU
39	DT	89	VAL
39	DT	96	ARG
39	DT	108	ARG
39	DT	113	LYS
39	DT	118	ARG
39	DT	125	ARG
40	DU	20	LEU
40	DU	36	ARG

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Mol	Chain	Res	Type
40	DU	74	LEU
40	DU	92	ARG
40	DU	95	LEU
40	DU	97	ASP
40	DU	104	GLN
40	DU	108	GLU
40	DU	112	ARG
41	DV	5	VAL
41	DV	15	GLU
41	DV	21	ARG
41	DV	24	LYS
41	DV	28	GLU
41	DV	46	VAL
41	DV	61	VAL
41	DV	62	LEU
41	DV	71	LEU
41	DV	72	VAL
41	DV	78	LYS
41	DV	79	VAL
41	DV	85	LYS
41	DV	95	LEU
42	DW	4	LYS
42	DW	11	ARG
42	DW	15	ARG
42	DW	17	VAL
42	DW	23	LEU
42	DW	51	LEU
42	DW	78	GLU
42	DW	92	ARG
43	DX	23	GLU
43	DX	57	LEU
43	DX	76	ARG
43	DX	88	LYS
44	DY	8	LYS
44	DY	30	VAL
44	DY	43	ASN
44	DY	61	ILE
44	DY	72	VAL
44	DY	85	VAL
44	DY	90	LEU
45	DZ	4	ARG
45	DZ	5	LEU

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Mol	Chain	Res	Type
45	DZ	18	LEU
45	DZ	23	LYS
45	DZ	33	LEU
45	DZ	46	LYS
45	DZ	50	GLN
45	DZ	70	LEU
45	DZ	72	ARG
45	DZ	76	LEU
45	DZ	91	LEU
45	DZ	122	ARG
45	DZ	131	ARG
45	DZ	144	LEU
45	DZ	149	SER
45	DZ	150	LEU
45	DZ	154	ASP
45	DZ	155	LEU
45	DZ	162	GLU
45	DZ	171	ILE
46	D0	7	LEU
46	D0	10	THR
46	D0	20	ARG
46	D0	24	LYS
46	D0	62	LEU
47	D1	30	VAL
47	D1	32	LYS
47	D1	33	LYS
47	D1	35	THR
47	D1	37	ILE
47	D1	46	LEU
47	D1	78	LYS
47	D1	85	LEU
47	D1	95	LEU
47	D1	97	LEU
48	D2	1	MET
48	D2	14	ARG
48	D2	28	LYS
48	D2	30	ARG
48	D2	32	LEU
48	D2	45	SER
48	D2	50	ILE
48	D2	53	LEU
48	D2	64	LEU

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Mol	Chain	Res	Type
48	D2	70	GLN
49	D3	8	LEU
49	D3	23	LEU
49	D3	31	LEU
49	D3	54	VAL
49	D3	58	VAL
50	D4	3	GLU
50	D4	8	LYS
50	D4	10	VAL
50	D4	13	ARG
50	D4	21	VAL
50	D4	22	ILE
50	D4	24	THR
50	D4	34	GLU
50	D4	35	VAL
50	D4	43	TYR
50	D4	44	THR
50	D4	50	VAL
50	D4	58	ARG
50	D4	61	ARG
50	D4	63	TYR
51	D5	6	VAL
51	D5	40	LYS
52	D6	6	ARG
52	D6	25	LYS
52	D6	28	ARG
52	D6	38	LYS
52	D6	48	VAL
53	D7	9	ARG
53	D7	10	ARG
53	D7	41	ARG
53	D7	43	THR
53	D7	48	LYS
54	D8	14	VAL
54	D8	30	ARG
54	D8	32	LEU
54	D8	34	TRP
54	D8	37	SER
54	D8	41	ILE
55	D9	4	ARG
55	D9	7	VAL
55	D9	12	ASP

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Mol	Chain	Res	Type
55	D9	26	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (155) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	40	HIS
2	AB	94	ASN
2	AB	135	GLN
3	AC	6	HIS
3	AC	28	GLN
3	AC	37	GLN
3	AC	104	GLN
3	AC	118	GLN
3	AC	136	GLN
3	AC	181	ASN
4	AD	45	GLN
4	AD	77	ASN
4	AD	123	HIS
4	AD	129	ASN
4	AD	160	GLN
4	AD	201	GLN
5	AE	20	GLN
6	AF	84	ASN
6	AF	100	ASN
7	AG	28	ASN
7	AG	56	GLN
7	AG	97	GLN
7	AG	148	ASN
8	AH	82	HIS
9	AI	31	GLN
9	AI	73	GLN
9	AI	124	GLN
11	AK	93	GLN
11	AK	104	GLN
11	AK	116	HIS
11	AK	117	ASN
12	AL	78	GLN
12	AL	80	HIS
14	AN	52	GLN
15	AO	28	GLN
16	AP	76	GLN
19	AS	65	ASN

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Mol	Chain	Res	Type
19	AS	83	HIS
20	AT	9	ASN
20	AT	45	GLN
20	AT	90	GLN
27	BD	115	GLN
27	BD	164	GLN
27	BD	166	GLN
27	BD	203	ASN
27	BD	253	GLN
28	BE	55	ASN
28	BE	143	ASN
29	BF	69	HIS
29	BF	75	HIS
29	BF	203	GLN
30	BG	26	GLN
30	BG	41	GLN
30	BG	138	GLN
32	BI	43	ASN
32	BI	105	HIS
33	BN	45	ASN
33	BN	133	GLN
35	BP	38	GLN
36	BQ	12	GLN
36	BQ	45	GLN
39	BT	43	GLN
39	BT	123	GLN
40	BU	81	HIS
40	BU	94	ASN
43	BX	82	GLN
44	BY	6	HIS
44	BY	43	ASN
44	BY	92	ASN
45	BZ	73	GLN
45	BZ	132	ASN
45	BZ	151	HIS
48	B2	9	GLN
48	B2	70	GLN
50	B4	40	HIS
50	B4	46	GLN
52	B6	46	HIS
55	B9	20	HIS
55	B9	36	GLN

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Mol	Chain	Res	Type
2	CB	19	HIS
2	CB	40	HIS
2	CB	76	GLN
2	CB	78	GLN
2	CB	94	ASN
2	CB	212	GLN
2	CB	224	GLN
3	CC	28	GLN
3	CC	31	HIS
3	CC	136	GLN
3	CC	162	GLN
4	CD	45	GLN
4	CD	77	ASN
4	CD	123	HIS
4	CD	125	HIS
4	CD	129	ASN
4	CD	160	GLN
4	CD	161	ASN
5	CE	38	GLN
5	CE	127	ASN
5	CE	130	ASN
5	CE	141	GLN
6	CF	7	ASN
6	CF	100	ASN
7	CG	28	ASN
7	CG	148	ASN
7	CG	153	HIS
8	CH	15	ASN
9	CI	23	ASN
9	CI	38	GLN
9	CI	58	HIS
9	CI	89	ASN
10	CJ	62	HIS
10	CJ	68	HIS
11	CK	22	HIS
11	CK	117	ASN
12	CL	78	GLN
15	CO	28	GLN
19	CS	14	HIS
19	CS	23	ASN
19	CS	56	GLN
19	CS	57	HIS

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Mol	Chain	Res	Type
19	CS	69	HIS
20	CT	9	ASN
27	DD	96	HIS
27	DD	116	GLN
27	DD	164	GLN
27	DD	166	GLN
27	DD	253	GLN
28	DE	35	GLN
29	DF	69	HIS
29	DF	75	HIS
29	DF	169	ASN
29	DF	203	GLN
30	DG	40	ASN
30	DG	41	GLN
30	DG	121	ASN
30	DG	138	GLN
32	DI	43	ASN
34	DO	89	ASN
35	DP	35	HIS
35	DP	38	GLN
36	DQ	141	GLN
37	DR	31	HIS
38	DS	68	GLN
39	DT	58	ASN
39	DT	123	GLN
41	DV	80	GLN
43	DX	31	HIS
44	DY	43	ASN
45	DZ	50	GLN
45	DZ	75	ASN
45	DZ	121	HIS
45	DZ	151	HIS
55	D9	20	HIS
55	D9	36	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1521 (98%)	388 (25%)	22 (1%)
1	CA	1501/1521 (98%)	392 (26%)	24 (1%)
22	AV	12/24 (50%)	4 (33%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	CV	11/24 (45%)	4 (36%)	0
23	AW	0/2	-	-
23	CW	0/2	-	-
24	AX	74/77 (96%)	25 (33%)	1 (1%)
24	CX	74/77 (96%)	26 (35%)	1 (1%)
25	BA	2811/2915 (96%)	539 (19%)	24 (0%)
25	DA	2791/2915 (95%)	623 (22%)	29 (1%)
26	BB	120/121 (99%)	19 (15%)	3 (2%)
26	DB	119/121 (98%)	36 (30%)	0
All	All	9008/9320 (96%)	2056 (22%)	104 (1%)

All (2056) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	6	G
1	AA	7	G
1	AA	9	G
1	AA	22	G
1	AA	29	G
1	AA	32	A
1	AA	39	G
1	AA	41	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	59	A
1	AA	61	G
1	AA	72	C
1	AA	73	G
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	92	C
1	AA	96	U
1	AA	97	G
1	AA	98	G
1	AA	115	G
1	AA	116	A
1	AA	120	A
1	AA	121	C
1	AA	129	U

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Mol	Chain	Res	Type
1	AA	129(A)	G
1	AA	131	C
1	AA	138	G
1	AA	143	A
1	AA	146	G
1	AA	152	A
1	AA	157	G
1	AA	163	C
1	AA	172	A
1	AA	173	U
1	AA	174	C
1	AA	180	U
1	AA	182	U
1	AA	189(A)	C
1	AA	189(D)	C
1	AA	189(F)	U
1	AA	189(G)	G
1	AA	189(H)	G
1	AA	189(I)	G
1	AA	189(K)	U
1	AA	189(L)	G
1	AA	195	A
1	AA	197	A
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	243	A
1	AA	247	G
1	AA	251	G
1	AA	264	U
1	AA	266	G
1	AA	267	C
1	AA	276	G
1	AA	289	G
1	AA	306	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	342	C
1	AA	346	G
1	AA	347	G
1	AA	348	G

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Mol	Chain	Res	Type
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	374	A
1	AA	382	A
1	AA	383	A
1	AA	384	G
1	AA	397	A
1	AA	398	C
1	AA	403	C
1	AA	405	U
1	AA	406	G
1	AA	409	G
1	AA	411	A
1	AA	412	A
1	AA	413	G
1	AA	414	A
1	AA	421	U
1	AA	424	G
1	AA	426	G
1	AA	429	U
1	AA	430	A
1	AA	434	U
1	AA	435	C
1	AA	436	C
1	AA	439	A
1	AA	441	A
1	AA	442	C
1	AA	443	C
1	AA	452	A
1	AA	453	A
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	483	C
1	AA	485	G
1	AA	491	G
1	AA	495	A

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Mol	Chain	Res	Type
1	AA	496	A
1	AA	498	U
1	AA	504	C
1	AA	505	G
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	520	A
1	AA	521	G
1	AA	524	G
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	544	G
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	567	G
1	AA	571	U
1	AA	572	A
1	AA	573	A
1	AA	575	G
1	AA	576	G
1	AA	577	G
1	AA	581	G
1	AA	582	U
1	AA	587	G
1	AA	590	C
1	AA	596	C
1	AA	600	C
1	AA	623	C
1	AA	625	G
1	AA	627	G
1	AA	629	G
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	653	A
1	AA	661	G

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Mol	Chain	Res	Type
1	AA	665	A
1	AA	671	G
1	AA	680	C
1	AA	687	A
1	AA	688	G
1	AA	692	U
1	AA	693	G
1	AA	695	A
1	AA	712	A
1	AA	723	U
1	AA	724	G
1	AA	730	G
1	AA	731	G
1	AA	733	A
1	AA	748	C
1	AA	749	C
1	AA	751	U
1	AA	754	C
1	AA	755	G
1	AA	759	A
1	AA	760	G
1	AA	764	C
1	AA	766	A
1	AA	774	G
1	AA	777	A
1	AA	787	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	798	G
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	821	G
1	AA	827	U
1	AA	828	A
1	AA	836	G
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	851	G
1	AA	853	G

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Mol	Chain	Res	Type
1	AA	859	A
1	AA	872	A
1	AA	884	U
1	AA	887	G
1	AA	902	G
1	AA	914	A
1	AA	919	A
1	AA	920	U
1	AA	925	G
1	AA	926	G
1	AA	927	G
1	AA	932	C
1	AA	934	C
1	AA	936	C
1	AA	942	G
1	AA	954	G
1	AA	958	A
1	AA	960	U
1	AA	961	U
1	AA	966	G
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	983	A
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	1001	A
1	AA	1002	G
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1009	G
1	AA	1010	G
1	AA	1016	A
1	AA	1020	U
1	AA	1021	G

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Mol	Chain	Res	Type
1	AA	1022	G
1	AA	1024	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1032	G
1	AA	1033	G
1	AA	1037	C
1	AA	1044	A
1	AA	1045	C
1	AA	1053	G
1	AA	1054	C
1	AA	1061	G
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1076	C
1	AA	1077	G
1	AA	1081	G
1	AA	1088	G
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1112	C
1	AA	1113	C
1	AA	1122	U
1	AA	1124	G
1	AA	1125	U
1	AA	1126	U
1	AA	1130	A
1	AA	1135	U
1	AA	1136	U
1	AA	1137	C

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Mol	Chain	Res	Type
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1146	A
1	AA	1152	A
1	AA	1157	A
1	AA	1159	U
1	AA	1163	C
1	AA	1166	G
1	AA	1168	A
1	AA	1169	A
1	AA	1179	A
1	AA	1180	A
1	AA	1181	G
1	AA	1183	A
1	AA	1184	G
1	AA	1191	A
1	AA	1194	U
1	AA	1196	U
1	AA	1197	G
1	AA	1199	U
1	AA	1200	C
1	AA	1202	G
1	AA	1206	G
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1217	C
1	AA	1224	G
1	AA	1225	A
1	AA	1227	A
1	AA	1228	C
1	AA	1238	A
1	AA	1255	G
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1262	C
1	AA	1268	A
1	AA	1270	C
1	AA	1273	G

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Mol	Chain	Res	Type
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1282	C
1	AA	1284	C
1	AA	1286	A
1	AA	1287	A
1	AA	1289	A
1	AA	1290	G
1	AA	1296	C
1	AA	1297	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1305	G
1	AA	1317	C
1	AA	1319	A
1	AA	1320	C
1	AA	1322	C
1	AA	1338	G
1	AA	1340	A
1	AA	1346	A
1	AA	1347	G
1	AA	1353	G
1	AA	1354	C
1	AA	1355	G
1	AA	1358	U
1	AA	1360	A
1	AA	1363	C
1	AA	1368	G
1	AA	1370	G
1	AA	1372	U
1	AA	1377	A
1	AA	1379	G
1	AA	1383	C
1	AA	1397	C
1	AA	1398	A
1	AA	1400	C
1	AA	1402	C
1	AA	1406	U
1	AA	1409	C
1	AA	1419	G

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Mol	Chain	Res	Type
1	AA	1425	U
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1447	A
1	AA	1452	C
1	AA	1457	G
1	AA	1459	C
1	AA	1487	G
1	AA	1489	G
1	AA	1490	C
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	14	A
22	AV	15	A
22	AV	19	U
22	AV	24	A
24	AX	6	G
24	AX	7	G
24	AX	9	G
24	AX	16	C
24	AX	17	C
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	25	C
24	AX	30	G
24	AX	31	G
24	AX	34	C
24	AX	42	G
24	AX	47	U

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Mol	Chain	Res	Type
24	AX	48	C
24	AX	52	G
24	AX	56	C
24	AX	58	A
24	AX	59	A
24	AX	60	U
24	AX	61	C
24	AX	64	G
24	AX	65	C
24	AX	67	C
24	AX	68	C
25	BA	10	G
25	BA	12	U
25	BA	27	G
25	BA	34	C
25	BA	37	C
25	BA	45	C
25	BA	50	U
25	BA	55	G
25	BA	61	G
25	BA	71	A
25	BA	72	U
25	BA	74	A
25	BA	75	G
25	BA	96	G
25	BA	100	G
25	BA	102	G
25	BA	118	A
25	BA	119	A
25	BA	120	U
25	BA	121	G
25	BA	125	G
25	BA	140	G
25	BA	154	G
25	BA	154(A)	C
25	BA	172	C
25	BA	175	G
25	BA	177	G
25	BA	182	A
25	BA	188	G
25	BA	196	A
25	BA	199	A

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Mol	Chain	Res	Type
25	BA	205	G
25	BA	215	G
25	BA	216	A
25	BA	221	A
25	BA	222	A
25	BA	223	A
25	BA	225	A
25	BA	226	G
25	BA	229	A
25	BA	233	A
25	BA	248	G
25	BA	271(E)	U
25	BA	271(I)	G
25	BA	271(K)	U
25	BA	271(L)	U
25	BA	271(M)	G
25	BA	271(N)	U
25	BA	271(O)	C
25	BA	271(S)	G
25	BA	272(A)	U
25	BA	272(B)	G
25	BA	272(G)	C
25	BA	272(I)	U
25	BA	279	C
25	BA	282	A
25	BA	311	A
25	BA	324	A
25	BA	329	G
25	BA	330	A
25	BA	333	G
25	BA	336	C
25	BA	352	G
25	BA	353	G
25	BA	357	A
25	BA	360	G
25	BA	363	G
25	BA	363(B)	G
25	BA	363(F)	A
25	BA	372	G
25	BA	383	U
25	BA	386	G
25	BA	391	G

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Mol	Chain	Res	Type
25	BA	396	G
25	BA	399	G
25	BA	407	G
25	BA	411	G
25	BA	412	A
25	BA	415	A
25	BA	428	A
25	BA	443	A
25	BA	444	C
25	BA	448	U
25	BA	449	A
25	BA	451	C
25	BA	457	A
25	BA	470	A
25	BA	481	G
25	BA	494	G
25	BA	504	U
25	BA	505	A
25	BA	508	G
25	BA	509	C
25	BA	528	A
25	BA	530	G
25	BA	531	C
25	BA	532	A
25	BA	533	G
25	BA	545	G
25	BA	549	G
25	BA	555	U
25	BA	563	G
25	BA	573	G
25	BA	574	C
25	BA	575	A
25	BA	593	G
25	BA	602	G
25	BA	603	A
25	BA	604	G
25	BA	607	U
25	BA	610	G
25	BA	614(A)	U
25	BA	614(B)	G
25	BA	615	G
25	BA	616	G

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Mol	Chain	Res	Type
25	BA	627	A
25	BA	637	A
25	BA	645	C
25	BA	646	A
25	BA	652(E)	G
25	BA	652(F)	G
25	BA	652(T)	C
25	BA	652(U)	G
25	BA	668	G
25	BA	669	G
25	BA	686	G
25	BA	717	G
25	BA	722	A
25	BA	730	C
25	BA	740	U
25	BA	746	A
25	BA	747	U
25	BA	764	A
25	BA	775	G
25	BA	776	G
25	BA	782	A
25	BA	783	A
25	BA	784	A
25	BA	785	G
25	BA	789	A
25	BA	792	G
25	BA	793	A
25	BA	805	G
25	BA	812	C
25	BA	819	A
25	BA	827	U
25	BA	830	G
25	BA	866	A
25	BA	877	U
25	BA	879	G
25	BA	880	G
25	BA	881	G
25	BA	882	G
25	BA	884	C
25	BA	885	C
25	BA	886	C
25	BA	887	A

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Mol	Chain	Res	Type
25	BA	888	C
25	BA	889	C
25	BA	890	A
25	BA	892	G
25	BA	896	A
25	BA	897	C
25	BA	907	U
25	BA	910	A
25	BA	932	G
25	BA	941	A
25	BA	945	A
25	BA	946	G
25	BA	958	U
25	BA	959	A
25	BA	961	C
25	BA	974	G
25	BA	975	C
25	BA	983	A
25	BA	996	A
25	BA	1012	U
25	BA	1013	C
25	BA	1020	A
25	BA	1022	G
25	BA	1025	G
25	BA	1026	U
25	BA	1033	U
25	BA	1038	C
25	BA	1039	G
25	BA	1041	C
25	BA	1044	G
25	BA	1045	A
25	BA	1046	A
25	BA	1047	G
25	BA	1048	A
25	BA	1051	G
25	BA	1107	G
25	BA	1108	U
25	BA	1109	C
25	BA	1110	G
25	BA	1112	G
25	BA	1119	C
25	BA	1129	A

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Mol	Chain	Res	Type
25	BA	1130	U
25	BA	1132	A
25	BA	1135	C
25	BA	1136	G
25	BA	1138	G
25	BA	1139	G
25	BA	1170	G
25	BA	1171	G
25	BA	1173	G
25	BA	1174	A
25	BA	1175	U
25	BA	1176	G
25	BA	1177	A
25	BA	1210	A
25	BA	1211	U
25	BA	1218	C
25	BA	1236	G
25	BA	1244	G
25	BA	1248	G
25	BA	1250	G
25	BA	1253	A
25	BA	1256	G
25	BA	1271	G
25	BA	1272	A
25	BA	1273	U
25	BA	1300	U
25	BA	1301	A
25	BA	1305	C
25	BA	1308	A
25	BA	1311	G
25	BA	1314	C
25	BA	1319	G
25	BA	1320	C
25	BA	1334	G
25	BA	1342	A
25	BA	1345	C
25	BA	1352	U
25	BA	1359	A
25	BA	1360	A
25	BA	1365	A
25	BA	1384	A
25	BA	1385	G

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Mol	Chain	Res	Type
25	BA	1386	C
25	BA	1395	A
25	BA	1416	G
25	BA	1417	C
25	BA	1420	U
25	BA	1421	G
25	BA	1422	G
25	BA	1428	C
25	BA	1429	G
25	BA	1445	A
25	BA	1449	A
25	BA	1450	G
25	BA	1455	G
25	BA	1459	G
25	BA	1467	C
25	BA	1471	A
25	BA	1478	G
25	BA	1482	G
25	BA	1486	A
25	BA	1490	A
25	BA	1493	C
25	BA	1504	C
25	BA	1507	A
25	BA	1508	A
25	BA	1509	C
25	BA	1509(A)	A
25	BA	1525	G
25	BA	1527	G
25	BA	1531	C
25	BA	1532	C
25	BA	1542	A
25	BA	1543	C
25	BA	1546	C
25	BA	1558	A
25	BA	1566	A
25	BA	1569	A
25	BA	1578	U
25	BA	1580	A
25	BA	1581	G
25	BA	1584	C
25	BA	1586	A
25	BA	1592	C

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Mol	Chain	Res	Type
25	BA	1607	C
25	BA	1608	A
25	BA	1609	A
25	BA	1634	A
25	BA	1635	G
25	BA	1646	C
25	BA	1647	G
25	BA	1648	C
25	BA	1651	G
25	BA	1654	A
25	BA	1664	A
25	BA	1667	G
25	BA	1674	G
25	BA	1683	C
25	BA	1688	U
25	BA	1696	G
25	BA	1700	A
25	BA	1701	A
25	BA	1703	G
25	BA	1721	G
25	BA	1722	A
25	BA	1739	U
25	BA	1740	G
25	BA	1746	G
25	BA	1756	G
25	BA	1762	A
25	BA	1763	G
25	BA	1764	G
25	BA	1772	G
25	BA	1773	A
25	BA	1780	A
25	BA	1782	C
25	BA	1786	A
25	BA	1791	A
25	BA	1800	C
25	BA	1801	G
25	BA	1816	G
25	BA	1836	C
25	BA	1837	C
25	BA	1839	G
25	BA	1847	A
25	BA	1851	U

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Mol	Chain	Res	Type
25	BA	1878	G
25	BA	1889	A
25	BA	1900	A
25	BA	1906	G
25	BA	1909	C
25	BA	1910	G
25	BA	1912	A
25	BA	1913	A
25	BA	1914	C
25	BA	1915	U
25	BA	1919	A
25	BA	1929	G
25	BA	1930	G
25	BA	1937	A
25	BA	1938	A
25	BA	1940	U
25	BA	1952	A
25	BA	1955	U
25	BA	1963	U
25	BA	1965	C
25	BA	1967	C
25	BA	1970	A
25	BA	1971	A
25	BA	1972	A
25	BA	1992	G
25	BA	1993	U
25	BA	1997	G
25	BA	2001	A
25	BA	2021	C
25	BA	2023	G
25	BA	2031	A
25	BA	2032	G
25	BA	2033	A
25	BA	2035	G
25	BA	2036	C
25	BA	2039	C
25	BA	2043	C
25	BA	2049	G
25	BA	2055	C
25	BA	2056	G
25	BA	2060	A
25	BA	2061	G

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Mol	Chain	Res	Type
25	BA	2062	A
25	BA	2063	C
25	BA	2067	G
25	BA	2069	G
25	BA	2093	G
25	BA	2097	C
25	BA	2099	U
25	BA	2100	G
25	BA	2109	U
25	BA	2111	C
25	BA	2113	U
25	BA	2118	U
25	BA	2119	A
25	BA	2120	G
25	BA	2121	G
25	BA	2127	G
25	BA	2130	U
25	BA	2132	U
25	BA	2133	G
25	BA	2134	A
25	BA	2135	A
25	BA	2136	C
25	BA	2137	C
25	BA	2138	C
25	BA	2140	C
25	BA	2141	G
25	BA	2142	C
25	BA	2143	C
25	BA	2145	C
25	BA	2147	G
25	BA	2148	G
25	BA	2151	G
25	BA	2156	G
25	BA	2157	G
25	BA	2158	A
25	BA	2159	G
25	BA	2160	G
25	BA	2165	G
25	BA	2169	A
25	BA	2171	A
25	BA	2172	U
25	BA	2173	A

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Mol	Chain	Res	Type
25	BA	2174	C
25	BA	2175	C
25	BA	2176	A
25	BA	2178	C
25	BA	2181	G
25	BA	2182	G
25	BA	2184	G
25	BA	2188	C
25	BA	2189	U
25	BA	2192	G
25	BA	2193	G
25	BA	2198	A
25	BA	2199	A
25	BA	2206	G
25	BA	2207	G
25	BA	2208	A
25	BA	2218	U
25	BA	2225	A
25	BA	2226	C
25	BA	2238	G
25	BA	2239	G
25	BA	2268	A
25	BA	2269	A
25	BA	2273	A
25	BA	2275	C
25	BA	2278	A
25	BA	2283	C
25	BA	2287	A
25	BA	2289	G
25	BA	2305	A
25	BA	2307	G
25	BA	2308	G
25	BA	2312	U
25	BA	2320	A
25	BA	2325	G
25	BA	2327	A
25	BA	2334	G
25	BA	2335	A
25	BA	2336	A
25	BA	2343	C
25	BA	2347	C
25	BA	2350	C

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Mol	Chain	Res	Type
25	BA	2361	A
25	BA	2383	G
25	BA	2384	G
25	BA	2385	C
25	BA	2405	G
25	BA	2406	U
25	BA	2410	G
25	BA	2414	G
25	BA	2424	C
25	BA	2425	A
25	BA	2428	G
25	BA	2429	G
25	BA	2430	A
25	BA	2435	A
25	BA	2438	U
25	BA	2439	A
25	BA	2441	C
25	BA	2448	A
25	BA	2468	G
25	BA	2469	A
25	BA	2471	C
25	BA	2476	A
25	BA	2478	A
25	BA	2483	C
25	BA	2487	G
25	BA	2490	G
25	BA	2502	G
25	BA	2504	U
25	BA	2505	G
25	BA	2518	A
25	BA	2525	G
25	BA	2529	G
25	BA	2554	U
25	BA	2555	U
25	BA	2564	A
25	BA	2566	A
25	BA	2567	G
25	BA	2573	C
25	BA	2582	G
25	BA	2585	U
25	BA	2602	A
25	BA	2609	U

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Mol	Chain	Res	Type
25	BA	2611	U
25	BA	2612	C
25	BA	2623	G
25	BA	2628	C
25	BA	2629	A
25	BA	2630	G
25	BA	2654	A
25	BA	2673	G
25	BA	2689	U
25	BA	2690	C
25	BA	2691	C
25	BA	2702	U
25	BA	2703	C
25	BA	2712(A)	A
25	BA	2713	A
25	BA	2714	G
25	BA	2726	U
25	BA	2733	A
25	BA	2739	U
25	BA	2751	G
25	BA	2758	A
25	BA	2764	A
25	BA	2765	A
25	BA	2766	G
25	BA	2769	C
25	BA	2778	A
25	BA	2790	A
25	BA	2791	C
25	BA	2792	G
25	BA	2793	G
25	BA	2794	C
25	BA	2802	G
25	BA	2808	U
25	BA	2818	G
25	BA	2820	A
25	BA	2821	A
25	BA	2835	A
25	BA	2846	G
25	BA	2872	G
25	BA	2873	A
25	BA	2880	C
25	BA	2886	G

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Mol	Chain	Res	Type
25	BA	2889	C
25	BA	2892	A
25	BA	2893	G
25	BA	2894	G
26	BB	2	C
26	BB	7	G
26	BB	9	G
26	BB	24	G
26	BB	32	C
26	BB	47	C
26	BB	51	G
26	BB	52	A
26	BB	53	A
26	BB	56	G
26	BB	57	A
26	BB	72	G
26	BB	73	A
26	BB	75	G
26	BB	85	G
26	BB	86	G
26	BB	89	G
26	BB	106	G
26	BB	110	G
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	59	A
1	CA	61	G
1	CA	66	G
1	CA	72	C
1	CA	73	G
1	CA	79	G
1	CA	80	G
1	CA	88	A

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Mol	Chain	Res	Type
1	CA	89	C
1	CA	91	C
1	CA	96	U
1	CA	97	G
1	CA	98	G
1	CA	115	G
1	CA	116	A
1	CA	120	A
1	CA	121	C
1	CA	129	U
1	CA	129(A)	G
1	CA	131	C
1	CA	146	G
1	CA	157	G
1	CA	163	C
1	CA	172	A
1	CA	173	U
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(D)	C
1	CA	189(F)	U
1	CA	189(G)	G
1	CA	189(H)	G
1	CA	189(I)	G
1	CA	189(J)	G
1	CA	189(K)	U
1	CA	189(L)	G
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	243	A
1	CA	247	G
1	CA	251	G
1	CA	264	U
1	CA	266	G
1	CA	267	C
1	CA	276	G
1	CA	289	G

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Mol	Chain	Res	Type
1	CA	306	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	342	C
1	CA	344	A
1	CA	346	G
1	CA	350	G
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	374	A
1	CA	382	A
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	403	C
1	CA	405	U
1	CA	406	G
1	CA	409	G
1	CA	411	A
1	CA	412	A
1	CA	413	G
1	CA	414	A
1	CA	421	U
1	CA	422	C
1	CA	424	G
1	CA	426	G
1	CA	429	U
1	CA	430	A
1	CA	434	U
1	CA	435	C
1	CA	436	C
1	CA	439	A
1	CA	441	A
1	CA	442	C
1	CA	443	C
1	CA	452	A
1	CA	453	A

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Mol	Chain	Res	Type
1	CA	461	A
1	CA	470	C
1	CA	471	G
1	CA	483	C
1	CA	485	G
1	CA	491	G
1	CA	495	A
1	CA	496	A
1	CA	498	U
1	CA	504	C
1	CA	505	G
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	520	A
1	CA	521	G
1	CA	527	G
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	536	C
1	CA	544	G
1	CA	547	A
1	CA	559	A
1	CA	560	U
1	CA	561	U
1	CA	567	G
1	CA	571	U
1	CA	572	A
1	CA	573	A
1	CA	575	G
1	CA	576	G
1	CA	577	G
1	CA	581	G
1	CA	582	U
1	CA	587	G
1	CA	590	C
1	CA	591	U
1	CA	596	C
1	CA	600	C
1	CA	623	C

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Mol	Chain	Res	Type
1	CA	625	G
1	CA	627	G
1	CA	629	G
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	650	G
1	CA	653	A
1	CA	661	G
1	CA	665	A
1	CA	671	G
1	CA	680	C
1	CA	692	U
1	CA	693	G
1	CA	695	A
1	CA	712	A
1	CA	723	U
1	CA	724	G
1	CA	730	G
1	CA	731	G
1	CA	733	A
1	CA	748	C
1	CA	749	C
1	CA	751	U
1	CA	754	C
1	CA	755	G
1	CA	759	A
1	CA	760	G
1	CA	764	C
1	CA	766	A
1	CA	774	G
1	CA	777	A
1	CA	787	A
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	798	G
1	CA	802	A
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	821	G

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Mol	Chain	Res	Type
1	CA	827	U
1	CA	828	A
1	CA	836	G
1	CA	840	C
1	CA	841	U
1	CA	848	C
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	868	C
1	CA	884	U
1	CA	902	G
1	CA	914	A
1	CA	919	A
1	CA	920	U
1	CA	925	G
1	CA	926	G
1	CA	927	G
1	CA	932	C
1	CA	934	C
1	CA	936	C
1	CA	942	G
1	CA	948	C
1	CA	954	G
1	CA	958	A
1	CA	960	U
1	CA	961	U
1	CA	966	G
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	983	A
1	CA	991	U
1	CA	992	U
1	CA	993	G
1	CA	996	A
1	CA	1001	A
1	CA	1001(A)	G

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Mol	Chain	Res	Type
1	CA	1002	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1010	G
1	CA	1016	A
1	CA	1020	U
1	CA	1022	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1029	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1030(D)	A
1	CA	1032	G
1	CA	1033	G
1	CA	1037	C
1	CA	1038	C
1	CA	1041	A
1	CA	1044	A
1	CA	1045	C
1	CA	1053	G
1	CA	1054	C
1	CA	1061	G
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1077	G
1	CA	1081	G
1	CA	1088	G
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1112	C
1	CA	1113	C

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Mol	Chain	Res	Type
1	CA	1117	G
1	CA	1122	U
1	CA	1124	G
1	CA	1125	U
1	CA	1126	U
1	CA	1129	C
1	CA	1130	A
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1156	G
1	CA	1157	A
1	CA	1159	U
1	CA	1163	C
1	CA	1168	A
1	CA	1169	A
1	CA	1179	A
1	CA	1180	A
1	CA	1181	G
1	CA	1183	A
1	CA	1184	G
1	CA	1194	U
1	CA	1196	U
1	CA	1197	G
1	CA	1199	U
1	CA	1200	C
1	CA	1202	G
1	CA	1206	G
1	CA	1212	U
1	CA	1213	A
1	CA	1214	C
1	CA	1217	C
1	CA	1224	G
1	CA	1225	A
1	CA	1227	A

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Mol	Chain	Res	Type
1	CA	1228	C
1	CA	1236	A
1	CA	1238	A
1	CA	1255	G
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1262	C
1	CA	1267	C
1	CA	1268	A
1	CA	1270	C
1	CA	1273	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1284	C
1	CA	1285	A
1	CA	1286	A
1	CA	1287	A
1	CA	1289	A
1	CA	1290	G
1	CA	1296	C
1	CA	1297	C
1	CA	1300	G
1	CA	1305	G
1	CA	1310	G
1	CA	1317	C
1	CA	1319	A
1	CA	1322	C
1	CA	1338	G
1	CA	1340	A
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1354	C
1	CA	1355	G
1	CA	1358	U
1	CA	1360	A
1	CA	1363	C

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Mol	Chain	Res	Type
1	CA	1363(A)	A
1	CA	1370	G
1	CA	1372	U
1	CA	1377	A
1	CA	1379	G
1	CA	1381	U
1	CA	1383	C
1	CA	1397	C
1	CA	1398	A
1	CA	1400	C
1	CA	1402	C
1	CA	1406	U
1	CA	1409	C
1	CA	1419	G
1	CA	1425	U
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1447	A
1	CA	1452	C
1	CA	1457	G
1	CA	1459	C
1	CA	1487	G
1	CA	1489	G
1	CA	1490	C
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G
1	CA	1497	G
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1517	G
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1532	U
22	CV	15	A
22	CV	19	U
22	CV	20	U
22	CV	24	A
24	CX	6	G

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Mol	Chain	Res	Type
24	CX	7	G
24	CX	9	G
24	CX	16	C
24	CX	17	C
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	25	C
24	CX	30	G
24	CX	31	G
24	CX	34	C
24	CX	42	G
24	CX	47	U
24	CX	48	C
24	CX	52	G
24	CX	56	C
24	CX	58	A
24	CX	59	A
24	CX	60	U
24	CX	61	C
24	CX	64	G
24	CX	65	C
24	CX	67	C
24	CX	68	C
24	CX	70	G
25	DA	7	G
25	DA	9	U
25	DA	10	G
25	DA	12	U
25	DA	13	A
25	DA	15	G
25	DA	34	C
25	DA	35	G
25	DA	45	C
25	DA	51	G
25	DA	63	U
25	DA	71	A
25	DA	74	A
25	DA	75	G
25	DA	78	A
25	DA	83	G
25	DA	84	A

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Mol	Chain	Res	Type
25	DA	90	U
25	DA	94(A)	G
25	DA	96	G
25	DA	118	A
25	DA	120	U
25	DA	139	G
25	DA	139(A)	G
25	DA	141	A
25	DA	154(A)	C
25	DA	157	U
25	DA	173	G
25	DA	181	A
25	DA	182	A
25	DA	188	G
25	DA	196	A
25	DA	205	G
25	DA	206	U
25	DA	214	G
25	DA	216	A
25	DA	221	A
25	DA	222	A
25	DA	225	A
25	DA	228	A
25	DA	229	A
25	DA	230	U
25	DA	233	A
25	DA	248	G
25	DA	271(D)	G
25	DA	271(I)	G
25	DA	271(K)	U
25	DA	271(L)	U
25	DA	271(M)	G
25	DA	271(N)	U
25	DA	271(O)	C
25	DA	272	G
25	DA	272(A)	U
25	DA	272(B)	G
25	DA	272(J)	C
25	DA	276	A
25	DA	277	C
25	DA	278	A
25	DA	282	A

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Mol	Chain	Res	Type
25	DA	283	A
25	DA	290	G
25	DA	292	C
25	DA	295	G
25	DA	308	G
25	DA	311	A
25	DA	316	C
25	DA	317	G
25	DA	319	C
25	DA	322	A
25	DA	327	G
25	DA	329	G
25	DA	330	A
25	DA	333	G
25	DA	342	G
25	DA	345	A
25	DA	352	G
25	DA	354	G
25	DA	363	G
25	DA	363(B)	G
25	DA	385	C
25	DA	386	G
25	DA	396	G
25	DA	403	U
25	DA	405	U
25	DA	406	G
25	DA	407	G
25	DA	411	G
25	DA	412	A
25	DA	415	A
25	DA	426	C
25	DA	428	A
25	DA	444	C
25	DA	454	A
25	DA	455	C
25	DA	456	C
25	DA	457	A
25	DA	470	A
25	DA	471	A
25	DA	479	A
25	DA	480	A
25	DA	481	G

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Mol	Chain	Res	Type
25	DA	484	C
25	DA	487	C
25	DA	504	U
25	DA	505	A
25	DA	508	G
25	DA	509	C
25	DA	527	C
25	DA	529	A
25	DA	530	G
25	DA	531	C
25	DA	532	A
25	DA	533	G
25	DA	536	A
25	DA	545	G
25	DA	562	U
25	DA	563	G
25	DA	566	U
25	DA	568	U
25	DA	573	G
25	DA	574	C
25	DA	575	A
25	DA	587	C
25	DA	588	U
25	DA	595	C
25	DA	603	A
25	DA	604	G
25	DA	607	U
25	DA	609	A
25	DA	610	G
25	DA	614(B)	G
25	DA	614(C)	A
25	DA	615	G
25	DA	616	G
25	DA	627	A
25	DA	637	A
25	DA	644	A
25	DA	645	C
25	DA	646	A
25	DA	647	G
25	DA	651	G
25	DA	652(B)	A
25	DA	652(C)	G

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Mol	Chain	Res	Type
25	DA	652(U)	G
25	DA	652(V)	C
25	DA	669	G
25	DA	686	G
25	DA	701	G
25	DA	708	C
25	DA	715	G
25	DA	717	G
25	DA	726	G
25	DA	730	C
25	DA	751	A
25	DA	753	C
25	DA	758	C
25	DA	759	G
25	DA	765	G
25	DA	771	G
25	DA	775	G
25	DA	776	G
25	DA	781	A
25	DA	782	A
25	DA	784	A
25	DA	785	G
25	DA	792	G
25	DA	801	G
25	DA	805	G
25	DA	812	C
25	DA	819	A
25	DA	827	U
25	DA	830	G
25	DA	843	G
25	DA	845	G
25	DA	847	U
25	DA	857	C
25	DA	859	G
25	DA	866	A
25	DA	869	G
25	DA	879	G
25	DA	880	G
25	DA	882	G
25	DA	884	C
25	DA	886	C
25	DA	887	A

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Mol	Chain	Res	Type
25	DA	888	C
25	DA	889	C
25	DA	890	A
25	DA	893	C
25	DA	896	A
25	DA	898	C
25	DA	900	A
25	DA	901	A
25	DA	910	A
25	DA	912	C
25	DA	915	C
25	DA	917	A
25	DA	932	G
25	DA	933	A
25	DA	936	C
25	DA	938	G
25	DA	941	A
25	DA	945	A
25	DA	946	G
25	DA	959	A
25	DA	961	C
25	DA	974	G
25	DA	975	C
25	DA	979	G
25	DA	980	A
25	DA	983	A
25	DA	989	G
25	DA	996	A
25	DA	1005	C
25	DA	1012	U
25	DA	1013	C
25	DA	1017	G
25	DA	1020	A
25	DA	1022	G
25	DA	1025	G
25	DA	1026	U
25	DA	1027	A
25	DA	1033	U
25	DA	1034	G
25	DA	1038	C
25	DA	1039	G
25	DA	1043	C

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Mol	Chain	Res	Type
25	DA	1114	G
25	DA	1117	G
25	DA	1121	C
25	DA	1122	G
25	DA	1126	A
25	DA	1128	A
25	DA	1130	U
25	DA	1135	C
25	DA	1136	G
25	DA	1139	G
25	DA	1142(A)	A
25	DA	1166	C
25	DA	1170	G
25	DA	1171	G
25	DA	1180	C
25	DA	1194	A
25	DA	1195	G
25	DA	1206	G
25	DA	1210	A
25	DA	1211	U
25	DA	1219	G
25	DA	1220	A
25	DA	1227	G
25	DA	1229	G
25	DA	1242	A
25	DA	1244	G
25	DA	1253	A
25	DA	1255	U
25	DA	1256	G
25	DA	1271	G
25	DA	1272	A
25	DA	1273	U
25	DA	1275	A
25	DA	1276	A
25	DA	1298	C
25	DA	1300	U
25	DA	1301	A
25	DA	1305	C
25	DA	1306	C
25	DA	1309	G
25	DA	1314	C
25	DA	1318	C

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Mol	Chain	Res	Type
25	DA	1321	A
25	DA	1341	U
25	DA	1342	A
25	DA	1352	U
25	DA	1359	A
25	DA	1360	A
25	DA	1365	A
25	DA	1368	G
25	DA	1370	C
25	DA	1373	A
25	DA	1380	G
25	DA	1384	A
25	DA	1385	G
25	DA	1386	C
25	DA	1391	U
25	DA	1395	A
25	DA	1412	A
25	DA	1416	G
25	DA	1417	C
25	DA	1420	U
25	DA	1421	G
25	DA	1427	A
25	DA	1428	C
25	DA	1437	C
25	DA	1445	A
25	DA	1446	C
25	DA	1449	A
25	DA	1450	G
25	DA	1459	G
25	DA	1467	C
25	DA	1471	A
25	DA	1472	A
25	DA	1473	G
25	DA	1482	G
25	DA	1490	A
25	DA	1493	C
25	DA	1497	U
25	DA	1508	A
25	DA	1509	C
25	DA	1509(A)	A
25	DA	1509(B)	A
25	DA	1531	C

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Mol	Chain	Res	Type
25	DA	1533	G
25	DA	1537	G
25	DA	1539	G
25	DA	1543	C
25	DA	1544	A
25	DA	1547	C
25	DA	1554	A
25	DA	1558	A
25	DA	1559	G
25	DA	1566	A
25	DA	1569	A
25	DA	1578	U
25	DA	1580	A
25	DA	1582	C
25	DA	1583	A
25	DA	1584	C
25	DA	1586	A
25	DA	1598	C
25	DA	1607	C
25	DA	1608	A
25	DA	1609	A
25	DA	1610	A
25	DA	1612	C
25	DA	1616	A
25	DA	1618	A
25	DA	1640	C
25	DA	1648	C
25	DA	1654	A
25	DA	1661	G
25	DA	1664	A
25	DA	1674	G
25	DA	1675	C
25	DA	1682	G
25	DA	1695	G
25	DA	1700	A
25	DA	1703	G
25	DA	1721	G
25	DA	1722	A
25	DA	1740	G
25	DA	1743	C
25	DA	1746	G
25	DA	1756	G

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Mol	Chain	Res	Type
25	DA	1758	G
25	DA	1762	A
25	DA	1763	G
25	DA	1764	G
25	DA	1773	A
25	DA	1780	A
25	DA	1782	C
25	DA	1791	A
25	DA	1800	C
25	DA	1801	G
25	DA	1806	C
25	DA	1812	A
25	DA	1816	G
25	DA	1823	G
25	DA	1833	U
25	DA	1835	G
25	DA	1847	A
25	DA	1848	A
25	DA	1866	C
25	DA	1877	A
25	DA	1878	G
25	DA	1881	C
25	DA	1889	A
25	DA	1900	A
25	DA	1906	G
25	DA	1913	A
25	DA	1914	C
25	DA	1926	U
25	DA	1927	A
25	DA	1929	G
25	DA	1930	G
25	DA	1936	A
25	DA	1937	A
25	DA	1938	A
25	DA	1955	U
25	DA	1963	U
25	DA	1965	C
25	DA	1967	C
25	DA	1970	A
25	DA	1971	A
25	DA	1972	A
25	DA	1981	A

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Mol	Chain	Res	Type
25	DA	1984	G
25	DA	1993	U
25	DA	1997	G
25	DA	2020	A
25	DA	2023	G
25	DA	2031	A
25	DA	2032	G
25	DA	2033	A
25	DA	2036	C
25	DA	2043	C
25	DA	2049	G
25	DA	2055	C
25	DA	2056	G
25	DA	2060	A
25	DA	2061	G
25	DA	2062	A
25	DA	2063	C
25	DA	2067	G
25	DA	2069	G
25	DA	2092	U
25	DA	2093	G
25	DA	2096	U
25	DA	2102	U
25	DA	2104	G
25	DA	2106	G
25	DA	2108	C
25	DA	2109	U
25	DA	2111	C
25	DA	2112	G
25	DA	2113	U
25	DA	2116	G
25	DA	2119	A
25	DA	2121	G
25	DA	2122	U
25	DA	2126	A
25	DA	2127	G
25	DA	2128	C
25	DA	2130	U
25	DA	2131	G
25	DA	2132	U
25	DA	2133	G
25	DA	2134	A

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Mol	Chain	Res	Type
25	DA	2135	A
25	DA	2136	C
25	DA	2137	C
25	DA	2138	C
25	DA	2139	C
25	DA	2140	C
25	DA	2142	C
25	DA	2143	C
25	DA	2144	U
25	DA	2146	C
25	DA	2148	G
25	DA	2149	G
25	DA	2150	U
25	DA	2152	G
25	DA	2153	G
25	DA	2154	G
25	DA	2155	G
25	DA	2156	G
25	DA	2157	G
25	DA	2158	A
25	DA	2162	G
25	DA	2163	C
25	DA	2164	C
25	DA	2165	G
25	DA	2166	G
25	DA	2167	U
25	DA	2168	G
25	DA	2169	A
25	DA	2170	A
25	DA	2172	U
25	DA	2173	A
25	DA	2177	C
25	DA	2178	C
25	DA	2181	G
25	DA	2185	C
25	DA	2187	G
25	DA	2188	C
25	DA	2189	U
25	DA	2192	G
25	DA	2193	G
25	DA	2196	C
25	DA	2198	A

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Mol	Chain	Res	Type
25	DA	2199	A
25	DA	2205	C
25	DA	2206	G
25	DA	2207	G
25	DA	2208	A
25	DA	2218	U
25	DA	2225	A
25	DA	2235	G
25	DA	2238	G
25	DA	2239	G
25	DA	2254	C
25	DA	2273	A
25	DA	2275	C
25	DA	2278	A
25	DA	2280	G
25	DA	2283	C
25	DA	2287	A
25	DA	2288	A
25	DA	2294	C
25	DA	2299	G
25	DA	2302	G
25	DA	2303	G
25	DA	2305	A
25	DA	2308	G
25	DA	2318	G
25	DA	2320	A
25	DA	2325	G
25	DA	2334	G
25	DA	2336	A
25	DA	2343	C
25	DA	2345	G
25	DA	2347	C
25	DA	2350	C
25	DA	2354	G
25	DA	2357	U
25	DA	2358	G
25	DA	2366	A
25	DA	2367	G
25	DA	2376	A
25	DA	2383	G
25	DA	2385	C
25	DA	2396	G

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Mol	Chain	Res	Type
25	DA	2401	U
25	DA	2402	C
25	DA	2403	C
25	DA	2406	U
25	DA	2410	G
25	DA	2422	A
25	DA	2423	U
25	DA	2425	A
25	DA	2427	C
25	DA	2428	G
25	DA	2429	G
25	DA	2430	A
25	DA	2431	U
25	DA	2435	A
25	DA	2439	A
25	DA	2440	C
25	DA	2441	C
25	DA	2448	A
25	DA	2459	A
25	DA	2469	A
25	DA	2474	C
25	DA	2476	A
25	DA	2478	A
25	DA	2479	G
25	DA	2480	C
25	DA	2487	G
25	DA	2492	U
25	DA	2494	G
25	DA	2502	G
25	DA	2505	G
25	DA	2506	U
25	DA	2507	C
25	DA	2518	A
25	DA	2525	G
25	DA	2554	U
25	DA	2564	A
25	DA	2566	A
25	DA	2567	G
25	DA	2573	C
25	DA	2578	G
25	DA	2582	G
25	DA	2586	C

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Mol	Chain	Res	Type
25	DA	2602	A
25	DA	2609	U
25	DA	2611	U
25	DA	2612	C
25	DA	2630	G
25	DA	2634	G
25	DA	2646	C
25	DA	2652	C
25	DA	2654	A
25	DA	2658	C
25	DA	2661	G
25	DA	2663	G
25	DA	2668	G
25	DA	2669	G
25	DA	2674	G
25	DA	2689	U
25	DA	2690	C
25	DA	2691	C
25	DA	2702	U
25	DA	2703	C
25	DA	2712(A)	A
25	DA	2713	A
25	DA	2714	G
25	DA	2720	U
25	DA	2721	A
25	DA	2726	U
25	DA	2733	A
25	DA	2746	U
25	DA	2751	G
25	DA	2752	C
25	DA	2757	A
25	DA	2758	A
25	DA	2760	C
25	DA	2761	G
25	DA	2764	A
25	DA	2765	A
25	DA	2766	G
25	DA	2778	A
25	DA	2780	G
25	DA	2789	C
25	DA	2794	C
25	DA	2802	G

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Mol	Chain	Res	Type
25	DA	2803	C
25	DA	2820	A
25	DA	2821	A
25	DA	2833	G
25	DA	2835	A
25	DA	2849	U
25	DA	2859	G
25	DA	2866	U
25	DA	2872	G
25	DA	2873	A
25	DA	2879	C
25	DA	2880	C
25	DA	2886	G
25	DA	2892	A
25	DA	2893	G
25	DA	2894	G
25	DA	2895	U
25	DA	2897	U
26	DB	2	C
26	DB	3	C
26	DB	4	C
26	DB	6	C
26	DB	7	G
26	DB	8	U
26	DB	13	A
26	DB	21	G
26	DB	24	G
26	DB	30	C
26	DB	31	C
26	DB	33	G
26	DB	35	U
26	DB	39	A
26	DB	41	U
26	DB	42	C
26	DB	45	A
26	DB	55	U
26	DB	56	G
26	DB	58	A
26	DB	59	A
26	DB	63	G
26	DB	64	C
26	DB	65	C

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Mol	Chain	Res	Type
26	DB	72	G
26	DB	73	A
26	DB	74	U
26	DB	75	G
26	DB	85	G
26	DB	86	G
26	DB	93	G
26	DB	101	G
26	DB	106	G
26	DB	108	U
26	DB	109	C
26	DB	110	G

All (104) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1165	C
1	AA	1190	G
1	AA	1201	A
1	AA	1256	A
1	AA	1285	A
1	AA	1299	A
1	AA	1442	G
1	AA	1492	A
24	AX	16	C
25	BA	71	A
25	BA	195	A
25	BA	278	A

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Mol	Chain	Res	Type
25	BA	746	A
25	BA	764	A
25	BA	827	U
25	BA	1046	A
25	BA	1047	G
25	BA	1174	A
25	BA	1175	U
25	BA	1176	G
25	BA	1210	A
25	BA	1300	U
25	BA	1420	U
25	BA	1530	C
25	BA	1992	G
25	BA	2126	A
25	BA	2181	G
25	BA	2183	C
25	BA	2198	A
25	BA	2238	G
25	BA	2406	U
25	BA	2689	U
25	BA	2893	G
26	BB	1	U
26	BB	52	A
26	BB	56	G
1	CA	5	U
1	CA	60	A
1	CA	65	U
1	CA	115	G
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	748	C
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1183	A

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Mol	Chain	Res	Type
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1279	A
1	CA	1442	G
1	CA	1492	A
24	CX	16	C
25	DA	34	C
25	DA	195	A
25	DA	271(K)	U
25	DA	271(M)	G
25	DA	277	C
25	DA	587	C
25	DA	752	A
25	DA	800	A
25	DA	856	C
25	DA	960	A
25	DA	1210	A
25	DA	1275	A
25	DA	1379	A
25	DA	1420	U
25	DA	1543	C
25	DA	1558	A
25	DA	1653	G
25	DA	1913	A
25	DA	1992	G
25	DA	2110	G
25	DA	2133	G
25	DA	2169	A
25	DA	2172	U
25	DA	2282	G
25	DA	2406	U
25	DA	2422	A
25	DA	2430	A
25	DA	2689	U
25	DA	2756	U

5.4 Non-standard residues in protein, DNA, RNA chains (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	4SU	AX	8	24	18,21,22	2.27	5 (27%)	25,30,33	1.65	5 (20%)
24	PSU	AX	55	24	18,21,22	1.38	3 (16%)	21,30,33	2.06	3 (14%)
24	31H	AX	76	56,24	31,34,35	1.24	3 (9%)	35,47,50	2.24	13 (37%)
24	5MC	CX	32	24	19,22,23	1.60	3 (15%)	26,32,35	1.12	2 (7%)
23	PPU	CW	76	23	37,40,41	1.30	5 (13%)	47,57,60	2.15	14 (29%)
24	31H	CX	76	24	31,34,35	1.29	3 (9%)	35,47,50	2.31	12 (34%)
23	PPU	AW	76	25,23	37,40,41	1.35	5 (13%)	47,57,60	2.24	15 (31%)
24	5MU	AX	54	56,24	19,22,23	1.37	5 (26%)	27,32,35	2.08	6 (22%)
24	5MC	AX	32	24	19,22,23	1.68	3 (15%)	26,32,35	1.31	3 (11%)
24	PSU	CX	55	24	18,21,22	1.36	2 (11%)	21,30,33	1.98	4 (19%)
24	4SU	CX	8	24	18,21,22	2.12	6 (33%)	25,30,33	1.56	5 (20%)
24	5MU	CX	54	24	19,22,23	1.28	5 (26%)	27,32,35	2.17	6 (22%)

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	4SU	AX	8	24	-	0/7/25/26	0/2/2/2
24	PSU	AX	55	24	-	1/7/25/26	0/2/2/2
24	31H	AX	76	56,24	-	5/22/40/41	0/3/3/3
24	5MC	CX	32	24	-	0/7/25/26	0/2/2/2
23	PPU	CW	76	23	-	5/25/43/44	0/4/4/4
24	31H	CX	76	24	-	10/22/40/41	0/3/3/3
23	PPU	AW	76	25,23	-	5/25/43/44	0/4/4/4
24	5MU	AX	54	56,24	-	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	-	1/7/25/26	0/2/2/2
24	4SU	CX	8	24	-	0/7/25/26	0/2/2/2
24	5MU	CX	54	24	-	0/7/25/26	0/2/2/2

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AX	32	5MC	C5-C4	6.11	1.48	1.44
24	CX	32	5MC	C5-C4	5.76	1.48	1.44
24	AX	8	4SU	C4-N3	-5.30	1.32	1.37
23	CW	76	PPU	C5-C4	5.03	1.48	1.39
23	AW	76	PPU	C5-C4	4.98	1.48	1.39
24	AX	8	4SU	C4-S4	-4.85	1.60	1.68
24	CX	8	4SU	C4-N3	-4.65	1.32	1.37
24	CX	8	4SU	C4-S4	-4.64	1.60	1.68
24	CX	76	31H	C5-N7	-4.18	1.31	1.39
24	AX	8	4SU	C2-N3	-4.10	1.30	1.38
24	AX	76	31H	C5-C4	-3.69	1.32	1.39
24	AX	76	31H	C5-N7	-3.67	1.32	1.39
24	CX	55	PSU	C6-C5	3.59	1.39	1.35
24	CX	8	4SU	C5-C4	-3.49	1.38	1.42
24	AX	55	PSU	C6-C5	3.37	1.39	1.35
24	AX	8	4SU	C5-C4	-3.27	1.38	1.42
23	AW	76	PPU	C5-C6	3.14	1.49	1.41
24	CX	8	4SU	O2-C2	2.95	1.28	1.23
24	CX	76	31H	C5-C6	-2.90	1.32	1.41
24	AX	54	5MU	C4-N3	-2.85	1.33	1.38
23	CW	76	PPU	C5-C6	2.83	1.48	1.41
24	AX	32	5MC	C6-C5	2.78	1.39	1.34
24	AX	54	5MU	C6-C5	2.77	1.39	1.34
24	CX	32	5MC	C6-C5	2.75	1.39	1.34
24	CX	54	5MU	C6-C5	2.56	1.38	1.34
24	CX	54	5MU	C4-N3	-2.49	1.34	1.38
23	CW	76	PPU	C5-N7	-2.48	1.34	1.39
24	AX	32	5MC	C6-N1	-2.45	1.33	1.38
24	AX	76	31H	C5-C6	-2.42	1.34	1.41
24	AX	55	PSU	C4-N3	-2.41	1.34	1.38
24	CX	8	4SU	C2-N1	2.39	1.42	1.38
23	AW	76	PPU	C5-N7	-2.32	1.34	1.39
24	CX	55	PSU	C4-N3	-2.32	1.34	1.38
24	CX	8	4SU	C2-N3	-2.23	1.34	1.38
24	AX	54	5MU	C4-C5	2.23	1.48	1.44
24	CX	76	31H	C5-C4	-2.20	1.35	1.39
23	CW	76	PPU	C8-N7	2.16	1.35	1.31
24	AX	54	5MU	C6-N1	-2.15	1.34	1.38
23	AW	76	PPU	C8-N7	2.12	1.35	1.31
23	CW	76	PPU	C6-N6	2.10	1.42	1.36
24	CX	54	5MU	C6-N1	-2.10	1.34	1.38
24	CX	32	5MC	C6-N1	-2.09	1.34	1.38
24	AX	8	4SU	O2-C2	2.09	1.26	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AX	54	5MU	C2-N3	-2.07	1.34	1.38
24	CX	54	5MU	C4-C5	2.07	1.48	1.44
24	CX	54	5MU	C2-N3	-2.03	1.34	1.38
24	AX	55	PSU	O4'-C1'	-2.02	1.41	1.43
23	AW	76	PPU	C6-N6	2.01	1.42	1.36

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	AX	55	PSU	N1-C2-N3	6.30	121.81	115.17
24	CX	55	PSU	N1-C2-N3	6.22	121.73	115.17
23	AW	76	PPU	C5-C4-N3	-6.18	118.21	126.72
23	CW	76	PPU	C5-C4-N3	-5.95	118.52	126.72
24	AX	76	31H	N1-C2-N3	-5.94	119.59	128.58
24	CX	76	31H	O4'-C1'-N9	5.81	119.26	108.09
24	CX	76	31H	N1-C2-N3	-5.63	120.06	128.58
24	AX	54	5MU	N3-C2-N1	5.55	122.12	114.89
24	CX	76	31H	C5-C4-N3	-5.26	119.47	126.72
23	AW	76	PPU	C3'-N3'-C	-5.25	115.22	123.20
24	CX	54	5MU	C4-N3-C2	-5.13	120.61	127.34
24	CX	54	5MU	N3-C2-N1	5.08	121.51	114.89
24	AX	54	5MU	C4-N3-C2	-5.03	120.75	127.34
24	AX	76	31H	O4'-C1'-N9	-5.02	98.44	108.09
24	AX	76	31H	C5-C4-N3	-4.99	119.84	126.72
24	CX	54	5MU	O4-C4-C5	-4.72	119.52	124.92
23	AW	76	PPU	N3-C4-N9	4.67	135.12	127.17
24	AX	32	5MC	C5-C6-N1	-4.52	118.41	123.31
23	CW	76	PPU	N3-C4-N9	4.45	134.73	127.17
23	CW	76	PPU	C2-N1-C6	4.44	122.68	111.83
23	CW	76	PPU	C3'-N3'-C	-4.28	116.69	123.20
23	AW	76	PPU	C2-N1-C6	4.28	122.28	111.83
23	CW	76	PPU	C10-N6-C6	-4.26	109.69	120.52
24	CX	54	5MU	C5-C4-N3	4.25	119.02	115.32
24	AX	8	4SU	C5-C4-N3	4.06	118.53	114.75
23	AW	76	PPU	C4-C5-N7	-4.06	105.94	110.58
24	CX	55	PSU	C4-N3-C2	-3.99	120.87	126.37
24	AX	55	PSU	C4-N3-C2	-3.95	120.93	126.37
24	AX	55	PSU	O2-C2-N1	-3.91	118.75	122.79
24	CX	8	4SU	C6-C5-C4	-3.86	116.61	119.95
24	CX	54	5MU	O2-C2-N1	-3.86	117.77	122.80
24	AX	54	5MU	C5-C4-N3	3.83	118.65	115.32
23	AW	76	PPU	C10-N6-C6	-3.76	110.95	120.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	AW	76	PPU	C2-N3-C4	3.76	121.01	111.83
23	CW	76	PPU	C4-C5-N7	-3.70	106.36	110.58
24	CX	76	31H	N9-C8-N7	-3.69	108.70	113.94
24	AX	54	5MU	O4-C4-C5	-3.64	120.75	124.92
24	CX	8	4SU	C1'-N1-C2	3.64	124.14	117.59
24	CX	76	31H	C2-N3-C4	3.59	120.60	111.83
23	CW	76	PPU	C2-N3-C4	3.59	120.59	111.83
24	AX	8	4SU	C6-C5-C4	-3.58	116.85	119.95
24	AX	8	4SU	O2-C2-N1	3.57	127.44	122.80
24	CX	32	5MC	C5-C6-N1	-3.48	119.53	123.31
24	CX	54	5MU	C5-C6-N1	-3.42	119.60	123.31
23	AW	76	PPU	N1-C6-N6	3.40	121.00	116.86
24	CX	76	31H	C5-N7-C8	3.38	108.76	103.45
23	CW	76	PPU	N1-C6-N6	3.37	120.96	116.86
24	CX	55	PSU	O2-C2-N1	-3.33	119.36	122.79
24	AX	76	31H	C2-N3-C4	3.32	119.94	111.83
24	AX	54	5MU	C5-C6-N1	-3.27	119.76	123.31
24	AX	76	31H	N9-C8-N7	-3.25	109.32	113.94
23	AW	76	PPU	C9-N6-C6	-3.16	112.48	120.52
23	CW	76	PPU	N3-C2-N1	-3.15	123.81	128.58
24	CX	8	4SU	C5-C4-N3	3.14	117.67	114.75
23	AW	76	PPU	N3-C2-N1	-3.12	123.86	128.58
24	CX	76	31H	N3-C4-N9	3.03	132.32	127.17
24	AX	76	31H	O2'-C2'-C3'	3.01	118.54	111.16
24	AX	8	4SU	S4-C4-N3	-3.01	117.05	120.20
24	AX	76	31H	C5-C4-N9	2.99	109.07	105.81
24	AX	54	5MU	O2-C2-N1	-2.96	118.94	122.80
23	AW	76	PPU	C5-N7-C8	2.79	107.83	103.45
24	AX	76	31H	C4'-O4'-C1'	-2.77	103.35	109.47
23	CW	76	PPU	CA-C-N3'	2.75	119.94	116.21
24	AX	76	31H	C6-C5-C4	2.71	120.87	117.18
24	AX	76	31H	C5-N7-C8	2.64	107.60	103.45
23	CW	76	PPU	C9-N6-C6	-2.64	113.81	120.52
24	CX	32	5MC	C5-C4-N3	-2.59	119.10	121.75
24	CX	76	31H	C4-C5-N7	-2.46	107.76	110.58
23	CW	76	PPU	C5-N7-C8	2.44	107.29	103.45
24	CX	8	4SU	O2-C2-N1	2.43	125.96	122.80
24	CX	76	31H	O2'-C2'-C3'	2.41	117.08	111.16
24	AX	32	5MC	C5-C4-N3	-2.40	119.30	121.75
23	CW	76	PPU	C10-N6-C9	-2.39	108.49	116.18
24	CX	8	4SU	C6-N1-C2	-2.39	118.09	121.00
24	AX	32	5MC	O2-C2-N3	-2.38	118.58	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	AX	8	4SU	O2-C2-N3	-2.38	117.10	121.49
23	AW	76	PPU	C10-N6-C9	-2.37	108.58	116.18
24	CX	55	PSU	C5-C6-N1	-2.31	118.94	122.14
24	CX	76	31H	C4'-O4'-C1'	-2.30	104.38	109.47
24	AX	76	31H	N3-C4-N9	2.30	131.08	127.17
24	CX	76	31H	CA-N-CN	-2.30	119.29	122.82
23	AW	76	PPU	CA-C-N3'	2.26	119.27	116.21
23	CW	76	PPU	C4-C5-C6	2.21	118.20	115.91
24	CX	76	31H	C5-C4-N9	2.20	108.20	105.81
24	AX	76	31H	OCN-CN-N	-2.18	119.68	125.32
23	AW	76	PPU	CM-OC-CZ	2.11	122.02	117.50
24	AX	76	31H	O4'-C1'-C2'	-2.06	102.20	106.62
23	AW	76	PPU	C4-N9-C8	2.02	107.86	105.74

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	AW	76	PPU	O4'-C4'-C5'-O5'
24	AX	76	31H	OCN-CN-N-CA
24	CX	76	31H	C-CA-CB-CG
24	CX	76	31H	OCN-CN-N-CA
24	CX	76	31H	CA-CB-CG-SD
23	AW	76	PPU	C3'-C4'-C5'-O5'
24	AX	76	31H	C3'-C4'-C5'-O5'
23	CW	76	PPU	C3'-C4'-C5'-O5'
24	CX	76	31H	C3'-C4'-C5'-O5'
24	AX	76	31H	O4'-C4'-C5'-O5'
23	CW	76	PPU	O4'-C4'-C5'-O5'
24	CX	76	31H	O4'-C4'-C5'-O5'
23	AW	76	PPU	N-CA-CB-CG
24	CX	76	31H	CB-CG-SD-CE
24	CX	76	31H	C4'-C5'-O5'-P
23	CW	76	PPU	C-CA-CB-CG
24	CX	76	31H	N3'-C-CA-N
24	CX	76	31H	O-C-CA-N
23	AW	76	PPU	C5-C6-N6-C9
23	CW	76	PPU	N-CA-CB-CG
24	AX	76	31H	C4'-C5'-O5'-P
23	CW	76	PPU	C5-C6-N6-C9
24	AX	55	PSU	O4'-C4'-C5'-O5'
23	AW	76	PPU	C-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
24	AX	76	31H	O-C-CA-N
24	CX	76	31H	O-C-CA-CB
24	CX	55	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	AX	55	PSU	1	0
24	AX	76	31H	3	0
23	CW	76	PPU	7	0
24	CX	76	31H	4	0
23	AW	76	PPU	5	0
24	CX	55	PSU	1	0
24	CX	8	4SU	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
57	SF4	AD	501	4	0,12,12	-	-	-		
57	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
57	SF4	AD	501	4	-	-	0/6/5/5
57	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.

No monomer is involved in short contacts.

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%)	0.51	48 (3%) 50 41	39, 74, 94, 105	0
1	CA	1503/1521 (98%)	0.61	86 (5%) 29 23	41, 75, 94, 105	0
2	AB	231/256 (90%)	1.05	27 (11%) 9 8	65, 82, 90, 96	0
2	CB	231/256 (90%)	1.45	50 (21%) 2 2	67, 83, 92, 96	0
3	AC	206/239 (86%)	0.94	18 (8%) 16 13	67, 78, 86, 94	0
3	CC	206/239 (86%)	1.31	31 (15%) 5 4	69, 80, 87, 92	0
4	AD	208/209 (99%)	1.02	24 (11%) 9 8	57, 72, 82, 86	0
4	CD	208/209 (99%)	1.14	24 (11%) 9 8	57, 73, 82, 87	0
5	AE	148/162 (91%)	0.80	12 (8%) 18 15	55, 71, 81, 86	0
5	CE	148/162 (91%)	1.01	13 (8%) 15 13	58, 73, 82, 89	0
6	AF	100/101 (99%)	0.74	6 (6%) 27 21	55, 71, 80, 82	0
6	CF	100/101 (99%)	0.57	2 (2%) 65 56	58, 73, 80, 82	0
7	AG	155/156 (99%)	0.81	15 (9%) 13 11	67, 76, 85, 94	0
7	CG	155/156 (99%)	1.08	21 (13%) 7 5	68, 78, 86, 96	0
8	AH	137/138 (99%)	0.56	3 (2%) 62 53	62, 72, 78, 86	0
8	CH	137/138 (99%)	0.94	9 (6%) 24 19	62, 73, 80, 88	0
9	AI	127/128 (99%)	1.39	24 (18%) 3 3	64, 82, 87, 90	0
9	CI	127/128 (99%)	2.16	64 (50%) 0 0	67, 83, 89, 91	0
10	AJ	97/105 (92%)	1.21	15 (15%) 5 4	63, 80, 89, 95	0
10	CJ	96/105 (91%)	2.01	49 (51%) 0 0	70, 86, 93, 100	0
11	AK	114/129 (88%)	0.87	7 (6%) 27 21	54, 72, 81, 83	0
11	CK	114/129 (88%)	0.67	3 (2%) 57 48	56, 72, 80, 83	0
12	AL	122/132 (92%)	0.74	6 (4%) 35 27	55, 65, 75, 78	0
12	CL	122/132 (92%)	0.83	5 (4%) 41 33	57, 67, 75, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	AM	123/126 (97%)	1.37	23 (18%) 3 3	64, 78, 86, 91	0
13	CM	122/126 (96%)	1.70	35 (28%) 1 1	68, 80, 88, 93	0
14	AN	60/61 (98%)	1.32	11 (18%) 3 3	65, 76, 83, 86	0
14	CN	60/61 (98%)	2.07	28 (46%) 0 0	69, 79, 84, 88	0
15	AO	88/89 (98%)	0.90	7 (7%) 18 15	56, 69, 80, 90	0
15	CO	88/89 (98%)	0.71	6 (6%) 23 18	56, 70, 80, 90	0
16	AP	82/88 (93%)	1.49	16 (19%) 3 2	58, 73, 83, 85	0
16	CP	82/88 (93%)	1.30	16 (19%) 3 2	58, 72, 82, 85	0
17	AQ	99/105 (94%)	1.11	7 (7%) 22 17	60, 70, 81, 85	0
17	CQ	99/105 (94%)	0.75	2 (2%) 65 56	57, 70, 80, 84	0
18	AR	68/88 (77%)	0.59	4 (5%) 28 22	60, 70, 81, 85	0
18	CR	68/88 (77%)	0.59	0 100 100	61, 72, 82, 86	0
19	AS	83/93 (89%)	1.22	10 (12%) 9 7	67, 81, 88, 96	0
19	CS	83/93 (89%)	1.52	21 (25%) 1 1	71, 83, 91, 97	0
20	AT	96/106 (90%)	1.10	15 (15%) 5 4	58, 72, 82, 89	0
20	CT	96/106 (90%)	0.95	9 (9%) 14 12	59, 72, 82, 88	0
21	AU	23/27 (85%)	1.46	5 (21%) 2 2	65, 75, 80, 86	0
21	CU	23/27 (85%)	1.78	7 (30%) 1 1	66, 76, 83, 87	0
22	AV	13/24 (54%)	1.97	6 (46%) 0 0	60, 92, 100, 100	0
22	CV	12/24 (50%)	1.91	7 (58%) 0 0	63, 93, 99, 99	0
23	AW	1/2 (50%)	-0.24	0 100 100	42, 42, 42, 42	0
23	CW	1/2 (50%)	0.94	0 100 100	59, 59, 59, 59	0
24	AX	71/77 (92%)	0.42	2 (2%) 55 46	37, 72, 84, 92	0
24	CX	71/77 (92%)	0.24	0 100 100	39, 73, 86, 92	0
25	BA	2819/2915 (96%)	-0.18	77 (2%) 56 47	23, 46, 89, 107	0
25	DA	2800/2915 (96%)	-0.14	50 (1%) 67 59	26, 50, 90, 107	0
26	BB	120/121 (99%)	0.10	0 100 100	40, 65, 76, 91	0
26	DB	120/121 (99%)	0.67	5 (4%) 40 32	44, 70, 81, 93	0
27	BD	275/276 (99%)	0.33	5 (1%) 67 59	24, 45, 61, 77	0
27	DD	275/276 (99%)	0.18	1 (0%) 88 85	27, 47, 63, 78	0
28	BE	204/206 (99%)	-0.07	1 (0%) 87 83	18, 44, 66, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	DE	204/206 (99%)	0.12	1 (0%) 87 83	32, 57, 72, 86	0
29	BF	203/210 (96%)	0.30	1 (0%) 87 83	26, 55, 74, 84	0
29	DF	203/210 (96%)	0.28	0 100 100	26, 58, 75, 85	0
30	BG	181/182 (99%)	1.02	25 (13%) 6 5	56, 70, 82, 91	0
30	DG	181/182 (99%)	1.37	36 (19%) 3 2	61, 73, 85, 91	0
31	BH	174/180 (96%)	0.47	5 (2%) 53 45	51, 66, 76, 82	0
31	DH	174/180 (96%)	0.82	7 (4%) 42 34	55, 69, 80, 85	0
32	BI	146/148 (98%)	0.75	3 (2%) 63 54	46, 74, 85, 87	0
32	DI	146/148 (98%)	1.25	25 (17%) 4 3	50, 75, 84, 87	0
33	BN	140/140 (100%)	0.26	4 (2%) 53 45	33, 53, 72, 80	0
33	DN	140/140 (100%)	0.26	0 100 100	36, 56, 72, 81	0
34	BO	122/122 (100%)	-0.19	1 (0%) 82 77	25, 43, 60, 76	0
34	DO	122/122 (100%)	0.30	1 (0%) 82 77	42, 59, 73, 77	0
35	BP	149/150 (99%)	0.37	1 (0%) 84 79	27, 57, 73, 87	0
35	DP	149/150 (99%)	0.33	1 (0%) 84 79	29, 59, 76, 86	0
36	BQ	141/141 (100%)	0.36	2 (1%) 73 65	35, 53, 64, 71	0
36	DQ	141/141 (100%)	0.52	3 (2%) 63 54	38, 56, 68, 76	0
37	BR	118/118 (100%)	-0.21	2 (1%) 69 61	25, 37, 56, 66	0
37	DR	118/118 (100%)	0.24	0 100 100	40, 54, 66, 76	0
38	BS	110/112 (98%)	0.00	0 100 100	40, 52, 63, 68	0
38	DS	110/112 (98%)	1.15	15 (13%) 7 5	57, 76, 86, 92	0
39	BT	131/146 (89%)	0.00	1 (0%) 82 77	32, 50, 74, 86	0
39	DT	131/146 (89%)	0.47	2 (1%) 72 64	44, 60, 75, 85	0
40	BU	116/118 (98%)	-0.30	1 (0%) 81 75	23, 35, 55, 76	0
40	DU	116/118 (98%)	0.39	4 (3%) 48 39	41, 61, 77, 87	0
41	BV	101/101 (100%)	-0.30	0 100 100	19, 43, 64, 76	0
41	DV	101/101 (100%)	0.35	0 100 100	44, 71, 80, 88	0
42	BW	112/113 (99%)	-0.33	0 100 100	21, 38, 53, 75	0
42	DW	112/113 (99%)	0.12	1 (0%) 81 75	31, 51, 69, 85	0
43	BX	95/96 (98%)	-0.03	1 (1%) 78 71	25, 43, 64, 82	0
43	DX	95/96 (98%)	0.59	5 (5%) 32 25	43, 62, 78, 91	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	BY	107/110 (97%)	0.10	0 100 100	36, 51, 69, 80	0
44	DY	107/110 (97%)	0.90	8 (7%) 20 16	55, 72, 81, 89	0
45	BZ	171/206 (83%)	0.30	3 (1%) 67 59	42, 63, 77, 92	0
45	DZ	174/206 (84%)	0.89	10 (5%) 29 23	61, 80, 90, 100	0
46	B0	83/85 (97%)	-0.07	0 100 100	16, 43, 56, 66	0
46	D0	83/85 (97%)	0.85	8 (9%) 13 11	44, 65, 74, 80	0
47	B1	97/98 (98%)	0.10	3 (3%) 51 42	27, 49, 70, 77	0
47	D1	97/98 (98%)	0.57	2 (2%) 63 54	38, 59, 75, 78	0
48	B2	70/72 (97%)	0.07	1 (1%) 73 65	37, 50, 66, 72	0
48	D2	70/72 (97%)	0.53	0 100 100	58, 70, 79, 85	0
49	B3	59/60 (98%)	-0.27	0 100 100	26, 41, 61, 72	0
49	D3	59/60 (98%)	0.29	2 (3%) 48 39	44, 64, 77, 80	0
50	B4	69/71 (97%)	1.01	8 (11%) 9 8	57, 76, 91, 94	0
50	D4	69/71 (97%)	1.55	18 (26%) 1 1	77, 87, 97, 104	0
51	B5	59/60 (98%)	-0.39	0 100 100	19, 38, 57, 78	0
51	D5	59/60 (98%)	0.04	0 100 100	31, 52, 69, 76	0
52	B6	53/54 (98%)	-0.19	0 100 100	29, 43, 60, 71	0
52	D6	53/54 (98%)	0.71	1 (1%) 66 58	50, 63, 75, 83	0
53	B7	48/49 (97%)	-0.15	0 100 100	20, 30, 53, 72	0
53	D7	48/49 (97%)	0.26	3 (6%) 26 20	35, 46, 71, 76	0
54	B8	64/65 (98%)	-0.10	0 100 100	27, 36, 47, 55	0
54	D8	64/65 (98%)	0.57	0 100 100	44, 58, 67, 75	0
55	B9	37/37 (100%)	0.18	1 (2%) 56 47	31, 52, 64, 69	0
55	D9	37/37 (100%)	0.56	0 100 100	44, 58, 67, 73	0
All	All	20634/21448 (96%)	0.42	1154 (5%) 30 23	16, 64, 87, 107	0

All (1154) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
9	CI	126	SER	7.5
13	CM	124	PRO	7.3
13	CM	123	ALA	6.9
5	CE	94	ALA	6.6
25	BA	2804	C	6.4

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Mol	Chain	Res	Type	RSRZ
9	CI	102	LEU	6.4
25	BA	2805	G	6.2
14	AN	2	ALA	6.1
25	BA	2803	C	5.9
14	CN	2	ALA	5.7
9	CI	9	ARG	5.6
4	AD	2	GLY	5.5
25	BA	2121	G	5.4
20	AT	103	GLY	5.2
13	AM	105	THR	5.1
9	CI	14	VAL	5.0
1	AA	1447	A	5.0
25	BA	2119	A	4.9
9	AI	106	ALA	4.9
1	CA	1532	U	4.9
16	AP	68	ASP	4.7
14	CN	18	VAL	4.7
9	CI	64	THR	4.7
50	D4	52	THR	4.7
25	BA	2792	G	4.6
1	CA	1202	G	4.6
25	BA	2793	G	4.5
9	CI	123	PRO	4.4
14	CN	59	ALA	4.4
9	CI	7	THR	4.4
13	AM	124	PRO	4.4
31	BH	2	SER	4.3
50	D4	54	GLY	4.3
9	CI	66	ARG	4.3
25	BA	2120	G	4.3
25	BA	2142	C	4.3
25	BA	2113	U	4.2
3	CC	13	GLY	4.2
1	AA	1446	U	4.2
10	CJ	71	LEU	4.2
22	CV	13	A	4.2
30	DG	19	LEU	4.2
4	CD	18	LYS	4.1
25	BA	2117	A	4.1
1	CA	1030(B)	C	4.1
9	CI	65	VAL	4.0
1	AA	1532	U	4.0

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Mol	Chain	Res	Type	RSRZ
9	CI	96	LEU	4.0
9	CI	125	TYR	4.0
9	AI	126	SER	4.0
14	CN	30	ALA	4.0
22	AV	24	A	4.0
50	B4	55	ARG	4.0
14	CN	21	TYR	4.0
25	BA	2179	C	4.0
4	AD	179	GLU	4.0
30	DG	173	LEU	3.9
2	AB	237	ALA	3.9
13	CM	33	ALA	3.9
38	DS	3	ARG	3.9
1	CA	1001(A)	G	3.9
27	BD	276	LYS	3.9
50	D4	51	ASP	3.9
7	CG	81	GLY	3.8
36	BQ	61	GLY	3.8
50	B4	49	PHE	3.8
50	D4	57	GLU	3.8
10	CJ	23	ILE	3.8
10	CJ	54	PHE	3.8
25	BA	2141	G	3.8
46	D0	71	ASP	3.8
21	CU	6	ARG	3.8
4	AD	21	LEU	3.8
3	CC	195	VAL	3.8
14	CN	3	ARG	3.8
22	AV	23	A	3.8
14	CN	25	VAL	3.7
30	BG	146	TYR	3.7
13	CM	102	ARG	3.7
25	BA	1026	U	3.7
2	CB	187	LEU	3.7
32	DI	13	GLY	3.7
30	BG	136	ARG	3.7
13	AM	121	LYS	3.7
31	DH	115	VAL	3.7
14	CN	5	ALA	3.7
20	CT	9	ASN	3.7
25	BA	2115	G	3.6
32	DI	14	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
9	CI	18	PHE	3.6
10	CJ	57	LYS	3.6
13	CM	122	LYS	3.6
5	AE	85	GLY	3.6
25	BA	2178	C	3.6
25	DA	2143	C	3.6
1	CA	1531	A	3.6
10	CJ	34	VAL	3.6
13	CM	7	VAL	3.6
1	AA	380	G	3.6
5	CE	17	ALA	3.6
10	CJ	27	ALA	3.6
2	CB	214	ILE	3.6
2	CB	164	VAL	3.6
9	CI	26	VAL	3.6
25	BA	2188	C	3.6
7	AG	79	ARG	3.5
25	DA	2894	G	3.5
9	CI	63	ILE	3.5
2	CB	7	VAL	3.5
7	AG	80	VAL	3.5
32	DI	3	VAL	3.5
21	CU	14	TRP	3.5
2	CB	97	TRP	3.5
1	AA	1452	C	3.5
25	BA	2108	C	3.5
3	AC	87	LEU	3.5
14	AN	15	LYS	3.5
2	CB	190	THR	3.5
50	D4	49	PHE	3.5
13	CM	6	GLY	3.5
2	CB	165	VAL	3.5
25	BA	2129	C	3.5
25	BA	2896	C	3.5
4	AD	20	TYR	3.5
7	CG	84	ASN	3.5
2	CB	70	PHE	3.4
14	CN	33	VAL	3.4
9	CI	21	PRO	3.4
4	CD	20	TYR	3.4
9	AI	114	TYR	3.4
1	CA	1250	A	3.4

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Mol	Chain	Res	Type	RSRZ
1	AA	103	C	3.4
3	CC	189	ALA	3.4
7	CG	83	ALA	3.4
9	CI	36	TYR	3.4
4	AD	110	PHE	3.4
20	CT	74	LYS	3.4
19	CS	9	VAL	3.4
25	BA	2112	G	3.4
38	DS	32	LEU	3.4
9	AI	66	ARG	3.4
50	D4	55	ARG	3.4
10	CJ	6	ILE	3.4
25	BA	2122	U	3.4
38	DS	7	TYR	3.4
2	AB	7	VAL	3.3
10	CJ	72	VAL	3.3
25	BA	2145	C	3.3
10	CJ	75	ILE	3.3
50	D4	56	VAL	3.3
1	CA	1115	C	3.3
25	BA	2794	C	3.3
25	BA	2168	G	3.3
25	DA	2116	G	3.3
50	D4	41	PRO	3.3
2	CB	22	LYS	3.3
14	CN	4	LYS	3.3
55	B9	17	ILE	3.3
2	CB	92	TYR	3.3
9	CI	105	ASP	3.3
19	AS	84	GLY	3.3
10	CJ	69	ASN	3.3
25	DA	2146	C	3.3
19	AS	48	THR	3.3
25	BA	2170	A	3.3
1	CA	1119	C	3.3
25	DA	2804	C	3.3
31	DH	101	ARG	3.3
16	CP	51	VAL	3.3
25	BA	2132	U	3.2
30	DG	172	LEU	3.2
2	CB	21	ARG	3.2
32	DI	18	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	CA	1237	C	3.2
25	DA	2145	C	3.2
2	CB	129	GLU	3.2
9	CI	5	TYR	3.2
25	DA	2147	G	3.2
5	CE	13	ILE	3.2
9	CI	46	ALA	3.2
25	DA	2133	G	3.2
9	CI	17	VAL	3.2
1	CA	1286	A	3.2
10	CJ	63	PHE	3.2
9	CI	127	LYS	3.2
1	AA	1024	G	3.2
1	CA	1220	G	3.2
25	BA	2133	G	3.2
30	BG	119	GLY	3.2
22	AV	13	A	3.1
16	CP	16	HIS	3.1
14	CN	15	LYS	3.1
21	AU	16	GLY	3.1
1	AA	1036	G	3.1
13	AM	94	ARG	3.1
25	DA	2112	G	3.1
8	CH	54	ASP	3.1
13	CM	112	GLY	3.1
9	CI	12	GLU	3.1
32	DI	85	GLU	3.1
3	CC	12	LEU	3.1
20	CT	24	LEU	3.1
13	AM	123	ALA	3.1
13	CM	75	ALA	3.1
2	AB	19	HIS	3.1
10	CJ	59	SER	3.1
30	DG	92	VAL	3.1
32	BI	91	SER	3.1
25	BA	888	C	3.1
9	AI	46	ALA	3.1
9	CI	43	ALA	3.1
19	CS	52	TYR	3.1
3	CC	207	VAL	3.1
4	AD	112	VAL	3.1
5	CE	90	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
46	D0	73	GLY	3.1
1	AA	630	G	3.1
1	AA	1456	G	3.1
1	CA	973	G	3.1
25	DA	171	G	3.1
2	CB	200	ILE	3.1
13	AM	56	LEU	3.1
8	AH	3	THR	3.1
25	BA	2174	C	3.1
30	BG	50	ALA	3.0
3	CC	167	TRP	3.0
6	AF	88	VAL	3.0
4	AD	3	ARG	3.0
25	BA	2160	G	3.0
9	AI	13	ALA	3.0
45	DZ	113	ALA	3.0
9	CI	69	GLY	3.0
2	CB	133	LYS	3.0
13	CM	78	ILE	3.0
9	CI	2	GLU	3.0
10	CJ	48	THR	3.0
1	CA	1236	A	3.0
14	CN	34	TYR	3.0
13	AM	22	ILE	3.0
13	CM	25	ILE	3.0
19	CS	84	GLY	3.0
30	BG	26	GLN	3.0
5	AE	95	ALA	3.0
2	AB	97	TRP	3.0
21	CU	9	ARG	3.0
9	CI	79	LEU	3.0
3	CC	191	THR	3.0
4	CD	164	ALA	3.0
50	B4	59	PHE	3.0
7	AG	78	ARG	2.9
14	CN	7	ILE	2.9
13	AM	87	TYR	2.9
16	AP	17	TYR	2.9
30	BG	25	TYR	2.9
30	BG	49	ASP	2.9
1	CA	1149	C	2.9
25	BA	2143	C	2.9

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Mol	Chain	Res	Type	RSRZ
43	DX	33	LYS	2.9
25	DA	2144	U	2.9
36	BQ	60	ARG	2.9
3	CC	14	ILE	2.9
9	CI	81	ILE	2.9
7	CG	154	TYR	2.9
25	BA	2169	A	2.9
10	CJ	12	ASP	2.9
10	AJ	72	VAL	2.9
26	DB	118	G	2.9
26	DB	119	G	2.9
7	AG	156	TRP	2.9
45	DZ	114	GLY	2.9
2	CB	131	PRO	2.9
1	AA	149	A	2.9
2	CB	93	VAL	2.9
3	CC	180	ALA	2.9
7	CG	80	VAL	2.9
14	CN	10	ALA	2.9
30	DG	28	VAL	2.9
1	CA	1038	C	2.9
9	CI	30	GLY	2.9
25	BA	2167	U	2.9
1	CA	1036	G	2.9
21	AU	23	PRO	2.9
24	AX	70	G	2.9
10	AJ	35	SER	2.9
14	AN	37	PHE	2.9
19	CS	14	HIS	2.9
20	AT	24	LEU	2.9
30	DG	20	ILE	2.9
32	DI	30	LEU	2.9
43	DX	92	LEU	2.9
2	CB	99	GLY	2.8
1	CA	1030	C	2.8
1	CA	1223	C	2.8
2	CB	236	TYR	2.8
44	DY	55	TYR	2.8
10	CJ	49	VAL	2.8
12	CL	51	ALA	2.8
26	DB	23	G	2.8
13	AM	106	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
20	CT	23	ARG	2.8
9	CI	75	ASP	2.8
5	CE	85	GLY	2.8
7	AG	82	GLY	2.8
10	CJ	31	GLY	2.8
50	D4	45	GLY	2.8
10	CJ	37	PRO	2.8
1	AA	163	C	2.8
7	AG	2	ALA	2.8
9	AI	41	VAL	2.8
7	CG	37	ASN	2.8
3	CC	57	ILE	2.8
5	CE	89	ILE	2.8
50	D4	40	HIS	2.8
38	DS	48	LEU	2.8
1	CA	1030(A)	G	2.8
25	DA	2115	G	2.8
50	B4	52	THR	2.8
13	CM	121	LYS	2.8
9	CI	82	ALA	2.8
25	BA	2897	U	2.8
25	DA	2897	U	2.8
10	CJ	76	ASN	2.8
10	CJ	88	LEU	2.8
14	CN	6	LEU	2.8
19	AS	57	HIS	2.8
30	DG	85	GLY	2.8
1	CA	1355	G	2.8
25	DA	2123	G	2.8
10	AJ	64	GLU	2.8
8	CH	53	VAL	2.8
3	AC	201	TYR	2.8
14	CN	20	ALA	2.8
32	BI	39	ALA	2.8
7	CG	38	LEU	2.8
13	CM	66	LEU	2.8
30	DG	175	LEU	2.8
4	CD	154	ASN	2.8
10	CJ	58	ASP	2.8
3	AC	4	LYS	2.8
1	AA	1030(B)	C	2.8
4	CD	109	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
12	AL	5	PRO	2.8
50	D4	47	GLN	2.7
4	AD	132	ARG	2.7
10	CJ	46	ARG	2.7
48	B2	69	ARG	2.7
3	AC	207	VAL	2.7
25	DA	229	A	2.7
44	DY	16	ALA	2.7
1	CA	1370	G	2.7
2	CB	199	TYR	2.7
7	AG	85	TYR	2.7
12	CL	69	TYR	2.7
19	CS	20	LEU	2.7
25	DA	2125	G	2.7
25	DA	2318	G	2.7
25	BA	2109	U	2.7
19	CS	2	PRO	2.7
9	CI	83	ARG	2.7
25	DA	2803	C	2.7
44	DY	57	GLN	2.7
4	AD	170	VAL	2.7
10	CJ	94	VAL	2.7
30	DG	31	VAL	2.7
2	CB	218	ALA	2.7
9	CI	101	PHE	2.7
20	AT	10	LEU	2.7
30	DG	29	TRP	2.7
30	DG	53	LEU	2.7
30	DG	90	LEU	2.7
32	DI	53	ALA	2.7
10	CJ	98	ILE	2.7
46	D0	75	LEU	2.7
1	CA	1363(A)	A	2.7
1	CA	1017	G	2.7
1	CA	1224	G	2.7
22	CV	22	U	2.7
3	AC	15	THR	2.7
7	CG	77	SER	2.7
13	AM	102	ARG	2.7
20	AT	25	ARG	2.7
50	B4	53	GLU	2.7
5	AE	94	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
7	CG	2	ALA	2.7
10	AJ	63	PHE	2.7
10	CJ	32	ALA	2.7
14	CN	44	LEU	2.7
19	CS	31	ILE	2.7
36	DQ	104	PHE	2.7
13	CM	64	TRP	2.7
2	CB	31	TYR	2.7
20	CT	73	HIS	2.7
1	CA	965	A	2.7
3	CC	155	GLY	2.7
8	CH	5	PRO	2.7
13	AM	88	ARG	2.7
1	AA	1001(A)	G	2.7
1	AA	1023	G	2.7
1	CA	951	G	2.7
1	CA	1190	G	2.7
26	DB	54	G	2.7
5	AE	100	VAL	2.7
4	CD	174	LEU	2.7
46	D0	69	PHE	2.7
50	D4	42	PHE	2.7
7	AG	153	HIS	2.7
14	CN	61	TRP	2.7
4	AD	138	TYR	2.7
27	BD	262	ARG	2.7
2	CB	234	PRO	2.7
9	CI	115	GLY	2.7
10	CJ	87	THR	2.7
16	CP	69	THR	2.7
40	BU	117	GLN	2.7
2	CB	163	PHE	2.6
27	BD	38	LYS	2.6
1	AA	1034	G	2.6
2	AB	48	MET	2.6
25	BA	2807	G	2.6
14	CN	29	ARG	2.6
20	AT	102	GLY	2.6
43	DX	86	GLY	2.6
2	CB	205	ASP	2.6
19	CS	71	LEU	2.6
15	AO	87	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
3	AC	189	ALA	2.6
30	BG	23	PHE	2.6
30	BG	178	PHE	2.6
30	DG	76	SER	2.6
32	DI	100	ALA	2.6
44	DY	1	MET	2.6
1	CA	1003	G	2.6
6	AF	63	TYR	2.6
15	AO	69	TYR	2.6
25	BA	2123	G	2.6
38	DS	36	TYR	2.6
17	AQ	80	GLY	2.6
1	CA	980	C	2.6
1	CA	1363	C	2.6
4	AD	157	LEU	2.6
4	CD	161	ASN	2.6
17	AQ	87	LYS	2.6
5	CE	82	VAL	2.6
13	CM	69	GLU	2.6
11	AK	81	ASP	2.6
25	BA	2114	A	2.6
4	AD	124	GLY	2.6
12	AL	29	GLY	2.6
50	D4	2	LYS	2.6
1	CA	1002	G	2.6
3	AC	55	VAL	2.6
9	CI	27	THR	2.6
15	CO	27	VAL	2.6
36	DQ	106	VAL	2.6
2	AB	120	ALA	2.6
12	CL	32	PHE	2.6
30	BG	116	ASP	2.6
10	CJ	62	HIS	2.6
12	CL	89	ARG	2.6
5	AE	23	GLY	2.6
11	AK	25	TYR	2.6
17	AQ	95	TYR	2.6
46	D0	76	GLY	2.6
38	DS	56	LEU	2.6
9	AI	63	ILE	2.6
9	CI	86	VAL	2.6
13	AM	7	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
16	CP	2	VAL	2.6
16	AP	82	GLN	2.6
30	BG	137	GLU	2.6
2	CB	123	ALA	2.6
1	AA	1002	G	2.5
1	AA	1106	G	2.5
1	CA	1034	G	2.5
25	DA	2110	G	2.5
25	DA	2805	G	2.5
28	BE	89	ASP	2.6
1	AA	1381	U	2.5
1	CA	1219	U	2.5
22	CV	20	U	2.5
25	DA	2172	U	2.5
2	AB	22	LYS	2.5
10	CJ	55	LYS	2.5
20	AT	21	LYS	2.5
19	AS	68	GLY	2.5
21	AU	21	TYR	2.5
30	BG	53	LEU	2.5
2	CB	39	ILE	2.5
10	AJ	75	ILE	2.5
12	AL	18	VAL	2.5
2	CB	134	GLU	2.5
3	CC	192	THR	2.5
32	DI	17	GLN	2.5
30	DG	57	ALA	2.5
35	DP	15	ARG	2.5
9	CI	71	SER	2.5
1	AA	154	C	2.5
1	CA	1045	C	2.5
8	CH	2	LEU	2.5
9	AI	72	GLY	2.5
30	BG	24	GLY	2.5
30	DG	139	LEU	2.5
2	CB	184	VAL	2.5
9	CI	62	TYR	2.5
50	D4	50	VAL	2.5
22	AV	14	A	2.5
21	AU	24	ARG	2.5
4	CD	144	ASP	2.5
9	AI	75	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
14	CN	60	SER	2.5
25	BA	2130	U	2.5
4	CD	194	LEU	2.5
10	CJ	8	LEU	2.5
30	DG	68	PRO	2.5
32	DI	90	GLY	2.5
1	AA	1030	C	2.5
1	CA	1155	G	2.5
16	CP	82	GLN	2.5
50	D4	44	THR	2.5
20	AT	23	ARG	2.5
20	AT	14	LYS	2.5
2	AB	160	ASP	2.5
10	CJ	16	LEU	2.5
10	AJ	31	GLY	2.5
38	DS	52	SER	2.5
44	DY	58	GLY	2.5
31	BH	123	PHE	2.5
14	AN	5	ALA	2.5
16	AP	22	THR	2.5
19	CS	24	ALA	2.5
39	BT	115	ARG	2.5
1	CA	1325	C	2.5
25	DA	2136	C	2.5
38	DS	21	THR	2.5
1	CA	1033	G	2.5
1	CA	1156	G	2.5
1	CA	1357	A	2.5
32	DI	11	ASN	2.5
2	CB	138	LEU	2.4
32	DI	116	LEU	2.4
13	CM	22	ILE	2.4
38	DS	46	VAL	2.4
1	CA	723	U	2.4
2	AB	117	GLU	2.4
9	CI	10	ARG	2.4
12	AL	89	ARG	2.4
17	AQ	78	GLU	2.4
31	BH	104	GLU	2.4
2	CB	62	ALA	2.4
14	AN	59	ALA	2.4
9	AI	7	THR	2.4

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Mol	Chain	Res	Type	RSRZ
21	CU	17	THR	2.4
10	CJ	68	HIS	2.4
2	CB	69	LEU	2.4
4	CD	181	MET	2.4
11	AK	117	ASN	2.4
13	CM	40	ASN	2.4
46	D0	62	LEU	2.4
1	AA	151	A	2.4
2	CB	185	ILE	2.4
37	BR	49	ASP	2.4
4	CD	170	VAL	2.4
13	AM	100	GLY	2.4
4	CD	73	ARG	2.4
14	AN	23	ARG	2.4
21	CU	24	ARG	2.4
2	AB	134	GLU	2.4
10	CJ	64	GLU	2.4
13	CM	73	GLU	2.4
30	BG	12	TYR	2.4
31	DH	83	TYR	2.4
2	AB	11	LEU	2.4
10	AJ	69	ASN	2.4
15	CO	19	PRO	2.4
20	CT	100	ILE	2.4
30	BG	77	ILE	2.4
30	DG	39	ILE	2.4
22	CV	21	C	2.4
25	DA	2142	C	2.4
2	CB	189	ASP	2.4
7	CG	61	VAL	2.4
16	CP	68	ASP	2.4
19	CS	60	VAL	2.4
30	DG	42	GLY	2.4
7	AG	4	ARG	2.4
53	D7	47	ARG	2.4
1	AA	585	G	2.4
1	CA	966	G	2.4
1	CA	1154	G	2.4
9	AI	2	GLU	2.4
14	CN	16	PHE	2.4
25	BA	652(C)	G	2.4
25	BA	2151	G	2.4

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Mol	Chain	Res	Type	RSRZ
7	CG	152	ALA	2.4
9	AI	119	ALA	2.4
13	AM	2	ALA	2.4
27	BD	2	ALA	2.4
30	DG	73	ALA	2.4
1	CA	950	U	2.4
32	DI	1	MET	2.4
9	CI	19	LEU	2.4
19	CS	49	ILE	2.4
30	DG	140	ILE	2.4
3	CC	7	PRO	2.4
4	AD	189	PRO	2.4
16	AP	15	PRO	2.4
19	AS	76	PRO	2.4
2	CB	100	GLY	2.4
2	CB	230	VAL	2.4
3	AC	2	GLY	2.4
5	CE	67	VAL	2.4
32	DI	92	VAL	2.4
50	B4	50	VAL	2.4
2	AB	30	ARG	2.4
7	CG	33	ASP	2.4
16	AP	35	LYS	2.4
44	DY	107	ASP	2.4
1	AA	1027	C	2.4
1	CA	1116	C	2.4
1	CA	1249	C	2.4
19	CS	74	PHE	2.4
4	AD	80	GLU	2.4
25	BA	2173	A	2.4
2	AB	188	ALA	2.4
5	CE	125	SER	2.4
4	AD	173	TRP	2.4
1	CA	630	G	2.4
3	AC	192	THR	2.4
3	CC	48	TYR	2.4
5	CE	10	MET	2.4
25	BA	2893	G	2.4
25	DA	2159	G	2.4
50	D4	43	TYR	2.4
2	AB	221	LEU	2.4
4	AD	155	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
13	CM	34	LEU	2.4
18	AR	79	LEU	2.4
9	CI	49	PRO	2.4
13	CM	31	LYS	2.3
2	CB	38	GLY	2.3
13	CM	119	GLY	2.3
30	BG	42	GLY	2.3
9	CI	33	PHE	2.3
2	AB	129	GLU	2.3
3	AC	200	ALA	2.3
9	CI	45	ALA	2.3
32	DI	146	ALA	2.3
1	AA	63	C	2.3
25	BA	2111	C	2.3
25	BA	2146	C	2.3
1	AA	1005	A	2.3
1	CA	1492	A	2.3
1	CA	1493	A	2.3
2	CB	140	HIS	2.3
5	AE	98	THR	2.3
5	CE	119	LEU	2.3
7	AG	151	TYR	2.3
9	CI	40	LEU	2.3
9	CI	56	LEU	2.3
10	CJ	42	THR	2.3
14	CN	22	THR	2.3
19	CS	30	LEU	2.3
21	AU	18	TYR	2.3
11	CK	32	ILE	2.3
15	AO	3	ILE	2.3
2	CB	169	LYS	2.3
3	CC	4	LYS	2.3
4	AD	169	LYS	2.3
9	AI	11	LYS	2.3
9	CI	78	LYS	2.3
13	AM	113	PRO	2.3
38	DS	57	LYS	2.3
47	B1	48	LYS	2.3
1	AA	148	G	2.3
1	AA	1030(A)	G	2.3
4	CD	140	VAL	2.3
9	AI	104	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
13	CM	104	ARG	2.3
25	BA	2802	G	2.3
3	CC	2	GLY	2.3
13	AM	6	GLY	2.3
13	AM	24	GLY	2.3
16	CP	10	GLY	2.3
2	AB	12	GLU	2.3
5	AE	117	ASP	2.3
7	CG	39	ALA	2.3
9	AI	94	ALA	2.3
17	CQ	97	SER	2.3
20	CT	19	SER	2.3
9	AI	64	THR	2.3
16	AP	69	THR	2.3
25	BA	2107	C	2.3
25	DA	2138	C	2.3
1	CA	968	A	2.3
3	CC	5	ILE	2.3
30	DG	52	ILE	2.3
13	AM	122	LYS	2.3
14	CN	9	LYS	2.3
3	CC	172	ARG	2.3
7	CG	79	ARG	2.3
15	CO	79	ARG	2.3
30	DG	32	PRO	2.3
7	AG	21	VAL	2.3
10	AJ	34	VAL	2.3
4	CD	130	GLY	2.3
9	CI	72	GLY	2.3
14	CN	38	GLY	2.3
1	CA	1310	G	2.3
5	AE	86	ALA	2.3
25	DA	1171	G	2.3
4	AD	102	ASP	2.3
43	DX	1	MET	2.3
9	CI	50	LEU	2.3
10	AJ	33	GLN	2.3
31	BH	103	LEU	2.3
4	AD	208	SER	2.3
4	CD	71	SER	2.3
19	CS	70	LYS	2.3
10	CJ	5	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
15	CO	68	ARG	2.3
30	DG	25	TYR	2.3
30	DG	136	ARG	2.3
43	DX	69	TYR	2.3
1	AA	101	A	2.3
1	CA	1275	A	2.3
13	CM	15	VAL	2.3
22	AV	15	A	2.3
25	DA	2108	C	2.3
30	DG	160	VAL	2.3
9	CI	6	GLY	2.3
31	DH	123	PHE	2.3
45	DZ	88	PHE	2.3
9	CI	15	ALA	2.3
3	CC	204	LEU	2.3
19	CS	12	ASP	2.3
32	DI	12	LEU	2.3
42	DW	36	LEU	2.3
1	AA	104	G	2.3
10	AJ	98	ILE	2.3
25	BA	2147	G	2.3
25	BA	2154	G	2.3
25	BA	2157	G	2.3
25	DA	2166	G	2.3
33	BN	71	ILE	2.3
4	CD	152	SER	2.3
10	CJ	19	SER	2.3
16	CP	45	THR	2.3
20	AT	11	SER	2.3
34	BO	49	ARG	2.3
50	B4	48	ARG	2.3
2	CB	167	PRO	2.3
30	DG	12	TYR	2.3
9	CI	28	VAL	2.3
16	CP	53	VAL	2.3
32	DI	127	VAL	2.3
38	DS	98	VAL	2.3
7	CG	132	GLY	2.3
13	AM	85	GLY	2.3
38	DS	45	GLY	2.3
25	DA	2122	U	2.3
25	BA	2135	A	2.2

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Mol	Chain	Res	Type	RSRZ
25	BA	2161	C	2.2
25	DA	277	C	2.2
25	DA	2111	C	2.2
25	DA	2896	C	2.2
7	AG	84	ASN	2.2
9	AI	52	ALA	2.2
30	DG	169	ALA	2.2
3	AC	188	LEU	2.2
17	CQ	98	LEU	2.2
12	AL	17	LYS	2.2
20	AT	18	GLN	2.2
40	DU	56	ASP	2.2
2	CB	58	ILE	2.2
3	AC	14	ILE	2.2
13	CM	9	ILE	2.2
50	D4	22	ILE	2.2
2	CB	194	PRO	2.2
27	BD	140	THR	2.2
13	CM	54	VAL	2.2
45	DZ	149	SER	2.2
1	AA	1026	G	2.2
1	CA	971	G	2.2
1	CA	1061	G	2.2
1	CA	1215	G	2.2
25	DA	2141	G	2.2
25	DA	2155	G	2.2
25	DA	2319	G	2.2
4	AD	167	GLY	2.2
11	CK	74	ALA	2.2
27	DD	2	ALA	2.2
30	DG	54	GLU	2.2
1	AA	1531	A	2.2
1	CA	949	A	2.2
2	AB	8	LYS	2.2
7	CG	28	ASN	2.2
10	AJ	78	ASN	2.2
13	CM	106	ASN	2.2
20	AT	58	LYS	2.2
5	AE	118	ILE	2.2
8	CH	70	GLN	2.2
9	CI	74	ILE	2.2
7	CG	32	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
10	CJ	45	ARG	2.2
14	CN	57	ARG	2.2
19	CS	13	ASP	2.2
21	CU	15	ARG	2.2
38	DS	95	HIS	2.2
6	AF	6	VAL	2.2
9	CI	98	PRO	2.2
30	DG	15	VAL	2.2
9	CI	4	TYR	2.2
9	CI	92	TYR	2.2
9	CI	114	TYR	2.2
2	AB	151	GLY	2.2
9	CI	68	GLY	2.2
10	CJ	36	GLY	2.2
15	AO	89	GLY	2.2
1	CA	1047	G	2.2
1	CA	1117	G	2.2
1	CA	1290	G	2.2
2	AB	180	LEU	2.2
7	AG	99	LEU	2.2
7	CG	12	LEU	2.2
26	DB	24	G	2.2
30	DG	50	ALA	2.2
10	CJ	43	ARG	2.2
11	AK	126	ARG	2.2
16	AP	65	GLN	2.2
1	AA	607	A	2.2
25	DA	2135	A	2.2
1	AA	1028	C	2.2
1	CA	1028	C	2.2
1	CA	1322	C	2.2
25	BA	2177	C	2.2
4	CD	134	ASP	2.2
7	AG	33	ASP	2.2
10	CJ	91	PRO	2.2
47	D1	68	PRO	2.2
49	D3	2	PRO	2.2
2	AB	14	GLY	2.2
2	AB	33	TYR	2.2
10	CJ	10	GLY	2.2
13	CM	100	GLY	2.2
53	D7	48	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
10	CJ	40	LEU	2.2
10	CJ	85	LEU	2.2
19	CS	15	LEU	2.2
43	BX	95	LEU	2.2
3	CC	121	ALA	2.2
3	CC	168	ALA	2.2
4	CD	195	ALA	2.2
14	AN	30	ALA	2.2
32	DI	46	ALA	2.2
7	CG	5	ARG	2.2
7	CG	78	ARG	2.2
14	AN	3	ARG	2.2
10	CJ	33	GLN	2.2
16	CP	76	GLN	2.2
25	BA	2144	U	2.2
1	AA	105	G	2.2
1	CA	963	G	2.2
1	CA	1131	G	2.2
1	CA	1139	G	2.2
20	AT	73	HIS	2.2
25	BA	614(B)	G	2.2
25	BA	2116	G	2.2
25	BA	2159	G	2.2
25	BA	2165	G	2.2
1	CA	975	A	2.2
3	CC	55	VAL	2.2
9	AI	109	VAL	2.2
11	AK	30	VAL	2.2
22	CV	23	A	2.2
25	DA	896	A	2.2
25	DA	2176	A	2.2
50	B4	56	VAL	2.2
1	AA	175	C	2.2
1	AA	1037	C	2.2
1	CA	1320	C	2.2
1	CA	1354	C	2.2
16	AP	1	MET	2.2
24	AX	71	C	2.2
25	DA	271(Z)	C	2.2
10	AJ	42	THR	2.2
32	DI	93	THR	2.2
34	DO	1	MET	2.2

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Mol	Chain	Res	Type	RSRZ
5	AE	114	GLY	2.2
11	CK	118	GLY	2.2
40	DU	61	TRP	2.2
9	CI	88	TYR	2.2
45	BZ	104	PHE	2.2
20	AT	72	LEU	2.2
28	DE	52	LEU	2.2
30	BG	3	LEU	2.2
47	D1	2	SER	2.2
9	CI	106	ALA	2.2
11	AK	92	GLU	2.2
30	BG	35	GLU	2.2
30	BG	54	GLU	2.2
30	DG	158	ALA	2.2
45	DZ	168	GLU	2.2
13	CM	39	ILE	2.1
45	BZ	171	ILE	2.1
1	CA	1364	U	2.1
16	AP	13	HIS	2.1
22	AV	19	U	2.1
25	DA	2132	U	2.1
13	AM	45	VAL	2.1
15	AO	27	VAL	2.1
17	AQ	10	VAL	2.1
45	DZ	42	VAL	2.1
45	DZ	68	PRO	2.1
1	AA	346	G	2.1
1	AA	377	G	2.1
1	AA	1030(C)	G	2.1
1	CA	1031	G	2.1
1	CA	1032	G	2.1
6	CF	54	LYS	2.1
1	CA	1035	A	2.1
1	CA	1233	G	2.1
1	CA	1530	G	2.1
2	CB	74	LYS	2.1
19	CS	32	LYS	2.1
25	BA	1913	A	2.1
25	BA	2125	G	2.1
25	BA	2152	G	2.1
25	BA	2181	G	2.1
25	DA	10	G	2.1

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Mol	Chain	Res	Type	RSRZ
25	DA	2793	G	2.1
38	DS	11	LYS	2.1
9	AI	30	GLY	2.1
30	BG	65	GLY	2.1
32	BI	90	GLY	2.1
1	CA	1336	C	2.1
1	CA	1362	C	2.1
3	AC	47	LEU	2.1
6	AF	45	LEU	2.1
9	CI	59	PHE	2.1
14	AN	21	TYR	2.1
16	CP	39	TYR	2.1
25	BA	2140	C	2.1
47	B1	98	LEU	2.1
40	DU	76	TYR	2.1
6	AF	49	ALA	2.1
9	CI	13	ALA	2.1
10	AJ	59	SER	2.1
13	CM	51	ALA	2.1
13	CM	118	ALA	2.1
14	AN	60	SER	2.1
44	DY	48	ALA	2.1
45	DZ	172	ALA	2.1
4	CD	141	ARG	2.1
10	CJ	61	GLU	2.1
14	CN	23	ARG	2.1
33	BN	115	ARG	2.1
30	DG	157	ILE	2.1
8	CH	95	VAL	2.1
3	CC	142	MET	2.1
14	AN	14	PRO	2.1
18	AR	84	LYS	2.1
16	AP	67	THR	2.1
19	CS	68	GLY	2.1
33	BN	81	GLY	2.1
2	CB	55	PHE	2.1
3	AC	91	LEU	2.1
6	CF	45	LEU	2.1
9	AI	59	PHE	2.1
30	DG	102	PHE	2.1
52	D6	42	TRP	2.1
1	CA	1213	A	2.1

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Mol	Chain	Res	Type	RSRZ
9	AI	10	ARG	2.1
9	CI	16	ARG	2.1
13	AM	108	ARG	2.1
13	CM	30	ALA	2.1
16	AP	32	TYR	2.1
20	CT	8	ARG	2.1
39	DT	130	ALA	2.1
3	AC	124	ILE	2.1
3	CC	8	ILE	2.1
3	CC	154	SER	2.1
4	AD	145	GLU	2.1
12	AL	16	GLU	2.1
13	AM	78	ILE	2.1
25	DA	1114	G	2.1
25	DA	2151	G	2.1
25	DA	2157	G	2.1
1	AA	153	C	2.1
19	CS	69	HIS	2.1
2	AB	165	VAL	2.1
3	CC	173	VAL	2.1
4	CD	165	MET	2.1
16	CP	14	ASN	2.1
20	AT	9	ASN	2.1
33	BN	9	VAL	2.1
8	CH	67	PRO	2.1
1	CA	1257	U	2.1
3	CC	159	GLY	2.1
5	CE	22	GLY	2.1
15	AO	56	LEU	2.1
19	AS	72	GLY	2.1
36	DQ	61	GLY	2.1
45	BZ	106	GLY	2.1
10	CJ	60	ARG	2.1
13	CM	88	ARG	2.1
19	AS	78	ARG	2.1
2	CB	225	ALA	2.1
3	CC	182	ILE	2.1
3	CC	184	TYR	2.1
5	CE	109	ILE	2.1
13	AM	51	ALA	2.1
16	CP	19	ILE	2.1
30	BG	73	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
30	BG	164	GLU	2.1
31	BH	58	GLU	2.1
1	AA	152	A	2.1
1	AA	1035	A	2.1
1	AA	1286	A	2.1
1	CA	978	A	2.1
1	CA	1285	A	2.1
14	CN	32	SER	2.1
19	AS	4	SER	2.1
25	BA	2801(A)	A	2.1
45	DZ	166	SER	2.1
5	AE	20	GLN	2.1
9	CI	124	GLN	2.1
1	AA	66	G	2.1
1	AA	1029	C	2.1
1	CA	1365	G	2.1
2	AB	101	MET	2.1
9	AI	28	VAL	2.1
12	CL	43	VAL	2.1
25	BA	1117	G	2.1
25	BA	1176	G	2.1
25	BA	2131	G	2.1
25	BA	2153	G	2.1
25	BA	2155	G	2.1
30	BG	5	VAL	2.1
50	D4	28	LYS	2.1
30	BG	34	LEU	2.1
2	AB	152	PHE	2.1
3	AC	9	GLY	2.1
16	CP	78	GLY	2.1
2	CB	166	ASP	2.1
8	AH	92	ARG	2.1
8	CH	30	ARG	2.1
9	AI	9	ARG	2.1
10	CJ	70	ARG	2.1
10	CJ	79	ARG	2.1
13	CM	29	ARG	2.1
15	AO	22	THR	2.1
30	DG	71	THR	2.1
46	D0	74	ARG	2.1
3	CC	71	ALA	2.1
4	CD	48	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
10	AJ	6	ILE	2.1
10	CJ	82	ILE	2.1
11	AK	42	TRP	2.1
19	AS	34	TRP	2.1
17	AQ	58	GLU	2.1
1	CA	1110	A	2.0
6	AF	90	VAL	2.0
17	AQ	5	VAL	2.0
25	BA	2790	A	2.0
30	DG	109	VAL	2.0
31	DH	17	VAL	2.0
32	DI	19	VAL	2.0
32	DI	145	VAL	2.0
32	DI	119	PRO	2.0
1	AA	1109	C	2.0
3	AC	178	LEU	2.0
4	AD	188	LEU	2.0
8	AH	2	LEU	2.0
10	CJ	65	LEU	2.0
16	CP	60	LEU	2.0
25	DA	2137	C	2.0
32	DI	5	LEU	2.0
35	BP	3	LEU	2.0
44	DY	90	LEU	2.0
1	AA	347	G	2.0
1	CA	1048	G	2.0
1	CA	1253	G	2.0
1	CA	1361	G	2.0
2	CB	152	PHE	2.0
7	AG	81	GLY	2.0
15	CO	15	PHE	2.0
15	CO	54	ARG	2.0
20	CT	101	GLY	2.0
21	CU	10	ARG	2.0
25	BA	2156	G	2.0
25	BA	2833	G	2.0
25	DA	2182	G	2.0
31	DH	132	ARG	2.0
38	DS	29	PHE	2.0
49	D3	29	ARG	2.0
2	CB	41	ILE	2.0
2	CB	54	THR	2.0

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Mol	Chain	Res	Type	RSRZ
7	CG	42	ILE	2.0
13	CM	105	THR	2.0
25	DA	1026	U	2.0
37	BR	69	ASP	2.0
45	DZ	146	ILE	2.0
9	CI	122	ALA	2.0
39	DT	131	ALA	2.0
30	DG	59	GLU	2.0
31	DH	116	GLU	2.0
32	DI	95	LYS	2.0
2	AB	124	SER	2.0
2	CB	71	VAL	2.0
3	AC	68	VAL	2.0
4	CD	160	GLN	2.0
9	CI	41	VAL	2.0
19	CS	11	VAL	2.0
5	AE	93	PRO	2.0
16	CP	46	PRO	2.0
1	CA	1016	A	2.0
4	AD	176	LEU	2.0
4	CD	162	LEU	2.0
13	CM	48	LEU	2.0
16	AP	49	LEU	2.0
18	AR	44	LEU	2.0
20	AT	13	LEU	2.0
22	CV	15	A	2.0
22	CV	24	A	2.0
32	DI	38	LEU	2.0
47	B1	97	LEU	2.0
10	AJ	29	ARG	2.0
16	AP	42	ARG	2.0
2	AB	99	GLY	2.0
3	CC	10	PHE	2.0
16	AP	80	PHE	2.0
18	AR	57	GLY	2.0
19	AS	74	PHE	2.0
1	CA	979	C	2.0
8	CH	111	ILE	2.0
4	AD	48	ALA	2.0
4	CD	111	ALA	2.0
10	CJ	100	THR	2.0
46	D0	43	THR	2.0

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Mol	Chain	Res	Type	RSRZ
2	CB	191	ASP	2.0
25	BA	12	U	2.0
25	BA	90	U	2.0
25	BA	2150	U	2.0
1	CA	306	G	2.0
14	CN	17	LYS	2.0
25	BA	2148	G	2.0
25	DA	271(M)	G	2.0
25	DA	2154	G	2.0
30	BG	48	GLU	2.0
29	BF	172	TRP	2.0
2	AB	236	TYR	2.0
40	DU	47	TYR	2.0
16	AP	2	VAL	2.0
53	D7	46	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	4SU	CX	8	20/21	0.85	0.11	65,84,90,94	0
24	5MU	CX	54	21/22	0.86	0.12	66,78,87,98	0
24	PSU	CX	55	20/21	0.86	0.11	59,68,84,85	0
24	PSU	AX	55	20/21	0.92	0.10	57,66,78,79	0
24	5MC	CX	32	21/22	0.92	0.12	52,69,78,83	0
24	4SU	AX	8	20/21	0.93	0.10	50,63,78,79	0
24	31H	CX	76	32/33	0.93	0.12	33,54,78,89	0
24	5MC	AX	32	21/22	0.94	0.11	46,61,70,75	0
24	5MU	AX	54	21/22	0.94	0.09	55,69,75,82	0
23	PPU	CW	76	37/38	0.96	0.11	31,50,63,70	0
24	31H	AX	76	32/33	0.96	0.12	27,44,76,98	0
23	PPU	AW	76	37/38	0.97	0.09	25,33,43,45	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
56	MG	DG	3001	1/1	0.55	0.21	81,81,81,81	0
56	MG	DA	3574	1/1	0.66	0.33	56,56,56,56	0
56	MG	CA	3138	1/1	0.69	0.17	58,58,58,58	0
56	MG	DA	3504	1/1	0.71	0.17	49,49,49,49	0
56	MG	DA	3247	1/1	0.73	0.15	49,49,49,49	0
56	MG	AA	3184	1/1	0.75	0.23	74,74,74,74	0
56	MG	AA	3056	1/1	0.75	0.29	69,69,69,69	0
56	MG	AA	3180	1/1	0.75	0.15	56,56,56,56	0
56	MG	CA	3105	1/1	0.76	0.25	84,84,84,84	0
56	MG	AA	3167	1/1	0.76	0.25	73,73,73,73	0
56	MG	BA	3580	1/1	0.76	0.13	62,62,62,62	0
56	MG	DA	3478	1/1	0.77	0.25	53,53,53,53	0
56	MG	CA	3126	1/1	0.77	0.15	73,73,73,73	0
56	MG	BA	3639	1/1	0.77	0.19	64,64,64,64	0
56	MG	CA	3119	1/1	0.77	0.12	48,48,48,48	0
56	MG	DA	3326	1/1	0.78	0.13	41,41,41,41	0
56	MG	DA	3354	1/1	0.78	0.16	51,51,51,51	0
56	MG	CA	3149	1/1	0.78	0.38	66,66,66,66	0
56	MG	DA	3271	1/1	0.79	0.17	55,55,55,55	0
56	MG	AA	3055	1/1	0.79	0.20	72,72,72,72	0
56	MG	CA	3068	1/1	0.79	0.20	74,74,74,74	0
56	MG	DA	3446	1/1	0.79	0.12	46,46,46,46	0
56	MG	AF	3001	1/1	0.80	0.18	52,52,52,52	0
56	MG	CA	3140	1/1	0.80	0.23	61,61,61,61	0
56	MG	DA	3475	1/1	0.80	0.14	41,41,41,41	0
56	MG	BA	3634	1/1	0.80	0.23	41,41,41,41	0
56	MG	CA	3108	1/1	0.80	0.20	59,59,59,59	0
56	MG	BA	3569	1/1	0.80	0.17	55,55,55,55	0
56	MG	BB	3009	1/1	0.80	0.18	67,67,67,67	0
56	MG	CA	3125	1/1	0.81	0.24	71,71,71,71	0
56	MG	BA	3631	1/1	0.81	0.13	41,41,41,41	0
56	MG	DA	3103	1/1	0.81	0.08	56,56,56,56	0
56	MG	DA	3443	1/1	0.81	0.12	49,49,49,49	0
56	MG	AA	3106	1/1	0.81	0.15	50,50,50,50	0
56	MG	DA	3366	1/1	0.82	0.12	43,43,43,43	0
56	MG	DA	3416	1/1	0.82	0.13	44,44,44,44	0
56	MG	BA	3536	1/1	0.82	0.21	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3497	1/1	0.82	0.14	34,34,34,34	0
56	MG	BA	3633	1/1	0.82	0.15	57,57,57,57	0
56	MG	BZ	3001	1/1	0.82	0.12	58,58,58,58	0
56	MG	CA	3016	1/1	0.82	0.16	68,68,68,68	0
56	MG	DA	3507	1/1	0.82	0.13	54,54,54,54	0
56	MG	DA	3566	1/1	0.82	0.15	61,61,61,61	0
56	MG	CA	3035	1/1	0.82	0.13	66,66,66,66	0
56	MG	DB	3006	1/1	0.82	0.13	55,55,55,55	0
56	MG	CA	3065	1/1	0.82	0.14	55,55,55,55	0
56	MG	DW	3002	1/1	0.82	0.11	60,60,60,60	0
56	MG	CA	3145	1/1	0.83	0.18	59,59,59,59	0
56	MG	DA	3518	1/1	0.83	0.19	53,53,53,53	0
56	MG	DA	3301	1/1	0.83	0.13	56,56,56,56	0
56	MG	DA	3302	1/1	0.83	0.10	43,43,43,43	0
56	MG	BA	3062	1/1	0.83	0.18	46,46,46,46	0
56	MG	CA	3104	1/1	0.83	0.29	74,74,74,74	0
56	MG	AA	3024	1/1	0.83	0.38	60,60,60,60	0
56	MG	DY	502	1/1	0.83	0.14	51,51,51,51	0
56	MG	BA	3466	1/1	0.84	0.26	49,49,49,49	0
56	MG	AA	3049	1/1	0.84	0.14	47,47,47,47	0
56	MG	CA	3151	1/1	0.84	0.20	50,50,50,50	0
56	MG	DA	3020	1/1	0.84	0.22	50,50,50,50	0
56	MG	DA	3474	1/1	0.84	0.11	62,62,62,62	0
56	MG	DA	3090	1/1	0.84	0.10	54,54,54,54	0
56	MG	BA	3505	1/1	0.84	0.23	46,46,46,46	0
56	MG	DA	3479	1/1	0.84	0.18	63,63,63,63	0
56	MG	DA	3150	1/1	0.84	0.35	55,55,55,55	0
56	MG	AA	3181	1/1	0.84	0.17	53,53,53,53	0
56	MG	AA	3109	1/1	0.84	0.22	44,44,44,44	0
56	MG	DA	3538	1/1	0.84	0.10	39,39,39,39	0
56	MG	DA	3300	1/1	0.84	0.18	58,58,58,58	0
56	MG	AA	3160	1/1	0.84	0.12	71,71,71,71	0
56	MG	AA	3086	1/1	0.84	0.37	61,61,61,61	0
56	MG	DB	3009	1/1	0.84	0.14	60,60,60,60	0
56	MG	CA	3139	1/1	0.84	0.15	67,67,67,67	0
56	MG	DA	3343	1/1	0.84	0.23	56,56,56,56	0
56	MG	BA	3331	1/1	0.84	0.12	59,59,59,59	0
56	MG	CA	3103	1/1	0.85	0.16	52,52,52,52	0
56	MG	CA	3129	1/1	0.85	0.11	55,55,55,55	0
56	MG	CA	3011	1/1	0.85	0.17	66,66,66,66	0
56	MG	DA	3539	1/1	0.85	0.16	52,52,52,52	0
56	MG	BA	3617	1/1	0.85	0.25	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3088	1/1	0.85	0.20	62,62,62,62	0
56	MG	BA	3632	1/1	0.85	0.25	54,54,54,54	0
56	MG	BA	3611	1/1	0.85	0.20	59,59,59,59	0
56	MG	DA	3485	1/1	0.85	0.18	60,60,60,60	0
56	MG	DA	3501	1/1	0.85	0.11	55,55,55,55	0
56	MG	DA	3381	1/1	0.85	0.20	56,56,56,56	0
56	MG	AA	3149	1/1	0.86	0.17	68,68,68,68	0
56	MG	AA	3027	1/1	0.86	0.21	71,71,71,71	0
56	MG	DA	3359	1/1	0.86	0.17	43,43,43,43	0
56	MG	BA	3043	1/1	0.86	0.20	36,36,36,36	0
56	MG	CA	3132	1/1	0.86	0.25	73,73,73,73	0
56	MG	DA	3398	1/1	0.86	0.14	51,51,51,51	0
56	MG	BA	3545	1/1	0.86	0.11	54,54,54,54	0
56	MG	BA	3557	1/1	0.86	0.18	42,42,42,42	0
56	MG	AA	3092	1/1	0.86	0.23	61,61,61,61	0
56	MG	BA	3244	1/1	0.86	0.21	46,46,46,46	0
56	MG	BA	3582	1/1	0.86	0.14	31,31,31,31	0
56	MG	CA	3036	1/1	0.86	0.14	56,56,56,56	0
56	MG	BA	3583	1/1	0.86	0.12	37,37,37,37	0
56	MG	DA	3058	1/1	0.86	0.20	45,45,45,45	0
56	MG	BA	3584	1/1	0.86	0.14	44,44,44,44	0
56	MG	CA	3083	1/1	0.86	0.22	66,66,66,66	0
56	MG	DA	3135	1/1	0.86	0.12	47,47,47,47	0
56	MG	CA	3084	1/1	0.86	0.13	72,72,72,72	0
56	MG	BA	3601	1/1	0.86	0.15	50,50,50,50	0
56	MG	DA	3251	1/1	0.86	0.22	62,62,62,62	0
56	MG	DA	3557	1/1	0.86	0.13	62,62,62,62	0
56	MG	DA	3561	1/1	0.86	0.14	63,63,63,63	0
56	MG	AA	3013	1/1	0.86	0.25	58,58,58,58	0
56	MG	DA	3568	1/1	0.86	0.11	60,60,60,60	0
56	MG	DA	3274	1/1	0.86	0.13	56,56,56,56	0
56	MG	DA	3580	1/1	0.86	0.10	58,58,58,58	0
56	MG	DB	3005	1/1	0.86	0.11	56,56,56,56	0
56	MG	AA	3054	1/1	0.86	0.17	65,65,65,65	0
56	MG	BA	3483	1/1	0.86	0.14	47,47,47,47	0
56	MG	BA	3496	1/1	0.86	0.16	31,31,31,31	0
56	MG	DQ	3003	1/1	0.86	0.13	50,50,50,50	0
56	MG	DA	3309	1/1	0.86	0.13	60,60,60,60	0
56	MG	CA	3121	1/1	0.86	0.15	61,61,61,61	0
56	MG	BA	3307	1/1	0.87	0.08	63,63,63,63	0
56	MG	BA	3585	1/1	0.87	0.25	50,50,50,50	0
56	MG	BA	3510	1/1	0.87	0.19	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3019	1/1	0.87	0.34	71,71,71,71	0
56	MG	CA	3034	1/1	0.87	0.24	67,67,67,67	0
56	MG	AA	3061	1/1	0.87	0.22	62,62,62,62	0
56	MG	BA	3395	1/1	0.87	0.10	54,54,54,54	0
56	MG	CA	3049	1/1	0.87	0.18	51,51,51,51	0
56	MG	DA	3325	1/1	0.87	0.12	54,54,54,54	0
56	MG	BA	3412	1/1	0.87	0.11	48,48,48,48	0
56	MG	CA	3067	1/1	0.87	0.19	63,63,63,63	0
56	MG	AA	3171	1/1	0.87	0.10	62,62,62,62	0
56	MG	CA	3078	1/1	0.87	0.18	66,66,66,66	0
56	MG	BA	3574	1/1	0.87	0.19	55,55,55,55	0
56	MG	DA	3022	1/1	0.87	0.19	39,39,39,39	0
56	MG	BA	3211	1/1	0.87	0.22	29,29,29,29	0
56	MG	BA	3229	1/1	0.87	0.20	54,54,54,54	0
56	MG	DA	3425	1/1	0.87	0.10	37,37,37,37	0
56	MG	DA	3428	1/1	0.87	0.15	33,33,33,33	0
56	MG	DF	303	1/1	0.87	0.17	57,57,57,57	0
56	MG	DA	3437	1/1	0.87	0.15	48,48,48,48	0
56	MG	AA	3102	1/1	0.87	0.23	60,60,60,60	0
56	MG	BB	3010	1/1	0.87	0.09	77,77,77,77	0
56	MG	BB	3015	1/1	0.87	0.10	48,48,48,48	0
56	MG	DA	3467	1/1	0.88	0.14	47,47,47,47	0
56	MG	DA	3470	1/1	0.88	0.30	52,52,52,52	0
56	MG	DA	3252	1/1	0.88	0.12	53,53,53,53	0
56	MG	AA	3121	1/1	0.88	0.14	40,40,40,40	0
56	MG	AA	3003	1/1	0.88	0.12	57,57,57,57	0
56	MG	DA	3275	1/1	0.88	0.12	45,45,45,45	0
56	MG	CA	3041	1/1	0.88	0.18	67,67,67,67	0
56	MG	DA	3496	1/1	0.88	0.10	46,46,46,46	0
56	MG	CA	3133	1/1	0.88	0.19	68,68,68,68	0
56	MG	CA	3048	1/1	0.88	0.39	52,52,52,52	0
56	MG	AA	3057	1/1	0.88	0.29	67,67,67,67	0
56	MG	BB	3003	1/1	0.88	0.09	61,61,61,61	0
56	MG	DA	3526	1/1	0.88	0.14	64,64,64,64	0
56	MG	AA	3058	1/1	0.88	0.19	62,62,62,62	0
56	MG	AA	3023	1/1	0.88	0.30	71,71,71,71	0
56	MG	DA	3347	1/1	0.88	0.09	41,41,41,41	0
56	MG	BA	3553	1/1	0.88	0.49	48,48,48,48	0
56	MG	BG	3003	1/1	0.88	0.09	41,41,41,41	0
56	MG	DA	3567	1/1	0.88	0.11	41,41,41,41	0
56	MG	BA	3094	1/1	0.88	0.14	45,45,45,45	0
56	MG	DA	3373	1/1	0.88	0.09	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3003	1/1	0.88	0.21	65,65,65,65	0
56	MG	DA	3585	1/1	0.88	0.09	37,37,37,37	0
56	MG	CA	3009	1/1	0.88	0.17	55,55,55,55	0
56	MG	BA	3612	1/1	0.88	0.18	51,51,51,51	0
56	MG	DA	3420	1/1	0.88	0.09	46,46,46,46	0
56	MG	AA	3176	1/1	0.88	0.14	60,60,60,60	0
56	MG	DA	3147	1/1	0.88	0.20	47,47,47,47	0
56	MG	DN	5001	1/1	0.88	0.12	65,65,65,65	0
56	MG	AA	3045	1/1	0.88	0.25	60,60,60,60	0
56	MG	CA	3021	1/1	0.88	0.14	52,52,52,52	0
56	MG	BA	3576	1/1	0.88	0.13	48,48,48,48	0
56	MG	AA	3042	1/1	0.89	0.20	54,54,54,54	0
56	MG	AA	3164	1/1	0.89	0.14	61,61,61,61	0
56	MG	BA	3306	1/1	0.89	0.17	54,54,54,54	0
56	MG	DA	3412	1/1	0.89	0.19	53,53,53,53	0
56	MG	CA	3004	1/1	0.89	0.11	51,51,51,51	0
56	MG	AA	3016	1/1	0.89	0.16	49,49,49,49	0
56	MG	BA	3323	1/1	0.89	0.11	61,61,61,61	0
56	MG	BA	3578	1/1	0.89	0.12	59,59,59,59	0
56	MG	BA	3579	1/1	0.89	0.10	46,46,46,46	0
56	MG	BA	3036	1/1	0.89	0.13	56,56,56,56	0
56	MG	CA	3025	1/1	0.89	0.11	48,48,48,48	0
56	MG	CA	3033	1/1	0.89	0.28	52,52,52,52	0
56	MG	BA	3357	1/1	0.89	0.10	30,30,30,30	0
56	MG	DA	3066	1/1	0.89	0.13	49,49,49,49	0
56	MG	DA	3083	1/1	0.89	0.09	48,48,48,48	0
56	MG	BA	3367	1/1	0.89	0.12	49,49,49,49	0
56	MG	DA	3100	1/1	0.89	0.09	34,34,34,34	0
56	MG	BA	3387	1/1	0.89	0.21	49,49,49,49	0
56	MG	DA	3109	1/1	0.89	0.08	50,50,50,50	0
56	MG	AA	3169	1/1	0.89	0.15	71,71,71,71	0
56	MG	BA	3593	1/1	0.89	0.23	39,39,39,39	0
56	MG	BA	3401	1/1	0.89	0.14	32,32,32,32	0
56	MG	DA	3173	1/1	0.89	0.15	54,54,54,54	0
56	MG	DA	3191	1/1	0.89	0.14	53,53,53,53	0
56	MG	CA	3055	1/1	0.89	0.11	62,62,62,62	0
56	MG	BA	3605	1/1	0.89	0.08	46,46,46,46	0
56	MG	DA	3545	1/1	0.89	0.16	58,58,58,58	0
56	MG	BA	3056	1/1	0.89	0.13	46,46,46,46	0
56	MG	AA	3002	1/1	0.89	0.23	43,43,43,43	0
56	MG	BA	3469	1/1	0.89	0.09	28,28,28,28	0
56	MG	CA	3082	1/1	0.89	0.32	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3619	1/1	0.89	0.12	30,30,30,30	0
56	MG	BA	3075	1/1	0.89	0.31	58,58,58,58	0
56	MG	BA	3495	1/1	0.89	0.23	48,48,48,48	0
56	MG	DA	3307	1/1	0.89	0.09	53,53,53,53	0
56	MG	BA	3090	1/1	0.89	0.16	44,44,44,44	0
56	MG	AA	3142	1/1	0.89	0.17	60,60,60,60	0
56	MG	DB	3007	1/1	0.89	0.09	38,38,38,38	0
56	MG	BA	3111	1/1	0.89	0.08	27,27,27,27	0
56	MG	DA	3337	1/1	0.89	0.07	42,42,42,42	0
56	MG	CA	3118	1/1	0.89	0.15	78,78,78,78	0
56	MG	BA	3192	1/1	0.89	0.26	58,58,58,58	0
56	MG	BA	3523	1/1	0.89	0.10	50,50,50,50	0
56	MG	AA	3073	1/1	0.89	0.24	50,50,50,50	0
56	MG	BA	3213	1/1	0.89	0.20	21,21,21,21	0
56	MG	BA	3609	1/1	0.90	0.10	44,44,44,44	0
56	MG	DA	3399	1/1	0.90	0.08	40,40,40,40	0
56	MG	DA	3402	1/1	0.90	0.11	63,63,63,63	0
56	MG	BA	3488	1/1	0.90	0.22	36,36,36,36	0
56	MG	BA	3237	1/1	0.90	0.21	57,57,57,57	0
56	MG	DA	3067	1/1	0.90	0.24	53,53,53,53	0
56	MG	AA	3093	1/1	0.90	0.14	45,45,45,45	0
56	MG	BA	3246	1/1	0.90	0.20	56,56,56,56	0
56	MG	DA	3098	1/1	0.90	0.09	46,46,46,46	0
56	MG	BA	3503	1/1	0.90	0.13	30,30,30,30	0
56	MG	BA	3293	1/1	0.90	0.11	17,17,17,17	0
56	MG	DA	3108	1/1	0.90	0.10	46,46,46,46	0
56	MG	CA	3072	1/1	0.90	0.22	57,57,57,57	0
56	MG	BA	3044	1/1	0.90	0.15	30,30,30,30	0
56	MG	AA	3038	1/1	0.90	0.23	53,53,53,53	0
56	MG	AA	3062	1/1	0.90	0.30	58,58,58,58	0
56	MG	DA	3163	1/1	0.90	0.26	31,31,31,31	0
56	MG	DA	3166	1/1	0.90	0.16	35,35,35,35	0
56	MG	DA	3487	1/1	0.90	0.09	50,50,50,50	0
56	MG	AA	3041	1/1	0.90	0.20	52,52,52,52	0
56	MG	DA	3500	1/1	0.90	0.17	46,46,46,46	0
56	MG	BB	3005	1/1	0.90	0.18	30,30,30,30	0
56	MG	DA	3211	1/1	0.90	0.17	35,35,35,35	0
56	MG	BA	3549	1/1	0.90	0.16	57,57,57,57	0
56	MG	DA	3515	1/1	0.90	0.09	64,64,64,64	0
56	MG	BA	3350	1/1	0.90	0.14	59,59,59,59	0
56	MG	AA	3113	1/1	0.90	0.21	53,53,53,53	0
56	MG	DA	3530	1/1	0.90	0.14	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3531	1/1	0.90	0.11	69,69,69,69	0
56	MG	BA	3567	1/1	0.90	0.09	53,53,53,53	0
56	MG	BA	3359	1/1	0.90	0.10	54,54,54,54	0
56	MG	DA	3541	1/1	0.90	0.11	57,57,57,57	0
56	MG	DA	3544	1/1	0.90	0.12	51,51,51,51	0
56	MG	AA	3085	1/1	0.90	0.23	63,63,63,63	0
56	MG	CA	3123	1/1	0.90	0.17	66,66,66,66	0
56	MG	BA	3373	1/1	0.90	0.13	41,41,41,41	0
56	MG	BA	3381	1/1	0.90	0.18	31,31,31,31	0
56	MG	AA	3010	1/1	0.90	0.20	60,60,60,60	0
56	MG	CA	3013	1/1	0.90	0.16	53,53,53,53	0
56	MG	AA	3015	1/1	0.90	0.12	56,56,56,56	0
56	MG	CA	3137	1/1	0.90	0.14	66,66,66,66	0
56	MG	DA	3584	1/1	0.90	0.13	61,61,61,61	0
56	MG	BA	3206	1/1	0.90	0.21	41,41,41,41	0
56	MG	BA	3403	1/1	0.90	0.13	18,18,18,18	0
56	MG	AA	3185	1/1	0.90	0.08	64,64,64,64	0
56	MG	DA	3351	1/1	0.90	0.09	46,46,46,46	0
56	MG	BA	3415	1/1	0.90	0.15	54,54,54,54	0
56	MG	AA	3151	1/1	0.90	0.18	45,45,45,45	0
56	MG	AA	3035	1/1	0.90	0.23	65,65,65,65	0
56	MG	DA	3371	1/1	0.90	0.07	46,46,46,46	0
56	MG	DA	3017	1/1	0.90	0.25	46,46,46,46	0
56	MG	DA	3375	1/1	0.90	0.12	49,49,49,49	0
56	MG	BA	3230	1/1	0.90	0.07	40,40,40,40	0
56	MG	DA	3340	1/1	0.91	0.11	47,47,47,47	0
56	MG	CA	3120	1/1	0.91	0.17	51,51,51,51	0
56	MG	AA	3110	1/1	0.91	0.12	60,60,60,60	0
56	MG	AA	3012	1/1	0.91	0.10	64,64,64,64	0
56	MG	AA	3119	1/1	0.91	0.16	57,57,57,57	0
56	MG	BA	3235	1/1	0.91	0.09	51,51,51,51	0
56	MG	BH	3001	1/1	0.91	0.19	56,56,56,56	0
56	MG	BO	5001	1/1	0.91	0.18	62,62,62,62	0
56	MG	AA	3076	1/1	0.91	0.14	52,52,52,52	0
56	MG	BA	3404	1/1	0.91	0.16	38,38,38,38	0
56	MG	BA	3405	1/1	0.91	0.11	26,26,26,26	0
56	MG	CA	3007	1/1	0.91	0.07	50,50,50,50	0
56	MG	AA	3126	1/1	0.91	0.29	54,54,54,54	0
56	MG	AA	3006	1/1	0.91	0.11	67,67,67,67	0
56	MG	DA	3406	1/1	0.91	0.09	50,50,50,50	0
56	MG	CA	3148	1/1	0.91	0.11	57,57,57,57	0
56	MG	CA	3012	1/1	0.91	0.18	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3423	1/1	0.91	0.11	47,47,47,47	0
56	MG	DA	3424	1/1	0.91	0.14	30,30,30,30	0
56	MG	CA	3152	1/1	0.91	0.13	75,75,75,75	0
56	MG	BA	3428	1/1	0.91	0.08	58,58,58,58	0
56	MG	CA	3018	1/1	0.91	0.10	43,43,43,43	0
56	MG	BA	3443	1/1	0.91	0.09	44,44,44,44	0
56	MG	DA	3445	1/1	0.91	0.13	48,48,48,48	0
56	MG	DA	3028	1/1	0.91	0.10	47,47,47,47	0
56	MG	BA	3278	1/1	0.91	0.08	50,50,50,50	0
56	MG	AA	3018	1/1	0.91	0.16	50,50,50,50	0
56	MG	DA	3473	1/1	0.91	0.10	50,50,50,50	0
56	MG	BA	3476	1/1	0.91	0.07	51,51,51,51	0
56	MG	DA	3070	1/1	0.91	0.30	49,49,49,49	0
56	MG	DA	3477	1/1	0.91	0.09	42,42,42,42	0
56	MG	DA	3076	1/1	0.91	0.07	43,43,43,43	0
56	MG	BA	3596	1/1	0.91	0.15	56,56,56,56	0
56	MG	DA	3483	1/1	0.91	0.10	54,54,54,54	0
56	MG	DA	3484	1/1	0.91	0.12	34,34,34,34	0
56	MG	DA	3088	1/1	0.91	0.06	39,39,39,39	0
56	MG	BA	3600	1/1	0.91	0.20	68,68,68,68	0
56	MG	BA	3480	1/1	0.91	0.17	43,43,43,43	0
56	MG	BA	3604	1/1	0.91	0.07	28,28,28,28	0
56	MG	BA	3297	1/1	0.91	0.08	39,39,39,39	0
56	MG	BA	3300	1/1	0.91	0.15	39,39,39,39	0
56	MG	DA	3506	1/1	0.91	0.11	65,65,65,65	0
56	MG	CA	3050	1/1	0.91	0.21	67,67,67,67	0
56	MG	AA	3019	1/1	0.91	0.27	62,62,62,62	0
56	MG	DA	3516	1/1	0.91	0.08	61,61,61,61	0
56	MG	AA	3153	1/1	0.91	0.17	50,50,50,50	0
56	MG	CA	3066	1/1	0.91	0.21	43,43,43,43	0
56	MG	BA	3112	1/1	0.91	0.14	40,40,40,40	0
56	MG	BA	3125	1/1	0.91	0.14	51,51,51,51	0
56	MG	BA	3626	1/1	0.91	0.15	50,50,50,50	0
56	MG	CA	3077	1/1	0.91	0.18	44,44,44,44	0
56	MG	DA	3192	1/1	0.91	0.12	51,51,51,51	0
56	MG	DA	3206	1/1	0.91	0.08	50,50,50,50	0
56	MG	BA	3627	1/1	0.91	0.13	54,54,54,54	0
56	MG	DA	3552	1/1	0.91	0.17	49,49,49,49	0
56	MG	DA	3213	1/1	0.91	0.12	34,34,34,34	0
56	MG	BA	3629	1/1	0.91	0.17	60,60,60,60	0
56	MG	BA	3140	1/1	0.91	0.17	33,33,33,33	0
56	MG	BA	3507	1/1	0.91	0.11	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3257	1/1	0.91	0.11	55,55,55,55	0
56	MG	CA	3085	1/1	0.91	0.13	52,52,52,52	0
56	MG	DA	3578	1/1	0.91	0.10	47,47,47,47	0
56	MG	DA	3272	1/1	0.91	0.10	57,57,57,57	0
56	MG	CA	3090	1/1	0.91	0.17	66,66,66,66	0
56	MG	CA	3091	1/1	0.91	0.19	66,66,66,66	0
56	MG	DB	3004	1/1	0.91	0.11	36,36,36,36	0
56	MG	BA	3171	1/1	0.91	0.09	44,44,44,44	0
56	MG	BA	3513	1/1	0.91	0.08	60,60,60,60	0
56	MG	AA	3156	1/1	0.91	0.10	61,61,61,61	0
56	MG	BA	3642	1/1	0.91	0.20	47,47,47,47	0
56	MG	DB	3012	1/1	0.91	0.13	53,53,53,53	0
56	MG	CA	3113	1/1	0.91	0.14	57,57,57,57	0
56	MG	CA	3114	1/1	0.91	0.14	80,80,80,80	0
56	MG	AA	3187	1/1	0.91	0.13	33,33,33,33	0
56	MG	DA	3327	1/1	0.91	0.14	34,34,34,34	0
56	MG	DA	3328	1/1	0.91	0.13	48,48,48,48	0
56	MG	AA	3158	1/1	0.91	0.11	54,54,54,54	0
56	MG	D8	5002	1/1	0.91	0.17	64,64,64,64	0
56	MG	BD	302	1/1	0.92	0.09	45,45,45,45	0
56	MG	BA	3347	1/1	0.92	0.14	53,53,53,53	0
56	MG	BA	3130	1/1	0.92	0.09	40,40,40,40	0
56	MG	BA	3550	1/1	0.92	0.17	44,44,44,44	0
56	MG	BW	3002	1/1	0.92	0.13	57,57,57,57	0
56	MG	CA	3131	1/1	0.92	0.10	65,65,65,65	0
56	MG	DA	3346	1/1	0.92	0.10	33,33,33,33	0
56	MG	BY	502	1/1	0.92	0.08	35,35,35,35	0
56	MG	BY	503	1/1	0.92	0.07	42,42,42,42	0
56	MG	DA	3352	1/1	0.92	0.07	45,45,45,45	0
56	MG	CA	3136	1/1	0.92	0.08	53,53,53,53	0
56	MG	BA	3013	1/1	0.92	0.08	35,35,35,35	0
56	MG	DA	3360	1/1	0.92	0.09	39,39,39,39	0
56	MG	DA	3361	1/1	0.92	0.15	38,38,38,38	0
56	MG	BA	3141	1/1	0.92	0.10	45,45,45,45	0
56	MG	BA	3019	1/1	0.92	0.23	49,49,49,49	0
56	MG	BA	3023	1/1	0.92	0.10	40,40,40,40	0
56	MG	BA	3571	1/1	0.92	0.16	50,50,50,50	0
56	MG	AA	3154	1/1	0.92	0.19	51,51,51,51	0
56	MG	DA	3386	1/1	0.92	0.17	48,48,48,48	0
56	MG	BA	3575	1/1	0.92	0.08	55,55,55,55	0
56	MG	AA	3125	1/1	0.92	0.21	41,41,41,41	0
56	MG	AA	3179	1/1	0.92	0.21	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3004	1/1	0.92	0.18	51,51,51,51	0
56	MG	DA	3409	1/1	0.92	0.22	53,53,53,53	0
56	MG	DA	3009	1/1	0.92	0.08	42,42,42,42	0
56	MG	BA	3046	1/1	0.92	0.13	29,29,29,29	0
56	MG	DA	3418	1/1	0.92	0.10	29,29,29,29	0
56	MG	AA	3112	1/1	0.92	0.19	94,94,94,94	0
56	MG	DA	3021	1/1	0.92	0.11	55,55,55,55	0
56	MG	AA	3159	1/1	0.92	0.07	56,56,56,56	0
56	MG	BA	3074	1/1	0.92	0.11	45,45,45,45	0
56	MG	DA	3432	1/1	0.92	0.18	33,33,33,33	0
56	MG	DA	3032	1/1	0.92	0.17	42,42,42,42	0
56	MG	DA	3438	1/1	0.92	0.15	38,38,38,38	0
56	MG	DA	3050	1/1	0.92	0.10	41,41,41,41	0
56	MG	DA	3052	1/1	0.92	0.08	49,49,49,49	0
56	MG	BA	3408	1/1	0.92	0.09	56,56,56,56	0
56	MG	DA	3454	1/1	0.92	0.11	64,64,64,64	0
56	MG	DA	3465	1/1	0.92	0.13	38,38,38,38	0
56	MG	BA	3241	1/1	0.92	0.29	26,26,26,26	0
56	MG	AA	3004	1/1	0.92	0.15	67,67,67,67	0
56	MG	BA	3594	1/1	0.92	0.13	37,37,37,37	0
56	MG	DA	3075	1/1	0.92	0.13	41,41,41,41	0
56	MG	BA	3077	1/1	0.92	0.22	37,37,37,37	0
56	MG	BA	3254	1/1	0.92	0.12	45,45,45,45	0
56	MG	BA	3437	1/1	0.92	0.26	58,58,58,58	0
56	MG	BA	3602	1/1	0.92	0.10	31,31,31,31	0
56	MG	DA	3092	1/1	0.92	0.21	45,45,45,45	0
56	MG	BA	3265	1/1	0.92	0.27	47,47,47,47	0
56	MG	CA	3059	1/1	0.92	0.20	58,58,58,58	0
56	MG	CA	3062	1/1	0.92	0.13	57,57,57,57	0
56	MG	DA	3494	1/1	0.92	0.13	49,49,49,49	0
56	MG	BA	3449	1/1	0.92	0.08	47,47,47,47	0
56	MG	BA	3084	1/1	0.92	0.13	34,34,34,34	0
56	MG	DA	3113	1/1	0.92	0.12	41,41,41,41	0
56	MG	DA	3503	1/1	0.92	0.07	38,38,38,38	0
56	MG	DA	3118	1/1	0.92	0.17	49,49,49,49	0
56	MG	DA	3121	1/1	0.92	0.11	50,50,50,50	0
56	MG	DA	3125	1/1	0.92	0.10	47,47,47,47	0
56	MG	DA	3508	1/1	0.92	0.07	38,38,38,38	0
56	MG	DA	3510	1/1	0.92	0.14	53,53,53,53	0
56	MG	DA	3127	1/1	0.92	0.10	41,41,41,41	0
56	MG	AA	3079	1/1	0.92	0.33	49,49,49,49	0
56	MG	AA	3105	1/1	0.92	0.15	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3071	1/1	0.92	0.30	51,51,51,51	0
56	MG	DA	3162	1/1	0.92	0.19	57,57,57,57	0
56	MG	BA	3098	1/1	0.92	0.23	56,56,56,56	0
56	MG	AA	3124	1/1	0.92	0.13	30,30,30,30	0
56	MG	BA	3624	1/1	0.92	0.13	49,49,49,49	0
56	MG	DA	3178	1/1	0.92	0.18	46,46,46,46	0
56	MG	CA	3081	1/1	0.92	0.12	56,56,56,56	0
56	MG	BA	3001	1/1	0.92	0.15	35,35,35,35	0
56	MG	DA	3201	1/1	0.92	0.13	51,51,51,51	0
56	MG	DA	3553	1/1	0.92	0.15	46,46,46,46	0
56	MG	BA	3309	1/1	0.92	0.09	32,32,32,32	0
56	MG	BA	3316	1/1	0.92	0.09	61,61,61,61	0
56	MG	DA	3563	1/1	0.92	0.11	60,60,60,60	0
56	MG	BA	3124	1/1	0.92	0.15	58,58,58,58	0
56	MG	DA	3236	1/1	0.92	0.14	47,47,47,47	0
56	MG	DA	3239	1/1	0.92	0.15	56,56,56,56	0
56	MG	DA	3242	1/1	0.92	0.17	60,60,60,60	0
56	MG	CA	3086	1/1	0.92	0.17	68,68,68,68	0
56	MG	BA	3498	1/1	0.92	0.16	37,37,37,37	0
56	MG	BA	3324	1/1	0.92	0.10	53,53,53,53	0
56	MG	CA	3096	1/1	0.92	0.13	61,61,61,61	0
56	MG	DA	3592	1/1	0.92	0.30	52,52,52,52	0
56	MG	DA	3263	1/1	0.92	0.07	39,39,39,39	0
56	MG	DA	3269	1/1	0.92	0.14	43,43,43,43	0
56	MG	BA	3328	1/1	0.92	0.10	39,39,39,39	0
56	MG	BA	3329	1/1	0.92	0.09	30,30,30,30	0
56	MG	BA	3002	1/1	0.92	0.11	39,39,39,39	0
56	MG	CA	3107	1/1	0.92	0.23	56,56,56,56	0
56	MG	DE	3001	1/1	0.92	0.07	43,43,43,43	0
56	MG	BA	3675	1/1	0.92	0.25	33,33,33,33	0
56	MG	BA	3339	1/1	0.92	0.11	34,34,34,34	0
56	MG	BA	3515	1/1	0.92	0.10	25,25,25,25	0
56	MG	BA	3340	1/1	0.92	0.08	42,42,42,42	0
56	MG	BA	3524	1/1	0.92	0.08	57,57,57,57	0
56	MG	DA	3323	1/1	0.92	0.07	35,35,35,35	0
56	MG	D7	101	1/1	0.92	0.40	51,51,51,51	0
56	MG	BA	3345	1/1	0.92	0.15	41,41,41,41	0
56	MG	BU	205	1/1	0.93	0.11	53,53,53,53	0
56	MG	BV	201	1/1	0.93	0.25	36,36,36,36	0
56	MG	BA	3561	1/1	0.93	0.09	55,55,55,55	0
56	MG	BA	3565	1/1	0.93	0.12	51,51,51,51	0
56	MG	BA	3566	1/1	0.93	0.11	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3329	1/1	0.93	0.07	48,48,48,48	0
56	MG	BA	3398	1/1	0.93	0.12	41,41,41,41	0
56	MG	B0	104	1/1	0.93	0.21	48,48,48,48	0
56	MG	BA	3064	1/1	0.93	0.15	30,30,30,30	0
56	MG	BA	3073	1/1	0.93	0.10	14,14,14,14	0
56	MG	AA	3065	1/1	0.93	0.20	48,48,48,48	0
56	MG	AA	3107	1/1	0.93	0.22	36,36,36,36	0
56	MG	CE	202	1/1	0.93	0.10	68,68,68,68	0
56	MG	CF	3001	1/1	0.93	0.11	45,45,45,45	0
56	MG	CJ	5001	1/1	0.93	0.07	60,60,60,60	0
56	MG	CK	3001	1/1	0.93	0.14	50,50,50,50	0
56	MG	CX	101	1/1	0.93	0.18	48,48,48,48	0
56	MG	DA	3365	1/1	0.93	0.07	29,29,29,29	0
56	MG	AA	3066	1/1	0.93	0.22	46,46,46,46	0
56	MG	AE	3001	1/1	0.93	0.06	71,71,71,71	0
56	MG	BA	3261	1/1	0.93	0.15	53,53,53,53	0
56	MG	CA	3015	1/1	0.93	0.10	43,43,43,43	0
56	MG	BA	3416	1/1	0.93	0.12	64,64,64,64	0
56	MG	DA	3384	1/1	0.93	0.16	52,52,52,52	0
56	MG	BA	3088	1/1	0.93	0.09	42,42,42,42	0
56	MG	DA	3392	1/1	0.93	0.09	54,54,54,54	0
56	MG	DA	3025	1/1	0.93	0.09	41,41,41,41	0
56	MG	BA	3425	1/1	0.93	0.16	53,53,53,53	0
56	MG	AA	3039	1/1	0.93	0.07	45,45,45,45	0
56	MG	DA	3033	1/1	0.93	0.15	37,37,37,37	0
56	MG	DA	3408	1/1	0.93	0.11	28,28,28,28	0
56	MG	DA	3039	1/1	0.93	0.24	51,51,51,51	0
56	MG	DA	3044	1/1	0.93	0.05	47,47,47,47	0
56	MG	DA	3414	1/1	0.93	0.07	42,42,42,42	0
56	MG	DA	3047	1/1	0.93	0.17	41,41,41,41	0
56	MG	BA	3288	1/1	0.93	0.11	48,48,48,48	0
56	MG	CA	3028	1/1	0.93	0.07	52,52,52,52	0
56	MG	DA	3423	1/1	0.93	0.09	40,40,40,40	0
56	MG	CA	3029	1/1	0.93	0.18	48,48,48,48	0
56	MG	DA	3065	1/1	0.93	0.22	49,49,49,49	0
56	MG	CA	3032	1/1	0.93	0.12	68,68,68,68	0
56	MG	BA	3586	1/1	0.93	0.23	45,45,45,45	0
56	MG	BA	3588	1/1	0.93	0.12	51,51,51,51	0
56	MG	BA	3441	1/1	0.93	0.08	44,44,44,44	0
56	MG	DA	3441	1/1	0.93	0.21	45,45,45,45	0
56	MG	BA	3093	1/1	0.93	0.08	40,40,40,40	0
56	MG	DA	3444	1/1	0.93	0.20	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3595	1/1	0.93	0.09	47,47,47,47	0
56	MG	CA	3043	1/1	0.93	0.16	60,60,60,60	0
56	MG	DA	3450	1/1	0.93	0.10	37,37,37,37	0
56	MG	DA	3089	1/1	0.93	0.20	33,33,33,33	0
56	MG	DA	3459	1/1	0.93	0.18	38,38,38,38	0
56	MG	CA	3044	1/1	0.93	0.13	56,56,56,56	0
56	MG	DA	3091	1/1	0.93	0.12	45,45,45,45	0
56	MG	DA	3469	1/1	0.93	0.16	33,33,33,33	0
56	MG	BA	3447	1/1	0.93	0.15	55,55,55,55	0
56	MG	DA	3472	1/1	0.93	0.08	53,53,53,53	0
56	MG	DA	3096	1/1	0.93	0.06	29,29,29,29	0
56	MG	DA	3097	1/1	0.93	0.07	46,46,46,46	0
56	MG	BA	3597	1/1	0.93	0.11	43,43,43,43	0
56	MG	AK	3001	1/1	0.93	0.15	43,43,43,43	0
56	MG	BA	3298	1/1	0.93	0.07	28,28,28,28	0
56	MG	DA	3106	1/1	0.93	0.06	43,43,43,43	0
56	MG	DA	3481	1/1	0.93	0.07	41,41,41,41	0
56	MG	CA	3057	1/1	0.93	0.12	41,41,41,41	0
56	MG	AX	3002	1/1	0.93	0.12	56,56,56,56	0
56	MG	BA	3472	1/1	0.93	0.13	34,34,34,34	0
56	MG	BA	3106	1/1	0.93	0.11	40,40,40,40	0
56	MG	DA	3488	1/1	0.93	0.08	41,41,41,41	0
56	MG	AX	3007	1/1	0.93	0.18	60,60,60,60	0
56	MG	AA	3128	1/1	0.93	0.15	57,57,57,57	0
56	MG	AA	3131	1/1	0.93	0.10	55,55,55,55	0
56	MG	DA	3132	1/1	0.93	0.05	35,35,35,35	0
56	MG	BA	3615	1/1	0.93	0.10	42,42,42,42	0
56	MG	DA	3145	1/1	0.93	0.04	31,31,31,31	0
56	MG	BA	3616	1/1	0.93	0.10	34,34,34,34	0
56	MG	AA	3136	1/1	0.93	0.13	56,56,56,56	0
56	MG	DA	3155	1/1	0.93	0.24	45,45,45,45	0
56	MG	DA	3158	1/1	0.93	0.15	36,36,36,36	0
56	MG	BA	3016	1/1	0.93	0.24	50,50,50,50	0
56	MG	AA	3111	1/1	0.93	0.20	45,45,45,45	0
56	MG	AA	3170	1/1	0.93	0.12	54,54,54,54	0
56	MG	BA	3165	1/1	0.93	0.25	43,43,43,43	0
56	MG	BA	3334	1/1	0.93	0.10	32,32,32,32	0
56	MG	DA	3187	1/1	0.93	0.08	46,46,46,46	0
56	MG	DA	3534	1/1	0.93	0.12	54,54,54,54	0
56	MG	DA	3535	1/1	0.93	0.10	22,22,22,22	0
56	MG	BA	3028	1/1	0.93	0.08	41,41,41,41	0
56	MG	BA	3172	1/1	0.93	0.17	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3195	1/1	0.93	0.10	38,38,38,38	0
56	MG	BA	3191	1/1	0.93	0.11	33,33,33,33	0
56	MG	AA	3147	1/1	0.93	0.09	67,67,67,67	0
56	MG	BA	3638	1/1	0.93	0.10	32,32,32,32	0
56	MG	BA	3517	1/1	0.93	0.12	40,40,40,40	0
56	MG	DA	3223	1/1	0.93	0.17	47,47,47,47	0
56	MG	DA	3559	1/1	0.93	0.10	55,55,55,55	0
56	MG	DA	3230	1/1	0.93	0.14	41,41,41,41	0
56	MG	DA	3232	1/1	0.93	0.08	38,38,38,38	0
56	MG	BA	3199	1/1	0.93	0.12	32,32,32,32	0
56	MG	BA	3673	1/1	0.93	0.10	37,37,37,37	0
56	MG	AA	3148	1/1	0.93	0.07	56,56,56,56	0
56	MG	DA	3569	1/1	0.93	0.10	55,55,55,55	0
56	MG	DA	3245	1/1	0.93	0.19	46,46,46,46	0
56	MG	BA	3532	1/1	0.93	0.08	53,53,53,53	0
56	MG	DA	3249	1/1	0.93	0.11	34,34,34,34	0
56	MG	DA	3582	1/1	0.93	0.14	38,38,38,38	0
56	MG	CA	3110	1/1	0.93	0.13	64,64,64,64	0
56	MG	BB	3004	1/1	0.93	0.11	49,49,49,49	0
56	MG	DA	3587	1/1	0.93	0.17	53,53,53,53	0
56	MG	AA	3059	1/1	0.93	0.19	54,54,54,54	0
56	MG	DA	3593	1/1	0.93	0.13	51,51,51,51	0
56	MG	DA	3259	1/1	0.93	0.17	42,42,42,42	0
56	MG	DA	3260	1/1	0.93	0.16	36,36,36,36	0
56	MG	DA	3261	1/1	0.93	0.15	49,49,49,49	0
56	MG	BB	3006	1/1	0.93	0.09	49,49,49,49	0
56	MG	AA	3051	1/1	0.93	0.17	49,49,49,49	0
56	MG	DB	3010	1/1	0.93	0.23	60,60,60,60	0
56	MG	BA	3220	1/1	0.93	0.11	31,31,31,31	0
56	MG	AA	3020	1/1	0.93	0.07	49,49,49,49	0
56	MG	DA	3273	1/1	0.93	0.11	31,31,31,31	0
56	MG	CA	3122	1/1	0.93	0.19	54,54,54,54	0
56	MG	AA	3183	1/1	0.93	0.20	55,55,55,55	0
56	MG	BE	305	1/1	0.93	0.11	51,51,51,51	0
56	MG	DT	5001	1/1	0.93	0.08	42,42,42,42	0
56	MG	BF	303	1/1	0.93	0.11	20,20,20,20	0
56	MG	BA	3554	1/1	0.93	0.14	47,47,47,47	0
56	MG	BA	3234	1/1	0.93	0.20	57,57,57,57	0
56	MG	BA	3559	1/1	0.93	0.16	52,52,52,52	0
56	MG	CA	3109	1/1	0.94	0.13	50,50,50,50	0
56	MG	BA	3087	1/1	0.94	0.06	36,36,36,36	0
56	MG	CA	3112	1/1	0.94	0.17	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3260	1/1	0.94	0.15	49,49,49,49	0
56	MG	BA	3471	1/1	0.94	0.14	35,35,35,35	0
56	MG	DA	3281	1/1	0.94	0.08	56,56,56,56	0
56	MG	DA	3288	1/1	0.94	0.12	64,64,64,64	0
56	MG	CA	3116	1/1	0.94	0.14	59,59,59,59	0
56	MG	CA	3117	1/1	0.94	0.18	42,42,42,42	0
56	MG	AX	3006	1/1	0.94	0.10	54,54,54,54	0
56	MG	DA	3306	1/1	0.94	0.06	38,38,38,38	0
56	MG	AA	3166	1/1	0.94	0.11	53,53,53,53	0
56	MG	BA	3635	1/1	0.94	0.13	63,63,63,63	0
56	MG	DA	3310	1/1	0.94	0.07	41,41,41,41	0
56	MG	DA	3316	1/1	0.94	0.17	57,57,57,57	0
56	MG	DA	3320	1/1	0.94	0.08	46,46,46,46	0
56	MG	BA	3478	1/1	0.94	0.08	47,47,47,47	0
56	MG	BA	3266	1/1	0.94	0.15	29,29,29,29	0
56	MG	BA	3092	1/1	0.94	0.15	44,44,44,44	0
56	MG	BA	3645	1/1	0.94	0.07	66,66,66,66	0
56	MG	BA	3649	1/1	0.94	0.10	50,50,50,50	0
56	MG	BA	3652	1/1	0.94	0.17	49,49,49,49	0
56	MG	DA	3330	1/1	0.94	0.10	42,42,42,42	0
56	MG	BA	3654	1/1	0.94	0.21	64,64,64,64	0
56	MG	DA	3338	1/1	0.94	0.10	36,36,36,36	0
56	MG	BA	3667	1/1	0.94	0.34	38,38,38,38	0
56	MG	BA	3484	1/1	0.94	0.10	46,46,46,46	0
56	MG	BA	3283	1/1	0.94	0.16	57,57,57,57	0
56	MG	BA	3491	1/1	0.94	0.11	39,39,39,39	0
56	MG	BA	3493	1/1	0.94	0.09	40,40,40,40	0
56	MG	BA	3494	1/1	0.94	0.15	34,34,34,34	0
56	MG	BA	3285	1/1	0.94	0.12	48,48,48,48	0
56	MG	AA	3047	1/1	0.94	0.14	45,45,45,45	0
56	MG	AA	3074	1/1	0.94	0.17	38,38,38,38	0
56	MG	AA	3026	1/1	0.94	0.13	40,40,40,40	0
56	MG	BB	3017	1/1	0.94	0.09	40,40,40,40	0
56	MG	BA	3500	1/1	0.94	0.09	35,35,35,35	0
56	MG	BA	3101	1/1	0.94	0.07	30,30,30,30	0
56	MG	BE	306	1/1	0.94	0.07	32,32,32,32	0
56	MG	AA	3017	1/1	0.94	0.13	63,63,63,63	0
56	MG	BF	304	1/1	0.94	0.10	37,37,37,37	0
56	MG	BF	305	1/1	0.94	0.17	61,61,61,61	0
56	MG	DA	3003	1/1	0.94	0.24	47,47,47,47	0
56	MG	BG	3002	1/1	0.94	0.07	27,27,27,27	0
56	MG	DA	3393	1/1	0.94	0.06	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3396	1/1	0.94	0.07	45,45,45,45	0
56	MG	AA	3081	1/1	0.94	0.13	44,44,44,44	0
56	MG	AA	3178	1/1	0.94	0.12	62,62,62,62	0
56	MG	BA	3308	1/1	0.94	0.12	52,52,52,52	0
56	MG	BP	201	1/1	0.94	0.18	36,36,36,36	0
56	MG	BP	203	1/1	0.94	0.13	47,47,47,47	0
56	MG	BA	3116	1/1	0.94	0.07	50,50,50,50	0
56	MG	DA	3410	1/1	0.94	0.21	64,64,64,64	0
56	MG	BA	3311	1/1	0.94	0.09	39,39,39,39	0
56	MG	DA	3030	1/1	0.94	0.12	30,30,30,30	0
56	MG	BA	3117	1/1	0.94	0.22	40,40,40,40	0
56	MG	BX	102	1/1	0.94	0.09	38,38,38,38	0
56	MG	DA	3419	1/1	0.94	0.15	59,59,59,59	0
56	MG	AA	3053	1/1	0.94	0.16	50,50,50,50	0
56	MG	DA	3421	1/1	0.94	0.10	52,52,52,52	0
56	MG	BA	3527	1/1	0.94	0.09	40,40,40,40	0
56	MG	AA	3043	1/1	0.94	0.08	53,53,53,53	0
56	MG	B0	101	1/1	0.94	0.12	71,71,71,71	0
56	MG	B0	102	1/1	0.94	0.11	42,42,42,42	0
56	MG	DA	3431	1/1	0.94	0.13	61,61,61,61	0
56	MG	DA	3056	1/1	0.94	0.06	36,36,36,36	0
56	MG	DA	3434	1/1	0.94	0.15	41,41,41,41	0
56	MG	DA	3435	1/1	0.94	0.14	33,33,33,33	0
56	MG	BA	3126	1/1	0.94	0.13	45,45,45,45	0
56	MG	DA	3064	1/1	0.94	0.12	48,48,48,48	0
56	MG	BA	3543	1/1	0.94	0.12	47,47,47,47	0
56	MG	BA	3040	1/1	0.94	0.10	43,43,43,43	0
56	MG	BA	3136	1/1	0.94	0.07	44,44,44,44	0
56	MG	AA	3087	1/1	0.94	0.07	62,62,62,62	0
56	MG	DA	3071	1/1	0.94	0.08	36,36,36,36	0
56	MG	BA	3338	1/1	0.94	0.06	48,48,48,48	0
56	MG	DA	3452	1/1	0.94	0.14	56,56,56,56	0
56	MG	AA	3044	1/1	0.94	0.25	50,50,50,50	0
56	MG	DA	3458	1/1	0.94	0.15	34,34,34,34	0
56	MG	DA	3082	1/1	0.94	0.33	58,58,58,58	0
56	MG	DA	3460	1/1	0.94	0.08	50,50,50,50	0
56	MG	BA	3145	1/1	0.94	0.09	30,30,30,30	0
56	MG	DA	3466	1/1	0.94	0.07	38,38,38,38	0
56	MG	BA	3558	1/1	0.94	0.12	59,59,59,59	0
56	MG	BA	3344	1/1	0.94	0.09	35,35,35,35	0
56	MG	BA	3153	1/1	0.94	0.14	39,39,39,39	0
56	MG	BA	3164	1/1	0.94	0.08	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3348	1/1	0.94	0.07	31,31,31,31	0
56	MG	DA	3093	1/1	0.94	0.11	46,46,46,46	0
56	MG	AA	3034	1/1	0.94	0.30	54,54,54,54	0
56	MG	CA	3026	1/1	0.94	0.19	44,44,44,44	0
56	MG	BA	3048	1/1	0.94	0.13	47,47,47,47	0
56	MG	BA	3050	1/1	0.94	0.15	44,44,44,44	0
56	MG	BA	3177	1/1	0.94	0.08	44,44,44,44	0
56	MG	DA	3105	1/1	0.94	0.05	36,36,36,36	0
56	MG	BA	3183	1/1	0.94	0.16	35,35,35,35	0
56	MG	BA	3186	1/1	0.94	0.12	39,39,39,39	0
56	MG	DA	3486	1/1	0.94	0.16	37,37,37,37	0
56	MG	BA	3188	1/1	0.94	0.13	39,39,39,39	0
56	MG	BA	3393	1/1	0.94	0.09	49,49,49,49	0
56	MG	DA	3492	1/1	0.94	0.09	44,44,44,44	0
56	MG	CA	3039	1/1	0.94	0.19	50,50,50,50	0
56	MG	BA	3394	1/1	0.94	0.15	35,35,35,35	0
56	MG	AA	3069	1/1	0.94	0.15	50,50,50,50	0
56	MG	BA	3396	1/1	0.94	0.12	38,38,38,38	0
56	MG	DA	3131	1/1	0.94	0.10	46,46,46,46	0
56	MG	BA	3058	1/1	0.94	0.11	43,43,43,43	0
56	MG	BA	3400	1/1	0.94	0.18	45,45,45,45	0
56	MG	DA	3137	1/1	0.94	0.06	37,37,37,37	0
56	MG	AA	3157	1/1	0.94	0.08	55,55,55,55	0
56	MG	CA	3053	1/1	0.94	0.14	44,44,44,44	0
56	MG	DA	3514	1/1	0.94	0.07	40,40,40,40	0
56	MG	BA	3587	1/1	0.94	0.07	42,42,42,42	0
56	MG	DA	3152	1/1	0.94	0.11	34,34,34,34	0
56	MG	AD	502	1/1	0.94	0.27	55,55,55,55	0
56	MG	DA	3524	1/1	0.94	0.11	51,51,51,51	0
56	MG	DA	3525	1/1	0.94	0.06	44,44,44,44	0
56	MG	BA	3590	1/1	0.94	0.16	55,55,55,55	0
56	MG	DA	3529	1/1	0.94	0.13	41,41,41,41	0
56	MG	CA	3060	1/1	0.94	0.23	50,50,50,50	0
56	MG	BA	3210	1/1	0.94	0.24	24,24,24,24	0
56	MG	DA	3164	1/1	0.94	0.12	36,36,36,36	0
56	MG	DA	3165	1/1	0.94	0.14	34,34,34,34	0
56	MG	CA	3063	1/1	0.94	0.35	53,53,53,53	0
56	MG	DA	3171	1/1	0.94	0.13	51,51,51,51	0
56	MG	DA	3172	1/1	0.94	0.07	35,35,35,35	0
56	MG	DA	3543	1/1	0.94	0.11	63,63,63,63	0
56	MG	CA	3064	1/1	0.94	0.10	60,60,60,60	0
56	MG	BA	3066	1/1	0.94	0.12	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3548	1/1	0.94	0.16	40,40,40,40	0
56	MG	DA	3549	1/1	0.94	0.07	41,41,41,41	0
56	MG	DA	3183	1/1	0.94	0.07	37,37,37,37	0
56	MG	BA	3070	1/1	0.94	0.09	30,30,30,30	0
56	MG	DA	3554	1/1	0.94	0.07	68,68,68,68	0
56	MG	BA	3217	1/1	0.94	0.19	29,29,29,29	0
56	MG	AA	3122	1/1	0.94	0.09	58,58,58,58	0
56	MG	DA	3560	1/1	0.94	0.11	51,51,51,51	0
56	MG	BA	3599	1/1	0.94	0.06	46,46,46,46	0
56	MG	DA	3198	1/1	0.94	0.11	54,54,54,54	0
56	MG	DA	3565	1/1	0.94	0.10	51,51,51,51	0
56	MG	DA	3199	1/1	0.94	0.07	52,52,52,52	0
56	MG	AA	3096	1/1	0.94	0.15	53,53,53,53	0
56	MG	BA	3422	1/1	0.94	0.10	46,46,46,46	0
56	MG	AA	3097	1/1	0.94	0.13	49,49,49,49	0
56	MG	AA	3098	1/1	0.94	0.21	48,48,48,48	0
56	MG	DA	3576	1/1	0.94	0.10	36,36,36,36	0
56	MG	DA	3217	1/1	0.94	0.06	39,39,39,39	0
56	MG	DA	3218	1/1	0.94	0.07	33,33,33,33	0
56	MG	DA	3581	1/1	0.94	0.10	53,53,53,53	0
56	MG	BA	3426	1/1	0.94	0.07	43,43,43,43	0
56	MG	DA	3226	1/1	0.94	0.07	27,27,27,27	0
56	MG	BA	3607	1/1	0.94	0.19	51,51,51,51	0
56	MG	BA	3079	1/1	0.94	0.05	46,46,46,46	0
56	MG	DA	3233	1/1	0.94	0.21	36,36,36,36	0
56	MG	DA	3234	1/1	0.94	0.10	45,45,45,45	0
56	MG	DA	3594	1/1	0.94	0.18	48,48,48,48	0
56	MG	DB	3002	1/1	0.94	0.12	50,50,50,50	0
56	MG	DA	3235	1/1	0.94	0.14	42,42,42,42	0
56	MG	BA	3429	1/1	0.94	0.13	41,41,41,41	0
56	MG	BA	3430	1/1	0.94	0.09	29,29,29,29	0
56	MG	DA	3240	1/1	0.94	0.12	54,54,54,54	0
56	MG	CA	3089	1/1	0.94	0.12	40,40,40,40	0
56	MG	BA	3081	1/1	0.94	0.14	42,42,42,42	0
56	MG	BA	3239	1/1	0.94	0.21	52,52,52,52	0
56	MG	CA	3093	1/1	0.94	0.21	72,72,72,72	0
56	MG	DE	3002	1/1	0.94	0.10	35,35,35,35	0
56	MG	CA	3094	1/1	0.94	0.16	67,67,67,67	0
56	MG	BA	3082	1/1	0.94	0.10	47,47,47,47	0
56	MG	CA	3097	1/1	0.94	0.13	67,67,67,67	0
56	MG	DQ	3001	1/1	0.94	0.06	48,48,48,48	0
56	MG	BA	3446	1/1	0.94	0.12	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3621	1/1	0.94	0.08	30,30,30,30	0
56	MG	DV	3002	1/1	0.94	0.06	43,43,43,43	0
56	MG	AX	3003	1/1	0.94	0.19	50,50,50,50	0
56	MG	BA	3086	1/1	0.94	0.15	39,39,39,39	0
56	MG	DA	3264	1/1	0.94	0.15	47,47,47,47	0
56	MG	BA	3463	1/1	0.94	0.06	43,43,43,43	0
56	MG	BB	3014	1/1	0.95	0.08	35,35,35,35	0
56	MG	BA	3327	1/1	0.95	0.06	44,44,44,44	0
56	MG	BA	3166	1/1	0.95	0.06	35,35,35,35	0
56	MG	DA	3305	1/1	0.95	0.09	30,30,30,30	0
56	MG	AA	3134	1/1	0.95	0.22	52,52,52,52	0
56	MG	BE	303	1/1	0.95	0.15	41,41,41,41	0
56	MG	CA	3142	1/1	0.95	0.12	42,42,42,42	0
56	MG	CA	3143	1/1	0.95	0.13	42,42,42,42	0
56	MG	CA	3144	1/1	0.95	0.12	56,56,56,56	0
56	MG	BA	3330	1/1	0.95	0.16	44,44,44,44	0
56	MG	BA	3518	1/1	0.95	0.19	41,41,41,41	0
56	MG	AA	3021	1/1	0.95	0.13	41,41,41,41	0
56	MG	BA	3332	1/1	0.95	0.09	61,61,61,61	0
56	MG	BA	3526	1/1	0.95	0.13	25,25,25,25	0
56	MG	CE	201	1/1	0.95	0.14	52,52,52,52	0
56	MG	BA	3173	1/1	0.95	0.17	45,45,45,45	0
56	MG	BA	3174	1/1	0.95	0.04	29,29,29,29	0
56	MG	DA	3333	1/1	0.95	0.07	38,38,38,38	0
56	MG	BA	3533	1/1	0.95	0.08	45,45,45,45	0
56	MG	BA	3176	1/1	0.95	0.08	47,47,47,47	0
56	MG	BA	3537	1/1	0.95	0.21	58,58,58,58	0
56	MG	BA	3539	1/1	0.95	0.12	58,58,58,58	0
56	MG	BA	3540	1/1	0.95	0.13	46,46,46,46	0
56	MG	AA	3009	1/1	0.95	0.09	54,54,54,54	0
56	MG	DA	3349	1/1	0.95	0.13	46,46,46,46	0
56	MG	BV	202	1/1	0.95	0.08	36,36,36,36	0
56	MG	DA	3018	1/1	0.95	0.10	39,39,39,39	0
56	MG	DA	3353	1/1	0.95	0.06	32,32,32,32	0
56	MG	BA	3180	1/1	0.95	0.09	33,33,33,33	0
56	MG	DA	3356	1/1	0.95	0.06	31,31,31,31	0
56	MG	DA	3357	1/1	0.95	0.07	33,33,33,33	0
56	MG	BW	3004	1/1	0.95	0.13	30,30,30,30	0
56	MG	BA	3078	1/1	0.95	0.13	53,53,53,53	0
56	MG	BA	3010	1/1	0.95	0.07	33,33,33,33	0
56	MG	BA	3187	1/1	0.95	0.12	37,37,37,37	0
56	MG	BA	3012	1/1	0.95	0.09	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3368	1/1	0.95	0.05	25,25,25,25	0
56	MG	DA	3369	1/1	0.95	0.11	45,45,45,45	0
56	MG	BA	3556	1/1	0.95	0.09	41,41,41,41	0
56	MG	BA	3352	1/1	0.95	0.07	32,32,32,32	0
56	MG	BA	3356	1/1	0.95	0.10	46,46,46,46	0
56	MG	DA	3041	1/1	0.95	0.06	35,35,35,35	0
56	MG	DA	3382	1/1	0.95	0.14	50,50,50,50	0
56	MG	DA	3043	1/1	0.95	0.08	30,30,30,30	0
56	MG	B5	503	1/1	0.95	0.20	47,47,47,47	0
56	MG	CA	3001	1/1	0.95	0.08	72,72,72,72	0
56	MG	BA	3189	1/1	0.95	0.18	26,26,26,26	0
56	MG	DA	3394	1/1	0.95	0.07	41,41,41,41	0
56	MG	AA	3174	1/1	0.95	0.12	55,55,55,55	0
56	MG	BA	3563	1/1	0.95	0.14	47,47,47,47	0
56	MG	BA	3362	1/1	0.95	0.08	30,30,30,30	0
56	MG	DA	3059	1/1	0.95	0.07	33,33,33,33	0
56	MG	DA	3405	1/1	0.95	0.16	45,45,45,45	0
56	MG	DA	3062	1/1	0.95	0.19	42,42,42,42	0
56	MG	BA	3365	1/1	0.95	0.12	41,41,41,41	0
56	MG	AA	3080	1/1	0.95	0.20	39,39,39,39	0
56	MG	BA	3018	1/1	0.95	0.15	47,47,47,47	0
56	MG	BA	3374	1/1	0.95	0.07	29,29,29,29	0
56	MG	DA	3069	1/1	0.95	0.06	35,35,35,35	0
56	MG	DA	3415	1/1	0.95	0.10	40,40,40,40	0
56	MG	BA	3572	1/1	0.95	0.07	59,59,59,59	0
56	MG	DA	3417	1/1	0.95	0.10	40,40,40,40	0
56	MG	BA	3376	1/1	0.95	0.09	39,39,39,39	0
56	MG	DA	3073	1/1	0.95	0.16	51,51,51,51	0
56	MG	AA	3068	1/1	0.95	0.11	31,31,31,31	0
56	MG	BA	3384	1/1	0.95	0.07	28,28,28,28	0
56	MG	DA	3078	1/1	0.95	0.15	46,46,46,46	0
56	MG	CA	3024	1/1	0.95	0.10	64,64,64,64	0
56	MG	BA	3021	1/1	0.95	0.09	37,37,37,37	0
56	MG	BA	3390	1/1	0.95	0.10	47,47,47,47	0
56	MG	DA	3430	1/1	0.95	0.15	30,30,30,30	0
56	MG	CA	3027	1/1	0.95	0.24	64,64,64,64	0
56	MG	AA	3114	1/1	0.95	0.15	56,56,56,56	0
56	MG	BA	3581	1/1	0.95	0.05	34,34,34,34	0
56	MG	BA	3026	1/1	0.95	0.24	46,46,46,46	0
56	MG	AA	3150	1/1	0.95	0.20	51,51,51,51	0
56	MG	BA	3218	1/1	0.95	0.19	38,38,38,38	0
56	MG	AA	3116	1/1	0.95	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
56	MG	BA	3222	1/1	0.95	0.12	45,45,45,45	0
56	MG	BA	3223	1/1	0.95	0.19	51,51,51,51	0
56	MG	CA	3040	1/1	0.95	0.24	52,52,52,52	0
56	MG	BA	3224	1/1	0.95	0.12	45,45,45,45	0
56	MG	AA	3182	1/1	0.95	0.19	57,57,57,57	0
56	MG	BA	3591	1/1	0.95	0.08	36,36,36,36	0
56	MG	CA	3045	1/1	0.95	0.14	52,52,52,52	0
56	MG	DA	3456	1/1	0.95	0.08	34,34,34,34	0
56	MG	DA	3111	1/1	0.95	0.21	39,39,39,39	0
56	MG	CA	3046	1/1	0.95	0.07	41,41,41,41	0
56	MG	DA	3114	1/1	0.95	0.05	37,37,37,37	0
56	MG	CA	3047	1/1	0.95	0.21	51,51,51,51	0
56	MG	DA	3120	1/1	0.95	0.15	33,33,33,33	0
56	MG	BA	3592	1/1	0.95	0.08	52,52,52,52	0
56	MG	DA	3468	1/1	0.95	0.10	55,55,55,55	0
56	MG	DA	3123	1/1	0.95	0.07	51,51,51,51	0
56	MG	BA	3042	1/1	0.95	0.08	33,33,33,33	0
56	MG	DA	3471	1/1	0.95	0.07	50,50,50,50	0
56	MG	DA	3126	1/1	0.95	0.16	42,42,42,42	0
56	MG	BA	3232	1/1	0.95	0.06	41,41,41,41	0
56	MG	DA	3128	1/1	0.95	0.07	42,42,42,42	0
56	MG	DA	3129	1/1	0.95	0.18	54,54,54,54	0
56	MG	BA	3102	1/1	0.95	0.08	49,49,49,49	0
56	MG	AA	3083	1/1	0.95	0.12	59,59,59,59	0
56	MG	BA	3107	1/1	0.95	0.05	21,21,21,21	0
56	MG	DA	3480	1/1	0.95	0.06	32,32,32,32	0
56	MG	CA	3058	1/1	0.95	0.17	56,56,56,56	0
56	MG	DA	3141	1/1	0.95	0.05	42,42,42,42	0
56	MG	DA	3144	1/1	0.95	0.06	38,38,38,38	0
56	MG	BA	3108	1/1	0.95	0.08	38,38,38,38	0
56	MG	DA	3146	1/1	0.95	0.08	34,34,34,34	0
56	MG	BA	3110	1/1	0.95	0.11	31,31,31,31	0
56	MG	BA	3242	1/1	0.95	0.23	46,46,46,46	0
56	MG	DA	3491	1/1	0.95	0.06	40,40,40,40	0
56	MG	DA	3151	1/1	0.95	0.07	34,34,34,34	0
56	MG	AA	3120	1/1	0.95	0.08	47,47,47,47	0
56	MG	AA	3100	1/1	0.95	0.14	35,35,35,35	0
56	MG	DA	3156	1/1	0.95	0.07	38,38,38,38	0
56	MG	BA	3047	1/1	0.95	0.18	41,41,41,41	0
56	MG	BA	3256	1/1	0.95	0.24	41,41,41,41	0
56	MG	BA	3435	1/1	0.95	0.11	36,36,36,36	0
56	MG	AA	3001	1/1	0.95	0.11	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3069	1/1	0.95	0.10	34,34,34,34	0
56	MG	AA	3123	1/1	0.95	0.15	38,38,38,38	0
56	MG	DA	3509	1/1	0.95	0.06	36,36,36,36	0
56	MG	DA	3170	1/1	0.95	0.19	38,38,38,38	0
56	MG	DA	3512	1/1	0.95	0.10	36,36,36,36	0
56	MG	BA	3051	1/1	0.95	0.14	41,41,41,41	0
56	MG	CA	3073	1/1	0.95	0.18	57,57,57,57	0
56	MG	CA	3074	1/1	0.95	0.26	48,48,48,48	0
56	MG	DA	3517	1/1	0.95	0.18	47,47,47,47	0
56	MG	CA	3076	1/1	0.95	0.22	48,48,48,48	0
56	MG	DA	3520	1/1	0.95	0.08	34,34,34,34	0
56	MG	DA	3179	1/1	0.95	0.14	20,20,20,20	0
56	MG	AA	3071	1/1	0.95	0.04	36,36,36,36	0
56	MG	DA	3185	1/1	0.95	0.06	32,32,32,32	0
56	MG	BA	3268	1/1	0.95	0.30	39,39,39,39	0
56	MG	CA	3079	1/1	0.95	0.30	55,55,55,55	0
56	MG	BA	3448	1/1	0.95	0.09	42,42,42,42	0
56	MG	DA	3533	1/1	0.95	0.07	60,60,60,60	0
56	MG	DA	3193	1/1	0.95	0.17	49,49,49,49	0
56	MG	DA	3194	1/1	0.95	0.10	47,47,47,47	0
56	MG	BA	3620	1/1	0.95	0.12	41,41,41,41	0
56	MG	DA	3197	1/1	0.95	0.13	38,38,38,38	0
56	MG	DA	3540	1/1	0.95	0.15	46,46,46,46	0
56	MG	AE	3002	1/1	0.95	0.10	38,38,38,38	0
56	MG	BA	3623	1/1	0.95	0.06	48,48,48,48	0
56	MG	BA	3061	1/1	0.95	0.20	44,44,44,44	0
56	MG	DA	3204	1/1	0.95	0.06	37,37,37,37	0
56	MG	BA	3137	1/1	0.95	0.12	30,30,30,30	0
56	MG	DA	3207	1/1	0.95	0.14	39,39,39,39	0
56	MG	DA	3551	1/1	0.95	0.08	52,52,52,52	0
56	MG	BA	3286	1/1	0.95	0.10	32,32,32,32	0
56	MG	DA	3212	1/1	0.95	0.17	39,39,39,39	0
56	MG	BA	3287	1/1	0.95	0.09	46,46,46,46	0
56	MG	AA	3048	1/1	0.95	0.22	42,42,42,42	0
56	MG	CA	3092	1/1	0.95	0.15	54,54,54,54	0
56	MG	DA	3222	1/1	0.95	0.06	36,36,36,36	0
56	MG	BA	3474	1/1	0.95	0.12	53,53,53,53	0
56	MG	DA	3225	1/1	0.95	0.06	33,33,33,33	0
56	MG	AA	3014	1/1	0.95	0.16	49,49,49,49	0
56	MG	BA	3296	1/1	0.95	0.06	25,25,25,25	0
56	MG	AA	3165	1/1	0.95	0.07	43,43,43,43	0
56	MG	CA	3099	1/1	0.95	0.20	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3101	1/1	0.95	0.14	53,53,53,53	0
56	MG	DA	3571	1/1	0.95	0.14	48,48,48,48	0
56	MG	BA	3146	1/1	0.95	0.08	31,31,31,31	0
56	MG	BA	3149	1/1	0.95	0.10	50,50,50,50	0
56	MG	DA	3577	1/1	0.95	0.12	35,35,35,35	0
56	MG	DA	3237	1/1	0.95	0.09	39,39,39,39	0
56	MG	DA	3238	1/1	0.95	0.11	42,42,42,42	0
56	MG	BA	3641	1/1	0.95	0.15	33,33,33,33	0
56	MG	BA	3486	1/1	0.95	0.14	21,21,21,21	0
56	MG	BA	3643	1/1	0.95	0.07	42,42,42,42	0
56	MG	DA	3243	1/1	0.95	0.06	50,50,50,50	0
56	MG	DA	3244	1/1	0.95	0.07	48,48,48,48	0
56	MG	BA	3644	1/1	0.95	0.07	41,41,41,41	0
56	MG	BA	3301	1/1	0.95	0.09	46,46,46,46	0
56	MG	BA	3646	1/1	0.95	0.10	23,23,23,23	0
56	MG	DB	3001	1/1	0.95	0.13	40,40,40,40	0
56	MG	BA	3150	1/1	0.95	0.11	32,32,32,32	0
56	MG	BA	3151	1/1	0.95	0.05	34,34,34,34	0
56	MG	DA	3256	1/1	0.95	0.06	45,45,45,45	0
56	MG	BA	3069	1/1	0.95	0.06	47,47,47,47	0
56	MG	BA	3662	1/1	0.95	0.11	36,36,36,36	0
56	MG	BA	3154	1/1	0.95	0.17	40,40,40,40	0
56	MG	BA	3671	1/1	0.95	0.12	48,48,48,48	0
56	MG	BA	3156	1/1	0.95	0.12	48,48,48,48	0
56	MG	BA	3314	1/1	0.95	0.12	36,36,36,36	0
56	MG	BA	3162	1/1	0.95	0.13	39,39,39,39	0
56	MG	DE	3003	1/1	0.95	0.11	40,40,40,40	0
56	MG	DF	301	1/1	0.95	0.20	44,44,44,44	0
56	MG	BA	3318	1/1	0.95	0.07	44,44,44,44	0
56	MG	AA	3108	1/1	0.95	0.19	54,54,54,54	0
56	MG	AA	3089	1/1	0.95	0.11	36,36,36,36	0
56	MG	DP	3001	1/1	0.95	0.11	44,44,44,44	0
56	MG	BB	3007	1/1	0.95	0.09	35,35,35,35	0
56	MG	BA	3325	1/1	0.95	0.09	42,42,42,42	0
56	MG	DA	3277	1/1	0.95	0.09	48,48,48,48	0
56	MG	BA	3509	1/1	0.95	0.12	23,23,23,23	0
56	MG	DA	3286	1/1	0.95	0.07	35,35,35,35	0
56	MG	DA	3287	1/1	0.95	0.12	38,38,38,38	0
56	MG	BB	3013	1/1	0.95	0.15	57,57,57,57	0
56	MG	D8	5001	1/1	0.95	0.14	50,50,50,50	0
56	MG	DA	3292	1/1	0.95	0.12	45,45,45,45	0
56	MG	DA	3255	1/1	0.96	0.22	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3637	1/1	0.96	0.13	24,24,24,24	0
56	MG	AA	3104	1/1	0.96	0.09	56,56,56,56	0
56	MG	CA	3115	1/1	0.96	0.06	62,62,62,62	0
56	MG	BA	3267	1/1	0.96	0.07	40,40,40,40	0
56	MG	BA	3142	1/1	0.96	0.05	40,40,40,40	0
56	MG	BA	3450	1/1	0.96	0.06	45,45,45,45	0
56	MG	BA	3451	1/1	0.96	0.06	48,48,48,48	0
56	MG	DA	3265	1/1	0.96	0.26	51,51,51,51	0
56	MG	DA	3266	1/1	0.96	0.07	46,46,46,46	0
56	MG	DA	3268	1/1	0.96	0.08	38,38,38,38	0
56	MG	BA	3458	1/1	0.96	0.07	60,60,60,60	0
56	MG	BA	3459	1/1	0.96	0.13	42,42,42,42	0
56	MG	BA	3460	1/1	0.96	0.06	57,57,57,57	0
56	MG	BA	3270	1/1	0.96	0.12	21,21,21,21	0
56	MG	BA	3271	1/1	0.96	0.12	49,49,49,49	0
56	MG	BA	3653	1/1	0.96	0.08	33,33,33,33	0
56	MG	BA	3277	1/1	0.96	0.12	32,32,32,32	0
56	MG	DA	3278	1/1	0.96	0.10	50,50,50,50	0
56	MG	CA	3130	1/1	0.96	0.15	57,57,57,57	0
56	MG	DA	3282	1/1	0.96	0.05	30,30,30,30	0
56	MG	DA	3285	1/1	0.96	0.12	52,52,52,52	0
56	MG	BA	3655	1/1	0.96	0.09	18,18,18,18	0
56	MG	BA	3659	1/1	0.96	0.10	28,28,28,28	0
56	MG	BA	3660	1/1	0.96	0.09	49,49,49,49	0
56	MG	DA	3291	1/1	0.96	0.07	38,38,38,38	0
56	MG	CA	3134	1/1	0.96	0.12	53,53,53,53	0
56	MG	DA	3295	1/1	0.96	0.07	61,61,61,61	0
56	MG	DA	3298	1/1	0.96	0.05	32,32,32,32	0
56	MG	CA	3135	1/1	0.96	0.23	62,62,62,62	0
56	MG	BA	3470	1/1	0.96	0.09	48,48,48,48	0
56	MG	BA	3057	1/1	0.96	0.06	38,38,38,38	0
56	MG	BA	3668	1/1	0.96	0.13	26,26,26,26	0
56	MG	BA	3280	1/1	0.96	0.12	48,48,48,48	0
56	MG	BA	3473	1/1	0.96	0.10	37,37,37,37	0
56	MG	DA	3308	1/1	0.96	0.08	29,29,29,29	0
56	MG	AA	3031	1/1	0.96	0.07	60,60,60,60	0
56	MG	BA	3284	1/1	0.96	0.12	41,41,41,41	0
56	MG	BA	3147	1/1	0.96	0.10	35,35,35,35	0
56	MG	BA	3148	1/1	0.96	0.06	25,25,25,25	0
56	MG	DA	3321	1/1	0.96	0.08	45,45,45,45	0
56	MG	DA	3322	1/1	0.96	0.07	23,23,23,23	0
56	MG	AL	201	1/1	0.96	0.05	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AM	3001	1/1	0.96	0.07	54,54,54,54	0
56	MG	BB	3008	1/1	0.96	0.10	21,21,21,21	0
56	MG	BA	3485	1/1	0.96	0.14	64,64,64,64	0
56	MG	CA	3153	1/1	0.96	0.11	37,37,37,37	0
56	MG	CA	3154	1/1	0.96	0.18	62,62,62,62	0
56	MG	BA	3292	1/1	0.96	0.11	43,43,43,43	0
56	MG	DA	3331	1/1	0.96	0.06	41,41,41,41	0
56	MG	DA	3332	1/1	0.96	0.06	43,43,43,43	0
56	MG	AA	3033	1/1	0.96	0.25	48,48,48,48	0
56	MG	BA	3295	1/1	0.96	0.08	61,61,61,61	0
56	MG	BA	3492	1/1	0.96	0.09	42,42,42,42	0
56	MG	BB	3016	1/1	0.96	0.05	24,24,24,24	0
56	MG	CT	3001	1/1	0.96	0.12	50,50,50,50	0
56	MG	DA	3344	1/1	0.96	0.14	31,31,31,31	0
56	MG	BA	3152	1/1	0.96	0.06	39,39,39,39	0
56	MG	AA	3072	1/1	0.96	0.13	39,39,39,39	0
56	MG	BD	304	1/1	0.96	0.20	28,28,28,28	0
56	MG	AX	3005	1/1	0.96	0.25	42,42,42,42	0
56	MG	DA	3011	1/1	0.96	0.08	38,38,38,38	0
56	MG	DA	3015	1/1	0.96	0.09	41,41,41,41	0
56	MG	AA	3005	1/1	0.96	0.07	37,37,37,37	0
56	MG	BA	3157	1/1	0.96	0.13	34,34,34,34	0
56	MG	BF	301	1/1	0.96	0.10	56,56,56,56	0
56	MG	BA	3158	1/1	0.96	0.12	33,33,33,33	0
56	MG	AA	3129	1/1	0.96	0.06	35,35,35,35	0
56	MG	DA	3023	1/1	0.96	0.06	37,37,37,37	0
56	MG	DA	3024	1/1	0.96	0.12	36,36,36,36	0
56	MG	BA	3163	1/1	0.96	0.07	31,31,31,31	0
56	MG	DA	3367	1/1	0.96	0.10	47,47,47,47	0
56	MG	DA	3026	1/1	0.96	0.12	34,34,34,34	0
56	MG	DA	3027	1/1	0.96	0.07	30,30,30,30	0
56	MG	DA	3370	1/1	0.96	0.13	44,44,44,44	0
56	MG	BA	3504	1/1	0.96	0.10	39,39,39,39	0
56	MG	DA	3029	1/1	0.96	0.10	40,40,40,40	0
56	MG	AA	3130	1/1	0.96	0.10	50,50,50,50	0
56	MG	DA	3377	1/1	0.96	0.11	37,37,37,37	0
56	MG	AA	3091	1/1	0.96	0.06	36,36,36,36	0
56	MG	BA	3076	1/1	0.96	0.04	29,29,29,29	0
56	MG	DA	3034	1/1	0.96	0.21	46,46,46,46	0
56	MG	DA	3038	1/1	0.96	0.05	30,30,30,30	0
56	MG	BA	3169	1/1	0.96	0.09	39,39,39,39	0
56	MG	BA	3512	1/1	0.96	0.10	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BQ	201	1/1	0.96	0.14	52,52,52,52	0
56	MG	BQ	203	1/1	0.96	0.19	33,33,33,33	0
56	MG	DA	3045	1/1	0.96	0.17	48,48,48,48	0
56	MG	BU	202	1/1	0.96	0.07	40,40,40,40	0
56	MG	BU	203	1/1	0.96	0.15	32,32,32,32	0
56	MG	DA	3404	1/1	0.96	0.05	46,46,46,46	0
56	MG	DA	3051	1/1	0.96	0.07	50,50,50,50	0
56	MG	BA	3317	1/1	0.96	0.08	35,35,35,35	0
56	MG	DA	3054	1/1	0.96	0.21	45,45,45,45	0
56	MG	DA	3055	1/1	0.96	0.07	34,34,34,34	0
56	MG	BA	3514	1/1	0.96	0.10	32,32,32,32	0
56	MG	BA	3003	1/1	0.96	0.05	49,49,49,49	0
56	MG	BA	3516	1/1	0.96	0.08	43,43,43,43	0
56	MG	DA	3060	1/1	0.96	0.06	45,45,45,45	0
56	MG	BA	3319	1/1	0.96	0.12	39,39,39,39	0
56	MG	DA	3063	1/1	0.96	0.05	31,31,31,31	0
56	MG	BX	101	1/1	0.96	0.10	46,46,46,46	0
56	MG	BA	3005	1/1	0.96	0.06	29,29,29,29	0
56	MG	BA	3521	1/1	0.96	0.07	54,54,54,54	0
56	MG	BA	3009	1/1	0.96	0.06	34,34,34,34	0
56	MG	BA	3080	1/1	0.96	0.09	29,29,29,29	0
56	MG	BA	3525	1/1	0.96	0.07	46,46,46,46	0
56	MG	AA	3132	1/1	0.96	0.11	50,50,50,50	0
56	MG	DA	3072	1/1	0.96	0.08	33,33,33,33	0
56	MG	DA	3429	1/1	0.96	0.08	35,35,35,35	0
56	MG	AA	3133	1/1	0.96	0.06	38,38,38,38	0
56	MG	B0	105	1/1	0.96	0.08	43,43,43,43	0
56	MG	B4	502	1/1	0.96	0.05	61,61,61,61	0
56	MG	DA	3077	1/1	0.96	0.07	34,34,34,34	0
56	MG	B5	502	1/1	0.96	0.11	34,34,34,34	0
56	MG	DA	3436	1/1	0.96	0.06	27,27,27,27	0
56	MG	AA	3060	1/1	0.96	0.14	55,55,55,55	0
56	MG	BA	3182	1/1	0.96	0.13	30,30,30,30	0
56	MG	DA	3439	1/1	0.96	0.09	28,28,28,28	0
56	MG	DA	3440	1/1	0.96	0.12	52,52,52,52	0
56	MG	DA	3087	1/1	0.96	0.15	35,35,35,35	0
56	MG	AA	3135	1/1	0.96	0.07	46,46,46,46	0
56	MG	BA	3184	1/1	0.96	0.05	37,37,37,37	0
56	MG	CA	3005	1/1	0.96	0.08	42,42,42,42	0
56	MG	BA	3185	1/1	0.96	0.08	43,43,43,43	0
56	MG	DA	3447	1/1	0.96	0.07	33,33,33,33	0
56	MG	DA	3449	1/1	0.96	0.09	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3335	1/1	0.96	0.10	40,40,40,40	0
56	MG	BA	3017	1/1	0.96	0.11	40,40,40,40	0
56	MG	DA	3094	1/1	0.96	0.09	35,35,35,35	0
56	MG	DA	3095	1/1	0.96	0.09	47,47,47,47	0
56	MG	DA	3457	1/1	0.96	0.10	38,38,38,38	0
56	MG	AA	3052	1/1	0.96	0.21	60,60,60,60	0
56	MG	AA	3175	1/1	0.96	0.19	53,53,53,53	0
56	MG	BA	3343	1/1	0.96	0.12	27,27,27,27	0
56	MG	DA	3099	1/1	0.96	0.12	37,37,37,37	0
56	MG	AA	3137	1/1	0.96	0.07	79,79,79,79	0
56	MG	DA	3101	1/1	0.96	0.08	46,46,46,46	0
56	MG	DA	3102	1/1	0.96	0.20	51,51,51,51	0
56	MG	CA	3017	1/1	0.96	0.09	41,41,41,41	0
56	MG	BA	3190	1/1	0.96	0.24	31,31,31,31	0
56	MG	BA	3555	1/1	0.96	0.08	42,42,42,42	0
56	MG	BA	3346	1/1	0.96	0.09	43,43,43,43	0
56	MG	CA	3022	1/1	0.96	0.12	34,34,34,34	0
56	MG	AA	3177	1/1	0.96	0.15	32,32,32,32	0
56	MG	DA	3112	1/1	0.96	0.08	24,24,24,24	0
56	MG	AA	3138	1/1	0.96	0.08	50,50,50,50	0
56	MG	BA	3349	1/1	0.96	0.10	46,46,46,46	0
56	MG	DA	3115	1/1	0.96	0.08	36,36,36,36	0
56	MG	DA	3117	1/1	0.96	0.16	43,43,43,43	0
56	MG	BA	3560	1/1	0.96	0.13	55,55,55,55	0
56	MG	BA	3195	1/1	0.96	0.14	47,47,47,47	0
56	MG	BA	3562	1/1	0.96	0.05	46,46,46,46	0
56	MG	DA	3122	1/1	0.96	0.14	45,45,45,45	0
56	MG	BA	3095	1/1	0.96	0.04	33,33,33,33	0
56	MG	BA	3564	1/1	0.96	0.10	29,29,29,29	0
56	MG	BA	3202	1/1	0.96	0.06	30,30,30,30	0
56	MG	BA	3205	1/1	0.96	0.14	40,40,40,40	0
56	MG	BA	3358	1/1	0.96	0.10	39,39,39,39	0
56	MG	DA	3493	1/1	0.96	0.12	45,45,45,45	0
56	MG	CA	3038	1/1	0.96	0.14	44,44,44,44	0
56	MG	DA	3495	1/1	0.96	0.12	45,45,45,45	0
56	MG	BA	3096	1/1	0.96	0.15	44,44,44,44	0
56	MG	DA	3498	1/1	0.96	0.07	48,48,48,48	0
56	MG	DA	3499	1/1	0.96	0.07	45,45,45,45	0
56	MG	BA	3361	1/1	0.96	0.09	45,45,45,45	0
56	MG	BA	3027	1/1	0.96	0.07	28,28,28,28	0
56	MG	DA	3136	1/1	0.96	0.13	36,36,36,36	0
56	MG	CA	3042	1/1	0.96	0.16	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3505	1/1	0.96	0.05	44,44,44,44	0
56	MG	DA	3139	1/1	0.96	0.20	39,39,39,39	0
56	MG	BA	3573	1/1	0.96	0.14	44,44,44,44	0
56	MG	AA	3141	1/1	0.96	0.09	47,47,47,47	0
56	MG	BA	3031	1/1	0.96	0.24	46,46,46,46	0
56	MG	BA	3105	1/1	0.96	0.07	32,32,32,32	0
56	MG	BA	3577	1/1	0.96	0.13	57,57,57,57	0
56	MG	BA	3034	1/1	0.96	0.16	24,24,24,24	0
56	MG	BA	3375	1/1	0.96	0.21	51,51,51,51	0
56	MG	BA	3219	1/1	0.96	0.05	20,20,20,20	0
56	MG	AA	3094	1/1	0.96	0.19	49,49,49,49	0
56	MG	CA	3054	1/1	0.96	0.13	44,44,44,44	0
56	MG	BA	3383	1/1	0.96	0.06	33,33,33,33	0
56	MG	DA	3521	1/1	0.96	0.22	51,51,51,51	0
56	MG	DA	3523	1/1	0.96	0.08	40,40,40,40	0
56	MG	DA	3159	1/1	0.96	0.12	31,31,31,31	0
56	MG	DA	3161	1/1	0.96	0.07	24,24,24,24	0
56	MG	CA	3056	1/1	0.96	0.19	40,40,40,40	0
56	MG	DA	3527	1/1	0.96	0.13	43,43,43,43	0
56	MG	BA	3221	1/1	0.96	0.18	41,41,41,41	0
56	MG	AA	3144	1/1	0.96	0.15	42,42,42,42	0
56	MG	BA	3388	1/1	0.96	0.04	54,54,54,54	0
56	MG	BA	3389	1/1	0.96	0.17	35,35,35,35	0
56	MG	DA	3167	1/1	0.96	0.06	51,51,51,51	0
56	MG	BA	3041	1/1	0.96	0.10	42,42,42,42	0
56	MG	DA	3536	1/1	0.96	0.06	56,56,56,56	0
56	MG	DA	3537	1/1	0.96	0.12	47,47,47,47	0
56	MG	BA	3392	1/1	0.96	0.10	41,41,41,41	0
56	MG	AA	3146	1/1	0.96	0.11	41,41,41,41	0
56	MG	BA	3226	1/1	0.96	0.25	32,32,32,32	0
56	MG	DA	3174	1/1	0.96	0.09	44,44,44,44	0
56	MG	DA	3175	1/1	0.96	0.08	47,47,47,47	0
56	MG	AA	3025	1/1	0.96	0.11	37,37,37,37	0
56	MG	AA	3036	1/1	0.96	0.12	41,41,41,41	0
56	MG	BA	3231	1/1	0.96	0.18	41,41,41,41	0
56	MG	BA	3045	1/1	0.96	0.11	34,34,34,34	0
56	MG	DA	3550	1/1	0.96	0.10	46,46,46,46	0
56	MG	DA	3186	1/1	0.96	0.06	41,41,41,41	0
56	MG	CA	3070	1/1	0.96	0.08	39,39,39,39	0
56	MG	DA	3189	1/1	0.96	0.20	31,31,31,31	0
56	MG	DA	3190	1/1	0.96	0.10	34,34,34,34	0
56	MG	DA	3555	1/1	0.96	0.10	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3556	1/1	0.96	0.12	36,36,36,36	0
56	MG	BA	3120	1/1	0.96	0.08	44,44,44,44	0
56	MG	BA	3402	1/1	0.96	0.14	28,28,28,28	0
56	MG	BA	3598	1/1	0.96	0.12	48,48,48,48	0
56	MG	BA	3121	1/1	0.96	0.25	43,43,43,43	0
56	MG	CA	3075	1/1	0.96	0.15	53,53,53,53	0
56	MG	BA	3236	1/1	0.96	0.07	42,42,42,42	0
56	MG	AA	3037	1/1	0.96	0.06	51,51,51,51	0
56	MG	BA	3406	1/1	0.96	0.14	39,39,39,39	0
56	MG	BA	3603	1/1	0.96	0.07	49,49,49,49	0
56	MG	DA	3203	1/1	0.96	0.09	21,21,21,21	0
56	MG	DA	3570	1/1	0.96	0.06	52,52,52,52	0
56	MG	CA	3080	1/1	0.96	0.09	41,41,41,41	0
56	MG	DA	3572	1/1	0.96	0.10	51,51,51,51	0
56	MG	DA	3573	1/1	0.96	0.16	45,45,45,45	0
56	MG	BA	3407	1/1	0.96	0.10	43,43,43,43	0
56	MG	DA	3575	1/1	0.96	0.16	49,49,49,49	0
56	MG	BA	3238	1/1	0.96	0.21	47,47,47,47	0
56	MG	DA	3208	1/1	0.96	0.11	43,43,43,43	0
56	MG	DA	3210	1/1	0.96	0.06	37,37,37,37	0
56	MG	DA	3579	1/1	0.96	0.11	54,54,54,54	0
56	MG	BA	3410	1/1	0.96	0.09	43,43,43,43	0
56	MG	AA	3067	1/1	0.96	0.30	42,42,42,42	0
56	MG	BA	3240	1/1	0.96	0.18	43,43,43,43	0
56	MG	DA	3583	1/1	0.96	0.05	43,43,43,43	0
56	MG	DA	3214	1/1	0.96	0.14	30,30,30,30	0
56	MG	DA	3215	1/1	0.96	0.07	31,31,31,31	0
56	MG	AA	3101	1/1	0.96	0.29	53,53,53,53	0
56	MG	DA	3590	1/1	0.96	0.18	38,38,38,38	0
56	MG	CA	3087	1/1	0.96	0.06	33,33,33,33	0
56	MG	DA	3219	1/1	0.96	0.11	33,33,33,33	0
56	MG	DA	3220	1/1	0.96	0.08	43,43,43,43	0
56	MG	DA	3221	1/1	0.96	0.06	33,33,33,33	0
56	MG	CA	3088	1/1	0.96	0.14	41,41,41,41	0
56	MG	DB	3003	1/1	0.96	0.06	29,29,29,29	0
56	MG	BA	3127	1/1	0.96	0.06	45,45,45,45	0
56	MG	BA	3128	1/1	0.96	0.17	29,29,29,29	0
56	MG	BA	3245	1/1	0.96	0.12	27,27,27,27	0
56	MG	BA	3618	1/1	0.96	0.20	54,54,54,54	0
56	MG	BA	3129	1/1	0.96	0.10	42,42,42,42	0
56	MG	BA	3427	1/1	0.96	0.10	49,49,49,49	0
56	MG	BA	3252	1/1	0.96	0.10	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DD	301	1/1	0.96	0.11	43,43,43,43	0
56	MG	AA	3028	1/1	0.96	0.12	39,39,39,39	0
56	MG	CA	3098	1/1	0.96	0.14	42,42,42,42	0
56	MG	BA	3255	1/1	0.96	0.23	32,32,32,32	0
56	MG	CA	3100	1/1	0.96	0.15	56,56,56,56	0
56	MG	BA	3434	1/1	0.96	0.08	43,43,43,43	0
56	MG	CA	3102	1/1	0.96	0.16	30,30,30,30	0
56	MG	DA	3241	1/1	0.96	0.16	36,36,36,36	0
56	MG	BA	3135	1/1	0.96	0.10	36,36,36,36	0
56	MG	AA	3103	1/1	0.96	0.10	51,51,51,51	0
56	MG	BA	3630	1/1	0.96	0.08	47,47,47,47	0
56	MG	DR	202	1/1	0.96	0.06	32,32,32,32	0
56	MG	BA	3439	1/1	0.96	0.13	30,30,30,30	0
56	MG	DU	201	1/1	0.96	0.12	41,41,41,41	0
56	MG	DV	3001	1/1	0.96	0.13	45,45,45,45	0
56	MG	BA	3052	1/1	0.96	0.05	27,27,27,27	0
56	MG	BA	3263	1/1	0.96	0.22	64,64,64,64	0
56	MG	BA	3444	1/1	0.96	0.08	34,34,34,34	0
56	MG	D0	5001	1/1	0.96	0.06	39,39,39,39	0
56	MG	D3	3001	1/1	0.96	0.19	70,70,70,70	0
56	MG	BA	3053	1/1	0.96	0.10	31,31,31,31	0
56	MG	DA	3253	1/1	0.96	0.05	26,26,26,26	0
56	MG	DA	3254	1/1	0.96	0.11	46,46,46,46	0
59	K	AX	3001	1/1	0.96	0.06	48,48,48,48	0
59	K	DA	3001	1/1	0.96	0.05	48,48,48,48	0
56	MG	DA	3363	1/1	0.97	0.04	36,36,36,36	0
56	MG	DA	3364	1/1	0.97	0.07	37,37,37,37	0
56	MG	BB	3018	1/1	0.97	0.05	30,30,30,30	0
56	MG	BA	3322	1/1	0.97	0.10	40,40,40,40	0
56	MG	DA	3119	1/1	0.97	0.16	37,37,37,37	0
56	MG	BD	303	1/1	0.97	0.21	37,37,37,37	0
56	MG	BA	3118	1/1	0.97	0.09	45,45,45,45	0
56	MG	BD	305	1/1	0.97	0.09	38,38,38,38	0
56	MG	BD	307	1/1	0.97	0.05	27,27,27,27	0
56	MG	BD	308	1/1	0.97	0.07	35,35,35,35	0
56	MG	DA	3374	1/1	0.97	0.07	35,35,35,35	0
56	MG	BE	301	1/1	0.97	0.11	45,45,45,45	0
56	MG	DA	3376	1/1	0.97	0.06	38,38,38,38	0
56	MG	BE	302	1/1	0.97	0.28	36,36,36,36	0
56	MG	BA	3233	1/1	0.97	0.17	41,41,41,41	0
56	MG	BA	3431	1/1	0.97	0.06	44,44,44,44	0
56	MG	DA	3130	1/1	0.97	0.24	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3432	1/1	0.97	0.06	37,37,37,37	0
56	MG	DA	3387	1/1	0.97	0.05	53,53,53,53	0
56	MG	BA	3167	1/1	0.97	0.08	46,46,46,46	0
56	MG	DA	3133	1/1	0.97	0.06	53,53,53,53	0
56	MG	DA	3134	1/1	0.97	0.19	33,33,33,33	0
56	MG	DA	3395	1/1	0.97	0.04	41,41,41,41	0
56	MG	BA	3568	1/1	0.97	0.07	42,42,42,42	0
56	MG	DA	3397	1/1	0.97	0.05	18,18,18,18	0
56	MG	BA	3168	1/1	0.97	0.09	47,47,47,47	0
56	MG	BA	3570	1/1	0.97	0.07	36,36,36,36	0
56	MG	DA	3138	1/1	0.97	0.11	33,33,33,33	0
56	MG	BG	3001	1/1	0.97	0.10	71,71,71,71	0
56	MG	AA	3077	1/1	0.97	0.08	39,39,39,39	0
56	MG	BA	3170	1/1	0.97	0.12	34,34,34,34	0
56	MG	DA	3407	1/1	0.97	0.06	40,40,40,40	0
56	MG	AA	3099	1/1	0.97	0.17	33,33,33,33	0
56	MG	BN	3001	1/1	0.97	0.06	57,57,57,57	0
56	MG	BA	3123	1/1	0.97	0.06	36,36,36,36	0
56	MG	DA	3411	1/1	0.97	0.04	36,36,36,36	0
56	MG	DA	3149	1/1	0.97	0.14	41,41,41,41	0
56	MG	BA	3011	1/1	0.97	0.03	30,30,30,30	0
56	MG	BP	202	1/1	0.97	0.32	31,31,31,31	0
56	MG	BA	3333	1/1	0.97	0.09	35,35,35,35	0
56	MG	DA	3153	1/1	0.97	0.09	42,42,42,42	0
56	MG	AA	3152	1/1	0.97	0.11	57,57,57,57	0
56	MG	AA	3172	1/1	0.97	0.10	69,69,69,69	0
56	MG	BR	3003	1/1	0.97	0.11	39,39,39,39	0
56	MG	BA	3337	1/1	0.97	0.05	37,37,37,37	0
56	MG	DA	3422	1/1	0.97	0.05	63,63,63,63	0
56	MG	DA	3160	1/1	0.97	0.13	44,44,44,44	0
56	MG	BA	3243	1/1	0.97	0.09	45,45,45,45	0
56	MG	CA	3124	1/1	0.97	0.13	52,52,52,52	0
56	MG	BA	3014	1/1	0.97	0.14	35,35,35,35	0
56	MG	BA	3179	1/1	0.97	0.04	27,27,27,27	0
56	MG	CA	3127	1/1	0.97	0.13	49,49,49,49	0
56	MG	BA	3342	1/1	0.97	0.05	35,35,35,35	0
56	MG	AA	3078	1/1	0.97	0.08	34,34,34,34	0
56	MG	BA	3461	1/1	0.97	0.16	52,52,52,52	0
56	MG	BA	3249	1/1	0.97	0.07	48,48,48,48	0
56	MG	BA	3464	1/1	0.97	0.06	41,41,41,41	0
56	MG	BX	103	1/1	0.97	0.08	25,25,25,25	0
56	MG	BA	3251	1/1	0.97	0.08	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3467	1/1	0.97	0.10	20,20,20,20	0
56	MG	DA	3176	1/1	0.97	0.12	29,29,29,29	0
56	MG	BA	3468	1/1	0.97	0.06	32,32,32,32	0
56	MG	DA	3442	1/1	0.97	0.18	42,42,42,42	0
56	MG	BA	3181	1/1	0.97	0.04	37,37,37,37	0
56	MG	BA	3253	1/1	0.97	0.18	47,47,47,47	0
56	MG	DA	3184	1/1	0.97	0.13	30,30,30,30	0
56	MG	AA	3063	1/1	0.97	0.19	39,39,39,39	0
56	MG	CA	3141	1/1	0.97	0.11	54,54,54,54	0
56	MG	AA	3155	1/1	0.97	0.10	61,61,61,61	0
56	MG	DA	3188	1/1	0.97	0.04	25,25,25,25	0
56	MG	BA	3131	1/1	0.97	0.06	36,36,36,36	0
56	MG	DA	3453	1/1	0.97	0.08	31,31,31,31	0
56	MG	BA	3257	1/1	0.97	0.04	29,29,29,29	0
56	MG	DA	3455	1/1	0.97	0.14	45,45,45,45	0
56	MG	BA	3258	1/1	0.97	0.14	30,30,30,30	0
56	MG	CA	3146	1/1	0.97	0.05	42,42,42,42	0
56	MG	B7	3001	1/1	0.97	0.06	45,45,45,45	0
56	MG	B7	3004	1/1	0.97	0.05	34,34,34,34	0
56	MG	CA	3150	1/1	0.97	0.07	62,62,62,62	0
56	MG	DA	3461	1/1	0.97	0.10	33,33,33,33	0
56	MG	DA	3463	1/1	0.97	0.07	28,28,28,28	0
56	MG	DA	3464	1/1	0.97	0.12	46,46,46,46	0
56	MG	B8	5001	1/1	0.97	0.09	36,36,36,36	0
56	MG	B9	502	1/1	0.97	0.07	41,41,41,41	0
56	MG	BA	3259	1/1	0.97	0.12	35,35,35,35	0
56	MG	CA	3002	1/1	0.97	0.08	43,43,43,43	0
56	MG	BA	3132	1/1	0.97	0.10	25,25,25,25	0
56	MG	BA	3133	1/1	0.97	0.04	33,33,33,33	0
56	MG	BA	3360	1/1	0.97	0.07	21,21,21,21	0
56	MG	CA	3006	1/1	0.97	0.24	37,37,37,37	0
56	MG	AA	3139	1/1	0.97	0.06	36,36,36,36	0
56	MG	DA	3209	1/1	0.97	0.06	38,38,38,38	0
56	MG	CA	3008	1/1	0.97	0.22	31,31,31,31	0
56	MG	BA	3020	1/1	0.97	0.10	33,33,33,33	0
56	MG	DA	3002	1/1	0.97	0.10	33,33,33,33	0
56	MG	CA	3010	1/1	0.97	0.06	53,53,53,53	0
56	MG	BA	3487	1/1	0.97	0.10	17,17,17,17	0
56	MG	DA	3006	1/1	0.97	0.06	33,33,33,33	0
56	MG	DA	3216	1/1	0.97	0.08	37,37,37,37	0
56	MG	DA	3007	1/1	0.97	0.05	39,39,39,39	0
56	MG	BA	3606	1/1	0.97	0.09	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3010	1/1	0.97	0.08	36,36,36,36	0
56	MG	BA	3363	1/1	0.97	0.10	29,29,29,29	0
56	MG	DA	3014	1/1	0.97	0.07	33,33,33,33	0
56	MG	DA	3489	1/1	0.97	0.13	49,49,49,49	0
56	MG	CA	3014	1/1	0.97	0.09	39,39,39,39	0
56	MG	BA	3608	1/1	0.97	0.16	45,45,45,45	0
56	MG	BA	3089	1/1	0.97	0.07	37,37,37,37	0
56	MG	DA	3019	1/1	0.97	0.06	40,40,40,40	0
56	MG	DA	3227	1/1	0.97	0.21	49,49,49,49	0
56	MG	DA	3228	1/1	0.97	0.08	51,51,51,51	0
56	MG	BA	3610	1/1	0.97	0.08	47,47,47,47	0
56	MG	BA	3366	1/1	0.97	0.06	34,34,34,34	0
56	MG	BA	3138	1/1	0.97	0.10	35,35,35,35	0
56	MG	CA	3020	1/1	0.97	0.28	46,46,46,46	0
56	MG	DA	3502	1/1	0.97	0.10	39,39,39,39	0
56	MG	BA	3613	1/1	0.97	0.08	45,45,45,45	0
56	MG	BA	3614	1/1	0.97	0.05	55,55,55,55	0
56	MG	CA	3023	1/1	0.97	0.08	38,38,38,38	0
56	MG	BA	3368	1/1	0.97	0.07	42,42,42,42	0
56	MG	BA	3370	1/1	0.97	0.09	29,29,29,29	0
56	MG	AA	3064	1/1	0.97	0.18	45,45,45,45	0
56	MG	BA	3269	1/1	0.97	0.05	34,34,34,34	0
56	MG	DA	3031	1/1	0.97	0.04	21,21,21,21	0
56	MG	DA	3511	1/1	0.97	0.14	53,53,53,53	0
56	MG	BA	3054	1/1	0.97	0.14	42,42,42,42	0
56	MG	BA	3499	1/1	0.97	0.09	35,35,35,35	0
56	MG	CA	3030	1/1	0.97	0.09	41,41,41,41	0
56	MG	DA	3246	1/1	0.97	0.17	38,38,38,38	0
56	MG	DA	3035	1/1	0.97	0.12	46,46,46,46	0
56	MG	DA	3248	1/1	0.97	0.20	52,52,52,52	0
56	MG	DA	3037	1/1	0.97	0.10	40,40,40,40	0
56	MG	CA	3031	1/1	0.97	0.08	52,52,52,52	0
56	MG	BA	3193	1/1	0.97	0.19	48,48,48,48	0
56	MG	DA	3040	1/1	0.97	0.14	34,34,34,34	0
56	MG	BA	3622	1/1	0.97	0.11	45,45,45,45	0
56	MG	BA	3501	1/1	0.97	0.09	44,44,44,44	0
56	MG	BA	3502	1/1	0.97	0.10	33,33,33,33	0
56	MG	BA	3276	1/1	0.97	0.06	42,42,42,42	0
56	MG	DA	3258	1/1	0.97	0.19	49,49,49,49	0
56	MG	DA	3046	1/1	0.97	0.17	34,34,34,34	0
56	MG	DA	3532	1/1	0.97	0.06	51,51,51,51	0
56	MG	CA	3037	1/1	0.97	0.06	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3048	1/1	0.97	0.07	41,41,41,41	0
56	MG	DA	3262	1/1	0.97	0.06	39,39,39,39	0
56	MG	DA	3049	1/1	0.97	0.04	40,40,40,40	0
56	MG	BA	3194	1/1	0.97	0.03	23,23,23,23	0
56	MG	BA	3055	1/1	0.97	0.07	13,13,13,13	0
56	MG	BA	3385	1/1	0.97	0.06	20,20,20,20	0
56	MG	DA	3267	1/1	0.97	0.15	47,47,47,47	0
56	MG	DA	3053	1/1	0.97	0.12	41,41,41,41	0
56	MG	BA	3386	1/1	0.97	0.14	32,32,32,32	0
56	MG	DA	3270	1/1	0.97	0.06	37,37,37,37	0
56	MG	BA	3197	1/1	0.97	0.10	19,19,19,19	0
56	MG	DA	3547	1/1	0.97	0.09	41,41,41,41	0
56	MG	BA	3282	1/1	0.97	0.15	31,31,31,31	0
56	MG	DA	3057	1/1	0.97	0.04	30,30,30,30	0
56	MG	BA	3144	1/1	0.97	0.12	44,44,44,44	0
56	MG	BA	3201	1/1	0.97	0.07	41,41,41,41	0
56	MG	BA	3636	1/1	0.97	0.04	32,32,32,32	0
56	MG	DA	3061	1/1	0.97	0.05	35,35,35,35	0
56	MG	DA	3279	1/1	0.97	0.05	27,27,27,27	0
56	MG	BA	3391	1/1	0.97	0.08	37,37,37,37	0
56	MG	AA	3046	1/1	0.97	0.10	42,42,42,42	0
56	MG	BA	3024	1/1	0.97	0.17	32,32,32,32	0
56	MG	DA	3558	1/1	0.97	0.05	39,39,39,39	0
56	MG	BA	3025	1/1	0.97	0.10	37,37,37,37	0
56	MG	CA	3051	1/1	0.97	0.09	66,66,66,66	0
56	MG	CA	3052	1/1	0.97	0.06	39,39,39,39	0
56	MG	DA	3290	1/1	0.97	0.06	36,36,36,36	0
56	MG	DA	3564	1/1	0.97	0.05	36,36,36,36	0
56	MG	DA	3068	1/1	0.97	0.08	35,35,35,35	0
56	MG	BA	3060	1/1	0.97	0.10	42,42,42,42	0
56	MG	AA	3082	1/1	0.97	0.20	57,57,57,57	0
56	MG	DA	3296	1/1	0.97	0.05	28,28,28,28	0
56	MG	BA	3212	1/1	0.97	0.14	28,28,28,28	0
56	MG	DA	3299	1/1	0.97	0.06	50,50,50,50	0
56	MG	AA	3145	1/1	0.97	0.07	35,35,35,35	0
56	MG	BA	3214	1/1	0.97	0.14	28,28,28,28	0
56	MG	DA	3074	1/1	0.97	0.04	29,29,29,29	0
56	MG	DA	3303	1/1	0.97	0.06	43,43,43,43	0
56	MG	BA	3103	1/1	0.97	0.10	42,42,42,42	0
56	MG	BA	3651	1/1	0.97	0.05	42,42,42,42	0
56	MG	BA	3529	1/1	0.97	0.10	33,33,33,33	0
56	MG	BA	3531	1/1	0.97	0.05	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3029	1/1	0.97	0.12	52,52,52,52	0
56	MG	BA	3030	1/1	0.97	0.45	43,43,43,43	0
56	MG	DA	3313	1/1	0.97	0.07	40,40,40,40	0
56	MG	DA	3314	1/1	0.97	0.17	54,54,54,54	0
56	MG	DA	3084	1/1	0.97	0.07	39,39,39,39	0
56	MG	DA	3317	1/1	0.97	0.09	53,53,53,53	0
56	MG	DA	3318	1/1	0.97	0.12	43,43,43,43	0
56	MG	DA	3586	1/1	0.97	0.10	47,47,47,47	0
56	MG	DA	3319	1/1	0.97	0.18	38,38,38,38	0
56	MG	DA	3588	1/1	0.97	0.10	21,21,21,21	0
56	MG	DA	3589	1/1	0.97	0.06	33,33,33,33	0
56	MG	BA	3067	1/1	0.97	0.09	34,34,34,34	0
56	MG	DA	3591	1/1	0.97	0.09	42,42,42,42	0
56	MG	BA	3302	1/1	0.97	0.10	55,55,55,55	0
56	MG	BA	3661	1/1	0.97	0.06	38,38,38,38	0
56	MG	BA	3155	1/1	0.97	0.20	27,27,27,27	0
56	MG	DA	3324	1/1	0.97	0.08	52,52,52,52	0
56	MG	BA	3666	1/1	0.97	0.16	35,35,35,35	0
56	MG	AA	3095	1/1	0.97	0.13	55,55,55,55	0
56	MG	BA	3409	1/1	0.97	0.07	28,28,28,28	0
56	MG	BA	3670	1/1	0.97	0.14	34,34,34,34	0
56	MG	BA	3544	1/1	0.97	0.12	25,25,25,25	0
56	MG	BA	3033	1/1	0.97	0.08	33,33,33,33	0
56	MG	DB	3008	1/1	0.97	0.08	35,35,35,35	0
56	MG	BA	3546	1/1	0.97	0.06	57,57,57,57	0
56	MG	BB	3001	1/1	0.97	0.08	36,36,36,36	0
56	MG	DB	3011	1/1	0.97	0.06	29,29,29,29	0
56	MG	BA	3547	1/1	0.97	0.05	60,60,60,60	0
56	MG	DA	3335	1/1	0.97	0.12	36,36,36,36	0
56	MG	DD	302	1/1	0.97	0.11	39,39,39,39	0
56	MG	BA	3548	1/1	0.97	0.07	30,30,30,30	0
56	MG	BA	3072	1/1	0.97	0.10	24,24,24,24	0
56	MG	DA	3339	1/1	0.97	0.09	32,32,32,32	0
56	MG	DE	3004	1/1	0.97	0.09	48,48,48,48	0
56	MG	BA	3413	1/1	0.97	0.10	26,26,26,26	0
56	MG	DA	3341	1/1	0.97	0.07	25,25,25,25	0
56	MG	DA	3342	1/1	0.97	0.14	37,37,37,37	0
56	MG	AA	3008	1/1	0.97	0.24	55,55,55,55	0
56	MG	DA	3104	1/1	0.97	0.17	35,35,35,35	0
56	MG	BA	3227	1/1	0.97	0.06	32,32,32,32	0
56	MG	DQ	3002	1/1	0.97	0.18	38,38,38,38	0
56	MG	BA	3418	1/1	0.97	0.06	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3348	1/1	0.97	0.07	25,25,25,25	0
56	MG	DA	3107	1/1	0.97	0.19	46,46,46,46	0
56	MG	BA	3419	1/1	0.97	0.07	20,20,20,20	0
56	MG	BB	3012	1/1	0.97	0.10	44,44,44,44	0
56	MG	DA	3110	1/1	0.97	0.12	42,42,42,42	0
56	MG	BA	3315	1/1	0.97	0.15	31,31,31,31	0
56	MG	DA	3355	1/1	0.97	0.04	36,36,36,36	0
56	MG	BA	3228	1/1	0.97	0.08	40,40,40,40	0
56	MG	BA	3113	1/1	0.97	0.18	41,41,41,41	0
56	MG	DA	3358	1/1	0.97	0.10	45,45,45,45	0
56	MG	AA	3032	1/1	0.97	0.11	42,42,42,42	0
56	MG	AA	3186	1/1	0.97	0.12	55,55,55,55	0
58	ZN	B4	501	1/1	0.97	0.06	106,106,106,106	0
58	ZN	D4	501	1/1	0.97	0.08	141,141,141,141	0
56	MG	DA	3116	1/1	0.97	0.10	29,29,29,29	0
56	MG	DA	3362	1/1	0.97	0.07	43,43,43,43	0
56	MG	BA	3004	1/1	0.98	0.06	23,23,23,23	0
56	MG	BA	3203	1/1	0.98	0.13	35,35,35,35	0
56	MG	B0	103	1/1	0.98	0.07	33,33,33,33	0
56	MG	DA	3448	1/1	0.98	0.14	29,29,29,29	0
56	MG	BA	3204	1/1	0.98	0.12	35,35,35,35	0
56	MG	AA	3070	1/1	0.98	0.16	33,33,33,33	0
56	MG	DA	3451	1/1	0.98	0.05	30,30,30,30	0
56	MG	B3	101	1/1	0.98	0.12	35,35,35,35	0
56	MG	B3	102	1/1	0.98	0.15	22,22,22,22	0
56	MG	BA	3326	1/1	0.98	0.05	28,28,28,28	0
56	MG	BA	3068	1/1	0.98	0.04	39,39,39,39	0
56	MG	BA	3519	1/1	0.98	0.07	53,53,53,53	0
56	MG	BA	3520	1/1	0.98	0.06	24,24,24,24	0
56	MG	B7	3002	1/1	0.98	0.05	35,35,35,35	0
56	MG	B7	3003	1/1	0.98	0.06	28,28,28,28	0
56	MG	BA	3208	1/1	0.98	0.16	25,25,25,25	0
56	MG	BA	3522	1/1	0.98	0.06	52,52,52,52	0
56	MG	DA	3462	1/1	0.98	0.06	35,35,35,35	0
56	MG	BA	3628	1/1	0.98	0.07	38,38,38,38	0
56	MG	BA	3209	1/1	0.98	0.18	26,26,26,26	0
56	MG	BA	3022	1/1	0.98	0.04	26,26,26,26	0
56	MG	BA	3414	1/1	0.98	0.06	31,31,31,31	0
56	MG	BA	3006	1/1	0.98	0.12	36,36,36,36	0
56	MG	DA	3276	1/1	0.98	0.18	50,50,50,50	0
56	MG	BA	3099	1/1	0.98	0.20	32,32,32,32	0
56	MG	BA	3528	1/1	0.98	0.05	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3262	1/1	0.98	0.09	24,24,24,24	0
56	MG	DA	3280	1/1	0.98	0.07	50,50,50,50	0
56	MG	BA	3007	1/1	0.98	0.03	32,32,32,32	0
56	MG	BA	3420	1/1	0.98	0.05	24,24,24,24	0
56	MG	DA	3283	1/1	0.98	0.04	38,38,38,38	0
56	MG	DA	3476	1/1	0.98	0.03	32,32,32,32	0
56	MG	DA	3284	1/1	0.98	0.04	23,23,23,23	0
56	MG	BA	3421	1/1	0.98	0.07	36,36,36,36	0
56	MG	BA	3535	1/1	0.98	0.05	47,47,47,47	0
56	MG	BA	3640	1/1	0.98	0.06	33,33,33,33	0
56	MG	BA	3264	1/1	0.98	0.15	35,35,35,35	0
56	MG	DA	3482	1/1	0.98	0.05	46,46,46,46	0
56	MG	DA	3124	1/1	0.98	0.09	29,29,29,29	0
56	MG	BA	3336	1/1	0.98	0.06	43,43,43,43	0
56	MG	BA	3538	1/1	0.98	0.14	55,55,55,55	0
56	MG	DA	3294	1/1	0.98	0.04	37,37,37,37	0
56	MG	BA	3134	1/1	0.98	0.10	40,40,40,40	0
56	MG	BA	3215	1/1	0.98	0.10	32,32,32,32	0
56	MG	DA	3297	1/1	0.98	0.08	38,38,38,38	0
56	MG	DA	3490	1/1	0.98	0.06	34,34,34,34	0
56	MG	CA	3147	1/1	0.98	0.08	52,52,52,52	0
56	MG	BA	3542	1/1	0.98	0.07	51,51,51,51	0
56	MG	BA	3216	1/1	0.98	0.23	33,33,33,33	0
56	MG	BA	3650	1/1	0.98	0.04	31,31,31,31	0
56	MG	AN	502	1/1	0.98	0.18	53,53,53,53	0
56	MG	BA	3341	1/1	0.98	0.05	32,32,32,32	0
56	MG	DA	3497	1/1	0.98	0.11	45,45,45,45	0
56	MG	DA	3304	1/1	0.98	0.10	32,32,32,32	0
56	MG	AA	3168	1/1	0.98	0.14	56,56,56,56	0
56	MG	BA	3104	1/1	0.98	0.04	42,42,42,42	0
56	MG	BA	3049	1/1	0.98	0.09	43,43,43,43	0
56	MG	BA	3657	1/1	0.98	0.07	24,24,24,24	0
56	MG	BA	3658	1/1	0.98	0.06	27,27,27,27	0
56	MG	BA	3272	1/1	0.98	0.07	37,37,37,37	0
56	MG	DA	3311	1/1	0.98	0.08	43,43,43,43	0
56	MG	DA	3142	1/1	0.98	0.10	37,37,37,37	0
56	MG	DA	3143	1/1	0.98	0.05	27,27,27,27	0
56	MG	DA	3315	1/1	0.98	0.10	43,43,43,43	0
56	MG	BA	3273	1/1	0.98	0.05	29,29,29,29	0
56	MG	BA	3551	1/1	0.98	0.05	48,48,48,48	0
56	MG	BA	3274	1/1	0.98	0.08	47,47,47,47	0
56	MG	BA	3665	1/1	0.98	0.05	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3513	1/1	0.98	0.06	32,32,32,32	0
56	MG	DA	3148	1/1	0.98	0.04	47,47,47,47	0
56	MG	BA	3175	1/1	0.98	0.10	33,33,33,33	0
56	MG	AA	3075	1/1	0.98	0.12	39,39,39,39	0
56	MG	DA	3005	1/1	0.98	0.06	26,26,26,26	0
56	MG	AX	3004	1/1	0.98	0.11	39,39,39,39	0
56	MG	DA	3519	1/1	0.98	0.05	42,42,42,42	0
56	MG	BA	3351	1/1	0.98	0.04	33,33,33,33	0
56	MG	DA	3008	1/1	0.98	0.03	38,38,38,38	0
56	MG	DA	3522	1/1	0.98	0.09	44,44,44,44	0
56	MG	BA	3279	1/1	0.98	0.07	38,38,38,38	0
56	MG	BA	3353	1/1	0.98	0.06	39,39,39,39	0
56	MG	BA	3674	1/1	0.98	0.05	54,54,54,54	0
56	MG	DA	3012	1/1	0.98	0.11	30,30,30,30	0
56	MG	DA	3013	1/1	0.98	0.06	37,37,37,37	0
56	MG	DA	3528	1/1	0.98	0.04	37,37,37,37	0
56	MG	BA	3354	1/1	0.98	0.05	42,42,42,42	0
56	MG	BA	3355	1/1	0.98	0.04	31,31,31,31	0
56	MG	DA	3016	1/1	0.98	0.15	31,31,31,31	0
56	MG	DA	3336	1/1	0.98	0.08	22,22,22,22	0
56	MG	BB	3002	1/1	0.98	0.12	41,41,41,41	0
56	MG	BA	3178	1/1	0.98	0.17	26,26,26,26	0
56	MG	BA	3281	1/1	0.98	0.12	51,51,51,51	0
56	MG	DA	3168	1/1	0.98	0.11	39,39,39,39	0
56	MG	DA	3169	1/1	0.98	0.04	38,38,38,38	0
56	MG	BA	3453	1/1	0.98	0.04	27,27,27,27	0
56	MG	BA	3456	1/1	0.98	0.12	33,33,33,33	0
56	MG	BA	3457	1/1	0.98	0.06	29,29,29,29	0
56	MG	BA	3225	1/1	0.98	0.05	31,31,31,31	0
56	MG	BA	3029	1/1	0.98	0.07	12,12,12,12	0
56	MG	AA	3030	1/1	0.98	0.09	47,47,47,47	0
56	MG	BB	3011	1/1	0.98	0.05	45,45,45,45	0
56	MG	DA	3546	1/1	0.98	0.06	40,40,40,40	0
56	MG	DA	3177	1/1	0.98	0.06	52,52,52,52	0
56	MG	AA	3162	1/1	0.98	0.06	40,40,40,40	0
56	MG	BA	3032	1/1	0.98	0.04	40,40,40,40	0
56	MG	DA	3180	1/1	0.98	0.06	30,30,30,30	0
56	MG	DA	3181	1/1	0.98	0.05	40,40,40,40	0
56	MG	DA	3182	1/1	0.98	0.05	38,38,38,38	0
56	MG	BA	3015	1/1	0.98	0.04	27,27,27,27	0
56	MG	BA	3364	1/1	0.98	0.05	29,29,29,29	0
56	MG	BA	3114	1/1	0.98	0.12	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3291	1/1	0.98	0.08	14,14,14,14	0
56	MG	AA	3050	1/1	0.98	0.04	24,24,24,24	0
56	MG	BD	301	1/1	0.98	0.11	30,30,30,30	0
56	MG	BA	3085	1/1	0.98	0.10	27,27,27,27	0
56	MG	DA	3036	1/1	0.98	0.04	38,38,38,38	0
56	MG	CA	3061	1/1	0.98	0.10	45,45,45,45	0
56	MG	DA	3562	1/1	0.98	0.06	42,42,42,42	0
56	MG	BA	3369	1/1	0.98	0.09	33,33,33,33	0
56	MG	BA	3035	1/1	0.98	0.15	21,21,21,21	0
56	MG	BA	3371	1/1	0.98	0.06	25,25,25,25	0
56	MG	BD	306	1/1	0.98	0.10	36,36,36,36	0
56	MG	DA	3196	1/1	0.98	0.06	33,33,33,33	0
56	MG	DA	3042	1/1	0.98	0.04	32,32,32,32	0
56	MG	DA	3372	1/1	0.98	0.06	21,21,21,21	0
56	MG	BA	3372	1/1	0.98	0.07	29,29,29,29	0
56	MG	BA	3475	1/1	0.98	0.07	45,45,45,45	0
56	MG	DA	3200	1/1	0.98	0.08	28,28,28,28	0
56	MG	BA	3119	1/1	0.98	0.08	29,29,29,29	0
56	MG	DA	3202	1/1	0.98	0.13	24,24,24,24	0
56	MG	DA	3378	1/1	0.98	0.08	31,31,31,31	0
56	MG	DA	3380	1/1	0.98	0.04	33,33,33,33	0
56	MG	BA	3477	1/1	0.98	0.06	50,50,50,50	0
56	MG	AA	3173	1/1	0.98	0.12	32,32,32,32	0
56	MG	BE	304	1/1	0.98	0.07	13,13,13,13	0
56	MG	DA	3385	1/1	0.98	0.03	45,45,45,45	0
56	MG	BA	3038	1/1	0.98	0.06	30,30,30,30	0
56	MG	BA	3299	1/1	0.98	0.07	36,36,36,36	0
56	MG	DA	3389	1/1	0.98	0.04	42,42,42,42	0
56	MG	DA	3391	1/1	0.98	0.04	42,42,42,42	0
56	MG	BA	3377	1/1	0.98	0.07	31,31,31,31	0
56	MG	BA	3589	1/1	0.98	0.06	27,27,27,27	0
56	MG	BA	3380	1/1	0.98	0.09	17,17,17,17	0
56	MG	BA	3122	1/1	0.98	0.20	39,39,39,39	0
56	MG	BA	3382	1/1	0.98	0.09	27,27,27,27	0
56	MG	AA	3007	1/1	0.98	0.13	30,30,30,30	0
56	MG	BA	3489	1/1	0.98	0.17	41,41,41,41	0
56	MG	BA	3490	1/1	0.98	0.07	38,38,38,38	0
56	MG	DA	3400	1/1	0.98	0.17	38,38,38,38	0
56	MG	DA	3401	1/1	0.98	0.09	55,55,55,55	0
56	MG	DA	3596	1/1	0.98	0.12	54,54,54,54	0
56	MG	BA	3063	1/1	0.98	0.11	47,47,47,47	0
56	MG	DA	3403	1/1	0.98	0.04	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BN	3002	1/1	0.98	0.04	27,27,27,27	0
56	MG	BA	3304	1/1	0.98	0.09	43,43,43,43	0
56	MG	BA	3305	1/1	0.98	0.07	28,28,28,28	0
56	MG	BA	3091	1/1	0.98	0.14	19,19,19,19	0
56	MG	BA	3159	1/1	0.98	0.14	27,27,27,27	0
56	MG	BP	204	1/1	0.98	0.08	31,31,31,31	0
56	MG	BA	3196	1/1	0.98	0.10	17,17,17,17	0
56	MG	BQ	202	1/1	0.98	0.04	14,14,14,14	0
56	MG	BA	3160	1/1	0.98	0.09	29,29,29,29	0
56	MG	BR	3001	1/1	0.98	0.04	31,31,31,31	0
56	MG	DA	3229	1/1	0.98	0.16	38,38,38,38	0
56	MG	BR	3002	1/1	0.98	0.04	23,23,23,23	0
56	MG	DA	3231	1/1	0.98	0.05	37,37,37,37	0
56	MG	BA	3198	1/1	0.98	0.07	34,34,34,34	0
56	MG	CA	3095	1/1	0.98	0.11	56,56,56,56	0
56	MG	BA	3312	1/1	0.98	0.05	18,18,18,18	0
56	MG	DE	3005	1/1	0.98	0.06	20,20,20,20	0
56	MG	BA	3313	1/1	0.98	0.06	17,17,17,17	0
56	MG	DF	302	1/1	0.98	0.05	41,41,41,41	0
56	MG	BU	204	1/1	0.98	0.12	29,29,29,29	0
56	MG	BA	3161	1/1	0.98	0.04	39,39,39,39	0
56	MG	BA	3247	1/1	0.98	0.19	48,48,48,48	0
56	MG	BA	3248	1/1	0.98	0.14	21,21,21,21	0
56	MG	DA	3426	1/1	0.98	0.07	35,35,35,35	0
56	MG	DA	3427	1/1	0.98	0.08	25,25,25,25	0
56	MG	DA	3080	1/1	0.98	0.07	29,29,29,29	0
56	MG	DR	201	1/1	0.98	0.23	36,36,36,36	0
56	MG	DA	3081	1/1	0.98	0.07	44,44,44,44	0
56	MG	BW	3001	1/1	0.98	0.05	25,25,25,25	0
56	MG	BA	3200	1/1	0.98	0.08	25,25,25,25	0
56	MG	BA	3399	1/1	0.98	0.08	42,42,42,42	0
56	MG	DA	3433	1/1	0.98	0.10	33,33,33,33	0
56	MG	DW	3001	1/1	0.98	0.09	38,38,38,38	0
56	MG	DA	3085	1/1	0.98	0.16	40,40,40,40	0
56	MG	DA	3086	1/1	0.98	0.07	41,41,41,41	0
56	MG	BA	3506	1/1	0.98	0.04	39,39,39,39	0
56	MG	CA	3106	1/1	0.98	0.14	40,40,40,40	0
56	MG	BA	3250	1/1	0.98	0.08	33,33,33,33	0
56	MG	DA	3250	1/1	0.98	0.05	37,37,37,37	0
56	MG	BA	3508	1/1	0.98	0.06	25,25,25,25	0
57	SF4	CD	501	8/8	0.98	0.04	58,71,82,82	0
56	MG	AA	3084	1/1	0.98	0.08	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	ZN	CN	501	1/1	0.98	0.04	82,82,82,82	0
56	MG	BA	3320	1/1	0.98	0.05	44,44,44,44	0
58	ZN	D9	501	1/1	0.98	0.06	54,54,54,54	0
56	MG	CA	3111	1/1	0.98	0.08	43,43,43,43	0
56	MG	BA	3321	1/1	0.98	0.06	53,53,53,53	0
56	MG	AA	3040	1/1	0.99	0.12	27,27,27,27	0
56	MG	AA	3127	1/1	0.99	0.09	68,68,68,68	0
56	MG	BA	3289	1/1	0.99	0.07	28,28,28,28	0
56	MG	BA	3290	1/1	0.99	0.04	36,36,36,36	0
56	MG	BA	3207	1/1	0.99	0.14	36,36,36,36	0
56	MG	BA	3083	1/1	0.99	0.09	34,34,34,34	0
56	MG	BA	3530	1/1	0.99	0.08	36,36,36,36	0
56	MG	BA	3479	1/1	0.99	0.07	45,45,45,45	0
56	MG	AA	3022	1/1	0.99	0.04	39,39,39,39	0
56	MG	BA	3481	1/1	0.99	0.09	31,31,31,31	0
56	MG	BA	3534	1/1	0.99	0.09	20,20,20,20	0
56	MG	BA	3482	1/1	0.99	0.03	23,23,23,23	0
56	MG	BA	3294	1/1	0.99	0.04	32,32,32,32	0
56	MG	BF	302	1/1	0.99	0.03	45,45,45,45	0
56	MG	BA	3647	1/1	0.99	0.02	30,30,30,30	0
56	MG	DA	3413	1/1	0.99	0.07	24,24,24,24	0
56	MG	BA	3648	1/1	0.99	0.05	28,28,28,28	0
56	MG	BA	3433	1/1	0.99	0.04	33,33,33,33	0
56	MG	DA	3334	1/1	0.99	0.03	24,24,24,24	0
56	MG	BA	3065	1/1	0.99	0.08	29,29,29,29	0
56	MG	BA	3397	1/1	0.99	0.03	30,30,30,30	0
56	MG	BA	3436	1/1	0.99	0.04	35,35,35,35	0
56	MG	BA	3541	1/1	0.99	0.02	26,26,26,26	0
56	MG	AA	3090	1/1	0.99	0.10	28,28,28,28	0
56	MG	BA	3438	1/1	0.99	0.05	33,33,33,33	0
56	MG	BA	3656	1/1	0.99	0.07	12,12,12,12	0
56	MG	BA	3109	1/1	0.99	0.04	36,36,36,36	0
56	MG	BA	3440	1/1	0.99	0.05	38,38,38,38	0
56	MG	AA	3115	1/1	0.99	0.03	35,35,35,35	0
56	MG	DA	3345	1/1	0.99	0.08	33,33,33,33	0
56	MG	AA	3011	1/1	0.99	0.05	24,24,24,24	0
56	MG	AA	3140	1/1	0.99	0.05	31,31,31,31	0
56	MG	DA	3595	1/1	0.99	0.04	43,43,43,43	0
56	MG	BA	3445	1/1	0.99	0.03	22,22,22,22	0
56	MG	BA	3664	1/1	0.99	0.12	30,30,30,30	0
56	MG	DA	3350	1/1	0.99	0.09	36,36,36,36	0
56	MG	BA	3008	1/1	0.99	0.07	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3071	1/1	0.99	0.09	32,32,32,32	0
56	MG	DA	3205	1/1	0.99	0.17	32,32,32,32	0
56	MG	BA	3303	1/1	0.99	0.06	31,31,31,31	0
56	MG	BU	201	1/1	0.99	0.11	32,32,32,32	0
56	MG	BA	3139	1/1	0.99	0.04	31,31,31,31	0
56	MG	BA	3669	1/1	0.99	0.05	29,29,29,29	0
56	MG	BA	3115	1/1	0.99	0.05	34,34,34,34	0
56	MG	DA	3140	1/1	0.99	0.09	37,37,37,37	0
56	MG	BA	3037	1/1	0.99	0.04	24,24,24,24	0
56	MG	BA	3672	1/1	0.99	0.04	46,46,46,46	0
56	MG	BA	3452	1/1	0.99	0.08	38,38,38,38	0
56	MG	BV	203	1/1	0.99	0.03	24,24,24,24	0
56	MG	BA	3275	1/1	0.99	0.05	39,39,39,39	0
56	MG	BA	3454	1/1	0.99	0.08	21,21,21,21	0
56	MG	DA	3289	1/1	0.99	0.09	26,26,26,26	0
56	MG	DA	3079	1/1	0.99	0.04	54,54,54,54	0
56	MG	BW	3003	1/1	0.99	0.06	27,27,27,27	0
56	MG	BA	3455	1/1	0.99	0.03	21,21,21,21	0
56	MG	DA	3293	1/1	0.99	0.07	34,34,34,34	0
56	MG	AA	3161	1/1	0.99	0.09	66,66,66,66	0
56	MG	BA	3411	1/1	0.99	0.09	25,25,25,25	0
56	MG	BA	3143	1/1	0.99	0.15	36,36,36,36	0
56	MG	DA	3224	1/1	0.99	0.10	22,22,22,22	0
56	MG	BA	3310	1/1	0.99	0.05	35,35,35,35	0
56	MG	BA	3039	1/1	0.99	0.07	31,31,31,31	0
56	MG	BA	3511	1/1	0.99	0.05	38,38,38,38	0
56	MG	DA	3157	1/1	0.99	0.07	40,40,40,40	0
56	MG	DA	3379	1/1	0.99	0.03	26,26,26,26	0
56	MG	AA	3117	1/1	0.99	0.04	47,47,47,47	0
56	MG	BA	3462	1/1	0.99	0.03	44,44,44,44	0
56	MG	AA	3163	1/1	0.99	0.03	49,49,49,49	0
56	MG	DA	3383	1/1	0.99	0.06	47,47,47,47	0
56	MG	BA	3417	1/1	0.99	0.09	24,24,24,24	0
56	MG	BA	3625	1/1	0.99	0.05	25,25,25,25	0
56	MG	BA	3465	1/1	0.99	0.05	37,37,37,37	0
56	MG	BA	3097	1/1	0.99	0.12	53,53,53,53	0
56	MG	D5	502	1/1	0.99	0.20	36,36,36,36	0
56	MG	DA	3388	1/1	0.99	0.03	35,35,35,35	0
56	MG	AA	3118	1/1	0.99	0.11	36,36,36,36	0
56	MG	DA	3390	1/1	0.99	0.04	41,41,41,41	0
57	SF4	AD	501	8/8	0.99	0.04	50,63,78,83	0
56	MG	BA	3059	1/1	0.99	0.04	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	ZN	AN	501	1/1	0.99	0.04	67,67,67,67	0
58	ZN	BY	501	1/1	0.99	0.02	51,51,51,51	0
56	MG	BA	3100	1/1	0.99	0.06	29,29,29,29	0
56	MG	DA	3312	1/1	0.99	0.03	47,47,47,47	0
58	ZN	DY	501	1/1	0.99	0.04	92,92,92,92	0
56	MG	AA	3143	1/1	0.99	0.05	32,32,32,32	0
58	ZN	D5	501	1/1	0.99	0.04	67,67,67,67	0
58	ZN	D6	501	1/1	0.99	0.06	68,68,68,68	0
56	MG	AX	3008	1/1	0.99	0.08	23,23,23,23	0
56	MG	BA	3424	1/1	0.99	0.06	38,38,38,38	0
56	MG	CA	3128	1/1	0.99	0.03	39,39,39,39	0
58	ZN	B6	501	1/1	1.00	0.01	45,45,45,45	0
58	ZN	B9	501	1/1	1.00	0.03	45,45,45,45	0
56	MG	BA	3663	1/1	1.00	0.01	20,20,20,20	0
56	MG	BA	3378	1/1	1.00	0.06	16,16,16,16	0
56	MG	DA	3542	1/1	1.00	0.03	30,30,30,30	0
56	MG	BA	3552	1/1	1.00	0.03	31,31,31,31	0
56	MG	BA	3379	1/1	1.00	0.05	31,31,31,31	0
56	MG	DA	3154	1/1	1.00	0.07	24,24,24,24	0
56	MG	BA	3442	1/1	1.00	0.05	20,20,20,20	0
58	ZN	B5	501	1/1	1.00	0.02	42,42,42,42	0

6.5 Other polymers (i)

There are no such residues in this entry.