Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:50 AM UTC

PDB ID	:	4W2I / pdb_00004w2i
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in complex with negamycin, mRNA and three deacylated tRNAs in the A, P and E sites
Authors	:	Polikanov, Y.S.; Szal, T.; Jiang, F.; Gupta, P.; Matsuda, R.; Shiozuka, M.; Steitz, T.A.; Vazquez-Laslop, N.; Mankin, A.S.
Deposited on	:	2014-09-12
Resolution	:	2.70 Å(reported)

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

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

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

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

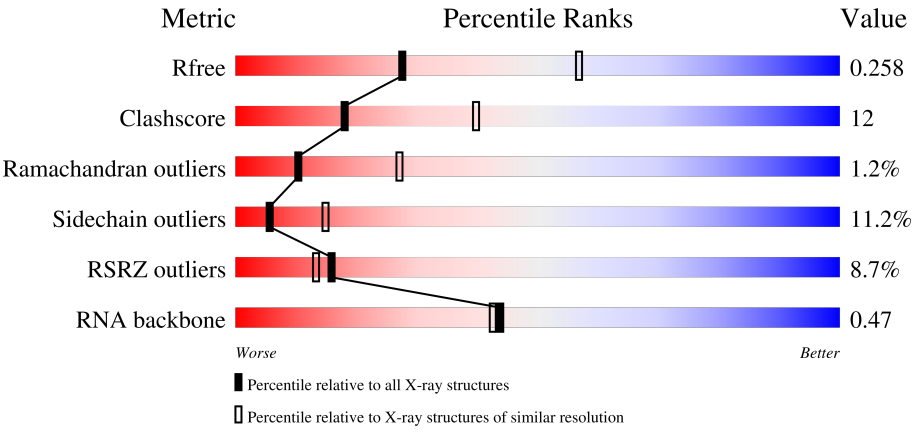
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)
RNA backbone	3983	1044 (2.90-2.50)

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	4% 51% 37% 11% .
1	CA	1521	7% 46% 42% 11% .
2	AB	256	20% 45% 35% 10% 10%
2	CB	256	29% 41% 37% 11% 10%

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Mol	Chain	Length	Quality of chain
3	AC	239	16% 51% 32% 14%
3	CC	239	36% 50% 30% 6% 14%
4	AD	209	14% 56% 39%
4	CD	209	4% 65% 31%
5	AE	162	6% 56% 33% 9%
5	CE	162	21% 56% 31% 9%
6	AF	101	8% 69% 24% 6%
6	CF	101	2% 60% 30% 9%
7	AG	156	13% 71% 25%
7	CG	156	11% 67% 29%
8	AH	138	7% 65% 32%
8	CH	138	9% 58% 38%
9	AI	128	24% 61% 32% 6%
9	CI	128	47% 52% 42% 5%
10	AJ	105	30% 51% 34% 7% 8%
10	CJ	105	69% 43% 41% 8% 9%
11	AK	129	3% 65% 20% 12%
11	CK	129	7% 58% 28% 12%
12	AL	132	6% 66% 23% 8%
12	CL	132	5% 66% 24% 8%
13	AM	126	10% 60% 29% 8%
13	CM	126	23% 48% 44%
14	AN	61	23% 56% 36% 7%
14	CN	61	61% 57% 34% 7%
15	AO	89	6% 62% 31% 6%

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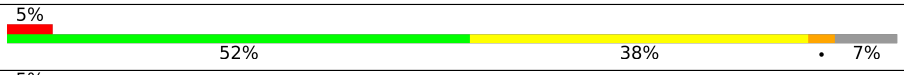
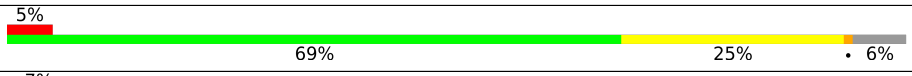
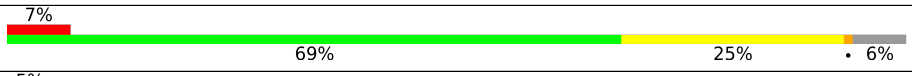
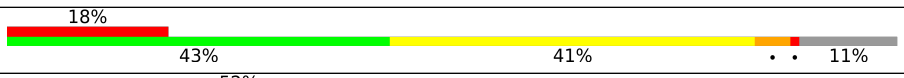
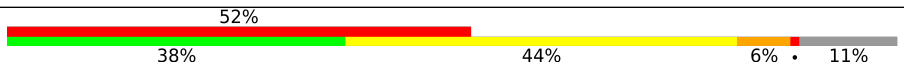
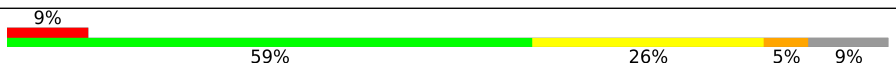
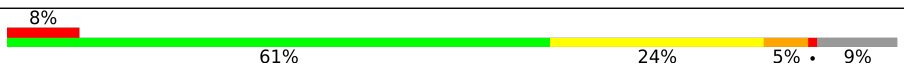
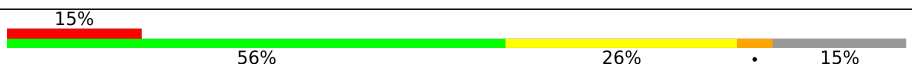
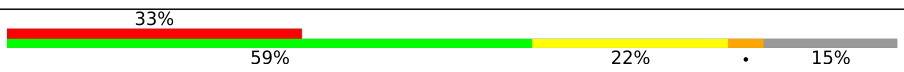
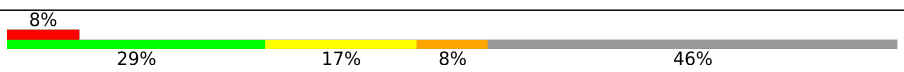
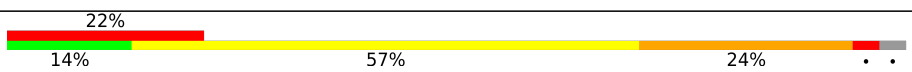
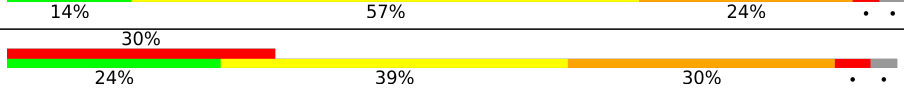
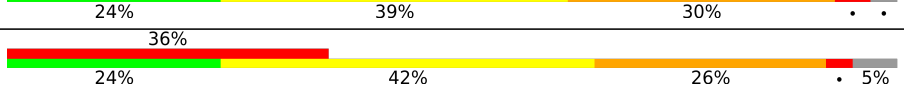
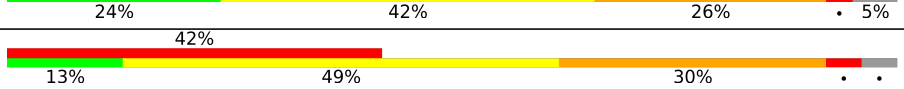
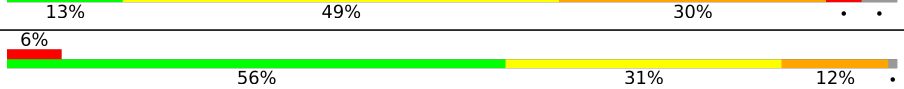
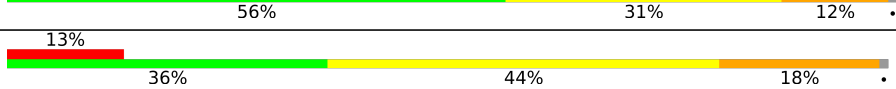
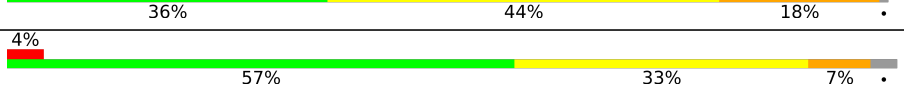
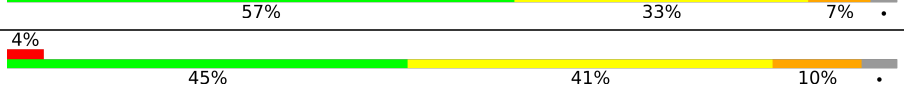
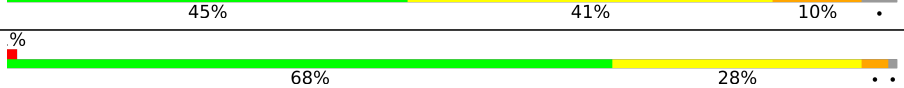
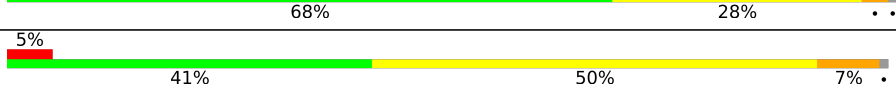
Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AW	76	
23	AY	76	
23	CW	76	
23	CY	76	
24	AX	77	
24	CX	77	
25	BA	2915	
25	DA	2915	
26	BB	121	
26	DB	121	

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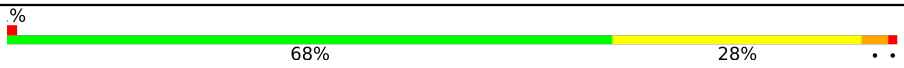
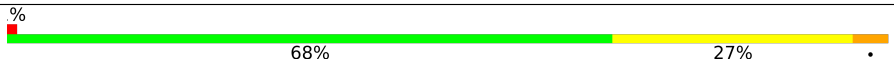
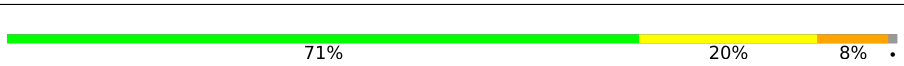
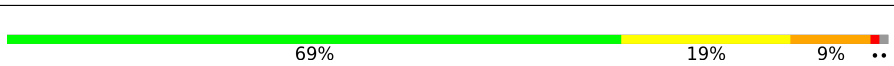
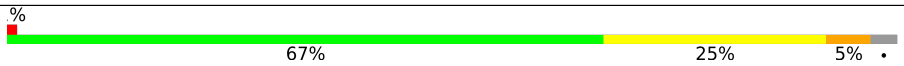
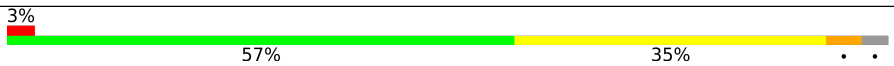
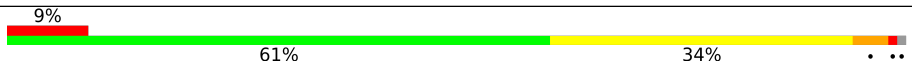
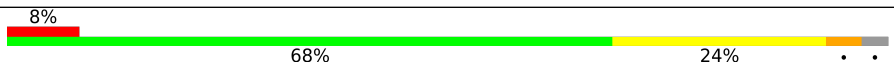
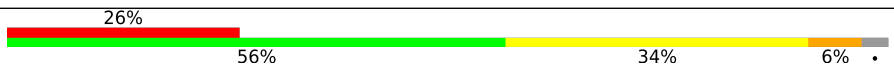
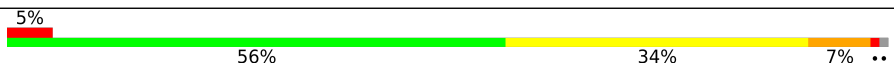
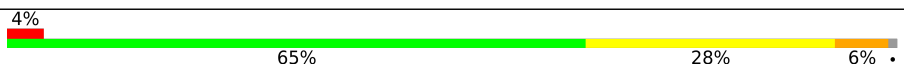
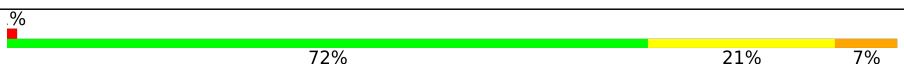
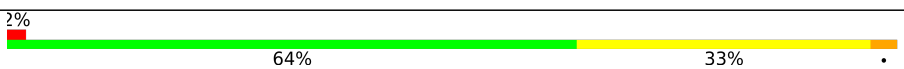
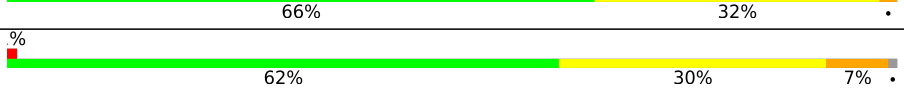
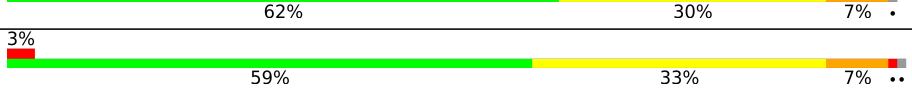
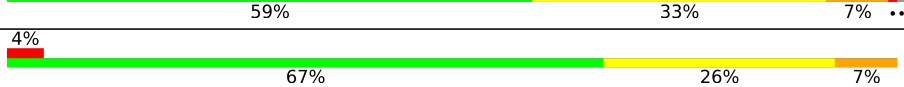
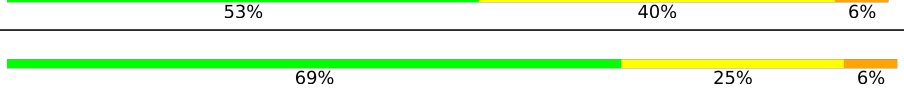
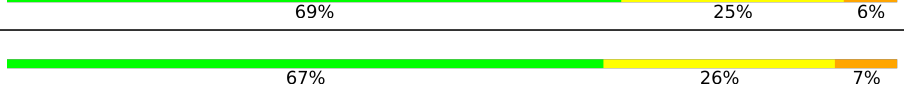
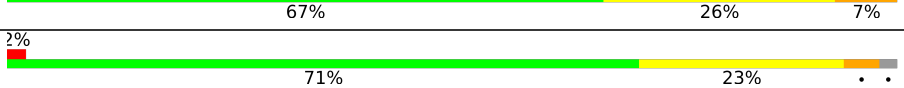
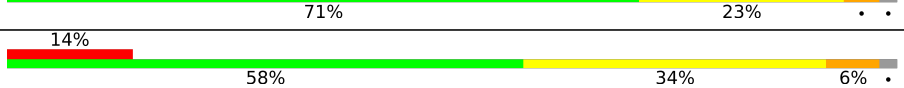
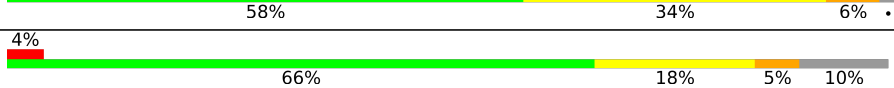
Mol	Chain	Length	Quality of chain
27	BD	276	
27	DD	276	
28	BE	206	
28	DE	206	
29	BF	210	
29	DF	210	
30	BG	182	
30	DG	182	
31	BH	180	
31	DH	180	
32	BI	148	
32	DI	148	
33	BN	140	
33	DN	140	
34	BO	122	
34	DO	122	
35	BP	150	
35	DP	150	
36	BQ	141	
36	DQ	141	
37	BR	118	
37	DR	118	
38	BS	112	
38	DS	112	
39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

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Mol	Chain	Length	Quality of chain
39	DT	146	5% 59% 25% 6% 10%
40	BU	118	% 72% 20% 6%
40	DU	118	5% 67% 27%
41	BV	101	% 68% 27% 5%
41	DV	101	8% 63% 28% 8%
42	BW	113	% 68% 27%
42	DW	113	71% 25%
43	BX	96	% 76% 21%
43	DX	96	9% 71% 27%
44	BY	110	4% 64% 29% 5%
44	DY	110	23% 64% 32%
45	BZ	206	15% 44% 31% 7% 17%
45	DZ	206	31% 43% 34% 6% 16%
46	B0	85	7% 85% 9%
46	D0	85	12% 71% 25%
47	B1	98	2% 70% 29%
47	D1	98	% 70% 26%
48	B2	72	3% 67% 26%
48	D2	72	7% 68% 26%
49	B3	60	73% 23%
49	D3	60	8% 58% 33% 7%
50	B4	71	18% 44% 34% 18%
50	D4	71	35% 35% 54% 8%
51	B5	60	63% 28% 7%
51	D5	60	72% 25%

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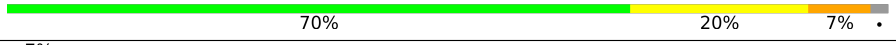
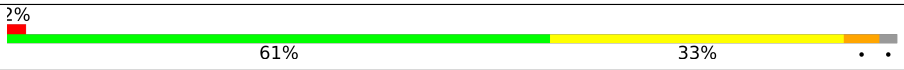
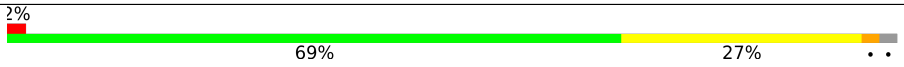
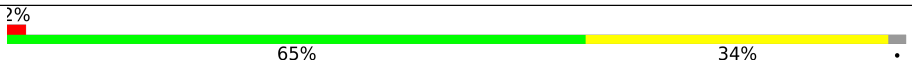
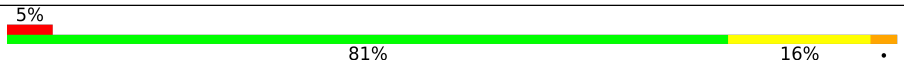
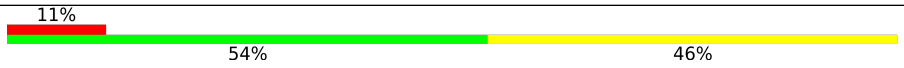
Mol	Chain	Length	Quality of chain
52	B6	54	
52	D6	54	
53	B7	49	
53	D7	49	
54	B8	65	
54	D8	65	
55	B9	37	
55	D9	37	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	AA	3075	-	-	-	X
56	MG	CA	3054	-	-	-	X
57	NEG	AA	3216	-	-	X	-

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 297376 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	1496	Total	C	N	O	P	0	0	0
			32163	14314	5963	10390	1496			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

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

- Molecule 3 is a protein called 30S Ribosomal Protein S3.

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

- Molecule 4 is a protein called 30S Ribosomal Protein S4.

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

- Molecule 5 is a protein called 30S Ribosomal Protein S5.

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

- Molecule 6 is a protein called 30S Ribosomal Protein S6.

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

- Molecule 7 is a protein called 30S Ribosomal Protein S7.

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

- Molecule 8 is a protein called 30S Ribosomal Protein S8.

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

- Molecule 9 is a protein called 30S Ribosomal Protein S9.

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

- Molecule 10 is a protein called 30S Ribosomal Protein S10.

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

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

- Molecule 11 is a protein called 30S Ribosomal Protein S11.

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

- Molecule 12 is a protein called 30S Ribosomal Protein S12.

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

- Molecule 13 is a protein called 30S Ribosomal Protein S13.

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

- Molecule 14 is a protein called 30S Ribosomal Protein S14.

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 A/P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AW	74	Total	C	N	O	P	S	0	0	0
			1588	713	285	515	73	2			
23	AY	74	Total	C	N	O	P	S	0	0	0
			1581	707	285	515	73	1			
23	CW	72	Total	C	N	O	P	S	0	0	0
			1541	688	278	502	72	1			
23	CY	73	Total	C	N	O	P	S	0	0	0
			1561	698	283	507	72	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2822	Total	C	N	O	P	0	0	0
			60792	27054	11380	19537	2821			
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			
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			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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			
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			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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
			558	352	102	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
			517	331	102	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	218	Total	Mg	0	0
			218	218		
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	AM	1	Total	Mg	0	0
			1	1		
56	AN	3	Total	Mg	0	0
			3	3		
56	AO	1	Total	Mg	0	0
			1	1		
56	AV	3	Total	Mg	0	0
			3	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	AW	4	Total Mg 4 4	0	0
56	AX	11	Total Mg 11 11	0	0
56	AY	3	Total Mg 3 3	0	0
56	BA	785	Total Mg 785 785	0	0
56	BB	18	Total Mg 18 18	0	0
56	BD	11	Total Mg 11 11	0	0
56	BE	8	Total Mg 8 8	0	0
56	BF	11	Total Mg 11 11	0	0
56	BG	2	Total Mg 2 2	0	0
56	BN	6	Total Mg 6 6	0	0
56	BO	1	Total Mg 1 1	0	0
56	BP	4	Total Mg 4 4	0	0
56	BQ	5	Total Mg 5 5	0	0
56	BR	3	Total Mg 3 3	0	0
56	BT	1	Total Mg 1 1	0	0
56	BU	9	Total Mg 9 9	0	0
56	BV	7	Total Mg 7 7	0	0
56	BW	4	Total Mg 4 4	0	0
56	BX	2	Total Mg 2 2	0	0
56	BY	1	Total Mg 1 1	0	0
56	BZ	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	B0	3	Total Mg 3 3	0	0
56	B1	1	Total Mg 1 1	0	0
56	B2	1	Total Mg 1 1	0	0
56	B3	2	Total Mg 2 2	0	0
56	B4	1	Total Mg 1 1	0	0
56	B5	5	Total Mg 5 5	0	0
56	B6	1	Total Mg 1 1	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	172	Total Mg 172 172	0	0
56	CD	1	Total Mg 1 1	0	0
56	CE	1	Total Mg 1 1	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	CN	1	Total Mg 1 1	0	0
56	CT	1	Total Mg 1 1	0	0
56	CV	1	Total Mg 1 1	0	0
56	CW	2	Total Mg 2 2	0	0
56	CX	2	Total Mg 2 2	0	0

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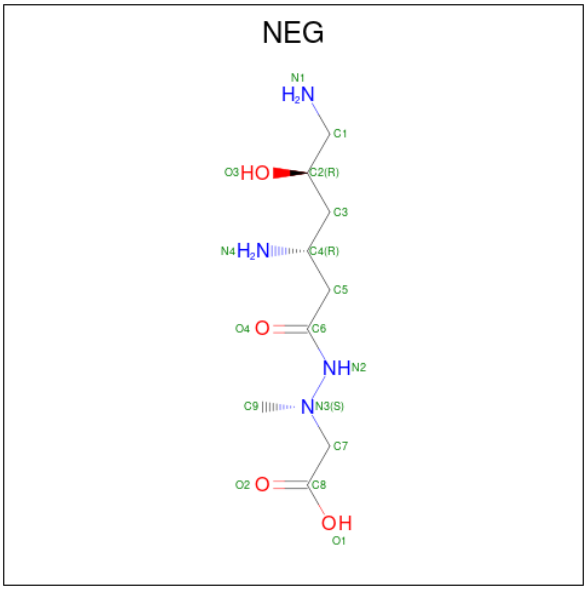
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	CY	1	Total Mg 1 1	0	0
56	DA	623	Total Mg 623 623	0	0
56	DB	12	Total Mg 12 12	0	0
56	DD	9	Total Mg 9 9	0	0
56	DE	4	Total Mg 4 4	0	0
56	DF	6	Total Mg 6 6	0	0
56	DG	1	Total Mg 1 1	0	0
56	DN	1	Total Mg 1 1	0	0
56	DO	2	Total Mg 2 2	0	0
56	DP	1	Total Mg 1 1	0	0
56	DQ	4	Total Mg 4 4	0	0
56	DR	2	Total Mg 2 2	0	0
56	DU	3	Total Mg 3 3	0	0
56	DV	3	Total Mg 3 3	0	0
56	DW	4	Total Mg 4 4	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	1	Total Mg 1 1	0	0

- Molecule 57 is NEGAMYCIN (CCD ID: NEG) (formula: $C_9H_{20}N_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
57	AA	1	Total	C	N	O	0	0
			17	9	4	4		
57	AA	1	Total	C	N	O	0	0
			17	9	4	4		
57	AA	1	Total	C	N	O	0	0
			17	9	4	4		
57	AA	1	Total	C	N	O	0	0
			17	9	4	4		
57	AA	1	Total	C	N	O	0	0
			17	9	4	4		
57	AA	1	Total	C	N	O	0	0
			17	9	4	4		
57	AA	1	Total	C	N	O	0	0
			17	9	4	4		
57	AW	1	Total	C	N	O	0	0
			17	9	4	4		
57	AX	1	Total	C	N	O	0	0
			17	9	4	4		
57	CA	1	Total	C	N	O	0	0
			17	9	4	4		
57	CA	1	Total	C	N	O	0	0
			17	9	4	4		
57	CA	1	Total	C	N	O	0	0
			17	9	4	4		
57	CA	1	Total	C	N	O	0	0
			17	9	4	4		

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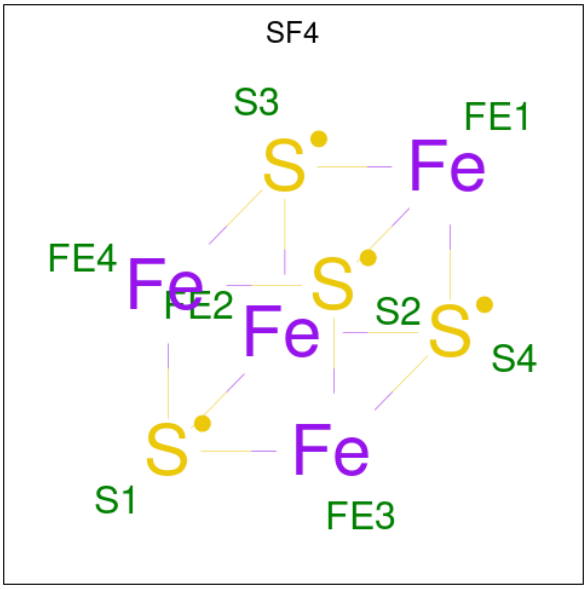
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	CA	1	Total C N O 17 9 4 4	0	0
57	CA	1	Total C N O 17 9 4 4	0	0
57	CA	1	Total C N O 17 9 4 4	0	0
57	CA	1	Total C N O 17 9 4 4	0	0
57	CW	1	Total C N O 17 9 4 4	0	0
57	CX	1	Total C N O 17 9 4 4	0	0

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



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

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	AN	1	Total Zn 1 1	0	0

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

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

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

- Molecule 61 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	AA	247	Total O 247 247	0	0
61	AD	1	Total O 1 1	0	0
61	AE	2	Total O 2 2	0	0
61	AL	2	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	AM	2	Total O 2 2	0	0
61	AO	1	Total O 1 1	0	0
61	AV	3	Total O 3 3	0	0
61	AW	13	Total O 13 13	0	0
61	AX	11	Total O 11 11	0	0
61	AY	1	Total O 1 1	0	0
61	BA	1396	Total O 1396 1396	0	0
61	BB	34	Total O 34 34	0	0
61	BD	12	Total O 12 12	0	0
61	BE	11	Total O 11 11	0	0
61	BF	5	Total O 5 5	0	0
61	BG	3	Total O 3 3	0	0
61	BI	1	Total O 1 1	0	0
61	BN	1	Total O 1 1	0	0
61	BO	2	Total O 2 2	0	0
61	BP	23	Total O 23 23	0	0
61	BQ	3	Total O 3 3	0	0
61	BR	1	Total O 1 1	0	0
61	BT	2	Total O 2 2	0	0
61	BU	3	Total O 3 3	0	0
61	BV	2	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	BW	1	Total O 1 1	0	0
61	BX	2	Total O 2 2	0	0
61	BZ	1	Total O 1 1	0	0
61	B0	8	Total O 8 8	0	0
61	B3	1	Total O 1 1	0	0
61	B5	6	Total O 6 6	0	0
61	B6	1	Total O 1 1	0	0
61	B7	2	Total O 2 2	0	0
61	B8	7	Total O 7 7	0	0
61	CA	184	Total O 184 184	0	0
61	CJ	2	Total O 2 2	0	0
61	CP	1	Total O 1 1	0	0
61	CV	2	Total O 2 2	0	0
61	CW	3	Total O 3 3	0	0
61	CX	6	Total O 6 6	0	0
61	DA	960	Total O 960 960	0	0
61	DB	8	Total O 8 8	0	0
61	DD	16	Total O 16 16	0	0
61	DE	9	Total O 9 9	0	0
61	DF	5	Total O 5 5	0	0
61	DN	3	Total O 3 3	0	0

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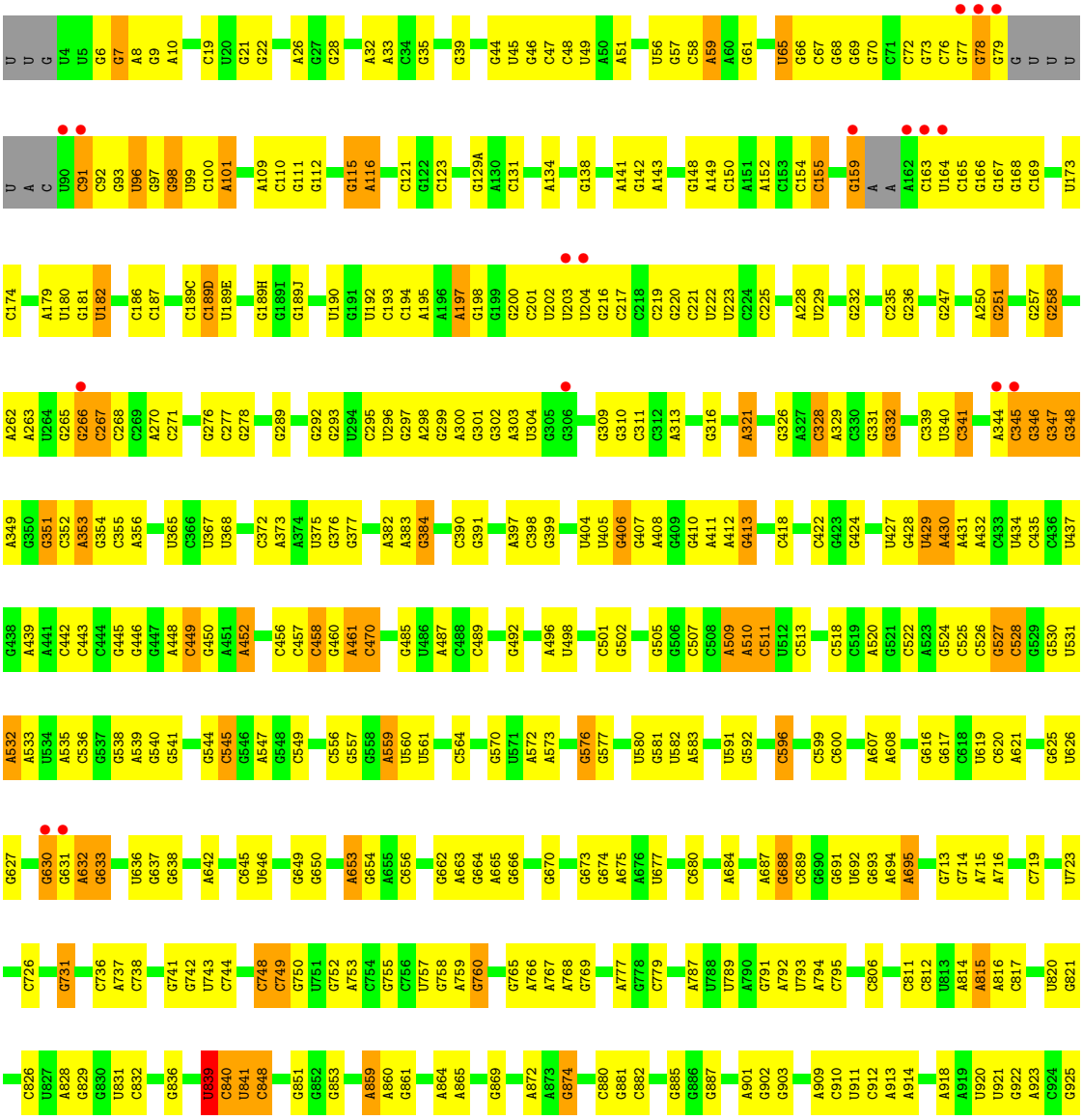
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	DO	2	Total O 2 2	0	0
61	DP	15	Total O 15 15	0	0
61	DQ	1	Total O 1 1	0	0
61	DR	1	Total O 1 1	0	0
61	DU	1	Total O 1 1	0	0
61	DW	1	Total O 1 1	0	0
61	DX	1	Total O 1 1	0	0
61	DY	2	Total O 2 2	0	0
61	D0	8	Total O 8 8	0	0
61	D1	4	Total O 4 4	0	0
61	D7	2	Total O 2 2	0	0
61	D8	1	Total O 1 1	0	0

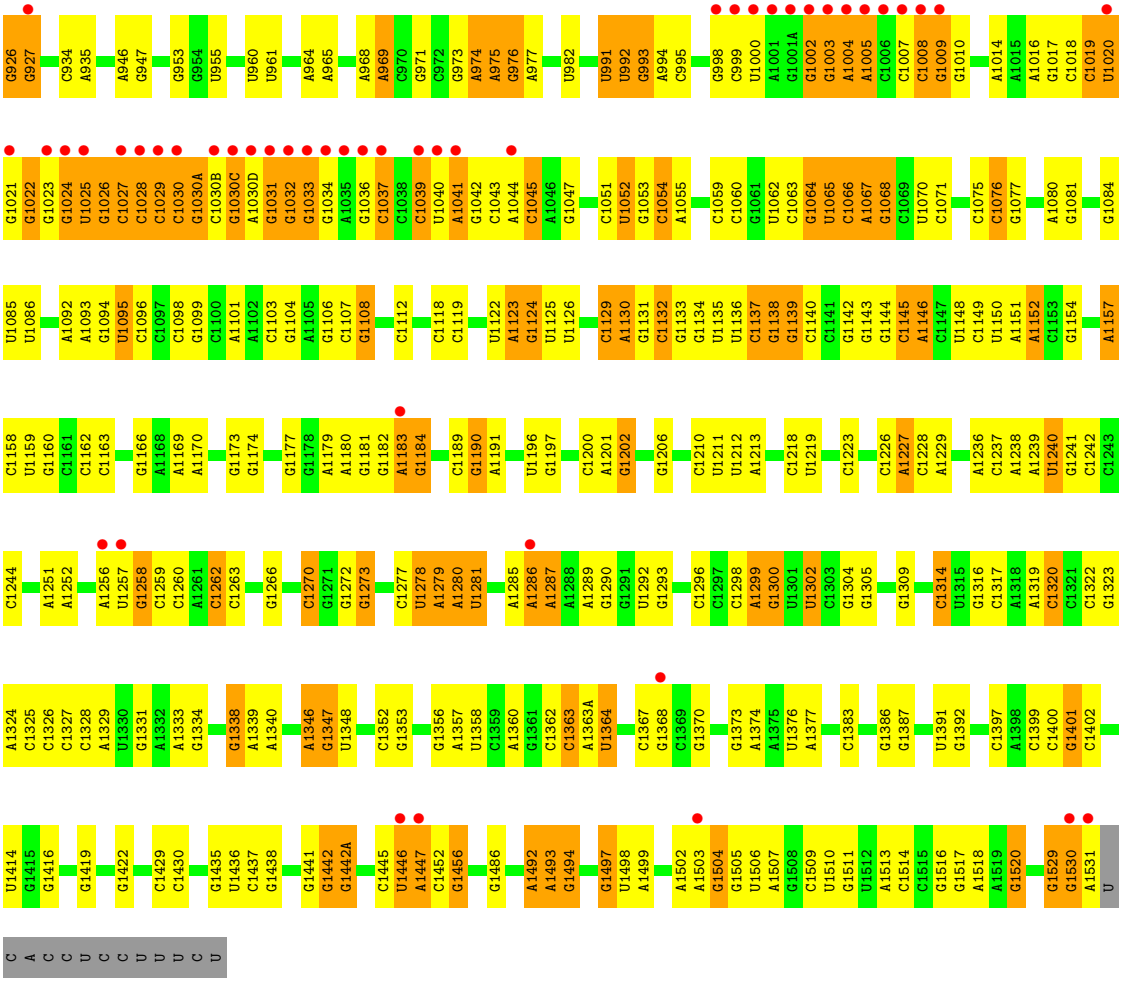
3 Residue-property plots (i)

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

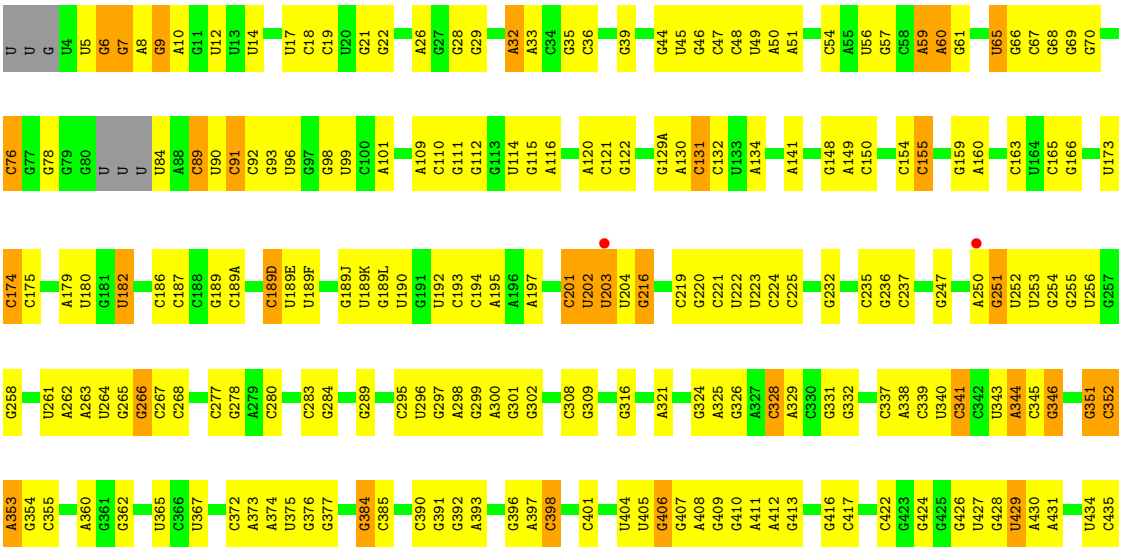
Chain AA:

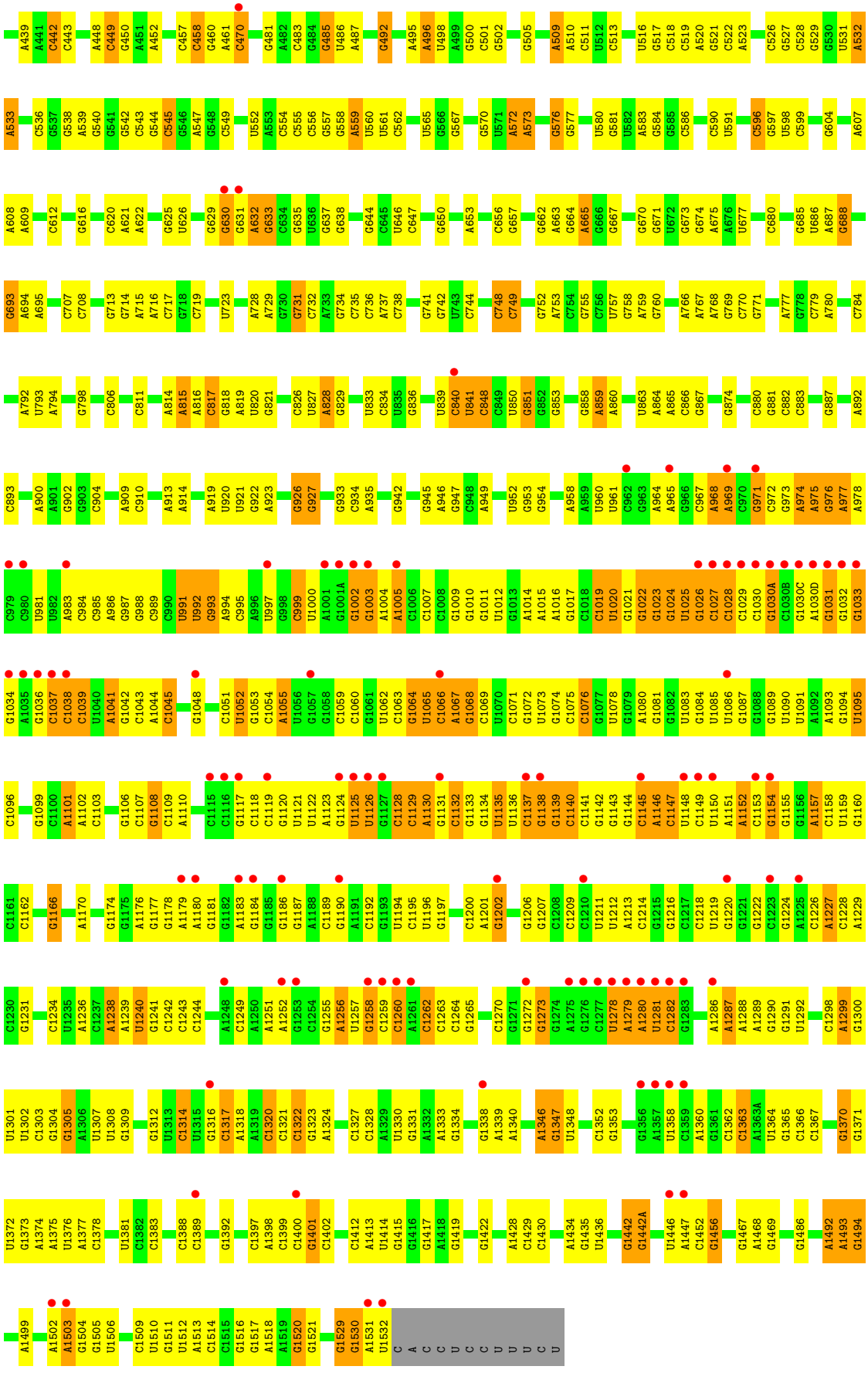




• Molecule 1: 16S Ribosomal RNA

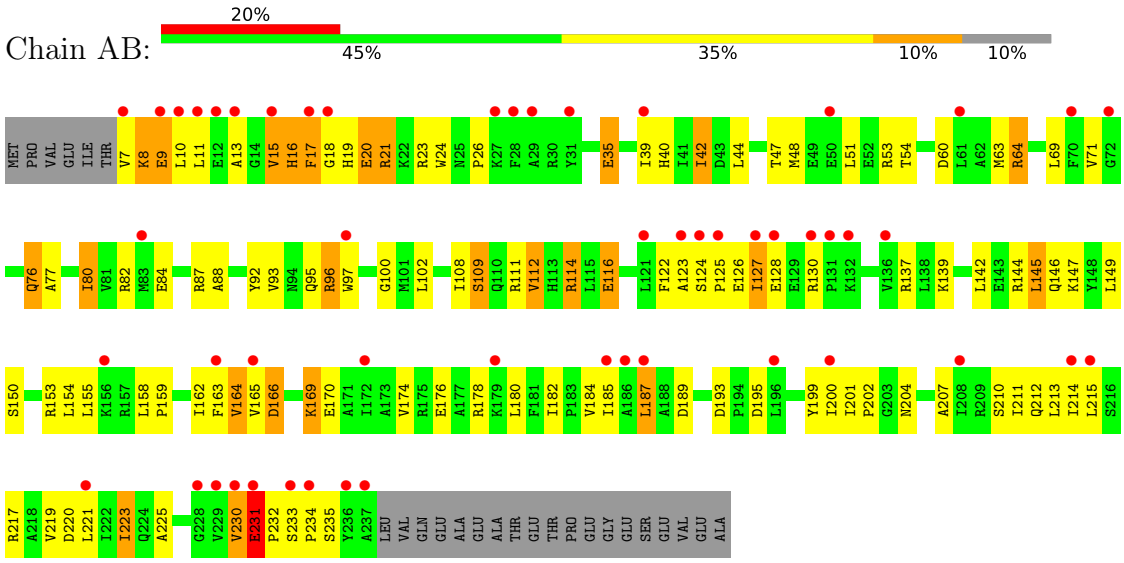
Chain CA:




A439 A441 C442 C443 A448 C449 G450 A451 A452 C457 C458 G460 A461 C470 G481 A482 C483 G484 G485 U486 A487 G492 A495 A496 U498 A499 G500 C501 G502 G505 A509 A510 C511 U512 C513 U516 G517 C518 C519 A520 G521 C522 A523 C526 G527 C528 G529 G530 U531 A532
A533 C536 G537 G538 A539 G540 G541 G542 C543 G544 C545 G546 A547 G548 C549 U552 A553 C554 C555 C556 G557 G558 A559 U560 U561 C562 U565 G566 G567 G570 U571 A572 A573 G576 G577 U580 G581 U582 A583 G584 G585 C586 C590 U591 C596 G597 U598 C599 G604 A607
A608 A609 C612 G616 C620 A621 A622 G625 U626 G629 G630 G631 A632 G633 C634 G635 U636 G637 G638 G644 C645 U646 C647 G650 A653 C656 G657 G662 A663 G664 A665 G666 G667 G670 G671 U672 G673 G674 A675 A676 U677 C680 G685 U686 A687 G688
G693 A694 A695 C707 C708 G713 G714 A715 A716 C717 G718 C719 U723 A728 A729 G730 G731 C732 A733 G734 C735 C736 A737 C738 G741 G742 U743 C744 C748 C749 G752 A753 C754 G755 G756 U757 G758 A759 G760 A766 A767 A768 G769 C770 G771 A777 G778 C779 A780 C784
A792 U793 A794 G798 C806 C811 A814 A815 A816 C817 G818 A819 U820 G821 C826 U827 A828 G829 U833 C834 U835 G836 U839 C840 U841 C848 C849 U850 G851 G852 G853 G858 A859 A860 U863 A864 A865 C866 G867 G874 C880 G881 C882 C883 G887 A892
C893 A900 A901 G902 G903 C904 A909 C910 A913 A914 A919 U920 U921 G922 A923 G926 G927 G933 C934 A935 G942 G945 A946 G947 G948 A949 U952 G953 G954 A958 A959 U960 U961 C962 G963 A964 A965 G966 C967 A968 A969 C970 G971 C972 G973 A974 A975 G976 A977 A978
C979 Q980 U981 U982 A983 C984 C985 A986 G987 G988 C989 C990 U991 U992 G993 A994 C995 A996 U997 G998 C999 U1000 A1001 G1001A G1002 G1003 A1004 A1005 C1006 C1007 C1008 G1009 G1010 G1011 U1012 G1013 A1014 A1015 A1016 G1017 C1018 C1019 U1020 G1021 G1022 G1023 G1024 U1025 G1026 C1027 C1028 C1029 C1030 G1030A C1030B G1030C A1030D G1031 G1032 G1033
G1034 A1035 G1036 C1037 C1038 C1039 U1040 A1041 G1042 C1043 A1044 C1045 G1048 C1051 U1052 G1053 C1054 A1055 U1056 G1057 G1058 C1059 C1060 G1061 U1062 C1063 G1064 U1065 C1066 A1067 G1068 C1069 U1070 C1071 G1072 U1073 G1074 C1075 C1076 G1077 U1078 G1079 A1080 G1081 G1082 U1083 G1084 U1085 U1086 G1087 G1088 G1089 U1090 U1091 A1092 A1093 G1094 U1095
C1096 G1099 C1100 A1101 A1102 C1103 G1106 C1107 G1108 C1109 A1110 C1115 C1116 G1117 C1118 C1119 G1120 U1121 U1122 A1123 G1124 U1125 U1126 G1127 C1128 C1129 A1130 G1131 C1132 G1133 G1134 U1135 U1136 C1137 G1138 G1139 C1140 C1141 G1142 G1143 G1144 C1145 A1146 C1147 U1148 C1149 U1150 A1151 A1152 C1153 G1154 G1155 G1156 A1157 C1158 U1159 G1160
C1161 C1162 G1166 A1170 G1174 G1175 A1176 G1177 G1178 A1179 A1180 G1181 G1182 A1183 G1184 G1185 G1186 G1187 A1188 C1189 G1190 A1191 C1192 G1193 U1194 C1195 U1196 G1197 C1200 A1201 G1202 G1206 G1207 C1208 C1209 C1210 U1211 U1212 A1213 C1214 G1215 G1216 C1217 C1218 U1219 G1220 G1221 G1222 C1223 G1224 A1225 C1226 A1227 C1228 A1229
C1230 G1231 C1234 U1235 A1236 C1237 A1238 A1239 U1240 G1241 C1242 C1243 C1244 A1248 C1249 A1250 A1251 A1252 G1253 C1254 G1255 A1256 U1257 G1258 C1259 C1260 A1261 C1262 C1263 C1264 G1265 C1270 G1271 G1272 G1273 G1274 A1275 G1276 C1277 U1278 A1279 A1280 U1281 C1282 G1283 A1286 A1287 A1288 A1289 G1290 G1291 U1292 C1298 A1299 G1300
U1301 U1302 C1303 G1304 G1305 A1306 U1307 U1308 G1309 G1312 U1313 C1314 U1315 G1316 C1317 A1318 A1319 C1320 C1321 C1322 G1323 A1324 C1327 C1328 A1329 U1330 G1331 A1332 A1333 G1334 G1338 A1339 A1340 A1346 G1347 U1348 C1352 G1353 G1356 A1357 U1358 C1359 A1360 G1361 C1362 C1363 A1363A U1364 G1365 C1366 C1367 G1370 G1371
U1372 G1373 A1374 A1375 U1376 A1377 C1378 U1381 C1382 C1383 C1388 C1389 G1392 C1397 A1398 C1399 C1400 G1401 C1402 C1412 A1413 U1414 G1415 G1416 G1417 A1418 G1419 G1422 A1428 C1429 C1430 A1434 G1435 U1436 G1442 G1442A U1446 A1447 C1452 G1456 G1467 A1468 G1469 G1486 A1492 A1493 G1494
A1499 A1502 A1503 G1504 G1505 U1506 C1509 U1510 G1511 U1512 A1513 C1514 C1515 G1516 G1517 A1518 A1519 G1520 G1521 G1529 G1530 A1531 U1532 C A C C U C C U U U C U

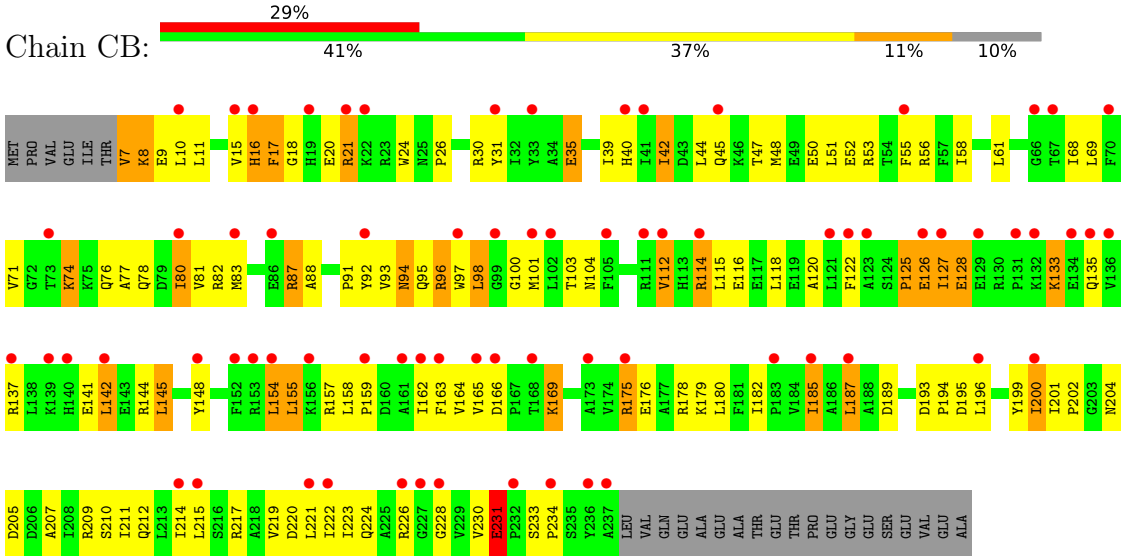
• Molecule 2: 30S Ribosomal Protein S2

Chain AB:



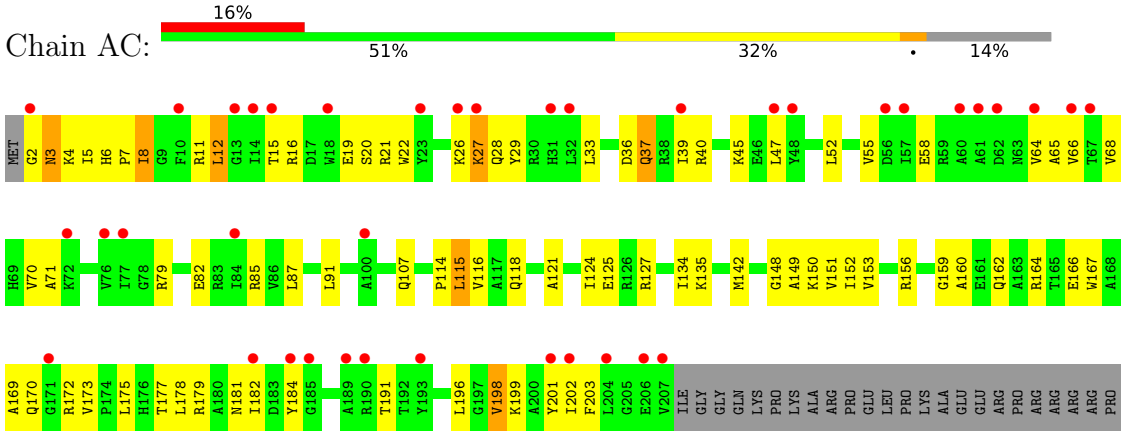
• Molecule 2: 30S Ribosomal Protein S2

Chain CB:



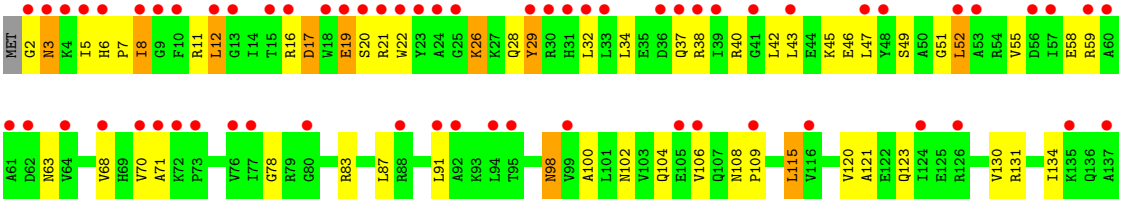
• Molecule 3: 30S Ribosomal Protein S3

Chain AC:



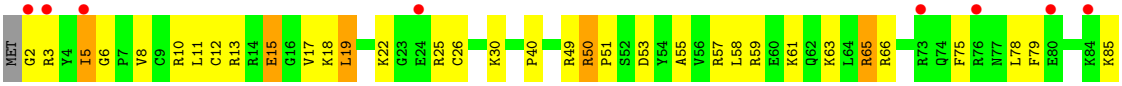
• Molecule 3: 30S Ribosomal Protein S3

Chain CC:



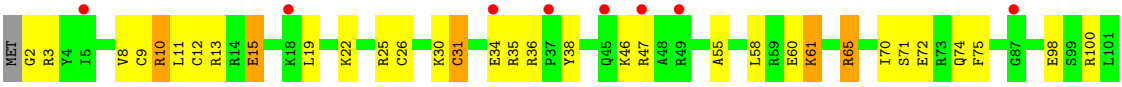
• Molecule 4: 30S Ribosomal Protein S4

Chain AD:



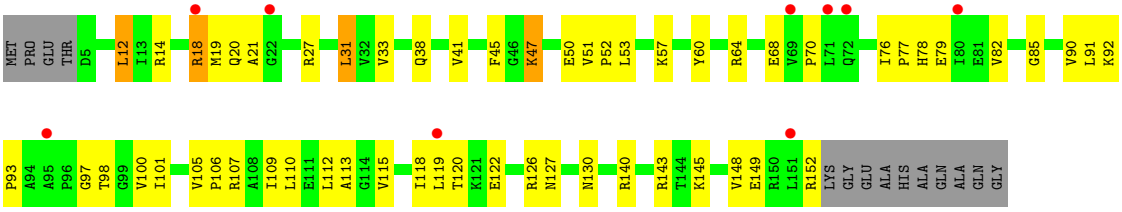
• Molecule 4: 30S Ribosomal Protein S4

Chain CD:



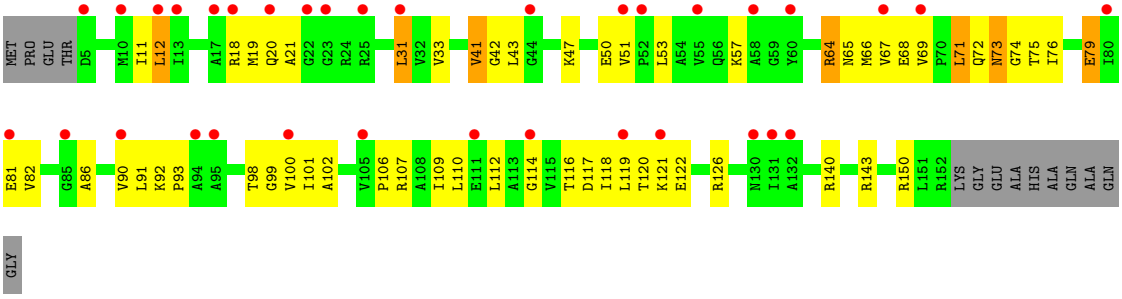
• Molecule 5: 30S Ribosomal Protein S5

Chain AE:



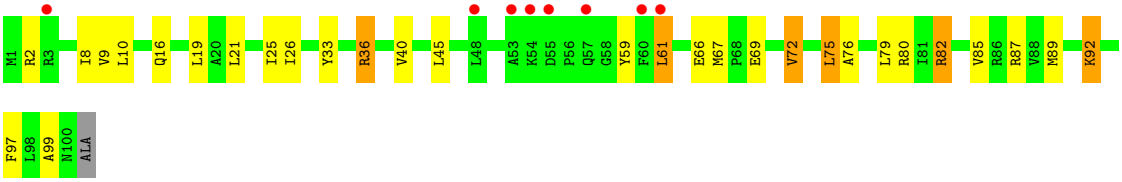
• Molecule 5: 30S Ribosomal Protein S5

Chain CE:



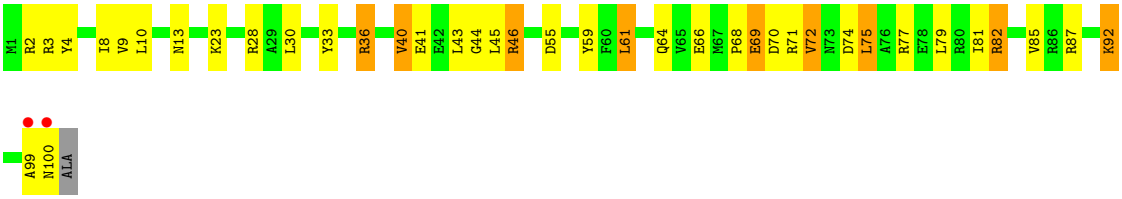
• Molecule 6: 30S Ribosomal Protein S6

Chain AF:



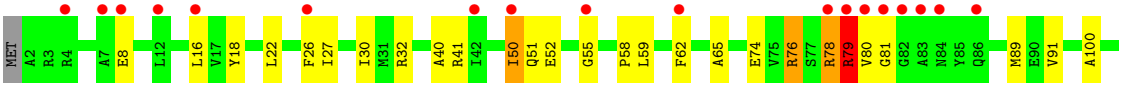
• Molecule 6: 30S Ribosomal Protein S6

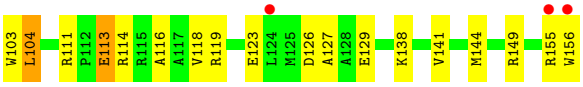
Chain CF:



• Molecule 7: 30S Ribosomal Protein S7

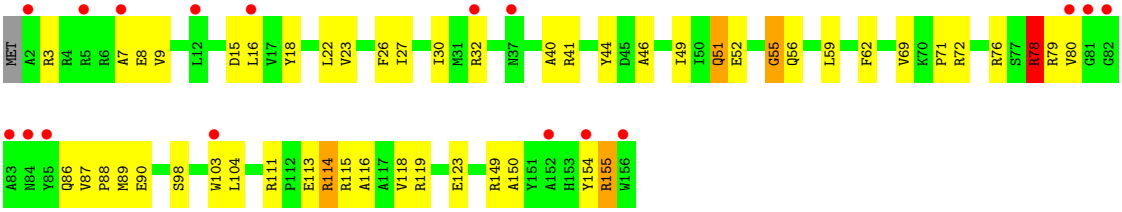
Chain AG:





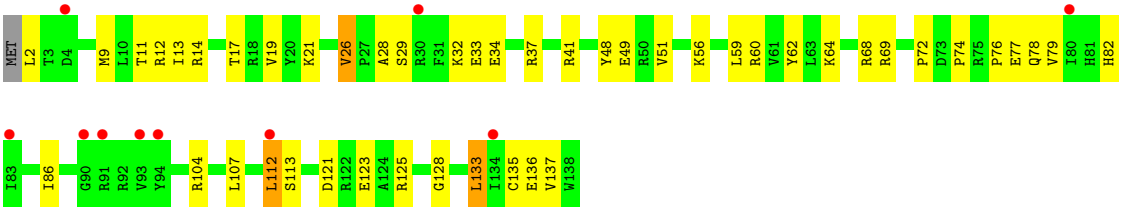
• Molecule 7: 30S Ribosomal Protein S7

Chain CG:



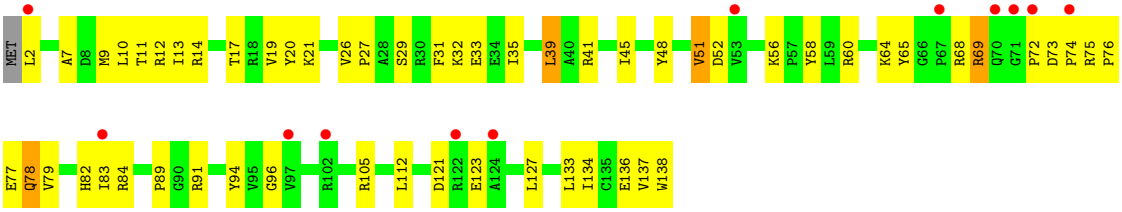
• Molecule 8: 30S Ribosomal Protein S8

Chain AH:



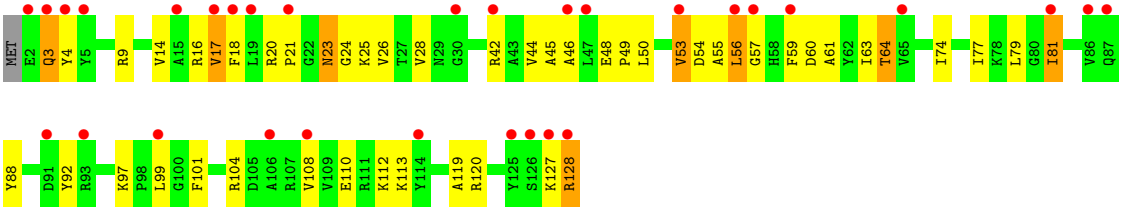
• Molecule 8: 30S Ribosomal Protein S8

Chain CH:



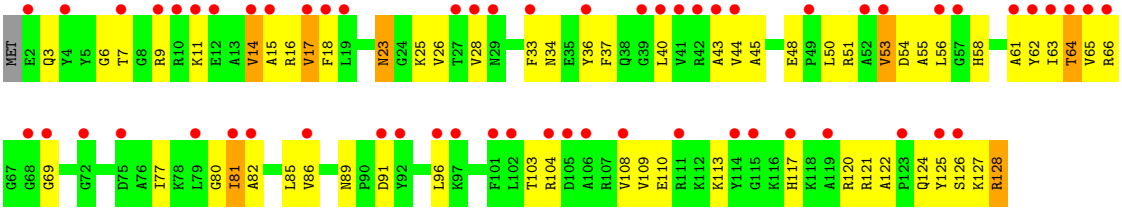
• Molecule 9: 30S Ribosomal Protein S9

Chain AI:



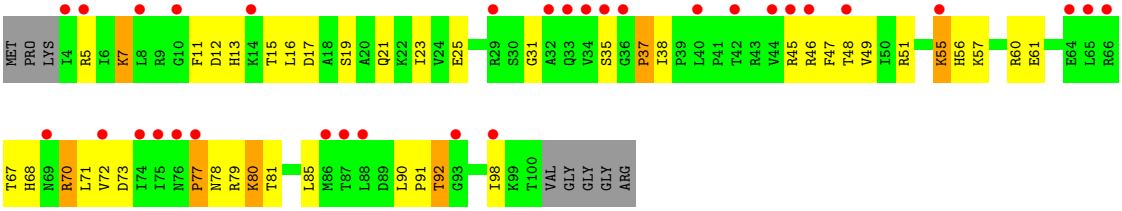
• Molecule 9: 30S Ribosomal Protein S9

Chain CI:



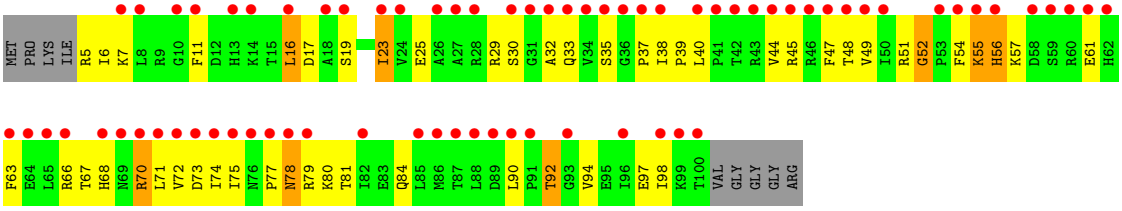
• Molecule 10: 30S Ribosomal Protein S10

Chain AJ:



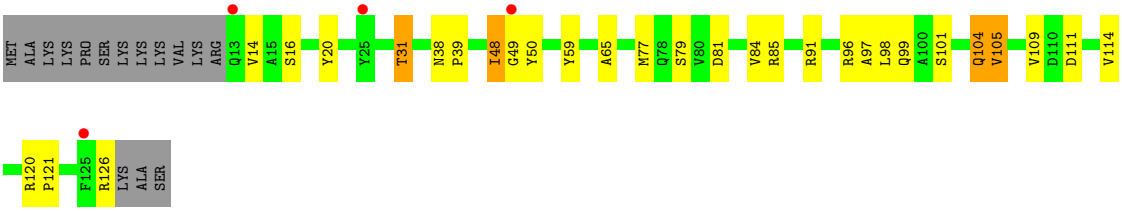
• Molecule 10: 30S Ribosomal Protein S10

Chain CJ:



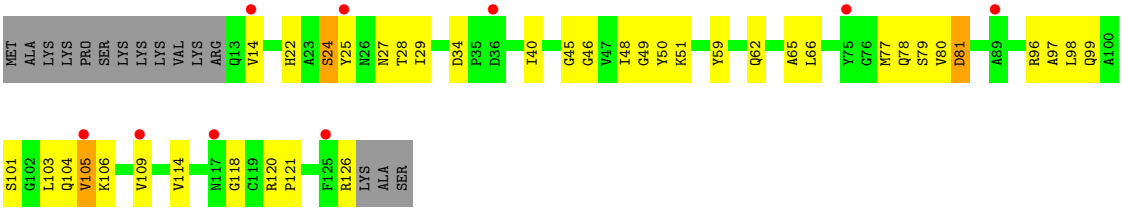
• Molecule 11: 30S Ribosomal Protein S11

Chain AK:



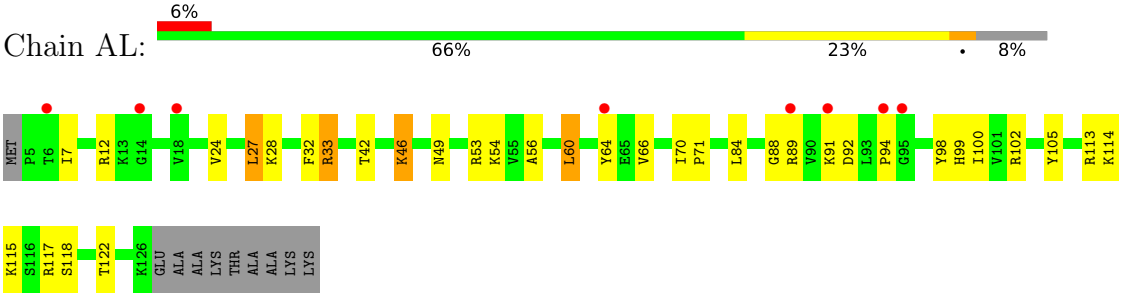
• Molecule 11: 30S Ribosomal Protein S11

Chain CK:



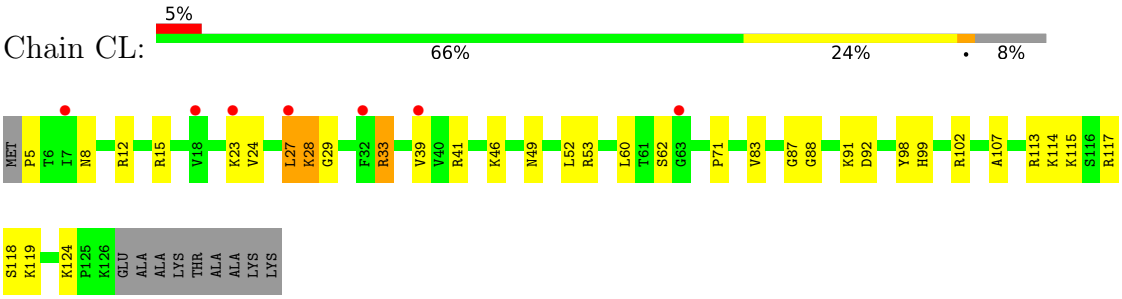
• Molecule 12: 30S Ribosomal Protein S12

Chain AL:



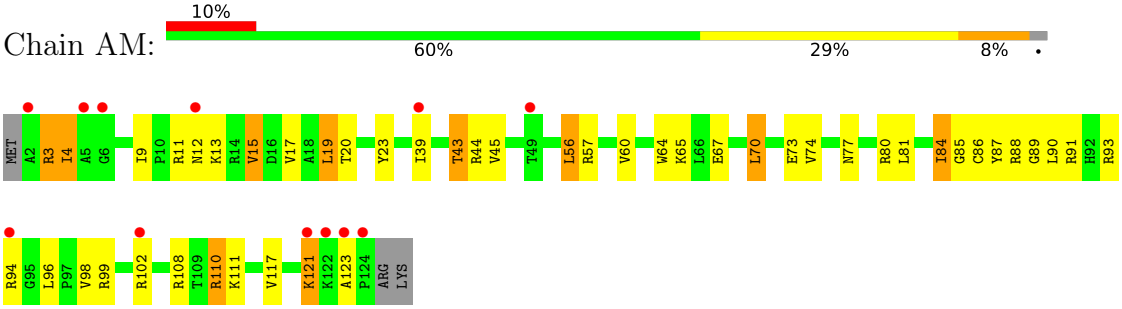
• Molecule 12: 30S Ribosomal Protein S12

Chain CL:



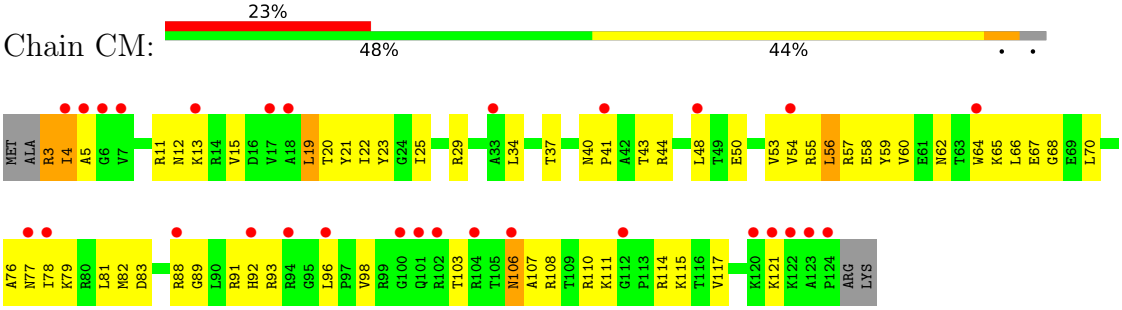
• Molecule 13: 30S Ribosomal Protein S13

Chain AM:



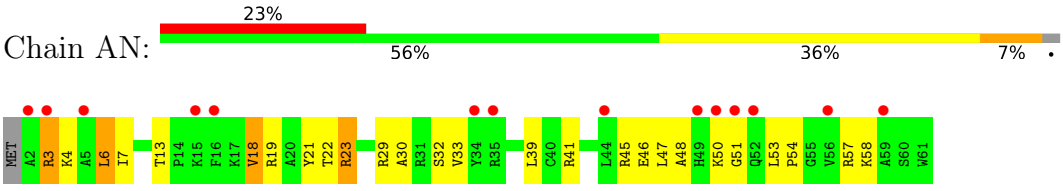
• Molecule 13: 30S Ribosomal Protein S13

Chain CM:



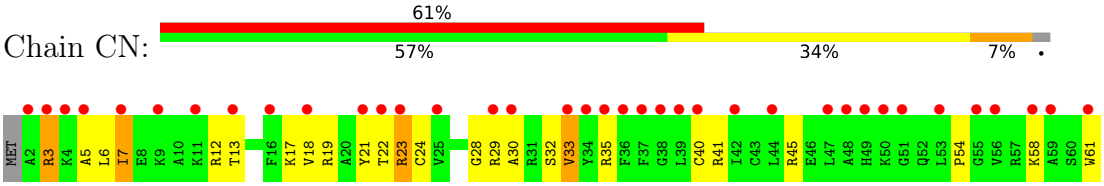
• Molecule 14: 30S Ribosomal Protein S14

Chain AN:



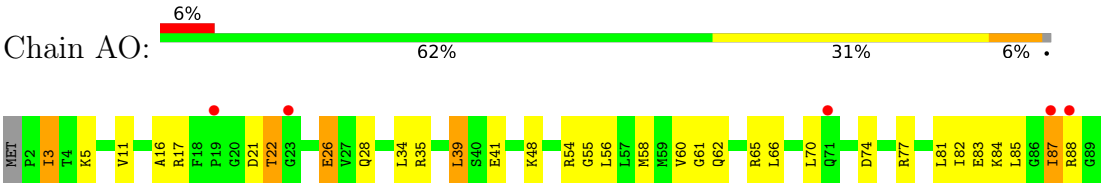
• Molecule 14: 30S Ribosomal Protein S14

Chain CN:



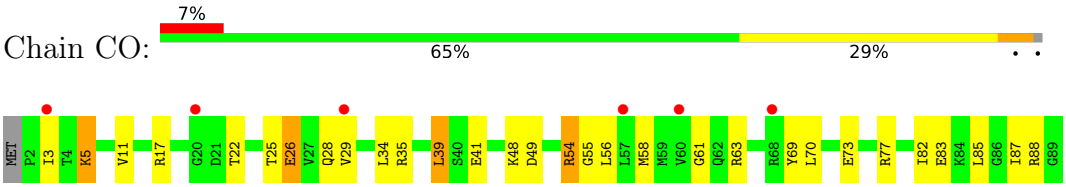
• Molecule 15: 30S Ribosomal Protein S15

Chain AO:



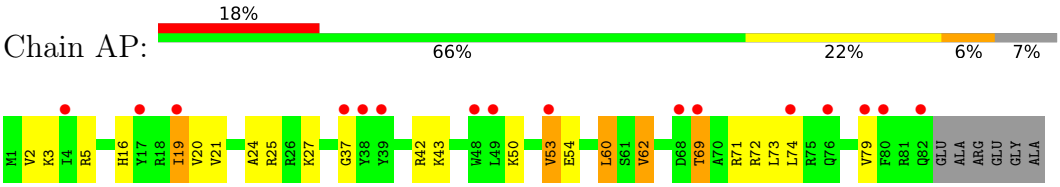
• Molecule 15: 30S Ribosomal Protein S15

Chain CO:



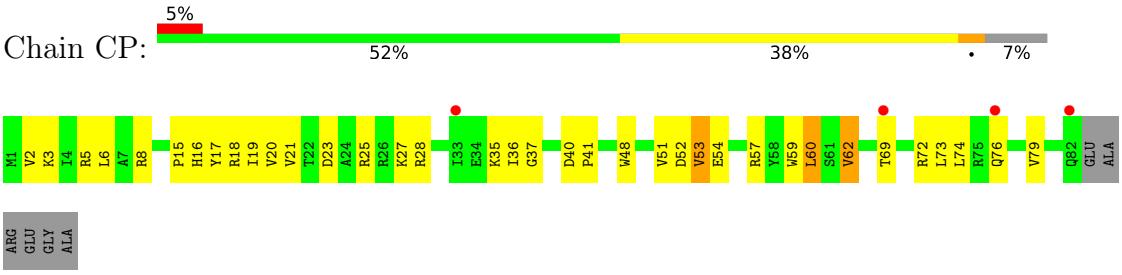
• Molecule 16: 30S Ribosomal Protein S16

Chain AP:



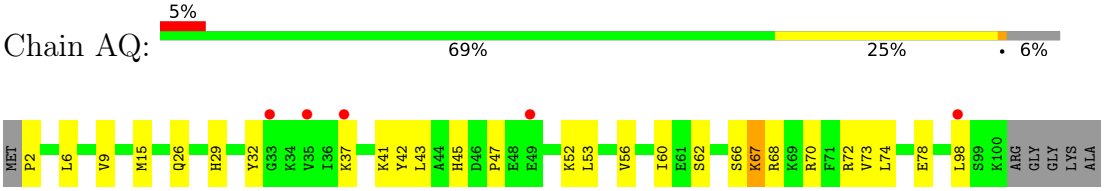
• Molecule 16: 30S Ribosomal Protein S16

Chain CP:



• Molecule 17: 30S Ribosomal Protein S17

Chain AQ:

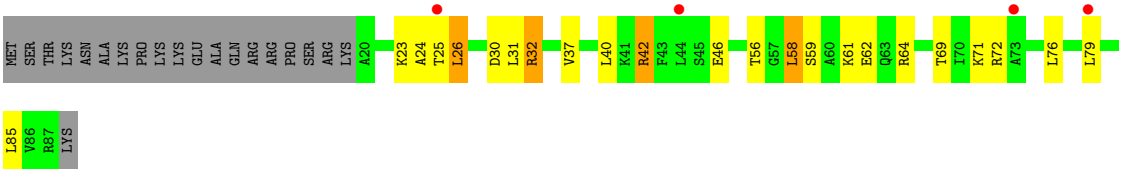


• Molecule 17: 30S Ribosomal Protein S17

Chain CQ:

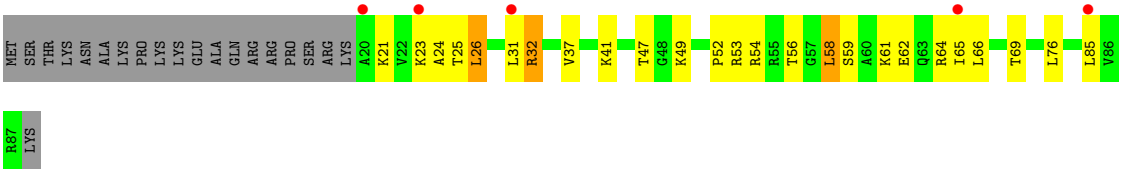
• Molecule 18: 30S Ribosomal Protein S18

Chain AR:



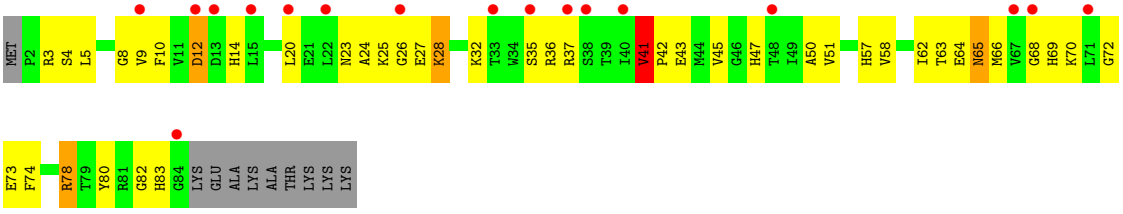
• Molecule 18: 30S Ribosomal Protein S18

Chain CR:



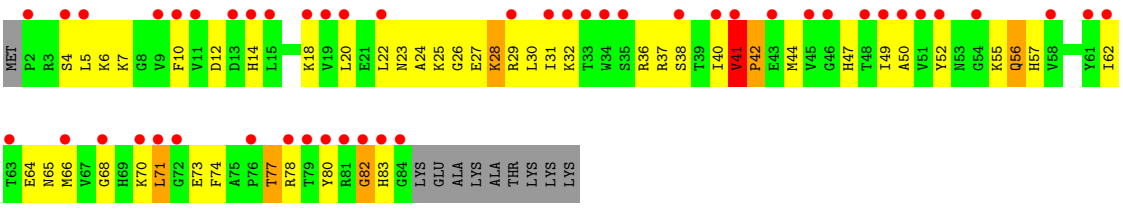
• Molecule 19: 30S Ribosomal Protein S19

Chain AS:



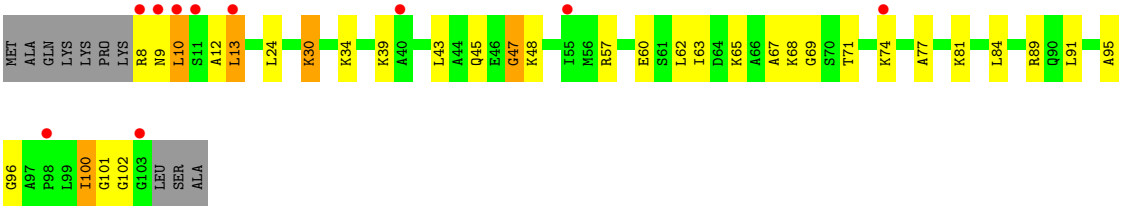
• Molecule 19: 30S Ribosomal Protein S19

Chain CS:

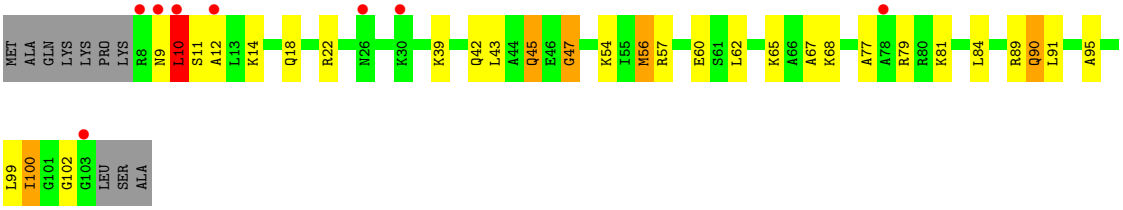


• Molecule 20: 30S Ribosomal Protein S20

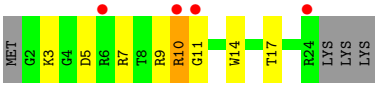
Chain AT:



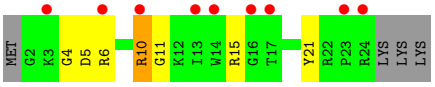
• Molecule 20: 30S Ribosomal Protein S20



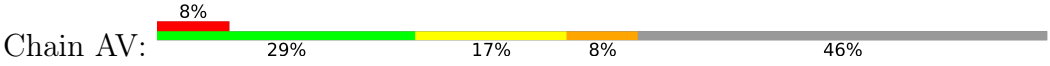
• Molecule 21: 30S Ribosomal Protein THX

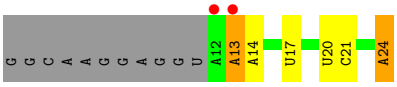


• Molecule 21: 30S Ribosomal Protein THX

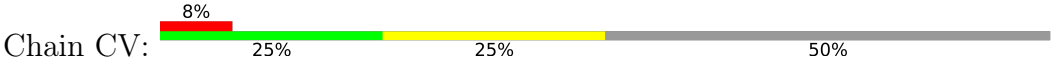


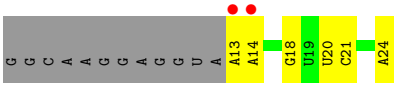
• Molecule 22: mRNA



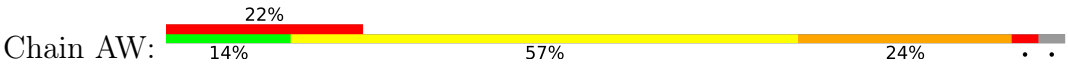


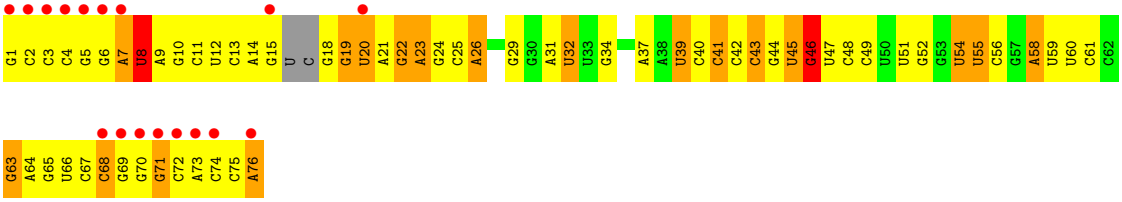
• Molecule 22: mRNA





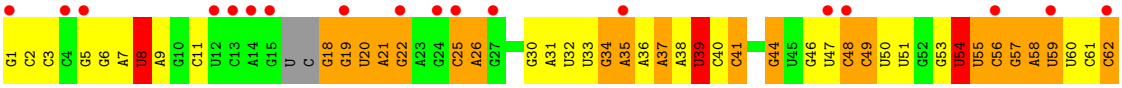
• Molecule 23: A/P-site tRNA

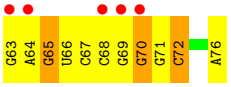




• Molecule 23: A/P-site tRNA

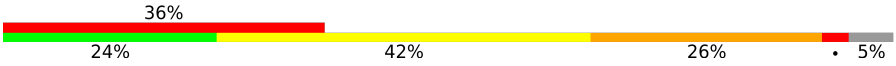
Chain AY:

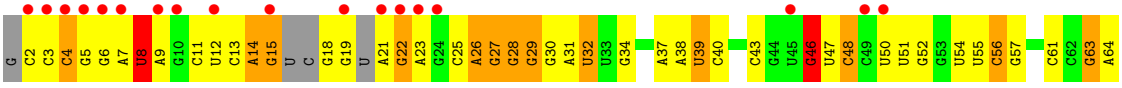


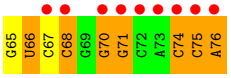


• Molecule 23: A/P-site tRNA

Chain CW:

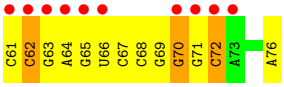






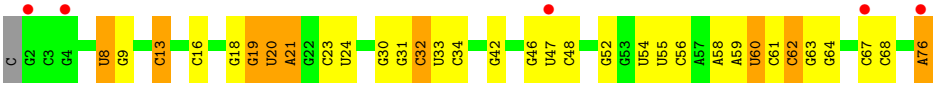
• Molecule 23: A/P-site tRNA

Chain CY:



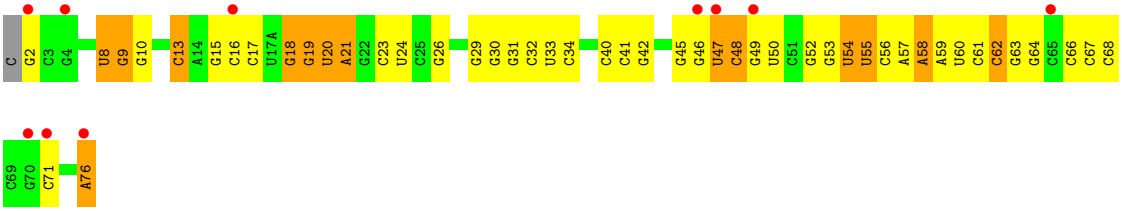
• Molecule 24: E-site tRNA

Chain AX:



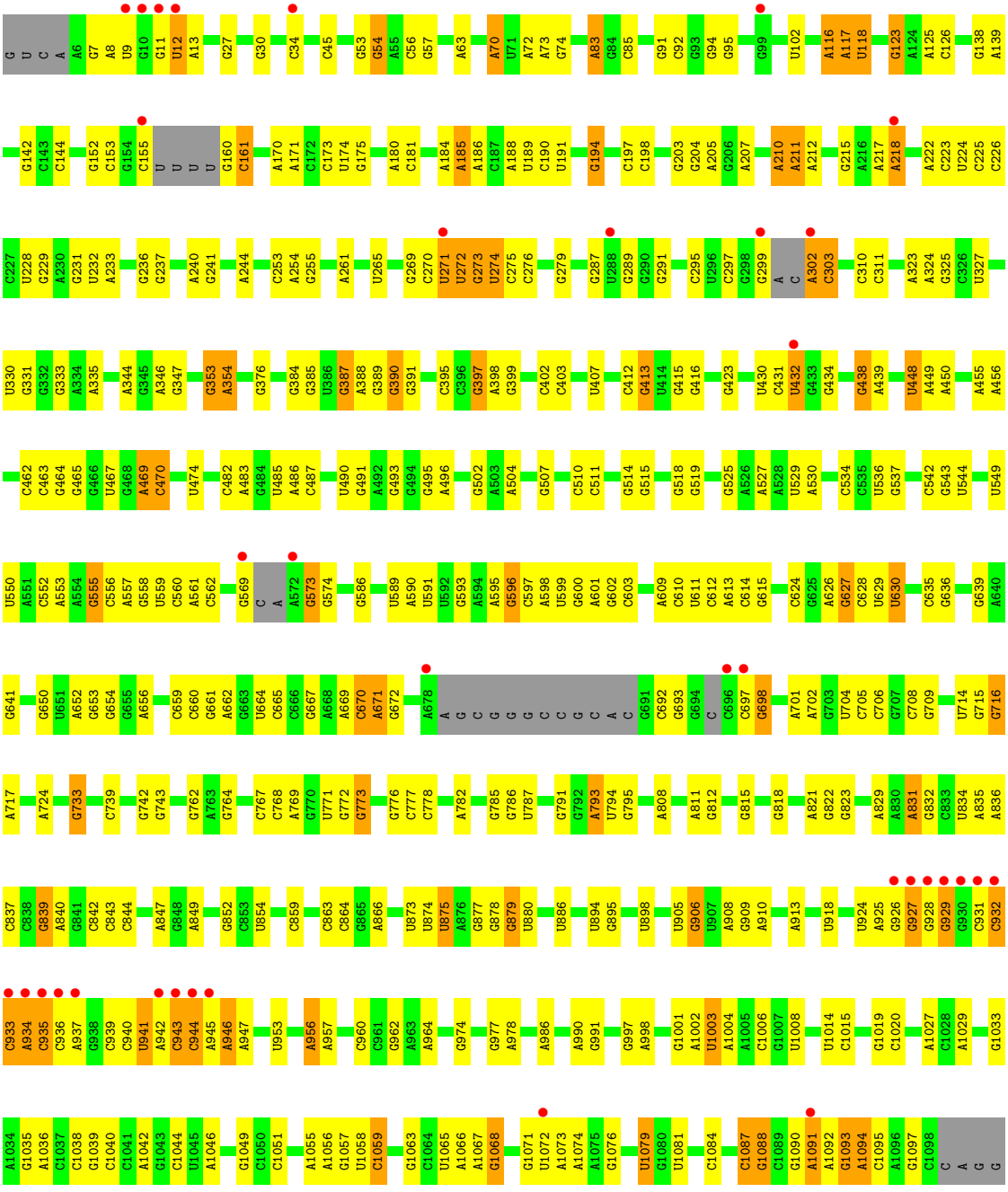
• Molecule 24: E-site tRNA

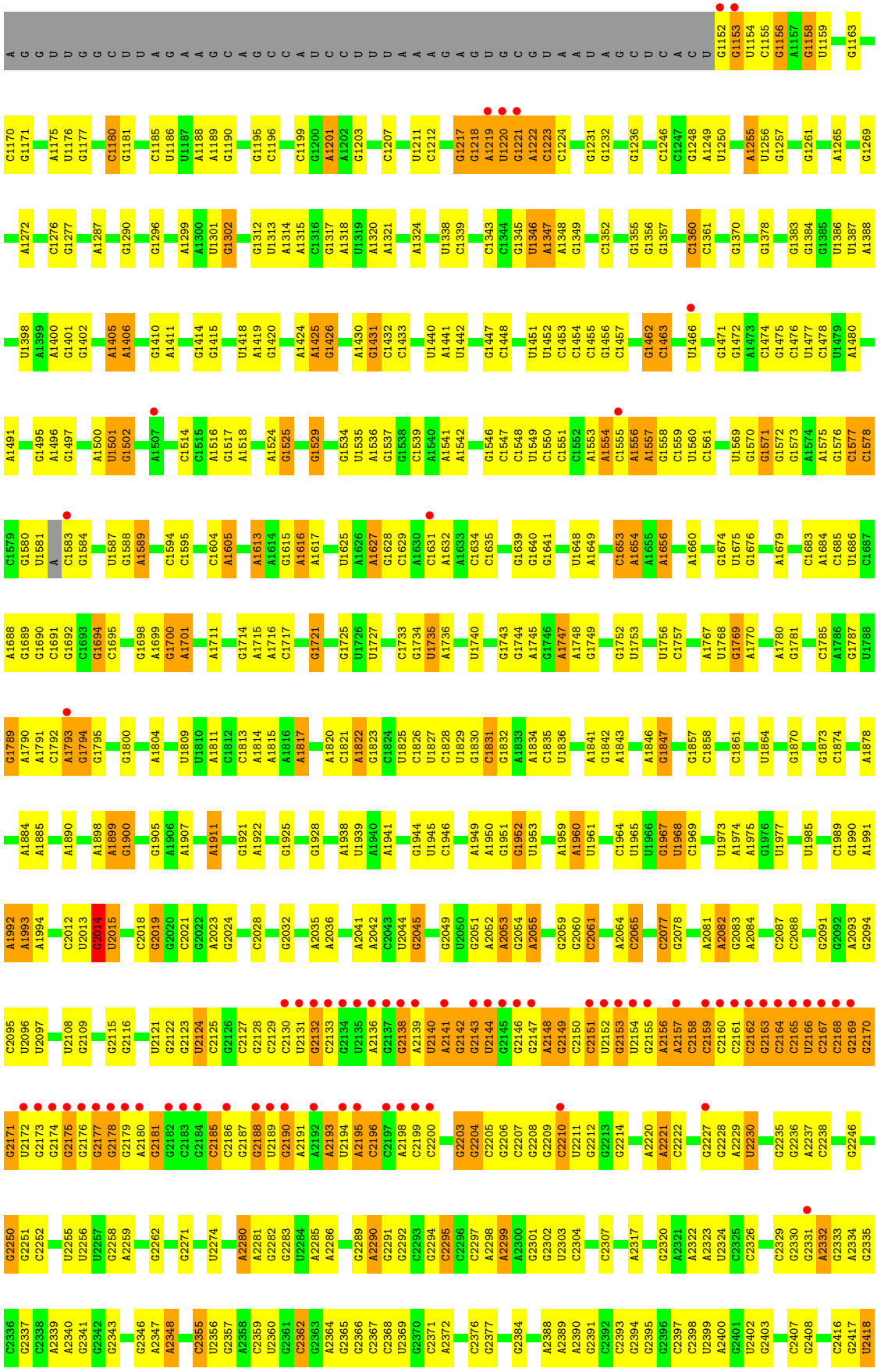
Chain CX:

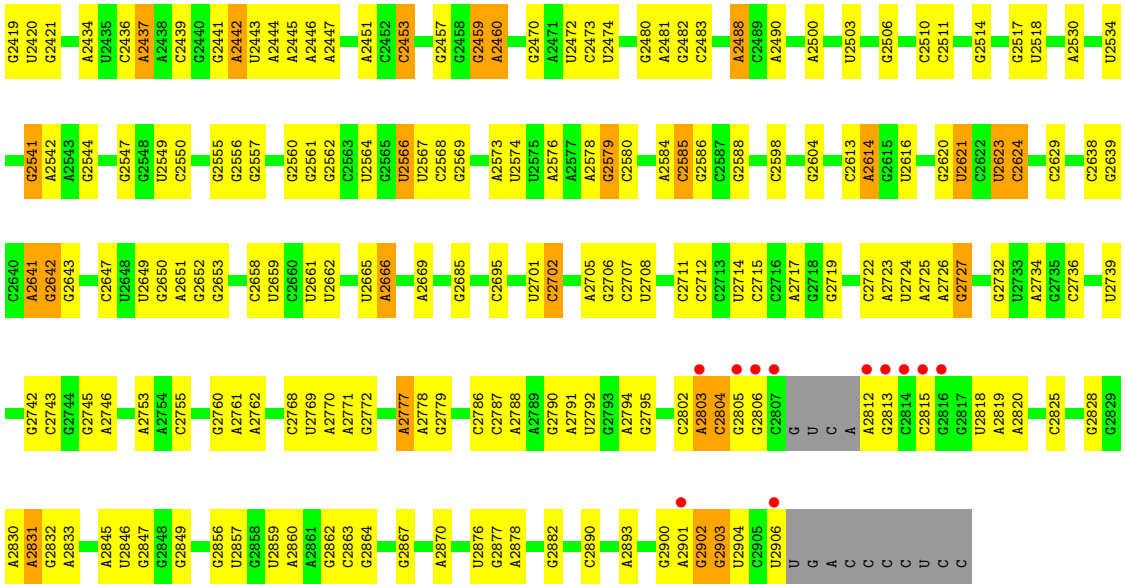


• Molecule 25: 23S Ribosomal RNA

Chain BA:

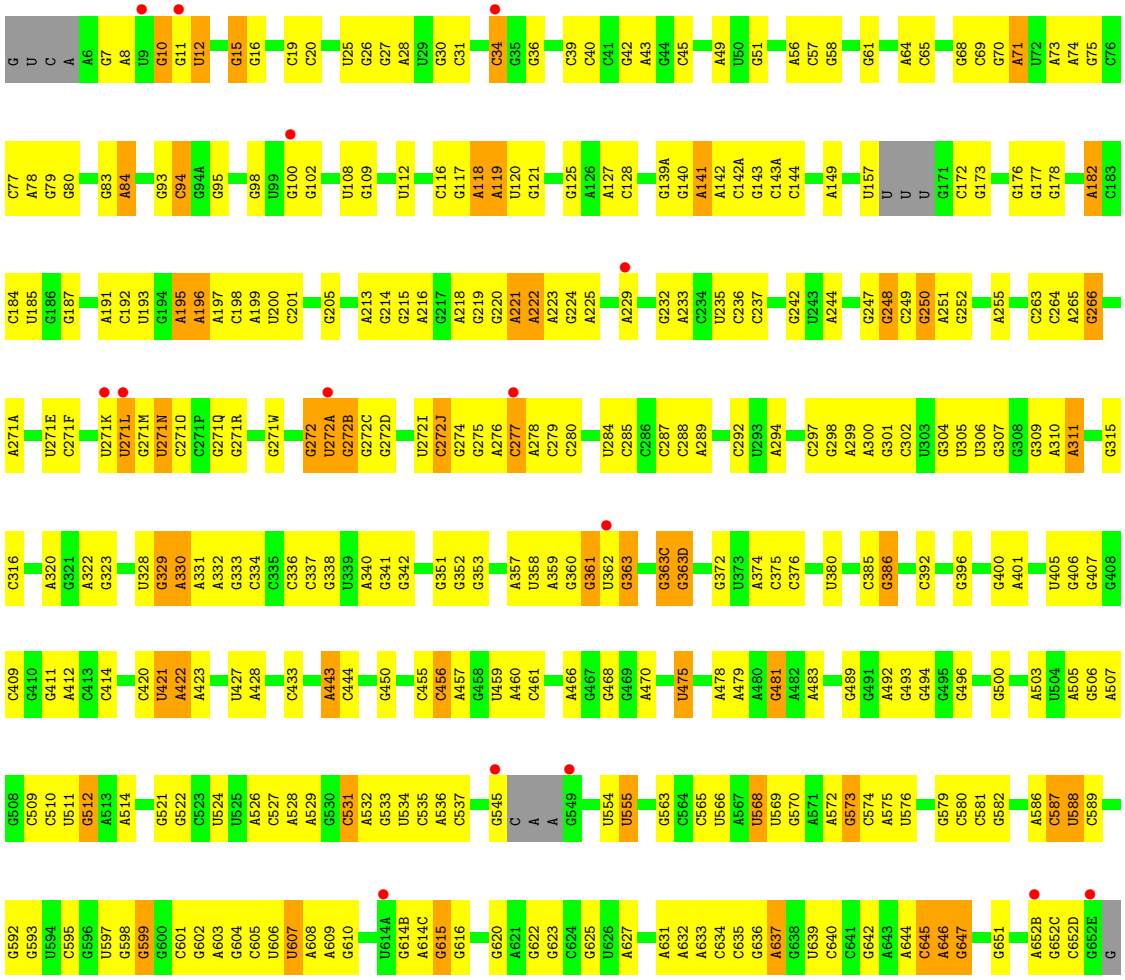


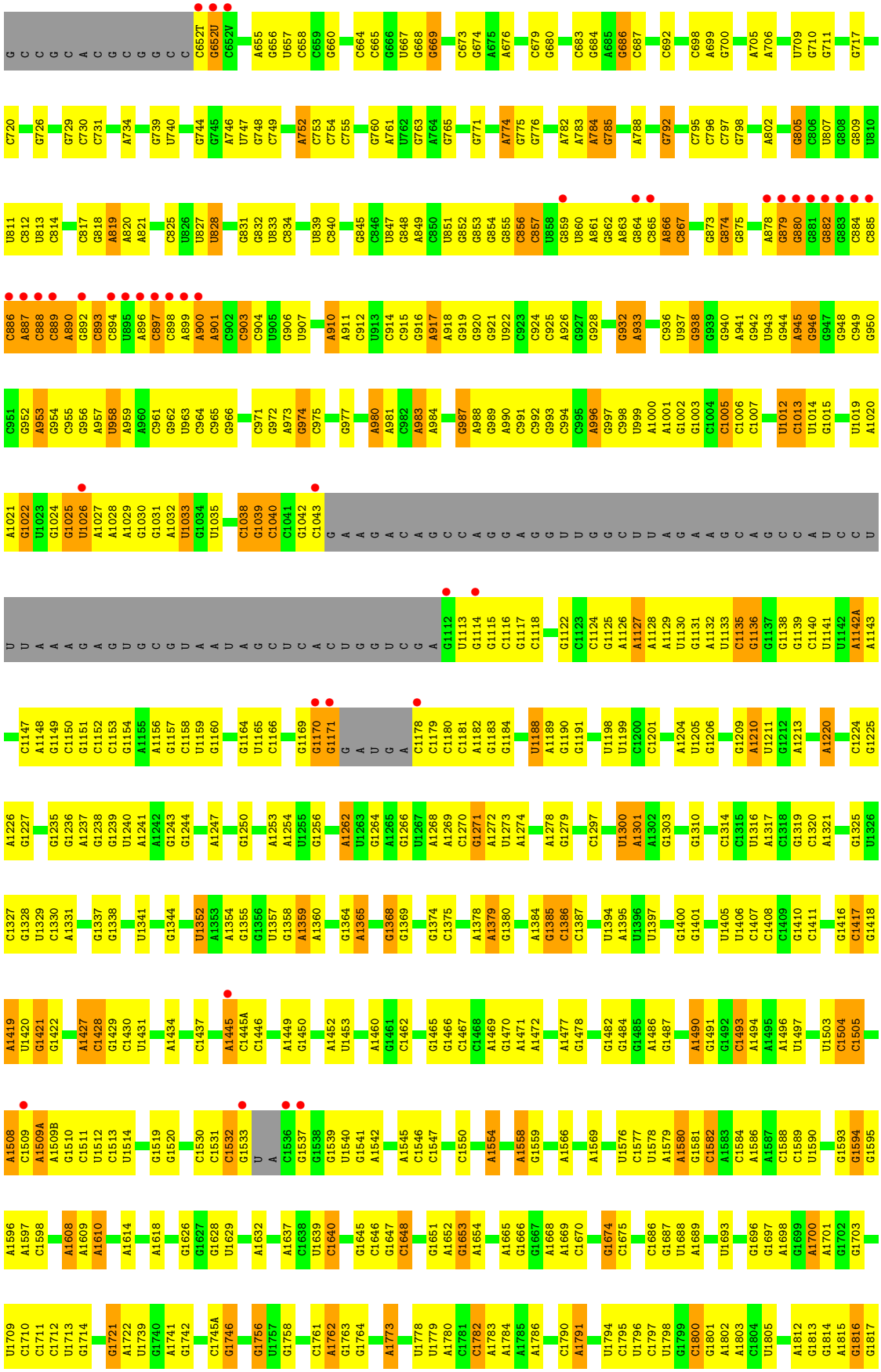


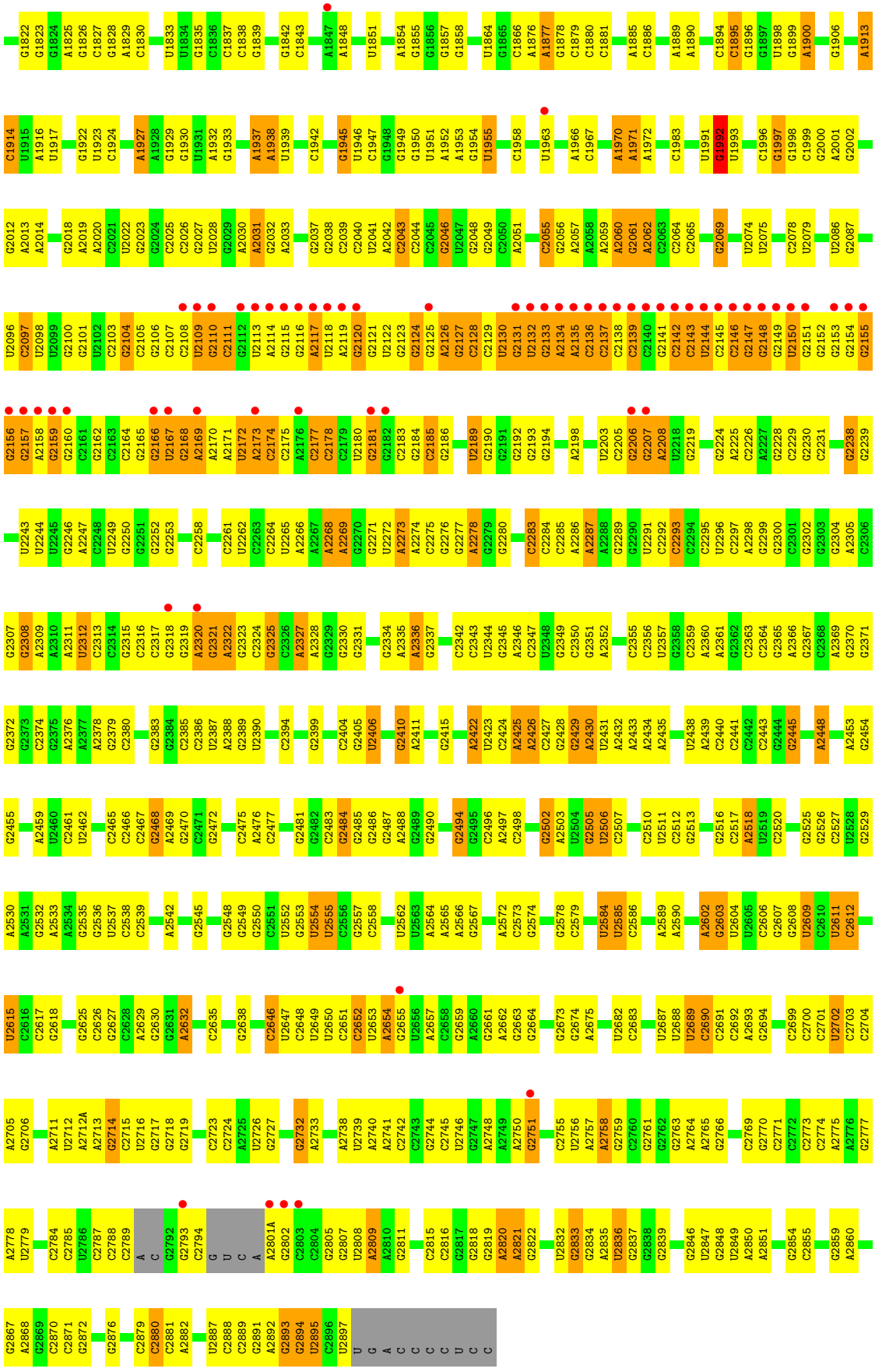


• Molecule 25: 23S Ribosomal RNA

Chain DA:

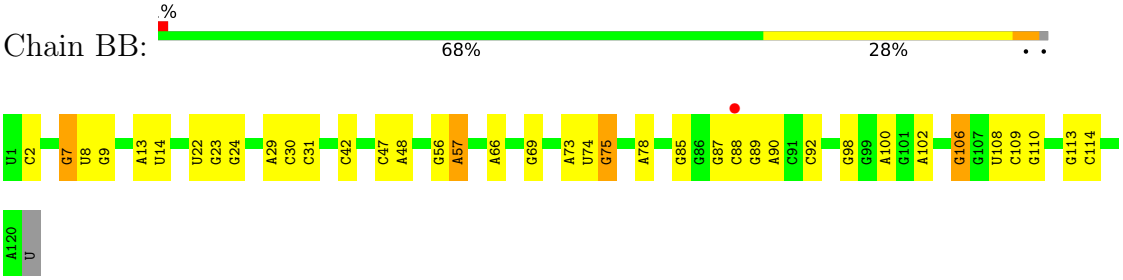






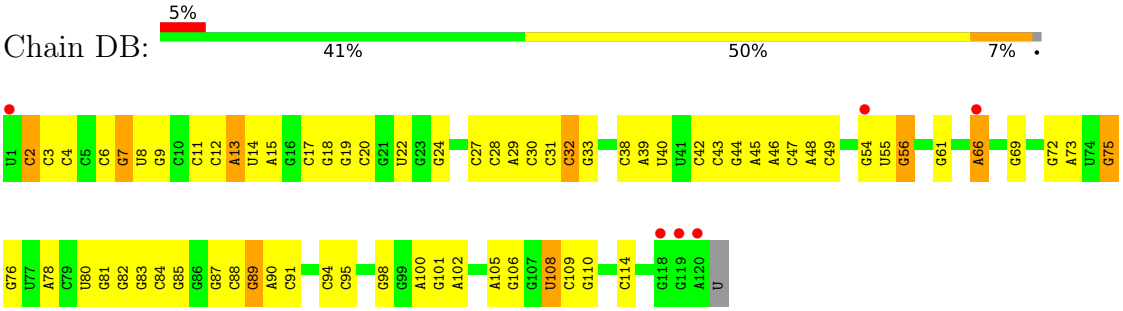
• Molecule 26: 5S Ribosomal RNA

Chain BB:



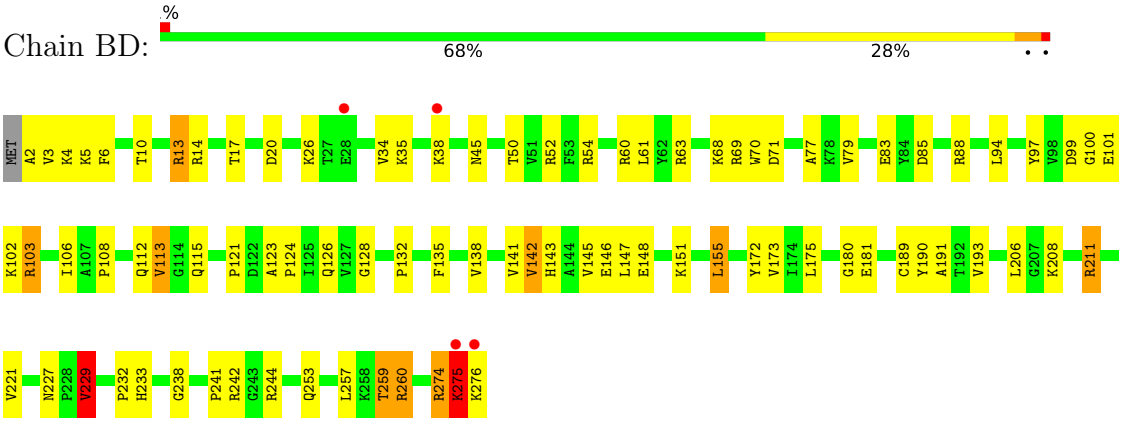
• Molecule 26: 5S Ribosomal RNA

Chain DB:



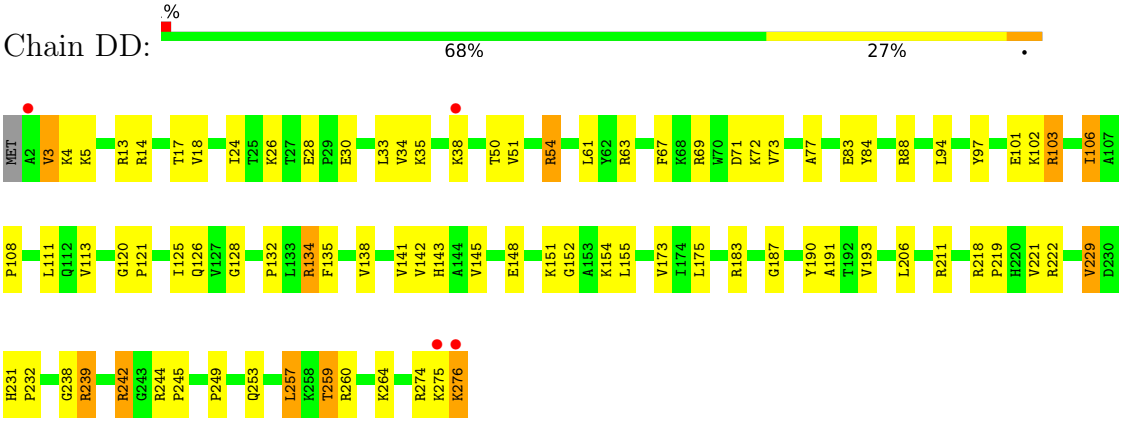
• Molecule 27: 50S Ribosomal Protein L2

Chain BD:



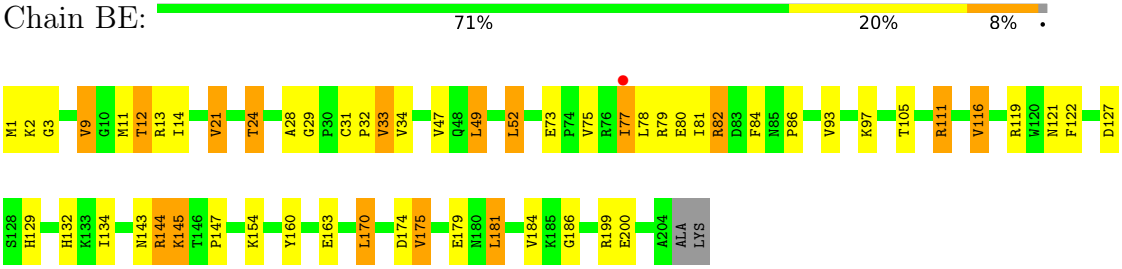
• Molecule 27: 50S Ribosomal Protein L2

Chain DD:



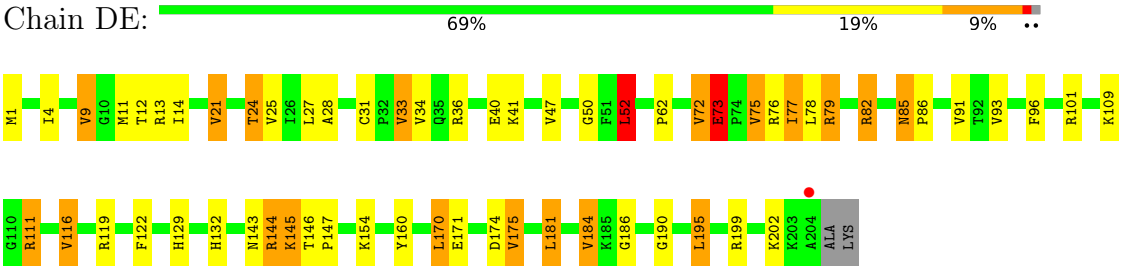
• Molecule 28: 50S Ribosomal Protein L3

Chain BE:



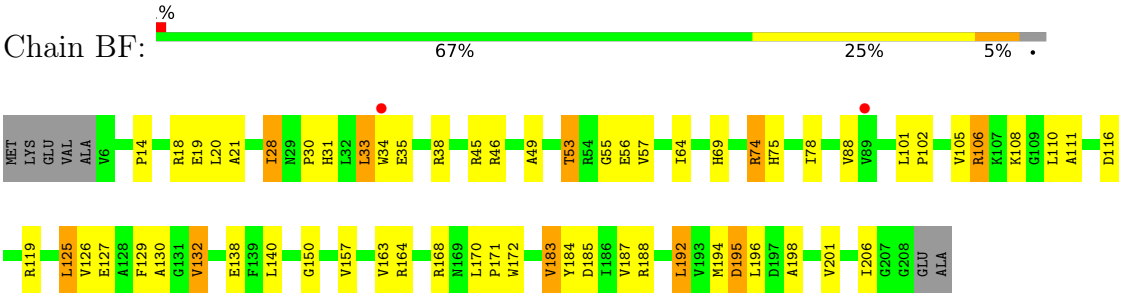
• Molecule 28: 50S Ribosomal Protein L3

Chain DE:



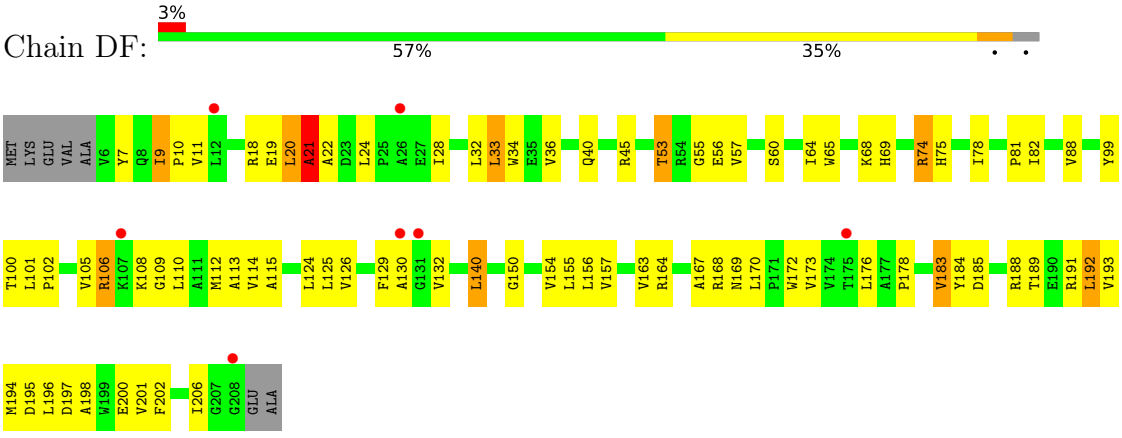
• Molecule 29: 50S Ribosomal Protein L4

Chain BF:



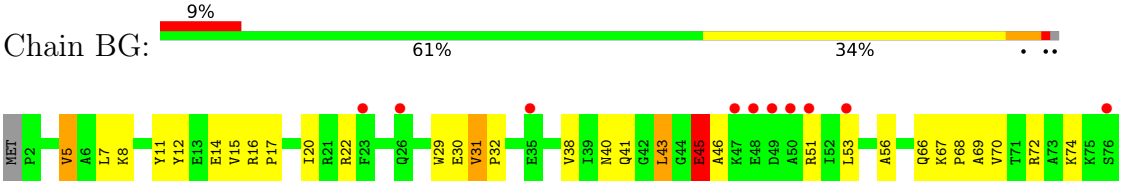
• Molecule 29: 50S Ribosomal Protein L4

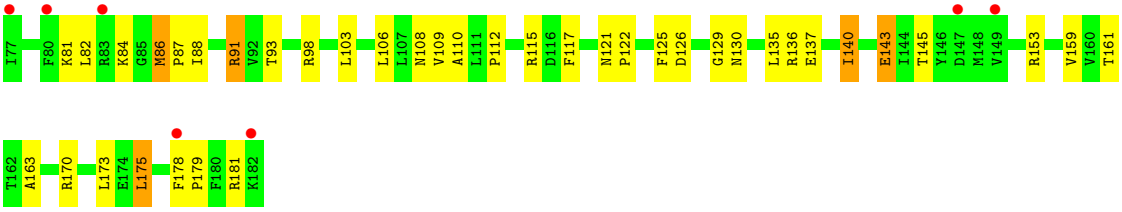
Chain DF:



• Molecule 30: 50S Ribosomal Protein L5

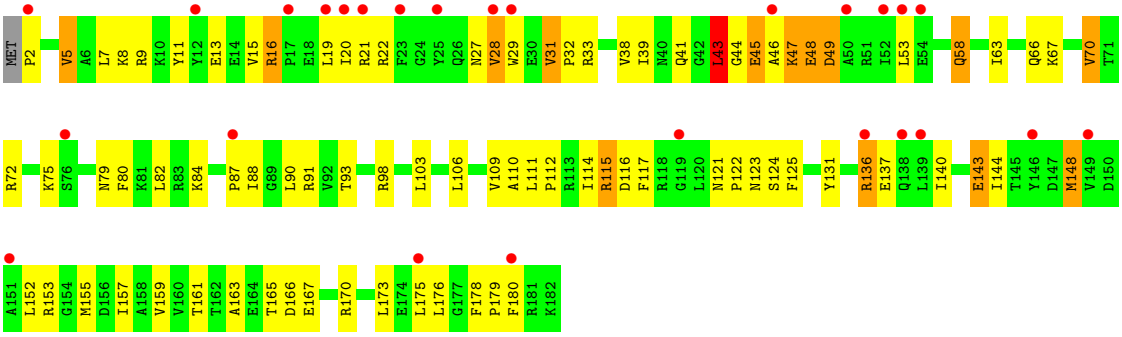
Chain BG:





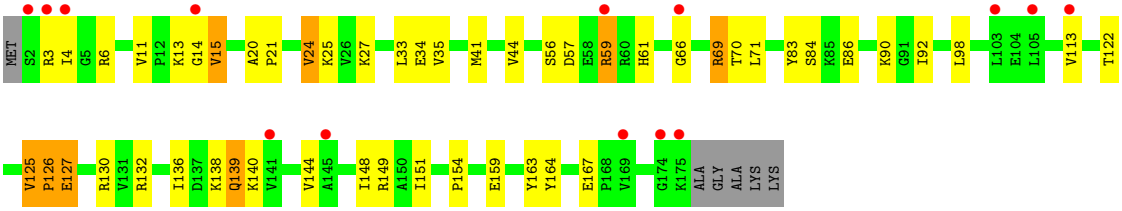
• Molecule 30: 50S Ribosomal Protein L5

Chain DG:



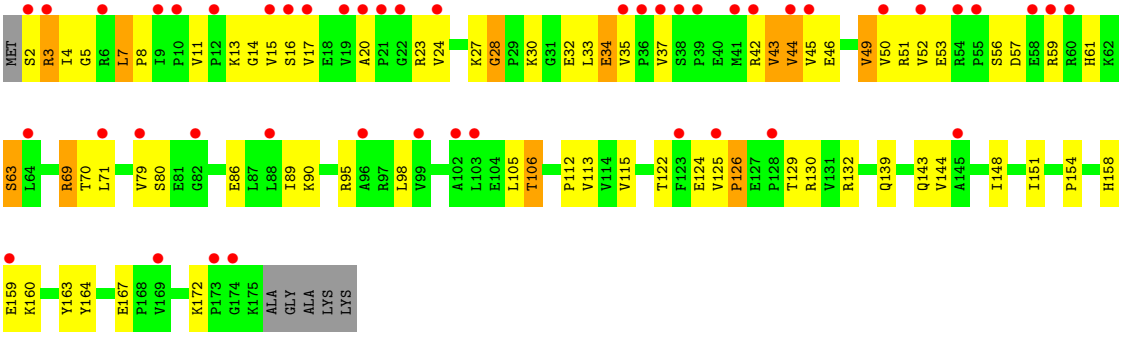
• Molecule 31: 50S Ribosomal Protein L6

Chain BH:



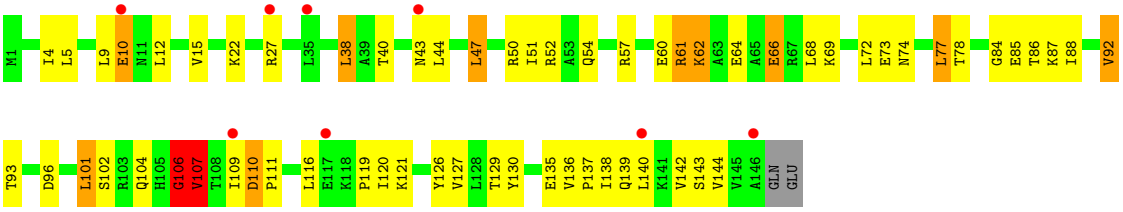
• Molecule 31: 50S Ribosomal Protein L6

Chain DH:

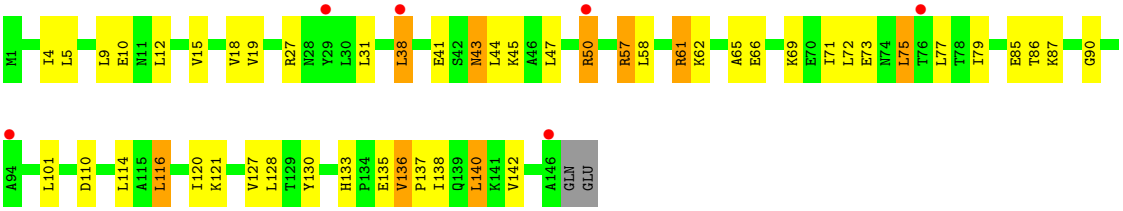


• Molecule 32: 50S Ribosomal Protein L9

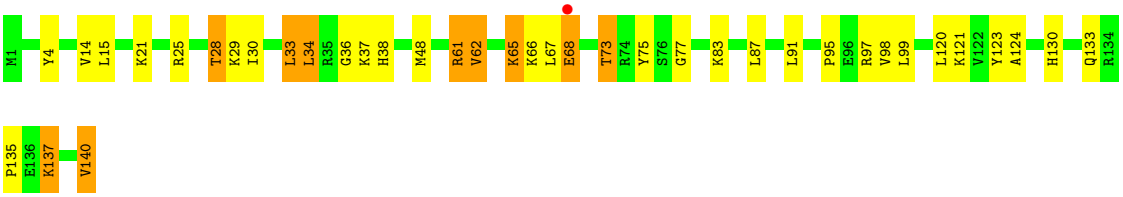
Chain BI:



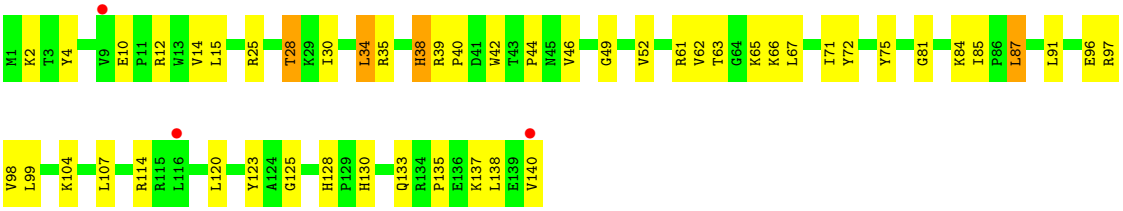
• Molecule 32: 50S Ribosomal Protein L9



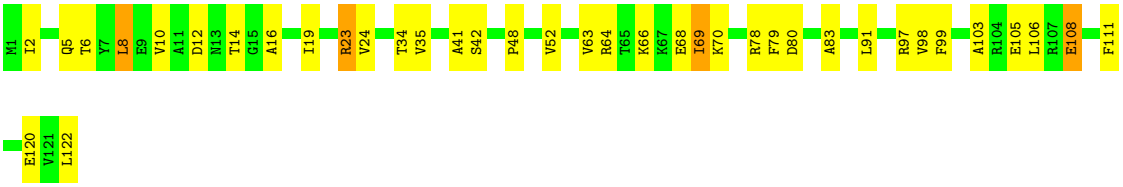
• Molecule 33: 50S Ribosomal Protein L13



• Molecule 33: 50S Ribosomal Protein L13

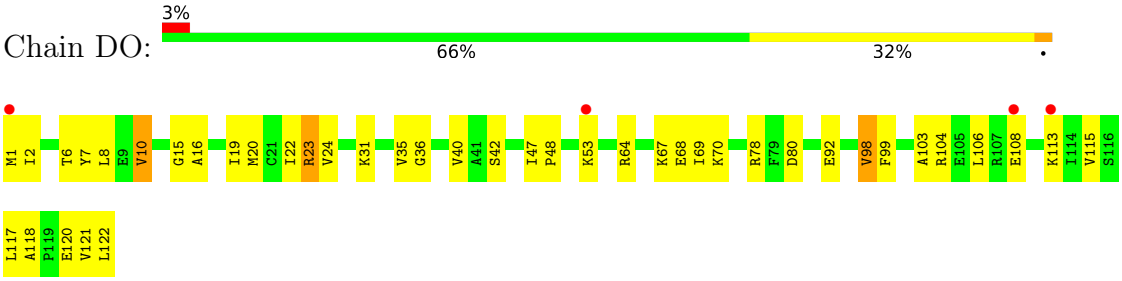


• Molecule 34: 50S Ribosomal Protein L14



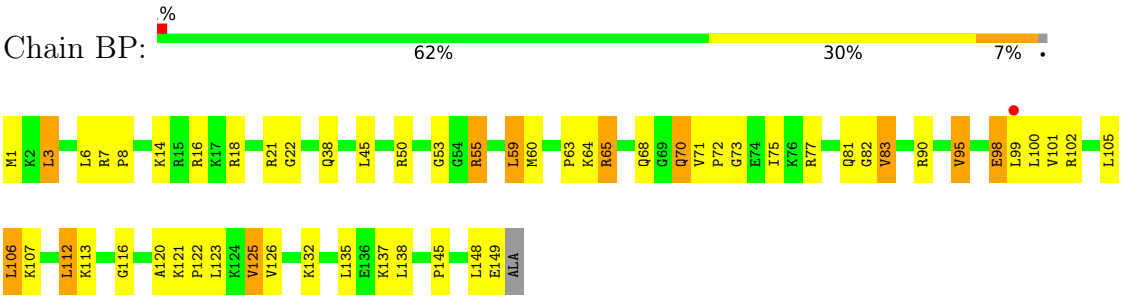
• Molecule 34: 50S Ribosomal Protein L14

Chain DO:



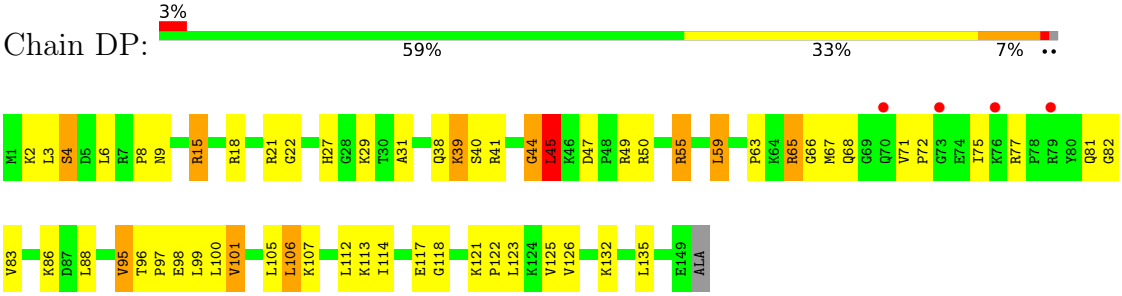
• Molecule 35: 50S Ribosomal Protein L15

Chain BP:



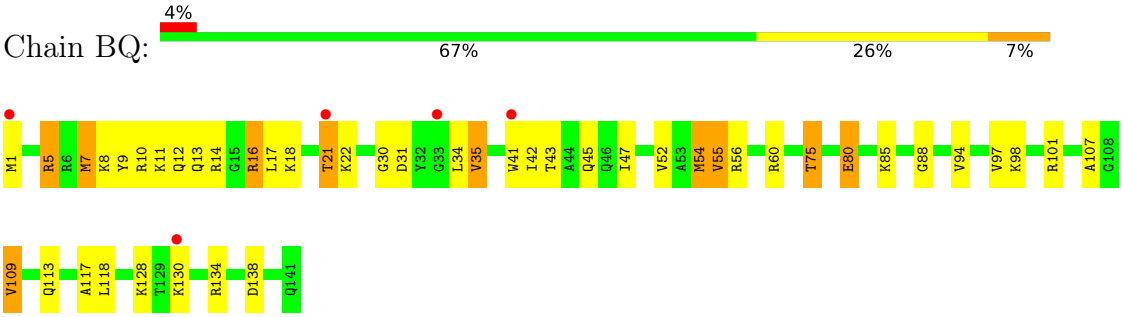
• Molecule 35: 50S Ribosomal Protein L15

Chain DP:



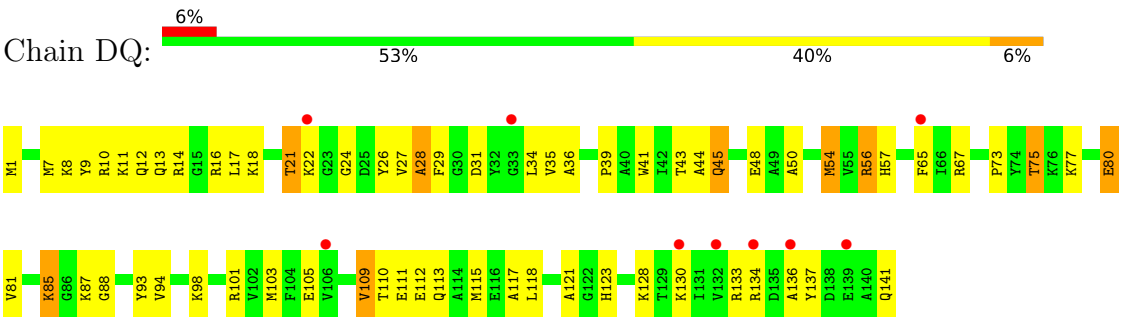
• Molecule 36: 50S Ribosomal Protein L16

Chain BQ:



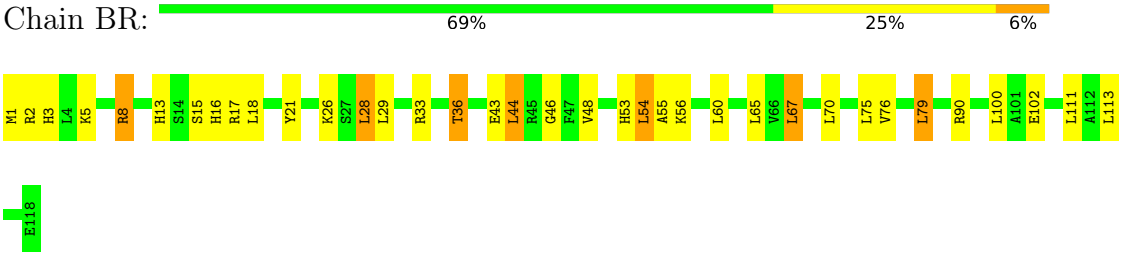
• Molecule 36: 50S Ribosomal Protein L16

Chain DQ:



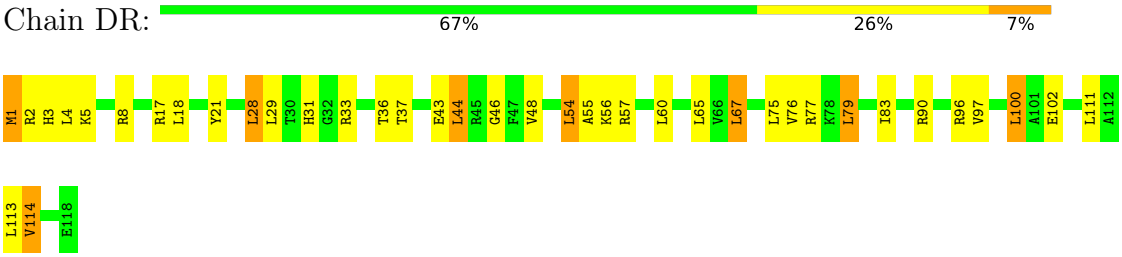
• Molecule 37: 50S Ribosomal Protein L17

Chain BR:



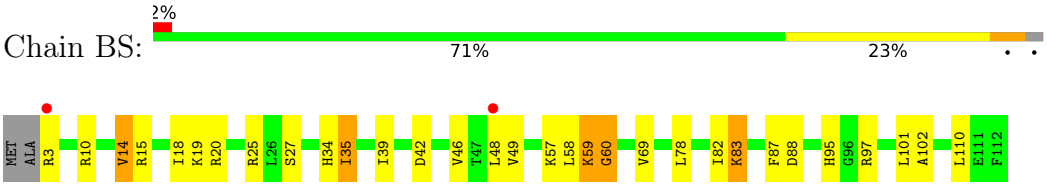
• Molecule 37: 50S Ribosomal Protein L17

Chain DR:



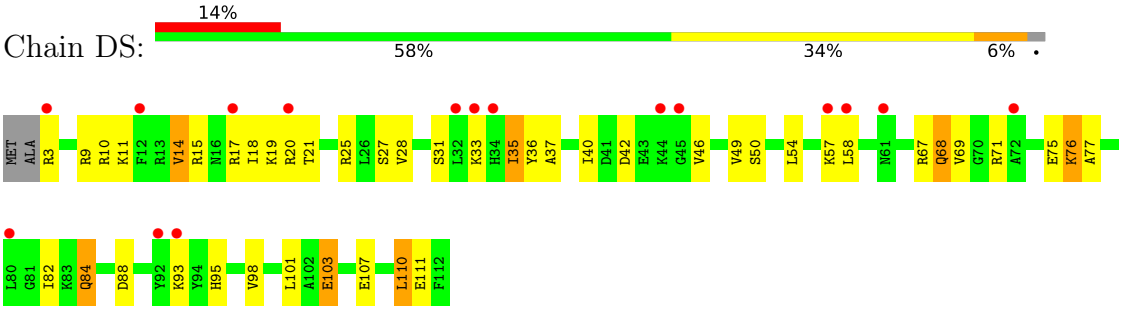
• Molecule 38: 50S Ribosomal Protein L18

Chain BS:



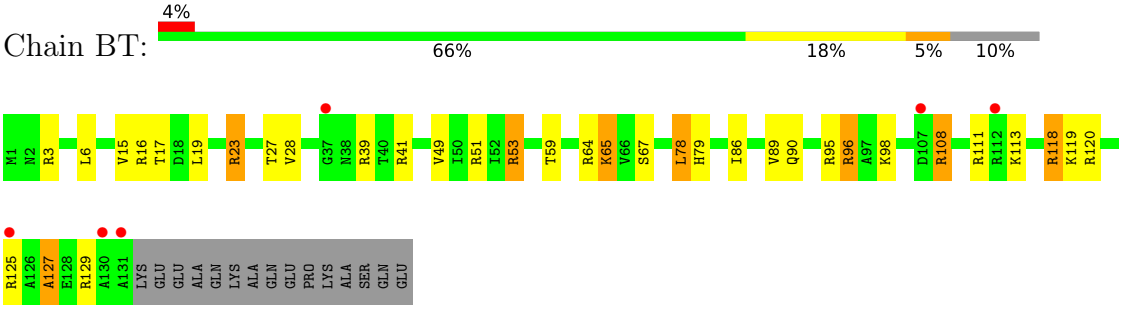
• Molecule 38: 50S Ribosomal Protein L18

Chain DS:



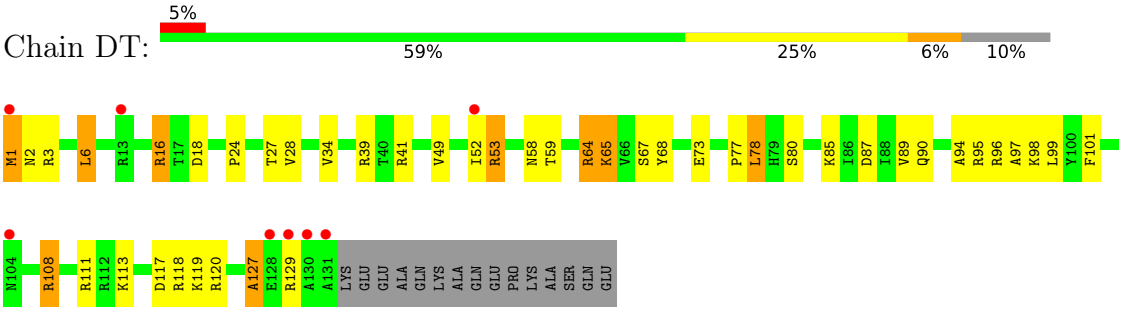
• Molecule 39: 50S Ribosomal Protein L19

Chain BT:



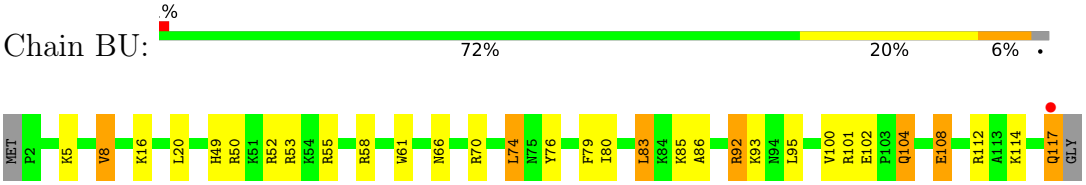
• Molecule 39: 50S Ribosomal Protein L19

Chain DT:



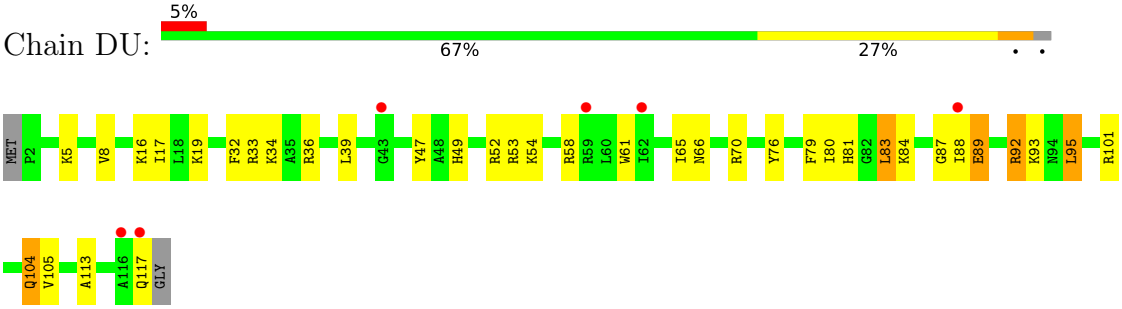
• Molecule 40: 50S Ribosomal Protein L20

Chain BU:



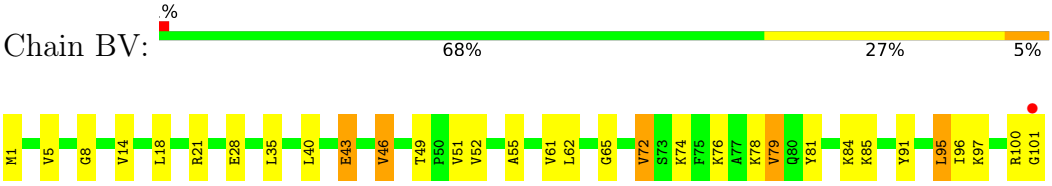
• Molecule 40: 50S Ribosomal Protein L20

Chain DU:



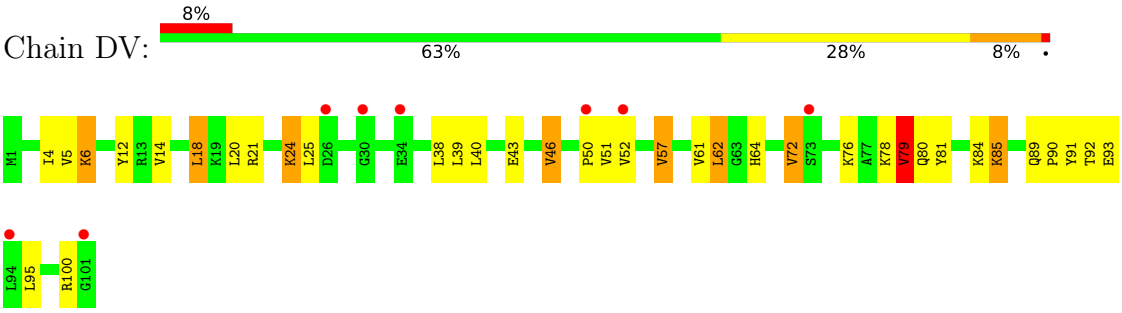
• Molecule 41: 50S Ribosomal Protein L21

Chain BV:



• Molecule 41: 50S Ribosomal Protein L21

Chain DV:



• Molecule 42: 50S Ribosomal Protein L22

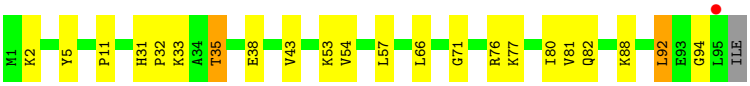
Chain BW:

• Molecule 42: 50S Ribosomal Protein L22

Chain DW:

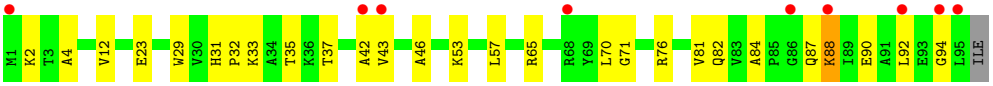
• Molecule 43: 50S Ribosomal Protein L23

Chain BX:



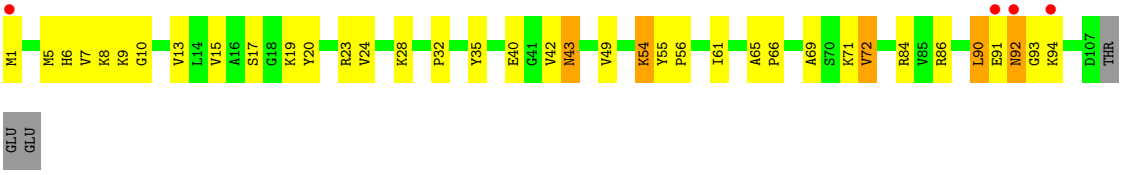
• Molecule 43: 50S Ribosomal Protein L23

Chain DX:



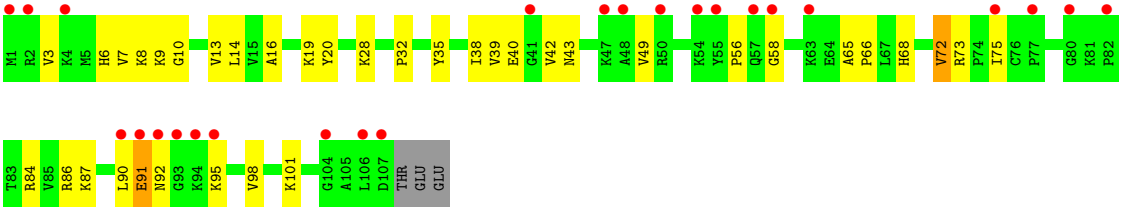
• Molecule 44: 50S Ribosomal Protein L24

Chain BY:



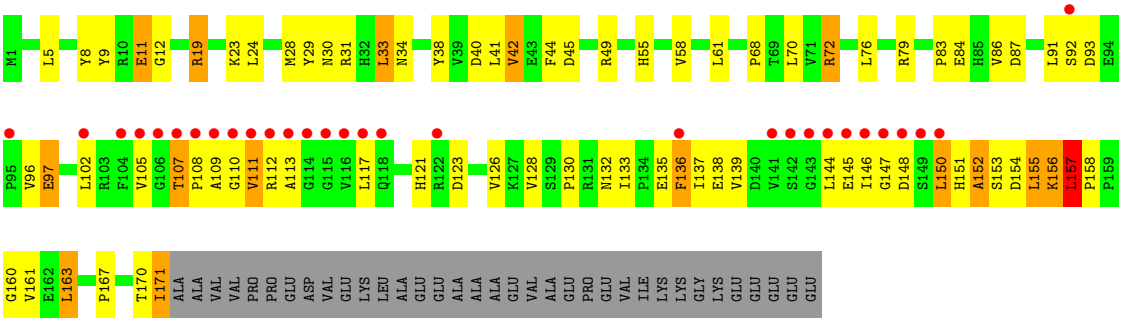
• Molecule 44: 50S Ribosomal Protein L24

Chain DY:



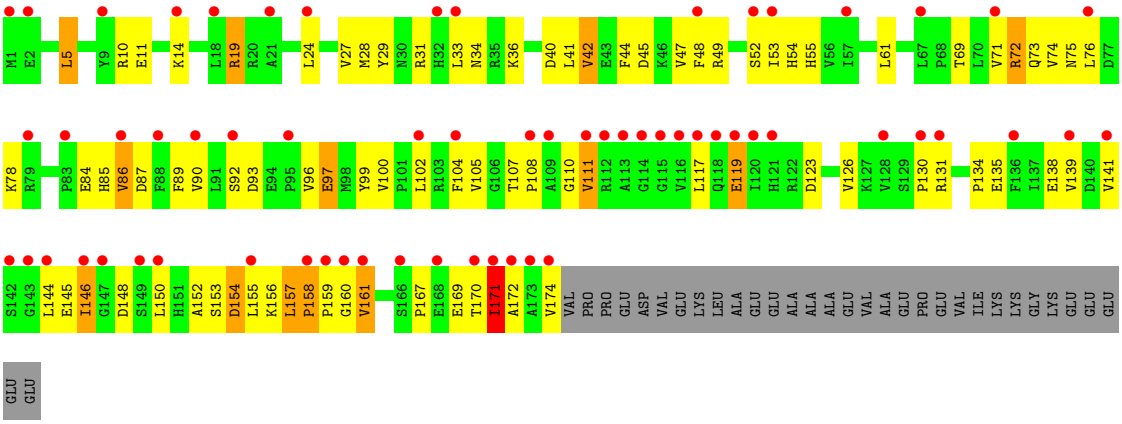
• Molecule 45: 50S Ribosomal Protein L25

Chain BZ:



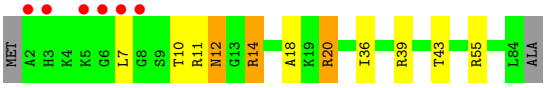
• Molecule 45: 50S Ribosomal Protein L25

Chain DZ:



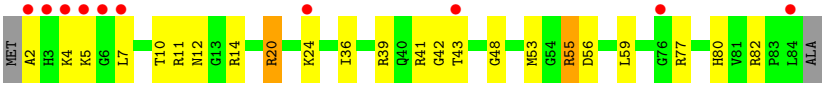
• Molecule 46: 50S Ribosomal Protein L27

Chain B0:



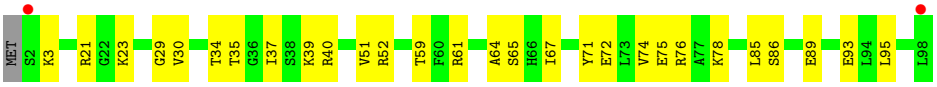
• Molecule 46: 50S Ribosomal Protein L27

Chain D0:



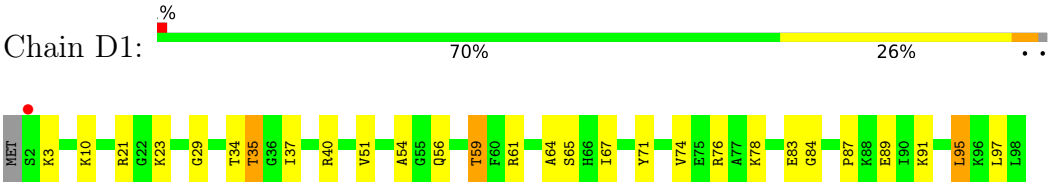
• Molecule 47: 50S Ribosomal Protein L28

Chain B1:



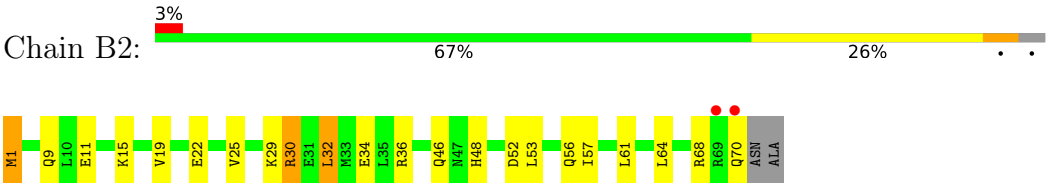
• Molecule 47: 50S Ribosomal Protein L28

Chain D1:



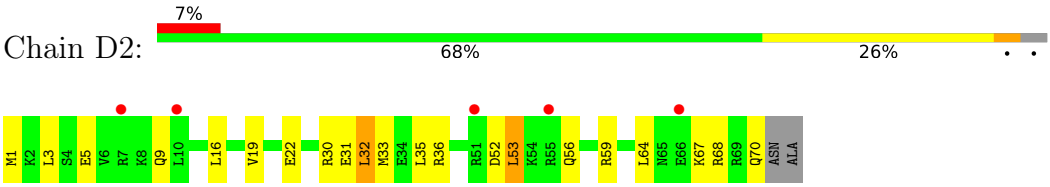
• Molecule 48: 50S Ribosomal Protein L29

Chain B2:



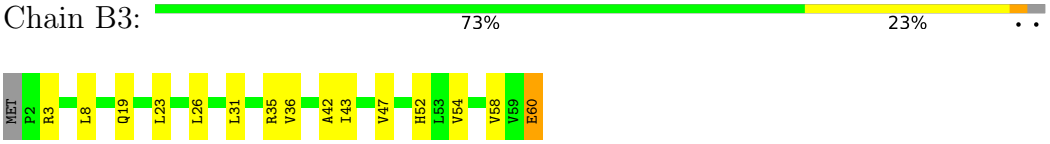
• Molecule 48: 50S Ribosomal Protein L29

Chain D2:



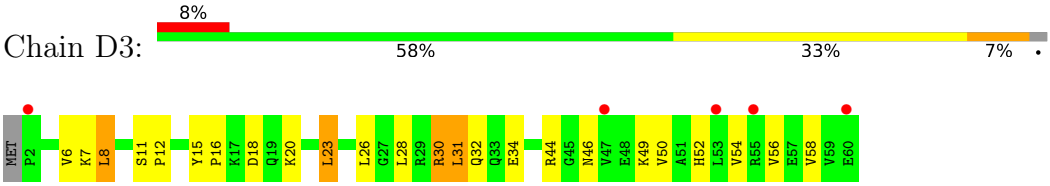
• Molecule 49: 50S Ribosomal Protein L30

Chain B3:



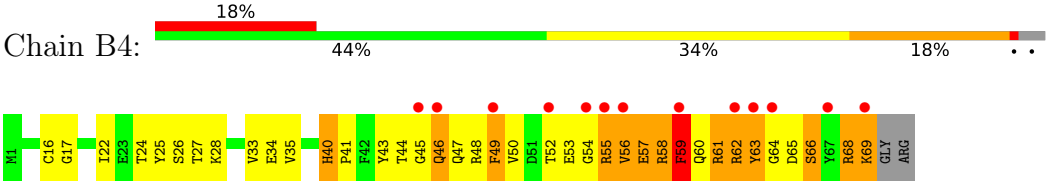
• Molecule 49: 50S Ribosomal Protein L30

Chain D3:



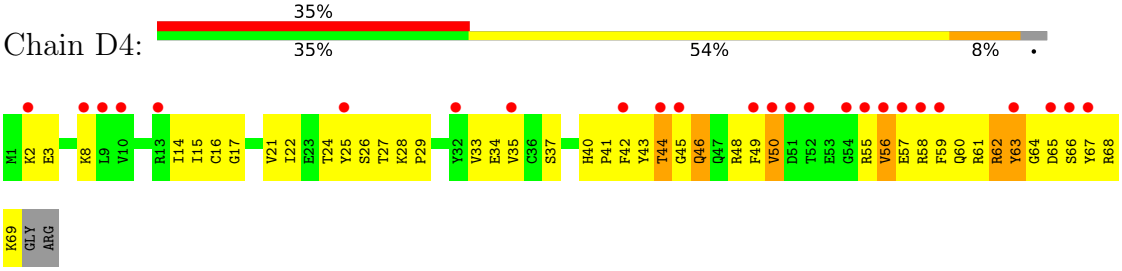
• Molecule 50: 50S Ribosomal Protein L31

Chain B4:



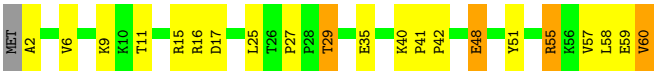
• Molecule 50: 50S Ribosomal Protein L31

Chain D4:



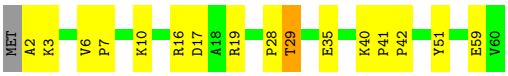
• Molecule 51: 50S Ribosomal Protein L32

Chain B5:



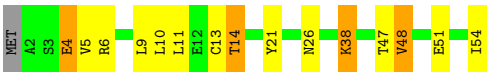
• Molecule 51: 50S Ribosomal Protein L32

Chain D5:



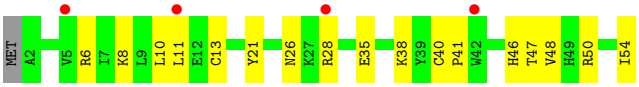
• Molecule 52: 50S Ribosomal Protein L33

Chain B6:



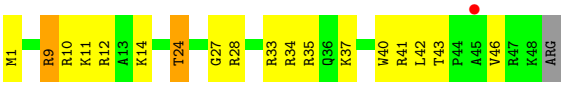
• Molecule 52: 50S Ribosomal Protein L33

Chain D6:



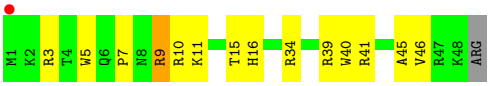
• Molecule 53: 50S Ribosomal Protein L34

Chain B7:



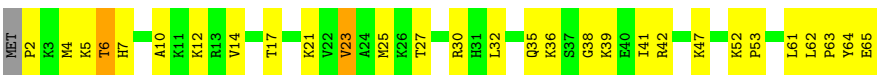
• Molecule 53: 50S Ribosomal Protein L34

Chain D7:



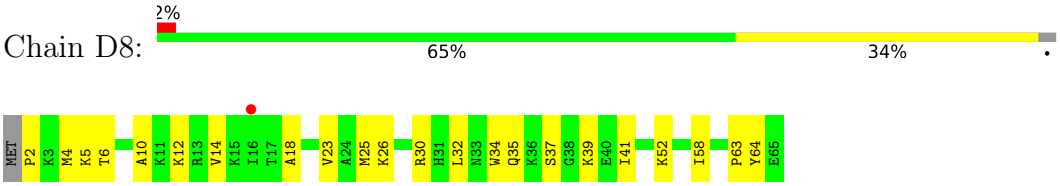
• Molecule 54: 50S Ribosomal Protein L35

Chain B8:



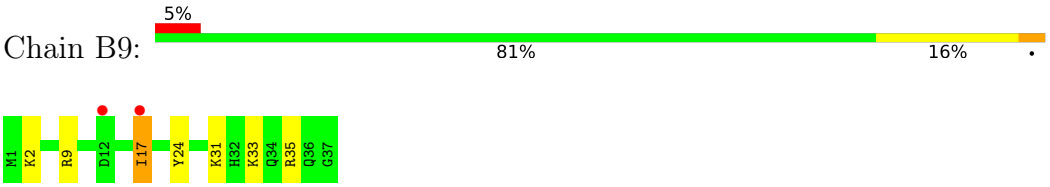
• Molecule 54: 50S Ribosomal Protein L35

Chain D8:



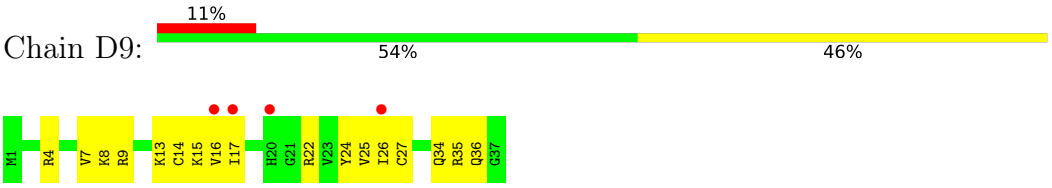
• Molecule 55: 50S Ribosomal Protein L36

Chain B9:



• Molecule 55: 50S Ribosomal Protein L36

Chain D9:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	208.25Å 443.61Å 619.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	124.25 – 2.70 124.25 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.2 (124.25-2.70) 97.2 (124.25-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.28 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.210 , 0.257 0.212 , 0.258	Depositor DCC
R_{free} test set	75600 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å^2)	54.2	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 57.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	297376	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.74% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 7MG, 5MC, K, ZN, PSU, 5MU, NEG, MIA, SF4, 4SU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	AA	0.25	0/36002	0.45	1/56188 (0.0%)
1	CA	0.24	0/36170	0.46	0/56452
2	AB	0.40	0/1881	1.02	10/2542 (0.4%)
2	CB	0.42	0/1860	1.03	7/2518 (0.3%)
3	AC	0.40	0/1576	0.85	1/2130 (0.0%)
3	CC	0.40	0/1566	0.91	4/2119 (0.2%)
4	AD	0.39	0/1689	0.88	2/2267 (0.1%)
4	CD	0.41	0/1704	0.89	3/2284 (0.1%)
5	AE	0.45	0/1145	0.90	1/1543 (0.1%)
5	CE	0.42	0/1149	0.96	2/1548 (0.1%)
6	AF	0.41	0/819	0.76	0/1111
6	CF	0.39	0/829	0.74	0/1123
7	AG	0.39	0/1250	0.87	1/1679 (0.1%)
7	CG	0.37	0/1254	0.92	4/1683 (0.2%)
8	AH	0.39	0/1108	0.85	0/1494
8	CH	0.38	0/1108	0.85	4/1494 (0.3%)
9	AI	0.40	0/1002	0.91	0/1346
9	CI	0.40	0/997	0.89	1/1343 (0.1%)
10	AJ	0.39	0/722	0.91	1/982 (0.1%)
10	CJ	0.44	0/727	0.97	4/988 (0.4%)
11	AK	0.42	0/844	0.83	0/1145
11	CK	0.42	0/848	0.85	0/1149
12	AL	0.45	0/946	0.81	0/1274
12	CL	0.40	0/946	0.92	3/1274 (0.2%)
13	AM	0.40	0/969	0.93	1/1302 (0.1%)
13	CM	0.40	0/961	0.93	1/1291 (0.1%)
14	AN	0.38	0/501	0.84	2/664 (0.3%)
14	CN	0.41	0/501	0.87	2/664 (0.3%)
15	AO	0.45	0/739	0.87	1/985 (0.1%)
15	CO	0.38	0/739	0.79	0/985
16	AP	0.43	0/697	0.87	1/939 (0.1%)
16	CP	0.41	0/693	0.77	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	AQ	0.39	0/836	0.80	1/1117 (0.1%)
17	CQ	0.37	0/836	0.81	0/1117
18	AR	0.41	0/560	0.79	0/746
18	CR	0.36	0/560	0.78	0/746
19	AS	0.37	0/667	0.90	2/900 (0.2%)
19	CS	0.46	0/661	1.03	3/893 (0.3%)
20	AT	0.38	0/730	0.91	0/965
20	CT	0.41	0/729	0.90	1/965 (0.1%)
21	AU	0.36	0/203	0.87	0/266
21	CU	0.41	0/203	0.83	0/266
22	AV	0.26	0/310	0.37	0/480
22	CV	0.24	0/282	0.42	0/437
23	AW	0.30	1/1602 (0.1%)	0.48	0/2493
23	AY	0.31	1/1602 (0.1%)	0.50	0/2493
23	CW	0.29	0/1556	0.45	0/2418
23	CY	0.31	1/1579 (0.1%)	0.49	0/2455
24	AX	0.31	0/1725	0.47	0/2689
24	CX	0.29	1/1725 (0.1%)	0.46	0/2689
25	BA	0.36	0/68083	0.49	1/106274 (0.0%)
25	DA	0.27	0/67542	0.48	1/105428 (0.0%)
26	BB	0.30	0/2878	0.50	0/4490
26	DB	0.26	0/2878	0.43	0/4490
27	BD	0.56	0/2186	0.91	4/2944 (0.1%)
27	DD	0.49	0/2186	0.88	0/2944
28	BE	0.59	0/1592	0.88	0/2149
28	DE	0.47	0/1592	0.96	9/2149 (0.4%)
29	BF	0.53	0/1619	0.89	0/2193
29	DF	0.43	0/1615	0.90	3/2188 (0.1%)
30	BG	0.42	0/1450	0.87	3/1959 (0.2%)
30	DG	0.39	0/1449	0.93	1/1958 (0.1%)
31	BH	0.49	0/1356	0.86	3/1834 (0.2%)
31	DH	0.43	0/1356	0.97	6/1834 (0.3%)
32	BI	0.41	0/1100	0.95	4/1501 (0.3%)
32	DI	0.39	0/1076	0.88	2/1471 (0.1%)
33	BN	0.52	0/1144	0.83	0/1543
33	DN	0.39	0/1144	0.88	2/1543 (0.1%)
34	BO	0.54	0/943	0.91	0/1269
34	DO	0.42	0/943	0.84	0/1269
35	BP	0.52	0/1152	0.85	2/1533 (0.1%)
35	DP	0.43	0/1152	0.96	5/1533 (0.3%)
36	BQ	0.53	0/1143	0.80	1/1527 (0.1%)
36	DQ	0.44	0/1143	0.85	1/1527 (0.1%)
37	BR	0.55	0/982	0.88	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
37	DR	0.44	0/982	0.81	0/1312
38	BS	0.46	0/887	0.82	0/1180
38	DS	0.37	0/880	0.89	0/1172
39	BT	0.50	0/1105	0.85	0/1477
39	DT	0.41	0/1097	0.80	0/1468
40	BU	0.56	0/977	0.85	0/1301
40	DU	0.39	0/977	0.80	0/1301
41	BV	0.53	0/782	0.85	0/1049
41	DV	0.37	0/782	0.80	0/1049
42	BW	0.59	0/897	0.85	0/1205
42	DW	0.45	0/897	0.81	0/1205
43	BX	0.54	0/764	0.85	0/1025
43	DX	0.44	0/764	0.87	0/1025
44	BY	0.47	0/819	0.90	1/1095 (0.1%)
44	DY	0.38	0/819	0.85	1/1095 (0.1%)
45	BZ	0.45	0/1379	0.99	6/1873 (0.3%)
45	DZ	0.41	0/1390	0.98	5/1890 (0.3%)
46	B0	0.52	0/662	0.90	2/881 (0.2%)
46	D0	0.37	0/662	0.81	2/881 (0.2%)
47	B1	0.52	0/762	0.86	0/1014
47	D1	0.43	0/762	0.85	0/1014
48	B2	0.49	0/590	0.85	0/781
48	D2	0.33	0/590	0.75	0/781
49	B3	0.51	0/474	0.93	0/635
49	D3	0.36	0/469	0.83	0/630
50	B4	0.46	0/571	1.16	7/768 (0.9%)
50	D4	0.46	0/545	0.98	0/737
51	B5	0.57	0/469	0.94	1/635 (0.2%)
51	D5	0.44	0/469	0.82	0/635
52	B6	0.53	0/460	0.77	0/613
52	D6	0.41	0/456	0.70	0/608
53	B7	0.58	0/426	0.78	0/561
53	D7	0.51	0/426	0.81	1/561 (0.2%)
54	B8	0.56	0/525	0.82	0/691
54	D8	0.45	0/525	0.80	0/691
55	B9	0.50	0/310	0.79	0/407
55	D9	0.41	0/310	0.86	0/407
All	All	0.35	4/316673 (0.0%)	0.61	138/474091 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	1
7	AG	0	1
7	CG	0	1
38	BS	0	1
All	All	0	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AY	8	4SU	O3'-P	5.81	1.62	1.56
23	CY	8	4SU	O3'-P	5.76	1.62	1.56
24	CX	8	4SU	O3'-P	5.19	1.61	1.56
23	AW	8	4SU	O3'-P	5.14	1.61	1.56

All (138) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	CB	231	GLU	CA-C-N	-12.95	107.78	120.21
2	CB	231	GLU	C-N-CA	-12.95	107.78	120.21
2	AB	231	GLU	CA-C-N	-11.36	109.17	120.31
2	AB	231	GLU	C-N-CA	-11.36	109.17	120.31
45	BZ	107	THR	CA-C-N	9.64	130.03	119.90
45	BZ	107	THR	C-N-CA	9.64	130.03	119.90
2	AB	128	GLU	N-CA-C	-8.47	103.06	112.72
19	CS	41	VAL	CA-C-N	8.10	129.97	119.84
19	CS	41	VAL	C-N-CA	8.10	129.97	119.84
8	CH	73	ASP	CA-C-N	7.73	127.91	119.87
8	CH	73	ASP	C-N-CA	7.73	127.91	119.87
28	DE	72	VAL	CA-C-N	7.69	135.55	121.70
28	DE	72	VAL	C-N-CA	7.69	135.55	121.70
12	CL	119	LYS	N-CA-C	-7.49	100.64	110.53
13	AM	84	ILE	N-CA-C	7.42	122.81	112.50
19	CS	82	GLY	N-CA-C	7.30	120.90	110.46
35	DP	44	GLY	CA-C-N	7.13	134.53	121.70
35	DP	44	GLY	C-N-CA	7.13	134.53	121.70
50	B4	59	PHE	N-CA-C	-7.11	102.92	112.94
3	AC	29	TYR	N-CA-C	-7.10	104.60	113.55
45	DZ	171	ILE	N-CA-C	7.04	118.09	111.48
45	BZ	157	LEU	CA-C-N	6.99	127.58	120.38
45	BZ	157	LEU	C-N-CA	6.99	127.58	120.38
15	AO	87	ILE	N-CA-C	6.98	118.04	111.48
25	BA	2014	G	C2'-C3'-O3'	6.92	119.88	109.50
2	CB	228	GLY	N-CA-C	6.89	119.41	110.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	CC	108	ASN	CA-C-N	6.84	126.47	119.56
3	CC	108	ASN	C-N-CA	6.84	126.47	119.56
35	DP	22	GLY	CA-C-N	6.84	126.64	119.05
35	DP	22	GLY	C-N-CA	6.84	126.64	119.05
31	DH	11	VAL	CA-C-N	6.83	126.76	120.21
31	DH	11	VAL	C-N-CA	6.83	126.76	120.21
50	B4	52	THR	N-CA-C	-6.82	101.20	110.68
46	B0	12	ASN	N-CA-C	6.77	120.85	112.59
7	AG	78	ARG	N-CA-C	6.73	119.20	107.49
50	B4	40	HIS	CA-C-N	6.73	128.25	119.84
50	B4	40	HIS	C-N-CA	6.73	128.25	119.84
50	B4	60	GLN	N-CA-C	-6.66	105.55	113.21
3	CC	29	TYR	N-CA-C	-6.65	105.17	113.55
30	BG	31	VAL	CA-C-N	6.61	128.10	119.84
30	BG	31	VAL	C-N-CA	6.61	128.10	119.84
30	BG	45	GLU	N-CA-C	-6.60	104.16	111.82
7	CG	8	GLU	N-CA-C	6.54	119.25	110.35
32	DI	44	LEU	N-CA-C	-6.53	104.00	112.23
45	DZ	14	LYS	CA-C-N	6.49	126.18	119.56
45	DZ	14	LYS	C-N-CA	6.49	126.18	119.56
4	AD	50	ARG	CA-C-N	6.39	126.34	119.76
4	AD	50	ARG	C-N-CA	6.39	126.34	119.76
31	BH	127	GLU	CA-C-N	-6.38	113.19	119.64
31	BH	127	GLU	C-N-CA	-6.38	113.19	119.64
31	DH	28	GLY	CA-C-N	6.35	125.85	119.24
31	DH	28	GLY	C-N-CA	6.35	125.85	119.24
45	DZ	158	PRO	CA-C-N	6.31	126.33	119.90
45	DZ	158	PRO	C-N-CA	6.31	126.33	119.90
2	AB	123	ALA	N-CA-C	-6.31	105.45	113.02
29	DF	9	ILE	N-CA-C	6.25	114.86	107.73
32	BI	106	GLY	CA-C-N	6.15	132.76	121.70
32	BI	106	GLY	C-N-CA	6.15	132.76	121.70
14	AN	13	THR	CA-C-N	6.13	126.10	120.21
14	AN	13	THR	C-N-CA	6.13	126.10	120.21
14	CN	13	THR	CA-C-N	6.12	126.31	120.31
14	CN	13	THR	C-N-CA	6.12	126.31	120.31
30	DG	48	GLU	N-CA-C	-6.10	105.87	113.55
12	CL	28	LYS	N-CA-C	6.09	119.50	111.28
25	DA	1992	G	C2'-C3'-O3'	6.08	118.62	109.50
28	DE	190	GLY	CA-C-N	6.04	126.01	120.03
28	DE	190	GLY	C-N-CA	6.04	126.01	120.03
9	CI	96	LEU	N-CA-C	-6.04	107.74	114.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
27	BD	275	LYS	N-CA-C	5.99	123.55	110.80
27	BD	274	ARG	N-CA-C	5.95	118.23	110.43
50	B4	65	ASP	N-CA-C	-5.91	106.12	113.15
4	CD	171	GLY	CA-C-N	5.91	126.06	119.32
4	CD	171	GLY	C-N-CA	5.91	126.06	119.32
10	CJ	52	GLY	CA-C-N	5.88	125.98	119.87
10	CJ	52	GLY	C-N-CA	5.88	125.98	119.87
44	DY	91	GLU	N-CA-C	-5.83	105.66	112.89
2	AB	166	ASP	CA-C-N	5.83	125.52	119.05
2	AB	166	ASP	C-N-CA	5.83	125.52	119.05
31	DH	7	LEU	CA-C-N	5.82	126.31	120.14
31	DH	7	LEU	C-N-CA	5.82	126.31	120.14
50	B4	68	ARG	N-CA-C	5.81	118.48	110.35
2	AB	9	GLU	N-CA-C	5.80	123.16	110.80
7	CG	69	VAL	N-CA-C	-5.79	107.12	113.43
19	AS	41	VAL	CA-C-N	5.74	127.01	119.84
19	AS	41	VAL	C-N-CA	5.74	127.01	119.84
29	DF	21	ALA	CA-C-N	5.73	132.02	121.70
29	DF	21	ALA	C-N-CA	5.73	132.02	121.70
2	CB	193	ASP	CA-C-N	5.72	125.19	119.24
2	CB	193	ASP	C-N-CA	5.72	125.19	119.24
46	B0	14	ARG	N-CA-C	5.71	119.27	110.42
28	DE	77	ILE	N-CA-C	5.70	116.33	108.12
20	CT	11	SER	N-CA-C	-5.70	105.92	112.92
44	BY	92	ASN	N-CA-C	5.69	118.21	111.33
5	CE	98	THR	N-CA-C	5.64	117.12	110.97
10	AJ	80	LYS	N-CA-C	-5.63	105.14	112.23
45	BZ	158	PRO	CA-C-N	5.63	126.87	119.84
45	BZ	158	PRO	C-N-CA	5.63	126.87	119.84
46	D0	82	ARG	CA-C-N	5.60	125.62	119.90
46	D0	82	ARG	C-N-CA	5.60	125.62	119.90
31	BH	92	ILE	N-CA-C	5.59	115.79	110.42
8	CH	134	ILE	N-CA-C	5.56	115.65	110.42
36	BQ	22	LYS	N-CA-C	-5.49	105.38	111.36
2	AB	193	ASP	CA-C-N	5.47	124.66	118.97
2	AB	193	ASP	C-N-CA	5.47	124.66	118.97
35	DP	40	SER	N-CA-C	-5.45	105.36	112.23
13	CM	106	ASN	N-CA-C	5.44	117.81	111.02
27	BD	238	GLY	N-CA-C	-5.37	102.58	112.62
7	CG	78	ARG	N-CA-C	5.37	116.83	107.49
32	BI	110	ASP	CA-C-N	5.33	125.14	119.28
32	BI	110	ASP	C-N-CA	5.33	125.14	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	DE	52	LEU	CA-C-N	5.32	125.24	119.76
28	DE	52	LEU	C-N-CA	5.32	125.24	119.76
1	AA	839	U	P-O3'-C3'	5.29	128.13	120.20
28	DE	85	ASN	CA-C-N	5.28	125.18	119.85
28	DE	85	ASN	C-N-CA	5.28	125.18	119.85
17	AQ	67	LYS	N-CA-C	-5.28	102.58	110.23
4	CD	178	VAL	N-CA-C	5.27	115.99	110.62
12	CL	23	LYS	N-CA-C	-5.26	106.91	113.38
51	B5	27	PRO	O-C-N	5.25	123.73	121.31
2	AB	23	ARG	N-CA-C	-5.24	105.12	112.25
33	DN	125	GLY	CA-C-N	5.20	124.81	119.56
33	DN	125	GLY	C-N-CA	5.20	124.81	119.56
16	AP	62	VAL	N-CA-C	-5.16	107.72	112.83
53	D7	45	ALA	N-CA-C	5.11	116.66	111.14
32	DI	71	ILE	N-CA-C	5.06	115.28	110.42
10	CJ	90	LEU	CA-C-N	5.06	126.17	119.84
10	CJ	90	LEU	C-N-CA	5.06	126.17	119.84
36	DQ	28	ALA	N-CA-C	5.06	121.58	110.80
35	BP	22	GLY	CA-C-N	5.06	124.23	118.97
35	BP	22	GLY	C-N-CA	5.06	124.23	118.97
5	CE	68	GLU	N-CA-C	5.05	117.17	111.11
7	CG	114	ARG	N-CA-C	5.02	116.45	110.97
2	CB	112	VAL	N-CA-C	-5.02	104.71	111.44
27	BD	229	VAL	CB-CA-C	-5.02	104.38	112.16
8	CH	96	GLY	N-CA-C	-5.02	105.90	112.82
2	CB	114	ARG	N-CA-C	-5.01	105.49	112.45
5	AE	98	THR	N-CA-C	5.01	116.43	110.97
3	CC	19	GLU	N-CA-C	-5.00	106.86	113.12

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	8	LYS	Peptide
7	AG	79	ARG	Peptide
38	BS	58	LEU	Peptide
7	CG	78	ARG	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	32163	0	16234	556	0
1	CA	32312	0	16308	638	0
2	AB	1846	0	1867	79	0
2	CB	1825	0	1828	100	0
3	AC	1552	0	1546	56	0
3	CC	1542	0	1517	59	0
4	AD	1659	0	1676	66	0
4	CD	1674	0	1714	45	0
5	AE	1129	0	1185	37	0
5	CE	1133	0	1191	40	0
6	AF	806	0	793	23	0
6	CF	816	0	808	29	0
7	AG	1231	0	1238	27	0
7	CG	1235	0	1249	38	0
8	AH	1088	0	1126	35	0
8	CH	1088	0	1126	40	0
9	AI	983	0	986	39	0
9	CI	978	0	966	46	0
10	AJ	709	0	650	32	0
10	CJ	714	0	672	48	0
11	AK	829	0	825	17	0
11	CK	833	0	836	21	0
12	AL	930	0	980	28	0
12	CL	930	0	980	31	0
13	AM	958	0	1002	42	0
13	CM	950	0	988	45	0
14	AN	492	0	529	22	0
14	CN	492	0	529	25	0
15	AO	728	0	760	22	0
15	CO	728	0	760	24	0
16	AP	681	0	697	21	0
16	CP	677	0	686	22	0
17	AQ	823	0	891	18	0
17	CQ	823	0	891	20	0
18	AR	555	0	618	17	0
18	CR	555	0	618	18	0
19	AS	652	0	662	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	CS	646	0	644	38	0
20	AT	728	0	798	21	0
20	CT	727	0	796	18	0
21	AU	199	0	208	6	0
21	CU	199	0	208	5	0
22	AV	277	0	140	8	0
22	CV	252	0	130	6	0
23	AW	1588	0	820	68	0
23	AY	1581	0	805	59	0
23	CW	1541	0	784	46	0
23	CY	1561	0	796	64	0
24	AX	1625	0	828	14	0
24	CX	1625	0	828	31	0
25	BA	60792	0	30654	821	0
25	DA	60311	0	30412	1131	0
26	BB	2573	0	1306	23	0
26	DB	2573	0	1306	65	0
27	BD	2136	0	2218	68	0
27	DD	2136	0	2218	70	0
28	BE	1559	0	1618	36	0
28	DE	1559	0	1618	54	0
29	BF	1584	0	1625	43	0
29	DF	1580	0	1619	64	0
30	BG	1425	0	1443	42	0
30	DG	1424	0	1434	63	0
31	BH	1330	0	1407	31	0
31	DH	1330	0	1407	42	0
32	BI	1085	0	1114	38	0
32	DI	1061	0	1080	22	0
33	BN	1117	0	1184	24	0
33	DN	1117	0	1184	31	0
34	BO	933	0	996	23	0
34	DO	933	0	996	28	0
35	BP	1135	0	1212	48	0
35	DP	1135	0	1212	48	0
36	BQ	1122	0	1179	38	0
36	DQ	1122	0	1179	63	0
37	BR	968	0	1033	20	0
37	DR	968	0	1033	31	0
38	BS	877	0	938	20	0
38	DS	870	0	923	28	0
39	BT	1091	0	1151	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	DT	1083	0	1136	34	0
40	BU	959	0	1019	27	0
40	DU	959	0	1019	31	0
41	BV	771	0	830	17	0
41	DV	771	0	830	20	0
42	BW	886	0	940	21	0
42	DW	886	0	939	18	0
43	BX	750	0	814	17	0
43	DX	750	0	814	18	0
44	BY	806	0	881	28	0
44	DY	806	0	881	29	0
45	BZ	1349	0	1355	52	0
45	DZ	1360	0	1363	65	0
46	B0	653	0	674	13	0
46	D0	653	0	674	22	0
47	B1	755	0	826	18	0
47	D1	755	0	826	18	0
48	B2	588	0	643	11	0
48	D2	588	0	643	12	0
49	B3	469	0	518	6	0
49	D3	464	0	514	16	0
50	B4	558	0	544	30	0
50	D4	532	0	503	30	0
51	B5	455	0	465	15	0
51	D5	455	0	465	11	0
52	B6	453	0	473	10	0
52	D6	449	0	469	10	0
53	B7	418	0	467	20	0
53	D7	418	0	467	13	0
54	B8	517	0	582	26	0
54	D8	517	0	582	17	0
55	B9	307	0	335	4	0
55	D9	307	0	335	13	0
56	AA	218	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	AM	1	0	0	0	0
56	AN	3	0	0	0	0
56	AO	1	0	0	0	0
56	AV	3	0	0	0	0
56	AW	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	AX	11	0	0	0	0
56	AY	3	0	0	0	0
56	B0	3	0	0	0	0
56	B1	1	0	0	0	0
56	B2	1	0	0	0	0
56	B3	2	0	0	0	0
56	B4	1	0	0	0	0
56	B5	5	0	0	0	0
56	B6	1	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	785	0	0	0	0
56	BB	18	0	0	0	0
56	BD	11	0	0	0	0
56	BE	8	0	0	0	0
56	BF	11	0	0	0	0
56	BG	2	0	0	0	0
56	BN	6	0	0	0	0
56	BO	1	0	0	0	0
56	BP	4	0	0	0	0
56	BQ	5	0	0	0	0
56	BR	3	0	0	0	0
56	BT	1	0	0	0	0
56	BU	9	0	0	0	0
56	BV	7	0	0	0	0
56	BW	4	0	0	0	0
56	BX	2	0	0	0	0
56	BY	1	0	0	0	0
56	BZ	1	0	0	0	0
56	CA	172	0	0	0	0
56	CD	1	0	0	0	0
56	CE	1	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	CN	1	0	0	0	0
56	CT	1	0	0	0	0
56	CV	1	0	0	0	0
56	CW	2	0	0	0	0
56	CX	2	0	0	0	0
56	CY	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	1	0	0	0	0
56	DA	623	0	0	0	0
56	DB	12	0	0	0	0
56	DD	9	0	0	0	0
56	DE	4	0	0	0	0
56	DF	6	0	0	0	0
56	DG	1	0	0	0	0
56	DN	1	0	0	0	0
56	DO	2	0	0	0	0
56	DP	1	0	0	0	0
56	DQ	4	0	0	0	0
56	DR	2	0	0	0	0
56	DU	3	0	0	0	0
56	DV	3	0	0	0	0
56	DW	4	0	0	0	0
56	DY	1	0	0	0	0
57	AA	119	0	133	18	0
57	AW	17	0	19	2	0
57	AX	17	0	19	3	0
57	CA	136	0	152	13	0
57	CW	17	0	19	1	0
57	CX	17	0	19	5	0
58	AD	8	0	0	0	0
58	CD	8	0	0	0	0
59	AN	1	0	0	0	0
59	B4	1	0	0	0	0
59	B5	1	0	0	0	0
59	B6	1	0	0	0	0
59	B9	1	0	0	0	0
59	BY	1	0	0	0	0
59	CN	1	0	0	0	0
59	D4	1	0	0	0	0
59	D5	1	0	0	0	0
59	D6	1	0	0	0	0
59	D9	1	0	0	0	0
59	DY	1	0	0	0	0
60	AX	1	0	0	0	0
60	CX	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	AA	247	0	0	9	0
61	AD	1	0	0	0	0
61	AE	2	0	0	0	0
61	AL	2	0	0	0	0
61	AM	2	0	0	0	0
61	AO	1	0	0	0	0
61	AV	3	0	0	0	0
61	AW	13	0	0	2	0
61	AX	11	0	0	2	0
61	AY	1	0	0	0	0
61	B0	8	0	0	0	0
61	B3	1	0	0	0	0
61	B5	6	0	0	1	0
61	B6	1	0	0	0	0
61	B7	2	0	0	1	0
61	B8	7	0	0	1	0
61	BA	1396	0	0	65	0
61	BB	34	0	0	1	0
61	BD	12	0	0	2	0
61	BE	11	0	0	3	0
61	BF	5	0	0	0	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BN	1	0	0	0	0
61	BO	2	0	0	0	0
61	BP	23	0	0	1	0
61	BQ	3	0	0	0	0
61	BR	1	0	0	0	0
61	BT	2	0	0	0	0
61	BU	3	0	0	0	0
61	BV	2	0	0	0	0
61	BW	1	0	0	1	0
61	BX	2	0	0	0	0
61	BZ	1	0	0	1	0
61	CA	184	0	0	14	0
61	CJ	2	0	0	2	0
61	CP	1	0	0	0	0
61	CV	2	0	0	0	0
61	CW	3	0	0	1	0
61	CX	6	0	0	0	0
61	D0	8	0	0	1	0
61	D1	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	D7	2	0	0	0	0
61	D8	1	0	0	0	0
61	DA	960	0	0	63	0
61	DB	8	0	0	0	0
61	DD	16	0	0	2	0
61	DE	9	0	0	0	0
61	DF	5	0	0	0	0
61	DN	3	0	0	0	0
61	DO	2	0	0	0	0
61	DP	15	0	0	0	0
61	DQ	1	0	0	1	0
61	DR	1	0	0	0	0
61	DU	1	0	0	0	0
61	DW	1	0	0	0	0
61	DX	1	0	0	0	0
61	DY	2	0	0	0	0
All	All	297376	0	196603	5695	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 12.

All (5695) 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)
23:CW:27:G:H1	23:CW:43:C:N4	1.53	1.07
23:CY:7:A:N6	23:CY:66:U:H3	1.50	1.07
23:AY:49:C:N4	23:AY:65:G:H1	1.56	1.03
23:CY:15:G:N2	23:CY:48:C:H42	1.55	1.03
53:B7:24:THR:HG22	53:B7:27:GLY:H	1.24	1.02
23:AW:7:A:N6	23:AW:66:U:H3	1.56	1.01
1:AA:72:C:H42	1:AA:97:G:H1	1.05	1.00
1:AA:1028:C:H42	1:AA:1033:G:H1	1.09	1.00
1:AA:999:C:N4	1:AA:1042:G:H1	1.58	1.00
43:BX:31:HIS:HD2	43:BX:33:LYS:H	1.10	0.99
1:CA:1002:G:H1	1:CA:1038:C:H42	0.99	0.99
23:CY:15:G:H22	23:CY:48:C:N4	1.60	0.99
1:CA:1000:U:H3	1:CA:1041:A:N6	1.62	0.98
38:DS:35:ILE:HD11	38:DS:101:LEU:HD12	1.43	0.98
23:CY:19:G:H1	23:CY:56:C:H42	0.98	0.98
25:DA:1798:U:H5'	27:DD:259:THR:HG22	1.47	0.97
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.46	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:78:G:H1	1:AA:91:C:H42	1.09	0.96
1:CA:1002:G:H1	1:CA:1038:C:N4	1.64	0.96
25:BA:2158:C:N4	25:BA:2177:G:H1	1.63	0.96
1:CA:1422:G:H5"	34:DO:48:PRO:HB3	1.46	0.95
57:AA:3221:NEG:H71	25:BA:786:G:H1	1.28	0.95
1:CA:201:C:H42	1:CA:216:G:H1	1.04	0.95
1:AA:376:G:H5"	16:AP:5:ARG:HG2	1.50	0.94
25:BA:1829:U:H5'	27:BD:259:THR:HG22	1.48	0.94
46:B0:11:ARG:O	46:B0:14:ARG:NH2	2.02	0.93
25:DA:2123:G:H1	25:DA:2175:C:H42	0.95	0.93
46:B0:10:THR:HG22	46:B0:12:ASN:H	1.31	0.93
25:BA:2122:G:H1	25:BA:2211:U:H3	1.17	0.93
2:CB:87:ARG:HE	2:CB:233:SER:HB3	1.30	0.93
25:DA:2318:G:H21	38:DS:3:ARG:HH12	1.17	0.93
23:AY:7:A:H61	23:AY:66:U:H3	1.05	0.92
25:DA:2096:U:H3	25:DA:2193:G:H1	1.17	0.92
1:CA:1162:C:H42	1:CA:1174:G:H1	1.17	0.92
1:AA:998:G:H1	1:AA:1043:C:H42	1.17	0.92
23:AY:19:G:H1	23:AY:56:C:H42	1.17	0.92
25:BA:2146:G:H1	25:BA:2196:C:H42	0.97	0.91
25:BA:2146:G:H1	25:BA:2196:C:N4	1.67	0.91
1:CA:1000:U:H3	1:CA:1041:A:H61	0.93	0.91
23:CY:19:G:H1	23:CY:56:C:N4	1.69	0.91
25:DA:2123:G:H1	25:DA:2175:C:N4	1.69	0.91
25:DA:2130:U:H4'	25:DA:2133:G:H4'	1.50	0.91
1:AA:953:G:H5'	1:AA:965:A:H61	1.34	0.91
23:AY:26:A:H61	23:AY:44:G:H1	0.92	0.91
25:BA:1736:A:H62	25:BA:1745:A:H2	1.15	0.91
23:AW:11:C:N4	23:AW:24:G:H1	1.68	0.90
25:BA:1405:A:N1	25:BA:1418:U:N3	2.19	0.90
1:CA:1086:U:H3	1:CA:1099:G:H22	1.17	0.90
23:AW:29:G:H1	23:AW:41:C:H42	1.15	0.90
23:AW:11:C:H42	23:AW:24:G:H1	0.96	0.90
23:AY:26:A:N6	23:AY:44:G:H1	1.68	0.90
25:BA:2128:G:H1	25:BA:2205:C:H42	1.19	0.90
25:BA:537:G:N7	61:BA:4902:HOH:O	2.05	0.89
23:AW:7:A:H61	23:AW:66:U:H3	0.96	0.89
25:DA:2138:C:H42	25:DA:2153:G:H1	1.21	0.89
1:CA:1003:G:N2	1:CA:1025:U:O4	2.06	0.88
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.55	0.88
25:DA:740:U:OP2	61:DA:4494:HOH:O	1.91	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2139:C:H42	25:DA:2152:G:H1	1.19	0.88
33:DN:123:TYR:HH	33:DN:130:HIS:HE2	1.17	0.88
1:AA:1003:G:N2	1:AA:1004:A:N3	2.22	0.88
25:DA:2689:U:H4'	25:DA:2690:C:H5'	1.53	0.88
25:BA:2123:G:H1	25:BA:2210:C:H42	1.16	0.88
1:CA:770:C:OP1	61:CA:4102:HOH:O	1.91	0.88
23:AY:49:C:H42	23:AY:65:G:H1	0.91	0.88
46:D0:11:ARG:O	46:D0:14:ARG:NH2	2.08	0.87
25:BA:656:A:OP1	35:BP:65:ARG:NH1	2.07	0.87
1:AA:538:G:H5"	12:AL:114:LYS:HB2	1.56	0.87
2:AB:17:PHE:HB2	2:AB:44:LEU:HD21	1.56	0.87
1:AA:999:C:H42	1:AA:1042:G:H1	0.87	0.87
1:AA:1158:C:H5	1:AA:1181:G:H1	1.20	0.86
23:CY:15:G:H22	23:CY:48:C:H42	0.88	0.86
25:DA:880:G:N2	25:DA:898:C:O2	2.08	0.86
25:BA:2163:G:O6	25:BA:2172:U:O2	1.94	0.86
23:CY:43:C:H2'	23:CY:44:G:H8	1.39	0.86
25:DA:2046:G:H5'	51:D5:19:ARG:HA	1.57	0.86
34:DO:35:VAL:HG11	34:DO:103:ALA:HB3	1.56	0.86
1:CA:1024:G:H2'	1:CA:1025:U:H5"	1.58	0.86
1:AA:975:A:H4'	1:AA:976:G:H5"	1.57	0.86
3:AC:52:LEU:HD21	3:AC:55:VAL:HG23	1.58	0.86
23:CW:27:G:H1	23:CW:43:C:H42	0.90	0.85
25:BA:2695:C:O2	34:BO:70:LYS:NZ	2.09	0.85
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.58	0.85
36:DQ:21:THR:HG21	36:DQ:101:ARG:HD3	1.57	0.85
25:BA:615:G:O6	61:BA:4976:HOH:O	1.94	0.85
27:DD:238:GLY:O	61:DD:408:HOH:O	1.93	0.85
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.59	0.85
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.57	0.85
39:BT:65:LYS:HE2	39:BT:67:SER:HB2	1.59	0.85
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.10	0.85
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.10	0.84
25:DA:1204:A:H2	25:DA:1241:A:H62	1.21	0.84
23:CW:27:G:N2	23:CW:43:C:N3	2.25	0.84
25:DA:1670:C:OP1	61:DA:4090:HOH:O	1.93	0.84
1:CA:999:C:H42	1:CA:1042:G:H1	1.22	0.84
25:BA:2123:G:H1	25:BA:2210:C:N4	1.74	0.83
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.60	0.83
1:AA:664:G:H22	1:AA:741:G:H1	1.25	0.83
1:AA:1502:A:H2	1:AA:1505:G:H1	1.24	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1221:G:H1'	25:BA:1222:A:H5'	1.60	0.83
23:CW:7:A:N1	23:CW:66:U:O4	2.12	0.83
25:DA:2100:G:H1	25:DA:2189:U:H3	1.27	0.83
1:CA:953:G:H5'	1:CA:965:A:H61	1.43	0.82
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.12	0.82
1:CA:1502:A:H2	1:CA:1505:G:H1	1.25	0.82
25:DA:198:C:OP2	61:DA:4556:HOH:O	1.97	0.82
25:BA:325:G:OP2	44:BY:84:ARG:NH2	2.13	0.82
23:CY:50:U:H3	23:CY:64:A:N6	1.77	0.82
39:DT:65:LYS:HE2	39:DT:67:SER:HB2	1.61	0.82
1:AA:72:C:N4	1:AA:97:G:H1	1.76	0.82
23:AW:6:G:H1	23:AW:67:C:H42	1.27	0.82
25:DA:962:G:OP1	61:DA:4554:HOH:O	1.98	0.82
1:CA:975:A:H4'	1:CA:976:G:H5"	1.62	0.82
25:DA:1689:A:H62	25:DA:1698:A:H2	1.23	0.82
48:B2:22:GLU:OE2	48:B2:68:ARG:NH2	2.13	0.82
43:DX:31:HIS:HD2	43:DX:33:LYS:H	1.25	0.82
23:AY:7:A:N6	23:AY:66:U:H3	1.76	0.81
23:AY:49:C:N3	23:AY:65:G:N2	2.28	0.81
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.13	0.81
25:BA:739:C:O2'	27:BD:38:LYS:NZ	2.14	0.81
25:BA:1378:G:OP1	61:BA:4738:HOH:O	1.98	0.81
44:BY:92:ASN:HB3	44:BY:94:LYS:H	1.45	0.81
25:BA:1577:C:O2'	25:BA:1578:C:O5'	1.98	0.81
35:BP:98:GLU:OE1	35:BP:102:ARG:NH1	2.12	0.81
1:CA:1089:G:H1	1:CA:1096:C:H42	1.28	0.81
23:AW:19:G:H1	23:AW:56:C:H42	1.25	0.81
32:BI:92:VAL:HG13	32:BI:120:ILE:HB	1.60	0.81
27:BD:17:THR:O	27:BD:211:ARG:NH2	2.13	0.81
25:DA:2807:G:N1	25:DA:2893:G:O6	2.13	0.81
1:AA:1422:G:H5"	34:BO:48:PRO:HB3	1.61	0.81
27:BD:180:GLY:HA3	27:BD:275:LYS:HG3	1.61	0.81
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HA	1.61	0.81
36:DQ:27:VAL:O	36:DQ:29:PHE:N	2.13	0.81
25:DA:994:C:OP1	40:DU:53:ARG:NH2	2.12	0.80
25:DA:2683:C:OP1	39:DT:53:ARG:NH2	2.13	0.80
46:D0:10:THR:HG22	46:D0:12:ASN:H	1.44	0.80
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.44	0.80
25:DA:2162:G:H4'	25:DA:2172:U:H2'	1.63	0.80
1:CA:26:A:N6	1:CA:558:G:O2'	2.14	0.80
25:DA:2148:G:H2'	25:DA:2149:G:H8	1.44	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2683:C:O2	34:DO:70:LYS:NZ	2.15	0.80
25:BA:2158:C:N3	25:BA:2177:G:N2	2.28	0.80
61:BA:5365:HOH:O	37:BR:3:HIS:NE2	2.15	0.80
1:CA:670:G:OP2	57:CA:3173:NEG:N2	2.14	0.80
1:AA:999:C:N3	1:AA:1042:G:N2	2.28	0.80
43:BX:31:HIS:CD2	43:BX:33:LYS:H	1.98	0.80
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.15	0.80
25:DA:568:U:O4	61:DA:4175:HOH:O	1.99	0.79
1:AA:677:U:H3	1:AA:713:G:H22	1.29	0.79
25:BA:2146:G:N2	25:BA:2196:C:N3	2.28	0.79
45:BZ:72:ARG:NH2	45:BZ:97:GLU:O	2.15	0.79
1:AA:1086:U:H3	1:AA:1099:G:H22	1.30	0.79
23:AY:50:U:O4	23:AY:64:A:N1	2.15	0.79
25:BA:1249:A:H2	25:BA:1287:A:H62	1.28	0.79
25:DA:948:G:OP1	61:DA:4554:HOH:O	2.01	0.79
51:D5:16:ARG:NH1	51:D5:17:ASP:OD1	2.16	0.79
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.15	0.79
43:BX:35:THR:HG22	43:BX:38:GLU:H	1.48	0.79
1:CA:1162:C:N4	1:CA:1174:G:H1	1.78	0.79
25:DA:2287:A:H62	25:DA:2344:U:H3	1.28	0.79
1:CA:1166:G:N2	1:CA:1170:A:OP2	2.16	0.79
25:BA:431:C:H4'	25:BA:432:U:H5'	1.65	0.79
29:DF:185:ASP:HA	29:DF:188:ARG:HD3	1.64	0.79
3:CC:179:ARG:NH1	3:CC:206:GLU:OE1	2.16	0.78
27:BD:71:ASP:HB3	27:BD:103:ARG:HH22	1.46	0.78
25:DA:1019:U:H3	25:DA:1142(A):A:H62	1.30	0.78
25:DA:2789:C:O2	25:DA:2894:G:N1	2.15	0.78
23:AY:25:C:O2'	23:AY:26:A:O5'	2.00	0.78
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.65	0.78
25:DA:847:U:O4	25:DA:933:A:N6	2.17	0.78
25:DA:1147:C:H2'	25:DA:1148:A:H8	1.49	0.78
25:DA:831:G:O2'	35:DP:38:GLN:NE2	2.17	0.78
13:CM:82:MET:HE2	13:CM:92:HIS:HB3	1.64	0.78
23:CY:51:U:H3	23:CY:63:G:H1	1.32	0.78
23:AY:26:A:N1	23:AY:44:G:N2	2.29	0.78
2:AB:15:VAL:O	2:AB:16:HIS:ND1	2.17	0.78
2:AB:201:ILE:HG21	2:AB:214:ILE:HG21	1.65	0.78
23:AW:19:G:N2	23:AW:56:C:N3	2.32	0.78
25:BA:2164:C:N3	25:BA:2171:G:O6	2.17	0.78
42:BW:14:PRO:HG2	42:BW:78:GLU:HG2	1.65	0.78
25:DA:2805:G:H2'	25:DA:2807:G:C8	2.18	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BS:25:ARG:NH1	38:BS:42:ASP:OD1	2.16	0.77
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.17	0.77
25:BA:1361:C:OP2	61:BA:4738:HOH:O	2.01	0.77
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.17	0.77
7:AG:50:ILE:HD11	7:AG:58:PRO:HA	1.66	0.77
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.66	0.77
1:AA:316:G:OP2	1:AA:351:G:O2'	2.03	0.77
1:AA:310:G:OP2	16:AP:27:LYS:NZ	2.15	0.77
1:AA:1028:C:N4	1:AA:1033:G:H1	1.80	0.77
25:BA:297:C:O2	25:BA:387:G:N2	2.18	0.77
25:BA:2158:C:N4	25:BA:2177:G:N1	2.30	0.77
1:AA:1007:C:N3	1:AA:1022:G:O6	2.16	0.77
25:BA:1313:U:OP1	61:BA:5106:HOH:O	2.02	0.77
52:D6:10:LEU:HG	52:D6:54:ILE:HG13	1.66	0.77
25:DA:1783:A:OP1	61:DA:4494:HOH:O	2.02	0.77
1:AA:1183:A:H3'	1:AA:1184:G:H5"	1.67	0.77
25:BA:2188:G:N7	25:BA:2190:G:N2	2.33	0.77
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.17	0.77
2:AB:18:GLY:HA2	2:AB:42:ILE:HG13	1.67	0.76
30:BG:161:THR:HG22	30:BG:163:ALA:H	1.49	0.76
5:CE:33:VAL:HG21	5:CE:109:ILE:HA	1.65	0.76
25:DA:2355:C:H1'	46:D0:39:ARG:HH21	1.49	0.76
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.50	0.76
25:BA:1500:A:OP2	61:BA:4166:HOH:O	2.03	0.76
8:CH:69:ARG:NH2	8:CH:75:ARG:O	2.19	0.76
23:AW:67:C:O2'	23:AW:68:C:O4'	2.03	0.76
36:BQ:21:THR:HG21	36:BQ:101:ARG:HD3	1.66	0.76
1:CA:1075:C:OP1	2:CB:179:LYS:NZ	2.19	0.76
25:DA:792:G:O6	61:DA:4447:HOH:O	2.03	0.76
26:BB:8:U:O3'	38:BS:25:ARG:NH2	2.18	0.76
25:DA:1171:G:N2	25:DA:1178:C:N3	2.34	0.76
25:BA:2831:A:OP2	61:BA:5365:HOH:O	2.04	0.76
25:BA:1001:G:OP2	36:BQ:14:ARG:NH2	2.18	0.76
34:BO:35:VAL:HG11	34:BO:103:ALA:HB3	1.66	0.76
25:DA:631:A:OP1	35:DP:65:ARG:NH1	2.18	0.76
1:AA:78:G:H1	1:AA:91:C:N4	1.83	0.76
13:AM:121:LYS:HE3	13:AM:121:LYS:H	1.50	0.76
2:CB:178:ARG:HE	8:CH:74:PRO:HG3	1.50	0.76
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	1.68	0.76
45:DZ:72:ARG:NH2	45:DZ:97:GLU:O	2.18	0.76
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2142:C:N3	25:DA:2149:G:O6	2.18	0.76
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.68	0.76
23:AW:29:G:H1	23:AW:41:C:N4	1.83	0.76
23:CY:19:G:N2	23:CY:56:C:N3	2.28	0.76
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.67	0.76
1:AA:1029:C:O2	1:AA:1032:G:N1	2.19	0.75
1:CA:664:G:H22	1:CA:741:G:H1	1.34	0.75
25:BA:1189:A:OP2	61:BA:5287:HOH:O	2.04	0.75
1:AA:167:G:H2'	1:AA:168:G:H8	1.50	0.75
1:AA:189(D):C:O2	1:AA:189(H):G:N1	2.19	0.75
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.30	0.75
1:AA:339:C:OP2	34:BO:97:ARG:NH1	2.20	0.75
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.01	0.75
25:DA:587:C:OP2	35:DP:21:ARG:NH2	2.18	0.75
40:DU:76:TYR:OH	40:DU:92:ARG:NH1	2.20	0.75
1:CA:1083:U:OP2	61:CA:4096:HOH:O	2.04	0.75
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.68	0.75
25:DA:1958:C:OP2	61:DA:4662:HOH:O	2.05	0.75
1:AA:347:G:O2'	1:AA:348:G:OP1	2.04	0.75
1:AA:1007:C:O2	1:AA:1022:G:N1	2.20	0.75
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.19	0.75
25:BA:787:U:OP2	61:BA:4795:HOH:O	2.05	0.75
1:CA:677:U:H3	1:CA:713:G:H22	1.34	0.75
57:CA:3174:NEG:H72	25:DA:1945:G:OP1	1.86	0.75
1:AA:1008:C:N3	1:AA:1021:G:O6	2.19	0.74
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.69	0.74
25:BA:388:A:H2'	25:BA:389:G:H8	1.51	0.74
1:CA:1026:G:H5'	1:CA:1027:C:O5'	1.87	0.74
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.16	0.74
25:DA:1171:G:H1	25:DA:1178:C:H42	1.35	0.74
57:CA:3175:NEG:H72	25:DA:739:G:H1	1.52	0.74
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.70	0.74
57:AX:3013:NEG:N2	25:BA:2334:A:OP2	2.20	0.74
40:BU:76:TYR:OH	40:BU:92:ARG:NH1	2.20	0.74
5:AE:33:VAL:HG21	5:AE:109:ILE:HA	1.70	0.74
25:DA:143:G:H4'	43:DX:35:THR:HG21	1.69	0.74
47:D1:51:VAL:HG11	47:D1:74:VAL:HG21	1.70	0.74
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.68	0.74
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.68	0.74
25:DA:2246:G:N7	61:DA:4073:HOH:O	2.21	0.74
43:DX:31:HIS:CD2	43:DX:33:LYS:H	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:654:G:OP2	61:AA:4213:HOH:O	2.06	0.74
25:BA:30:G:OP2	40:BU:5:LYS:NZ	2.20	0.74
25:BA:2169:G:H3'	25:BA:2170:G:H5"	1.67	0.74
25:DA:309:G:N3	25:DA:329:G:O2'	2.19	0.74
1:AA:345:C:OP2	39:BT:39:ARG:NH2	2.20	0.73
45:BZ:151:HIS:O	45:BZ:153:SER:N	2.19	0.73
20:CT:43:LEU:O	20:CT:47:GLY:N	2.21	0.73
24:CX:21:A:H61	24:CX:46:G:H2'	1.50	0.73
25:DA:195:A:N7	61:DA:4556:HOH:O	2.21	0.73
25:DA:1762:A:N1	61:DA:4559:HOH:O	2.20	0.73
25:DA:2615:U:OP1	61:DA:4297:HOH:O	2.04	0.73
1:AA:522:C:H41	12:AL:53:ARG:HH22	1.34	0.73
29:BF:185:ASP:OD1	29:BF:188:ARG:NH1	2.20	0.73
1:CA:1002:G:N2	1:CA:1038:C:N3	2.31	0.73
25:DA:323:G:HO2'	25:DA:1205:U:H3	1.35	0.73
28:DE:72:VAL:HA	28:DE:73:GLU:HB3	1.69	0.73
38:DS:50:SER:O	38:DS:76:LYS:NZ	2.21	0.73
3:CC:34:LEU:HG	3:CC:38:ARG:HH12	1.53	0.73
25:DA:2143:C:H42	25:DA:2148:G:H1	1.34	0.73
2:AB:16:HIS:O	2:AB:18:GLY:N	2.21	0.73
42:BW:31:GLU:OE1	61:BW:4001:HOH:O	2.07	0.73
25:DA:1271:G:OP2	61:DA:4489:HOH:O	2.06	0.73
1:CA:1256:A:OP2	3:CC:26:LYS:NZ	2.21	0.73
23:CW:74:C:N4	25:DA:2507:C:O2'	2.21	0.73
25:DA:1310:G:OP2	53:D7:9:ARG:NH1	2.18	0.73
10:AJ:7:LYS:HG3	10:AJ:71:LEU:HD13	1.68	0.73
25:BA:692:C:N4	25:BA:698:G:O6	2.18	0.73
25:BA:2832:G:OP2	61:BA:5365:HOH:O	2.05	0.73
39:DT:16:ARG:NH1	39:DT:18:ASP:OD1	2.21	0.73
19:AS:9:VAL:HG21	50:B4:61:ARG:HH12	1.53	0.73
27:BD:2:ALA:N	27:BD:20:ASP:OD2	2.21	0.73
23:CY:43:C:H2'	23:CY:44:G:C8	2.23	0.73
25:DA:2138:C:N4	25:DA:2153:G:H1	1.87	0.73
1:AA:266:G:H5"	1:AA:268:C:H41	1.54	0.72
1:AA:998:G:H1	1:AA:1043:C:N4	1.87	0.72
45:BZ:117:LEU:HD11	45:BZ:144:LEU:HB3	1.70	0.72
25:DA:2632:A:HO2'	25:DA:2811:G:HO2'	1.33	0.72
1:CA:345:C:OP2	39:DT:39:ARG:NH2	2.22	0.72
25:DA:271(L):U:OP1	32:DI:50:ARG:NH2	2.23	0.72
28:BE:111:ARG:HG3	28:BE:160:TYR:CD2	2.23	0.72
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:18:G:O2'	23:CW:57:G:N2	2.22	0.72
25:BA:139:A:H8	25:BA:1454:C:HO2'	1.38	0.72
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.21	0.72
25:DA:1971:A:OP2	27:DD:242:ARG:NH2	2.22	0.72
26:DB:15:A:OP2	26:DB:69:G:N2	2.21	0.72
1:AA:953:G:H5'	1:AA:965:A:N6	2.05	0.72
23:AY:19:G:N2	23:AY:56:C:N3	2.33	0.72
25:DA:527:C:OP1	61:DA:4468:HOH:O	2.07	0.72
25:DA:1937:A:OP1	61:DA:4724:HOH:O	2.07	0.72
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.04	0.72
23:CY:76:A:H62	25:DA:2422:A:H5'	1.55	0.72
9:AI:16:ARG:HB2	9:AI:64:THR:HG22	1.71	0.72
25:BA:303:C:H42	25:BA:385:G:H1	1.35	0.72
25:BA:1044:C:OP1	61:BA:4747:HOH:O	2.06	0.72
2:CB:30:ARG:HH21	2:CB:194:PRO:HB2	1.55	0.72
25:DA:971:C:OP2	61:DA:4840:HOH:O	2.06	0.72
25:BA:1094:A:OP2	25:BA:1155:C:N4	2.18	0.72
4:CD:157:LEU:O	4:CD:161:ASN:ND2	2.23	0.72
25:DA:271(W):G:N7	61:DA:4937:HOH:O	2.23	0.72
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.72	0.71
25:DA:848:G:H2'	25:DA:849:A:C8	2.25	0.71
57:AA:3216:NEG:HN42	57:AA:3216:NEG:H11	1.55	0.71
23:AY:19:G:H1	23:AY:56:C:N4	1.88	0.71
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.89	0.71
25:DA:2589:A:OP1	61:DA:4444:HOH:O	2.08	0.71
29:DF:21:ALA:HB3	29:DF:22:ALA:HA	1.72	0.71
1:CA:377:G:OP1	16:CP:3:LYS:HD2	1.91	0.71
1:CA:771:G:N7	61:CA:4043:HOH:O	2.22	0.71
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.24	0.71
49:D3:8:LEU:HD13	49:D3:31:LEU:HD23	1.72	0.71
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.23	0.71
25:DA:2308:G:O6	25:DA:2311:A:N6	2.20	0.71
1:AA:1064:G:N2	1:AA:1190:G:O2'	2.23	0.71
1:AA:1025:U:O2	1:AA:1036:G:O6	2.08	0.71
41:BV:95:LEU:HD13	41:BV:97:LYS:HD3	1.72	0.71
23:CW:2:C:N3	23:CW:71:G:O6	2.23	0.71
25:DA:2057:A:OP2	61:DA:4194:HOH:O	2.07	0.71
25:BA:1740:U:O2'	27:BD:14:ARG:NH2	2.24	0.71
25:DA:2819:G:N7	61:DA:4367:HOH:O	2.23	0.71
25:DA:2832:U:OP2	61:DA:4429:HOH:O	2.09	0.71
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:81:ILE:HD11	27:DD:125:ILE:HB	1.71	0.71
25:DA:2425:A:H4'	25:DA:2426:A:H5"	1.71	0.71
25:DA:2805:G:H2'	25:DA:2807:G:H8	1.54	0.71
36:DQ:111:GLU:OE2	36:DQ:133:ARG:NH2	2.21	0.71
25:BA:2163:G:N7	25:BA:2173:G:N3	2.37	0.71
41:DV:40:LEU:HB2	41:DV:46:VAL:HG13	1.71	0.71
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.55	0.70
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.71	0.70
25:BA:232:U:OP1	54:B8:6:THR:OG1	2.09	0.70
28:BE:105:THR:OG1	28:BE:199:ARG:NH2	2.24	0.70
1:CA:953:G:H5'	1:CA:965:A:N6	2.05	0.70
25:DA:1816:G:O6	27:DD:35:LYS:NZ	2.22	0.70
25:DA:2169:A:H2'	25:DA:2170:A:C8	2.26	0.70
25:DA:1153:C:OP1	40:DU:92:ARG:NH1	2.20	0.70
30:DG:161:THR:HG22	30:DG:163:ALA:H	1.57	0.70
25:BA:1814:A:N7	61:BA:5073:HOH:O	2.25	0.70
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.71	0.70
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.18	0.70
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.74	0.70
25:DA:2141:G:O6	25:DA:2150:U:O2	2.08	0.70
1:AA:166:G:H2'	1:AA:167:G:H8	1.56	0.70
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.71	0.70
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.25	0.70
52:B6:10:LEU:HG	52:B6:54:ILE:HG13	1.71	0.70
1:CA:14:U:OP2	61:CA:4074:HOH:O	2.09	0.70
23:CY:50:U:H3	23:CY:64:A:H61	1.37	0.70
25:DA:783:A:OP2	61:DA:4444:HOH:O	2.10	0.70
25:DA:2139:C:N4	25:DA:2152:G:H1	1.88	0.70
1:AA:1414:U:H3	1:AA:1486:G:H1	1.39	0.70
35:BP:1:MET:HE2	35:BP:6:LEU:HD23	1.72	0.70
47:B1:85:LEU:HD22	47:B1:89:GLU:HG3	1.73	0.70
1:CA:673:G:H2'	1:CA:674:G:C8	2.27	0.70
25:DA:2148:G:H2'	25:DA:2149:G:C8	2.27	0.70
1:AA:839:U:H3'	1:AA:840:C:H6	1.56	0.70
1:AA:1030(A):G:O2'	1:AA:1030(C):G:N7	2.24	0.70
1:AA:1320:C:O2	19:AS:36:ARG:NH2	2.25	0.70
25:BA:2128:G:H1	25:BA:2205:C:N4	1.89	0.70
29:DF:53:THR:HG22	29:DF:56:GLU:HG3	1.72	0.70
25:DA:572:A:OP2	41:DV:78:LYS:NZ	2.24	0.70
45:DZ:117:LEU:HA	45:DZ:174:VAL:HA	1.71	0.70
1:AA:1003:G:H2'	1:AA:1004:A:H4'	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:591:U:O4	61:BA:4289:HOH:O	2.06	0.70
25:BA:778:C:OP2	61:BA:4877:HOH:O	2.10	0.70
2:CB:158:LEU:HD23	2:CB:182:ILE:HD11	1.74	0.70
47:B1:86:SER:OG	47:B1:89:GLU:OE1	2.08	0.69
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.56	0.69
25:DA:2124:G:N2	25:DA:2174:C:N3	2.39	0.69
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.72	0.69
1:CA:1278:U:H5'	1:CA:1279:A:O4'	1.92	0.69
25:BA:327:U:O4	61:BA:4758:HOH:O	2.07	0.69
25:BA:610:C:OP2	35:BP:21:ARG:NH2	2.25	0.69
15:CO:70:LEU:HD11	15:CO:77:ARG:HB2	1.73	0.69
25:DA:2317:C:N4	25:DA:2318:G:O6	2.25	0.69
1:AA:353:A:H8	1:AA:353:A:H5'	1.57	0.69
2:CB:87:ARG:NH2	2:CB:220:ASP:OD1	2.26	0.69
25:DA:2120:G:H2'	25:DA:2121:G:H8	1.57	0.69
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.55	0.69
10:AJ:5:ARG:HD3	10:AJ:71:LEU:HD11	1.73	0.69
27:DD:71:ASP:HB3	27:DD:103:ARG:HH22	1.57	0.69
49:B3:3:ARG:NH1	49:B3:60:GLU:OE2	2.23	0.69
1:CA:1029:C:N4	1:CA:1032:G:N1	2.41	0.69
10:CJ:74:ILE:HD11	10:CJ:81:THR:HG21	1.75	0.69
23:CY:62:C:H2'	23:CY:63:G:H8	1.58	0.69
28:DE:47:VAL:HG11	28:DE:86:PRO:HD2	1.72	0.69
23:AW:19:G:H1	23:AW:56:C:N4	1.91	0.69
25:BA:1604:C:OP2	25:BA:1605:A:O2'	2.10	0.69
1:AA:109:A:N1	61:AA:4202:HOH:O	2.25	0.69
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.75	0.69
25:BA:934:A:O2'	25:BA:935:C:OP2	2.10	0.69
1:CA:839:U:H5"	1:CA:840:C:H5	1.57	0.69
1:CA:1119:C:H42	1:CA:1154:G:H1	1.41	0.69
25:DA:1798:U:OP2	27:DD:274:ARG:NH2	2.26	0.69
29:DF:101:LEU:O	29:DF:106:ARG:NH1	2.26	0.69
39:DT:64:ARG:HB2	39:DT:73:GLU:HG2	1.75	0.69
46:D0:2:ALA:N	61:D0:204:HOH:O	2.26	0.69
57:AA:3221:NEG:H71	25:BA:786:G:N1	2.05	0.68
25:BA:709:G:H5"	35:BP:16:ARG:HG2	1.74	0.68
33:BN:123:TYR:HH	33:BN:130:HIS:HE2	1.37	0.68
25:DA:2031:A:N3	25:DA:2455:G:O2'	2.25	0.68
25:BA:2320:G:O6	25:BA:2323:A:N6	2.18	0.68
25:BA:2649:U:H5"	28:BE:82:ARG:HH21	1.58	0.68
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.22	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.25	0.68
25:DA:11:G:H2'	25:DA:12:U:H5"	1.75	0.68
45:DZ:111:VAL:HG21	45:DZ:117:LEU:HB2	1.75	0.68
1:AA:1191:A:OP1	3:AC:4:LYS:NZ	2.25	0.68
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.56	0.68
25:DA:468:G:N7	53:D7:39:ARG:NH2	2.41	0.68
45:DZ:144:LEU:HD22	45:DZ:174:VAL:HG23	1.73	0.68
25:BA:2459:G:OP2	61:BA:4656:HOH:O	2.11	0.68
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.26	0.68
25:DA:900:A:H2'	25:DA:901:A:H8	1.59	0.68
30:DG:5:VAL:HG22	30:DG:8:LYS:H	1.57	0.68
38:DS:84:GLN:H	38:DS:111:GLU:HB2	1.58	0.68
25:BA:650:G:N7	35:BP:107:LYS:NZ	2.41	0.68
25:BA:2460:A:OP1	61:BA:5152:HOH:O	2.11	0.68
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.74	0.68
23:CY:21:A:H61	23:CY:46:7MG:H2'	1.59	0.68
25:DA:1814:G:O3'	27:DD:54:ARG:NH2	2.27	0.68
1:AA:166:G:H2'	1:AA:167:G:C8	2.28	0.68
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.26	0.68
1:AA:1029:C:N3	1:AA:1032:G:O6	2.27	0.68
6:AF:89:MET:HE1	18:AR:72:ARG:HB3	1.76	0.68
45:BZ:91:LEU:HD12	45:BZ:130:PRO:HG3	1.76	0.68
1:AA:1008:C:N3	1:AA:1021:G:C6	2.62	0.68
7:AG:78:ARG:HH12	7:AG:79:ARG:HD2	1.58	0.68
29:BF:185:ASP:HA	29:BF:188:ARG:HD3	1.75	0.68
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.09	0.68
25:DA:2049:G:N7	61:DA:4134:HOH:O	2.25	0.68
1:AA:596:C:OP2	61:AA:4080:HOH:O	2.12	0.68
1:AA:1036:G:H21	1:AA:1037:C:H1'	1.59	0.68
27:BD:69:ARG:NH2	27:BD:128:GLY:O	2.27	0.68
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.74	0.68
25:DA:987:G:O2'	25:DA:1000:A:N3	2.25	0.68
25:DA:1721:G:N1	25:DA:1739:U:OP2	2.27	0.68
25:DA:2430:A:OP2	61:DA:4563:HOH:O	2.12	0.68
31:DH:46:GLU:HB2	31:DH:49:VAL:HG12	1.75	0.68
23:CY:76:A:N6	25:DA:2422:A:H5'	2.09	0.68
25:DA:248:G:OP1	61:DA:4656:HOH:O	2.12	0.68
25:DA:1030:G:OP2	36:DQ:128:LYS:NZ	2.27	0.68
55:D9:25:VAL:HB	55:D9:34:GLN:HB2	1.76	0.68
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.39	0.67
25:BA:1170:C:OP1	61:BA:4982:HOH:O	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BE:127:ASP:OD2	61:BE:401:HOH:O	2.11	0.67
1:CA:532:A:O2'	1:CA:533:A:OP1	2.12	0.67
9:CI:53:VAL:O	9:CI:55:ALA:N	2.27	0.67
25:DA:607:U:OP1	29:DF:102:PRO:HA	1.94	0.67
1:AA:1008:C:C4	1:AA:1021:G:O6	2.47	0.67
25:BA:354:A:H2	25:BA:1255:A:HO2'	1.42	0.67
1:CA:316:G:OP2	1:CA:351:G:O2'	2.13	0.67
26:DB:54:G:H21	30:DG:29:TRP:HE1	1.41	0.67
27:DD:148:GLU:HB2	27:DD:151:LYS:HD2	1.76	0.67
1:AA:1026:G:H3'	1:AA:1027:C:H6	1.60	0.67
25:BA:2291:G:N7	46:B0:14:ARG:NH1	2.41	0.67
25:DA:1031:G:H21	55:D9:36:GLN:HE22	1.42	0.67
37:DR:56:LYS:NZ	37:DR:90:ARG:O	2.27	0.67
1:AA:1320:C:H5'	19:AS:70:LYS:HG3	1.76	0.67
25:BA:932:C:H3'	25:BA:933:C:H5"	1.76	0.67
39:BT:39:ARG:HH12	39:BT:41:ARG:HD3	1.59	0.67
1:CA:999:C:N4	1:CA:1042:G:H1	1.92	0.67
25:DA:1237:A:OP1	61:DA:4737:HOH:O	2.10	0.67
25:BA:1480:A:H61	25:BA:1605:A:H62	1.40	0.67
29:BF:157:VAL:HB	29:BF:194:MET:HG2	1.75	0.67
25:DA:2584:U:H2'	25:DA:2585:U:H2'	1.77	0.67
25:DA:2836:U:H2'	25:DA:2837:G:C8	2.30	0.67
29:DF:24:LEU:HD23	29:DF:115:ALA:HA	1.76	0.67
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.11	0.67
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.10	0.67
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.77	0.67
25:BA:2252:C:OP2	61:BA:4455:HOH:O	2.11	0.67
25:BA:2877:G:OP2	39:BT:119:LYS:NZ	2.27	0.67
35:BP:116:GLY:O	35:BP:137:LYS:NZ	2.25	0.67
1:CA:1417:G:O6	61:CA:4052:HOH:O	2.11	0.67
25:DA:832:G:OP1	61:DA:4546:HOH:O	2.12	0.67
29:DF:64:ILE:HG21	29:DF:78:ILE:HG23	1.77	0.67
1:CA:1089:G:H1	1:CA:1096:C:N4	1.92	0.67
25:DA:1647:G:OP1	61:DA:4489:HOH:O	2.11	0.67
29:DF:157:VAL:HB	29:DF:194:MET:HG2	1.77	0.67
37:DR:36:THR:HG22	37:DR:37:THR:H	1.58	0.67
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.12	0.67
25:BA:1055:A:OP2	33:BN:37:LYS:NZ	2.26	0.67
57:CX:3004:NEG:N1	25:DA:2330:G:N7	2.43	0.67
9:AI:53:VAL:O	9:AI:55:ALA:N	2.28	0.67
31:BH:86:GLU:OE2	31:BH:132:ARG:NH2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1183:G:H5"	49:D3:30:ARG:HH12	1.60	0.67
25:DA:2518:A:OP2	61:DA:4293:HOH:O	2.13	0.67
28:DE:111:ARG:HD3	37:DR:1:MET:HE1	1.77	0.67
25:BA:1067:A:H8	25:BA:1068:G:H5"	1.58	0.67
25:BA:2307:C:OP1	38:BS:10:ARG:NH1	2.28	0.67
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.28	0.67
25:DA:361:G:H21	25:DA:362:U:H3	1.43	0.67
25:DA:2327:A:H2'	25:DA:2328:A:C8	2.30	0.67
25:DA:2472:G:H2'	25:DA:2475:C:H42	1.60	0.67
25:DA:2530:A:OP2	25:DA:2535:G:N2	2.28	0.67
25:DA:2867:G:OP2	39:DT:119:LYS:NZ	2.27	0.67
1:AA:653:A:OP1	8:AH:56:LYS:NZ	2.28	0.66
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.77	0.66
18:AR:32:ARG:HA	18:AR:69:THR:HG21	1.76	0.66
10:CJ:11:PHE:HE1	10:CJ:67:THR:HG22	1.59	0.66
25:DA:1266:G:O5'	42:DW:15:ARG:NH2	2.28	0.66
25:DA:2318:G:N2	38:DS:3:ARG:HH12	1.93	0.66
1:AA:993:G:O6	1:AA:1045:C:N4	2.28	0.66
25:BA:2081:A:OP2	61:BA:4459:HOH:O	2.13	0.66
1:CA:1029:C:N3	1:CA:1032:G:N2	2.44	0.66
25:DA:1022:G:H22	25:DA:1142(A):A:H2	1.43	0.66
32:DI:110:ASP:H	32:DI:130:TYR:HH	1.43	0.66
25:BA:273:G:H4'	25:BA:274:U:OP1	1.94	0.66
25:BA:542:C:OP1	51:B5:16:ARG:NH2	2.29	0.66
25:DA:576:U:OP1	61:DA:4452:HOH:O	2.13	0.66
45:DZ:104:PHE:HA	45:DZ:139:VAL:HB	1.78	0.66
1:AA:347:G:H2'	1:AA:348:G:O4'	1.95	0.66
25:BA:2015:U:OP2	61:BA:5370:HOH:O	2.12	0.66
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.27	0.66
24:CX:64:G:O2'	36:DQ:10:ARG:NH2	2.28	0.66
37:DR:55:ALA:HB2	37:DR:79:LEU:HD13	1.76	0.66
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.76	0.66
25:BA:2286:A:OP1	61:BA:5335:HOH:O	2.13	0.66
25:DA:1508:A:H4'	25:DA:1509(A):A:C4	2.31	0.66
29:DF:184:TYR:CE2	29:DF:188:ARG:HD2	2.31	0.66
3:AC:8:ILE:HG23	3:AC:16:ARG:HG2	1.78	0.66
23:AW:10:G:N1	23:AW:25:C:O2	2.24	0.66
25:DA:1815:A:P	27:DD:54:ARG:HH22	2.18	0.66
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.28	0.66
25:BA:1065:U:HO2'	25:BA:1067:A:H2	1.42	0.66
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:154:ASP:N	45:DZ:154:ASP:OD1	2.28	0.66
9:AI:50:LEU:HD13	9:AI:56:LEU:HA	1.78	0.66
28:BE:11:MET:HG2	28:BE:24:THR:HB	1.78	0.66
32:BI:72:LEU:C	32:BI:74:ASN:H	2.03	0.66
25:DA:223:A:O2'	25:DA:420:C:O2	2.13	0.66
25:DA:1796:U:H2'	25:DA:1797:C:C6	2.31	0.66
28:DE:36:ARG:HG2	28:DE:47:VAL:HG12	1.78	0.66
28:DE:73:GLU:HG3	28:DE:73:GLU:O	1.96	0.66
1:AA:1158:C:H5	1:AA:1181:G:N1	1.92	0.66
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.78	0.66
7:AG:111:ARG:HD2	7:AG:123:GLU:HB2	1.78	0.66
25:BA:2299:A:H62	25:BA:2356:U:H3	1.42	0.66
1:CA:1229:A:OP2	13:CM:114:ARG:NH1	2.29	0.66
25:DA:304:G:O6	61:DA:4467:HOH:O	2.10	0.66
26:DB:13:A:N1	26:DB:69:G:O2'	2.25	0.66
32:DI:90:GLY:O	32:DI:121:LYS:NZ	2.24	0.66
36:DQ:1:MET:HG3	36:DQ:44:ALA:HB1	1.77	0.66
1:AA:346:G:OP1	39:BT:41:ARG:NH1	2.26	0.66
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.30	0.66
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.11	0.66
5:AE:68:GLU:HG2	5:AE:70:PRO:HD3	1.78	0.65
57:AX:3013:NEG:O3	57:AX:3013:NEG:N4	2.29	0.65
25:BA:185:A:H62	35:BP:38:GLN:HE22	1.44	0.65
25:BA:2164:C:H2'	25:BA:2165:C:C6	2.31	0.65
13:CM:3:ARG:HA	50:D4:34:GLU:HG2	1.77	0.65
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.77	0.65
25:DA:1190:G:H2'	25:DA:1191:G:H8	1.61	0.65
27:DD:67:PHE:HE1	27:DD:106:ILE:HD12	1.61	0.65
57:AW:3004:NEG:H91	25:BA:1965:U:H3'	1.77	0.65
25:BA:1424:A:OP1	53:B7:10:ARG:NH2	2.29	0.65
1:CA:1309:G:O2'	13:CM:77:ASN:ND2	2.29	0.65
7:CG:78:ARG:NH1	7:CG:154:TYR:O	2.29	0.65
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.30	0.65
26:BB:48:A:H4'	38:BS:95:HIS:HD2	1.61	0.65
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.61	0.65
25:DA:71:A:N7	43:DX:31:HIS:HE1	1.94	0.65
25:DA:323:G:O2'	25:DA:1205:U:N3	2.25	0.65
25:DA:857:C:OP2	46:D0:77:ARG:NH2	2.29	0.65
27:DD:26:LYS:NZ	27:DD:30:GLU:OE1	2.30	0.65
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.77	0.65
1:CA:1521:G:N3	61:CA:4036:HOH:O	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.78	0.65
25:DA:687:C:OP2	61:DA:4709:HOH:O	2.13	0.65
26:DB:66:A:H61	26:DB:109:C:H5'	1.61	0.65
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.78	0.65
23:AY:53:G:C4	23:AY:54:5MU:H72	2.31	0.65
2:CB:24:TRP:CZ3	2:CB:26:PRO:HA	2.31	0.65
1:CA:942:G:H21	9:CI:124:GLN:NE2	1.94	0.65
25:DA:1300:U:H4'	25:DA:1301:A:H5"	1.78	0.65
25:BA:70:A:N7	43:BX:31:HIS:HE1	1.94	0.65
25:BA:1814:A:OP1	61:BA:4796:HOH:O	2.15	0.65
24:CX:21:A:N6	24:CX:46:G:H2'	2.11	0.65
48:D2:16:LEU:O	48:D2:67:LYS:NZ	2.30	0.65
1:AA:96:U:H2'	1:AA:97:G:C8	2.32	0.65
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.30	0.65
25:BA:241:G:OP1	35:BP:50:ARG:NH1	2.29	0.65
44:BY:17:SER:OG	44:BY:71:LYS:NZ	2.28	0.65
25:DA:307:G:N2	25:DA:310:A:O5'	2.29	0.65
45:DZ:92:SER:OG	45:DZ:93:ASP:N	2.29	0.65
54:D8:6:THR:HG22	54:D8:63:PRO:HD2	1.79	0.65
1:AA:1026:G:O6	1:AA:1034:G:N2	2.30	0.64
25:BA:743:G:N7	61:BA:4543:HOH:O	2.28	0.64
45:BZ:28:MET:HE1	45:BZ:61:LEU:HD21	1.77	0.64
1:CA:405:U:O4	4:CD:2:GLY:N	2.31	0.64
25:DA:144:C:H5'	43:DX:2:LYS:HE2	1.80	0.64
1:AA:1132:C:H2'	1:AA:1133:G:H8	1.61	0.64
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.79	0.64
25:BA:465:G:N7	61:BA:5330:HOH:O	2.29	0.64
25:BA:2121:U:H3	25:BA:2212:G:H1	1.44	0.64
27:BD:206:LEU:HD22	27:BD:211:ARG:HG2	1.79	0.64
1:CA:35:G:O2'	12:CL:118:SER:O	2.13	0.64
57:CA:3173:NEG:H11	57:CA:3173:NEG:H51	1.78	0.64
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.62	0.64
3:AC:82:GLU:HG2	3:AC:85:ARG:HH21	1.60	0.64
25:BA:2357:G:OP2	61:BA:4075:HOH:O	2.13	0.64
26:BB:87:G:N2	26:BB:90:A:OP2	2.28	0.64
36:BQ:18:LYS:O	36:BQ:98:LYS:NZ	2.25	0.64
38:DS:15:ARG:O	38:DS:19:LYS:HG2	1.97	0.64
25:BA:611:U:H2'	25:BA:612:C:C6	2.32	0.64
27:BD:52:ARG:NH2	61:BD:411:HOH:O	2.30	0.64
10:CJ:78:ASN:O	10:CJ:80:LYS:N	2.30	0.64
45:DZ:24:LEU:HB2	45:DZ:41:LEU:HD23	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:9:ASN:O	20:AT:10:LEU:HB2	1.96	0.64
23:AW:76:A:HO2'	25:BA:2518:U:HO2'	1.45	0.64
25:BA:1093:G:H2'	25:BA:1156:G:H22	1.63	0.64
25:BA:1219:A:H4'	25:BA:1220:U:OP1	1.98	0.64
23:CY:7:A:H61	23:CY:66:U:H3	0.74	0.64
25:DA:2646:C:OP2	25:DA:2732:G:O2'	2.15	0.64
1:AA:167:G:H2'	1:AA:168:G:C8	2.32	0.64
57:AA:3216:NEG:O1	61:AA:4240:HOH:O	2.13	0.64
2:AB:212:GLN:NE2	2:AB:234:PRO:O	2.30	0.64
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.33	0.64
8:AH:29:SER:HB3	8:AH:32:LYS:HG3	1.78	0.64
5:CE:11:ILE:HB	5:CE:31:LEU:HB3	1.78	0.64
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.79	0.64
27:DD:69:ARG:NH2	27:DD:128:GLY:O	2.31	0.64
29:DF:185:ASP:OD1	29:DF:188:ARG:NH1	2.30	0.64
50:D4:62:ARG:O	50:D4:64:GLY:N	2.30	0.64
1:AA:1002:G:H3'	1:AA:1003:G:C8	2.32	0.64
9:AI:77:ILE:O	9:AI:81:ILE:HG22	1.98	0.64
24:AX:21:A:H61	24:AX:46:G:H2'	1.63	0.64
23:AY:2:C:H42	23:AY:71:G:H1	1.46	0.64
25:BA:894:U:OP2	61:BA:4526:HOH:O	2.15	0.64
1:CA:538:G:H5"	12:CL:114:LYS:HB2	1.79	0.64
5:CE:92:LYS:HB3	5:CE:119:LEU:HB2	1.80	0.64
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.80	0.64
25:DA:2123:G:N2	25:DA:2175:C:N3	2.42	0.64
30:DG:39:ILE:HG12	30:DG:157:ILE:HG12	1.80	0.64
25:BA:2149:G:H21	25:BA:2195:A:H1'	1.62	0.64
25:BA:2365:G:N7	61:BA:4567:HOH:O	2.30	0.64
25:DA:1159:U:H2'	25:DA:1160:G:H8	1.62	0.64
42:DW:18:ARG:NH1	42:DW:76:VAL:O	2.31	0.64
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.78	0.64
23:AW:10:G:O6	23:AW:25:C:N3	2.31	0.64
30:BG:108:ASN:HB3	50:B4:22:ILE:HD13	1.80	0.64
47:B1:51:VAL:HG11	47:B1:74:VAL:HG21	1.79	0.64
1:CA:1132:C:H2'	1:CA:1133:G:H8	1.63	0.64
2:CB:96:ARG:HD2	2:CB:98:LEU:HD22	1.79	0.64
7:CG:113:GLU:HG3	7:CG:118:VAL:HG12	1.80	0.64
11:CK:98:LEU:O	11:CK:101:SER:OG	2.13	0.64
25:DA:1800:C:OP2	27:DD:183:ARG:NH2	2.30	0.64
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.80	0.64
23:AW:7:A:N1	23:AW:66:U:O2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.13	0.64
25:DA:1648:C:OP1	61:DA:4489:HOH:O	2.15	0.64
25:DA:2723:C:H5"	37:DR:1:MET:HE2	1.79	0.64
1:AA:1112:C:H1'	3:AC:179:ARG:HG2	1.80	0.63
19:AS:27:GLU:HB3	19:AS:28:LYS:HB3	1.79	0.63
25:BA:1189:A:OP1	33:BN:25:ARG:NH2	2.30	0.63
28:BE:47:VAL:HG21	28:BE:86:PRO:HD2	1.80	0.63
27:DD:276:LYS:HD3	27:DD:276:LYS:H	1.61	0.63
32:DI:72:LEU:HA	32:DI:75:LEU:HD22	1.78	0.63
25:BA:671:A:H2'	25:BA:672:G:O4'	1.98	0.63
25:BA:2297:C:OP2	52:B6:6:ARG:NH1	2.29	0.63
50:B4:55:ARG:HB2	50:B4:56:VAL:O	1.99	0.63
2:CB:47:THR:HA	2:CB:202:PRO:HG2	1.80	0.63
24:CX:47:U:H3'	24:CX:48:C:H5'	1.81	0.63
23:CY:25:C:O2'	23:CY:26:A:O5'	2.16	0.63
25:DA:811:U:O4	61:DA:4886:HOH:O	2.12	0.63
25:DA:2124:G:N1	25:DA:2174:C:N4	2.46	0.63
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.31	0.63
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.31	0.63
20:AT:43:LEU:O	20:AT:47:GLY:N	2.31	0.63
1:CA:148:G:H2'	1:CA:149:A:H8	1.63	0.63
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.14	0.63
23:CY:31:A:N1	23:CY:39:PSU:O2	2.31	0.63
25:DA:184:C:H2'	25:DA:185:U:C6	2.32	0.63
25:DA:2727:G:O2'	34:DO:70:LYS:NZ	2.31	0.63
36:DQ:57:HIS:HD2	36:DQ:117:ALA:HB2	1.61	0.63
1:CA:1129:C:OP1	9:CI:16:ARG:NH1	2.31	0.63
2:CB:15:VAL:HG13	2:CB:209:ARG:HB3	1.81	0.63
25:DA:1149:G:H2'	25:DA:1150:C:C6	2.34	0.63
25:DA:1470:G:N2	25:DA:1520:G:OP2	2.30	0.63
25:DA:1842:G:O2'	27:DD:253:GLN:NE2	2.31	0.63
53:D7:34:ARG:NH1	53:D7:41:ARG:O	2.31	0.63
1:AA:165:C:H2'	1:AA:166:G:C8	2.33	0.63
25:BA:630:U:OP1	29:BF:102:PRO:HA	1.98	0.63
61:CW:4001:HOH:O	25:DA:2602:A:N6	2.31	0.63
25:DA:299:A:H5"	44:DY:86:ARG:HH21	1.64	0.63
25:DA:2839:G:H5'	37:DR:46:GLY:HA2	1.80	0.63
28:DE:1:MET:HE3	28:DE:199:ARG:HD2	1.79	0.63
45:DZ:153:SER:HB3	45:DZ:167:PRO:HB3	1.79	0.63
1:AA:511:C:OP2	4:AD:49:ARG:NH1	2.31	0.63
27:BD:148:GLU:HB2	27:BD:151:LYS:HD2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.46	0.63
1:CA:1301:U:O2'	1:CA:1302:U:H5'	1.98	0.63
25:DA:2166:G:H3'	25:DA:2167:U:H5"	1.80	0.63
7:AG:78:ARG:NH1	7:AG:79:ARG:HD2	2.14	0.63
25:BA:1388:A:OP2	61:BA:4364:HOH:O	2.15	0.63
25:BA:1829:U:OP2	27:BD:274:ARG:NH2	2.29	0.63
25:BA:2210:C:OP1	25:BA:2210:C:H4'	1.97	0.63
45:BZ:110:GLY:HA3	45:BZ:145:GLU:HA	1.81	0.63
1:CA:1292:U:OP2	7:CG:41:ARG:NH2	2.31	0.63
1:AA:26:A:O2'	4:AD:209:ARG:NH2	2.31	0.63
1:AA:1292:U:OP2	7:AG:41:ARG:NH2	2.30	0.63
20:AT:10:LEU:HD13	20:AT:12:ALA:HB2	1.81	0.63
25:BA:1039:G:OP1	40:BU:50:ARG:NH2	2.31	0.63
39:BT:95:ARG:HG2	39:BT:95:ARG:HH11	1.63	0.63
45:BZ:92:SER:OG	45:BZ:93:ASP:N	2.32	0.63
1:CA:920:U:H2'	1:CA:921:U:C6	2.33	0.63
2:CB:17:PHE:HB2	2:CB:44:LEU:HD11	1.79	0.63
25:DA:998:C:OP1	40:DU:92:ARG:NH2	2.32	0.63
35:DP:88:LEU:HD11	35:DP:114:ILE:HD12	1.80	0.63
37:DR:97:VAL:HG22	37:DR:114:VAL:HG13	1.80	0.63
1:CA:1346:A:N1	1:CA:1374:A:H5"	2.14	0.63
30:DG:144:ILE:HA	30:DG:148:MET:HE1	1.81	0.63
40:DU:49:HIS:HA	40:DU:52:ARG:HB3	1.81	0.63
42:DW:71:VAL:HA	42:DW:107:LEU:HD12	1.81	0.63
50:D4:24:THR:OG1	50:D4:25:TYR:N	2.29	0.63
1:AA:70:G:H1	1:AA:99:U:H3	1.46	0.62
1:AA:1007:C:N3	1:AA:1022:G:C6	2.67	0.62
25:BA:2820:A:N6	25:BA:2900:G:O2'	2.31	0.62
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.34	0.62
25:DA:2357:U:OP1	46:D0:20:ARG:NH1	2.28	0.62
1:AA:59:A:N1	61:AA:4113:HOH:O	2.31	0.62
23:AW:25:C:H2'	23:AW:26:A:H8	1.64	0.62
1:CA:1118:C:H2'	1:CA:1119:C:C6	2.34	0.62
3:CC:52:LEU:HD21	3:CC:55:VAL:HG23	1.80	0.62
5:CE:143:ARG:NH1	8:CH:77:GLU:OE1	2.32	0.62
25:DA:2472:G:N1	25:DA:2477:C:OP1	2.27	0.62
1:AA:67:C:H2'	1:AA:68:G:C8	2.35	0.62
9:AI:17:VAL:HG23	9:AI:63:ILE:HG12	1.82	0.62
35:BP:16:ARG:NH1	61:BP:314:HOH:O	2.31	0.62
35:BP:50:ARG:HD3	54:B8:7:HIS:CD2	2.34	0.62
35:BP:63:PRO:HG2	54:B8:25:MET:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CY:25:C:H2'	23:CY:26:A:H8	1.62	0.62
25:DA:2744:G:N2	31:DH:143:GLN:OE1	2.32	0.62
1:AA:141:A:H1'	1:AA:182:U:O2	2.00	0.62
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.32	0.62
23:AW:11:C:N3	23:AW:24:G:N2	2.41	0.62
25:BA:553:A:N1	25:BA:2064:A:H2'	2.15	0.62
1:CA:545:C:OP2	4:CD:65:ARG:NH2	2.31	0.62
1:CA:977:A:O2'	1:CA:981:U:N3	2.32	0.62
23:CW:14:A:H61	23:CW:21:A:H2	1.48	0.62
25:DA:1405:U:H2'	25:DA:1406:U:C6	2.34	0.62
25:DA:2297:C:O2	25:DA:2321:G:N2	2.33	0.62
1:AA:1173:G:H2'	1:AA:1174:G:H8	1.64	0.62
3:AC:116:VAL:HG21	3:AC:202:ILE:HD11	1.81	0.62
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.81	0.62
44:DY:16:ALA:HB2	44:DY:73:ARG:HG3	1.82	0.62
7:AG:113:GLU:HG2	7:AG:119:ARG:HG2	1.81	0.62
61:BA:5296:HOH:O	38:BS:3:ARG:HG2	1.99	0.62
25:DA:994:C:O2'	25:DA:996:A:OP1	2.16	0.62
27:DD:132:PRO:HD3	27:DD:190:TYR:CZ	2.34	0.62
1:AA:532:A:N6	1:AA:1206:G:O2'	2.32	0.62
9:AI:49:PRO:HG3	9:AI:101:PHE:HD2	1.63	0.62
25:BA:536:U:OP2	61:BA:4902:HOH:O	2.16	0.62
1:CA:411:A:OP2	4:CD:25:ARG:NH2	2.32	0.62
2:CB:207:ALA:O	2:CB:210:SER:OG	2.15	0.62
25:DA:1996:C:H4'	25:DA:1997:G:OP1	2.00	0.62
25:DA:2506:U:OP1	28:DE:144:ARG:NH2	2.33	0.62
25:BA:1091:A:H1'	25:BA:1093:G:N3	2.13	0.62
27:BD:71:ASP:HB3	27:BD:103:ARG:NH2	2.13	0.62
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.14	0.62
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.16	0.62
25:DA:2120:G:H2'	25:DA:2121:G:C8	2.34	0.62
45:DZ:55:HIS:CE1	45:DZ:135:GLU:HG3	2.35	0.62
50:D4:44:THR:O	50:D4:46:GLN:N	2.32	0.62
25:DA:796:C:H2'	25:DA:797:C:C6	2.35	0.62
25:DA:2166:G:N7	25:DA:2168:G:N2	2.48	0.62
27:DD:132:PRO:HG2	27:DD:135:PHE:CD2	2.34	0.62
47:D1:64:ALA:HA	47:D1:67:ILE:HG13	1.80	0.62
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.32	0.62
1:AA:673:G:H2'	1:AA:674:G:C8	2.34	0.62
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.32	0.62
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:196:A:H62	35:DP:38:GLN:HE22	1.47	0.62
25:DA:582:G:OP2	61:DA:4953:HOH:O	2.16	0.62
25:DA:2171:A:N3	25:DA:2172:U:N3	2.48	0.62
26:DB:106:G:H5"	45:DZ:31:ARG:HG2	1.82	0.62
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.62	0.61
25:BA:2045:G:H5'	25:BA:2629:C:H4'	1.81	0.61
25:BA:2059:G:O6	61:BA:4774:HOH:O	2.13	0.61
32:BI:92:VAL:HG11	32:BI:144:VAL:HG11	1.82	0.61
38:BS:15:ARG:O	38:BS:19:LYS:HG2	2.00	0.61
45:BZ:111:VAL:C	45:BZ:113:ALA:H	2.08	0.61
45:BZ:138:GLU:H	45:BZ:156:LYS:NZ	1.98	0.61
25:BA:709:G:OP1	61:BA:4752:HOH:O	2.16	0.61
25:BA:1613:A:OP1	27:BD:211:ARG:NH1	2.34	0.61
1:CA:1239:A:H62	1:CA:1299:A:H62	1.48	0.61
1:CA:1317:C:N3	19:CS:37:ARG:NH2	2.45	0.61
23:CW:15:G:N2	23:CW:21:A:N3	2.48	0.61
23:CW:56:C:C5	25:DA:897:C:H1'	2.35	0.61
25:DA:1250:G:N7	35:DP:18:ARG:NH2	2.48	0.61
25:DA:2103:C:N3	25:DA:2186:G:O6	2.33	0.61
1:AA:1124:G:N7	1:AA:1145:C:O2'	2.26	0.61
23:AW:54:5MU:OP2	36:BQ:60:ARG:NH1	2.34	0.61
25:BA:1218:G:O2'	25:BA:1219:A:O5'	2.19	0.61
2:CB:7:VAL:HG12	2:CB:8:LYS:HG2	1.80	0.61
4:CD:152:SER:O	4:CD:155:LEU:HB2	2.00	0.61
11:CK:99:GLN:HG2	11:CK:105:VAL:HG21	1.83	0.61
25:DA:287:C:H2'	25:DA:288:C:H6	1.65	0.61
47:D1:59:THR:O	47:D1:91:LYS:NZ	2.33	0.61
1:AA:278:G:OP2	17:AQ:41:LYS:NZ	2.30	0.61
2:AB:211:ILE:HG22	2:AB:215:LEU:HD12	1.80	0.61
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.83	0.61
23:AY:21:A:O2'	23:AY:22:G:O4'	2.19	0.61
25:BA:794:U:O2'	42:BW:92:ARG:NH2	2.33	0.61
25:BA:2164:C:O2	25:BA:2171:G:N1	2.25	0.61
43:BX:11:PRO:HB3	43:BX:92:LEU:HD11	1.83	0.61
53:B7:34:ARG:NH1	53:B7:41:ARG:O	2.34	0.61
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.33	0.61
25:DA:2079:U:O3'	47:D1:35:THR:OG1	2.19	0.61
25:DA:2134:A:O2'	25:DA:2159:G:N3	2.33	0.61
25:DA:2193:G:H2'	25:DA:2194:G:H8	1.64	0.61
23:AW:6:G:H1	23:AW:67:C:N4	1.96	0.61
23:AW:68:C:H2'	23:AW:69:G:H8	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:302:A:O2'	25:BA:303:C:OP1	2.19	0.61
25:BA:2367:C:H1'	46:B0:39:ARG:HH21	1.65	0.61
57:CA:3177:NEG:N3	25:DA:15:G:OP2	2.33	0.61
3:CC:40:ARG:NH2	3:CC:55:VAL:O	2.33	0.61
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.36	0.61
37:DR:67:LEU:HD13	37:DR:76:VAL:HG21	1.81	0.61
25:BA:2123:G:N2	25:BA:2210:C:N3	2.39	0.61
3:CC:11:ARG:NH2	3:CC:177:THR:O	2.32	0.61
3:CC:134:ILE:HG23	3:CC:151:VAL:HB	1.82	0.61
13:CM:79:LYS:NZ	13:CM:83:ASP:OD2	2.23	0.61
25:DA:299:A:H5"	44:DY:86:ARG:NH2	2.16	0.61
25:DA:601:C:OP1	29:DF:108:LYS:NZ	2.33	0.61
25:DA:1005:C:H2'	25:DA:1006:C:C6	2.36	0.61
25:DA:2445:G:OP1	29:DF:74:ARG:NH2	2.29	0.61
32:DI:110:ASP:N	32:DI:130:TYR:OH	2.27	0.61
57:AA:3218:NEG:H11	57:AA:3218:NEG:H51	1.81	0.61
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.19	0.61
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.83	0.61
2:AB:127:ILE:HG13	2:AB:130:ARG:HH11	1.66	0.61
19:AS:45:VAL:HA	19:AS:62:ILE:HG22	1.83	0.61
25:BA:1071:G:C4	25:BA:1180:C:H1'	2.35	0.61
25:BA:2825:C:H5'	51:B5:29:THR:HG21	1.81	0.61
29:BF:101:LEU:O	29:BF:106:ARG:NH1	2.33	0.61
1:CA:596:C:O2	1:CA:644:G:N2	2.19	0.61
6:CF:68:PRO:HB2	6:CF:71:ARG:HG3	1.83	0.61
10:CJ:47:PHE:N	10:CJ:63:PHE:O	2.32	0.61
12:CL:71:PRO:O	12:CL:102:ARG:NH1	2.34	0.61
16:CP:72:ARG:HH21	16:CP:73:LEU:HD21	1.64	0.61
25:DA:807:U:OP2	35:DP:41:ARG:NH2	2.33	0.61
25:DA:911:A:H2'	36:DQ:9:TYR:OH	2.00	0.61
29:DF:53:THR:HG23	29:DF:55:GLY:H	1.66	0.61
38:DS:68:GLN:HE21	38:DS:71:ARG:HD3	1.66	0.61
27:BD:147:LEU:HD13	27:BD:155:LEU:HD21	1.83	0.61
28:BE:31:CYS:HB3	28:BE:49:LEU:HG	1.82	0.61
1:CA:8:A:H5'	5:CE:101:ILE:HG22	1.80	0.61
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.66	0.61
1:CA:1004:A:H3'	1:CA:1005:A:C5'	2.30	0.61
17:CQ:6:LEU:HG	17:CQ:23:VAL:HG11	1.80	0.61
23:CW:25:C:H2'	23:CW:26:A:C8	2.36	0.61
25:DA:361:G:N2	25:DA:362:U:H3	1.98	0.61
25:DA:1020:A:N1	25:DA:1141:U:O2'	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1165:U:H2'	25:DA:1166:C:C6	2.35	0.61
25:DA:2062:A:OP1	61:DA:4163:HOH:O	2.16	0.61
1:AA:955:U:O2'	19:AS:83:HIS:HD2	1.83	0.61
1:AA:1239:A:H62	1:AA:1299:A:N6	1.99	0.61
1:AA:1416:G:N7	61:AA:4106:HOH:O	2.32	0.61
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.35	0.61
13:AM:84:ILE:HD12	19:AS:74:PHE:CE2	2.36	0.61
25:BA:2285:A:H2'	25:BA:2286:A:C8	2.34	0.61
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.34	0.61
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.32	0.61
1:CA:815:A:N7	1:CA:1509:C:O2'	2.28	0.61
25:DA:279:C:N3	25:DA:361:G:N2	2.48	0.61
29:DF:126:VAL:HG21	29:DF:129:PHE:CZ	2.35	0.61
45:DZ:145:GLU:HG3	45:DZ:146:ILE:N	2.15	0.61
1:AA:1505:G:O2'	22:AV:13:A:O2'	2.19	0.60
25:BA:1346:U:H4'	25:BA:1347:A:H5"	1.83	0.60
25:DA:2193:G:H2'	25:DA:2194:G:C8	2.36	0.60
25:DA:2299:G:N1	25:DA:2318:G:N7	2.49	0.60
1:AA:411:A:OP2	4:AD:25:ARG:NH2	2.32	0.60
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.85	0.60
4:AD:188:LEU:HD23	4:AD:188:LEU:H	1.65	0.60
41:BV:40:LEU:HB2	41:BV:46:VAL:HG13	1.83	0.60
1:CA:1178:G:N2	1:CA:1181:G:OP2	2.32	0.60
23:CY:71:G:H4'	25:DA:1851:U:H4'	1.83	0.60
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.35	0.60
25:BA:2339:A:H2'	25:BA:2340:A:C8	2.36	0.60
25:BA:2804:C:H2'	25:BA:2805:G:H8	1.66	0.60
32:BI:40:THR:O	32:BI:44:LEU:HB2	2.02	0.60
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.11	0.60
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.19	0.60
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.84	0.60
35:DP:95:VAL:HA	35:DP:99:LEU:HD21	1.83	0.60
1:AA:96:U:H2'	1:AA:97:G:H8	1.66	0.60
1:AA:1030(C):G:N7	1:AA:1031:G:N2	2.49	0.60
14:AN:3:ARG:HB3	14:AN:3:ARG:HH21	1.66	0.60
25:DA:531:C:N4	61:DA:4155:HOH:O	2.33	0.60
25:DA:1188:U:H4'	41:DV:79:VAL:HG22	1.82	0.60
2:AB:178:ARG:HG2	8:AH:72:PRO:HA	1.81	0.60
5:AE:60:TYR:CE1	5:AE:64:ARG:HD3	2.35	0.60
25:BA:2139:A:O3'	25:BA:2140:U:H3'	2.01	0.60
1:CA:353:A:H5'	1:CA:353:A:H8	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:972:C:O2'	10:CJ:55:LYS:O	2.18	0.60
15:CO:11:VAL:HG21	15:CO:34:LEU:HD22	1.83	0.60
19:CS:14:HIS:O	19:CS:18:LYS:HG3	2.00	0.60
25:DA:625:G:N7	35:DP:107:LYS:NZ	2.44	0.60
49:D3:12:PRO:HB2	49:D3:20:LYS:HG2	1.82	0.60
1:AA:1237:C:HO2'	1:AA:1300:G:H1	1.48	0.60
25:BA:1003:U:H5"	36:BQ:14:ARG:HD3	1.84	0.60
35:BP:126:VAL:HG12	35:BP:148:LEU:HD22	1.82	0.60
25:DA:2133:G:N2	25:DA:2157:G:H1'	2.16	0.60
1:AA:1008:C:O2	1:AA:1021:G:N1	2.35	0.60
23:AW:5:G:H2'	23:AW:6:G:C8	2.36	0.60
25:BA:2348:A:H61	46:B0:43:THR:CG2	2.15	0.60
25:DA:1532:C:N4	25:DA:1537:G:O6	2.34	0.60
25:DA:2298:A:H2'	25:DA:2299:G:O4'	2.02	0.60
35:DP:59:LEU:HD21	54:D8:10:ALA:HA	1.84	0.60
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.36	0.60
57:AA:3220:NEG:H71	25:BA:1967:G:OP1	2.02	0.60
17:AQ:67:LYS:HA	17:AQ:70:ARG:HH12	1.67	0.60
25:BA:2331:G:H22	38:BS:3:ARG:NE	1.98	0.60
1:CA:572:A:OP1	61:CA:4050:HOH:O	2.16	0.60
25:DA:588:U:H2'	25:DA:589:C:C6	2.36	0.60
25:DA:2557:G:H2'	25:DA:2558:C:C6	2.37	0.60
25:BA:1312:G:O5'	42:BW:15:ARG:NH2	2.35	0.60
25:BA:1345:G:OP1	61:BA:4801:HOH:O	2.15	0.60
25:BA:2343:G:O2'	25:BA:2348:A:N1	2.34	0.60
6:CF:45:LEU:HD12	6:CF:59:TYR:HD2	1.67	0.60
25:DA:2048:G:OP1	61:DA:4296:HOH:O	2.16	0.60
25:DA:2273:A:H2'	25:DA:2274:A:C8	2.36	0.60
28:DE:116:VAL:HG13	28:DE:122:PHE:HB2	1.84	0.60
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.33	0.60
25:BA:1232:G:H5"	41:BV:81:TYR:CE1	2.37	0.60
25:BA:1356:G:OP2	53:B7:9:ARG:NH1	2.28	0.60
1:CA:1148:U:O2'	9:CI:66:ARG:NH2	2.28	0.60
1:CA:1240:U:OP2	7:CG:116:ALA:N	2.35	0.60
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.16	0.60
24:CX:23:C:H2'	24:CX:24:U:C6	2.37	0.60
25:DA:500:G:N1	25:DA:503:A:OP2	2.35	0.60
25:DA:2331:G:O2'	25:DA:2336:A:N1	2.30	0.60
30:DG:109:VAL:HG21	50:D4:14:ILE:HG21	1.83	0.60
36:DQ:22:LYS:O	45:DZ:78:LYS:NZ	2.35	0.60
36:DQ:65:PHE:HB2	36:DQ:105:GLU:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:138:GLU:HB2	45:DZ:156:LYS:HD2	1.83	0.60
1:AA:815:A:N7	1:AA:1509:C:O2'	2.34	0.59
50:B4:57:GLU:HB3	50:B4:58:ARG:HG2	1.82	0.59
25:DA:2059:A:O2'	29:DF:69:HIS:HD2	1.84	0.59
1:AA:976:G:H5'	1:AA:1358:U:O2'	2.01	0.59
1:AA:1149:C:H2'	1:AA:1150:U:H6	1.67	0.59
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.29	0.59
4:AD:107:ARG:HH22	4:AD:194:LEU:HD13	1.67	0.59
7:AG:76:ARG:HB3	7:AG:156:TRP:HH2	1.67	0.59
40:BU:66:ASN:O	40:BU:70:ARG:HG3	2.02	0.59
6:CF:100:ASN:HD21	18:CR:23:LYS:HG2	1.67	0.59
10:CJ:61:GLU:OE2	14:CN:45:ARG:NE	2.33	0.59
24:CX:40:C:H2'	24:CX:41:C:H6	1.67	0.59
26:DB:66:A:N6	26:DB:108:U:H3'	2.17	0.59
28:DE:111:ARG:HG3	28:DE:160:TYR:CD2	2.38	0.59
33:DN:4:TYR:HB2	40:DU:101:ARG:NH1	2.16	0.59
39:DT:27:THR:HB	39:DT:90:GLN:HB3	1.84	0.59
45:DZ:126:VAL:HG11	45:DZ:161:VAL:HG23	1.84	0.59
1:AA:1129:C:H5"	9:AI:16:ARG:HH12	1.67	0.59
6:AF:67:MET:HE1	6:AF:75:LEU:HD12	1.83	0.59
25:BA:1700:G:H3'	37:BR:2:ARG:HD3	1.83	0.59
1:CA:1378:C:O2	7:CG:76:ARG:NH2	2.36	0.59
5:CE:20:GLN:NE2	5:CE:21:ALA:O	2.35	0.59
11:CK:48:ILE:O	11:CK:50:TYR:N	2.35	0.59
19:CS:22:LEU:HD22	19:CS:31:ILE:HD11	1.85	0.59
25:DA:958:U:OP2	36:DQ:14:ARG:NH1	2.35	0.59
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.25	0.59
23:AW:51:U:H2'	23:AW:52:G:H8	1.67	0.59
27:BD:108:PRO:HB3	27:BD:143:HIS:CE1	2.37	0.59
53:B7:34:ARG:NH2	61:B7:201:HOH:O	2.33	0.59
1:CA:664:G:P	18:CR:64:ARG:HH21	2.25	0.59
30:DG:9:ARG:NH1	30:DG:13:GLU:OE1	2.35	0.59
25:BA:1049:G:O2'	25:BA:1056:A:N1	2.28	0.59
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.67	0.59
8:CH:7:ALA:O	8:CH:11:THR:OG1	2.14	0.59
25:DA:65:C:O2'	25:DA:456:C:N3	2.29	0.59
25:DA:692:C:O2'	27:DD:38:LYS:NZ	2.35	0.59
25:DA:1021:A:H62	25:DA:1141:U:H3	1.50	0.59
25:DA:2771:C:H5"	28:DE:202:LYS:HD3	1.83	0.59
36:DQ:109:VAL:HG13	36:DQ:113:GLN:HB3	1.84	0.59
1:AA:1008:C:C2	1:AA:1021:G:N1	2.71	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1735:U:O2	25:BA:1747:A:H5'	2.03	0.59
25:BA:1744:G:OP2	25:BA:1745:A:O2'	2.20	0.59
16:CP:23:ASP:OD1	16:CP:25:ARG:HD3	2.02	0.59
25:DA:639:U:H2'	25:DA:640:C:C6	2.38	0.59
25:DA:1830:C:OP2	61:DA:4606:HOH:O	2.15	0.59
1:AA:382:A:H2'	1:AA:383:A:C8	2.38	0.59
1:AA:1003:G:C2'	1:AA:1004:A:H4'	2.32	0.59
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.02	0.59
3:AC:8:ILE:HD13	3:AC:184:TYR:HB3	1.85	0.59
8:AH:51:VAL:HG21	8:AH:60:ARG:HH11	1.68	0.59
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	1.83	0.59
23:AW:1:G:H2'	23:AW:2:C:H6	1.68	0.59
25:BA:956:A:H62	36:BQ:12:GLN:HA	1.68	0.59
27:BD:132:PRO:HG2	27:BD:135:PHE:CD2	2.38	0.59
8:CH:51:VAL:HG11	8:CH:60:ARG:HH12	1.68	0.59
25:DA:2497:A:OP1	61:DA:4078:HOH:O	2.17	0.59
26:DB:11:C:H3'	26:DB:12:C:H6	1.66	0.59
1:AA:920:U:H2'	1:AA:921:U:C6	2.38	0.59
3:AC:3:ASN:N	3:AC:3:ASN:OD1	2.35	0.59
1:CA:976:G:H5'	1:CA:1358:U:O2'	2.02	0.59
4:CD:61:LYS:NZ	4:CD:207:TYR:OH	2.35	0.59
25:DA:1131:G:O6	25:DA:2040:C:H1'	2.03	0.59
25:DA:2701:C:OP1	61:DA:4911:HOH:O	2.16	0.59
25:BA:1827:U:H2'	25:BA:1828:C:C6	2.38	0.59
25:BA:2604:G:OP1	61:BA:4828:HOH:O	2.16	0.59
32:BI:130:TYR:HB3	32:BI:138:ILE:HB	1.84	0.59
50:B4:44:THR:O	50:B4:46:GLN:N	2.36	0.59
52:B6:13:CYS:SG	52:B6:47:THR:HG21	2.43	0.59
1:CA:1053:G:N7	1:CA:1200:C:H5"	2.18	0.59
1:CA:1119:C:N4	1:CA:1154:G:H1	2.00	0.59
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.84	0.59
23:CW:39:PSU:H2'	23:CW:40:C:H6	1.66	0.59
23:CW:50:U:O4	23:CW:64:A:N1	2.36	0.59
25:DA:2787:C:H1'	28:DE:62:PRO:HG3	1.85	0.59
27:DD:242:ARG:N	27:DD:242:ARG:HD3	2.17	0.59
28:DE:28:ALA:HB3	28:DE:93:VAL:HG12	1.85	0.59
45:DZ:28:MET:HE1	45:DZ:61:LEU:HD21	1.83	0.59
45:DZ:100:VAL:HG21	45:DZ:134:PRO:HG2	1.83	0.59
5:AE:152:ARG:NH2	8:AH:107:LEU:O	2.35	0.59
10:AJ:21:GLN:NE2	10:AJ:25:GLU:OE2	2.34	0.59
25:BA:2511:C:OP1	61:BA:5152:HOH:O	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.37	0.59
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.35	0.59
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.85	0.59
13:CM:65:LYS:N	50:D4:50:VAL:HG21	2.18	0.59
13:CM:92:HIS:CE1	13:CM:98:VAL:HG21	2.37	0.59
25:DA:2404:C:O3'	35:DP:77:ARG:NH2	2.35	0.59
31:DH:89:ILE:O	31:DH:129:THR:HG23	2.01	0.59
32:BI:72:LEU:O	32:BI:74:ASN:N	2.34	0.58
38:BS:34:HIS:O	38:BS:97:ARG:NH2	2.36	0.58
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.85	0.58
23:CY:76:A:O2'	25:DA:2394:C:N3	2.30	0.58
25:DA:1012:U:H5	33:DN:28:THR:HG21	1.68	0.58
39:DT:53:ARG:HB3	39:DT:53:ARG:HH11	1.67	0.58
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.70	0.58
25:BA:1546:G:N2	27:BD:99:ASP:O	2.32	0.58
25:BA:1648:U:O4	61:BA:4364:HOH:O	2.09	0.58
25:BA:2132:G:O2'	25:BA:2142:G:OP2	2.21	0.58
25:BA:2190:G:C6	25:BA:2193:A:H8	2.20	0.58
1:CA:1052:U:H5"	1:CA:1053:G:OP2	2.03	0.58
23:CY:55:PSU:N3	23:CY:58:A:N7	2.51	0.58
25:DA:108:U:H2'	25:DA:109:G:C8	2.38	0.58
25:DA:1169:G:H1	25:DA:1180:C:H42	1.50	0.58
25:DA:2103:C:H2'	25:DA:2104:G:C8	2.38	0.58
38:DS:103:GLU:O	38:DS:107:GLU:HG3	2.02	0.58
1:AA:345:C:O2	1:AA:345:C:H2'	2.01	0.58
1:AA:946:A:O2'	1:AA:1333:A:N3	2.30	0.58
25:BA:11:G:H2'	25:BA:12:U:H5"	1.85	0.58
25:BA:661:G:OP1	35:BP:132:LYS:HE2	2.02	0.58
25:BA:927:G:H2'	25:BA:928:G:H8	1.69	0.58
25:BA:2804:C:H2'	25:BA:2805:G:C8	2.38	0.58
1:CA:864:A:H5'	5:CE:86:ALA:HB2	1.85	0.58
2:CB:120:ALA:O	2:CB:122:PHE:N	2.30	0.58
57:CW:3002:NEG:N3	25:DA:1942:C:OP1	2.36	0.58
23:CY:9:A:OP2	23:CY:13:C:N4	2.35	0.58
25:DA:361:G:N3	25:DA:362:U:N3	2.51	0.58
25:DA:376:C:OP1	61:DA:4657:HOH:O	2.17	0.58
26:DB:24:G:N2	26:DB:27:C:N3	2.39	0.58
26:DB:80:U:H2'	26:DB:81:G:C8	2.38	0.58
29:DF:192:LEU:HD13	29:DF:194:MET:HE2	1.85	0.58
37:DR:33:ARG:HD2	37:DR:113:LEU:HD13	1.86	0.58
43:DX:43:VAL:HG21	43:DX:81:VAL:HG11	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:51:U:H3	23:AW:63:G:H1	1.51	0.58
25:BA:908:A:OP2	61:BA:4344:HOH:O	2.17	0.58
25:BA:1220:U:O3'	25:BA:1221:G:H4'	2.03	0.58
32:BI:129:THR:HG22	32:BI:139:GLN:HE22	1.68	0.58
33:BN:30:ILE:HG22	33:BN:34:LEU:HD22	1.84	0.58
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.38	0.58
2:CB:21:ARG:HA	2:CB:39:ILE:HA	1.84	0.58
25:DA:1803:A:O2'	27:DD:259:THR:HG21	2.02	0.58
25:DA:2689:U:P	25:DA:2719:G:H22	2.26	0.58
30:DG:38:VAL:HG22	30:DG:93:THR:HG23	1.84	0.58
47:D1:10:LYS:NZ	47:D1:65:SER:OG	2.37	0.58
1:AA:731:G:H5'	1:AA:766:A:H4'	1.86	0.58
1:AA:982:U:H5"	14:AN:6:LEU:HD21	1.85	0.58
20:AT:60:GLU:HG3	20:AT:81:LYS:HD2	1.85	0.58
25:BA:331:G:H21	25:BA:354:A:H62	1.51	0.58
50:B4:53:GLU:C	50:B4:55:ARG:H	2.10	0.58
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.17	0.58
23:CY:51:U:O2	23:CY:63:G:N2	2.34	0.58
25:DA:330:A:H2	25:DA:1210:A:HO2'	1.50	0.58
25:DA:1025:G:C4	25:DA:1135:C:H1'	2.39	0.58
25:DA:2365:G:O6	54:D8:39:LYS:HE3	2.04	0.58
25:DA:2748:A:H5'	31:DH:4:ILE:HD12	1.85	0.58
26:DB:33:G:H5'	30:DG:2:PRO:HD3	1.86	0.58
29:DF:7:TYR:O	29:DF:22:ALA:N	2.36	0.58
45:DZ:117:LEU:HD11	45:DZ:144:LEU:HD13	1.85	0.58
1:AA:78:G:N2	1:AA:91:C:N3	2.51	0.58
1:AA:1151:A:HO2'	1:AA:1152:A:H8	1.51	0.58
23:AW:76:A:H5"	25:BA:2614:A:H61	1.68	0.58
26:BB:13:A:N1	26:BB:69:G:O2'	2.31	0.58
1:CA:1099:G:OP2	2:CB:144:ARG:NH2	2.37	0.58
1:CA:1456:G:O3'	20:CT:39:LYS:NZ	2.37	0.58
25:DA:247:G:H4'	25:DA:386:G:C5	2.39	0.58
25:DA:400:G:N7	61:DA:4648:HOH:O	2.32	0.58
25:DA:1713:U:H2'	25:DA:1714:G:H8	1.69	0.58
25:DA:2612:C:OP2	51:D5:2:ALA:N	2.36	0.58
26:DB:3:C:H2'	26:DB:4:C:C6	2.39	0.58
42:DW:11:ARG:HD2	42:DW:82:LEU:HD12	1.85	0.58
2:AB:87:ARG:CZ	2:AB:233:SER:HB3	2.34	0.58
23:AY:26:A:N6	23:AY:44:G:N1	2.37	0.58
25:BA:1441:A:OP1	61:BA:5091:HOH:O	2.17	0.58
1:CA:662:G:H2'	1:CA:663:A:C8	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:128:GLU:HG3	2:CB:135:GLN:HE22	1.68	0.58
25:DA:997:G:OP1	40:DU:92:ARG:HG2	2.03	0.58
32:DI:31:LEU:HD21	32:DI:38:LEU:HG	1.85	0.58
34:DO:98:VAL:HG22	34:DO:118:ALA:HA	1.86	0.58
45:DZ:45:ASP:OD1	45:DZ:49:ARG:NH1	2.35	0.58
1:AA:1039:C:H2'	1:AA:1040:U:C6	2.38	0.58
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.19	0.58
6:AF:97:PHE:HD2	18:AR:31:LEU:HD12	1.69	0.58
25:BA:139:A:H8	25:BA:1454:C:O2'	1.87	0.58
36:BQ:43:THR:HG22	36:BQ:94:VAL:HG12	1.86	0.58
45:BZ:24:LEU:HB2	45:BZ:41:LEU:HD23	1.85	0.58
1:CA:17:U:H2'	1:CA:18:C:C6	2.39	0.58
25:DA:320:A:H4'	25:DA:322:A:C8	2.38	0.58
25:DA:1140:C:O3'	33:DN:25:ARG:NH1	2.37	0.58
25:DA:1429:G:H2'	25:DA:1430:C:C6	2.38	0.58
25:DA:2537:U:H2'	25:DA:2538:C:C6	2.38	0.58
32:DI:4:ILE:HG12	32:DI:18:VAL:HG22	1.86	0.58
1:AA:142:G:H2'	1:AA:143:A:H8	1.69	0.58
24:AX:21:A:N6	24:AX:46:G:H2'	2.19	0.58
25:BA:1830:G:O2'	27:BD:181:GLU:OE2	2.18	0.58
25:BA:2235:G:OP1	27:BD:172:TYR:OH	2.18	0.58
27:BD:132:PRO:HD3	27:BD:190:TYR:CZ	2.39	0.58
41:BV:5:VAL:HG21	41:BV:35:LEU:HD23	1.85	0.58
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.77	0.58
19:CS:49:ILE:HD13	19:CS:62:ILE:HD13	1.84	0.58
25:DA:981:A:N1	25:DA:2027:G:O2'	2.36	0.58
25:DA:1262:A:H2	51:D5:10:LYS:HD2	1.69	0.58
45:DZ:105:VAL:N	45:DZ:139:VAL:O	2.36	0.58
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.84	0.58
23:AW:8:4SU:O5'	23:AW:8:4SU:H6	2.04	0.58
25:BA:1201:A:OP1	40:BU:55:ARG:HD3	2.04	0.58
25:BA:1781:G:O2'	25:BA:2870:A:N1	2.37	0.58
4:CD:140:VAL:HG11	4:CD:146:ILE:HD11	1.85	0.58
25:DA:322:A:OP1	29:DF:168:ARG:HD2	2.04	0.58
25:DA:1434:A:H61	25:DA:1558:A:H62	1.50	0.58
25:DA:2144:U:H1'	25:DA:2148:G:H22	1.69	0.58
1:AA:222:U:H2'	1:AA:223:U:C6	2.38	0.57
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.25	0.57
25:DA:646:A:H2'	25:DA:647:G:O4'	2.03	0.57
25:DA:839:U:H2'	25:DA:840:C:C6	2.38	0.57
25:DA:1773:A:H5"	61:DA:4621:HOH:O	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:53:ILE:HD13	45:DZ:99:TYR:HB2	1.85	0.57
29:BF:184:TYR:CE2	29:BF:188:ARG:HD2	2.39	0.57
49:B3:19:GLN:OE1	49:B3:52:HIS:NE2	2.36	0.57
1:CA:1015:A:H1'	1:CA:1219:U:H5'	1.86	0.57
25:DA:193:U:OP1	61:DA:4562:HOH:O	2.17	0.57
25:DA:2125:G:N1	25:DA:2172:U:OP2	2.33	0.57
25:DA:2143:C:N4	25:DA:2148:G:H1	2.02	0.57
25:DA:2438:U:O2'	25:DA:2440:C:OP1	2.18	0.57
31:DH:17:VAL:HG11	31:DH:50:VAL:HG21	1.84	0.57
33:DN:15:LEU:HB3	33:DN:137:LYS:HA	1.85	0.57
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.36	0.57
23:AY:67:C:H2'	23:AY:68:C:C6	2.39	0.57
25:BA:236:G:H4'	25:BA:413:G:C5	2.38	0.57
25:BA:664:U:H2'	25:BA:665:C:C6	2.40	0.57
1:CA:1126:U:H3	10:CJ:40:LEU:HD11	1.67	0.57
1:CA:1222:G:OP1	19:CS:77:THR:HG21	2.05	0.57
2:CB:178:ARG:NH2	8:CH:68:ARG:HH12	2.01	0.57
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.27	0.57
25:DA:1038:C:H42	25:DA:1117:G:H1	1.51	0.57
25:DA:1866:C:H2'	25:DA:1876:A:O4'	2.04	0.57
1:AA:138:G:H1	1:AA:225:C:H42	1.50	0.57
1:AA:859:A:OP2	1:AA:869:G:N1	2.31	0.57
25:BA:2041:A:OP2	51:B5:9:LYS:NZ	2.38	0.57
25:BA:2348:A:H61	46:B0:43:THR:HG22	1.70	0.57
23:CW:27:G:H2'	23:CW:28:G:H8	1.69	0.57
25:DA:845:G:OP2	25:DA:845:G:N2	2.29	0.57
25:DA:1358:G:O2'	25:DA:1359:A:H5"	2.03	0.57
45:DZ:53:ILE:HG22	45:DZ:71:VAL:O	2.04	0.57
47:D1:76:ARG:NH1	47:D1:97:LEU:O	2.37	0.57
50:D4:33:VAL:HG12	50:D4:35:VAL:H	1.69	0.57
25:BA:672:G:N3	25:BA:2362:C:O2'	2.38	0.57
37:BR:28:LEU:HD12	37:BR:48:VAL:HG21	1.85	0.57
25:DA:652(T):C:H2'	25:DA:652(U):G:C8	2.40	0.57
25:DA:1593:G:H2'	25:DA:1594:G:C8	2.40	0.57
25:DA:2001:A:H4'	25:DA:2689:U:H2'	1.86	0.57
25:DA:2638:G:OP1	28:DE:82:ARG:NH2	2.38	0.57
28:DE:12:THR:HG22	28:DE:13:ARG:H	1.69	0.57
30:DG:136:ARG:HD2	30:DG:137:GLU:HG3	1.86	0.57
45:DZ:44:PHE:CZ	45:DZ:86:VAL:HG11	2.39	0.57
1:AA:1132:C:H2'	1:AA:1133:G:C8	2.39	0.57
2:AB:76:GLN:CD	2:AB:76:GLN:H	2.13	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.87	0.57
9:AI:20:ARG:O	9:AI:60:ASP:N	2.36	0.57
9:AI:110:GLU:OE2	9:AI:113:LYS:NZ	2.36	0.57
17:AQ:45:HIS:NE2	17:AQ:47:PRO:HG3	2.19	0.57
50:B4:63:TYR:N	50:B4:64:GLY:HA2	2.19	0.57
54:B8:62:LEU:HB3	54:B8:65:GLU:HG2	1.87	0.57
1:CA:1151:A:O2'	1:CA:1152:A:H8	1.87	0.57
4:CD:61:LYS:HZ1	4:CD:72:GLU:CD	2.11	0.57
23:CY:7:A:N1	23:CY:66:U:O2	2.38	0.57
25:DA:1998:G:O2'	25:DA:2724:C:O2'	2.23	0.57
25:DA:2274:A:O2'	25:DA:2276:G:OP1	2.21	0.57
25:DA:2539:C:H4'	55:D9:35:ARG:HH22	1.70	0.57
42:DW:14:PRO:HG2	42:DW:78:GLU:HG2	1.85	0.57
1:AA:152:A:N6	1:AA:169:C:N3	2.52	0.57
1:AA:748:C:H4'	1:AA:749:C:O5'	2.05	0.57
1:CA:67:C:H2'	1:CA:68:G:C8	2.40	0.57
25:DA:279:C:H2'	25:DA:280:C:H6	1.68	0.57
25:DA:492:A:H2'	25:DA:493:G:O4'	2.04	0.57
25:DA:602:G:O2'	25:DA:655:A:N6	2.37	0.57
25:DA:1794:U:H2'	25:DA:1795:C:C6	2.40	0.57
36:DQ:85:LYS:HG2	46:D0:7:LEU:HB3	1.85	0.57
43:DX:88:LYS:NZ	43:DX:90:GLU:OE1	2.38	0.57
25:BA:997:G:OP1	36:BQ:16:ARG:NH2	2.38	0.57
25:BA:1296:G:N7	35:BP:18:ARG:NH2	2.53	0.57
25:DA:1786:A:H1'	25:DA:1938:A:N6	2.19	0.57
31:DH:27:LYS:NZ	31:DH:32:GLU:OE2	2.37	0.57
32:DI:27:ARG:HD2	47:D1:71:TYR:CE1	2.39	0.57
10:AJ:16:LEU:HD22	10:AJ:68:HIS:HB2	1.86	0.57
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.38	0.57
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HB3	1.86	0.57
18:CR:32:ARG:HA	18:CR:69:THR:HG21	1.86	0.57
25:DA:1352:U:OP1	61:DA:4149:HOH:O	2.18	0.57
25:DA:2336:A:H61	46:D0:43:THR:HG22	1.69	0.57
29:DF:11:VAL:HG22	29:DF:125:LEU:HB2	1.87	0.57
39:DT:59:THR:HG23	39:DT:78:LEU:HB3	1.86	0.57
1:AA:134:A:H61	16:AP:25:ARG:NH1	2.02	0.57
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.38	0.57
25:BA:602:G:H2'	25:BA:603:C:C6	2.40	0.57
25:BA:2761:A:H5'	31:BH:4:ILE:HD12	1.86	0.57
32:BI:93:THR:OG1	32:BI:96:ASP:OD1	2.22	0.57
1:CA:620:C:H2'	1:CA:621:A:O4'	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:946:A:H2'	1:CA:947:G:C8	2.40	0.57
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.86	0.57
25:DA:251:A:H2'	25:DA:252:G:O4'	2.05	0.57
25:DA:644:A:H4'	25:DA:645:C:C5	2.40	0.57
30:DG:106:LEU:HA	30:DG:110:ALA:HB3	1.86	0.57
34:DO:115:VAL:HG13	34:DO:121:VAL:HG21	1.87	0.57
36:DQ:31:ASP:OD1	36:DQ:134:ARG:NH1	2.38	0.57
1:AA:1002:G:O6	1:AA:1003:G:N2	2.38	0.56
4:AD:88:VAL:HG22	5:AE:97:GLY:HA2	1.86	0.56
23:AW:25:C:H2'	23:AW:26:A:C8	2.39	0.56
25:BA:1355:G:O6	61:BA:4959:HOH:O	2.18	0.56
25:BA:2122:G:H2'	25:BA:2123:G:C8	2.40	0.56
1:CA:201:C:N4	1:CA:216:G:H1	1.87	0.56
18:CR:47:THR:HG23	18:CR:49:LYS:HG3	1.87	0.56
25:DA:2142:C:H2'	25:DA:2143:C:C6	2.40	0.56
43:DX:53:LYS:HB3	43:DX:82:GLN:HB3	1.86	0.56
1:AA:1027:C:H2'	1:AA:1028:C:C5	2.41	0.56
25:BA:181:C:O2'	25:BA:849:A:N3	2.38	0.56
36:BQ:31:ASP:HA	36:BQ:134:ARG:HH11	1.69	0.56
1:CA:570:G:OP2	57:CA:3171:NEG:H12	2.04	0.56
24:CX:55:PSU:N3	24:CX:58:A:OP2	2.30	0.56
1:AA:356:A:N3	1:AA:368:U:O2'	2.33	0.56
1:AA:662:G:H2'	1:AA:663:A:C8	2.39	0.56
6:AF:82:ARG:HB3	6:AF:85:VAL:HG23	1.87	0.56
13:AM:88:ARG:HG3	13:AM:98:VAL:HG11	1.86	0.56
35:BP:121:LYS:O	35:BP:123:LEU:N	2.39	0.56
38:BS:27:SER:HA	38:BS:88:ASP:HB3	1.87	0.56
55:B9:17:ILE:HG22	55:B9:24:TYR:HB2	1.88	0.56
1:CA:757:U:H2'	1:CA:758:G:O4'	2.06	0.56
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.71	0.56
2:CB:74:LYS:NZ	2:CB:205:ASP:O	2.38	0.56
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.69	0.56
19:CS:42:PRO:HG3	50:D4:61:ARG:HG2	1.87	0.56
23:CY:10:G:H1	23:CY:25:C:H42	1.51	0.56
25:DA:866:A:H2	25:DA:867:C:C4	2.23	0.56
25:DA:1406:U:H2'	25:DA:1407:C:C6	2.40	0.56
25:DA:2183:C:H2'	25:DA:2184:G:H8	1.70	0.56
26:DB:75:G:N2	45:DZ:73:GLN:OE1	2.36	0.56
26:DB:105:A:OP1	45:DZ:72:ARG:NH1	2.39	0.56
1:AA:28:G:O2'	1:AA:296:U:OP1	2.22	0.56
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:231:GLU:HB3	2:AB:232:PRO:HD3	1.86	0.56
6:AF:2:ARG:NE	6:AF:69:GLU:HG2	2.20	0.56
23:AW:51:U:H2'	23:AW:52:G:C8	2.41	0.56
28:BE:47:VAL:HG23	28:BE:84:PHE:O	2.04	0.56
52:B6:6:ARG:NH1	52:B6:26:ASN:HB2	2.20	0.56
53:B7:24:THR:HG22	53:B7:27:GLY:N	2.08	0.56
1:CA:434:U:H2'	1:CA:435:C:C6	2.39	0.56
1:CA:1074:G:OP1	5:CE:64:ARG:NH2	2.39	0.56
1:CA:1202:G:O4'	14:CN:29:ARG:NH1	2.38	0.56
7:CG:18:TYR:HB3	7:CG:59:LEU:HD13	1.88	0.56
25:DA:746:A:H2'	25:DA:2612:C:H5"	1.87	0.56
25:DA:864:G:H1	25:DA:912:C:H5	1.52	0.56
25:DA:1007:C:OP1	33:DN:35:ARG:NH1	2.38	0.56
25:DA:1513:C:H2'	25:DA:1514:U:C6	2.41	0.56
25:DA:2134:A:H3'	25:DA:2135:A:C8	2.41	0.56
25:DA:2153:G:H2'	25:DA:2154:G:C8	2.41	0.56
25:DA:2815:C:H2'	25:DA:2816:C:H6	1.70	0.56
28:DE:11:MET:HG2	28:DE:24:THR:HB	1.88	0.56
45:DZ:73:GLN:O	45:DZ:87:ASP:N	2.37	0.56
47:D1:3:LYS:HB2	47:D1:61:ARG:HH12	1.70	0.56
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.41	0.56
25:BA:1425:A:H4'	25:BA:1426:G:OP2	2.05	0.56
25:BA:2389:A:H2'	25:BA:2390:A:C8	2.41	0.56
28:BE:24:THR:HG22	28:BE:186:GLY:O	2.05	0.56
28:BE:174:ASP:OD1	28:BE:175:VAL:N	2.39	0.56
1:CA:1000:U:O2	1:CA:1041:A:N1	2.38	0.56
1:CA:1240:U:N3	7:CG:30:ILE:O	2.26	0.56
25:DA:1970:A:H4'	25:DA:1971:A:OP1	2.06	0.56
36:DQ:24:GLY:HA2	36:DQ:67:ARG:NH2	2.21	0.56
1:AA:49:U:O4	1:AA:365:U:H5	1.89	0.56
1:AA:489:C:OP1	4:AD:132:ARG:NH2	2.38	0.56
1:AA:1190:G:O2'	1:AA:1191:A:OP2	2.22	0.56
3:AC:156:ARG:NE	3:AC:160:ALA:O	2.37	0.56
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	1.85	0.56
23:AY:19:G:H3'	23:AY:20:U:H5'	1.87	0.56
25:BA:2132:G:OP1	25:BA:2167:C:N4	2.38	0.56
32:BI:106:GLY:HA2	32:BI:107:VAL:O	2.06	0.56
35:BP:50:ARG:HD3	54:B8:7:HIS:HD2	1.69	0.56
1:CA:337:C:H2'	1:CA:338:A:C8	2.41	0.56
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.38	0.56
26:DB:55:U:O2'	30:DG:27:ASN:ND2	2.29	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:35:GLU:HB2	2:AB:40:HIS:HD2	1.70	0.56
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.36	0.56
45:BZ:138:GLU:H	45:BZ:156:LYS:HZ2	1.53	0.56
1:CA:10:A:OP2	5:CE:126:ARG:HD2	2.06	0.56
7:CG:111:ARG:HD2	7:CG:123:GLU:HB2	1.87	0.56
8:CH:14:ARG:NH2	8:CH:83:ILE:O	2.36	0.56
25:DA:1400:G:H2'	25:DA:1401:G:C8	2.41	0.56
25:DA:2105:C:H2'	25:DA:2106:G:C8	2.41	0.56
25:DA:2590:A:O3'	27:DD:239:ARG:NH2	2.39	0.56
31:DH:90:LYS:NZ	31:DH:159:GLU:OE1	2.38	0.56
36:DQ:81:VAL:HB	46:D0:7:LEU:HD21	1.88	0.56
23:AW:18:G:H4'	23:AW:60:U:C5	2.41	0.56
25:BA:1324:A:OP1	37:BR:36:THR:HG23	2.06	0.56
45:BZ:152:ALA:H	45:BZ:171:ILE:HG12	1.69	0.56
1:CA:45:U:H2'	1:CA:46:G:C8	2.40	0.56
3:CC:43:LEU:HD21	3:CC:91:LEU:HD13	1.86	0.56
3:CC:109:PRO:HB3	3:CC:115:LEU:HD23	1.88	0.56
8:CH:64:LYS:HG2	8:CH:79:VAL:HG21	1.88	0.56
25:DA:1805:U:O2	27:DD:50:THR:HB	2.05	0.56
25:DA:2602:A:H4'	25:DA:2603:G:O5'	2.06	0.56
29:DF:167:ALA:HB1	29:DF:173:VAL:HG11	1.88	0.56
1:AA:692:U:O2'	1:AA:694:A:N7	2.31	0.56
8:AH:64:LYS:HG2	8:AH:79:VAL:HG21	1.88	0.56
13:AM:57:ARG:HH11	13:AM:57:ARG:HG3	1.70	0.56
25:BA:553:A:C2	25:BA:2064:A:H2'	2.39	0.56
25:BA:918:U:OP1	36:BQ:5:ARG:HD3	2.05	0.56
25:BA:1785:C:OP1	39:BT:96:ARG:NH1	2.39	0.56
28:BE:9:VAL:HB	39:BT:3:ARG:HG2	1.88	0.56
31:BH:90:LYS:HD3	31:BH:159:GLU:HG2	1.88	0.56
1:CA:1144:G:N2	1:CA:1146:A:H62	2.04	0.56
2:CB:45:GLN:HA	2:CB:48:MET:HE2	1.86	0.56
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.32	0.56
23:CY:1:G:H2'	23:CY:2:C:C6	2.41	0.56
25:DA:1796:U:H2'	25:DA:1797:C:H6	1.69	0.56
25:DA:2133:G:H22	25:DA:2157:G:H1'	1.69	0.56
30:DG:11:TYR:HA	30:DG:15:VAL:HB	1.87	0.56
31:DH:154:PRO:HB3	31:DH:163:TYR:CZ	2.41	0.56
35:DP:38:GLN:HG2	35:DP:45:LEU:HD23	1.87	0.56
1:AA:1027:C:N3	1:AA:1034:G:C6	2.74	0.56
25:BA:1475:G:H2'	25:BA:1476:C:C6	2.40	0.56
30:BG:15:VAL:HG22	30:BG:175:LEU:HB3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CH:9:MET:HG3	8:CH:26:VAL:HG11	1.87	0.56
10:CJ:30:SER:O	10:CJ:81:THR:HG23	2.05	0.56
23:CY:18:G:N2	23:CY:55:PSU:N3	2.53	0.56
25:DA:1190:G:H2'	25:DA:1191:G:C8	2.41	0.56
45:DZ:69:THR:HG22	45:DZ:90:VAL:HA	1.88	0.56
1:AA:545:C:O2'	1:AA:549:C:OP1	2.21	0.55
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.39	0.55
13:AM:84:ILE:HD12	19:AS:74:PHE:HE2	1.71	0.55
25:BA:1059:C:OP2	61:BA:5284:HOH:O	2.18	0.55
25:BA:1410:G:P	47:B1:3:LYS:HG3	2.46	0.55
25:BA:2044:U:O2'	25:BA:2629:C:H5'	2.06	0.55
1:CA:1004:A:H62	1:CA:1037:C:H3'	1.69	0.55
3:CC:164:ARG:HG2	3:CC:165:THR:H	1.71	0.55
5:CE:42:GLY:HA2	5:CE:65:ASN:O	2.06	0.55
27:DD:26:LYS:HE2	27:DD:28:GLU:O	2.05	0.55
29:DF:150:GLY:HA2	29:DF:172:TRP:CD2	2.42	0.55
29:DF:154:VAL:HG22	29:DF:191:ARG:HB2	1.87	0.55
1:AA:736:C:H2'	1:AA:737:A:C8	2.42	0.55
1:AA:1142:G:H2'	1:AA:1143:G:O4'	2.06	0.55
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.31	0.55
23:AY:76:A:N6	25:BA:2434:A:O4'	2.38	0.55
28:BE:29:GLY:HA3	61:BE:406:HOH:O	2.06	0.55
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	1.88	0.55
25:DA:182:A:N3	25:DA:433:C:O2'	2.35	0.55
32:DI:130:TYR:HB3	32:DI:138:ILE:HB	1.88	0.55
38:DS:14:VAL:O	38:DS:18:ILE:HG12	2.06	0.55
1:AA:1129:C:O2'	1:AA:1139:G:N7	2.37	0.55
23:AW:58:A:O2'	23:AW:60:U:OP2	2.19	0.55
25:BA:847:A:H8	25:BA:847:A:OP1	1.89	0.55
1:CA:160:A:H1'	1:CA:344:A:C5	2.41	0.55
1:CA:674:G:H2'	1:CA:675:A:H8	1.70	0.55
1:CA:1131:G:H1	1:CA:1143:G:H21	1.54	0.55
4:CD:108:LEU:HD13	4:CD:174:LEU:HD13	1.88	0.55
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.06	0.55
23:CW:52:G:H5"	36:DQ:56:ARG:HH22	1.70	0.55
25:DA:2134:A:O2'	25:DA:2135:A:OP1	2.25	0.55
25:DA:2180:U:H2'	25:DA:2181:G:O4'	2.05	0.55
26:DB:46:A:H2'	26:DB:47:C:H6	1.72	0.55
30:DG:43:LEU:HD11	30:DG:153:ARG:HG2	1.89	0.55
43:DX:65:ARG:HB2	43:DX:70:LEU:HD23	1.89	0.55
1:AA:1173:G:H2'	1:AA:1174:G:C8	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1190:G:OP1	3:AC:5:ILE:N	2.36	0.55
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.71	0.55
12:AL:46:LYS:HD2	12:AL:94:PRO:HG3	1.89	0.55
19:AS:10:PHE:HE2	19:AS:37:ARG:HD3	1.71	0.55
23:AY:6:G:O6	23:AY:7:A:N6	2.39	0.55
25:BA:2303:U:H2'	25:BA:2304:C:C6	2.42	0.55
25:BA:2457:G:OP1	29:BF:74:ARG:NH2	2.34	0.55
1:CA:1179:A:H4'	9:CI:103:THR:HA	1.87	0.55
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.89	0.55
25:DA:1688:U:O2	25:DA:1700:A:H5'	2.06	0.55
25:DA:1946:U:H2'	25:DA:1947:C:C6	2.41	0.55
25:DA:2378:A:H2'	38:DS:21:THR:HG21	1.88	0.55
37:DR:36:THR:HG22	37:DR:37:THR:N	2.20	0.55
55:D9:22:ARG:NH1	55:D9:24:TYR:OH	2.40	0.55
1:AA:839:U:H3'	1:AA:840:C:C6	2.40	0.55
1:AA:1278:U:H5'	1:AA:1279:A:O4'	2.06	0.55
4:AD:173:TRP:HB2	4:AD:187:ARG:O	2.07	0.55
25:BA:346:A:OP1	29:BF:168:ARG:HD2	2.07	0.55
25:BA:794:U:O2	25:BA:2036:A:H1'	2.06	0.55
27:BD:242:ARG:HD3	27:BD:242:ARG:N	2.22	0.55
45:BZ:55:HIS:CE1	45:BZ:135:GLU:HG3	2.41	0.55
47:B1:23:LYS:HB3	47:B1:29:GLY:HA3	1.89	0.55
47:B1:89:GLU:O	47:B1:93:GLU:HG2	2.06	0.55
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.42	0.55
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.88	0.55
10:CJ:55:LYS:O	10:CJ:57:LYS:N	2.39	0.55
23:CW:52:G:H5"	36:DQ:56:ARG:NH2	2.21	0.55
28:DE:77:ILE:HD13	28:DE:195:LEU:HD13	1.87	0.55
36:DQ:18:LYS:O	36:DQ:98:LYS:NZ	2.27	0.55
44:DY:87:LYS:HB3	44:DY:95:LYS:HD3	1.87	0.55
1:AA:525:C:OP1	12:AL:89:ARG:NH1	2.39	0.55
1:AA:1190:G:HO2'	1:AA:1191:A:P	2.30	0.55
25:BA:53:G:O2'	53:B7:35:ARG:HD3	2.06	0.55
25:BA:1067:A:H62	25:BA:1186:U:H3	1.54	0.55
25:BA:2568:C:H2'	25:BA:2569:G:O4'	2.07	0.55
39:BT:27:THR:HB	39:BT:90:GLN:HB3	1.89	0.55
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.39	0.55
1:CA:1256:A:P	3:CC:26:LYS:HZ2	2.30	0.55
10:CJ:61:GLU:OE1	14:CN:58:LYS:NZ	2.38	0.55
25:DA:84:A:N1	25:DA:98:G:O2'	2.33	0.55
25:DA:2131:G:OP1	25:DA:2132:U:O2'	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2291:U:H2'	25:DA:2292:C:C6	2.41	0.55
31:DH:20:ALA:HB3	31:DH:23:ARG:HG3	1.88	0.55
39:DT:99:LEU:HD22	39:DT:101:PHE:HE1	1.71	0.55
45:DZ:54:HIS:NE2	45:DZ:123:ASP:OD2	2.39	0.55
1:AA:262:A:H2'	1:AA:263:A:C8	2.42	0.55
23:AW:19:G:N1	23:AW:56:C:N4	2.47	0.55
25:BA:354:A:H2	25:BA:1255:A:O2'	1.88	0.55
35:BP:64:LYS:HE3	54:B8:12:LYS:HD3	1.88	0.55
1:CA:328:C:H4'	1:CA:329:A:H5'	1.89	0.55
1:CA:344:A:H5'	1:CA:345:C:C5	2.41	0.55
1:CA:1085:U:H3'	1:CA:1086:U:C5	2.42	0.55
23:CW:39:PSU:H2'	23:CW:40:C:C6	2.42	0.55
24:CX:2:G:O6	24:CX:71:C:N3	2.40	0.55
25:DA:307:G:N1	25:DA:310:A:OP2	2.40	0.55
25:DA:528:A:C2	25:DA:2042:A:H2'	2.42	0.55
25:DA:819:A:C4	25:DA:1189:A:C2	2.94	0.55
25:DA:2114:A:N6	25:DA:2119:A:N7	2.54	0.55
48:D2:22:GLU:OE2	48:D2:68:ARG:NH2	2.27	0.55
25:BA:215:G:H21	25:BA:217:A:H62	1.53	0.55
25:BA:1033:G:O2'	25:BA:1046:A:N3	2.37	0.55
25:BA:1040:C:OP1	40:BU:53:ARG:NH2	2.39	0.55
25:BA:2849:G:H5'	37:BR:46:GLY:HA2	1.89	0.55
1:CA:1162:C:N3	1:CA:1174:G:N2	2.48	0.55
2:CB:16:HIS:O	2:CB:18:GLY:N	2.39	0.55
8:CH:21:LYS:O	8:CH:65:TYR:OH	2.21	0.55
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.41	0.55
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.88	0.55
25:DA:1264:G:H2'	25:DA:2014:A:N6	2.22	0.55
26:DB:14:U:O3'	26:DB:108:U:O2'	2.25	0.55
34:DO:1:MET:HG3	34:DO:67:LYS:HG2	1.88	0.55
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.89	0.55
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.07	0.55
25:BA:261:A:N1	25:BA:291:G:O2'	2.38	0.55
25:BA:1065:U:O2'	25:BA:1067:A:H2	1.89	0.55
31:BH:25:LYS:HG2	31:BH:34:GLU:HG2	1.88	0.55
1:CA:9:G:H2'	1:CA:10:A:H8	1.72	0.55
1:CA:999:C:H2'	1:CA:1000:U:C6	2.42	0.55
1:CA:1132:C:H2'	1:CA:1133:G:C8	2.42	0.55
1:CA:1503:A:C4	22:CV:13:A:N6	2.74	0.55
6:CF:69:GLU:CD	6:CF:69:GLU:H	2.15	0.55
9:CI:125:TYR:HD1	9:CI:126:SER:N	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:108:PRO:HB2	45:DZ:111:VAL:HG23	1.89	0.55
1:AA:181:G:H4'	1:AA:182:U:H5'	1.89	0.55
1:AA:649:G:H2'	1:AA:650:G:H8	1.73	0.55
5:AE:148:VAL:HG21	8:AH:107:LEU:HB3	1.88	0.55
25:BA:388:A:H2'	25:BA:389:G:C8	2.39	0.55
25:BA:1269:G:N2	25:BA:1272:A:OP2	2.29	0.55
25:BA:2340:A:H2'	25:BA:2341:G:C8	2.41	0.55
30:BG:115:ARG:HB3	30:BG:136:ARG:HH22	1.70	0.55
32:BI:77:LEU:HG	32:BI:101:LEU:HD23	1.89	0.55
1:CA:973:G:H3'	1:CA:974:A:H5"	1.88	0.55
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.07	0.55
1:CA:1154:G:H2'	1:CA:1155:G:C8	2.42	0.55
1:CA:1288:A:N3	1:CA:1352:C:O2'	2.36	0.55
20:CT:65:LYS:HA	20:CT:68:LYS:HD3	1.89	0.55
25:DA:2136:C:O2'	25:DA:2137:C:O5'	2.24	0.55
1:AA:1223:C:OP2	19:AS:78:ARG:NH2	2.40	0.54
25:BA:432:U:H6	25:BA:432:U:H5"	1.72	0.54
37:BR:67:LEU:HD13	37:BR:76:VAL:HG21	1.87	0.54
44:BY:28:LYS:HD2	44:BY:40:GLU:HG3	1.89	0.54
51:B5:58:LEU:HD23	51:B5:60:VAL:HG23	1.89	0.54
1:CA:1158:C:O2'	2:CB:133:LYS:NZ	2.40	0.54
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.43	0.54
10:CJ:7:LYS:HG3	10:CJ:71:LEU:HD13	1.88	0.54
13:CM:88:ARG:HG3	13:CM:98:VAL:HG11	1.89	0.54
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.06	0.54
23:CY:1:G:H1	23:CY:72:C:H42	1.55	0.54
25:DA:2483:C:H2'	25:DA:2484:G:O4'	2.06	0.54
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.87	0.54
25:BA:469:A:H1'	25:BA:1246:C:O4'	2.07	0.54
39:BT:59:THR:HG23	39:BT:78:LEU:HB3	1.89	0.54
3:CC:20:SER:HB3	3:CC:22:TRP:HE1	1.72	0.54
31:DH:42:ARG:NH1	31:DH:53:GLU:OE2	2.40	0.54
41:DV:72:VAL:HG13	41:DV:85:LYS:HB3	1.89	0.54
1:AA:35:G:O2'	12:AL:118:SER:O	2.20	0.54
1:AA:544:G:OP1	4:AD:59:ARG:NH2	2.32	0.54
1:AA:630:G:H2'	1:AA:631:G:H8	1.72	0.54
2:AB:84:GLU:HB3	2:AB:219:VAL:HG21	1.90	0.54
8:AH:19:VAL:HG23	8:AH:21:LYS:HD3	1.89	0.54
24:AX:8:4SU:O5'	24:AX:8:4SU:H6	2.07	0.54
25:BA:1067:A:C8	25:BA:1068:G:H5"	2.40	0.54
2:CB:98:LEU:HG	2:CB:101:MET:HE3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.89	0.54
23:CW:27:G:H2'	23:CW:28:G:C8	2.42	0.54
23:CY:5:G:H1	23:CY:68:C:H42	1.54	0.54
23:CY:9:A:O3'	23:CY:45:U:O2'	2.24	0.54
25:DA:84:A:H5"	44:DY:8:LYS:HE3	1.90	0.54
25:DA:566:U:H5"	35:DP:29:LYS:HE3	1.89	0.54
25:DA:574:C:N3	28:DE:145:LYS:NZ	2.51	0.54
25:DA:1429:G:H2'	25:DA:1430:C:H6	1.72	0.54
25:DA:2153:G:H2'	25:DA:2154:G:H8	1.72	0.54
25:DA:2183:C:H2'	25:DA:2184:G:C8	2.43	0.54
27:DD:108:PRO:HB3	27:DD:143:HIS:CE1	2.42	0.54
55:D9:14:CYS:HA	55:D9:27:CYS:HB2	1.87	0.54
1:AA:8:A:N6	4:AD:205:GLU:O	2.39	0.54
1:AA:1052:U:H5"	1:AA:1053:G:OP2	2.08	0.54
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.37	0.54
25:BA:704:U:H2'	25:BA:705:C:C6	2.43	0.54
25:BA:714:U:O2	54:B8:2:PRO:HD2	2.07	0.54
25:BA:2162:C:O2	25:BA:2173:G:C2	2.61	0.54
25:BA:2812:A:N3	25:BA:2904:U:H1'	2.22	0.54
33:BN:62:VAL:CG1	33:BN:66:LYS:HB2	2.38	0.54
35:BP:83:VAL:HG13	35:BP:112:LEU:HD21	1.88	0.54
1:CA:340:U:H2'	1:CA:341:C:C6	2.42	0.54
23:CY:15:G:N1	23:CY:48:C:N3	2.45	0.54
25:DA:2022:U:O2'	25:DA:2617:C:H5'	2.08	0.54
40:DU:66:ASN:O	40:DU:70:ARG:HG3	2.06	0.54
47:D1:3:LYS:HB2	47:D1:61:ARG:NH1	2.23	0.54
50:D4:59:PHE:HA	50:D4:60:GLN:C	2.32	0.54
1:AA:100:C:H2'	1:AA:101:A:C8	2.43	0.54
1:AA:461:A:O2'	1:AA:470:C:H5'	2.07	0.54
1:AA:539:A:OP2	12:AL:115:LYS:NZ	2.40	0.54
17:AQ:43:LEU:HD12	17:AQ:68:ARG:HG2	1.90	0.54
35:BP:100:LEU:HD12	35:BP:112:LEU:HD11	1.90	0.54
43:BX:43:VAL:HG21	43:BX:81:VAL:HG11	1.89	0.54
43:BX:53:LYS:HB3	43:BX:82:GLN:HB3	1.90	0.54
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.74	0.54
3:CC:164:ARG:NH1	3:CC:166:GLU:OE1	2.41	0.54
25:DA:2154:G:H2'	25:DA:2155:G:H5'	1.89	0.54
25:DA:2611:U:H5'	25:DA:2611:U:H6	1.72	0.54
50:D4:14:ILE:HB	50:D4:22:ILE:HB	1.90	0.54
4:AD:178:VAL:HG12	4:AD:179:GLU:H	1.72	0.54
25:BA:2162:C:N3	25:BA:2173:G:C6	2.76	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2398:C:H2'	25:BA:2399:U:C6	2.43	0.54
25:BA:2416:C:O3'	35:BP:77:ARG:NH2	2.37	0.54
38:BS:14:VAL:O	38:BS:18:ILE:HG12	2.07	0.54
45:BZ:145:GLU:H	45:BZ:148:ASP:HB2	1.73	0.54
1:CA:736:C:H2'	1:CA:737:A:C8	2.41	0.54
1:CA:997:U:H3	1:CA:1044:A:H61	1.53	0.54
8:CH:121:ASP:N	8:CH:121:ASP:OD1	2.39	0.54
9:CI:45:ALA:HA	9:CI:48:GLU:HB2	1.89	0.54
10:CJ:63:PHE:HE1	14:CN:58:LYS:HG2	1.73	0.54
20:CT:57:ARG:HH22	20:CT:100:ILE:HD12	1.72	0.54
23:CW:4:C:H42	23:CW:68:C:H42	1.55	0.54
23:CW:26:A:H2'	23:CW:27:G:C8	2.42	0.54
25:DA:882:G:O6	25:DA:893:C:N4	2.41	0.54
25:DA:1693:U:O2'	27:DD:14:ARG:NH2	2.41	0.54
25:DA:2155:G:C5	25:DA:2156:G:H1'	2.43	0.54
25:DA:2503:A:O2'	25:DA:2505:G:OP2	2.17	0.54
28:DE:36:ARG:HD3	28:DE:85:ASN:HD21	1.73	0.54
35:DP:121:LYS:O	35:DP:123:LEU:N	2.40	0.54
45:DZ:157:LEU:HB3	45:DZ:161:VAL:HG13	1.90	0.54
1:AA:664:G:N2	1:AA:741:G:H1	2.02	0.54
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	1.89	0.54
25:BA:1065:U:H3	25:BA:1188:A:H62	1.56	0.54
25:BA:1553:A:O2'	25:BA:1554:A:O4'	2.26	0.54
40:BU:79:PHE:CE2	40:BU:83:LEU:HD21	2.43	0.54
50:B4:33:VAL:HG12	50:B4:35:VAL:H	1.73	0.54
1:CA:664:G:N2	1:CA:741:G:H1	2.03	0.54
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.23	0.54
4:CD:112:VAL:HG13	4:CD:161:ASN:OD1	2.08	0.54
9:CI:50:LEU:HD21	9:CI:81:ILE:HD11	1.90	0.54
25:DA:332:A:O2'	25:DA:334:C:OP2	2.20	0.54
25:DA:1802:A:N1	25:DA:1822:G:H1'	2.23	0.54
30:DG:115:ARG:HG3	30:DG:136:ARG:HH21	1.73	0.54
33:DN:4:TYR:HB2	40:DU:101:ARG:HH12	1.72	0.54
33:DN:15:LEU:HB2	33:DN:135:PRO:HB2	1.89	0.54
1:AA:991:U:O2'	1:AA:992:U:OP2	2.24	0.54
1:AA:1502:A:H2	1:AA:1505:G:N1	2.01	0.54
7:AG:113:GLU:HG3	7:AG:118:VAL:HG12	1.89	0.54
16:AP:19:ILE:HG22	16:AP:37:GLY:C	2.33	0.54
23:AY:7:A:O2'	23:AY:49:C:H5'	2.07	0.54
23:AY:63:G:H2'	23:AY:64:A:O4'	2.08	0.54
25:BA:397:G:OP1	25:BA:430:U:N3	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:909:G:H2'	25:BA:910:A:O4'	2.08	0.54
25:BA:1248:G:OP2	25:BA:1249:A:O2'	2.21	0.54
34:BO:91:LEU:HB3	34:BO:111:PHE:CE1	2.43	0.54
36:BQ:14:ARG:HG2	36:BQ:41:TRP:HH2	1.73	0.54
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.42	0.54
1:CA:671:G:H5'	6:CF:77:ARG:HH22	1.73	0.54
1:CA:728:A:H2'	1:CA:729:A:C8	2.43	0.54
1:CA:1029:C:N4	1:CA:1032:G:C6	2.76	0.54
1:CA:1299:A:H2'	1:CA:1299:A:N3	2.23	0.54
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.42	0.54
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.08	0.54
25:DA:10:G:H2'	25:DA:11:G:H8	1.72	0.54
41:DV:43:GLU:N	41:DV:43:GLU:OE2	2.41	0.54
1:AA:382:A:H2'	1:AA:383:A:H8	1.73	0.54
9:AI:26:VAL:HG22	9:AI:61:ALA:HB3	1.90	0.54
23:AY:62:C:H2'	23:AY:63:G:H8	1.71	0.54
37:BR:56:LYS:NZ	37:BR:90:ARG:O	2.41	0.54
1:CA:1002:G:C4	1:CA:1003:G:C8	2.96	0.54
12:CL:46:LYS:NZ	12:CL:91:LYS:O	2.40	0.54
25:DA:918:A:H5"	26:DB:98:G:O2'	2.08	0.54
25:DA:1006:C:C2	25:DA:1138:G:N2	2.76	0.54
25:DA:1220:A:OP2	40:DU:19:LYS:NZ	2.30	0.54
25:DA:1669:A:H5"	25:DA:2550:G:OP1	2.07	0.54
28:DE:72:VAL:HA	28:DE:73:GLU:CB	2.37	0.54
42:DW:79:GLY:HA3	42:DW:100:THR:HG22	1.90	0.54
52:D6:13:CYS:SG	52:D6:47:THR:HG21	2.47	0.54
6:AF:97:PHE:CD2	18:AR:31:LEU:HD12	2.43	0.54
8:AH:34:GLU:OE1	8:AH:37:ARG:NH1	2.41	0.54
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.08	0.54
25:BA:54:G:O2'	25:BA:125:A:N1	2.38	0.54
25:BA:843:C:H2'	25:BA:844:C:C6	2.43	0.54
25:BA:1314:A:H2'	25:BA:1315:A:O4'	2.08	0.54
29:BF:195:ASP:HB3	29:BF:198:ALA:H	1.70	0.54
54:B8:42:ARG:HD2	61:B8:206:HOH:O	2.08	0.54
1:CA:84:U:H4'	1:CA:89:C:N3	2.23	0.54
14:CN:21:TYR:HE2	14:CN:23:ARG:NE	2.05	0.54
25:DA:1697:G:OP2	25:DA:1698:A:O2'	2.22	0.54
25:DA:2108:C:H2'	25:DA:2109:U:H5'	1.89	0.54
30:DG:49:ASP:N	30:DG:49:ASP:OD1	2.40	0.54
33:DN:67:LEU:HD13	33:DN:87:LEU:HD13	1.89	0.54
41:DV:24:LYS:HG3	41:DV:64:HIS:HD2	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:D4:16:CYS:SG	50:D4:17:GLY:N	2.81	0.54
50:D4:26:SER:OG	50:D4:27:THR:N	2.41	0.54
1:AA:1509:C:H2'	1:AA:1510:U:O4'	2.08	0.53
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.23	0.53
19:AS:20:LEU:HD23	19:AS:23:ASN:HD22	1.74	0.53
23:AW:19:G:H4'	23:AW:20:U:OP1	2.08	0.53
25:DA:890:A:H2'	25:DA:892:G:H8	1.72	0.53
25:DA:2846:G:N7	61:DA:4362:HOH:O	2.33	0.53
27:DD:232:PRO:O	61:DD:404:HOH:O	2.19	0.53
1:AA:527:G:O2'	1:AA:535:A:N1	2.29	0.53
1:AA:714:G:H2'	1:AA:715:A:C8	2.44	0.53
1:AA:1399:C:C2	1:AA:1502:A:N6	2.76	0.53
51:B5:48:GLU:O	51:B5:60:VAL:HG11	2.08	0.53
8:CH:41:ARG:NH2	8:CH:123:GLU:OE2	2.40	0.53
25:DA:315:G:H2'	25:DA:316:C:C6	2.43	0.53
25:DA:1952:A:OP1	34:DO:42:SER:OG	2.24	0.53
25:DA:2552:U:H2'	25:DA:2554:U:H5"	1.91	0.53
36:DQ:16:ARG:HG2	36:DQ:18:LYS:HE2	1.89	0.53
1:AA:194:C:O3'	20:AT:68:LYS:HD2	2.08	0.53
1:AA:390:C:H2'	1:AA:391:G:C8	2.43	0.53
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.43	0.53
2:AB:71:VAL:HB	2:AB:164:VAL:HG13	1.90	0.53
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HD23	1.90	0.53
10:AJ:78:ASN:O	10:AJ:80:LYS:N	2.40	0.53
24:AX:64:G:O2'	36:BQ:10:ARG:NH2	2.41	0.53
23:AY:2:C:N4	23:AY:71:G:H1	2.05	0.53
25:BA:272:U:H4'	32:BI:50:ARG:HH12	1.73	0.53
25:BA:1211:U:H2'	25:BA:1212:C:C6	2.44	0.53
34:BO:2:ILE:HD12	34:BO:6:THR:HG21	1.90	0.53
37:BR:33:ARG:NH2	51:B5:57:VAL:O	2.38	0.53
51:B5:16:ARG:NH1	51:B5:17:ASP:OD1	2.42	0.53
1:CA:1004:A:H5"	1:CA:1025:U:C5	2.42	0.53
6:CF:33:TYR:HE1	6:CF:74:ASP:HB3	1.74	0.53
19:CS:30:LEU:HD11	19:CS:50:ALA:HB2	1.90	0.53
25:DA:30:G:H2'	25:DA:31:C:C6	2.43	0.53
27:DD:71:ASP:HB3	27:DD:103:ARG:NH2	2.23	0.53
28:DE:72:VAL:HG22	28:DE:73:GLU:HG2	1.91	0.53
30:DG:11:TYR:HB2	30:DG:176:LEU:HD21	1.90	0.53
30:DG:46:ALA:HB2	30:DG:53:LEU:HD12	1.90	0.53
3:AC:124:ILE:HD12	3:AC:196:LEU:HD12	1.90	0.53
4:AD:18:LYS:NZ	4:AD:26:CYS:O	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1834:A:O2'	27:BD:259:THR:HG21	2.08	0.53
25:BA:1874:C:H5'	27:BD:253:GLN:NE2	2.23	0.53
25:BA:2584:A:N7	28:BE:145:LYS:HB2	2.23	0.53
29:BF:53:THR:HG22	29:BF:55:GLY:H	1.73	0.53
51:B5:11:THR:HG23	51:B5:15:ARG:HB3	1.90	0.53
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.89	0.53
57:CA:3174:NEG:H2	25:DA:1954:G:H3'	1.91	0.53
2:CB:144:ARG:NH2	2:CB:148:TYR:OH	2.41	0.53
8:CH:19:VAL:HG23	8:CH:21:LYS:HD3	1.90	0.53
8:CH:68:ARG:NH1	8:CH:74:PRO:HB3	2.24	0.53
24:CX:53:G:H3'	24:CX:54:5MU:H73	1.90	0.53
23:CY:36:A:H2'	23:CY:37:MIA:O4'	2.08	0.53
25:DA:200:U:O2	25:DA:386:G:N2	2.41	0.53
25:DA:300:A:P	44:DY:86:ARG:HH22	2.32	0.53
25:DA:1462:C:H4'	25:DA:2703:C:H5'	1.91	0.53
25:DA:2693:A:H2'	25:DA:2694:G:H8	1.74	0.53
38:DS:27:SER:HA	38:DS:88:ASP:HB3	1.90	0.53
1:AA:757:U:H2'	1:AA:758:G:O4'	2.08	0.53
1:AA:1239:A:H4'	1:AA:1240:U:H5"	1.90	0.53
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.43	0.53
13:AM:93:ARG:HB3	25:BA:935:C:OP1	2.08	0.53
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.41	0.53
25:BA:1076:G:OP2	36:BQ:128:LYS:NZ	2.42	0.53
25:BA:1715:A:H4'	25:BA:1716:A:O5'	2.09	0.53
45:BZ:126:VAL:HG11	45:BZ:161:VAL:HG23	1.90	0.53
50:B4:59:PHE:C	50:B4:61:ARG:H	2.14	0.53
1:CA:1106:G:H5"	3:CC:172:ARG:HG2	1.90	0.53
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.44	0.53
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.41	0.53
25:DA:568:U:H5'	25:DA:945:A:C6	2.44	0.53
34:DO:120:GLU:HB2	39:DT:68:TYR:HE2	1.74	0.53
39:DT:117:ASP:OD2	39:DT:120:ARG:NE	2.29	0.53
45:DZ:117:LEU:HD23	45:DZ:119:GLU:HG2	1.91	0.53
1:AA:973:G:H3'	1:AA:974:A:H5"	1.91	0.53
1:AA:1352:C:OP1	21:AU:3:LYS:NZ	2.34	0.53
7:AG:78:ARG:NH1	7:AG:79:ARG:HH21	2.07	0.53
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.08	0.53
25:BA:1846:A:OP2	27:BD:54:ARG:NH2	2.37	0.53
42:BW:25:ARG:NH2	42:BW:74:ALA:O	2.38	0.53
1:CA:21:G:H2'	1:CA:22:G:C8	2.44	0.53
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.89	0.53
25:DA:906:G:N2	25:DA:907:U:O2	2.41	0.53
25:DA:1653:G:H3'	37:DR:2:ARG:HD3	1.90	0.53
25:DA:2359:C:H2'	25:DA:2360:A:O4'	2.09	0.53
25:DA:2627:G:N2	25:DA:2777:G:OP2	2.41	0.53
3:AC:33:LEU:HD12	3:AC:37:GLN:HE22	1.74	0.53
8:AH:13:ILE:O	8:AH:17:THR:HG23	2.09	0.53
25:BA:2407:C:O2'	47:B1:30:VAL:HG22	2.08	0.53
25:BA:2420:U:H2'	25:BA:2421:G:C8	2.43	0.53
54:B8:63:PRO:HG2	54:B8:64:TYR:CE2	2.44	0.53
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.41	0.53
1:CA:520:A:N1	1:CA:536:C:H1'	2.24	0.53
1:CA:1307:U:H2'	1:CA:1308:U:C6	2.44	0.53
5:CE:50:GLU:HB2	5:CE:53:LEU:HD13	1.90	0.53
15:CO:25:THR:HG21	15:CO:70:LEU:HB2	1.91	0.53
25:DA:1550:C:H5'	25:DA:1742:G:N2	2.24	0.53
25:DA:2061:G:H5"	25:DA:2503:A:C2	2.44	0.53
41:DV:6:LYS:HB2	41:DV:38:LEU:HD21	1.91	0.53
9:AI:28:VAL:HA	9:AI:63:ILE:O	2.08	0.53
21:AU:3:LYS:HB3	21:AU:14:TRP:CG	2.43	0.53
25:BA:1074:A:N6	25:BA:1171:G:H2'	2.24	0.53
36:BQ:109:VAL:HG13	36:BQ:113:GLN:HB3	1.90	0.53
1:CA:376:G:H5"	16:CP:5:ARG:HB2	1.90	0.53
1:CA:1324:A:O4'	1:CA:1362:C:H4'	2.09	0.53
24:CX:50:U:H3	24:CX:64:G:H1	1.56	0.53
23:CY:59:U:O5'	23:CY:59:U:H6	1.92	0.53
25:DA:331:A:OP1	25:DA:1209:G:N2	2.40	0.53
25:DA:566:U:P	41:DV:80:GLN:HE21	2.32	0.53
25:DA:2808:U:C2'	25:DA:2809:A:H5'	2.39	0.53
29:DF:24:LEU:HD21	29:DF:114:VAL:HG12	1.91	0.53
31:DH:90:LYS:HD2	31:DH:163:TYR:CD1	2.43	0.53
35:DP:2:LYS:NZ	35:DP:4:SER:OG	2.36	0.53
5:AE:45:PHE:CD2	5:AE:47:LYS:HE2	2.44	0.53
43:BX:5:TYR:CZ	48:B2:30:ARG:HB2	2.44	0.53
52:B6:14:THR:HB	52:B6:48:VAL:O	2.09	0.53
1:CA:222:U:H2'	1:CA:223:U:C6	2.43	0.53
3:CC:42:LEU:O	3:CC:46:GLU:HG2	2.09	0.53
3:CC:150:LYS:HG3	3:CC:169:ALA:HB2	1.91	0.53
13:CM:3:ARG:HE	13:CM:4:ILE:HG22	1.74	0.53
25:DA:140:G:N2	25:DA:1596:A:H4'	2.24	0.53
25:DA:885:C:H2'	25:DA:886:C:H4'	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:903:C:H2'	25:DA:904:C:C6	2.43	0.53
25:DA:1013:C:H2'	25:DA:1014:U:H6	1.74	0.53
29:DF:34:TRP:CE2	35:DP:8:PRO:HG3	2.44	0.53
39:DT:85:LYS:NZ	39:DT:87:ASP:OD2	2.42	0.53
1:AA:642:A:N3	8:AH:113:SER:OG	2.41	0.53
23:AY:40:C:H2'	23:AY:41:C:H6	1.73	0.53
25:BA:1431:G:O2'	25:BA:1442:U:O2	2.22	0.53
25:BA:2762:A:P	31:BH:3:ARG:HH21	2.32	0.53
40:BU:58:ARG:HA	40:BU:61:TRP:CE3	2.44	0.53
44:BY:92:ASN:N	44:BY:93:GLY:HA2	2.24	0.53
1:CA:988:G:H2'	1:CA:989:C:O4'	2.09	0.53
57:CA:3174:NEG:H11	25:DA:1955:U:OP2	2.08	0.53
2:CB:95:GLN:HB2	2:CB:148:TYR:HD1	1.74	0.53
17:CQ:95:TYR:HA	17:CQ:98:LEU:HD12	1.90	0.53
23:CW:28:G:C2	23:CW:29:G:H1'	2.44	0.53
23:CY:9:A:H5'	23:CY:46:7MG:O4'	2.08	0.53
25:DA:375:C:H2'	25:DA:376:C:C6	2.44	0.53
30:DG:114:ILE:HG23	30:DG:136:ARG:NH2	2.24	0.53
37:DR:2:ARG:NH1	37:DR:5:LYS:O	2.42	0.53
4:AD:22:LYS:HB2	4:AD:26:CYS:SG	2.48	0.52
5:AE:33:VAL:HG13	5:AE:112:LEU:HD12	1.90	0.52
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.91	0.52
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.91	0.52
20:AT:57:ARG:HH12	20:AT:100:ILE:HD12	1.73	0.52
23:AY:8:4SU:H4'	23:AY:48:C:H4'	1.91	0.52
25:BA:1255:A:H5"	25:BA:1257:G:O4'	2.09	0.52
25:BA:1787:G:H4'	25:BA:1789:G:O4'	2.10	0.52
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.41	0.52
57:CA:3175:NEG:C7	25:DA:739:G:H1	2.21	0.52
13:CM:23:TYR:O	13:CM:67:GLU:N	2.41	0.52
25:DA:272:G:H4'	25:DA:272(A):U:H5"	1.91	0.52
25:DA:1027:A:C2	25:DA:2488:A:H5'	2.45	0.52
25:DA:1300:U:H4'	25:DA:1301:A:C5'	2.39	0.52
25:DA:1864:U:OP1	25:DA:2410:G:O2'	2.25	0.52
25:DA:2689:U:OP1	25:DA:2719:G:N1	2.37	0.52
28:DE:12:THR:HG23	39:DT:58:ASN:OD1	2.10	0.52
36:DQ:85:LYS:HB2	46:D0:7:LEU:HD12	1.91	0.52
1:AA:458:C:H2'	1:AA:460:G:O4'	2.08	0.52
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.40	0.52
2:AB:174:VAL:HG13	2:AB:184:VAL:HG11	1.91	0.52
20:AT:57:ARG:HH22	20:AT:100:ILE:HD12	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2162:C:H2'	25:BA:2173:G:N2	2.24	0.52
8:CH:56:LYS:HB2	8:CH:58:TYR:HE1	1.74	0.52
19:CS:12:ASP:HB2	19:CS:38:SER:OG	2.09	0.52
23:CW:76:A:H8	25:DA:2602:A:H61	1.56	0.52
25:DA:184:C:H2'	25:DA:185:U:H6	1.74	0.52
25:DA:337:C:H2'	25:DA:338:G:O4'	2.09	0.52
25:DA:651:G:H4'	54:D8:18:ALA:HB3	1.91	0.52
25:DA:679:C:H2'	25:DA:680:G:H8	1.75	0.52
25:DA:910:A:H62	36:DQ:12:GLN:HA	1.73	0.52
25:DA:1166:C:H1'	25:DA:1184:G:N2	2.23	0.52
36:DQ:111:GLU:CD	36:DQ:133:ARG:HH21	2.15	0.52
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.91	0.52
25:BA:139:A:C8	25:BA:1454:C:O2'	2.60	0.52
25:BA:742:G:OP1	25:BA:1426:G:O2'	2.25	0.52
25:BA:2584:A:N7	28:BE:144:ARG:HD2	2.25	0.52
1:CA:1031:G:H2'	1:CA:1032:G:C8	2.45	0.52
23:CY:25:C:H2'	23:CY:26:A:C8	2.44	0.52
25:DA:1278:A:OP1	37:DR:36:THR:HG23	2.08	0.52
25:DA:2142:C:O2	25:DA:2149:G:N1	2.29	0.52
25:DA:2472:G:H2'	25:DA:2475:C:N4	2.24	0.52
29:DF:34:TRP:CZ2	35:DP:8:PRO:HG3	2.45	0.52
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.24	0.52
3:AC:164:ARG:HD2	3:AC:166:GLU:HG2	1.91	0.52
12:AL:117:ARG:HB3	12:AL:122:THR:HB	1.92	0.52
25:BA:63:A:O3'	43:BX:71:GLY:HA3	2.10	0.52
25:BA:191:U:OP1	61:BA:4936:HOH:O	2.19	0.52
25:BA:2159:C:N3	25:BA:2176:G:O6	2.41	0.52
25:BA:2236:G:H4'	25:BA:2238:C:C2	2.45	0.52
27:BD:121:PRO:HB3	27:BD:135:PHE:CE2	2.44	0.52
36:BQ:85:LYS:HG2	46:B0:7:LEU:HB3	1.92	0.52
1:CA:748:C:H4'	1:CA:749:C:O5'	2.10	0.52
16:CP:19:ILE:HG22	16:CP:36:ILE:HG13	1.91	0.52
19:CS:28:LYS:HZ2	19:CS:28:LYS:HB3	1.75	0.52
25:DA:1151:G:H4'	40:DU:81:HIS:CG	2.45	0.52
25:DA:1374:G:H2'	25:DA:1375:C:C6	2.45	0.52
25:DA:1608:A:H1'	25:DA:1610:A:OP2	2.08	0.52
25:DA:2055:C:H1'	28:DE:145:LYS:HE2	1.90	0.52
25:DA:2386:C:H4'	46:D0:56:ASP:HA	1.92	0.52
25:DA:2882:A:OP1	37:DR:96:ARG:NE	2.31	0.52
29:DF:178:PRO:HB3	29:DF:198:ALA:HA	1.91	0.52
30:DG:72:ARG:NH1	30:DG:87:PRO:HG3	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DO:2:ILE:HD12	34:DO:6:THR:HG21	1.90	0.52
25:BA:1093:G:H2'	25:BA:1156:G:N2	2.25	0.52
1:CA:1317:C:H42	14:CN:19:ARG:HH21	1.57	0.52
1:CA:1317:C:OP1	14:CN:17:LYS:HG2	2.10	0.52
2:CB:30:ARG:NH2	2:CB:195:ASP:OD1	2.43	0.52
2:CB:158:LEU:HD21	2:CB:180:LEU:HD13	1.90	0.52
3:CC:3:ASN:N	3:CC:3:ASN:OD1	2.41	0.52
10:CJ:5:ARG:N	61:CJ:5101:HOH:O	2.42	0.52
25:DA:108:U:H2'	25:DA:109:G:H8	1.75	0.52
25:DA:117:G:OP2	25:DA:119:A:O2'	2.27	0.52
25:DA:521:G:H2'	25:DA:522:G:H8	1.75	0.52
25:DA:1427:A:H4'	25:DA:1428:C:O5'	2.08	0.52
25:DA:1477:A:H2'	25:DA:1478:G:O4'	2.09	0.52
25:DA:2625:G:H2'	25:DA:2626:C:O4'	2.10	0.52
26:DB:114:C:H4'	38:DS:46:VAL:HG22	1.90	0.52
34:DO:80:ASP:OD1	39:DT:64:ARG:NH2	2.43	0.52
44:DY:90:LEU:HB3	44:DY:92:ASN:H	1.75	0.52
1:AA:1080:A:H5'	5:AE:14:ARG:HH21	1.73	0.52
13:AM:123:ALA:HB2	23:AW:39:PSU:H1'	1.91	0.52
25:BA:223:C:H2'	25:BA:224:U:H6	1.74	0.52
25:BA:776:G:C6	27:BD:208:LYS:HB2	2.45	0.52
25:BA:1343:C:O2'	25:BA:1348:A:N1	2.41	0.52
25:BA:2163:G:C4	25:BA:2164:C:H1'	2.44	0.52
40:BU:114:LYS:HA	40:BU:117:GLN:HE21	1.73	0.52
41:BV:76:LYS:HB2	41:BV:81:TYR:HB3	1.92	0.52
1:CA:554:C:H2'	1:CA:555:C:C6	2.44	0.52
1:CA:1239:A:H62	1:CA:1299:A:N6	2.07	0.52
2:CB:137:ARG:HB3	2:CB:137:ARG:CZ	2.39	0.52
3:CC:148:GLY:HA3	3:CC:172:ARG:O	2.10	0.52
25:DA:1932:A:H2'	25:DA:1933:G:O4'	2.09	0.52
25:DA:2117:A:N6	25:DA:2171:A:N1	2.58	0.52
26:DB:19:G:H2'	26:DB:20:C:O4'	2.10	0.52
45:DZ:5:LEU:HD23	45:DZ:47:VAL:HG21	1.91	0.52
1:AA:10:A:HO2'	1:AA:507:C:HO2'	1.58	0.52
1:AA:1024:G:H2'	1:AA:1025:U:H5"	1.92	0.52
1:AA:1145:C:H4'	1:AA:1146:A:H5'	1.91	0.52
5:AE:110:LEU:HD13	5:AE:118:ILE:HD13	1.90	0.52
10:AJ:13:HIS:HA	10:AJ:16:LEU:HB3	1.91	0.52
25:BA:1921:G:H2'	25:BA:1921:G:N3	2.23	0.52
25:BA:2021:C:H4'	25:BA:2736:C:O2	2.09	0.52
25:BA:2262:G:OP1	36:BQ:85:LYS:NZ	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2274:U:OP1	25:BA:2399:U:O2'	2.20	0.52
36:BQ:35:VAL:HG13	36:BQ:130:LYS:HB3	1.90	0.52
45:BZ:70:LEU:HG	45:BZ:91:LEU:HD21	1.91	0.52
50:B4:16:CYS:SG	50:B4:17:GLY:N	2.83	0.52
1:CA:1346:A:N6	1:CA:1375:A:OP2	2.43	0.52
9:CI:51:ARG:HG2	9:CI:56:LEU:HD21	1.92	0.52
20:CT:10:LEU:HD22	20:CT:12:ALA:HB2	1.91	0.52
25:DA:1341:U:OP1	25:DA:1397:U:N3	2.34	0.52
25:DA:1665:A:H4'	34:DO:67:LYS:HB2	1.92	0.52
28:DE:72:VAL:HG13	28:DE:73:GLU:O	2.10	0.52
30:DG:15:VAL:HG13	30:DG:175:LEU:HD23	1.91	0.52
32:DI:140:LEU:HD13	32:DI:142:VAL:HG22	1.91	0.52
36:DQ:16:ARG:HG3	36:DQ:17:LEU:H	1.75	0.52
44:DY:28:LYS:HD2	44:DY:40:GLU:HG3	1.92	0.52
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.45	0.52
57:AA:3216:NEG:H11	57:AA:3216:NEG:N4	2.24	0.52
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.43	0.52
19:AS:20:LEU:HA	19:AS:23:ASN:HD22	1.75	0.52
25:BA:1185:C:O3'	33:BN:25:ARG:NH1	2.43	0.52
25:BA:1501:U:O2'	25:BA:1502:G:N7	2.37	0.52
25:BA:2846:U:H2'	25:BA:2847:G:C8	2.45	0.52
31:BH:69:ARG:HG3	31:BH:70:THR:N	2.24	0.52
1:CA:839:U:H5"	1:CA:840:C:C5	2.43	0.52
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.90	0.52
39:DT:95:ARG:HG2	39:DT:95:ARG:HH11	1.75	0.52
50:D4:59:PHE:HA	50:D4:61:ARG:N	2.24	0.52
1:AA:841:U:C5	1:AA:848:C:H1'	2.45	0.52
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.91	0.52
25:BA:927:G:H2'	25:BA:928:G:C8	2.44	0.52
36:BQ:16:ARG:HG3	36:BQ:17:LEU:H	1.75	0.52
1:CA:91:C:H2'	1:CA:92:C:C6	2.45	0.52
1:CA:309:G:O2'	1:CA:607:A:N1	2.40	0.52
1:CA:1004:A:C8	1:CA:1005:A:H4'	2.40	0.52
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.09	0.52
25:DA:744:G:OP1	28:DE:132:HIS:ND1	2.35	0.52
25:DA:1991:U:H2'	25:DA:1992:G:H5"	1.91	0.52
1:AA:56:U:H2'	1:AA:57:G:C8	2.45	0.52
1:AA:72:C:N3	1:AA:97:G:N2	2.46	0.52
1:AA:292:G:C5	1:AA:293:G:H1'	2.44	0.52
1:AA:636:U:H5"	17:AQ:2:PRO:HG3	1.91	0.52
1:AA:1152:A:H5'	10:AJ:13:HIS:CG	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BO:80:ASP:OD2	39:BT:64:ARG:NH2	2.42	0.52
45:BZ:157:LEU:C	45:BZ:161:VAL:HG11	2.35	0.52
1:CA:1028:C:N3	1:CA:1033:G:C6	2.78	0.52
1:CA:1401:G:C2	1:CA:1402:C:H1'	2.45	0.52
2:CB:122:PHE:HA	2:CB:127:ILE:HD12	1.90	0.52
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.44	0.52
19:CS:20:LEU:HA	19:CS:23:ASN:HD22	1.75	0.52
23:CW:25:C:H2'	23:CW:26:A:H8	1.74	0.52
40:DU:79:PHE:HE2	40:DU:95:LEU:HD21	1.75	0.52
1:AA:405:U:O4	4:AD:2:GLY:N	2.43	0.51
1:AA:741:G:H2'	1:AA:742:G:O4'	2.09	0.51
1:AA:1060:C:OP1	14:AN:45:ARG:NH2	2.39	0.51
1:AA:1302:U:C5	13:AM:17:VAL:HG21	2.45	0.51
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.45	0.51
25:BA:1320:A:N3	25:BA:1343:C:H1'	2.24	0.51
25:BA:1809:U:H2'	25:BA:1815:A:N6	2.25	0.51
25:BA:2474:U:H1'	25:BA:2503:U:O4	2.10	0.51
47:B1:64:ALA:HA	47:B1:67:ILE:HG13	1.92	0.51
50:B4:26:SER:OG	50:B4:27:THR:N	2.43	0.51
1:CA:817:C:OP2	61:CA:4058:HOH:O	2.19	0.51
1:CA:1027:C:H2'	1:CA:1028:C:C5	2.45	0.51
25:DA:528:A:N1	25:DA:2042:A:H2'	2.25	0.51
25:DA:2815:C:H2'	25:DA:2816:C:C6	2.45	0.51
26:DB:66:A:H61	26:DB:108:U:H3'	1.75	0.51
29:DF:192:LEU:HD22	29:DF:194:MET:HG3	1.91	0.51
33:DN:38:HIS:CE1	33:DN:39:ARG:HG3	2.45	0.51
1:AA:154:C:H2'	1:AA:155:C:H6	1.76	0.51
1:AA:383:A:C5	1:AA:384:G:H1'	2.45	0.51
1:AA:921:U:O2	5:AE:19:MET:HB2	2.10	0.51
8:AH:49:GLU:HG2	8:AH:62:TYR:HE1	1.75	0.51
23:AY:1:G:H2'	23:AY:2:C:C6	2.45	0.51
31:BH:84:SER:OG	31:BH:132:ARG:NH1	2.43	0.51
42:BW:14:PRO:HG2	42:BW:78:GLU:CG	2.38	0.51
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.45	0.51
57:CA:3174:NEG:N3	25:DA:1946:U:OP2	2.44	0.51
3:CC:134:ILE:HG22	3:CC:168:ALA:HB3	1.93	0.51
25:DA:855:G:C6	25:DA:856:C:C4	2.98	0.51
25:DA:890:A:H2'	25:DA:892:G:C8	2.44	0.51
25:DA:1316:U:H2'	25:DA:1317:A:C8	2.45	0.51
25:DA:1386:C:H2'	25:DA:1387:C:C6	2.45	0.51
25:DA:2850:A:N7	25:DA:2868:A:O2'	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DE:101:ARG:CZ	28:DE:171:GLU:HB2	2.40	0.51
45:DZ:29:TYR:HB3	45:DZ:34:ASN:HD22	1.76	0.51
1:AA:449:C:H5"	1:AA:450:G:OP2	2.10	0.51
1:AA:1392:G:H21	1:AA:1502:A:H8	1.57	0.51
3:AC:153:VAL:HG22	3:AC:198:VAL:HG13	1.91	0.51
3:AC:162:GLN:NE2	22:AV:24:A:O2'	2.44	0.51
23:AW:43:C:H2'	23:AW:44:G:C8	2.45	0.51
25:BA:174:U:H4'	25:BA:207:A:H4'	1.91	0.51
25:BA:514:G:O2'	42:BW:49:LYS:NZ	2.31	0.51
25:BA:1065:U:OP1	25:BA:1081:U:O2'	2.28	0.51
25:BA:2255:U:H2'	25:BA:2256:U:C6	2.46	0.51
25:BA:2724:U:H2'	25:BA:2727:G:H5"	1.92	0.51
40:BU:79:PHE:O	40:BU:83:LEU:HD22	2.10	0.51
1:CA:324:G:OP2	61:CA:4084:HOH:O	2.19	0.51
4:CD:173:TRP:HB2	4:CD:187:ARG:O	2.10	0.51
23:CY:62:C:H2'	23:CY:63:G:C8	2.42	0.51
25:DA:19:C:H2'	25:DA:20:C:C6	2.45	0.51
25:DA:252:G:P	35:DP:50:ARG:HH12	2.33	0.51
25:DA:265:A:H1'	25:DA:266:G:O4'	2.11	0.51
25:DA:1235:G:C6	25:DA:1236:G:N1	2.78	0.51
25:DA:1815:A:H8	25:DA:1815:A:OP1	1.92	0.51
25:DA:2882:A:H5'	37:DR:96:ARG:HG3	1.90	0.51
40:DU:83:LEU:HD12	40:DU:88:ILE:HD12	1.92	0.51
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.26	0.51
2:AB:71:VAL:HG12	2:AB:170:GLU:HG3	1.91	0.51
2:AB:80:ILE:HG13	2:AB:212:GLN:HG2	1.92	0.51
9:AI:45:ALA:HA	9:AI:48:GLU:HB2	1.91	0.51
15:AO:70:LEU:HD11	15:AO:77:ARG:HB2	1.92	0.51
23:AY:34:G:H3'	23:AY:35:A:H8	1.75	0.51
23:AY:63:G:C2	23:AY:64:A:H1'	2.44	0.51
25:BA:1221:G:H1'	25:BA:1222:A:C5'	2.34	0.51
25:BA:2087:C:H2'	25:BA:2088:C:C6	2.45	0.51
25:BA:2802:C:O2	25:BA:2903:G:N1	2.38	0.51
31:BH:98:LEU:HD13	31:BH:125:VAL:HG23	1.92	0.51
31:BH:113:VAL:HG11	31:BH:151:ILE:HD13	1.92	0.51
32:BI:126:TYR:HB2	32:BI:142:VAL:HG23	1.91	0.51
1:CA:266:G:H5"	1:CA:268:C:H41	1.75	0.51
1:CA:374:A:C6	1:CA:375:U:C4	2.99	0.51
1:CA:663:A:O3'	18:CR:64:ARG:NH2	2.43	0.51
1:CA:1119:C:N3	1:CA:1154:G:N2	2.59	0.51
3:CC:20:SER:HB3	3:CC:22:TRP:NE1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:87:LEU:O	3:CC:91:LEU:N	2.38	0.51
25:DA:357:A:H2'	25:DA:358:U:C6	2.46	0.51
25:DA:1998:G:HO2'	25:DA:2724:C:HO2'	1.59	0.51
25:DA:2124:G:H1	25:DA:2173:A:N6	2.08	0.51
25:DA:2252:G:H2'	25:DA:2253:G:C8	2.46	0.51
25:DA:2808:U:H2'	25:DA:2809:A:H5'	1.93	0.51
27:DD:108:PRO:HG2	27:DD:111:LEU:HB2	1.92	0.51
37:DR:21:TYR:OH	37:DR:43:GLU:HG2	2.10	0.51
45:DZ:171:ILE:HD12	45:DZ:172:ALA:H	1.76	0.51
1:AA:1053:G:N7	1:AA:1200:C:H5"	2.26	0.51
1:AA:1106:G:H5"	3:AC:172:ARG:HG2	1.92	0.51
4:AD:53:ASP:O	4:AD:57:ARG:HG3	2.10	0.51
4:AD:129:ASN:OD1	4:AD:145:GLU:N	2.34	0.51
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.36	0.51
25:BA:211:A:H5"	25:BA:448:U:OP1	2.11	0.51
25:BA:502:G:H4'	25:BA:527:A:N1	2.26	0.51
25:BA:599:U:O4	61:BA:4870:HOH:O	2.18	0.51
25:BA:1793:A:H2'	61:BA:5168:HOH:O	2.09	0.51
25:BA:2574:U:O2'	34:BO:23:ARG:HD3	2.11	0.51
25:BA:2787:C:OP2	61:BA:4638:HOH:O	2.19	0.51
26:BB:57:A:H4'	30:BG:30:GLU:HG3	1.92	0.51
29:BF:30:PRO:HB3	35:BP:1:MET:HE1	1.92	0.51
14:CN:23:ARG:NH1	14:CN:30:ALA:HB2	2.26	0.51
25:DA:84:A:H5'	44:DY:8:LYS:HG2	1.92	0.51
25:DA:684:G:OP1	53:D7:16:HIS:ND1	2.41	0.51
25:DA:2123:G:H2'	25:DA:2124:G:H8	1.75	0.51
25:DA:2292:C:P	38:DS:17:ARG:HH12	2.33	0.51
1:AA:632:A:H3'	1:AA:633:G:H8	1.74	0.51
1:AA:1054:C:C5	23:AW:34:G:H1'	2.46	0.51
1:AA:1177:G:OP2	9:AI:97:LYS:NZ	2.35	0.51
19:AS:68:GLY:H	50:B4:58:ARG:NH1	2.09	0.51
25:BA:118:U:OP2	61:BA:4148:HOH:O	2.20	0.51
25:BA:2282:G:OP2	61:BA:4725:HOH:O	2.19	0.51
25:BA:2624:C:OP2	51:B5:2:ALA:N	2.44	0.51
31:BH:59:ARG:HB2	31:BH:59:ARG:HH11	1.74	0.51
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.10	0.51
23:CY:21:A:N6	23:CY:46:7MG:H81	2.25	0.51
25:DA:785:G:OP2	61:DA:4179:HOH:O	2.19	0.51
25:DA:821:A:H2'	25:DA:946:G:H5"	1.91	0.51
25:DA:1337:G:H2'	25:DA:1338:G:O4'	2.11	0.51
25:DA:2502:G:N7	61:DA:4672:HOH:O	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DG:80:PHE:O	30:DG:82:LEU:N	2.43	0.51
38:DS:67:ARG:O	38:DS:71:ARG:HG3	2.10	0.51
1:AA:65:U:H5'	1:AA:65:U:H6	1.75	0.51
1:AA:1064:G:H1'	1:AA:1190:G:N2	2.25	0.51
25:BA:561:A:H2'	25:BA:562:C:C6	2.46	0.51
25:BA:906:G:O2'	25:BA:962:G:O6	2.17	0.51
25:BA:1823:G:O2'	25:BA:1861:C:OP1	2.25	0.51
25:BA:2320:G:O2'	25:BA:2322:A:N7	2.37	0.51
25:BA:2639:G:O2'	25:BA:2794:A:N1	2.41	0.51
25:BA:2707:C:H2'	25:BA:2708:U:C6	2.46	0.51
45:BZ:132:ASN:ND2	45:BZ:160:GLY:HA3	2.26	0.51
47:B1:3:LYS:HB2	47:B1:61:ARG:NH1	2.25	0.51
1:CA:738:C:OP1	6:CF:2:ARG:NH1	2.43	0.51
1:CA:1189:C:OP1	10:CJ:51:ARG:NH2	2.44	0.51
1:CA:1456:G:O6	20:CT:54:LYS:NZ	2.44	0.51
25:DA:11:G:N7	61:DA:4541:HOH:O	2.35	0.51
25:DA:1012:U:C5	33:DN:28:THR:HG21	2.46	0.51
25:DA:2880:C:O3'	37:DR:90:ARG:NH1	2.44	0.51
1:AA:328:C:H4'	1:AA:329:A:H5'	1.92	0.51
1:AA:413:G:N2	1:AA:428:G:H1'	2.26	0.51
1:AA:750:G:H1'	15:AO:22:THR:HG23	1.92	0.51
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.44	0.51
3:AC:156:ARG:NH2	3:AC:159:GLY:O	2.37	0.51
5:AE:143:ARG:NH1	8:AH:77:GLU:OE1	2.44	0.51
12:AL:84:LEU:HB2	12:AL:105:TYR:CE2	2.45	0.51
23:AW:52:G:H5"	36:BQ:56:ARG:HH12	1.74	0.51
25:BA:302:A:H2'	25:BA:303:C:C6	2.46	0.51
25:BA:1495:G:O2'	25:BA:1575:A:N1	2.42	0.51
25:BA:2173:G:H2'	25:BA:2174:G:C8	2.46	0.51
44:BY:6:HIS:HE1	44:BY:72:VAL:O	1.94	0.51
54:B8:6:THR:HG23	54:B8:63:PRO:HD2	1.92	0.51
1:CA:49:U:O4	1:CA:365:U:H5	1.93	0.51
1:CA:345:C:H4'	1:CA:346:G:C4	2.45	0.51
1:CA:866:C:C4	1:CA:867:G:H1'	2.45	0.51
1:CA:1122:U:C4	1:CA:1123:A:N7	2.78	0.51
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.33	0.51
10:CJ:11:PHE:CE1	10:CJ:67:THR:HG22	2.44	0.51
25:DA:191:A:H2'	25:DA:192:C:C6	2.45	0.51
25:DA:705:A:H2'	25:DA:706:A:O4'	2.11	0.51
25:DA:987:G:H5"	25:DA:988:A:OP2	2.09	0.51
25:DA:1159:U:H2'	25:DA:1160:G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2123:G:H2'	25:DA:2124:G:C8	2.46	0.51
25:DA:2206:G:H3'	25:DA:2207:G:C8	2.46	0.51
32:DI:12:LEU:HD22	32:DI:19:VAL:HG21	1.92	0.51
48:D2:9:GLN:HE22	48:D2:56:GLN:HB3	1.76	0.51
1:AA:1000:U:O4	1:AA:1041:A:N1	2.43	0.51
23:AW:26:A:N1	23:AW:44:G:N2	2.59	0.51
23:AW:66:U:H2'	23:AW:67:C:C6	2.46	0.51
25:BA:27:G:N2	25:BA:537:G:H1'	2.26	0.51
25:BA:1890:A:N6	25:BA:1905:G:O2'	2.42	0.51
25:BA:2506:G:O2'	36:BQ:80:GLU:HA	2.11	0.51
26:BB:92:C:OP1	45:BZ:79:ARG:NH1	2.42	0.51
27:BD:85:ASP:OD2	27:BD:88:ARG:NH1	2.40	0.51
39:BT:23:ARG:HG3	39:BT:120:ARG:NH1	2.26	0.51
9:CI:18:PHE:HB2	9:CI:62:TYR:HB3	1.93	0.51
16:CP:52:ASP:O	16:CP:54:GLU:N	2.39	0.51
1:AA:92:C:H2'	1:AA:93:G:C8	2.46	0.51
7:AG:78:ARG:HH12	7:AG:79:ARG:HH21	1.58	0.51
18:AR:24:ALA:C	18:AR:26:LEU:H	2.19	0.51
19:AS:51:VAL:O	19:AS:58:VAL:N	2.36	0.51
25:BA:1223:C:H2'	25:BA:1224:C:H6	1.74	0.51
25:BA:1864:U:O2'	25:BA:1991:A:N1	2.41	0.51
25:BA:2324:U:H5'	30:BG:88:ILE:HD11	1.93	0.51
1:CA:637:G:H2'	1:CA:638:G:H8	1.75	0.51
1:CA:859:A:H2'	1:CA:860:A:O4'	2.10	0.51
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.45	0.51
1:CA:1388:C:H2'	1:CA:1389:C:C6	2.46	0.51
4:CD:191:ARG:NH1	4:CD:194:LEU:O	2.44	0.51
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.26	0.51
23:CY:71:G:H2'	23:CY:72:C:C6	2.46	0.51
25:DA:83:G:OP1	44:DY:95:LYS:NZ	2.44	0.51
25:DA:698:C:O2'	25:DA:734:A:N6	2.43	0.51
25:DA:2086:U:H2'	25:DA:2087:G:C8	2.46	0.51
25:DA:2285:C:OP2	52:D6:6:ARG:NH1	2.43	0.51
25:DA:2849:U:H4'	25:DA:2868:A:C2	2.46	0.51
26:DB:11:C:H3'	26:DB:12:C:C6	2.44	0.51
27:DD:145:VAL:HG13	27:DD:191:ALA:HB2	1.92	0.51
35:DP:63:PRO:HG2	54:D8:25:MET:HB2	1.92	0.51
36:DQ:43:THR:HA	36:DQ:94:VAL:HG12	1.93	0.51
41:DV:14:VAL:HA	41:DV:18:LEU:HD12	1.92	0.51
1:AA:321:A:N7	1:AA:328:C:O2'	2.40	0.50
1:AA:1149:C:H2'	1:AA:1150:U:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:56:C:H5	25:BA:943:C:O4'	1.94	0.50
23:AY:37:MIA:H2'	23:AY:38:A:C8	2.46	0.50
23:AY:38:A:H2'	23:AY:39:PSU:O4'	2.12	0.50
25:BA:310:C:H2'	25:BA:311:C:H6	1.75	0.50
25:BA:667:G:N2	25:BA:670:C:OP2	2.44	0.50
25:BA:927:G:N2	25:BA:944:C:N3	2.58	0.50
25:BA:1410:G:OP2	47:B1:3:LYS:HG3	2.11	0.50
25:BA:2060:G:H2'	25:BA:2061:C:O4'	2.11	0.50
35:BP:81:GLN:NE2	35:BP:105:LEU:O	2.44	0.50
45:BZ:152:ALA:HA	45:BZ:155:LEU:HD23	1.92	0.50
7:CG:27:ILE:HD12	7:CG:40:ALA:HA	1.94	0.50
10:CJ:16:LEU:HD12	10:CJ:68:HIS:HB2	1.92	0.50
25:DA:642:G:H4'	25:DA:2349:G:H4'	1.93	0.50
25:DA:2019:A:H4'	40:DU:34:LYS:HD2	1.92	0.50
25:DA:2166:G:H3'	25:DA:2167:U:C5'	2.40	0.50
25:DA:2788:C:O2'	25:DA:2809:A:N3	2.43	0.50
32:DI:43:ASN:HD22	32:DI:43:ASN:C	2.19	0.50
39:DT:16:ARG:HB3	39:DT:16:ARG:HH11	1.77	0.50
25:BA:929:G:N2	25:BA:941:U:O2	2.44	0.50
25:BA:1066:A:N1	25:BA:1186:U:O2'	2.43	0.50
25:BA:1153:G:N3	25:BA:1153:G:H2'	2.27	0.50
25:BA:1525:G:O2'	25:BA:1605:A:N1	2.40	0.50
25:BA:2130:C:H2'	25:BA:2131:U:C6	2.47	0.50
25:BA:2420:U:H2'	25:BA:2421:G:H8	1.76	0.50
38:BS:10:ARG:O	38:BS:14:VAL:HG13	2.11	0.50
1:CA:1502:A:H2	1:CA:1505:G:N1	2.01	0.50
1:CA:1516:G:H2'	1:CA:1518:A:OP2	2.10	0.50
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.46	0.50
24:CX:47:U:H3'	24:CX:48:C:C5'	2.41	0.50
25:DA:1213:A:N3	25:DA:1238:G:O2'	2.37	0.50
25:DA:1779:U:H2'	61:DA:4904:HOH:O	2.10	0.50
25:DA:2108:C:C2'	25:DA:2109:U:H5'	2.42	0.50
25:DA:2224:G:H4'	25:DA:2226:C:C2	2.46	0.50
1:AA:620:C:C2	4:AD:135:LEU:HG	2.47	0.50
1:AA:839:U:O2'	1:AA:840:C:H5'	2.11	0.50
4:AD:111:ALA:HB2	4:AD:120:LEU:HD12	1.92	0.50
13:AM:121:LYS:H	13:AM:121:LYS:CE	2.21	0.50
25:BA:667:G:H21	25:BA:671:A:H2	1.60	0.50
25:BA:715:G:H5'	25:BA:716:G:OP2	2.11	0.50
25:BA:1272:A:OP1	41:BV:84:LYS:HE2	2.12	0.50
42:BW:88:ARG:HG3	42:BW:92:ARG:HH21	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1150:U:O2	10:CJ:39:PRO:HG2	2.12	0.50
12:CL:113:ARG:NE	12:CL:115:LYS:O	2.36	0.50
16:CP:40:ASP:HB3	16:CP:48:TRP:HB2	1.93	0.50
25:DA:71:A:H5"	25:DA:73:A:C8	2.45	0.50
25:DA:1899:G:N3	25:DA:1899:G:H2'	2.27	0.50
25:DA:2304:G:H22	25:DA:2312:U:H3	1.58	0.50
26:DB:66:A:N6	26:DB:109:C:H5'	2.25	0.50
30:DG:41:GLN:HG2	30:DG:155:MET:HB3	1.93	0.50
31:DH:28:GLY:HA3	31:DH:79:VAL:HB	1.94	0.50
42:DW:35:ILE:HG23	51:D5:28:PRO:HD2	1.93	0.50
44:DY:3:VAL:HB	44:DY:32:PRO:HB3	1.93	0.50
1:AA:110:C:H2'	1:AA:111:G:O4'	2.12	0.50
1:AA:418:C:H1'	1:AA:540:G:O2'	2.11	0.50
45:BZ:138:GLU:O	45:BZ:156:LYS:HD3	2.11	0.50
50:B4:54:GLY:C	50:B4:56:VAL:HA	2.36	0.50
50:B4:64:GLY:C	50:B4:66:SER:H	2.19	0.50
1:CA:431:A:OP1	61:CA:4124:HOH:O	2.19	0.50
1:CA:798:G:O6	61:CA:4041:HOH:O	2.17	0.50
1:CA:1068:G:H8	1:CA:1068:G:OP2	1.95	0.50
4:CD:8:VAL:HA	4:CD:11:LEU:HD13	1.93	0.50
25:DA:304:G:H2'	25:DA:305:U:C6	2.46	0.50
25:DA:307:G:N7	61:DA:4268:HOH:O	2.35	0.50
25:DA:443:A:H1'	25:DA:1201:C:O4'	2.11	0.50
25:DA:1647:G:H3'	25:DA:1647:G:OP2	2.12	0.50
25:DA:1813:G:H1'	27:DD:50:THR:OG1	2.11	0.50
25:DA:2097:C:H2'	25:DA:2098:U:O4'	2.11	0.50
25:DA:2130:U:H3	25:DA:2159:G:N2	2.10	0.50
25:DA:2146:C:H4'	25:DA:2147:G:H5'	1.94	0.50
37:DR:100:LEU:HD11	37:DR:113:LEU:HD23	1.93	0.50
49:D3:23:LEU:HD13	49:D3:50:VAL:HG11	1.92	0.50
4:AD:8:VAL:HA	4:AD:11:LEU:HD13	1.92	0.50
9:AI:99:LEU:HB3	9:AI:101:PHE:HE1	1.75	0.50
18:AR:56:THR:HB	18:AR:58:LEU:HD22	1.92	0.50
23:AY:40:C:H2'	23:AY:41:C:C6	2.46	0.50
1:CA:828:A:N6	1:CA:858:G:O2'	2.44	0.50
1:CA:947:G:H1	1:CA:1234:C:H42	1.58	0.50
1:CA:1120:G:C5	1:CA:1154:G:N2	2.80	0.50
1:CA:1376:U:OP1	7:CG:98:SER:OG	2.25	0.50
3:CC:63:ASN:HB2	3:CC:98:ASN:HB2	1.92	0.50
3:CC:131:ARG:NE	3:CC:166:GLU:OE2	2.44	0.50
19:CS:41:VAL:N	19:CS:44:MET:SD	2.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:7:G:H2'	25:DA:8:A:C8	2.46	0.50
25:DA:906:G:O3'	36:DQ:67:ARG:NH2	2.44	0.50
25:DA:924:C:H2'	25:DA:925:C:C6	2.46	0.50
25:DA:2207:G:O2'	25:DA:2208:A:OP1	2.29	0.50
25:DA:2854:G:H2'	25:DA:2855:C:C6	2.47	0.50
26:DB:38:C:O4'	38:DS:95:HIS:NE2	2.44	0.50
29:DF:197:ASP:O	29:DF:200:GLU:HB2	2.11	0.50
31:DH:30:LYS:HG3	31:DH:80:SER:O	2.11	0.50
47:D1:34:THR:HG21	47:D1:37:ILE:HG13	1.93	0.50
49:D3:7:LYS:HE3	49:D3:32:GLN:NE2	2.27	0.50
1:AA:302:G:O2'	1:AA:556:C:H5"	2.12	0.50
1:AA:528:C:H41	12:AL:49:ASN:CG	2.19	0.50
1:AA:1002:G:N3	1:AA:1003:G:H1'	2.27	0.50
57:AA:3220:NEG:O4	57:AA:3220:NEG:H72	2.09	0.50
2:AB:20:GLU:HA	2:AB:21:ARG:NH2	2.27	0.50
2:AB:163:PHE:HA	2:AB:185:ILE:HG13	1.93	0.50
4:AD:134:ASP:O	4:AD:136:PRO:HD3	2.11	0.50
7:AG:18:TYR:HB3	7:AG:59:LEU:HD13	1.93	0.50
25:BA:1014:U:H2'	25:BA:1015:C:C6	2.47	0.50
25:BA:1524:A:H2'	25:BA:1525:G:O4'	2.12	0.50
27:BD:77:ALA:HB2	27:BD:97:TYR:CD1	2.47	0.50
28:BE:179:GLU:HB3	28:BE:181:LEU:HD22	1.92	0.50
29:BF:192:LEU:HD22	29:BF:194:MET:HG3	1.92	0.50
30:BG:143:GLU:O	50:B4:28:LYS:NZ	2.38	0.50
33:BN:62:VAL:HG13	33:BN:66:LYS:HB2	1.92	0.50
34:BO:64:ARG:HB2	34:BO:83:ALA:HB3	1.94	0.50
51:B5:35:GLU:HG3	51:B5:51:TYR:CB	2.42	0.50
1:CA:130:A:O2'	1:CA:131:C:O5'	2.30	0.50
1:CA:573:A:N3	1:CA:883:C:O2'	2.41	0.50
1:CA:833:U:H2'	1:CA:834:C:H6	1.76	0.50
1:CA:1028:C:C4	1:CA:1033:G:O6	2.64	0.50
1:CA:1059:C:OP2	3:CC:199:LYS:NZ	2.30	0.50
1:CA:1187:G:H5'	9:CI:113:LYS:HE2	1.93	0.50
1:CA:1494:G:H4'	25:DA:1913:A:N7	2.27	0.50
2:CB:103:THR:HA	2:CB:180:LEU:HD11	1.94	0.50
25:DA:460:A:P	53:D7:41:ARG:HH22	2.34	0.50
25:DA:774:A:N3	25:DA:774:A:H2'	2.27	0.50
25:DA:1141:U:OP2	33:DN:63:THR:OG1	2.29	0.50
27:DD:17:THR:O	27:DD:211:ARG:NH2	2.38	0.50
1:AA:975:A:H5'	1:AA:975:A:H8	1.77	0.50
1:AA:993:G:H2'	1:AA:995:C:H41	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:220:ASP:O	2:AB:223:ILE:HG12	2.12	0.50
23:AW:65:G:H2'	23:AW:66:U:C6	2.47	0.50
25:BA:186:A:N6	25:BA:2442:A:H2'	2.25	0.50
25:BA:504:A:N1	25:BA:525:G:H4'	2.27	0.50
25:BA:1067:A:C8	25:BA:1067:A:H3'	2.45	0.50
25:BA:1343:C:OP2	61:BA:4481:HOH:O	2.19	0.50
28:BE:47:VAL:HG21	28:BE:86:PRO:CD	2.41	0.50
1:CA:78:G:O6	1:CA:91:C:N3	2.44	0.50
1:CA:865:A:H5'	1:CA:1078:U:C5	2.47	0.50
1:CA:983:A:N1	1:CA:1222:G:N2	2.60	0.50
6:CF:4:TYR:CE1	6:CF:92:LYS:HG3	2.46	0.50
23:CW:7:A:H3'	23:CW:8:4SU:H6	1.94	0.50
23:CY:76:A:N3	25:DA:2394:C:N4	2.56	0.50
25:DA:289:A:N6	25:DA:351:G:O2'	2.44	0.50
25:DA:839:U:H2'	25:DA:840:C:H6	1.77	0.50
25:DA:2061:G:OP1	29:DF:68:LYS:NZ	2.44	0.50
25:DA:2127:G:H2'	25:DA:2128:C:H5'	1.93	0.50
25:DA:2774:C:H2'	25:DA:2775:A:O4'	2.10	0.50
25:DA:2876:G:H4'	39:DT:2:ASN:ND2	2.27	0.50
28:DE:77:ILE:HG21	28:DE:195:LEU:HD13	1.94	0.50
39:DT:108:ARG:HG2	39:DT:111:ARG:HH12	1.76	0.50
54:D8:4:MET:HE3	54:D8:63:PRO:HG3	1.92	0.50
1:AA:1008:C:O2'	1:AA:1009:G:OP1	2.23	0.50
1:AA:1202:G:N2	14:AN:46:GLU:OE1	2.44	0.50
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.47	0.50
23:AW:9:A:N3	23:AW:45:U:H2'	2.27	0.50
25:BA:1452:U:H2'	25:BA:1453:C:C6	2.47	0.50
25:BA:1553:A:O2'	25:BA:1554:A:O5'	2.27	0.50
25:BA:1993:A:OP2	27:BD:242:ARG:NH2	2.39	0.50
25:BA:2051:G:H2'	25:BA:2053:A:OP1	2.11	0.50
30:BG:46:ALA:HB2	30:BG:53:LEU:HD12	1.93	0.50
39:BT:19:LEU:HD22	39:BT:86:ILE:HG13	1.93	0.50
1:CA:219:C:H2'	1:CA:220:G:O4'	2.11	0.50
1:CA:554:C:H2'	1:CA:555:C:H6	1.77	0.50
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.93	0.50
2:CB:178:ARG:NE	8:CH:74:PRO:HG3	2.25	0.50
10:CJ:16:LEU:HD23	10:CJ:94:VAL:HG22	1.94	0.50
23:CW:75:C:H2'	23:CW:76:A:C4	2.47	0.50
25:DA:478:A:N1	25:DA:500:G:H4'	2.27	0.50
25:DA:900:A:H2'	25:DA:901:A:C8	2.43	0.50
25:DA:1639:U:H2'	25:DA:1640:C:H5"	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2134:A:C2	25:DA:2159:G:H4'	2.47	0.50
25:DA:2557:G:H2'	25:DA:2558:C:H6	1.76	0.50
25:DA:2655:G:O2'	25:DA:2664:G:O6	2.25	0.50
30:DG:170:ARG:HH21	30:DG:180:PHE:HB2	1.76	0.50
34:DO:120:GLU:HG2	34:DO:122:LEU:HG	1.93	0.50
36:DQ:50:ALA:HB1	36:DQ:121:ALA:HB1	1.94	0.50
48:D2:1:MET:N	48:D2:52:ASP:OD1	2.38	0.50
1:AA:1030(B):C:C3'	1:AA:1030(C):G:H5'	2.42	0.50
1:AA:1144:G:N2	1:AA:1146:A:H62	2.09	0.50
3:AC:15:THR:CG2	3:AC:181:ASN:HA	2.41	0.50
19:AS:36:ARG:HB3	19:AS:72:GLY:HA3	1.93	0.50
23:AY:34:G:H3'	23:AY:35:A:C8	2.47	0.50
25:BA:180:A:H2'	25:BA:181:C:C6	2.47	0.50
25:BA:469:A:C5	29:BF:45:ARG:HD2	2.46	0.50
25:BA:1002:A:N1	25:BA:2470:G:H4'	2.27	0.50
25:BA:2334:A:H2'	25:BA:2335:G:O4'	2.12	0.50
25:BA:2711:C:H2'	25:BA:2712:C:O4'	2.12	0.50
26:BB:66:A:H61	26:BB:108:U:H2'	1.76	0.50
36:BQ:54:MET:HG3	36:BQ:117:ALA:HB1	1.92	0.50
40:BU:108:GLU:O	40:BU:112:ARG:HG2	2.12	0.50
1:CA:109:A:C6	1:CA:326:G:C6	3.00	0.50
1:CA:460:G:O6	1:CA:470:C:H5"	2.12	0.50
1:CA:1007:C:N3	1:CA:1022:G:O6	2.45	0.50
1:CA:1048:G:OP1	14:CN:3:ARG:NH2	2.45	0.50
1:CA:1399:C:C2	1:CA:1502:A:N6	2.80	0.50
3:CC:22:TRP:CD2	3:CC:59:ARG:HD2	2.46	0.50
23:CW:21:A:H1'	23:CW:48:C:N4	2.27	0.50
29:DF:197:ASP:OD2	29:DF:198:ALA:N	2.45	0.50
1:AA:625:G:H4'	16:AP:16:HIS:CD2	2.47	0.49
1:AA:691:G:H2'	1:AA:692:U:C6	2.47	0.49
2:AB:93:VAL:HG21	2:AB:97:TRP:CD1	2.46	0.49
6:AF:21:LEU:O	6:AF:25:ILE:HG12	2.12	0.49
13:AM:23:TYR:HB3	13:AM:67:GLU:HA	1.93	0.49
13:AM:80:ARG:HH22	19:AS:69:HIS:HE1	1.60	0.49
25:BA:333:G:N3	25:BA:353:G:O2'	2.44	0.49
25:BA:555:G:C5	25:BA:2044:U:H5"	2.46	0.49
28:BE:14:ILE:HG13	28:BE:21:VAL:HG13	1.94	0.49
35:BP:82:GLY:HA2	35:BP:113:LYS:O	2.11	0.49
1:CA:1304:G:C6	1:CA:1305:G:N1	2.80	0.49
4:CD:196:LEU:C	4:CD:198:VAL:H	2.20	0.49
6:CF:46:ARG:HH11	6:CF:46:ARG:HB2	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2692:C:OP2	61:DA:4608:HOH:O	2.20	0.49
28:DE:170:LEU:HB3	28:DE:184:VAL:HG22	1.94	0.49
31:DH:8:PRO:HB3	31:DH:51:ARG:HG2	1.94	0.49
52:D6:6:ARG:NH1	52:D6:26:ASN:HB2	2.27	0.49
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.41	0.49
1:AA:1401:G:C2	1:AA:1402:C:H1'	2.47	0.49
2:AB:20:GLU:HA	2:AB:21:ARG:HH21	1.77	0.49
2:AB:223:ILE:HD12	2:AB:230:VAL:HG12	1.94	0.49
5:AE:127:ASN:HB3	5:AE:130:ASN:HB2	1.94	0.49
25:BA:553:A:C2	25:BA:2065:C:H4'	2.47	0.49
25:BA:2221:A:OP2	25:BA:2222:C:H5	1.94	0.49
25:BA:2863:C:H2'	25:BA:2864:G:C8	2.47	0.49
28:BE:12:THR:HG22	28:BE:13:ARG:H	1.76	0.49
48:B2:1:MET:N	48:B2:52:ASP:OD2	2.30	0.49
51:B5:55:ARG:NH1	51:B5:57:VAL:HG22	2.27	0.49
1:CA:688:G:H5'	11:CK:46:GLY:C	2.37	0.49
1:CA:1226:C:H2'	13:CM:103:THR:HB	1.94	0.49
6:CF:45:LEU:HD12	6:CF:59:TYR:CD2	2.47	0.49
25:DA:361:G:N3	25:DA:362:U:C4	2.80	0.49
25:DA:526:A:N3	25:DA:2044:C:H1'	2.28	0.49
25:DA:1254:A:C6	29:DF:82:ILE:HD11	2.47	0.49
25:DA:1827:C:OP2	27:DD:222:ARG:NH1	2.44	0.49
25:DA:1843:C:H5'	27:DD:253:GLN:NE2	2.27	0.49
26:DB:46:A:H2'	26:DB:47:C:C6	2.46	0.49
36:DQ:35:VAL:HG13	36:DQ:130:LYS:HB3	1.93	0.49
38:DS:37:ALA:HB2	38:DS:101:LEU:HD11	1.93	0.49
1:AA:232:G:H1'	1:AA:262:A:N1	2.27	0.49
1:AA:922:G:H2'	1:AA:923:A:C8	2.47	0.49
23:AW:67:C:O2'	23:AW:68:C:O5'	2.24	0.49
25:BA:1451:U:H2'	25:BA:1452:U:C6	2.47	0.49
25:BA:2402:U:P	54:B8:35:GLN:HE22	2.34	0.49
1:CA:779:C:O2'	11:CK:120:ARG:HD3	2.12	0.49
1:CA:881:G:OP1	12:CL:12:ARG:NH2	2.44	0.49
1:CA:974:A:P	14:CN:29:ARG:HH21	2.35	0.49
12:CL:117:ARG:NH2	12:CL:124:LYS:HB2	2.27	0.49
19:CS:52:TYR:HB2	19:CS:57:HIS:CE1	2.47	0.49
25:DA:866:A:H5"	25:DA:867:C:OP2	2.12	0.49
25:DA:2307:G:H8	25:DA:2307:G:OP1	1.96	0.49
31:DH:69:ARG:HG3	31:DH:70:THR:N	2.27	0.49
36:DQ:34:LEU:HB2	36:DQ:118:LEU:HD22	1.94	0.49
37:DR:1:MET:HE3	37:DR:3:HIS:CE1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:250:A:H4'	1:AA:251:G:O5'	2.13	0.49
1:AA:456:C:H2'	1:AA:457:C:C6	2.47	0.49
1:AA:1239:A:H62	1:AA:1299:A:H62	1.60	0.49
1:AA:1499:A:H1'	1:AA:1520:G:H5'	1.95	0.49
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.44	0.49
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.77	0.49
14:AN:21:TYR:OH	14:AN:23:ARG:NH2	2.45	0.49
17:AQ:62:SER:OG	17:AQ:72:ARG:HD3	2.12	0.49
20:AT:65:LYS:HA	20:AT:68:LYS:HD3	1.94	0.49
23:AW:56:C:OP1	25:BA:943:C:H5'	2.12	0.49
31:BH:33:LEU:HD21	31:BH:136:ILE:HG13	1.94	0.49
52:B6:11:LEU:HB2	52:B6:21:TYR:HB2	1.93	0.49
1:CA:141:A:H1'	1:CA:182:U:O2	2.13	0.49
1:CA:1004:A:H2'	1:CA:1038:C:H1'	1.94	0.49
1:CA:1095:U:P	1:CA:1108:G:H1	2.35	0.49
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.13	0.49
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.13	0.49
57:CA:3174:NEG:N1	25:DA:1949:G:O6	2.44	0.49
4:CD:164:ALA:O	4:CD:168:ARG:NH2	2.46	0.49
9:CI:127:LYS:O	9:CI:128:ARG:HG2	2.12	0.49
12:CL:39:VAL:HG11	12:CL:41:ARG:HH11	1.78	0.49
15:CO:82:ILE:HB	15:CO:87:ILE:HB	1.94	0.49
23:CY:7:A:N6	23:CY:66:U:N3	2.27	0.49
25:DA:34:C:H2'	25:DA:34:C:O2	2.12	0.49
25:DA:586:A:N1	25:DA:809:G:O2'	2.39	0.49
25:DA:2364:C:H2'	25:DA:2365:G:O4'	2.12	0.49
25:DA:2657:A:O3'	31:DH:160:LYS:NZ	2.44	0.49
25:DA:2848:G:C8	39:DT:97:ALA:HB2	2.48	0.49
30:DG:170:ARG:HH21	30:DG:180:PHE:CB	2.24	0.49
35:DP:38:GLN:O	35:DP:39:LYS:CB	2.60	0.49
36:DQ:111:GLU:O	36:DQ:115:MET:HG2	2.12	0.49
43:DX:92:LEU:C	43:DX:94:GLY:H	2.21	0.49
1:AA:8:A:H5'	5:AE:101:ILE:HG22	1.94	0.49
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.26	0.49
2:AB:127:ILE:HG13	2:AB:130:ARG:NH1	2.27	0.49
7:AG:74:GLU:HG2	7:AG:91:VAL:HG22	1.95	0.49
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	1.92	0.49
25:BA:8:A:H2'	25:BA:9:U:C6	2.47	0.49
25:BA:552:C:C5	25:BA:2792:U:H2'	2.48	0.49
25:BA:653:G:H2'	25:BA:654:G:C8	2.48	0.49
25:BA:957:A:H2'	36:BQ:9:TYR:OH	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BE:116:VAL:HG13	28:BE:122:PHE:HB2	1.95	0.49
1:CA:814:A:H2'	1:CA:816:A:H5"	1.95	0.49
3:CC:100:ALA:O	3:CC:102:ASN:ND2	2.42	0.49
24:CX:17:C:OP1	24:CX:61:C:H5'	2.12	0.49
25:DA:19:C:H2'	25:DA:20:C:H6	1.77	0.49
25:DA:116:C:H2'	25:DA:117:G:O4'	2.12	0.49
25:DA:1486:A:H2'	25:DA:1487:G:C8	2.47	0.49
25:DA:2405:G:O2'	25:DA:2411:A:N6	2.44	0.49
25:DA:2846:G:H2'	25:DA:2847:U:O4'	2.13	0.49
26:DB:22:U:H3	26:DB:61:G:H1	1.59	0.49
30:DG:179:PRO:HG3	50:D4:43:TYR:OH	2.12	0.49
35:DP:47:ASP:OD2	35:DP:49:ARG:NH2	2.46	0.49
44:DY:86:ARG:HB2	44:DY:98:VAL:HG23	1.94	0.49
45:DZ:92:SER:O	45:DZ:130:PRO:HG2	2.12	0.49
1:AA:309:G:H1'	1:AA:608:A:C2	2.47	0.49
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.11	0.49
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	1.94	0.49
12:AL:56:ALA:HB2	12:AL:70:ILE:HD11	1.93	0.49
17:AQ:29:HIS:CE1	17:AQ:32:TYR:HD2	2.31	0.49
19:AS:65:ASN:HD22	19:AS:66:MET:N	2.10	0.49
23:AY:58:A:H4'	23:AY:59:U:OP1	2.13	0.49
25:BA:1587:U:H2'	25:BA:1588:G:O4'	2.12	0.49
25:BA:2470:G:O2'	25:BA:2472:U:O4	2.27	0.49
25:BA:2760:G:O6	25:BA:2768:C:H5"	2.12	0.49
61:BA:4092:HOH:O	36:BQ:75:THR:HG23	2.12	0.49
42:BW:68:ARG:HD3	42:BW:111:HIS:HA	1.94	0.49
1:CA:529:G:O6	12:CL:49:ASN:HA	2.12	0.49
1:CA:576:G:O6	1:CA:880:C:O2'	2.23	0.49
1:CA:1220:G:O3'	19:CS:36:ARG:HD3	2.12	0.49
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.27	0.49
24:CX:10:G:N2	24:CX:26:G:H1'	2.27	0.49
25:DA:489:G:N7	42:DW:49:LYS:NZ	2.60	0.49
25:DA:1686:C:H2'	25:DA:1687:G:O4'	2.12	0.49
25:DA:1803:A:N1	25:DA:1822:G:O2'	2.46	0.49
25:DA:2043:C:H1'	25:DA:2779:U:O4	2.11	0.49
26:DB:17:C:H2'	26:DB:18:G:O4'	2.12	0.49
29:DF:21:ALA:CB	29:DF:22:ALA:HA	2.41	0.49
45:DZ:138:GLU:H	45:DZ:156:LYS:HD3	1.76	0.49
1:AA:431:A:H2'	1:AA:432:A:O4'	2.13	0.49
1:AA:620:C:H2'	1:AA:621:A:O4'	2.13	0.49
1:AA:688:G:H2'	1:AA:689:C:H6	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.19	0.49
8:AH:112:LEU:HB3	8:AH:133:LEU:HA	1.95	0.49
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.44	0.49
25:BA:2116:G:P	32:BI:22:LYS:HD2	2.53	0.49
25:BA:2556:G:H2'	25:BA:2557:G:O4'	2.13	0.49
35:BP:59:LEU:HD21	54:B8:10:ALA:HA	1.95	0.49
35:BP:101:VAL:HA	35:BP:106:LEU:O	2.12	0.49
43:BX:31:HIS:HD2	43:BX:33:LYS:N	1.94	0.49
1:CA:404:U:H2'	1:CA:405:U:C6	2.48	0.49
1:CA:1154:G:H2'	1:CA:1155:G:H8	1.76	0.49
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.95	0.49
3:CC:71:ALA:HA	3:CC:106:VAL:HB	1.95	0.49
4:CD:12:CYS:SG	4:CD:19:LEU:HB2	2.52	0.49
5:CE:110:LEU:HD13	5:CE:118:ILE:HG21	1.95	0.49
9:CI:17:VAL:HG23	9:CI:63:ILE:HG12	1.94	0.49
11:CK:81:ASP:OD1	11:CK:106:LYS:HE2	2.13	0.49
45:DZ:171:ILE:HD12	45:DZ:172:ALA:N	2.28	0.49
1:AA:576:G:O6	1:AA:880:C:O2'	2.26	0.49
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.12	0.49
3:AC:71:ALA:HB2	3:AC:115:LEU:HD21	1.95	0.49
5:AE:78:HIS:HD1	8:AH:104:ARG:HD2	1.78	0.49
12:AL:88:GLY:O	12:AL:99:HIS:HD2	1.95	0.49
25:BA:70:A:H5"	25:BA:72:A:C8	2.48	0.49
25:BA:733:G:C4	53:B7:11:LYS:HG2	2.47	0.49
25:BA:1068:G:OP2	33:BN:65:LYS:NZ	2.46	0.49
25:BA:2549:U:H2'	25:BA:2550:C:C6	2.47	0.49
25:BA:2859:U:O4	39:BT:23:ARG:NH2	2.38	0.49
29:BF:164:ARG:O	29:BF:168:ARG:HB2	2.12	0.49
30:BG:126:ASP:OD2	30:BG:130:ASN:ND2	2.44	0.49
31:BH:24:VAL:HG22	31:BH:35:VAL:HB	1.93	0.49
1:CA:976:G:H22	1:CA:1363:C:H5"	1.77	0.49
1:CA:993:G:O6	1:CA:1045:C:N4	2.39	0.49
1:CA:1121:U:C4	1:CA:1122:U:C4	3.00	0.49
10:CJ:5:ARG:O	10:CJ:98:ILE:HA	2.13	0.49
25:DA:569:U:O2'	25:DA:983:A:N1	2.34	0.49
25:DA:861:A:N6	25:DA:916:G:O2'	2.46	0.49
25:DA:2177:C:H2'	25:DA:2178:C:O4'	2.13	0.49
27:DD:3:VAL:HG13	27:DD:17:THR:HB	1.95	0.49
29:DF:109:GLY:O	29:DF:113:ALA:N	2.46	0.49
29:DF:129:PHE:CD2	29:DF:163:VAL:HG21	2.47	0.49
36:DQ:26:TYR:O	36:DQ:67:ARG:NH1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:45:ASP:CG	45:DZ:49:ARG:HH11	2.21	0.49
1:AA:116:A:H61	1:AA:313:A:H1'	1.76	0.49
1:AA:922:G:C6	1:AA:923:A:C6	3.01	0.49
1:AA:946:A:H2'	1:AA:947:G:C8	2.48	0.49
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.48	0.49
25:BA:407:U:OP1	61:BA:4340:HOH:O	2.20	0.49
25:BA:1338:U:H2'	25:BA:1339:C:C6	2.48	0.49
25:BA:2096:U:H2'	25:BA:2097:U:C6	2.47	0.49
25:BA:2116:G:OP1	32:BI:22:LYS:HD2	2.13	0.49
25:BA:2143:G:H1	25:BA:2199:C:H42	1.61	0.49
25:BA:2150:C:H2'	25:BA:2151:C:C6	2.48	0.49
29:BF:53:THR:CG2	29:BF:55:GLY:H	2.25	0.49
53:B7:24:THR:O	53:B7:28:ARG:HG3	2.12	0.49
54:B8:23:VAL:HG11	54:B8:47:LYS:HD3	1.95	0.49
1:CA:597:G:N2	8:CH:94:TYR:OH	2.44	0.49
1:CA:881:G:H2'	1:CA:882:C:O4'	2.12	0.49
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.12	0.49
1:CA:1085:U:H3'	1:CA:1086:U:H5	1.77	0.49
1:CA:1227:A:N3	19:CS:83:HIS:HB3	2.28	0.49
3:CC:28:GLN:O	3:CC:32:LEU:HD23	2.12	0.49
25:DA:36:G:N3	25:DA:450:G:O2'	2.43	0.49
25:DA:527:C:C4	25:DA:2779:U:H2'	2.47	0.49
25:DA:597:U:H2'	25:DA:598:G:C8	2.48	0.49
25:DA:2292:C:O2'	25:DA:2293:C:H5'	2.13	0.49
25:DA:2320:A:H2'	25:DA:2320:A:N3	2.28	0.49
25:DA:2453:A:N7	61:DA:4348:HOH:O	2.35	0.49
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.95	0.49
27:BD:34:VAL:HG12	27:BD:63:ARG:HG3	1.95	0.49
37:BR:55:ALA:HB2	37:BR:79:LEU:HD13	1.95	0.49
42:BW:58:ALA:HB1	42:BW:64:MET:HB2	1.95	0.49
1:CA:481:G:O2'	1:CA:483:C:N4	2.44	0.49
1:CA:1158:C:O3'	2:CB:133:LYS:NZ	2.45	0.49
1:CA:1194:U:H2'	1:CA:1195:C:C6	2.47	0.49
13:CM:68:GLY:HA3	30:DG:116:ASP:OD1	2.13	0.49
25:DA:185:U:H4'	25:DA:218:A:H4'	1.94	0.49
25:DA:456:C:H4'	61:DA:4011:HOH:O	2.13	0.49
25:DA:825:C:O2	35:DP:55:ARG:NH2	2.41	0.49
25:DA:952:G:OP1	36:DQ:16:ARG:NH2	2.46	0.49
25:DA:1127:A:O2'	25:DA:2518:A:OP1	2.28	0.49
25:DA:1274:A:N3	25:DA:1297:C:H1'	2.28	0.49
25:DA:1939:U:OP1	25:DA:2604:U:O2'	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DB:31:C:H4'	30:DG:29:TRP:CZ2	2.48	0.49
28:DE:170:LEU:HB3	28:DE:184:VAL:CG2	2.43	0.49
39:DT:77:PRO:HB2	39:DT:80:SER:HB2	1.94	0.49
42:DW:2:GLU:OE2	42:DW:72:LYS:NZ	2.27	0.49
44:DY:7:VAL:HG21	44:DY:72:VAL:HG12	1.95	0.49
1:AA:1009:G:H1'	1:AA:1021:G:C2	2.48	0.48
1:AA:1149:C:OP2	9:AI:9:ARG:NH2	2.41	0.48
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.95	0.48
3:AC:142:MET:HG3	3:AC:170:GLN:HB3	1.94	0.48
14:AN:48:ALA:HB2	14:AN:53:LEU:HD12	1.94	0.48
23:AY:2:C:N3	23:AY:71:G:N2	2.61	0.48
25:BA:467:U:O2	29:BF:46:ARG:NH2	2.38	0.48
25:BA:1476:C:H2'	25:BA:1477:U:C6	2.48	0.48
25:BA:2053:A:C6	25:BA:2510:C:H1'	2.47	0.48
25:BA:2138:G:H2'	25:BA:2139:A:C5	2.48	0.48
31:BH:4:ILE:O	31:BH:69:ARG:HG2	2.13	0.48
40:BU:49:HIS:HA	40:BU:52:ARG:HB3	1.95	0.48
40:BU:86:ALA:O	41:BV:49:THR:HG23	2.12	0.48
45:BZ:132:ASN:HD22	45:BZ:160:GLY:HA3	1.78	0.48
51:B5:17:ASP:OD2	61:B5:4005:HOH:O	2.20	0.48
54:B8:4:MET:HE3	54:B8:63:PRO:HG3	1.95	0.48
1:CA:29:G:O2'	1:CA:295:C:H4'	2.13	0.48
1:CA:500:G:O5'	12:CL:124:LYS:NZ	2.46	0.48
1:CA:532:A:H2	1:CA:1206:G:H21	1.60	0.48
5:CE:41:VAL:O	5:CE:66:MET:HA	2.13	0.48
15:CO:5:LYS:HZ2	15:CO:5:LYS:H	1.61	0.48
25:DA:142:A:N1	25:DA:1595:G:O2'	2.31	0.48
25:DA:879:G:H3'	25:DA:880:G:H8	1.77	0.48
25:DA:1114:G:H2'	25:DA:1115:G:H8	1.76	0.48
31:DH:24:VAL:HG13	31:DH:37:VAL:HG21	1.94	0.48
34:DO:64:ARG:NH2	34:DO:99:PHE:O	2.46	0.48
35:DP:101:VAL:HG23	35:DP:106:LEU:HD13	1.95	0.48
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.94	0.48
1:AA:570:G:H1'	1:AA:820:U:C4	2.48	0.48
23:AW:76:A:H5"	25:BA:2614:A:N6	2.27	0.48
23:AY:50:U:H3	23:AY:64:A:H2	1.54	0.48
25:BA:173:C:H2'	25:BA:174:U:C6	2.48	0.48
25:BA:611:U:O4	25:BA:717:A:H1'	2.11	0.48
25:BA:705:C:H2'	25:BA:706:C:C6	2.47	0.48
25:BA:933:C:OP1	25:BA:933:C:H4'	2.12	0.48
25:BA:1038:C:OP1	41:BV:74:LYS:NZ	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1576:G:C6	25:BA:1577:C:N4	2.81	0.48
29:BF:102:PRO:HB2	29:BF:105:VAL:HG23	1.95	0.48
1:CA:174:C:H2'	1:CA:175:C:H6	1.78	0.48
1:CA:179:A:H2'	1:CA:180:U:C6	2.48	0.48
1:CA:1298:C:H2'	7:CG:114:ARG:HH12	1.77	0.48
2:CB:91:PRO:HG2	2:CB:155:LEU:HD23	1.94	0.48
6:CF:43:LEU:HD23	6:CF:46:ARG:HH22	1.77	0.48
17:CQ:32:TYR:O	17:CQ:34:LYS:N	2.42	0.48
25:DA:30:G:OP2	40:DU:5:LYS:NZ	2.38	0.48
25:DA:39:C:H2'	25:DA:40:C:C6	2.48	0.48
25:DA:910:A:C5	36:DQ:13:GLN:HG3	2.48	0.48
25:DA:1147:C:H2'	25:DA:1148:A:C8	2.39	0.48
25:DA:1794:U:H2'	25:DA:1795:C:H6	1.77	0.48
25:DA:2356:C:H2'	25:DA:2357:U:O4'	2.12	0.48
25:DA:2611:U:C4	51:D5:3:LYS:HG2	2.48	0.48
28:DE:27:LEU:HD22	39:DT:1:MET:HE3	1.94	0.48
1:AA:1130:A:O3'	9:AI:20:ARG:NH2	2.46	0.48
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.47	0.48
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.47	0.48
13:AM:19:LEU:HD21	13:AM:56:LEU:HD11	1.95	0.48
25:BA:390:G:H2'	25:BA:391:G:C8	2.48	0.48
25:BA:1952:G:O2'	25:BA:1990:G:O6	2.25	0.48
40:BU:102:GLU:HA	40:BU:104:GLN:HE22	1.79	0.48
1:CA:975:A:N1	10:CJ:48:THR:HB	2.28	0.48
1:CA:1236:A:O2'	1:CA:1304:G:H4'	2.13	0.48
1:CA:1291:G:C6	1:CA:1292:U:C4	3.01	0.48
2:CB:82:ARG:HG3	2:CB:92:TYR:OH	2.14	0.48
2:CB:128:GLU:HG3	2:CB:135:GLN:NE2	2.28	0.48
25:DA:479:A:N3	25:DA:481:G:H5"	2.28	0.48
25:DA:784:A:C8	25:DA:792:G:C5	3.01	0.48
25:DA:875:G:C2	25:DA:903:C:C2	3.02	0.48
25:DA:910:A:N3	25:DA:2264:C:O2'	2.44	0.48
25:DA:1639:U:O2'	25:DA:2699:C:H4'	2.13	0.48
28:DE:9:VAL:HG13	28:DE:25:VAL:O	2.13	0.48
41:DV:76:LYS:HB2	41:DV:81:TYR:HB3	1.95	0.48
1:AA:445:G:H2'	1:AA:446:G:C8	2.48	0.48
1:AA:926:G:H5"	1:AA:927:G:O5'	2.13	0.48
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.14	0.48
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.33	0.48
57:AA:3221:NEG:H71	25:BA:786:G:H22	1.78	0.48
3:AC:121:ALA:O	3:AC:125:GLU:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:145:LYS:O	5:AE:149:GLU:HG2	2.14	0.48
12:AL:60:LEU:HD21	12:AL:66:VAL:HG22	1.95	0.48
23:AW:29:G:N2	23:AW:41:C:N3	2.49	0.48
25:BA:347:G:C8	29:BF:171:PRO:HG3	2.49	0.48
25:BA:415:G:O2'	25:BA:416:G:N7	2.43	0.48
25:BA:2094:G:H2'	25:BA:2095:C:O4'	2.13	0.48
1:CA:187:C:O2'	20:CT:89:ARG:NH2	2.45	0.48
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.14	0.48
2:CB:155:LEU:HD21	2:CB:159:PRO:HG3	1.95	0.48
6:CF:44:GLY:HA2	6:CF:59:TYR:CZ	2.49	0.48
8:CH:56:LYS:HB2	8:CH:58:TYR:CE1	2.47	0.48
25:DA:64:A:O3'	43:DX:71:GLY:HA3	2.14	0.48
25:DA:684:G:N7	61:DA:4006:HOH:O	2.35	0.48
25:DA:833:U:O2	35:DP:55:ARG:NH2	2.47	0.48
25:DA:2105:C:H2'	25:DA:2106:G:H8	1.78	0.48
44:DY:20:TYR:CE1	44:DY:43:ASN:HA	2.48	0.48
4:AD:173:TRP:CD1	4:AD:173:TRP:H	2.31	0.48
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.46	0.48
9:AI:23:ASN:HD22	9:AI:25:LYS:HG2	1.77	0.48
25:BA:225:C:H2'	25:BA:226:C:C6	2.49	0.48
25:BA:1249:A:H2	25:BA:1287:A:N6	2.04	0.48
25:BA:2576:A:C2	25:BA:2659:U:H4'	2.49	0.48
26:BB:22:U:H2'	26:BB:23:G:C8	2.48	0.48
30:BG:106:LEU:HA	30:BG:110:ALA:HB3	1.96	0.48
32:BI:78:THR:HA	32:BI:143:SER:HG	1.78	0.48
1:CA:814:A:N7	1:CA:816:A:C4	2.81	0.48
1:CA:1298:C:OP2	7:CG:114:ARG:NH2	2.44	0.48
8:CH:13:ILE:O	8:CH:17:THR:HG23	2.13	0.48
24:CX:64:G:H4'	36:DQ:10:ARG:NH1	2.29	0.48
25:DA:511:U:O4	25:DA:512:G:N1	2.46	0.48
25:DA:1165:U:H2'	25:DA:1166:C:H6	1.77	0.48
25:DA:1262:A:C2	51:D5:10:LYS:HD2	2.48	0.48
25:DA:1316:U:H2'	25:DA:1317:A:H8	1.77	0.48
25:DA:2469:A:H2'	25:DA:2470:G:O4'	2.13	0.48
25:DA:2562:U:H1'	34:DO:23:ARG:HH11	1.78	0.48
25:DA:2785:C:OP1	28:DE:41:LYS:NZ	2.36	0.48
26:DB:76:G:N2	26:DB:101:G:O6	2.36	0.48
26:DB:88:C:H2'	26:DB:89:G:O4'	2.14	0.48
44:DY:9:LYS:HA	44:DY:10:GLY:HA2	1.55	0.48
45:DZ:145:GLU:H	45:DZ:148:ASP:HB2	1.79	0.48
46:D0:53:MET:HG3	46:D0:59:LEU:HD23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:164:U:H2'	1:AA:165:C:C6	2.49	0.48
13:AM:13:LYS:HA	13:AM:44:ARG:HH11	1.79	0.48
61:AX:3108:HOH:O	25:BA:2614:A:OP1	2.20	0.48
25:BA:116:A:C8	25:BA:117:A:C8	3.01	0.48
25:BA:898:U:O2'	49:B3:42:ALA:O	2.32	0.48
25:BA:1223:C:H2'	25:BA:1224:C:C6	2.48	0.48
25:BA:2132:G:H5"	25:BA:2167:C:H42	1.77	0.48
1:CA:109:A:H2'	1:CA:326:G:N2	2.28	0.48
1:CA:501:C:H2'	1:CA:502:G:H8	1.79	0.48
1:CA:958:A:N6	19:CS:77:THR:O	2.47	0.48
15:CO:5:LYS:H	15:CO:5:LYS:NZ	2.11	0.48
25:DA:271(A):A:N1	25:DA:272(D):G:O2'	2.42	0.48
25:DA:962:G:H2'	25:DA:963:U:O4'	2.13	0.48
25:DA:1005:C:H2'	25:DA:1006:C:H6	1.76	0.48
25:DA:2590:A:OP2	27:DD:238:GLY:HA2	2.13	0.48
27:DD:121:PRO:HB3	27:DD:135:PHE:CE2	2.48	0.48
35:DP:82:GLY:HA2	35:DP:113:LYS:O	2.13	0.48
36:DQ:137:TYR:O	36:DQ:141:GLN:HG2	2.14	0.48
41:DV:24:LYS:CG	41:DV:64:HIS:HD2	2.27	0.48
1:AA:297:G:H4'	1:AA:557:G:H4'	1.95	0.48
1:AA:582:U:C2	1:AA:760:G:C6	3.01	0.48
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.14	0.48
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.13	0.48
1:AA:1266:G:N2	1:AA:1270:C:N3	2.62	0.48
2:AB:48:MET:HA	2:AB:51:LEU:HD12	1.95	0.48
2:AB:187:LEU:HA	2:AB:201:ILE:HB	1.95	0.48
3:AC:33:LEU:O	3:AC:37:GLN:NE2	2.46	0.48
6:AF:9:VAL:HB	6:AF:87:ARG:HB2	1.95	0.48
25:BA:1199:C:OP1	40:BU:92:ARG:NH1	2.46	0.48
37:BR:21:TYR:OH	37:BR:43:GLU:HG2	2.13	0.48
1:CA:193:C:H2'	1:CA:194:C:C6	2.48	0.48
1:CA:646:U:H2'	1:CA:647:C:C6	2.49	0.48
1:CA:737:A:H2'	1:CA:738:C:C6	2.49	0.48
1:CA:1003:G:H2'	1:CA:1004:A:O4'	2.14	0.48
10:CJ:6:ILE:HG12	10:CJ:98:ILE:HG13	1.96	0.48
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.13	0.48
24:CX:2:G:OP1	46:D0:5:LYS:NZ	2.46	0.48
25:DA:322:A:OP2	29:DF:169:ASN:HB2	2.13	0.48
25:DA:852:G:H2'	25:DA:853:G:H8	1.78	0.48
25:DA:1169:G:H2'	25:DA:1170:G:C8	2.49	0.48
25:DA:1452:A:O2'	25:DA:1453:U:H2'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1950:G:N1	25:DA:1954:G:O2'	2.35	0.48
25:DA:2139:C:N3	25:DA:2152:G:N2	2.58	0.48
25:DA:2265:U:H4'	36:DQ:13:GLN:HE22	1.78	0.48
25:DA:2472:G:H1	25:DA:2477:C:P	2.35	0.48
46:D0:48:GLY:HA3	46:D0:80:HIS:ND1	2.29	0.48
1:AA:509:A:O2'	1:AA:510:A:OP1	2.27	0.48
1:AA:1014:A:C2	1:AA:1219:U:H1'	2.49	0.48
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.94	0.48
4:AD:107:ARG:NH2	4:AD:194:LEU:HD22	2.28	0.48
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.94	0.48
13:AM:11:ARG:C	13:AM:13:LYS:H	2.21	0.48
22:AV:20:U:H2'	22:AV:21:C:C6	2.48	0.48
25:BA:895:G:O6	25:BA:974:G:H2'	2.14	0.48
25:BA:1074:A:H61	25:BA:1171:G:H2'	1.79	0.48
25:BA:2163:G:C5	25:BA:2164:C:H1'	2.48	0.48
25:BA:2172:U:C4	25:BA:2173:G:N7	2.82	0.48
25:BA:2258:G:H2'	25:BA:2259:A:C8	2.48	0.48
30:BG:66:GLN:OE1	30:BG:98:ARG:NE	2.39	0.48
31:BH:3:ARG:HG2	31:BH:6:ARG:HG2	1.95	0.48
1:CA:1320:C:O4'	19:CS:73:GLU:HG3	2.14	0.48
6:CF:70:ASP:N	6:CF:70:ASP:OD1	2.45	0.48
23:CY:10:G:H1	23:CY:25:C:N4	2.11	0.48
25:DA:938:G:OP2	54:D8:52:LYS:NZ	2.44	0.48
25:DA:1301:A:H2	25:DA:1626:G:N3	2.12	0.48
25:DA:1434:A:H61	25:DA:1558:A:N6	2.12	0.48
25:DA:1637:A:H4'	25:DA:2711:A:O2'	2.13	0.48
25:DA:2135:A:H61	25:DA:2157:G:N2	2.12	0.48
39:DT:24:PRO:HD3	39:DT:52:ILE:HD12	1.95	0.48
49:D3:26:LEU:HD21	49:D3:46:ASN:HB2	1.95	0.48
1:AA:1309:G:O2'	13:AM:77:ASN:ND2	2.47	0.48
1:AA:1346:A:N1	1:AA:1374:A:H5"	2.28	0.48
2:AB:158:LEU:HD12	2:AB:182:ILE:HD11	1.96	0.48
4:AD:164:ALA:C	4:AD:168:ARG:HH11	2.22	0.48
25:BA:1195:G:H2'	25:BA:1196:C:C6	2.49	0.48
25:BA:2717:A:O2'	25:BA:2862:G:OP1	2.31	0.48
25:BA:2772:G:N7	61:BA:4272:HOH:O	2.35	0.48
26:BB:88:C:H2'	26:BB:89:G:O4'	2.14	0.48
30:BG:45:GLU:H	30:BG:45:GLU:HG2	1.50	0.48
34:BO:64:ARG:NH2	34:BO:99:PHE:O	2.47	0.48
34:BO:69:ILE:HD11	34:BO:105:GLU:CD	2.38	0.48
34:BO:120:GLU:HG2	34:BO:122:LEU:HG	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:637:G:H2'	1:CA:638:G:C8	2.49	0.48
1:CA:758:G:H4'	1:CA:880:C:H4'	1.95	0.48
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.47	0.48
25:DA:1124:C:H2'	25:DA:1125:G:O4'	2.14	0.48
25:DA:2001:A:H2'	25:DA:2002:G:C8	2.49	0.48
28:DE:31:CYS:HB2	28:DE:91:VAL:HB	1.96	0.48
33:DN:128:HIS:CE1	33:DN:135:PRO:HG2	2.48	0.48
1:AA:911:U:H2'	1:AA:912:C:C6	2.49	0.48
2:AB:95:GLN:HG3	2:AB:147:LYS:HD3	1.95	0.48
14:AN:3:ARG:HB3	14:AN:3:ARG:NH2	2.29	0.48
23:AW:26:A:H61	23:AW:44:G:H1	1.61	0.48
23:AW:72:C:H5'	61:AW:4009:HOH:O	2.13	0.48
25:BA:207:A:C2	25:BA:224:U:H4'	2.49	0.48
25:BA:818:G:OP1	53:B7:14:LYS:NZ	2.44	0.48
25:BA:1973:U:O2'	25:BA:1975:A:N7	2.46	0.48
25:BA:2658:C:OP2	25:BA:2745:G:O2'	2.19	0.48
44:BY:90:LEU:HB3	44:BY:92:ASN:H	1.79	0.48
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.49	0.48
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.49	0.48
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.95	0.48
9:CI:16:ARG:N	9:CI:64:THR:O	2.41	0.48
23:CY:47:U:O2'	23:CY:48:C:H5'	2.13	0.48
25:DA:989:G:H4'	25:DA:990:A:OP1	2.12	0.48
25:DA:1003:G:N2	25:DA:1153:C:C2	2.81	0.48
25:DA:1639:U:C2'	25:DA:1640:C:H5"	2.44	0.48
25:DA:1711:C:H2'	25:DA:1712:C:C6	2.48	0.48
25:DA:2345:G:H4'	25:DA:2346:A:H5"	1.96	0.48
25:DA:2512:C:H2'	25:DA:2513:G:O4'	2.13	0.48
33:DN:12:ARG:HH21	33:DN:138:LEU:HD11	1.78	0.48
33:DN:42:TRP:CH2	33:DN:44:PRO:HB3	2.48	0.48
35:DP:101:VAL:HA	35:DP:106:LEU:O	2.14	0.48
50:D4:46:GLN:C	50:D4:48:ARG:H	2.22	0.48
1:AA:625:G:H2'	1:AA:626:U:C6	2.49	0.47
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.38	0.47
2:AB:145:LEU:HD12	2:AB:149:LEU:HD12	1.96	0.47
4:AD:162:LEU:HD12	4:AD:181:MET:HE3	1.96	0.47
10:AJ:57:LYS:HE2	10:AJ:60:ARG:NH2	2.29	0.47
19:AS:28:LYS:HB3	19:AS:28:LYS:HZ2	1.79	0.47
25:BA:1547:C:O4'	27:BD:100:GLY:HA2	2.14	0.47
36:BQ:42:ILE:HD13	36:BQ:97:VAL:HB	1.96	0.47
1:CA:148:G:H2'	1:CA:149:A:C8	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:509:A:H5”	4:CD:55:ALA:HB2	1.95	0.47
1:CA:1069:C:O2’	1:CA:1192:C:H1’	2.14	0.47
1:CA:1226:C:H4’	19:CS:80:TYR:CZ	2.49	0.47
1:CA:1240:U:OP2	7:CG:115:ARG:HA	2.13	0.47
1:CA:1312:G:H5’	19:CS:5:LEU:HD21	1.96	0.47
1:CA:1371:G:O3’	9:CI:69:GLY:HA3	2.14	0.47
5:CE:81:GLU:HG2	5:CE:90:VAL:HG13	1.96	0.47
5:CE:90:VAL:O	5:CE:120:THR:HA	2.14	0.47
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.47	0.47
11:CK:79:SER:OG	11:CK:106:LYS:NZ	2.47	0.47
15:CO:5:LYS:HB2	15:CO:5:LYS:HZ3	1.79	0.47
25:DA:784:A:C6	27:DD:229:VAL:HG11	2.49	0.47
27:DD:26:LYS:HB3	27:DD:83:GLU:HG2	1.95	0.47
1:AA:501:C:H2’	1:AA:502:G:C8	2.49	0.47
4:AD:6:GLY:O	4:AD:115:ARG:NH1	2.45	0.47
4:AD:15:GLU:OE2	4:AD:66:ARG:NH1	2.47	0.47
4:AD:25:ARG:NH1	4:AD:30:LYS:HB3	2.30	0.47
25:BA:1152:G:H4’	25:BA:1153:G:OP2	2.14	0.47
25:BA:1580:G:N2	25:BA:1583:C:H41	2.11	0.47
25:BA:2331:G:H4’	25:BA:2332:A:OP1	2.13	0.47
26:BB:29:A:H2’	26:BB:30:C:C6	2.49	0.47
29:BF:150:GLY:HA2	29:BF:172:TRP:CD2	2.49	0.47
45:BZ:153:SER:HB3	45:BZ:167:PRO:HB3	1.96	0.47
1:CA:426:G:OP1	4:CD:36:ARG:HD2	2.14	0.47
1:CA:486:U:H2’	1:CA:487:A:C8	2.49	0.47
1:CA:596:C:N3	1:CA:644:G:N1	2.47	0.47
1:CA:953:G:C2	1:CA:954:G:H1’	2.50	0.47
2:CB:125:PRO:C	2:CB:127:ILE:H	2.23	0.47
23:CW:7:A:N1	23:CW:66:U:C4	2.80	0.47
23:CY:56:C:H2’	23:CY:57:G:H8	1.79	0.47
25:DA:287:C:H2’	25:DA:288:C:C6	2.47	0.47
25:DA:1013:C:H2’	25:DA:1014:U:C6	2.49	0.47
25:DA:2025:C:H2’	25:DA:2026:C:C6	2.49	0.47
25:DA:2135:A:H61	25:DA:2157:G:H21	1.61	0.47
25:DA:2147:G:H2’	25:DA:2148:G:O4’	2.14	0.47
25:DA:2207:G:H8	25:DA:2207:G:OP1	1.96	0.47
26:DB:42:C:O2’	30:DG:67:LYS:O	2.32	0.47
29:DF:65:TRP:CZ2	29:DF:75:HIS:HD2	2.32	0.47
35:DP:81:GLN:NE2	35:DP:105:LEU:O	2.47	0.47
1:AA:142:G:H2’	1:AA:143:A:C8	2.49	0.47
1:AA:404:U:H5’	4:AD:122:ARG:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:452:A:O3'	16:AP:72:ARG:HD2	2.14	0.47
1:AA:1280:A:O2'	1:AA:1281:U:H5"	2.14	0.47
57:AA:3220:NEG:N3	25:BA:1968:U:OP2	2.48	0.47
23:AY:25:C:O2'	23:AY:26:A:O4'	2.32	0.47
25:BA:1073:A:C2	25:BA:2500:A:H5'	2.49	0.47
25:BA:2169:G:C3'	25:BA:2170:G:H5"	2.42	0.47
28:BE:24:THR:HG23	28:BE:184:VAL:HG12	1.96	0.47
32:BI:93:THR:H	32:BI:96:ASP:HB2	1.79	0.47
45:BZ:58:VAL:HG12	45:BZ:68:PRO:HA	1.95	0.47
45:BZ:111:VAL:HG12	45:BZ:112:ARG:H	1.79	0.47
57:CA:3175:NEG:H72	25:DA:739:G:N1	2.24	0.47
3:CC:120:VAL:HA	3:CC:123:GLN:HB2	1.96	0.47
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.96	0.47
23:CW:22:G:N7	23:CW:46:7MG:N2	2.60	0.47
25:DA:565:C:H2'	25:DA:566:U:O4'	2.14	0.47
25:DA:700:G:O2'	25:DA:1632:A:N3	2.40	0.47
25:DA:1033:U:OP1	55:D9:9:ARG:NH2	2.47	0.47
25:DA:1153:C:H2'	25:DA:1154:G:O4'	2.14	0.47
25:DA:1158:C:H4'	49:D3:32:GLN:HB2	1.97	0.47
25:DA:1181:C:H2'	25:DA:1182:A:C8	2.50	0.47
26:DB:105:A:H2'	26:DB:106:G:O4'	2.14	0.47
34:DO:104:ARG:CZ	39:DT:34:VAL:HG11	2.44	0.47
1:AA:545:C:OP1	4:AD:61:LYS:NZ	2.47	0.47
1:AA:993:G:O2'	1:AA:994:A:N7	2.47	0.47
9:AI:24:GLY:HA3	9:AI:57:GLY:HA2	1.95	0.47
23:AY:19:G:H5"	23:AY:20:U:C5	2.49	0.47
25:BA:223:C:H2'	25:BA:224:U:C6	2.49	0.47
25:BA:287:G:O6	25:BA:448:U:O2'	2.25	0.47
25:BA:390:G:H2'	25:BA:391:G:H8	1.78	0.47
25:BA:878:G:O2'	35:BP:38:GLN:NE2	2.47	0.47
45:BZ:163:LEU:HD23	45:BZ:167:PRO:HG3	1.96	0.47
1:CA:250:A:H4'	1:CA:251:G:O5'	2.12	0.47
2:CB:52:GLU:HG2	2:CB:56:ARG:NH2	2.30	0.47
15:CO:17:ARG:HH11	15:CO:17:ARG:HG3	1.80	0.47
22:CV:20:U:H2'	22:CV:21:C:C6	2.49	0.47
57:CX:3004:NEG:H71	25:DA:2323:G:N7	2.29	0.47
25:DA:570:G:H2'	25:DA:2030:A:C5	2.49	0.47
25:DA:1300:U:C2	25:DA:1626:G:C6	3.01	0.47
25:DA:2315:G:H2'	25:DA:2316:C:C6	2.49	0.47
26:DB:40:U:C6	50:D4:2:LYS:HE3	2.49	0.47
26:DB:72:G:O2'	26:DB:105:A:N6	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DR:28:LEU:HD12	37:DR:48:VAL:HG21	1.96	0.47
45:DZ:141:VAL:HG12	45:DZ:144:LEU:HD12	1.96	0.47
1:AA:277:C:H5"	17:AQ:68:ARG:NH2	2.30	0.47
1:AA:1130:A:H5'	9:AI:18:PHE:CE2	2.49	0.47
1:AA:1392:G:N2	1:AA:1502:A:H8	2.13	0.47
2:AB:16:HIS:HD2	2:AB:204:ASN:H	1.62	0.47
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.97	0.47
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.15	0.47
4:AD:178:VAL:O	4:AD:180:GLY:N	2.45	0.47
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.47	0.47
19:AS:12:ASP:HB3	19:AS:14:HIS:CD2	2.50	0.47
23:AY:58:A:H1'	23:AY:60:U:OP2	2.14	0.47
30:BG:74:LYS:O	30:BG:84:LYS:NZ	2.47	0.47
1:CA:976:G:OP1	14:CN:32:SER:N	2.42	0.47
1:CA:1241:G:H2'	1:CA:1242:C:C6	2.49	0.47
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.96	0.47
1:CA:1414:U:H3	1:CA:1486:G:H1	1.62	0.47
3:CC:130:VAL:O	3:CC:134:ILE:HG12	2.14	0.47
13:CM:50:GLU:O	13:CM:54:VAL:HG22	2.14	0.47
25:DA:272(B):G:H2'	25:DA:272(C):G:C8	2.50	0.47
25:DA:1239:G:H2'	25:DA:1240:U:O4'	2.14	0.47
25:DA:1354:A:H2'	25:DA:1355:G:O4'	2.14	0.47
25:DA:2461:C:H2'	25:DA:2462:U:C6	2.50	0.47
25:DA:2494:G:O2'	36:DQ:80:GLU:HA	2.14	0.47
25:DA:2602:A:H4'	25:DA:2603:G:C5'	2.45	0.47
25:DA:2693:A:H2'	25:DA:2694:G:C8	2.49	0.47
25:DA:2847:U:OP1	39:DT:98:LYS:HE2	2.14	0.47
28:DE:24:THR:HG23	28:DE:184:VAL:HG12	1.96	0.47
30:DG:179:PRO:HB2	50:D4:42:PHE:HE1	1.79	0.47
1:AA:1004:A:C6	1:AA:1037:C:C4	3.03	0.47
1:AA:1125:U:H4'	10:AJ:5:ARG:NH2	2.29	0.47
5:AE:77:PRO:HG2	5:AE:78:HIS:HD2	1.78	0.47
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.14	0.47
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.15	0.47
19:AS:80:TYR:CZ	19:AS:82:GLY:HA2	2.49	0.47
23:AW:46:7MG:H5"	61:AW:4003:HOH:O	2.15	0.47
25:BA:1699:A:OP1	37:BR:8:ARG:NH1	2.47	0.47
25:BA:2159:C:O2	25:BA:2176:G:N1	2.36	0.47
25:BA:2162:C:C2	25:BA:2173:G:C2	3.03	0.47
25:BA:2482:G:O6	25:BA:2488:A:O2'	2.30	0.47
29:BF:53:THR:HB	29:BF:56:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BN:91:LEU:HG	33:BN:98:VAL:HG21	1.97	0.47
34:BO:68:GLU:HB3	34:BO:78:ARG:HB2	1.95	0.47
36:BQ:31:ASP:HA	36:BQ:134:ARG:NH1	2.29	0.47
38:BS:35:ILE:HG12	38:BS:101:LEU:HD12	1.95	0.47
44:BY:54:LYS:H	44:BY:56:PRO:HD3	1.79	0.47
50:B4:44:THR:O	50:B4:44:THR:OG1	2.25	0.47
1:CA:9:G:H2'	1:CA:10:A:C8	2.48	0.47
1:CA:625:G:H2'	1:CA:626:U:C6	2.50	0.47
1:CA:1075:C:C2'	1:CA:1076:C:H5'	2.44	0.47
1:CA:1090:U:H2'	1:CA:1091:U:C6	2.49	0.47
1:CA:1392:G:N2	1:CA:1502:A:H8	2.12	0.47
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.95	0.47
6:CF:99:ALA:HB2	18:CR:31:LEU:HD21	1.97	0.47
8:CH:91:ARG:HD3	17:CQ:32:TYR:O	2.15	0.47
10:CJ:45:ARG:HG2	10:CJ:47:PHE:CZ	2.49	0.47
16:CP:19:ILE:N	16:CP:37:GLY:O	2.46	0.47
16:CP:59:TRP:HA	16:CP:62:VAL:HG12	1.95	0.47
25:DA:601:C:O2'	25:DA:605:C:H5"	2.14	0.47
25:DA:731:C:OP1	61:DA:4599:HOH:O	2.21	0.47
25:DA:2513:G:N2	28:DE:143:ASN:OD1	2.47	0.47
27:DD:145:VAL:HG11	27:DD:175:LEU:HD11	1.97	0.47
32:DI:41:GLU:O	32:DI:45:LYS:HG3	2.14	0.47
33:DN:34:LEU:O	33:DN:49:GLY:HA3	2.14	0.47
1:AA:21:G:OP1	61:AA:4122:HOH:O	2.20	0.47
1:AA:345:C:H4'	1:AA:346:G:C4	2.50	0.47
1:AA:434:U:H2'	1:AA:435:C:C6	2.50	0.47
1:AA:632:A:H5'	1:AA:633:G:OP2	2.14	0.47
1:AA:765:G:N1	1:AA:812:C:O2'	2.38	0.47
1:AA:1286:A:C8	1:AA:1287:A:H4'	2.49	0.47
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.14	0.47
1:AA:1386:G:H2'	1:AA:1387:G:H8	1.79	0.47
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.50	0.47
9:AI:26:VAL:HG13	9:AI:63:ILE:HD12	1.97	0.47
19:AS:23:ASN:HA	19:AS:27:GLU:CD	2.40	0.47
25:BA:397:G:H4'	25:BA:398:A:OP2	2.14	0.47
25:BA:518:G:H2'	25:BA:519:G:O4'	2.14	0.47
25:BA:560:C:O3'	40:BU:53:ARG:NH1	2.47	0.47
25:BA:840:A:OP2	25:BA:2093:A:O2'	2.31	0.47
25:BA:1405:A:H2'	25:BA:1406:A:H5'	1.96	0.47
25:BA:1529:G:O6	25:BA:1553:A:N6	2.48	0.47
25:BA:1559:C:H2'	25:BA:1560:U:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2108:U:H2'	25:BA:2109:G:C8	2.50	0.47
25:BA:2124:U:H2'	25:BA:2125:C:C6	2.50	0.47
25:BA:2141:A:O2'	25:BA:2142:G:H5'	2.14	0.47
25:BA:2158:C:H41	25:BA:2178:G:N2	2.12	0.47
25:BA:2168:C:O2'	25:BA:2169:G:OP2	2.29	0.47
25:BA:2190:G:C6	25:BA:2193:A:C8	3.02	0.47
25:BA:2376:C:H2'	25:BA:2377:G:O4'	2.15	0.47
25:BA:2803:A:H2'	25:BA:2803:A:N3	2.28	0.47
27:BD:275:LYS:HB3	27:BD:276:LYS:H	1.24	0.47
31:BH:13:LYS:HA	31:BH:14:GLY:HA2	1.67	0.47
31:BH:56:SER:OG	31:BH:57:ASP:N	2.47	0.47
32:BI:135:GLU:C	32:BI:137:PRO:HD3	2.40	0.47
1:CA:130:A:H1'	1:CA:263:A:O2'	2.14	0.47
1:CA:632:A:H5'	1:CA:633:G:OP2	2.15	0.47
1:CA:779:C:H2'	1:CA:780:A:O4'	2.15	0.47
1:CA:949:A:N7	13:CM:106:ASN:ND2	2.63	0.47
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.47	0.47
1:CA:1255:G:HO2'	1:CA:1258:G:HO2'	1.62	0.47
3:CC:70:VAL:N	3:CC:106:VAL:HG23	2.30	0.47
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.55	0.47
8:CH:39:LEU:HB3	8:CH:45:ILE:HG12	1.95	0.47
8:CH:51:VAL:HG12	8:CH:52:ASP:H	1.80	0.47
13:CM:91:ARG:O	13:CM:96:LEU:N	2.44	0.47
24:CX:13:C:O2'	25:DA:1924:C:H4'	2.15	0.47
25:DA:359:A:H2'	25:DA:360:G:O4'	2.14	0.47
25:DA:632:A:H2'	25:DA:633:A:C8	2.49	0.47
25:DA:673:C:H5"	29:DF:81:PRO:HD2	1.96	0.47
25:DA:747:U:O2	25:DA:2014:A:H1'	2.14	0.47
25:DA:1114:G:H2'	25:DA:1115:G:C8	2.49	0.47
25:DA:1127:A:H2'	25:DA:2518:A:H2	1.80	0.47
25:DA:1761:C:H3'	25:DA:1762:A:H5"	1.97	0.47
25:DA:2572:A:C8	28:DE:144:ARG:HD2	2.50	0.47
26:DB:28:C:H2'	26:DB:29:A:C8	2.50	0.47
28:DE:174:ASP:OD1	28:DE:175:VAL:N	2.48	0.47
35:DP:15:ARG:HD3	35:DP:15:ARG:N	2.30	0.47
35:DP:39:LYS:HB2	35:DP:45:LEU:HG	1.96	0.47
36:DQ:18:LYS:HE3	36:DQ:18:LYS:HB2	1.72	0.47
1:AA:69:G:H2'	1:AA:70:G:C8	2.50	0.47
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.50	0.47
23:AY:36:A:H2'	23:AY:37:MIA:O4'	2.14	0.47
25:BA:793:A:H2'	25:BA:2624:C:H5"	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1654:A:H1'	25:BA:1656:A:OP2	2.15	0.47
25:BA:1873:G:O2'	27:BD:253:GLN:NE2	2.47	0.47
25:BA:2388:A:H2'	25:BA:2389:A:O4'	2.15	0.47
29:BF:125:LEU:HD12	29:BF:194:MET:HB2	1.97	0.47
33:BN:4:TYR:CD2	40:BU:100:VAL:HG11	2.50	0.47
43:BX:32:PRO:HA	43:BX:77:LYS:HB2	1.96	0.47
43:BX:92:LEU:C	43:BX:94:GLY:H	2.23	0.47
44:BY:19:LYS:HE2	44:BY:20:TYR:CE1	2.50	0.47
55:B9:2:LYS:HE2	55:B9:31:LYS:O	2.15	0.47
1:CA:396:G:O2'	1:CA:398:C:OP1	2.17	0.47
1:CA:994:A:N7	1:CA:1216:G:H4'	2.30	0.47
1:CA:1028:C:C2	1:CA:1033:G:N1	2.82	0.47
1:CA:1109:C:H2'	1:CA:1110:A:O4'	2.15	0.47
1:CA:1239:A:H4'	1:CA:1240:U:H5"	1.97	0.47
1:CA:1262:C:H2'	1:CA:1263:C:C6	2.50	0.47
2:CB:16:HIS:CB	2:CB:204:ASN:HB3	2.31	0.47
3:CC:173:VAL:O	3:CC:175:LEU:HD12	2.15	0.47
10:CJ:32:ALA:CB	10:CJ:33:GLN:HA	2.38	0.47
23:CW:11:C:H2'	23:CW:12:U:H6	1.80	0.47
25:DA:570:G:H2'	25:DA:2030:A:N7	2.30	0.47
25:DA:873:G:H1'	36:DQ:29:PHE:HE2	1.79	0.47
25:DA:919:G:C6	25:DA:2268:A:C6	3.03	0.47
25:DA:921:G:H2'	25:DA:922:U:C6	2.49	0.47
25:DA:942:G:OP1	35:DP:39:LYS:NZ	2.48	0.47
25:DA:2206:G:H8	25:DA:2207:G:N7	2.11	0.47
31:DH:3:ARG:NH1	31:DH:5:GLY:H	2.13	0.47
54:D8:63:PRO:HG2	54:D8:64:TYR:CE2	2.50	0.47
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	1.97	0.47
4:AD:196:LEU:C	4:AD:198:VAL:H	2.22	0.47
8:AH:121:ASP:HB2	8:AH:125:ARG:NH2	2.30	0.47
16:AP:19:ILE:N	16:AP:37:GLY:O	2.48	0.47
57:AX:3013:NEG:H92	25:BA:2335:G:N7	2.30	0.47
25:BA:834:U:H5"	25:BA:835:A:H5'	1.97	0.47
25:BA:1727:U:O2'	25:BA:1794:G:N7	2.35	0.47
25:BA:1733:C:H2'	25:BA:1734:G:O4'	2.15	0.47
25:BA:2585:C:H3'	61:BA:5300:HOH:O	2.13	0.47
25:BA:2795:G:OP2	61:BA:4927:HOH:O	2.20	0.47
35:BP:95:VAL:HG13	35:BP:125:VAL:HG12	1.97	0.47
36:BQ:7:MET:HB2	36:BQ:7:MET:HE3	1.63	0.47
47:B1:72:GLU:O	47:B1:76:ARG:HG3	2.15	0.47
52:B6:4:GLU:HG3	52:B6:5:VAL:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B6:9:LEU:HA	52:B6:54:ILE:HB	1.96	0.47
1:CA:69:G:H2'	1:CA:70:G:H8	1.79	0.47
1:CA:391:G:C6	1:CA:392:G:C5	3.03	0.47
1:CA:1142:G:H2'	1:CA:1143:G:O4'	2.14	0.47
1:CA:1298:C:H4'	1:CA:1299:A:H5'	1.96	0.47
5:CE:71:LEU:HG	5:CE:114:GLY:O	2.14	0.47
16:CP:72:ARG:NH2	16:CP:73:LEU:HD21	2.29	0.47
23:CW:8:4SU:H1'	23:CW:48:C:H1'	1.97	0.47
57:CX:3004:NEG:N1	25:DA:2330:G:O6	2.47	0.47
25:DA:192:C:O2'	25:DA:802:A:N3	2.47	0.47
25:DA:752:A:P	53:D7:3:ARG:HH22	2.38	0.47
25:DA:828:U:H4'	25:DA:831:G:N1	2.29	0.47
25:DA:932:G:H4'	25:DA:933:A:O5'	2.14	0.47
25:DA:953:A:C2	25:DA:954:G:C8	3.03	0.47
25:DA:1126:A:H8	25:DA:1126:A:OP1	1.97	0.47
25:DA:1266:G:O2'	25:DA:2012:G:O6	2.23	0.47
25:DA:1486:A:H2'	25:DA:1487:G:H8	1.80	0.47
25:DA:1922:G:H2'	25:DA:1923:U:O4'	2.15	0.47
25:DA:2124:G:C6	25:DA:2174:C:N4	2.81	0.47
25:DA:2811:G:N2	25:DA:2891:G:H1'	2.29	0.47
26:DB:40:U:H2'	50:D4:2:LYS:HE3	1.97	0.47
29:DF:113:ALA:HB2	29:DF:183:VAL:HB	1.97	0.47
32:DI:66:GLU:OE2	32:DI:69:LYS:HD3	2.15	0.47
1:AA:44:G:C2	1:AA:45:U:H1'	2.50	0.47
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.44	0.47
25:BA:886:U:H1'	25:BA:1236:G:H1'	1.96	0.47
25:BA:1400:A:H2'	25:BA:1401:G:O4'	2.15	0.47
25:BA:1714:G:O2'	25:BA:2013:U:O4	2.27	0.47
25:BA:2055:A:OP1	61:BA:4435:HOH:O	2.20	0.47
31:BH:154:PRO:HB3	31:BH:163:TYR:CZ	2.50	0.47
33:BN:95:PRO:HG2	33:BN:124:ALA:HB2	1.97	0.47
42:BW:18:ARG:NH1	42:BW:76:VAL:O	2.48	0.47
45:BZ:107:THR:HA	45:BZ:108:PRO:HD3	1.55	0.47
45:BZ:121:HIS:HB3	45:BZ:123:ASP:O	2.14	0.47
1:CA:501:C:H2'	1:CA:502:G:C8	2.50	0.47
1:CA:657:G:H21	15:CO:22:THR:HG1	1.62	0.47
1:CA:926:G:H5"	1:CA:927:G:O5'	2.15	0.47
7:CG:78:ARG:CZ	7:CG:79:ARG:HH12	2.28	0.47
10:CJ:44:VAL:HG13	10:CJ:66:ARG:HG2	1.97	0.47
23:CY:23:A:O5'	23:CY:23:A:H8	1.98	0.47
25:DA:10:G:O2'	25:DA:2801(A):A:N6	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:26:G:H1'	25:DA:514:A:N6	2.30	0.47
25:DA:459:U:H5"	53:D7:40:TRP:CD2	2.50	0.47
27:DD:34:VAL:HG12	27:DD:63:ARG:HG3	1.96	0.47
28:DE:14:ILE:HG13	28:DE:21:VAL:HG13	1.96	0.47
39:DT:94:ALA:HB1	39:DT:99:LEU:HD21	1.97	0.47
1:AA:148:G:H2'	1:AA:149:A:H8	1.81	0.46
1:AA:309:G:O2'	1:AA:607:A:N1	2.47	0.46
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.50	0.46
10:AJ:5:ARG:NE	10:AJ:73:ASP:OD1	2.25	0.46
25:BA:231:G:C8	54:B8:5:LYS:HG2	2.50	0.46
25:BA:1462:G:O2'	25:BA:1463:C:OP2	2.28	0.46
25:BA:2170:G:H5'	25:BA:2170:G:C8	2.51	0.46
25:BA:2190:G:O6	25:BA:2193:A:H2'	2.16	0.46
37:BR:67:LEU:CD1	37:BR:76:VAL:HG21	2.45	0.46
41:BV:14:VAL:HB	41:BV:96:ILE:HG13	1.97	0.46
44:BY:5:MET:HE2	44:BY:5:MET:HB2	1.66	0.46
44:BY:13:VAL:HB	44:BY:72:VAL:HG13	1.96	0.46
45:BZ:45:ASP:O	45:BZ:49:ARG:HG3	2.14	0.46
54:B8:23:VAL:HG13	54:B8:47:LYS:HB3	1.95	0.46
1:CA:997:U:H3	1:CA:1044:A:N6	2.13	0.46
4:CD:13:ARG:HB3	4:CD:38:TYR:O	2.15	0.46
13:CM:34:LEU:HD13	13:CM:41:PRO:HA	1.97	0.46
20:CT:60:GLU:HG3	20:CT:81:LYS:HD2	1.97	0.46
25:DA:363(C):G:H2'	25:DA:363(D):G:H8	1.80	0.46
25:DA:888:C:H5"	25:DA:889:C:OP2	2.14	0.46
25:DA:949:C:H2'	25:DA:950:G:C8	2.50	0.46
25:DA:1032:A:H2	25:DA:1122:G:H22	1.62	0.46
25:DA:2252:G:H2'	25:DA:2253:G:H8	1.80	0.46
25:DA:2291:U:OP1	25:DA:2380:C:O2'	2.29	0.46
26:DB:3:C:H2'	26:DB:4:C:H6	1.78	0.46
26:DB:87:G:N2	26:DB:90:A:OP2	2.47	0.46
30:DG:15:VAL:HG22	30:DG:175:LEU:HB3	1.97	0.46
55:D9:15:LYS:HE2	55:D9:17:ILE:HD13	1.97	0.46
1:AA:376:G:O3'	16:AP:5:ARG:HD2	2.15	0.46
1:AA:1026:G:O2'	1:AA:1027:C:OP1	2.27	0.46
4:AD:12:CYS:SG	4:AD:19:LEU:HB2	2.55	0.46
16:AP:60:LEU:HD12	16:AP:60:LEU:HA	1.80	0.46
19:AS:9:VAL:HG21	50:B4:61:ARG:NH1	2.27	0.46
23:AY:21:A:O2'	23:AY:22:G:OP1	2.26	0.46
23:AY:56:C:H2'	23:AY:57:G:O4'	2.14	0.46
25:BA:1067:A:H8	25:BA:1067:A:H3'	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1068:G:N7	33:BN:66:LYS:HE2	2.30	0.46
25:BA:1079:U:OP1	55:B9:9:ARG:NH2	2.48	0.46
25:BA:1834:A:H4'	27:BD:259:THR:HG23	1.97	0.46
25:BA:2018:C:H4'	25:BA:2019:G:OP1	2.15	0.46
25:BA:2859:U:H4'	25:BA:2878:A:C2	2.50	0.46
29:BF:172:TRP:H	29:BF:172:TRP:CD1	2.32	0.46
39:BT:118:ARG:HH22	39:BT:125:ARG:HH12	1.64	0.46
42:BW:79:GLY:HA3	42:BW:100:THR:HG22	1.96	0.46
1:CA:1014:A:C2	1:CA:1219:U:H1'	2.49	0.46
1:CA:1103:C:H5"	2:CB:98:LEU:HD13	1.97	0.46
3:CC:47:LEU:O	3:CC:51:GLY:N	2.47	0.46
10:CJ:49:VAL:HG23	14:CN:41:ARG:HD2	1.97	0.46
25:DA:338:G:O6	61:DA:4110:HOH:O	2.19	0.46
25:DA:608:A:OP1	29:DF:100:THR:OG1	2.27	0.46
25:DA:1226:A:OP1	41:DV:84:LYS:HE2	2.15	0.46
25:DA:1484:G:H1	25:DA:1505:C:H42	1.63	0.46
25:DA:1826:G:H4'	27:DD:242:ARG:CZ	2.46	0.46
25:DA:2243:U:H2'	25:DA:2244:U:C6	2.50	0.46
25:DA:2424:C:O2	25:DA:2429:G:O2'	2.26	0.46
45:DZ:158:PRO:HA	45:DZ:159:PRO:HD3	1.78	0.46
1:AA:456:C:H2'	1:AA:457:C:H6	1.81	0.46
1:AA:1262:C:H2'	1:AA:1263:C:C6	2.50	0.46
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.15	0.46
25:BA:160:G:O2'	25:BA:161:C:H5'	2.15	0.46
25:BA:2148:A:N7	25:BA:2185:C:H1'	2.29	0.46
25:BA:2371:C:H2'	25:BA:2372:A:O4'	2.14	0.46
26:BB:75:G:H5"	26:BB:75:G:H8	1.79	0.46
26:BB:102:A:N7	61:BB:3117:HOH:O	2.35	0.46
32:BI:12:LEU:HA	32:BI:12:LEU:HD23	1.78	0.46
42:BW:46:PHE:O	42:BW:50:VAL:HG23	2.16	0.46
1:CA:449:C:H5"	1:CA:450:G:OP2	2.15	0.46
1:CA:768:A:OP2	61:CA:4023:HOH:O	2.21	0.46
1:CA:1025:U:H3	1:CA:1036:G:H1	1.63	0.46
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.30	0.46
2:CB:92:TYR:CE2	2:CB:94:ASN:HB2	2.50	0.46
24:CX:76:A:H3'	25:DA:2585:U:C5	2.49	0.46
25:DA:1576:U:H2'	25:DA:1577:C:H6	1.79	0.46
25:DA:2060:A:N3	61:DA:4401:HOH:O	2.36	0.46
25:DA:2738:A:OP2	61:DA:4493:HOH:O	2.19	0.46
26:DB:24:G:N7	26:DB:56:G:H2'	2.30	0.46
1:AA:1019:C:H2'	1:AA:1020:U:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1030:C:N3	1:AA:1031:G:C2	2.84	0.46
1:AA:1063:C:OP2	1:AA:1064:G:O2'	2.24	0.46
1:AA:1367:C:H4'	10:AJ:48:THR:HG21	1.98	0.46
2:AB:169:LYS:O	2:AB:169:LYS:HD3	2.15	0.46
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.44	0.46
15:AO:39:LEU:HB3	15:AO:56:LEU:HD13	1.96	0.46
25:BA:1405:A:H2	25:BA:1418:U:O4	1.98	0.46
25:BA:1974:A:OP1	34:BO:42:SER:OG	2.26	0.46
26:BB:31:C:H4'	30:BG:29:TRP:CZ2	2.51	0.46
29:BF:116:ASP:OD2	35:BP:1:MET:HB3	2.16	0.46
31:BH:56:SER:HB3	31:BH:61:HIS:ND1	2.31	0.46
36:BQ:52:VAL:O	36:BQ:55:VAL:HG12	2.16	0.46
50:B4:69:LYS:HB2	50:B4:69:LYS:HZ2	1.80	0.46
1:CA:375:U:C4	1:CA:376:G:N7	2.83	0.46
1:CA:716:A:N3	11:CK:118:GLY:HA2	2.29	0.46
1:CA:826:C:H2'	1:CA:827:U:C6	2.51	0.46
1:CA:892:A:H2'	1:CA:893:C:C6	2.51	0.46
1:CA:933:G:OP2	7:CG:3:ARG:HB2	2.14	0.46
1:CA:1103:C:P	2:CB:96:ARG:HH22	2.38	0.46
4:CD:71:SER:OG	4:CD:74:GLN:HB2	2.15	0.46
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.97	0.46
9:CI:89:ASN:C	9:CI:89:ASN:HD22	2.23	0.46
23:CW:31:A:H2'	23:CW:32:PSU:O4'	2.15	0.46
25:DA:271(Q):G:H2'	25:DA:271(R):G:H8	1.80	0.46
25:DA:385:C:O2	35:DP:71:VAL:HG21	2.16	0.46
25:DA:468:G:H5"	29:DF:60:SER:HB2	1.96	0.46
25:DA:1130:U:O2	25:DA:2025:C:H5"	2.15	0.46
25:DA:1278:A:H2'	25:DA:1279:G:C8	2.51	0.46
25:DA:1889:A:H2'	25:DA:1890:A:C8	2.50	0.46
25:DA:2104:G:H1	25:DA:2185:C:H42	1.63	0.46
25:DA:2173:A:H2'	25:DA:2174:C:O4'	2.15	0.46
25:DA:2371:G:N3	52:D6:46:HIS:HE1	2.14	0.46
25:DA:2466:C:OP1	55:D9:4:ARG:HB2	2.16	0.46
25:DA:2740:A:N6	25:DA:2763:G:O2'	2.48	0.46
27:DD:152:GLY:O	27:DD:154:LYS:HG2	2.15	0.46
29:DF:102:PRO:HB2	29:DF:105:VAL:HG23	1.97	0.46
30:DG:44:GLY:O	30:DG:47:LYS:HB2	2.16	0.46
30:DG:63:ILE:HA	30:DG:143:GLU:HG3	1.96	0.46
1:AA:189(D):C:O2	1:AA:189(H):G:C6	2.68	0.46
1:AA:501:C:H2'	1:AA:502:G:H8	1.81	0.46
1:AA:927:G:OP2	1:AA:927:G:H4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.31	0.46
15:AO:62:GLN:HE21	15:AO:66:LEU:HD13	1.81	0.46
17:AQ:15:MET:HE1	17:AQ:43:LEU:HD22	1.96	0.46
25:BA:287:G:N7	25:BA:448:U:H2'	2.30	0.46
25:BA:627:G:OP2	35:BP:90:ARG:NH1	2.48	0.46
25:BA:2357:G:N3	25:BA:2393:C:H2'	2.30	0.46
25:BA:2639:G:N2	25:BA:2790:G:OP2	2.48	0.46
36:BQ:16:ARG:HG2	36:BQ:18:LYS:HE2	1.97	0.46
54:B8:52:LYS:N	54:B8:53:PRO:HD2	2.31	0.46
1:CA:69:G:H2'	1:CA:70:G:C8	2.51	0.46
1:CA:232:G:H1'	1:CA:262:A:N1	2.30	0.46
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.97	0.46
1:CA:1027:C:OP1	1:CA:1027:C:H4'	2.15	0.46
4:CD:3:ARG:HD3	4:CD:118:ARG:CD	2.45	0.46
18:CR:24:ALA:O	18:CR:26:LEU:N	2.41	0.46
19:CS:24:ALA:O	19:CS:26:GLY:N	2.49	0.46
24:CX:23:C:H2'	24:CX:24:U:H6	1.79	0.46
25:DA:42:G:H2'	25:DA:43:A:O4'	2.16	0.46
25:DA:597:U:H2'	25:DA:598:G:H8	1.80	0.46
25:DA:920:G:H2'	25:DA:921:G:H8	1.81	0.46
25:DA:994:C:OP2	40:DU:54:LYS:NZ	2.42	0.46
25:DA:1628:G:H2'	25:DA:1629:U:C6	2.50	0.46
25:DA:1916:A:H2'	25:DA:1917:U:O4'	2.16	0.46
29:DF:202:PHE:O	29:DF:206:ILE:HG12	2.15	0.46
40:DU:17:ILE:HG13	40:DU:32:PHE:HE1	1.80	0.46
1:AA:228:A:H2'	1:AA:229:U:O4'	2.16	0.46
1:AA:377:G:OP1	16:AP:3:LYS:HD2	2.15	0.46
1:AA:859:A:H2'	1:AA:860:A:O4'	2.15	0.46
1:AA:1223:C:P	19:AS:78:ARG:HH21	2.39	0.46
5:AE:90:VAL:O	5:AE:120:THR:HA	2.15	0.46
8:AH:82:HIS:NE2	8:AH:136:GLU:OE2	2.47	0.46
25:BA:12:U:H2'	25:BA:12:U:O2	2.14	0.46
25:BA:210:A:N1	25:BA:254:A:O2'	2.41	0.46
25:BA:1831:C:OP1	27:BD:260:ARG:NH2	2.48	0.46
27:BD:145:VAL:HG11	27:BD:175:LEU:HD11	1.98	0.46
31:BH:11:VAL:HG13	31:BH:15:VAL:HG22	1.96	0.46
32:BI:77:LEU:HB2	32:BI:142:VAL:HG12	1.98	0.46
35:BP:99:LEU:HD22	35:BP:102:ARG:HH22	1.80	0.46
42:BW:68:ARG:HH11	42:BW:112:GLY:H	1.64	0.46
44:BY:6:HIS:H	44:BY:6:HIS:CD2	2.33	0.46
46:B0:18:ALA:HB3	46:B0:20:ARG:NH2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:784:C:H4'	25:DA:1837:C:OP1	2.16	0.46
1:CA:833:U:H2'	1:CA:834:C:C6	2.51	0.46
2:CB:16:HIS:HA	2:CB:204:ASN:HD22	1.80	0.46
5:CE:41:VAL:HG23	5:CE:67:VAL:HG13	1.97	0.46
7:CG:71:PRO:HG3	7:CG:103:TRP:CH2	2.51	0.46
7:CG:149:ARG:HD2	11:CK:59:TYR:CE1	2.50	0.46
15:CO:69:TYR:CZ	15:CO:73:GLU:HG3	2.51	0.46
25:DA:729:G:O2'	25:DA:763:G:H4'	2.14	0.46
25:DA:853:G:H2'	25:DA:854:G:C8	2.51	0.46
25:DA:1127:A:H2'	25:DA:2518:A:C2	2.49	0.46
25:DA:1131:G:C2	25:DA:1132:A:C4	3.03	0.46
25:DA:1198:U:H2'	25:DA:1199:U:C6	2.50	0.46
25:DA:1467:C:C5	25:DA:1546:C:H2'	2.51	0.46
25:DA:2154:G:C2	25:DA:2155:G:C8	3.03	0.46
25:DA:2277:G:OP2	46:D0:10:THR:HG21	2.16	0.46
29:DF:155:LEU:HD11	29:DF:176:LEU:HD12	1.97	0.46
45:DZ:40:ASP:OD2	45:DZ:42:VAL:HG13	2.15	0.46
45:DZ:48:PHE:HE1	45:DZ:71:VAL:HG11	1.81	0.46
50:D4:64:GLY:C	50:D4:66:SER:H	2.23	0.46
1:AA:155:C:N3	1:AA:167:G:N1	2.63	0.46
1:AA:632:A:H3'	1:AA:633:G:C8	2.50	0.46
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.16	0.46
1:AA:1031:G:H2'	1:AA:1032:G:C8	2.51	0.46
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.51	0.46
2:AB:111:ARG:HH21	2:AB:114:ARG:HD2	1.80	0.46
3:AC:5:ILE:HG12	3:AC:6:HIS:H	1.80	0.46
25:BA:7:G:H2'	25:BA:8:A:O4'	2.15	0.46
25:BA:895:G:N9	25:BA:978:A:H8	2.14	0.46
25:BA:1035:G:H4'	25:BA:1036:A:OP1	2.16	0.46
25:BA:2556:G:H1'	25:BA:2658:C:H4'	1.96	0.46
34:BO:2:ILE:HG13	34:BO:8:LEU:HD11	1.97	0.46
34:BO:34:THR:OG1	34:BO:35:VAL:N	2.48	0.46
44:BY:35:TYR:CE2	44:BY:69:ALA:HB3	2.51	0.46
1:CA:767:A:H2'	1:CA:768:A:O4'	2.16	0.46
3:CC:131:ARG:NH1	5:CE:50:GLU:HG3	2.30	0.46
4:CD:150:GLU:HA	4:CD:153:ARG:HE	1.80	0.46
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	1.97	0.46
12:CL:53:ARG:NH1	12:CL:92:ASP:OD2	2.36	0.46
15:CO:29:VAL:HG13	15:CO:63:ARG:HG3	1.97	0.46
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.98	0.46
18:CR:61:LYS:O	18:CR:65:ILE:HG12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:51:U:H2'	23:CW:52:G:C8	2.51	0.46
23:CY:23:A:C6	23:CY:24:G:C6	3.04	0.46
25:DA:483:A:O2'	44:DY:49:VAL:O	2.30	0.46
25:DA:528:A:OP2	33:DN:114:ARG:NH1	2.48	0.46
25:DA:599:G:H5'	35:DP:9:ASN:ND2	2.31	0.46
25:DA:606:U:H4'	25:DA:658:C:H4'	1.96	0.46
25:DA:1027:A:C6	25:DA:1126:A:C4	3.04	0.46
25:DA:2249:U:N3	25:DA:2253:G:OP2	2.45	0.46
27:DD:5:LYS:HE3	27:DD:5:LYS:HB3	1.58	0.46
1:AA:749:C:H2'	1:AA:750:G:H8	1.81	0.46
1:AA:1027:C:O2	1:AA:1034:G:C2	2.69	0.46
2:AB:24:TRP:CZ3	2:AB:26:PRO:HA	2.50	0.46
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.98	0.46
12:AL:28:LYS:HE2	12:AL:64:TYR:HE1	1.81	0.46
23:AY:71:G:H2'	23:AY:72:C:C6	2.51	0.46
25:BA:601:A:OP1	25:BA:1301:U:O2'	2.29	0.46
25:BA:1357:G:O6	53:B7:9:ARG:NH2	2.49	0.46
25:BA:1548:C:H2'	25:BA:1549:U:C6	2.51	0.46
25:BA:2021:C:H5"	25:BA:2736:C:O2'	2.16	0.46
25:BA:2160:C:H2'	25:BA:2161:C:C6	2.51	0.46
25:BA:2166:U:O2'	25:BA:2167:C:H2'	2.16	0.46
25:BA:2541:G:H5"	25:BA:2542:A:H5"	1.96	0.46
25:BA:2753:A:C6	25:BA:2777:A:C8	3.04	0.46
34:BO:19:ILE:HB	34:BO:41:ALA:HB1	1.98	0.46
45:BZ:111:VAL:O	45:BZ:113:ALA:N	2.46	0.46
54:B8:17:THR:OG1	54:B8:21:LYS:HB2	2.16	0.46
1:CA:26:A:O2'	4:CD:209:ARG:NH2	2.43	0.46
1:CA:56:U:H2'	1:CA:57:G:C8	2.51	0.46
1:CA:110:C:H2'	1:CA:111:G:O4'	2.16	0.46
1:CA:346:G:OP1	39:DT:41:ARG:NH2	2.47	0.46
1:CA:977:A:C2	1:CA:1224:G:C5	3.04	0.46
1:CA:1118:C:H1'	1:CA:1179:A:C4	2.51	0.46
1:CA:1314:C:OP1	19:CS:6:LYS:NZ	2.45	0.46
1:CA:1429:C:H2'	1:CA:1430:C:C6	2.51	0.46
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.16	0.46
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.16	0.46
23:CW:51:U:H2'	23:CW:52:G:H8	1.80	0.46
25:DA:31:C:OP1	61:DA:4533:HOH:O	2.20	0.46
25:DA:919:G:N2	25:DA:2269:A:OP2	2.48	0.46
25:DA:1653:G:O3'	37:DR:2:ARG:HB2	2.16	0.46
25:DA:1670:C:O2	28:DE:129:HIS:NE2	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2206:G:C8	25:DA:2207:G:N7	2.84	0.46
31:DH:126:PRO:HB2	31:DH:130:ARG:HD2	1.96	0.46
34:DO:36:GLY:HA2	34:DO:106:LEU:HD23	1.97	0.46
42:DW:33:ARG:NH2	42:DW:52:GLU:OE1	2.42	0.46
44:DY:43:ASN:CG	44:DY:65:ALA:HB3	2.41	0.46
47:D1:56:GLN:NE2	47:D1:87:PRO:HD3	2.31	0.46
1:AA:976:G:OP1	14:AN:32:SER:N	2.48	0.46
1:AA:1227:A:OP2	13:AM:111:LYS:HE3	2.16	0.46
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.40	0.46
25:BA:659:C:H2'	25:BA:660:C:C6	2.51	0.46
25:BA:1500:A:O2'	25:BA:1501:U:H2'	2.16	0.46
25:BA:1813:C:H1'	25:BA:2621:U:H5"	1.97	0.46
28:BE:28:ALA:HB3	28:BE:93:VAL:HG12	1.98	0.46
31:BH:3:ARG:CG	31:BH:6:ARG:HG2	2.46	0.46
32:BI:93:THR:HG22	32:BI:119:PRO:HB3	1.98	0.46
1:CA:220:G:H2'	1:CA:221:C:H5'	1.98	0.46
1:CA:667:G:O2'	15:CO:49:ASP:OD1	2.22	0.46
1:CA:693:G:H2'	1:CA:694:A:C8	2.51	0.46
1:CA:1320:C:OP1	19:CS:70:LYS:HE3	2.16	0.46
3:CC:143:GLU:C	3:CC:145:GLY:H	2.24	0.46
6:CF:30:LEU:HD23	6:CF:75:LEU:HD21	1.98	0.46
9:CI:55:ALA:HA	9:CI:58:HIS:HD2	1.81	0.46
25:DA:573:G:O2'	25:DA:574:C:H3'	2.16	0.46
25:DA:1028:A:N3	25:DA:2486:G:O2'	2.46	0.46
25:DA:1490:A:O2'	25:DA:1491:G:H5'	2.15	0.46
25:DA:1885:A:H2'	25:DA:1886:C:O4'	2.16	0.46
25:DA:2758:A:C2	25:DA:2759:G:H1'	2.51	0.46
1:AA:129(A):G:C6	1:AA:189(E):U:H4'	2.51	0.46
1:AA:865:A:C2	1:AA:918:A:H4'	2.50	0.46
2:AB:16:HIS:C	2:AB:18:GLY:H	2.20	0.46
2:AB:48:MET:HA	2:AB:51:LEU:HB2	1.98	0.46
12:AL:42:THR:HG22	12:AL:54:LYS:HD2	1.98	0.46
13:AM:3:ARG:O	13:AM:57:ARG:NH1	2.49	0.46
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.49	0.46
24:AX:59:A:H2'	24:AX:60:U:H5'	1.98	0.46
25:BA:324:A:P	44:BY:86:ARG:HH22	2.39	0.46
25:BA:629:U:H4'	25:BA:705:C:H4'	1.96	0.46
25:BA:1095:C:H1'	25:BA:1159:U:H4'	1.98	0.46
25:BA:1843:A:O2'	27:BD:45:ASN:N	2.45	0.46
25:BA:2156:A:O2'	25:BA:2157:A:OP1	2.29	0.46
25:BA:2302:G:C2	25:BA:2355:C:O2	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BB:74:U:H2'	26:BB:75:G:O4'	2.16	0.46
27:BD:26:LYS:HB3	27:BD:83:GLU:HG2	1.98	0.46
45:BZ:136:PHE:O	45:BZ:137:ILE:HG13	2.16	0.46
50:B4:62:ARG:HD3	50:B4:62:ARG:HA	1.68	0.46
1:CA:516:U:O2'	1:CA:519:C:N3	2.43	0.46
1:CA:630:G:H2'	1:CA:631:G:H8	1.81	0.46
1:CA:1073:U:O2'	2:CB:104:ASN:OD1	2.25	0.46
9:CI:33:PHE:CE1	9:CI:43:ALA:HB1	2.51	0.46
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.98	0.46
20:CT:56:MET:HG3	20:CT:57:ARG:N	2.31	0.46
20:CT:90:GLN:HE21	20:CT:90:GLN:HB2	1.48	0.46
25:DA:218:A:C2	25:DA:235:U:H4'	2.51	0.46
25:DA:271(Q):G:H2'	25:DA:271(R):G:C8	2.51	0.46
25:DA:275:G:H2'	25:DA:276:A:O4'	2.16	0.46
25:DA:674:G:O2'	29:DF:74:ARG:HD3	2.16	0.46
25:DA:864:G:C6	25:DA:865:C:N4	2.84	0.46
25:DA:1545:A:H2'	25:DA:1546:C:O4'	2.15	0.46
25:DA:2019:A:C4'	40:DU:34:LYS:HD2	2.46	0.46
25:DA:2674:G:H2'	25:DA:2675:A:C8	2.51	0.46
31:DH:56:SER:HB3	31:DH:61:HIS:ND1	2.31	0.46
1:AA:45:U:H2'	1:AA:46:G:C8	2.51	0.45
1:AA:1031:G:H2'	1:AA:1032:G:H8	1.81	0.45
8:AH:33:GLU:HG2	8:AH:48:TYR:CE2	2.52	0.45
19:AS:32:LYS:HA	19:AS:50:ALA:HB3	1.96	0.45
19:AS:64:GLU:HB3	50:B4:59:PHE:HE2	1.80	0.45
20:AT:30:LYS:HD2	20:AT:71:THR:HG23	1.98	0.45
24:AX:23:C:H2'	24:AX:24:U:C6	2.51	0.45
25:BA:943:C:C4	25:BA:944:C:N4	2.85	0.45
25:BA:1154:U:O2'	25:BA:1155:C:O4'	2.34	0.45
25:BA:1594:C:H2'	25:BA:1595:C:C6	2.51	0.45
25:BA:1841:A:H2'	25:BA:1842:G:O4'	2.16	0.45
25:BA:2151:C:N3	25:BA:2181:G:O6	2.49	0.45
25:BA:2156:A:OP2	25:BA:2178:G:N1	2.48	0.45
25:BA:2162:C:H1'	25:BA:2174:G:N2	2.31	0.45
25:BA:2705:A:H2'	25:BA:2706:G:C8	2.50	0.45
25:BA:2724:U:OP1	25:BA:2727:G:H4'	2.15	0.45
25:BA:2742:G:H2'	25:BA:2743:C:O4'	2.16	0.45
30:BG:72:ARG:NH1	30:BG:87:PRO:HG3	2.32	0.45
32:BI:10:GLU:H	32:BI:10:GLU:HG3	1.56	0.45
32:BI:129:THR:HG22	32:BI:139:GLN:NE2	2.31	0.45
33:BN:21:LYS:NZ	33:BN:140:VAL:OXT	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:892:A:O2'	1:CA:1415:G:H4'	2.16	0.45
1:CA:1071:C:H2'	1:CA:1072:G:H8	1.81	0.45
2:CB:53:ARG:O	2:CB:56:ARG:HB3	2.15	0.45
2:CB:100:GLY:N	2:CB:176:GLU:OE2	2.38	0.45
2:CB:189:ASP:OD1	2:CB:189:ASP:N	2.45	0.45
9:CI:26:VAL:HG22	9:CI:61:ALA:HB3	1.97	0.45
13:CM:20:THR:HA	13:CM:25:ILE:HG22	1.98	0.45
13:CM:64:TRP:HB2	13:CM:66:LEU:HD21	1.98	0.45
18:CR:53:ARG:HA	18:CR:56:THR:OG1	2.16	0.45
25:DA:7:G:H2'	25:DA:8:A:H8	1.81	0.45
25:DA:301:G:OP2	44:DY:84:ARG:NH2	2.48	0.45
25:DA:320:A:H4'	25:DA:322:A:N7	2.31	0.45
25:DA:615:G:OP1	29:DF:40:GLN:HG2	2.16	0.45
25:DA:749:C:O2	25:DA:1618:A:H2'	2.16	0.45
25:DA:1005:C:C2	25:DA:1143:A:C5	3.04	0.45
25:DA:1446:C:H42	25:DA:1465:G:H1	1.63	0.45
25:DA:2262:U:H4'	25:DA:2328:A:C2	2.51	0.45
26:DB:8:U:O2'	38:DS:40:ILE:HD13	2.16	0.45
30:DG:41:GLN:HB3	30:DG:43:LEU:HD22	1.97	0.45
30:DG:173:LEU:HD22	30:DG:178:PHE:CE1	2.51	0.45
31:DH:13:LYS:HA	31:DH:14:GLY:HA2	1.69	0.45
35:DP:59:LEU:HD23	54:D8:58:ILE:HD13	1.96	0.45
36:DQ:54:MET:H	36:DQ:54:MET:HG2	1.55	0.45
36:DQ:136:ALA:HB1	45:DZ:52:SER:HB3	1.98	0.45
1:AA:149:A:H2'	1:AA:150:C:C6	2.51	0.45
1:AA:715:A:H2'	1:AA:716:A:C8	2.51	0.45
1:AA:975:A:H4'	1:AA:976:G:C5'	2.38	0.45
1:AA:1007:C:C2	1:AA:1022:G:N1	2.84	0.45
1:AA:1010:G:N2	1:AA:1020:U:H1'	2.31	0.45
1:AA:1151:A:O2'	1:AA:1152:A:H8	1.99	0.45
2:AB:231:GLU:HB3	2:AB:232:PRO:CD	2.44	0.45
4:AD:155:LEU:O	4:AD:159:ARG:HG3	2.15	0.45
9:AI:4:TYR:CE2	9:AI:88:TYR:HA	2.51	0.45
12:AL:32:PHE:O	12:AL:33:ARG:HD2	2.16	0.45
19:AS:24:ALA:O	19:AS:26:GLY:N	2.49	0.45
23:AY:18:G:C2	23:AY:58:A:C5	3.03	0.45
25:BA:1387:U:O2	43:BX:80:ILE:HD12	2.16	0.45
25:BA:1634:C:H2'	25:BA:1635:C:C6	2.52	0.45
25:BA:1749:G:N7	61:BA:5038:HOH:O	2.36	0.45
25:BA:1847:G:O6	27:BD:35:LYS:NZ	2.38	0.45
28:BE:2:LYS:HG3	28:BE:200:GLU:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BS:39:ILE:HB	38:BS:49:VAL:HG13	1.98	0.45
54:B8:23:VAL:CG1	54:B8:47:LYS:HD3	2.46	0.45
1:CA:562:C:H1'	12:CL:15:ARG:HB3	1.98	0.45
1:CA:863:U:H2'	1:CA:865:A:OP2	2.17	0.45
1:CA:964:A:N3	1:CA:969:A:O2'	2.39	0.45
2:CB:166:ASP:OD2	2:CB:169:LYS:HB2	2.16	0.45
25:DA:524:U:H4'	25:DA:555:U:H4'	1.97	0.45
25:DA:536:A:H2'	25:DA:537:C:C6	2.51	0.45
25:DA:839:U:H1'	25:DA:1191:G:H1'	1.97	0.45
25:DA:918:A:H1'	26:DB:80:U:H1'	1.98	0.45
25:DA:1270:C:O2'	25:DA:1325:G:H2'	2.16	0.45
25:DA:1576:U:H2'	25:DA:1577:C:C6	2.50	0.45
25:DA:2702:U:H4'	25:DA:2703:C:OP1	2.15	0.45
36:DQ:57:HIS:CD2	36:DQ:117:ALA:HB2	2.45	0.45
38:DS:25:ARG:HD3	38:DS:42:ASP:OD2	2.15	0.45
41:DV:25:LEU:H	41:DV:92:THR:HG1	1.64	0.45
47:D1:91:LYS:HG2	47:D1:95:LEU:HD22	1.98	0.45
1:AA:197:A:C5	1:AA:221:C:H4'	2.51	0.45
1:AA:292:G:N7	1:AA:293:G:H1'	2.30	0.45
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.51	0.45
57:AA:3220:NEG:H71	25:BA:1967:G:P	2.56	0.45
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.97	0.45
2:AB:207:ALA:O	2:AB:210:SER:HB3	2.17	0.45
3:AC:22:TRP:CE2	14:AN:54:PRO:HG3	2.51	0.45
4:AD:63:LYS:HG3	4:AD:198:VAL:HG22	1.97	0.45
6:AF:19:LEU:HD11	6:AF:59:TYR:CE2	2.52	0.45
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.51	0.45
16:AP:3:LYS:HG3	16:AP:24:ALA:HB2	1.97	0.45
25:BA:125:A:H5"	25:BA:126:C:C6	2.50	0.45
25:BA:215:G:N2	25:BA:217:A:H62	2.13	0.45
25:BA:595:A:OP2	41:BV:78:LYS:NZ	2.50	0.45
25:BA:791:G:OP1	61:BA:4785:HOH:O	2.21	0.45
25:BA:1627:A:H8	25:BA:1627:A:OP2	1.99	0.45
25:BA:1836:U:O2	27:BD:50:THR:HB	2.15	0.45
25:BA:1911:A:O2'	25:BA:2109:G:H5'	2.16	0.45
37:BR:54:LEU:HD12	37:BR:54:LEU:HA	1.84	0.45
46:B0:10:THR:HG22	46:B0:12:ASN:N	2.14	0.45
1:CA:509:A:N3	1:CA:543:C:O2'	2.44	0.45
1:CA:1095:U:H2'	1:CA:1096:C:C6	2.51	0.45
1:CA:1328:C:O2'	13:CM:29:ARG:NH2	2.47	0.45
4:CD:134:ASP:O	4:CD:136:PRO:HD3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CJ:23:ILE:HD13	10:CJ:23:ILE:HA	1.79	0.45
11:CK:65:ALA:HB3	11:CK:97:ALA:HB3	1.97	0.45
19:CS:66:MET:HB2	19:CS:74:PHE:CZ	2.52	0.45
23:CY:69:G:H2'	23:CY:70:G:O4'	2.16	0.45
25:DA:340:A:H2'	25:DA:341:G:O4'	2.17	0.45
25:DA:937:U:H2'	25:DA:938:G:O4'	2.16	0.45
25:DA:940:G:N3	25:DA:1191:G:H4'	2.31	0.45
25:DA:1778:U:H2'	25:DA:1784:A:N6	2.30	0.45
25:DA:1946:U:H2'	25:DA:1947:C:H6	1.80	0.45
25:DA:2342:C:O2'	25:DA:2374:C:OP1	2.29	0.45
25:DA:2554:U:H2'	25:DA:2555:U:C6	2.51	0.45
25:DA:2741:A:H2'	25:DA:2742:C:O4'	2.16	0.45
30:DG:137:GLU:HG2	30:DG:152:LEU:HD22	1.99	0.45
1:AA:814:A:H2'	1:AA:816:A:H5"	1.99	0.45
1:AA:1095:U:P	1:AA:1108:G:H1	2.39	0.45
15:AO:85:LEU:HA	15:AO:85:LEU:HD23	1.84	0.45
25:BA:463:C:H2'	25:BA:464:G:C8	2.51	0.45
25:BA:543:G:H2'	25:BA:544:U:C6	2.51	0.45
25:BA:559:U:H2'	25:BA:560:C:C6	2.51	0.45
25:BA:1685:C:H5"	25:BA:2722:C:O2'	2.15	0.45
25:BA:2856:G:H2'	25:BA:2857:U:O4'	2.16	0.45
25:BA:2867:G:N2	25:BA:2870:A:OP2	2.38	0.45
29:BF:20:LEU:HD22	29:BF:21:ALA:H	1.82	0.45
32:BI:61:ARG:HH11	32:BI:61:ARG:HA	1.82	0.45
38:BS:59:LYS:HB2	38:BS:60:GLY:H	1.52	0.45
40:BU:76:TYR:CE1	40:BU:80:ILE:HG13	2.52	0.45
1:CA:59:A:H5"	1:CA:60:A:H5"	1.98	0.45
1:CA:131:C:H2'	1:CA:132:C:C6	2.52	0.45
1:CA:302:G:N3	1:CA:556:C:H4'	2.31	0.45
1:CA:1055:A:C5	1:CA:1206:G:C2	3.04	0.45
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.51	0.45
2:CB:91:PRO:HG3	2:CB:154:LEU:HD12	1.99	0.45
2:CB:223:ILE:HA	2:CB:226:ARG:HG2	1.99	0.45
3:CC:37:GLN:HA	3:CC:40:ARG:HG3	1.98	0.45
5:CE:73:ASN:OD1	5:CE:73:ASN:N	2.50	0.45
13:CM:25:ILE:HD12	13:CM:66:LEU:HD22	1.98	0.45
17:CQ:56:VAL:HB	17:CQ:78:GLU:HB3	1.99	0.45
18:CR:21:LYS:HD3	18:CR:21:LYS:HA	1.72	0.45
25:DA:7:G:OP1	33:DN:130:HIS:HE1	1.99	0.45
25:DA:748:G:C8	42:DW:89:ALA:HB1	2.51	0.45
25:DA:771:G:OP1	53:D7:10:ARG:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2074:U:H2'	25:DA:2075:U:C6	2.51	0.45
26:DB:106:G:C5'	45:DZ:31:ARG:HG2	2.47	0.45
27:DD:218:ARG:HB3	27:DD:219:PRO:HD2	1.98	0.45
31:DH:113:VAL:HG11	31:DH:151:ILE:HD13	1.99	0.45
33:DN:138:LEU:HD23	33:DN:138:LEU:HA	1.66	0.45
40:DU:89:GLU:HB2	41:DV:50:PRO:HB2	1.97	0.45
43:DX:4:ALA:HB1	43:DX:42:ALA:HA	1.98	0.45
1:AA:179:A:H2'	1:AA:180:U:C6	2.51	0.45
1:AA:666:G:H5'	1:AA:726:C:H1'	1.98	0.45
1:AA:692:U:H1'	1:AA:695:A:N7	2.32	0.45
1:AA:826:C:H4'	8:AH:12:ARG:HG2	1.97	0.45
4:AD:112:VAL:HG23	4:AD:116:GLN:OE1	2.16	0.45
9:AI:99:LEU:HB3	9:AI:101:PHE:CD1	2.52	0.45
57:AW:3004:NEG:N3	25:BA:1964:C:OP1	2.50	0.45
25:BA:1296:G:OP2	35:BP:21:ARG:NH1	2.47	0.45
25:BA:1679:A:OP2	61:BA:4905:HOH:O	2.21	0.45
25:BA:1725:G:H5"	25:BA:1725:G:N3	2.31	0.45
25:BA:1938:A:H2'	25:BA:1939:U:O4'	2.17	0.45
25:BA:2755:C:OP1	55:B9:35:ARG:NH1	2.48	0.45
29:BF:18:ARG:NH2	29:BF:127:GLU:OE1	2.50	0.45
30:BG:69:ALA:HB3	30:BG:91:ARG:HH21	1.82	0.45
35:BP:138:LEU:HD23	35:BP:145:PRO:HG3	1.97	0.45
36:BQ:11:LYS:HE2	36:BQ:88:GLY:O	2.16	0.45
39:BT:15:VAL:HG13	39:BT:79:HIS:CE1	2.51	0.45
49:B3:43:ILE:O	49:B3:47:VAL:HG23	2.16	0.45
50:B4:62:ARG:C	50:B4:64:GLY:HA2	2.42	0.45
1:CA:65:U:H5'	1:CA:65:U:H6	1.81	0.45
1:CA:840:C:H4'	1:CA:841:U:OP1	2.17	0.45
1:CA:952:U:H2'	1:CA:953:G:H8	1.82	0.45
2:CB:98:LEU:HD23	2:CB:98:LEU:H	1.81	0.45
5:CE:93:PRO:HG2	8:CH:105:ARG:NE	2.31	0.45
9:CI:89:ASN:HD22	9:CI:91:ASP:H	1.64	0.45
10:CJ:25:GLU:O	10:CJ:29:ARG:HG2	2.15	0.45
14:CN:24:CYS:HB3	14:CN:29:ARG:H	1.81	0.45
23:CW:9:A:H4'	23:CW:46:7MG:O4'	2.16	0.45
23:CY:18:G:C2	23:CY:55:PSU:O4	2.70	0.45
25:DA:554:U:O2'	25:DA:555:U:H5'	2.15	0.45
25:DA:1024:G:OP1	25:DA:1026:U:H5'	2.16	0.45
25:DA:1184:G:OP1	49:D3:30:ARG:HD2	2.16	0.45
25:DA:2141:G:O4'	25:DA:2151:G:N2	2.50	0.45
25:DA:2283:C:H2'	25:DA:2284:C:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2750:A:H8	25:DA:2750:A:OP1	2.00	0.45
26:DB:94:C:H2'	26:DB:95:C:C6	2.52	0.45
31:DH:7:LEU:HA	31:DH:8:PRO:HD3	1.75	0.45
45:DZ:152:ALA:HB3	45:DZ:169:GLU:HB3	1.97	0.45
1:AA:189(C):C:H2'	1:AA:189(D):C:O4'	2.17	0.45
1:AA:522:C:H41	12:AL:53:ARG:NH2	2.06	0.45
3:AC:79:ARG:O	3:AC:82:GLU:HB2	2.17	0.45
15:AO:3:ILE:O	15:AO:3:ILE:HG12	2.16	0.45
18:AR:59:SER:OG	18:AR:62:GLU:HG2	2.17	0.45
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.41	0.45
20:AT:67:ALA:C	20:AT:69:GLY:H	2.25	0.45
25:BA:1186:U:H4'	25:BA:1188:A:O4'	2.17	0.45
25:BA:1419:A:H2'	25:BA:1420:G:O4'	2.16	0.45
25:BA:1537:G:O2'	27:BD:101:GLU:HB2	2.16	0.45
25:BA:2028:C:O2'	25:BA:2833:A:N3	2.48	0.45
25:BA:2418:U:H2'	25:BA:2418:U:OP2	2.17	0.45
32:BI:66:GLU:HA	32:BI:69:LYS:HB3	1.99	0.45
33:BN:15:LEU:HB2	33:BN:135:PRO:HB2	1.97	0.45
44:BY:92:ASN:HB3	44:BY:94:LYS:N	2.23	0.45
1:CA:19:C:H5"	5:CE:86:ALA:HB3	1.97	0.45
1:CA:149:A:H2'	1:CA:150:C:C6	2.52	0.45
1:CA:1400:C:H4'	22:CV:18:G:C5	2.52	0.45
2:CB:93:VAL:HG21	2:CB:97:TRP:HE1	1.80	0.45
2:CB:114:ARG:O	2:CB:118:LEU:HG	2.16	0.45
9:CI:37:PHE:HD1	9:CI:40:LEU:HD12	1.81	0.45
11:CK:101:SER:OG	11:CK:103:LEU:HD23	2.17	0.45
12:CL:88:GLY:O	12:CL:99:HIS:HD2	1.98	0.45
25:DA:679:C:H2'	25:DA:680:G:C8	2.51	0.45
25:DA:1509(B):A:H2'	25:DA:1510:G:C8	2.52	0.45
25:DA:2238:G:H2'	25:DA:2238:G:N3	2.32	0.45
26:DB:91:C:OP2	36:DQ:16:ARG:NH1	2.49	0.45
28:DE:33:VAL:HG21	28:DE:36:ARG:HE	1.82	0.45
34:DO:98:VAL:HG13	34:DO:117:LEU:HB3	1.99	0.45
35:DP:97:PRO:HD3	35:DP:126:VAL:O	2.16	0.45
45:DZ:171:ILE:H	45:DZ:171:ILE:HG13	1.68	0.45
1:AA:860:A:H2'	1:AA:861:G:O4'	2.17	0.45
1:AA:881:G:H2'	1:AA:882:C:O4'	2.16	0.45
1:AA:1309:G:OP2	13:AM:99:ARG:NH2	2.50	0.45
2:AB:146:GLN:O	2:AB:150:SER:HB3	2.17	0.45
10:AJ:19:SER:OG	10:AJ:91:PRO:HD2	2.16	0.45
23:AY:76:A:H4'	47:B1:30:VAL:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:613:A:H2'	25:BA:614:C:O4'	2.17	0.45
25:BA:815:G:O2'	25:BA:1425:A:N1	2.41	0.45
25:BA:1218:G:H2'	25:BA:1218:G:OP2	2.17	0.45
25:BA:2174:G:H2'	25:BA:2175:G:O4'	2.17	0.45
25:BA:2443:U:O2'	25:BA:2445:A:N7	2.46	0.45
25:BA:2588:G:H1'	61:BA:5252:HOH:O	2.17	0.45
25:BA:2651:A:H2'	25:BA:2652:G:O4'	2.16	0.45
27:BD:132:PRO:HG2	27:BD:135:PHE:HD2	1.79	0.45
28:BE:121:ASN:ND2	61:BE:409:HOH:O	2.50	0.45
34:BO:8:LEU:HB2	34:BO:19:ILE:HG13	1.99	0.45
35:BP:63:PRO:HD3	54:B8:27:THR:HG22	1.99	0.45
42:BW:19:LEU:HB3	51:B5:25:LEU:HD11	1.99	0.45
44:BY:1:MET:HE3	44:BY:1:MET:HB2	1.81	0.45
1:CA:1149:C:OP1	9:CI:14:VAL:HG11	2.17	0.45
2:CB:50:GLU:HB3	2:CB:200:ILE:O	2.17	0.45
3:CC:47:LEU:HD12	3:CC:68:VAL:HG11	1.99	0.45
6:CF:82:ARG:HD2	6:CF:82:ARG:HA	1.74	0.45
13:CM:11:ARG:C	13:CM:13:LYS:H	2.24	0.45
13:CM:50:GLU:HA	13:CM:53:VAL:HB	1.99	0.45
19:CS:68:GLY:H	50:D4:58:ARG:HH11	1.64	0.45
23:CY:55:PSU:N3	23:CY:58:A:C8	2.85	0.45
25:DA:1022:G:N7	33:DN:66:LYS:HE2	2.32	0.45
25:DA:1614:A:C2	42:DW:93:ALA:HB2	2.52	0.45
25:DA:1854:A:H2'	25:DA:1855:G:O4'	2.17	0.45
25:DA:2296:U:OP2	38:DS:9:ARG:NH2	2.40	0.45
25:DA:2723:C:OP2	28:DE:109:LYS:NZ	2.47	0.45
27:DD:13:ARG:HA	27:DD:13:ARG:HD2	1.83	0.45
27:DD:73:VAL:HG13	27:DD:120:GLY:HA3	1.99	0.45
38:DS:28:VAL:HG11	38:DS:98:VAL:HG13	1.98	0.45
40:DU:81:HIS:O	40:DU:84:LYS:HB3	2.16	0.45
45:DZ:145:GLU:HB3	45:DZ:148:ASP:CG	2.41	0.45
1:AA:449:C:O2	16:AP:42:ARG:HD2	2.17	0.45
1:AA:964:A:N3	1:AA:969:A:O2'	2.48	0.45
3:AC:12:LEU:HD11	14:AN:51:GLY:HA2	1.99	0.45
7:AG:149:ARG:HD2	11:AK:59:TYR:CZ	2.52	0.45
25:BA:323:A:H5"	44:BY:86:ARG:HH21	1.82	0.45
25:BA:463:C:H2'	25:BA:464:G:H8	1.81	0.45
25:BA:768:C:H2'	25:BA:769:A:C8	2.52	0.45
25:BA:895:G:N3	25:BA:978:A:H1'	2.32	0.45
25:BA:1456:G:H2'	25:BA:1457:C:C6	2.51	0.45
25:BA:2013:U:H2'	25:BA:2014:G:H5"	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2081:A:O2'	29:BF:69:HIS:HD2	1.99	0.45
25:BA:2198:A:H2'	25:BA:2199:C:C6	2.52	0.45
25:BA:2902:G:H4'	25:BA:2903:G:O5'	2.17	0.45
27:BD:68:LYS:HD3	27:BD:70:TRP:CH2	2.52	0.45
31:BH:83:TYR:CE2	31:BH:138:LYS:HB2	2.52	0.45
32:BI:130:TYR:N	32:BI:138:ILE:O	2.43	0.45
47:B1:3:LYS:HB2	47:B1:61:ARG:HH12	1.81	0.45
47:B1:34:THR:HG21	47:B1:37:ILE:HG13	1.99	0.45
50:B4:46:GLN:HA	50:B4:48:ARG:HH21	1.82	0.45
1:CA:362:G:N2	1:CA:365:U:OP2	2.49	0.45
1:CA:539:A:H2'	1:CA:540:G:C8	2.51	0.45
1:CA:1259:C:C4	1:CA:1260:C:H1'	2.52	0.45
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.17	0.45
25:DA:222:A:H3'	25:DA:421:U:H5'	1.99	0.45
25:DA:251:A:C4	25:DA:252:G:H1'	2.51	0.45
25:DA:861:A:C2	25:DA:917:A:C4	3.05	0.45
25:DA:1379:A:H4'	25:DA:1380:G:OP2	2.16	0.45
25:DA:2390:U:P	54:D8:35:GLN:HE22	2.40	0.45
41:DV:21:ARG:HG2	41:DV:91:TYR:CD2	2.52	0.45
1:AA:340:U:H2'	1:AA:341:C:C6	2.52	0.45
1:AA:1131:G:P	9:AI:20:ARG:HH22	2.40	0.45
4:AD:163:GLU:O	4:AD:166:LYS:HG2	2.16	0.45
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.32	0.45
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.17	0.45
16:AP:3:LYS:O	16:AP:21:VAL:HA	2.17	0.45
25:BA:85:C:H4'	25:BA:102:U:H1'	1.99	0.45
25:BA:573:G:H2'	25:BA:574:G:O4'	2.17	0.45
25:BA:1177:G:N2	33:BN:73:THR:HG23	2.32	0.45
25:BA:1221:G:N2	25:BA:1223:C:OP1	2.50	0.45
25:BA:2860:A:OP2	25:BA:2876:U:H5	2.00	0.45
50:B4:56:VAL:O	50:B4:57:GLU:O	2.34	0.45
1:CA:309:G:H1'	1:CA:608:A:C2	2.52	0.45
1:CA:850:U:H2'	1:CA:851:G:H5"	1.99	0.45
6:CF:23:LYS:HG2	6:CF:61:LEU:HD21	1.99	0.45
13:CM:78:ILE:HA	13:CM:81:LEU:HD12	1.99	0.45
23:CW:25:C:O2'	23:CW:26:A:H5'	2.16	0.45
25:DA:201:C:O2'	25:DA:251:A:N1	2.48	0.45
25:DA:588:U:O5'	25:DA:588:U:H6	2.00	0.45
25:DA:866:A:N6	25:DA:914:C:C4	2.85	0.45
25:DA:977:G:N3	25:DA:1001:A:H2	2.15	0.45
25:DA:1039:G:C6	25:DA:1040:C:C4	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1181:C:H2'	25:DA:1182:A:H8	1.82	0.45
25:DA:1364:G:P	47:D1:3:LYS:HG3	2.57	0.45
25:DA:2274:A:C5	25:DA:2276:G:C8	3.05	0.45
25:DA:2653:U:H5"	25:DA:2654:A:OP2	2.17	0.45
25:DA:2741:A:N6	25:DA:2763:G:O2'	2.47	0.45
43:DX:46:ALA:HB1	48:D2:33:MET:HE1	1.98	0.45
49:D3:46:ASN:O	49:D3:50:VAL:HG22	2.17	0.45
3:AC:173:VAL:O	3:AC:175:LEU:HD12	2.16	0.45
4:AD:166:LYS:HB2	4:AD:168:ARG:NH2	2.32	0.45
8:AH:11:THR:HG23	8:AH:14:ARG:NH1	2.32	0.45
23:AW:75:C:H2'	23:AW:76:A:C4	2.52	0.45
25:BA:2661:U:H2'	25:BA:2662:U:C6	2.51	0.45
34:BO:16:ALA:HB2	34:BO:52:VAL:HG21	1.98	0.45
39:BT:16:ARG:HH21	39:BT:19:LEU:HD11	1.81	0.45
45:BZ:19:ARG:NH1	45:BZ:84:GLU:O	2.49	0.45
1:CA:192:U:H2'	1:CA:193:C:C6	2.52	0.45
1:CA:299:G:H2'	1:CA:300:A:C8	2.52	0.45
1:CA:586:C:O3'	8:CH:89:PRO:HB3	2.17	0.45
1:CA:1179:A:H2'	1:CA:1180:A:O4'	2.17	0.45
2:CB:7:VAL:HB	2:CB:8:LYS:H	1.62	0.45
2:CB:87:ARG:NH1	2:CB:219:VAL:HG12	2.32	0.45
8:CH:31:PHE:O	8:CH:35:ILE:HG13	2.17	0.45
10:CJ:78:ASN:C	10:CJ:80:LYS:H	2.25	0.45
24:CX:49:G:C2	24:CX:66:C:C2	3.05	0.45
25:DA:27:G:N2	25:DA:512:G:H1'	2.32	0.45
25:DA:127:A:H5"	25:DA:128:C:C6	2.52	0.45
25:DA:636:G:OP1	35:DP:132:LYS:HE2	2.17	0.45
25:DA:1782:C:H1'	25:DA:2609:U:H5"	1.99	0.45
25:DA:2370:G:H2'	25:DA:2371:G:C8	2.51	0.45
30:DG:45:GLU:H	30:DG:45:GLU:HG2	1.39	0.45
30:DG:123:ASN:C	30:DG:125:PHE:H	2.26	0.45
32:DI:114:LEU:HD11	32:DI:128:LEU:HD13	1.98	0.45
40:DU:76:TYR:CZ	40:DU:80:ILE:HG13	2.52	0.45
44:DY:6:HIS:HE1	44:DY:72:VAL:O	2.00	0.45
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.53	0.44
1:AA:1437:C:H2'	1:AA:1438:G:C8	2.52	0.44
4:AD:100:ARG:HB3	4:AD:102:ASP:OD1	2.17	0.44
15:AO:54:ARG:HG2	15:AO:58:MET:HE2	1.99	0.44
25:BA:254:A:H1'	25:BA:255:G:O4'	2.18	0.44
25:BA:1534:G:H2'	25:BA:1535:U:O4'	2.18	0.44
25:BA:1674:G:H2'	25:BA:1675:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BE:170:LEU:HB3	28:BE:184:VAL:HG22	1.97	0.44
33:BN:15:LEU:HD12	33:BN:137:LYS:HG2	1.99	0.44
45:BZ:150:LEU:HB3	45:BZ:171:ILE:HD11	1.99	0.44
1:CA:278:G:OP2	17:CQ:41:LYS:NZ	2.41	0.44
1:CA:390:C:H2'	1:CA:391:G:C8	2.53	0.44
1:CA:742:G:P	15:CO:35:ARG:HH22	2.40	0.44
20:CT:91:LEU:HD23	20:CT:91:LEU:HA	1.82	0.44
24:CX:15:G:H2'	24:CX:59:A:N1	2.32	0.44
24:CX:19:G:H4'	24:CX:20:U:OP2	2.17	0.44
23:CY:25:C:O2'	23:CY:26:A:O4'	2.34	0.44
25:DA:30:G:C6	25:DA:31:C:C4	3.06	0.44
25:DA:392:C:H5"	25:DA:409:C:H5"	2.00	0.44
25:DA:664:C:H2'	25:DA:665:C:C6	2.52	0.44
25:DA:936:C:H2'	25:DA:937:U:C6	2.52	0.44
25:DA:1038:C:N4	25:DA:1117:G:H1	2.14	0.44
25:DA:1378:A:OP1	53:D7:10:ARG:NH2	2.50	0.44
25:DA:2427:C:H5"	25:DA:2428:G:OP1	2.17	0.44
25:DA:2475:C:H42	25:DA:2529:G:H22	1.65	0.44
25:DA:2850:A:C2	25:DA:2851:A:C4	3.05	0.44
28:DE:24:THR:HG22	28:DE:186:GLY:O	2.17	0.44
30:DG:70:VAL:HA	30:DG:90:LEU:HD23	1.98	0.44
31:DH:44:VAL:O	31:DH:50:VAL:HA	2.17	0.44
36:DQ:36:ALA:HB2	36:DQ:103:MET:SD	2.57	0.44
50:D4:56:VAL:HG13	50:D4:57:GLU:H	1.81	0.44
1:AA:600:C:H4'	8:AH:128:GLY:O	2.17	0.44
1:AA:645:C:H2'	1:AA:646:U:C6	2.52	0.44
1:AA:674:G:H2'	1:AA:675:A:C8	2.52	0.44
1:AA:903:G:OP1	61:AA:4042:HOH:O	2.21	0.44
23:AW:24:G:C6	23:AW:25:C:N3	2.85	0.44
25:BA:491:G:OP1	53:B7:12:ARG:NH2	2.50	0.44
25:BA:2555:G:H2'	25:BA:2556:G:O4'	2.17	0.44
25:BA:2707:C:H2'	25:BA:2708:U:H6	1.82	0.44
26:BB:14:U:O3'	26:BB:108:U:O2'	2.35	0.44
27:BD:145:VAL:HB	27:BD:155:LEU:HB2	1.99	0.44
27:BD:232:PRO:HB3	27:BD:244:ARG:CZ	2.48	0.44
28:BE:31:CYS:HA	28:BE:32:PRO:HD2	1.89	0.44
30:BG:11:TYR:HA	30:BG:15:VAL:HB	1.99	0.44
30:BG:14:GLU:O	30:BG:17:PRO:HD2	2.18	0.44
30:BG:38:VAL:HG22	30:BG:93:THR:HG23	1.99	0.44
32:BI:47:LEU:O	32:BI:51:ILE:HG13	2.17	0.44
33:BN:4:TYR:HB2	40:BU:101:ARG:NH1	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BZ:109:ALA:HB3	45:BZ:145:GLU:OE2	2.17	0.44
1:CA:567:G:O6	12:CL:5:PRO:HD3	2.17	0.44
1:CA:598:U:H4'	8:CH:94:TYR:CG	2.53	0.44
1:CA:1256:A:N1	1:CA:1278:U:H1'	2.31	0.44
1:CA:1505:G:H4'	22:CV:13:A:H2	1.82	0.44
3:CC:19:GLU:HB3	3:CC:40:ARG:HH22	1.82	0.44
6:CF:46:ARG:HB2	6:CF:46:ARG:NH1	2.31	0.44
6:CF:82:ARG:HB2	6:CF:85:VAL:HG23	1.98	0.44
10:CJ:47:PHE:HB2	10:CJ:63:PHE:HB2	1.99	0.44
25:DA:620:G:H8	25:DA:622:G:O6	2.00	0.44
25:DA:711:G:H1	25:DA:720:C:H42	1.65	0.44
25:DA:820:A:H1'	25:DA:943:U:H1'	1.99	0.44
25:DA:919:G:C6	25:DA:920:G:C5	3.05	0.44
25:DA:1419:A:C8	25:DA:1421:G:C6	3.06	0.44
25:DA:1651:G:C6	25:DA:1652:A:C5	3.05	0.44
25:DA:2324:C:H5"	25:DA:2325:G:H5'	2.00	0.44
26:DB:2:C:H2'	26:DB:3:C:H6	1.82	0.44
31:DH:23:ARG:NH1	31:DH:34:GLU:OE2	2.50	0.44
35:DP:86:LYS:HB3	35:DP:118:GLY:HA3	1.97	0.44
37:DR:44:LEU:HD22	37:DR:48:VAL:HG23	1.98	0.44
1:AA:219:C:H2'	1:AA:220:G:O4'	2.17	0.44
1:AA:626:U:C2	1:AA:627:G:C8	3.05	0.44
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.48	0.44
1:AA:1392:G:N2	1:AA:1502:A:C8	2.85	0.44
4:AD:50:ARG:HA	4:AD:51:PRO:HD3	1.76	0.44
11:AK:120:ARG:HA	11:AK:121:PRO:HD3	1.83	0.44
19:AS:12:ASP:OD1	19:AS:35:SER:HB3	2.17	0.44
23:AY:18:G:H1	23:AY:55:PSU:H1'	1.82	0.44
25:BA:197:C:H2'	25:BA:198:C:C6	2.53	0.44
25:BA:1447:G:H2'	25:BA:1448:C:O4'	2.18	0.44
25:BA:2130:C:H2'	25:BA:2131:U:H6	1.80	0.44
30:BG:122:PRO:HD3	30:BG:181:ARG:HG2	1.99	0.44
32:BI:62:LYS:HE3	32:BI:62:LYS:HB2	1.78	0.44
41:BV:97:LYS:HA	41:BV:97:LYS:HD2	1.81	0.44
52:B6:9:LEU:HD13	52:B6:51:GLU:HG3	2.00	0.44
14:CN:22:THR:HB	14:CN:33:VAL:HG11	1.99	0.44
23:CY:50:U:O2	23:CY:64:A:N1	2.50	0.44
25:DA:639:U:H2'	25:DA:640:C:H6	1.82	0.44
25:DA:668:G:H5'	25:DA:669:G:OP2	2.17	0.44
25:DA:795:C:H2'	25:DA:796:C:C6	2.52	0.44
25:DA:898:C:C5	25:DA:899:A:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:942:G:H4'	25:DA:1190:G:H5'	2.00	0.44
25:DA:2149:G:H5"	25:DA:2150:U:OP2	2.17	0.44
27:DD:4:LYS:HB3	27:DD:18:VAL:HG23	2.00	0.44
27:DD:67:PHE:CE1	27:DD:106:ILE:HD12	2.47	0.44
29:DF:33:LEU:HD13	29:DF:112:MET:HE2	1.98	0.44
31:DH:3:ARG:HH12	31:DH:5:GLY:HA3	1.82	0.44
38:DS:110:LEU:HD12	38:DS:110:LEU:HA	1.82	0.44
44:DY:14:LEU:HB2	44:DY:75:ILE:HD11	1.99	0.44
46:D0:12:ASN:HA	46:D0:14:ARG:HH21	1.81	0.44
50:D4:46:GLN:HA	50:D4:48:ARG:NH1	2.33	0.44
55:D9:7:VAL:HG12	55:D9:34:GLN:HB3	1.98	0.44
1:AA:1002:G:C6	1:AA:1003:G:C2	3.05	0.44
1:AA:1004:A:N1	1:AA:1037:C:N4	2.65	0.44
1:AA:1008:C:C2	1:AA:1021:G:C6	3.06	0.44
1:AA:1236:A:H4'	1:AA:1304:G:H4'	1.99	0.44
1:AA:1258:G:H2'	1:AA:1259:C:C6	2.52	0.44
1:AA:1298:C:OP2	7:AG:114:ARG:NH2	2.49	0.44
4:AD:152:SER:O	4:AD:155:LEU:HB2	2.17	0.44
6:AF:8:ILE:HD12	6:AF:26:ILE:HD13	1.99	0.44
14:AN:21:TYR:HE2	14:AN:23:ARG:NE	2.15	0.44
25:BA:190:C:O2'	25:BA:240:A:N1	2.46	0.44
25:BA:344:A:H4'	25:BA:346:A:C8	2.52	0.44
25:BA:624:C:OP1	29:BF:108:LYS:HE3	2.18	0.44
25:BA:767:C:H2'	25:BA:768:C:H6	1.83	0.44
25:BA:956:A:N1	25:BA:2289:G:H1'	2.32	0.44
25:BA:1476:C:H2'	25:BA:1477:U:H6	1.81	0.44
25:BA:2331:G:OP1	25:BA:2331:G:H3'	2.17	0.44
26:BB:42:C:OP1	30:BG:67:LYS:NZ	2.48	0.44
35:BP:50:ARG:HH21	54:B8:7:HIS:HD2	1.63	0.44
35:BP:99:LEU:HD22	35:BP:102:ARG:NH2	2.32	0.44
1:CA:265:G:H5'	17:CQ:64:PRO:O	2.17	0.44
1:CA:570:G:H1'	1:CA:820:U:C4	2.52	0.44
1:CA:991:U:HO2'	1:CA:992:U:C5'	2.30	0.44
4:CD:100:ARG:HB3	4:CD:102:ASP:OD1	2.18	0.44
6:CF:13:ASN:ND2	6:CF:55:ASP:OD2	2.51	0.44
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.17	0.44
9:CI:17:VAL:HG11	9:CI:81:ILE:HA	1.99	0.44
13:CM:19:LEU:HB3	13:CM:25:ILE:HG21	1.99	0.44
17:CQ:3:LYS:HB3	17:CQ:61:GLU:HB3	1.99	0.44
23:CY:57:G:N3	23:CY:57:G:H2'	2.32	0.44
25:DA:141:A:C8	25:DA:1408:C:O2'	2.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:686:G:N2	25:DA:788:A:H61	2.16	0.44
25:DA:879:G:C6	25:DA:899:A:H1'	2.53	0.44
25:DA:996:A:C2	25:DA:997:G:C8	3.05	0.44
25:DA:1817:G:OP1	27:DD:88:ARG:NH2	2.43	0.44
25:DA:2363:C:O2	46:D0:39:ARG:NH2	2.42	0.44
31:DH:2:SER:O	31:DH:3:ARG:HG2	2.17	0.44
31:DH:59:ARG:O	31:DH:63:SER:OG	2.35	0.44
42:DW:82:LEU:HD22	42:DW:84:ARG:HH22	1.83	0.44
45:DZ:159:PRO:HA	45:DZ:160:GLY:HA2	1.67	0.44
51:D5:35:GLU:HG3	51:D5:51:TYR:CG	2.53	0.44
1:AA:138:G:H1	1:AA:225:C:N4	2.14	0.44
1:AA:192:U:H2'	1:AA:193:C:H6	1.83	0.44
1:AA:836:G:OP1	18:AR:61:LYS:NZ	2.40	0.44
1:AA:1047:G:H5"	14:AN:4:LYS:HD2	1.99	0.44
1:AA:1272:G:H2'	1:AA:1273:G:O4'	2.18	0.44
57:AA:3216:NEG:H91	23:AW:34:G:H5'	1.99	0.44
2:AB:71:VAL:HA	2:AB:93:VAL:HG23	2.00	0.44
3:AC:47:LEU:HD12	3:AC:68:VAL:HG11	2.00	0.44
6:AF:36:ARG:NH1	6:AF:66:GLU:OE1	2.51	0.44
7:AG:22:LEU:HG	7:AG:62:PHE:HE2	1.82	0.44
25:BA:831:A:C8	25:BA:839:G:C5	3.06	0.44
27:BD:5:LYS:HB3	27:BD:5:LYS:HE3	1.63	0.44
41:BV:65:GLY:HA3	41:BV:91:TYR:CZ	2.53	0.44
6:CF:2:ARG:NE	6:CF:69:GLU:HG2	2.32	0.44
8:CH:29:SER:HB3	8:CH:32:LYS:HG3	1.99	0.44
9:CI:117:HIS:HB2	9:CI:121:ARG:HG3	2.00	0.44
10:CJ:54:PHE:O	10:CJ:56:HIS:N	2.46	0.44
14:CN:3:ARG:O	14:CN:7:ILE:HG23	2.17	0.44
23:CY:24:G:C6	23:CY:25:C:N4	2.85	0.44
25:DA:30:G:C5	25:DA:31:C:C4	3.05	0.44
25:DA:80:G:O2'	25:DA:294:A:N1	2.41	0.44
25:DA:955:C:N4	25:DA:956:G:C6	2.86	0.44
25:DA:1169:G:H1	25:DA:1180:C:N4	2.13	0.44
25:DA:2745:C:H2'	25:DA:2746:U:O4'	2.17	0.44
28:DE:170:LEU:HD12	28:DE:170:LEU:HA	1.81	0.44
30:DG:11:TYR:CZ	30:DG:16:ARG:HG2	2.53	0.44
53:D7:11:LYS:HE3	53:D7:15:THR:OG1	2.18	0.44
1:AA:353:A:H5'	1:AA:353:A:C8	2.44	0.44
1:AA:446:G:N2	1:AA:489:C:N3	2.66	0.44
4:AD:162:LEU:HD23	4:AD:162:LEU:HA	1.74	0.44
7:AG:144:MET:HE2	7:AG:144:MET:HB3	1.77	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AX:19:G:H4'	24:AX:20:U:OP2	2.18	0.44
25:BA:275:C:H2'	25:BA:276:C:C6	2.53	0.44
25:BA:412:C:O2	35:BP:71:VAL:HG21	2.17	0.44
25:BA:771:U:H2'	25:BA:772:G:O4'	2.18	0.44
25:BA:1820:A:H2'	25:BA:1821:C:O4'	2.17	0.44
25:BA:2292:G:O2'	25:BA:2400:A:N1	2.43	0.44
31:BH:126:PRO:HB2	31:BH:127:GLU:H	1.64	0.44
32:BI:4:ILE:HG21	32:BI:47:LEU:HG	2.00	0.44
36:BQ:18:LYS:HE3	36:BQ:18:LYS:HB2	1.71	0.44
45:BZ:146:ILE:HA	45:BZ:147:GLY:HA2	1.79	0.44
1:CA:76:C:H42	1:CA:93:G:H1	1.66	0.44
1:CA:375:U:O3'	16:CP:6:LEU:HB2	2.18	0.44
1:CA:1014:A:N3	1:CA:1219:U:H1'	2.33	0.44
1:CA:1042:G:H2'	1:CA:1043:C:O4'	2.18	0.44
1:CA:1152:A:O2'	1:CA:1153:C:H5'	2.17	0.44
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.18	0.44
57:CA:3177:NEG:H32	25:DA:16:G:N7	2.33	0.44
2:CB:15:VAL:CG1	2:CB:209:ARG:HB3	2.46	0.44
3:CC:17:ASP:N	3:CC:17:ASP:OD1	2.50	0.44
10:CJ:52:GLY:O	14:CN:41:ARG:NH2	2.38	0.44
18:CR:58:LEU:HD23	18:CR:66:LEU:HD22	1.99	0.44
25:DA:307:G:O2'	25:DA:309:G:N7	2.40	0.44
25:DA:1022:G:OP2	33:DN:65:LYS:NZ	2.45	0.44
25:DA:2467:C:H4'	36:DQ:123:HIS:CG	2.53	0.44
25:DA:2468:G:C2	25:DA:2481:G:N3	2.86	0.44
25:DA:2516:G:C6	25:DA:2517:C:C4	3.06	0.44
25:DA:2526:G:H5'	25:DA:2742:C:O2'	2.18	0.44
25:DA:2682:U:O2'	39:DT:58:ASN:ND2	2.50	0.44
25:DA:2699:C:H2'	25:DA:2700:C:O4'	2.18	0.44
25:DA:2769:C:H2'	25:DA:2770:G:O4'	2.18	0.44
32:DI:116:LEU:HD21	32:DI:120:ILE:HG13	2.00	0.44
35:DP:6:LEU:HA	35:DP:6:LEU:HD23	1.79	0.44
36:DQ:31:ASP:HA	36:DQ:134:ARG:HH11	1.81	0.44
39:DT:127:ALA:C	39:DT:129:ARG:N	2.74	0.44
1:AA:509:A:H5"	4:AD:55:ALA:HB2	2.00	0.44
1:AA:664:G:P	18:AR:64:ARG:HH21	2.40	0.44
1:AA:998:G:N2	1:AA:1043:C:N3	2.55	0.44
3:AC:82:GLU:HG2	3:AC:85:ARG:NH2	2.30	0.44
19:AS:41:VAL:O	19:AS:43:GLU:N	2.50	0.44
24:AX:59:A:C2'	24:AX:60:U:H5'	2.47	0.44
23:AY:59:U:H3'	23:AY:60:U:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:217:A:H8	25:BA:218:A:H5'	1.82	0.44
25:BA:1302:G:O2'	29:BF:75:HIS:HE1	2.01	0.44
25:BA:1688:A:H2'	25:BA:1689:G:O4'	2.18	0.44
25:BA:1822:A:H8	25:BA:1822:A:OP2	2.01	0.44
25:BA:2023:A:H2'	25:BA:2024:G:C8	2.52	0.44
25:BA:2136:A:C2	25:BA:2190:G:H1'	2.53	0.44
25:BA:2170:G:O2'	25:BA:2171:G:OP2	2.30	0.44
25:BA:2403:G:O6	25:BA:2437:A:H8	2.00	0.44
26:BB:106:G:H5'	45:BZ:31:ARG:HG2	1.99	0.44
32:BI:38:LEU:H	32:BI:38:LEU:HD12	1.82	0.44
41:BV:1:MET:HB2	41:BV:43:GLU:OE2	2.18	0.44
1:CA:7:G:H21	5:CE:121:LYS:HG2	1.83	0.44
1:CA:527:G:O6	12:CL:49:ASN:ND2	2.51	0.44
1:CA:921:U:O2	5:CE:19:MET:HB2	2.17	0.44
1:CA:1009:G:H22	1:CA:1021:G:H1'	1.81	0.44
1:CA:1051:C:H2'	1:CA:1052:U:C6	2.53	0.44
1:CA:1249:C:H4'	9:CI:36:TYR:OH	2.18	0.44
6:CF:36:ARG:NH2	6:CF:66:GLU:OE2	2.51	0.44
9:CI:16:ARG:HB2	9:CI:64:THR:HB	2.00	0.44
25:DA:118:A:H1'	25:DA:178:G:O4'	2.18	0.44
25:DA:280:C:C2	25:DA:362:U:O4	2.71	0.44
25:DA:297:C:H2'	25:DA:298:G:O4'	2.17	0.44
25:DA:760:G:H2'	25:DA:761:A:O4'	2.18	0.44
25:DA:1540:U:H2'	25:DA:1541:G:O4'	2.17	0.44
25:DA:1645:G:H5"	25:DA:1646:C:O4'	2.18	0.44
25:DA:1709:U:H2'	25:DA:1710:C:C6	2.52	0.44
25:DA:1825:A:OP1	27:DD:249:PRO:HD3	2.17	0.44
25:DA:2230:G:C6	25:DA:2231:C:C4	3.06	0.44
25:DA:2659:G:OP1	31:DH:158:HIS:NE2	2.45	0.44
25:DA:2801(A):A:H1'	25:DA:2895:U:H1'	2.00	0.44
26:DB:6:C:H2'	26:DB:7:G:O4'	2.18	0.44
26:DB:39:A:O2'	26:DB:46:A:N1	2.46	0.44
29:DF:20:LEU:HD12	29:DF:125:LEU:HD13	2.00	0.44
34:DO:68:GLU:HB3	34:DO:78:ARG:HB2	2.00	0.44
36:DQ:24:GLY:HA2	36:DQ:67:ARG:HH22	1.81	0.44
43:DX:12:VAL:HG22	43:DX:29:TRP:CE2	2.53	0.44
50:D4:15:ILE:O	50:D4:33:VAL:N	2.50	0.44
54:D8:63:PRO:HG2	54:D8:64:TYR:CD2	2.53	0.44
1:AA:591:U:H2'	1:AA:592:G:C8	2.52	0.44
1:AA:976:G:N2	1:AA:1363:C:OP2	2.25	0.44
3:AC:149:ALA:HA	3:AC:201:TYR:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:168:ARG:CD	4:AD:168:ARG:H	2.31	0.44
6:AF:36:ARG:CB	6:AF:36:ARG:HH11	2.31	0.44
11:AK:77:MET:HE2	11:AK:77:MET:HB2	1.90	0.44
25:BA:83:A:H5"	44:BY:8:LYS:HG2	1.99	0.44
25:BA:486:A:H2'	25:BA:487:C:O4'	2.18	0.44
25:BA:515:G:N7	42:BW:49:LYS:NZ	2.65	0.44
25:BA:692:C:H2'	25:BA:693:G:O4'	2.18	0.44
25:BA:863:C:H2'	25:BA:864:C:H6	1.83	0.44
25:BA:2165:C:C2	25:BA:2171:G:C2	3.05	0.44
25:BA:2203:G:O2'	25:BA:2204:G:OP1	2.34	0.44
25:BA:2642:G:H2'	25:BA:2643:G:C8	2.53	0.44
26:BB:89:G:H2'	26:BB:90:A:C8	2.52	0.44
27:BD:70:TRP:HB3	27:BD:190:TYR:CE1	2.53	0.44
27:BD:145:VAL:HG12	27:BD:146:GLU:O	2.18	0.44
28:BE:144:ARG:HB3	28:BE:145:LYS:H	1.52	0.44
36:BQ:34:LEU:HB2	36:BQ:118:LEU:HD22	1.99	0.44
38:BS:46:VAL:HG12	38:BS:48:LEU:HD12	1.99	0.44
39:BT:118:ARG:HD2	39:BT:118:ARG:HA	1.49	0.44
48:B2:11:GLU:O	48:B2:15:LYS:HG3	2.18	0.44
1:CA:6:G:H4'	1:CA:298:A:H4'	1.99	0.44
1:CA:255:G:H1'	17:CQ:16:GLN:NE2	2.32	0.44
5:CE:76:ILE:O	5:CE:93:PRO:HB3	2.17	0.44
25:DA:660:G:H5'	29:DF:99:TYR:CE2	2.52	0.44
25:DA:817:C:H2'	25:DA:818:G:O4'	2.18	0.44
25:DA:848:G:C4	25:DA:933:A:H8	2.36	0.44
25:DA:992:C:OP1	40:DU:47:TYR:OH	2.24	0.44
25:DA:1019:U:OP1	25:DA:1035:U:O2'	2.32	0.44
25:DA:1510:G:H2'	25:DA:1511:C:O4'	2.18	0.44
25:DA:1596:A:H2'	25:DA:1597:A:O4'	2.17	0.44
25:DA:2032:G:OP2	25:DA:2454:G:O2'	2.29	0.44
25:DA:2162:G:H4'	25:DA:2172:U:C2'	2.42	0.44
25:DA:2387:U:H1'	46:D0:41:ARG:HE	1.82	0.44
26:DB:32:C:H2'	26:DB:33:G:O4'	2.18	0.44
37:DR:31:HIS:C	37:DR:33:ARG:H	2.26	0.44
38:DS:77:ALA:HB1	38:DS:82:ILE:HB	2.00	0.44
1:AA:59:A:H3'	1:AA:331:G:H22	1.82	0.44
1:AA:738:C:OP2	6:AF:92:LYS:NZ	2.40	0.44
1:AA:831:U:H2'	1:AA:832:C:C6	2.52	0.44
1:AA:1070:U:OP1	5:AE:18:ARG:NH1	2.51	0.44
1:AA:1399:C:C2	1:AA:1401:G:C5	3.06	0.44
2:AB:77:ALA:HB2	2:AB:165:VAL:HG11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AJ:11:PHE:CE1	10:AJ:67:THR:HG22	2.52	0.44
23:AY:8:4SU:H1'	23:AY:48:C:O2	2.18	0.44
25:BA:270:C:H4'	25:BA:271:U:OP1	2.18	0.44
25:BA:791:G:OP1	28:BE:132:HIS:ND1	2.48	0.44
25:BA:932:C:H3'	25:BA:933:C:C5'	2.47	0.44
25:BA:1405:A:N3	25:BA:1405:A:H5'	2.33	0.44
25:BA:1558:G:H2'	25:BA:1559:C:O4'	2.18	0.44
25:BA:1653:C:H4'	25:BA:1654:A:O5'	2.18	0.44
25:BA:2077:C:O2	61:BA:4428:HOH:O	2.21	0.44
25:BA:2169:G:N3	25:BA:2170:G:H5"	2.33	0.44
25:BA:2369:U:OP1	46:B0:20:ARG:HD3	2.17	0.44
25:BA:2377:G:O6	54:B8:39:LYS:HE3	2.18	0.44
29:BF:196:LEU:HD23	29:BF:196:LEU:HA	1.76	0.44
50:B4:47:GLN:C	50:B4:49:PHE:H	2.25	0.44
53:B7:35:ARG:HG3	53:B7:42:LEU:HD11	2.00	0.44
1:CA:280:C:N3	17:CQ:39:SER:N	2.66	0.44
1:CA:337:C:H2'	1:CA:338:A:H8	1.80	0.44
1:CA:532:A:H2	1:CA:1206:G:N2	2.15	0.44
1:CA:1069:C:H4'	1:CA:1192:C:O2	2.17	0.44
1:CA:1145:C:H4'	1:CA:1146:A:H5'	1.99	0.44
1:CA:1347:G:H22	1:CA:1373:G:H2'	1.83	0.44
7:CG:46:ALA:HA	7:CG:49:ILE:HD12	1.99	0.44
14:CN:23:ARG:HG3	14:CN:28:GLY:O	2.18	0.44
16:CP:17:TYR:HE2	16:CP:41:PRO:HG3	1.83	0.44
25:DA:272(J):C:H42	25:DA:363:G:H1	1.65	0.44
25:DA:466:A:N3	25:DA:683:C:H1'	2.33	0.44
25:DA:506:G:O3'	25:DA:507:A:H8	2.01	0.44
25:DA:1310:G:OP2	53:D7:9:ARG:HD2	2.17	0.44
25:DA:1838:C:N4	25:DA:1898:U:H2'	2.33	0.44
25:DA:2051:A:H5'	25:DA:2578:G:O4'	2.18	0.44
25:DA:2153:G:C2	25:DA:2154:G:C5	3.06	0.44
25:DA:2321:G:O2'	25:DA:2322:A:OP1	2.29	0.44
35:DP:65:ARG:HD3	35:DP:66:GLY:N	2.33	0.44
45:DZ:75:ASN:O	45:DZ:84:GLU:N	2.29	0.44
1:AA:909:A:H2'	1:AA:910:C:O4'	2.18	0.43
1:AA:1325:C:O2'	1:AA:1326:C:H5'	2.17	0.43
9:AI:79:LEU:HD22	9:AI:104:ARG:HB2	1.99	0.43
13:AM:11:ARG:O	13:AM:13:LYS:N	2.50	0.43
16:AP:72:ARG:NH2	16:AP:73:LEU:HD21	2.33	0.43
25:BA:212:A:O4'	25:BA:449:A:H5'	2.18	0.43
25:BA:2705:A:H2'	25:BA:2706:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2722:C:H2'	25:BA:2723:A:C8	2.53	0.43
25:BA:2787:C:H2'	25:BA:2788:A:O4'	2.18	0.43
26:BB:7:G:H8	26:BB:7:G:H5"	1.83	0.43
45:BZ:145:GLU:O	45:BZ:148:ASP:N	2.39	0.43
50:B4:16:CYS:HA	50:B4:33:VAL:O	2.18	0.43
50:B4:24:THR:OG1	50:B4:25:TYR:N	2.50	0.43
1:CA:922:G:C6	1:CA:923:A:C6	3.06	0.43
2:CB:35:GLU:HB2	2:CB:40:HIS:HD2	1.83	0.43
6:CF:8:ILE:HD11	6:CF:79:LEU:HD13	1.99	0.43
7:CG:150:ALA:HA	11:CK:59:TYR:HB3	1.99	0.43
9:CI:110:GLU:OE2	9:CI:113:LYS:NZ	2.51	0.43
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.99	0.43
11:CK:24:SER:OG	11:CK:25:TYR:N	2.46	0.43
14:CN:24:CYS:HB2	14:CN:40:CYS:HB3	2.00	0.43
23:CW:38:A:C6	23:CW:39:PSU:C2	3.05	0.43
23:CY:27:G:H2'	23:CY:28:G:C8	2.53	0.43
25:DA:236:C:H2'	25:DA:237:C:C6	2.53	0.43
25:DA:248:G:C2	25:DA:2431:U:H4'	2.53	0.43
25:DA:251:A:C5	25:DA:252:G:H1'	2.53	0.43
25:DA:964:C:O2'	25:DA:2273:A:N3	2.41	0.43
25:DA:1417:C:H2'	25:DA:1418:G:O4'	2.18	0.43
25:DA:2532:G:C6	25:DA:2533:A:C6	3.05	0.43
25:DA:2705:A:H2'	25:DA:2706:G:O4'	2.18	0.43
25:DA:2820:A:O5'	37:DR:4:LEU:HD23	2.17	0.43
25:DA:2833:G:H4'	25:DA:2834:G:OP2	2.18	0.43
26:DB:48:A:H2'	26:DB:49:C:C6	2.53	0.43
27:DD:134:ARG:HG3	27:DD:187:GLY:O	2.18	0.43
28:DE:9:VAL:HG22	28:DE:25:VAL:HB	1.99	0.43
31:DH:98:LEU:HD12	31:DH:98:LEU:HA	1.91	0.43
40:DU:65:ILE:HD11	40:DU:95:LEU:HB3	2.00	0.43
44:DY:19:LYS:HE2	44:DY:20:TYR:CE1	2.53	0.43
45:DZ:110:GLY:HA3	45:DZ:174:VAL:HG21	1.99	0.43
49:D3:16:PRO:HB2	49:D3:18:ASP:OD1	2.16	0.43
50:D4:40:HIS:HA	50:D4:41:PRO:HD2	1.84	0.43
52:D6:11:LEU:HB2	52:D6:21:TYR:HB2	2.00	0.43
1:AA:236:G:H5"	17:AQ:42:TYR:OH	2.17	0.43
1:AA:377:G:P	16:AP:5:ARG:HD2	2.58	0.43
1:AA:779:C:O2'	11:AK:120:ARG:HD3	2.18	0.43
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.33	0.43
57:AA:3221:NEG:H11	25:BA:786:G:O6	2.17	0.43
2:AB:166:ASP:O	2:AB:170:GLU:N	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:150:LYS:HG3	3:AC:169:ALA:HB2	2.00	0.43
25:BA:2560:G:H2'	25:BA:2561:G:O4'	2.17	0.43
30:BG:16:ARG:O	30:BG:20:ILE:HG13	2.18	0.43
32:BI:27:ARG:HD2	47:B1:71:TYR:CE1	2.54	0.43
33:BN:33:LEU:HD12	33:BN:33:LEU:HA	1.87	0.43
38:BS:83:LYS:HE2	38:BS:83:LYS:HB2	1.91	0.43
42:BW:65:LEU:HD12	42:BW:68:ARG:HE	1.83	0.43
48:B2:25:VAL:HG11	48:B2:61:LEU:HD21	1.98	0.43
1:CA:44:G:H2'	1:CA:45:U:O4'	2.18	0.43
1:CA:189(K):U:H2'	1:CA:189(L):G:C8	2.54	0.43
1:CA:495:A:H4'	1:CA:496:A:OP1	2.18	0.43
1:CA:581:G:OP1	15:CO:61:GLY:HA3	2.18	0.43
1:CA:818:G:O2'	1:CA:819:A:H5'	2.18	0.43
1:CA:1075:C:H2'	1:CA:1076:C:H5'	1.99	0.43
1:CA:1327:C:O2'	1:CA:1328:C:H5'	2.18	0.43
2:CB:125:PRO:O	2:CB:127:ILE:N	2.51	0.43
5:CE:99:GLY:HA2	5:CE:116:THR:O	2.18	0.43
6:CF:4:TYR:HE1	6:CF:92:LYS:HG3	1.83	0.43
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.17	0.43
8:CH:12:ARG:CZ	8:CH:27:PRO:HD3	2.49	0.43
13:CM:5:ALA:CB	13:CM:22:ILE:HD12	2.48	0.43
15:CO:85:LEU:HB3	15:CO:87:ILE:HG13	2.00	0.43
23:CW:63:G:H2'	23:CW:64:A:C8	2.53	0.43
25:DA:70:G:H5"	25:DA:112:U:O2	2.18	0.43
25:DA:118:A:H3'	25:DA:119:A:H5"	2.00	0.43
25:DA:176:G:O2'	25:DA:177:G:H5'	2.18	0.43
25:DA:1116:C:H2'	25:DA:1117:G:C8	2.53	0.43
25:DA:1357:U:H2'	25:DA:1358:G:O4'	2.18	0.43
25:DA:1466:G:O3'	25:DA:1546:C:O2'	2.35	0.43
25:DA:1530:C:H42	25:DA:1539:G:H1	1.64	0.43
25:DA:1580:A:H5'	25:DA:1581:G:OP2	2.18	0.43
25:DA:1894:C:C2'	25:DA:1895:C:H5'	2.48	0.43
25:DA:2265:U:C4	25:DA:2266:A:C5	3.06	0.43
25:DA:2773:C:H2'	25:DA:2774:C:H6	1.83	0.43
40:DU:104:GLN:OE1	40:DU:105:VAL:HG23	2.18	0.43
1:AA:872:A:C8	1:AA:874:G:C8	3.07	0.43
1:AA:1028:C:N3	1:AA:1033:G:N2	2.53	0.43
1:AA:1106:G:C6	1:AA:1107:C:C4	3.06	0.43
7:AG:89:MET:SD	7:AG:155:ARG:HB2	2.58	0.43
23:AY:20:U:H3'	23:AY:20:U:OP2	2.17	0.43
25:BA:91:G:H2'	25:BA:92:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1716:A:H5"	25:BA:2562:G:OP1	2.18	0.43
25:BA:1821:C:H2'	25:BA:1822:A:C5	2.53	0.43
25:BA:1944:G:H2'	25:BA:1945:U:C6	2.53	0.43
25:BA:1992:A:H4'	25:BA:1993:A:OP1	2.18	0.43
25:BA:2132:G:N3	25:BA:2142:G:H1'	2.33	0.43
25:BA:2638:C:H2'	25:BA:2639:G:O4'	2.18	0.43
29:BF:28:ILE:HD13	29:BF:119:ARG:HE	1.83	0.43
32:BI:54:GLN:HG3	32:BI:57:ARG:NH2	2.34	0.43
38:BS:87:PHE:CE1	38:BS:102:ALA:HB2	2.53	0.43
1:CA:130:A:H5'	17:CQ:63:ARG:HE	1.84	0.43
1:CA:253:U:H2'	1:CA:254:G:C8	2.54	0.43
1:CA:984:C:H2'	1:CA:985:C:H6	1.83	0.43
1:CA:1010:G:H22	1:CA:1020:U:H1'	1.81	0.43
1:CA:1381:U:O2'	7:CG:79:ARG:HG3	2.18	0.43
1:CA:1392:G:N2	1:CA:1502:A:C8	2.87	0.43
2:CB:118:LEU:HD13	2:CB:142:LEU:HB2	2.01	0.43
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.18	0.43
9:CI:50:LEU:HD23	9:CI:85:LEU:HD11	2.00	0.43
12:CL:8:ASN:O	12:CL:12:ARG:HG3	2.19	0.43
25:DA:93:G:H2'	25:DA:94:C:C6	2.53	0.43
25:DA:299:A:N1	25:DA:322:A:O2'	2.36	0.43
25:DA:311:A:C6	25:DA:328:U:C4	3.06	0.43
25:DA:752:A:OP1	53:D7:3:ARG:NH2	2.45	0.43
25:DA:853:G:H2'	25:DA:854:G:H8	1.82	0.43
25:DA:925:C:H2'	25:DA:926:A:H8	1.83	0.43
25:DA:972:G:C6	25:DA:973:A:C6	3.06	0.43
25:DA:1268:A:H2'	25:DA:1269:A:O4'	2.18	0.43
25:DA:1445:A:OP2	25:DA:1445(A):C:N4	2.39	0.43
25:DA:2143:C:H2'	25:DA:2144:U:O4'	2.18	0.43
25:DA:2228:G:C6	25:DA:2229:C:C4	3.06	0.43
25:DA:2406:U:C2	35:DP:72:PRO:HG2	2.54	0.43
26:DB:2:C:H2'	26:DB:3:C:C6	2.53	0.43
28:DE:101:ARG:NH2	28:DE:171:GLU:HB2	2.33	0.43
28:DE:181:LEU:HD21	39:DT:6:LEU:HD12	2.00	0.43
31:DH:24:VAL:HG22	31:DH:35:VAL:HB	2.00	0.43
41:DV:12:TYR:CD2	41:DV:20:LEU:HD21	2.52	0.43
1:AA:97:G:H2'	1:AA:98:G:O4'	2.18	0.43
1:AA:109:A:C6	1:AA:326:G:C6	3.06	0.43
1:AA:375:U:OP1	16:AP:69:THR:HG21	2.18	0.43
1:AA:865:A:H2	1:AA:918:A:H4'	1.83	0.43
1:AA:1139:G:N2	1:AA:1143:G:C6	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1239:A:C4	1:AA:1298:C:N4	2.86	0.43
1:AA:1429:C:H2'	1:AA:1430:C:C6	2.53	0.43
5:AE:77:PRO:HG2	5:AE:78:HIS:CD2	2.52	0.43
12:AL:113:ARG:O	12:AL:114:LYS:HD2	2.19	0.43
15:AO:82:ILE:HD12	15:AO:88:ARG:HB2	2.00	0.43
25:BA:9:U:O4	25:BA:2641:A:H2	2.02	0.43
25:BA:925:A:N6	25:BA:946:A:C8	2.87	0.43
25:BA:1834:A:H2'	25:BA:1835:C:O4'	2.19	0.43
40:BU:74:LEU:H	40:BU:74:LEU:HD12	1.82	0.43
45:BZ:105:VAL:N	45:BZ:139:VAL:O	2.46	0.43
48:B2:29:LYS:HG2	48:B2:57:ILE:HD13	1.99	0.43
1:CA:384:G:H2'	1:CA:385:C:C6	2.54	0.43
1:CA:953:G:H2'	1:CA:954:G:O4'	2.18	0.43
1:CA:1186:G:H21	14:CN:61:TRP:C	2.27	0.43
2:CB:196:LEU:HD12	2:CB:196:LEU:HA	1.86	0.43
4:CD:112:VAL:HG22	4:CD:116:GLN:OE1	2.19	0.43
7:CG:90:GLU:H	7:CG:90:GLU:CD	2.25	0.43
8:CH:20:TYR:CE2	8:CH:75:ARG:HG2	2.54	0.43
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	2.00	0.43
11:CK:80:VAL:O	11:CK:106:LYS:N	2.50	0.43
16:CP:15:PRO:O	16:CP:16:HIS:ND1	2.51	0.43
18:CR:24:ALA:C	18:CR:26:LEU:H	2.26	0.43
25:DA:182:A:H2	25:DA:433:C:O2	2.00	0.43
25:DA:479:A:O2'	25:DA:481:G:H5'	2.18	0.43
25:DA:889:C:O2'	25:DA:890:A:O5'	2.35	0.43
25:DA:953:A:C6	25:DA:965:C:N3	2.86	0.43
25:DA:1857:G:O2'	25:DA:1885:A:N6	2.46	0.43
25:DA:1857:G:C6	25:DA:1858:G:C6	3.06	0.43
25:DA:2364:C:OP1	46:D0:55:ARG:HD3	2.19	0.43
25:DA:2870:C:H2'	25:DA:2871:C:O4'	2.19	0.43
27:DD:77:ALA:HB2	27:DD:97:TYR:CD2	2.53	0.43
35:DP:44:GLY:CA	35:DP:45:LEU:HB2	2.48	0.43
40:DU:58:ARG:HA	40:DU:61:TRP:CE3	2.54	0.43
43:DX:35:THR:HG22	43:DX:37:THR:H	1.83	0.43
1:AA:44:G:C6	1:AA:45:U:C2	3.07	0.43
1:AA:524:G:H2'	1:AA:525:C:C6	2.52	0.43
1:AA:1027:C:C2	1:AA:1034:G:N1	2.87	0.43
1:AA:1304:G:C6	1:AA:1305:G:N1	2.86	0.43
1:AA:1498:U:O2'	22:AV:17:U:OP1	2.29	0.43
2:AB:112:VAL:O	2:AB:116:GLU:HB2	2.19	0.43
4:AD:61:LYS:HA	4:AD:203:VAL:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AR:26:LEU:HD13	18:AR:26:LEU:HA	1.88	0.43
23:AY:69:G:H2'	23:AY:70:G:O4'	2.18	0.43
25:BA:384:G:H2'	25:BA:385:G:H8	1.82	0.43
25:BA:1698:G:H2'	25:BA:1699:A:O4'	2.18	0.43
25:BA:1874:C:H5'	27:BD:253:GLN:HE22	1.83	0.43
25:BA:1911:A:N1	25:BA:2246:G:H1'	2.34	0.43
25:BA:1968:U:H2'	25:BA:1969:C:C6	2.53	0.43
25:BA:2283:G:OP1	46:B0:18:ALA:HB1	2.19	0.43
25:BA:2364:A:N6	25:BA:2377:G:O2'	2.51	0.43
25:BA:2818:U:O2'	25:BA:2819:A:H5'	2.19	0.43
30:BG:12:TYR:HA	30:BG:16:ARG:HG3	1.99	0.43
50:B4:40:HIS:HA	50:B4:41:PRO:HD2	1.76	0.43
1:CA:501:C:H1'	1:CA:549:C:H1'	2.01	0.43
1:CA:707:C:H2'	1:CA:708:C:C6	2.52	0.43
1:CA:811:C:H4'	1:CA:900:A:N6	2.34	0.43
1:CA:839:U:O2'	1:CA:840:C:OP1	2.29	0.43
1:CA:978:A:O2'	1:CA:1322:C:N3	2.46	0.43
1:CA:1005:A:H1'	1:CA:1025:U:C2	2.53	0.43
2:CB:96:ARG:HH11	2:CB:98:LEU:HA	1.82	0.43
7:CG:15:ASP:OD2	7:CG:44:TYR:OH	2.27	0.43
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.84	0.43
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.53	0.43
57:CX:3004:NEG:N2	25:DA:2322:A:OP2	2.52	0.43
25:DA:77:C:OP1	48:D2:59:ARG:HD3	2.18	0.43
25:DA:851:U:H5'	49:D3:49:LYS:HD2	1.99	0.43
25:DA:949:C:H2'	25:DA:950:G:H8	1.84	0.43
25:DA:2107:C:H2'	25:DA:2108:C:O4'	2.18	0.43
26:DB:66:A:N6	26:DB:109:C:OP2	2.51	0.43
28:DE:146:THR:HA	28:DE:147:PRO:HA	1.89	0.43
35:DP:99:LEU:HD12	35:DP:100:LEU:HD23	2.00	0.43
37:DR:21:TYR:CZ	37:DR:43:GLU:HG2	2.52	0.43
1:AA:411:A:OP2	4:AD:30:LYS:HD2	2.17	0.43
1:AA:520:A:N1	1:AA:536:C:H1'	2.33	0.43
1:AA:767:A:H2'	1:AA:768:A:O4'	2.18	0.43
1:AA:1064:G:H1'	1:AA:1190:G:H21	1.83	0.43
1:AA:1299:A:H5"	1:AA:1299:A:N3	2.34	0.43
1:AA:1360:A:H8	1:AA:1360:A:OP1	2.00	0.43
2:AB:137:ARG:CZ	2:AB:137:ARG:HB3	2.48	0.43
2:AB:178:ARG:NH2	8:AH:74:PRO:HB3	2.27	0.43
6:AF:8:ILE:HD11	6:AF:79:LEU:HD13	2.01	0.43
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:85:LEU:HB3	15:AO:87:ILE:HG13	1.99	0.43
23:AW:26:A:N6	23:AW:44:G:H1	2.15	0.43
24:AX:13:C:O2'	25:BA:1946:C:H4'	2.18	0.43
25:BA:589:U:H2'	25:BA:590:A:O4'	2.19	0.43
25:BA:596:G:O2'	25:BA:597:C:H3'	2.19	0.43
25:BA:2534:U:O2'	25:BA:2659:U:OP1	2.27	0.43
29:BF:132:VAL:HA	29:BF:138:GLU:HB3	2.01	0.43
38:BS:48:LEU:HD23	38:BS:82:ILE:HD11	2.00	0.43
44:BY:92:ASN:OD1	44:BY:94:LYS:HG3	2.19	0.43
50:B4:59:PHE:HA	50:B4:61:ARG:HG2	2.01	0.43
1:CA:1004:A:C2	1:CA:1038:C:C4	3.06	0.43
1:CA:1106:G:H2'	1:CA:1107:C:C6	2.54	0.43
2:CB:48:MET:HA	2:CB:51:LEU:HD12	2.01	0.43
7:CG:113:GLU:CG	7:CG:119:ARG:HG2	2.45	0.43
16:CP:60:LEU:HD13	16:CP:60:LEU:HA	1.80	0.43
23:CW:11:C:H2'	23:CW:12:U:C6	2.53	0.43
24:CX:8:4SU:H1'	24:CX:48:C:O2	2.18	0.43
24:CX:55:PSU:O2'	24:CX:57:A:N7	2.42	0.43
25:DA:372:G:H8	47:D1:65:SER:O	2.02	0.43
25:DA:938:G:OP1	54:D8:52:LYS:HD2	2.18	0.43
25:DA:1151:G:C2	25:DA:1152:C:C2	3.07	0.43
25:DA:2126:A:H61	25:DA:2172:U:H5'	1.83	0.43
25:DA:2203:U:O2'	25:DA:2205:C:H5'	2.18	0.43
25:DA:2751:G:H8	31:DH:2:SER:HA	1.83	0.43
25:DA:2889:C:H3'	25:DA:2891:G:C8	2.53	0.43
27:DD:132:PRO:HG2	27:DD:135:PHE:HD2	1.80	0.43
29:DF:20:LEU:HD22	29:DF:21:ALA:H	1.84	0.43
30:DG:75:LYS:C	30:DG:84:LYS:HB2	2.43	0.43
36:DQ:22:LYS:HB3	36:DQ:22:LYS:HE2	1.81	0.43
42:DW:46:PHE:O	42:DW:50:VAL:HG23	2.18	0.43
45:DZ:108:PRO:HB3	45:DZ:144:LEU:HB3	2.00	0.43
45:DZ:145:GLU:HG3	45:DZ:146:ILE:H	1.81	0.43
50:D4:62:ARG:HA	50:D4:62:ARG:HD3	1.73	0.43
1:AA:1026:G:HO2'	1:AA:1027:C:P	2.41	0.43
1:AA:1363(A):A:H4'	1:AA:1364:U:H2'	2.01	0.43
1:AA:1429:C:H2'	1:AA:1430:C:H6	1.83	0.43
4:AD:78:LEU:HD23	4:AD:78:LEU:HA	1.84	0.43
4:AD:79:PHE:CE1	4:AD:204:ILE:HD13	2.53	0.43
8:AH:28:ALA:HA	8:AH:59:LEU:HG	2.00	0.43
13:AM:65:LYS:NZ	13:AM:73:GLU:HG3	2.34	0.43
13:AM:86:CYS:HB2	19:AS:73:GLU:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:74:LEU:HG	16:AP:79:VAL:HG21	1.99	0.43
23:AW:22:G:HO2'	23:AW:23:A:P	2.42	0.43
25:BA:344:A:H4'	25:BA:346:A:N7	2.33	0.43
25:BA:599:U:H2'	25:BA:600:G:C8	2.54	0.43
25:BA:1576:G:O2'	25:BA:1577:C:H5'	2.18	0.43
25:BA:1769:G:H2'	25:BA:1770:A:H8	1.84	0.43
32:BI:88:ILE:O	32:BI:121:LYS:NZ	2.50	0.43
33:BN:28:THR:HG22	33:BN:29:LYS:N	2.33	0.43
34:BO:108:GLU:H	34:BO:108:GLU:HG3	1.48	0.43
36:BQ:30:GLY:HA2	36:BQ:107:ALA:HB2	2.00	0.43
1:CA:32:A:C2	1:CA:33:A:C4	3.06	0.43
1:CA:70:G:H1	1:CA:99:U:H3	1.67	0.43
1:CA:986:A:H2'	1:CA:987:G:O4'	2.18	0.43
1:CA:1011:G:N2	1:CA:1019:C:H1'	2.34	0.43
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.53	0.43
2:CB:61:LEU:HD23	2:CB:68:ILE:HD11	2.00	0.43
7:CG:87:VAL:HG11	7:CG:155:ARG:HA	2.00	0.43
7:CG:88:PRO:HG3	7:CG:149:ARG:HA	2.01	0.43
9:CI:127:LYS:HE3	9:CI:127:LYS:HB2	1.87	0.43
13:CM:19:LEU:HD12	13:CM:19:LEU:HA	1.90	0.43
13:CM:91:ARG:HA	13:CM:91:ARG:HD2	1.92	0.43
24:CX:53:G:H2'	24:CX:54:5MU:C6	2.54	0.43
25:DA:676:A:H1'	25:DA:2443:C:H1'	2.00	0.43
25:DA:997:G:O2'	25:DA:998:C:H5'	2.18	0.43
25:DA:1131:G:H8	25:DA:2025:C:H4'	1.84	0.43
25:DA:1756:G:H4'	25:DA:1758:G:O4'	2.19	0.43
25:DA:2206:G:H3'	25:DA:2207:G:N7	2.34	0.43
30:DG:9:ARG:HH11	30:DG:13:GLU:CD	2.25	0.43
36:DQ:75:THR:HG21	36:DQ:87:LYS:NZ	2.34	0.43
36:DQ:77:LYS:HE2	61:DQ:3101:HOH:O	2.18	0.43
41:DV:62:LEU:HD23	41:DV:93:GLU:HG2	2.00	0.43
48:D2:31:GLU:O	48:D2:35:LEU:HG	2.19	0.43
1:AA:831:U:H2'	1:AA:832:C:H6	1.83	0.43
1:AA:1329:A:N7	21:AU:7:ARG:NH2	2.65	0.43
13:AM:80:ARG:HH22	19:AS:69:HIS:CE1	2.36	0.43
15:AO:26:GLU:HB3	15:AO:81:LEU:HD13	2.01	0.43
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.19	0.43
20:AT:13:LEU:H	20:AT:13:LEU:HG	1.45	0.43
23:AY:8:4SU:H4'	23:AY:48:C:C4'	2.48	0.43
25:BA:549:U:H2'	25:BA:550:U:C6	2.54	0.43
25:BA:864:C:O2'	25:BA:886:U:H5"	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1683:C:H2'	25:BA:1684:A:C8	2.54	0.43
25:BA:1701:A:C1'	25:BA:2833:A:H5'	2.49	0.43
25:BA:2032:G:O6	61:BA:4615:HOH:O	2.21	0.43
27:BD:101:GLU:OE1	27:BD:103:ARG:NH1	2.45	0.43
27:BD:102:LYS:C	27:BD:103:ARG:HG2	2.43	0.43
28:BE:143:ASN:HD22	28:BE:147:PRO:CD	2.32	0.43
33:BN:68:GLU:H	33:BN:68:GLU:HG2	1.65	0.43
1:CA:59:A:H3'	1:CA:331:G:H22	1.83	0.43
1:CA:253:U:H2'	1:CA:254:G:H8	1.83	0.43
1:CA:261:U:OP2	20:CT:79:ARG:NH2	2.52	0.43
1:CA:741:G:H2'	1:CA:742:G:O4'	2.19	0.43
1:CA:993:G:N3	1:CA:993:G:H2'	2.34	0.43
1:CA:1012:U:O2	1:CA:1017:G:O6	2.36	0.43
1:CA:1434:A:H2'	1:CA:1435:G:O4'	2.19	0.43
2:CB:118:LEU:HB3	2:CB:142:LEU:HD12	2.01	0.43
2:CB:211:ILE:H	2:CB:211:ILE:HG13	1.66	0.43
3:CC:6:HIS:HA	3:CC:7:PRO:HD3	1.85	0.43
3:CC:32:LEU:HD13	3:CC:32:LEU:HA	1.86	0.43
3:CC:71:ALA:HB1	3:CC:109:PRO:HG3	2.01	0.43
10:CJ:6:ILE:HA	10:CJ:97:GLU:O	2.19	0.43
25:DA:644:A:C2	25:DA:2369:A:H1'	2.54	0.43
25:DA:813:U:H2'	25:DA:814:C:C6	2.54	0.43
25:DA:928:G:H8	25:DA:928:G:O5'	2.01	0.43
25:DA:1588:C:H2'	25:DA:1589:C:C6	2.54	0.43
25:DA:1711:C:H2'	25:DA:1712:C:H6	1.84	0.43
25:DA:1823:G:OP1	27:DD:54:ARG:NH1	2.52	0.43
25:DA:2484:G:C2	25:DA:2485:G:C8	3.07	0.43
29:DF:9:ILE:HA	29:DF:10:PRO:HD3	1.85	0.43
30:DG:79:ASN:OD1	30:DG:79:ASN:N	2.51	0.43
34:DO:31:LYS:HZ3	34:DO:31:LYS:HG2	1.64	0.43
36:DQ:73:PRO:HA	36:DQ:93:TYR:CD1	2.54	0.43
1:AA:299:G:H8	1:AA:299:G:O5'	2.02	0.43
1:AA:713:G:H2'	1:AA:714:G:C8	2.53	0.43
11:AK:38:ASN:HA	11:AK:39:PRO:HD3	1.87	0.43
13:AM:93:ARG:HG2	25:BA:935:C:O4'	2.19	0.43
13:AM:94:ARG:CZ	19:AS:80:TYR:HD2	2.32	0.43
13:AM:121:LYS:HZ2	23:AW:40:C:H5"	1.84	0.43
14:AN:39:LEU:HD11	14:AN:47:LEU:HD12	2.00	0.43
20:AT:30:LYS:O	20:AT:34:LYS:HG3	2.19	0.43
23:AW:31:A:H2'	23:AW:32:PSU:O4'	2.19	0.43
24:AX:61:C:H2'	24:AX:62:C:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:274:U:H5	32:BI:52:ARG:HD3	1.84	0.43
25:BA:552:C:C4	25:BA:2792:U:H2'	2.54	0.43
25:BA:1769:G:H2'	25:BA:1770:A:C8	2.54	0.43
25:BA:1884:A:H2'	25:BA:1885:A:C8	2.53	0.43
26:BB:29:A:H2'	26:BB:30:C:O4'	2.19	0.43
36:BQ:35:VAL:HA	36:BQ:101:ARG:O	2.18	0.43
40:BU:50:ARG:HH12	41:BV:72:VAL:HA	1.83	0.43
42:BW:48:ALA:O	42:BW:52:GLU:HB2	2.19	0.43
43:BX:92:LEU:HD12	43:BX:92:LEU:HA	1.75	0.43
45:BZ:130:PRO:HA	45:BZ:133:ILE:HG13	2.00	0.43
1:CA:154:C:H2'	1:CA:155:C:C6	2.54	0.43
1:CA:308:C:H2'	1:CA:309:G:C8	2.54	0.43
1:CA:927:G:OP2	1:CA:927:G:H4'	2.19	0.43
1:CA:1371:G:C6	1:CA:1372:U:C4	3.07	0.43
1:CA:1494:G:H4'	25:DA:1913:A:C8	2.54	0.43
2:CB:24:TRP:CD1	2:CB:24:TRP:H	2.36	0.43
2:CB:219:VAL:HA	2:CB:222:ILE:HG12	2.00	0.43
3:CC:19:GLU:HB3	3:CC:40:ARG:NH2	2.33	0.43
11:CK:45:GLY:O	11:CK:50:TYR:HB2	2.18	0.43
15:CO:48:LYS:HD3	15:CO:48:LYS:HA	1.60	0.43
15:CO:54:ARG:HH11	15:CO:58:MET:CE	2.32	0.43
16:CP:18:ARG:HG2	16:CP:35:LYS:HE3	2.00	0.43
25:DA:460:A:H2'	25:DA:461:C:O4'	2.18	0.43
25:DA:754:C:H2'	25:DA:755:C:C6	2.54	0.43
25:DA:1422:G:H4'	25:DA:1493:C:OP1	2.18	0.43
25:DA:1745(A):C:H5'	25:DA:1746:G:OP2	2.18	0.43
25:DA:2031:A:C6	25:DA:2498:C:H1'	2.53	0.43
25:DA:2100:G:C6	25:DA:2190:G:C6	3.06	0.43
25:DA:2716:U:O2'	25:DA:2717:G:H5'	2.18	0.43
25:DA:2881:C:H2'	25:DA:2882:A:O4'	2.19	0.43
32:DI:27:ARG:HD2	47:D1:71:TYR:CZ	2.54	0.43
36:DQ:45:GLN:CD	36:DQ:45:GLN:H	2.25	0.43
42:DW:12:ILE:O	42:DW:101:SER:OG	2.31	0.43
45:DZ:19:ARG:HE	45:DZ:19:ARG:HB2	1.42	0.43
55:D9:17:ILE:HD12	55:D9:17:ILE:HA	1.94	0.43
1:AA:407:G:H2'	1:AA:408:A:C8	2.54	0.43
3:AC:87:LEU:O	3:AC:91:LEU:N	2.40	0.43
9:AI:9:ARG:HG2	9:AI:14:VAL:HG13	2.01	0.43
11:AK:104:GLN:HE21	11:AK:104:GLN:HB3	1.55	0.43
25:BA:402:C:H2'	25:BA:403:C:C6	2.54	0.43
25:BA:1556:A:H5'	25:BA:1557:A:OP2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1615:G:H5'	27:BD:60:ARG:HA	2.01	0.43
25:BA:1717:C:O2	28:BE:129:HIS:NE2	2.44	0.43
25:BA:2156:A:OP2	25:BA:2178:G:N2	2.52	0.43
25:BA:2221:A:H5"	25:BA:2222:C:OP2	2.19	0.43
25:BA:2230:U:O4'	47:B1:52:ARG:NH2	2.51	0.43
25:BA:2332:A:N3	25:BA:2332:A:H2'	2.34	0.43
25:BA:2623:U:H5'	25:BA:2623:U:H6	1.84	0.43
30:BG:117:PHE:HZ	30:BG:179:PRO:HG2	1.83	0.43
1:CA:392:G:H2'	1:CA:393:A:C8	2.54	0.43
1:CA:604:G:C2	1:CA:635:G:C5	3.07	0.43
1:CA:662:G:H2'	1:CA:663:A:H8	1.82	0.43
1:CA:828:A:H5"	1:CA:859:A:N1	2.34	0.43
1:CA:1074:G:O2'	1:CA:1101:A:N1	2.44	0.43
2:CB:92:TYR:HE2	2:CB:94:ASN:HB2	1.83	0.43
2:CB:201:ILE:HG21	2:CB:214:ILE:HG21	2.01	0.43
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.84	0.43
3:CC:8:ILE:HG23	3:CC:16:ARG:HG2	2.01	0.43
3:CC:121:ALA:HB2	3:CC:198:VAL:HG21	2.00	0.43
3:CC:184:TYR:HA	3:CC:200:ALA:O	2.19	0.43
10:CJ:16:LEU:HD23	10:CJ:16:LEU:HA	1.87	0.43
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.33	0.43
13:CM:108:ARG:HA	13:CM:108:ARG:HD3	1.86	0.43
24:CX:18:G:O2'	24:CX:19:G:H5'	2.18	0.43
25:DA:271(E):U:H2'	25:DA:271(F):C:C6	2.53	0.43
25:DA:493:G:H2'	25:DA:494:G:O4'	2.18	0.43
25:DA:622:G:H2'	25:DA:623:G:H8	1.84	0.43
25:DA:864:G:H4'	26:DB:102:A:H4'	2.00	0.43
25:DA:1029:A:N1	25:DA:2465:C:O2'	2.40	0.43
25:DA:1140:C:OP2	33:DN:66:LYS:NZ	2.40	0.43
25:DA:2064:C:H2'	25:DA:2065:C:C6	2.53	0.43
25:DA:2114:A:H2'	25:DA:2114:A:N3	2.33	0.43
29:DF:106:ARG:H	29:DF:106:ARG:HG2	1.51	0.43
32:DI:133:HIS:HD2	32:DI:136:VAL:HG23	1.84	0.43
45:DZ:45:ASP:O	45:DZ:49:ARG:HG3	2.19	0.43
1:AA:192:U:H2'	1:AA:193:C:C6	2.54	0.42
1:AA:616:G:O2'	1:AA:617:G:H5'	2.19	0.42
1:AA:619:U:N3	4:AD:134:ASP:OD1	2.32	0.42
1:AA:1002:G:C6	1:AA:1003:G:N3	2.87	0.42
2:AB:24:TRP:CD1	2:AB:24:TRP:H	2.36	0.42
4:AD:65:ARG:HG2	4:AD:75:PHE:CD2	2.54	0.42
13:AM:108:ARG:HA	13:AM:108:ARG:HD3	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:95:G:OP1	48:B2:46:GLN:NE2	2.47	0.42
25:BA:399:G:H8	47:B1:65:SER:O	2.02	0.42
25:BA:1207:C:O2'	41:BV:8:GLY:HA2	2.19	0.42
25:BA:1276:C:H2'	25:BA:1277:G:C8	2.54	0.42
25:BA:1701:A:O4'	25:BA:2833:A:H5'	2.19	0.42
25:BA:1898:A:H2'	25:BA:1899:A:C8	2.54	0.42
25:BA:2166:U:C2	25:BA:2170:G:N1	2.88	0.42
29:BF:183:VAL:O	29:BF:187:VAL:HG23	2.19	0.42
30:BG:143:GLU:H	30:BG:143:GLU:CD	2.26	0.42
31:BH:164:TYR:HB2	31:BH:167:GLU:HB2	2.00	0.42
32:BI:84:GLY:O	32:BI:86:THR:N	2.51	0.42
33:BN:75:TYR:CE2	33:BN:77:GLY:HA2	2.53	0.42
45:BZ:41:LEU:HD21	45:BZ:83:PRO:HG2	2.00	0.42
50:B4:53:GLU:C	50:B4:55:ARG:N	2.77	0.42
1:CA:277:C:OP1	17:CQ:41:LYS:HE2	2.19	0.42
1:CA:343:U:O2'	1:CA:344:A:H2'	2.18	0.42
1:CA:892:A:C6	1:CA:893:C:C4	3.07	0.42
1:CA:1028:C:O2	1:CA:1034:G:H1'	2.18	0.42
1:CA:1328:C:OP1	21:CU:21:TYR:OH	2.32	0.42
7:CG:23:VAL:O	7:CG:27:ILE:HG12	2.19	0.42
20:CT:14:LYS:O	20:CT:18:GLN:HG3	2.19	0.42
25:DA:139(A):G:O2'	25:DA:140:G:H5'	2.18	0.42
25:DA:224:G:H2'	25:DA:225:A:O4'	2.18	0.42
25:DA:276:A:H5"	25:DA:277:C:H5'	2.01	0.42
25:DA:336:C:HO2'	44:DY:35:TYR:HH	1.67	0.42
25:DA:637:A:H8	35:DP:117:GLU:HG3	1.84	0.42
25:DA:676:A:H2	25:DA:2069:G:N3	2.17	0.42
25:DA:945:A:C4	25:DA:2448:A:C2	3.07	0.42
25:DA:952:G:C4	25:DA:966:G:C2	3.07	0.42
25:DA:1032:A:O3'	55:D9:16:VAL:HG11	2.19	0.42
25:DA:1394:U:H2'	25:DA:1395:A:O4'	2.19	0.42
25:DA:1430:C:H2'	25:DA:1431:U:C6	2.54	0.42
25:DA:1469:A:H2'	25:DA:1470:G:O4'	2.19	0.42
25:DA:2299:G:H2'	25:DA:2300:G:H8	1.84	0.42
25:DA:2689:U:C4'	25:DA:2690:C:H5'	2.37	0.42
29:DF:11:VAL:HB	29:DF:18:ARG:HB3	2.01	0.42
36:DQ:11:LYS:HE3	36:DQ:88:GLY:O	2.19	0.42
42:DW:4:LYS:HB2	42:DW:106:ILE:HG12	2.00	0.42
45:DZ:97:GLU:H	45:DZ:97:GLU:HG2	1.58	0.42
1:AA:405:U:OP2	4:AD:3:ARG:NH2	2.52	0.42
3:AC:39:ILE:HG23	3:AC:91:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:48:ILE:O	11:AK:50:TYR:N	2.51	0.42
17:AQ:56:VAL:HB	17:AQ:78:GLU:HB3	2.01	0.42
25:BA:384:G:H2'	25:BA:385:G:C8	2.54	0.42
25:BA:449:A:H2'	25:BA:450:A:C8	2.54	0.42
25:BA:1231:G:OP1	61:BA:4357:HOH:O	2.22	0.42
25:BA:2250:G:N3	25:BA:2250:G:H2'	2.33	0.42
25:BA:2564:U:H2'	25:BA:2566:U:H5"	2.00	0.42
30:BG:179:PRO:HG3	50:B4:43:TYR:OH	2.19	0.42
35:BP:3:LEU:HD12	35:BP:3:LEU:HA	1.91	0.42
39:BT:127:ALA:O	39:BT:129:ARG:N	2.51	0.42
40:BU:85:LYS:HB3	40:BU:85:LYS:HE2	1.82	0.42
41:BV:55:ALA:HB2	41:BV:101:GLY:HA2	2.01	0.42
1:CA:54:C:H2'	1:CA:352:C:H41	1.84	0.42
1:CA:416:G:C5	1:CA:417:C:C4	3.07	0.42
1:CA:685:G:C2	1:CA:686:U:C4	3.07	0.42
1:CA:971:G:H1'	1:CA:1365:G:O2'	2.19	0.42
5:CE:75:THR:OG1	5:CE:117:ASP:O	2.23	0.42
8:CH:69:ARG:HG3	8:CH:76:PRO:HA	2.01	0.42
19:CS:10:PHE:HE1	19:CS:37:ARG:HD3	1.84	0.42
23:CW:70:G:H8	23:CW:70:G:OP2	2.02	0.42
25:DA:172:C:H2'	25:DA:173:G:C8	2.55	0.42
25:DA:443:A:N7	29:DF:45:ARG:HG2	2.34	0.42
25:DA:1814:G:H4'	27:DD:51:VAL:HG21	2.00	0.42
25:DA:2258:C:O2'	25:DA:2427:C:OP2	2.30	0.42
25:DA:2662:A:H8	25:DA:2662:A:O5'	2.02	0.42
25:DA:2859:G:H2'	25:DA:2860:A:C8	2.55	0.42
26:DB:83:G:H4'	49:D3:52:HIS:CG	2.54	0.42
26:DB:91:C:H5'	36:DQ:18:LYS:HA	2.01	0.42
27:DD:206:LEU:HD22	27:DD:211:ARG:HG2	2.01	0.42
27:DD:245:PRO:HB2	27:DD:253:GLN:HG2	2.00	0.42
33:DN:30:ILE:HG23	33:DN:52:VAL:HG11	2.01	0.42
33:DN:34:LEU:HD23	33:DN:107:LEU:HD21	2.01	0.42
33:DN:71:ILE:HG21	33:DN:84:LYS:HB3	2.01	0.42
34:DO:120:GLU:HB2	39:DT:68:TYR:CE2	2.54	0.42
42:DW:18:ARG:HG3	42:DW:76:VAL:HB	1.99	0.42
46:D0:55:ARG:HE	46:D0:55:ARG:HB2	1.54	0.42
49:D3:6:VAL:HG13	49:D3:56:VAL:HG22	2.01	0.42
1:AA:530:G:O6	22:AV:21:C:H1'	2.19	0.42
1:AA:1092:A:H2'	1:AA:1093:A:C8	2.54	0.42
1:AA:1338:G:C6	1:AA:1339:A:C6	3.07	0.42
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.92	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.19	0.42
10:AJ:81:THR:O	10:AJ:85:LEU:N	2.37	0.42
13:AM:11:ARG:HA	13:AM:45:VAL:HB	2.01	0.42
13:AM:60:VAL:HG22	13:AM:64:TRP:HZ3	1.83	0.42
15:AO:11:VAL:HG21	15:AO:34:LEU:HD22	2.00	0.42
25:BA:776:G:C5	27:BD:208:LYS:HB2	2.54	0.42
25:BA:879:G:N3	35:BP:53:GLY:HA3	2.35	0.42
25:BA:946:A:H2'	25:BA:947:A:O4'	2.19	0.42
25:BA:1057:G:OP2	40:BU:66:ASN:ND2	2.37	0.42
25:BA:1583:C:H2'	25:BA:1584:G:O4'	2.18	0.42
25:BA:1899:A:H3'	25:BA:1900:G:O4'	2.19	0.42
25:BA:2162:C:H1'	25:BA:2174:G:H22	1.84	0.42
27:BD:4:LYS:HE2	27:BD:6:PHE:CE1	2.55	0.42
28:BE:47:VAL:O	28:BE:80:GLU:HA	2.19	0.42
31:BH:4:ILE:HG22	31:BH:69:ARG:HG2	2.01	0.42
31:BH:139:GLN:HG3	31:BH:140:LYS:N	2.34	0.42
32:BI:54:GLN:HG3	32:BI:57:ARG:HH22	1.83	0.42
37:BR:44:LEU:HD22	37:BR:48:VAL:HG23	2.01	0.42
44:BY:9:LYS:HA	44:BY:10:GLY:HA2	1.66	0.42
44:BY:43:ASN:HD22	44:BY:43:ASN:HA	1.68	0.42
1:CA:154:C:C2'	1:CA:155:C:H5'	2.49	0.42
1:CA:340:U:H2'	1:CA:341:C:H6	1.85	0.42
1:CA:608:A:H2'	1:CA:609:A:O4'	2.18	0.42
1:CA:841:U:C5	1:CA:848:C:H1'	2.55	0.42
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.52	0.42
2:CB:77:ALA:HB2	2:CB:211:ILE:HD13	2.01	0.42
19:CS:27:GLU:HB3	19:CS:28:LYS:HB3	2.01	0.42
19:CS:32:LYS:HA	19:CS:50:ALA:HB3	2.01	0.42
25:DA:27:G:O2'	25:DA:28:A:OP2	2.35	0.42
25:DA:1614:A:P	25:DA:1614:A:H8	2.43	0.42
25:DA:2469:A:C6	25:DA:2470:G:C4	3.08	0.42
25:DA:2564:A:OP1	25:DA:2648:C:O2'	2.30	0.42
25:DA:2646:C:H2'	25:DA:2647:U:O4'	2.20	0.42
33:DN:91:LEU:HG	33:DN:98:VAL:HG21	1.99	0.42
47:D1:83:GLU:HA	47:D1:84:GLY:HA2	1.67	0.42
50:D4:57:GLU:HA	50:D4:58:ARG:HA	1.75	0.42
1:AA:872:A:C4	1:AA:874:G:N7	2.87	0.42
1:AA:881:G:P	12:AL:12:ARG:HH22	2.42	0.42
1:AA:1007:C:H6	1:AA:1007:C:O5'	2.02	0.42
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.19	0.42
1:AA:1493:A:H5"	1:AA:1494:G:OP2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:10:ARG:HB2	4:AD:40:PRO:HG3	2.02	0.42
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	2.00	0.42
6:AF:16:GLN:CD	6:AF:16:GLN:H	2.27	0.42
7:AG:111:ARG:HB3	7:AG:111:ARG:HH11	1.84	0.42
8:AH:86:ILE:HG12	8:AH:135:CYS:HA	2.01	0.42
13:AM:90:LEU:O	13:AM:93:ARG:HB2	2.18	0.42
23:AW:56:C:C5	25:BA:943:C:O4'	2.72	0.42
25:BA:310:C:H2'	25:BA:311:C:C6	2.53	0.42
25:BA:515:G:H8	25:BA:515:G:OP1	2.03	0.42
25:BA:1495:G:H4'	25:BA:1589:A:OP1	2.19	0.42
25:BA:1694:G:H3'	25:BA:1694:G:OP2	2.19	0.42
25:BA:1817:A:H1'	25:BA:1960:A:N6	2.34	0.42
25:BA:2298:A:H4'	25:BA:2299:A:O4'	2.19	0.42
25:BA:2333:G:H5"	25:BA:2334:A:OP2	2.19	0.42
43:BX:54:VAL:HG22	43:BX:81:VAL:HG12	2.02	0.42
54:B8:36:LYS:HB2	54:B8:41:ILE:CD1	2.49	0.42
1:CA:28:G:O2'	1:CA:296:U:OP1	2.26	0.42
1:CA:36:C:O2'	12:CL:117:ARG:NH2	2.51	0.42
1:CA:338:A:H2'	1:CA:339:C:O4'	2.20	0.42
1:CA:607:A:H2'	1:CA:608:A:O4'	2.19	0.42
8:CH:33:GLU:HG2	8:CH:48:TYR:CE1	2.54	0.42
10:CJ:74:ILE:HG22	61:CJ:5101:HOH:O	2.19	0.42
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.52	0.42
23:CW:7:A:C6	23:CW:66:U:O4	2.72	0.42
23:CY:76:A:H62	25:DA:2422:A:C5'	2.29	0.42
25:DA:528:A:H2	25:DA:2043:C:H5'	1.84	0.42
25:DA:569:U:C4	25:DA:570:G:C6	3.07	0.42
25:DA:601:C:O2	25:DA:605:C:H4'	2.20	0.42
25:DA:1022:G:C5	25:DA:1140:C:C4	3.08	0.42
25:DA:1224:C:C4	25:DA:1225:G:C6	3.08	0.42
25:DA:2261:C:H1'	25:DA:2388:A:N3	2.34	0.42
25:DA:2372:G:H1'	52:D6:46:HIS:CE1	2.54	0.42
25:DA:2661:G:H2'	25:DA:2662:A:C8	2.55	0.42
25:DA:2746:U:O4	25:DA:2755:C:H4'	2.18	0.42
25:DA:2815:C:H5'	51:D5:29:THR:HG21	2.02	0.42
25:DA:2849:U:OP2	39:DT:95:ARG:NH1	2.53	0.42
26:DB:89:G:C6	26:DB:90:A:C6	3.08	0.42
27:DD:33:LEU:HD23	27:DD:33:LEU:HA	1.85	0.42
27:DD:231:HIS:ND1	27:DD:232:PRO:HD2	2.34	0.42
31:DH:164:TYR:HB2	31:DH:167:GLU:HB2	2.01	0.42
34:DO:7:TYR:CE1	34:DO:20:MET:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DR:17:ARG:HG2	37:DR:21:TYR:CE2	2.55	0.42
1:AA:292:G:O2'	1:AA:608:A:N6	2.51	0.42
1:AA:437:U:O2'	4:AD:125:HIS:HE1	2.03	0.42
1:AA:1003:G:N2	1:AA:1004:A:H1'	2.33	0.42
1:AA:1017:G:H2'	1:AA:1018:C:C6	2.54	0.42
1:AA:1080:A:H5'	5:AE:14:ARG:NH2	2.35	0.42
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	2.01	0.42
20:AT:48:LYS:HA	20:AT:48:LYS:HD3	1.80	0.42
22:AV:13:A:H3'	22:AV:14:A:H5"	2.02	0.42
23:AW:1:G:H2'	23:AW:2:C:C6	2.51	0.42
23:AW:52:G:H5"	36:BQ:56:ARG:NH1	2.34	0.42
23:AY:7:A:HO2'	23:AY:49:C:H5'	1.85	0.42
25:BA:225:C:H2'	25:BA:226:C:H6	1.84	0.42
25:BA:495:G:O6	53:B7:37:LYS:NZ	2.47	0.42
25:BA:964:A:H5"	26:BB:98:G:O2'	2.20	0.42
25:BA:1639:G:H2'	25:BA:1640:G:C8	2.54	0.42
25:BA:1756:U:H2'	25:BA:1757:C:C6	2.54	0.42
25:BA:1817:A:H8	61:BA:4001:HOH:O	2.02	0.42
25:BA:1825:U:H2'	25:BA:1826:C:C6	2.53	0.42
25:BA:2164:C:N3	25:BA:2171:G:C6	2.87	0.42
25:BA:2331:G:H22	38:BS:3:ARG:CZ	2.33	0.42
37:BR:33:ARG:HD2	37:BR:113:LEU:HD13	2.01	0.42
37:BR:53:HIS:O	37:BR:56:LYS:HB2	2.19	0.42
1:CA:407:G:H2'	1:CA:408:A:C8	2.54	0.42
1:CA:517:G:N1	1:CA:533:A:OP2	2.42	0.42
1:CA:522:C:H41	12:CL:53:ARG:NH2	2.05	0.42
1:CA:945:G:C2	1:CA:946:A:C8	3.07	0.42
1:CA:1011:G:C6	1:CA:1012:U:C2	3.07	0.42
1:CA:1362:C:H2'	1:CA:1363:C:H5"	2.02	0.42
8:CH:77:GLU:HG3	8:CH:78:GLN:N	2.34	0.42
8:CH:138:TRP:CD1	8:CH:138:TRP:C	2.98	0.42
9:CI:82:ALA:HA	9:CI:85:LEU:HD12	2.01	0.42
20:CT:67:ALA:HB2	20:CT:77:ALA:HB2	2.02	0.42
25:DA:266:G:N2	25:DA:427:U:H1'	2.35	0.42
25:DA:828:U:C5	25:DA:2247:A:H4'	2.54	0.42
25:DA:833:U:H2'	25:DA:834:C:C6	2.54	0.42
25:DA:898:C:H3'	25:DA:899:A:C8	2.54	0.42
25:DA:983:A:C6	25:DA:984:A:N1	2.88	0.42
25:DA:1328:G:O2'	25:DA:1329:U:H2'	2.19	0.42
25:DA:1422:G:H1'	25:DA:1496:A:N1	2.35	0.42
26:DB:43:C:H2'	26:DB:45:A:N7	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DB:81:G:C6	26:DB:82:G:C5	3.07	0.42
27:DD:275:LYS:HA	27:DD:275:LYS:HD2	1.86	0.42
28:DE:144:ARG:HB3	28:DE:145:LYS:H	1.44	0.42
29:DF:164:ARG:O	29:DF:168:ARG:HB2	2.20	0.42
30:DG:47:LYS:HB3	30:DG:48:GLU:H	1.62	0.42
31:DH:106:THR:HG23	31:DH:112:PRO:HB3	2.01	0.42
40:DU:83:LEU:O	40:DU:87:GLY:N	2.52	0.42
41:DV:4:ILE:HD12	41:DV:39:LEU:HB3	2.02	0.42
43:DX:31:HIS:HA	43:DX:32:PRO:HD3	1.91	0.42
44:DY:39:VAL:HB	44:DY:42:VAL:HB	2.02	0.42
45:DZ:27:VAL:HG12	45:DZ:85:HIS:HE1	1.83	0.42
52:D6:35:GLU:HG2	52:D6:50:ARG:HD3	2.00	0.42
1:AA:7:G:H5'	1:AA:298:A:O4'	2.17	0.42
1:AA:526:C:P	12:AL:91:LYS:HE3	2.60	0.42
1:AA:1441:G:H5"	1:AA:1442:G:O5'	2.19	0.42
10:AJ:90:LEU:HA	10:AJ:91:PRO:HD3	1.92	0.42
11:AK:97:ALA:O	11:AK:101:SER:HB3	2.19	0.42
13:AM:15:VAL:HG22	13:AM:43:THR:O	2.20	0.42
25:BA:1949:A:C6	25:BA:1950:A:C6	3.08	0.42
25:BA:2152:U:H4'	25:BA:2155:G:H4'	2.02	0.42
25:BA:2329:C:H2'	25:BA:2330:G:O4'	2.18	0.42
25:BA:2453:C:OP2	25:BA:2598:C:O2'	2.37	0.42
25:BA:2566:U:H2'	25:BA:2567:U:C6	2.54	0.42
35:BP:120:ALA:HB1	35:BP:138:LEU:HA	2.02	0.42
1:CA:189:G:H2'	1:CA:189(A):C:C6	2.55	0.42
1:CA:428:G:OP2	4:CD:10:ARG:NH1	2.52	0.42
1:CA:612:C:O2	1:CA:629:G:N2	2.53	0.42
1:CA:922:G:N3	1:CA:1398:A:H2	2.18	0.42
1:CA:1289:A:H2'	1:CA:1290:G:H5'	2.02	0.42
1:CA:1346:A:H61	1:CA:1374:A:H3'	1.85	0.42
1:CA:1499:A:H1'	1:CA:1520:G:H5'	2.01	0.42
5:CE:79:GLU:CD	5:CE:79:GLU:H	2.28	0.42
13:CM:40:ASN:HB3	13:CM:43:THR:HG23	2.02	0.42
13:CM:65:LYS:HA	50:D4:50:VAL:HG11	2.00	0.42
18:CR:52:PRO:O	18:CR:56:THR:HG23	2.20	0.42
23:CW:76:A:OP2	25:DA:2602:A:N6	2.53	0.42
25:DA:142(A):C:H2'	25:DA:143:G:O4'	2.20	0.42
25:DA:263:C:H2'	25:DA:264:C:O4'	2.20	0.42
25:DA:656:G:H2'	25:DA:657:U:O4'	2.19	0.42
25:DA:892:G:C4	25:DA:893:C:H1'	2.54	0.42
25:DA:990:A:H5"	25:DA:991:C:OP1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1453:U:OP1	37:DR:77:ARG:NH1	2.46	0.42
25:DA:1814:G:H5"	27:DD:54:ARG:HH21	1.84	0.42
25:DA:2302:G:C6	25:DA:2315:G:C6	3.08	0.42
25:DA:2356:C:O3'	46:D0:20:ARG:HD3	2.19	0.42
25:DA:2370:G:C6	25:DA:2371:G:C6	3.08	0.42
27:DD:102:LYS:C	27:DD:103:ARG:HG2	2.45	0.42
30:DG:111:LEU:HB2	30:DG:112:PRO:HD3	2.01	0.42
31:DH:86:GLU:HG3	31:DH:132:ARG:NH2	2.34	0.42
31:DH:115:VAL:HG11	31:DH:148:ILE:HD13	2.01	0.42
39:DT:127:ALA:C	39:DT:129:ARG:H	2.27	0.42
47:D1:23:LYS:HB3	47:D1:29:GLY:HA3	2.01	0.42
48:D2:53:LEU:HD23	48:D2:53:LEU:HA	1.67	0.42
52:D6:40:CYS:HA	52:D6:41:PRO:HD3	1.87	0.42
1:AA:397:A:O2'	1:AA:399:G:OP2	2.35	0.42
1:AA:1237:C:O2'	1:AA:1300:G:N1	2.36	0.42
1:AA:1529:G:H4'	1:AA:1530:G:OP2	2.19	0.42
2:AB:77:ALA:CB	2:AB:165:VAL:HG11	2.50	0.42
2:AB:80:ILE:HG13	2:AB:212:GLN:HA	2.01	0.42
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.19	0.42
3:AC:182:ILE:HD13	3:AC:203:PHE:HA	2.02	0.42
15:AO:56:LEU:HD21	25:BA:762:G:C2	2.55	0.42
18:AR:42:ARG:HH21	18:AR:42:ARG:HB3	1.85	0.42
25:BA:485:U:H5"	53:B7:40:TRP:CD2	2.55	0.42
25:BA:701:A:O2'	25:BA:702:A:H5'	2.20	0.42
25:BA:875:U:H4'	25:BA:878:G:N1	2.35	0.42
25:BA:1347:A:O2'	25:BA:1348:A:H3'	2.19	0.42
25:BA:1471:G:H2'	25:BA:1472:G:C8	2.54	0.42
25:BA:2127:C:H2'	25:BA:2128:G:C8	2.55	0.42
25:BA:2665:U:H2'	25:BA:2666:A:C8	2.55	0.42
45:BZ:152:ALA:H	45:BZ:171:ILE:CG1	2.33	0.42
1:CA:203:U:H2'	1:CA:203:U:OP2	2.20	0.42
1:CA:1025:U:O2'	1:CA:1026:G:C8	2.72	0.42
1:CA:1512:U:H2'	1:CA:1513:A:C8	2.54	0.42
3:CC:164:ARG:HG2	3:CC:165:THR:N	2.33	0.42
16:CP:48:TRP:HH2	16:CP:76:GLN:HE22	1.67	0.42
17:CQ:45:HIS:HA	17:CQ:69:LYS:HE3	2.01	0.42
18:CR:56:THR:HB	18:CR:58:LEU:HD22	2.01	0.42
25:DA:244:A:C2	25:DA:255:A:C4	3.08	0.42
25:DA:247:G:H4'	25:DA:386:G:C6	2.55	0.42
25:DA:271(N):U:H3'	25:DA:271(O):C:H5'	2.02	0.42
25:DA:328:U:H4'	44:DY:68:HIS:CG	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:475:U:H4'	25:DA:510:C:H5'	2.01	0.42
25:DA:593:G:H4'	54:D8:4:MET:HE2	2.02	0.42
25:DA:709:U:H2'	25:DA:710:G:H8	1.84	0.42
25:DA:1031:G:H5"	55:D9:8:LYS:HE3	2.01	0.42
25:DA:1675:C:O5'	25:DA:1675:C:H6	2.01	0.42
25:DA:1913:A:H4'	25:DA:1914:C:C5'	2.50	0.42
25:DA:2018:G:H2'	25:DA:2019:A:O4'	2.20	0.42
25:DA:2027:G:H2'	25:DA:2028:U:O4'	2.19	0.42
25:DA:2124:G:C2	25:DA:2174:C:N3	2.88	0.42
25:DA:2526:G:C5	25:DA:2527:C:C5	3.07	0.42
26:DB:80:U:H2'	26:DB:81:G:H8	1.84	0.42
30:DG:33:ARG:O	30:DG:161:THR:HG23	2.19	0.42
38:DS:68:GLN:HE21	38:DS:68:GLN:HA	1.84	0.42
45:DZ:29:TYR:HB3	45:DZ:34:ASN:ND2	2.35	0.42
45:DZ:107:THR:HA	45:DZ:108:PRO:HD3	1.81	0.42
1:AA:737:A:H2'	1:AA:738:C:C6	2.54	0.42
1:AA:787:A:N1	1:AA:795:C:N4	2.66	0.42
1:AA:1051:C:H2'	1:AA:1052:U:C6	2.55	0.42
1:AA:1148:U:O4'	9:AI:16:ARG:HD2	2.19	0.42
57:AA:3216:NEG:H93	61:AA:4239:HOH:O	2.19	0.42
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.84	0.42
3:AC:135:LYS:HZ3	5:AE:52:PRO:HG2	1.85	0.42
20:AT:100:ILE:HB	20:AT:101:GLY:H	1.69	0.42
23:AW:68:C:C2	23:AW:69:G:C8	3.08	0.42
25:BA:142:G:O2'	43:BX:35:THR:HG21	2.19	0.42
25:BA:624:C:O2'	25:BA:628:C:OP1	2.28	0.42
25:BA:653:G:H2'	25:BA:654:G:H8	1.85	0.42
25:BA:1091:A:OP1	25:BA:1091:A:H4'	2.19	0.42
25:BA:1218:G:O2'	25:BA:1219:A:O4'	2.26	0.42
25:BA:1370:G:N7	61:BA:4365:HOH:O	2.36	0.42
25:BA:1550:C:H2'	25:BA:1551:C:C6	2.54	0.42
25:BA:1660:A:P	25:BA:1660:A:H8	2.43	0.42
25:BA:1961:U:OP1	25:BA:2616:U:O2'	2.30	0.42
25:BA:2863:C:H2'	25:BA:2864:G:H8	1.85	0.42
27:BD:233:HIS:HA	61:BD:405:HOH:O	2.20	0.42
30:BG:67:LYS:HG2	30:BG:68:PRO:HD2	2.02	0.42
30:BG:121:ASN:HA	30:BG:122:PRO:HD3	1.80	0.42
34:BO:66:LYS:HA	34:BO:79:PHE:O	2.20	0.42
40:BU:20:LEU:HD23	40:BU:20:LEU:HA	1.83	0.42
45:BZ:23:LYS:HB3	45:BZ:38:TYR:CD1	2.55	0.42
45:BZ:40:ASP:OD2	45:BZ:42:VAL:HG13	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BZ:44:PHE:CZ	45:BZ:86:VAL:HG11	2.55	0.42
46:B0:43:THR:HG23	46:B0:43:THR:O	2.20	0.42
1:CA:130:A:H5'	17:CQ:63:ARG:NE	2.34	0.42
1:CA:134:A:H1'	1:CA:325:A:C5	2.54	0.42
1:CA:154:C:H2'	1:CA:155:C:H6	1.84	0.42
1:CA:165:C:H2'	1:CA:166:G:C8	2.54	0.42
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.32	0.42
1:CA:448:A:OP2	1:CA:485:G:N2	2.31	0.42
1:CA:909:A:H2'	1:CA:910:C:O4'	2.20	0.42
1:CA:967:C:H2'	1:CA:968:A:C8	2.55	0.42
1:CA:975:A:H4'	1:CA:976:G:C5'	2.41	0.42
1:CA:1529:G:H4'	1:CA:1530:G:OP2	2.20	0.42
3:CC:5:ILE:HD11	10:CJ:61:GLU:OE1	2.19	0.42
11:CK:62:GLN:O	11:CK:66:LEU:HG	2.20	0.42
12:CL:83:VAL:HG23	12:CL:107:ALA:HB2	2.01	0.42
13:CM:81:LEU:HD13	13:CM:88:ARG:HG2	2.02	0.42
19:CS:40:ILE:HA	19:CS:44:MET:SD	2.60	0.42
25:DA:645:C:O2	25:DA:645:C:H2'	2.20	0.42
25:DA:988:A:O5'	49:D3:11:SER:HB2	2.20	0.42
25:DA:1002:G:N2	25:DA:1154:G:H1'	2.34	0.42
25:DA:1170:G:N2	25:DA:1179:C:O2	2.53	0.42
25:DA:1503:U:H2'	25:DA:1504:C:C6	2.55	0.42
25:DA:1951:U:O2'	25:DA:1953:A:N7	2.49	0.42
25:DA:2026:C:H2'	25:DA:2027:G:O4'	2.20	0.42
25:DA:2126:A:N3	25:DA:2127:G:H1'	2.35	0.42
25:DA:2331:G:N3	25:DA:2336:A:C2	2.88	0.42
25:DA:2510:C:C4	25:DA:2511:U:C4	3.08	0.42
25:DA:2887:U:H2'	25:DA:2888:C:C6	2.55	0.42
31:DH:16:SER:OG	31:DH:27:LYS:HB2	2.20	0.42
48:D2:32:LEU:HD13	48:D2:36:ARG:NH1	2.34	0.42
1:AA:769:G:H4'	1:AA:1513:A:H4'	2.02	0.42
1:AA:840:C:H4'	1:AA:841:U:OP1	2.19	0.42
1:AA:1149:C:P	9:AI:9:ARG:HH21	2.42	0.42
1:AA:1437:C:H2'	1:AA:1438:G:H8	1.84	0.42
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.84	0.42
15:AO:55:GLY:HA2	15:AO:58:MET:HE3	2.02	0.42
18:AR:40:LEU:HB3	18:AR:79:LEU:HD11	2.02	0.42
23:AW:70:G:H2'	23:AW:71:G:O4'	2.20	0.42
23:AY:25:C:O2'	23:AY:26:A:H8	2.02	0.42
25:BA:831:A:O4'	27:BD:227:ASN:ND2	2.52	0.42
25:BA:880:U:O2	35:BP:55:ARG:NH2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1261:G:OP1	40:BU:8:VAL:HG22	2.20	0.42
25:BA:1360:C:H5'	25:BA:1360:C:H6	1.85	0.42
25:BA:2417:G:O2'	25:BA:2418:U:OP1	2.33	0.42
25:BA:2418:U:H2'	25:BA:2418:U:H6	1.69	0.42
25:BA:2901:A:C6	25:BA:2902:G:C6	3.08	0.42
28:BE:33:VAL:HB	28:BE:47:VAL:CG1	2.50	0.42
28:BE:52:LEU:HD12	28:BE:77:ILE:HD11	2.01	0.42
29:BF:33:LEU:HD12	29:BF:33:LEU:HA	1.88	0.42
30:BG:129:GLY:O	30:BG:161:THR:HB	2.19	0.42
31:BH:144:VAL:O	31:BH:148:ILE:HG13	2.20	0.42
49:B3:3:ARG:CZ	49:B3:36:VAL:HG11	2.50	0.42
1:CA:324:G:N7	61:CA:4083:HOH:O	2.37	0.42
1:CA:406:G:H21	4:CD:119:GLN:HE22	1.68	0.42
1:CA:457:C:H2'	1:CA:458:C:C6	2.55	0.42
1:CA:457:C:H2'	1:CA:458:C:H6	1.85	0.42
1:CA:616:G:OP2	4:CD:141:ARG:NH2	2.43	0.42
1:CA:993:G:H2'	1:CA:995:C:H41	1.85	0.42
1:CA:1060:C:N4	3:CC:2:GLY:HA2	2.35	0.42
1:CA:1288:A:H2'	1:CA:1289:A:O4'	2.20	0.42
1:CA:1318:A:H4'	19:CS:10:PHE:CE1	2.55	0.42
1:CA:1321:C:OP2	1:CA:1322:C:O2'	2.29	0.42
2:CB:31:TYR:HE2	2:CB:194:PRO:HB3	1.85	0.42
2:CB:83:MET:HB3	2:CB:234:PRO:HG2	2.02	0.42
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	2.02	0.42
8:CH:20:TYR:HA	8:CH:65:TYR:CE2	2.55	0.42
9:CI:23:ASN:ND2	9:CI:25:LYS:HG2	2.35	0.42
13:CM:76:ALA:HA	13:CM:79:LYS:HB3	2.00	0.42
24:CX:9:G:N3	24:CX:45:G:H2'	2.34	0.42
57:CX:3004:NEG:C8	57:CX:3004:NEG:HN41	2.33	0.42
25:DA:56:A:H2'	25:DA:57:C:O4'	2.19	0.42
25:DA:68:G:H2'	25:DA:69:C:O4'	2.20	0.42
25:DA:219:G:C6	25:DA:220:G:C6	3.08	0.42
25:DA:954:G:C5	25:DA:955:C:C5	3.08	0.42
25:DA:1164:G:C2	25:DA:1165:U:C2	3.07	0.42
25:DA:1877:A:OP2	25:DA:1877:A:H8	2.03	0.42
25:DA:2037:G:H2'	25:DA:2038:G:C8	2.55	0.42
25:DA:2126:A:N6	25:DA:2162:G:O2'	2.52	0.42
25:DA:2323:G:H2'	25:DA:2324:C:O4'	2.20	0.42
25:DA:2635:C:OP1	28:DE:79:ARG:NH2	2.52	0.42
25:DA:2649:U:H2'	25:DA:2650:U:C6	2.55	0.42
27:DD:134:ARG:HG3	27:DD:134:ARG:H	1.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DD:232:PRO:HB3	27:DD:244:ARG:CZ	2.49	0.42
30:DG:44:GLY:HA2	30:DG:88:ILE:HG22	2.01	0.42
32:DI:61:ARG:HD3	32:DI:61:ARG:HA	1.64	0.42
36:DQ:35:VAL:HG12	36:DQ:130:LYS:O	2.19	0.42
1:AA:200:G:H1	1:AA:217:C:H42	1.67	0.42
1:AA:811:C:O2'	1:AA:901:A:N1	2.43	0.42
1:AA:1044:A:C5	1:AA:1045:C:H1'	2.54	0.42
1:AA:1445:C:C4	1:AA:1446:U:C4	3.08	0.42
57:AA:3216:NEG:C9	23:AW:34:G:H5'	2.50	0.42
25:BA:56:C:H2'	25:BA:57:G:O4'	2.20	0.42
25:BA:233:A:C2	25:BA:244:A:C4	3.08	0.42
25:BA:491:G:P	53:B7:12:ARG:HH22	2.43	0.42
25:BA:593:G:H2'	25:BA:2052:A:N7	2.35	0.42
25:BA:956:A:C5	36:BQ:13:GLN:HG3	2.55	0.42
25:BA:1356:G:OP2	53:B7:9:ARG:HD2	2.20	0.42
25:BA:1432:C:H2'	25:BA:1433:C:C6	2.55	0.42
25:BA:1577:C:O2'	25:BA:1578:C:P	2.78	0.42
25:BA:1577:C:O2'	25:BA:1578:C:H6	2.03	0.42
25:BA:1857:G:H2'	25:BA:1858:C:O4'	2.19	0.42
25:BA:2161:C:C4	25:BA:2162:C:C5	3.08	0.42
25:BA:2163:G:C2	25:BA:2164:C:H1'	2.54	0.42
25:BA:2732:G:OP2	61:BA:4924:HOH:O	2.22	0.42
26:BB:78:A:C2	26:BB:100:A:C4	3.07	0.42
29:BF:64:ILE:HG21	29:BF:78:ILE:HG23	2.02	0.42
30:BG:109:VAL:C	30:BG:112:PRO:HD2	2.45	0.42
44:BY:20:TYR:CE1	44:BY:43:ASN:HA	2.55	0.42
45:BZ:29:TYR:HB3	45:BZ:34:ASN:ND2	2.35	0.42
45:BZ:128:VAL:HG23	45:BZ:160:GLY:O	2.19	0.42
49:B3:26:LEU:O	49:B3:35:ARG:NE	2.51	0.42
1:CA:526:C:OP1	12:CL:91:LYS:HE3	2.19	0.42
1:CA:590:C:H2'	1:CA:591:U:C6	2.55	0.42
1:CA:714:G:H2'	1:CA:715:A:C8	2.55	0.42
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.20	0.42
1:CA:1256:A:H61	1:CA:1278:U:C2'	2.32	0.42
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.55	0.42
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.55	0.42
6:CF:3:ARG:HD3	6:CF:64:GLN:NE2	2.35	0.42
15:CO:26:GLU:CD	15:CO:77:ARG:HE	2.28	0.42
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.55	0.42
25:DA:622:G:H2'	25:DA:623:G:C8	2.54	0.42
25:DA:699:A:H4'	25:DA:1554:A:N6	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:863:A:P	36:DQ:22:LYS:HG3	2.59	0.42
25:DA:1028:A:H62	25:DA:1125:G:H2'	1.85	0.42
25:DA:1741:A:H2'	25:DA:1742:G:O4'	2.20	0.42
25:DA:2360:A:C2	25:DA:2361:A:H1'	2.55	0.42
25:DA:2690:C:OP1	37:DR:17:ARG:NH1	2.31	0.42
33:DN:75:TYR:HA	33:DN:81:GLY:O	2.20	0.42
38:DS:11:LYS:O	38:DS:15:ARG:HG3	2.19	0.42
38:DS:36:TYR:OH	38:DS:54:LEU:HD22	2.20	0.42
45:DZ:146:ILE:H	45:DZ:146:ILE:HG13	1.66	0.42
50:D4:15:ILE:HD13	50:D4:21:VAL:HG13	2.01	0.42
1:AA:19:C:H4'	1:AA:864:A:O4'	2.20	0.41
1:AA:1129:C:C5'	9:AI:16:ARG:HH12	2.30	0.41
1:AA:1516:G:H2'	1:AA:1518:A:OP2	2.20	0.41
6:AF:61:LEU:HD12	6:AF:61:LEU:HA	1.85	0.41
8:AH:26:VAL:HG22	8:AH:59:LEU:HB2	2.01	0.41
22:AV:20:U:H2'	22:AV:21:C:H6	1.84	0.41
25:BA:1440:U:H4'	25:BA:1649:A:H4'	2.02	0.41
25:BA:1616:A:H2'	25:BA:1617:A:O4'	2.19	0.41
25:BA:2647:C:O2'	28:BE:80:GLU:OE1	2.28	0.41
25:BA:2658:C:H2'	25:BA:2659:U:O4'	2.20	0.41
27:BD:112:GLN:O	27:BD:115:GLN:HG2	2.20	0.41
32:BI:110:ASP:HA	32:BI:111:PRO:HD2	1.87	0.41
42:BW:2:GLU:OE2	42:BW:72:LYS:NZ	2.34	0.41
1:CA:50:A:N1	1:CA:360:A:O2'	2.39	0.41
1:CA:192:U:H2'	1:CA:193:C:H6	1.85	0.41
1:CA:224:C:H2'	1:CA:225:C:C6	2.55	0.41
1:CA:300:A:H1'	1:CA:565:U:O2	2.20	0.41
1:CA:904:C:OP2	61:CA:4139:HOH:O	2.21	0.41
1:CA:1096:C:O2	1:CA:1170:A:O2'	2.35	0.41
1:CA:1129:C:H1'	1:CA:1130:A:N7	2.35	0.41
1:CA:1135:U:H2'	1:CA:1137:C:O2	2.20	0.41
4:CD:31:CYS:O	4:CD:35:ARG:HG3	2.19	0.41
7:CG:51:GLN:HE21	7:CG:51:GLN:HB3	1.57	0.41
12:CL:113:ARG:O	12:CL:114:LYS:HD2	2.19	0.41
23:CW:21:A:N6	23:CW:46:7MG:N3	2.67	0.41
25:DA:422:A:H2'	25:DA:423:A:C8	2.55	0.41
25:DA:709:U:H2'	25:DA:710:G:C8	2.55	0.41
25:DA:1169:G:H22	25:DA:1180:C:H42	1.68	0.41
25:DA:2287:A:C4	25:DA:2289:G:C8	3.08	0.41
25:DA:2287:A:N6	25:DA:2344:U:H3	2.06	0.41
25:DA:2330:G:H21	46:D0:42:GLY:N	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2548:G:H2'	25:DA:2549:G:O4'	2.20	0.41
25:DA:2687:U:H2'	25:DA:2688:U:O4'	2.20	0.41
25:DA:2703:C:H2'	25:DA:2704:C:H6	1.84	0.41
26:DB:54:G:H21	30:DG:29:TRP:NE1	2.15	0.41
28:DE:4:ILE:HG22	28:DE:96:PHE:HE2	1.85	0.41
31:DH:129:THR:O	31:DH:129:THR:HG22	2.20	0.41
1:AA:583:A:N6	1:AA:758:G:O2'	2.51	0.41
1:AA:1162:C:H2'	1:AA:1163:C:C6	2.55	0.41
1:AA:1258:G:H2'	1:AA:1259:C:H6	1.84	0.41
2:AB:114:ARG:HG2	2:AB:145:LEU:HD21	2.02	0.41
3:AC:5:ILE:HG12	3:AC:6:HIS:N	2.34	0.41
7:AG:76:ARG:HB3	7:AG:156:TRP:CH2	2.52	0.41
8:AH:9:MET:SD	8:AH:32:LYS:HB3	2.60	0.41
9:AI:21:PRO:HA	9:AI:59:PHE:HA	2.02	0.41
13:AM:17:VAL:O	13:AM:20:THR:OG1	2.26	0.41
13:AM:70:LEU:O	13:AM:74:VAL:HG23	2.20	0.41
25:BA:144:C:H5'	43:BX:2:LYS:HE2	2.02	0.41
25:BA:194:G:O6	47:B1:39:LYS:NZ	2.47	0.41
25:BA:469:A:C6	29:BF:45:ARG:HD2	2.55	0.41
25:BA:821:A:H2'	25:BA:821:A:N3	2.35	0.41
25:BA:873:U:H4'	35:BP:55:ARG:HB2	2.02	0.41
25:BA:940:C:H2'	25:BA:941:U:O4'	2.20	0.41
25:BA:1087:C:H5'	25:BA:1088:G:OP2	2.20	0.41
25:BA:1792:C:C2'	25:BA:1793:A:H5'	2.50	0.41
25:BA:2901:A:C2'	25:BA:2902:G:H5'	2.51	0.41
29:BF:31:HIS:NE2	29:BF:35:GLU:OE2	2.49	0.41
31:BH:3:ARG:HH22	31:BH:66:GLY:HA3	1.85	0.41
31:BH:149:ARG:NH1	31:BH:167:GLU:OE1	2.53	0.41
34:BO:12:ASP:OD1	34:BO:14:THR:OG1	2.24	0.41
45:BZ:11:GLU:HB3	45:BZ:12:GLY:H	1.77	0.41
1:CA:694:A:O2'	23:CY:38:A:O2'	2.32	0.41
1:CA:731:G:H5'	1:CA:766:A:H4'	2.02	0.41
1:CA:973:G:OP1	10:CJ:57:LYS:NZ	2.38	0.41
1:CA:981:U:H5'	14:CN:21:TYR:CZ	2.55	0.41
1:CA:1120:G:N7	1:CA:1154:G:N2	2.68	0.41
1:CA:1140:C:H2'	1:CA:1141:C:H6	1.84	0.41
1:CA:1370:G:N7	9:CI:109:VAL:HG11	2.36	0.41
24:CX:29:G:C6	24:CX:30:G:C5	3.08	0.41
23:CY:21:A:N6	23:CY:46:7MG:H2'	2.32	0.41
25:DA:57:C:H2'	25:DA:58:G:O4'	2.20	0.41
25:DA:117:G:C6	25:DA:119:A:C6	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:250:G:C6	25:DA:251:A:C6	3.07	0.41
25:DA:284:U:H2'	25:DA:285:C:C6	2.55	0.41
25:DA:360:G:H2'	25:DA:361:G:O4'	2.20	0.41
25:DA:942:G:C6	25:DA:943:U:C4	3.08	0.41
25:DA:1028:A:H2'	25:DA:1029:A:C8	2.55	0.41
25:DA:1368:G:C2	25:DA:1369:G:C8	3.08	0.41
25:DA:2250:G:O2'	25:DA:2496:C:OP1	2.31	0.41
29:DF:32:LEU:O	29:DF:36:VAL:HG23	2.20	0.41
30:DG:103:LEU:HA	30:DG:103:LEU:HD23	1.77	0.41
44:DY:6:HIS:H	44:DY:6:HIS:CD2	2.37	0.41
51:D5:41:PRO:HA	51:D5:42:PRO:HD2	1.86	0.41
1:AA:33:A:N3	12:AL:32:PHE:HE2	2.19	0.41
1:AA:115:G:H4'	1:AA:116:A:O5'	2.20	0.41
1:AA:159:G:H3'	1:AA:344:A:C2	2.54	0.41
3:AC:82:GLU:HA	3:AC:85:ARG:HH21	1.84	0.41
15:AO:48:LYS:HD2	15:AO:48:LYS:HA	1.83	0.41
23:AY:50:U:C4	23:AY:64:A:N1	2.88	0.41
25:BA:354:A:H2	25:BA:1255:A:C2'	2.33	0.41
25:BA:1477:U:H2'	25:BA:1478:C:C6	2.55	0.41
25:BA:1715:A:O2'	25:BA:1721:G:N7	2.47	0.41
29:BF:126:VAL:HG21	29:BF:129:PHE:CZ	2.55	0.41
31:BH:27:LYS:HE2	31:BH:27:LYS:HB3	1.87	0.41
32:BI:77:LEU:CB	32:BI:142:VAL:HG12	2.50	0.41
44:BY:5:MET:HE1	44:BY:32:PRO:HA	2.03	0.41
1:CA:114:U:H1'	1:CA:353:A:H1'	2.02	0.41
1:CA:744:C:O2'	1:CA:851:G:N2	2.53	0.41
1:CA:1002:G:C4	1:CA:1003:G:H8	2.37	0.41
1:CA:1024:G:H2'	1:CA:1024:G:N3	2.36	0.41
1:CA:1328:C:O2'	13:CM:29:ARG:NE	2.52	0.41
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.35	0.41
4:CD:11:LEU:O	4:CD:15:GLU:HB2	2.20	0.41
13:CM:57:ARG:NH1	50:D4:34:GLU:HA	2.35	0.41
13:CM:89:GLY:O	13:CM:93:ARG:N	2.53	0.41
17:CQ:6:LEU:HD12	17:CQ:6:LEU:HA	1.86	0.41
25:DA:993:G:C6	25:DA:994:C:C4	3.09	0.41
25:DA:1015:G:O6	25:DA:1148:A:N6	2.53	0.41
25:DA:1268:A:C2	25:DA:2013:A:C4	3.08	0.41
30:DG:125:PHE:HB3	30:DG:166:ASP:CG	2.45	0.41
31:DH:164:TYR:N	31:DH:167:GLU:OE1	2.37	0.41
37:DR:54:LEU:HD12	37:DR:54:LEU:HA	1.95	0.41
41:DV:89:GLN:HA	41:DV:90:PRO:HD3	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:D2:3:LEU:HD23	48:D2:3:LEU:HA	1.81	0.41
1:AA:168:G:O2'	1:AA:169:C:H5'	2.20	0.41
1:AA:198:G:C5	1:AA:220:G:C2	3.08	0.41
1:AA:266:G:O2'	1:AA:267:C:OP2	2.32	0.41
1:AA:332:G:OP2	20:AT:10:LEU:HD12	2.19	0.41
1:AA:670:G:OP2	57:AA:3219:NEG:H91	2.21	0.41
1:AA:674:G:H2'	1:AA:675:A:H8	1.85	0.41
1:AA:719:C:N4	18:AR:71:LYS:HE2	2.35	0.41
1:AA:1055:A:H2'	3:AC:156:ARG:HD2	2.01	0.41
1:AA:1063:C:H3'	1:AA:1064:G:H2'	2.02	0.41
1:AA:1219:U:OP1	14:AN:19:ARG:NH2	2.44	0.41
57:AA:3217:NEG:O4	57:AA:3217:NEG:N4	2.51	0.41
3:AC:33:LEU:O	3:AC:36:ASP:HB2	2.20	0.41
4:AD:17:VAL:HG11	4:AD:197:PRO:HG3	2.02	0.41
4:AD:85:LYS:HG3	4:AD:86:LYS:H	1.86	0.41
11:AK:85:ARG:HG2	11:AK:111:ASP:O	2.20	0.41
19:AS:65:ASN:HD22	19:AS:65:ASN:C	2.29	0.41
23:AW:5:G:C2	23:AW:6:G:C4	3.08	0.41
25:BA:733:G:N2	25:BA:835:A:H61	2.18	0.41
25:BA:785:G:H3'	25:BA:786:G:C8	2.55	0.41
25:BA:1067:A:H61	25:BA:1188:A:N6	2.19	0.41
25:BA:1094:A:N1	25:BA:1158:G:O2'	2.39	0.41
25:BA:1154:U:O2'	25:BA:1155:C:H6	2.03	0.41
25:BA:2290:A:OP2	46:B0:12:ASN:ND2	2.48	0.41
25:BA:2702:C:OP1	37:BR:17:ARG:NH1	2.33	0.41
25:BA:2786:C:H2'	25:BA:2787:C:H6	1.84	0.41
27:BD:70:TRP:HB3	27:BD:190:TYR:CZ	2.55	0.41
30:BG:86:MET:HA	30:BG:87:PRO:HD3	1.94	0.41
1:CA:12:U:H4'	1:CA:526:C:O2'	2.20	0.41
1:CA:202:U:H3'	1:CA:203:U:C6	2.55	0.41
1:CA:256:U:OP1	17:CQ:17:LYS:NZ	2.42	0.41
1:CA:283:C:C2	1:CA:284:G:C8	3.09	0.41
1:CA:1243:C:OP1	21:CU:10:ARG:HB3	2.21	0.41
1:CA:1264:C:H2'	1:CA:1265:G:H8	1.86	0.41
1:CA:1279:A:O2'	1:CA:1282:C:N4	2.54	0.41
3:CC:178:LEU:HD13	3:CC:178:LEU:HA	1.91	0.41
4:CD:150:GLU:O	4:CD:153:ARG:HG2	2.20	0.41
9:CI:34:ASN:OD1	9:CI:34:ASN:N	2.53	0.41
11:CK:120:ARG:HA	11:CK:121:PRO:HD3	1.76	0.41
18:CR:76:LEU:HD12	18:CR:76:LEU:HA	1.85	0.41
19:CS:56:GLN:HE21	19:CS:56:GLN:HB3	1.71	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CV:20:U:H2'	22:CV:21:C:H6	1.84	0.41
24:CX:18:G:C5	24:CX:57:A:C6	3.09	0.41
23:CY:12:U:C2	23:CY:13:C:H1'	2.55	0.41
25:DA:265:A:C8	25:DA:266:G:H1'	2.55	0.41
25:DA:568:U:H5'	25:DA:945:A:N6	2.36	0.41
25:DA:699:A:H2'	25:DA:700:G:O4'	2.21	0.41
25:DA:963:U:H5"	61:DA:4078:HOH:O	2.20	0.41
25:DA:974:G:N2	25:DA:989:G:H1'	2.35	0.41
25:DA:1593:G:H2'	25:DA:1594:G:H8	1.85	0.41
25:DA:2038:G:H2'	25:DA:2039:C:O4'	2.19	0.41
25:DA:2114:A:O2'	25:DA:2167:U:H1'	2.20	0.41
25:DA:2147:G:N1	25:DA:2148:G:N3	2.69	0.41
25:DA:2286:A:H4'	25:DA:2287:A:O4'	2.21	0.41
25:DA:2313:C:H4'	30:DG:91:ARG:HG3	2.02	0.41
25:DA:2562:U:O2'	34:DO:23:ARG:HD3	2.20	0.41
30:DG:19:LEU:HD22	30:DG:32:PRO:HG2	2.02	0.41
30:DG:43:LEU:HD12	30:DG:45:GLU:HG3	2.02	0.41
30:DG:66:GLN:NE2	30:DG:93:THR:O	2.46	0.41
35:DP:96:THR:H	35:DP:99:LEU:HG	1.85	0.41
45:DZ:111:VAL:HG22	45:DZ:174:VAL:HG13	2.03	0.41
1:AA:637:G:H2'	1:AA:638:G:C8	2.55	0.41
1:AA:1098:C:P	2:AB:144:ARG:HH21	2.44	0.41
1:AA:1169:A:C6	1:AA:1170:A:C6	3.08	0.41
1:AA:1296:C:H4'	1:AA:1302:U:C5	2.56	0.41
1:AA:1352:C:H2'	1:AA:1353:G:C8	2.56	0.41
5:AE:31:LEU:HD23	5:AE:31:LEU:HA	1.65	0.41
10:AJ:77:PRO:HB2	10:AJ:78:ASN:H	1.63	0.41
13:AM:96:LEU:O	13:AM:110:ARG:NH1	2.46	0.41
15:AO:16:ALA:HB1	15:AO:21:ASP:HB3	2.03	0.41
23:AY:8:4SU:H6	23:AY:8:4SU:OP2	2.21	0.41
25:BA:330:U:H2'	25:BA:331:G:O4'	2.20	0.41
25:BA:438:G:C5	35:BP:72:PRO:HB3	2.55	0.41
25:BA:708:C:HO2'	35:BP:14:LYS:H	1.66	0.41
25:BA:854:U:O2'	25:BA:2082:A:N1	2.52	0.41
25:BA:1790:A:H1'	25:BA:2723:A:C2	2.54	0.41
25:BA:2846:U:C4	25:BA:2893:A:N6	2.89	0.41
29:BF:170:LEU:HD23	29:BF:172:TRP:CZ2	2.55	0.41
30:BG:5:VAL:HG22	30:BG:8:LYS:H	1.85	0.41
30:BG:16:ARG:HB2	30:BG:17:PRO:HD3	2.02	0.41
37:BR:13:HIS:CE1	37:BR:16:HIS:HB2	2.55	0.41
45:BZ:8:TYR:HB2	45:BZ:38:TYR:CE2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:B8:7:HIS:HB3	54:B8:61:LEU:HB3	2.02	0.41
1:CA:707:C:H2'	1:CA:708:C:H6	1.86	0.41
1:CA:841:U:OP1	1:CA:841:U:H6	2.02	0.41
1:CA:1031:G:H2'	1:CA:1032:G:H8	1.84	0.41
1:CA:1067:A:H8	1:CA:1067:A:O5'	2.03	0.41
1:CA:1316:G:N7	19:CS:7:LYS:NZ	2.61	0.41
2:CB:93:VAL:HG21	2:CB:97:TRP:NE1	2.35	0.41
9:CI:121:ARG:NH1	9:CI:122:ALA:O	2.53	0.41
23:CY:22:G:N7	23:CY:46:7MG:C2	2.89	0.41
25:DA:305:U:H2'	25:DA:306:U:C6	2.55	0.41
25:DA:699:A:H4'	25:DA:1554:A:H61	1.85	0.41
25:DA:817:C:O2'	25:DA:839:U:OP1	2.26	0.41
25:DA:918:A:N3	26:DB:80:U:H4'	2.36	0.41
25:DA:954:G:O2'	25:DA:2274:A:N1	2.49	0.41
25:DA:1589:C:H2'	25:DA:1590:U:C6	2.55	0.41
25:DA:2139:C:C4	25:DA:2153:G:C2	3.08	0.41
25:DA:2144:U:N3	25:DA:2146:C:N3	2.69	0.41
25:DA:2295:C:OP1	38:DS:10:ARG:NH1	2.54	0.41
30:DG:16:ARG:NE	30:DG:31:VAL:HG11	2.35	0.41
32:DI:135:GLU:C	32:DI:137:PRO:HD3	2.46	0.41
34:DO:8:LEU:HB2	34:DO:19:ILE:HG13	2.01	0.41
44:DY:38:ILE:HD13	44:DY:66:PRO:HA	2.02	0.41
1:AA:429:U:H1'	1:AA:430:A:H5"	2.02	0.41
1:AA:974:A:P	14:AN:29:ARG:HH21	2.44	0.41
1:AA:1084:G:C5	1:AA:1085:U:C4	3.08	0.41
7:AG:103:TRP:CH2	7:AG:141:VAL:HG21	2.56	0.41
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.46	0.41
24:AX:32:5MC:HM52	24:AX:33:U:O4	2.20	0.41
25:BA:635:C:H2'	25:BA:636:G:O4'	2.21	0.41
25:BA:669:A:H4'	25:BA:670:C:H5	1.85	0.41
25:BA:998:A:OP2	36:BQ:16:ARG:NE	2.40	0.41
25:BA:1640:G:H2'	25:BA:1641:G:O4'	2.21	0.41
25:BA:1690:G:H2'	25:BA:1691:C:O4'	2.20	0.41
25:BA:2143:G:H2'	25:BA:2144:U:C6	2.56	0.41
25:BA:2902:G:H5"	25:BA:2903:G:O4'	2.21	0.41
26:BB:113:G:H2'	26:BB:114:C:C6	2.56	0.41
30:BG:103:LEU:HD23	30:BG:103:LEU:HA	1.78	0.41
31:BH:149:ARG:HH12	31:BH:167:GLU:CD	2.28	0.41
48:B2:48:HIS:O	48:B2:52:ASP:HB2	2.21	0.41
1:CA:179:A:H2'	1:CA:180:U:H6	1.85	0.41
1:CA:264:U:H2'	1:CA:265:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:543:C:O2'	1:CA:544:G:H5'	2.20	0.41
1:CA:665:A:N3	1:CA:732:C:H2'	2.36	0.41
1:CA:1023:G:C4	1:CA:1024:G:C8	3.09	0.41
7:CG:115:ARG:HG2	7:CG:118:VAL:HG23	2.03	0.41
9:CI:15:ALA:HB2	9:CI:65:VAL:HG23	2.02	0.41
11:CK:77:MET:HE2	11:CK:77:MET:HB2	1.76	0.41
23:CW:27:G:O5'	23:CW:27:G:H8	2.04	0.41
24:CX:64:G:H4'	36:DQ:10:ARG:CZ	2.51	0.41
25:DA:304:G:H2'	25:DA:305:U:H6	1.86	0.41
25:DA:974:G:C4	25:DA:989:G:C2	3.09	0.41
25:DA:1243:G:H2'	25:DA:1244:G:O4'	2.20	0.41
25:DA:1790:C:H5"	25:DA:1791:A:OP1	2.19	0.41
25:DA:2118:U:N3	25:DA:2149:G:H1'	2.36	0.41
25:DA:2127:G:C6	25:DA:2128:C:C5	3.08	0.41
25:DA:2265:U:C4'	36:DQ:13:GLN:HE22	2.34	0.41
25:DA:2468:G:O2'	25:DA:2481:G:N2	2.51	0.41
26:DB:28:C:H2'	26:DB:29:A:H8	1.86	0.41
26:DB:84:C:OP1	49:D3:15:TYR:OH	2.29	0.41
30:DG:31:VAL:HA	30:DG:32:PRO:HD2	1.85	0.41
31:DH:144:VAL:O	31:DH:148:ILE:HG12	2.21	0.41
35:DP:121:LYS:HB3	35:DP:123:LEU:HG	2.02	0.41
43:DX:31:HIS:CD2	43:DX:33:LYS:HB2	2.56	0.41
1:AA:266:G:O3'	17:AQ:67:LYS:HB2	2.21	0.41
1:AA:347:G:HO2'	1:AA:348:G:P	2.36	0.41
1:AA:448:A:C4	1:AA:487:A:C2	3.09	0.41
1:AA:1316:G:H4'	14:AN:18:VAL:HG13	2.02	0.41
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.21	0.41
13:AM:4:ILE:HD12	13:AM:57:ARG:HA	2.02	0.41
18:AR:24:ALA:O	18:AR:26:LEU:N	2.47	0.41
25:BA:174:U:H2'	25:BA:175:G:C8	2.56	0.41
25:BA:490:U:H2'	25:BA:491:G:O4'	2.20	0.41
25:BA:670:C:H5'	25:BA:671:A:OP2	2.21	0.41
25:BA:1036:A:OP1	25:BA:1203:G:H5"	2.20	0.41
25:BA:1188:A:C4	25:BA:1190:G:C8	3.09	0.41
25:BA:1217:G:C5	25:BA:1218:G:C8	3.09	0.41
25:BA:1386:U:H4'	25:BA:1387:U:OP2	2.20	0.41
25:BA:2128:G:N2	25:BA:2205:C:N3	2.58	0.41
30:BG:173:LEU:HD22	30:BG:178:PHE:CE1	2.55	0.41
34:BO:63:VAL:HG12	34:BO:106:LEU:HD11	2.03	0.41
44:BY:65:ALA:HA	44:BY:66:PRO:HD3	1.90	0.41
1:CA:193:C:H2'	1:CA:194:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1493:A:H5"	1:CA:1494:G:OP2	2.21	0.41
5:CE:31:LEU:HD23	5:CE:31:LEU:HA	1.77	0.41
13:CM:56:LEU:O	13:CM:60:VAL:HG12	2.21	0.41
15:CO:55:GLY:HA2	15:CO:58:MET:CE	2.50	0.41
25:DA:143:G:H2'	25:DA:143(A):C:C6	2.55	0.41
25:DA:414:C:H4'	25:DA:1879:C:O2	2.20	0.41
25:DA:848:G:C2	25:DA:933:A:H1'	2.55	0.41
25:DA:954:G:C6	25:DA:955:C:C4	3.09	0.41
25:DA:1227:G:OP2	40:DU:16:LYS:NZ	2.43	0.41
25:DA:2271:G:C5	25:DA:2272:U:C5	3.09	0.41
25:DA:2366:A:H2'	25:DA:2367:G:O4'	2.21	0.41
25:DA:2415:G:O3'	35:DP:66:GLY:HA2	2.19	0.41
25:DA:2516:G:O6	25:DA:2517:C:N4	2.54	0.41
28:DE:12:THR:HG22	28:DE:13:ARG:N	2.35	0.41
30:DG:16:ARG:O	30:DG:20:ILE:HG13	2.20	0.41
30:DG:121:ASN:HA	30:DG:122:PRO:HD3	1.78	0.41
40:DU:17:ILE:HG23	40:DU:39:LEU:HD12	2.02	0.41
1:AA:123:C:OP1	1:AA:311:C:O2'	2.29	0.41
1:AA:580:U:H2'	1:AA:581:G:O4'	2.20	0.41
1:AA:923:A:O2'	1:AA:1399:C:OP2	2.34	0.41
1:AA:1003:G:C2	1:AA:1004:A:N3	2.89	0.41
2:AB:13:ALA:HA	2:AB:17:PHE:HB3	2.03	0.41
3:AC:20:SER:HB3	3:AC:22:TRP:NE1	2.36	0.41
3:AC:27:LYS:HA	3:AC:27:LYS:HD2	1.72	0.41
17:AQ:45:HIS:O	17:AQ:73:VAL:HG23	2.21	0.41
19:AS:12:ASP:C	19:AS:14:HIS:H	2.28	0.41
22:AV:14:A:C2	23:AY:34:G:C2	3.09	0.41
23:AW:18:G:O6	23:AW:55:PSU:H1'	2.21	0.41
25:BA:842:C:H2'	25:BA:843:C:C6	2.56	0.41
25:BA:1027:A:N1	25:BA:2049:G:O2'	2.45	0.41
25:BA:1401:G:H2'	25:BA:1402:G:O4'	2.21	0.41
25:BA:1454:C:H2'	25:BA:1455:C:C6	2.55	0.41
25:BA:1735:U:O2'	25:BA:1747:A:N7	2.41	0.41
25:BA:1814:A:H5'	25:BA:2620:G:H4'	2.03	0.41
25:BA:2052:A:H4'	25:BA:2053:A:C8	2.56	0.41
25:BA:2148:A:H4'	25:BA:2149:G:OP1	2.21	0.41
25:BA:2294:G:OP1	25:BA:2295:C:H1'	2.21	0.41
28:BE:78:LEU:O	28:BE:79:ARG:HG2	2.21	0.41
39:BT:108:ARG:HA	39:BT:111:ARG:NH1	2.36	0.41
1:CA:448:A:P	1:CA:485:G:H22	2.43	0.41
1:CA:892:A:H2'	1:CA:893:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1019:C:H2'	1:CA:1020:U:O4'	2.21	0.41
1:CA:1229:A:OP2	13:CM:114:ARG:HD3	2.20	0.41
3:CC:42:LEU:HA	3:CC:45:LYS:HZ3	1.86	0.41
3:CC:71:ALA:CA	3:CC:106:VAL:HB	2.51	0.41
6:CF:61:LEU:HD12	6:CF:61:LEU:HA	1.88	0.41
24:CX:61:C:H2'	24:CX:62:C:H6	1.86	0.41
25:DA:121:G:H4'	25:DA:149:A:H5'	2.01	0.41
25:DA:820:A:C2	25:DA:821:A:C4	3.08	0.41
25:DA:860:U:O2'	25:DA:861:A:H5'	2.20	0.41
25:DA:1797:C:H4'	27:DD:257:LEU:O	2.21	0.41
25:DA:1839:G:C8	25:DA:1927:A:H1'	2.56	0.41
25:DA:2415:G:O2'	35:DP:67:MET:HG3	2.21	0.41
25:DA:2545:G:N3	25:DA:2565:A:H2	2.19	0.41
25:DA:2553:G:H5"	25:DA:2554:U:OP2	2.20	0.41
25:DA:2821:A:C2	25:DA:2822:G:C4	3.09	0.41
27:DD:72:LYS:NZ	27:DD:101:GLU:OE2	2.45	0.41
30:DG:16:ARG:HE	30:DG:31:VAL:HG11	1.85	0.41
30:DG:28:VAL:O	30:DG:31:VAL:HG12	2.21	0.41
32:DI:57:ARG:HH22	32:DI:58:LEU:HD12	1.84	0.41
33:DN:96:GLU:H	33:DN:96:GLU:CD	2.28	0.41
35:DP:27:HIS:O	35:DP:31:ALA:HA	2.21	0.41
49:D3:6:VAL:HG12	49:D3:28:LEU:HD11	2.02	0.41
1:AA:57:G:H2'	1:AA:58:C:C6	2.56	0.41
1:AA:265:G:H2'	1:AA:267:C:H5	1.85	0.41
1:AA:270:A:H2'	1:AA:271:C:C6	2.56	0.41
1:AA:276:G:O3'	17:AQ:68:ARG:NH1	2.54	0.41
1:AA:348:G:C2'	1:AA:349:A:H5'	2.51	0.41
1:AA:377:G:OP1	16:AP:5:ARG:HD2	2.21	0.41
1:AA:526:C:OP1	12:AL:91:LYS:HE3	2.21	0.41
1:AA:540:G:H2'	1:AA:541:G:O4'	2.21	0.41
1:AA:564:C:H5'	17:AQ:32:TYR:CE1	2.56	0.41
1:AA:925:G:H1'	1:AA:1502:A:C4	2.56	0.41
1:AA:1003:G:H2'	1:AA:1004:A:C4'	2.49	0.41
1:AA:1210:C:N4	1:AA:1211:U:O4	2.54	0.41
1:AA:1229:A:O3'	24:AX:30:G:H5"	2.20	0.41
1:AA:1292:U:H2'	1:AA:1293:G:C8	2.56	0.41
1:AA:1325:C:H4'	21:AU:17:THR:HG21	2.02	0.41
2:AB:17:PHE:HA	2:AB:44:LEU:HD11	2.03	0.41
3:AC:82:GLU:HA	3:AC:85:ARG:HE	1.86	0.41
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.91	0.41
5:AE:45:PHE:CE2	5:AE:47:LYS:HE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:99:ALA:HB1	18:AR:23:LYS:HZ2	1.85	0.41
8:AH:69:ARG:HG3	8:AH:76:PRO:HA	2.03	0.41
12:AL:7:ILE:HD13	12:AL:7:ILE:HA	1.85	0.41
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.84	0.41
23:AW:54:5MU:H2'	23:AW:55:PSU:O4'	2.21	0.41
23:AY:55:PSU:C2	23:AY:57:G:H5'	2.56	0.41
25:BA:123:G:N2	53:B7:9:ARG:HB3	2.36	0.41
25:BA:672:G:H8	25:BA:672:G:O5'	2.04	0.41
25:BA:782:A:N7	25:BA:808:A:H2	2.19	0.41
25:BA:905:U:O2	25:BA:2280:A:H2'	2.20	0.41
25:BA:1321:A:O2'	25:BA:1692:G:N3	2.53	0.41
25:BA:1414:G:C2	25:BA:1415:G:C8	3.09	0.41
25:BA:1541:A:C6	25:BA:1542:A:C6	3.09	0.41
25:BA:1594:C:H2'	25:BA:1595:C:H6	1.84	0.41
25:BA:2271:G:C8	25:BA:2439:C:C4	3.09	0.41
25:BA:2584:A:O5'	25:BA:2586:G:H4'	2.21	0.41
27:BD:79:VAL:HG12	27:BD:113:VAL:HA	2.03	0.41
27:BD:123:ALA:HA	27:BD:124:PRO:HD3	1.93	0.41
27:BD:146:GLU:HB2	27:BD:189:CYS:HB3	2.02	0.41
29:BF:129:PHE:CD1	29:BF:163:VAL:HG21	2.55	0.41
30:BG:41:GLN:NE2	30:BG:153:ARG:HB3	2.36	0.41
30:BG:125:PHE:CZ	30:BG:170:ARG:HA	2.56	0.41
33:BN:121:LYS:HG2	33:BN:130:HIS:NE2	2.36	0.41
35:BP:38:GLN:HG2	35:BP:45:LEU:HD23	2.02	0.41
39:BT:51:ARG:HG3	39:BT:98:LYS:HD2	2.02	0.41
45:BZ:30:ASN:OD1	45:BZ:33:LEU:HD23	2.21	0.41
48:B2:32:LEU:HD13	48:B2:36:ARG:NH1	2.35	0.41
52:B6:21:TYR:CD1	52:B6:38:LYS:HG2	2.56	0.41
1:CA:89:C:H2'	1:CA:90:U:O4'	2.21	0.41
1:CA:174:C:H2'	1:CA:175:C:C6	2.55	0.41
1:CA:189(D):C:H2'	1:CA:189(E):U:O4'	2.21	0.41
1:CA:297:G:H4'	1:CA:557:G:H4'	2.03	0.41
1:CA:735:C:H2'	1:CA:736:C:C6	2.56	0.41
1:CA:977:A:H2	1:CA:1224:G:C6	2.38	0.41
1:CA:1126:U:N3	10:CJ:40:LEU:HD11	2.34	0.41
1:CA:1137:C:H5"	1:CA:1138:G:OP1	2.21	0.41
1:CA:1148:U:H2'	1:CA:1149:C:O4'	2.21	0.41
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.21	0.41
1:CA:1287:A:C6	1:CA:1288:A:C6	3.09	0.41
1:CA:1400:C:H5'	22:CV:18:G:C6	2.56	0.41
1:CA:1428:A:H2'	1:CA:1429:C:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1434:A:H61	1:CA:1467:G:H1'	1.86	0.41
2:CB:8:LYS:HG3	2:CB:9:GLU:H	1.85	0.41
3:CC:180:ALA:O	3:CC:181:ASN:C	2.64	0.41
4:CD:166:LYS:HD3	4:CD:166:LYS:HA	1.91	0.41
7:CG:89:MET:SD	7:CG:155:ARG:HB2	2.61	0.41
7:CG:111:ARG:HB3	7:CG:111:ARG:HH11	1.86	0.41
13:CM:43:THR:OG1	13:CM:48:LEU:HD21	2.21	0.41
15:CO:85:LEU:HD23	15:CO:85:LEU:HA	1.94	0.41
16:CP:74:LEU:O	16:CP:79:VAL:HG23	2.20	0.41
18:CR:59:SER:OG	18:CR:62:GLU:HG2	2.20	0.41
20:CT:42:GLN:O	20:CT:45:GLN:HB3	2.21	0.41
23:CW:14:A:H2'	23:CW:15:G:O4'	2.21	0.41
23:CY:34:G:C6	23:CY:35:A:C6	3.08	0.41
25:DA:27:G:C2	25:DA:512:G:N3	2.88	0.41
25:DA:300:A:N1	25:DA:333:G:O2'	2.48	0.41
25:DA:307:G:H22	25:DA:310:A:P	2.43	0.41
25:DA:534:U:H2'	25:DA:535:C:C6	2.56	0.41
25:DA:918:A:C5	25:DA:919:G:H1'	2.55	0.41
25:DA:956:G:H2'	25:DA:957:A:H2'	2.03	0.41
25:DA:980:A:C4	25:DA:1136:G:O4'	2.74	0.41
25:DA:1330:C:O2'	25:DA:1331:A:H5'	2.21	0.41
25:DA:1668:A:C8	25:DA:1674:G:C6	3.09	0.41
25:DA:1880:C:H2'	25:DA:1881:C:H6	1.86	0.41
25:DA:1900:A:N1	25:DA:1970:A:C6	2.89	0.41
25:DA:1999:C:H2'	25:DA:2000:G:O4'	2.20	0.41
25:DA:2110:G:H1'	25:DA:2111:C:OP1	2.21	0.41
25:DA:2167:U:O2	25:DA:2167:U:H2'	2.20	0.41
25:DA:2278:A:OP1	36:DQ:11:LYS:HD2	2.21	0.41
25:DA:2552:U:C2	25:DA:2554:U:H5'	2.56	0.41
25:DA:2572:A:O5'	25:DA:2574:G:H4'	2.20	0.41
25:DA:2607:G:H2'	25:DA:2608:G:O4'	2.21	0.41
25:DA:2712:U:H2'	25:DA:2714:G:H5"	2.03	0.41
26:DB:28:C:H5"	38:DS:31:SER:HB3	2.03	0.41
26:DB:44:G:OP1	30:DG:98:ARG:NH2	2.44	0.41
28:DE:52:LEU:HB3	28:DE:76:ARG:HD3	2.02	0.41
29:DF:33:LEU:HD12	29:DF:33:LEU:HA	1.77	0.41
29:DF:172:TRP:CD1	29:DF:172:TRP:H	2.38	0.41
31:DH:98:LEU:HB2	31:DH:125:VAL:HG23	2.02	0.41
33:DN:104:LYS:HA	33:DN:107:LEU:HD12	2.02	0.41
34:DO:10:VAL:HG21	34:DO:16:ALA:HB3	2.03	0.41
36:DQ:17:LEU:HB3	36:DQ:39:PRO:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DQ:29:PHE:HB2	36:DQ:105:GLU:OE2	2.20	0.41
41:DV:5:VAL:CG1	41:DV:57:VAL:HG21	2.50	0.41
43:DX:84:ALA:HB3	43:DX:87:GLN:NE2	2.36	0.41
55:D9:22:ARG:NH1	55:D9:35:ARG:HD2	2.36	0.41
1:AA:262:A:C6	1:AA:263:A:C6	3.08	0.41
1:AA:684:A:H1'	11:AK:39:PRO:HD2	2.02	0.41
1:AA:743:U:H2'	1:AA:744:C:C6	2.55	0.41
1:AA:1095:U:H2'	1:AA:1096:C:O4'	2.21	0.41
1:AA:1226:C:H4'	19:AS:80:TYR:OH	2.20	0.41
5:AE:76:ILE:O	5:AE:93:PRO:HB3	2.21	0.41
9:AI:113:LYS:HD2	9:AI:119:ALA:O	2.21	0.41
10:AJ:5:ARG:O	10:AJ:98:ILE:HA	2.21	0.41
25:BA:2128:G:H2'	25:BA:2129:C:C6	2.56	0.41
25:BA:2148:A:N3	25:BA:2149:G:H1'	2.36	0.41
25:BA:2172:U:N3	25:BA:2173:G:N7	2.69	0.41
25:BA:2360:U:O4	25:BA:2394:G:N1	2.54	0.41
25:BA:2579:G:H2'	25:BA:2580:C:C6	2.56	0.41
25:BA:2650:G:P	28:BE:82:ARG:HH22	2.44	0.41
27:BD:10:THR:OG1	27:BD:13:ARG:HG2	2.21	0.41
27:BD:13:ARG:HD2	27:BD:13:ARG:HA	1.76	0.41
30:BG:56:ALA:HA	30:BG:153:ARG:HH21	1.86	0.41
48:B2:30:ARG:O	48:B2:34:GLU:HG3	2.20	0.41
1:CA:401:C:H1'	1:CA:622:A:H1'	2.04	0.41
1:CA:442:C:H42	1:CA:492:G:H1	1.68	0.41
1:CA:717:C:O2'	1:CA:734:G:O4'	2.28	0.41
1:CA:984:C:H2'	1:CA:985:C:C6	2.56	0.41
1:CA:1206:G:C6	1:CA:1207:G:C5	3.09	0.41
1:CA:1272:G:H2'	1:CA:1273:G:O4'	2.21	0.41
2:CB:16:HIS:HB3	2:CB:210:SER:CB	2.51	0.41
2:CB:175:ARG:HB3	2:CB:175:ARG:NH1	2.36	0.41
5:CE:72:GLN:O	5:CE:75:THR:HG22	2.21	0.41
23:CY:18:G:N2	23:CY:55:PSU:C4	2.89	0.41
25:DA:83:G:N1	25:DA:102:G:O2'	2.44	0.41
25:DA:187:G:N3	25:DA:1365:A:H2	2.19	0.41
25:DA:374:A:C2	25:DA:401:A:C4	3.09	0.41
25:DA:581:C:H2'	25:DA:582:G:C8	2.56	0.41
25:DA:634:C:H2'	25:DA:635:C:C6	2.56	0.41
25:DA:1002:G:H2'	25:DA:1003:G:O4'	2.21	0.41
25:DA:1344:G:C6	25:DA:1385:G:N7	2.89	0.41
25:DA:1983:C:H4'	25:DA:2606:C:H4'	2.03	0.41
25:DA:2651:C:C2'	25:DA:2652:C:H5'	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2704:C:H2'	25:DA:2705:A:O4'	2.21	0.41
26:DB:78:A:C2	26:DB:100:A:C4	3.09	0.41
28:DE:50:GLY:CA	28:DE:75:VAL:HG11	2.50	0.41
29:DF:156:LEU:HD21	29:DF:163:VAL:HG12	2.02	0.41
30:DG:58:GLN:HA	30:DG:58:GLN:OE1	2.21	0.41
33:DN:39:ARG:HA	33:DN:40:PRO:HD3	1.90	0.41
33:DN:72:TYR:N	33:DN:85:ILE:O	2.52	0.41
37:DR:79:LEU:HD23	37:DR:83:ILE:HD12	2.03	0.41
40:DU:113:ALA:O	40:DU:117:GLN:HG2	2.21	0.41
1:AA:22:G:H4'	1:AA:885:G:C8	2.57	0.40
1:AA:295:C:H2'	1:AA:296:U:O4'	2.21	0.40
1:AA:649:G:H2'	1:AA:650:G:C8	2.55	0.40
1:AA:791:G:N2	1:AA:1497:G:O3'	2.54	0.40
1:AA:1053:G:H3'	57:AA:3216:NEG:H72	2.02	0.40
1:AA:1059:C:OP2	3:AC:199:LYS:NZ	2.42	0.40
1:AA:1327:C:O2'	1:AA:1328:C:H5'	2.21	0.40
1:AA:1399:C:H4'	1:AA:1400:C:O5'	2.21	0.40
1:AA:1446:U:O2'	1:AA:1447:A:O5'	2.40	0.40
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.20	0.40
3:AC:152:ILE:HG23	3:AC:167:TRP:HB3	2.03	0.40
4:AD:148:VAL:HG12	4:AD:149:ALA:O	2.21	0.40
4:AD:173:TRP:HE1	4:AD:193:ASP:HB3	1.86	0.40
10:AJ:12:ASP:OD2	10:AJ:15:THR:HG23	2.21	0.40
23:AW:9:A:H1'	23:AW:45:U:O2'	2.20	0.40
23:AW:75:C:H2'	23:AW:76:A:N9	2.36	0.40
25:BA:831:A:C6	27:BD:229:VAL:HG11	2.56	0.40
25:BA:1541:A:H2'	25:BA:1542:A:C8	2.55	0.40
25:BA:1572:G:C6	25:BA:1573:G:C2	3.09	0.40
25:BA:1727:U:O2	25:BA:1794:G:H3'	2.20	0.40
25:BA:2204:G:C2	25:BA:2205:C:C2	3.09	0.40
25:BA:2324:U:O2'	30:BG:40:ASN:ND2	2.49	0.40
25:BA:2368:C:H2'	25:BA:2369:U:O4'	2.21	0.40
30:BG:31:VAL:HA	30:BG:32:PRO:HD2	1.75	0.40
33:BN:36:GLY:HA2	33:BN:38:HIS:CE1	2.56	0.40
36:BQ:42:ILE:HG22	36:BQ:47:ILE:HG13	2.02	0.40
37:BR:2:ARG:NH1	37:BR:5:LYS:O	2.54	0.40
39:BT:127:ALA:C	39:BT:129:ARG:N	2.79	0.40
41:BV:21:ARG:HG2	41:BV:91:TYR:CD1	2.56	0.40
54:B8:6:THR:HG22	54:B8:62:LEU:HA	2.03	0.40
1:CA:120:A:O2'	1:CA:122:G:OP1	2.27	0.40
1:CA:583:A:H2'	1:CA:584:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1055:A:H8	1:CA:1055:A:OP2	2.04	0.40
1:CA:1065:U:H1'	1:CA:1066:C:OP2	2.21	0.40
1:CA:1144:G:H21	1:CA:1146:A:H62	1.69	0.40
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.56	0.40
1:CA:1216:G:H5"	14:CN:5:ALA:HB2	2.03	0.40
2:CB:112:VAL:O	2:CB:116:GLU:N	2.34	0.40
5:CE:41:VAL:O	5:CE:67:VAL:HG12	2.20	0.40
16:CP:8:ARG:HG3	16:CP:17:TYR:CE1	2.56	0.40
23:CY:52:G:C2	23:CY:53:G:H1'	2.55	0.40
25:DA:247:G:O6	54:D8:12:LYS:NZ	2.50	0.40
25:DA:805:G:C4'	35:DP:38:GLN:HB2	2.51	0.40
25:DA:874:G:H2'	25:DA:875:G:O4'	2.21	0.40
25:DA:1148:A:O2'	25:DA:1149:G:H5'	2.21	0.40
25:DA:1472:A:N6	25:DA:1519:G:H1'	2.36	0.40
25:DA:1800:C:OP1	27:DD:264:LYS:NZ	2.48	0.40
28:DE:181:LEU:HD12	28:DE:181:LEU:HA	1.84	0.40
45:DZ:10:ARG:HG3	45:DZ:36:LYS:HB3	2.03	0.40
45:DZ:29:TYR:O	45:DZ:89:PHE:HD1	2.04	0.40
48:D2:1:MET:SD	48:D2:56:GLN:NE2	2.94	0.40
50:D4:28:LYS:HA	50:D4:29:PRO:HD3	1.89	0.40
53:D7:5:TRP:CD1	53:D7:7:PRO:HD3	2.56	0.40
1:AA:303:A:H2'	1:AA:304:U:O4'	2.21	0.40
1:AA:1003:G:C2	1:AA:1004:A:H1'	2.55	0.40
1:AA:1289:A:H2'	1:AA:1290:G:H5'	2.03	0.40
1:AA:1324:A:O4'	1:AA:1362:C:H4'	2.22	0.40
4:AD:103:ASN:O	4:AD:107:ARG:HG2	2.21	0.40
11:AK:65:ALA:HB3	11:AK:97:ALA:HB3	2.04	0.40
11:AK:98:LEU:O	11:AK:101:SER:OG	2.30	0.40
12:AL:24:VAL:HG13	12:AL:98:TYR:CE1	2.56	0.40
13:AM:80:ARG:NH2	19:AS:69:HIS:CE1	2.89	0.40
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	2.03	0.40
25:BA:228:U:H2'	25:BA:229:G:O4'	2.21	0.40
25:BA:493:G:OP1	53:B7:33:ARG:NH1	2.55	0.40
25:BA:831:A:C5	27:BD:229:VAL:HG21	2.55	0.40
25:BA:863:C:H2'	25:BA:864:C:C6	2.55	0.40
25:BA:1684:A:H5'	25:BA:1791:A:O2'	2.21	0.40
25:BA:2152:U:H2'	25:BA:2153:G:N2	2.35	0.40
25:BA:2186:C:H5	25:BA:2187:G:C4	2.39	0.40
25:BA:2402:U:O2'	25:BA:2403:G:H5'	2.21	0.40
25:BA:2564:U:C2	25:BA:2566:U:H5'	2.57	0.40
30:BG:137:GLU:HB2	30:BG:140:ILE:HD13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BP:70:GLN:O	35:BP:73:GLY:N	2.49	0.40
36:BQ:134:ARG:HA	36:BQ:138:ASP:OD2	2.21	0.40
37:BR:26:LYS:HE2	37:BR:70:LEU:O	2.21	0.40
42:BW:86:LEU:HD22	42:BW:96:ILE:HD11	2.02	0.40
44:BY:15:VAL:HG21	44:BY:42:VAL:HG11	2.02	0.40
51:B5:59:GLU:HG2	51:B5:60:VAL:N	2.36	0.40
1:CA:353:A:H5'	1:CA:353:A:C8	2.52	0.40
1:CA:946:A:C6	1:CA:947:G:C6	3.08	0.40
1:CA:975:A:H8	1:CA:975:A:H5'	1.87	0.40
1:CA:976:G:C8	1:CA:1358:U:C2	3.08	0.40
1:CA:1004:A:N6	1:CA:1037:C:C2	2.89	0.40
7:CG:114:ARG:H	7:CG:114:ARG:HG2	1.64	0.40
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.54	0.40
10:CJ:6:ILE:HB	10:CJ:72:VAL:CG2	2.51	0.40
19:CS:28:LYS:HB2	19:CS:29:ARG:CB	2.51	0.40
21:CU:6:ARG:HG2	21:CU:15:ARG:HD2	2.03	0.40
23:CY:30:G:H2'	23:CY:31:A:H8	1.86	0.40
25:DA:49:A:H5"	25:DA:51:G:O4'	2.21	0.40
25:DA:235:U:H2'	25:DA:236:C:C6	2.57	0.40
25:DA:886:C:H3'	25:DA:887:A:H5"	2.02	0.40
25:DA:1581:G:H2'	25:DA:1582:C:O4'	2.20	0.40
25:DA:2040:C:H2'	25:DA:2041:U:O4'	2.21	0.40
25:DA:2335:A:C8	25:DA:2337:G:C5	3.08	0.40
25:DA:2820:A:C6	37:DR:4:LEU:HD11	2.57	0.40
26:DB:94:C:H2'	26:DB:95:C:H6	1.85	0.40
28:DE:9:VAL:HB	39:DT:3:ARG:HG2	2.04	0.40
29:DF:20:LEU:HA	29:DF:20:LEU:HD23	1.76	0.40
30:DG:124:SER:HB2	30:DG:131:TYR:CE1	2.57	0.40
34:DO:92:GLU:OE2	34:DO:113:LYS:NZ	2.30	0.40
36:DQ:41:TRP:HB3	36:DQ:94:VAL:HG21	2.02	0.40
40:DU:83:LEU:HB3	40:DU:88:ILE:HB	2.02	0.40
45:DZ:53:ILE:H	45:DZ:53:ILE:HG13	1.64	0.40
52:D6:8:LYS:HD3	54:D8:34:TRP:CD2	2.56	0.40
1:AA:109:A:C8	1:AA:326:G:H2'	2.57	0.40
1:AA:179:A:H2'	1:AA:180:U:H6	1.87	0.40
1:AA:427:U:H1'	1:AA:541:G:OP1	2.21	0.40
1:AA:1137:C:H5"	1:AA:1138:G:OP1	2.21	0.40
1:AA:1367:C:H2'	1:AA:1368:G:O4'	2.21	0.40
2:AB:54:THR:HG23	2:AB:199:TYR:HB3	2.02	0.40
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.22	0.40
2:AB:122:PHE:HE1	2:AB:139:LYS:N	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:170:GLU:O	2:AB:174:VAL:HG23	2.22	0.40
5:AE:113:ALA:HB3	5:AE:115:VAL:HG23	2.03	0.40
13:AM:19:LEU:HA	13:AM:19:LEU:HD13	1.74	0.40
23:AW:4:C:H2'	23:AW:5:G:H8	1.85	0.40
25:BA:152:G:H2'	25:BA:153:C:C6	2.56	0.40
25:BA:772:G:C6	25:BA:773:G:N1	2.89	0.40
25:BA:1314:A:C2	25:BA:2035:A:C4	3.10	0.40
25:BA:1570:G:H2'	25:BA:1571:G:O4'	2.21	0.40
25:BA:2132:G:H5"	25:BA:2167:C:N4	2.36	0.40
25:BA:2544:G:O2'	25:BA:2669:A:N1	2.50	0.40
27:BD:142:VAL:HG13	27:BD:191:ALA:HB1	2.03	0.40
29:BF:14:PRO:HD2	29:BF:127:GLU:OE2	2.21	0.40
32:BI:102:SER:O	32:BI:106:GLY:HA3	2.21	0.40
35:BP:59:LEU:HD13	35:BP:60:MET:HE2	2.02	0.40
42:BW:71:VAL:HA	42:BW:107:LEU:HD12	2.03	0.40
44:BY:49:VAL:HG21	44:BY:61:ILE:HG23	2.02	0.40
44:BY:54:LYS:HA	44:BY:55:TYR:HA	1.79	0.40
45:BZ:87:ASP:OD2	61:BZ:3101:HOH:O	2.22	0.40
45:BZ:121:HIS:HB2	45:BZ:171:ILE:HG22	2.04	0.40
53:B7:33:ARG:HH11	53:B7:33:ARG:HD2	1.75	0.40
1:CA:552:U:O3'	12:CL:87:GLY:HA3	2.21	0.40
1:CA:580:U:H2'	1:CA:581:G:O4'	2.20	0.40
1:CA:674:G:H2'	1:CA:675:A:C8	2.52	0.40
1:CA:971:G:P	1:CA:1231:G:H21	2.43	0.40
1:CA:1038:C:O2'	1:CA:1039:C:H5'	2.21	0.40
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.56	0.40
1:CA:1091:U:C2	1:CA:1093:A:OP2	2.75	0.40
1:CA:1330:U:H4'	13:CM:23:TYR:CE1	2.56	0.40
2:CB:180:LEU:HD23	2:CB:180:LEU:HA	1.89	0.40
8:CH:39:LEU:HD13	8:CH:39:LEU:HA	1.87	0.40
8:CH:82:HIS:NE2	8:CH:136:GLU:OE2	2.53	0.40
9:CI:28:VAL:HA	9:CI:63:ILE:O	2.21	0.40
16:CP:40:ASP:HB3	16:CP:48:TRP:CB	2.51	0.40
23:CW:52:G:C6	23:CW:63:G:C6	3.10	0.40
23:CW:66:U:C4	23:CW:67:C:C2	3.09	0.40
25:DA:58:G:O2'	25:DA:73:A:N1	2.50	0.40
25:DA:242:G:C8	54:D8:5:LYS:HG2	2.56	0.40
25:DA:302:C:OP1	44:DY:101:LYS:NZ	2.40	0.40
25:DA:667:U:O2	54:D8:2:PRO:HD2	2.20	0.40
25:DA:861:A:H2'	25:DA:862:G:O4'	2.22	0.40
25:DA:990:A:H1'	25:DA:1156:A:N3	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1028:A:N6	25:DA:1125:G:H2'	2.37	0.40
25:DA:1418:G:H2'	25:DA:1579:A:H62	1.85	0.40
25:DA:2432:A:C6	25:DA:2433:A:C6	3.09	0.40
25:DA:2615:U:N1	51:D5:7:PRO:HA	2.36	0.40
25:DA:2715:C:H2'	25:DA:2716:U:C6	2.57	0.40
25:DA:2784:C:H2'	25:DA:2785:C:C6	2.57	0.40
29:DF:18:ARG:HG2	29:DF:19:GLU:H	1.86	0.40
29:DF:124:LEU:HB3	29:DF:193:VAL:HG22	2.03	0.40
31:DH:43:VAL:HG13	31:DH:52:VAL:HG22	2.03	0.40
34:DO:15:GLY:O	34:DO:47:ILE:HG12	2.22	0.40
34:DO:22:ILE:HG12	34:DO:40:VAL:O	2.22	0.40
44:DY:56:PRO:C	44:DY:58:GLY:H	2.30	0.40
1:AA:187:C:O2'	20:AT:89:ARG:NH2	2.53	0.40
1:AA:257:G:H2'	1:AA:258:G:O4'	2.21	0.40
1:AA:684:A:O2'	11:AK:39:PRO:O	2.40	0.40
1:AA:789:U:O2'	1:AA:791:G:N7	2.50	0.40
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.56	0.40
2:AB:108:ILE:HD13	2:AB:108:ILE:HA	1.92	0.40
7:AG:65:ALA:HB1	7:AG:127:ALA:HB3	2.03	0.40
19:AS:27:GLU:HG2	19:AS:47:HIS:CE1	2.56	0.40
20:AT:63:ILE:HG22	20:AT:77:ALA:HB1	2.03	0.40
23:AW:55:PSU:O3'	25:BA:943:C:H4'	2.21	0.40
24:AX:76:A:H1'	61:AX:3101:HOH:O	2.21	0.40
23:AY:49:C:N4	23:AY:65:G:N1	2.38	0.40
25:BA:470:C:H4'	29:BF:49:ALA:HB2	2.03	0.40
25:BA:1516:A:H2'	25:BA:1517:G:O4'	2.20	0.40
25:BA:1752:G:C6	25:BA:1753:U:C4	3.10	0.40
25:BA:1780:A:H2'	25:BA:1781:G:O4'	2.21	0.40
25:BA:2012:C:H2'	25:BA:2013:U:O4'	2.21	0.40
25:BA:2573:A:H2'	25:BA:2574:U:O4'	2.21	0.40
28:BE:3:GLY:HA3	28:BE:81:ILE:HD12	2.03	0.40
29:BF:34:TRP:CH2	35:BP:8:PRO:HB3	2.56	0.40
29:BF:111:ALA:HB2	29:BF:206:ILE:HG21	2.04	0.40
30:BG:126:ASP:HB2	30:BG:130:ASN:O	2.21	0.40
31:BH:20:ALA:HB1	31:BH:21:PRO:HD2	2.03	0.40
40:BU:16:LYS:HB3	40:BU:16:LYS:HE2	1.95	0.40
40:BU:76:TYR:CZ	40:BU:80:ILE:HG13	2.56	0.40
48:B2:9:GLN:HE22	48:B2:56:GLN:HB3	1.85	0.40
54:B8:38:GLY:O	54:B8:42:ARG:HB2	2.21	0.40
1:CA:521:G:O2'	1:CA:522:C:H5'	2.21	0.40
1:CA:555:C:H2'	1:CA:556:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:836:G:C6	1:CA:851:G:C5	3.10	0.40
1:CA:919:A:O2'	1:CA:1080:A:N1	2.38	0.40
1:CA:954:G:H21	1:CA:1227:A:H62	1.68	0.40
1:CA:1338:G:C6	1:CA:1339:A:C6	3.10	0.40
2:CB:77:ALA:CB	2:CB:165:VAL:HG11	2.51	0.40
8:CH:82:HIS:HE2	8:CH:136:GLU:HG3	1.85	0.40
16:CP:57:ARG:HH21	16:CP:79:VAL:HA	1.87	0.40
25:DA:25:U:C4	25:DA:26:G:C6	3.09	0.40
25:DA:64:A:H2'	25:DA:65:C:O4'	2.20	0.40
25:DA:221:A:N1	25:DA:265:A:O2'	2.50	0.40
25:DA:579:G:H2'	25:DA:580:C:C6	2.56	0.40
25:DA:581:C:OP2	40:DU:33:ARG:HD3	2.20	0.40
25:DA:609:A:C8	25:DA:610:G:C8	3.09	0.40
25:DA:1803:A:H4'	27:DD:259:THR:HG23	2.02	0.40
25:DA:2617:C:C2'	25:DA:2618:G:H5'	2.51	0.40
25:DA:2784:C:H2'	25:DA:2785:C:H6	1.86	0.40
29:DF:140:LEU:HD21	29:DF:170:LEU:HD11	2.03	0.40
29:DF:184:TYR:O	29:DF:188:ARG:HG3	2.21	0.40
32:DI:62:LYS:HA	32:DI:65:ALA:HB3	2.03	0.40
44:DY:13:VAL:HB	44:DY:72:VAL:HG13	2.02	0.40
48:D2:1:MET:HG2	48:D2:5:GLU:OE1	2.21	0.40
1:AA:299:G:C6	1:AA:300:A:C6	3.10	0.40
1:AA:864:A:H2'	1:AA:865:A:C8	2.57	0.40
2:AB:82:ARG:HG3	2:AB:92:TYR:CZ	2.57	0.40
6:AF:8:ILE:HG22	6:AF:10:LEU:HD22	2.03	0.40
7:AG:100:ALA:O	7:AG:104:LEU:HB2	2.22	0.40
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.55	0.40
10:AJ:85:LEU:HD23	10:AJ:85:LEU:HA	1.97	0.40
13:AM:81:LEU:O	13:AM:89:GLY:HA3	2.22	0.40
25:BA:117:A:H4'	25:BA:118:U:OP1	2.21	0.40
25:BA:510:C:H2'	25:BA:511:C:C6	2.57	0.40
25:BA:1383:G:H2'	25:BA:1384:G:O4'	2.20	0.40
25:BA:1925:G:OP1	27:BD:241:PRO:HB2	2.22	0.40
25:BA:2331:G:N2	38:BS:3:ARG:HA	2.37	0.40
33:BN:61:ARG:HG3	33:BN:62:VAL:H	1.87	0.40
39:BT:53:ARG:O	39:BT:59:THR:HA	2.22	0.40
44:BY:7:VAL:HG21	44:BY:72:VAL:HG12	2.04	0.40
45:BZ:9:TYR:OH	45:BZ:61:LEU:HD23	2.21	0.40
51:B5:41:PRO:HA	51:B5:42:PRO:HD2	1.82	0.40
1:CA:236:G:C6	1:CA:237:C:C4	3.09	0.40
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:584:G:H5'	17:CQ:91:ARG:HH22	1.86	0.40
1:CA:1118:C:OP1	9:CI:9:ARG:HD2	2.20	0.40
1:CA:1238:A:C2	1:CA:1303:C:H4'	2.57	0.40
4:CD:70:ILE:HG23	4:CD:75:PHE:HB2	2.04	0.40
19:CS:38:SER:HB2	19:CS:71:LEU:HD22	2.02	0.40
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.21	0.40
25:DA:172:C:H2'	25:DA:173:G:H8	1.86	0.40
25:DA:797:C:H2'	25:DA:798:G:O4'	2.22	0.40
25:DA:864:G:OP2	36:DQ:22:LYS:HE3	2.21	0.40
25:DA:999:U:H5"	25:DA:1154:G:O6	2.22	0.40
25:DA:1410:G:H2'	25:DA:1411:C:C6	2.56	0.40
25:DA:1665:A:H2'	25:DA:1666:G:O4'	2.21	0.40
25:DA:2078:C:C4	25:DA:2079:U:C4	3.10	0.40
25:DA:2283:C:C2	25:DA:2389:G:C2	3.09	0.40
25:DA:2318:G:H21	38:DS:3:ARG:NH1	2.00	0.40
27:DD:24:ILE:HD13	27:DD:84:TYR:HB2	2.03	0.40
29:DF:195:ASP:OD1	29:DF:196:LEU:N	2.54	0.40
42:DW:43:GLY:O	42:DW:47:VAL:HG23	2.22	0.40
45:DZ:55:HIS:HE1	45:DZ:135:GLU:HG3	1.80	0.40
47:D1:54:ALA:HB1	47:D1:83:GLU:HG3	2.03	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%)	196 (86%)	24 (10%)	9 (4%)	2 5
2	CB	229/256 (90%)	195 (85%)	24 (10%)	10 (4%)	2 4
3	AC	204/239 (85%)	182 (89%)	18 (9%)	4 (2%)	6 16
3	CC	204/239 (85%)	182 (89%)	19 (9%)	3 (2%)	8 22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	AD	206/209 (99%)	193 (94%)	12 (6%)	1 (0%)	24 48
4	CD	206/209 (99%)	196 (95%)	8 (4%)	2 (1%)	12 32
5	AE	146/162 (90%)	135 (92%)	10 (7%)	1 (1%)	18 41
5	CE	146/162 (90%)	135 (92%)	10 (7%)	1 (1%)	18 41
6	AF	98/101 (97%)	95 (97%)	3 (3%)	0	100 100
6	CF	98/101 (97%)	95 (97%)	2 (2%)	1 (1%)	12 32
7	AG	153/156 (98%)	141 (92%)	9 (6%)	3 (2%)	6 16
7	CG	153/156 (98%)	143 (94%)	7 (5%)	3 (2%)	6 16
8	AH	135/138 (98%)	130 (96%)	4 (3%)	1 (1%)	18 41
8	CH	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	18 41
9	AI	125/128 (98%)	113 (90%)	10 (8%)	2 (2%)	7 20
9	CI	125/128 (98%)	112 (90%)	10 (8%)	3 (2%)	4 12
10	AJ	95/105 (90%)	82 (86%)	7 (7%)	6 (6%)	1 2
10	CJ	94/105 (90%)	81 (86%)	7 (7%)	6 (6%)	1 1
11	AK	112/129 (87%)	106 (95%)	4 (4%)	2 (2%)	6 18
11	CK	112/129 (87%)	106 (95%)	4 (4%)	2 (2%)	6 18
12	AL	120/132 (91%)	117 (98%)	3 (2%)	0	100 100
12	CL	120/132 (91%)	116 (97%)	4 (3%)	0	100 100
13	AM	121/126 (96%)	109 (90%)	11 (9%)	1 (1%)	16 37
13	CM	120/126 (95%)	107 (89%)	11 (9%)	2 (2%)	7 19
14	AN	58/61 (95%)	57 (98%)	1 (2%)	0	100 100
14	CN	58/61 (95%)	57 (98%)	1 (2%)	0	100 100
15	AO	86/89 (97%)	83 (96%)	3 (4%)	0	100 100
15	CO	86/89 (97%)	82 (95%)	3 (4%)	1 (1%)	10 27
16	AP	80/88 (91%)	76 (95%)	3 (4%)	1 (1%)	9 25
16	CP	80/88 (91%)	76 (95%)	3 (4%)	1 (1%)	9 25
17	AQ	97/105 (92%)	92 (95%)	5 (5%)	0	100 100
17	CQ	97/105 (92%)	93 (96%)	3 (3%)	1 (1%)	12 32
18	AR	66/88 (75%)	65 (98%)	0	1 (2%)	8 22
18	CR	66/88 (75%)	65 (98%)	0	1 (2%)	8 22
19	AS	81/93 (87%)	71 (88%)	8 (10%)	2 (2%)	4 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
19	CS	81/93 (87%)	69 (85%)	10 (12%)	2 (2%)	4 11
20	AT	94/106 (89%)	86 (92%)	2 (2%)	6 (6%)	1 1
20	CT	94/106 (89%)	87 (93%)	1 (1%)	6 (6%)	1 1
21	AU	21/27 (78%)	19 (90%)	2 (10%)	0	100 100
21	CU	21/27 (78%)	18 (86%)	3 (14%)	0	100 100
27	BD	273/276 (99%)	257 (94%)	15 (6%)	1 (0%)	30 54
27	DD	273/276 (99%)	255 (93%)	16 (6%)	2 (1%)	18 41
28	BE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	24 48
28	DE	202/206 (98%)	195 (96%)	5 (2%)	2 (1%)	12 32
29	BF	201/210 (96%)	199 (99%)	1 (0%)	1 (0%)	24 48
29	DF	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	12 32
30	BG	179/182 (98%)	167 (93%)	10 (6%)	2 (1%)	11 29
30	DG	179/182 (98%)	166 (93%)	10 (6%)	3 (2%)	7 19
31	BH	172/180 (96%)	163 (95%)	8 (5%)	1 (1%)	21 44
31	DH	172/180 (96%)	162 (94%)	9 (5%)	1 (1%)	21 44
32	BI	144/148 (97%)	128 (89%)	12 (8%)	4 (3%)	4 9
32	DI	144/148 (97%)	130 (90%)	12 (8%)	2 (1%)	9 23
33	BN	138/140 (99%)	134 (97%)	4 (3%)	0	100 100
33	DN	138/140 (99%)	133 (96%)	4 (3%)	1 (1%)	18 41
34	BO	120/122 (98%)	114 (95%)	5 (4%)	1 (1%)	16 37
34	DO	120/122 (98%)	115 (96%)	5 (4%)	0	100 100
35	BP	147/150 (98%)	140 (95%)	6 (4%)	1 (1%)	18 41
35	DP	147/150 (98%)	137 (93%)	7 (5%)	3 (2%)	6 16
36	BQ	139/141 (99%)	133 (96%)	6 (4%)	0	100 100
36	DQ	139/141 (99%)	133 (96%)	5 (4%)	1 (1%)	18 41
37	BR	116/118 (98%)	110 (95%)	6 (5%)	0	100 100
37	DR	116/118 (98%)	110 (95%)	6 (5%)	0	100 100
38	BS	108/112 (96%)	102 (94%)	5 (5%)	1 (1%)	14 35
38	DS	108/112 (96%)	102 (94%)	5 (5%)	1 (1%)	14 35
39	BT	129/146 (88%)	121 (94%)	7 (5%)	1 (1%)	16 37
39	DT	129/146 (88%)	124 (96%)	4 (3%)	1 (1%)	16 37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
40	BU	114/118 (97%)	112 (98%)	2 (2%)	0	100 100
40	DU	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
41	BV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	12 32
41	DV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	12 32
42	BW	110/113 (97%)	108 (98%)	2 (2%)	0	100 100
42	DW	110/113 (97%)	110 (100%)	0	0	100 100
43	BX	93/96 (97%)	90 (97%)	3 (3%)	0	100 100
43	DX	93/96 (97%)	89 (96%)	4 (4%)	0	100 100
44	BY	105/110 (96%)	98 (93%)	6 (6%)	1 (1%)	12 32
44	DY	105/110 (96%)	100 (95%)	5 (5%)	0	100 100
45	BZ	169/206 (82%)	145 (86%)	21 (12%)	3 (2%)	6 18
45	DZ	172/206 (84%)	153 (89%)	18 (10%)	1 (1%)	21 44
46	B0	81/85 (95%)	79 (98%)	2 (2%)	0	100 100
46	D0	81/85 (95%)	77 (95%)	3 (4%)	1 (1%)	10 27
47	B1	95/98 (97%)	93 (98%)	2 (2%)	0	100 100
47	D1	95/98 (97%)	93 (98%)	2 (2%)	0	100 100
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%)	56 (98%)	1 (2%)	0	100 100
49	D3	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
50	B4	67/71 (94%)	50 (75%)	12 (18%)	5 (8%)	1 1
50	D4	67/71 (94%)	51 (76%)	8 (12%)	8 (12%)	0 0
51	B5	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
51	D5	57/60 (95%)	57 (100%)	0	0	100 100
52	B6	51/54 (94%)	49 (96%)	2 (4%)	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 14
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%)	34 (97%)	1 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
55	D9	35/37 (95%)	34 (97%)	1 (3%)	0	100 100
All	All	11409/12128 (94%)	10706 (94%)	562 (5%)	141 (1%)	10 27

All (141) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	16	HIS
2	AB	17	PHE
2	AB	231	GLU
7	AG	80	VAL
9	AI	44	VAL
9	AI	54	ASP
10	AJ	31	GLY
10	AJ	56	HIS
10	AJ	77	PRO
10	AJ	79	ARG
20	AT	10	LEU
27	BD	275	LYS
29	BF	130	ALA
30	BG	43	LEU
31	BH	126	PRO
32	BI	107	VAL
45	BZ	152	ALA
50	B4	45	GLY
50	B4	55	ARG
50	B4	57	GLU
50	B4	62	ARG
2	CB	10	LEU
2	CB	16	HIS
2	CB	17	PHE
2	CB	231	GLU
4	CD	46	LYS
7	CG	80	VAL
9	CI	54	ASP
10	CJ	55	LYS
10	CJ	56	HIS
10	CJ	79	ARG
20	CT	95	ALA
20	CT	99	LEU
28	DE	73	GLU
29	DF	21	ALA
29	DF	130	ALA

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Mol	Chain	Res	Type
30	DG	43	LEU
30	DG	47	LYS
31	DH	126	PRO
32	DI	10	GLU
36	DQ	28	ALA
50	D4	45	GLY
50	D4	62	ARG
50	D4	63	TYR
50	D4	68	ARG
53	D7	46	VAL
2	AB	126	GLU
3	AC	107	GLN
7	AG	55	GLY
7	AG	81	GLY
10	AJ	55	LYS
11	AK	49	GLY
13	AM	12	ASN
18	AR	25	THR
19	AS	42	PRO
20	AT	47	GLY
20	AT	96	GLY
32	BI	85	GLU
32	BI	106	GLY
39	BT	127	ALA
41	BV	79	VAL
45	BZ	163	LEU
2	CB	8	LYS
2	CB	20	GLU
2	CB	126	GLU
7	CG	7	ALA
7	CG	55	GLY
9	CI	44	VAL
10	CJ	75	ILE
10	CJ	78	ASN
11	CK	49	GLY
19	CS	25	LYS
20	CT	10	LEU
20	CT	47	GLY
20	CT	100	ILE
27	DD	3	VAL
27	DD	239	ARG
35	DP	39	LYS

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Mol	Chain	Res	Type
39	DT	127	ALA
41	DV	79	VAL
5	AE	85	GLY
19	AS	25	LYS
20	AT	95	ALA
20	AT	102	GLY
8	CH	133	LEU
9	CI	11	LYS
13	CM	59	TYR
19	CS	42	PRO
32	DI	85	GLU
50	D4	49	PHE
2	AB	213	LEU
3	AC	26	LYS
8	AH	133	LEU
28	BE	52	LEU
32	BI	73	GLU
50	B4	49	PHE
3	CC	26	LYS
4	CD	47	ARG
13	CM	12	ASN
15	CO	88	ARG
18	CR	25	THR
28	DE	52	LEU
33	DN	2	LYS
38	DS	84	GLN
46	D0	4	LYS
50	D4	55	ARG
2	AB	9	GLU
2	AB	10	LEU
3	AC	65	ALA
3	AC	66	VAL
4	AD	166	LYS
20	AT	100	ILE
30	BG	51	ARG
34	BO	5	GLN
44	BY	54	LYS
3	CC	144	SER
3	CC	181	ASN
11	CK	105	VAL
50	D4	46	GLN
50	D4	65	ASP

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Mol	Chain	Res	Type
10	AJ	37	PRO
35	BP	122	PRO
45	BZ	157	LEU
2	CB	21	ARG
2	CB	127	ILE
10	CJ	37	PRO
30	DG	117	PHE
35	DP	45	LEU
45	DZ	157	LEU
16	AP	53	VAL
2	CB	125	PRO
17	CQ	33	GLY
6	CF	40	VAL
20	CT	102	GLY
35	DP	122	PRO
11	AK	105	VAL
16	CP	53	VAL
38	BS	60	GLY
5	CE	69	VAL
2	AB	124	SER
2	AB	125	PRO

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%)	157 (82%)	35 (18%)	2 5
2	CB	187/220 (85%)	156 (83%)	31 (17%)	2 6
3	AC	143/188 (76%)	128 (90%)	15 (10%)	6 17
3	CC	140/188 (74%)	123 (88%)	17 (12%)	5 12
4	AD	170/181 (94%)	158 (93%)	12 (7%)	13 33
4	CD	173/181 (96%)	157 (91%)	16 (9%)	8 22
5	AE	113/123 (92%)	101 (89%)	12 (11%)	6 17
5	CE	114/123 (93%)	100 (88%)	14 (12%)	4 12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
6	AF	83/90 (92%)	76 (92%)	7 (8%)	10 26
6	CF	85/90 (94%)	73 (86%)	12 (14%)	3 9
7	AG	119/127 (94%)	107 (90%)	12 (10%)	7 18
7	CG	120/127 (94%)	110 (92%)	10 (8%)	10 26
8	AH	114/119 (96%)	109 (96%)	5 (4%)	25 53
8	CH	114/119 (96%)	104 (91%)	10 (9%)	9 23
9	AI	90/99 (91%)	78 (87%)	12 (13%)	4 10
9	CI	89/99 (90%)	78 (88%)	11 (12%)	4 11
10	AJ	66/92 (72%)	61 (92%)	5 (8%)	12 30
10	CJ	69/92 (75%)	63 (91%)	6 (9%)	9 24
11	AK	82/99 (83%)	72 (88%)	10 (12%)	5 12
11	CK	83/99 (84%)	73 (88%)	10 (12%)	5 12
12	AL	97/109 (89%)	93 (96%)	4 (4%)	27 56
12	CL	97/109 (89%)	93 (96%)	4 (4%)	27 56
13	AM	93/101 (92%)	81 (87%)	12 (13%)	4 10
13	CM	92/101 (91%)	82 (89%)	10 (11%)	6 16
14	AN	49/50 (98%)	40 (82%)	9 (18%)	1 4
14	CN	49/50 (98%)	42 (86%)	7 (14%)	3 8
15	AO	78/80 (98%)	70 (90%)	8 (10%)	7 18
15	CO	78/80 (98%)	71 (91%)	7 (9%)	9 23
16	AP	69/74 (93%)	60 (87%)	9 (13%)	4 10
16	CP	68/74 (92%)	61 (90%)	7 (10%)	7 18
17	AQ	94/97 (97%)	87 (93%)	7 (7%)	13 32
17	CQ	94/97 (97%)	89 (95%)	5 (5%)	20 46
18	AR	59/77 (77%)	51 (86%)	8 (14%)	3 9
18	CR	59/77 (77%)	53 (90%)	6 (10%)	7 18
19	AS	69/80 (86%)	63 (91%)	6 (9%)	9 24
19	CS	67/80 (84%)	59 (88%)	8 (12%)	5 13
20	AT	70/82 (85%)	63 (90%)	7 (10%)	7 19
20	CT	70/82 (85%)	64 (91%)	6 (9%)	10 25
21	AU	18/22 (82%)	16 (89%)	2 (11%)	6 15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
21	CU	18/22 (82%)	17 (94%)	1 (6%)	19 44
27	BD	215/218 (99%)	195 (91%)	20 (9%)	8 21
27	DD	215/218 (99%)	194 (90%)	21 (10%)	7 19
28	BE	164/166 (99%)	140 (85%)	24 (15%)	3 8
28	DE	164/166 (99%)	141 (86%)	23 (14%)	3 9
29	BF	160/166 (96%)	143 (89%)	17 (11%)	6 17
29	DF	159/166 (96%)	144 (91%)	15 (9%)	8 21
30	BG	143/156 (92%)	127 (89%)	16 (11%)	6 15
30	DG	142/156 (91%)	122 (86%)	20 (14%)	3 9
31	BH	144/148 (97%)	133 (92%)	11 (8%)	12 30
31	DH	144/148 (97%)	125 (87%)	19 (13%)	4 10
32	BI	110/124 (89%)	86 (78%)	24 (22%)	1 3
32	DI	104/124 (84%)	84 (81%)	20 (19%)	1 4
33	BN	118/119 (99%)	99 (84%)	19 (16%)	2 6
33	DN	118/119 (99%)	104 (88%)	14 (12%)	5 13
34	BO	100/100 (100%)	93 (93%)	7 (7%)	14 34
34	DO	100/100 (100%)	93 (93%)	7 (7%)	14 34
35	BP	115/116 (99%)	99 (86%)	16 (14%)	3 9
35	DP	115/116 (99%)	98 (85%)	17 (15%)	3 8
36	BQ	111/111 (100%)	98 (88%)	13 (12%)	5 13
36	DQ	111/111 (100%)	98 (88%)	13 (12%)	5 13
37	BR	101/101 (100%)	84 (83%)	17 (17%)	2 6
37	DR	101/101 (100%)	84 (83%)	17 (17%)	2 6
38	BS	87/88 (99%)	78 (90%)	9 (10%)	7 18
38	DS	85/88 (97%)	71 (84%)	14 (16%)	2 6
39	BT	115/127 (91%)	102 (89%)	13 (11%)	5 14
39	DT	113/127 (89%)	99 (88%)	14 (12%)	4 11
40	BU	93/94 (99%)	84 (90%)	9 (10%)	8 20
40	DU	93/94 (99%)	85 (91%)	8 (9%)	10 25
41	BV	80/82 (98%)	67 (84%)	13 (16%)	2 6
41	DV	80/82 (98%)	66 (82%)	14 (18%)	2 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
42	BW	90/92 (98%)	81 (90%)	9 (10%)	7 19
42	DW	90/92 (98%)	82 (91%)	8 (9%)	9 23
43	BX	77/78 (99%)	71 (92%)	6 (8%)	11 29
43	DX	77/78 (99%)	73 (95%)	4 (5%)	21 47
44	BY	85/91 (93%)	79 (93%)	6 (7%)	13 33
44	DY	85/91 (93%)	83 (98%)	2 (2%)	43 72
45	BZ	145/179 (81%)	127 (88%)	18 (12%)	4 11
45	DZ	145/179 (81%)	123 (85%)	22 (15%)	3 7
46	B0	65/67 (97%)	62 (95%)	3 (5%)	24 51
46	D0	65/67 (97%)	61 (94%)	4 (6%)	16 39
47	B1	80/83 (96%)	73 (91%)	7 (9%)	9 23
47	D1	80/83 (96%)	73 (91%)	7 (9%)	9 23
48	B2	65/67 (97%)	58 (89%)	7 (11%)	6 16
48	D2	65/67 (97%)	59 (91%)	6 (9%)	8 22
49	B3	51/52 (98%)	45 (88%)	6 (12%)	5 13
49	D3	50/52 (96%)	42 (84%)	8 (16%)	2 6
50	B4	60/63 (95%)	49 (82%)	11 (18%)	2 5
50	D4	53/63 (84%)	44 (83%)	9 (17%)	2 6
51	B5	50/52 (96%)	44 (88%)	6 (12%)	5 12
51	D5	50/52 (96%)	46 (92%)	4 (8%)	11 28
52	B6	51/52 (98%)	47 (92%)	4 (8%)	11 29
52	D6	50/52 (96%)	47 (94%)	3 (6%)	17 41
53	B7	41/42 (98%)	36 (88%)	5 (12%)	5 12
53	D7	41/42 (98%)	40 (98%)	1 (2%)	43 72
54	B8	54/55 (98%)	49 (91%)	5 (9%)	8 21
54	D8	54/55 (98%)	47 (87%)	7 (13%)	4 10
55	B9	34/34 (100%)	32 (94%)	2 (6%)	18 42
55	D9	34/34 (100%)	32 (94%)	2 (6%)	18 42
All	All	9321/10066 (93%)	8280 (89%)	1041 (11%)	6 15

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

Mol	Chain	Res	Type
2	AB	7	VAL
2	AB	8	LYS
2	AB	11	LEU
2	AB	15	VAL
2	AB	19	HIS
2	AB	20	GLU
2	AB	21	ARG
2	AB	35	GLU
2	AB	39	ILE
2	AB	42	ILE
2	AB	53	ARG
2	AB	64	ARG
2	AB	76	GLN
2	AB	80	ILE
2	AB	96	ARG
2	AB	109	SER
2	AB	112	VAL
2	AB	114	ARG
2	AB	116	GLU
2	AB	127	ILE
2	AB	142	LEU
2	AB	145	LEU
2	AB	153	ARG
2	AB	154	LEU
2	AB	155	LEU
2	AB	164	VAL
2	AB	169	LYS
2	AB	187	LEU
2	AB	200	ILE
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	8	ILE
3	AC	12	LEU
3	AC	21	ARG
3	AC	27	LYS
3	AC	28	GLN
3	AC	37	GLN
3	AC	45	LYS

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Mol	Chain	Res	Type
3	AC	64	VAL
3	AC	70	VAL
3	AC	115	LEU
3	AC	127	ARG
3	AC	178	LEU
3	AC	191	THR
3	AC	198	VAL
4	AD	5	ILE
4	AD	15	GLU
4	AD	19	LEU
4	AD	58	LEU
4	AD	65	ARG
4	AD	112	VAL
4	AD	127	THR
4	AD	135	LEU
4	AD	157	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	182	LYS
5	AE	12	LEU
5	AE	18	ARG
5	AE	27	ARG
5	AE	31	LEU
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	51	VAL
5	AE	57	LYS
5	AE	79	GLU
5	AE	82	VAL
5	AE	91	LEU
6	AF	36	ARG
6	AF	40	VAL
6	AF	61	LEU
6	AF	72	VAL
6	AF	75	LEU
6	AF	82	ARG
6	AF	92	LYS
7	AG	8	GLU
7	AG	16	LEU
7	AG	32	ARG
7	AG	50	ILE

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Mol	Chain	Res	Type
7	AG	51	GLN
7	AG	52	GLU
7	AG	76	ARG
7	AG	79	ARG
7	AG	104	LEU
7	AG	113	GLU
7	AG	129	GLU
7	AG	138	LYS
8	AH	2	LEU
8	AH	26	VAL
8	AH	78	GLN
8	AH	112	LEU
8	AH	137	VAL
9	AI	3	GLN
9	AI	17	VAL
9	AI	23	ASN
9	AI	42	ARG
9	AI	53	VAL
9	AI	56	LEU
9	AI	64	THR
9	AI	81	ILE
9	AI	108	VAL
9	AI	112	LYS
9	AI	127	LYS
9	AI	128	ARG
10	AJ	7	LYS
10	AJ	23	ILE
10	AJ	46	ARG
10	AJ	70	ARG
10	AJ	92	THR
11	AK	14	VAL
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	81	ASP
11	AK	96	ARG
11	AK	104	GLN
11	AK	109	VAL
11	AK	114	VAL
11	AK	126	ARG
12	AL	27	LEU
12	AL	33	ARG

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Mol	Chain	Res	Type
12	AL	46	LYS
12	AL	60	LEU
13	AM	3	ARG
13	AM	4	ILE
13	AM	15	VAL
13	AM	19	LEU
13	AM	39	ILE
13	AM	43	THR
13	AM	56	LEU
13	AM	70	LEU
13	AM	102	ARG
13	AM	110	ARG
13	AM	117	VAL
13	AM	121	LYS
14	AN	3	ARG
14	AN	6	LEU
14	AN	7	ILE
14	AN	18	VAL
14	AN	22	THR
14	AN	23	ARG
14	AN	33	VAL
14	AN	50	LYS
14	AN	57	ARG
15	AO	3	ILE
15	AO	5	LYS
15	AO	22	THR
15	AO	26	GLU
15	AO	39	LEU
15	AO	41	GLU
15	AO	83	GLU
15	AO	84	LYS
16	AP	2	VAL
16	AP	19	ILE
16	AP	20	VAL
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	62	VAL
16	AP	69	THR
16	AP	71	ARG
17	AQ	6	LEU
17	AQ	9	VAL

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Mol	Chain	Res	Type
17	AQ	52	LYS
17	AQ	53	LEU
17	AQ	60	ILE
17	AQ	74	LEU
17	AQ	98	LEU
18	AR	26	LEU
18	AR	32	ARG
18	AR	37	VAL
18	AR	42	ARG
18	AR	46	GLU
18	AR	58	LEU
18	AR	76	LEU
18	AR	85	LEU
19	AS	5	LEU
19	AS	12	ASP
19	AS	28	LYS
19	AS	41	VAL
19	AS	65	ASN
19	AS	78	ARG
20	AT	8	ARG
20	AT	13	LEU
20	AT	24	LEU
20	AT	30	LYS
20	AT	62	LEU
20	AT	74	LYS
20	AT	84	LEU
21	AU	9	ARG
21	AU	10	ARG
27	BD	3	VAL
27	BD	13	ARG
27	BD	61	LEU
27	BD	94	LEU
27	BD	103	ARG
27	BD	106	ILE
27	BD	113	VAL
27	BD	126	GLN
27	BD	138	VAL
27	BD	141	VAL
27	BD	142	VAL
27	BD	155	LEU
27	BD	173	VAL
27	BD	193	VAL

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Mol	Chain	Res	Type
27	BD	211	ARG
27	BD	221	VAL
27	BD	229	VAL
27	BD	257	LEU
27	BD	259	THR
27	BD	260	ARG
28	BE	1	MET
28	BE	9	VAL
28	BE	12	THR
28	BE	21	VAL
28	BE	24	THR
28	BE	33	VAL
28	BE	34	VAL
28	BE	49	LEU
28	BE	73	GLU
28	BE	75	VAL
28	BE	77	ILE
28	BE	82	ARG
28	BE	97	LYS
28	BE	111	ARG
28	BE	116	VAL
28	BE	119	ARG
28	BE	134	ILE
28	BE	144	ARG
28	BE	145	LYS
28	BE	154	LYS
28	BE	163	GLU
28	BE	170	LEU
28	BE	175	VAL
28	BE	181	LEU
29	BF	19	GLU
29	BF	28	ILE
29	BF	33	LEU
29	BF	38	ARG
29	BF	53	THR
29	BF	57	VAL
29	BF	74	ARG
29	BF	88	VAL
29	BF	106	ARG
29	BF	110	LEU
29	BF	125	LEU
29	BF	132	VAL

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Mol	Chain	Res	Type
29	BF	140	LEU
29	BF	183	VAL
29	BF	192	LEU
29	BF	195	ASP
29	BF	201	VAL
30	BG	5	VAL
30	BG	7	LEU
30	BG	22	ARG
30	BG	43	LEU
30	BG	45	GLU
30	BG	70	VAL
30	BG	81	LYS
30	BG	82	LEU
30	BG	86	MET
30	BG	91	ARG
30	BG	135	LEU
30	BG	140	ILE
30	BG	143	GLU
30	BG	145	THR
30	BG	159	VAL
30	BG	175	LEU
31	BH	15	VAL
31	BH	24	VAL
31	BH	41	MET
31	BH	44	VAL
31	BH	59	ARG
31	BH	69	ARG
31	BH	71	LEU
31	BH	122	THR
31	BH	125	VAL
31	BH	130	ARG
31	BH	139	GLN
32	BI	5	LEU
32	BI	9	LEU
32	BI	10	GLU
32	BI	15	VAL
32	BI	38	LEU
32	BI	43	ASN
32	BI	47	LEU
32	BI	60	GLU
32	BI	61	ARG
32	BI	62	LYS

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Mol	Chain	Res	Type
32	BI	64	GLU
32	BI	66	GLU
32	BI	68	LEU
32	BI	77	LEU
32	BI	87	LYS
32	BI	92	VAL
32	BI	101	LEU
32	BI	104	GLN
32	BI	107	VAL
32	BI	109	ILE
32	BI	116	LEU
32	BI	127	VAL
32	BI	136	VAL
32	BI	140	LEU
33	BN	14	VAL
33	BN	28	THR
33	BN	33	LEU
33	BN	34	LEU
33	BN	48	MET
33	BN	61	ARG
33	BN	62	VAL
33	BN	65	LYS
33	BN	67	LEU
33	BN	68	GLU
33	BN	73	THR
33	BN	83	LYS
33	BN	87	LEU
33	BN	97	ARG
33	BN	99	LEU
33	BN	120	LEU
33	BN	133	GLN
33	BN	137	LYS
33	BN	140	VAL
34	BO	8	LEU
34	BO	10	VAL
34	BO	23	ARG
34	BO	24	VAL
34	BO	69	ILE
34	BO	98	VAL
34	BO	108	GLU
35	BP	3	LEU
35	BP	7	ARG

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Mol	Chain	Res	Type
35	BP	55	ARG
35	BP	59	LEU
35	BP	65	ARG
35	BP	68	GLN
35	BP	70	GLN
35	BP	75	ILE
35	BP	83	VAL
35	BP	95	VAL
35	BP	98	GLU
35	BP	106	LEU
35	BP	112	LEU
35	BP	125	VAL
35	BP	135	LEU
35	BP	149	GLU
36	BQ	1	MET
36	BQ	5	ARG
36	BQ	7	MET
36	BQ	8	LYS
36	BQ	16	ARG
36	BQ	21	THR
36	BQ	35	VAL
36	BQ	45	GLN
36	BQ	54	MET
36	BQ	55	VAL
36	BQ	75	THR
36	BQ	80	GLU
36	BQ	109	VAL
37	BR	1	MET
37	BR	8	ARG
37	BR	15	SER
37	BR	18	LEU
37	BR	28	LEU
37	BR	29	LEU
37	BR	36	THR
37	BR	44	LEU
37	BR	54	LEU
37	BR	60	LEU
37	BR	65	LEU
37	BR	67	LEU
37	BR	75	LEU
37	BR	79	LEU
37	BR	100	LEU

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Mol	Chain	Res	Type
37	BR	102	GLU
37	BR	111	LEU
38	BS	14	VAL
38	BS	20	ARG
38	BS	35	ILE
38	BS	57	LYS
38	BS	59	LYS
38	BS	69	VAL
38	BS	78	LEU
38	BS	83	LYS
38	BS	110	LEU
39	BT	6	LEU
39	BT	17	THR
39	BT	23	ARG
39	BT	28	VAL
39	BT	49	VAL
39	BT	53	ARG
39	BT	65	LYS
39	BT	78	LEU
39	BT	89	VAL
39	BT	96	ARG
39	BT	108	ARG
39	BT	113	LYS
39	BT	118	ARG
40	BU	8	VAL
40	BU	74	LEU
40	BU	83	LEU
40	BU	92	ARG
40	BU	93	LYS
40	BU	95	LEU
40	BU	104	GLN
40	BU	108	GLU
40	BU	117	GLN
41	BV	18	LEU
41	BV	28	GLU
41	BV	43	GLU
41	BV	46	VAL
41	BV	51	VAL
41	BV	52	VAL
41	BV	61	VAL
41	BV	62	LEU
41	BV	72	VAL

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Mol	Chain	Res	Type
41	BV	79	VAL
41	BV	85	LYS
41	BV	95	LEU
41	BV	100	ARG
42	BW	4	LYS
42	BW	11	ARG
42	BW	17	VAL
42	BW	19	LEU
42	BW	23	LEU
42	BW	51	LEU
42	BW	68	ARG
42	BW	100	THR
42	BW	107	LEU
43	BX	35	THR
43	BX	57	LEU
43	BX	66	LEU
43	BX	76	ARG
43	BX	88	LYS
43	BX	92	LEU
44	BY	23	ARG
44	BY	24	VAL
44	BY	43	ASN
44	BY	72	VAL
44	BY	90	LEU
44	BY	91	GLU
45	BZ	5	LEU
45	BZ	11	GLU
45	BZ	19	ARG
45	BZ	33	LEU
45	BZ	42	VAL
45	BZ	72	ARG
45	BZ	76	LEU
45	BZ	96	VAL
45	BZ	97	GLU
45	BZ	102	LEU
45	BZ	111	VAL
45	BZ	136	PHE
45	BZ	150	LEU
45	BZ	154	ASP
45	BZ	155	LEU
45	BZ	156	LYS
45	BZ	170	THR

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Mol	Chain	Res	Type
45	BZ	171	ILE
46	B0	20	ARG
46	B0	36	ILE
46	B0	55	ARG
47	B1	21	ARG
47	B1	35	THR
47	B1	40	ARG
47	B1	59	THR
47	B1	75	GLU
47	B1	78	LYS
47	B1	95	LEU
48	B2	1	MET
48	B2	19	VAL
48	B2	30	ARG
48	B2	32	LEU
48	B2	53	LEU
48	B2	64	LEU
48	B2	70	GLN
49	B3	8	LEU
49	B3	23	LEU
49	B3	31	LEU
49	B3	54	VAL
49	B3	58	VAL
49	B3	60	GLU
50	B4	34	GLU
50	B4	46	GLN
50	B4	50	VAL
50	B4	56	VAL
50	B4	58	ARG
50	B4	59	PHE
50	B4	61	ARG
50	B4	63	TYR
50	B4	66	SER
50	B4	68	ARG
50	B4	69	LYS
51	B5	6	VAL
51	B5	29	THR
51	B5	40	LYS
51	B5	48	GLU
51	B5	55	ARG
51	B5	60	VAL
52	B6	4	GLU

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Mol	Chain	Res	Type
52	B6	14	THR
52	B6	38	LYS
52	B6	48	VAL
53	B7	1	MET
53	B7	9	ARG
53	B7	24	THR
53	B7	43	THR
53	B7	46	VAL
54	B8	6	THR
54	B8	14	VAL
54	B8	23	VAL
54	B8	30	ARG
54	B8	32	LEU
55	B9	17	ILE
55	B9	33	LYS
2	CB	7	VAL
2	CB	11	LEU
2	CB	35	GLU
2	CB	42	ILE
2	CB	71	VAL
2	CB	74	LYS
2	CB	76	GLN
2	CB	80	ILE
2	CB	81	VAL
2	CB	87	ARG
2	CB	94	ASN
2	CB	96	ARG
2	CB	98	LEU
2	CB	115	LEU
2	CB	126	GLU
2	CB	128	GLU
2	CB	133	LYS
2	CB	142	LEU
2	CB	145	LEU
2	CB	154	LEU
2	CB	155	LEU
2	CB	157	ARG
2	CB	164	VAL
2	CB	169	LYS
2	CB	175	ARG
2	CB	185	ILE
2	CB	187	LEU

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Mol	Chain	Res	Type
2	CB	200	ILE
2	CB	217	ARG
2	CB	221	LEU
2	CB	224	GLN
3	CC	3	ASN
3	CC	8	ILE
3	CC	12	LEU
3	CC	17	ASP
3	CC	21	ARG
3	CC	49	SER
3	CC	52	LEU
3	CC	98	ASN
3	CC	104	GLN
3	CC	115	LEU
3	CC	152	ILE
3	CC	154	SER
3	CC	178	LEU
3	CC	191	THR
3	CC	195	VAL
3	CC	198	VAL
3	CC	207	VAL
4	CD	10	ARG
4	CD	15	GLU
4	CD	31	CYS
4	CD	34	GLU
4	CD	58	LEU
4	CD	61	LYS
4	CD	65	ARG
4	CD	108	LEU
4	CD	127	THR
4	CD	135	LEU
4	CD	157	LEU
4	CD	170	VAL
4	CD	181	MET
4	CD	187	ARG
4	CD	188	LEU
4	CD	194	LEU
5	CE	12	LEU
5	CE	18	ARG
5	CE	31	LEU
5	CE	41	VAL
5	CE	47	LYS

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Mol	Chain	Res	Type
5	CE	51	VAL
5	CE	57	LYS
5	CE	64	ARG
5	CE	71	LEU
5	CE	73	ASN
5	CE	79	GLU
5	CE	82	VAL
5	CE	91	LEU
5	CE	150	ARG
6	CF	10	LEU
6	CF	28	ARG
6	CF	36	ARG
6	CF	40	VAL
6	CF	41	GLU
6	CF	46	ARG
6	CF	61	LEU
6	CF	69	GLU
6	CF	72	VAL
6	CF	75	LEU
6	CF	82	ARG
6	CF	92	LYS
7	CG	9	VAL
7	CG	16	LEU
7	CG	32	ARG
7	CG	51	GLN
7	CG	52	GLU
7	CG	56	GLN
7	CG	72	ARG
7	CG	86	GLN
7	CG	104	LEU
7	CG	155	ARG
8	CH	2	LEU
8	CH	10	LEU
8	CH	39	LEU
8	CH	51	VAL
8	CH	69	ARG
8	CH	78	GLN
8	CH	84	ARG
8	CH	112	LEU
8	CH	127	LEU
8	CH	137	VAL
9	CI	3	GLN

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Mol	Chain	Res	Type
9	CI	7	THR
9	CI	14	VAL
9	CI	17	VAL
9	CI	23	ASN
9	CI	53	VAL
9	CI	64	THR
9	CI	81	ILE
9	CI	86	VAL
9	CI	108	VAL
9	CI	128	ARG
10	CJ	16	LEU
10	CJ	19	SER
10	CJ	23	ILE
10	CJ	70	ARG
10	CJ	84	GLN
10	CJ	92	THR
11	CK	14	VAL
11	CK	24	SER
11	CK	51	LYS
11	CK	78	GLN
11	CK	81	ASP
11	CK	96	ARG
11	CK	104	GLN
11	CK	109	VAL
11	CK	114	VAL
11	CK	126	ARG
12	CL	27	LEU
12	CL	33	ARG
12	CL	52	LEU
12	CL	60	LEU
13	CM	3	ARG
13	CM	4	ILE
13	CM	15	VAL
13	CM	19	LEU
13	CM	56	LEU
13	CM	70	LEU
13	CM	110	ARG
13	CM	115	LYS
13	CM	117	VAL
13	CM	121	LYS
14	CN	3	ARG
14	CN	6	LEU

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Mol	Chain	Res	Type
14	CN	7	ILE
14	CN	12	ARG
14	CN	18	VAL
14	CN	23	ARG
14	CN	33	VAL
15	CO	3	ILE
15	CO	5	LYS
15	CO	26	GLU
15	CO	39	LEU
15	CO	41	GLU
15	CO	54	ARG
15	CO	83	GLU
16	CP	2	VAL
16	CP	20	VAL
16	CP	21	VAL
16	CP	27	LYS
16	CP	60	LEU
16	CP	62	VAL
16	CP	69	THR
17	CQ	6	LEU
17	CQ	9	VAL
17	CQ	53	LEU
17	CQ	74	LEU
17	CQ	96	GLU
18	CR	26	LEU
18	CR	32	ARG
18	CR	37	VAL
18	CR	41	LYS
18	CR	58	LEU
18	CR	85	LEU
19	CS	28	LYS
19	CS	41	VAL
19	CS	56	GLN
19	CS	64	GLU
19	CS	65	ASN
19	CS	71	LEU
19	CS	77	THR
19	CS	78	ARG
20	CT	10	LEU
20	CT	45	GLN
20	CT	56	MET
20	CT	62	LEU

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Mol	Chain	Res	Type
20	CT	84	LEU
20	CT	90	GLN
21	CU	10	ARG
27	DD	54	ARG
27	DD	61	LEU
27	DD	94	LEU
27	DD	103	ARG
27	DD	106	ILE
27	DD	113	VAL
27	DD	126	GLN
27	DD	134	ARG
27	DD	138	VAL
27	DD	141	VAL
27	DD	142	VAL
27	DD	155	LEU
27	DD	173	VAL
27	DD	193	VAL
27	DD	221	VAL
27	DD	229	VAL
27	DD	242	ARG
27	DD	257	LEU
27	DD	259	THR
27	DD	260	ARG
27	DD	276	LYS
28	DE	9	VAL
28	DE	21	VAL
28	DE	24	THR
28	DE	33	VAL
28	DE	34	VAL
28	DE	40	GLU
28	DE	52	LEU
28	DE	73	GLU
28	DE	75	VAL
28	DE	78	LEU
28	DE	79	ARG
28	DE	82	ARG
28	DE	111	ARG
28	DE	116	VAL
28	DE	119	ARG
28	DE	144	ARG
28	DE	145	LYS
28	DE	154	LYS

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Mol	Chain	Res	Type
28	DE	170	LEU
28	DE	175	VAL
28	DE	181	LEU
28	DE	184	VAL
28	DE	195	LEU
29	DF	20	LEU
29	DF	28	ILE
29	DF	33	LEU
29	DF	53	THR
29	DF	57	VAL
29	DF	74	ARG
29	DF	88	VAL
29	DF	106	ARG
29	DF	110	LEU
29	DF	132	VAL
29	DF	140	LEU
29	DF	183	VAL
29	DF	189	THR
29	DF	192	LEU
29	DF	201	VAL
30	DG	5	VAL
30	DG	7	LEU
30	DG	16	ARG
30	DG	21	ARG
30	DG	22	ARG
30	DG	28	VAL
30	DG	31	VAL
30	DG	43	LEU
30	DG	45	GLU
30	DG	49	ASP
30	DG	58	GLN
30	DG	70	VAL
30	DG	115	ARG
30	DG	136	ARG
30	DG	140	ILE
30	DG	143	GLU
30	DG	148	MET
30	DG	159	VAL
30	DG	165	THR
30	DG	167	GLU
31	DH	3	ARG
31	DH	15	VAL

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Mol	Chain	Res	Type
31	DH	33	LEU
31	DH	34	GLU
31	DH	43	VAL
31	DH	44	VAL
31	DH	45	VAL
31	DH	49	VAL
31	DH	57	ASP
31	DH	63	SER
31	DH	69	ARG
31	DH	71	LEU
31	DH	95	ARG
31	DH	105	LEU
31	DH	106	THR
31	DH	122	THR
31	DH	124	GLU
31	DH	139	GLN
31	DH	172	LYS
32	DI	5	LEU
32	DI	9	LEU
32	DI	15	VAL
32	DI	38	LEU
32	DI	43	ASN
32	DI	47	LEU
32	DI	50	ARG
32	DI	57	ARG
32	DI	61	ARG
32	DI	73	GLU
32	DI	75	LEU
32	DI	77	LEU
32	DI	79	ILE
32	DI	86	THR
32	DI	87	LYS
32	DI	101	LEU
32	DI	116	LEU
32	DI	127	VAL
32	DI	136	VAL
32	DI	140	LEU
33	DN	10	GLU
33	DN	14	VAL
33	DN	28	THR
33	DN	34	LEU
33	DN	38	HIS

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Mol	Chain	Res	Type
33	DN	46	VAL
33	DN	61	ARG
33	DN	62	VAL
33	DN	87	LEU
33	DN	97	ARG
33	DN	99	LEU
33	DN	120	LEU
33	DN	133	GLN
33	DN	140	VAL
34	DO	10	VAL
34	DO	23	ARG
34	DO	24	VAL
34	DO	53	LYS
34	DO	69	ILE
34	DO	98	VAL
34	DO	108	GLU
35	DP	3	LEU
35	DP	4	SER
35	DP	15	ARG
35	DP	45	LEU
35	DP	55	ARG
35	DP	59	LEU
35	DP	65	ARG
35	DP	68	GLN
35	DP	75	ILE
35	DP	83	VAL
35	DP	95	VAL
35	DP	98	GLU
35	DP	101	VAL
35	DP	106	LEU
35	DP	112	LEU
35	DP	125	VAL
35	DP	135	LEU
36	DQ	7	MET
36	DQ	8	LYS
36	DQ	21	THR
36	DQ	45	GLN
36	DQ	48	GLU
36	DQ	54	MET
36	DQ	56	ARG
36	DQ	75	THR
36	DQ	80	GLU

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Mol	Chain	Res	Type
36	DQ	85	LYS
36	DQ	109	VAL
36	DQ	110	THR
36	DQ	112	GLU
37	DR	1	MET
37	DR	8	ARG
37	DR	18	LEU
37	DR	28	LEU
37	DR	29	LEU
37	DR	44	LEU
37	DR	54	LEU
37	DR	57	ARG
37	DR	60	LEU
37	DR	65	LEU
37	DR	67	LEU
37	DR	75	LEU
37	DR	79	LEU
37	DR	100	LEU
37	DR	102	GLU
37	DR	111	LEU
37	DR	114	VAL
38	DS	14	VAL
38	DS	20	ARG
38	DS	33	LYS
38	DS	35	ILE
38	DS	49	VAL
38	DS	57	LYS
38	DS	58	LEU
38	DS	68	GLN
38	DS	69	VAL
38	DS	75	GLU
38	DS	76	LYS
38	DS	93	LYS
38	DS	103	GLU
38	DS	110	LEU
39	DT	1	MET
39	DT	6	LEU
39	DT	16	ARG
39	DT	28	VAL
39	DT	49	VAL
39	DT	53	ARG
39	DT	64	ARG

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Mol	Chain	Res	Type
39	DT	65	LYS
39	DT	78	LEU
39	DT	89	VAL
39	DT	96	ARG
39	DT	108	ARG
39	DT	113	LYS
39	DT	118	ARG
40	DU	8	VAL
40	DU	36	ARG
40	DU	83	LEU
40	DU	89	GLU
40	DU	92	ARG
40	DU	93	LYS
40	DU	95	LEU
40	DU	104	GLN
41	DV	6	LYS
41	DV	18	LEU
41	DV	24	LYS
41	DV	46	VAL
41	DV	51	VAL
41	DV	52	VAL
41	DV	57	VAL
41	DV	61	VAL
41	DV	62	LEU
41	DV	72	VAL
41	DV	79	VAL
41	DV	85	LYS
41	DV	95	LEU
41	DV	100	ARG
42	DW	4	LYS
42	DW	11	ARG
42	DW	17	VAL
42	DW	23	LEU
42	DW	51	LEU
42	DW	68	ARG
42	DW	100	THR
42	DW	107	LEU
43	DX	23	GLU
43	DX	57	LEU
43	DX	76	ARG
43	DX	88	LYS
44	DY	72	VAL

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Mol	Chain	Res	Type
44	DY	91	GLU
45	DZ	5	LEU
45	DZ	11	GLU
45	DZ	19	ARG
45	DZ	33	LEU
45	DZ	42	VAL
45	DZ	72	ARG
45	DZ	74	VAL
45	DZ	76	LEU
45	DZ	86	VAL
45	DZ	96	VAL
45	DZ	97	GLU
45	DZ	102	LEU
45	DZ	111	VAL
45	DZ	119	GLU
45	DZ	131	ARG
45	DZ	146	ILE
45	DZ	150	LEU
45	DZ	154	ASP
45	DZ	155	LEU
45	DZ	161	VAL
45	DZ	170	THR
45	DZ	171	ILE
46	D0	20	ARG
46	D0	24	LYS
46	D0	36	ILE
46	D0	55	ARG
47	D1	21	ARG
47	D1	35	THR
47	D1	40	ARG
47	D1	59	THR
47	D1	78	LYS
47	D1	89	GLU
47	D1	95	LEU
48	D2	19	VAL
48	D2	30	ARG
48	D2	32	LEU
48	D2	53	LEU
48	D2	64	LEU
48	D2	70	GLN
49	D3	8	LEU
49	D3	23	LEU

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Mol	Chain	Res	Type
49	D3	30	ARG
49	D3	31	LEU
49	D3	34	GLU
49	D3	44	ARG
49	D3	54	VAL
49	D3	58	VAL
50	D4	3	GLU
50	D4	8	LYS
50	D4	37	SER
50	D4	44	THR
50	D4	50	VAL
50	D4	56	VAL
50	D4	63	TYR
50	D4	67	TYR
50	D4	69	LYS
51	D5	6	VAL
51	D5	29	THR
51	D5	40	LYS
51	D5	59	GLU
52	D6	28	ARG
52	D6	38	LYS
52	D6	48	VAL
53	D7	9	ARG
54	D8	14	VAL
54	D8	23	VAL
54	D8	26	LYS
54	D8	30	ARG
54	D8	32	LEU
54	D8	37	SER
54	D8	41	ILE
55	D9	13	LYS
55	D9	26	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (154) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	40	HIS
2	AB	212	GLN
3	AC	37	GLN
3	AC	104	GLN
3	AC	108	ASN
3	AC	136	GLN

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Mol	Chain	Res	Type
3	AC	162	GLN
3	AC	181	ASN
4	AD	77	ASN
4	AD	123	HIS
4	AD	125	HIS
4	AD	160	GLN
5	AE	38	GLN
5	AE	56	GLN
5	AE	65	ASN
5	AE	141	GLN
6	AF	73	ASN
6	AF	100	ASN
7	AG	13	GLN
7	AG	28	ASN
7	AG	51	GLN
7	AG	97	GLN
9	AI	23	ASN
9	AI	34	ASN
10	AJ	56	HIS
11	AK	93	GLN
11	AK	104	GLN
11	AK	116	HIS
12	AL	78	GLN
12	AL	99	HIS
13	AM	77	ASN
14	AN	49	HIS
15	AO	9	GLN
15	AO	13	GLN
15	AO	28	GLN
15	AO	62	GLN
16	AP	16	HIS
19	AS	23	ASN
19	AS	65	ASN
19	AS	69	HIS
19	AS	83	HIS
20	AT	45	GLN
20	AT	75	ASN
27	BD	87	ASN
27	BD	164	GLN
27	BD	253	GLN
28	BE	85	ASN
29	BF	69	HIS

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Mol	Chain	Res	Type
29	BF	169	ASN
29	BF	203	GLN
32	BI	43	ASN
32	BI	54	GLN
32	BI	74	ASN
32	BI	139	GLN
33	BN	94	HIS
34	BO	3	GLN
34	BO	89	ASN
35	BP	38	GLN
35	BP	70	GLN
36	BQ	45	GLN
38	BS	68	GLN
39	BT	84	GLN
39	BT	123	GLN
40	BU	81	HIS
40	BU	117	GLN
43	BX	31	HIS
43	BX	82	GLN
44	BY	6	HIS
44	BY	43	ASN
45	BZ	55	HIS
48	B2	70	GLN
49	B3	32	GLN
52	B6	20	ASN
54	B8	35	GLN
55	B9	36	GLN
2	CB	16	HIS
2	CB	76	GLN
2	CB	94	ASN
2	CB	135	GLN
3	CC	69	HIS
3	CC	104	GLN
3	CC	123	GLN
3	CC	136	GLN
4	CD	45	GLN
4	CD	74	GLN
4	CD	77	ASN
4	CD	123	HIS
4	CD	125	HIS
4	CD	160	GLN
4	CD	161	ASN

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Mol	Chain	Res	Type
5	CE	65	ASN
5	CE	141	GLN
6	CF	73	ASN
6	CF	100	ASN
7	CG	11	GLN
7	CG	28	ASN
7	CG	51	GLN
7	CG	56	GLN
7	CG	97	GLN
7	CG	148	ASN
8	CH	78	GLN
9	CI	23	ASN
9	CI	31	GLN
9	CI	58	HIS
9	CI	89	ASN
9	CI	124	GLN
11	CK	93	GLN
11	CK	104	GLN
12	CL	78	GLN
12	CL	99	HIS
13	CM	40	ASN
13	CM	77	ASN
15	CO	28	GLN
16	CP	13	HIS
16	CP	16	HIS
16	CP	76	GLN
19	CS	23	ASN
19	CS	47	HIS
19	CS	69	HIS
20	CT	45	GLN
20	CT	75	ASN
20	CT	90	GLN
27	DD	164	GLN
27	DD	253	GLN
28	DE	85	ASN
28	DE	180	ASN
29	DF	69	HIS
29	DF	75	HIS
29	DF	169	ASN
29	DF	203	GLN
32	DI	43	ASN
32	DI	133	HIS

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Mol	Chain	Res	Type
34	DO	89	ASN
35	DP	38	GLN
35	DP	70	GLN
36	DQ	13	GLN
36	DQ	57	HIS
36	DQ	123	HIS
38	DS	68	GLN
39	DT	58	ASN
39	DT	123	GLN
41	DV	80	GLN
43	DX	31	HIS
43	DX	82	GLN
44	DY	43	ASN
44	DY	92	ASN
45	DZ	34	ASN
45	DZ	55	HIS
45	DZ	118	GLN
45	DZ	121	HIS
47	D1	56	GLN
50	D4	60	GLN
54	D8	35	GLN
55	D9	36	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1493/1521 (98%)	281 (18%)	27 (1%)
1	CA	1501/1521 (98%)	281 (18%)	24 (1%)
22	AV	12/24 (50%)	2 (16%)	0
22	CV	11/24 (45%)	2 (18%)	0
23	AW	72/76 (94%)	31 (43%)	1 (1%)
23	AY	73/76 (96%)	33 (45%)	4 (5%)
23	CW	69/76 (90%)	30 (43%)	2 (2%)
23	CY	71/76 (93%)	32 (45%)	1 (1%)
24	AX	75/77 (97%)	21 (28%)	2 (2%)
24	CX	75/77 (97%)	21 (28%)	1 (1%)
25	BA	2814/2915 (96%)	456 (16%)	28 (0%)
25	DA	2791/2915 (95%)	520 (18%)	29 (1%)
26	BB	119/121 (98%)	13 (10%)	2 (1%)
26	DB	119/121 (98%)	14 (11%)	0
All	All	9295/9620 (96%)	1737 (18%)	121 (1%)

All (1737) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	7	G
1	AA	9	G
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	59	A
1	AA	61	G
1	AA	65	U
1	AA	66	G
1	AA	73	G
1	AA	76	C
1	AA	77	G
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	96	U
1	AA	98	G
1	AA	101	A
1	AA	112	G
1	AA	115	G
1	AA	116	A
1	AA	121	C
1	AA	131	C
1	AA	155	C
1	AA	159	G
1	AA	163	C
1	AA	173	U
1	AA	174	C
1	AA	182	U
1	AA	186	C
1	AA	189(D)	C
1	AA	189(J)	G
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U

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Mol	Chain	Res	Type
1	AA	216	G
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	341	C
1	AA	345	C
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	351	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	384	G
1	AA	398	C
1	AA	406	G
1	AA	412	A
1	AA	413	G
1	AA	422	C
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	439	A
1	AA	442	C
1	AA	443	C
1	AA	449	C
1	AA	452	A
1	AA	458	C
1	AA	461	A
1	AA	470	C
1	AA	485	G

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Mol	Chain	Res	Type
1	AA	492	G
1	AA	496	A
1	AA	498	U
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	527	G
1	AA	528	C
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	545	C
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	577	G
1	AA	596	C
1	AA	599	C
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	653	A
1	AA	665	A
1	AA	680	C
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	695	A
1	AA	723	U
1	AA	731	G
1	AA	749	C
1	AA	752	G
1	AA	753	A
1	AA	755	G
1	AA	759	A

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Mol	Chain	Res	Type
1	AA	760	G
1	AA	777	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	806	C
1	AA	815	A
1	AA	817	C
1	AA	821	G
1	AA	828	A
1	AA	829	G
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	874	G
1	AA	887	G
1	AA	902	G
1	AA	914	A
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	935	A
1	AA	960	U
1	AA	961	U
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	991	U
1	AA	992	U
1	AA	993	G
1	AA	1002	G
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1009	G

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Mol	Chain	Res	Type
1	AA	1019	C
1	AA	1020	U
1	AA	1022	G
1	AA	1023	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	1031	G
1	AA	1032	G
1	AA	1033	G
1	AA	1037	C
1	AA	1039	C
1	AA	1041	A
1	AA	1045	C
1	AA	1052	U
1	AA	1054	C
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1094	G
1	AA	1095	U
1	AA	1101	A
1	AA	1108	G
1	AA	1123	A
1	AA	1124	G
1	AA	1126	U
1	AA	1129	C
1	AA	1130	A
1	AA	1132	C
1	AA	1134	G
1	AA	1135	U
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G

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Mol	Chain	Res	Type
1	AA	1139	G
1	AA	1140	C
1	AA	1145	C
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1157	A
1	AA	1159	U
1	AA	1160	G
1	AA	1166	G
1	AA	1183	A
1	AA	1184	G
1	AA	1196	U
1	AA	1197	G
1	AA	1202	G
1	AA	1212	U
1	AA	1213	A
1	AA	1227	A
1	AA	1228	C
1	AA	1238	A
1	AA	1240	U
1	AA	1244	C
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1262	C
1	AA	1270	C
1	AA	1273	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1281	U
1	AA	1286	A
1	AA	1287	A
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1314	C
1	AA	1317	C
1	AA	1320	C
1	AA	1322	C

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Mol	Chain	Res	Type
1	AA	1338	G
1	AA	1340	A
1	AA	1346	A
1	AA	1347	G
1	AA	1363	C
1	AA	1364	U
1	AA	1370	G
1	AA	1383	C
1	AA	1397	C
1	AA	1401	G
1	AA	1419	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1456	G
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
22	AV	13	A
22	AV	24	A
23	AW	3	C
23	AW	7	A
23	AW	8	4SU
23	AW	12	U
23	AW	13	C
23	AW	14	A
23	AW	15	G
23	AW	19	G
23	AW	20	U
23	AW	21	A
23	AW	22	G

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Mol	Chain	Res	Type
23	AW	23	A
23	AW	26	A
23	AW	41	C
23	AW	42	C
23	AW	43	C
23	AW	45	U
23	AW	46	7MG
23	AW	47	U
23	AW	48	C
23	AW	49	C
23	AW	58	A
23	AW	59	U
23	AW	61	C
23	AW	63	G
23	AW	64	A
23	AW	68	C
23	AW	71	G
23	AW	73	A
23	AW	74	C
23	AW	76	A
24	AX	9	G
24	AX	13	C
24	AX	16	C
24	AX	18	G
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	31	G
24	AX	34	C
24	AX	42	G
24	AX	47	U
24	AX	48	C
24	AX	52	G
24	AX	56	C
24	AX	58	A
24	AX	60	U
24	AX	62	C
24	AX	63	G
24	AX	67	C
24	AX	68	C
24	AX	76	A
23	AY	3	C

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Mol	Chain	Res	Type
23	AY	5	G
23	AY	8	4SU
23	AY	9	A
23	AY	11	C
23	AY	19	G
23	AY	20	U
23	AY	21	A
23	AY	22	G
23	AY	25	C
23	AY	26	A
23	AY	30	G
23	AY	31	A
23	AY	33	U
23	AY	34	G
23	AY	35	A
23	AY	39	PSU
23	AY	41	C
23	AY	44	G
23	AY	47	U
23	AY	48	C
23	AY	49	C
23	AY	51	U
23	AY	54	5MU
23	AY	56	C
23	AY	57	G
23	AY	58	A
23	AY	59	U
23	AY	61	C
23	AY	62	C
23	AY	65	G
23	AY	70	G
23	AY	72	C
25	BA	12	U
25	BA	13	A
25	BA	34	C
25	BA	45	C
25	BA	54	G
25	BA	70	A
25	BA	73	A
25	BA	74	G
25	BA	83	A
25	BA	94	G

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Mol	Chain	Res	Type
25	BA	116	A
25	BA	117	A
25	BA	118	U
25	BA	123	G
25	BA	138	G
25	BA	155	C
25	BA	161	C
25	BA	170	A
25	BA	171	A
25	BA	185	A
25	BA	188	A
25	BA	189	U
25	BA	194	G
25	BA	203	G
25	BA	204	G
25	BA	205	A
25	BA	210	A
25	BA	211	A
25	BA	218	A
25	BA	222	A
25	BA	237	G
25	BA	253	C
25	BA	265	U
25	BA	269	G
25	BA	271	U
25	BA	272	U
25	BA	273	G
25	BA	274	U
25	BA	279	G
25	BA	289	G
25	BA	295	C
25	BA	299	G
25	BA	303	C
25	BA	335	A
25	BA	353	G
25	BA	354	A
25	BA	376	G
25	BA	387	G
25	BA	390	G
25	BA	395	C
25	BA	397	G
25	BA	413	G

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Mol	Chain	Res	Type
25	BA	423	G
25	BA	432	U
25	BA	434	G
25	BA	438	G
25	BA	439	A
25	BA	448	U
25	BA	455	A
25	BA	456	A
25	BA	462	C
25	BA	469	A
25	BA	470	C
25	BA	474	U
25	BA	482	C
25	BA	483	A
25	BA	496	A
25	BA	507	G
25	BA	529	U
25	BA	530	A
25	BA	534	C
25	BA	555	G
25	BA	556	C
25	BA	557	A
25	BA	558	G
25	BA	569	G
25	BA	573	G
25	BA	586	G
25	BA	596	G
25	BA	598	A
25	BA	609	A
25	BA	626	A
25	BA	627	G
25	BA	630	U
25	BA	639	G
25	BA	641	G
25	BA	652	A
25	BA	662	A
25	BA	670	C
25	BA	671	A
25	BA	697	C
25	BA	698	G
25	BA	716	G
25	BA	724	A

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Mol	Chain	Res	Type
25	BA	733	G
25	BA	764	G
25	BA	773	G
25	BA	777	C
25	BA	795	G
25	BA	811	A
25	BA	812	G
25	BA	822	G
25	BA	823	G
25	BA	829	A
25	BA	831	A
25	BA	832	G
25	BA	836	A
25	BA	837	C
25	BA	839	G
25	BA	852	G
25	BA	859	C
25	BA	866	A
25	BA	874	U
25	BA	875	U
25	BA	877	G
25	BA	879	G
25	BA	906	G
25	BA	913	A
25	BA	924	U
25	BA	926	G
25	BA	927	G
25	BA	929	G
25	BA	931	C
25	BA	932	C
25	BA	933	C
25	BA	934	A
25	BA	935	C
25	BA	936	C
25	BA	937	A
25	BA	939	C
25	BA	941	U
25	BA	942	A
25	BA	943	C
25	BA	944	C
25	BA	945	A
25	BA	946	A

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Mol	Chain	Res	Type
25	BA	953	U
25	BA	956	A
25	BA	960	C
25	BA	977	G
25	BA	986	A
25	BA	990	A
25	BA	991	G
25	BA	1003	U
25	BA	1004	A
25	BA	1006	C
25	BA	1008	U
25	BA	1019	G
25	BA	1020	C
25	BA	1029	A
25	BA	1042	A
25	BA	1051	C
25	BA	1058	U
25	BA	1059	C
25	BA	1063	G
25	BA	1068	G
25	BA	1072	U
25	BA	1079	U
25	BA	1084	C
25	BA	1087	C
25	BA	1088	G
25	BA	1090	G
25	BA	1091	A
25	BA	1092	A
25	BA	1093	G
25	BA	1094	A
25	BA	1097	G
25	BA	1153	G
25	BA	1156	G
25	BA	1158	G
25	BA	1163	G
25	BA	1175	A
25	BA	1176	U
25	BA	1180	C
25	BA	1181	G
25	BA	1201	A
25	BA	1217	G
25	BA	1218	G

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Mol	Chain	Res	Type
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1222	A
25	BA	1223	C
25	BA	1250	U
25	BA	1255	A
25	BA	1256	U
25	BA	1265	A
25	BA	1290	G
25	BA	1299	A
25	BA	1302	G
25	BA	1317	G
25	BA	1318	A
25	BA	1346	U
25	BA	1347	A
25	BA	1349	G
25	BA	1352	C
25	BA	1360	C
25	BA	1398	U
25	BA	1405	A
25	BA	1406	A
25	BA	1411	A
25	BA	1426	G
25	BA	1430	A
25	BA	1431	G
25	BA	1462	G
25	BA	1463	C
25	BA	1466	U
25	BA	1474	C
25	BA	1491	A
25	BA	1496	A
25	BA	1497	G
25	BA	1501	U
25	BA	1502	G
25	BA	1514	C
25	BA	1518	A
25	BA	1525	G
25	BA	1529	G
25	BA	1536	A
25	BA	1539	C
25	BA	1554	A

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Mol	Chain	Res	Type
25	BA	1555	C
25	BA	1556	A
25	BA	1557	A
25	BA	1561	C
25	BA	1569	U
25	BA	1571	G
25	BA	1578	C
25	BA	1581	U
25	BA	1589	A
25	BA	1605	A
25	BA	1613	A
25	BA	1616	A
25	BA	1625	U
25	BA	1627	A
25	BA	1628	G
25	BA	1629	C
25	BA	1631	C
25	BA	1632	A
25	BA	1653	C
25	BA	1654	A
25	BA	1656	A
25	BA	1676	G
25	BA	1686	U
25	BA	1694	G
25	BA	1695	C
25	BA	1701	A
25	BA	1711	A
25	BA	1721	G
25	BA	1735	U
25	BA	1743	G
25	BA	1747	A
25	BA	1748	A
25	BA	1767	A
25	BA	1768	U
25	BA	1769	G
25	BA	1789	G
25	BA	1793	A
25	BA	1794	G
25	BA	1795	G
25	BA	1800	G
25	BA	1804	A
25	BA	1811	A

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Mol	Chain	Res	Type
25	BA	1817	A
25	BA	1822	A
25	BA	1831	C
25	BA	1832	G
25	BA	1847	G
25	BA	1870	G
25	BA	1878	A
25	BA	1899	A
25	BA	1900	G
25	BA	1907	A
25	BA	1911	A
25	BA	1922	A
25	BA	1928	G
25	BA	1941	A
25	BA	1951	G
25	BA	1952	G
25	BA	1953	U
25	BA	1959	A
25	BA	1960	A
25	BA	1967	G
25	BA	1968	U
25	BA	1977	U
25	BA	1985	U
25	BA	1989	C
25	BA	1992	A
25	BA	1993	A
25	BA	1994	A
25	BA	2014	G
25	BA	2015	U
25	BA	2019	G
25	BA	2042	A
25	BA	2045	G
25	BA	2053	A
25	BA	2054	G
25	BA	2055	A
25	BA	2061	C
25	BA	2065	C
25	BA	2077	C
25	BA	2078	G
25	BA	2082	A
25	BA	2083	G
25	BA	2084	A

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Mol	Chain	Res	Type
25	BA	2091	G
25	BA	2115	G
25	BA	2124	U
25	BA	2132	G
25	BA	2133	C
25	BA	2138	G
25	BA	2140	U
25	BA	2141	A
25	BA	2142	G
25	BA	2143	G
25	BA	2144	U
25	BA	2147	G
25	BA	2149	G
25	BA	2151	C
25	BA	2153	G
25	BA	2154	U
25	BA	2156	A
25	BA	2157	A
25	BA	2158	C
25	BA	2159	C
25	BA	2162	C
25	BA	2163	G
25	BA	2164	C
25	BA	2165	C
25	BA	2166	U
25	BA	2167	C
25	BA	2168	C
25	BA	2169	G
25	BA	2170	G
25	BA	2171	G
25	BA	2175	G
25	BA	2177	G
25	BA	2178	G
25	BA	2179	G
25	BA	2180	A
25	BA	2181	G
25	BA	2185	C
25	BA	2188	G
25	BA	2189	U
25	BA	2190	G
25	BA	2191	A
25	BA	2193	A

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Mol	Chain	Res	Type
25	BA	2194	U
25	BA	2195	A
25	BA	2196	C
25	BA	2200	C
25	BA	2203	G
25	BA	2204	G
25	BA	2206	G
25	BA	2207	C
25	BA	2208	G
25	BA	2209	G
25	BA	2210	C
25	BA	2214	G
25	BA	2220	A
25	BA	2221	A
25	BA	2227	G
25	BA	2228	G
25	BA	2229	A
25	BA	2230	U
25	BA	2237	A
25	BA	2250	G
25	BA	2251	G
25	BA	2280	A
25	BA	2281	A
25	BA	2290	A
25	BA	2295	C
25	BA	2299	A
25	BA	2301	G
25	BA	2317	A
25	BA	2326	C
25	BA	2332	A
25	BA	2337	G
25	BA	2346	G
25	BA	2348	A
25	BA	2355	C
25	BA	2359	C
25	BA	2362	C
25	BA	2366	G
25	BA	2384	G
25	BA	2391	G
25	BA	2395	G
25	BA	2397	C
25	BA	2408	G

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Mol	Chain	Res	Type
25	BA	2418	U
25	BA	2419	G
25	BA	2436	C
25	BA	2437	A
25	BA	2441	G
25	BA	2442	A
25	BA	2444	A
25	BA	2446	A
25	BA	2447	A
25	BA	2451	A
25	BA	2453	C
25	BA	2459	G
25	BA	2460	A
25	BA	2473	C
25	BA	2480	G
25	BA	2481	A
25	BA	2483	C
25	BA	2488	A
25	BA	2490	A
25	BA	2514	G
25	BA	2517	G
25	BA	2530	A
25	BA	2541	G
25	BA	2547	G
25	BA	2566	U
25	BA	2578	A
25	BA	2579	G
25	BA	2585	C
25	BA	2614	A
25	BA	2621	U
25	BA	2623	U
25	BA	2624	C
25	BA	2641	A
25	BA	2642	G
25	BA	2653	G
25	BA	2666	A
25	BA	2685	G
25	BA	2701	U
25	BA	2702	C
25	BA	2714	U
25	BA	2715	C
25	BA	2719	G

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Mol	Chain	Res	Type
25	BA	2725	A
25	BA	2726	A
25	BA	2727	G
25	BA	2734	A
25	BA	2739	U
25	BA	2746	A
25	BA	2770	A
25	BA	2771	A
25	BA	2777	A
25	BA	2778	A
25	BA	2779	G
25	BA	2791	A
25	BA	2803	A
25	BA	2804	C
25	BA	2806	G
25	BA	2813	G
25	BA	2815	C
25	BA	2828	G
25	BA	2830	A
25	BA	2831	A
25	BA	2845	A
25	BA	2882	G
25	BA	2890	C
25	BA	2902	G
25	BA	2903	G
25	BA	2906	U
26	BB	2	C
26	BB	7	G
26	BB	9	G
26	BB	24	G
26	BB	47	C
26	BB	56	G
26	BB	57	A
26	BB	73	A
26	BB	75	G
26	BB	85	G
26	BB	106	G
26	BB	109	C
26	BB	110	G
1	CA	5	U
1	CA	6	G
1	CA	7	G

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Mol	Chain	Res	Type
1	CA	9	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	59	A
1	CA	61	G
1	CA	65	U
1	CA	66	G
1	CA	76	C
1	CA	89	C
1	CA	91	C
1	CA	96	U
1	CA	98	G
1	CA	101	A
1	CA	112	G
1	CA	115	G
1	CA	116	A
1	CA	121	C
1	CA	131	C
1	CA	155	C
1	CA	159	G
1	CA	163	C
1	CA	173	U
1	CA	174	C
1	CA	182	U
1	CA	186	C
1	CA	189(D)	C
1	CA	189(F)	U
1	CA	189(J)	G
1	CA	190	U
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	202	U
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	247	G
1	CA	251	G
1	CA	252	U

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Mol	Chain	Res	Type
1	CA	258	G
1	CA	266	G
1	CA	267	C
1	CA	289	G
1	CA	301	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	341	C
1	CA	344	A
1	CA	346	G
1	CA	351	G
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	409	G
1	CA	412	A
1	CA	413	G
1	CA	422	C
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	439	A
1	CA	442	C
1	CA	443	C
1	CA	449	C
1	CA	452	A
1	CA	458	C
1	CA	461	A
1	CA	470	C
1	CA	485	G
1	CA	492	G
1	CA	496	A
1	CA	498	U

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Mol	Chain	Res	Type
1	CA	505	G
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	528	C
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	545	C
1	CA	547	A
1	CA	559	A
1	CA	560	U
1	CA	561	U
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	577	G
1	CA	596	C
1	CA	599	C
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	650	G
1	CA	653	A
1	CA	665	A
1	CA	680	C
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	695	A
1	CA	723	U
1	CA	731	G
1	CA	749	C
1	CA	752	G
1	CA	753	A
1	CA	755	G
1	CA	759	A
1	CA	760	G
1	CA	777	A
1	CA	792	A
1	CA	793	U

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Mol	Chain	Res	Type
1	CA	794	A
1	CA	806	C
1	CA	815	A
1	CA	817	C
1	CA	821	G
1	CA	828	A
1	CA	829	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	874	G
1	CA	887	G
1	CA	902	G
1	CA	914	A
1	CA	926	G
1	CA	927	G
1	CA	934	C
1	CA	935	A
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	991	U
1	CA	992	U
1	CA	993	G
1	CA	999	C
1	CA	1002	G
1	CA	1003	G
1	CA	1005	A
1	CA	1019	C
1	CA	1020	U
1	CA	1022	G
1	CA	1023	G
1	CA	1024	G

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Mol	Chain	Res	Type
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1031	G
1	CA	1033	G
1	CA	1037	C
1	CA	1038	C
1	CA	1039	C
1	CA	1041	A
1	CA	1045	C
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1087	G
1	CA	1094	G
1	CA	1095	U
1	CA	1101	A
1	CA	1108	G
1	CA	1117	G
1	CA	1124	G
1	CA	1125	U
1	CA	1126	U
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1145	C
1	CA	1146	A

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Mol	Chain	Res	Type
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1157	A
1	CA	1159	U
1	CA	1160	G
1	CA	1166	G
1	CA	1183	A
1	CA	1184	G
1	CA	1196	U
1	CA	1197	G
1	CA	1202	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1227	A
1	CA	1228	C
1	CA	1238	A
1	CA	1240	U
1	CA	1244	C
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1262	C
1	CA	1270	C
1	CA	1273	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1287	A
1	CA	1299	A
1	CA	1300	G
1	CA	1305	G
1	CA	1314	C
1	CA	1317	C
1	CA	1320	C
1	CA	1322	C
1	CA	1340	A
1	CA	1346	A

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Mol	Chain	Res	Type
1	CA	1347	G
1	CA	1363	C
1	CA	1364	U
1	CA	1370	G
1	CA	1383	C
1	CA	1397	C
1	CA	1401	G
1	CA	1419	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1446	U
1	CA	1447	A
1	CA	1452	C
1	CA	1456	G
1	CA	1492	A
1	CA	1493	A
1	CA	1494	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	1531	A
1	CA	1532	U
22	CV	14	A
22	CV	24	A
23	CW	3	C
23	CW	5	G
23	CW	6	G
23	CW	8	4SU
23	CW	13	C
23	CW	14	A
23	CW	15	G
23	CW	19	G
23	CW	22	G
23	CW	23	A
23	CW	26	A
23	CW	27	G
23	CW	28	G
23	CW	29	G

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Mol	Chain	Res	Type
23	CW	30	G
23	CW	34	G
23	CW	46	7MG
23	CW	47	U
23	CW	48	C
23	CW	56	C
23	CW	61	C
23	CW	63	G
23	CW	65	G
23	CW	66	U
23	CW	68	C
23	CW	70	G
23	CW	71	G
23	CW	74	C
23	CW	75	C
23	CW	76	A
24	CX	9	G
24	CX	13	C
24	CX	16	C
24	CX	18	G
24	CX	19	G
24	CX	20	U
24	CX	21	A
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	60	U
24	CX	62	C
24	CX	63	G
24	CX	67	C
24	CX	68	C
24	CX	76	A
23	CY	3	C
23	CY	8	4SU
23	CY	11	C
23	CY	13	C
23	CY	19	G

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Mol	Chain	Res	Type
23	CY	23	A
23	CY	26	A
23	CY	30	G
23	CY	31	A
23	CY	33	U
23	CY	34	G
23	CY	35	A
23	CY	37	MIA
23	CY	39	PSU
23	CY	41	C
23	CY	44	G
23	CY	46	7MG
23	CY	47	U
23	CY	49	C
23	CY	51	U
23	CY	53	G
23	CY	54	5MU
23	CY	56	C
23	CY	57	G
23	CY	58	A
23	CY	59	U
23	CY	61	C
23	CY	62	C
23	CY	65	G
23	CY	67	C
23	CY	70	G
23	CY	72	C
25	DA	10	G
25	DA	12	U
25	DA	15	G
25	DA	34	C
25	DA	45	C
25	DA	61	G
25	DA	71	A
25	DA	74	A
25	DA	75	G
25	DA	78	A
25	DA	79	G
25	DA	84	A
25	DA	94	C
25	DA	95	G
25	DA	100	G

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Mol	Chain	Res	Type
25	DA	118	A
25	DA	119	A
25	DA	120	U
25	DA	125	G
25	DA	141	A
25	DA	157	U
25	DA	182	A
25	DA	196	A
25	DA	197	A
25	DA	199	A
25	DA	205	G
25	DA	213	A
25	DA	214	G
25	DA	215	G
25	DA	216	A
25	DA	221	A
25	DA	222	A
25	DA	229	A
25	DA	232	G
25	DA	233	A
25	DA	248	G
25	DA	250	G
25	DA	266	G
25	DA	271(K)	U
25	DA	271(L)	U
25	DA	271(M)	G
25	DA	271(N)	U
25	DA	272	G
25	DA	272(A)	U
25	DA	272(B)	G
25	DA	272(I)	U
25	DA	272(J)	C
25	DA	274	G
25	DA	277	C
25	DA	278	A
25	DA	292	C
25	DA	311	A
25	DA	329	G
25	DA	330	A
25	DA	342	G
25	DA	352	G
25	DA	353	G

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Mol	Chain	Res	Type
25	DA	361	G
25	DA	363	G
25	DA	363(C)	G
25	DA	363(D)	G
25	DA	380	U
25	DA	386	G
25	DA	396	G
25	DA	405	U
25	DA	406	G
25	DA	407	G
25	DA	411	G
25	DA	412	A
25	DA	421	U
25	DA	422	A
25	DA	428	A
25	DA	443	A
25	DA	444	C
25	DA	455	C
25	DA	456	C
25	DA	457	A
25	DA	470	A
25	DA	475	U
25	DA	481	G
25	DA	496	G
25	DA	505	A
25	DA	509	C
25	DA	512	G
25	DA	529	A
25	DA	531	C
25	DA	532	A
25	DA	533	G
25	DA	545	G
25	DA	555	U
25	DA	563	G
25	DA	568	U
25	DA	573	G
25	DA	575	A
25	DA	587	C
25	DA	588	U
25	DA	592	G
25	DA	595	C
25	DA	599	G

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Mol	Chain	Res	Type
25	DA	603	A
25	DA	604	G
25	DA	607	U
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	645	C
25	DA	646	A
25	DA	647	G
25	DA	652(B)	A
25	DA	652(C)	G
25	DA	652(D)	C
25	DA	652(U)	G
25	DA	669	G
25	DA	686	G
25	DA	717	G
25	DA	726	G
25	DA	730	C
25	DA	752	A
25	DA	753	C
25	DA	765	G
25	DA	774	A
25	DA	775	G
25	DA	776	G
25	DA	782	A
25	DA	784	A
25	DA	785	G
25	DA	792	G
25	DA	805	G
25	DA	812	C
25	DA	819	A
25	DA	827	U
25	DA	828	U
25	DA	857	C
25	DA	859	G
25	DA	866	A
25	DA	867	C
25	DA	874	G
25	DA	878	A

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Mol	Chain	Res	Type
25	DA	879	G
25	DA	880	G
25	DA	882	G
25	DA	884	C
25	DA	886	C
25	DA	887	A
25	DA	888	C
25	DA	889	C
25	DA	890	A
25	DA	893	C
25	DA	894	C
25	DA	896	A
25	DA	897	C
25	DA	900	A
25	DA	901	A
25	DA	903	C
25	DA	910	A
25	DA	915	C
25	DA	917	A
25	DA	932	G
25	DA	933	A
25	DA	938	G
25	DA	941	A
25	DA	944	G
25	DA	945	A
25	DA	946	G
25	DA	953	A
25	DA	958	U
25	DA	959	A
25	DA	961	C
25	DA	974	G
25	DA	975	C
25	DA	980	A
25	DA	983	A
25	DA	987	G
25	DA	996	A
25	DA	1005	C
25	DA	1012	U
25	DA	1013	C
25	DA	1022	G
25	DA	1025	G
25	DA	1026	U

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Mol	Chain	Res	Type
25	DA	1033	U
25	DA	1038	C
25	DA	1039	G
25	DA	1040	C
25	DA	1042	G
25	DA	1043	C
25	DA	1113	U
25	DA	1118	C
25	DA	1127	A
25	DA	1128	A
25	DA	1129	A
25	DA	1133	U
25	DA	1135	C
25	DA	1136	G
25	DA	1139	G
25	DA	1142(A)	A
25	DA	1157	G
25	DA	1170	G
25	DA	1171	G
25	DA	1188	U
25	DA	1206	G
25	DA	1210	A
25	DA	1211	U
25	DA	1220	A
25	DA	1247	A
25	DA	1253	A
25	DA	1256	G
25	DA	1262	A
25	DA	1271	G
25	DA	1272	A
25	DA	1273	U
25	DA	1300	U
25	DA	1301	A
25	DA	1303	G
25	DA	1314	C
25	DA	1319	G
25	DA	1320	C
25	DA	1321	A
25	DA	1327	C
25	DA	1352	U
25	DA	1359	A
25	DA	1360	A

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Mol	Chain	Res	Type
25	DA	1365	A
25	DA	1368	G
25	DA	1379	A
25	DA	1384	A
25	DA	1385	G
25	DA	1386	C
25	DA	1416	G
25	DA	1417	C
25	DA	1419	A
25	DA	1420	U
25	DA	1421	G
25	DA	1428	C
25	DA	1437	C
25	DA	1445	A
25	DA	1449	A
25	DA	1450	G
25	DA	1460	A
25	DA	1471	A
25	DA	1482	G
25	DA	1490	A
25	DA	1493	C
25	DA	1494	A
25	DA	1497	U
25	DA	1504	C
25	DA	1505	C
25	DA	1508	A
25	DA	1509	C
25	DA	1509(A)	A
25	DA	1512	U
25	DA	1531	C
25	DA	1532	C
25	DA	1533	G
25	DA	1542	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

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Mol	Chain	Res	Type
25	DA	1584	C
25	DA	1586	A
25	DA	1594	G
25	DA	1598	C
25	DA	1608	A
25	DA	1609	A
25	DA	1610	A
25	DA	1640	C
25	DA	1648	C
25	DA	1654	A
25	DA	1674	G
25	DA	1696	G
25	DA	1700	A
25	DA	1701	A
25	DA	1703	G
25	DA	1721	G
25	DA	1722	A
25	DA	1746	G
25	DA	1756	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	1812	A
25	DA	1816	G
25	DA	1828	G
25	DA	1829	A
25	DA	1833	U
25	DA	1835	G
25	DA	1848	A
25	DA	1877	A
25	DA	1878	G
25	DA	1895	C
25	DA	1896	G
25	DA	1900	A
25	DA	1906	G
25	DA	1913	A

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Mol	Chain	Res	Type
25	DA	1914	C
25	DA	1927	A
25	DA	1929	G
25	DA	1930	G
25	DA	1937	A
25	DA	1938	A
25	DA	1945	G
25	DA	1955	U
25	DA	1963	U
25	DA	1966	A
25	DA	1967	C
25	DA	1970	A
25	DA	1971	A
25	DA	1972	A
25	DA	1993	U
25	DA	1997	G
25	DA	2020	A
25	DA	2023	G
25	DA	2031	A
25	DA	2033	A
25	DA	2043	C
25	DA	2046	G
25	DA	2055	C
25	DA	2056	G
25	DA	2060	A
25	DA	2061	G
25	DA	2062	A
25	DA	2069	G
25	DA	2097	C
25	DA	2101	G
25	DA	2104	G
25	DA	2109	U
25	DA	2110	G
25	DA	2111	C
25	DA	2113	U
25	DA	2115	G
25	DA	2116	G
25	DA	2117	A
25	DA	2120	G
25	DA	2122	U
25	DA	2124	G
25	DA	2126	A

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Mol	Chain	Res	Type
25	DA	2127	G
25	DA	2128	C
25	DA	2129	C
25	DA	2130	U
25	DA	2131	G
25	DA	2132	U
25	DA	2133	G
25	DA	2134	A
25	DA	2135	A
25	DA	2136	C
25	DA	2137	C
25	DA	2139	C
25	DA	2142	C
25	DA	2143	C
25	DA	2144	U
25	DA	2145	C
25	DA	2146	C
25	DA	2147	G
25	DA	2148	G
25	DA	2150	U
25	DA	2155	G
25	DA	2156	G
25	DA	2157	G
25	DA	2158	A
25	DA	2159	G
25	DA	2160	G
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	2172	U
25	DA	2173	A
25	DA	2174	C
25	DA	2177	C
25	DA	2178	C
25	DA	2181	G
25	DA	2185	C
25	DA	2189	U
25	DA	2192	G
25	DA	2198	A

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Mol	Chain	Res	Type
25	DA	2206	G
25	DA	2207	G
25	DA	2208	A
25	DA	2219	G
25	DA	2225	A
25	DA	2238	G
25	DA	2239	G
25	DA	2268	A
25	DA	2269	A
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	2293	C
25	DA	2305	A
25	DA	2308	G
25	DA	2309	A
25	DA	2312	U
25	DA	2319	G
25	DA	2320	A
25	DA	2321	G
25	DA	2322	A
25	DA	2325	G
25	DA	2327	A
25	DA	2334	G
25	DA	2336	A
25	DA	2343	C
25	DA	2347	C
25	DA	2350	C
25	DA	2352	A
25	DA	2376	A
25	DA	2379	G
25	DA	2383	G
25	DA	2385	C
25	DA	2399	G
25	DA	2406	U
25	DA	2410	G
25	DA	2422	A
25	DA	2423	U
25	DA	2425	A

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Mol	Chain	Res	Type
25	DA	2426	A
25	DA	2429	G
25	DA	2430	A
25	DA	2434	A
25	DA	2435	A
25	DA	2439	A
25	DA	2441	C
25	DA	2445	G
25	DA	2448	A
25	DA	2459	A
25	DA	2468	G
25	DA	2476	A
25	DA	2484	G
25	DA	2487	G
25	DA	2490	G
25	DA	2494	G
25	DA	2502	G
25	DA	2505	G
25	DA	2506	U
25	DA	2518	A
25	DA	2520	C
25	DA	2525	G
25	DA	2536	G
25	DA	2542	A
25	DA	2554	U
25	DA	2555	U
25	DA	2566	A
25	DA	2567	G
25	DA	2573	C
25	DA	2579	C
25	DA	2584	U
25	DA	2585	U
25	DA	2586	C
25	DA	2602	A
25	DA	2603	G
25	DA	2609	U
25	DA	2611	U
25	DA	2612	C
25	DA	2615	U
25	DA	2629	A
25	DA	2630	G
25	DA	2632	A

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Mol	Chain	Res	Type
25	DA	2646	C
25	DA	2652	C
25	DA	2654	A
25	DA	2663	G
25	DA	2673	G
25	DA	2689	U
25	DA	2690	C
25	DA	2691	C
25	DA	2702	U
25	DA	2712(A)	A
25	DA	2713	A
25	DA	2714	G
25	DA	2718	G
25	DA	2726	U
25	DA	2732	G
25	DA	2733	A
25	DA	2739	U
25	DA	2751	G
25	DA	2757	A
25	DA	2758	A
25	DA	2761	G
25	DA	2764	A
25	DA	2765	A
25	DA	2766	G
25	DA	2778	A
25	DA	2793	G
25	DA	2794	C
25	DA	2802	G
25	DA	2809	A
25	DA	2818	G
25	DA	2820	A
25	DA	2821	A
25	DA	2833	G
25	DA	2835	A
25	DA	2836	U
25	DA	2872	G
25	DA	2879	C
25	DA	2880	C
25	DA	2892	A
25	DA	2893	G
25	DA	2894	G
25	DA	2895	U

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Mol	Chain	Res	Type
25	DA	2897	U
26	DB	2	C
26	DB	7	G
26	DB	9	G
26	DB	13	A
26	DB	30	C
26	DB	32	C
26	DB	56	G
26	DB	66	A
26	DB	73	A
26	DB	75	G
26	DB	85	G
26	DB	89	G
26	DB	108	U
26	DB	110	G

All (121) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	266	G
1	AA	345	C
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	793	U
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1008	C
1	AA	1026	G
1	AA	1027	C
1	AA	1029	C
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1190	G
1	AA	1201	A
1	AA	1212	U

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Mol	Chain	Res	Type
1	AA	1256	A
1	AA	1285	A
1	AA	1442	G
1	AA	1492	A
23	AW	22	G
24	AX	20	U
24	AX	47	U
23	AY	18	G
23	AY	21	A
23	AY	25	C
23	AY	58	A
25	BA	184	A
25	BA	185	A
25	BA	273	G
25	BA	302	A
25	BA	793	A
25	BA	811	A
25	BA	1019	G
25	BA	1093	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1255	A
25	BA	1425	A
25	BA	1577	C
25	BA	1700	G
25	BA	2014	G
25	BA	2140	U
25	BA	2148	A
25	BA	2156	A
25	BA	2166	U
25	BA	2170	G
25	BA	2203	G
25	BA	2347	A
25	BA	2418	U
25	BA	2613	C
25	BA	2701	U
25	BA	2769	U
25	BA	2902	G
26	BB	56	G
26	BB	109	C
1	CA	60	A

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Mol	Chain	Res	Type
1	CA	115	G
1	CA	251	G
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	687	A
1	CA	748	C
1	CA	793	U
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1027	C
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1183	A
1	CA	1201	A
1	CA	1256	A
1	CA	1442	G
1	CA	1492	A
23	CW	4	C
23	CW	13	C
24	CX	20	U
23	CY	18	G
25	DA	195	A
25	DA	196	A
25	DA	249	C
25	DA	271(K)	U
25	DA	277	C
25	DA	587	C
25	DA	752	A
25	DA	774	A
25	DA	827	U
25	DA	856	C
25	DA	900	A
25	DA	1210	A
25	DA	1300	U
25	DA	1301	A
25	DA	1427	A

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Mol	Chain	Res	Type
25	DA	1493	C
25	DA	1558	A
25	DA	1653	G
25	DA	1913	A
25	DA	1992	G
25	DA	2110	G
25	DA	2126	A
25	DA	2134	A
25	DA	2321	G
25	DA	2351	G
25	DA	2422	A
25	DA	2602	A
25	DA	2689	U
25	DA	2756	U

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

36 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	PSU	AX	55	24	18,21,22	1.38	2 (11%)	21,30,33	2.04	4 (19%)
23	PSU	CW	55	23	18,21,22	1.43	2 (11%)	21,30,33	1.95	3 (14%)
23	PSU	AY	32	23	18,21,22	1.35	2 (11%)	21,30,33	2.05	4 (19%)
23	4SU	CY	8	23	18,21,22	1.79	4 (22%)	25,30,33	2.13	5 (20%)
23	MIA	AW	37	23	28,31,32	2.31	6 (21%)	38,44,47	2.84	14 (36%)
23	4SU	AY	8	23	18,21,22	1.69	4 (22%)	25,30,33	1.82	4 (16%)
23	7MG	CY	46	23	23,26,27	1.41	5 (21%)	27,39,42	2.46	5 (18%)
23	5MU	CW	54	23	19,22,23	1.36	4 (21%)	27,32,35	1.69	6 (22%)
24	5MC	CX	32	24	19,22,23	1.69	3 (15%)	26,32,35	1.30	3 (11%)
23	PSU	CY	39	23	18,21,22	1.39	2 (11%)	21,30,33	2.30	3 (14%)
24	4SU	CX	8	24	18,21,22	2.18	5 (27%)	25,30,33	1.50	6 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
24	5MU	AX	54	24	19,22,23	1.36	4 (21%)	27,32,35	1.97	7 (25%)
23	PSU	AW	39	23	18,21,22	1.44	3 (16%)	21,30,33	1.65	4 (19%)
23	7MG	CW	46	23	23,26,27	1.30	4 (17%)	27,39,42	2.71	7 (25%)
23	PSU	AY	55	23	18,21,22	1.34	2 (11%)	21,30,33	2.11	4 (19%)
23	PSU	CW	39	23	18,21,22	1.38	2 (11%)	21,30,33	2.03	4 (19%)
23	4SU	AW	8	23	18,21,22	1.76	4 (22%)	25,30,33	1.81	5 (20%)
23	PSU	CY	32	23	18,21,22	1.36	2 (11%)	21,30,33	1.90	4 (19%)
23	5MU	AW	54	23	19,22,23	1.40	5 (26%)	27,32,35	1.91	6 (22%)
23	PSU	AW	32	23	18,21,22	1.36	2 (11%)	21,30,33	1.88	3 (14%)
23	7MG	AW	46	23	23,26,27	1.38	5 (21%)	27,39,42	2.54	7 (25%)
23	MIA	AY	37	23	21,24,32	1.63	3 (14%)	30,35,47	1.98	9 (30%)
23	PSU	AY	39	23	18,21,22	1.57	4 (22%)	21,30,33	2.14	5 (23%)
23	4SU	CW	8	23	18,21,22	1.68	4 (22%)	25,30,33	2.34	5 (20%)
23	PSU	CW	32	23	18,21,22	1.38	2 (11%)	21,30,33	1.95	3 (14%)
24	5MC	AX	32	24	19,22,23	1.59	3 (15%)	26,32,35	1.26	2 (7%)
23	MIA	CY	37	23	21,24,32	1.67	4 (19%)	30,35,47	2.03	8 (26%)
24	5MU	CX	54	24	19,22,23	1.39	4 (21%)	27,32,35	2.29	8 (29%)
23	7MG	AY	46	23	23,26,27	1.37	4 (17%)	27,39,42	2.65	7 (25%)
24	PSU	CX	55	24	18,21,22	1.37	2 (11%)	21,30,33	1.92	5 (23%)
23	5MU	AY	54	23	19,22,23	1.53	5 (26%)	27,32,35	1.65	6 (22%)
23	PSU	CY	55	23	18,21,22	1.49	3 (16%)	21,30,33	1.94	5 (23%)
23	MIA	CW	37	23	21,24,32	1.57	4 (19%)	30,35,47	2.11	8 (26%)
23	5MU	CY	54	23	19,22,23	1.39	5 (26%)	27,32,35	2.19	8 (29%)
24	4SU	AX	8	24	18,21,22	2.34	5 (27%)	25,30,33	1.61	5 (20%)
23	PSU	AW	55	23	18,21,22	1.31	2 (11%)	21,30,33	1.78	4 (19%)

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	PSU	AX	55	24	-	0/7/25/26	0/2/2/2
23	PSU	CW	55	23	-	0/7/25/26	0/2/2/2
23	PSU	AY	32	23	-	0/7/25/26	0/2/2/2
23	4SU	CY	8	23	-	2/7/25/26	0/2/2/2
23	MIA	AW	37	23	-	1/15/33/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	4SU	AY	8	23	-	2/7/25/26	0/2/2/2
23	7MG	CY	46	23	-	2/7/37/38	0/3/3/3
23	5MU	CW	54	23	-	0/7/25/26	0/2/2/2
24	5MC	CX	32	24	-	0/7/25/26	0/2/2/2
23	PSU	CY	39	23	-	2/7/25/26	0/2/2/2
24	4SU	CX	8	24	-	1/7/25/26	0/2/2/2
24	5MU	AX	54	24	-	0/7/25/26	0/2/2/2
23	PSU	AW	39	23	-	0/7/25/26	0/2/2/2
23	7MG	CW	46	23	-	2/7/37/38	0/3/3/3
23	PSU	AY	55	23	-	2/7/25/26	0/2/2/2
23	PSU	CW	39	23	-	0/7/25/26	0/2/2/2
23	4SU	AW	8	23	-	0/7/25/26	0/2/2/2
23	PSU	CY	32	23	-	0/7/25/26	0/2/2/2
23	5MU	AW	54	23	-	0/7/25/26	0/2/2/2
23	PSU	AW	32	23	-	0/7/25/26	0/2/2/2
23	7MG	AW	46	23	-	4/7/37/38	0/3/3/3
23	MIA	AY	37	23	-	0/7/25/34	0/3/3/3
23	PSU	AY	39	23	-	2/7/25/26	0/2/2/2
23	4SU	CW	8	23	-	0/7/25/26	0/2/2/2
23	PSU	CW	32	23	-	0/7/25/26	0/2/2/2
24	5MC	AX	32	24	-	0/7/25/26	0/2/2/2
23	MIA	CY	37	23	-	3/7/25/34	0/3/3/3
24	5MU	CX	54	24	-	0/7/25/26	0/2/2/2
23	7MG	AY	46	23	-	2/7/37/38	0/3/3/3
24	PSU	CX	55	24	-	0/7/25/26	0/2/2/2
23	5MU	AY	54	23	-	2/7/25/26	0/2/2/2
23	PSU	CY	55	23	-	1/7/25/26	0/2/2/2
23	MIA	CW	37	23	-	0/7/25/34	0/3/3/3
23	5MU	CY	54	23	-	2/7/25/26	0/2/2/2
24	4SU	AX	8	24	-	0/7/25/26	0/2/2/2
23	PSU	AW	55	23	-	0/7/25/26	0/2/2/2

All (126) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C2-S10	-6.96	1.70	1.75
23	AW	37	MIA	C13-C14	6.78	1.52	1.32
24	CX	32	5MC	C5-C4	6.09	1.48	1.44
24	AX	8	4SU	C4-N3	-5.83	1.31	1.37
24	AX	32	5MC	C5-C4	5.49	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CX	8	4SU	C4-N3	-5.36	1.32	1.37
23	CY	37	MIA	C5-C4	5.29	1.48	1.39
23	AY	37	MIA	C5-C4	5.12	1.48	1.39
23	CW	37	MIA	C5-C4	4.91	1.47	1.39
24	AX	8	4SU	C4-S4	-4.69	1.60	1.68
23	CW	8	4SU	C4-S4	-4.68	1.60	1.68
23	CY	8	4SU	C4-S4	-4.64	1.60	1.68
23	AW	37	MIA	C5-C4	4.58	1.47	1.39
24	CX	8	4SU	C4-S4	-4.57	1.60	1.68
23	AW	8	4SU	C4-S4	-4.50	1.60	1.68
23	AY	8	4SU	C4-S4	-4.37	1.61	1.68
23	CW	55	PSU	C6-C5	4.29	1.40	1.35
23	CY	55	PSU	C6-C5	3.94	1.39	1.35
23	AY	39	PSU	C6-C5	3.93	1.39	1.35
24	AX	8	4SU	C2-N3	-3.92	1.31	1.38
23	CY	32	PSU	C6-C5	3.89	1.39	1.35
24	CX	55	PSU	C6-C5	3.88	1.39	1.35
23	AW	55	PSU	C6-C5	3.86	1.39	1.35
24	CX	8	4SU	C2-N3	-3.65	1.31	1.38
23	AY	55	PSU	C6-C5	3.64	1.39	1.35
23	CW	32	PSU	C6-C5	3.60	1.39	1.35
23	AW	39	PSU	C6-C5	3.57	1.39	1.35
23	CY	39	PSU	C6-C5	3.55	1.39	1.35
23	CW	39	PSU	C6-C5	3.54	1.39	1.35
23	AY	46	7MG	C5-C4	3.52	1.48	1.37
23	AW	32	PSU	C6-C5	3.52	1.39	1.35
23	AY	32	PSU	C6-C5	3.52	1.39	1.35
24	AX	8	4SU	C5-C4	-3.44	1.38	1.42
24	AX	55	PSU	C6-C5	3.43	1.39	1.35
23	CY	46	7MG	C5-C4	3.42	1.48	1.37
23	AW	46	7MG	C4-N9	-3.39	1.33	1.37
23	AW	46	7MG	C5-C4	3.37	1.48	1.37
23	CW	46	7MG	C5-C4	3.35	1.47	1.37
23	CY	46	7MG	C4-N9	-3.28	1.33	1.37
24	AX	32	5MC	C6-C5	3.15	1.39	1.34
23	CY	55	PSU	C4-N3	-3.09	1.33	1.38
23	AY	54	5MU	C4-N3	-3.00	1.33	1.38
23	AW	39	PSU	C4-N3	-2.97	1.33	1.38
23	CY	37	MIA	C5-C6	2.94	1.49	1.41
23	AW	8	4SU	C4-N3	-2.92	1.34	1.37
24	CX	8	4SU	C5-C4	-2.92	1.39	1.42
23	AY	54	5MU	C2-N3	-2.91	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	54	5MU	C6-C5	2.90	1.39	1.34
23	CW	37	MIA	C5-C6	2.90	1.49	1.41
24	CX	32	5MC	C6-C5	2.86	1.39	1.34
23	AY	37	MIA	C5-C6	2.83	1.48	1.41
23	CY	8	4SU	C4-N3	-2.83	1.34	1.37
23	CY	8	4SU	C5-C4	-2.80	1.39	1.42
23	AY	8	4SU	C4-N3	-2.78	1.34	1.37
24	CX	54	5MU	C6-C5	2.76	1.39	1.34
23	CY	54	5MU	C2-N1	2.75	1.42	1.38
23	AY	54	5MU	C6-C5	2.73	1.39	1.34
24	CX	54	5MU	C4-C5	2.71	1.49	1.44
23	CY	8	4SU	C2-N1	2.68	1.42	1.38
24	AX	54	5MU	C4-N3	-2.64	1.33	1.38
23	AW	8	4SU	C5-C4	-2.64	1.39	1.42
23	AY	54	5MU	C2-N1	2.64	1.42	1.38
23	AW	37	MIA	C5-C6	2.63	1.48	1.41
24	AX	55	PSU	C4-N3	-2.62	1.33	1.38
24	AX	54	5MU	C6-C5	2.61	1.38	1.34
23	AW	54	5MU	C4-N3	-2.61	1.34	1.38
23	AY	46	7MG	C4-N9	-2.61	1.34	1.37
23	CW	39	PSU	C4-N3	-2.61	1.34	1.38
23	AY	37	MIA	C8-N7	2.59	1.36	1.31
23	CW	8	4SU	C5-C4	-2.58	1.39	1.42
23	AY	46	7MG	C8-N9	2.58	1.47	1.45
23	CW	54	5MU	C6-C5	2.57	1.38	1.34
23	AY	39	PSU	O4'-C1'	-2.56	1.40	1.43
23	CW	32	PSU	C4-N3	-2.56	1.34	1.38
23	AY	32	PSU	C4-N3	-2.55	1.34	1.38
23	CY	54	5MU	C6-C5	2.54	1.38	1.34
23	AW	37	MIA	C8-N7	2.54	1.36	1.31
23	CY	37	MIA	C8-N7	2.54	1.36	1.31
23	CY	46	7MG	C8-N9	2.52	1.47	1.45
23	AY	39	PSU	C4-N3	-2.52	1.34	1.38
23	AW	32	PSU	C4-N3	-2.51	1.34	1.38
23	AY	8	4SU	C5-C4	-2.51	1.39	1.42
24	AX	8	4SU	O2-C2	2.49	1.27	1.23
23	CW	46	7MG	C5-C6	2.48	1.49	1.43
23	CY	54	5MU	C4-C5	2.47	1.48	1.44
23	AW	8	4SU	C2-N1	2.47	1.42	1.38
23	CW	37	MIA	C8-N7	2.46	1.36	1.31
24	CX	54	5MU	C4-N3	-2.46	1.34	1.38
23	CW	46	7MG	C4-N9	-2.45	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CW	8	4SU	C4-N3	-2.41	1.35	1.37
23	CW	54	5MU	C4-N3	-2.40	1.34	1.38
23	AW	37	MIA	C5-N7	-2.39	1.34	1.39
23	AY	55	PSU	C4-N3	-2.37	1.34	1.38
23	CW	54	5MU	C4-C5	2.33	1.48	1.44
24	CX	54	5MU	C6-N1	-2.31	1.34	1.38
23	CW	8	4SU	C2-N1	2.29	1.42	1.38
23	AY	39	PSU	C2-N1	-2.28	1.33	1.36
23	CW	55	PSU	C4-N3	-2.27	1.34	1.38
24	AX	54	5MU	C4-C5	2.27	1.48	1.44
23	CY	32	PSU	C4-N3	-2.26	1.34	1.38
24	AX	32	5MC	C6-N1	-2.26	1.34	1.38
23	AW	54	5MU	C2-N1	2.25	1.42	1.38
23	AW	54	5MU	C4-C5	2.22	1.48	1.44
23	CW	46	7MG	C8-N9	2.22	1.47	1.45
23	AY	8	4SU	C2-N1	2.22	1.41	1.38
24	CX	55	PSU	C4-N3	-2.22	1.34	1.38
23	CW	54	5MU	C2-N1	2.21	1.41	1.38
23	CY	46	7MG	C6-N1	-2.16	1.34	1.38
23	CY	54	5MU	C4-N3	-2.16	1.34	1.38
23	AW	46	7MG	C5-C6	2.15	1.48	1.43
24	CX	32	5MC	C6-N1	-2.15	1.34	1.38
23	AY	54	5MU	C4-C5	2.13	1.48	1.44
23	AW	54	5MU	C6-N1	-2.12	1.34	1.38
23	CY	39	PSU	C4-N3	-2.11	1.34	1.38
23	AW	39	PSU	C2-N3	-2.11	1.34	1.37
23	CY	54	5MU	C6-N1	-2.11	1.34	1.38
23	AY	46	7MG	C5-C6	2.10	1.48	1.43
23	AW	55	PSU	C4-N3	-2.10	1.34	1.38
24	CX	8	4SU	C6-C5	2.09	1.39	1.35
23	CY	46	7MG	C5-C6	2.09	1.48	1.43
23	CY	55	PSU	C2-N3	-2.07	1.34	1.37
23	AW	46	7MG	C8-N9	2.06	1.47	1.45
23	CY	37	MIA	C5-N7	-2.04	1.35	1.39
23	CW	37	MIA	C5-N7	-2.03	1.35	1.39
24	AX	54	5MU	C2-N1	2.01	1.41	1.38
23	AW	46	7MG	C6-N1	-2.00	1.35	1.38

All (196) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	AW	37	MIA	C12-C13-C14	-10.43	108.30	127.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	AY	46	7MG	N9-C4-N3	9.05	138.72	125.46
23	CW	46	7MG	N9-C4-N3	8.86	138.44	125.46
23	AW	46	7MG	N9-C4-N3	8.24	137.53	125.46
23	CY	46	7MG	N9-C4-N3	7.84	136.95	125.46
23	AW	37	MIA	C5-C4-N3	-7.31	119.48	127.18
23	CY	39	PSU	N1-C2-N3	7.06	122.62	115.17
23	CW	8	4SU	C4-N3-C2	-6.71	120.88	127.31
23	AY	55	PSU	N1-C2-N3	6.43	121.95	115.17
23	AY	32	PSU	N1-C2-N3	6.40	121.92	115.17
23	CW	39	PSU	N1-C2-N3	6.36	121.88	115.17
24	AX	55	PSU	N1-C2-N3	6.34	121.86	115.17
23	AY	39	PSU	N1-C2-N3	6.32	121.83	115.17
23	CY	55	PSU	N1-C2-N3	6.13	121.63	115.17
23	CW	32	PSU	N1-C2-N3	6.04	121.54	115.17
23	CW	55	PSU	N1-C2-N3	5.98	121.48	115.17
23	CW	37	MIA	C5-C4-N3	-5.98	118.48	126.72
24	CX	55	PSU	N1-C2-N3	5.92	121.41	115.17
23	CW	46	7MG	C5-C4-N3	-5.89	117.08	128.13
23	CY	8	4SU	C4-N3-C2	-5.84	121.72	127.31
23	AW	32	PSU	N1-C2-N3	5.76	121.24	115.17
23	CY	37	MIA	C5-C4-N3	-5.72	118.84	126.72
24	CX	54	5MU	C4-N3-C2	-5.72	119.84	127.34
23	CY	32	PSU	N1-C2-N3	5.69	121.17	115.17
23	AW	46	7MG	N9-C8-N7	-5.58	95.48	103.37
23	CW	8	4SU	C5-C4-N3	5.53	119.90	114.75
23	AW	37	MIA	N3-C4-N9	5.51	133.99	126.99
24	CX	54	5MU	N3-C2-N1	5.48	122.03	114.89
23	AY	46	7MG	C5-C4-N3	-5.48	117.85	128.13
23	AY	37	MIA	C5-C4-N3	-5.36	119.34	126.72
23	CY	8	4SU	C5-C4-N3	5.28	119.67	114.75
23	AW	39	PSU	N1-C2-N3	5.23	120.68	115.17
23	CW	46	7MG	N9-C8-N7	-5.17	96.06	103.37
23	CY	46	7MG	N9-C8-N7	-5.15	96.08	103.37
23	CW	46	7MG	C2-N3-C4	5.11	121.10	112.30
23	AY	8	4SU	C4-N3-C2	-5.11	122.42	127.31
23	CY	39	PSU	O2-C2-N1	-5.09	117.54	122.79
23	CY	54	5MU	C4-N3-C2	-5.07	120.70	127.34
23	AW	55	PSU	N1-C2-N3	5.02	120.46	115.17
23	AW	46	7MG	C5-C4-N3	-4.98	118.78	128.13
23	AY	46	7MG	N9-C8-N7	-4.94	96.37	103.37
23	CW	8	4SU	C5-C4-S4	-4.91	118.69	124.31
23	AW	54	5MU	N3-C2-N1	4.88	121.25	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CY	54	5MU	C5-C4-N3	4.88	119.57	115.32
23	AW	8	4SU	C5-C4-N3	4.86	119.27	114.75
23	CY	46	7MG	C5-C4-N3	-4.82	119.09	128.13
23	AY	46	7MG	C2-N3-C4	4.71	120.41	112.30
23	CW	37	MIA	N3-C4-N9	4.70	135.17	127.17
24	AX	54	5MU	C4-N3-C2	-4.64	121.25	127.34
23	CY	37	MIA	N3-C4-N9	4.64	135.06	127.17
23	AW	8	4SU	C4-N3-C2	-4.63	122.87	127.31
23	CY	54	5MU	O4-C4-C5	-4.58	119.68	124.92
23	AW	54	5MU	C4-N3-C2	-4.56	121.37	127.34
24	AX	54	5MU	N3-C2-N1	4.54	120.80	114.89
24	CX	54	5MU	C5-C4-N3	4.50	119.23	115.32
23	CY	39	PSU	C4-N3-C2	-4.48	120.20	126.37
23	AY	39	PSU	O2-C2-N1	-4.48	118.17	122.79
23	CY	8	4SU	C5-C4-S4	-4.36	119.33	124.31
23	AY	8	4SU	C5-C4-N3	4.32	118.77	114.75
23	CY	54	5MU	N3-C2-N1	4.31	120.50	114.89
23	AY	37	MIA	N3-C4-N9	4.27	134.44	127.17
24	AX	54	5MU	C5-C4-N3	4.27	119.03	115.32
23	AW	46	7MG	C2-N3-C4	4.25	119.62	112.30
23	AW	37	MIA	C16-C14-C13	-4.20	110.06	122.66
23	AY	32	PSU	C4-N3-C2	-4.20	120.59	126.37
23	AY	55	PSU	C4-N3-C2	-4.18	120.61	126.37
23	CW	39	PSU	C4-N3-C2	-4.15	120.66	126.37
23	CW	8	4SU	N3-C2-N1	4.15	120.29	114.89
23	CY	46	7MG	C2-N3-C4	4.15	119.44	112.30
24	AX	32	5MC	C5-C6-N1	-4.12	118.83	123.31
24	CX	55	PSU	C4-N3-C2	-4.11	120.71	126.37
24	AX	55	PSU	C4-N3-C2	-4.07	120.77	126.37
24	CX	54	5MU	C5-C6-N1	-3.99	118.97	123.31
24	AX	8	4SU	C6-C5-C4	-3.99	116.50	119.95
23	CW	37	MIA	C2-N3-C4	3.97	121.54	111.83
23	CW	32	PSU	C4-N3-C2	-3.95	120.93	126.37
23	AY	55	PSU	O2-C2-N1	-3.92	118.75	122.79
23	CW	37	MIA	N3-C2-N1	-3.91	122.66	128.58
24	CX	54	5MU	O4-C4-C5	-3.90	120.45	124.92
23	AW	37	MIA	C15-C14-C13	-3.88	111.01	122.66
23	AY	54	5MU	C5-C4-N3	3.81	118.64	115.32
23	CW	55	PSU	O2-C2-N1	-3.79	118.88	122.79
23	AW	54	5MU	O4-C4-C5	-3.77	120.60	124.92
23	CY	32	PSU	C4-N3-C2	-3.73	121.23	126.37
23	CW	54	5MU	C5-C4-N3	3.73	118.56	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CW	54	5MU	O4-C4-C5	-3.70	120.69	124.92
23	CY	37	MIA	C2-N3-C4	3.69	120.85	111.83
23	AW	55	PSU	C4-N3-C2	-3.66	121.33	126.37
23	AW	54	5MU	C5-C4-N3	3.66	118.50	115.32
23	AW	32	PSU	C4-N3-C2	-3.65	121.34	126.37
23	AY	37	MIA	N3-C2-N1	-3.63	123.08	128.58
24	AX	54	5MU	O4-C4-C5	-3.62	120.78	124.92
23	CY	8	4SU	N3-C2-N1	3.61	119.59	114.89
23	AY	54	5MU	N3-C2-N1	3.60	119.58	114.89
23	CY	37	MIA	N3-C2-N1	-3.60	123.13	128.58
23	CW	37	MIA	C4-C5-N7	-3.57	106.50	110.58
24	CX	54	5MU	O2-C2-N1	-3.57	118.15	122.80
23	AY	37	MIA	C2-N3-C4	3.54	120.48	111.83
23	AY	8	4SU	C5-C4-S4	-3.54	120.26	124.31
23	AY	8	4SU	N3-C2-N1	3.53	119.48	114.89
23	CW	54	5MU	C4-N3-C2	-3.53	122.72	127.34
23	CW	55	PSU	C4-N3-C2	-3.52	121.52	126.37
24	CX	32	5MC	C5-C6-N1	-3.49	119.52	123.31
23	AW	37	MIA	C6-C5-N7	3.49	136.23	132.43
23	CW	54	5MU	N3-C2-N1	3.48	119.43	114.89
23	AY	37	MIA	C4-C5-N7	-3.47	106.61	110.58
23	AY	32	PSU	O2-C2-N1	-3.46	119.22	122.79
23	CY	37	MIA	C4-C5-N7	-3.44	106.65	110.58
23	AW	8	4SU	C5-C4-S4	-3.41	120.41	124.31
23	AW	37	MIA	C4-C5-N7	-3.41	106.69	110.58
23	AW	37	MIA	C2-N3-C4	3.39	121.16	112.29
24	AX	8	4SU	O2-C2-N1	3.34	127.14	122.80
23	CY	55	PSU	C4-N3-C2	-3.33	121.78	126.37
23	AY	54	5MU	C4-N3-C2	-3.30	123.01	127.34
23	CY	54	5MU	C5-C6-N1	-3.30	119.73	123.31
24	AX	55	PSU	O2-C2-N1	-3.30	119.39	122.79
23	CW	32	PSU	O2-C2-N1	-3.28	119.40	122.79
23	AY	54	5MU	C5-C6-N1	-3.28	119.75	123.31
23	AW	32	PSU	O2-C2-N1	-3.27	119.42	122.79
23	CW	46	7MG	C5-C6-N1	3.27	116.69	110.94
23	AY	39	PSU	C6-C5-C4	-3.27	115.97	118.17
23	AY	39	PSU	C4-N3-C2	-3.26	121.88	126.37
24	AX	54	5MU	C5-C6-N1	-3.26	119.77	123.31
23	CY	32	PSU	O2-C2-N1	-3.25	119.44	122.79
24	CX	8	4SU	C5-C4-N3	3.22	117.75	114.75
23	AY	54	5MU	O4-C4-C5	-3.17	121.29	124.92
23	AW	54	5MU	C5-C6-N1	-3.14	119.90	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	AW	8	4SU	N3-C2-N1	3.09	118.91	114.89
23	CW	39	PSU	O2-C2-N1	-3.05	119.64	122.79
24	AX	8	4SU	S4-C4-N3	-2.96	117.10	120.20
24	CX	32	5MC	C5-C4-N3	-2.91	118.77	121.75
23	AW	39	PSU	C4-N3-C2	-2.91	122.36	126.37
24	AX	8	4SU	C5-C4-N3	2.88	117.43	114.75
23	CW	8	4SU	O2-C2-N1	-2.86	119.08	122.80
24	CX	8	4SU	O2-C2-N1	2.86	126.51	122.80
24	CX	32	5MC	O2-C2-N3	-2.84	117.85	122.33
24	CX	8	4SU	S4-C4-N3	-2.78	117.29	120.20
24	AX	32	5MC	C5-C4-N3	-2.78	118.91	121.75
23	AW	46	7MG	C5-C6-N1	2.76	115.81	110.94
24	AX	54	5MU	O2-C2-N1	-2.73	119.24	122.80
23	AY	37	MIA	C4-N9-C8	2.71	108.58	105.74
23	CW	37	MIA	C5-N7-C8	2.70	107.70	103.45
23	CY	55	PSU	C6-C5-C4	-2.67	116.37	118.17
24	CX	8	4SU	C1'-N1-C2	2.63	122.32	117.59
24	CX	8	4SU	O2-C2-N3	-2.63	116.64	121.49
23	AY	46	7MG	C5-C6-N1	2.62	115.54	110.94
23	CY	54	5MU	C1'-N1-C6	-2.60	116.86	121.15
23	AW	54	5MU	O2-C2-N1	-2.58	119.44	122.80
23	AW	37	MIA	N3-C2-N1	-2.57	122.31	127.00
23	AY	37	MIA	C5-N7-C8	2.54	107.44	103.45
23	CW	54	5MU	C5M-C5-C4	2.54	121.49	118.78
23	CY	54	5MU	C5M-C5-C4	2.53	121.49	118.78
23	CY	37	MIA	C4-N9-C8	2.53	108.40	105.74
23	AW	37	MIA	C2-N1-C6	2.52	122.33	117.54
23	AW	37	MIA	C4-N9-C8	2.51	108.38	105.74
23	CY	37	MIA	C5-N7-C8	2.50	107.38	103.45
23	AW	37	MIA	C5-N7-C8	2.50	107.38	103.45
23	CW	37	MIA	C4-N9-C8	2.48	108.34	105.74
23	AY	54	5MU	O2-C2-N3	-2.46	116.95	121.49
23	CY	55	PSU	O2-C2-N1	-2.43	120.29	122.79
24	CX	8	4SU	C6-C5-C4	-2.41	117.87	119.95
23	AW	8	4SU	C1'-N1-C2	2.40	121.91	117.59
23	CY	46	7MG	C5-C6-N1	2.40	115.17	110.94
23	AY	39	PSU	C6-N1-C2	-2.40	120.47	122.69
23	CY	32	PSU	C6-C5-C4	-2.39	116.56	118.17
23	CW	54	5MU	C5-C6-N1	-2.38	120.72	123.31
24	CX	55	PSU	O2-C2-N1	-2.38	120.34	122.79
24	AX	55	PSU	C5-C6-N1	-2.37	118.85	122.14
23	CY	54	5MU	C1'-N1-C2	2.35	121.81	117.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	AW	55	PSU	O2-C2-N1	-2.33	120.38	122.79
24	AX	8	4SU	C1'-N1-C2	2.32	121.76	117.59
24	CX	55	PSU	C5-C6-N1	-2.31	118.93	122.14
23	AY	46	7MG	C5-C4-N9	-2.28	103.41	106.33
23	CW	39	PSU	C5-C6-N1	-2.24	119.03	122.14
23	AY	46	7MG	O6-C6-C5	-2.24	122.13	127.62
23	CY	8	4SU	C1'-N1-C2	2.22	121.58	117.59
24	AX	54	5MU	C5M-C5-C4	2.18	121.11	118.78
23	AY	32	PSU	C5-C6-N1	-2.15	119.15	122.14
23	CW	46	7MG	O6-C6-C5	-2.15	122.35	127.62
23	CY	55	PSU	O2-C2-N3	-2.13	118.08	121.86
23	AY	37	MIA	C6-C5-N7	2.11	136.16	132.09
23	AY	55	PSU	O4'-C1'-C2'	2.10	108.06	105.15
23	CW	46	7MG	C2-N1-C6	-2.10	121.30	125.11
23	AY	37	MIA	C2-N1-C6	2.09	122.17	118.73
24	CX	54	5MU	C5M-C5-C4	2.09	121.01	118.78
23	CW	37	MIA	C6-C5-N7	2.08	136.10	132.09
23	AW	37	MIA	N6-C6-N1	2.08	121.12	118.33
23	AW	46	7MG	C5-C4-N9	-2.07	103.68	106.33
23	AW	55	PSU	C6-C5-C4	-2.06	116.78	118.17
23	AW	37	MIA	N9-C8-N7	-2.05	111.03	113.94
24	CX	55	PSU	O2-C2-N3	-2.03	118.25	121.86
23	CY	37	MIA	C2-N1-C6	2.03	122.06	118.73
23	AW	39	PSU	O2-C2-N1	-2.02	120.70	122.79
23	AW	46	7MG	O6-C6-C5	-2.02	122.66	127.62
24	CX	54	5MU	C5M-C5-C6	-2.01	120.13	122.85
23	AW	39	PSU	C5-C6-N1	-2.00	119.36	122.14

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	AW	37	MIA	C12-C13-C14-C16
23	AY	46	7MG	C2'-C1'-N9-C8
23	AY	55	PSU	C2'-C1'-C5-C4
23	CY	54	5MU	C3'-C4'-C5'-O5'
23	CY	54	5MU	O4'-C4'-C5'-O5'
23	AY	39	PSU	O4'-C4'-C5'-O5'
23	AY	54	5MU	O4'-C4'-C5'-O5'
23	CY	8	4SU	C3'-C4'-C5'-O5'
23	CY	8	4SU	O4'-C4'-C5'-O5'
23	CY	37	MIA	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
23	CY	37	MIA	O4'-C4'-C5'-O5'
23	CY	39	PSU	O4'-C4'-C5'-O5'
23	AY	39	PSU	C3'-C4'-C5'-O5'
23	CY	39	PSU	C3'-C4'-C5'-O5'
23	CW	46	7MG	C2'-C1'-N9-C8
23	AY	54	5MU	C3'-C4'-C5'-O5'
23	AY	8	4SU	O4'-C4'-C5'-O5'
23	AY	8	4SU	C3'-C4'-C5'-O5'
23	CY	46	7MG	C2'-C1'-N9-C8
23	AY	55	PSU	O4'-C1'-C5-C4
23	CY	37	MIA	C4'-C5'-O5'-P
23	AY	46	7MG	C3'-C4'-C5'-O5'
23	CY	46	7MG	O4'-C1'-N9-C8
23	AW	46	7MG	C4'-C5'-O5'-P
23	AW	46	7MG	C2'-C1'-N9-C8
23	CY	55	PSU	C2'-C1'-C5-C6
23	AW	46	7MG	C3'-C4'-C5'-O5'
23	CW	46	7MG	O4'-C1'-N9-C8
23	AW	46	7MG	O4'-C4'-C5'-O5'
24	CX	8	4SU	C2'-C1'-N1-C2

There are no ring outliers.

24 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	AY	8	4SU	4	0
23	CY	46	7MG	5	0
23	CY	39	PSU	1	0
24	CX	8	4SU	1	0
23	AW	39	PSU	1	0
23	CW	46	7MG	3	0
23	AY	55	PSU	2	0
23	CW	39	PSU	3	0
23	AW	8	4SU	1	0
23	AW	54	5MU	2	0
23	AW	32	PSU	1	0
23	AW	46	7MG	1	0
23	AY	37	MIA	2	0
23	AY	39	PSU	1	0
23	CW	8	4SU	2	0
23	CW	32	PSU	1	0
24	AX	32	5MC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	CY	37	MIA	1	0
24	CX	54	5MU	2	0
24	CX	55	PSU	2	0
23	AY	54	5MU	1	0
23	CY	55	PSU	5	0
24	AX	8	4SU	1	0
23	AW	55	PSU	3	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2048 ligands modelled in this entry, 2027 are monoatomic - leaving 21 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	NEG	CA	3170	56	14,16,16	7.77	1 (7%)	12,20,20	1.09	1 (8%)
58	SF4	CD	302	4	0,12,12	-	-	-		
57	NEG	CA	3176	-	14,16,16	7.71	1 (7%)	12,20,20	1.50	2 (16%)
57	NEG	CA	3171	-	14,16,16	7.30	1 (7%)	12,20,20	2.55	3 (25%)
57	NEG	AA	3222	-	14,16,16	7.58	1 (7%)	12,20,20	1.66	1 (8%)
57	NEG	AA	3216	56	14,16,16	7.98	1 (7%)	12,20,20	2.29	2 (16%)
57	NEG	CX	3004	-	14,16,16	7.66	1 (7%)	12,20,20	2.04	2 (16%)
57	NEG	CA	3174	-	14,16,16	7.12	1 (7%)	12,20,20	4.26	4 (33%)
57	NEG	CA	3173	-	14,16,16	7.54	1 (7%)	12,20,20	2.16	2 (16%)
57	NEG	CA	3175	-	14,16,16	7.82	1 (7%)	12,20,20	2.37	4 (33%)
57	NEG	AA	3218	56	14,16,16	7.74	1 (7%)	12,20,20	1.92	3 (25%)
57	NEG	AA	3220	-	14,16,16	7.21	1 (7%)	12,20,20	2.09	4 (33%)
57	NEG	AA	3221	-	14,16,16	8.17	1 (7%)	12,20,20	1.59	1 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
57	NEG	CA	3177	-	14,16,16	6.82	1 (7%)	12,20,20	3.84	5 (41%)
57	NEG	CW	3002	-	14,16,16	7.34	1 (7%)	12,20,20	1.38	2 (16%)
57	NEG	AW	3004	-	14,16,16	7.31	1 (7%)	12,20,20	1.34	1 (8%)
57	NEG	AX	3013	-	14,16,16	8.09	2 (14%)	12,20,20	2.53	3 (25%)
57	NEG	AA	3217	-	14,16,16	7.23	1 (7%)	12,20,20	2.25	3 (25%)
57	NEG	AA	3219	-	14,16,16	7.42	1 (7%)	12,20,20	2.31	3 (25%)
58	SF4	AD	501	4	0,12,12	-	-	-		
57	NEG	CA	3172	-	14,16,16	7.93	1 (7%)	12,20,20	2.14	2 (16%)

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	NEG	CA	3170	56	-	5/18/18/18	-
58	SF4	CD	302	4	-	-	0/6/5/5
57	NEG	CA	3176	-	-	3/18/18/18	-
57	NEG	CA	3171	-	-	4/18/18/18	-
57	NEG	AA	3222	-	-	3/18/18/18	-
57	NEG	AA	3216	56	-	3/18/18/18	-
57	NEG	CX	3004	-	-	5/18/18/18	-
57	NEG	CA	3174	-	-	1/18/18/18	-
57	NEG	CA	3173	-	-	4/18/18/18	-
57	NEG	CA	3175	-	-	7/18/18/18	-
57	NEG	AA	3218	56	-	4/18/18/18	-
57	NEG	AA	3220	-	-	5/18/18/18	-
57	NEG	AA	3221	-	-	6/18/18/18	-
57	NEG	CA	3177	-	-	4/18/18/18	-
57	NEG	CW	3002	-	-	1/18/18/18	-
57	NEG	AW	3004	-	-	3/18/18/18	-
57	NEG	AX	3013	-	-	7/18/18/18	-
57	NEG	AA	3217	-	-	3/18/18/18	-
57	NEG	AA	3219	-	-	4/18/18/18	-
58	SF4	AD	501	4	-	-	0/6/5/5
57	NEG	CA	3172	-	-	4/18/18/18	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	AA	3221	NEG	N2-N3	-30.41	1.11	1.41
57	AX	3013	NEG	N2-N3	-30.05	1.11	1.41
57	AA	3216	NEG	N2-N3	-29.74	1.11	1.41
57	CA	3172	NEG	N2-N3	-29.54	1.12	1.41
57	CA	3175	NEG	N2-N3	-29.11	1.12	1.41
57	CA	3170	NEG	N2-N3	-28.92	1.12	1.41
57	AA	3218	NEG	N2-N3	-28.79	1.12	1.41
57	CA	3176	NEG	N2-N3	-28.71	1.12	1.41
57	CX	3004	NEG	N2-N3	-28.55	1.13	1.41
57	AA	3222	NEG	N2-N3	-28.25	1.13	1.41
57	CA	3173	NEG	N2-N3	-28.06	1.13	1.41
57	AA	3219	NEG	N2-N3	-27.62	1.14	1.41
57	CW	3002	NEG	N2-N3	-27.30	1.14	1.41
57	AW	3004	NEG	N2-N3	-27.24	1.14	1.41
57	CA	3171	NEG	N2-N3	-27.18	1.14	1.41
57	AA	3217	NEG	N2-N3	-26.90	1.14	1.41
57	AA	3220	NEG	N2-N3	-26.81	1.14	1.41
57	CA	3174	NEG	N2-N3	-26.49	1.15	1.41
57	CA	3177	NEG	N2-N3	-25.33	1.16	1.41
57	AX	3013	NEG	O1-C8	-2.03	1.24	1.30

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	CA	3174	NEG	C9-N3-N2	10.94	119.34	109.09
57	CA	3177	NEG	C9-N3-N2	9.82	118.29	109.09
57	CA	3174	NEG	C6-N2-N3	8.14	128.42	120.29
57	AA	3216	NEG	C9-N3-N2	6.96	115.60	109.09
57	CA	3177	NEG	C6-N2-N3	6.92	127.21	120.29
57	CA	3171	NEG	C9-N3-N2	6.56	115.23	109.09
57	CA	3175	NEG	C6-N2-N3	6.35	126.64	120.29
57	CX	3004	NEG	C3-C2-C1	-6.26	106.45	111.87
57	AA	3217	NEG	C9-N3-N2	6.13	114.83	109.09
57	CA	3172	NEG	C6-N2-N3	-5.90	114.40	120.29
57	AX	3013	NEG	C9-N3-N2	5.38	114.13	109.09
57	AX	3013	NEG	C7-N3-N2	-5.17	102.11	109.51
57	AA	3222	NEG	C7-N3-N2	5.05	116.74	109.51
57	AA	3218	NEG	C3-C2-C1	4.97	116.18	111.87
57	CA	3173	NEG	C3-C2-C1	4.86	116.08	111.87
57	CA	3174	NEG	C3-C2-C1	-4.63	107.86	111.87
57	AA	3221	NEG	C7-N3-N2	-4.54	103.00	109.51
57	CA	3171	NEG	C6-N2-N3	4.54	124.83	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	CA	3173	NEG	C9-N3-N2	4.53	113.33	109.09
57	AA	3219	NEG	C6-N2-N3	4.52	124.81	120.29
57	AA	3219	NEG	C9-N3-N2	4.50	113.31	109.09
57	AA	3220	NEG	C6-N2-N3	4.24	124.53	120.29
57	CA	3176	NEG	C6-N2-N3	-3.90	116.40	120.29
57	AX	3013	NEG	C6-N2-N3	-3.81	116.48	120.29
57	CA	3177	NEG	C7-N3-N2	3.81	114.96	109.51
57	AA	3220	NEG	C9-N3-N2	3.68	112.54	109.09
57	CA	3172	NEG	C3-C2-C1	-3.60	108.76	111.87
57	AA	3219	NEG	C7-N3-N2	3.59	114.66	109.51
57	AA	3218	NEG	C6-N2-N3	-3.47	116.83	120.29
57	CA	3175	NEG	C9-N3-N2	3.10	111.99	109.09
57	AA	3217	NEG	C6-N2-N3	2.92	123.21	120.29
57	CA	3170	NEG	C9-N3-N2	2.89	111.79	109.09
57	AA	3216	NEG	C7-N3-N2	-2.81	105.48	109.51
57	AW	3004	NEG	C6-N2-N3	-2.80	117.49	120.29
57	CX	3004	NEG	C9-N3-N2	2.49	111.42	109.09
57	CA	3177	NEG	C3-C2-C1	-2.33	109.85	111.87
57	CA	3171	NEG	O4-C6-N2	2.31	126.33	123.32
57	AA	3220	NEG	C7-N3-N2	2.24	112.72	109.51
57	CA	3175	NEG	O4-C6-C5	-2.22	118.29	121.54
57	CA	3175	NEG	O4-C6-N2	-2.20	120.45	123.32
57	CA	3177	NEG	O4-C6-N2	2.18	126.16	123.32
57	CW	3002	NEG	C6-N2-N3	-2.17	118.13	120.29
57	CA	3176	NEG	C7-N3-N2	2.10	112.52	109.51
57	AA	3220	NEG	O4-C6-C5	-2.05	118.53	121.54
57	CA	3174	NEG	O4-C6-N2	2.05	126.00	123.32
57	CW	3002	NEG	C7-N3-N2	2.05	112.45	109.51
57	AA	3218	NEG	C3-C4-C5	2.03	117.02	111.20
57	AA	3217	NEG	O4-C6-C5	-2.02	118.59	121.54

There are no chirality outliers.

All (76) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	AA	3217	NEG	N3-C7-C8-O1
57	AA	3217	NEG	N3-C7-C8-O2
57	AA	3219	NEG	N3-C7-C8-O1
57	AA	3219	NEG	N3-C7-C8-O2
57	AA	3220	NEG	C6-N2-N3-C7
57	AA	3221	NEG	N3-C7-C8-O1
57	AA	3221	NEG	N3-C7-C8-O2

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Mol	Chain	Res	Type	Atoms
57	AA	3222	NEG	C6-N2-N3-C9
57	AX	3013	NEG	N3-C7-C8-O1
57	AX	3013	NEG	N3-C7-C8-O2
57	CA	3171	NEG	N3-C7-C8-O1
57	CA	3171	NEG	N3-C7-C8-O2
57	CA	3172	NEG	N3-C7-C8-O1
57	CA	3172	NEG	N3-C7-C8-O2
57	CA	3173	NEG	N3-C7-C8-O1
57	CA	3173	NEG	N3-C7-C8-O2
57	CA	3174	NEG	C6-N2-N3-C9
57	CA	3175	NEG	C8-C7-N3-N2
57	CA	3175	NEG	C6-N2-N3-C7
57	CA	3175	NEG	C6-N2-N3-C9
57	CA	3177	NEG	N3-C7-C8-O1
57	CA	3177	NEG	N3-C7-C8-O2
57	CA	3177	NEG	C6-N2-N3-C9
57	CX	3004	NEG	N3-C7-C8-O1
57	CX	3004	NEG	N3-C7-C8-O2
57	AA	3218	NEG	C6-N2-N3-C7
57	AA	3222	NEG	C8-C7-N3-N2
57	AA	3216	NEG	N3-C7-C8-O1
57	AA	3216	NEG	N3-C7-C8-O2
57	AA	3218	NEG	N3-C7-C8-O1
57	AA	3218	NEG	N3-C7-C8-O2
57	CA	3170	NEG	N3-C7-C8-O1
57	CA	3170	NEG	N3-C7-C8-O2
57	CA	3175	NEG	N3-C7-C8-O1
57	CA	3176	NEG	N3-C7-C8-O1
57	CA	3176	NEG	N3-C7-C8-O2
57	CA	3170	NEG	C4-C5-C6-O4
57	AA	3219	NEG	C6-N2-N3-C7
57	CA	3177	NEG	C6-N2-N3-C7
57	AX	3013	NEG	C2-C3-C4-N4
57	AA	3220	NEG	N3-C7-C8-O2
57	AW	3004	NEG	N3-C7-C8-O2
57	AA	3217	NEG	C6-N2-N3-C7
57	AA	3222	NEG	C6-N2-N3-C7
57	CA	3171	NEG	C6-N2-N3-C7
57	AA	3221	NEG	O4-C6-N2-N3
57	AX	3013	NEG	O4-C6-N2-N3
57	CA	3173	NEG	O4-C6-N2-N3
57	CA	3175	NEG	O4-C6-N2-N3

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Mol	Chain	Res	Type	Atoms
57	CX	3004	NEG	O4-C6-N2-N3
57	AA	3216	NEG	C8-C7-N3-N2
57	AX	3013	NEG	C8-C7-N3-N2
57	CA	3172	NEG	C8-C7-N3-N2
57	CA	3170	NEG	C4-C5-C6-N2
57	AA	3220	NEG	N3-C7-C8-O1
57	AW	3004	NEG	N3-C7-C8-O1
57	CA	3175	NEG	N3-C7-C8-O2
57	AA	3218	NEG	C8-C7-N3-C9
57	AA	3219	NEG	C8-C7-N3-C9
57	AA	3220	NEG	C8-C7-N3-C9
57	AA	3221	NEG	C8-C7-N3-C9
57	AW	3004	NEG	C8-C7-N3-C9
57	CA	3171	NEG	C8-C7-N3-C9
57	CA	3176	NEG	C8-C7-N3-C9
57	CW	3002	NEG	C8-C7-N3-C9
57	AA	3220	NEG	C2-C3-C4-C5
57	CA	3172	NEG	C2-C3-C4-C5
57	CX	3004	NEG	C2-C3-C4-C5
57	CA	3170	NEG	C8-C7-N3-N2
57	AA	3221	NEG	C4-C5-C6-O4
57	AX	3013	NEG	C4-C5-C6-O4
57	AA	3221	NEG	C5-C6-N2-N3
57	AX	3013	NEG	C5-C6-N2-N3
57	CA	3173	NEG	C5-C6-N2-N3
57	CA	3175	NEG	C5-C6-N2-N3
57	CX	3004	NEG	C5-C6-N2-N3

There are no ring outliers.

15 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	CA	3171	NEG	1	0
57	AA	3216	NEG	7	0
57	CX	3004	NEG	5	0
57	CA	3174	NEG	5	0
57	CA	3173	NEG	2	0
57	CA	3175	NEG	3	0
57	AA	3218	NEG	1	0
57	AA	3220	NEG	4	0
57	AA	3221	NEG	4	0
57	CA	3177	NEG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	CW	3002	NEG	1	0
57	AW	3004	NEG	2	0
57	AX	3013	NEG	3	0
57	AA	3217	NEG	1	0
57	AA	3219	NEG	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AA	1496/1521 (98%)	0.48	64 (4%) 40 36	36, 68, 97, 112	0
1	CA	1503/1521 (98%)	0.66	100 (6%) 24 21	38, 71, 97, 111	0
2	AB	231/256 (90%)	1.30	52 (22%) 2 2	67, 83, 93, 99	0
2	CB	231/256 (90%)	1.69	73 (31%) 1 1	69, 85, 94, 100	0
3	AC	206/239 (86%)	1.25	39 (18%) 3 3	65, 78, 88, 96	0
3	CC	206/239 (86%)	1.85	85 (41%) 0 0	68, 80, 90, 96	0
4	AD	208/209 (99%)	1.04	29 (13%) 6 5	53, 68, 80, 87	0
4	CD	208/209 (99%)	0.82	9 (4%) 40 36	54, 67, 80, 90	0
5	AE	148/162 (91%)	0.79	9 (6%) 27 24	54, 70, 81, 86	0
5	CE	148/162 (91%)	1.46	34 (22%) 2 2	57, 72, 82, 88	0
6	AF	100/101 (99%)	1.05	8 (8%) 18 15	53, 67, 78, 87	0
6	CF	100/101 (99%)	0.65	2 (2%) 65 62	54, 68, 80, 87	0
7	AG	155/156 (99%)	1.10	21 (13%) 7 6	62, 75, 86, 95	0
7	CG	155/156 (99%)	0.98	17 (10%) 10 9	63, 77, 86, 99	0
8	AH	137/138 (99%)	0.98	10 (7%) 21 18	57, 70, 78, 85	0
8	CH	137/138 (99%)	1.08	12 (8%) 15 13	60, 72, 81, 85	0
9	AI	127/128 (99%)	1.55	31 (24%) 2 1	57, 82, 90, 94	0
9	CI	127/128 (99%)	2.05	60 (47%) 0 0	65, 84, 91, 95	0
10	AJ	97/105 (92%)	1.70	32 (32%) 1 1	63, 85, 94, 98	0
10	CJ	96/105 (91%)	2.59	72 (75%) 0 0	65, 86, 94, 99	0
11	AK	114/129 (88%)	0.68	4 (3%) 47 43	47, 66, 78, 84	0
11	CK	114/129 (88%)	0.71	9 (7%) 18 16	49, 68, 79, 85	0
12	AL	122/132 (92%)	0.55	8 (6%) 24 21	48, 57, 69, 79	0
12	CL	122/132 (92%)	0.91	7 (5%) 29 26	50, 60, 71, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	AM	123/126 (97%)	0.97	12 (9%) 13 11	52, 70, 84, 96	0
13	CM	122/126 (96%)	1.59	29 (23%) 2 1	70, 83, 93, 99	0
14	AN	60/61 (98%)	1.57	14 (23%) 2 2	64, 77, 83, 89	0
14	CN	60/61 (98%)	2.62	37 (61%) 0 0	67, 80, 87, 90	0
15	AO	88/89 (98%)	0.76	5 (5%) 29 26	49, 66, 77, 84	0
15	CO	88/89 (98%)	0.78	6 (6%) 23 20	51, 67, 79, 85	0
16	AP	82/88 (93%)	1.34	16 (19%) 3 2	53, 67, 78, 82	0
16	CP	82/88 (93%)	1.07	4 (4%) 35 31	54, 66, 77, 82	0
17	AQ	99/105 (94%)	0.91	5 (5%) 33 29	53, 69, 81, 83	0
17	CQ	99/105 (94%)	0.85	7 (7%) 22 19	55, 70, 81, 85	0
18	AR	68/88 (77%)	0.74	4 (5%) 28 25	54, 67, 80, 82	0
18	CR	68/88 (77%)	0.83	5 (7%) 20 18	54, 69, 81, 85	0
19	AS	83/93 (89%)	1.29	17 (20%) 2 2	68, 80, 88, 97	0
19	CS	83/93 (89%)	2.31	48 (57%) 0 0	71, 82, 91, 97	0
20	AT	96/106 (90%)	0.88	10 (10%) 11 10	57, 69, 85, 90	0
20	CT	96/106 (90%)	0.89	8 (8%) 17 14	56, 69, 85, 90	0
21	AU	23/27 (85%)	1.23	4 (17%) 4 3	62, 71, 78, 81	0
21	CU	23/27 (85%)	1.93	9 (39%) 1 0	65, 74, 80, 83	0
22	AV	13/24 (54%)	0.79	2 (15%) 5 4	51, 61, 91, 97	0
22	CV	12/24 (50%)	1.24	2 (16%) 4 3	55, 65, 91, 92	0
23	AW	67/76 (88%)	1.46	17 (25%) 1 1	50, 93, 102, 108	0
23	AY	67/76 (88%)	1.61	23 (34%) 1 1	37, 101, 106, 107	0
23	CW	65/76 (85%)	2.02	27 (41%) 0 0	69, 100, 108, 110	0
23	CY	66/76 (86%)	1.82	32 (48%) 0 0	40, 101, 106, 107	0
24	AX	72/77 (93%)	0.67	5 (6%) 23 20	45, 69, 85, 96	0
24	CX	72/77 (93%)	1.02	10 (13%) 6 5	46, 72, 87, 98	0
25	BA	2822/2915 (96%)	-0.15	117 (4%) 41 37	22, 42, 94, 110	0
25	DA	2800/2915 (96%)	0.01	114 (4%) 41 37	25, 47, 96, 113	0
26	BB	120/121 (99%)	0.29	1 (0%) 82 81	41, 61, 72, 92	0
26	DB	120/121 (99%)	0.94	6 (5%) 34 30	48, 67, 78, 93	0
27	BD	275/276 (99%)	0.08	4 (1%) 72 70	21, 38, 55, 86	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
27	DD	275/276 (99%)	0.08	4 (1%) 72 70	23, 41, 57, 85	0
28	BE	204/206 (99%)	0.21	1 (0%) 87 86	19, 45, 67, 84	0
28	DE	204/206 (99%)	0.12	1 (0%) 87 86	22, 49, 69, 84	0
29	BF	203/210 (96%)	0.26	2 (0%) 79 78	23, 50, 74, 95	0
29	DF	203/210 (96%)	0.38	7 (3%) 48 44	25, 55, 77, 95	0
30	BG	181/182 (99%)	0.83	17 (9%) 14 12	52, 68, 82, 94	0
30	DG	181/182 (99%)	1.26	26 (14%) 6 5	57, 72, 84, 92	0
31	BH	174/180 (96%)	0.93	14 (8%) 18 15	51, 69, 80, 87	0
31	DH	174/180 (96%)	1.48	47 (27%) 1 1	57, 74, 84, 88	0
32	BI	146/148 (98%)	0.88	8 (5%) 30 27	45, 71, 84, 88	0
32	DI	146/148 (98%)	0.85	6 (4%) 41 37	46, 72, 84, 89	0
33	BN	140/140 (100%)	0.43	1 (0%) 84 83	32, 48, 69, 78	0
33	DN	140/140 (100%)	0.60	3 (2%) 63 61	38, 53, 72, 79	0
34	BO	122/122 (100%)	-0.19	0 100 100	23, 39, 59, 65	0
34	DO	122/122 (100%)	0.54	4 (3%) 49 45	43, 58, 72, 84	0
35	BP	149/150 (99%)	0.44	1 (0%) 84 83	23, 53, 76, 82	0
35	DP	149/150 (99%)	0.52	4 (2%) 56 53	28, 57, 78, 83	0
36	BQ	141/141 (100%)	0.65	5 (3%) 47 43	32, 53, 69, 81	0
36	DQ	141/141 (100%)	0.97	9 (6%) 25 22	36, 58, 73, 82	0
37	BR	118/118 (100%)	-0.19	0 100 100	19, 33, 48, 59	0
37	DR	118/118 (100%)	0.24	0 100 100	32, 51, 65, 78	0
38	BS	110/112 (98%)	0.06	2 (1%) 67 65	36, 50, 67, 72	0
38	DS	110/112 (98%)	1.26	16 (14%) 6 5	64, 77, 88, 94	0
39	BT	131/146 (89%)	0.04	6 (4%) 37 34	28, 41, 69, 88	0
39	DT	131/146 (89%)	0.72	8 (6%) 27 24	45, 60, 78, 88	0
40	BU	116/118 (98%)	-0.40	1 (0%) 81 80	17, 29, 43, 67	0
40	DU	116/118 (98%)	0.78	6 (5%) 33 29	36, 64, 80, 89	0
41	BV	101/101 (100%)	-0.32	1 (0%) 79 78	18, 36, 55, 73	0
41	DV	101/101 (100%)	0.98	8 (7%) 18 16	42, 77, 87, 93	0
42	BW	112/113 (99%)	-0.39	1 (0%) 81 80	17, 29, 52, 89	0
42	DW	112/113 (99%)	0.28	0 100 100	35, 49, 71, 91	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
43	BX	95/96 (98%)	-0.25	1 (1%) 78 76	15, 33, 65, 84	0
43	DX	95/96 (98%)	0.73	9 (9%) 14 11	38, 57, 76, 84	0
44	BY	107/110 (97%)	0.20	4 (3%) 45 41	33, 48, 75, 84	0
44	DY	107/110 (97%)	1.29	25 (23%) 2 2	54, 70, 86, 93	0
45	BZ	171/206 (83%)	1.14	30 (17%) 4 3	38, 69, 102, 108	0
45	DZ	174/206 (84%)	1.96	63 (36%) 1 0	71, 88, 101, 108	0
46	B0	83/85 (97%)	0.10	6 (7%) 21 18	25, 37, 67, 83	0
46	D0	83/85 (97%)	1.17	10 (12%) 9 7	46, 69, 81, 91	0
47	B1	97/98 (98%)	0.12	2 (2%) 63 61	19, 40, 69, 76	0
47	D1	97/98 (98%)	0.19	1 (1%) 79 78	33, 53, 77, 79	0
48	B2	70/72 (97%)	0.06	2 (2%) 53 50	32, 42, 62, 80	0
48	D2	70/72 (97%)	0.95	5 (7%) 22 19	54, 70, 81, 84	0
49	B3	59/60 (98%)	-0.16	0 100 100	22, 36, 55, 80	0
49	D3	59/60 (98%)	0.88	5 (8%) 16 14	52, 67, 82, 85	0
50	B4	69/71 (97%)	0.87	13 (18%) 3 3	53, 73, 93, 94	0
50	D4	69/71 (97%)	1.80	25 (36%) 1 0	76, 87, 99, 107	0
51	B5	59/60 (98%)	-0.46	0 100 100	18, 31, 46, 68	0
51	D5	59/60 (98%)	0.20	0 100 100	28, 50, 68, 77	0
52	B6	53/54 (98%)	-0.16	0 100 100	29, 40, 59, 67	0
52	D6	53/54 (98%)	0.86	4 (7%) 20 17	47, 61, 75, 79	0
53	B7	48/49 (97%)	-0.24	1 (2%) 63 61	16, 25, 55, 66	0
53	D7	48/49 (97%)	0.03	1 (2%) 63 61	28, 37, 62, 71	0
54	B8	64/65 (98%)	-0.35	0 100 100	23, 32, 43, 58	0
54	D8	64/65 (98%)	0.51	1 (1%) 70 68	43, 57, 65, 71	0
55	B9	37/37 (100%)	0.33	2 (5%) 31 27	31, 50, 69, 75	0
55	D9	37/37 (100%)	1.12	4 (10%) 11 9	49, 60, 73, 77	0
All	All	20900/21748 (96%)	0.54	1810 (8%) 16 13	15, 62, 92, 113	0

All (1810) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
14	CN	38	GLY	8.6
7	CG	82	GLY	8.4

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Mol	Chain	Res	Type	RSRZ
13	CM	124	PRO	8.4
45	DZ	116	VAL	7.8
13	CM	123	ALA	7.6
45	BZ	111	VAL	7.5
50	D4	56	VAL	7.3
45	BZ	144	LEU	7.2
25	BA	931	C	7.1
13	AM	123	ALA	6.9
10	CJ	63	PHE	6.6
25	DA	2155	G	6.3
7	CG	83	ALA	6.3
25	BA	932	C	6.2
13	CM	122	LYS	6.2
45	BZ	108	PRO	6.1
10	CJ	47	PHE	6.1
45	DZ	115	GLY	5.9
10	CJ	65	LEU	5.9
45	BZ	115	GLY	5.9
14	CN	39	LEU	5.7
45	BZ	116	VAL	5.6
9	CI	102	LEU	5.5
45	DZ	113	ALA	5.4
13	CM	102	ARG	5.3
45	BZ	113	ALA	5.3
14	AN	2	ALA	5.3
3	CC	190	ARG	5.2
25	DA	885	C	5.2
7	AG	83	ALA	5.2
31	BH	2	SER	5.2
25	DA	883	G	5.2
46	B0	5	LYS	5.1
46	D0	2	ALA	5.1
22	CV	13	A	5.1
23	CW	73	A	5.1
7	AG	79	ARG	5.1
9	AI	126	SER	5.1
45	DZ	149	SER	5.1
25	BA	2168	C	5.1
9	CI	105	ASP	5.1
45	DZ	144	LEU	5.0
45	DZ	114	GLY	5.0
27	BD	276	LYS	5.0

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Mol	Chain	Res	Type	RSRZ
25	DA	2154	G	5.0
25	DA	2138	C	5.0
1	AA	1003	G	5.0
25	BA	2806	G	5.0
45	DZ	150	LEU	4.9
7	CG	84	ASN	4.9
23	AW	1	G	4.9
26	DB	1	U	4.9
27	BD	275	LYS	4.9
3	CC	207	VAL	4.9
2	AB	237	ALA	4.8
45	DZ	170	THR	4.8
20	CT	103	GLY	4.8
1	AA	1001(A)	G	4.8
1	AA	1002	G	4.8
13	CM	121	LYS	4.8
9	CI	106	ALA	4.8
14	CN	2	ALA	4.8
6	AF	55	ASP	4.8
1	CA	1030(A)	G	4.8
10	CJ	40	LEU	4.8
25	DA	2140	C	4.7
39	BT	37	GLY	4.7
25	BA	943	C	4.7
25	BA	2167	C	4.7
10	CJ	37	PRO	4.7
13	AM	124	PRO	4.7
23	CW	76	A	4.7
1	CA	1030(B)	C	4.6
25	BA	944	C	4.6
9	CI	11	LYS	4.6
32	BI	146	ALA	4.6
45	BZ	114	GLY	4.5
50	D4	67	TYR	4.5
19	CS	80	TYR	4.5
1	AA	630	G	4.5
25	DA	2139	C	4.5
31	BH	174	GLY	4.5
50	D4	49	PHE	4.5
25	BA	2166	U	4.4
9	AI	2	GLU	4.4
23	CW	72	C	4.4

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Mol	Chain	Res	Type	RSRZ
25	DA	1536	C	4.4
2	CB	237	ALA	4.4
10	CJ	32	ALA	4.4
13	CM	120	LYS	4.4
39	BT	131	ALA	4.3
50	B4	63	TYR	4.3
45	BZ	146	ILE	4.3
45	DZ	111	VAL	4.3
1	CA	1117	G	4.3
23	CW	74	C	4.3
46	D0	7	LEU	4.3
23	CW	71	G	4.3
25	BA	2137	G	4.3
9	CI	2	GLU	4.3
14	CN	34	TYR	4.3
18	AR	79	LEU	4.3
3	CC	189	ALA	4.3
7	AG	82	GLY	4.3
2	AB	12	GLU	4.3
25	BA	2163	G	4.3
25	DA	1533	G	4.3
2	CB	121	LEU	4.2
44	DY	107	ASP	4.2
2	CB	163	PHE	4.2
2	AB	165	VAL	4.2
10	CJ	34	VAL	4.2
27	DD	276	LYS	4.2
10	CJ	71	LEU	4.2
25	DA	2159	G	4.2
1	CA	1149	C	4.2
2	AB	13	ALA	4.2
45	DZ	172	ALA	4.2
25	DA	896	A	4.2
5	CE	22	GLY	4.2
47	B1	2	SER	4.2
23	AW	73	A	4.2
2	CB	21	ARG	4.2
7	AG	80	VAL	4.2
10	CJ	88	LEU	4.2
25	BA	2176	G	4.2
9	AI	15	ALA	4.1
39	DT	130	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
17	CQ	100	LYS	4.1
36	DQ	22	LYS	4.1
19	CS	84	GLY	4.1
42	BW	112	GLY	4.1
1	AA	1008	C	4.1
23	AW	4	C	4.1
25	BA	942	A	4.1
45	DZ	109	ALA	4.1
50	D4	57	GLU	4.1
1	AA	1036	G	4.1
2	CB	236	TYR	4.1
10	AJ	4	ILE	4.1
44	DY	80	GLY	4.0
25	BA	2169	G	4.0
1	AA	1257	U	4.0
1	CA	1281	U	4.0
25	BA	2165	C	4.0
21	CU	16	GLY	4.0
9	AI	19	LEU	4.0
32	BI	27	ARG	4.0
13	AM	2	ALA	4.0
3	CC	39	ILE	4.0
45	BZ	143	GLY	4.0
19	CS	13	ASP	4.0
1	CA	1532	U	4.0
3	CC	32	LEU	3.9
7	CG	81	GLY	3.9
14	CN	51	GLY	3.9
45	DZ	117	LEU	3.9
46	B0	6	GLY	3.9
46	B0	7	LEU	3.9
45	DZ	174	VAL	3.9
3	CC	60	ALA	3.9
39	BT	130	ALA	3.9
46	B0	3	HIS	3.9
8	AH	93	VAL	3.9
25	BA	2141	A	3.9
25	DA	884	C	3.9
19	CS	29	ARG	3.9
14	CN	49	HIS	3.9
30	BG	80	PHE	3.9
9	CI	86	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
20	CT	9	ASN	3.9
43	DX	68	ARG	3.9
9	AI	81	ILE	3.9
50	D4	59	PHE	3.9
10	AJ	77	PRO	3.8
25	DA	2156	G	3.8
10	CJ	35	SER	3.8
3	CC	6	HIS	3.8
14	AN	59	ALA	3.8
45	BZ	109	ALA	3.8
45	DZ	143	GLY	3.8
10	AJ	46	ARG	3.8
7	CG	85	TYR	3.8
44	DY	1	MET	3.8
1	AA	1447	A	3.8
45	BZ	141	VAL	3.8
20	CT	8	ARG	3.8
19	CS	31	ILE	3.8
1	AA	1000	U	3.8
1	CA	1260	C	3.8
20	AT	55	ILE	3.8
31	DH	2	SER	3.8
14	CN	36	PHE	3.8
21	CU	23	PRO	3.8
16	AP	68	ASP	3.7
10	CJ	48	THR	3.7
1	CA	1035	A	3.7
1	AA	204	U	3.7
25	DA	886	C	3.7
3	CC	198	VAL	3.7
14	CN	18	VAL	3.7
15	CO	60	VAL	3.7
45	DZ	71	VAL	3.7
19	AS	68	GLY	3.7
36	DQ	33	GLY	3.7
1	CA	1036	G	3.7
1	AA	1007	C	3.7
30	BG	51	ARG	3.7
44	DY	55	TYR	3.7
1	AA	1531	A	3.6
10	CJ	62	HIS	3.6
13	CM	78	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
46	D0	4	LYS	3.6
23	CW	70	G	3.6
25	BA	2175	G	3.6
10	CJ	54	PHE	3.6
5	CE	100	VAL	3.6
45	DZ	171	ILE	3.6
25	BA	1072	U	3.6
3	CC	2	GLY	3.6
1	CA	1276	G	3.6
1	CA	1277	C	3.6
14	CN	37	PHE	3.6
24	AX	67	C	3.6
31	DH	52	VAL	3.6
43	DX	43	VAL	3.6
3	CC	62	ASP	3.6
25	BA	12	U	3.6
5	CE	20	GLN	3.6
19	CS	22	LEU	3.6
10	CJ	55	LYS	3.6
23	AW	74	C	3.6
23	CW	3	C	3.6
25	BA	930	G	3.6
14	CN	22	THR	3.6
10	CJ	49	VAL	3.6
3	CC	188	LEU	3.6
19	CS	15	LEU	3.6
3	AC	39	ILE	3.5
25	BA	2183	C	3.5
17	AQ	33	GLY	3.5
45	BZ	110	GLY	3.5
3	AC	18	TRP	3.5
10	CJ	33	GLN	3.5
14	CN	33	VAL	3.5
47	D1	2	SER	3.5
25	DA	229	A	3.5
14	CN	7	ILE	3.5
14	CN	35	ARG	3.5
19	CS	79	THR	3.5
50	D4	65	ASP	3.5
3	CC	53	ALA	3.5
10	CJ	36	GLY	3.5
9	AI	127	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
25	BA	2146	G	3.5
25	BA	2174	G	3.5
25	DA	2112	G	3.5
10	CJ	43	ARG	3.5
14	CN	29	ARG	3.5
38	DS	20	ARG	3.5
25	DA	895	U	3.5
2	CB	131	PRO	3.5
45	DZ	108	PRO	3.5
45	BZ	118	GLN	3.5
19	CS	9	VAL	3.5
1	AA	1027	C	3.5
10	CJ	46	ARG	3.5
25	BA	2162	C	3.5
45	DZ	146	ILE	3.5
23	CY	15	G	3.5
8	CH	71	GLY	3.5
30	DG	20	ILE	3.4
19	CS	33	THR	3.4
19	CS	48	THR	3.4
1	CA	1033	G	3.4
18	CR	20	ALA	3.4
23	AY	15	G	3.4
25	DA	1171	G	3.4
19	CS	43	GLU	3.4
10	AJ	33	GLN	3.4
9	CI	66	ARG	3.4
14	CN	21	TYR	3.4
25	BA	696	C	3.4
25	DA	2145	C	3.4
49	D3	2	PRO	3.4
14	CN	44	LEU	3.4
1	CA	1125	U	3.4
1	AA	1503	A	3.4
25	BA	934	A	3.4
5	AE	95	ALA	3.4
7	AG	8	GLU	3.4
13	AM	6	GLY	3.4
20	AT	10	LEU	3.4
48	B2	70	GLN	3.4
2	AB	28	PHE	3.4
25	DA	888	C	3.4

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Mol	Chain	Res	Type	RSRZ
2	CB	22	LYS	3.4
46	D0	5	LYS	3.4
1	AA	1001	A	3.4
48	D2	66	GLU	3.4
48	B2	69	ARG	3.4
1	AA	1039	C	3.3
1	CA	1030	C	3.3
1	CA	1126	U	3.3
23	AW	3	C	3.3
25	BA	9	U	3.3
2	CB	111	ARG	3.3
7	CG	16	LEU	3.3
9	CI	56	LEU	3.3
10	AJ	8	LEU	3.3
10	CJ	90	LEU	3.3
31	DH	21	PRO	3.3
2	CB	140	HIS	3.3
45	BZ	147	GLY	3.3
25	BA	2195	A	3.3
25	DA	652(B)	A	3.3
45	DZ	21	ALA	3.3
10	CJ	76	ASN	3.3
30	BG	76	SER	3.3
1	AA	1006	C	3.3
25	BA	933	C	3.3
8	CH	2	LEU	3.3
2	CB	123	ALA	3.3
10	AJ	76	ASN	3.3
3	AC	62	ASP	3.3
2	AB	127	ILE	3.3
25	BA	2816	G	3.3
9	CI	10	ARG	3.3
10	AJ	45	ARG	3.3
19	AS	48	THR	3.3
30	DG	136	ARG	3.3
5	AE	151	LEU	3.3
31	DH	39	PRO	3.3
45	BZ	106	GLY	3.3
1	CA	1116	C	3.3
25	BA	2186	C	3.3
3	CC	64	VAL	3.3
9	AI	18	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
45	DZ	141	VAL	3.3
1	AA	1035	A	3.3
1	CA	1531	A	3.3
5	AE	18	ARG	3.3
25	BA	10	G	3.3
25	BA	926	G	3.3
25	DA	2802	G	3.3
7	CG	154	TYR	3.3
10	CJ	86	MET	3.3
19	CS	82	GLY	3.3
2	AB	7	VAL	3.3
4	AD	170	VAL	3.3
6	AF	60	PHE	3.3
55	B9	17	ILE	3.3
23	CW	4	C	3.2
25	BA	2814	C	3.2
25	DA	2143	C	3.2
4	AD	181	MET	3.2
9	CI	96	LEU	3.2
31	DH	64	LEU	3.2
9	CI	64	THR	3.2
50	D4	63	TYR	3.2
9	CI	101	PHE	3.2
25	BA	2145	G	3.2
25	DA	882	G	3.2
25	DA	2141	G	3.2
12	CL	18	VAL	3.2
45	DZ	104	PHE	3.2
9	AI	93	ARG	3.2
19	CS	81	ARG	3.2
2	AB	234	PRO	3.2
9	CI	49	PRO	3.2
10	CJ	14	LYS	3.2
23	AW	72	C	3.2
19	AS	84	GLY	3.2
19	CS	54	GLY	3.2
3	CC	201	TYR	3.2
9	CI	114	TYR	3.2
9	CI	17	VAL	3.2
1	CA	1034	G	3.2
4	CD	49	ARG	3.2
23	AY	69	G	3.2

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Mol	Chain	Res	Type	RSRZ
25	BA	2147	G	3.2
25	BA	2178	G	3.2
25	DA	11	G	3.2
25	DA	2160	G	3.2
3	AC	27	LYS	3.2
38	DS	57	LYS	3.2
3	CC	12	LEU	3.2
4	AD	179	GLU	3.2
30	DG	53	LEU	3.2
45	BZ	117	LEU	3.2
3	CC	95	THR	3.2
3	AC	13	GLY	3.2
25	DA	34	C	3.2
9	AI	17	VAL	3.2
10	AJ	34	VAL	3.2
33	DN	9	VAL	3.2
1	CA	1030(D)	A	3.2
1	CA	1286	A	3.2
31	DH	60	ARG	3.2
46	D0	3	HIS	3.2
23	AW	15	G	3.2
24	CX	70	G	3.2
3	AC	60	ALA	3.2
10	AJ	32	ALA	3.2
2	CB	165	VAL	3.2
30	DG	28	VAL	3.2
1	CA	1119	C	3.1
3	AC	15	THR	3.1
10	AJ	87	THR	3.1
3	CC	22	TRP	3.1
2	CB	161	ALA	3.1
15	CO	3	ILE	3.1
9	AI	86	VAL	3.1
19	CS	41	VAL	3.1
50	D4	10	VAL	3.1
1	AA	159	G	3.1
1	CA	1030(C)	G	3.1
25	BA	2143	G	3.1
25	DA	2116	G	3.1
9	AI	91	ASP	3.1
2	AB	61	LEU	3.1
23	CW	75	C	3.1

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Mol	Chain	Res	Type	RSRZ
2	CB	183	PRO	3.1
8	CH	72	PRO	3.1
7	CG	152	ALA	3.1
9	CI	44	VAL	3.1
11	CK	125	PHE	3.1
1	AA	1025	U	3.1
19	CS	18	LYS	3.1
14	CN	47	LEU	3.1
25	BA	11	G	3.1
25	DA	2131	G	3.1
2	CB	234	PRO	3.1
10	CJ	77	PRO	3.1
1	AA	999	C	3.1
11	AK	49	GLY	3.1
2	CB	185	ILE	3.1
24	AX	76	A	3.1
27	DD	275	LYS	3.1
9	CI	28	VAL	3.1
50	B4	56	VAL	3.1
55	D9	16	VAL	3.1
5	CE	31	LEU	3.1
25	BA	2135	U	3.1
1	AA	1032	G	3.1
1	CA	1356	G	3.1
5	CE	23	GLY	3.1
23	AY	24	G	3.1
23	CY	34	G	3.1
14	CN	48	ALA	3.1
19	CS	49	ILE	3.1
19	CS	62	ILE	3.1
39	DT	131	ALA	3.1
2	CB	97	TRP	3.1
35	DP	79	ARG	3.1
23	CY	72	C	3.1
25	DA	2146	C	3.1
23	AW	7	A	3.0
8	AH	112	LEU	3.0
3	CC	19	GLU	3.0
10	CJ	64	GLU	3.0
25	DA	1026	U	3.0
38	DS	45	GLY	3.0
45	BZ	107	THR	3.0

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Mol	Chain	Res	Type	RSRZ
3	CC	5	ILE	3.0
21	AU	6	ARG	3.0
7	AG	26	PHE	3.0
1	AA	1023	G	3.0
4	CD	137	SER	3.0
25	DA	2115	G	3.0
25	DA	2147	G	3.0
25	DA	2157	G	3.0
3	CC	91	LEU	3.0
43	DX	95	LEU	3.0
1	CA	1029	C	3.0
2	AB	236	TYR	3.0
25	DA	277	C	3.0
3	AC	56	ASP	3.0
4	AD	160	GLN	3.0
14	AN	15	LYS	3.0
4	CD	87	GLY	3.0
19	CS	68	GLY	3.0
29	DF	175	THR	3.0
50	B4	54	GLY	3.0
2	CB	136	VAL	3.0
45	DZ	86	VAL	3.0
50	B4	59	PHE	3.0
9	CI	79	LEU	3.0
30	BG	48	GLU	3.0
1	AA	1024	G	3.0
8	AH	4	ASP	3.0
23	CY	70	G	3.0
25	BA	2160	C	3.0
3	CC	21	ARG	3.0
25	BA	2139	A	3.0
25	DA	2119	A	3.0
40	DU	59	ARG	3.0
3	CC	9	GLY	3.0
9	CI	7	THR	3.0
9	CI	39	GLY	3.0
13	AM	49	THR	3.0
19	CS	46	GLY	3.0
31	DH	22	GLY	3.0
46	D0	6	GLY	3.0
19	CS	45	VAL	3.0
45	DZ	136	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
43	BX	95	LEU	3.0
43	DX	92	LEU	3.0
45	BZ	150	LEU	3.0
9	CI	97	LYS	3.0
13	AM	122	LYS	3.0
14	AN	50	LYS	3.0
16	AP	82	GLN	3.0
13	AM	102	ARG	3.0
14	CN	3	ARG	3.0
21	CU	13	ILE	3.0
1	CA	1202	G	3.0
25	BA	929	G	3.0
25	DA	2149	G	3.0
45	DZ	173	ALA	3.0
46	B0	2	ALA	3.0
5	CE	55	VAL	3.0
5	CE	12	LEU	2.9
10	CJ	61	GLU	2.9
10	CJ	41	PRO	2.9
19	CS	2	PRO	2.9
5	CE	13	ILE	2.9
14	CN	30	ALA	2.9
32	DI	146	ALA	2.9
2	AB	163	PHE	2.9
3	CC	10	PHE	2.9
19	AS	9	VAL	2.9
45	DZ	88	PHE	2.9
2	AB	187	LEU	2.9
10	AJ	40	LEU	2.9
30	BG	53	LEU	2.9
35	BP	99	LEU	2.9
1	AA	162	A	2.9
1	CA	1253	G	2.9
1	CA	1282	C	2.9
23	CY	62	C	2.9
25	BA	935	C	2.9
25	BA	1152	G	2.9
25	DA	881	G	2.9
25	DA	2137	C	2.9
23	CW	23	A	2.9
25	DA	899	A	2.9
25	DA	2117	A	2.9

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Mol	Chain	Res	Type	RSRZ
25	DA	2207	G	2.9
45	BZ	145	GLU	2.9
30	DG	17	PRO	2.9
23	AY	47	U	2.9
25	BA	2154	U	2.9
14	CN	40	CYS	2.9
3	CC	193	TYR	2.9
11	CK	75	TYR	2.9
53	B7	45	ALA	2.9
2	AB	230	VAL	2.9
3	AC	66	VAL	2.9
52	D6	5	VAL	2.9
4	AD	157	LEU	2.9
6	AF	61	LEU	2.9
19	CS	71	LEU	2.9
2	CB	134	GLU	2.9
1	AA	1030(D)	A	2.9
23	AW	2	C	2.9
23	CW	2	C	2.9
25	BA	1555	C	2.9
25	BA	1583	C	2.9
25	DA	897	C	2.9
25	DA	2114	A	2.9
44	DY	50	ARG	2.9
1	AA	927	G	2.9
1	CA	1127	G	2.9
23	CW	24	G	2.9
23	CY	5	G	2.9
23	CY	18	G	2.9
25	BA	288	U	2.9
25	BA	927	G	2.9
25	BA	2172	U	2.9
25	DA	2148	G	2.9
10	AJ	75	ILE	2.9
10	AJ	72	VAL	2.9
6	AF	54	LYS	2.9
10	CJ	56	HIS	2.9
10	CJ	91	PRO	2.9
2	CB	101	MET	2.9
4	AD	201	GLN	2.9
50	D4	66	SER	2.9
25	BA	432	U	2.9

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Mol	Chain	Res	Type	RSRZ
25	BA	2133	C	2.9
25	DA	2158	A	2.9
1	CA	1031	G	2.9
3	CC	149	ALA	2.9
7	CG	7	ALA	2.9
23	AY	70	G	2.9
25	DA	2751	G	2.9
30	DG	19	LEU	2.9
55	D9	20	HIS	2.9
13	CM	94	ARG	2.8
10	AJ	35	SER	2.8
30	BG	182	LYS	2.8
5	AE	119	LEU	2.8
5	CE	119	LEU	2.8
9	CI	27	THR	2.8
32	DI	38	LEU	2.8
19	CS	19	VAL	2.8
23	CW	7	A	2.8
25	BA	2192	A	2.8
25	DA	2144	U	2.8
1	CA	1400	C	2.8
1	AA	1033	G	2.8
1	CA	1154	G	2.8
23	CW	15	G	2.8
25	BA	1153	G	2.8
25	DA	1114	G	2.8
10	CJ	23	ILE	2.8
7	AG	84	ASN	2.8
3	CC	25	GLY	2.8
13	CM	6	GLY	2.8
36	BQ	33	GLY	2.8
2	CB	142	LEU	2.8
3	CC	137	ALA	2.8
9	AI	4	TYR	2.8
7	CG	80	VAL	2.8
31	DH	17	VAL	2.8
31	DH	169	VAL	2.8
36	DQ	106	VAL	2.8
3	CC	88	ARG	2.8
9	CI	104	ARG	2.8
10	CJ	28	ARG	2.8
15	CO	68	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
23	AY	14	A	2.8
25	BA	572	A	2.8
44	DY	57	GLN	2.8
10	CJ	75	ILE	2.8
13	CM	64	TRP	2.8
1	AA	306	G	2.8
1	CA	1124	G	2.8
23	AW	71	G	2.8
25	BA	2153	G	2.8
25	DA	652(U)	G	2.8
25	DA	2206	G	2.8
7	AG	124	LEU	2.8
44	DY	90	LEU	2.8
19	CS	63	THR	2.8
5	CE	67	VAL	2.8
9	AI	53	VAL	2.8
9	CI	53	VAL	2.8
10	CJ	72	VAL	2.8
45	BZ	105	VAL	2.8
45	DZ	1	MET	2.8
31	DH	55	PRO	2.8
48	D2	7	ARG	2.8
6	AF	57	GLN	2.8
45	DZ	118	GLN	2.8
25	BA	271	U	2.8
25	BA	2144	U	2.8
30	BG	77	ILE	2.8
1	CA	962	C	2.8
1	CA	1027	C	2.8
2	AB	97	TRP	2.8
2	AB	10	LEU	2.8
9	CI	40	LEU	2.8
43	DX	86	GLY	2.8
50	D4	51	ASP	2.8
2	CB	67	THR	2.8
3	CC	61	ALA	2.8
14	AN	56	VAL	2.8
16	AP	80	PHE	2.8
50	D4	50	VAL	2.8
1	AA	631	G	2.8
10	CJ	79	ARG	2.8
23	AW	6	G	2.8

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Mol	Chain	Res	Type	RSRZ
23	CW	19	G	2.8
25	DA	2133	G	2.8
12	AL	94	PRO	2.7
16	CP	82	GLN	2.7
2	AB	215	LEU	2.7
4	AD	137	SER	2.7
19	CS	5	LEU	2.7
20	AT	13	LEU	2.7
13	CM	100	GLY	2.7
25	BA	2157	A	2.7
25	DA	2135	A	2.7
45	DZ	160	GLY	2.7
50	D4	54	GLY	2.7
2	CB	19	HIS	2.7
2	AB	186	ALA	2.7
3	AC	189	ALA	2.7
4	AD	111	ALA	2.7
9	CI	12	GLU	2.7
14	CN	13	THR	2.7
19	CS	10	PHE	2.7
2	CB	148	TYR	2.7
12	CL	23	LYS	2.7
27	BD	38	LYS	2.7
38	DS	44	LYS	2.7
1	AA	1021	G	2.7
1	CA	1002	G	2.7
23	AW	69	G	2.7
23	AW	70	G	2.7
25	BA	2134	G	2.7
25	DA	545	G	2.7
3	CC	124	ILE	2.7
7	AG	50	ILE	2.7
9	CI	63	ILE	2.7
15	AO	87	ILE	2.7
4	AD	154	ASN	2.7
19	CS	38	SER	2.7
20	AT	9	ASN	2.7
41	DV	30	GLY	2.7
8	AH	91	ARG	2.7
9	AI	59	PHE	2.7
11	CK	105	VAL	2.7
11	CK	109	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
30	DG	50	ALA	2.7
1	CA	250	A	2.7
1	CA	1357	A	2.7
23	AW	76	A	2.7
25	DA	887	A	2.7
25	DA	1847	A	2.7
30	DG	2	PRO	2.7
4	CD	18	LYS	2.7
9	CI	36	TYR	2.7
23	AW	68	C	2.7
23	AY	25	C	2.7
25	BA	2151	C	2.7
25	DA	2136	C	2.7
2	AB	221	LEU	2.7
9	CI	19	LEU	2.7
19	CS	66	MET	2.7
45	DZ	76	LEU	2.7
49	D3	53	LEU	2.7
1	AA	1031	G	2.7
9	CI	117	HIS	2.7
10	AJ	93	GLY	2.7
19	CS	14	HIS	2.7
25	BA	2132	G	2.7
25	DA	2153	G	2.7
26	DB	54	G	2.7
44	DY	93	GLY	2.7
9	CI	29	ASN	2.7
2	CB	152	PHE	2.7
9	CI	43	ALA	2.7
31	DH	20	ALA	2.7
4	AD	84	LYS	2.7
19	CS	76	PRO	2.7
9	CI	92	TYR	2.7
25	BA	2803	A	2.7
3	CC	8	ILE	2.7
1	AA	1029	C	2.7
23	CY	61	C	2.7
25	DA	652(V)	C	2.7
25	DA	2142	C	2.7
2	CB	196	LEU	2.7
3	CC	43	LEU	2.7
10	CJ	8	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
14	CN	53	LEU	2.7
44	DY	106	LEU	2.7
3	CC	38	ARG	2.7
4	AD	73	ARG	2.7
10	AJ	10	GLY	2.7
31	DH	6	ARG	2.7
50	D4	58	ARG	2.7
10	CJ	69	ASN	2.7
14	CN	61	TRP	2.7
21	CU	14	TRP	2.7
31	DH	38	SER	2.7
45	BZ	149	SER	2.7
3	AC	76	VAL	2.7
7	CG	2	ALA	2.7
9	AI	65	VAL	2.7
9	CI	52	ALA	2.7
10	AJ	48	THR	2.7
13	CM	18	ALA	2.7
17	CQ	23	VAL	2.7
38	DS	72	ALA	2.7
10	CJ	58	ASP	2.7
1	AA	1530	G	2.6
1	CA	1001(A)	G	2.6
8	CH	70	GLN	2.6
25	DA	100	G	2.6
25	DA	2166	G	2.6
24	CX	47	U	2.6
30	DG	25	TYR	2.6
8	CH	83	ILE	2.6
10	CJ	82	ILE	2.6
45	DZ	120	ILE	2.6
53	D7	1	MET	2.6
2	AB	11	LEU	2.6
2	AB	196	LEU	2.6
30	DG	139	LEU	2.6
39	BT	112	ARG	2.6
49	D3	55	ARG	2.6
2	AB	72	GLY	2.6
3	CC	197	GLY	2.6
12	CL	63	GLY	2.6
41	BV	101	GLY	2.6
1	CA	1028	C	2.6

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Mol	Chain	Res	Type	RSRZ
1	CA	1259	C	2.6
2	AB	156	LYS	2.6
10	CJ	7	LYS	2.6
19	CS	32	LYS	2.6
25	BA	2807	C	2.6
10	CJ	78	ASN	2.6
11	CK	117	ASN	2.6
2	AB	15	VAL	2.6
9	CI	82	ALA	2.6
10	CJ	27	ALA	2.6
45	DZ	52	SER	2.6
45	DZ	90	VAL	2.6
45	DZ	92	SER	2.6
52	D6	42	TRP	2.6
11	AK	125	PHE	2.6
2	AB	208	ILE	2.6
40	DU	88	ILE	2.6
25	BA	2805	G	2.6
25	DA	271(K)	U	2.6
25	DA	2125	G	2.6
3	AC	32	LEU	2.6
10	CJ	16	LEU	2.6
30	BG	83	ARG	2.6
3	AC	26	LYS	2.6
3	AC	171	GLY	2.6
25	DA	2801(A)	A	2.6
9	CI	15	ALA	2.6
9	CI	65	VAL	2.6
1	AA	1028	C	2.6
36	BQ	1	MET	2.6
2	CB	33	TYR	2.6
2	CB	154	LEU	2.6
2	CB	187	LEU	2.6
3	CC	196	LEU	2.6
5	CE	60	TYR	2.6
10	AJ	88	LEU	2.6
10	CJ	85	LEU	2.6
46	D0	84	LEU	2.6
2	CB	40	HIS	2.6
3	CC	30	ARG	2.6
5	CE	18	ARG	2.6
10	CJ	60	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
14	AN	35	ARG	2.6
1	CA	1150	U	2.6
1	CA	1358	U	2.6
14	CN	50	LYS	2.6
50	D4	2	LYS	2.6
13	CM	112	GLY	2.6
20	AT	103	GLY	2.6
44	DY	104	GLY	2.6
1	CA	1138	G	2.6
1	CA	1184	G	2.6
25	BA	2155	G	2.6
25	DA	2110	G	2.6
25	DA	2318	G	2.6
2	CB	232	PRO	2.6
9	AI	106	ALA	2.6
11	CK	89	ALA	2.6
20	AT	98	PRO	2.6
31	DH	125	VAL	2.6
45	DZ	158	PRO	2.6
45	DZ	142	SER	2.6
1	CA	1183	A	2.6
19	AS	12	ASP	2.6
23	CY	36	A	2.6
1	AA	345	C	2.6
10	AJ	65	LEU	2.6
25	DA	1043	C	2.6
10	AJ	66	ARG	2.6
12	AL	91	LYS	2.6
44	BY	94	LYS	2.6
3	CC	194	GLY	2.6
15	AO	23	GLY	2.6
44	DY	58	GLY	2.6
25	DA	362	U	2.6
10	CJ	26	ALA	2.6
27	DD	2	ALA	2.6
38	DS	12	PHE	2.6
39	DT	104	ASN	2.6
30	DG	76	SER	2.5
50	B4	52	THR	2.5
1	AA	1009	G	2.5
3	CC	36	ASP	2.5
23	AY	63	G	2.5

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Mol	Chain	Res	Type	RSRZ
23	CW	5	G	2.5
23	CY	52	G	2.5
25	BA	1221	G	2.5
25	BA	2177	G	2.5
39	DT	1	MET	2.5
41	DV	26	ASP	2.5
3	AC	57	ILE	2.5
16	CP	33	ILE	2.5
1	AA	1005	A	2.5
45	DZ	33	LEU	2.5
45	DZ	67	LEU	2.5
48	D2	10	LEU	2.5
9	CI	9	ARG	2.5
12	AL	89	ARG	2.5
10	CJ	68	HIS	2.5
3	CC	48	TYR	2.5
19	CS	52	TYR	2.5
25	BA	2130	C	2.5
25	BA	2197	C	2.5
10	CJ	93	GLY	2.5
19	CS	72	GLY	2.5
5	CE	52	PRO	2.5
17	AQ	35	VAL	2.5
45	DZ	130	PRO	2.5
3	AC	10	PHE	2.5
31	DH	145	ALA	2.5
45	BZ	104	PHE	2.5
50	B4	46	GLN	2.5
1	CA	997	U	2.5
23	AW	20	U	2.5
31	DH	41	MET	2.5
10	CJ	96	ILE	2.5
3	CC	4	LYS	2.5
10	AJ	5	ARG	2.5
18	CR	31	LEU	2.5
19	CS	70	LYS	2.5
34	DO	113	LYS	2.5
50	B4	69	LYS	2.5
50	D4	8	LYS	2.5
1	AA	77	G	2.5
23	AY	1	G	2.5
23	CY	1	G	2.5

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Mol	Chain	Res	Type	RSRZ
1	CA	1280	A	2.5
9	CI	4	TYR	2.5
22	AV	13	A	2.5
23	AY	35	A	2.5
25	BA	1507	A	2.5
3	CC	13	GLY	2.5
9	CI	57	GLY	2.5
9	CI	115	GLY	2.5
43	DX	94	GLY	2.5
31	DH	10	PRO	2.5
44	DY	77	PRO	2.5
45	DZ	159	PRO	2.5
10	AJ	44	VAL	2.5
12	AL	18	VAL	2.5
14	CN	25	VAL	2.5
36	DQ	132	VAL	2.5
2	CB	105	PHE	2.5
1	AA	163	C	2.5
1	CA	979	C	2.5
25	BA	2210	C	2.5
3	CC	3	ASN	2.5
16	AP	69	THR	2.5
3	AC	72	LYS	2.5
2	CB	114	ARG	2.5
3	AC	47	LEU	2.5
4	AD	76	ARG	2.5
13	CM	88	ARG	2.5
13	CM	104	ARG	2.5
16	AP	19	ILE	2.5
4	AD	194	LEU	2.5
45	DZ	121	HIS	2.5
32	DI	29	TYR	2.5
50	D4	25	TYR	2.5
14	AN	51	GLY	2.5
50	B4	64	GLY	2.5
45	BZ	95	PRO	2.5
45	DZ	95	PRO	2.5
1	AA	78	G	2.5
1	AA	1183	A	2.5
19	AS	67	VAL	2.5
24	CX	76	A	2.5
25	BA	2198	A	2.5

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Mol	Chain	Res	Type	RSRZ
25	BA	2227	G	2.5
25	BA	2813	G	2.5
25	DA	880	G	2.5
25	DA	2169	A	2.5
5	CE	17	ALA	2.5
11	AK	13	GLN	2.5
31	DH	24	VAL	2.5
30	DG	151	ALA	2.5
10	CJ	87	THR	2.5
2	AB	121	LEU	2.5
2	AB	233	SER	2.5
2	CB	200	ILE	2.5
3	AC	14	ILE	2.5
7	AG	4	ARG	2.5
10	CJ	74	ILE	2.5
31	DH	9	ILE	2.5
39	DT	52	ILE	2.5
39	DT	129	ARG	2.5
23	AY	48	C	2.5
25	BA	34	C	2.5
23	CW	12	U	2.5
25	DA	9	U	2.5
25	DA	614(A)	U	2.5
2	CB	31	TYR	2.5
3	CC	23	TYR	2.5
19	CS	61	TYR	2.5
35	DP	73	GLY	2.5
40	DU	43	GLY	2.5
3	CC	68	VAL	2.5
3	CC	70	VAL	2.5
5	CE	105	VAL	2.5
31	DH	19	VAL	2.5
3	AC	100	ALA	2.5
4	AD	110	PHE	2.5
5	CE	94	ALA	2.5
13	AM	121	LYS	2.4
14	CN	11	LYS	2.4
38	DS	33	LYS	2.4
16	CP	69	THR	2.4
50	D4	44	THR	2.4
7	AG	78	ARG	2.4
25	BA	945	A	2.4

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Mol	Chain	Res	Type	RSRZ
31	DH	3	ARG	2.4
50	B4	55	ARG	2.4
2	AB	185	ILE	2.4
3	CC	204	LEU	2.4
7	CG	12	LEU	2.4
18	CR	65	ILE	2.4
55	D9	17	ILE	2.4
1	CA	1032	G	2.4
1	CA	1220	G	2.4
23	CW	6	G	2.4
23	CW	22	G	2.4
23	CY	63	G	2.4
23	CY	71	G	2.4
25	BA	2179	G	2.4
25	BA	2331	G	2.4
3	CC	31	HIS	2.4
5	CE	5	ASP	2.4
19	AS	13	ASP	2.4
45	BZ	148	ASP	2.4
23	CW	68	C	2.4
25	DA	2803	C	2.4
2	CB	159	PRO	2.4
5	CE	85	GLY	2.4
23	CY	47	U	2.4
24	AX	47	U	2.4
25	BA	2131	U	2.4
25	DA	272(A)	U	2.4
13	CM	41	PRO	2.4
46	D0	76	GLY	2.4
16	AP	17	TYR	2.4
16	CP	76	GLN	2.4
17	AQ	37	LYS	2.4
19	CS	58	VAL	2.4
3	CC	200	ALA	2.4
14	AN	16	PHE	2.4
30	BG	50	ALA	2.4
4	AD	168	ARG	2.4
21	CU	24	ARG	2.4
31	BH	3	ARG	2.4
32	DI	76	THR	2.4
45	BZ	112	ARG	2.4
50	D4	13	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
10	AJ	74	ILE	2.4
12	CL	7	ILE	2.4
44	BY	92	ASN	2.4
45	BZ	142	SER	2.4
1	CA	1261	A	2.4
1	CA	1503	A	2.4
7	AG	156	TRP	2.4
10	CJ	89	ASP	2.4
25	BA	1793	A	2.4
17	AQ	49	GLU	2.4
41	DV	34	GLU	2.4
1	AA	79	G	2.4
1	CA	1131	G	2.4
23	CY	57	G	2.4
25	DA	1170	G	2.4
2	CB	228	GLY	2.4
4	AD	2	GLY	2.4
10	CJ	53	PRO	2.4
44	DY	41	GLY	2.4
44	DY	94	LYS	2.4
2	AB	229	VAL	2.4
3	CC	106	VAL	2.4
10	CJ	24	VAL	2.4
16	AP	39	TYR	2.4
25	BA	155	C	2.4
25	BA	697	C	2.4
25	DA	889	C	2.4
3	CC	24	ALA	2.4
3	CC	71	ALA	2.4
3	CC	92	ALA	2.4
7	AG	62	PHE	2.4
4	AD	118	ARG	2.4
8	CH	124	ALA	2.4
9	CI	119	ALA	2.4
14	CN	59	ALA	2.4
23	CW	45	U	2.4
31	BH	145	ALA	2.4
31	DH	123	PHE	2.4
32	DI	50	ARG	2.4
10	CJ	100	THR	2.4
31	BH	103	LEU	2.4
50	D4	9	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
7	CG	37	ASN	2.4
10	CJ	13	HIS	2.4
14	AN	49	HIS	2.4
9	CI	126	SER	2.4
10	CJ	59	SER	2.4
2	AB	231	GLU	2.4
2	CB	126	GLU	2.4
19	CS	34	TRP	2.4
10	AJ	86	MET	2.4
1	CA	965	A	2.4
20	CT	30	LYS	2.4
25	BA	302	A	2.4
9	AI	30	GLY	2.4
9	CI	123	PRO	2.4
29	DF	107	LYS	2.4
38	DS	93	LYS	2.4
16	AP	37	GLY	2.4
29	DF	208	GLY	2.4
2	CB	112	VAL	2.4
14	CN	56	VAL	2.4
31	DH	37	VAL	2.4
31	DH	44	VAL	2.4
1	AA	1368	G	2.4
1	CA	1190	G	2.4
2	AB	130	ARG	2.4
3	AC	184	TYR	2.4
3	CC	29	TYR	2.4
7	CG	5	ARG	2.4
9	CI	125	TYR	2.4
20	CT	78	ALA	2.4
23	CW	10	G	2.4
23	CY	19	G	2.4
25	BA	2190	G	2.4
25	DA	1537	G	2.4
25	DA	2151	G	2.4
31	BH	59	ARG	2.4
3	CC	52	LEU	2.4
4	AD	120	LEU	2.4
13	CM	4	ILE	2.4
14	AN	44	LEU	2.4
18	CR	85	LEU	2.4
28	BE	77	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
31	DH	71	LEU	2.4
38	DS	58	LEU	2.4
1	AA	1037	C	2.4
1	CA	203	U	2.4
1	CA	1137	C	2.4
23	CY	13	C	2.4
25	DA	894	C	2.4
39	DT	128	GLU	2.4
2	AB	83	MET	2.4
27	DD	38	LYS	2.4
31	DH	36	PRO	2.4
9	CI	68	GLY	2.4
50	D4	45	GLY	2.4
2	CB	135	GLN	2.4
4	AD	191	ARG	2.4
8	AH	30	ARG	2.4
10	CJ	66	ARG	2.4
12	CL	39	VAL	2.4
21	CU	6	ARG	2.4
1	AA	344	A	2.4
1	CA	1225	A	2.4
1	CA	1447	A	2.4
2	AB	17	PHE	2.4
22	AV	12	A	2.4
23	CY	7	A	2.4
23	CY	35	A	2.4
10	CJ	18	ALA	2.4
50	D4	42	PHE	2.4
18	AR	44	LEU	2.3
19	AS	20	LEU	2.3
31	BH	105	LEU	2.3
5	CE	131	ILE	2.3
45	DZ	53	ILE	2.3
12	AL	6	THR	2.3
1	AA	1040	U	2.3
1	CA	1026	G	2.3
1	CA	1278	U	2.3
25	BA	2188	G	2.3
25	DA	2132	U	2.3
25	DA	2181	G	2.3
1	CA	1037	C	2.3
1	CA	1038	C	2.3

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Mol	Chain	Res	Type	RSRZ
2	CB	132	LYS	2.3
14	CN	9	LYS	2.3
19	AS	38	SER	2.3
23	CW	67	C	2.3
23	CY	4	C	2.3
25	BA	2161	C	2.3
30	BG	49	ASP	2.3
2	AB	125	PRO	2.3
4	AD	3	ARG	2.3
5	AE	72	GLN	2.3
14	CN	55	GLY	2.3
9	CI	111	ARG	2.3
19	CS	78	ARG	2.3
44	DY	2	ARG	2.3
45	DZ	112	ARG	2.3
2	AB	136	VAL	2.3
3	CC	76	VAL	2.3
31	DH	50	VAL	2.3
31	DH	79	VAL	2.3
33	DN	140	VAL	2.3
2	CB	70	PHE	2.3
3	CC	94	LEU	2.3
4	AD	117	ALA	2.3
5	CE	95	ALA	2.3
7	AG	12	LEU	2.3
13	CM	33	ALA	2.3
30	BG	178	PHE	2.3
31	DH	102	ALA	2.3
45	BZ	136	PHE	2.3
50	B4	49	PHE	2.3
13	CM	48	LEU	2.3
45	DZ	102	LEU	2.3
3	AC	182	ILE	2.3
3	CC	182	ILE	2.3
2	AB	31	TYR	2.3
14	AN	34	TYR	2.3
25	BA	2180	A	2.3
26	DB	120	A	2.3
2	AB	128	GLU	2.3
5	CE	10	MET	2.3
10	AJ	64	GLU	2.3
35	DP	76	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	CA	1086	U	2.3
25	DA	2118	U	2.3
39	BT	107	ASP	2.3
1	AA	1030(C)	G	2.3
1	CA	630	G	2.3
1	CA	1048	G	2.3
4	CD	37	PRO	2.3
7	CG	156	TRP	2.3
23	AW	5	G	2.3
23	CY	6	G	2.3
23	CY	22	G	2.3
26	DB	118	G	2.3
5	CE	25	ARG	2.3
5	CE	114	GLY	2.3
10	AJ	36	GLY	2.3
20	AT	8	ARG	2.3
25	BA	2164	C	2.3
40	BU	117	GLN	2.3
45	DZ	79	ARG	2.3
48	D2	51	ARG	2.3
3	CC	116	VAL	2.3
2	CB	122	PHE	2.3
3	CC	47	LEU	2.3
3	CC	146	ALA	2.3
3	CC	168	ALA	2.3
19	CS	20	LEU	2.3
20	CT	10	LEU	2.3
31	DH	88	LEU	2.3
43	DX	42	ALA	2.3
2	CB	80	ILE	2.3
4	CD	5	ILE	2.3
4	CD	34	GLU	2.3
10	AJ	55	LYS	2.3
36	DQ	130	LYS	2.3
44	DY	47	LYS	2.3
38	DS	61	ASN	2.3
25	BA	678	A	2.3
31	DH	16	SER	2.3
45	BZ	92	SER	2.3
3	CC	59	ARG	2.3
4	AD	122	ARG	2.3
9	AI	3	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
9	AI	87	GLN	2.3
16	AP	48	TRP	2.3
31	DH	42	ARG	2.3
31	DH	59	ARG	2.3
40	DU	117	GLN	2.3
1	AA	164	U	2.3
25	DA	2109	U	2.3
5	CE	51	VAL	2.3
5	CE	69	VAL	2.3
13	CM	7	VAL	2.3
2	AB	70	PHE	2.3
9	AI	47	LEU	2.3
3	CC	77	ILE	2.3
4	AD	158	ILE	2.3
5	CE	80	ILE	2.3
9	AI	46	ALA	2.3
28	DE	204	ALA	2.3
19	CS	83	HIS	2.3
23	AY	68	C	2.3
24	CX	4	G	2.3
25	BA	299	G	2.3
25	BA	936	C	2.3
25	BA	2138	G	2.3
30	DG	52	ILE	2.3
1	AA	1030(B)	C	2.3
1	CA	470	C	2.3
1	CA	1066	C	2.3
3	AC	31	HIS	2.3
25	DA	898	C	2.3
2	AB	27	LYS	2.3
10	CJ	99	LYS	2.3
45	DZ	14	LYS	2.3
46	D0	43	THR	2.3
9	AI	5	TYR	2.3
2	AB	9	GLU	2.3
30	BG	35	GLU	2.3
44	BY	91	GLU	2.3
2	CB	175	ARG	2.3
4	CD	47	ARG	2.3
9	CI	75	ASP	2.3
10	CJ	70	ARG	2.3
10	CJ	73	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
15	AO	19	PRO	2.3
17	CQ	99	SER	2.3
38	BS	3	ARG	2.3
41	DV	50	PRO	2.3
1	CA	1005	A	2.3
14	AN	52	GLN	2.3
35	DP	70	GLN	2.3
3	AC	185	GLY	2.3
9	CI	69	GLY	2.3
10	CJ	31	GLY	2.3
46	B0	8	GLY	2.3
3	CC	33	LEU	2.3
30	DG	149	VAL	2.3
47	B1	98	LEU	2.3
2	CB	55	PHE	2.3
1	CA	1148	U	2.2
1	CA	1446	U	2.2
2	CB	127	ILE	2.2
3	CC	57	ILE	2.2
4	AD	164	ALA	2.2
19	CS	50	ALA	2.2
44	DY	48	ALA	2.2
4	AD	169	LYS	2.2
20	AT	74	LYS	2.2
44	DY	63	LYS	2.2
10	CJ	42	THR	2.2
4	AD	24	GLU	2.2
27	BD	28	GLU	2.2
31	DH	58	GLU	2.2
32	BI	117	GLU	2.2
33	BN	68	GLU	2.2
3	AC	23	TYR	2.2
8	AH	94	TYR	2.2
9	AI	125	TYR	2.2
25	DA	865	C	2.2
1	CA	631	G	2.2
1	CA	1186	G	2.2
25	BA	2173	G	2.2
25	DA	879	G	2.2
25	DA	2182	G	2.2
7	CG	32	ARG	2.2
9	AI	128	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
14	AN	3	ARG	2.2
14	CN	23	ARG	2.2
19	AS	37	ARG	2.2
21	AU	10	ARG	2.2
2	AB	131	PRO	2.2
3	CC	73	PRO	2.2
30	DG	87	PRO	2.2
3	CC	154	SER	2.2
2	CB	99	GLY	2.2
10	CJ	10	GLY	2.2
12	AL	95	GLY	2.2
15	CO	20	GLY	2.2
9	AI	99	LEU	2.2
29	DF	12	LEU	2.2
41	DV	52	VAL	2.2
2	AB	123	ALA	2.2
2	CB	41	ILE	2.2
3	AC	77	ILE	2.2
6	AF	53	ALA	2.2
13	AM	5	ALA	2.2
14	CN	58	LYS	2.2
18	CR	23	LYS	2.2
20	CT	12	ALA	2.2
22	CV	14	A	2.2
25	BA	937	A	2.2
25	DA	2134	A	2.2
29	DF	130	ALA	2.2
40	DU	62	ILE	2.2
43	DX	88	LYS	2.2
2	CB	83	MET	2.2
45	DZ	32	HIS	2.2
1	AA	90	U	2.2
2	CB	86	GLU	2.2
3	AC	67	THR	2.2
3	AC	206	GLU	2.2
23	AY	59	U	2.2
44	DY	91	GLU	2.2
3	AC	48	TYR	2.2
3	AC	201	TYR	2.2
17	CQ	95	TYR	2.2
50	B4	67	TYR	2.2
8	CH	122	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
39	BT	125	ARG	2.2
45	DZ	131	ARG	2.2
1	AA	1030	C	2.2
1	CA	980	C	2.2
7	AG	86	GLN	2.2
16	AP	76	GLN	2.2
23	AY	13	C	2.2
23	AY	56	C	2.2
25	BA	2199	C	2.2
25	BA	2815	C	2.2
26	BB	88	C	2.2
3	CC	56	ASP	2.2
1	CA	971	G	2.2
9	AI	57	GLY	2.2
9	CI	72	GLY	2.2
19	CS	4	SER	2.2
19	AS	71	LEU	2.2
23	CY	65	G	2.2
25	BA	2182	G	2.2
25	DA	1112	G	2.2
30	DG	119	GLY	2.2
50	B4	45	GLY	2.2
3	AC	204	LEU	2.2
3	CC	178	LEU	2.2
16	AP	49	LEU	2.2
45	DZ	24	LEU	2.2
3	CC	135	LYS	2.2
29	BF	89	VAL	2.2
30	BG	47	LYS	2.2
30	BG	149	VAL	2.2
31	DH	45	VAL	2.2
36	BQ	130	LYS	2.2
46	D0	24	LYS	2.2
8	AH	80	ILE	2.2
8	AH	83	ILE	2.2
14	CN	16	PHE	2.2
38	DS	34	HIS	2.2
30	DG	54	GLU	2.2
49	D3	60	GLU	2.2
1	AA	1044	A	2.2
1	CA	1001	A	2.2
1	CA	1179	A	2.2

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Mol	Chain	Res	Type	RSRZ
23	AY	64	A	2.2
25	BA	1091	A	2.2
25	BA	1219	A	2.2
25	BA	2136	A	2.2
25	DA	2173	A	2.2
3	AC	193	TYR	2.2
9	AI	114	TYR	2.2
9	CI	62	TYR	2.2
23	AY	12	U	2.2
25	BA	2189	U	2.2
50	D4	32	TYR	2.2
3	CC	109	PRO	2.2
2	CB	45	GLN	2.2
3	CC	41	GLY	2.2
10	CJ	30	SER	2.2
14	CN	4	LYS	2.2
19	AS	15	LEU	2.2
19	AS	26	GLY	2.2
19	AS	35	SER	2.2
41	DV	73	SER	2.2
44	DY	4	LYS	2.2
3	AC	64	VAL	2.2
8	CH	53	VAL	2.2
16	AP	79	VAL	2.2
2	CB	16	HIS	2.2
2	CB	214	ILE	2.2
9	CI	33	PHE	2.2
10	CJ	98	ILE	2.2
25	BA	2159	C	2.2
25	BA	2200	C	2.2
36	DQ	65	PHE	2.2
44	DY	75	ILE	2.2
40	DU	116	ALA	2.2
4	AD	80	GLU	2.2
5	CE	111	GLU	2.2
17	CQ	49	GLU	2.2
23	AY	5	G	2.2
23	AY	22	G	2.2
24	CX	46	G	2.2
25	BA	99	G	2.2
25	BA	2184	G	2.2
25	DA	549	G	2.2

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Mol	Chain	Res	Type	RSRZ
45	DZ	168	GLU	2.2
2	CB	168	THR	2.2
2	CB	137	ARG	2.2
2	CB	153	ARG	2.2
13	AM	94	ARG	2.2
30	DG	21	ARG	2.2
1	CA	983	A	2.2
1	CA	1180	A	2.2
5	CE	130	ASN	2.2
10	AJ	69	ASN	2.2
12	AL	64	TYR	2.2
16	AP	38	TYR	2.2
17	CQ	2	PRO	2.2
25	DA	900	A	2.2
1	AA	203	U	2.2
2	AB	132	LYS	2.2
2	CB	156	LYS	2.2
3	CC	72	LYS	2.2
25	BA	1220	U	2.2
25	BA	1466	U	2.2
25	DA	271(L)	U	2.2
2	CB	227	GLY	2.2
7	AG	55	GLY	2.2
7	AG	81	GLY	2.2
8	AH	90	GLY	2.2
21	AU	11	GLY	2.2
31	DH	103	LEU	2.2
45	BZ	102	LEU	2.2
52	D6	11	LEU	2.2
2	AB	214	ILE	2.2
2	CB	15	VAL	2.2
3	AC	202	ILE	2.2
3	AC	207	VAL	2.2
8	AH	134	ILE	2.2
9	AI	108	VAL	2.2
31	DH	35	VAL	2.2
45	DZ	166	SER	2.2
9	CI	81	ILE	2.2
13	AM	39	ILE	2.2
14	CN	42	ILE	2.2
19	CS	40	ILE	2.2
10	CJ	11	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
12	CL	32	PHE	2.2
30	DG	23	PHE	2.2
2	AB	29	ALA	2.1
20	AT	40	ALA	2.1
32	DI	94	ALA	2.1
5	CE	81	GLU	2.1
31	DH	159	GLU	2.1
2	CB	226	ARG	2.1
6	AF	3	ARG	2.1
7	AG	155	ARG	2.1
9	AI	42	ARG	2.1
23	AY	4	C	2.1
50	D4	52	THR	2.1
1	AA	266	G	2.1
1	CA	1258	G	2.1
1	CA	1316	G	2.1
1	CA	1338	G	2.1
23	AY	19	G	2.1
23	CY	10	G	2.1
24	CX	2	G	2.1
25	BA	928	G	2.1
25	DA	892	G	2.1
10	AJ	14	LYS	2.1
13	AM	12	ASN	2.1
13	CM	106	ASN	2.1
15	AO	71	GLN	2.1
2	CB	221	LEU	2.1
6	AF	48	LEU	2.1
16	AP	74	LEU	2.1
1	AA	1041	A	2.1
2	CB	66	GLY	2.1
12	AL	14	GLY	2.1
25	DA	2320	A	2.1
41	DV	101	GLY	2.1
2	AB	39	ILE	2.1
3	CC	20	SER	2.1
3	CC	151	VAL	2.1
9	CI	91	ASP	2.1
13	CM	92	HIS	2.1
10	CJ	19	SER	2.1
10	CJ	44	VAL	2.1
19	CS	51	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
23	CY	12	U	2.1
23	CY	66	U	2.1
25	BA	2194	U	2.1
31	BH	169	VAL	2.1
45	DZ	161	VAL	2.1
45	DZ	48	PHE	2.1
6	CF	99	ALA	2.1
9	CI	61	ALA	2.1
14	CN	5	ALA	2.1
18	AR	73	ALA	2.1
30	DG	46	ALA	2.1
2	CB	129	GLU	2.1
32	BI	10	GLU	2.1
3	CC	126	ARG	2.1
3	CC	140	ARG	2.1
9	CI	42	ARG	2.1
10	CJ	45	ARG	2.1
31	DH	54	ARG	2.1
38	DS	3	ARG	2.1
45	BZ	122	ARG	2.1
10	AJ	42	THR	2.1
19	AS	33	THR	2.1
36	BQ	21	THR	2.1
1	CA	1153	C	2.1
1	CA	1389	C	2.1
24	CX	65	C	2.1
24	CX	71	C	2.1
25	DA	2108	C	2.1
30	DG	138	GLN	2.1
9	AI	56	LEU	2.1
19	AS	22	LEU	2.1
32	BI	35	LEU	2.1
32	BI	43	ASN	2.1
32	BI	140	LEU	2.1
38	DS	80	LEU	2.1
43	DX	1	MET	2.1
2	AB	18	GLY	2.1
45	DZ	147	GLY	2.1
1	AA	998	G	2.1
1	CA	1283	G	2.1
2	AB	200	ILE	2.1
2	CB	166	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
4	AD	5	ILE	2.1
7	AG	42	ILE	2.1
9	CI	41	VAL	2.1
10	AJ	98	ILE	2.1
11	CK	36	ASP	2.1
24	AX	4	G	2.1
25	BA	569	G	2.1
25	DA	859	G	2.1
25	DA	864	G	2.1
31	BH	141	VAL	2.1
50	D4	35	VAL	2.1
54	D8	16	ILE	2.1
55	B9	12	ASP	2.1
2	AB	124	SER	2.1
20	AT	11	SER	2.1
30	BG	23	PHE	2.1
30	DG	180	PHE	2.1
1	CA	1275	A	2.1
1	CA	1502	A	2.1
2	CB	173	ALA	2.1
23	CW	9	A	2.1
23	CW	21	A	2.1
23	CW	50	U	2.1
23	CY	14	A	2.1
23	CY	73	A	2.1
25	BA	2152	U	2.1
25	BA	2812	A	2.1
25	DA	878	A	2.1
25	DA	2113	U	2.1
25	DA	2167	U	2.1
34	DO	108	GLU	2.1
45	DZ	119	GLU	2.1
3	AC	190	ARG	2.1
3	CC	18	TRP	2.1
4	AD	115	ARG	2.1
7	CG	103	TRP	2.1
29	BF	34	TRP	2.1
30	DG	29	TRP	2.1
38	DS	17	ARG	2.1
5	CE	121	LYS	2.1
13	CM	13	LYS	2.1
31	DH	173	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
4	CD	45	GLN	2.1
7	AG	16	LEU	2.1
12	CL	27	LEU	2.1
38	BS	48	LEU	2.1
2	AB	228	GLY	2.1
2	CB	92	TYR	2.1
3	CC	171	GLY	2.1
5	AE	22	GLY	2.1
11	CK	25	TYR	2.1
30	DG	146	TYR	2.1
45	DZ	9	TYR	2.1
1	CA	1115	C	2.1
1	CA	1210	C	2.1
1	CA	1223	C	2.1
2	CB	222	ILE	2.1
5	AE	80	ILE	2.1
5	CE	90	VAL	2.1
16	AP	53	VAL	2.1
19	CS	11	VAL	2.1
23	AY	62	C	2.1
25	BA	1631	C	2.1
31	BH	113	VAL	2.1
31	DH	15	VAL	2.1
55	D9	26	ILE	2.1
30	BG	147	ASP	2.1
5	CE	58	ALA	2.1
5	CE	132	ALA	2.1
8	CH	102	ARG	2.1
14	AN	5	ALA	2.1
29	DF	26	ALA	2.1
36	DQ	134	ARG	2.1
1	AA	1004	A	2.1
1	AA	1256	A	2.1
1	CA	1248	A	2.1
2	CB	139	LYS	2.1
25	DA	2120	G	2.1
25	DA	2655	G	2.1
25	DA	2793	G	2.1
26	DB	119	G	2.1
18	AR	25	THR	2.1
23	CY	58	A	2.1
23	CY	64	A	2.1

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Mol	Chain	Res	Type	RSRZ
25	BA	2901	A	2.1
25	DA	1445	A	2.1
25	DA	1963	U	2.1
31	BH	175	LYS	2.1
9	AI	21	PRO	2.1
44	DY	82	PRO	2.1
44	BY	1	MET	2.1
2	CB	10	LEU	2.1
17	AQ	98	LEU	2.1
30	DG	175	LEU	2.1
33	DN	116	LEU	2.1
41	DV	94	LEU	2.1
45	DZ	18	LEU	2.1
6	CF	100	ASN	2.1
13	CM	77	ASN	2.1
44	DY	92	ASN	2.1
3	CC	80	GLY	2.1
29	DF	131	GLY	2.1
31	BH	66	GLY	2.1
30	DG	12	TYR	2.1
5	AE	69	VAL	2.1
13	CM	17	VAL	2.1
31	DH	99	VAL	2.1
45	DZ	128	VAL	2.1
49	D3	47	VAL	2.1
2	AB	50	GLU	2.0
3	CC	16	ARG	2.0
10	AJ	29	ARG	2.0
15	AO	88	ARG	2.0
36	DQ	136	ALA	2.0
36	DQ	139	GLU	2.0
45	DZ	2	GLU	2.0
50	B4	62	ARG	2.0
50	D4	55	ARG	2.0
7	AG	7	ALA	2.0
1	AA	91	C	2.0
1	CA	840	C	2.0
1	CA	1145	C	2.0
21	CU	3	LYS	2.0
23	CW	49	C	2.0
24	CX	16	C	2.0
25	DA	1509	C	2.0

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Mol	Chain	Res	Type	RSRZ
34	DO	53	LYS	2.0
44	DY	54	LYS	2.0
44	DY	95	LYS	2.0
2	CB	73	THR	2.0
3	CC	15	THR	2.0
31	DH	12	PRO	2.0
45	DZ	83	PRO	2.0
2	CB	215	LEU	2.0
5	AE	71	LEU	2.0
13	CM	101	GLN	2.0
17	CQ	98	LEU	2.0
25	BA	2906	U	2.0
25	DA	2150	U	2.0
30	BG	26	GLN	2.0
45	DZ	155	LEU	2.0
1	AA	1034	G	2.0
1	AA	1286	A	2.0
1	CA	969	A	2.0
1	CA	1003	G	2.0
1	CA	1057	G	2.0
1	CA	1252	A	2.0
1	CA	1272	G	2.0
1	CA	1279	A	2.0
23	AY	27	G	2.0
23	CY	27	G	2.0
24	AX	2	G	2.0
24	CX	49	G	2.0
25	DA	652(E)	G	2.0
26	DB	66	A	2.0
20	CT	26	ASN	2.0
2	AB	172	ILE	2.0
3	AC	84	ILE	2.0
10	CJ	38	ILE	2.0
10	CJ	50	ILE	2.0
16	AP	4	ILE	2.0
19	AS	40	ILE	2.0
31	BH	14	GLY	2.0
31	DH	82	GLY	2.0
32	BI	109	ILE	2.0
3	CC	99	VAL	2.0
8	CH	97	VAL	2.0
9	CI	108	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
11	CK	14	VAL	2.0
38	DS	92	TYR	2.0
45	DZ	139	VAL	2.0
3	CC	105	GLU	2.0
9	CI	18	PHE	2.0
48	D2	55	ARG	2.0
2	AB	179	LYS	2.0
3	AC	61	ALA	2.0
13	CM	5	ALA	2.0
31	DH	96	ALA	2.0
19	CS	35	SER	2.0
21	CU	17	THR	2.0
34	DO	1	MET	2.0
36	BQ	41	TRP	2.0
8	CH	67	PRO	2.0
8	CH	74	PRO	2.0
31	DH	128	PRO	2.0
1	CA	1359	C	2.0
2	CB	102	LEU	2.0
3	CC	37	GLN	2.0
13	CM	96	LEU	2.0
15	CO	57	LEU	2.0
23	CY	25	C	2.0
25	DA	652(T)	C	2.0
25	DA	1178	C	2.0
38	DS	32	LEU	2.0
1	AA	1020	U	2.0
1	AA	1446	U	2.0
2	CB	162	ILE	2.0
3	AC	2	GLY	2.0
5	CE	44	GLY	2.0
31	BH	4	ILE	2.0
31	DH	174	GLY	2.0
45	DZ	57	ILE	2.0
9	CI	14	VAL	2.0
13	CM	54	VAL	2.0
15	CO	29	VAL	2.0
21	AU	24	ARG	2.0
21	CU	10	ARG	2.0
25	BA	218	A	2.0
25	DA	2176	A	2.0
39	DT	13	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
52	D6	28	ARG	2.0
11	AK	25	TYR	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
23	7MG	CY	46	24/25	0.46	0.17	91,105,113,139	0
23	7MG	CW	46	24/25	0.51	0.18	93,104,114,127	0
23	PSU	CY	55	20/21	0.54	0.19	91,104,118,129	0
23	7MG	AW	46	24/25	0.59	0.15	74,94,116,138	0
23	4SU	CY	8	20/21	0.59	0.15	95,103,122,140	0
23	7MG	AY	46	24/25	0.63	0.14	92,100,111,135	0
23	4SU	CW	8	20/21	0.64	0.16	85,105,116,130	0
23	5MU	CY	54	21/22	0.65	0.17	88,99,111,135	0
23	PSU	AY	55	20/21	0.65	0.14	88,103,115,132	0
23	PSU	CY	32	20/21	0.69	0.14	83,95,100,107	0
23	PSU	CW	55	20/21	0.69	0.14	76,95,105,108	0
23	5MU	AY	54	21/22	0.70	0.14	85,97,115,141	0
23	PSU	CY	39	20/21	0.71	0.14	79,92,100,112	0
23	4SU	AY	8	20/21	0.72	0.11	99,105,115,127	0
23	4SU	AW	8	20/21	0.76	0.14	81,89,100,121	0
23	MIA	AY	37	22/30	0.76	0.17	82,91,103,118	0
23	MIA	CY	37	22/30	0.77	0.12	75,93,102,117	0
23	PSU	AW	55	20/21	0.80	0.13	57,85,93,93	0
24	PSU	CX	55	20/21	0.81	0.12	62,70,83,92	0
23	PSU	CW	32	20/21	0.84	0.17	62,82,97,97	0
23	PSU	AY	39	20/21	0.86	0.14	76,89,100,102	0
23	5MU	CW	54	21/22	0.87	0.13	72,81,90,93	0
23	PSU	AY	32	20/21	0.88	0.12	83,93,99,105	0
24	4SU	CX	8	20/21	0.88	0.14	73,82,90,90	0
24	5MC	CX	32	21/22	0.89	0.12	63,72,77,80	0
24	5MU	CX	54	21/22	0.89	0.12	69,80,89,95	0
24	PSU	AX	55	20/21	0.91	0.10	60,68,83,92	0
24	5MU	AX	54	21/22	0.92	0.10	60,70,77,80	0
23	MIA	CW	37	22/30	0.92	0.11	53,72,83,85	0
23	5MU	AW	54	21/22	0.93	0.10	57,76,85,89	0
23	PSU	CW	39	20/21	0.93	0.14	62,79,88,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
24	4SU	AX	8	20/21	0.94	0.10	47,62,81,87	0
24	5MC	AX	32	21/22	0.95	0.11	38,56,66,77	0
23	PSU	AW	32	20/21	0.95	0.09	39,59,64,65	0
23	MIA	AW	37	29/30	0.96	0.10	36,49,67,72	0
23	PSU	AW	39	20/21	0.96	0.08	37,57,68,72	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3578	1/1	0.49	0.19	71,71,71,71	0
56	MG	DA	3601	1/1	0.50	0.18	75,75,75,75	0
56	MG	AY	3003	1/1	0.51	0.28	78,78,78,78	0
56	MG	DA	3572	1/1	0.53	0.14	70,70,70,70	0
56	MG	BA	3737	1/1	0.59	0.22	68,68,68,68	0
56	MG	CA	3126	1/1	0.60	0.28	76,76,76,76	0
56	MG	DA	3365	1/1	0.62	0.23	54,54,54,54	0
56	MG	DY	502	1/1	0.62	0.19	86,86,86,86	0
56	MG	AA	3168	1/1	0.63	0.17	76,76,76,76	0
56	MG	DA	3417	1/1	0.63	0.26	71,71,71,71	0
56	MG	DA	3605	1/1	0.64	0.14	53,53,53,53	0
56	MG	BA	3692	1/1	0.64	0.26	73,73,73,73	0
56	MG	BA	3322	1/1	0.65	0.27	58,58,58,58	0
56	MG	CA	3054	1/1	0.65	0.50	65,65,65,65	0
56	MG	BA	3453	1/1	0.66	0.14	59,59,59,59	0
56	MG	AA	3198	1/1	0.66	0.23	82,82,82,82	0
56	MG	BA	3703	1/1	0.67	0.17	56,56,56,56	0
56	MG	DA	3042	1/1	0.67	0.19	71,71,71,71	0
56	MG	BA	3550	1/1	0.67	0.40	74,74,74,74	0
56	MG	AA	3179	1/1	0.67	0.19	85,85,85,85	0
56	MG	DA	3522	1/1	0.67	0.27	57,57,57,57	0
56	MG	CA	3007	1/1	0.68	0.26	69,69,69,69	0
56	MG	CA	3124	1/1	0.68	0.36	90,90,90,90	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3558	1/1	0.69	0.22	72,72,72,72	0
56	MG	CA	3075	1/1	0.69	0.20	53,53,53,53	0
56	MG	DA	3569	1/1	0.69	0.32	75,75,75,75	0
56	MG	BA	3714	1/1	0.69	0.26	73,73,73,73	0
56	MG	DA	3501	1/1	0.70	0.35	67,67,67,67	0
56	MG	CA	3145	1/1	0.70	0.20	62,62,62,62	0
56	MG	AY	3001	1/1	0.71	0.30	92,92,92,92	0
56	MG	DA	3242	1/1	0.71	0.12	56,56,56,56	0
56	MG	AA	3113	1/1	0.72	0.19	57,57,57,57	0
56	MG	CJ	5001	1/1	0.72	0.20	75,75,75,75	0
56	MG	CA	3051	1/1	0.72	0.27	78,78,78,78	0
56	MG	DA	3517	1/1	0.72	0.17	60,60,60,60	0
56	MG	CA	3143	1/1	0.72	0.29	59,59,59,59	0
56	MG	DA	3526	1/1	0.72	0.22	64,64,64,64	0
56	MG	BA	3327	1/1	0.73	0.25	74,74,74,74	0
56	MG	CA	3125	1/1	0.73	0.19	76,76,76,76	0
56	MG	BA	3154	1/1	0.73	0.27	58,58,58,58	0
56	MG	BA	3480	1/1	0.73	0.19	29,29,29,29	0
56	MG	DD	309	1/1	0.73	0.15	65,65,65,65	0
56	MG	BB	3015	1/1	0.73	0.12	54,54,54,54	0
56	MG	BA	3700	1/1	0.74	0.26	73,73,73,73	0
56	MG	AA	3093	1/1	0.74	0.19	58,58,58,58	0
56	MG	DA	3528	1/1	0.74	0.23	70,70,70,70	0
56	MG	CA	3036	1/1	0.74	0.21	69,69,69,69	0
56	MG	CA	3113	1/1	0.74	0.16	79,79,79,79	0
56	MG	BB	3007	1/1	0.75	0.14	84,84,84,84	0
56	MG	BA	3508	1/1	0.75	0.16	61,61,61,61	0
56	MG	BA	3544	1/1	0.75	0.23	57,57,57,57	0
56	MG	AX	3006	1/1	0.75	0.30	80,80,80,80	0
56	MG	DB	3009	1/1	0.75	0.24	70,70,70,70	0
56	MG	BA	3400	1/1	0.75	0.20	53,53,53,53	0
56	MG	BA	3608	1/1	0.75	0.21	68,68,68,68	0
56	MG	BA	3555	1/1	0.76	0.17	49,49,49,49	0
56	MG	CA	3150	1/1	0.76	0.18	80,80,80,80	0
56	MG	BA	3532	1/1	0.76	0.20	73,73,73,73	0
56	MG	AA	3188	1/1	0.76	0.17	69,69,69,69	0
56	MG	AY	3002	1/1	0.76	0.19	70,70,70,70	0
56	MG	DA	3247	1/1	0.76	0.10	51,51,51,51	0
56	MG	DA	3330	1/1	0.76	0.14	54,54,54,54	0
56	MG	DA	3349	1/1	0.76	0.15	46,46,46,46	0
56	MG	BA	3751	1/1	0.76	0.17	51,51,51,51	0
56	MG	DA	3602	1/1	0.76	0.20	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	3760	1/1	0.76	0.26	78,78,78,78	0
56	MG	DA	3433	1/1	0.76	0.11	58,58,58,58	0
56	MG	DA	3489	1/1	0.76	0.11	53,53,53,53	0
56	MG	DA	3491	1/1	0.76	0.12	69,69,69,69	0
56	MG	BA	3419	1/1	0.77	0.16	50,50,50,50	0
56	MG	AA	3112	1/1	0.77	0.21	53,53,53,53	0
56	MG	DA	3079	1/1	0.77	0.24	60,60,60,60	0
56	MG	DA	3163	1/1	0.77	0.28	63,63,63,63	0
56	MG	AA	3075	1/1	0.77	0.56	81,81,81,81	0
56	MG	BA	3610	1/1	0.77	0.28	64,64,64,64	0
56	MG	AA	3122	1/1	0.77	0.12	74,74,74,74	0
56	MG	AA	3206	1/1	0.77	0.19	62,62,62,62	0
56	MG	CA	3134	1/1	0.77	0.15	78,78,78,78	0
56	MG	DA	3411	1/1	0.77	0.16	43,43,43,43	0
56	MG	CA	3027	1/1	0.77	0.16	64,64,64,64	0
56	MG	AA	3138	1/1	0.77	0.20	73,73,73,73	0
56	MG	DA	3621	1/1	0.77	0.20	73,73,73,73	0
56	MG	DA	3463	1/1	0.77	0.13	53,53,53,53	0
56	MG	DA	3476	1/1	0.77	0.15	62,62,62,62	0
56	MG	AA	3014	1/1	0.77	0.16	64,64,64,64	0
56	MG	CA	3046	1/1	0.78	0.36	68,68,68,68	0
56	MG	DA	3036	1/1	0.78	0.13	48,48,48,48	0
56	MG	AX	3002	1/1	0.78	0.35	71,71,71,71	0
56	MG	AA	3192	1/1	0.78	0.17	71,71,71,71	0
56	MG	BA	3168	1/1	0.78	0.22	57,57,57,57	0
56	MG	BA	3591	1/1	0.78	0.18	58,58,58,58	0
56	MG	CA	3121	1/1	0.78	0.14	88,88,88,88	0
56	MG	DA	3553	1/1	0.78	0.30	45,45,45,45	0
56	MG	DA	3257	1/1	0.78	0.18	58,58,58,58	0
56	MG	CA	3123	1/1	0.78	0.28	77,77,77,77	0
56	MG	BA	3771	1/1	0.78	0.18	73,73,73,73	0
56	MG	AA	3183	1/1	0.78	0.18	63,63,63,63	0
56	MG	AA	3008	1/1	0.78	0.25	53,53,53,53	0
56	MG	BB	3016	1/1	0.78	0.21	63,63,63,63	0
56	MG	BA	3519	1/1	0.78	0.21	56,56,56,56	0
56	MG	BA	3331	1/1	0.78	0.15	51,51,51,51	0
56	MG	DA	3470	1/1	0.78	0.21	65,65,65,65	0
56	MG	BA	3395	1/1	0.78	0.17	65,65,65,65	0
56	MG	BA	3307	1/1	0.79	0.12	57,57,57,57	0
56	MG	DA	3524	1/1	0.79	0.21	58,58,58,58	0
56	MG	BA	3445	1/1	0.79	0.28	53,53,53,53	0
56	MG	BA	3081	1/1	0.79	0.15	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	DA	3425	1/1	0.79	0.38	69,69,69,69	0
56	MG	DA	3085	1/1	0.79	0.21	65,65,65,65	0
56	MG	DA	3436	1/1	0.79	0.17	63,63,63,63	0
56	MG	DA	3094	1/1	0.79	0.15	55,55,55,55	0
56	MG	DA	3581	1/1	0.79	0.29	67,67,67,67	0
56	MG	BA	3470	1/1	0.79	0.29	46,46,46,46	0
56	MG	BA	3730	1/1	0.79	0.15	45,45,45,45	0
56	MG	DA	3483	1/1	0.79	0.12	64,64,64,64	0
56	MG	CA	3068	1/1	0.79	0.23	77,77,77,77	0
56	MG	BA	3731	1/1	0.79	0.14	57,57,57,57	0
56	MG	CA	3004	1/1	0.79	0.17	69,69,69,69	0
56	MG	BA	3402	1/1	0.79	0.20	67,67,67,67	0
57	NEG	CA	3171	17/17	0.79	0.23	53,72,80,85	0
56	MG	BA	3682	1/1	0.80	0.29	73,73,73,73	0
56	MG	BP	204	1/1	0.80	0.18	54,54,54,54	0
56	MG	BA	3735	1/1	0.80	0.12	41,41,41,41	0
56	MG	BA	3736	1/1	0.80	0.12	73,73,73,73	0
56	MG	DA	3561	1/1	0.80	0.14	65,65,65,65	0
56	MG	CA	3021	1/1	0.80	0.22	66,66,66,66	0
56	MG	DA	3090	1/1	0.80	0.33	67,67,67,67	0
56	MG	BA	3435	1/1	0.80	0.14	52,52,52,52	0
56	MG	AA	3106	1/1	0.80	0.18	62,62,62,62	0
56	MG	DA	3178	1/1	0.80	0.12	45,45,45,45	0
56	MG	DA	3200	1/1	0.80	0.26	52,52,52,52	0
56	MG	BA	3539	1/1	0.80	0.18	58,58,58,58	0
56	MG	BA	3707	1/1	0.80	0.25	62,62,62,62	0
56	MG	BA	3484	1/1	0.80	0.27	64,64,64,64	0
56	MG	DA	3513	1/1	0.80	0.11	58,58,58,58	0
56	MG	CA	3148	1/1	0.80	0.19	72,72,72,72	0
57	NEG	AA	3217	17/17	0.80	0.20	45,55,78,95	0
56	MG	AA	3082	1/1	0.80	0.33	70,70,70,70	0
56	MG	CA	3069	1/1	0.81	0.30	75,75,75,75	0
56	MG	AA	3186	1/1	0.81	0.31	65,65,65,65	0
56	MG	BA	3373	1/1	0.81	0.17	35,35,35,35	0
56	MG	BA	3243	1/1	0.81	0.26	57,57,57,57	0
56	MG	BA	3303	1/1	0.81	0.16	27,27,27,27	0
56	MG	BA	3401	1/1	0.81	0.13	67,67,67,67	0
56	MG	BN	3002	1/1	0.81	0.14	53,53,53,53	0
56	MG	BA	3710	1/1	0.81	0.24	51,51,51,51	0
56	MG	DA	3276	1/1	0.81	0.11	57,57,57,57	0
56	MG	BU	201	1/1	0.81	0.20	29,29,29,29	0
56	MG	DA	3340	1/1	0.81	0.16	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	3562	1/1	0.81	0.14	67,67,67,67	0
56	MG	DA	3564	1/1	0.81	0.22	64,64,64,64	0
56	MG	CA	3139	1/1	0.81	0.22	63,63,63,63	0
56	MG	BA	3580	1/1	0.81	0.15	61,61,61,61	0
56	MG	DA	3573	1/1	0.81	0.12	69,69,69,69	0
56	MG	DA	3381	1/1	0.81	0.18	55,55,55,55	0
56	MG	BA	3723	1/1	0.81	0.14	41,41,41,41	0
56	MG	AA	3003	1/1	0.81	0.30	79,79,79,79	0
56	MG	AA	3136	1/1	0.81	0.18	59,59,59,59	0
56	MG	CA	3159	1/1	0.81	0.25	60,60,60,60	0
56	MG	AA	3030	1/1	0.81	0.28	65,65,65,65	0
56	MG	DA	3459	1/1	0.81	0.09	63,63,63,63	0
56	MG	BA	3634	1/1	0.81	0.12	50,50,50,50	0
56	MG	DO	201	1/1	0.81	0.17	59,59,59,59	0
56	MG	BA	3638	1/1	0.81	0.12	47,47,47,47	0
56	MG	BA	3741	1/1	0.81	0.15	68,68,68,68	0
56	MG	BA	3652	1/1	0.81	0.14	25,25,25,25	0
57	NEG	CA	3174	17/17	0.81	0.22	38,53,68,69	0
56	MG	AA	3047	1/1	0.82	0.22	68,68,68,68	0
56	MG	B4	502	1/1	0.82	0.24	73,73,73,73	0
56	MG	DA	3001	1/1	0.82	0.13	49,49,49,49	0
56	MG	BA	3566	1/1	0.82	0.11	28,28,28,28	0
56	MG	DA	3039	1/1	0.82	0.12	50,50,50,50	0
56	MG	BA	3543	1/1	0.82	0.20	62,62,62,62	0
56	MG	DA	3054	1/1	0.82	0.12	59,59,59,59	0
56	MG	AF	3001	1/1	0.82	0.14	48,48,48,48	0
56	MG	DA	3081	1/1	0.82	0.17	53,53,53,53	0
56	MG	CA	3026	1/1	0.82	0.15	61,61,61,61	0
56	MG	BA	3725	1/1	0.82	0.24	63,63,63,63	0
56	MG	CA	3128	1/1	0.82	0.37	72,72,72,72	0
56	MG	BA	3727	1/1	0.82	0.21	57,57,57,57	0
56	MG	DA	3582	1/1	0.82	0.21	65,65,65,65	0
56	MG	DA	3466	1/1	0.82	0.12	46,46,46,46	0
56	MG	BA	3429	1/1	0.82	0.13	71,71,71,71	0
56	MG	DA	3474	1/1	0.82	0.17	55,55,55,55	0
56	MG	DA	3180	1/1	0.82	0.23	50,50,50,50	0
56	MG	BA	3153	1/1	0.82	0.29	56,56,56,56	0
56	MG	DA	3220	1/1	0.82	0.11	45,45,45,45	0
56	MG	DE	302	1/1	0.82	0.11	30,30,30,30	0
56	MG	DA	3221	1/1	0.82	0.13	56,56,56,56	0
56	MG	BA	3702	1/1	0.82	0.18	60,60,60,60	0
56	MG	BA	3630	1/1	0.82	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	DA	3514	1/1	0.82	0.12	67,67,67,67	0
56	MG	BR	202	1/1	0.82	0.17	51,51,51,51	0
57	NEG	CX	3004	17/17	0.82	0.15	32,64,79,84	0
56	MG	BA	3134	1/1	0.83	0.22	57,57,57,57	0
56	MG	BA	3724	1/1	0.83	0.17	84,84,84,84	0
56	MG	CA	3055	1/1	0.83	0.24	63,63,63,63	0
56	MG	AA	3202	1/1	0.83	0.17	63,63,63,63	0
56	MG	BA	3639	1/1	0.83	0.21	55,55,55,55	0
56	MG	DA	3287	1/1	0.83	0.24	50,50,50,50	0
56	MG	DA	3291	1/1	0.83	0.17	41,41,41,41	0
56	MG	AA	3068	1/1	0.83	0.40	70,70,70,70	0
56	MG	CA	3098	1/1	0.83	0.17	59,59,59,59	0
56	MG	DA	3342	1/1	0.83	0.13	55,55,55,55	0
56	MG	CA	3110	1/1	0.83	0.29	62,62,62,62	0
56	MG	DA	3354	1/1	0.83	0.16	56,56,56,56	0
56	MG	BA	3515	1/1	0.83	0.12	57,57,57,57	0
56	MG	DA	3050	1/1	0.83	0.31	60,60,60,60	0
56	MG	CA	3118	1/1	0.83	0.24	61,61,61,61	0
56	MG	BA	3689	1/1	0.83	0.23	68,68,68,68	0
56	MG	BA	3157	1/1	0.83	0.30	59,59,59,59	0
56	MG	DA	3597	1/1	0.83	0.21	56,56,56,56	0
56	MG	DA	3430	1/1	0.83	0.12	51,51,51,51	0
56	MG	BA	3586	1/1	0.83	0.10	58,58,58,58	0
56	MG	BA	3356	1/1	0.83	0.15	24,24,24,24	0
56	MG	DA	3091	1/1	0.83	0.13	57,57,57,57	0
56	MG	DB	3005	1/1	0.83	0.51	77,77,77,77	0
56	MG	DB	3007	1/1	0.83	0.23	67,67,67,67	0
56	MG	BA	3600	1/1	0.83	0.14	59,59,59,59	0
56	MG	DA	3114	1/1	0.83	0.19	53,53,53,53	0
56	MG	DA	3122	1/1	0.83	0.34	71,71,71,71	0
56	MG	DA	3131	1/1	0.83	0.30	63,63,63,63	0
56	MG	DQ	3004	1/1	0.83	0.17	65,65,65,65	0
56	MG	AA	3210	1/1	0.83	0.24	65,65,65,65	0
56	MG	BA	3077	1/1	0.83	0.21	59,59,59,59	0
56	MG	CA	3136	1/1	0.83	0.18	73,73,73,73	0
57	NEG	CA	3172	17/17	0.83	0.18	61,76,83,84	0
56	MG	AX	3012	1/1	0.83	0.30	66,66,66,66	0
57	NEG	CA	3177	17/17	0.83	0.18	36,63,74,81	0
56	MG	CA	3048	1/1	0.83	0.26	54,54,54,54	0
56	MG	DA	3166	1/1	0.84	0.19	57,57,57,57	0
56	MG	DA	3176	1/1	0.84	0.09	49,49,49,49	0
56	MG	BA	3633	1/1	0.84	0.10	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3011	1/1	0.84	0.31	71,71,71,71	0
56	MG	DA	3195	1/1	0.84	0.21	56,56,56,56	0
56	MG	AA	3042	1/1	0.84	0.13	52,52,52,52	0
56	MG	AA	3044	1/1	0.84	0.26	67,67,67,67	0
56	MG	AA	3004	1/1	0.84	0.15	67,67,67,67	0
56	MG	DA	3226	1/1	0.84	0.12	70,70,70,70	0
56	MG	CA	3141	1/1	0.84	0.21	61,61,61,61	0
56	MG	BA	3295	1/1	0.84	0.16	66,66,66,66	0
56	MG	DA	3545	1/1	0.84	0.13	68,68,68,68	0
56	MG	BA	3662	1/1	0.84	0.14	56,56,56,56	0
56	MG	BA	3740	1/1	0.84	0.12	49,49,49,49	0
56	MG	BA	3086	1/1	0.84	0.22	67,67,67,67	0
56	MG	BA	3502	1/1	0.84	0.10	62,62,62,62	0
56	MG	AA	3027	1/1	0.84	0.16	58,58,58,58	0
56	MG	CA	3056	1/1	0.84	0.18	74,74,74,74	0
56	MG	BA	3585	1/1	0.84	0.19	61,61,61,61	0
56	MG	BA	3415	1/1	0.84	0.13	62,62,62,62	0
56	MG	CA	3073	1/1	0.84	0.32	70,70,70,70	0
56	MG	AA	3074	1/1	0.84	0.41	59,59,59,59	0
56	MG	DA	3596	1/1	0.84	0.13	64,64,64,64	0
56	MG	CA	3087	1/1	0.84	0.14	65,65,65,65	0
56	MG	DA	3599	1/1	0.84	0.23	72,72,72,72	0
56	MG	DA	3385	1/1	0.84	0.20	55,55,55,55	0
56	MG	DA	3394	1/1	0.84	0.12	50,50,50,50	0
56	MG	DA	3604	1/1	0.84	0.24	58,58,58,58	0
56	MG	DA	3398	1/1	0.84	0.22	73,73,73,73	0
56	MG	DA	3620	1/1	0.84	0.21	71,71,71,71	0
56	MG	DA	3405	1/1	0.84	0.16	76,76,76,76	0
56	MG	DA	3059	1/1	0.84	0.10	49,49,49,49	0
56	MG	CA	3090	1/1	0.84	0.16	70,70,70,70	0
56	MG	CA	3097	1/1	0.84	0.13	66,66,66,66	0
56	MG	DA	3429	1/1	0.84	0.17	57,57,57,57	0
56	MG	DA	3082	1/1	0.84	0.15	48,48,48,48	0
56	MG	BA	3527	1/1	0.84	0.12	58,58,58,58	0
56	MG	BE	308	1/1	0.84	0.14	34,34,34,34	0
56	MG	DA	3437	1/1	0.84	0.11	47,47,47,47	0
56	MG	D5	502	1/1	0.84	0.13	50,50,50,50	0
56	MG	BA	3530	1/1	0.84	0.10	56,56,56,56	0
57	NEG	AA	3222	17/17	0.84	0.18	30,45,63,66	0
56	MG	BA	3713	1/1	0.84	0.39	68,68,68,68	0
56	MG	AA	3011	1/1	0.84	0.22	66,66,66,66	0
56	MG	BA	3613	1/1	0.84	0.16	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	3628	1/1	0.84	0.17	55,55,55,55	0
56	MG	BA	3155	1/1	0.84	0.28	63,63,63,63	0
56	MG	CA	3131	1/1	0.85	0.20	62,62,62,62	0
56	MG	AA	3154	1/1	0.85	0.17	67,67,67,67	0
56	MG	BA	3681	1/1	0.85	0.19	47,47,47,47	0
56	MG	DA	3397	1/1	0.85	0.11	50,50,50,50	0
56	MG	AA	3155	1/1	0.85	0.22	60,60,60,60	0
56	MG	DA	3144	1/1	0.85	0.20	60,60,60,60	0
56	MG	CA	3057	1/1	0.85	0.12	73,73,73,73	0
56	MG	BA	3601	1/1	0.85	0.21	72,72,72,72	0
56	MG	DA	3577	1/1	0.85	0.19	72,72,72,72	0
56	MG	BA	3482	1/1	0.85	0.23	27,27,27,27	0
56	MG	DA	3426	1/1	0.85	0.19	53,53,53,53	0
56	MG	BA	3338	1/1	0.85	0.15	39,39,39,39	0
56	MG	BA	3340	1/1	0.85	0.17	34,34,34,34	0
56	MG	BA	3503	1/1	0.85	0.16	43,43,43,43	0
56	MG	AA	3015	1/1	0.85	0.19	56,56,56,56	0
56	MG	CA	3012	1/1	0.85	0.22	56,56,56,56	0
56	MG	BA	3370	1/1	0.85	0.10	51,51,51,51	0
56	MG	CA	3105	1/1	0.85	0.16	76,76,76,76	0
56	MG	BA	3712	1/1	0.85	0.12	35,35,35,35	0
56	MG	BA	3572	1/1	0.85	0.19	55,55,55,55	0
56	MG	BB	3001	1/1	0.85	0.20	56,56,56,56	0
56	MG	DB	3001	1/1	0.85	0.24	56,56,56,56	0
56	MG	DA	3058	1/1	0.85	0.10	48,48,48,48	0
56	MG	DA	3283	1/1	0.85	0.11	53,53,53,53	0
56	MG	CA	3040	1/1	0.85	0.17	70,70,70,70	0
56	MG	CA	3122	1/1	0.85	0.21	70,70,70,70	0
56	MG	DA	3318	1/1	0.85	0.10	60,60,60,60	0
56	MG	DA	3508	1/1	0.85	0.10	68,68,68,68	0
56	MG	DA	3323	1/1	0.85	0.13	44,44,44,44	0
56	MG	CA	3042	1/1	0.85	0.20	61,61,61,61	0
56	MG	CA	3043	1/1	0.85	0.26	56,56,56,56	0
56	MG	AA	3069	1/1	0.85	0.29	59,59,59,59	0
56	MG	DA	3086	1/1	0.85	0.28	42,42,42,42	0
56	MG	BA	3389	1/1	0.85	0.13	51,51,51,51	0
56	MG	AA	3193	1/1	0.85	0.19	69,69,69,69	0
56	MG	DA	3533	1/1	0.85	0.14	50,50,50,50	0
56	MG	DA	3534	1/1	0.85	0.28	59,59,59,59	0
56	MG	DA	3540	1/1	0.85	0.10	65,65,65,65	0
56	MG	DA	3460	1/1	0.86	0.10	64,64,64,64	0
56	MG	BA	3257	1/1	0.86	0.14	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	BA	3687	1/1	0.86	0.24	56,56,56,56	0
56	MG	BE	301	1/1	0.86	0.15	36,36,36,36	0
56	MG	DA	3151	1/1	0.86	0.21	52,52,52,52	0
56	MG	AE	3002	1/1	0.86	0.18	67,67,67,67	0
56	MG	BG	3002	1/1	0.86	0.09	52,52,52,52	0
56	MG	DA	3175	1/1	0.86	0.21	43,43,43,43	0
56	MG	AA	3174	1/1	0.86	0.10	59,59,59,59	0
56	MG	DA	3500	1/1	0.86	0.12	56,56,56,56	0
56	MG	BA	3694	1/1	0.86	0.12	57,57,57,57	0
56	MG	BA	3697	1/1	0.86	0.08	34,34,34,34	0
56	MG	BA	3304	1/1	0.86	0.15	21,21,21,21	0
56	MG	DA	3197	1/1	0.86	0.10	57,57,57,57	0
56	MG	DA	3199	1/1	0.86	0.35	57,57,57,57	0
56	MG	BA	3438	1/1	0.86	0.15	44,44,44,44	0
56	MG	DA	3207	1/1	0.86	0.18	58,58,58,58	0
56	MG	BA	3442	1/1	0.86	0.11	31,31,31,31	0
56	MG	CA	3005	1/1	0.86	0.20	62,62,62,62	0
56	MG	DA	3223	1/1	0.86	0.20	63,63,63,63	0
56	MG	BA	3444	1/1	0.86	0.13	37,37,37,37	0
56	MG	BA	3577	1/1	0.86	0.17	62,62,62,62	0
56	MG	DA	3542	1/1	0.86	0.11	65,65,65,65	0
56	MG	AN	502	1/1	0.86	0.25	56,56,56,56	0
56	MG	DA	3252	1/1	0.86	0.09	43,43,43,43	0
56	MG	BA	3109	1/1	0.86	0.17	49,49,49,49	0
56	MG	CA	3142	1/1	0.86	0.25	69,69,69,69	0
56	MG	BA	3112	1/1	0.86	0.12	50,50,50,50	0
56	MG	DA	3285	1/1	0.86	0.12	43,43,43,43	0
56	MG	BA	3715	1/1	0.86	0.11	48,48,48,48	0
56	MG	CA	3028	1/1	0.86	0.23	53,53,53,53	0
56	MG	DA	3574	1/1	0.86	0.13	68,68,68,68	0
56	MG	DA	3575	1/1	0.86	0.21	58,58,58,58	0
56	MG	DA	3298	1/1	0.86	0.12	57,57,57,57	0
56	MG	DA	3311	1/1	0.86	0.14	54,54,54,54	0
56	MG	BA	3329	1/1	0.86	0.13	57,57,57,57	0
56	MG	DA	3322	1/1	0.86	0.09	46,46,46,46	0
56	MG	AA	3176	1/1	0.86	0.20	69,69,69,69	0
56	MG	AA	3088	1/1	0.86	0.19	63,63,63,63	0
56	MG	CX	3003	1/1	0.86	0.15	64,64,64,64	0
56	MG	CY	3001	1/1	0.86	0.18	63,63,63,63	0
56	MG	DA	3345	1/1	0.86	0.12	57,57,57,57	0
56	MG	DA	3603	1/1	0.86	0.19	45,45,45,45	0
56	MG	BA	3494	1/1	0.86	0.15	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	3128	1/1	0.86	0.22	60,60,60,60	0
56	MG	DA	3606	1/1	0.86	0.11	54,54,54,54	0
56	MG	AA	3159	1/1	0.86	0.12	70,70,70,70	0
56	MG	DA	3377	1/1	0.86	0.12	48,48,48,48	0
56	MG	BA	3615	1/1	0.86	0.34	41,41,41,41	0
56	MG	BA	3504	1/1	0.86	0.30	57,57,57,57	0
56	MG	AA	3209	1/1	0.86	0.22	62,62,62,62	0
56	MG	BA	3512	1/1	0.86	0.12	65,65,65,65	0
56	MG	AA	3146	1/1	0.86	0.23	65,65,65,65	0
56	MG	DA	3061	1/1	0.86	0.12	63,63,63,63	0
56	MG	BA	3746	1/1	0.86	0.26	71,71,71,71	0
56	MG	BA	3189	1/1	0.86	0.17	55,55,55,55	0
56	MG	DR	3002	1/1	0.86	0.12	55,55,55,55	0
56	MG	BA	3755	1/1	0.86	0.13	42,42,42,42	0
56	MG	BA	3199	1/1	0.86	0.33	55,55,55,55	0
56	MG	BA	3765	1/1	0.86	0.15	59,59,59,59	0
57	NEG	AA	3220	17/17	0.86	0.13	29,49,59,65	0
56	MG	BA	3208	1/1	0.86	0.14	47,47,47,47	0
56	MG	CA	3093	1/1	0.86	0.14	57,57,57,57	0
56	MG	BA	3242	1/1	0.86	0.23	58,58,58,58	0
56	MG	DA	3103	1/1	0.86	0.17	60,60,60,60	0
57	NEG	CA	3175	17/17	0.86	0.25	48,61,79,89	0
56	MG	DA	3458	1/1	0.86	0.09	56,56,56,56	0
56	MG	BA	3031	1/1	0.86	0.21	49,49,49,49	0
56	MG	AA	3029	1/1	0.87	0.17	60,60,60,60	0
56	MG	BA	3247	1/1	0.87	0.14	49,49,49,49	0
56	MG	AA	3203	1/1	0.87	0.32	62,62,62,62	0
56	MG	BA	3559	1/1	0.87	0.13	66,66,66,66	0
56	MG	DA	3488	1/1	0.87	0.23	66,66,66,66	0
56	MG	BA	3561	1/1	0.87	0.12	64,64,64,64	0
56	MG	BA	3069	1/1	0.87	0.24	46,46,46,46	0
56	MG	DA	3496	1/1	0.87	0.25	51,51,51,51	0
56	MG	BA	3300	1/1	0.87	0.14	55,55,55,55	0
56	MG	AA	3048	1/1	0.87	0.25	55,55,55,55	0
56	MG	AA	3130	1/1	0.87	0.23	74,74,74,74	0
56	MG	BA	3582	1/1	0.87	0.16	63,63,63,63	0
56	MG	BA	3305	1/1	0.87	0.26	61,61,61,61	0
56	MG	BA	3465	1/1	0.87	0.14	20,20,20,20	0
56	MG	CA	3025	1/1	0.87	0.23	64,64,64,64	0
56	MG	DA	3523	1/1	0.87	0.15	62,62,62,62	0
56	MG	BA	3588	1/1	0.87	0.17	62,62,62,62	0
56	MG	DA	3246	1/1	0.87	0.18	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	AA	3134	1/1	0.87	0.24	73,73,73,73	0
56	MG	CA	3146	1/1	0.87	0.25	80,80,80,80	0
56	MG	BA	3597	1/1	0.87	0.12	51,51,51,51	0
56	MG	DA	3539	1/1	0.87	0.11	64,64,64,64	0
56	MG	CA	3031	1/1	0.87	0.26	71,71,71,71	0
56	MG	CA	3152	1/1	0.87	0.15	58,58,58,58	0
56	MG	CA	3153	1/1	0.87	0.16	62,62,62,62	0
56	MG	DA	3550	1/1	0.87	0.17	61,61,61,61	0
56	MG	AA	3224	1/1	0.87	0.18	61,61,61,61	0
56	MG	AA	3050	1/1	0.87	0.15	65,65,65,65	0
56	MG	BA	3729	1/1	0.87	0.22	55,55,55,55	0
56	MG	BA	3602	1/1	0.87	0.11	61,61,61,61	0
56	MG	CA	3045	1/1	0.87	0.27	68,68,68,68	0
56	MG	DA	3030	1/1	0.87	0.18	54,54,54,54	0
56	MG	AA	3111	1/1	0.87	0.13	65,65,65,65	0
56	MG	DA	3329	1/1	0.87	0.16	62,62,62,62	0
56	MG	AA	3184	1/1	0.87	0.17	75,75,75,75	0
56	MG	BA	3333	1/1	0.87	0.10	39,39,39,39	0
56	MG	CA	3052	1/1	0.87	0.17	65,65,65,65	0
56	MG	AA	3139	1/1	0.87	0.18	50,50,50,50	0
56	MG	DA	3348	1/1	0.87	0.13	46,46,46,46	0
56	MG	DA	3057	1/1	0.87	0.19	54,54,54,54	0
56	MG	BA	3616	1/1	0.87	0.09	43,43,43,43	0
56	MG	DA	3363	1/1	0.87	0.12	61,61,61,61	0
56	MG	AX	3004	1/1	0.87	0.20	67,67,67,67	0
56	MG	DA	3367	1/1	0.87	0.09	44,44,44,44	0
56	MG	DA	3369	1/1	0.87	0.14	47,47,47,47	0
56	MG	AX	3005	1/1	0.87	0.22	66,66,66,66	0
56	MG	DA	3066	1/1	0.87	0.10	39,39,39,39	0
56	MG	CA	3067	1/1	0.87	0.18	57,57,57,57	0
56	MG	DA	3615	1/1	0.87	0.25	59,59,59,59	0
56	MG	AA	3041	1/1	0.87	0.19	64,64,64,64	0
56	MG	BA	3183	1/1	0.87	0.24	47,47,47,47	0
56	MG	BA	3637	1/1	0.87	0.21	34,34,34,34	0
56	MG	AX	3009	1/1	0.87	0.22	72,72,72,72	0
56	MG	DA	3087	1/1	0.87	0.10	49,49,49,49	0
56	MG	AA	3149	1/1	0.87	0.12	71,71,71,71	0
56	MG	DA	3422	1/1	0.87	0.31	52,52,52,52	0
56	MG	AA	3087	1/1	0.87	0.17	59,59,59,59	0
56	MG	DA	3093	1/1	0.87	0.15	59,59,59,59	0
56	MG	BA	3209	1/1	0.87	0.23	57,57,57,57	0
56	MG	BB	3013	1/1	0.87	0.17	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	BA	3670	1/1	0.87	0.25	55,55,55,55	0
56	MG	D0	101	1/1	0.87	0.17	73,73,73,73	0
56	MG	CA	3103	1/1	0.87	0.16	78,78,78,78	0
56	MG	BA	3235	1/1	0.87	0.23	65,65,65,65	0
57	NEG	AA	3218	17/17	0.87	0.16	57,72,76,91	0
56	MG	DA	3442	1/1	0.87	0.14	46,46,46,46	0
56	MG	DA	3453	1/1	0.87	0.20	77,77,77,77	0
56	MG	DA	3456	1/1	0.87	0.10	50,50,50,50	0
56	MG	AA	3116	1/1	0.87	0.14	57,57,57,57	0
57	NEG	CA	3173	17/17	0.87	0.16	54,76,85,86	0
56	MG	BE	307	1/1	0.87	0.18	71,71,71,71	0
56	MG	CA	3117	1/1	0.87	0.26	71,71,71,71	0
56	MG	BA	3418	1/1	0.87	0.15	57,57,57,57	0
57	NEG	CW	3002	17/17	0.87	0.20	41,56,78,84	0
56	MG	DA	3169	1/1	0.87	0.17	61,61,61,61	0
56	MG	BA	3505	1/1	0.88	0.16	54,54,54,54	0
56	MG	BD	303	1/1	0.88	0.18	45,45,45,45	0
56	MG	CA	3120	1/1	0.88	0.19	70,70,70,70	0
56	MG	AA	3208	1/1	0.88	0.33	67,67,67,67	0
56	MG	DA	3184	1/1	0.88	0.35	56,56,56,56	0
56	MG	BA	3509	1/1	0.88	0.16	46,46,46,46	0
56	MG	DA	3494	1/1	0.88	0.17	55,55,55,55	0
56	MG	BA	3653	1/1	0.88	0.10	23,23,23,23	0
56	MG	BA	3323	1/1	0.88	0.29	60,60,60,60	0
56	MG	BA	3665	1/1	0.88	0.11	45,45,45,45	0
56	MG	BO	5001	1/1	0.88	0.15	70,70,70,70	0
56	MG	AA	3020	1/1	0.88	0.29	53,53,53,53	0
56	MG	AA	3032	1/1	0.88	0.19	62,62,62,62	0
56	MG	BA	3521	1/1	0.88	0.16	28,28,28,28	0
56	MG	DA	3224	1/1	0.88	0.17	27,27,27,27	0
56	MG	BA	3526	1/1	0.88	0.13	38,38,38,38	0
56	MG	B6	101	1/1	0.88	0.20	49,49,49,49	0
56	MG	BA	3118	1/1	0.88	0.13	46,46,46,46	0
56	MG	AA	3126	1/1	0.88	0.18	65,65,65,65	0
56	MG	BA	3151	1/1	0.88	0.26	51,51,51,51	0
56	MG	CA	3009	1/1	0.88	0.24	55,55,55,55	0
56	MG	DA	3260	1/1	0.88	0.13	36,36,36,36	0
56	MG	BA	3695	1/1	0.88	0.14	39,39,39,39	0
56	MG	DA	3541	1/1	0.88	0.29	46,46,46,46	0
56	MG	CA	3147	1/1	0.88	0.10	51,51,51,51	0
56	MG	AA	3017	1/1	0.88	0.16	49,49,49,49	0
56	MG	DA	3546	1/1	0.88	0.12	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3343	1/1	0.88	0.13	44,44,44,44	0
56	MG	BA	3701	1/1	0.88	0.23	66,66,66,66	0
56	MG	DA	3554	1/1	0.88	0.14	45,45,45,45	0
56	MG	DA	3294	1/1	0.88	0.14	53,53,53,53	0
56	MG	AA	3095	1/1	0.88	0.14	63,63,63,63	0
56	MG	DA	3302	1/1	0.88	0.11	38,38,38,38	0
56	MG	DA	3565	1/1	0.88	0.14	48,48,48,48	0
56	MG	AA	3177	1/1	0.88	0.12	66,66,66,66	0
56	MG	BA	3156	1/1	0.88	0.20	64,64,64,64	0
56	MG	AV	102	1/1	0.88	0.21	52,52,52,52	0
56	MG	BA	3394	1/1	0.88	0.12	53,53,53,53	0
56	MG	AW	3001	1/1	0.88	0.17	67,67,67,67	0
56	MG	AA	3096	1/1	0.88	0.27	53,53,53,53	0
56	MG	BA	3570	1/1	0.88	0.31	57,57,57,57	0
56	MG	BA	3721	1/1	0.88	0.14	74,74,74,74	0
56	MG	BA	3187	1/1	0.88	0.14	42,42,42,42	0
56	MG	DA	3593	1/1	0.88	0.15	57,57,57,57	0
56	MG	DA	3047	1/1	0.88	0.10	46,46,46,46	0
56	MG	CA	3047	1/1	0.88	0.33	56,56,56,56	0
56	MG	DA	3598	1/1	0.88	0.38	63,63,63,63	0
56	MG	AA	3180	1/1	0.88	0.21	67,67,67,67	0
56	MG	AA	3101	1/1	0.88	0.20	52,52,52,52	0
56	MG	AA	3102	1/1	0.88	0.14	50,50,50,50	0
56	MG	AA	3019	1/1	0.88	0.19	53,53,53,53	0
56	MG	BA	3420	1/1	0.88	0.14	61,61,61,61	0
56	MG	BA	3215	1/1	0.88	0.16	47,47,47,47	0
56	MG	AA	3080	1/1	0.88	0.34	58,58,58,58	0
56	MG	AA	3058	1/1	0.88	0.28	63,63,63,63	0
56	MG	DA	3616	1/1	0.88	0.14	47,47,47,47	0
56	MG	DA	3617	1/1	0.88	0.26	55,55,55,55	0
56	MG	AA	3150	1/1	0.88	0.17	58,58,58,58	0
56	MG	AA	3196	1/1	0.88	0.17	66,66,66,66	0
56	MG	CA	3070	1/1	0.88	0.23	52,52,52,52	0
56	MG	BA	3256	1/1	0.88	0.15	25,25,25,25	0
56	MG	DA	3406	1/1	0.88	0.25	48,48,48,48	0
56	MG	DA	3409	1/1	0.88	0.10	41,41,41,41	0
56	MG	AA	3151	1/1	0.88	0.24	65,65,65,65	0
56	MG	CA	3080	1/1	0.88	0.21	62,62,62,62	0
56	MG	BA	3259	1/1	0.88	0.14	32,32,32,32	0
56	MG	DP	201	1/1	0.88	0.19	50,50,50,50	0
56	MG	BA	3294	1/1	0.88	0.14	45,45,45,45	0
56	MG	BA	3047	1/1	0.88	0.15	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	DU	3001	1/1	0.88	0.26	61,61,61,61	0
56	MG	DA	3109	1/1	0.88	0.12	47,47,47,47	0
56	MG	BA	3048	1/1	0.88	0.22	56,56,56,56	0
56	MG	DA	3119	1/1	0.88	0.14	50,50,50,50	0
56	MG	AA	3152	1/1	0.88	0.16	63,63,63,63	0
56	MG	DA	3125	1/1	0.88	0.25	56,56,56,56	0
57	NEG	AA	3219	17/17	0.88	0.16	61,71,78,79	0
56	MG	CA	3101	1/1	0.88	0.10	64,64,64,64	0
57	NEG	AA	3221	17/17	0.88	0.17	44,57,69,70	0
56	MG	DA	3135	1/1	0.88	0.31	44,44,44,44	0
57	NEG	CA	3170	17/17	0.88	0.20	58,72,83,86	0
56	MG	BA	3074	1/1	0.88	0.20	58,58,58,58	0
56	MG	DA	3147	1/1	0.88	0.08	49,49,49,49	0
56	MG	AA	3153	1/1	0.88	0.17	44,44,44,44	0
56	MG	CA	3109	1/1	0.88	0.20	67,67,67,67	0
56	MG	AA	3083	1/1	0.88	0.18	57,57,57,57	0
56	MG	DA	3167	1/1	0.88	0.38	51,51,51,51	0
56	MG	BA	3310	1/1	0.88	0.10	41,41,41,41	0
56	MG	DA	3473	1/1	0.88	0.10	60,60,60,60	0
56	MG	AN	503	1/1	0.89	0.16	59,59,59,59	0
56	MG	BB	3012	1/1	0.89	0.08	42,42,42,42	0
56	MG	BA	3631	1/1	0.89	0.20	63,63,63,63	0
56	MG	BA	3335	1/1	0.89	0.12	50,50,50,50	0
56	MG	CA	3119	1/1	0.89	0.16	84,84,84,84	0
56	MG	BA	3053	1/1	0.89	0.12	56,56,56,56	0
56	MG	BD	301	1/1	0.89	0.25	45,45,45,45	0
56	MG	DA	3188	1/1	0.89	0.20	61,61,61,61	0
56	MG	BA	3636	1/1	0.89	0.11	61,61,61,61	0
56	MG	DA	3498	1/1	0.89	0.16	66,66,66,66	0
56	MG	AN	504	1/1	0.89	0.22	56,56,56,56	0
56	MG	BA	3070	1/1	0.89	0.11	48,48,48,48	0
56	MG	DA	3502	1/1	0.89	0.14	47,47,47,47	0
56	MG	BA	3348	1/1	0.89	0.14	35,35,35,35	0
56	MG	DA	3205	1/1	0.89	0.08	45,45,45,45	0
56	MG	BF	307	1/1	0.89	0.13	46,46,46,46	0
56	MG	BA	3644	1/1	0.89	0.15	34,34,34,34	0
56	MG	DA	3520	1/1	0.89	0.14	61,61,61,61	0
56	MG	BA	3351	1/1	0.89	0.19	61,61,61,61	0
56	MG	BA	3071	1/1	0.89	0.20	48,48,48,48	0
56	MG	BA	3660	1/1	0.89	0.17	44,44,44,44	0
56	MG	BR	201	1/1	0.89	0.25	40,40,40,40	0
56	MG	AA	3086	1/1	0.89	0.16	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	3524	1/1	0.89	0.11	44,44,44,44	0
56	MG	B2	3001	1/1	0.89	0.12	54,54,54,54	0
56	MG	BA	3233	1/1	0.89	0.12	49,49,49,49	0
56	MG	BA	3675	1/1	0.89	0.16	39,39,39,39	0
56	MG	BA	3378	1/1	0.89	0.18	24,24,24,24	0
56	MG	BA	3381	1/1	0.89	0.13	33,33,33,33	0
56	MG	AV	103	1/1	0.89	0.19	70,70,70,70	0
56	MG	BA	3537	1/1	0.89	0.17	55,55,55,55	0
56	MG	BA	3241	1/1	0.89	0.26	59,59,59,59	0
56	MG	DA	3290	1/1	0.89	0.15	36,36,36,36	0
56	MG	CA	3154	1/1	0.89	0.28	62,62,62,62	0
56	MG	CA	3156	1/1	0.89	0.13	58,58,58,58	0
56	MG	DA	3297	1/1	0.89	0.11	70,70,70,70	0
56	MG	BA	3078	1/1	0.89	0.10	48,48,48,48	0
56	MG	CA	3016	1/1	0.89	0.21	56,56,56,56	0
56	MG	AA	3059	1/1	0.89	0.24	53,53,53,53	0
56	MG	BA	3546	1/1	0.89	0.14	57,57,57,57	0
56	MG	DA	3320	1/1	0.89	0.16	53,53,53,53	0
56	MG	BA	3698	1/1	0.89	0.16	59,59,59,59	0
56	MG	DA	3028	1/1	0.89	0.09	52,52,52,52	0
56	MG	AA	3103	1/1	0.89	0.16	59,59,59,59	0
56	MG	BA	3551	1/1	0.89	0.21	56,56,56,56	0
56	MG	DA	3579	1/1	0.89	0.12	69,69,69,69	0
56	MG	DA	3338	1/1	0.89	0.09	60,60,60,60	0
56	MG	BA	3254	1/1	0.89	0.12	56,56,56,56	0
56	MG	BA	3403	1/1	0.89	0.19	53,53,53,53	0
56	MG	DA	3344	1/1	0.89	0.07	54,54,54,54	0
56	MG	BA	3704	1/1	0.89	0.09	75,75,75,75	0
56	MG	BA	3706	1/1	0.89	0.13	52,52,52,52	0
56	MG	BA	3089	1/1	0.89	0.35	46,46,46,46	0
56	MG	DA	3352	1/1	0.89	0.13	45,45,45,45	0
56	MG	AA	3140	1/1	0.89	0.10	61,61,61,61	0
56	MG	DA	3355	1/1	0.89	0.12	53,53,53,53	0
56	MG	AA	3144	1/1	0.89	0.08	62,62,62,62	0
56	MG	BA	3276	1/1	0.89	0.16	40,40,40,40	0
56	MG	AA	3145	1/1	0.89	0.20	36,36,36,36	0
56	MG	DA	3614	1/1	0.89	0.08	34,34,34,34	0
56	MG	BA	3430	1/1	0.89	0.18	48,48,48,48	0
56	MG	DA	3373	1/1	0.89	0.23	51,51,51,51	0
56	MG	DA	3376	1/1	0.89	0.14	46,46,46,46	0
56	MG	DA	3068	1/1	0.89	0.15	52,52,52,52	0
56	MG	DA	3078	1/1	0.89	0.14	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3622	1/1	0.89	0.12	61,61,61,61	0
56	MG	AA	3057	1/1	0.89	0.24	58,58,58,58	0
56	MG	DB	3002	1/1	0.89	0.15	58,58,58,58	0
56	MG	DB	3003	1/1	0.89	0.10	62,62,62,62	0
56	MG	CA	3053	1/1	0.89	0.34	63,63,63,63	0
56	MG	BA	3147	1/1	0.89	0.23	60,60,60,60	0
56	MG	AA	3160	1/1	0.89	0.21	70,70,70,70	0
56	MG	BA	3152	1/1	0.89	0.17	48,48,48,48	0
56	MG	AA	3215	1/1	0.89	0.22	56,56,56,56	0
56	MG	BA	3590	1/1	0.89	0.15	38,38,38,38	0
56	MG	BA	3447	1/1	0.89	0.11	38,38,38,38	0
56	MG	BA	3596	1/1	0.89	0.11	52,52,52,52	0
56	MG	AA	3164	1/1	0.89	0.18	71,71,71,71	0
56	MG	BA	3460	1/1	0.89	0.23	45,45,45,45	0
56	MG	AA	3190	1/1	0.89	0.17	61,61,61,61	0
56	MG	BA	3312	1/1	0.89	0.14	41,41,41,41	0
56	MG	BA	3002	1/1	0.89	0.12	36,36,36,36	0
56	MG	D8	5001	1/1	0.89	0.17	52,52,52,52	0
56	MG	DA	3121	1/1	0.89	0.11	33,33,33,33	0
56	MG	BA	3019	1/1	0.89	0.16	38,38,38,38	0
56	MG	BA	3483	1/1	0.89	0.15	50,50,50,50	0
56	MG	BA	3159	1/1	0.89	0.13	45,45,45,45	0
56	MG	DA	3444	1/1	0.89	0.11	59,59,59,59	0
56	MG	DA	3450	1/1	0.89	0.09	50,50,50,50	0
57	NEG	AW	3004	17/17	0.89	0.15	37,50,72,73	0
57	NEG	AX	3013	17/17	0.89	0.17	29,49,69,70	0
56	MG	BA	3757	1/1	0.89	0.17	47,47,47,47	0
56	MG	DA	3139	1/1	0.89	0.32	59,59,59,59	0
56	MG	AA	3117	1/1	0.89	0.18	66,66,66,66	0
56	MG	BA	3618	1/1	0.89	0.17	64,64,64,64	0
56	MG	DA	3148	1/1	0.89	0.14	53,53,53,53	0
56	MG	BA	3620	1/1	0.89	0.18	42,42,42,42	0
56	MG	CA	3106	1/1	0.89	0.14	55,55,55,55	0
56	MG	AA	3170	1/1	0.89	0.12	66,66,66,66	0
56	MG	DA	3472	1/1	0.89	0.11	40,40,40,40	0
56	MG	CA	3013	1/1	0.90	0.07	52,52,52,52	0
56	MG	BA	3299	1/1	0.90	0.07	53,53,53,53	0
56	MG	CA	3018	1/1	0.90	0.18	69,69,69,69	0
56	MG	BA	3492	1/1	0.90	0.11	33,33,33,33	0
56	MG	BA	3205	1/1	0.90	0.12	45,45,45,45	0
56	MG	DA	3238	1/1	0.90	0.09	40,40,40,40	0
56	MG	DA	3241	1/1	0.90	0.17	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	AA	3115	1/1	0.90	0.23	61,61,61,61	0
56	MG	BA	3716	1/1	0.90	0.13	48,48,48,48	0
56	MG	BA	3391	1/1	0.90	0.10	36,36,36,36	0
56	MG	DA	3518	1/1	0.90	0.17	57,57,57,57	0
56	MG	CA	3155	1/1	0.90	0.25	61,61,61,61	0
56	MG	AA	3207	1/1	0.90	0.16	57,57,57,57	0
56	MG	BA	3605	1/1	0.90	0.28	69,69,69,69	0
56	MG	CA	3168	1/1	0.90	0.20	62,62,62,62	0
56	MG	DA	3279	1/1	0.90	0.07	51,51,51,51	0
56	MG	DA	3527	1/1	0.90	0.16	67,67,67,67	0
56	MG	BA	3213	1/1	0.90	0.17	48,48,48,48	0
56	MG	CN	101	1/1	0.90	0.20	69,69,69,69	0
56	MG	BA	3609	1/1	0.90	0.14	62,62,62,62	0
56	MG	BA	3306	1/1	0.90	0.14	51,51,51,51	0
56	MG	AO	3101	1/1	0.90	0.15	58,58,58,58	0
56	MG	DA	3013	1/1	0.90	0.17	49,49,49,49	0
56	MG	DA	3025	1/1	0.90	0.23	49,49,49,49	0
56	MG	BA	3221	1/1	0.90	0.16	47,47,47,47	0
56	MG	DA	3029	1/1	0.90	0.14	52,52,52,52	0
56	MG	BA	3223	1/1	0.90	0.13	42,42,42,42	0
56	MG	BA	3407	1/1	0.90	0.12	44,44,44,44	0
56	MG	AA	3063	1/1	0.90	0.27	56,56,56,56	0
56	MG	DA	3558	1/1	0.90	0.13	48,48,48,48	0
56	MG	BA	3522	1/1	0.90	0.27	59,59,59,59	0
56	MG	BA	3416	1/1	0.90	0.10	53,53,53,53	0
56	MG	DA	3048	1/1	0.90	0.20	58,58,58,58	0
56	MG	BA	3417	1/1	0.90	0.14	56,56,56,56	0
56	MG	BA	3234	1/1	0.90	0.29	52,52,52,52	0
56	MG	BA	3753	1/1	0.90	0.20	76,76,76,76	0
56	MG	BA	3754	1/1	0.90	0.17	36,36,36,36	0
56	MG	CA	3061	1/1	0.90	0.19	61,61,61,61	0
56	MG	CA	3064	1/1	0.90	0.27	67,67,67,67	0
56	MG	DA	3062	1/1	0.90	0.09	49,49,49,49	0
56	MG	CA	3065	1/1	0.90	0.39	73,73,73,73	0
56	MG	BA	3325	1/1	0.90	0.12	42,42,42,42	0
56	MG	BA	3756	1/1	0.90	0.17	56,56,56,56	0
56	MG	AA	3092	1/1	0.90	0.26	59,59,59,59	0
56	MG	DA	3588	1/1	0.90	0.18	57,57,57,57	0
56	MG	DA	3590	1/1	0.90	0.10	61,61,61,61	0
56	MG	DA	3360	1/1	0.90	0.16	47,47,47,47	0
56	MG	AA	3099	1/1	0.90	0.13	59,59,59,59	0
56	MG	AA	3031	1/1	0.90	0.14	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	AA	3167	1/1	0.90	0.14	71,71,71,71	0
56	MG	CA	3076	1/1	0.90	0.14	54,54,54,54	0
56	MG	CA	3079	1/1	0.90	0.16	61,61,61,61	0
56	MG	AA	3201	1/1	0.90	0.10	60,60,60,60	0
56	MG	CA	3081	1/1	0.90	0.18	51,51,51,51	0
56	MG	BA	3174	1/1	0.90	0.09	52,52,52,52	0
56	MG	BA	3180	1/1	0.90	0.08	46,46,46,46	0
56	MG	DA	3393	1/1	0.90	0.19	53,53,53,53	0
56	MG	AA	3127	1/1	0.90	0.26	52,52,52,52	0
56	MG	DA	3105	1/1	0.90	0.22	54,54,54,54	0
56	MG	BA	3554	1/1	0.90	0.10	56,56,56,56	0
56	MG	AA	3094	1/1	0.90	0.30	53,53,53,53	0
56	MG	DA	3116	1/1	0.90	0.06	58,58,58,58	0
56	MG	BA	3450	1/1	0.90	0.16	59,59,59,59	0
56	MG	AX	3010	1/1	0.90	0.17	54,54,54,54	0
56	MG	CA	3104	1/1	0.90	0.14	51,51,51,51	0
56	MG	DA	3418	1/1	0.90	0.16	55,55,55,55	0
56	MG	BA	3354	1/1	0.90	0.20	39,39,39,39	0
56	MG	DA	3130	1/1	0.90	0.29	52,52,52,52	0
56	MG	BA	3563	1/1	0.90	0.17	43,43,43,43	0
56	MG	DA	3427	1/1	0.90	0.28	61,61,61,61	0
56	MG	DB	3010	1/1	0.90	0.34	72,72,72,72	0
56	MG	BA	3686	1/1	0.90	0.23	61,61,61,61	0
56	MG	BA	3461	1/1	0.90	0.11	21,21,21,21	0
56	MG	DE	304	1/1	0.90	0.10	45,45,45,45	0
56	MG	DF	304	1/1	0.90	0.10	48,48,48,48	0
56	MG	BA	3464	1/1	0.90	0.23	53,53,53,53	0
56	MG	BN	3001	1/1	0.90	0.14	51,51,51,51	0
56	MG	DQ	3002	1/1	0.90	0.08	50,50,50,50	0
56	MG	BA	3691	1/1	0.90	0.13	60,60,60,60	0
56	MG	DA	3439	1/1	0.90	0.23	58,58,58,58	0
56	MG	DA	3441	1/1	0.90	0.09	39,39,39,39	0
56	MG	DU	3003	1/1	0.90	0.09	50,50,50,50	0
56	MG	DV	3003	1/1	0.90	0.14	62,62,62,62	0
56	MG	BA	3283	1/1	0.90	0.08	39,39,39,39	0
56	MG	DA	3161	1/1	0.90	0.13	57,57,57,57	0
56	MG	DA	3447	1/1	0.90	0.15	49,49,49,49	0
56	MG	BA	3573	1/1	0.90	0.13	53,53,53,53	0
56	MG	BA	3574	1/1	0.90	0.24	60,60,60,60	0
56	MG	BA	3576	1/1	0.90	0.14	56,56,56,56	0
56	MG	BA	3359	1/1	0.90	0.17	43,43,43,43	0
56	MG	BY	502	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	BA	3579	1/1	0.90	0.12	57,57,57,57	0
56	MG	DA	3462	1/1	0.90	0.08	36,36,36,36	0
56	MG	BA	3471	1/1	0.90	0.11	33,33,33,33	0
56	MG	BA	3475	1/1	0.90	0.15	52,52,52,52	0
56	MG	B7	104	1/1	0.90	0.12	55,55,55,55	0
56	MG	CA	3133	1/1	0.90	0.22	67,67,67,67	0
56	MG	BA	3584	1/1	0.90	0.11	47,47,47,47	0
56	MG	BA	3479	1/1	0.90	0.19	36,36,36,36	0
56	MG	BA	3360	1/1	0.90	0.21	41,41,41,41	0
56	MG	BA	3195	1/1	0.90	0.30	53,53,53,53	0
56	MG	BA	3148	1/1	0.90	0.15	50,50,50,50	0
56	MG	BA	3711	1/1	0.90	0.11	51,51,51,51	0
56	MG	DA	3216	1/1	0.90	0.12	52,52,52,52	0
56	MG	BA	3567	1/1	0.91	0.08	35,35,35,35	0
56	MG	DA	3461	1/1	0.91	0.08	49,49,49,49	0
56	MG	BA	3569	1/1	0.91	0.11	44,44,44,44	0
56	MG	BA	3690	1/1	0.91	0.11	44,44,44,44	0
56	MG	DA	3465	1/1	0.91	0.21	52,52,52,52	0
56	MG	BA	3087	1/1	0.91	0.08	63,63,63,63	0
56	MG	DA	3165	1/1	0.91	0.26	69,69,69,69	0
56	MG	BA	3466	1/1	0.91	0.24	52,52,52,52	0
56	MG	BA	3468	1/1	0.91	0.08	31,31,31,31	0
56	MG	DA	3168	1/1	0.91	0.23	41,41,41,41	0
56	MG	BX	101	1/1	0.91	0.16	48,48,48,48	0
56	MG	DA	3172	1/1	0.91	0.15	56,56,56,56	0
56	MG	DA	3485	1/1	0.91	0.13	60,60,60,60	0
56	MG	BA	3281	1/1	0.91	0.14	55,55,55,55	0
56	MG	BA	3363	1/1	0.91	0.19	53,53,53,53	0
56	MG	DA	3490	1/1	0.91	0.08	49,49,49,49	0
56	MG	DA	3177	1/1	0.91	0.14	54,54,54,54	0
56	MG	BA	3364	1/1	0.91	0.12	50,50,50,50	0
56	MG	DA	3495	1/1	0.91	0.10	57,57,57,57	0
56	MG	BA	3477	1/1	0.91	0.15	35,35,35,35	0
56	MG	AA	3105	1/1	0.91	0.09	66,66,66,66	0
56	MG	BA	3285	1/1	0.91	0.16	55,55,55,55	0
56	MG	DA	3193	1/1	0.91	0.17	57,57,57,57	0
56	MG	BA	3290	1/1	0.91	0.17	61,61,61,61	0
56	MG	DA	3504	1/1	0.91	0.14	55,55,55,55	0
56	MG	BA	3108	1/1	0.91	0.09	52,52,52,52	0
56	MG	BA	3387	1/1	0.91	0.16	43,43,43,43	0
56	MG	BA	3015	1/1	0.91	0.16	52,52,52,52	0
56	MG	BA	3298	1/1	0.91	0.12	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3496	1/1	0.91	0.11	53,53,53,53	0
56	MG	DA	3213	1/1	0.91	0.10	58,58,58,58	0
56	MG	AA	3100	1/1	0.91	0.15	53,53,53,53	0
56	MG	BA	3201	1/1	0.91	0.20	49,49,49,49	0
56	MG	BA	3599	1/1	0.91	0.17	59,59,59,59	0
56	MG	BA	3399	1/1	0.91	0.19	62,62,62,62	0
56	MG	CA	3149	1/1	0.91	0.19	61,61,61,61	0
56	MG	BA	3113	1/1	0.91	0.52	44,44,44,44	0
56	MG	DA	3532	1/1	0.91	0.17	53,53,53,53	0
56	MG	DA	3232	1/1	0.91	0.18	57,57,57,57	0
56	MG	DA	3233	1/1	0.91	0.17	40,40,40,40	0
56	MG	AA	3132	1/1	0.91	0.14	75,75,75,75	0
56	MG	BA	3040	1/1	0.91	0.28	60,60,60,60	0
56	MG	BA	3211	1/1	0.91	0.29	57,57,57,57	0
56	MG	BA	3406	1/1	0.91	0.15	50,50,50,50	0
56	MG	CA	3037	1/1	0.91	0.31	67,67,67,67	0
56	MG	BA	3135	1/1	0.91	0.15	51,51,51,51	0
56	MG	DA	3548	1/1	0.91	0.17	67,67,67,67	0
56	MG	CA	3162	1/1	0.91	0.14	57,57,57,57	0
56	MG	CA	3163	1/1	0.91	0.12	49,49,49,49	0
56	MG	DA	3270	1/1	0.91	0.15	47,47,47,47	0
56	MG	DA	3274	1/1	0.91	0.12	43,43,43,43	0
56	MG	DA	3275	1/1	0.91	0.10	51,51,51,51	0
56	MG	CA	3164	1/1	0.91	0.17	65,65,65,65	0
56	MG	CA	3167	1/1	0.91	0.10	55,55,55,55	0
56	MG	DA	3282	1/1	0.91	0.19	43,43,43,43	0
56	MG	DA	3568	1/1	0.91	0.11	61,61,61,61	0
56	MG	BA	3412	1/1	0.91	0.13	50,50,50,50	0
56	MG	DA	3284	1/1	0.91	0.21	40,40,40,40	0
56	MG	BA	3309	1/1	0.91	0.09	41,41,41,41	0
56	MG	CA	3044	1/1	0.91	0.15	62,62,62,62	0
56	MG	CW	3001	1/1	0.91	0.15	69,69,69,69	0
56	MG	CX	3002	1/1	0.91	0.26	67,67,67,67	0
56	MG	BA	3523	1/1	0.91	0.10	39,39,39,39	0
56	MG	BA	3734	1/1	0.91	0.10	24,24,24,24	0
56	MG	BA	3045	1/1	0.91	0.10	41,41,41,41	0
56	MG	DA	3002	1/1	0.91	0.10	51,51,51,51	0
56	MG	DA	3585	1/1	0.91	0.10	55,55,55,55	0
56	MG	DA	3306	1/1	0.91	0.07	57,57,57,57	0
56	MG	DA	3589	1/1	0.91	0.20	55,55,55,55	0
56	MG	DA	3003	1/1	0.91	0.25	55,55,55,55	0
56	MG	BA	3217	1/1	0.91	0.21	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	DA	3023	1/1	0.91	0.39	44,44,44,44	0
56	MG	CA	3049	1/1	0.91	0.14	54,54,54,54	0
56	MG	AA	3107	1/1	0.91	0.24	66,66,66,66	0
56	MG	BA	3738	1/1	0.91	0.12	41,41,41,41	0
56	MG	BA	3149	1/1	0.91	0.23	57,57,57,57	0
56	MG	DA	3334	1/1	0.91	0.19	51,51,51,51	0
56	MG	BA	3227	1/1	0.91	0.11	38,38,38,38	0
56	MG	BA	3742	1/1	0.91	0.11	44,44,44,44	0
56	MG	BA	3534	1/1	0.91	0.09	54,54,54,54	0
56	MG	BA	3749	1/1	0.91	0.10	38,38,38,38	0
56	MG	CA	3060	1/1	0.91	0.10	58,58,58,58	0
56	MG	AA	3120	1/1	0.91	0.17	72,72,72,72	0
56	MG	BA	3049	1/1	0.91	0.24	54,54,54,54	0
56	MG	DA	3350	1/1	0.91	0.08	61,61,61,61	0
56	MG	DA	3619	1/1	0.91	0.27	57,57,57,57	0
56	MG	DA	3055	1/1	0.91	0.17	44,44,44,44	0
56	MG	DA	3056	1/1	0.91	0.09	51,51,51,51	0
56	MG	BA	3542	1/1	0.91	0.22	66,66,66,66	0
56	MG	DA	3623	1/1	0.91	0.13	48,48,48,48	0
56	MG	AA	3214	1/1	0.91	0.25	69,69,69,69	0
56	MG	AA	3121	1/1	0.91	0.10	54,54,54,54	0
56	MG	BA	3641	1/1	0.91	0.18	46,46,46,46	0
56	MG	AA	3002	1/1	0.91	0.21	59,59,59,59	0
56	MG	BA	3651	1/1	0.91	0.08	38,38,38,38	0
56	MG	BA	3548	1/1	0.91	0.13	50,50,50,50	0
56	MG	DA	3072	1/1	0.91	0.27	60,60,60,60	0
56	MG	DB	3012	1/1	0.91	0.16	61,61,61,61	0
56	MG	BA	3776	1/1	0.91	0.40	52,52,52,52	0
56	MG	BA	3337	1/1	0.91	0.09	25,25,25,25	0
56	MG	BB	3003	1/1	0.91	0.07	37,37,37,37	0
56	MG	DF	302	1/1	0.91	0.23	60,60,60,60	0
56	MG	BB	3005	1/1	0.91	0.13	54,54,54,54	0
56	MG	DG	3001	1/1	0.91	0.13	55,55,55,55	0
56	MG	CA	3086	1/1	0.91	0.10	53,53,53,53	0
56	MG	BA	3655	1/1	0.91	0.11	29,29,29,29	0
56	MG	CA	3088	1/1	0.91	0.14	48,48,48,48	0
56	MG	DQ	3003	1/1	0.91	0.20	64,64,64,64	0
56	MG	BA	3656	1/1	0.91	0.13	34,34,34,34	0
56	MG	CA	3092	1/1	0.91	0.18	55,55,55,55	0
56	MG	BA	3658	1/1	0.91	0.14	41,41,41,41	0
56	MG	CA	3094	1/1	0.91	0.17	48,48,48,48	0
56	MG	DA	3098	1/1	0.91	0.23	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	CA	3096	1/1	0.91	0.18	51,51,51,51	0
56	MG	AA	3225	1/1	0.91	0.10	55,55,55,55	0
56	MG	DA	3106	1/1	0.91	0.27	56,56,56,56	0
56	MG	AA	3178	1/1	0.91	0.19	60,60,60,60	0
57	NEG	AA	3216	17/17	0.91	0.15	34,56,70,74	0
56	MG	CA	3099	1/1	0.91	0.09	82,82,82,82	0
56	MG	CA	3100	1/1	0.91	0.07	52,52,52,52	0
56	MG	BA	3449	1/1	0.91	0.15	59,59,59,59	0
56	MG	DA	3120	1/1	0.91	0.09	42,42,42,42	0
56	MG	BA	3668	1/1	0.91	0.11	42,42,42,42	0
56	MG	AA	3199	1/1	0.91	0.24	68,68,68,68	0
56	MG	DA	3124	1/1	0.91	0.18	43,43,43,43	0
56	MG	AA	3124	1/1	0.91	0.16	63,63,63,63	0
56	MG	BA	3676	1/1	0.91	0.14	55,55,55,55	0
56	MG	DA	3443	1/1	0.91	0.11	49,49,49,49	0
56	MG	CA	3107	1/1	0.91	0.14	63,63,63,63	0
56	MG	AA	3043	1/1	0.91	0.27	62,62,62,62	0
56	MG	BA	3258	1/1	0.91	0.10	57,57,57,57	0
56	MG	DA	3140	1/1	0.91	0.20	36,36,36,36	0
57	NEG	CA	3176	17/17	0.91	0.18	46,65,76,84	0
56	MG	CA	3111	1/1	0.91	0.30	69,69,69,69	0
56	MG	DA	3146	1/1	0.91	0.17	50,50,50,50	0
56	MG	AA	3091	1/1	0.91	0.23	62,62,62,62	0
56	MG	AA	3067	1/1	0.92	0.30	53,53,53,53	0
56	MG	DA	3471	1/1	0.92	0.16	58,58,58,58	0
56	MG	CA	3039	1/1	0.92	0.21	70,70,70,70	0
56	MG	CA	3157	1/1	0.92	0.13	57,57,57,57	0
56	MG	CA	3158	1/1	0.92	0.19	72,72,72,72	0
56	MG	DA	3475	1/1	0.92	0.11	32,32,32,32	0
56	MG	BA	3739	1/1	0.92	0.10	75,75,75,75	0
56	MG	DA	3206	1/1	0.92	0.18	45,45,45,45	0
56	MG	DA	3484	1/1	0.92	0.09	59,59,59,59	0
56	MG	BA	3462	1/1	0.92	0.13	59,59,59,59	0
56	MG	BA	3649	1/1	0.92	0.22	49,49,49,49	0
56	MG	BA	3365	1/1	0.92	0.12	47,47,47,47	0
56	MG	AA	3197	1/1	0.92	0.17	64,64,64,64	0
56	MG	BA	3748	1/1	0.92	0.10	63,63,63,63	0
56	MG	CA	3179	1/1	0.92	0.16	53,53,53,53	0
56	MG	AA	3141	1/1	0.92	0.15	67,67,67,67	0
56	MG	BA	3750	1/1	0.92	0.19	52,52,52,52	0
56	MG	BA	3375	1/1	0.92	0.10	52,52,52,52	0
56	MG	BA	3210	1/1	0.92	0.18	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	3564	1/1	0.92	0.11	49,49,49,49	0
56	MG	BA	3145	1/1	0.92	0.12	41,41,41,41	0
56	MG	BA	3212	1/1	0.92	0.25	47,47,47,47	0
56	MG	DA	3243	1/1	0.92	0.09	42,42,42,42	0
56	MG	DA	3244	1/1	0.92	0.17	58,58,58,58	0
56	MG	BA	3051	1/1	0.92	0.18	63,63,63,63	0
56	MG	BA	3758	1/1	0.92	0.08	38,38,38,38	0
56	MG	DA	3008	1/1	0.92	0.08	38,38,38,38	0
56	MG	DA	3010	1/1	0.92	0.09	55,55,55,55	0
56	MG	DA	3012	1/1	0.92	0.06	43,43,43,43	0
56	MG	DA	3261	1/1	0.92	0.10	60,60,60,60	0
56	MG	DA	3267	1/1	0.92	0.12	42,42,42,42	0
56	MG	BA	3667	1/1	0.92	0.21	64,64,64,64	0
56	MG	CA	3058	1/1	0.92	0.18	64,64,64,64	0
56	MG	DA	3024	1/1	0.92	0.27	43,43,43,43	0
56	MG	CA	3059	1/1	0.92	0.48	70,70,70,70	0
56	MG	DA	3027	1/1	0.92	0.18	43,43,43,43	0
56	MG	BA	3214	1/1	0.92	0.18	64,64,64,64	0
56	MG	BA	3393	1/1	0.92	0.17	48,48,48,48	0
56	MG	BA	3775	1/1	0.92	0.16	47,47,47,47	0
56	MG	AA	3009	1/1	0.92	0.08	64,64,64,64	0
56	MG	DA	3037	1/1	0.92	0.11	46,46,46,46	0
56	MG	BA	3780	1/1	0.92	0.29	45,45,45,45	0
56	MG	BA	3054	1/1	0.92	0.15	51,51,51,51	0
56	MG	DA	3292	1/1	0.92	0.14	36,36,36,36	0
56	MG	AA	3007	1/1	0.92	0.09	49,49,49,49	0
56	MG	AM	201	1/1	0.92	0.09	61,61,61,61	0
56	MG	AA	3045	1/1	0.92	0.48	68,68,68,68	0
56	MG	DA	3300	1/1	0.92	0.09	27,27,27,27	0
56	MG	CA	3074	1/1	0.92	0.11	62,62,62,62	0
56	MG	BB	3008	1/1	0.92	0.11	71,71,71,71	0
56	MG	DA	3308	1/1	0.92	0.10	57,57,57,57	0
56	MG	AA	3054	1/1	0.92	0.18	46,46,46,46	0
56	MG	DA	3317	1/1	0.92	0.07	47,47,47,47	0
56	MG	AA	3077	1/1	0.92	0.10	69,69,69,69	0
56	MG	DA	3571	1/1	0.92	0.15	49,49,49,49	0
56	MG	AA	3108	1/1	0.92	0.13	59,59,59,59	0
56	MG	DA	3321	1/1	0.92	0.21	58,58,58,58	0
56	MG	BA	3080	1/1	0.92	0.21	49,49,49,49	0
56	MG	CA	3082	1/1	0.92	0.16	41,41,41,41	0
56	MG	CA	3085	1/1	0.92	0.17	60,60,60,60	0
56	MG	BA	3007	1/1	0.92	0.13	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	3333	1/1	0.92	0.08	53,53,53,53	0
56	MG	BA	3328	1/1	0.92	0.12	56,56,56,56	0
56	MG	BD	307	1/1	0.92	0.17	38,38,38,38	0
56	MG	DA	3584	1/1	0.92	0.08	45,45,45,45	0
56	MG	BD	308	1/1	0.92	0.12	42,42,42,42	0
56	MG	BA	3011	1/1	0.92	0.12	51,51,51,51	0
56	MG	BE	303	1/1	0.92	0.32	61,61,61,61	0
56	MG	BE	304	1/1	0.92	0.12	42,42,42,42	0
56	MG	DA	3346	1/1	0.92	0.07	29,29,29,29	0
56	MG	DA	3595	1/1	0.92	0.14	34,34,34,34	0
56	MG	BA	3696	1/1	0.92	0.12	38,38,38,38	0
56	MG	BA	3510	1/1	0.92	0.10	43,43,43,43	0
56	MG	BA	3246	1/1	0.92	0.12	57,57,57,57	0
56	MG	BA	3514	1/1	0.92	0.10	50,50,50,50	0
56	MG	DA	3353	1/1	0.92	0.07	65,65,65,65	0
56	MG	AA	3189	1/1	0.92	0.15	56,56,56,56	0
56	MG	BA	3518	1/1	0.92	0.15	25,25,25,25	0
56	MG	BN	3004	1/1	0.92	0.32	60,60,60,60	0
56	MG	DA	3361	1/1	0.92	0.18	45,45,45,45	0
56	MG	DA	3096	1/1	0.92	0.19	29,29,29,29	0
56	MG	DA	3611	1/1	0.92	0.07	53,53,53,53	0
56	MG	DA	3613	1/1	0.92	0.15	57,57,57,57	0
56	MG	AA	3109	1/1	0.92	0.14	51,51,51,51	0
56	MG	BA	3097	1/1	0.92	0.22	33,33,33,33	0
56	MG	DA	3368	1/1	0.92	0.09	48,48,48,48	0
56	MG	BA	3705	1/1	0.92	0.09	52,52,52,52	0
56	MG	DA	3371	1/1	0.92	0.11	68,68,68,68	0
56	MG	BA	3424	1/1	0.92	0.11	51,51,51,51	0
56	MG	DA	3108	1/1	0.92	0.12	48,48,48,48	0
56	MG	BA	3030	1/1	0.92	0.18	50,50,50,50	0
56	MG	BU	208	1/1	0.92	0.19	35,35,35,35	0
56	MG	DA	3384	1/1	0.92	0.26	55,55,55,55	0
56	MG	AA	3175	1/1	0.92	0.11	54,54,54,54	0
56	MG	BA	3434	1/1	0.92	0.10	65,65,65,65	0
56	MG	BZ	3001	1/1	0.92	0.21	52,52,52,52	0
56	MG	DB	3006	1/1	0.92	0.07	63,63,63,63	0
56	MG	DA	3395	1/1	0.92	0.14	40,40,40,40	0
56	MG	B0	103	1/1	0.92	0.14	61,61,61,61	0
56	MG	BA	3611	1/1	0.92	0.13	23,23,23,23	0
56	MG	DA	3401	1/1	0.92	0.09	50,50,50,50	0
56	MG	BA	3341	1/1	0.92	0.11	59,59,59,59	0
56	MG	B5	101	1/1	0.92	0.32	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	DA	3126	1/1	0.92	0.14	51,51,51,51	0
56	MG	DF	301	1/1	0.92	0.09	49,49,49,49	0
56	MG	DA	3127	1/1	0.92	0.20	53,53,53,53	0
56	MG	DA	3414	1/1	0.92	0.13	46,46,46,46	0
56	MG	B5	104	1/1	0.92	0.13	55,55,55,55	0
56	MG	BA	3191	1/1	0.92	0.22	50,50,50,50	0
56	MG	BA	3260	1/1	0.92	0.13	52,52,52,52	0
56	MG	CA	3001	1/1	0.92	0.09	59,59,59,59	0
56	MG	BA	3617	1/1	0.92	0.10	46,46,46,46	0
56	MG	CA	3127	1/1	0.92	0.12	69,69,69,69	0
56	MG	BA	3717	1/1	0.92	0.10	34,34,34,34	0
56	MG	BA	3533	1/1	0.92	0.08	27,27,27,27	0
56	MG	DA	3432	1/1	0.92	0.13	43,43,43,43	0
56	MG	DV	3001	1/1	0.92	0.10	75,75,75,75	0
56	MG	BA	3261	1/1	0.92	0.15	49,49,49,49	0
56	MG	BA	3625	1/1	0.92	0.15	49,49,49,49	0
56	MG	BA	3265	1/1	0.92	0.23	55,55,55,55	0
56	MG	DA	3438	1/1	0.92	0.15	55,55,55,55	0
56	MG	BA	3726	1/1	0.92	0.14	61,61,61,61	0
56	MG	CA	3140	1/1	0.92	0.12	49,49,49,49	0
56	MG	BA	3446	1/1	0.92	0.20	40,40,40,40	0
56	MG	CA	3017	1/1	0.92	0.25	53,53,53,53	0
56	MG	BA	3541	1/1	0.92	0.28	31,31,31,31	0
56	MG	DA	3445	1/1	0.92	0.09	50,50,50,50	0
56	MG	CA	3019	1/1	0.92	0.11	45,45,45,45	0
56	MG	BA	3355	1/1	0.92	0.11	26,26,26,26	0
56	MG	DA	3451	1/1	0.92	0.15	56,56,56,56	0
56	MG	DA	3173	1/1	0.92	0.10	49,49,49,49	0
56	MG	BA	3111	1/1	0.92	0.11	45,45,45,45	0
56	MG	BA	3733	1/1	0.92	0.10	78,78,78,78	0
56	MG	AA	3079	1/1	0.92	0.27	66,66,66,66	0
56	MG	BA	3200	1/1	0.92	0.08	50,50,50,50	0
56	MG	CA	3151	1/1	0.92	0.12	59,59,59,59	0
56	MG	DA	3183	1/1	0.92	0.13	57,57,57,57	0
56	MG	BA	3459	1/1	0.92	0.13	56,56,56,56	0
56	MG	CA	3032	1/1	0.92	0.20	52,52,52,52	0
56	MG	AX	3003	1/1	0.92	0.12	74,74,74,74	0
56	MG	DA	3469	1/1	0.92	0.10	56,56,56,56	0
59	ZN	D4	501	1/1	0.92	0.07	137,137,137,137	0
60	K	AX	3001	1/1	0.92	0.11	73,73,73,73	0
60	K	CX	3001	1/1	0.92	0.15	84,84,84,84	0
56	MG	AW	3002	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	BA	3033	1/1	0.93	0.12	45,45,45,45	0
56	MG	DA	3196	1/1	0.93	0.18	49,49,49,49	0
56	MG	CA	3033	1/1	0.93	0.13	44,44,44,44	0
56	MG	CA	3034	1/1	0.93	0.22	46,46,46,46	0
56	MG	CA	3160	1/1	0.93	0.20	53,53,53,53	0
56	MG	CA	3035	1/1	0.93	0.27	52,52,52,52	0
56	MG	DA	3467	1/1	0.93	0.15	69,69,69,69	0
56	MG	DA	3468	1/1	0.93	0.08	54,54,54,54	0
56	MG	BA	3036	1/1	0.93	0.24	50,50,50,50	0
56	MG	AW	3003	1/1	0.93	0.16	44,44,44,44	0
56	MG	DA	3212	1/1	0.93	0.13	52,52,52,52	0
56	MG	CA	3165	1/1	0.93	0.21	57,57,57,57	0
56	MG	DA	3214	1/1	0.93	0.20	58,58,58,58	0
56	MG	BA	3116	1/1	0.93	0.16	68,68,68,68	0
56	MG	DA	3219	1/1	0.93	0.06	35,35,35,35	0
56	MG	AA	3046	1/1	0.93	0.19	50,50,50,50	0
56	MG	DA	3479	1/1	0.93	0.11	52,52,52,52	0
56	MG	CA	3169	1/1	0.93	0.20	49,49,49,49	0
56	MG	BA	3046	1/1	0.93	0.21	50,50,50,50	0
56	MG	CD	301	1/1	0.93	0.09	67,67,67,67	0
56	MG	DA	3486	1/1	0.93	0.10	47,47,47,47	0
56	MG	DA	3225	1/1	0.93	0.23	56,56,56,56	0
56	MG	AA	3061	1/1	0.93	0.11	44,44,44,44	0
56	MG	BA	3137	1/1	0.93	0.13	41,41,41,41	0
56	MG	BA	3643	1/1	0.93	0.23	38,38,38,38	0
56	MG	DA	3237	1/1	0.93	0.08	42,42,42,42	0
56	MG	BA	3139	1/1	0.93	0.17	52,52,52,52	0
56	MG	DA	3239	1/1	0.93	0.11	61,61,61,61	0
56	MG	BA	3645	1/1	0.93	0.18	47,47,47,47	0
56	MG	DA	3499	1/1	0.93	0.10	60,60,60,60	0
56	MG	BA	3222	1/1	0.93	0.19	60,60,60,60	0
56	MG	BA	3545	1/1	0.93	0.10	58,58,58,58	0
56	MG	BA	3141	1/1	0.93	0.20	55,55,55,55	0
56	MG	BA	3761	1/1	0.93	0.21	65,65,65,65	0
56	MG	DA	3007	1/1	0.93	0.29	53,53,53,53	0
56	MG	DA	3510	1/1	0.93	0.09	32,32,32,32	0
56	MG	BA	3224	1/1	0.93	0.23	55,55,55,55	0
56	MG	DA	3253	1/1	0.93	0.21	57,57,57,57	0
56	MG	DA	3515	1/1	0.93	0.09	56,56,56,56	0
56	MG	DA	3254	1/1	0.93	0.10	53,53,53,53	0
56	MG	DA	3255	1/1	0.93	0.15	50,50,50,50	0
56	MG	AA	3062	1/1	0.93	0.25	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3773	1/1	0.93	0.17	43,43,43,43	0
56	MG	BA	3231	1/1	0.93	0.14	42,42,42,42	0
56	MG	AA	3125	1/1	0.93	0.10	53,53,53,53	0
56	MG	BA	3451	1/1	0.93	0.13	53,53,53,53	0
56	MG	BA	3783	1/1	0.93	0.16	36,36,36,36	0
56	MG	AA	3035	1/1	0.93	0.17	69,69,69,69	0
56	MG	BB	3002	1/1	0.93	0.24	51,51,51,51	0
56	MG	DA	3277	1/1	0.93	0.09	52,52,52,52	0
56	MG	CA	3063	1/1	0.93	0.19	59,59,59,59	0
56	MG	BA	3663	1/1	0.93	0.13	26,26,26,26	0
56	MG	BA	3342	1/1	0.93	0.11	43,43,43,43	0
56	MG	CA	3066	1/1	0.93	0.25	58,58,58,58	0
56	MG	BA	3560	1/1	0.93	0.15	47,47,47,47	0
56	MG	DA	3543	1/1	0.93	0.13	63,63,63,63	0
56	MG	DA	3544	1/1	0.93	0.17	49,49,49,49	0
56	MG	AX	3007	1/1	0.93	0.32	66,66,66,66	0
56	MG	DA	3044	1/1	0.93	0.42	60,60,60,60	0
56	MG	DA	3046	1/1	0.93	0.14	30,30,30,30	0
56	MG	BA	3345	1/1	0.93	0.12	20,20,20,20	0
56	MG	DA	3293	1/1	0.93	0.12	59,59,59,59	0
56	MG	AA	3110	1/1	0.93	0.09	53,53,53,53	0
56	MG	DA	3555	1/1	0.93	0.21	48,48,48,48	0
56	MG	BA	3565	1/1	0.93	0.12	50,50,50,50	0
56	MG	BA	3677	1/1	0.93	0.09	63,63,63,63	0
56	MG	BB	3017	1/1	0.93	0.10	48,48,48,48	0
56	MG	DA	3563	1/1	0.93	0.11	45,45,45,45	0
56	MG	BB	3018	1/1	0.93	0.08	46,46,46,46	0
56	MG	BA	3060	1/1	0.93	0.10	61,61,61,61	0
56	MG	BA	3063	1/1	0.93	0.08	39,39,39,39	0
56	MG	BA	3568	1/1	0.93	0.13	39,39,39,39	0
56	MG	DA	3570	1/1	0.93	0.09	62,62,62,62	0
56	MG	DA	3316	1/1	0.93	0.11	48,48,48,48	0
56	MG	DA	3060	1/1	0.93	0.14	50,50,50,50	0
56	MG	BA	3244	1/1	0.93	0.35	53,53,53,53	0
56	MG	AE	3001	1/1	0.93	0.07	77,77,77,77	0
56	MG	AX	3011	1/1	0.93	0.17	62,62,62,62	0
56	MG	BA	3248	1/1	0.93	0.10	27,27,27,27	0
56	MG	BA	3252	1/1	0.93	0.20	61,61,61,61	0
56	MG	DA	3325	1/1	0.93	0.06	32,32,32,32	0
56	MG	DA	3073	1/1	0.93	0.15	50,50,50,50	0
56	MG	DA	3075	1/1	0.93	0.11	51,51,51,51	0
56	MG	DA	3332	1/1	0.93	0.12	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	3076	1/1	0.93	0.24	34,34,34,34	0
56	MG	DA	3077	1/1	0.93	0.08	40,40,40,40	0
56	MG	BA	3693	1/1	0.93	0.10	38,38,38,38	0
56	MG	BF	301	1/1	0.93	0.18	39,39,39,39	0
56	MG	DA	3592	1/1	0.93	0.08	57,57,57,57	0
56	MG	BF	303	1/1	0.93	0.11	36,36,36,36	0
56	MG	BF	306	1/1	0.93	0.30	41,41,41,41	0
56	MG	AA	3098	1/1	0.93	0.22	59,59,59,59	0
56	MG	BF	311	1/1	0.93	0.23	60,60,60,60	0
56	MG	AA	3129	1/1	0.93	0.12	77,77,77,77	0
56	MG	AA	3006	1/1	0.93	0.08	57,57,57,57	0
56	MG	BA	3161	1/1	0.93	0.14	40,40,40,40	0
56	MG	AA	3200	1/1	0.93	0.16	61,61,61,61	0
56	MG	BA	3171	1/1	0.93	0.13	58,58,58,58	0
56	MG	AA	3026	1/1	0.93	0.20	68,68,68,68	0
56	MG	DA	3097	1/1	0.93	0.19	52,52,52,52	0
56	MG	BQ	3001	1/1	0.93	0.39	52,52,52,52	0
56	MG	DA	3610	1/1	0.93	0.07	65,65,65,65	0
56	MG	BQ	3005	1/1	0.93	0.14	49,49,49,49	0
56	MG	DA	3612	1/1	0.93	0.22	38,38,38,38	0
56	MG	BA	3263	1/1	0.93	0.19	47,47,47,47	0
56	MG	BA	3587	1/1	0.93	0.14	58,58,58,58	0
56	MG	DA	3366	1/1	0.93	0.12	36,36,36,36	0
56	MG	BA	3495	1/1	0.93	0.15	44,44,44,44	0
56	MG	BA	3177	1/1	0.93	0.15	58,58,58,58	0
56	MG	CA	3112	1/1	0.93	0.23	59,59,59,59	0
56	MG	DA	3370	1/1	0.93	0.17	49,49,49,49	0
56	MG	BV	207	1/1	0.93	0.17	42,42,42,42	0
56	MG	CA	3114	1/1	0.93	0.11	52,52,52,52	0
56	MG	DA	3374	1/1	0.93	0.15	52,52,52,52	0
56	MG	BA	3498	1/1	0.93	0.07	70,70,70,70	0
56	MG	BA	3592	1/1	0.93	0.18	61,61,61,61	0
56	MG	DA	3378	1/1	0.93	0.22	51,51,51,51	0
56	MG	DA	3380	1/1	0.93	0.10	43,43,43,43	0
56	MG	BA	3500	1/1	0.93	0.10	37,37,37,37	0
56	MG	BA	3501	1/1	0.93	0.13	74,74,74,74	0
56	MG	DB	3008	1/1	0.93	0.09	62,62,62,62	0
56	MG	AA	3013	1/1	0.93	0.12	66,66,66,66	0
56	MG	DA	3387	1/1	0.93	0.12	47,47,47,47	0
56	MG	B3	3001	1/1	0.93	0.14	41,41,41,41	0
56	MG	DD	301	1/1	0.93	0.25	44,44,44,44	0
56	MG	DD	307	1/1	0.93	0.21	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	DD	308	1/1	0.93	0.20	45,45,45,45	0
56	MG	BA	3182	1/1	0.93	0.33	50,50,50,50	0
56	MG	DA	3129	1/1	0.93	0.18	42,42,42,42	0
56	MG	BA	3084	1/1	0.93	0.14	46,46,46,46	0
56	MG	BA	3186	1/1	0.93	0.30	59,59,59,59	0
56	MG	BA	3604	1/1	0.93	0.16	46,46,46,46	0
56	MG	DF	303	1/1	0.93	0.12	46,46,46,46	0
56	MG	DA	3403	1/1	0.93	0.19	54,54,54,54	0
56	MG	DF	305	1/1	0.93	0.11	45,45,45,45	0
56	MG	DF	306	1/1	0.93	0.38	55,55,55,55	0
56	MG	DA	3137	1/1	0.93	0.07	57,57,57,57	0
56	MG	DA	3138	1/1	0.93	0.09	46,46,46,46	0
56	MG	DA	3407	1/1	0.93	0.19	41,41,41,41	0
56	MG	BA	3287	1/1	0.93	0.07	21,21,21,21	0
56	MG	BA	3719	1/1	0.93	0.15	49,49,49,49	0
56	MG	DA	3413	1/1	0.93	0.13	40,40,40,40	0
56	MG	BA	3606	1/1	0.93	0.19	62,62,62,62	0
56	MG	DA	3416	1/1	0.93	0.07	39,39,39,39	0
56	MG	DU	3002	1/1	0.93	0.35	58,58,58,58	0
56	MG	AA	3182	1/1	0.93	0.11	76,76,76,76	0
56	MG	BA	3012	1/1	0.93	0.12	49,49,49,49	0
56	MG	DA	3421	1/1	0.93	0.12	55,55,55,55	0
56	MG	CA	3135	1/1	0.93	0.16	75,75,75,75	0
56	MG	AA	3073	1/1	0.93	0.25	60,60,60,60	0
56	MG	D3	3001	1/1	0.93	0.20	70,70,70,70	0
56	MG	DA	3158	1/1	0.93	0.11	55,55,55,55	0
56	MG	CA	3138	1/1	0.93	0.14	52,52,52,52	0
56	MG	CA	3010	1/1	0.93	0.15	60,60,60,60	0
56	MG	BA	3091	1/1	0.93	0.24	43,43,43,43	0
56	MG	DA	3431	1/1	0.93	0.12	44,44,44,44	0
56	MG	BA	3612	1/1	0.93	0.20	65,65,65,65	0
56	MG	AA	3028	1/1	0.93	0.18	46,46,46,46	0
56	MG	CA	3014	1/1	0.93	0.10	46,46,46,46	0
56	MG	BA	3614	1/1	0.93	0.14	54,54,54,54	0
56	MG	BA	3105	1/1	0.93	0.09	43,43,43,43	0
56	MG	BA	3408	1/1	0.93	0.15	71,71,71,71	0
56	MG	DA	3174	1/1	0.93	0.08	42,42,42,42	0
56	MG	BA	3107	1/1	0.93	0.30	49,49,49,49	0
56	MG	CA	3020	1/1	0.93	0.08	48,48,48,48	0
56	MG	BA	3413	1/1	0.93	0.15	53,53,53,53	0
56	MG	CA	3024	1/1	0.93	0.16	53,53,53,53	0
56	MG	DA	3446	1/1	0.93	0.07	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	3202	1/1	0.93	0.10	41,41,41,41	0
56	MG	DA	3449	1/1	0.93	0.14	49,49,49,49	0
56	MG	DA	3181	1/1	0.93	0.35	50,50,50,50	0
56	MG	AA	3033	1/1	0.93	0.28	45,45,45,45	0
56	MG	BA	3626	1/1	0.93	0.12	40,40,40,40	0
56	MG	DA	3187	1/1	0.93	0.08	41,41,41,41	0
56	MG	BA	3207	1/1	0.93	0.14	52,52,52,52	0
56	MG	BA	3396	1/1	0.94	0.10	24,24,24,24	0
56	MG	DA	3031	1/1	0.94	0.15	51,51,51,51	0
56	MG	DA	3035	1/1	0.94	0.19	39,39,39,39	0
56	MG	BA	3593	1/1	0.94	0.24	53,53,53,53	0
56	MG	DA	3481	1/1	0.94	0.16	51,51,51,51	0
56	MG	DA	3482	1/1	0.94	0.12	42,42,42,42	0
56	MG	BF	308	1/1	0.94	0.28	40,40,40,40	0
56	MG	CA	3077	1/1	0.94	0.10	36,36,36,36	0
56	MG	DA	3041	1/1	0.94	0.09	51,51,51,51	0
56	MG	AA	3097	1/1	0.94	0.19	45,45,45,45	0
56	MG	DA	3249	1/1	0.94	0.08	43,43,43,43	0
56	MG	AA	3213	1/1	0.94	0.12	44,44,44,44	0
56	MG	BA	3598	1/1	0.94	0.11	58,58,58,58	0
56	MG	BA	3061	1/1	0.94	0.18	48,48,48,48	0
56	MG	DA	3493	1/1	0.94	0.14	64,64,64,64	0
56	MG	CA	3083	1/1	0.94	0.06	58,58,58,58	0
56	MG	DA	3256	1/1	0.94	0.15	48,48,48,48	0
56	MG	AA	3023	1/1	0.94	0.11	51,51,51,51	0
56	MG	BN	3005	1/1	0.94	0.11	46,46,46,46	0
56	MG	BN	3006	1/1	0.94	0.20	54,54,54,54	0
56	MG	BA	3708	1/1	0.94	0.06	7,7,7,7	0
56	MG	AA	3024	1/1	0.94	0.08	49,49,49,49	0
56	MG	DA	3271	1/1	0.94	0.12	51,51,51,51	0
56	MG	BA	3404	1/1	0.94	0.06	59,59,59,59	0
56	MG	BQ	3003	1/1	0.94	0.10	67,67,67,67	0
56	MG	BA	3405	1/1	0.94	0.09	47,47,47,47	0
56	MG	BA	3511	1/1	0.94	0.12	31,31,31,31	0
56	MG	AA	3114	1/1	0.94	0.19	66,66,66,66	0
56	MG	DA	3065	1/1	0.94	0.14	56,56,56,56	0
56	MG	BT	201	1/1	0.94	0.25	49,49,49,49	0
56	MG	DA	3067	1/1	0.94	0.08	52,52,52,52	0
56	MG	BA	3513	1/1	0.94	0.13	42,42,42,42	0
56	MG	DA	3069	1/1	0.94	0.19	49,49,49,49	0
56	MG	DA	3071	1/1	0.94	0.20	43,43,43,43	0
56	MG	BU	206	1/1	0.94	0.32	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	AA	3085	1/1	0.94	0.25	63,63,63,63	0
56	MG	BV	204	1/1	0.94	0.10	39,39,39,39	0
56	MG	AA	3021	1/1	0.94	0.24	60,60,60,60	0
56	MG	DA	3529	1/1	0.94	0.09	55,55,55,55	0
56	MG	DA	3530	1/1	0.94	0.18	69,69,69,69	0
56	MG	BW	201	1/1	0.94	0.17	45,45,45,45	0
56	MG	BA	3076	1/1	0.94	0.07	58,58,58,58	0
56	MG	BA	3311	1/1	0.94	0.17	34,34,34,34	0
56	MG	DA	3536	1/1	0.94	0.10	39,39,39,39	0
56	MG	DA	3538	1/1	0.94	0.08	50,50,50,50	0
56	MG	DA	3080	1/1	0.94	0.18	48,48,48,48	0
56	MG	DA	3305	1/1	0.94	0.12	42,42,42,42	0
56	MG	CA	3108	1/1	0.94	0.20	56,56,56,56	0
56	MG	AA	3158	1/1	0.94	0.16	62,62,62,62	0
56	MG	BA	3313	1/1	0.94	0.07	32,32,32,32	0
56	MG	BA	3318	1/1	0.94	0.06	36,36,36,36	0
56	MG	AA	3137	1/1	0.94	0.10	49,49,49,49	0
56	MG	DA	3089	1/1	0.94	0.23	57,57,57,57	0
56	MG	AA	3071	1/1	0.94	0.15	52,52,52,52	0
56	MG	AA	3161	1/1	0.94	0.07	59,59,59,59	0
56	MG	BA	3619	1/1	0.94	0.09	49,49,49,49	0
56	MG	BA	3421	1/1	0.94	0.09	46,46,46,46	0
56	MG	DA	3095	1/1	0.94	0.11	54,54,54,54	0
56	MG	DA	3556	1/1	0.94	0.12	48,48,48,48	0
56	MG	DA	3326	1/1	0.94	0.10	31,31,31,31	0
56	MG	B7	103	1/1	0.94	0.12	69,69,69,69	0
56	MG	BA	3531	1/1	0.94	0.10	56,56,56,56	0
56	MG	B9	502	1/1	0.94	0.17	61,61,61,61	0
56	MG	DA	3100	1/1	0.94	0.22	45,45,45,45	0
56	MG	AA	3162	1/1	0.94	0.14	70,70,70,70	0
56	MG	DA	3567	1/1	0.94	0.10	52,52,52,52	0
56	MG	CA	3002	1/1	0.94	0.12	65,65,65,65	0
56	MG	AA	3194	1/1	0.94	0.10	66,66,66,66	0
56	MG	DA	3107	1/1	0.94	0.11	47,47,47,47	0
56	MG	DA	3343	1/1	0.94	0.12	57,57,57,57	0
56	MG	BA	3629	1/1	0.94	0.15	62,62,62,62	0
56	MG	CA	3006	1/1	0.94	0.25	50,50,50,50	0
56	MG	DA	3110	1/1	0.94	0.08	30,30,30,30	0
56	MG	DA	3111	1/1	0.94	0.06	49,49,49,49	0
56	MG	DA	3112	1/1	0.94	0.28	49,49,49,49	0
56	MG	BA	3240	1/1	0.94	0.14	43,43,43,43	0
56	MG	DA	3115	1/1	0.94	0.06	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	3023	1/1	0.94	0.08	38,38,38,38	0
56	MG	DA	3117	1/1	0.94	0.09	46,46,46,46	0
56	MG	CA	3129	1/1	0.94	0.15	49,49,49,49	0
56	MG	DA	3359	1/1	0.94	0.10	54,54,54,54	0
56	MG	BA	3165	1/1	0.94	0.10	53,53,53,53	0
56	MG	CA	3132	1/1	0.94	0.10	54,54,54,54	0
56	MG	AA	3163	1/1	0.94	0.29	53,53,53,53	0
56	MG	BA	3439	1/1	0.94	0.09	15,15,15,15	0
56	MG	AA	3037	1/1	0.94	0.20	55,55,55,55	0
56	MG	BA	3172	1/1	0.94	0.14	58,58,58,58	0
56	MG	BA	3092	1/1	0.94	0.06	27,27,27,27	0
56	MG	BA	3640	1/1	0.94	0.17	61,61,61,61	0
56	MG	BA	3032	1/1	0.94	0.15	32,32,32,32	0
56	MG	BA	3547	1/1	0.94	0.14	47,47,47,47	0
56	MG	DA	3372	1/1	0.94	0.07	67,67,67,67	0
56	MG	BA	3178	1/1	0.94	0.20	43,43,43,43	0
56	MG	BA	3549	1/1	0.94	0.14	53,53,53,53	0
56	MG	DA	3375	1/1	0.94	0.22	42,42,42,42	0
56	MG	CA	3144	1/1	0.94	0.10	54,54,54,54	0
56	MG	BA	3646	1/1	0.94	0.22	48,48,48,48	0
56	MG	DA	3607	1/1	0.94	0.09	60,60,60,60	0
56	MG	DA	3608	1/1	0.94	0.07	47,47,47,47	0
56	MG	BA	3647	1/1	0.94	0.13	48,48,48,48	0
56	MG	DA	3141	1/1	0.94	0.14	56,56,56,56	0
56	MG	DA	3142	1/1	0.94	0.16	55,55,55,55	0
56	MG	DA	3382	1/1	0.94	0.28	53,53,53,53	0
56	MG	BA	3253	1/1	0.94	0.11	30,30,30,30	0
56	MG	DA	3145	1/1	0.94	0.13	61,61,61,61	0
56	MG	BA	3098	1/1	0.94	0.08	51,51,51,51	0
56	MG	DA	3389	1/1	0.94	0.15	63,63,63,63	0
56	MG	DA	3618	1/1	0.94	0.16	57,57,57,57	0
56	MG	DA	3390	1/1	0.94	0.16	48,48,48,48	0
56	MG	BA	3255	1/1	0.94	0.28	56,56,56,56	0
56	MG	BA	3104	1/1	0.94	0.36	44,44,44,44	0
56	MG	BA	3762	1/1	0.94	0.15	58,58,58,58	0
56	MG	DA	3152	1/1	0.94	0.25	53,53,53,53	0
56	MG	DA	3153	1/1	0.94	0.06	40,40,40,40	0
56	MG	DA	3400	1/1	0.94	0.10	61,61,61,61	0
56	MG	AA	3039	1/1	0.94	0.20	57,57,57,57	0
56	MG	BA	3770	1/1	0.94	0.09	20,20,20,20	0
56	MG	AA	3060	1/1	0.94	0.10	42,42,42,42	0
56	MG	DA	3164	1/1	0.94	0.15	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3772	1/1	0.94	0.10	52,52,52,52	0
56	MG	AA	3169	1/1	0.94	0.09	57,57,57,57	0
56	MG	BA	3042	1/1	0.94	0.11	54,54,54,54	0
56	MG	DB	3011	1/1	0.94	0.08	49,49,49,49	0
56	MG	BA	3661	1/1	0.94	0.13	61,61,61,61	0
56	MG	CA	3041	1/1	0.94	0.14	63,63,63,63	0
56	MG	AA	3143	1/1	0.94	0.10	57,57,57,57	0
56	MG	BA	3362	1/1	0.94	0.12	25,25,25,25	0
56	MG	BA	3784	1/1	0.94	0.09	62,62,62,62	0
56	MG	DA	3419	1/1	0.94	0.16	59,59,59,59	0
56	MG	DE	303	1/1	0.94	0.11	40,40,40,40	0
56	MG	BA	3785	1/1	0.94	0.24	42,42,42,42	0
56	MG	BA	3262	1/1	0.94	0.10	51,51,51,51	0
56	MG	DA	3423	1/1	0.94	0.15	34,34,34,34	0
56	MG	DA	3424	1/1	0.94	0.19	35,35,35,35	0
56	MG	BA	3467	1/1	0.94	0.14	48,48,48,48	0
56	MG	AA	3173	1/1	0.94	0.24	55,55,55,55	0
56	MG	DA	3179	1/1	0.94	0.25	61,61,61,61	0
56	MG	BA	3197	1/1	0.94	0.20	46,46,46,46	0
56	MG	BA	3367	1/1	0.94	0.12	58,58,58,58	0
56	MG	AA	3040	1/1	0.94	0.07	41,41,41,41	0
56	MG	CF	3001	1/1	0.94	0.14	44,44,44,44	0
56	MG	BA	3371	1/1	0.94	0.14	50,50,50,50	0
56	MG	DA	3434	1/1	0.94	0.13	46,46,46,46	0
56	MG	DA	3435	1/1	0.94	0.20	59,59,59,59	0
56	MG	BA	3278	1/1	0.94	0.10	48,48,48,48	0
56	MG	DA	3190	1/1	0.94	0.17	58,58,58,58	0
56	MG	DA	3191	1/1	0.94	0.18	35,35,35,35	0
56	MG	CT	3001	1/1	0.94	0.13	50,50,50,50	0
56	MG	AA	3078	1/1	0.94	0.24	59,59,59,59	0
56	MG	DW	3003	1/1	0.94	0.11	71,71,71,71	0
56	MG	DW	3004	1/1	0.94	0.06	50,50,50,50	0
56	MG	AA	3022	1/1	0.94	0.17	58,58,58,58	0
56	MG	BA	3119	1/1	0.94	0.11	44,44,44,44	0
56	MG	BA	3688	1/1	0.94	0.08	24,24,24,24	0
56	MG	BA	3127	1/1	0.94	0.19	38,38,38,38	0
56	MG	DA	3202	1/1	0.94	0.21	51,51,51,51	0
56	MG	BA	3486	1/1	0.94	0.13	30,30,30,30	0
56	MG	BA	3490	1/1	0.94	0.06	66,66,66,66	0
56	MG	BA	3491	1/1	0.94	0.10	52,52,52,52	0
56	MG	DA	3208	1/1	0.94	0.32	61,61,61,61	0
56	MG	DA	3209	1/1	0.94	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	DA	3455	1/1	0.94	0.17	50,50,50,50	0
56	MG	DA	3211	1/1	0.94	0.34	49,49,49,49	0
56	MG	BA	3388	1/1	0.94	0.11	40,40,40,40	0
56	MG	BA	3128	1/1	0.94	0.11	46,46,46,46	0
56	MG	DA	3011	1/1	0.94	0.10	46,46,46,46	0
56	MG	BA	3132	1/1	0.94	0.16	42,42,42,42	0
56	MG	AA	3147	1/1	0.94	0.10	47,47,47,47	0
56	MG	DA	3015	1/1	0.94	0.19	49,49,49,49	0
56	MG	DA	3016	1/1	0.94	0.15	34,34,34,34	0
56	MG	DA	3022	1/1	0.94	0.10	50,50,50,50	0
56	MG	BA	3589	1/1	0.94	0.08	41,41,41,41	0
56	MG	BA	3297	1/1	0.94	0.10	45,45,45,45	0
56	MG	AA	3049	1/1	0.94	0.15	59,59,59,59	0
56	MG	DA	3229	1/1	0.94	0.11	49,49,49,49	0
56	MG	CA	3071	1/1	0.94	0.19	58,58,58,58	0
56	MG	CA	3072	1/1	0.94	0.13	57,57,57,57	0
56	MG	BF	305	1/1	0.94	0.20	40,40,40,40	0
56	MG	BA	3520	1/1	0.95	0.14	25,25,25,25	0
56	MG	DA	3492	1/1	0.95	0.12	51,51,51,51	0
56	MG	DA	3088	1/1	0.95	0.08	39,39,39,39	0
56	MG	B3	3002	1/1	0.95	0.10	65,65,65,65	0
56	MG	BA	3144	1/1	0.95	0.11	37,37,37,37	0
56	MG	BA	3216	1/1	0.95	0.15	53,53,53,53	0
56	MG	DA	3497	1/1	0.95	0.08	27,27,27,27	0
56	MG	B5	103	1/1	0.95	0.15	51,51,51,51	0
56	MG	BA	3732	1/1	0.95	0.13	57,57,57,57	0
56	MG	BA	3623	1/1	0.95	0.08	59,59,59,59	0
56	MG	B7	102	1/1	0.95	0.20	40,40,40,40	0
56	MG	BA	3034	1/1	0.95	0.09	34,34,34,34	0
56	MG	BA	3035	1/1	0.95	0.13	25,25,25,25	0
56	MG	DA	3507	1/1	0.95	0.09	54,54,54,54	0
56	MG	BA	3627	1/1	0.95	0.09	52,52,52,52	0
56	MG	DA	3301	1/1	0.95	0.10	60,60,60,60	0
56	MG	DA	3511	1/1	0.95	0.10	62,62,62,62	0
56	MG	DA	3102	1/1	0.95	0.08	50,50,50,50	0
56	MG	DA	3304	1/1	0.95	0.08	32,32,32,32	0
56	MG	AA	3072	1/1	0.95	0.20	48,48,48,48	0
56	MG	CA	3130	1/1	0.95	0.19	70,70,70,70	0
56	MG	BA	3085	1/1	0.95	0.12	50,50,50,50	0
56	MG	DA	3310	1/1	0.95	0.08	39,39,39,39	0
56	MG	CA	3003	1/1	0.95	0.14	65,65,65,65	0
56	MG	DA	3312	1/1	0.95	0.11	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3314	1/1	0.95	0.06	46,46,46,46	0
56	MG	BA	3039	1/1	0.95	0.15	34,34,34,34	0
56	MG	BA	3225	1/1	0.95	0.06	43,43,43,43	0
56	MG	BA	3632	1/1	0.95	0.15	53,53,53,53	0
56	MG	BA	3226	1/1	0.95	0.12	32,32,32,32	0
56	MG	CA	3008	1/1	0.95	0.11	45,45,45,45	0
56	MG	AA	3148	1/1	0.95	0.17	50,50,50,50	0
56	MG	BA	3635	1/1	0.95	0.07	56,56,56,56	0
56	MG	BA	3428	1/1	0.95	0.15	42,42,42,42	0
56	MG	BA	3229	1/1	0.95	0.06	38,38,38,38	0
56	MG	DA	3328	1/1	0.95	0.14	49,49,49,49	0
56	MG	BA	3088	1/1	0.95	0.10	46,46,46,46	0
56	MG	BA	3431	1/1	0.95	0.08	54,54,54,54	0
56	MG	AA	3191	1/1	0.95	0.09	49,49,49,49	0
56	MG	BA	3090	1/1	0.95	0.15	40,40,40,40	0
56	MG	DA	3123	1/1	0.95	0.12	40,40,40,40	0
56	MG	BA	3436	1/1	0.95	0.12	67,67,67,67	0
56	MG	DA	3339	1/1	0.95	0.16	46,46,46,46	0
56	MG	AA	3053	1/1	0.95	0.09	41,41,41,41	0
56	MG	DA	3341	1/1	0.95	0.08	54,54,54,54	0
56	MG	DA	3549	1/1	0.95	0.16	53,53,53,53	0
56	MG	BA	3236	1/1	0.95	0.07	34,34,34,34	0
56	MG	DA	3552	1/1	0.95	0.09	43,43,43,43	0
56	MG	AA	3010	1/1	0.95	0.06	22,22,22,22	0
56	MG	DA	3128	1/1	0.95	0.16	45,45,45,45	0
56	MG	CA	3022	1/1	0.95	0.12	53,53,53,53	0
56	MG	BA	3094	1/1	0.95	0.36	49,49,49,49	0
56	MG	DA	3557	1/1	0.95	0.16	67,67,67,67	0
56	MG	BA	3096	1/1	0.95	0.07	29,29,29,29	0
56	MG	DA	3559	1/1	0.95	0.10	49,49,49,49	0
56	MG	BA	3336	1/1	0.95	0.11	31,31,31,31	0
56	MG	BA	3769	1/1	0.95	0.12	52,52,52,52	0
56	MG	BA	3163	1/1	0.95	0.20	57,57,57,57	0
56	MG	BA	3448	1/1	0.95	0.27	60,60,60,60	0
56	MG	BA	3001	1/1	0.95	0.09	23,23,23,23	0
56	MG	BA	3245	1/1	0.95	0.09	47,47,47,47	0
56	MG	BA	3774	1/1	0.95	0.30	32,32,32,32	0
56	MG	CA	3161	1/1	0.95	0.15	59,59,59,59	0
56	MG	AA	3211	1/1	0.95	0.15	41,41,41,41	0
56	MG	BA	3659	1/1	0.95	0.11	24,24,24,24	0
56	MG	BA	3777	1/1	0.95	0.31	40,40,40,40	0
56	MG	BA	3778	1/1	0.95	0.07	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3149	1/1	0.95	0.25	48,48,48,48	0
56	MG	BA	3099	1/1	0.95	0.12	58,58,58,58	0
56	MG	DA	3576	1/1	0.95	0.12	46,46,46,46	0
56	MG	BA	3456	1/1	0.95	0.10	63,63,63,63	0
56	MG	BA	3562	1/1	0.95	0.18	37,37,37,37	0
56	MG	DA	3156	1/1	0.95	0.19	45,45,45,45	0
56	MG	BA	3100	1/1	0.95	0.12	46,46,46,46	0
56	MG	DA	3159	1/1	0.95	0.25	60,60,60,60	0
56	MG	DA	3583	1/1	0.95	0.10	44,44,44,44	0
56	MG	BA	3664	1/1	0.95	0.07	25,25,25,25	0
56	MG	CE	3001	1/1	0.95	0.12	73,73,73,73	0
56	MG	DA	3587	1/1	0.95	0.11	45,45,45,45	0
56	MG	BA	3344	1/1	0.95	0.10	36,36,36,36	0
56	MG	BA	3249	1/1	0.95	0.10	33,33,33,33	0
56	MG	CK	3001	1/1	0.95	0.12	47,47,47,47	0
56	MG	DA	3591	1/1	0.95	0.12	46,46,46,46	0
56	MG	DA	3379	1/1	0.95	0.14	38,38,38,38	0
56	MG	BA	3250	1/1	0.95	0.15	40,40,40,40	0
56	MG	DA	3594	1/1	0.95	0.18	52,52,52,52	0
56	MG	BA	3350	1/1	0.95	0.07	43,43,43,43	0
56	MG	BA	3671	1/1	0.95	0.07	33,33,33,33	0
56	MG	DA	3383	1/1	0.95	0.19	40,40,40,40	0
56	MG	CA	3050	1/1	0.95	0.10	55,55,55,55	0
56	MG	BB	3009	1/1	0.95	0.09	49,49,49,49	0
56	MG	DA	3600	1/1	0.95	0.13	55,55,55,55	0
56	MG	DA	3386	1/1	0.95	0.12	59,59,59,59	0
56	MG	BA	3672	1/1	0.95	0.23	37,37,37,37	0
56	MG	BA	3103	1/1	0.95	0.08	45,45,45,45	0
56	MG	AA	3056	1/1	0.95	0.19	56,56,56,56	0
56	MG	BA	3009	1/1	0.95	0.15	41,41,41,41	0
56	MG	DA	3006	1/1	0.95	0.20	42,42,42,42	0
56	MG	AA	3195	1/1	0.95	0.15	58,58,58,58	0
56	MG	BA	3469	1/1	0.95	0.14	49,49,49,49	0
56	MG	DA	3609	1/1	0.95	0.09	47,47,47,47	0
56	MG	BA	3683	1/1	0.95	0.26	50,50,50,50	0
56	MG	BA	3685	1/1	0.95	0.07	43,43,43,43	0
56	MG	BD	304	1/1	0.95	0.11	50,50,50,50	0
56	MG	DA	3402	1/1	0.95	0.13	57,57,57,57	0
56	MG	AA	3018	1/1	0.95	0.07	58,58,58,58	0
56	MG	BA	3056	1/1	0.95	0.15	26,26,26,26	0
56	MG	BA	3474	1/1	0.95	0.09	37,37,37,37	0
56	MG	DA	3019	1/1	0.95	0.08	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3192	1/1	0.95	0.17	49,49,49,49	0
56	MG	DA	3410	1/1	0.95	0.06	37,37,37,37	0
56	MG	BA	3361	1/1	0.95	0.08	29,29,29,29	0
56	MG	DA	3412	1/1	0.95	0.09	52,52,52,52	0
56	MG	DA	3194	1/1	0.95	0.14	52,52,52,52	0
56	MG	BA	3057	1/1	0.95	0.15	48,48,48,48	0
56	MG	BA	3059	1/1	0.95	0.07	40,40,40,40	0
56	MG	BA	3583	1/1	0.95	0.09	46,46,46,46	0
56	MG	BA	3013	1/1	0.95	0.22	46,46,46,46	0
56	MG	BA	3014	1/1	0.95	0.11	46,46,46,46	0
56	MG	BF	304	1/1	0.95	0.23	37,37,37,37	0
56	MG	DA	3204	1/1	0.95	0.09	47,47,47,47	0
56	MG	AA	3038	1/1	0.95	0.27	56,56,56,56	0
56	MG	BA	3064	1/1	0.95	0.11	46,46,46,46	0
56	MG	DA	3033	1/1	0.95	0.12	43,43,43,43	0
56	MG	BA	3264	1/1	0.95	0.09	19,19,19,19	0
56	MG	BA	3121	1/1	0.95	0.13	64,64,64,64	0
56	MG	DA	3210	1/1	0.95	0.14	35,35,35,35	0
56	MG	DD	302	1/1	0.95	0.08	40,40,40,40	0
56	MG	BF	310	1/1	0.95	0.07	44,44,44,44	0
56	MG	DA	3038	1/1	0.95	0.14	56,56,56,56	0
56	MG	BA	3699	1/1	0.95	0.06	39,39,39,39	0
56	MG	CA	3078	1/1	0.95	0.07	41,41,41,41	0
56	MG	DA	3215	1/1	0.95	0.29	53,53,53,53	0
56	MG	BA	3266	1/1	0.95	0.07	38,38,38,38	0
56	MG	BA	3271	1/1	0.95	0.16	39,39,39,39	0
56	MG	DA	3045	1/1	0.95	0.06	44,44,44,44	0
56	MG	BA	3274	1/1	0.95	0.07	29,29,29,29	0
56	MG	BN	3003	1/1	0.95	0.13	62,62,62,62	0
56	MG	BA	3384	1/1	0.95	0.08	43,43,43,43	0
56	MG	DA	3049	1/1	0.95	0.07	48,48,48,48	0
56	MG	CA	3084	1/1	0.95	0.11	46,46,46,46	0
56	MG	DN	5001	1/1	0.95	0.08	75,75,75,75	0
56	MG	DA	3228	1/1	0.95	0.10	29,29,29,29	0
56	MG	DA	3052	1/1	0.95	0.17	44,44,44,44	0
56	MG	DA	3053	1/1	0.95	0.18	61,61,61,61	0
56	MG	BA	3125	1/1	0.95	0.15	34,34,34,34	0
56	MG	BA	3497	1/1	0.95	0.10	24,24,24,24	0
56	MG	BA	3018	1/1	0.95	0.15	36,36,36,36	0
56	MG	BP	203	1/1	0.95	0.09	37,37,37,37	0
56	MG	BA	3279	1/1	0.95	0.10	52,52,52,52	0
56	MG	AA	3181	1/1	0.95	0.12	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3203	1/1	0.95	0.27	51,51,51,51	0
56	MG	BQ	3004	1/1	0.95	0.23	48,48,48,48	0
56	MG	BA	3130	1/1	0.95	0.10	44,44,44,44	0
56	MG	DA	3063	1/1	0.95	0.09	52,52,52,52	0
56	MG	BA	3286	1/1	0.95	0.05	48,48,48,48	0
56	MG	BA	3206	1/1	0.95	0.24	49,49,49,49	0
56	MG	BA	3506	1/1	0.95	0.07	43,43,43,43	0
56	MG	BA	3288	1/1	0.95	0.09	36,36,36,36	0
56	MG	BU	204	1/1	0.95	0.11	43,43,43,43	0
56	MG	AA	3005	1/1	0.95	0.25	55,55,55,55	0
56	MG	AA	3012	1/1	0.95	0.17	43,43,43,43	0
56	MG	DA	3258	1/1	0.95	0.05	24,24,24,24	0
56	MG	DA	3259	1/1	0.95	0.09	50,50,50,50	0
56	MG	BA	3075	1/1	0.95	0.11	48,48,48,48	0
56	MG	BV	205	1/1	0.95	0.31	37,37,37,37	0
56	MG	DA	3263	1/1	0.95	0.08	48,48,48,48	0
56	MG	DA	3264	1/1	0.95	0.10	44,44,44,44	0
56	MG	DA	3265	1/1	0.95	0.09	47,47,47,47	0
56	MG	BA	3136	1/1	0.95	0.20	49,49,49,49	0
56	MG	DA	3268	1/1	0.95	0.18	53,53,53,53	0
56	MG	DA	3480	1/1	0.95	0.13	48,48,48,48	0
56	MG	AA	3157	1/1	0.95	0.11	46,46,46,46	0
56	MG	AA	3172	1/1	0.95	0.14	44,44,44,44	0
56	MG	BX	102	1/1	0.95	0.10	40,40,40,40	0
56	MG	AA	3081	1/1	0.95	0.14	52,52,52,52	0
56	MG	BA	3301	1/1	0.95	0.07	55,55,55,55	0
56	MG	BA	3143	1/1	0.95	0.20	35,35,35,35	0
56	MG	DA	3487	1/1	0.95	0.07	37,37,37,37	0
56	MG	DA	3278	1/1	0.95	0.07	44,44,44,44	0
56	MG	B1	101	1/1	0.95	0.26	45,45,45,45	0
56	MG	BA	3728	1/1	0.95	0.09	65,65,65,65	0
56	MG	AA	3090	1/1	0.96	0.27	50,50,50,50	0
56	MG	BA	3669	1/1	0.96	0.12	45,45,45,45	0
56	MG	BA	3146	1/1	0.96	0.07	36,36,36,36	0
56	MG	DA	3505	1/1	0.96	0.07	41,41,41,41	0
56	MG	BA	3067	1/1	0.96	0.11	35,35,35,35	0
56	MG	BA	3068	1/1	0.96	0.22	56,56,56,56	0
56	MG	DA	3509	1/1	0.96	0.11	38,38,38,38	0
56	MG	DA	3315	1/1	0.96	0.05	28,28,28,28	0
56	MG	BB	3004	1/1	0.96	0.13	64,64,64,64	0
56	MG	BA	3674	1/1	0.96	0.18	42,42,42,42	0
56	MG	BA	3280	1/1	0.96	0.10	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	3038	1/1	0.96	0.10	31,31,31,31	0
56	MG	DA	3516	1/1	0.96	0.08	35,35,35,35	0
56	MG	BA	3101	1/1	0.96	0.14	36,36,36,36	0
56	MG	BA	3150	1/1	0.96	0.06	47,47,47,47	0
56	MG	DA	3519	1/1	0.96	0.05	78,78,78,78	0
56	MG	DA	3136	1/1	0.96	0.13	35,35,35,35	0
56	MG	DA	3324	1/1	0.96	0.14	46,46,46,46	0
56	MG	CA	3166	1/1	0.96	0.05	42,42,42,42	0
56	MG	BB	3010	1/1	0.96	0.14	51,51,51,51	0
56	MG	BA	3678	1/1	0.96	0.09	41,41,41,41	0
56	MG	BA	3679	1/1	0.96	0.07	47,47,47,47	0
56	MG	BB	3014	1/1	0.96	0.05	39,39,39,39	0
56	MG	DA	3331	1/1	0.96	0.04	46,46,46,46	0
56	MG	CA	3180	1/1	0.96	0.17	61,61,61,61	0
56	MG	BA	3680	1/1	0.96	0.08	32,32,32,32	0
56	MG	BA	3472	1/1	0.96	0.11	43,43,43,43	0
56	MG	DA	3337	1/1	0.96	0.05	42,42,42,42	0
56	MG	BA	3473	1/1	0.96	0.12	31,31,31,31	0
56	MG	BA	3578	1/1	0.96	0.10	49,49,49,49	0
56	MG	AA	3171	1/1	0.96	0.09	56,56,56,56	0
56	MG	BA	3372	1/1	0.96	0.11	33,33,33,33	0
56	MG	DA	3150	1/1	0.96	0.09	49,49,49,49	0
56	MG	BA	3581	1/1	0.96	0.07	47,47,47,47	0
56	MG	CV	101	1/1	0.96	0.14	56,56,56,56	0
56	MG	BD	305	1/1	0.96	0.11	41,41,41,41	0
56	MG	BD	306	1/1	0.96	0.14	22,22,22,22	0
56	MG	DA	3347	1/1	0.96	0.08	53,53,53,53	0
56	MG	DA	3157	1/1	0.96	0.20	58,58,58,58	0
56	MG	BA	3003	1/1	0.96	0.07	43,43,43,43	0
56	MG	BA	3219	1/1	0.96	0.10	39,39,39,39	0
56	MG	DA	3551	1/1	0.96	0.11	66,66,66,66	0
56	MG	BD	311	1/1	0.96	0.27	46,46,46,46	0
56	MG	BA	3377	1/1	0.96	0.13	39,39,39,39	0
56	MG	BA	3481	1/1	0.96	0.12	32,32,32,32	0
56	MG	BA	3037	1/1	0.96	0.28	33,33,33,33	0
56	MG	DA	3358	1/1	0.96	0.07	51,51,51,51	0
56	MG	BA	3380	1/1	0.96	0.15	59,59,59,59	0
56	MG	BA	3106	1/1	0.96	0.12	42,42,42,42	0
56	MG	CA	3062	1/1	0.96	0.34	65,65,65,65	0
56	MG	DA	3560	1/1	0.96	0.10	59,59,59,59	0
56	MG	DA	3362	1/1	0.96	0.10	22,22,22,22	0
56	MG	BA	3485	1/1	0.96	0.08	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	DA	3364	1/1	0.96	0.25	54,54,54,54	0
56	MG	DA	3170	1/1	0.96	0.27	39,39,39,39	0
56	MG	BA	3382	1/1	0.96	0.11	30,30,30,30	0
56	MG	DA	3566	1/1	0.96	0.09	51,51,51,51	0
56	MG	BA	3487	1/1	0.96	0.13	37,37,37,37	0
56	MG	BA	3073	1/1	0.96	0.16	25,25,25,25	0
56	MG	BA	3386	1/1	0.96	0.19	36,36,36,36	0
56	MG	DA	3017	1/1	0.96	0.07	46,46,46,46	0
56	MG	AA	3185	1/1	0.96	0.19	51,51,51,51	0
56	MG	BA	3296	1/1	0.96	0.11	47,47,47,47	0
56	MG	AD	502	1/1	0.96	0.26	58,58,58,58	0
56	MG	BA	3390	1/1	0.96	0.13	26,26,26,26	0
56	MG	BG	3001	1/1	0.96	0.12	42,42,42,42	0
56	MG	DA	3182	1/1	0.96	0.11	52,52,52,52	0
56	MG	BA	3041	1/1	0.96	0.08	51,51,51,51	0
56	MG	BA	3392	1/1	0.96	0.07	17,17,17,17	0
56	MG	DA	3186	1/1	0.96	0.16	41,41,41,41	0
56	MG	BA	3499	1/1	0.96	0.08	57,57,57,57	0
56	MG	BA	3603	1/1	0.96	0.14	28,28,28,28	0
56	MG	BA	3160	1/1	0.96	0.17	58,58,58,58	0
56	MG	DA	3032	1/1	0.96	0.08	40,40,40,40	0
56	MG	BA	3228	1/1	0.96	0.30	51,51,51,51	0
56	MG	DA	3586	1/1	0.96	0.12	49,49,49,49	0
56	MG	AA	3052	1/1	0.96	0.12	52,52,52,52	0
56	MG	BA	3302	1/1	0.96	0.10	46,46,46,46	0
56	MG	BP	201	1/1	0.96	0.14	36,36,36,36	0
56	MG	BP	202	1/1	0.96	0.14	36,36,36,36	0
56	MG	BA	3230	1/1	0.96	0.21	53,53,53,53	0
56	MG	DA	3040	1/1	0.96	0.08	47,47,47,47	0
56	MG	BA	3044	1/1	0.96	0.14	39,39,39,39	0
56	MG	DA	3201	1/1	0.96	0.23	56,56,56,56	0
56	MG	BA	3114	1/1	0.96	0.22	49,49,49,49	0
56	MG	DA	3203	1/1	0.96	0.13	46,46,46,46	0
56	MG	DA	3043	1/1	0.96	0.09	49,49,49,49	0
56	MG	BA	3166	1/1	0.96	0.12	47,47,47,47	0
56	MG	BA	3115	1/1	0.96	0.07	13,13,13,13	0
56	MG	BA	3308	1/1	0.96	0.17	38,38,38,38	0
56	MG	DA	3404	1/1	0.96	0.07	36,36,36,36	0
56	MG	BA	3720	1/1	0.96	0.06	28,28,28,28	0
56	MG	BA	3079	1/1	0.96	0.23	40,40,40,40	0
56	MG	BR	203	1/1	0.96	0.18	36,36,36,36	0
56	MG	BA	3722	1/1	0.96	0.10	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	CA	3095	1/1	0.96	0.06	47,47,47,47	0
56	MG	BA	3239	1/1	0.96	0.17	30,30,30,30	0
56	MG	AA	3034	1/1	0.96	0.33	56,56,56,56	0
56	MG	AA	3066	1/1	0.96	0.07	53,53,53,53	0
56	MG	BA	3409	1/1	0.96	0.11	43,43,43,43	0
56	MG	DA	3415	1/1	0.96	0.28	45,45,45,45	0
56	MG	BA	3120	1/1	0.96	0.13	45,45,45,45	0
56	MG	BA	3621	1/1	0.96	0.07	48,48,48,48	0
56	MG	CA	3102	1/1	0.96	0.08	48,48,48,48	0
56	MG	DA	3222	1/1	0.96	0.10	46,46,46,46	0
56	MG	BV	206	1/1	0.96	0.09	38,38,38,38	0
56	MG	BA	3622	1/1	0.96	0.08	48,48,48,48	0
56	MG	BA	3317	1/1	0.96	0.10	47,47,47,47	0
56	MG	BW	202	1/1	0.96	0.13	43,43,43,43	0
56	MG	DA	3064	1/1	0.96	0.17	52,52,52,52	0
56	MG	BW	203	1/1	0.96	0.08	42,42,42,42	0
56	MG	BW	204	1/1	0.96	0.17	41,41,41,41	0
56	MG	BA	3083	1/1	0.96	0.13	30,30,30,30	0
56	MG	DA	3234	1/1	0.96	0.10	42,42,42,42	0
56	MG	DA	3236	1/1	0.96	0.09	59,59,59,59	0
56	MG	BA	3319	1/1	0.96	0.12	38,38,38,38	0
56	MG	BA	3123	1/1	0.96	0.28	39,39,39,39	0
56	MG	BA	3181	1/1	0.96	0.10	48,48,48,48	0
56	MG	DA	3240	1/1	0.96	0.12	36,36,36,36	0
56	MG	BA	3324	1/1	0.96	0.08	44,44,44,44	0
56	MG	BA	3525	1/1	0.96	0.06	40,40,40,40	0
56	MG	DA	3074	1/1	0.96	0.13	49,49,49,49	0
56	MG	CA	3115	1/1	0.96	0.06	58,58,58,58	0
56	MG	DA	3440	1/1	0.96	0.12	49,49,49,49	0
56	MG	CA	3116	1/1	0.96	0.07	64,64,64,64	0
56	MG	BA	3124	1/1	0.96	0.07	33,33,33,33	0
56	MG	DD	303	1/1	0.96	0.08	60,60,60,60	0
56	MG	DD	304	1/1	0.96	0.11	56,56,56,56	0
56	MG	DD	305	1/1	0.96	0.19	32,32,32,32	0
56	MG	BA	3326	1/1	0.96	0.08	50,50,50,50	0
56	MG	DA	3251	1/1	0.96	0.10	47,47,47,47	0
56	MG	BA	3422	1/1	0.96	0.12	45,45,45,45	0
56	MG	AA	3076	1/1	0.96	0.13	45,45,45,45	0
56	MG	BA	3184	1/1	0.96	0.15	33,33,33,33	0
56	MG	BA	3126	1/1	0.96	0.20	48,48,48,48	0
56	MG	DA	3083	1/1	0.96	0.10	46,46,46,46	0
56	MG	DA	3084	1/1	0.96	0.15	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	3452	1/1	0.96	0.09	44,44,44,44	0
56	MG	AX	3008	1/1	0.96	0.14	52,52,52,52	0
56	MG	BA	3332	1/1	0.96	0.22	48,48,48,48	0
56	MG	BA	3432	1/1	0.96	0.07	48,48,48,48	0
56	MG	DA	3457	1/1	0.96	0.10	46,46,46,46	0
56	MG	AA	3118	1/1	0.96	0.06	40,40,40,40	0
56	MG	DA	3262	1/1	0.96	0.08	41,41,41,41	0
56	MG	AA	3051	1/1	0.96	0.10	64,64,64,64	0
56	MG	BA	3752	1/1	0.96	0.09	48,48,48,48	0
56	MG	BA	3192	1/1	0.96	0.10	56,56,56,56	0
56	MG	DA	3266	1/1	0.96	0.12	61,61,61,61	0
56	MG	BA	3131	1/1	0.96	0.20	35,35,35,35	0
56	MG	BA	3196	1/1	0.96	0.06	46,46,46,46	0
56	MG	DA	3269	1/1	0.96	0.09	46,46,46,46	0
56	MG	BA	3440	1/1	0.96	0.09	41,41,41,41	0
56	MG	BA	3339	1/1	0.96	0.07	31,31,31,31	0
56	MG	DV	3002	1/1	0.96	0.18	51,51,51,51	0
56	MG	DA	3273	1/1	0.96	0.08	36,36,36,36	0
56	MG	AA	3165	1/1	0.96	0.10	51,51,51,51	0
56	MG	BA	3650	1/1	0.96	0.06	38,38,38,38	0
56	MG	DA	3099	1/1	0.96	0.14	39,39,39,39	0
56	MG	BA	3025	1/1	0.96	0.19	37,37,37,37	0
56	MG	DA	3101	1/1	0.96	0.08	28,28,28,28	0
56	MG	BA	3026	1/1	0.96	0.13	41,41,41,41	0
56	MG	DA	3477	1/1	0.96	0.12	41,41,41,41	0
56	MG	BA	3028	1/1	0.96	0.21	48,48,48,48	0
56	MG	DA	3104	1/1	0.96	0.19	49,49,49,49	0
56	MG	BA	3768	1/1	0.96	0.14	48,48,48,48	0
56	MG	AA	3166	1/1	0.96	0.12	43,43,43,43	0
56	MG	DA	3286	1/1	0.96	0.13	39,39,39,39	0
56	MG	BA	3138	1/1	0.96	0.16	50,50,50,50	0
56	MG	DA	3289	1/1	0.96	0.10	23,23,23,23	0
56	MG	BA	3657	1/1	0.96	0.16	54,54,54,54	0
56	MG	BA	3346	1/1	0.96	0.08	28,28,28,28	0
56	MG	AA	3131	1/1	0.96	0.12	63,63,63,63	0
56	MG	BA	3140	1/1	0.96	0.14	41,41,41,41	0
56	MG	BA	3095	1/1	0.96	0.17	39,39,39,39	0
56	MG	DA	3296	1/1	0.96	0.09	38,38,38,38	0
56	MG	DA	3113	1/1	0.96	0.21	51,51,51,51	0
56	MG	AA	3089	1/1	0.96	0.22	54,54,54,54	0
56	MG	DA	3299	1/1	0.96	0.08	40,40,40,40	0
56	MG	BA	3269	1/1	0.96	0.16	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3270	1/1	0.96	0.12	47,47,47,47	0
56	MG	BA	3779	1/1	0.96	0.12	52,52,52,52	0
56	MG	AA	3104	1/1	0.96	0.12	44,44,44,44	0
59	ZN	D9	501	1/1	0.96	0.06	82,82,82,82	0
56	MG	BA	3781	1/1	0.96	0.07	42,42,42,42	0
56	MG	BA	3272	1/1	0.96	0.14	41,41,41,41	0
56	MG	BA	3185	1/1	0.97	0.14	38,38,38,38	0
56	MG	BA	3321	1/1	0.97	0.06	43,43,43,43	0
56	MG	BA	3379	1/1	0.97	0.11	22,22,22,22	0
56	MG	B0	101	1/1	0.97	0.10	49,49,49,49	0
56	MG	BA	3050	1/1	0.97	0.07	34,34,34,34	0
56	MG	DA	3009	1/1	0.97	0.15	46,46,46,46	0
56	MG	AA	3187	1/1	0.97	0.09	56,56,56,56	0
56	MG	BA	3188	1/1	0.97	0.25	41,41,41,41	0
56	MG	DA	3408	1/1	0.97	0.05	25,25,25,25	0
56	MG	AA	3036	1/1	0.97	0.07	24,24,24,24	0
56	MG	CA	3089	1/1	0.97	0.17	46,46,46,46	0
56	MG	DA	3014	1/1	0.97	0.09	37,37,37,37	0
56	MG	BA	3454	1/1	0.97	0.05	43,43,43,43	0
56	MG	DA	3132	1/1	0.97	0.07	39,39,39,39	0
56	MG	DA	3133	1/1	0.97	0.06	50,50,50,50	0
56	MG	DA	3134	1/1	0.97	0.12	60,60,60,60	0
56	MG	BA	3385	1/1	0.97	0.11	50,50,50,50	0
56	MG	BA	3457	1/1	0.97	0.06	46,46,46,46	0
56	MG	DA	3018	1/1	0.97	0.06	29,29,29,29	0
56	MG	B5	102	1/1	0.97	0.23	42,42,42,42	0
56	MG	BA	3528	1/1	0.97	0.06	29,29,29,29	0
56	MG	DA	3272	1/1	0.97	0.09	43,43,43,43	0
56	MG	BA	3529	1/1	0.97	0.20	57,57,57,57	0
56	MG	B5	106	1/1	0.97	0.07	55,55,55,55	0
56	MG	BA	3458	1/1	0.97	0.14	52,52,52,52	0
56	MG	DA	3143	1/1	0.97	0.08	35,35,35,35	0
56	MG	BA	3273	1/1	0.97	0.06	36,36,36,36	0
56	MG	DA	3428	1/1	0.97	0.21	50,50,50,50	0
56	MG	BA	3020	1/1	0.97	0.13	32,32,32,32	0
56	MG	BA	3055	1/1	0.97	0.14	30,30,30,30	0
56	MG	DA	3280	1/1	0.97	0.08	26,26,26,26	0
56	MG	B8	101	1/1	0.97	0.08	35,35,35,35	0
56	MG	BA	3277	1/1	0.97	0.09	40,40,40,40	0
56	MG	BB	3006	1/1	0.97	0.04	46,46,46,46	0
56	MG	BA	3535	1/1	0.97	0.10	46,46,46,46	0
56	MG	BA	3536	1/1	0.97	0.12	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	BA	3330	1/1	0.97	0.09	35,35,35,35	0
56	MG	DA	3288	1/1	0.97	0.09	43,43,43,43	0
56	MG	BA	3232	1/1	0.97	0.26	44,44,44,44	0
56	MG	DA	3154	1/1	0.97	0.06	43,43,43,43	0
56	MG	DA	3155	1/1	0.97	0.26	53,53,53,53	0
56	MG	BA	3193	1/1	0.97	0.04	24,24,24,24	0
56	MG	BA	3194	1/1	0.97	0.07	40,40,40,40	0
56	MG	BA	3334	1/1	0.97	0.04	23,23,23,23	0
56	MG	BA	3624	1/1	0.97	0.08	50,50,50,50	0
56	MG	DA	3160	1/1	0.97	0.20	51,51,51,51	0
56	MG	BA	3021	1/1	0.97	0.09	32,32,32,32	0
56	MG	DA	3448	1/1	0.97	0.08	40,40,40,40	0
56	MG	DA	3162	1/1	0.97	0.15	45,45,45,45	0
56	MG	BA	3102	1/1	0.97	0.10	47,47,47,47	0
56	MG	BA	3709	1/1	0.97	0.08	42,42,42,42	0
56	MG	BA	3397	1/1	0.97	0.12	29,29,29,29	0
56	MG	BA	3238	1/1	0.97	0.39	35,35,35,35	0
56	MG	DA	3454	1/1	0.97	0.10	47,47,47,47	0
56	MG	CA	3015	1/1	0.97	0.04	45,45,45,45	0
56	MG	BA	3129	1/1	0.97	0.12	49,49,49,49	0
56	MG	BA	3198	1/1	0.97	0.12	35,35,35,35	0
56	MG	BA	3022	1/1	0.97	0.24	41,41,41,41	0
56	MG	DA	3171	1/1	0.97	0.06	41,41,41,41	0
56	MG	DA	3051	1/1	0.97	0.14	54,54,54,54	0
56	MG	DA	3313	1/1	0.97	0.12	46,46,46,46	0
56	MG	BA	3476	1/1	0.97	0.14	37,37,37,37	0
56	MG	BA	3552	1/1	0.97	0.11	32,32,32,32	0
56	MG	DA	3464	1/1	0.97	0.07	51,51,51,51	0
56	MG	BA	3058	1/1	0.97	0.13	23,23,23,23	0
56	MG	BA	3718	1/1	0.97	0.11	49,49,49,49	0
56	MG	CA	3023	1/1	0.97	0.07	54,54,54,54	0
56	MG	BE	302	1/1	0.97	0.06	28,28,28,28	0
56	MG	BA	3478	1/1	0.97	0.10	36,36,36,36	0
56	MG	BA	3293	1/1	0.97	0.07	40,40,40,40	0
56	MG	BE	305	1/1	0.97	0.11	38,38,38,38	0
56	MG	BA	3008	1/1	0.97	0.05	27,27,27,27	0
56	MG	CA	3029	1/1	0.97	0.13	37,37,37,37	0
56	MG	CA	3030	1/1	0.97	0.20	51,51,51,51	0
56	MG	DA	3185	1/1	0.97	0.23	53,53,53,53	0
56	MG	BA	3082	1/1	0.97	0.14	27,27,27,27	0
56	MG	AA	3055	1/1	0.97	0.09	40,40,40,40	0
56	MG	BA	3010	1/1	0.97	0.18	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3137	1/1	0.97	0.07	52,52,52,52	0
56	MG	BA	3347	1/1	0.97	0.12	26,26,26,26	0
56	MG	BA	3642	1/1	0.97	0.20	38,38,38,38	0
56	MG	DA	3070	1/1	0.97	0.10	34,34,34,34	0
56	MG	BA	3062	1/1	0.97	0.12	35,35,35,35	0
56	MG	BA	3349	1/1	0.97	0.09	25,25,25,25	0
56	MG	BA	3110	1/1	0.97	0.19	49,49,49,49	0
56	MG	BA	3489	1/1	0.97	0.06	43,43,43,43	0
56	MG	BA	3170	1/1	0.97	0.09	30,30,30,30	0
56	MG	BA	3648	1/1	0.97	0.08	39,39,39,39	0
56	MG	BA	3352	1/1	0.97	0.10	22,22,22,22	0
56	MG	BA	3353	1/1	0.97	0.09	27,27,27,27	0
56	MG	BA	3571	1/1	0.97	0.07	40,40,40,40	0
56	MG	DE	301	1/1	0.97	0.32	50,50,50,50	0
56	MG	BA	3493	1/1	0.97	0.08	29,29,29,29	0
56	MG	BA	3043	1/1	0.97	0.06	34,34,34,34	0
56	MG	BA	3027	1/1	0.97	0.10	41,41,41,41	0
56	MG	BA	3575	1/1	0.97	0.10	48,48,48,48	0
56	MG	BA	3173	1/1	0.97	0.10	46,46,46,46	0
56	MG	BA	3358	1/1	0.97	0.09	30,30,30,30	0
56	MG	BA	3423	1/1	0.97	0.17	43,43,43,43	0
56	MG	BA	3745	1/1	0.97	0.09	27,27,27,27	0
56	MG	DA	3357	1/1	0.97	0.07	44,44,44,44	0
56	MG	BA	3065	1/1	0.97	0.14	33,33,33,33	0
56	MG	BA	3175	1/1	0.97	0.08	44,44,44,44	0
56	MG	BQ	3002	1/1	0.97	0.16	41,41,41,41	0
56	MG	DO	202	1/1	0.97	0.11	57,57,57,57	0
56	MG	BA	3176	1/1	0.97	0.15	41,41,41,41	0
56	MG	DQ	3001	1/1	0.97	0.06	57,57,57,57	0
56	MG	BA	3142	1/1	0.97	0.14	47,47,47,47	0
56	MG	DA	3217	1/1	0.97	0.05	43,43,43,43	0
56	MG	DA	3218	1/1	0.97	0.07	53,53,53,53	0
56	MG	DR	3001	1/1	0.97	0.17	55,55,55,55	0
56	MG	BA	3066	1/1	0.97	0.17	40,40,40,40	0
56	MG	DA	3512	1/1	0.97	0.07	52,52,52,52	0
56	MG	BA	3179	1/1	0.97	0.09	61,61,61,61	0
56	MG	BA	3666	1/1	0.97	0.04	11,11,11,11	0
56	MG	BA	3218	1/1	0.97	0.14	52,52,52,52	0
56	MG	AA	3119	1/1	0.97	0.10	36,36,36,36	0
56	MG	BA	3507	1/1	0.97	0.12	53,53,53,53	0
56	MG	DW	3002	1/1	0.97	0.17	32,32,32,32	0
56	MG	BU	202	1/1	0.97	0.26	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	3368	1/1	0.97	0.08	56,56,56,56	0
56	MG	DA	3227	1/1	0.97	0.07	47,47,47,47	0
56	MG	CA	3178	1/1	0.97	0.06	54,54,54,54	0
56	MG	BU	205	1/1	0.97	0.17	39,39,39,39	0
56	MG	DA	3230	1/1	0.97	0.12	23,23,23,23	0
56	MG	D7	101	1/1	0.97	0.20	33,33,33,33	0
56	MG	AA	3016	1/1	0.97	0.13	48,48,48,48	0
56	MG	AA	3204	1/1	0.97	0.17	44,44,44,44	0
56	MG	BU	209	1/1	0.97	0.27	41,41,41,41	0
56	MG	BV	201	1/1	0.97	0.08	26,26,26,26	0
56	MG	BV	202	1/1	0.97	0.17	34,34,34,34	0
56	MG	DA	3531	1/1	0.97	0.11	40,40,40,40	0
56	MG	BA	3673	1/1	0.97	0.11	22,22,22,22	0
56	MG	BA	3314	1/1	0.97	0.04	41,41,41,41	0
56	MG	AA	3205	1/1	0.97	0.06	66,66,66,66	0
56	MG	DA	3535	1/1	0.97	0.04	38,38,38,38	0
56	MG	BA	3766	1/1	0.97	0.07	43,43,43,43	0
56	MG	BA	3443	1/1	0.97	0.08	50,50,50,50	0
56	MG	CW	3003	1/1	0.97	0.07	64,64,64,64	0
56	MG	DA	3388	1/1	0.97	0.06	49,49,49,49	0
56	MG	BA	3594	1/1	0.97	0.12	37,37,37,37	0
56	MG	BA	3374	1/1	0.97	0.11	34,34,34,34	0
56	MG	DA	3391	1/1	0.97	0.11	40,40,40,40	0
56	MG	AA	3084	1/1	0.97	0.21	53,53,53,53	0
56	MG	DA	3248	1/1	0.97	0.07	39,39,39,39	0
56	MG	DA	3118	1/1	0.97	0.17	50,50,50,50	0
59	ZN	CN	102	1/1	0.97	0.06	82,82,82,82	0
56	MG	DA	3547	1/1	0.97	0.12	41,41,41,41	0
56	MG	DA	3396	1/1	0.97	0.07	27,27,27,27	0
56	MG	DA	3250	1/1	0.97	0.10	37,37,37,37	0
56	MG	BA	3516	1/1	0.97	0.10	36,36,36,36	0
56	MG	AA	3025	1/1	0.98	0.35	54,54,54,54	0
56	MG	BA	3220	1/1	0.98	0.08	45,45,45,45	0
56	MG	AW	3005	1/1	0.98	0.05	52,52,52,52	0
56	MG	BA	3441	1/1	0.98	0.06	37,37,37,37	0
56	MG	BA	3267	1/1	0.98	0.15	14,14,14,14	0
56	MG	BA	3398	1/1	0.98	0.06	37,37,37,37	0
56	MG	DA	3537	1/1	0.98	0.05	53,53,53,53	0
56	MG	BA	3488	1/1	0.98	0.04	28,28,28,28	0
56	MG	AA	3064	1/1	0.98	0.07	47,47,47,47	0
56	MG	BA	3162	1/1	0.98	0.06	37,37,37,37	0
56	MG	DB	3004	1/1	0.98	0.14	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3065	1/1	0.98	0.05	40,40,40,40	0
56	MG	BA	3204	1/1	0.98	0.09	35,35,35,35	0
56	MG	BA	3684	1/1	0.98	0.07	39,39,39,39	0
56	MG	DA	3295	1/1	0.98	0.12	34,34,34,34	0
56	MG	BA	3366	1/1	0.98	0.06	23,23,23,23	0
56	MG	DA	3020	1/1	0.98	0.09	33,33,33,33	0
56	MG	DA	3021	1/1	0.98	0.06	44,44,44,44	0
56	MG	BA	3538	1/1	0.98	0.06	43,43,43,43	0
56	MG	BA	3164	1/1	0.98	0.21	33,33,33,33	0
56	MG	BA	3540	1/1	0.98	0.06	28,28,28,28	0
56	MG	DA	3092	1/1	0.98	0.07	43,43,43,43	0
56	MG	DA	3303	1/1	0.98	0.07	44,44,44,44	0
56	MG	BU	203	1/1	0.98	0.11	34,34,34,34	0
56	MG	AA	3070	1/1	0.98	0.04	31,31,31,31	0
56	MG	BA	3369	1/1	0.98	0.11	23,23,23,23	0
56	MG	DA	3307	1/1	0.98	0.04	28,28,28,28	0
56	MG	BA	3452	1/1	0.98	0.04	41,41,41,41	0
56	MG	DA	3309	1/1	0.98	0.05	42,42,42,42	0
56	MG	BA	3275	1/1	0.98	0.10	45,45,45,45	0
56	MG	DA	3392	1/1	0.98	0.09	34,34,34,34	0
56	MG	BA	3006	1/1	0.98	0.04	26,26,26,26	0
56	MG	BA	3251	1/1	0.98	0.10	51,51,51,51	0
56	MG	BA	3747	1/1	0.98	0.06	50,50,50,50	0
56	MG	DA	3034	1/1	0.98	0.04	35,35,35,35	0
56	MG	DA	3478	1/1	0.98	0.05	54,54,54,54	0
56	MG	BV	203	1/1	0.98	0.08	31,31,31,31	0
56	MG	BD	302	1/1	0.98	0.07	33,33,33,33	0
56	MG	DA	3399	1/1	0.98	0.11	35,35,35,35	0
56	MG	BA	3595	1/1	0.98	0.06	65,65,65,65	0
56	MG	BA	3411	1/1	0.98	0.07	49,49,49,49	0
56	MG	DA	3319	1/1	0.98	0.07	21,21,21,21	0
56	MG	BA	3167	1/1	0.98	0.14	28,28,28,28	0
56	MG	DA	3245	1/1	0.98	0.05	28,28,28,28	0
56	MG	BA	3117	1/1	0.98	0.12	41,41,41,41	0
56	MG	AA	3001	1/1	0.98	0.10	37,37,37,37	0
56	MG	BA	3038	1/1	0.98	0.10	31,31,31,31	0
56	MG	BD	309	1/1	0.98	0.18	39,39,39,39	0
56	MG	BA	3282	1/1	0.98	0.04	59,59,59,59	0
56	MG	BA	3016	1/1	0.98	0.04	22,22,22,22	0
56	MG	DA	3580	1/1	0.98	0.07	44,44,44,44	0
56	MG	BA	3284	1/1	0.98	0.07	35,35,35,35	0
56	MG	BA	3556	1/1	0.98	0.15	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3557	1/1	0.98	0.09	58,58,58,58	0
56	MG	DW	3001	1/1	0.98	0.16	45,45,45,45	0
56	MG	B0	102	1/1	0.98	0.07	54,54,54,54	0
56	MG	BA	3315	1/1	0.98	0.08	40,40,40,40	0
56	MG	BA	3607	1/1	0.98	0.08	45,45,45,45	0
56	MG	BA	3316	1/1	0.98	0.09	58,58,58,58	0
56	MG	BA	3763	1/1	0.98	0.11	10,10,10,10	0
56	MG	BF	302	1/1	0.98	0.24	29,29,29,29	0
56	MG	DA	3420	1/1	0.98	0.05	40,40,40,40	0
56	MG	DA	3503	1/1	0.98	0.06	58,58,58,58	0
56	MG	DA	3189	1/1	0.98	0.06	42,42,42,42	0
56	MG	BA	3764	1/1	0.98	0.10	26,26,26,26	0
56	MG	BA	3383	1/1	0.98	0.19	49,49,49,49	0
56	MG	BA	3052	1/1	0.98	0.05	34,34,34,34	0
56	MG	BA	3767	1/1	0.98	0.07	31,31,31,31	0
56	MG	BA	3093	1/1	0.98	0.06	39,39,39,39	0
56	MG	BA	3425	1/1	0.98	0.07	31,31,31,31	0
56	MG	BF	309	1/1	0.98	0.13	40,40,40,40	0
56	MG	BA	3017	1/1	0.98	0.05	32,32,32,32	0
56	MG	DA	3198	1/1	0.98	0.14	32,32,32,32	0
56	MG	BA	3320	1/1	0.98	0.04	28,28,28,28	0
56	MG	DA	3351	1/1	0.98	0.04	40,40,40,40	0
56	MG	BA	3237	1/1	0.98	0.15	43,43,43,43	0
56	MG	BA	3029	1/1	0.98	0.13	44,44,44,44	0
56	MG	BA	3292	1/1	0.98	0.11	26,26,26,26	0
56	MG	BA	3433	1/1	0.98	0.06	48,48,48,48	0
56	MG	DA	3521	1/1	0.98	0.13	29,29,29,29	0
56	MG	DA	3356	1/1	0.98	0.05	47,47,47,47	0
56	MG	AA	3212	1/1	0.98	0.10	33,33,33,33	0
56	MG	BA	3158	1/1	0.98	0.05	47,47,47,47	0
58	SF4	CD	302	8/8	0.98	0.05	51,66,73,73	0
59	ZN	B4	501	1/1	0.98	0.05	86,86,86,86	0
56	MG	BA	3357	1/1	0.98	0.11	29,29,29,29	0
56	MG	DA	3004	1/1	0.98	0.11	18,18,18,18	0
59	ZN	D6	501	1/1	0.98	0.05	70,70,70,70	0
56	MG	DA	3005	1/1	0.98	0.11	39,39,39,39	0
56	MG	DA	3281	1/1	0.98	0.09	39,39,39,39	0
56	MG	BA	3437	1/1	0.98	0.04	55,55,55,55	0
56	MG	BA	3743	1/1	0.99	0.04	18,18,18,18	0
56	MG	BA	3744	1/1	0.99	0.08	27,27,27,27	0
56	MG	BA	3190	1/1	0.99	0.34	35,35,35,35	0
56	MG	BA	3291	1/1	0.99	0.12	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AV	101	1/1	0.99	0.04	47,47,47,47	0
56	MG	BU	207	1/1	0.99	0.20	22,22,22,22	0
56	MG	CA	3091	1/1	0.99	0.11	45,45,45,45	0
56	MG	B7	101	1/1	0.99	0.06	35,35,35,35	0
56	MG	BA	3426	1/1	0.99	0.07	29,29,29,29	0
56	MG	BA	3427	1/1	0.99	0.05	22,22,22,22	0
56	MG	AA	3123	1/1	0.99	0.07	25,25,25,25	0
56	MG	BA	3517	1/1	0.99	0.11	26,26,26,26	0
56	MG	BA	3024	1/1	0.99	0.14	19,19,19,19	0
56	MG	AA	3142	1/1	0.99	0.05	38,38,38,38	0
56	MG	DD	306	1/1	0.99	0.19	35,35,35,35	0
56	MG	BA	3410	1/1	0.99	0.05	33,33,33,33	0
56	MG	BA	3376	1/1	0.99	0.07	23,23,23,23	0
56	MG	DA	3327	1/1	0.99	0.03	32,32,32,32	0
56	MG	BA	3782	1/1	0.99	0.13	48,48,48,48	0
56	MG	DA	3525	1/1	0.99	0.04	33,33,33,33	0
56	MG	AA	3133	1/1	0.99	0.06	35,35,35,35	0
56	MG	BA	3169	1/1	0.99	0.12	28,28,28,28	0
56	MG	BD	310	1/1	0.99	0.06	45,45,45,45	0
56	MG	BA	3414	1/1	0.99	0.08	26,26,26,26	0
56	MG	BA	3759	1/1	0.99	0.06	29,29,29,29	0
56	MG	BA	3133	1/1	0.99	0.05	43,43,43,43	0
56	MG	DA	3335	1/1	0.99	0.03	41,41,41,41	0
56	MG	DA	3336	1/1	0.99	0.03	30,30,30,30	0
56	MG	BA	3122	1/1	0.99	0.04	42,42,42,42	0
56	MG	BA	3072	1/1	0.99	0.06	42,42,42,42	0
56	MG	AA	3223	1/1	0.99	0.04	52,52,52,52	0
56	MG	BE	306	1/1	0.99	0.10	15,15,15,15	0
56	MG	DA	3026	1/1	0.99	0.06	24,24,24,24	0
58	SF4	AD	501	8/8	0.99	0.06	52,60,68,71	0
56	MG	DA	3231	1/1	0.99	0.03	54,54,54,54	0
59	ZN	AN	501	1/1	0.99	0.05	65,65,65,65	0
56	MG	AA	3156	1/1	0.99	0.04	65,65,65,65	0
59	ZN	B5	105	1/1	0.99	0.10	52,52,52,52	0
56	MG	BA	3463	1/1	0.99	0.07	34,34,34,34	0
59	ZN	DY	501	1/1	0.99	0.04	88,88,88,88	0
56	MG	BA	3004	1/1	0.99	0.02	25,25,25,25	0
59	ZN	D5	501	1/1	0.99	0.05	57,57,57,57	0
56	MG	DA	3235	1/1	0.99	0.04	29,29,29,29	0
56	MG	BA	3005	1/1	0.99	0.06	41,41,41,41	0
56	MG	BA	3289	1/1	0.99	0.05	24,24,24,24	0
56	MG	BB	3011	1/1	0.99	0.05	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
59	ZN	B9	501	1/1	1.00	0.04	47,47,47,47	0
56	MG	BA	3455	1/1	1.00	0.05	28,28,28,28	0
56	MG	AA	3135	1/1	1.00	0.03	34,34,34,34	0
56	MG	BA	3553	1/1	1.00	0.09	49,49,49,49	0
56	MG	BA	3654	1/1	1.00	0.04	24,24,24,24	0
59	ZN	BY	501	1/1	1.00	0.03	60,60,60,60	0
56	MG	DA	3506	1/1	1.00	0.07	37,37,37,37	0
56	MG	BA	3268	1/1	1.00	0.09	40,40,40,40	0
59	ZN	B6	102	1/1	1.00	0.03	43,43,43,43	0

6.5 Other polymers (i)

There are no such residues in this entry.