Full wwPDB X-ray Structure Validation Report

Apr 18, 2026 – 01:44 PM UTC

PDB ID	:	1VY4 / pdb_00001vy4
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in the pre-attack state of peptide bond formation containing acylated tRNA-substrates in the A and P sites.
Authors	:	Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on	:	2014-05-13
Resolution	:	2.60 Å(reported)

This is a Full wwPDB 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:

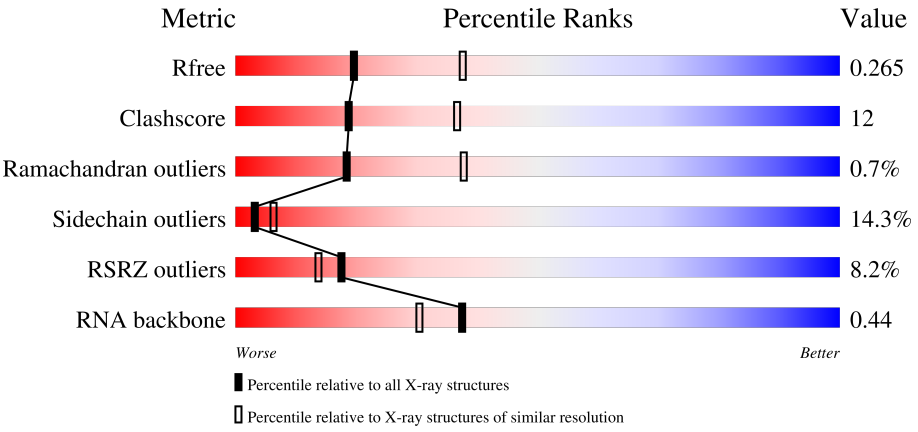
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 2.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)
RNA backbone	3983	1014 (2.84-2.36)

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

Mol	Chain	Length	Quality of chain
1	AA	1521	3% 49% 38% 11% ·
1	CA	1521	10% 43% 42% 14% ·
2	AB	256	17% 42% 38% 8% · 10%
2	CB	256	22% 36% 42% 12% · 10%

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Mol	Chain	Length	Quality of chain
3	AC	239	8% 50% 32% 14%
3	CC	239	35% 45% 33% 8% 14%
4	AD	209	11% 65% 28% 6%
4	CD	209	9% 57% 35% 8%
5	AE	162	10% 59% 28% 9%
5	CE	162	9% 50% 34% 7% 9%
6	AF	101	69% 23% 7%
6	CF	101	4% 65% 27% 7%
7	AG	156	15% 71% 21% 7%
7	CG	156	14% 66% 27% 6%
8	AH	138	11% 60% 33% 6%
8	CH	138	14% 50% 41% 8%
9	AI	128	21% 52% 39% 9%
9	CI	128	58% 41% 48% 9%
10	AJ	105	33% 56% 31% 5% 8%
10	CJ	105	34% 35% 50% 6% 9%
11	AK	129	5% 61% 22% 5% 12%
11	CK	129	8% 54% 33% 12%
12	AL	132	6% 60% 31% 8%
12	CL	132	27% 55% 31% 7% 8%
13	AM	126	8% 53% 33% 11%
13	CM	126	41% 36% 48% 13%
14	AN	61	7% 48% 44% 7%
14	CN	61	66% 41% 46% 11%
15	AO	89	4% 64% 29%

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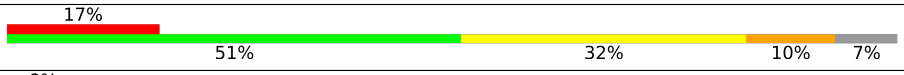
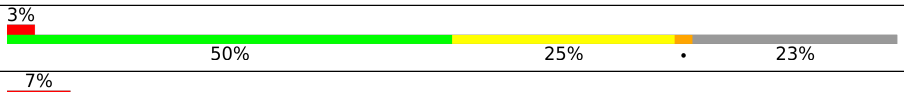
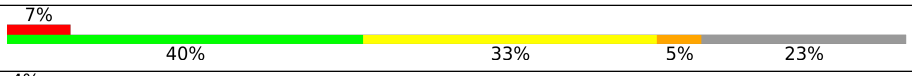
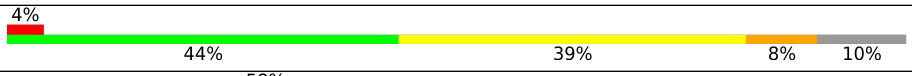
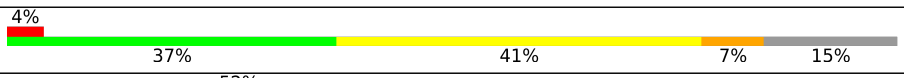
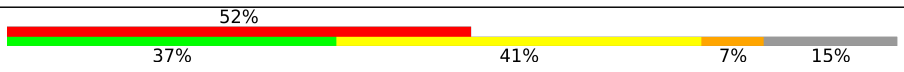
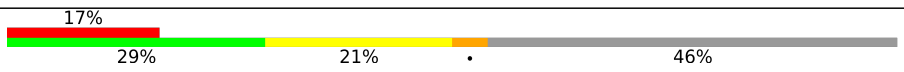
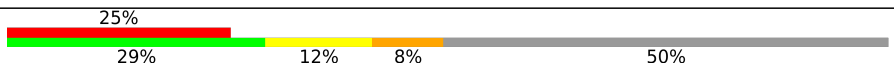
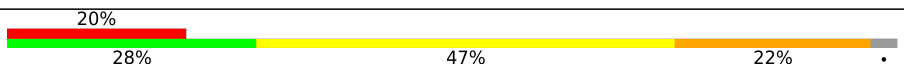
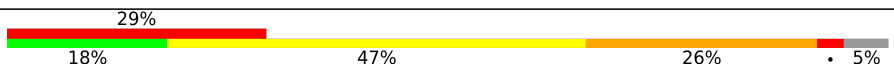
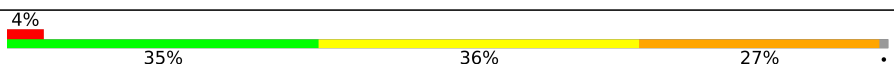
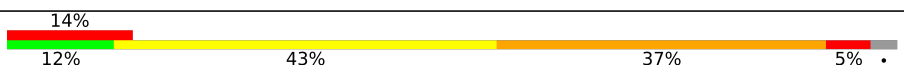
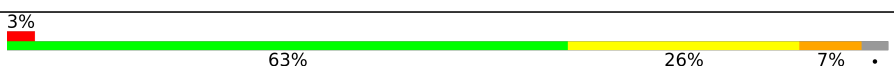
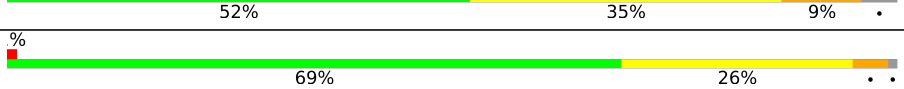
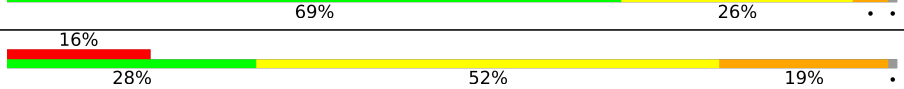
Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AW	76	
23	CW	76	
24	AX	77	
24	CX	77	
25	AY	76	
25	CY	76	
26	BA	2915	
26	DA	2915	
27	BB	121	
27	DB	121	

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Mol	Chain	Length	Quality of chain
28	BD	276	2% 78% 18%
28	DD	276	69% 26%
29	BE	206	73% 21%
29	DE	206	67% 24% 7%
30	BF	210	67% 25%
30	DF	210	2% 54% 37% 6%
31	BG	182	13% 64% 31%
31	DG	182	30% 42% 45% 13%
32	BH	180	7% 63% 30%
32	DH	180	16% 53% 38% 6%
33	BI	148	4% 57% 30% 9%
33	DI	148	9% 64% 27% 7%
34	BN	140	73% 21% 6%
34	DN	140	2% 65% 32%
35	BO	122	69% 28%
35	DO	122	64% 29% 7%
36	BP	150	3% 66% 27% 7%
36	DP	150	3% 60% 33% 6%
37	BQ	141	72% 26%
37	DQ	141	6% 60% 35%
38	BR	118	69% 25% 7%
38	DR	118	63% 31% 6%
39	BS	112	68% 23% 7%
39	DS	112	28% 51% 37% 11%
40	BT	146	3% 64% 21% 10%

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Mol	Chain	Length	Quality of chain
40	DT	146	3% 53% 34% 10%
41	BU	118	75% 22%
41	DU	118	2% 63% 33%
42	BV	101	70% 24% 6%
42	DV	101	7% 61% 32% 6%
43	BW	113	% 76% 19%
43	DW	113	2% 75% 22%
44	BX	96	% 73% 22%
44	DX	96	6% 63% 31% 5%
45	BY	110	5% 62% 31% 5%
45	DY	110	7% 62% 31% 5%
46	BZ	206	15% 49% 27% 7% 17%
46	DZ	206	15% 39% 37% 8% 16%
47	B0	85	8% 84% 9% 5%
47	D0	85	12% 68% 24% 6%
48	B1	98	4% 76% 21%
48	D1	98	2% 74% 19%
49	B2	72	3% 65% 29%
49	D2	72	% 62% 32%
50	B3	60	83% 10% 5%
50	D3	60	2% 63% 28% 7%
51	B4	71	14% 48% 31% 15%
51	D4	71	37% 42% 44% 10%
52	B5	60	2% 67% 28%
52	D5	60	2% 70% 27%

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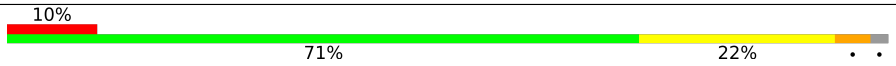
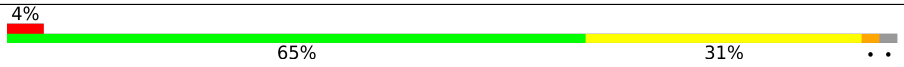
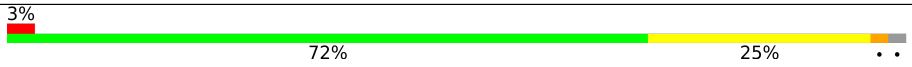
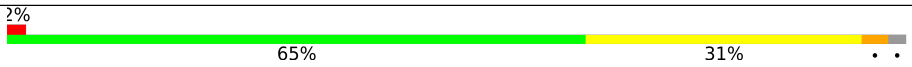
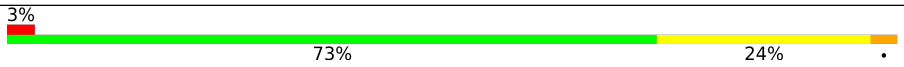
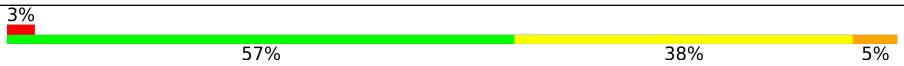
Mol	Chain	Length	Quality of chain
53	B6	54	
53	D6	54	
54	B7	49	
54	D7	49	
55	B8	65	
55	D8	65	
56	B9	37	
56	D9	37	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	PSU	CY	39	-	-	X	-
57	MG	DA	3079	-	-	-	X

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 297127 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	1497	Total	C	N	O	P	0	0	0
			32185	14324	5968	10396	1497			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1552	976	302	273	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1544	970	300	273	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1659	1040	326	286	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1678	1052	333	286	7			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			812	514	146	149	3			
6	CF	100	Total	C	N	O	S	0	0	0
			820	518	147	152	3			

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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	0	0	0
			986	626	193	167			
9	CI	127	Total	C	N	O	0	0	0
			978	619	190	169			

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

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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	CJ	96	Total	C	N	O	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
			833	519	156	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
			966	598	200	166	2			
13	CM	122	Total	C	N	O	S	0	0	0
			950	586	197	165	2			

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	84	Total	C	N	O	S	0	0	0
			661	423	122	114	2			
19	CS	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
20	CT	96	Total	C	N	O	S	0	0	0
			731	449	156	124	2			

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

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

- Molecule 22 is a RNA chain called mRNA.

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

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AW	74	Total	C	N	O	P	S	0	0	0
			1599	722	287	515	73	2			
23	CW	72	Total	C	N	O	P	S	0	0	0
			1552	697	280	502	72	1			

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
28	DD	275	Total	C	N	O	S	0	0	0
			2142	1352	426	361	3			

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BI	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
33	DI	146	Total	C	N	O	S	0	0	0
			1073	688	188	196	1			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BP	149	Total	C	N	O	S	0	0	0
			1139	709	231	196	3			
36	DP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AA	216	Total	Mg	0	0
			216	216		
57	AB	1	Total	Mg	0	0
			1	1		
57	AE	1	Total	Mg	0	0
			1	1		
57	AF	1	Total	Mg	0	0
			1	1		
57	AK	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	AL	2	Total Mg 2 2	0	0
57	AM	2	Total Mg 2 2	0	0
57	AN	2	Total Mg 2 2	0	0
57	AT	1	Total Mg 1 1	0	0
57	AU	1	Total Mg 1 1	0	0
57	AW	2	Total Mg 2 2	0	0
57	AX	15	Total Mg 15 15	0	0
57	AY	3	Total Mg 3 3	0	0
57	BA	814	Total Mg 814 814	0	0
57	BB	23	Total Mg 23 23	0	0
57	BD	10	Total Mg 10 10	0	0
57	BE	6	Total Mg 6 6	0	0
57	BF	11	Total Mg 11 11	0	0
57	BG	2	Total Mg 2 2	0	0
57	BH	1	Total Mg 1 1	0	0
57	BN	3	Total Mg 3 3	0	0
57	BO	1	Total Mg 1 1	0	0
57	BP	2	Total Mg 2 2	0	0
57	BQ	2	Total Mg 2 2	0	0
57	BR	2	Total Mg 2 2	0	0
57	BU	4	Total Mg 4 4	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	BV	5	Total Mg 5 5	0	0
57	BW	4	Total Mg 4 4	0	0
57	BX	1	Total Mg 1 1	0	0
57	BY	1	Total Mg 1 1	0	0
57	BZ	2	Total Mg 2 2	0	0
57	B0	2	Total Mg 2 2	0	0
57	B2	1	Total Mg 1 1	0	0
57	B4	1	Total Mg 1 1	0	0
57	B5	3	Total Mg 3 3	0	0
57	B6	2	Total Mg 2 2	0	0
57	B7	5	Total Mg 5 5	0	0
57	B8	2	Total Mg 2 2	0	0
57	B9	1	Total Mg 1 1	0	0
57	CA	169	Total Mg 169 169	0	0
57	CD	1	Total Mg 1 1	0	0
57	CE	2	Total Mg 2 2	0	0
57	CF	1	Total Mg 1 1	0	0
57	CJ	1	Total Mg 1 1	0	0
57	CK	1	Total Mg 1 1	0	0
57	CT	1	Total Mg 1 1	0	0
57	CW	1	Total Mg 1 1	0	0

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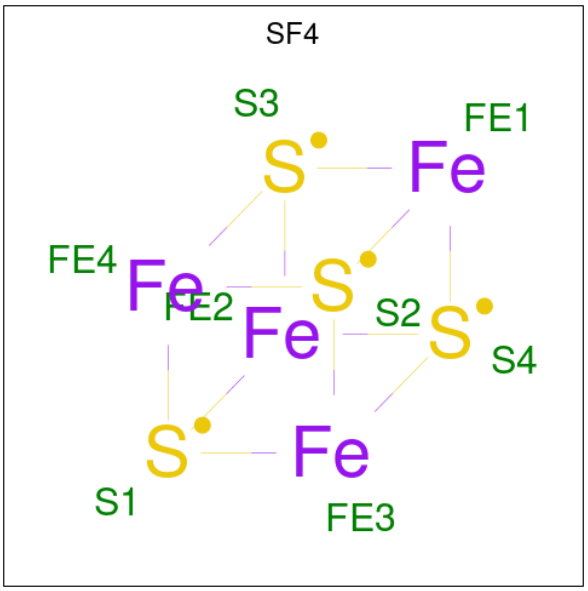
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	CX	2	Total Mg 2 2	0	0
57	DA	664	Total Mg 664 664	0	0
57	DB	13	Total Mg 13 13	0	0
57	DD	4	Total Mg 4 4	0	0
57	DE	7	Total Mg 7 7	0	0
57	DF	5	Total Mg 5 5	0	0
57	DG	1	Total Mg 1 1	0	0
57	DN	1	Total Mg 1 1	0	0
57	DO	2	Total Mg 2 2	0	0
57	DP	2	Total Mg 2 2	0	0
57	DQ	3	Total Mg 3 3	0	0
57	DR	1	Total Mg 1 1	0	0
57	DU	1	Total Mg 1 1	0	0
57	DV	1	Total Mg 1 1	0	0
57	DW	1	Total Mg 1 1	0	0
57	DY	1	Total Mg 1 1	0	0
57	D0	1	Total Mg 1 1	0	0
57	D3	1	Total Mg 1 1	0	0
57	D8	1	Total Mg 1 1	0	0

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



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

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

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

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

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

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

- Molecule 61 is water.

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

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

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

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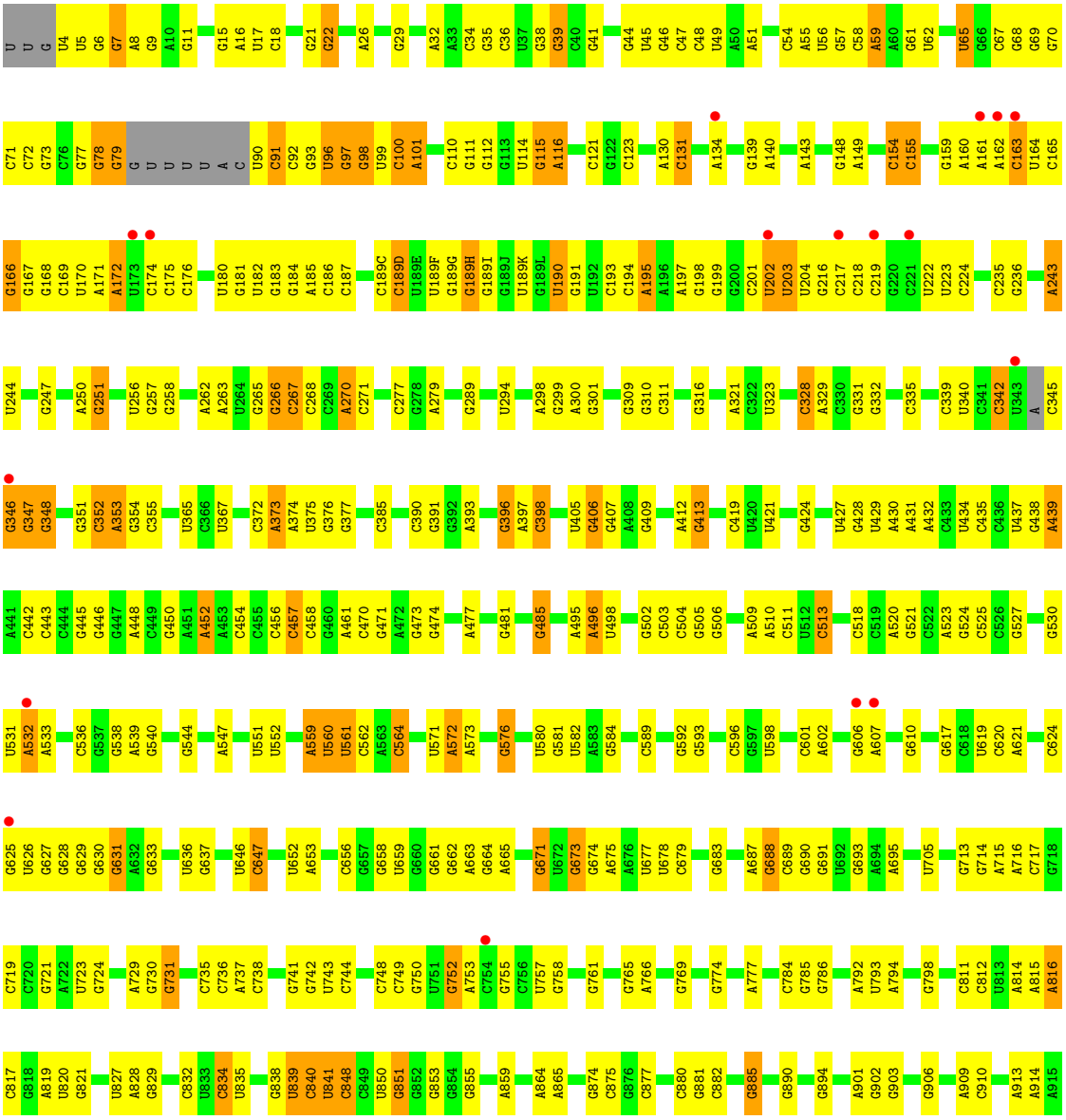
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	DT	4	Total O 4 4	0	0
61	DU	1	Total O 1 1	0	0
61	DV	1	Total O 1 1	0	0
61	DW	1	Total O 1 1	0	0
61	DX	2	Total O 2 2	0	0
61	DY	1	Total O 1 1	0	0
61	D0	4	Total O 4 4	0	0
61	D1	1	Total O 1 1	0	0
61	D3	2	Total O 2 2	0	0
61	D5	1	Total O 1 1	0	0
61	D6	1	Total O 1 1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

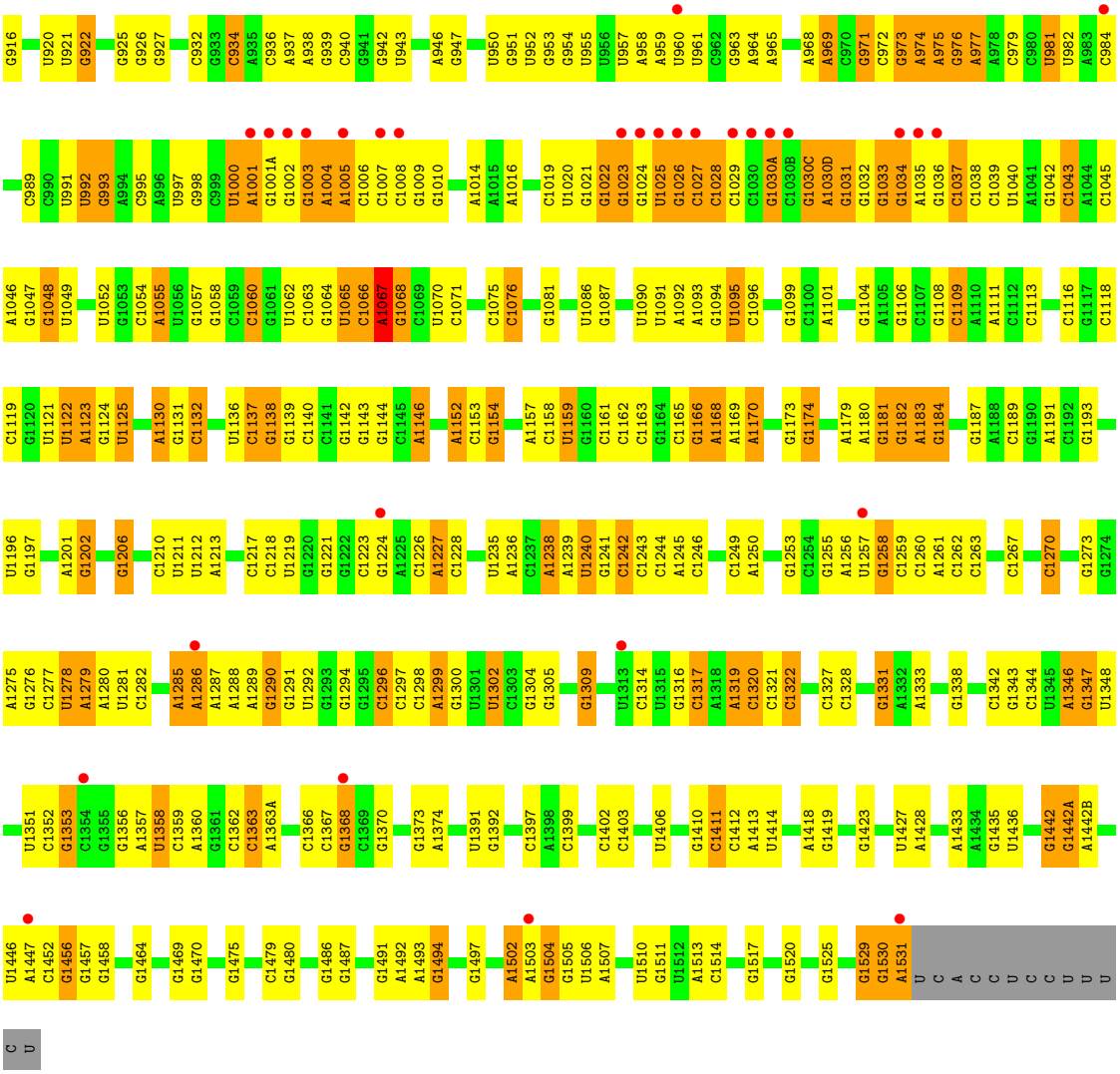
3 Residue-property plots (i)

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

- Molecule 1: 16S Ribosomal RNA

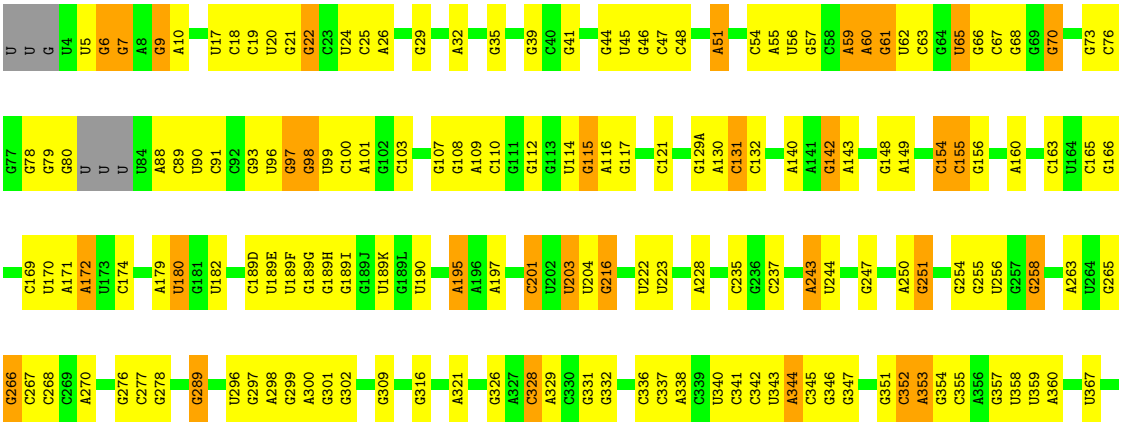
Chain AA:

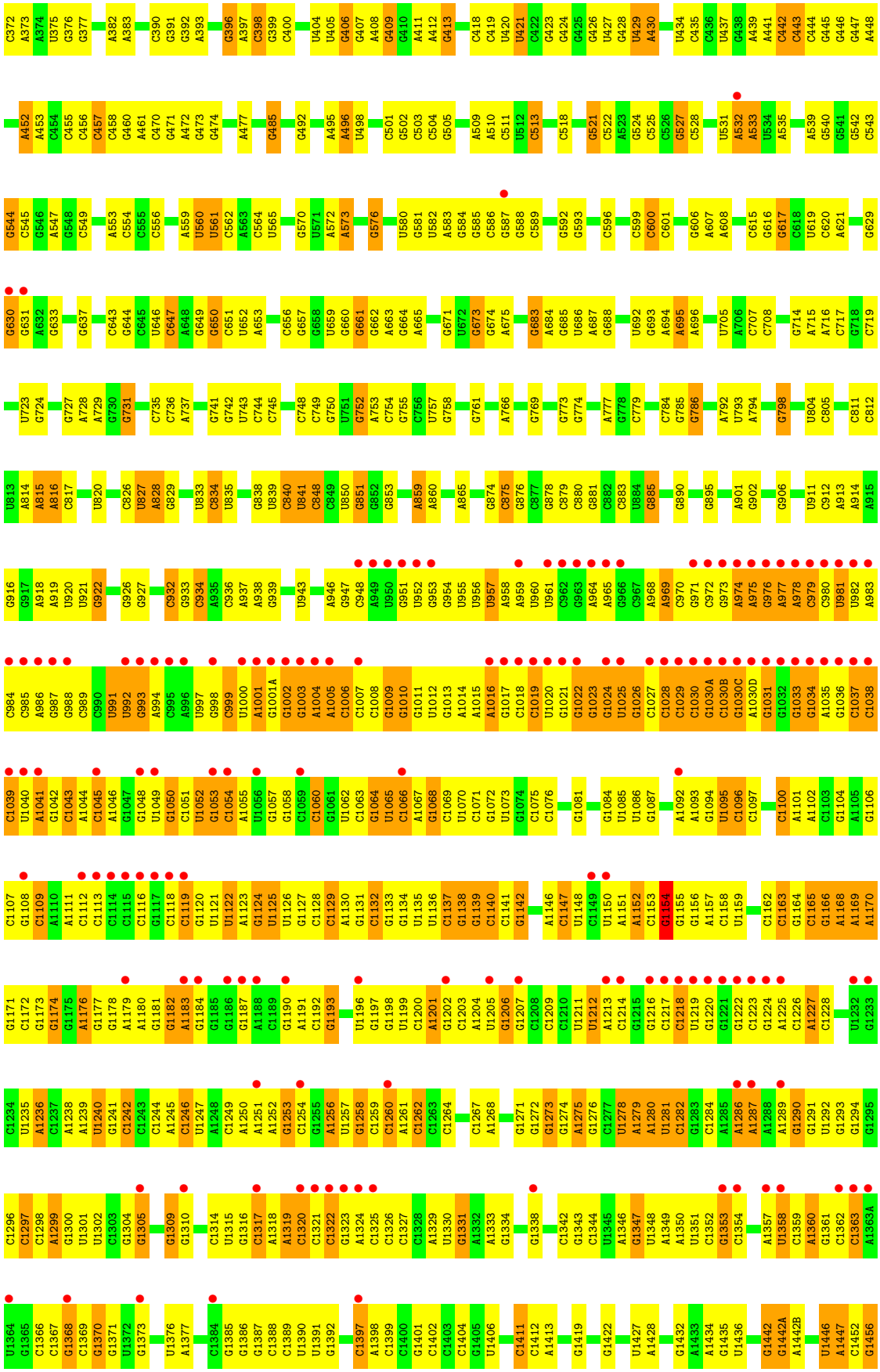




• Molecule 1: 16S Ribosomal RNA

Chain CA:

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A452 A453 C454 C455 C456 C457 C458 G460 A461 C470 G471 A472 G473 G474 A477 G485 G492 A495 A496 U498 C501 G502 C503 C504 G505 A509 A510 C511 U512 C513 C518 G521 C522 A523 G524 C525 C526 G527 C528 U531 A532 A533 U534 A535 A539 G540 G541 G542 C543
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• Molecule 2: 30S ribosomal protein S2

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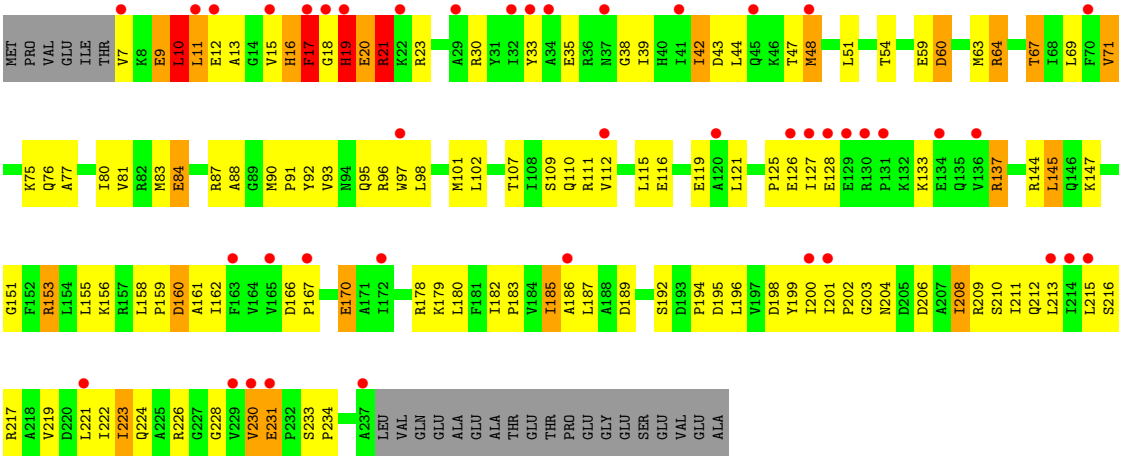
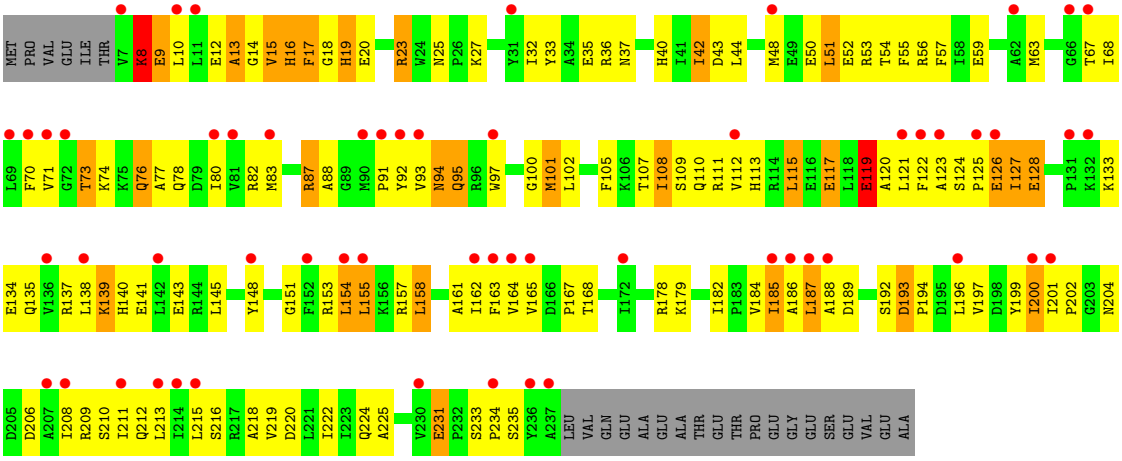


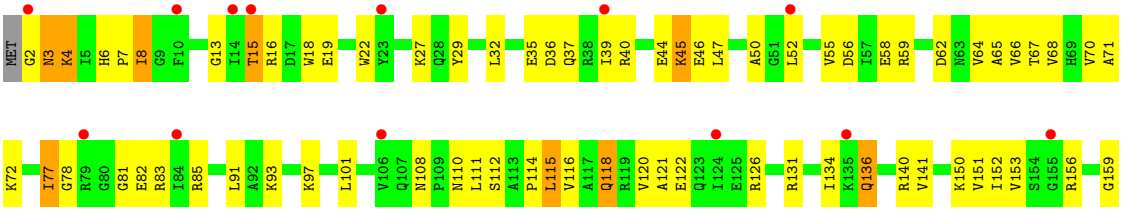
• Molecule 2: 30S ribosomal protein S2

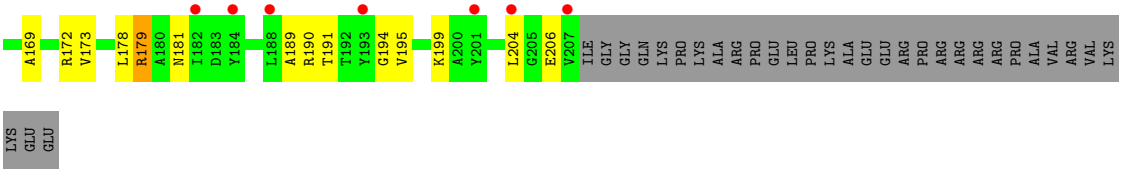
Chain CB:



• Molecule 3: 30S ribosomal protein S3

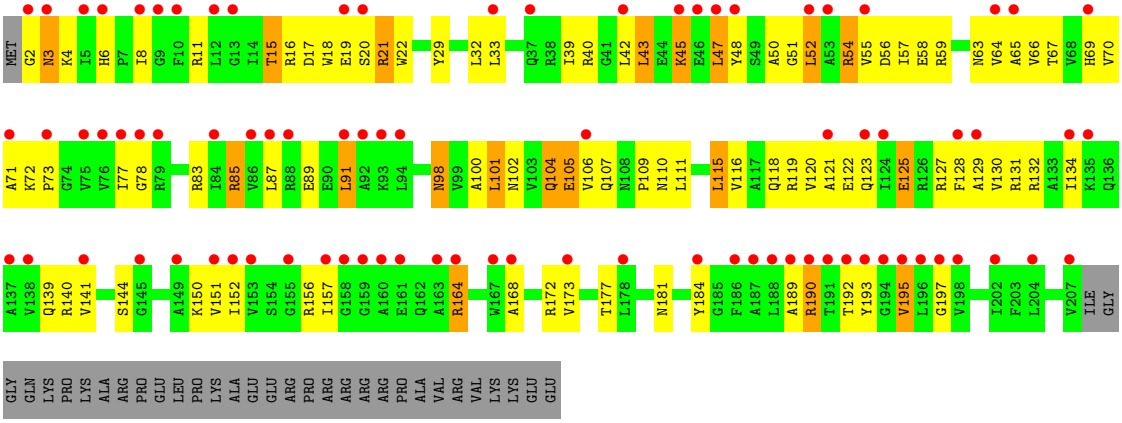
Chain AC:





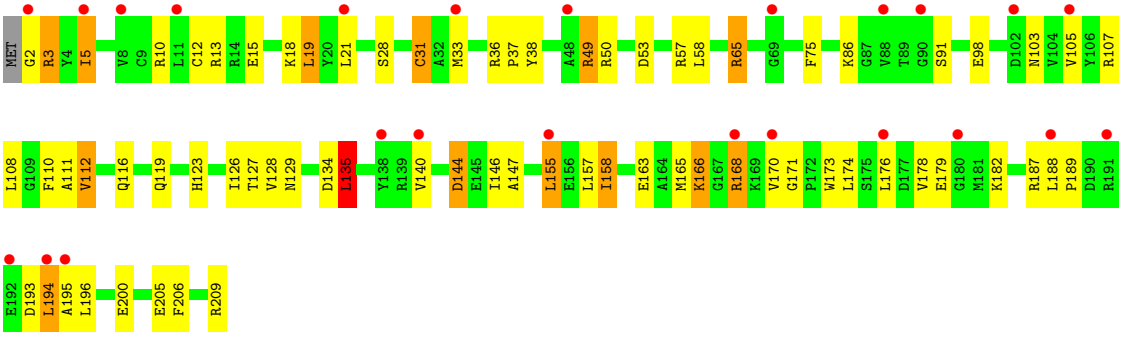
• Molecule 3: 30S ribosomal protein S3

Chain CC:



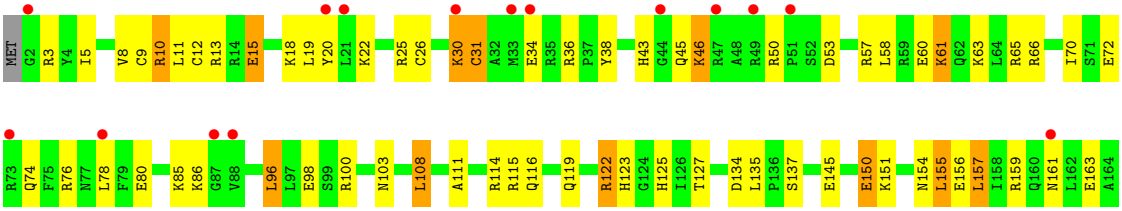
• Molecule 4: 30S ribosomal protein S4

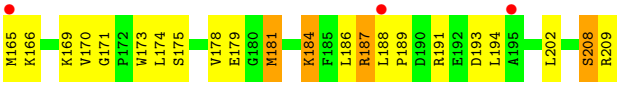
Chain AD:



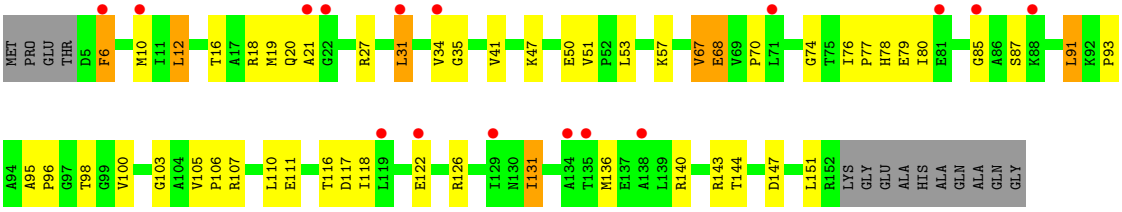
• Molecule 4: 30S ribosomal protein S4

Chain CD:

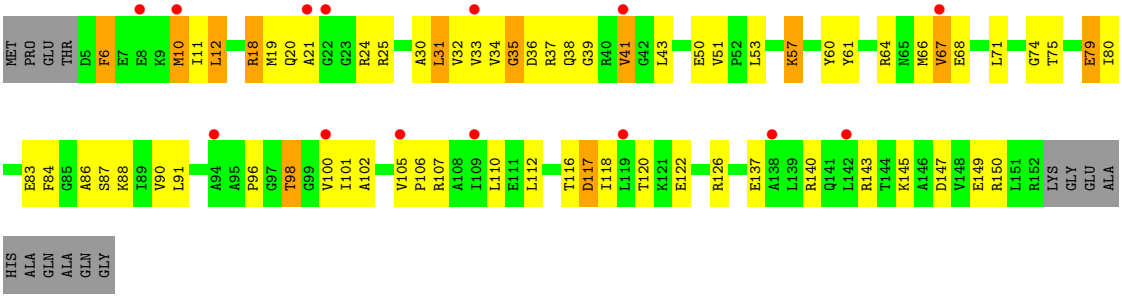




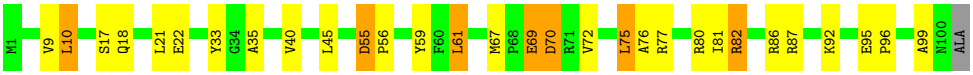
• Molecule 5: 30S ribosomal protein S5



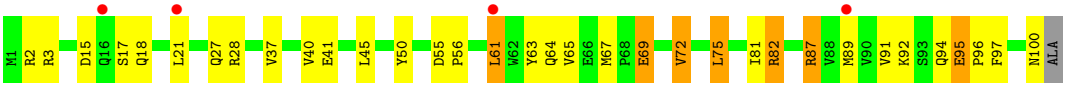
• Molecule 5: 30S ribosomal protein S5



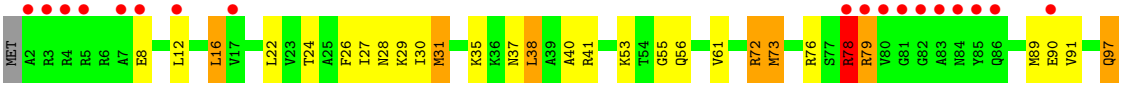
• Molecule 6: 30S ribosomal protein S6

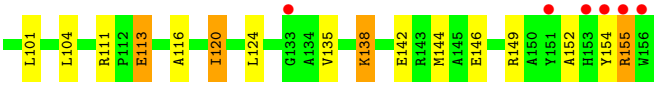


• Molecule 6: 30S ribosomal protein S6

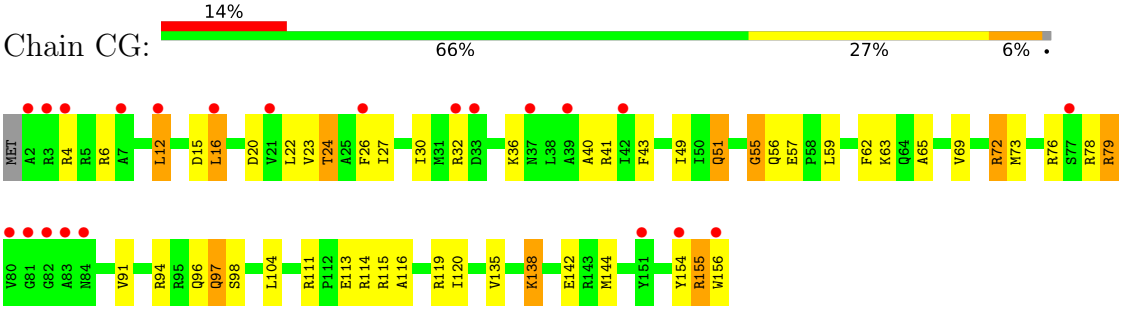


• Molecule 7: 30S ribosomal protein S7

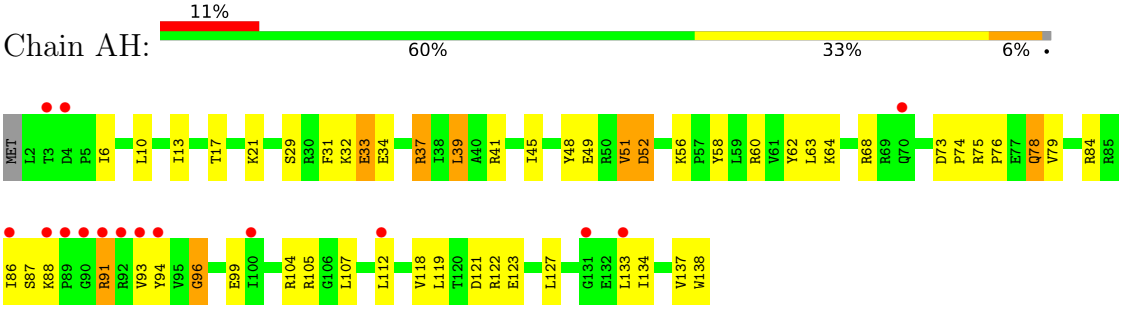




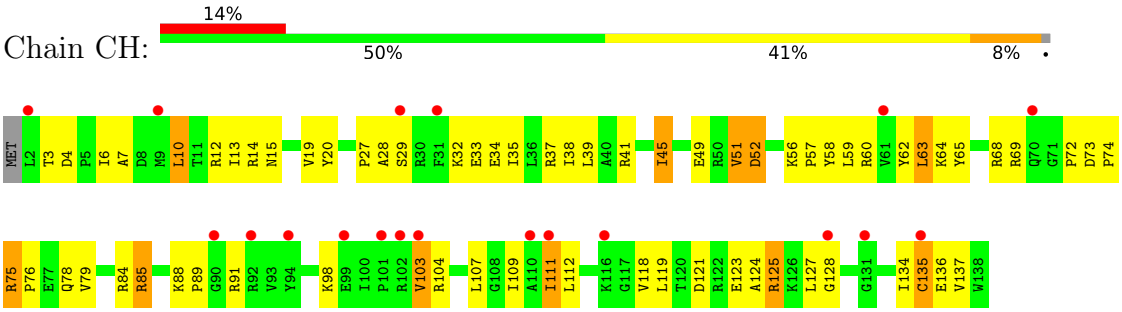
• Molecule 7: 30S ribosomal protein S7



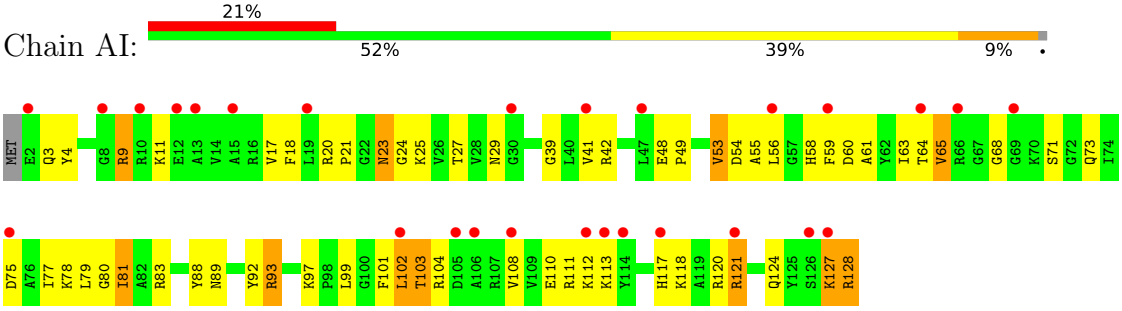
• Molecule 8: 30S ribosomal protein S8



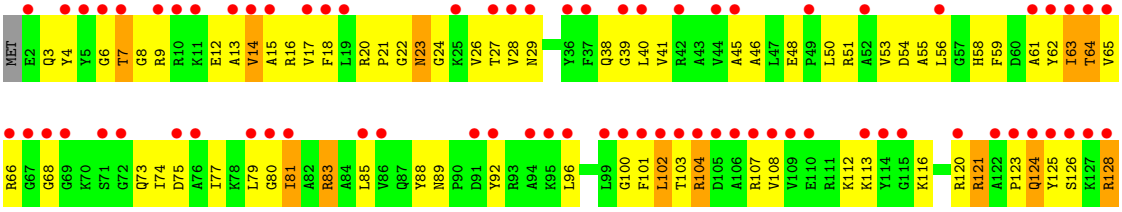
• Molecule 8: 30S ribosomal protein S8



• Molecule 9: 30S ribosomal protein S9

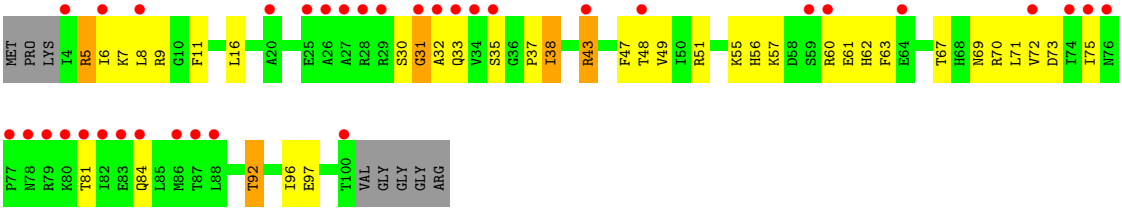


• Molecule 9: 30S ribosomal protein S9



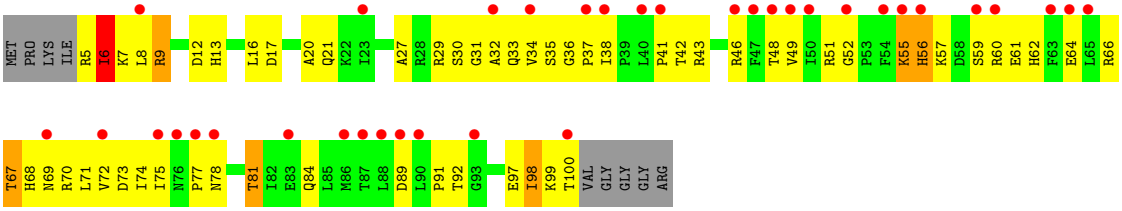
• Molecule 10: 30S ribosomal protein S10

Chain AJ:



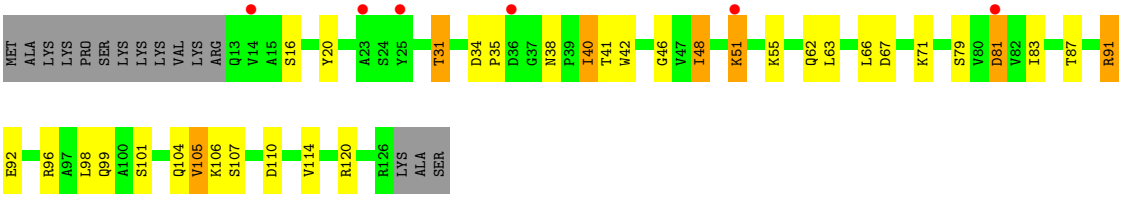
• Molecule 10: 30S ribosomal protein S10

Chain CJ:



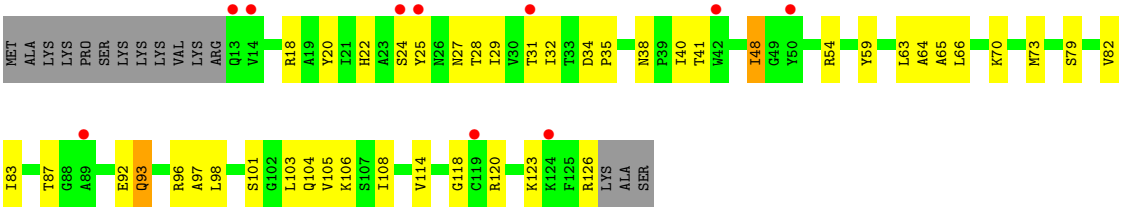
• Molecule 11: 30S ribosomal protein S11

Chain AK:



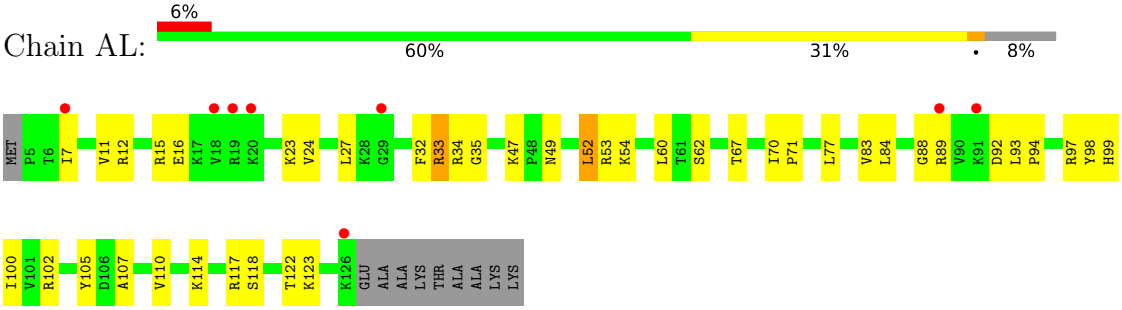
• Molecule 11: 30S ribosomal protein S11

Chain CK:



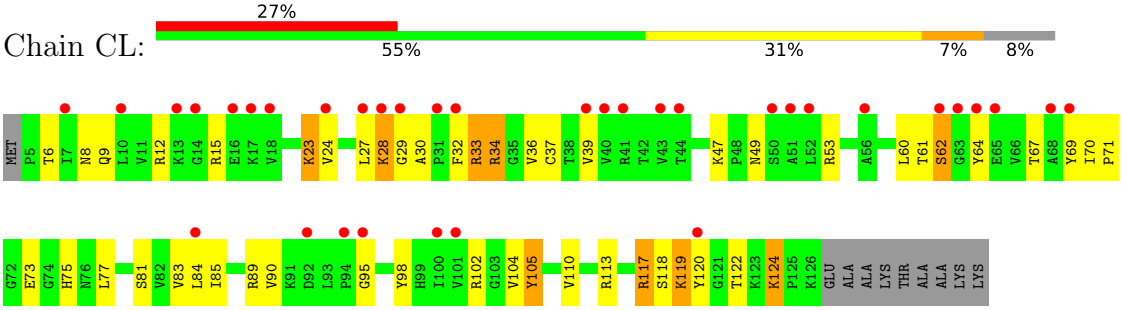
• Molecule 12: 30S ribosomal protein S12

Chain AL:



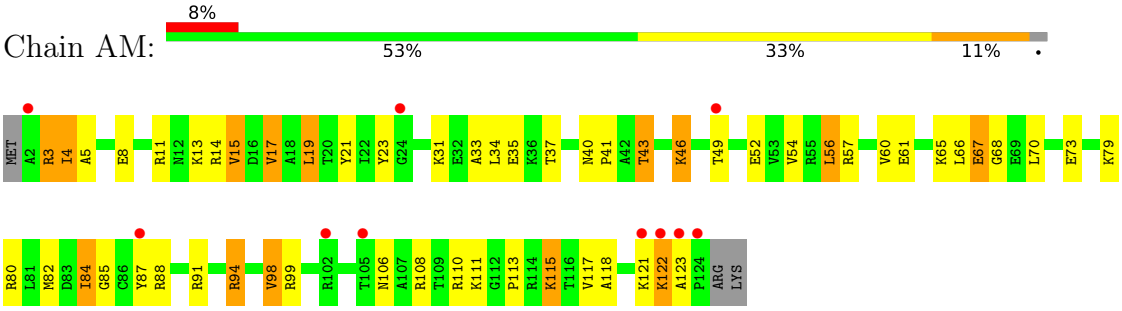
• Molecule 12: 30S ribosomal protein S12

Chain CL:



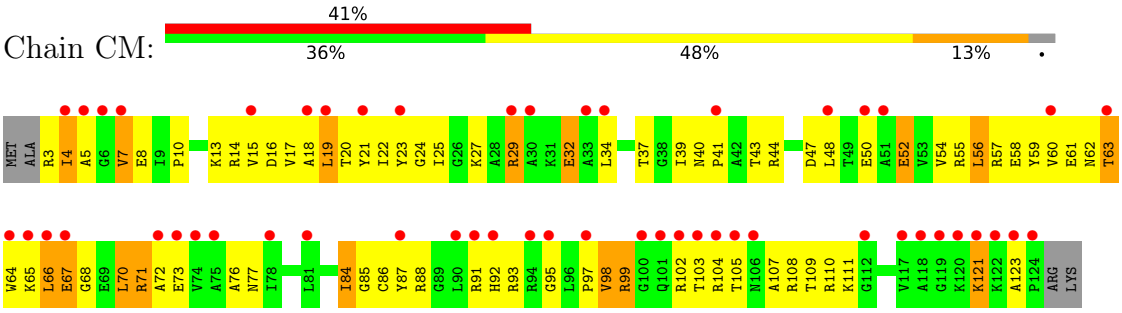
• Molecule 13: 30S ribosomal protein S13

Chain AM:



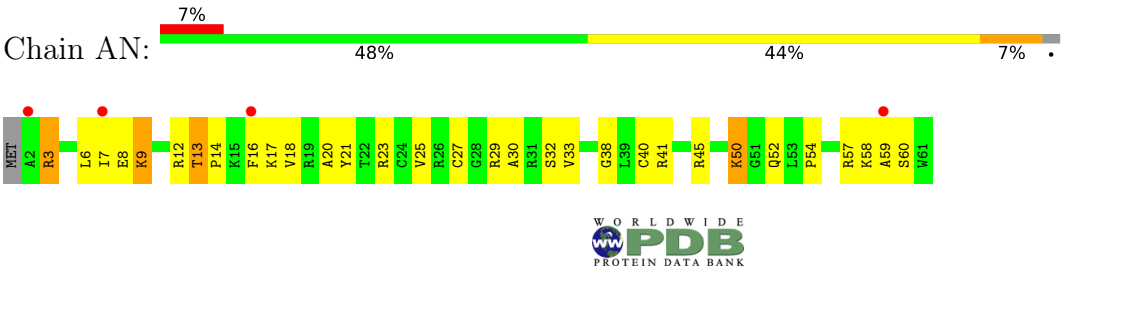
• Molecule 13: 30S ribosomal protein S13

Chain CM:



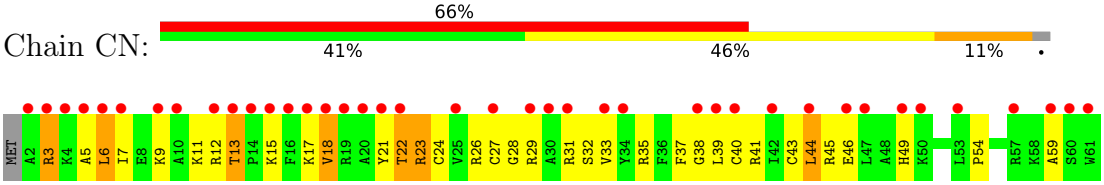
• Molecule 14: 30S ribosomal protein S14 type Z

Chain AN:



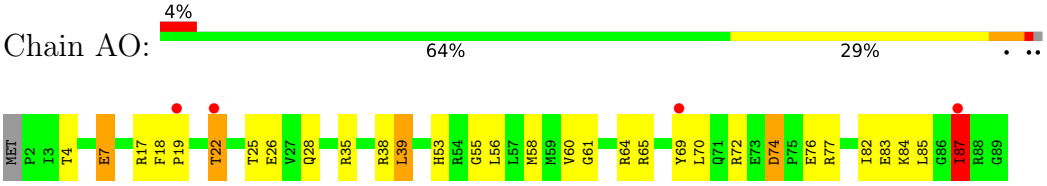
• Molecule 14: 30S ribosomal protein S14 type Z

Chain CN:



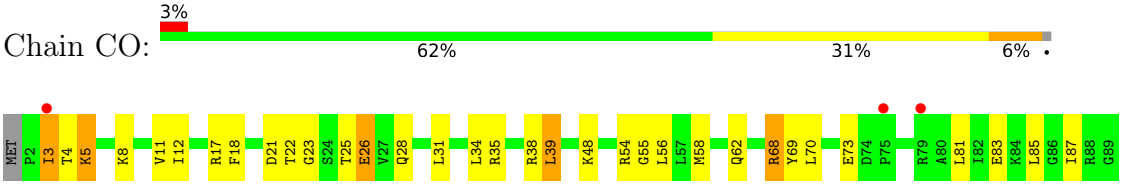
• Molecule 15: 30S ribosomal protein S15

Chain AO:



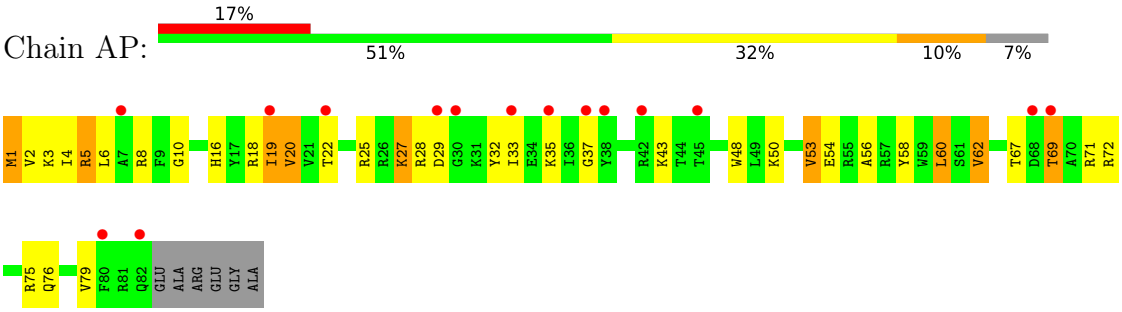
• Molecule 15: 30S ribosomal protein S15

Chain CO:



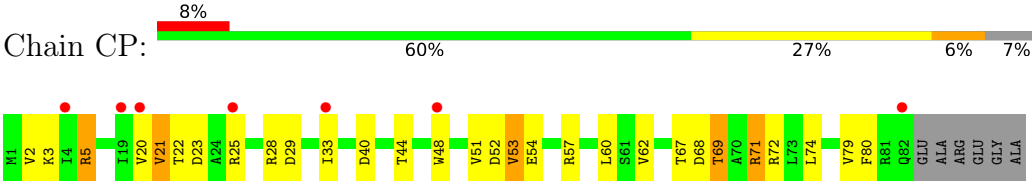
• Molecule 16: 30S ribosomal protein S16

Chain AP:



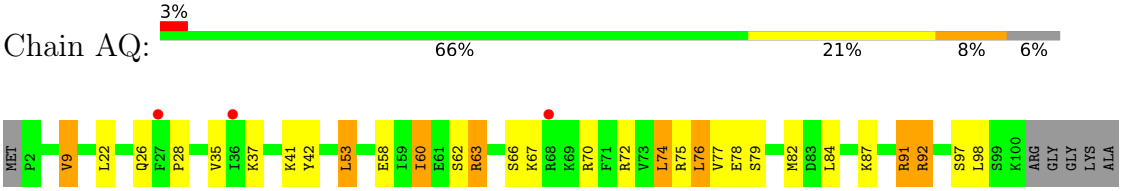
• Molecule 16: 30S ribosomal protein S16

Chain CP:



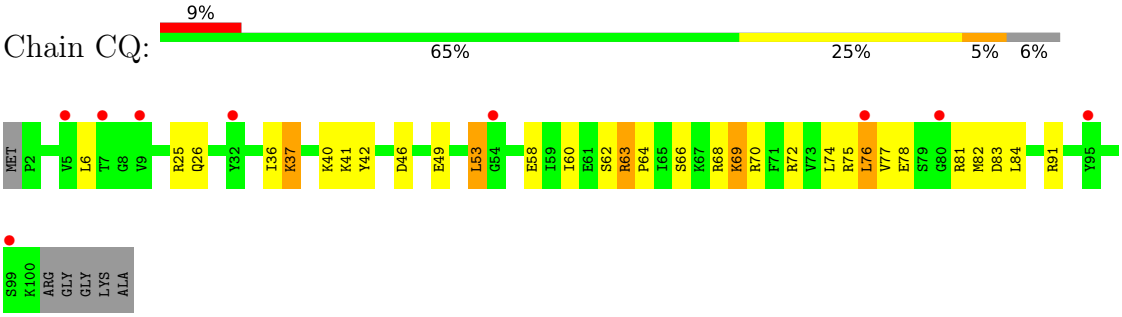
• Molecule 17: 30S ribosomal protein S17

Chain AQ:



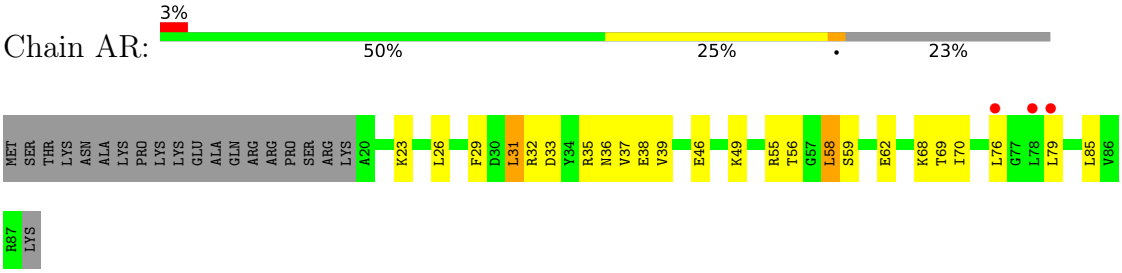
• Molecule 17: 30S ribosomal protein S17

Chain CQ:



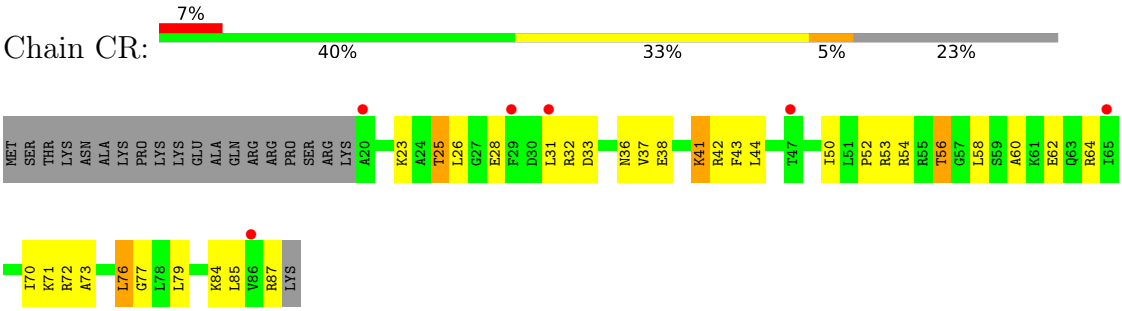
• Molecule 18: 30S ribosomal protein S18

Chain AR:



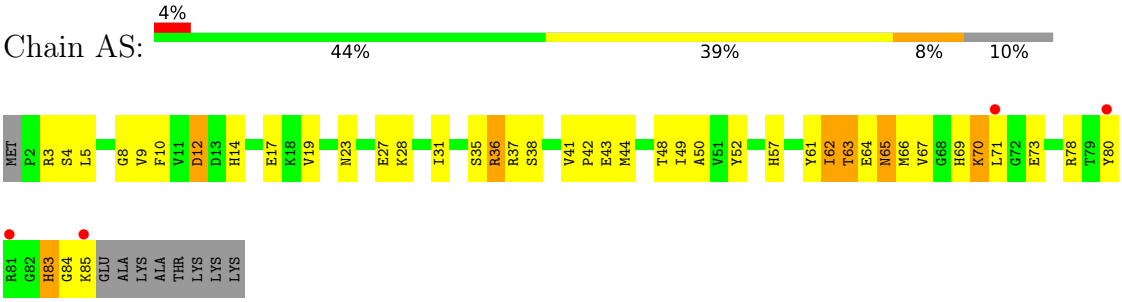
• Molecule 18: 30S ribosomal protein S18

Chain CR:



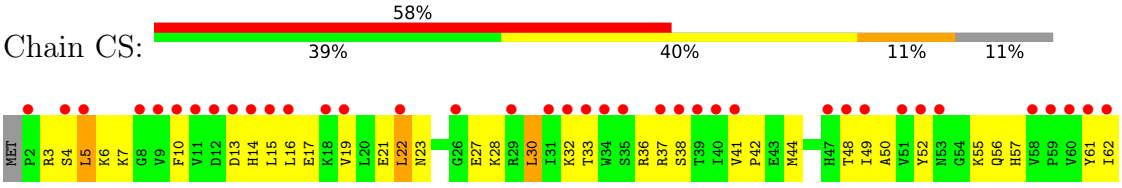
• Molecule 19: 30S ribosomal protein S19

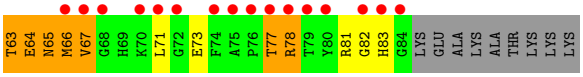
Chain AS:



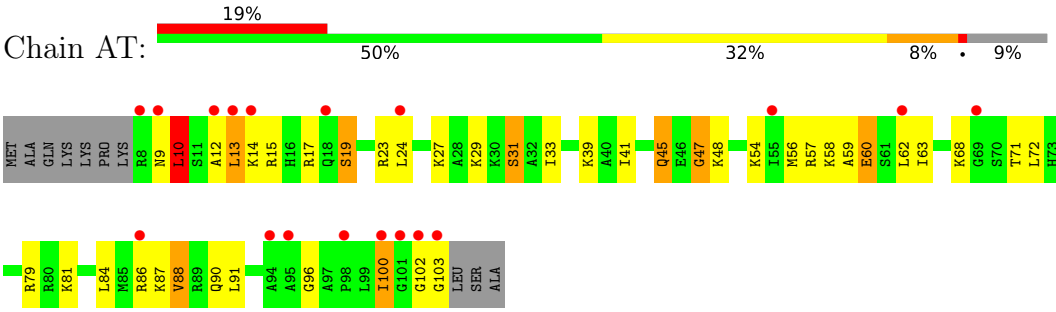
• Molecule 19: 30S ribosomal protein S19

Chain CS:

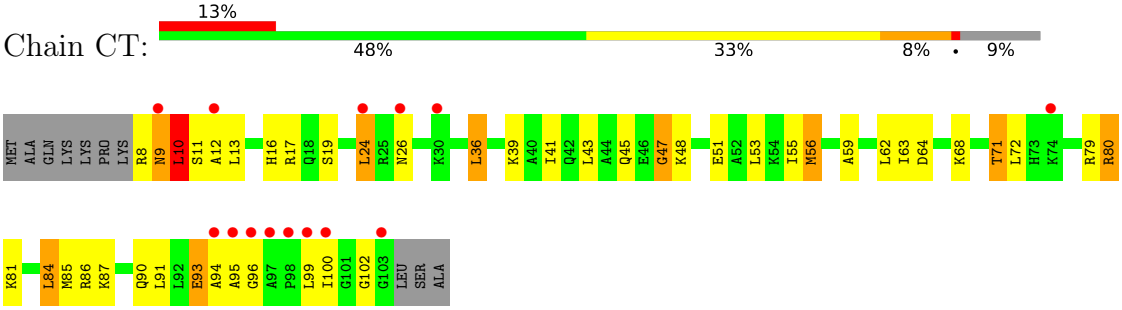




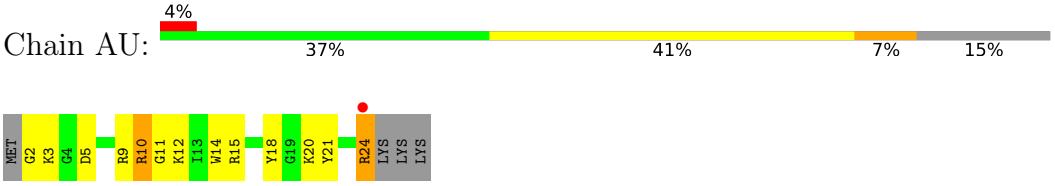
• Molecule 20: 30S ribosomal protein S20



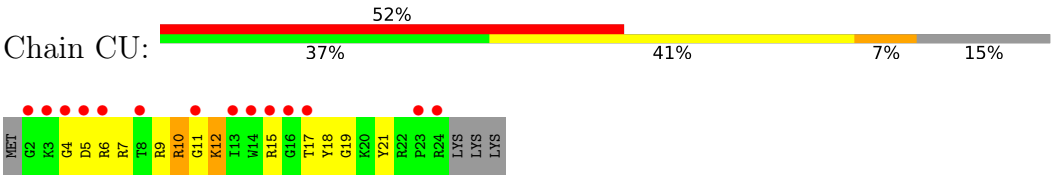
• Molecule 20: 30S ribosomal protein S20



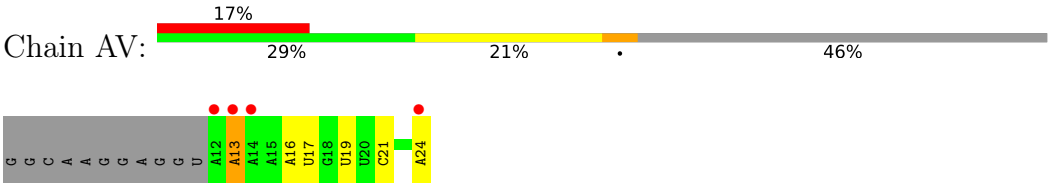
• Molecule 21: 30S ribosomal protein Thx



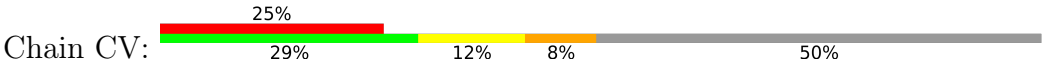
• Molecule 21: 30S ribosomal protein Thx

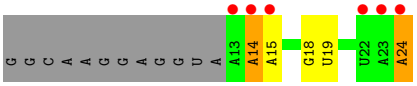


• Molecule 22: mRNA



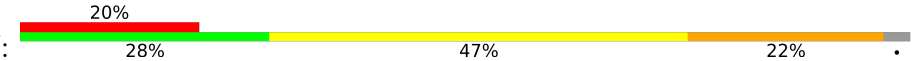
• Molecule 22: mRNA

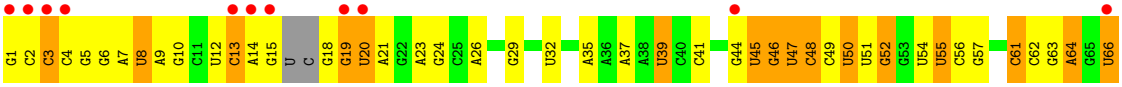


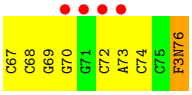


• Molecule 23: A-site tRNA

Chain AW:

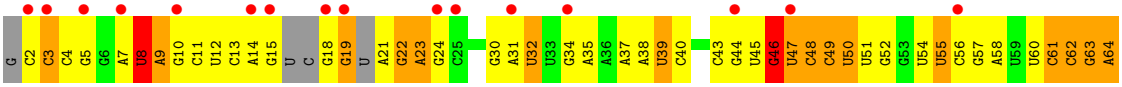


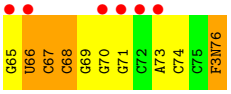




• Molecule 23: A-site tRNA

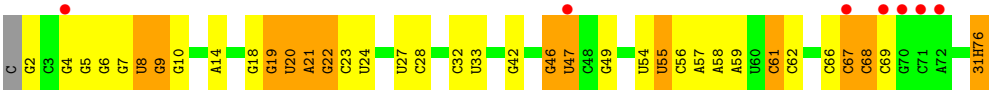
Chain CW:





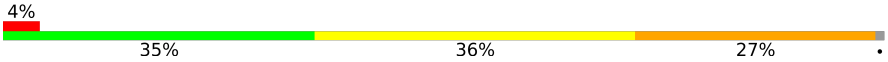
• Molecule 24: P-site tRNA

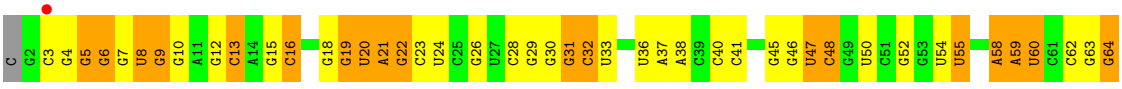
Chain AX:

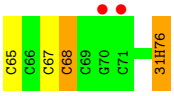


• Molecule 24: P-site tRNA

Chain CX:

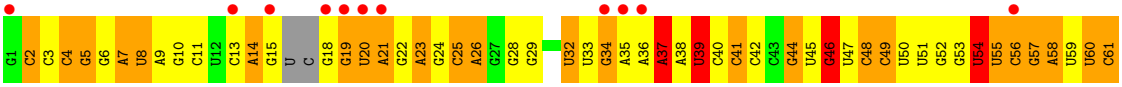






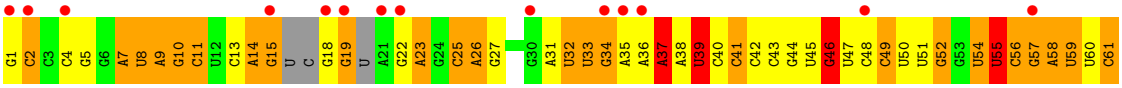
• Molecule 25: E-site tRNA

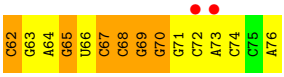
Chain AY:



• Molecule 25: E-site tRNA

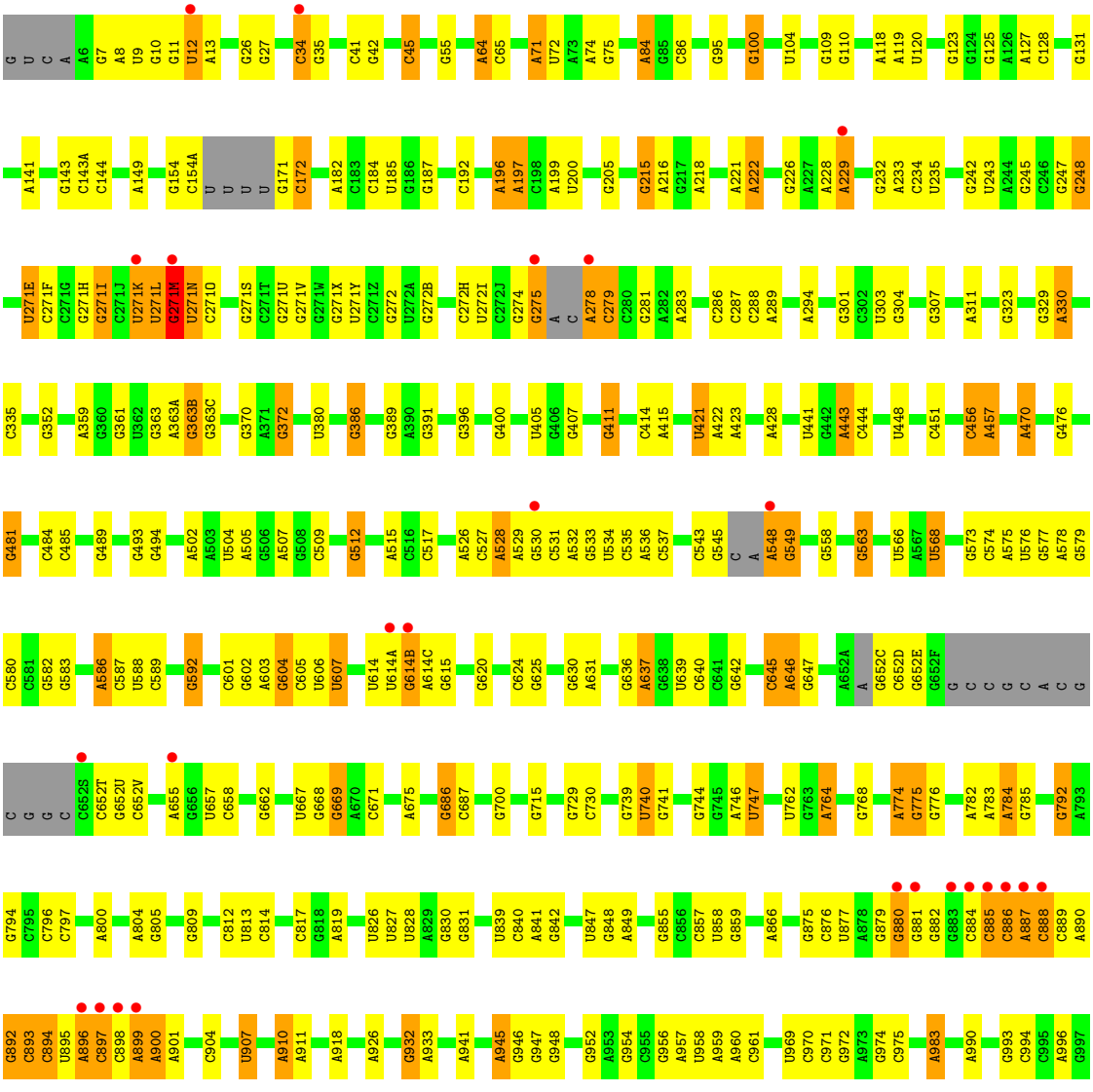
Chain CY:

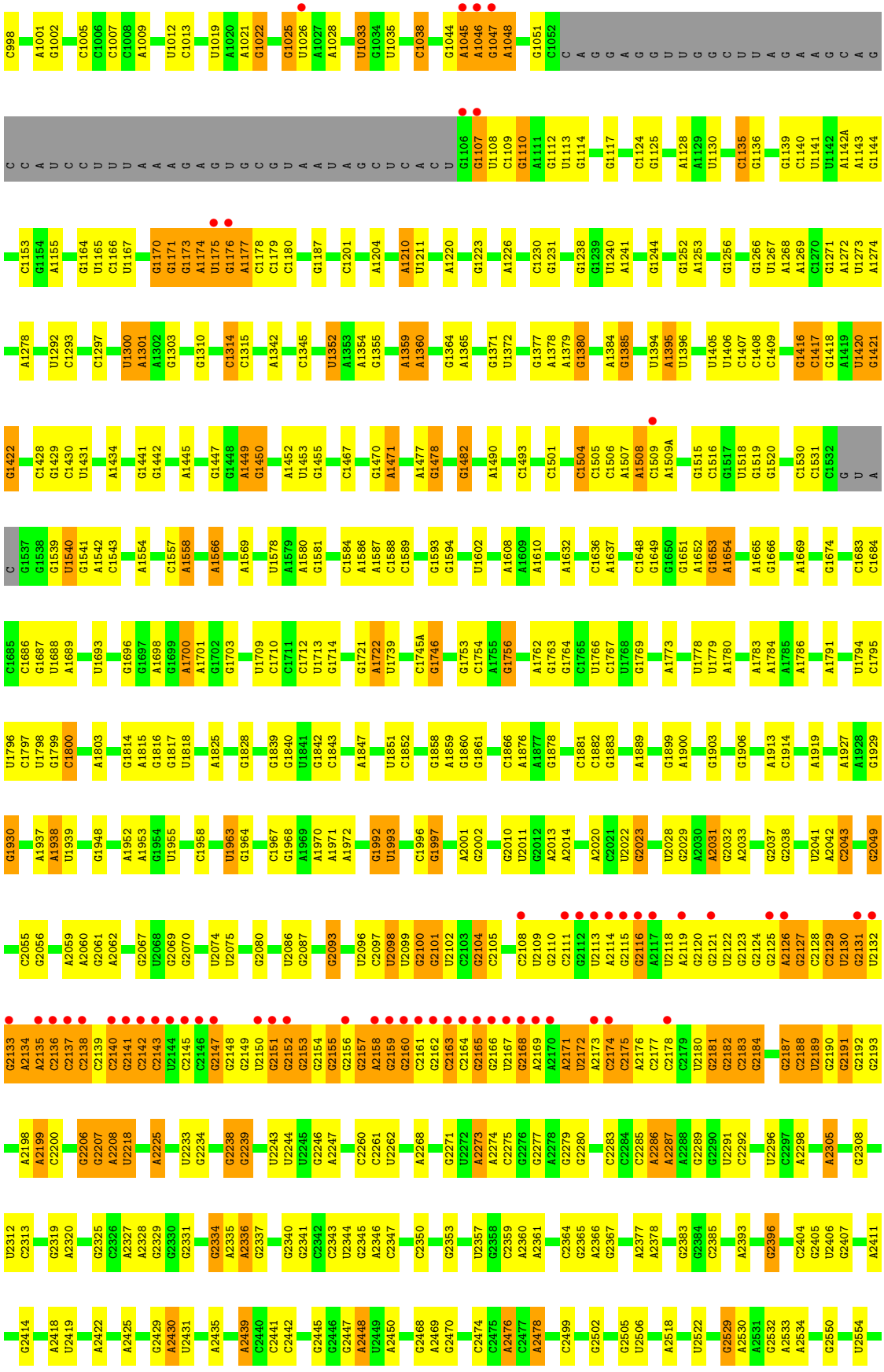




• Molecule 26: 23S Ribosomal RNA

Chain BA:

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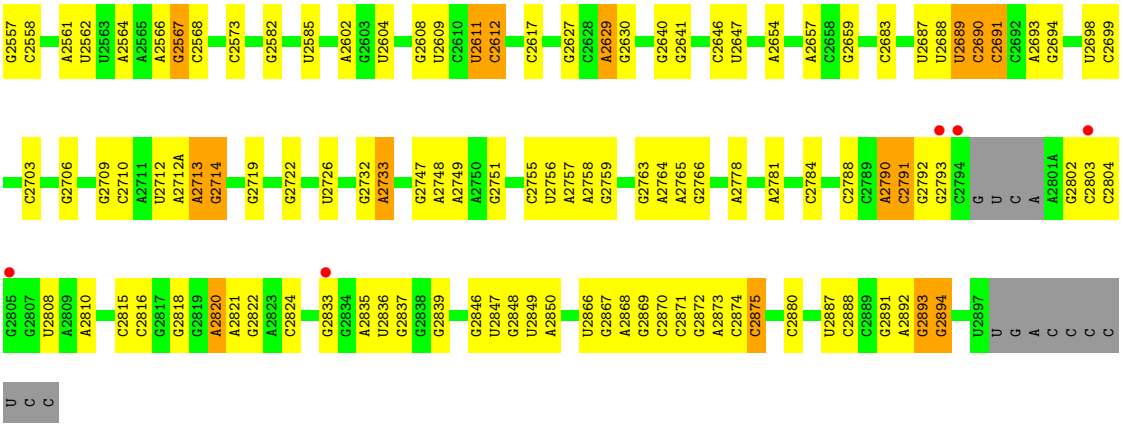
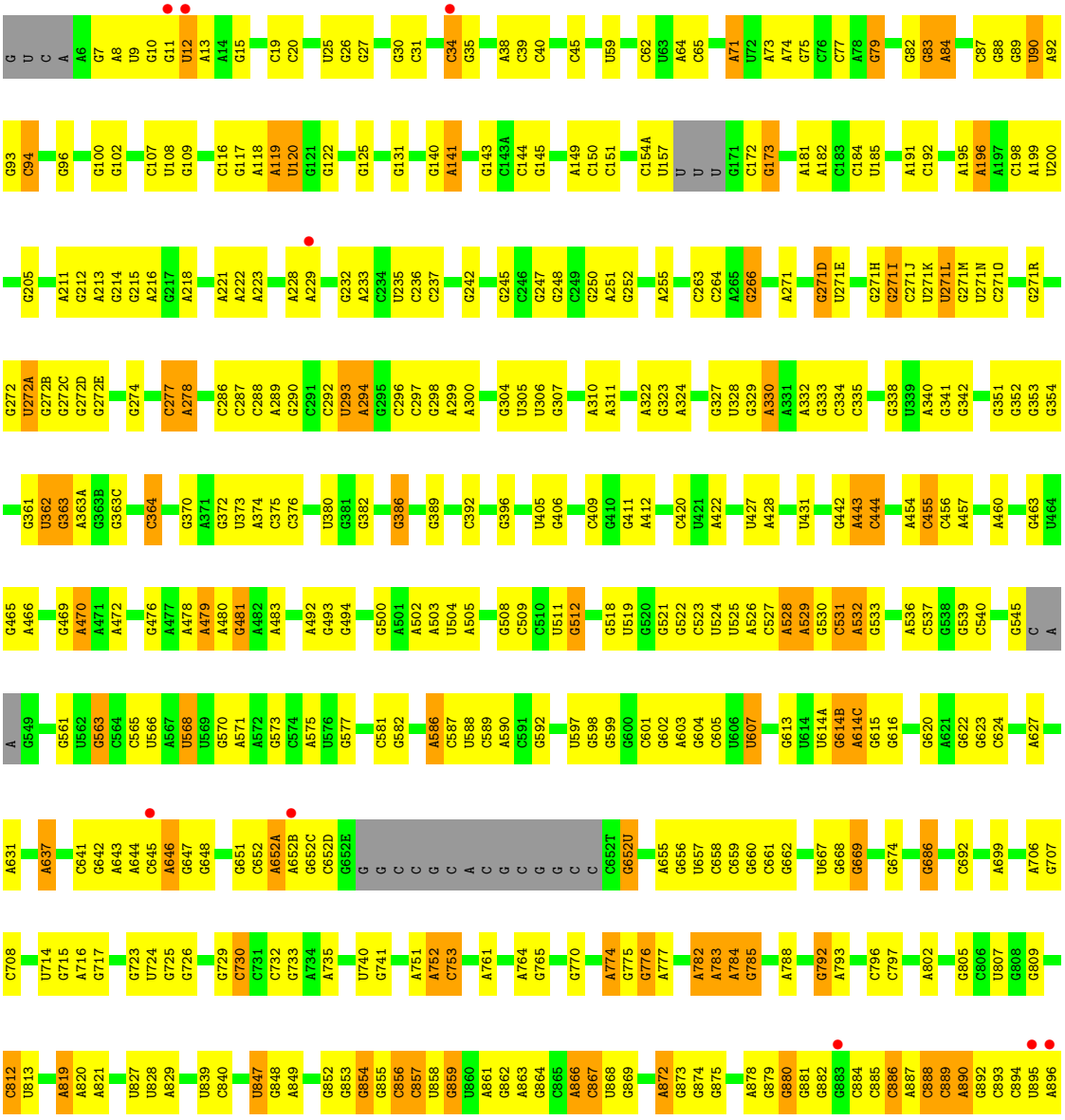
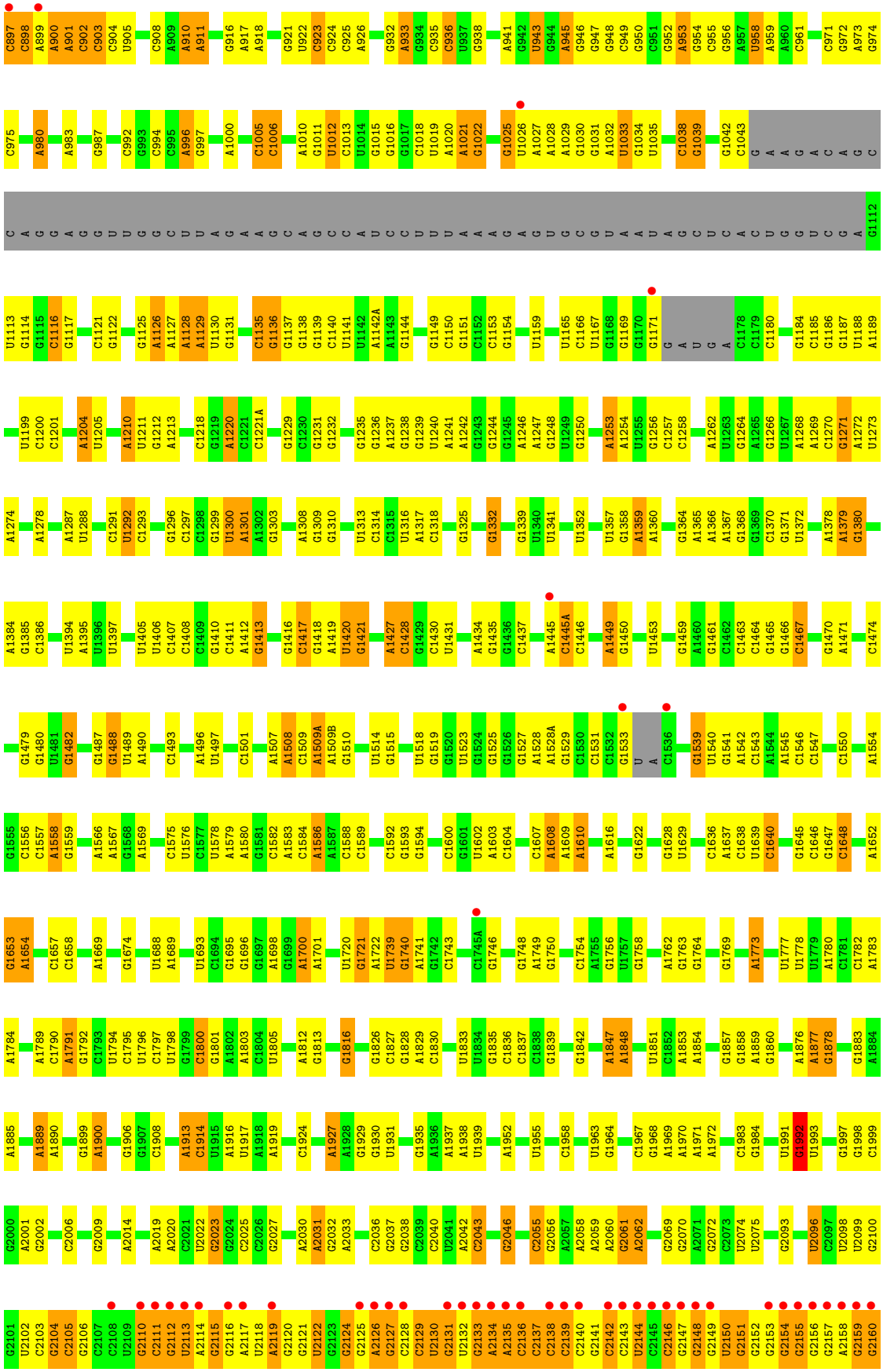


• Molecule 26: 23S Ribosomal RNA

Chain DA:

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C975 A980 A983 G987 C992 G993 C994 C995 A996 G997 A1000 C1005 C1006 A1010 G1011 U1012 C1013 U1014 G1015 G1016 G1017 C1018 U1019 A1020 A1021 G1022 G1025 U1026 A1027 A1028 A1029 G1030 G1031 A1032 U1033 G1034 U1035 C1038 G1039 G1042 C1043 G A A A G A C A G C
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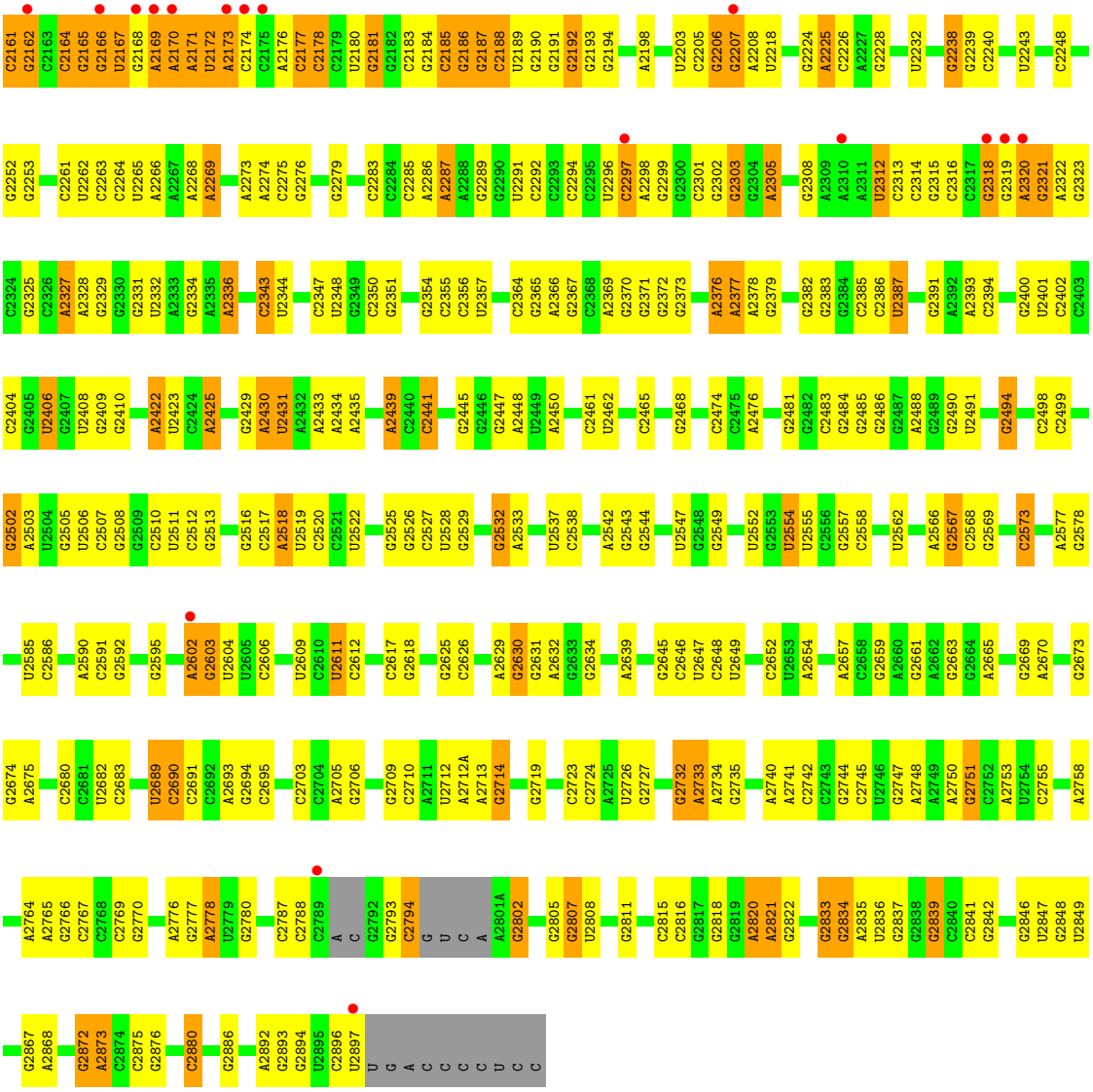
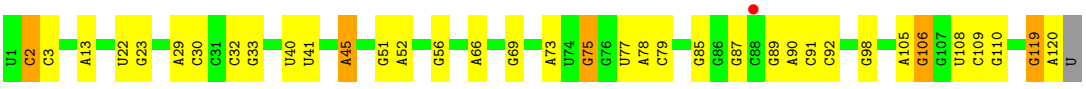


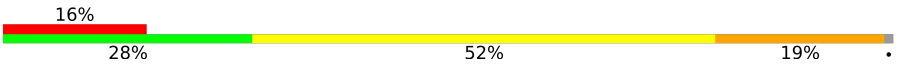
• Molecule 27: 5S Ribosomal RNA

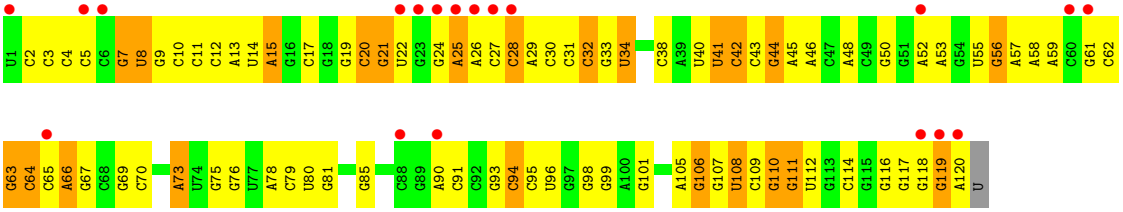
Chain BB:



• Molecule 27: 5S Ribosomal RNA

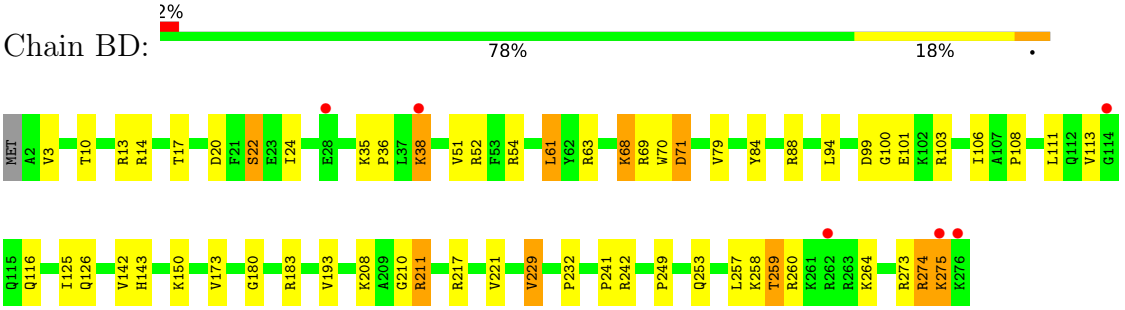
Chain DB:





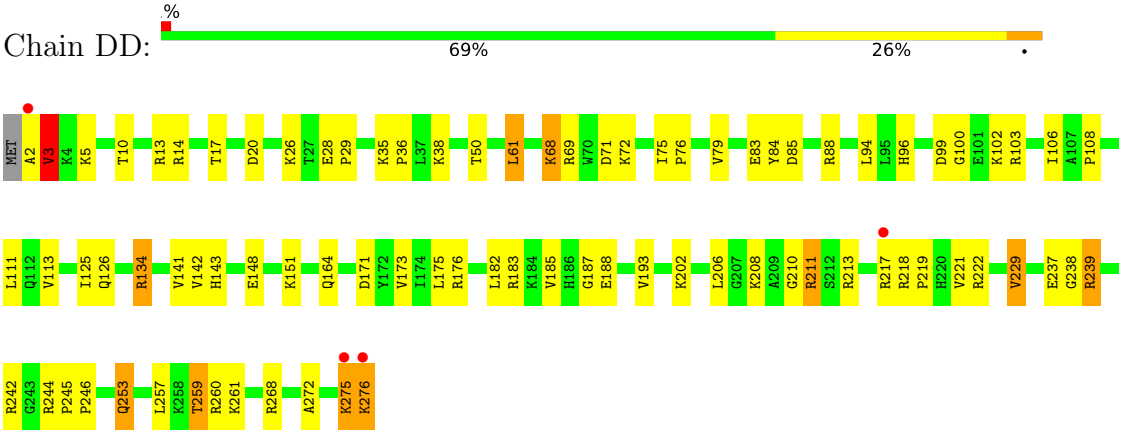
• Molecule 28: 50S ribosomal protein L2

Chain BD:



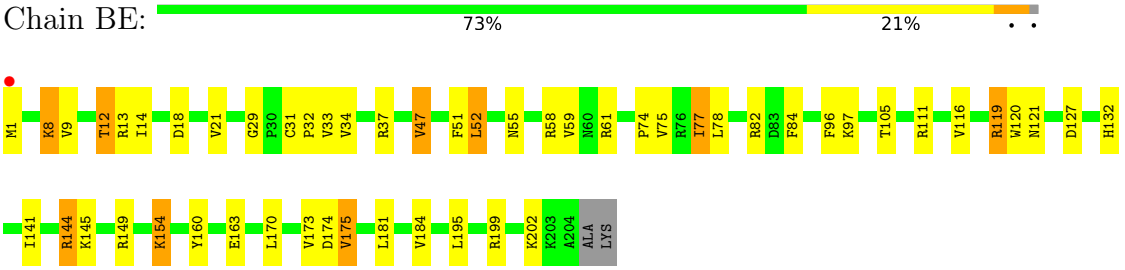
• Molecule 28: 50S ribosomal protein L2

Chain DD:



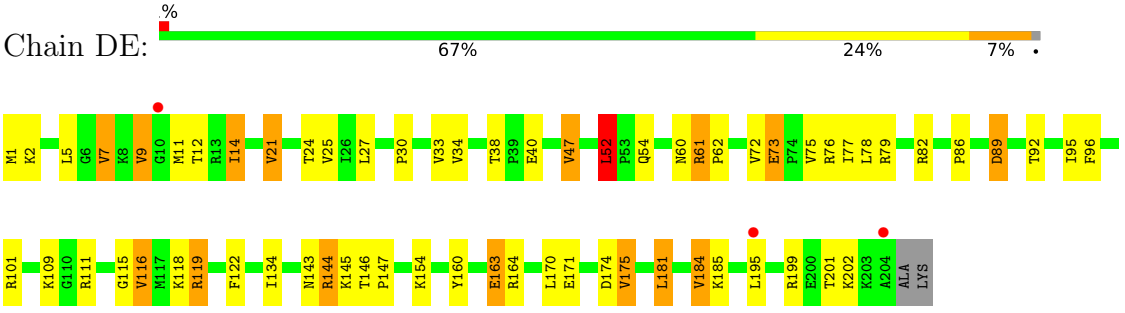
• Molecule 29: 50S ribosomal protein L3

Chain BE:



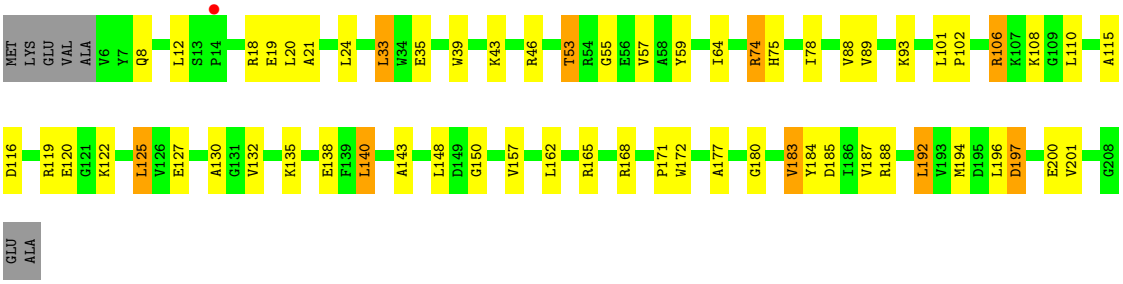
• Molecule 29: 50S ribosomal protein L3

Chain DE:



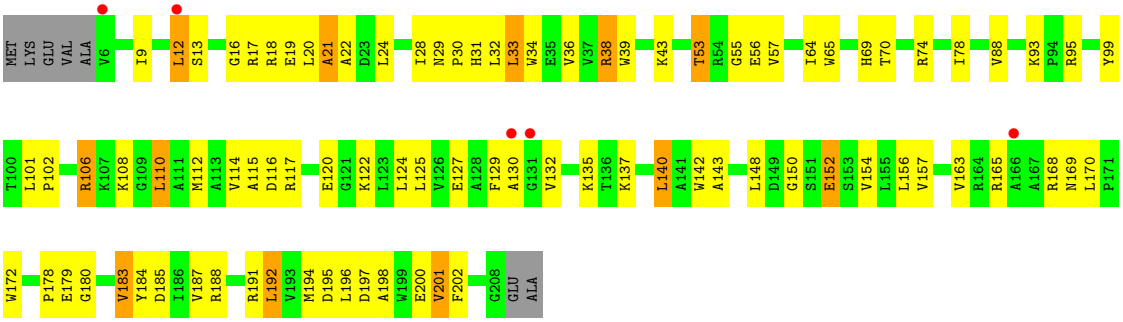
• Molecule 30: 50S ribosomal protein L4

Chain BF:



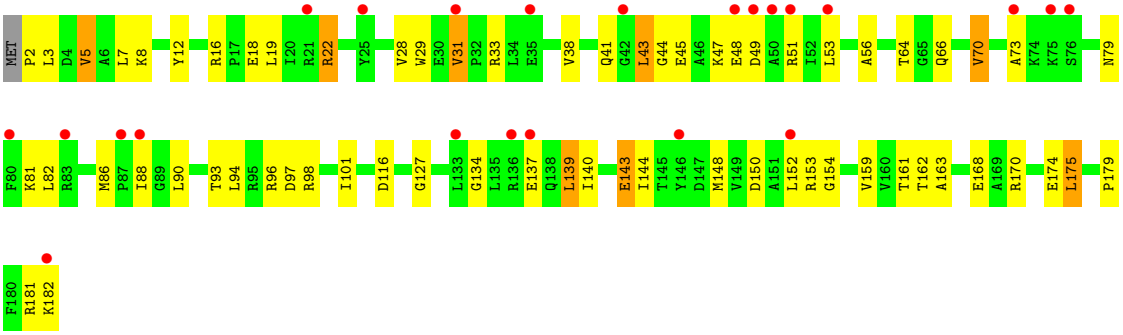
• Molecule 30: 50S ribosomal protein L4

Chain DF:



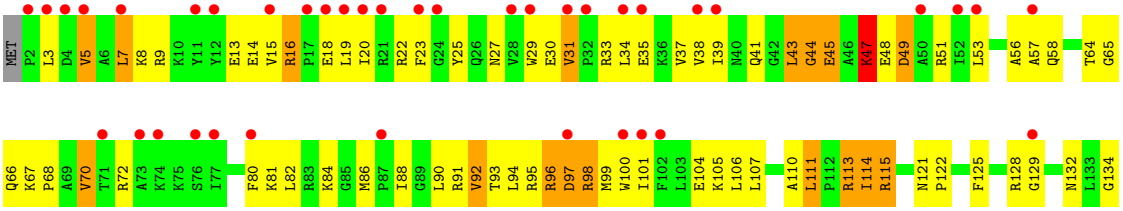
• Molecule 31: 50S ribosomal protein L5

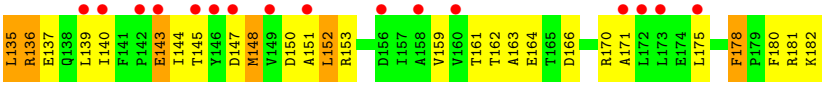
Chain BG:



• Molecule 31: 50S ribosomal protein L5

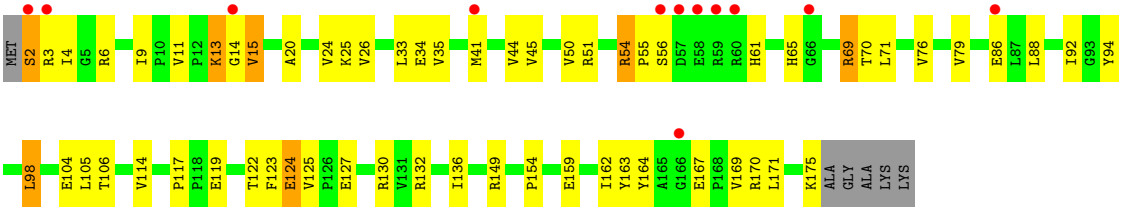
Chain DG:





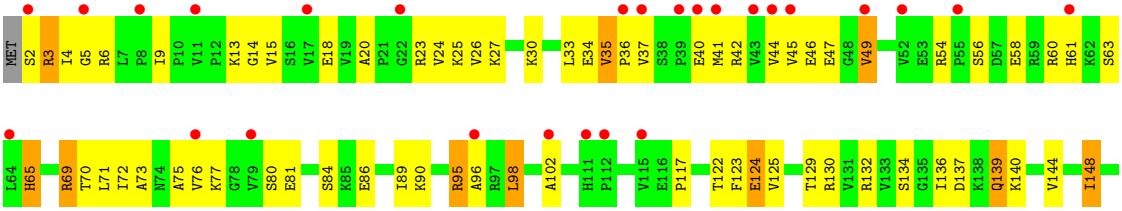
• Molecule 32: 50S ribosomal protein L6

Chain BH:



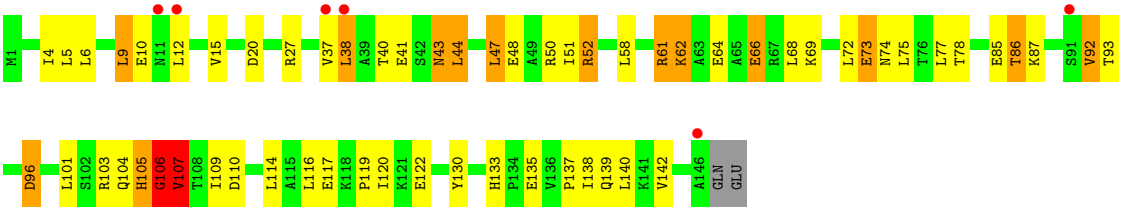
• Molecule 32: 50S ribosomal protein L6

Chain DH:



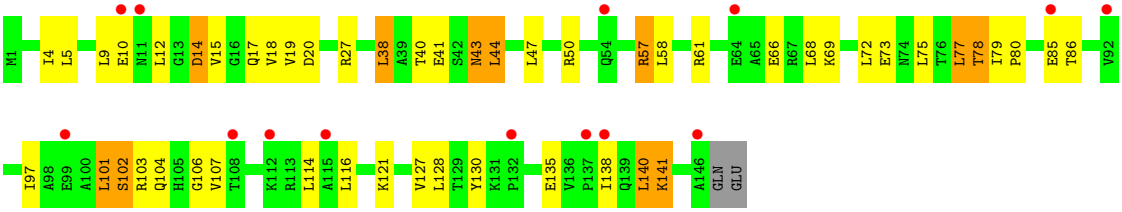
• Molecule 33: 50S ribosomal protein L9

Chain BI:



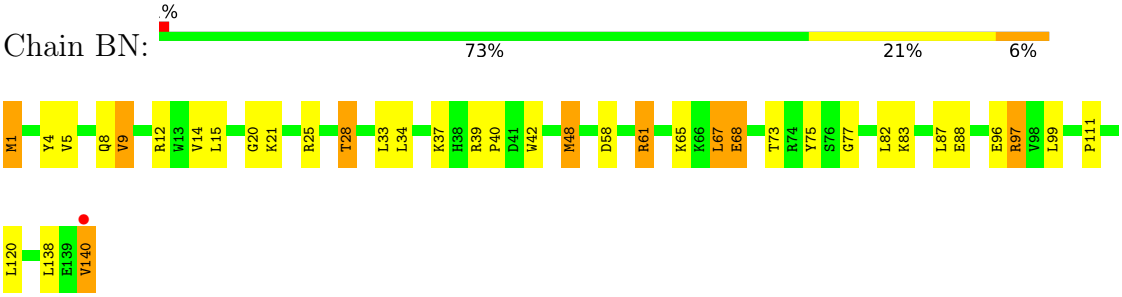
• Molecule 33: 50S ribosomal protein L9

Chain DI:



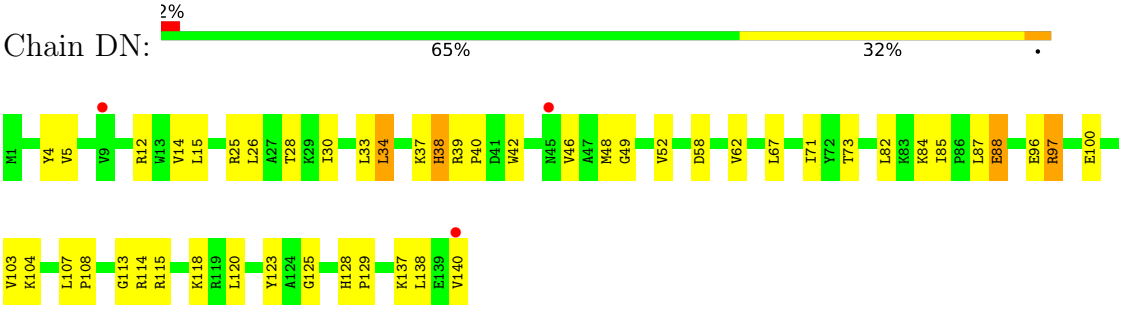
• Molecule 34: 50S ribosomal protein L13

Chain BN:



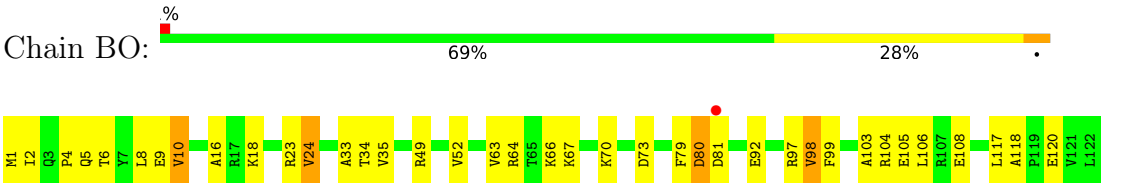
• Molecule 34: 50S ribosomal protein L13

Chain DN:



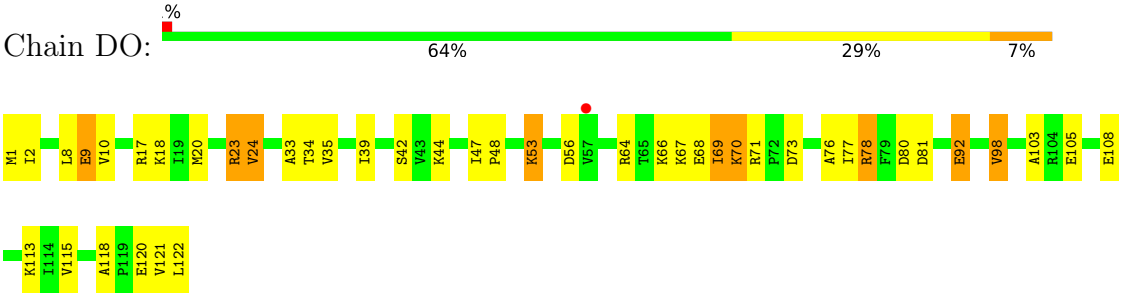
• Molecule 35: 50S ribosomal protein L14

Chain BO:



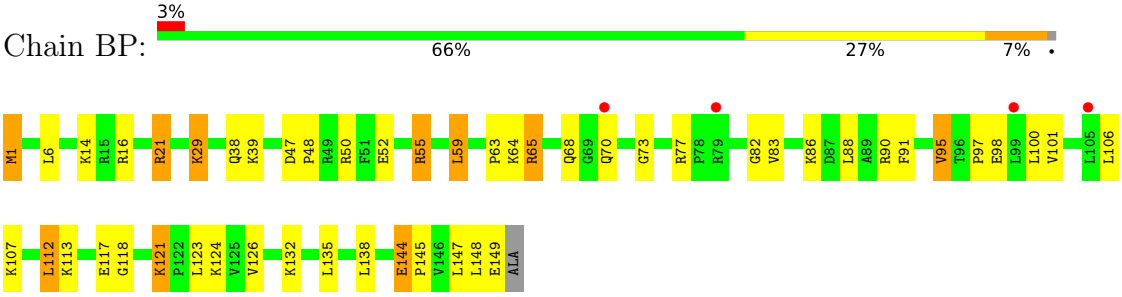
• Molecule 35: 50S ribosomal protein L14

Chain DO:



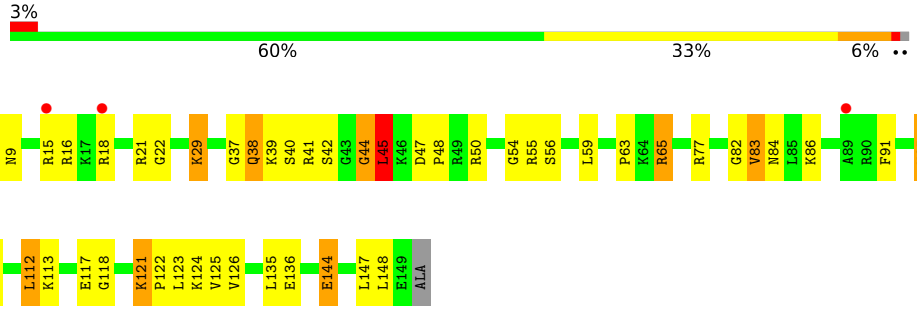
• Molecule 36: 50S ribosomal protein L15

Chain BP:



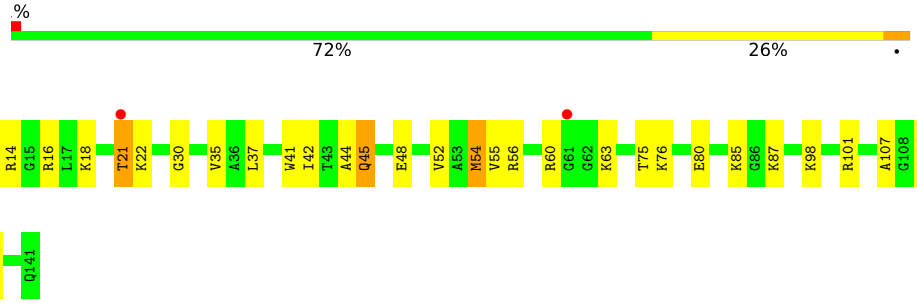
• Molecule 36: 50S ribosomal protein L15

Chain DP:



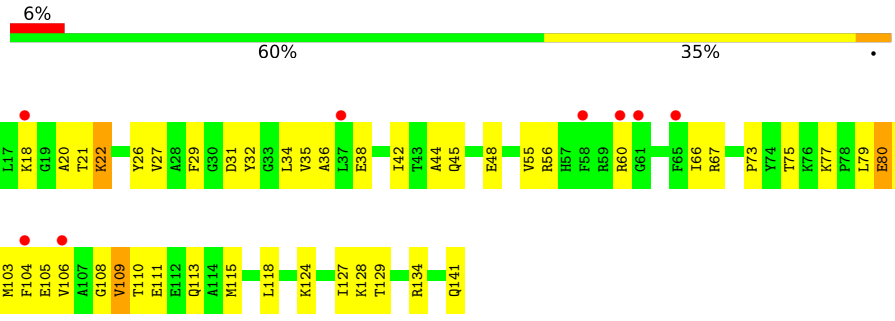
• Molecule 37: 50S ribosomal protein L16

Chain BQ:



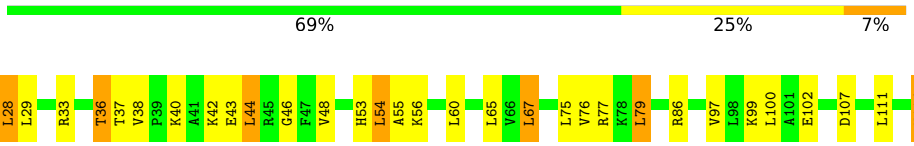
• Molecule 37: 50S ribosomal protein L16

Chain DQ:



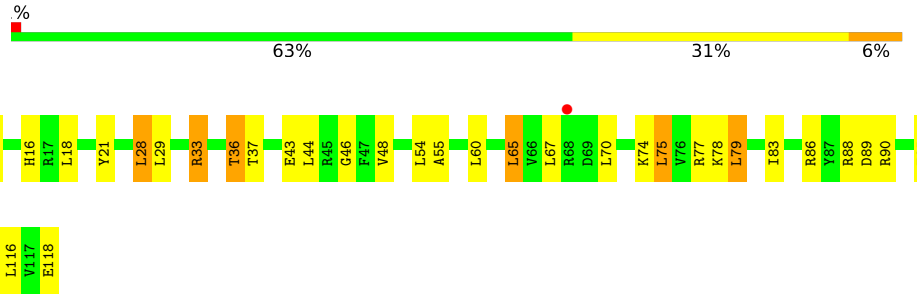
• Molecule 38: 50S ribosomal protein L17

Chain BR:



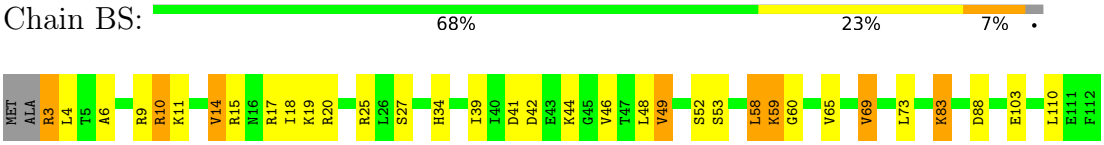
• Molecule 38: 50S ribosomal protein L17

Chain DR:



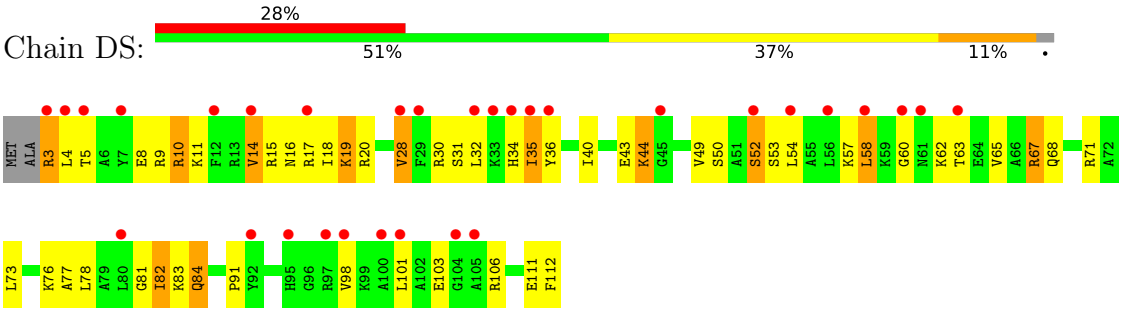
• Molecule 39: 50S ribosomal protein L18

Chain BS:



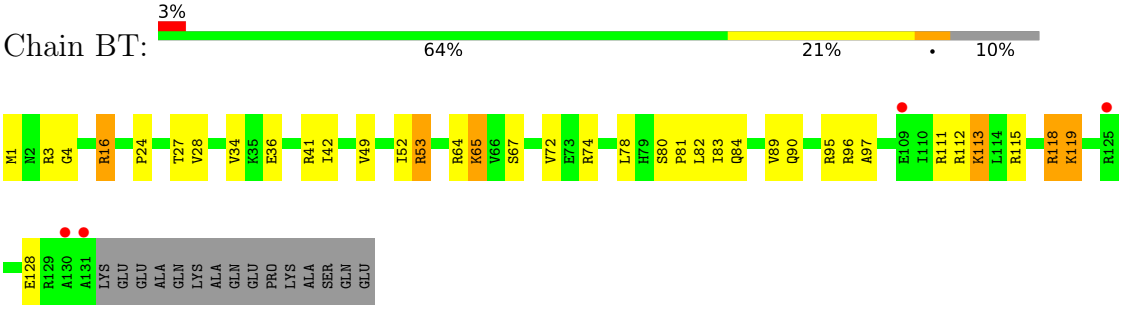
• Molecule 39: 50S ribosomal protein L18

Chain DS:



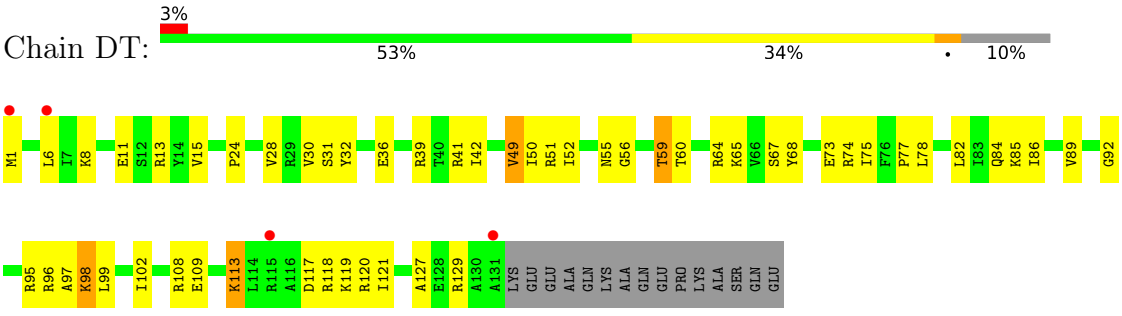
• Molecule 40: 50S ribosomal protein L19

Chain BT:



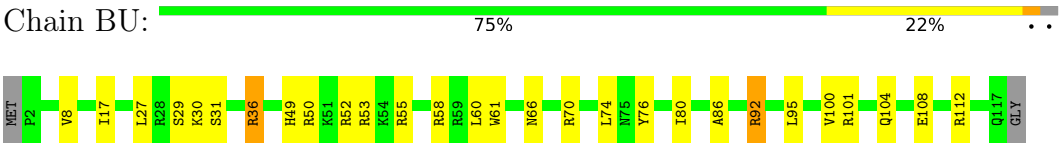
• Molecule 40: 50S ribosomal protein L19

Chain DT:



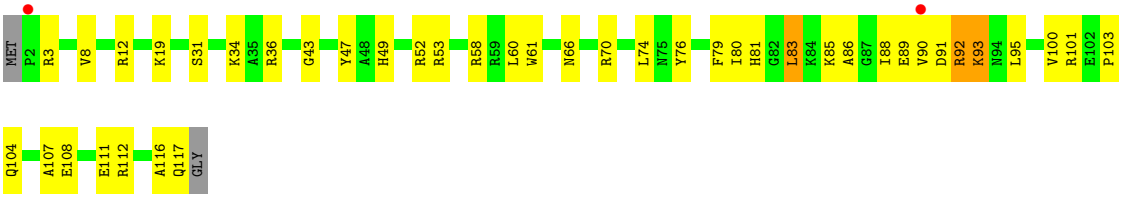
• Molecule 41: 50S ribosomal protein L20

Chain BU:

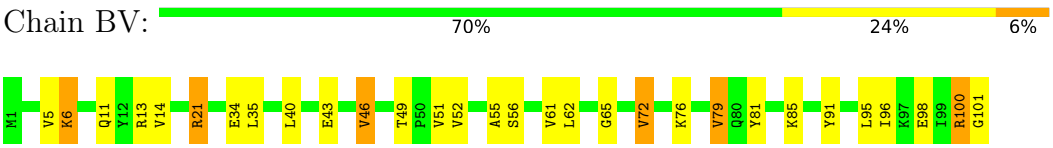


• Molecule 41: 50S ribosomal protein L20

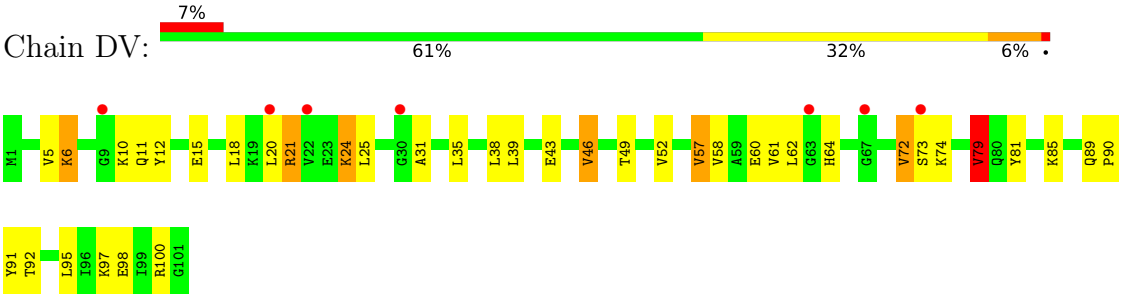
Chain DU:



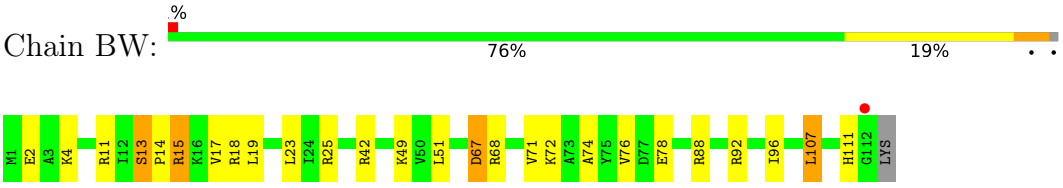
• Molecule 42: 50S ribosomal protein L21



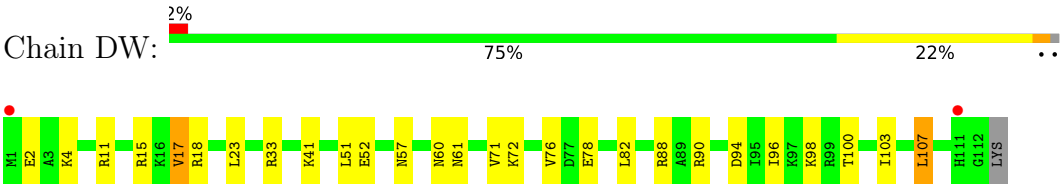
• Molecule 42: 50S ribosomal protein L21



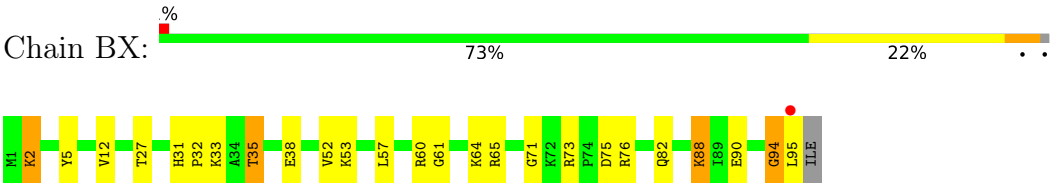
• Molecule 43: 50S ribosomal protein L22



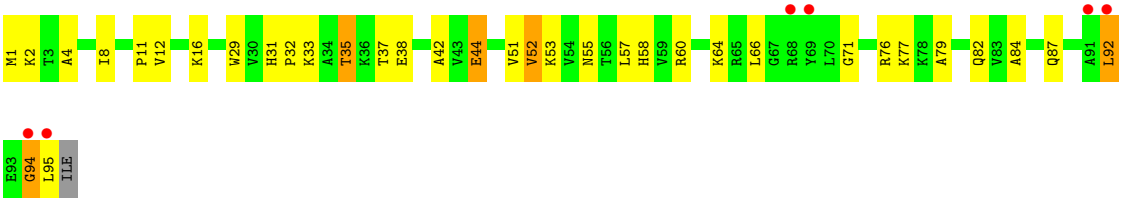
• Molecule 43: 50S ribosomal protein L22



• Molecule 44: 50S ribosomal protein L23

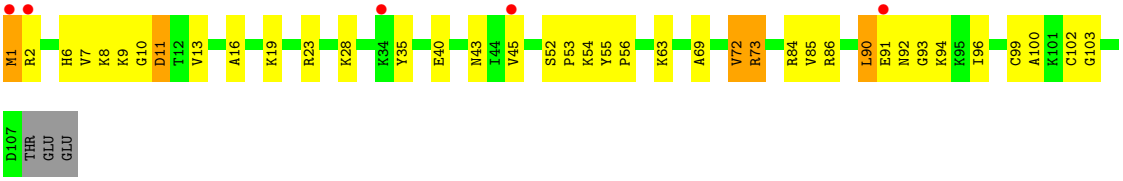


• Molecule 44: 50S ribosomal protein L23



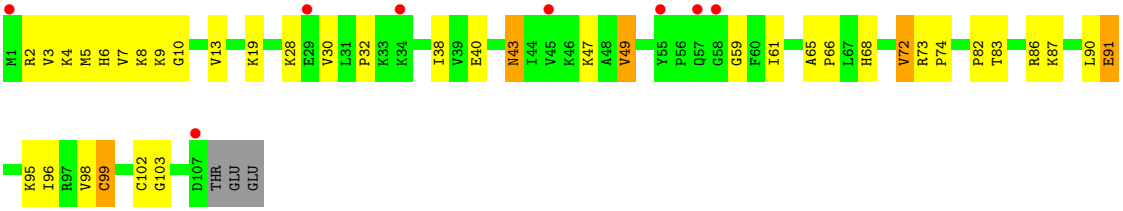
• Molecule 45: 50S ribosomal protein L24

Chain BY:



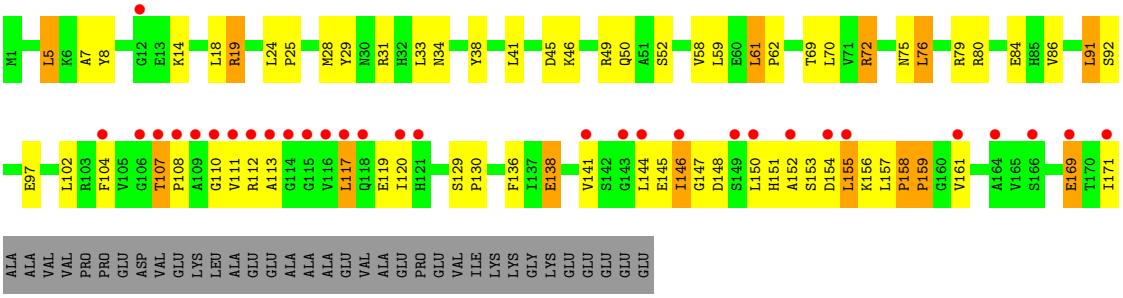
• Molecule 45: 50S ribosomal protein L24

Chain DY:



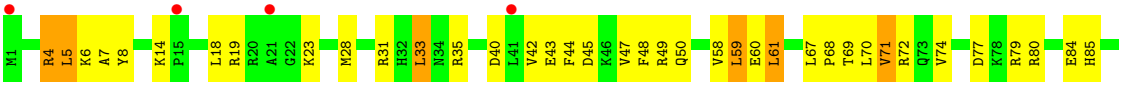
• Molecule 46: 50S ribosomal protein L25

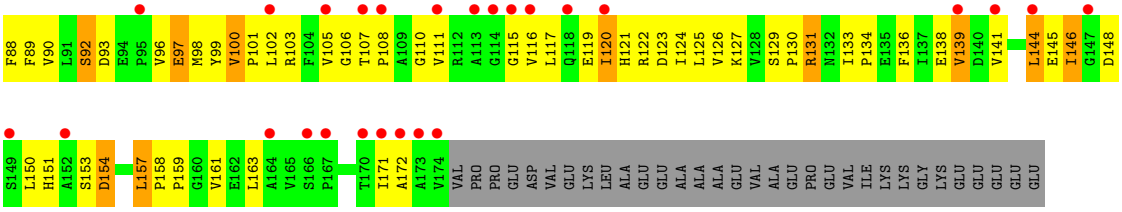
Chain BZ:



• Molecule 46: 50S ribosomal protein L25

Chain DZ:



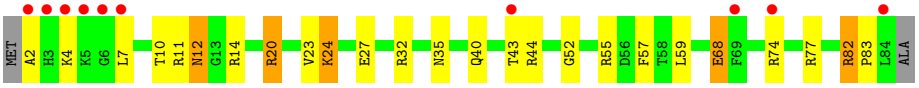


• Molecule 47: 50S ribosomal protein L27

Chain B0:

• Molecule 47: 50S ribosomal protein L27

Chain D0:

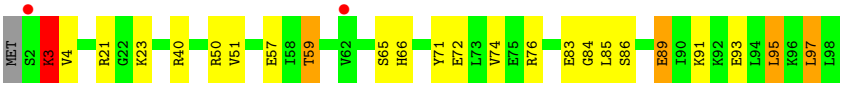


• Molecule 48: 50S ribosomal protein L28

Chain B1:

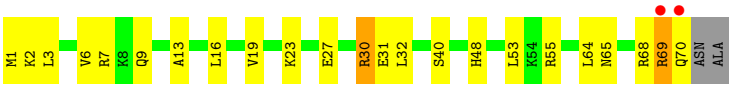
• Molecule 48: 50S ribosomal protein L28

Chain D1:



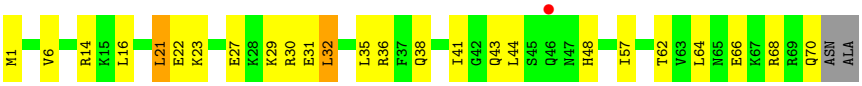
• Molecule 49: 50S ribosomal protein L29

Chain B2:



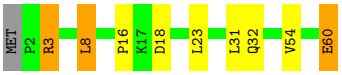
• Molecule 49: 50S ribosomal protein L29

Chain D2:



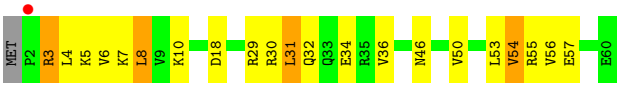
• Molecule 50: 50S ribosomal protein L30

Chain B3:



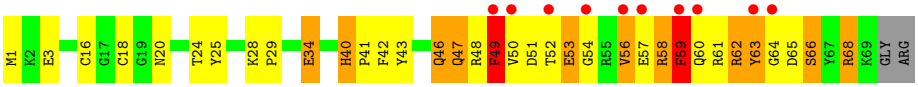
• Molecule 50: 50S ribosomal protein L30

Chain D3:



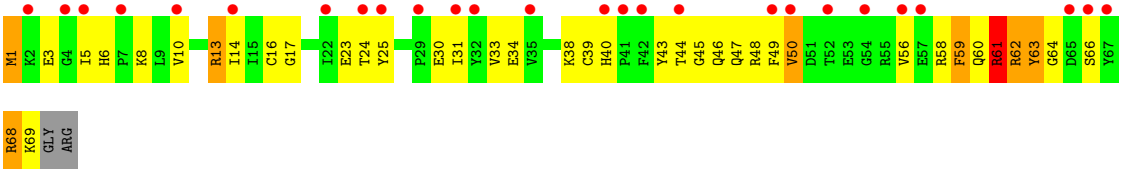
• Molecule 51: 50S ribosomal protein L31

Chain B4:



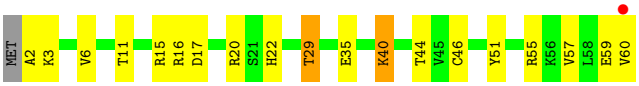
• Molecule 51: 50S ribosomal protein L31

Chain D4:



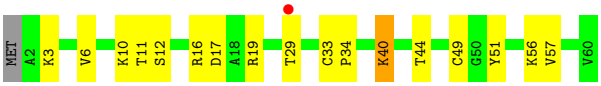
• Molecule 52: 50S ribosomal protein L32

Chain B5:



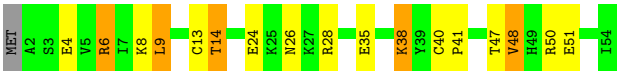
• Molecule 52: 50S ribosomal protein L32

Chain D5:



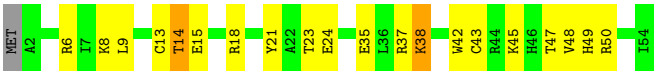
• Molecule 53: 50S ribosomal protein L33

Chain B6:



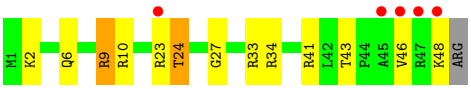
• Molecule 53: 50S ribosomal protein L33

Chain D6:



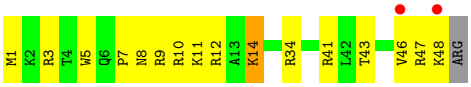
• Molecule 54: 50S ribosomal protein L34

Chain B7:



• Molecule 54: 50S ribosomal protein L34

Chain D7:

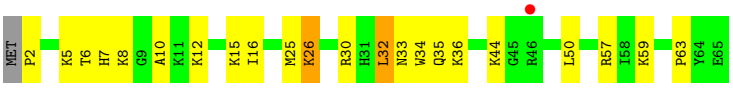


• Molecule 55: 50S ribosomal protein L35

Chain B8:

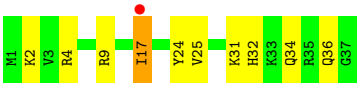
• Molecule 55: 50S ribosomal protein L35

Chain D8:



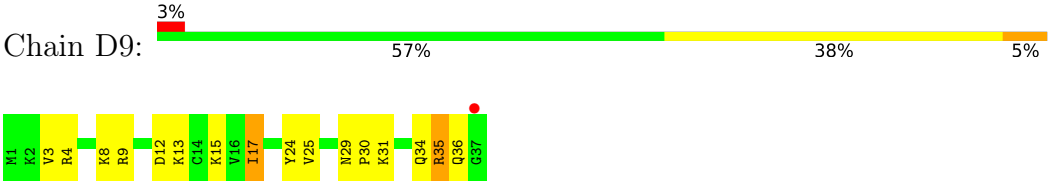
• Molecule 56: 50S ribosomal protein L36

Chain B9:



• Molecule 56: 50S ribosomal protein L36

Chain D9:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.45Å 448.85Å 619.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	151.90 – 2.60 151.90 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (151.90-2.60) 99.9 (151.90-2.60)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.22 (at 2.62Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.223 , 0.264 0.225 , 0.265	Depositor DCC
R_{free} test set	88430 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	56.4	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 59.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.40$, $< L^2 > = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	297127	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 4SU, K, SF4, MG, 5MC, 31H, F3N, PSU, 7MG, MIA, ZN, 5MU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	AA	0.22	0/36027	0.45	2/56227 (0.0%)
1	CA	0.22	0/36170	0.47	7/56452 (0.0%)
2	AB	0.40	0/1881	1.02	10/2542 (0.4%)
2	CB	0.46	0/1860	1.07	7/2518 (0.3%)
3	AC	0.39	0/1576	0.88	2/2130 (0.1%)
3	CC	0.41	0/1568	0.97	5/2122 (0.2%)
4	AD	0.39	0/1689	0.89	3/2267 (0.1%)
4	CD	0.39	0/1708	0.92	5/2289 (0.2%)
5	AE	0.43	0/1145	0.96	4/1543 (0.3%)
5	CE	0.43	0/1149	1.01	6/1548 (0.4%)
6	AF	0.38	0/825	0.79	0/1118
6	CF	0.38	0/833	0.83	2/1128 (0.2%)
7	AG	0.37	0/1250	0.83	1/1679 (0.1%)
7	CG	0.38	0/1254	0.91	3/1683 (0.2%)
8	AH	0.37	0/1108	0.88	1/1494 (0.1%)
8	CH	0.36	0/1108	0.87	2/1494 (0.1%)
9	AI	0.38	0/1005	0.90	0/1350
9	CI	0.40	0/997	0.96	2/1343 (0.1%)
10	AJ	0.38	0/722	0.91	0/982
10	CJ	0.46	0/727	1.06	4/988 (0.4%)
11	AK	0.39	0/848	0.86	1/1149 (0.1%)
11	CK	0.38	0/848	0.90	0/1149
12	AL	0.40	0/946	0.81	0/1274
12	CL	0.37	0/946	0.93	3/1274 (0.2%)
13	AM	0.40	0/977	0.94	2/1310 (0.2%)
13	CM	0.43	0/961	0.93	1/1291 (0.1%)
14	AN	0.40	0/501	0.83	0/664
14	CN	0.42	0/501	0.88	0/664
15	AO	0.39	0/739	0.87	3/985 (0.3%)
15	CO	0.37	0/739	0.86	0/985
16	AP	0.40	0/697	0.82	0/939
16	CP	0.39	0/693	0.82	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	AQ	0.35	0/836	0.85	0/1117
17	CQ	0.33	0/836	0.82	0/1117
18	AR	0.36	0/560	0.81	0/746
18	CR	0.36	0/560	0.82	0/746
19	AS	0.40	0/676	0.96	0/911
19	CS	0.48	0/661	1.15	2/893 (0.2%)
20	AT	0.38	0/730	0.95	1/965 (0.1%)
20	CT	0.38	0/733	0.92	3/969 (0.3%)
21	AU	0.32	0/203	0.79	0/266
21	CU	0.36	0/203	0.92	0/266
22	AV	0.22	0/310	0.41	0/480
22	CV	0.23	0/282	0.44	0/437
23	AW	0.29	1/1577 (0.1%)	0.53	0/2454
23	CW	0.31	0/1531	0.57	0/2379
24	AX	0.27	0/1700	0.43	0/2650
24	CX	0.26	1/1700 (0.1%)	0.45	0/2650
25	AY	0.33	0/1602	0.59	0/2493
25	CY	0.32	0/1579	0.57	0/2455
26	BA	0.28	0/68013	0.46	3/106165 (0.0%)
26	DA	0.23	0/67542	0.44	1/105428 (0.0%)
27	BB	0.23	0/2878	0.45	0/4490
27	DB	0.24	0/2878	0.44	0/4490
28	BD	0.48	0/2186	0.89	1/2944 (0.0%)
28	DD	0.43	0/2192	0.90	3/2951 (0.1%)
29	BE	0.50	0/1592	0.88	0/2149
29	DE	0.42	0/1592	0.88	0/2149
30	BF	0.46	0/1619	0.87	1/2193 (0.0%)
30	DF	0.40	0/1615	0.91	3/2188 (0.1%)
31	BG	0.40	0/1450	0.88	4/1959 (0.2%)
31	DG	0.41	0/1449	1.03	7/1958 (0.4%)
32	BH	0.44	0/1356	0.93	5/1834 (0.3%)
32	DH	0.39	0/1356	0.92	1/1834 (0.1%)
33	BI	0.38	0/1100	0.94	4/1501 (0.3%)
33	DI	0.39	0/1088	0.86	0/1484
34	BN	0.47	0/1144	0.85	0/1543
34	DN	0.38	0/1144	0.90	2/1543 (0.1%)
35	BO	0.48	0/943	0.86	0/1269
35	DO	0.41	0/943	0.84	0/1269
36	BP	0.46	0/1156	0.83	0/1537
36	DP	0.40	0/1152	0.92	7/1533 (0.5%)
37	BQ	0.46	0/1143	0.80	0/1527
37	DQ	0.40	0/1143	0.81	0/1527
38	BR	0.48	0/982	0.85	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	DR	0.42	0/982	0.79	0/1312
39	BS	0.40	0/887	0.91	1/1180 (0.1%)
39	DS	0.38	0/880	0.90	1/1172 (0.1%)
40	BT	0.44	0/1105	0.79	0/1477
40	DT	0.39	0/1097	0.81	0/1468
41	BU	0.49	0/977	0.84	0/1301
41	DU	0.39	0/977	0.81	0/1301
42	BV	0.46	0/782	0.84	0/1049
42	DV	0.38	0/782	0.85	0/1049
43	BW	0.50	0/897	0.88	2/1205 (0.2%)
43	DW	0.42	0/897	0.83	0/1205
44	BX	0.48	0/764	0.87	1/1025 (0.1%)
44	DX	0.41	0/764	0.89	1/1025 (0.1%)
45	BY	0.44	0/819	0.88	0/1095
45	DY	0.38	0/819	0.90	1/1095 (0.1%)
46	BZ	0.42	0/1379	0.99	5/1873 (0.3%)
46	DZ	0.39	0/1390	0.96	6/1890 (0.3%)
47	B0	0.44	0/662	0.84	1/881 (0.1%)
47	D0	0.38	0/662	0.94	3/881 (0.3%)
48	B1	0.46	0/762	0.82	0/1014
48	D1	0.41	0/762	0.79	0/1014
49	B2	0.41	0/590	0.84	1/781 (0.1%)
49	D2	0.35	0/590	0.77	0/781
50	B3	0.46	0/474	0.83	0/635
50	D3	0.35	0/469	0.89	0/630
51	B4	0.40	0/571	1.15	6/768 (0.8%)
51	D4	0.43	0/545	1.12	3/737 (0.4%)
52	B5	0.51	0/469	0.81	0/635
52	D5	0.42	0/469	0.80	0/635
53	B6	0.49	0/460	0.75	0/613
53	D6	0.37	0/456	0.75	0/608
54	B7	0.52	0/426	0.81	0/561
54	D7	0.48	0/426	0.87	0/561
55	B8	0.49	0/525	0.84	0/691
55	D8	0.38	0/525	0.79	0/691
56	B9	0.46	0/310	0.75	0/407
56	D9	0.38	0/310	0.81	0/407
All	All	0.30	2/316594 (0.0%)	0.60	156/473940 (0.0%)

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

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CX	8	4SU	O3'-P	5.16	1.61	1.56
23	AW	8	4SU	O3'-P	5.01	1.61	1.56

All (156) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
39	BS	60	GLY	N-CA-C	12.31	121.42	110.21
51	B4	60	GLN	N-CA-C	-9.45	101.68	113.02
2	CB	13	ALA	N-CA-C	8.91	123.72	113.02
2	AB	9	GLU	N-CA-C	8.85	122.39	110.35
13	AM	84	ILE	N-CA-C	8.80	120.59	111.00
46	BZ	107	THR	CA-C-N	8.54	129.07	119.93
46	BZ	107	THR	C-N-CA	8.54	129.07	119.93
2	AB	128	GLU	N-CA-C	-8.39	100.52	113.02
51	B4	52	THR	N-CA-C	-8.30	102.17	112.88
44	DX	94	GLY	N-CA-C	8.08	122.42	112.64
19	CS	67	VAL	N-CA-C	7.91	118.01	110.42
51	D4	68	ARG	N-CA-C	7.71	119.32	111.07
4	CD	171	GLY	CA-C-N	7.70	127.42	119.56
4	CD	171	GLY	C-N-CA	7.70	127.42	119.56
28	DD	275	LYS	N-CA-C	-7.52	97.57	109.23
39	DS	60	GLY	N-CA-C	7.44	121.26	111.52
1	CA	1119	C	N1-C2-O2	7.19	140.48	118.90
5	CE	11	ILE	N-CA-C	7.14	117.28	110.42
36	DP	44	GLY	CA-C-N	7.13	134.54	121.70
36	DP	44	GLY	C-N-CA	7.13	134.54	121.70
47	D0	82	ARG	CA-C-N	7.12	127.08	120.03
47	D0	82	ARG	C-N-CA	7.12	127.08	120.03
3	CC	139	GLN	N-CA-C	6.99	118.69	111.14
44	BX	94	GLY	N-CA-C	6.95	121.05	112.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	DY	91	GLU	N-CA-C	-6.87	104.37	112.89
46	BZ	158	PRO	CA-C-N	6.83	128.38	119.84
46	BZ	158	PRO	C-N-CA	6.83	128.38	119.84
2	CB	231	GLU	CA-C-N	-6.79	112.51	120.11
2	CB	231	GLU	C-N-CA	-6.79	112.51	120.11
20	CT	94	ALA	N-CA-C	-6.78	105.00	113.20
10	CJ	52	GLY	CA-C-N	6.72	126.31	119.19
10	CJ	52	GLY	C-N-CA	6.72	126.31	119.19
26	BA	1992	G	C2'-C3'-O3'	6.65	119.48	109.50
1	CA	1154	G	N1-C2-N2	-6.55	96.56	116.20
32	BH	20	ALA	CA-C-N	-6.49	111.73	119.84
32	BH	20	ALA	C-N-CA	-6.49	111.73	119.84
19	CS	82	GLY	N-CA-C	6.49	120.22	110.75
33	BI	110	ASP	CA-C-N	6.45	126.67	119.32
33	BI	110	ASP	C-N-CA	6.45	126.67	119.32
43	BW	13	SER	CA-C-N	6.40	126.62	119.32
43	BW	13	SER	C-N-CA	6.40	126.62	119.32
12	CL	119	LYS	N-CA-C	-6.33	101.57	110.50
31	DG	44	GLY	N-CA-C	-6.33	107.05	115.40
51	D4	61	ARG	N-CA-C	-6.31	104.48	111.36
28	DD	244	ARG	CA-C-N	-6.28	113.91	120.38
28	DD	244	ARG	C-N-CA	-6.28	113.91	120.38
13	CM	7	VAL	N-CA-C	6.26	117.85	108.96
28	BD	274	ARG	N-CA-C	6.16	119.17	110.23
51	B4	65	ASP	N-CA-C	-6.14	105.77	113.20
4	AD	166	LYS	N-CA-C	6.14	117.64	111.07
2	AB	166	ASP	CA-C-N	6.09	125.98	119.28
2	AB	166	ASP	C-N-CA	6.09	125.98	119.28
5	AE	98	THR	N-CA-C	6.05	117.54	111.07
49	B2	69	ARG	N-CA-C	6.03	117.55	110.97
2	AB	10	LEU	N-CA-C	5.97	123.51	110.80
3	CC	125	GLU	N-CA-C	-5.95	104.92	111.82
10	CJ	6	ILE	N-CA-C	5.94	116.67	108.12
9	CI	102	LEU	N-CA-C	5.91	119.68	112.23
31	BG	96	ARG	CB-CA-C	-5.90	109.78	116.63
20	AT	88	VAL	N-CA-C	5.90	116.08	110.42
5	CE	98	THR	N-CA-C	5.87	117.35	111.07
31	BG	127	GLY	N-CA-C	-5.86	106.64	114.25
20	CT	11	SER	N-CA-C	-5.84	105.73	112.92
8	AH	96	GLY	N-CA-C	-5.84	105.07	112.54
1	CA	1119	C	C2-N1-C1'	5.81	136.22	118.80
4	CD	178	VAL	N-CA-C	5.78	115.91	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	AB	23	ARG	N-CA-C	-5.78	106.04	112.57
46	DZ	139	VAL	N-CA-C	5.78	116.19	107.75
26	BA	271(M)	G	P-O3'-C3'	5.77	126.62	119.70
12	CL	28	LYS	N-CA-C	5.76	119.19	111.24
11	AK	40	ILE	N-CA-C	-5.75	106.62	111.56
46	DZ	129	SER	CA-C-N	5.73	126.11	119.47
46	DZ	129	SER	C-N-CA	5.73	126.11	119.47
7	CG	79	ARG	N-CA-C	5.71	122.97	110.80
1	CA	1154	G	N3-C2-N2	5.68	136.94	119.90
26	DA	1992	G	C2'-C3'-O3'	5.65	117.98	109.50
26	BA	271(M)	G	OP1-P-O3'	5.64	117.62	105.20
12	CL	105	TYR	CB-CA-C	-5.62	109.59	117.23
51	D4	59	PHE	N-CA-C	5.58	117.46	107.80
15	AO	74	ASP	CA-C-N	5.57	125.24	119.05
15	AO	74	ASP	C-N-CA	5.57	125.24	119.05
15	AO	87	ILE	N-CA-C	5.56	116.62	111.45
5	CE	105	VAL	CA-C-N	-5.54	113.96	119.56
5	CE	105	VAL	C-N-CA	-5.54	113.96	119.56
20	CT	99	LEU	N-CA-C	5.53	117.77	111.02
3	AC	4	LYS	N-CA-C	5.51	118.28	110.50
2	AB	38	GLY	N-CA-C	-5.51	106.41	114.61
33	BI	106	GLY	CA-C-N	5.50	131.61	121.70
33	BI	106	GLY	C-N-CA	5.50	131.61	121.70
34	DN	125	GLY	CA-C-N	5.50	126.35	120.47
34	DN	125	GLY	C-N-CA	5.50	126.35	120.47
46	DZ	106	GLY	N-CA-C	-5.49	106.54	112.08
4	CD	188	LEU	CA-C-N	5.48	125.80	119.93
4	CD	188	LEU	C-N-CA	5.48	125.80	119.93
36	DP	44	GLY	N-CA-C	-5.48	102.68	112.22
5	AE	76	ILE	CA-C-N	5.46	125.29	119.28
5	AE	76	ILE	C-N-CA	5.46	125.29	119.28
10	CJ	31	GLY	N-CA-C	-5.46	105.87	112.48
31	DG	65	GLY	N-CA-C	-5.46	106.67	115.08
32	BH	54	ARG	CA-C-N	5.46	125.29	119.28
32	BH	54	ARG	C-N-CA	5.46	125.29	119.28
30	BF	89	VAL	N-CA-C	5.44	115.53	110.42
51	B4	49	PHE	CB-CA-C	-5.40	110.33	116.54
5	CE	6	PHE	N-CA-C	5.38	118.76	110.42
1	AA	1067	A	C2'-C3'-O3'	5.37	117.55	109.50
6	CF	95	GLU	CA-C-N	5.36	125.36	119.89
6	CF	95	GLU	C-N-CA	5.36	125.36	119.89
51	B4	40	HIS	CA-C-N	5.35	126.53	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
51	B4	40	HIS	C-N-CA	5.35	126.53	119.84
5	AE	67	VAL	N-CA-C	5.35	116.43	108.46
47	B0	12	ASN	N-CA-C	5.34	118.81	112.72
32	DH	35	VAL	N-CA-C	5.33	113.81	107.73
31	BG	31	VAL	CA-C-N	5.32	125.31	119.89
31	BG	31	VAL	C-N-CA	5.32	125.31	119.89
30	DF	9	ILE	N-CA-C	5.31	113.67	107.89
13	AM	106	ASN	CB-CA-C	-5.31	110.44	116.54
47	D0	12	ASN	CB-CA-C	-5.30	109.44	117.07
36	DP	44	GLY	CA-C-O	-5.29	115.17	121.83
2	AB	21	ARG	N-CA-C	5.27	117.56	107.75
2	AB	75	LYS	N-CA-C	5.24	116.68	111.07
30	DF	21	ALA	CA-C-N	5.23	131.11	121.70
30	DF	21	ALA	C-N-CA	5.23	131.11	121.70
46	DZ	14	LYS	CA-C-N	5.22	125.53	119.47
46	DZ	14	LYS	C-N-CA	5.22	125.53	119.47
8	CH	75	ARG	CA-C-N	5.21	125.50	119.92
8	CH	75	ARG	C-N-CA	5.21	125.50	119.92
36	DP	22	GLY	CA-C-N	5.19	124.51	118.85
36	DP	22	GLY	C-N-CA	5.19	124.51	118.85
31	DG	96	ARG	CB-CA-C	-5.18	110.62	116.63
36	DP	38	GLN	N-CA-C	-5.16	103.68	110.43
1	CA	1119	C	C6-N1-C1'	-5.15	105.34	120.80
32	BH	9	ILE	N-CA-C	5.15	112.64	107.55
3	CC	77	ILE	N-CA-C	5.14	115.36	110.42
1	AA	1067	A	P-O3'-C3'	5.14	127.91	120.20
2	CB	193	ASP	CA-C-N	5.13	124.31	118.97
2	CB	193	ASP	C-N-CA	5.13	124.31	118.97
2	CB	119	GLU	N-CA-C	-5.12	106.54	112.89
3	CC	48	TYR	N-CA-C	-5.12	105.69	111.28
46	BZ	52	SER	CB-CA-C	-5.10	110.71	116.63
2	AB	71	VAL	N-CA-C	5.10	114.09	106.85
9	CI	63	ILE	N-CA-C	5.09	115.46	108.12
1	CA	1119	C	N3-C2-O2	-5.09	106.63	121.90
1	CA	1154	G	C5-C6-O6	5.09	143.86	128.60
31	DG	178	PHE	CA-C-N	5.07	127.92	120.46
31	DG	178	PHE	C-N-CA	5.07	127.92	120.46
3	CC	43	LEU	N-CA-C	5.07	117.59	111.40
7	AG	78	ARG	N-CA-C	5.06	117.21	107.44
2	CB	10	LEU	N-CA-C	5.05	118.93	112.87
7	CG	57	GLU	CA-C-N	5.05	125.08	119.32
7	CG	57	GLU	C-N-CA	5.05	125.08	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	AD	135	LEU	CA-C-N	5.04	124.70	119.56
4	AD	135	LEU	C-N-CA	5.04	124.70	119.56
5	CE	35	GLY	N-CA-C	5.02	118.39	110.91
3	AC	93	LYS	N-CA-C	-5.02	105.89	111.36
31	DG	31	VAL	CA-C-N	5.00	125.00	119.89
31	DG	31	VAL	C-N-CA	5.00	125.00	119.89

There are no chirality outliers.

All (10) planarity outliers are listed below:

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

5.2 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	32185	0	16245	538	0
1	CA	32312	0	16307	771	0
2	AB	1846	0	1867	85	0
2	CB	1825	0	1828	121	0
3	AC	1552	0	1546	61	0
3	CC	1544	0	1524	72	0
4	AD	1659	0	1676	56	0
4	CD	1678	0	1718	69	0
5	AE	1129	0	1185	31	0
5	CE	1133	0	1191	49	0
6	AF	812	0	804	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	CF	820	0	814	21	0
7	AG	1231	0	1238	24	0
7	CG	1235	0	1249	40	0
8	AH	1088	0	1126	35	0
8	CH	1088	0	1126	40	0
9	AI	986	0	995	44	0
9	CI	978	0	966	55	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	44	0
11	AK	833	0	836	21	0
11	CK	833	0	836	21	0
12	AL	930	0	980	27	0
12	CL	930	0	980	34	0
13	AM	966	0	1024	42	0
13	CM	950	0	988	73	0
14	AN	492	0	529	26	0
14	CN	492	0	529	32	0
15	AO	728	0	760	21	0
15	CO	728	0	760	23	0
16	AP	681	0	697	28	0
16	CP	677	0	686	22	0
17	AQ	823	0	891	26	0
17	CQ	823	0	891	21	0
18	AR	555	0	618	11	0
18	CR	555	0	618	26	0
19	AS	661	0	675	33	0
19	CS	646	0	644	41	0
20	AT	728	0	798	27	0
20	CT	731	0	807	28	0
21	AU	199	0	208	8	0
21	CU	199	0	208	9	0
22	AV	277	0	140	3	0
22	CV	252	0	130	6	0
23	AW	1599	0	830	42	0
23	CW	1552	0	794	53	0
24	AX	1635	0	839	23	0
24	CX	1635	0	839	36	0
25	AY	1581	0	805	85	0
25	CY	1561	0	796	94	0
26	BA	60729	0	30622	668	0
26	DA	60311	0	30412	887	0
27	BB	2573	0	1306	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	DB	2573	0	1306	79	0
28	BD	2136	0	2218	43	0
28	DD	2142	0	2229	60	0
29	BE	1559	0	1618	26	0
29	DE	1559	0	1618	41	0
30	BF	1584	0	1625	42	0
30	DF	1580	0	1619	63	0
31	BG	1425	0	1443	39	0
31	DG	1424	0	1434	93	0
32	BH	1330	0	1407	34	0
32	DH	1330	0	1407	44	0
33	BI	1085	0	1114	38	0
33	DI	1073	0	1106	22	0
34	BN	1117	0	1184	26	0
34	DN	1117	0	1184	27	0
35	BO	933	0	996	25	0
35	DO	933	0	996	32	0
36	BP	1139	0	1223	42	0
36	DP	1135	0	1212	54	0
37	BQ	1122	0	1179	30	0
37	DQ	1122	0	1179	41	0
38	BR	968	0	1033	22	0
38	DR	968	0	1033	30	0
39	BS	877	0	938	20	0
39	DS	870	0	923	35	0
40	BT	1091	0	1151	28	0
40	DT	1083	0	1136	39	0
41	BU	959	0	1019	18	0
41	DU	959	0	1018	30	0
42	BV	771	0	830	14	0
42	DV	771	0	830	25	0
43	BW	886	0	940	17	0
43	DW	886	0	940	13	0
44	BX	750	0	814	15	0
44	DX	750	0	814	28	0
45	BY	806	0	881	28	0
45	DY	806	0	881	30	0
46	BZ	1349	0	1355	45	0
46	DZ	1360	0	1363	74	0
47	B0	653	0	674	14	0
47	D0	653	0	674	22	0
48	B1	755	0	826	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	D1	755	0	826	18	0
49	B2	588	0	643	13	0
49	D2	588	0	643	15	0
50	B3	469	0	518	6	0
50	D3	464	0	514	13	0
51	B4	558	0	544	39	0
51	D4	532	0	503	30	0
52	B5	455	0	465	15	0
52	D5	455	0	465	13	0
53	B6	453	0	473	12	0
53	D6	449	0	469	12	0
54	B7	418	0	467	10	0
54	D7	418	0	467	13	0
55	B8	517	0	582	17	0
55	D8	517	0	582	16	0
56	B9	307	0	335	7	0
56	D9	307	0	335	11	0
57	AA	216	0	0	0	0
57	AB	1	0	0	0	0
57	AE	1	0	0	0	0
57	AF	1	0	0	0	0
57	AK	1	0	0	0	0
57	AL	2	0	0	0	0
57	AM	2	0	0	0	0
57	AN	2	0	0	0	0
57	AT	1	0	0	0	0
57	AU	1	0	0	0	0
57	AW	2	0	0	0	0
57	AX	15	0	0	0	0
57	AY	3	0	0	0	0
57	B0	2	0	0	0	0
57	B2	1	0	0	0	0
57	B4	1	0	0	0	0
57	B5	3	0	0	0	0
57	B6	2	0	0	0	0
57	B7	5	0	0	0	0
57	B8	2	0	0	0	0
57	B9	1	0	0	0	0
57	BA	814	0	0	0	0
57	BB	23	0	0	0	0
57	BD	10	0	0	0	0
57	BE	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	BF	11	0	0	0	0
57	BG	2	0	0	0	0
57	BH	1	0	0	0	0
57	BN	3	0	0	0	0
57	BO	1	0	0	0	0
57	BP	2	0	0	0	0
57	BQ	2	0	0	0	0
57	BR	2	0	0	0	0
57	BU	4	0	0	0	0
57	BV	5	0	0	0	0
57	BW	4	0	0	0	0
57	BX	1	0	0	0	0
57	BY	1	0	0	0	0
57	BZ	2	0	0	0	0
57	CA	169	0	0	0	0
57	CD	1	0	0	0	0
57	CE	2	0	0	0	0
57	CF	1	0	0	0	0
57	CJ	1	0	0	0	0
57	CK	1	0	0	0	0
57	CT	1	0	0	0	0
57	CW	1	0	0	0	0
57	CX	2	0	0	0	0
57	D0	1	0	0	0	0
57	D3	1	0	0	0	0
57	D8	1	0	0	0	0
57	DA	664	0	0	0	0
57	DB	13	0	0	0	0
57	DD	4	0	0	0	0
57	DE	7	0	0	0	0
57	DF	5	0	0	0	0
57	DG	1	0	0	0	0
57	DN	1	0	0	0	0
57	DO	2	0	0	0	0
57	DP	2	0	0	0	0
57	DQ	3	0	0	0	0
57	DR	1	0	0	0	0
57	DU	1	0	0	0	0
57	DV	1	0	0	0	0
57	DW	1	0	0	0	0
57	DY	1	0	0	0	0
58	AD	8	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	CD	8	0	0	1	0
59	AN	1	0	0	0	0
59	B4	1	0	0	0	0
59	B5	1	0	0	0	0
59	B6	1	0	0	0	0
59	B9	1	0	0	0	0
59	BY	1	0	0	0	0
59	CN	1	0	0	0	0
59	D4	1	0	0	0	0
59	D5	1	0	0	0	0
59	D6	1	0	0	0	0
59	D9	1	0	0	0	0
59	DY	1	0	0	0	0
60	AX	1	0	0	0	0
61	AA	210	0	0	13	0
61	AD	1	0	0	0	0
61	AE	2	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	2	0	0	1	0
61	AM	2	0	0	0	0
61	AV	2	0	0	0	0
61	AW	4	0	0	0	0
61	AX	4	0	0	0	0
61	AY	1	0	0	0	0
61	B0	6	0	0	0	0
61	B1	2	0	0	0	0
61	B3	2	0	0	0	0
61	B5	4	0	0	0	0
61	B6	2	0	0	0	0
61	B7	3	0	0	2	0
61	B8	13	0	0	0	0
61	B9	1	0	0	0	0
61	BA	1406	0	0	56	0
61	BB	37	0	0	1	0
61	BD	15	0	0	2	0
61	BE	17	0	0	4	0
61	BF	11	0	0	0	0
61	BG	3	0	0	0	0
61	BH	1	0	0	0	0
61	BI	1	0	0	0	0
61	BN	1	0	0	0	0
61	BO	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	BP	13	0	0	1	0
61	BQ	4	0	0	0	0
61	BR	2	0	0	0	0
61	BS	2	0	0	0	0
61	BT	2	0	0	0	0
61	BU	4	0	0	0	0
61	BV	2	0	0	0	0
61	BW	3	0	0	1	0
61	BX	3	0	0	0	0
61	BZ	1	0	0	0	0
61	CA	156	0	0	11	0
61	CE	2	0	0	0	0
61	CH	1	0	0	0	0
61	CJ	1	0	0	0	0
61	CK	1	0	0	0	0
61	CL	1	0	0	1	0
61	CT	1	0	0	0	0
61	CW	2	0	0	2	0
61	CX	2	0	0	0	0
61	CY	1	0	0	0	0
61	D0	4	0	0	0	0
61	D1	1	0	0	0	0
61	D3	2	0	0	0	0
61	D5	1	0	0	0	0
61	D6	1	0	0	0	0
61	D8	3	0	0	0	0
61	DA	989	0	0	44	0
61	DB	9	0	0	0	0
61	DD	18	0	0	3	0
61	DE	5	0	0	0	0
61	DF	4	0	0	0	0
61	DN	2	0	0	0	0
61	DP	12	0	0	4	0
61	DQ	1	0	0	0	0
61	DT	4	0	0	0	0
61	DU	1	0	0	0	0
61	DV	1	0	0	0	0
61	DW	1	0	0	0	0
61	DX	2	0	0	0	0
61	DY	1	0	0	0	0
All	All	297127	0	196404	5613	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 (5613) 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)
26:DA:2139:C:N4	26:DA:2152:G:H1	1.46	1.14
1:CA:999:C:N4	1:CA:1042:G:H1	1.48	1.12
25:AY:49:C:N4	25:AY:65:G:H1	1.51	1.09
1:CA:985:C:N4	1:CA:1220:G:H1	1.50	1.09
1:CA:998:G:H1	1:CA:1043:C:N4	1.51	1.09
25:CY:7:A:N6	25:CY:66:U:H3	1.54	1.06
26:DA:2138:C:N4	26:DA:2153:G:H1	1.53	1.04
25:AY:53:G:H1	25:AY:61:C:N4	1.56	1.04
26:BA:2136:C:N4	26:BA:2155:G:H1	1.57	1.02
45:BY:92:ASN:HB2	45:BY:94:LYS:H	1.21	1.02
26:BA:2102:U:H3	26:BA:2187:G:H1	1.06	1.00
1:CA:1245:A:H61	1:CA:1292:U:H3	1.09	1.00
1:CA:985:C:H42	1:CA:1220:G:H1	0.99	0.99
1:CA:1162:C:N4	1:CA:1174:G:H1	1.60	0.99
25:CY:10:G:H1	25:CY:25:C:H42	1.09	0.98
26:BA:2499:C:OP1	61:BA:5135:HOH:O	1.83	0.97
4:CD:15:GLU:HG3	4:CD:63:LYS:HG3	1.47	0.96
26:BA:2138:C:H42	26:BA:2153:G:H1	1.09	0.96
1:CA:1000:U:H3	1:CA:1041:A:N6	1.63	0.95
25:CY:50:U:H3	25:CY:64:A:H61	1.02	0.95
26:DA:2127:G:C6	26:DA:2161:C:N4	2.34	0.95
23:AW:26:A:H61	23:AW:44:G:H1	1.06	0.94
47:B0:11:ARG:O	47:B0:14:ARG:NH2	1.99	0.94
25:AY:29:G:H1	25:AY:41:C:N4	1.65	0.94
1:CA:76:C:N4	1:CA:93:G:H1	1.64	0.94
1:CA:1025:U:H3	1:CA:1036:G:H1	1.03	0.94
25:CY:22:G:N7	25:CY:46:7MG:N2	2.14	0.94
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.31	0.94
1:CA:501:C:OP1	12:CL:124:LYS:NZ	2.01	0.93
1:CA:1162:C:H42	1:CA:1174:G:H1	1.14	0.93
40:DT:55:ASN:H	40:DT:59:THR:HG22	1.29	0.93
26:BA:1798:U:H5'	28:BD:259:THR:HG22	1.50	0.93
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.47	0.93
23:AW:19:G:H1	23:AW:56:C:H42	1.17	0.93
1:CA:838:G:H1	1:CA:848:C:H42	1.10	0.93
35:BO:35:VAL:HG11	35:BO:103:ALA:HB3	1.51	0.92
26:BA:2121:G:H1	26:BA:2177:C:H42	1.13	0.92
46:DZ:5:LEU:HG	46:DZ:47:VAL:HG21	1.50	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:19:G:H1	25:CY:56:C:H42	1.12	0.92
25:CY:51:U:H3	25:CY:63:G:H1	1.17	0.91
23:AW:1:G:O6	23:AW:72:C:N3	2.04	0.91
26:DA:631:A:OP1	36:DP:65:ARG:NH1	2.04	0.91
26:DA:2121:G:H1	26:DA:2177:C:N4	1.68	0.91
1:CA:985:C:N3	1:CA:1220:G:N2	2.17	0.91
19:CS:42:PRO:HG3	51:D4:61:ARG:HG3	1.53	0.91
26:DA:2139:C:N4	26:DA:2152:G:N1	2.12	0.91
1:CA:1165:C:H42	1:CA:1171:G:H1	1.19	0.90
25:AY:53:G:H1	25:AY:61:C:H42	0.91	0.90
25:AY:29:G:H1	25:AY:41:C:H42	0.90	0.90
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.06	0.89
26:DA:2121:G:H1	26:DA:2177:C:H42	0.95	0.89
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.55	0.89
1:CA:1244:C:H42	1:CA:1293:G:H1	1.12	0.89
25:AY:49:C:N3	25:AY:65:G:N2	2.21	0.89
1:CA:999:C:N3	1:CA:1042:G:N2	2.21	0.89
25:CY:19:G:N2	25:CY:56:C:N3	2.20	0.89
26:DA:1798:U:H5'	28:DD:259:THR:HG22	1.55	0.89
25:CY:9:A:N6	25:CY:23:A:OP2	2.06	0.88
1:CA:998:G:N2	1:CA:1043:C:N3	2.20	0.88
1:AA:78:G:C6	1:AA:91:C:N4	2.40	0.88
25:AY:5:G:H1	25:AY:68:C:H42	1.16	0.88
46:DZ:110:GLY:HA3	46:DZ:145:GLU:HA	1.55	0.88
1:AA:1316:G:H22	1:AA:1319:A:H5"	1.39	0.88
27:DB:41:U:H5	31:DG:70:VAL:H	1.22	0.88
1:AA:78:G:C2	1:AA:91:C:N3	2.43	0.87
46:BZ:138:GLU:H	46:BZ:156:LYS:HD3	1.36	0.87
1:AA:1166:G:N2	1:AA:1170:A:OP2	2.06	0.87
23:AW:1:G:N1	23:AW:72:C:O2	2.07	0.87
41:DU:76:TYR:OH	41:DU:92:ARG:NH1	2.08	0.87
26:BA:1176:G:H1'	26:BA:1177:A:H5'	1.55	0.87
25:CY:15:G:H22	25:CY:48:C:H42	1.16	0.87
9:AI:17:VAL:HG21	9:AI:81:ILE:HG22	1.55	0.87
11:AK:48:ILE:HD12	11:AK:63:LEU:HB2	1.54	0.86
1:AA:1502:A:H2	1:AA:1505:G:H1	1.21	0.86
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.06	0.86
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.57	0.86
25:CY:50:U:H3	25:CY:64:A:N6	1.74	0.86
26:BA:2190:G:H2'	26:BA:2191:G:H5"	1.56	0.86
26:DA:2139:C:N3	26:DA:2152:G:N2	2.23	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:664:G:H22	1:AA:741:G:H1	1.23	0.86
26:DA:2136:C:N3	26:DA:2155:G:N2	2.24	0.86
1:CA:76:C:H42	1:CA:93:G:H1	0.91	0.86
26:DA:2136:C:N4	26:DA:2155:G:N1	2.24	0.85
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.10	0.85
26:DA:2807:G:N1	26:DA:2893:G:O6	2.08	0.85
26:BA:1310:G:OP2	54:B7:9:ARG:NH1	2.09	0.85
1:CA:1166:G:N2	1:CA:1170:A:OP2	2.09	0.85
46:BZ:72:ARG:NH2	46:BZ:97:GLU:O	2.10	0.84
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.58	0.84
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.42	0.84
26:DA:2297:C:N3	26:DA:2321:G:N1	2.25	0.84
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.59	0.84
26:BA:2134:A:H2'	26:BA:2135:A:C8	2.13	0.84
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.10	0.84
26:BA:631:A:OP1	36:BP:65:ARG:NH1	2.10	0.84
1:CA:1075:C:OP1	2:CB:179:LYS:NZ	2.10	0.84
26:DA:880:G:H22	26:DA:898:C:H1'	1.40	0.84
32:DH:46:GLU:HB2	32:DH:49:VAL:HG12	1.58	0.84
37:DQ:109:VAL:HG13	37:DQ:113:GLN:HB3	1.60	0.84
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.11	0.84
1:CA:958:A:N6	19:CS:77:THR:O	2.11	0.84
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.11	0.83
26:DA:1039:G:O6	26:DA:1116:C:N4	2.11	0.83
1:CA:201:C:H42	1:CA:216:G:H1	1.21	0.83
1:CA:1286:A:H8	1:CA:1287:A:H4'	1.43	0.83
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.11	0.83
30:DF:53:THR:HG22	30:DF:56:GLU:HG3	1.59	0.83
42:DV:24:LYS:HG2	42:DV:64:HIS:HD2	1.43	0.83
26:DA:1204:A:H2	26:DA:1241:A:H62	1.22	0.83
19:CS:30:LEU:HD11	19:CS:32:LYS:HG3	1.60	0.83
23:CW:49:C:N4	23:CW:65:G:O6	2.12	0.83
25:CY:31:A:N1	25:CY:39:PSU:O2	2.12	0.83
1:CA:1162:C:N3	1:CA:1174:G:N2	2.26	0.83
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.12	0.83
13:AM:122:LYS:HD3	13:AM:123:ALA:H	1.43	0.83
26:DA:2165:G:H22	26:DA:2172:U:H5	1.24	0.82
26:DA:652(D):C:N4	26:DA:652(U):G:O6	2.09	0.82
26:DA:2136:C:N4	26:DA:2155:G:H1	1.77	0.82
1:CA:1106:G:H5"	3:CC:172:ARG:HG2	1.62	0.82
4:CD:122:ARG:NH1	4:CD:134:ASP:O	2.12	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2136:C:N3	26:BA:2155:G:N2	2.27	0.82
40:BT:118:ARG:HH11	40:BT:118:ARG:HG3	1.45	0.82
1:CA:70:G:H1	1:CA:99:U:H3	1.28	0.82
1:CA:975:A:H4'	1:CA:976:G:H5"	1.60	0.82
26:DA:1019:U:H3	26:DA:1142(A):A:H62	1.26	0.82
26:DA:2136:C:C4	26:DA:2155:G:N1	2.47	0.82
26:BA:1314:C:OP1	61:BA:4634:HOH:O	1.98	0.82
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.12	0.82
1:CA:983:A:N1	1:CA:1222:G:N2	2.28	0.81
27:DB:22:U:H3	27:DB:61:G:H1	1.24	0.81
36:DP:96:THR:H	36:DP:99:LEU:HD21	1.43	0.81
2:AB:16:HIS:O	2:AB:18:GLY:N	2.13	0.81
1:CA:1133:G:H1	1:CA:1141:C:H42	1.24	0.81
9:CI:53:VAL:O	9:CI:55:ALA:N	2.12	0.81
26:DA:994:C:OP1	41:DU:53:ARG:NH2	2.12	0.81
1:AA:78:G:N1	1:AA:91:C:N4	2.29	0.81
25:AY:5:G:H1	25:AY:68:C:N4	1.78	0.81
3:AC:35:GLU:OE2	3:AC:59:ARG:NH2	2.14	0.81
1:CA:1030:C:H42	1:CA:1031:G:H1	1.24	0.81
1:CA:1318:A:H5"	19:CS:3:ARG:HH22	1.46	0.81
40:BT:16:ARG:NH2	40:BT:83:ILE:O	2.14	0.81
1:CA:1000:U:H3	1:CA:1041:A:H61	0.87	0.81
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.62	0.81
28:DD:276:LYS:HD3	28:DD:276:LYS:H	1.45	0.81
26:DA:2166:G:H3'	26:DA:2167:U:H5"	1.62	0.81
23:AW:26:A:N6	23:AW:44:G:H1	1.78	0.80
26:BA:2867:G:OP2	40:BT:119:LYS:NZ	2.14	0.80
25:CY:10:G:H1	25:CY:25:C:N4	1.78	0.80
1:AA:839:U:O2'	1:AA:840:C:OP1	2.00	0.80
25:AY:8:4SU:H4'	25:AY:48:C:H4'	1.64	0.80
26:BA:1779:U:OP2	61:BA:5167:HOH:O	1.99	0.80
25:CY:38:A:H3'	25:CY:39:PSU:H5'	1.62	0.80
46:DZ:45:ASP:OD2	46:DZ:49:ARG:NH1	2.14	0.80
1:AA:90:U:H2'	1:AA:91:C:H5"	1.63	0.80
23:CW:4:C:N3	23:CW:69:G:N2	2.29	0.80
31:DG:145:THR:HG23	31:DG:147:ASP:H	1.46	0.80
38:DR:97:VAL:HG22	38:DR:114:VAL:HG22	1.62	0.80
46:DZ:119:GLU:O	46:DZ:122:ARG:NH1	2.15	0.80
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.15	0.80
27:DB:7:G:O6	27:DB:114:C:N4	2.14	0.80
25:AY:53:G:N2	25:AY:61:C:N3	2.29	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:68:C:H2'	25:AY:69:G:H5'	1.63	0.80
26:BA:192:C:OP1	61:BA:4000:HOH:O	1.99	0.80
1:CA:878:G:H5'	8:CH:89:PRO:HG2	1.64	0.80
30:DF:53:THR:HG23	30:DF:55:GLY:H	1.47	0.79
1:AA:347:G:O2'	1:AA:348:G:OP1	2.00	0.79
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.16	0.79
1:CA:838:G:H1	1:CA:848:C:N4	1.79	0.79
26:BA:956:G:OP2	37:BQ:14:ARG:NH2	2.15	0.79
26:BA:2683:C:O2	35:BO:70:LYS:NZ	2.14	0.79
1:CA:589:C:O2	1:CA:650:G:N2	2.13	0.79
26:BA:2102:U:O2	26:BA:2187:G:N2	2.13	0.79
28:DD:238:GLY:O	61:DD:409:HOH:O	2.00	0.79
25:AY:15:G:H22	25:AY:48:C:H42	1.30	0.79
23:CW:4:C:N4	23:CW:69:G:N1	2.29	0.79
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.64	0.79
1:CA:1055:A:N7	1:CA:1200:C:N4	2.30	0.79
25:CY:4:C:H42	25:CY:69:G:H1	1.28	0.79
1:CA:1245:A:N6	1:CA:1292:U:H3	1.80	0.79
36:DP:100:LEU:HD12	36:DP:112:LEU:HD11	1.65	0.79
7:AG:38:LEU:HA	7:AG:41:ARG:HD2	1.65	0.78
26:DA:2127:G:C2	26:DA:2161:C:N3	2.52	0.78
1:AA:1027:C:C2	1:AA:1034:G:N1	2.52	0.78
26:BA:1800:C:OP2	28:BD:183:ARG:NH2	2.17	0.78
33:BI:92:VAL:HG13	33:BI:120:ILE:HB	1.65	0.78
6:CF:81:ILE:HD11	28:DD:125:ILE:HB	1.64	0.78
44:BX:31:HIS:HD2	44:BX:33:LYS:H	1.29	0.78
4:AD:155:LEU:HB3	4:AD:158:ILE:HD11	1.66	0.78
46:DZ:19:ARG:NH1	46:DZ:84:GLU:O	2.17	0.78
1:AA:266:G:H5"	1:AA:268:C:H41	1.47	0.78
1:CA:838:G:N2	1:CA:848:C:N3	2.30	0.78
1:CA:1028:C:N3	1:CA:1033:G:C6	2.52	0.78
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.64	0.78
26:BA:2136:C:H42	26:BA:2155:G:H1	0.83	0.78
1:CA:664:G:H22	1:CA:741:G:H1	1.29	0.78
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.65	0.77
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.84	0.77
31:BG:12:TYR:HA	31:BG:16:ARG:HG3	1.66	0.77
26:DA:2839:G:H5'	38:DR:46:GLY:HA2	1.64	0.77
27:DB:20:C:N4	27:DB:63:G:O6	2.17	0.77
1:AA:78:G:N2	1:AA:91:C:N3	2.33	0.77
26:BA:2138:C:N4	26:BA:2153:G:H1	1.81	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BI:104:GLN:O	33:BI:106:GLY:N	2.16	0.77
44:DX:60:ARG:HH12	54:D7:47:ARG:HH22	1.30	0.77
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.67	0.77
23:AW:50:U:H6	23:AW:50:U:H5'	1.48	0.77
25:AY:7:A:O2'	25:AY:49:C:H5'	1.85	0.77
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.66	0.77
1:AA:1027:C:N3	1:AA:1034:G:C6	2.53	0.77
25:AY:5:G:N2	25:AY:68:C:N3	2.31	0.77
26:BA:517:C:OP1	52:B5:16:ARG:NH2	2.18	0.77
26:DA:2037:G:O6	61:DA:4191:HOH:O	2.02	0.77
37:DQ:31:ASP:OD1	37:DQ:134:ARG:NH1	2.18	0.77
26:BA:1689:A:H62	26:BA:1698:A:H2	1.33	0.77
1:CA:1338:G:H21	24:CX:41:C:H1'	1.49	0.77
1:AA:1025:U:O2'	1:AA:1026:G:O4'	2.02	0.77
25:CY:19:G:H1	25:CY:56:C:N4	1.82	0.77
32:DH:24:VAL:HG13	32:DH:37:VAL:HG21	1.66	0.77
26:BA:2130:U:H4'	26:BA:2133:G:H4'	1.67	0.76
1:CA:1134:G:H1	1:CA:1140:C:H42	1.29	0.76
26:DA:370:G:N7	61:DA:3786:HOH:O	2.18	0.76
35:DO:35:VAL:HG11	35:DO:103:ALA:HB3	1.67	0.76
51:D4:40:HIS:HB3	51:D4:43:TYR:HB2	1.67	0.76
19:AS:27:GLU:HB3	19:AS:28:LYS:HA	1.65	0.76
1:CA:504:C:OP1	61:CA:3202:HOH:O	2.02	0.76
1:CA:1128:C:O2	1:CA:1147:C:N4	2.18	0.76
25:CY:51:U:O2	25:CY:63:G:N2	2.15	0.76
39:BS:39:ILE:HB	39:BS:49:VAL:HG13	1.68	0.76
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.65	0.76
26:BA:2162:G:H2'	26:BA:2163:C:H5"	1.65	0.76
44:BX:88:LYS:NZ	44:BX:90:GLU:OE1	2.18	0.76
24:CX:7:G:H5"	24:CX:8:4SU:H5	1.65	0.76
1:CA:1030:C:N4	1:CA:1031:G:H1	1.84	0.76
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.18	0.76
13:CM:84:ILE:O	13:CM:86:CYS:N	2.17	0.76
25:CY:49:C:H42	25:CY:65:G:H1	1.33	0.76
39:BS:25:ARG:NH1	39:BS:42:ASP:OD1	2.18	0.76
1:AA:998:G:H1	1:AA:1043:C:H42	1.30	0.76
26:BA:1506:C:H2'	26:BA:1507:A:H8	1.48	0.76
1:CA:76:C:N3	1:CA:93:G:N2	2.32	0.76
1:CA:1134:G:H1	1:CA:1140:C:N4	1.84	0.76
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.67	0.76
26:DA:1169:G:H1	26:DA:1180:C:H42	1.31	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2134:A:N3	26:DA:2159:G:O2'	2.17	0.76
31:DG:64:THR:HB	31:DG:94:LEU:HD21	1.67	0.76
3:AC:3:ASN:N	3:AC:3:ASN:OD1	2.18	0.75
26:BA:587:C:OP2	36:BP:21:ARG:NH2	2.20	0.75
55:D8:32:LEU:O	55:D8:36:LYS:NZ	2.18	0.75
26:BA:2121:G:H1	26:BA:2177:C:N4	1.84	0.75
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.19	0.75
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.51	0.75
46:DZ:126:VAL:HG11	46:DZ:161:VAL:HG23	1.67	0.75
36:BP:124:LYS:HG3	36:BP:144:GLU:HG2	1.69	0.75
26:DA:2113:U:H3	26:DA:2170:A:H61	1.33	0.75
25:CY:34:G:H2'	25:CY:35:A:C8	2.21	0.75
1:CA:35:G:O2'	12:CL:118:SER:O	2.05	0.75
4:AD:166:LYS:NZ	4:AD:179:GLU:OE2	2.20	0.75
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.15	0.75
1:CA:1244:C:N4	1:CA:1293:G:H1	1.83	0.75
1:CA:1502:A:H2	1:CA:1505:G:H1	1.32	0.75
48:D1:51:VAL:HG11	48:D1:74:VAL:HG21	1.68	0.75
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.19	0.75
25:AY:67:C:H2'	25:AY:68:C:C6	2.21	0.75
26:BA:2134:A:H2'	26:BA:2135:A:H8	1.49	0.75
25:CY:68:C:H2'	25:CY:69:G:H5'	1.69	0.75
26:DA:2122:U:O4	26:DA:2176:A:N1	2.20	0.75
3:CC:100:ALA:O	3:CC:102:ASN:ND2	2.20	0.75
1:CA:664:G:OP1	18:CR:64:ARG:NH2	2.19	0.75
1:CA:528:C:N4	12:CL:49:ASN:OD1	2.20	0.74
1:CA:953:G:H5'	1:CA:965:A:H61	1.51	0.74
3:CC:59:ARG:HG2	3:CC:64:VAL:HG13	1.68	0.74
25:CY:38:A:C3'	25:CY:39:PSU:H5'	2.16	0.74
26:DA:1842:G:O2'	28:DD:253:GLN:NE2	2.20	0.74
36:DP:42:SER:O	61:DP:303:HOH:O	2.05	0.74
46:DZ:77:ASP:OD1	46:DZ:80:ARG:NH1	2.18	0.74
26:BA:885:C:H3'	26:BA:886:C:H5"	1.70	0.74
26:BA:2116:G:N2	26:BA:2162:G:OP1	2.19	0.74
2:CB:125:PRO:O	2:CB:127:ILE:N	2.20	0.74
38:DR:33:ARG:NH2	52:D5:57:VAL:O	2.20	0.74
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.53	0.74
1:CA:1153:C:H42	1:CA:1154:G:H21	1.35	0.74
26:BA:279:C:H42	26:BA:361:G:H1	1.33	0.74
26:BA:1048:A:OP2	26:BA:1109:C:N4	2.21	0.74
1:AA:1007:C:N3	1:AA:1022:G:O6	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2287:A:H62	26:BA:2344:U:H3	1.31	0.74
26:BA:2353:G:N7	61:BA:4441:HOH:O	2.20	0.74
37:BQ:111:GLU:OE1	37:BQ:133:ARG:NH2	2.19	0.74
1:CA:1011:G:H1	1:CA:1018:C:H42	1.33	0.74
26:DA:2357:U:OP1	47:D0:20:ARG:NH1	2.19	0.74
46:DZ:154:ASP:N	46:DZ:154:ASP:OD1	2.20	0.74
1:AA:1086:U:H3	1:AA:1099:G:H22	1.35	0.74
26:BA:1842:G:O2'	28:BD:253:GLN:NE2	2.20	0.74
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.21	0.74
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.68	0.74
25:AY:49:C:H42	25:AY:65:G:H1	0.79	0.74
26:BA:2285:C:OP2	53:B6:6:ARG:NH1	2.20	0.74
1:CA:532:A:H61	3:CC:193:TYR:HB3	1.52	0.74
13:CM:5:ALA:HB1	13:CM:66:LEU:HD13	1.70	0.74
23:CW:30:G:H1	23:CW:40:C:H42	1.34	0.74
26:DA:11:G:N7	61:DA:4269:HOH:O	2.21	0.74
26:DA:2138:C:H42	26:DA:2153:G:H1	0.77	0.74
31:DG:106:LEU:HA	31:DG:110:ALA:HB3	1.70	0.74
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.20	0.73
30:DF:120:GLU:HB2	30:DF:122:LYS:HG2	1.68	0.73
1:CA:992:U:H6	1:CA:992:U:H5"	1.53	0.73
1:CA:1005:A:OP2	1:CA:1024:G:N2	2.19	0.73
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.68	0.73
2:CB:119:GLU:OE2	2:CB:153:ARG:NH1	2.22	0.73
24:CX:67:C:H2'	24:CX:68:C:H5'	1.69	0.73
50:D3:5:LYS:NZ	50:D3:34:GLU:OE2	2.19	0.73
1:AA:376:G:H5"	16:AP:5:ARG:HB3	1.70	0.73
32:BH:159:GLU:HG3	32:BH:169:VAL:HG11	1.68	0.73
1:CA:1054:C:C4	23:CW:34:G:H1'	2.23	0.73
52:B5:40:LYS:NZ	52:B5:44:THR:O	2.18	0.73
1:CA:345:C:OP2	40:DT:39:ARG:NH2	2.21	0.73
26:BA:993:G:OP1	41:BU:50:ARG:NH2	2.22	0.73
26:BA:847:U:OP2	61:BA:4392:HOH:O	2.06	0.73
26:BA:1602:U:O4	61:BA:4209:HOH:O	2.06	0.73
45:BY:92:ASN:HB2	45:BY:94:LYS:N	2.01	0.73
9:CI:8:GLY:HA3	9:CI:15:ALA:HB3	1.71	0.73
26:DA:952:G:OP1	37:DQ:16:ARG:NH2	2.21	0.73
23:AW:18:G:O2'	23:AW:57:G:N2	2.14	0.73
1:CA:1321:C:H5"	1:CA:1322:C:H2'	1.69	0.73
26:BA:243:U:OP1	55:B8:6:THR:OG1	2.07	0.73
56:B9:17:ILE:HG22	56:B9:24:TYR:HB2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:812:C:N3	61:AA:4038:HOH:O	2.20	0.73
23:AW:19:G:N2	23:AW:56:C:N3	2.36	0.73
26:DA:2127:G:N1	26:DA:2161:C:C4	2.57	0.73
27:BB:33:G:H5'	31:BG:2:PRO:HD3	1.70	0.73
1:CA:1323:G:N2	1:CA:1361:G:O2'	2.22	0.73
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.21	0.72
25:AY:56:C:H2'	25:AY:57:G:O4'	1.88	0.72
1:AA:504:C:OP1	61:AA:4184:HOH:O	2.07	0.72
1:CA:26:A:O2'	4:CD:209:ARG:NH2	2.22	0.72
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.06	0.72
26:DA:2138:C:N3	26:DA:2153:G:N2	2.34	0.72
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.07	0.72
1:CA:117:G:OP2	61:CA:3236:HOH:O	2.07	0.72
2:CB:95:GLN:HB2	2:CB:148:TYR:HD1	1.54	0.72
26:DA:191:A:N1	61:DA:4214:HOH:O	2.22	0.72
1:AA:975:A:H4'	1:AA:976:G:H5"	1.70	0.72
25:AY:33:U:H3'	25:AY:34:G:H5"	1.71	0.72
23:CW:19:G:H1	23:CW:56:C:H42	1.37	0.72
26:DA:740:U:OP2	61:DA:4209:HOH:O	2.07	0.72
44:DX:53:LYS:HB3	44:DX:82:GLN:HB3	1.69	0.72
51:B4:57:GLU:HB2	51:B4:58:ARG:HA	1.72	0.72
13:CM:5:ALA:HB3	13:CM:22:ILE:HD12	1.69	0.72
42:DV:98:GLU:OE1	42:DV:100:ARG:NH1	2.23	0.72
26:BA:65:C:O2	26:BA:456:C:N4	2.20	0.72
23:CW:50:U:O4	23:CW:64:A:N1	2.22	0.72
25:CY:7:A:H61	25:CY:66:U:H3	0.79	0.72
43:BW:15:ARG:NH1	61:BW:4002:HOH:O	2.21	0.72
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.23	0.72
46:DZ:28:MET:HE1	46:DZ:61:LEU:HD21	1.70	0.72
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.70	0.72
28:BD:17:THR:O	28:BD:211:ARG:NH2	2.23	0.72
46:BZ:117:LEU:HD11	46:BZ:144:LEU:HD22	1.71	0.72
23:CW:61:C:O2'	23:CW:62:C:O5'	2.07	0.72
25:CY:15:G:H22	25:CY:48:C:N4	1.87	0.72
26:DA:1250:G:OP2	36:DP:21:ARG:NH1	2.23	0.72
1:AA:310:G:OP2	16:AP:27:LYS:NZ	2.22	0.71
1:AA:934:C:OP1	61:AA:4086:HOH:O	2.08	0.71
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	1.71	0.71
2:CB:212:GLN:NE2	2:CB:234:PRO:O	2.23	0.71
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.72	0.71
23:AW:7:A:H61	23:AW:66:U:H3	1.36	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2049:G:N7	61:BA:5132:HOH:O	2.23	0.71
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.73	0.71
26:DA:2206:G:H3'	26:DA:2207:G:C8	2.25	0.71
49:D2:38:GLN:HB3	49:D2:44:LEU:HB2	1.72	0.71
26:BA:604:G:OP2	36:BP:90:ARG:NH1	2.24	0.71
1:CA:1011:G:H1	1:CA:1018:C:N4	1.89	0.71
26:DA:143:G:H4'	44:DX:35:THR:HG21	1.73	0.71
20:AT:57:ARG:HH12	20:AT:100:ILE:HD12	1.55	0.71
23:AW:19:G:H1	23:AW:56:C:N4	1.89	0.71
1:AA:1027:C:O2	1:AA:1034:G:C2	2.43	0.71
26:BA:1693:U:O2'	28:BD:14:ARG:NH2	2.23	0.71
26:DA:1449:A:O2'	26:DA:1529:G:N2	2.17	0.71
1:AA:538:G:H5"	12:AL:114:LYS:HB2	1.71	0.71
19:CS:77:THR:HG22	19:CS:78:ARG:HG2	1.71	0.71
26:DA:1800:C:OP2	28:DD:183:ARG:NH2	2.23	0.71
26:BA:1140:C:O3'	34:BN:25:ARG:NH1	2.23	0.71
1:CA:1465:C:OP2	40:DT:108:ARG:NH2	2.22	0.71
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.72	0.71
26:BA:899:A:O2'	26:BA:900:A:O5'	2.08	0.71
1:CA:986:A:O2'	19:CS:55:LYS:O	2.08	0.71
26:DA:2788:C:OP1	29:DE:61:ARG:NH2	2.23	0.71
28:DD:85:ASP:OD2	28:DD:88:ARG:NH1	2.21	0.71
4:CD:57:ARG:HH22	5:CE:107:ARG:HD3	1.55	0.71
5:CE:50:GLU:HB2	5:CE:53:LEU:HD13	1.73	0.71
27:DB:5:C:H42	27:DB:116:G:H1	1.39	0.71
6:AF:70:ASP:OD1	6:AF:70:ASP:N	2.24	0.70
39:DS:15:ARG:O	39:DS:19:LYS:HD3	1.90	0.70
26:BA:1380:G:OP2	61:BA:5119:HOH:O	2.09	0.70
1:CA:1366:C:O2'	10:CJ:60:ARG:NH2	2.24	0.70
31:DG:80:PHE:O	31:DG:82:LEU:N	2.22	0.70
33:DI:72:LEU:HD21	33:DI:107:VAL:HG11	1.74	0.70
26:BA:2239:G:OP2	61:BA:4313:HOH:O	2.08	0.70
26:BA:2448:A:OP1	61:BA:5135:HOH:O	2.09	0.70
54:B7:24:THR:HG22	54:B7:27:GLY:H	1.56	0.70
1:CA:999:C:H42	1:CA:1042:G:H1	0.74	0.70
1:CA:1128:C:O2'	1:CA:1147:C:N3	2.23	0.70
26:DA:1038:C:H42	26:DA:1117:G:H1	1.38	0.70
26:DA:2148:G:H2'	26:DA:2149:G:C8	2.27	0.70
17:AQ:75:ARG:NH1	17:AQ:76:LEU:O	2.25	0.70
1:CA:993:G:O6	1:CA:1045:C:N4	2.15	0.70
26:DA:900:A:H2'	26:DA:901:A:H8	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1689:A:H62	26:DA:1698:A:H2	1.40	0.70
3:AC:19:GLU:HB3	3:AC:40:ARG:HH22	1.57	0.70
25:AY:51:U:H2'	25:AY:52:G:H8	1.56	0.70
36:BP:126:VAL:HG12	36:BP:148:LEU:HD22	1.72	0.70
29:DE:111:ARG:HD3	38:DR:1:MET:HE1	1.72	0.70
32:DH:159:GLU:HG3	32:DH:169:VAL:HG11	1.74	0.70
33:DI:78:THR:O	33:DI:104:GLN:NE2	2.25	0.70
25:AY:15:G:N1	25:AY:48:C:N3	2.39	0.70
25:AY:22:G:N7	25:AY:46:7MG:O6	2.25	0.70
23:CW:4:C:N4	23:CW:69:G:C6	2.59	0.70
1:AA:1304:G:OP2	61:AA:4111:HOH:O	2.10	0.70
5:AE:6:PHE:HB2	5:AE:34:VAL:HG22	1.73	0.70
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.72	0.70
1:CA:953:G:H5'	1:CA:965:A:N6	2.07	0.70
27:DB:28:C:H2'	27:DB:29:A:H8	1.57	0.70
1:CA:582:U:OP1	15:CO:68:ARG:NH1	2.24	0.70
46:DZ:44:PHE:O	46:DZ:48:PHE:N	2.21	0.70
1:AA:1159:U:OP1	2:AB:133:LYS:NZ	2.25	0.69
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.20	0.69
26:BA:1238:G:OP2	61:BA:4983:HOH:O	2.10	0.69
1:CA:812:C:N3	61:CA:3212:HOH:O	2.25	0.69
2:CB:161:ALA:HB1	2:CB:185:ILE:HD11	1.74	0.69
10:CJ:5:ARG:N	10:CJ:73:ASP:HA	2.07	0.69
26:DA:2404:C:O3'	36:DP:77:ARG:NH2	2.25	0.69
28:BD:71:ASP:HB3	28:BD:103:ARG:HH22	1.57	0.69
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	1.72	0.69
26:DA:1033:U:OP1	56:D9:9:ARG:NH2	2.26	0.69
46:DZ:72:ARG:NH1	46:DZ:97:GLU:O	2.25	0.69
26:BA:1434:A:H61	26:BA:1558:A:H62	1.39	0.69
1:CA:798:G:O6	61:CA:3223:HOH:O	2.09	0.69
26:DA:300:A:OP1	45:DY:86:ARG:NH2	2.25	0.69
30:DF:197:ASP:OD1	30:DF:198:ALA:N	2.25	0.69
36:DP:91:PHE:O	36:DP:121:LYS:NZ	2.21	0.69
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.75	0.69
9:AI:110:GLU:OE2	9:AI:113:LYS:NZ	2.25	0.69
26:BA:1297:C:OP1	61:BA:4340:HOH:O	2.09	0.69
31:BG:41:GLN:NE2	31:BG:154:GLY:O	2.25	0.69
1:CA:67:C:H2'	1:CA:68:G:C8	2.28	0.69
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.56	0.69
1:CA:1359:C:O2	61:CA:3330:HOH:O	2.09	0.69
8:CH:12:ARG:HH12	8:CH:27:PRO:HD2	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:26:A:N1	25:CY:44:G:O6	2.26	0.69
26:DA:987:G:O2'	26:DA:1000:A:N3	2.25	0.69
1:AA:1423:G:OP1	35:BO:49:ARG:NH2	2.24	0.69
4:AD:49:ARG:H	4:AD:49:ARG:HE	1.38	0.69
26:BA:1385:G:O2'	26:BA:1396:U:O2	2.07	0.69
23:CW:56:C:H5	26:DA:897:C:H1'	1.56	0.69
26:DA:2166:G:H3'	26:DA:2167:U:C5'	2.22	0.69
26:DA:2176:A:H2'	26:DA:2177:C:C6	2.27	0.69
28:DD:275:LYS:HG3	28:DD:276:LYS:HA	1.73	0.69
30:BF:185:ASP:HA	30:BF:188:ARG:HD3	1.73	0.69
25:CY:69:G:H2'	25:CY:70:G:O4'	1.92	0.69
26:DA:878:A:N6	26:DA:899:A:O2'	2.22	0.69
26:DA:2119:A:H2	26:DA:2171:A:H5'	1.58	0.69
26:DA:2135:A:H2'	26:DA:2136:C:C6	2.27	0.69
19:AS:27:GLU:HB2	19:AS:28:LYS:HD2	1.74	0.69
44:BX:35:THR:HG22	44:BX:38:GLU:H	1.57	0.69
19:CS:27:GLU:HB3	19:CS:28:LYS:HA	1.75	0.69
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.58	0.69
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.75	0.69
26:BA:271(K):U:H1'	33:BI:50:ARG:HD2	1.74	0.69
29:BE:8:LYS:NZ	61:BE:416:HOH:O	2.18	0.69
48:B1:86:SER:OG	48:B1:89:GLU:OE1	2.08	0.69
1:CA:460:G:O6	1:CA:470:C:H5"	1.93	0.69
1:CA:1060:C:O2'	10:CJ:56:HIS:ND1	2.24	0.69
1:CA:1320:C:O4'	19:CS:73:GLU:HG2	1.93	0.69
1:CA:1329:A:OP2	21:CU:7:ARG:NH2	2.22	0.69
12:CL:124:LYS:HB2	12:CL:124:LYS:HZ2	1.57	0.69
25:CY:5:G:H1	25:CY:68:C:H42	1.40	0.69
26:DA:89:G:H3'	26:DA:90:U:H5"	1.75	0.69
26:DA:568:U:H5'	26:DA:945:A:N1	2.08	0.69
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.23	0.69
25:AY:76:A:N6	26:BA:2422:A:O4'	2.26	0.69
26:DA:1420:U:O2'	26:DA:1421:G:OP1	2.10	0.69
2:AB:21:ARG:HB3	2:AB:39:ILE:HG12	1.75	0.69
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.74	0.69
26:BA:952:G:OP1	37:BQ:16:ARG:NH2	2.26	0.69
46:DZ:93:ASP:HA	46:DZ:131:ARG:HH22	1.57	0.69
23:AW:50:U:H3	23:AW:64:A:H61	1.39	0.68
26:BA:1840:G:N7	61:BA:4310:HOH:O	2.26	0.68
47:B0:10:THR:HG22	47:B0:12:ASN:H	1.57	0.68
20:CT:43:LEU:O	20:CT:47:GLY:N	2.17	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:838:G:H1	1:AA:848:C:H42	1.40	0.68
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.27	0.68
31:DG:113:ARG:NH1	31:DG:139:LEU:O	2.26	0.68
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.40	0.68
14:AN:3:ARG:HB3	14:AN:3:ARG:HH21	1.57	0.68
26:BA:1143:A:OP1	34:BN:25:ARG:NH2	2.26	0.68
26:BA:1714:G:H1	26:BA:1745(A):C:H42	1.41	0.68
33:BI:38:LEU:H	33:BI:38:LEU:HD12	1.58	0.68
25:CY:62:C:H2'	25:CY:63:G:H8	1.58	0.68
26:DA:741:G:OP2	61:DA:4210:HOH:O	2.12	0.68
26:DA:1816:G:O6	28:DD:35:LYS:NZ	2.20	0.68
51:D4:44:THR:O	51:D4:46:GLN:N	2.27	0.68
1:AA:953:G:H5'	1:AA:965:A:H61	1.56	0.68
37:BQ:18:LYS:O	37:BQ:98:LYS:NZ	2.22	0.68
8:CH:12:ARG:NH1	8:CH:27:PRO:HD2	2.09	0.68
26:DA:2128:C:H42	26:DA:2160:G:H1	1.42	0.68
26:DA:2502:G:N7	61:DA:4405:HOH:O	2.26	0.68
26:DA:2689:U:H4'	26:DA:2690:C:H5'	1.75	0.68
30:DF:143:ALA:HB1	30:DF:148:LEU:HB2	1.74	0.68
47:D0:40:GLN:HE21	47:D0:57:PHE:HB3	1.58	0.68
25:AY:69:G:H2'	25:AY:70:G:O4'	1.94	0.68
26:BA:2123:G:H1	26:BA:2175:C:H42	1.40	0.68
1:CA:1002:G:H1	1:CA:1038:C:N4	1.91	0.68
1:CA:1166:G:H5"	1:CA:1166:G:H8	1.59	0.68
26:DA:1593:G:H2'	26:DA:1594:G:C8	2.28	0.68
26:DA:2171:A:N3	26:DA:2172:U:N3	2.41	0.68
38:DR:33:ARG:NH1	38:DR:115:GLU:OE2	2.26	0.68
1:AA:339:C:OP2	35:BO:97:ARG:NH1	2.26	0.68
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.26	0.68
26:BA:543:C:N4	26:BA:549:G:O6	2.18	0.68
26:BA:1783:A:N7	61:BA:5029:HOH:O	2.27	0.68
26:DA:2183:C:H2'	26:DA:2184:G:H8	1.59	0.68
30:DF:21:ALA:HB3	30:DF:22:ALA:HA	1.75	0.68
1:AA:838:G:H1	1:AA:848:C:N4	1.91	0.68
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.76	0.68
26:BA:548:A:O2'	26:BA:549:G:OP1	2.10	0.68
27:BB:2:C:O2	27:BB:119:G:N2	2.20	0.68
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.93	0.68
23:CW:43:C:H2'	23:CW:44:G:C8	2.29	0.68
1:AA:123:C:OP1	1:AA:311:C:O2'	2.11	0.68
26:BA:2447:G:OP2	61:BA:4544:HOH:O	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BZ:145:GLU:O	46:BZ:148:ASP:N	2.26	0.68
1:CA:750:G:N3	15:CO:23:GLY:HA3	2.08	0.68
26:DA:1189:A:OP2	61:DA:4174:HOH:O	2.12	0.68
29:DE:111:ARG:HG3	29:DE:160:TYR:CD2	2.29	0.68
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.26	0.68
1:CA:344:A:H5"	1:CA:345:C:H5	1.59	0.68
27:DB:55:U:O2'	31:DG:27:ASN:ND2	2.26	0.68
39:DS:58:LEU:HD11	39:DS:65:VAL:HA	1.75	0.68
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.12	0.67
26:BA:602:G:O2'	26:BA:655:A:N6	2.27	0.67
33:BI:106:GLY:HA2	33:BI:107:VAL:O	1.93	0.67
35:BO:2:ILE:HD12	35:BO:6:THR:HG21	1.73	0.67
50:B3:8:LEU:HD13	50:B3:31:LEU:HD23	1.75	0.67
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.57	0.67
1:CA:1309:G:OP1	13:CM:88:ARG:NH1	2.26	0.67
4:CD:173:TRP:HB3	4:CD:187:ARG:HE	1.59	0.67
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.42	0.67
1:AA:572:A:OP1	61:AA:4084:HOH:O	2.11	0.67
26:BA:2059:A:OP2	61:BA:4315:HOH:O	2.11	0.67
26:BA:2328:A:H2'	26:BA:2329:G:C8	2.28	0.67
12:CL:124:LYS:NZ	12:CL:124:LYS:HB2	2.08	0.67
1:AA:1158:C:H5	1:AA:1181:G:H1	1.42	0.67
9:AI:53:VAL:O	9:AI:55:ALA:N	2.27	0.67
19:CS:27:GLU:HB2	19:CS:28:LYS:HD3	1.77	0.67
25:CY:15:G:N2	25:CY:48:C:H42	1.90	0.67
42:DV:43:GLU:N	42:DV:43:GLU:OE2	2.27	0.67
52:D5:16:ARG:NH1	52:D5:17:ASP:OD1	2.27	0.67
1:AA:347:G:H2'	1:AA:348:G:O4'	1.94	0.67
3:CC:91:LEU:HD23	3:CC:101:LEU:HD22	1.76	0.67
8:CH:4:ASP:OD2	8:CH:85:ARG:NH1	2.27	0.67
26:DA:526:A:OP1	61:DA:4183:HOH:O	2.12	0.67
26:DA:2121:G:N2	26:DA:2177:C:N3	2.36	0.67
1:AA:1028:C:H2'	1:AA:1029:C:H4'	1.77	0.67
3:CC:129:ALA:HB3	3:CC:132:ARG:HB2	1.77	0.67
26:DA:2518:A:OP2	61:DA:3991:HOH:O	2.12	0.67
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.76	0.67
26:BA:1452:A:OP2	61:BA:3995:HOH:O	2.12	0.67
1:CA:1310:G:OP1	13:CM:77:ASN:ND2	2.27	0.67
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.77	0.67
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.77	0.67
26:DA:2224:G:OP1	28:DD:268:ARG:NE	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2562:U:H1'	35:DO:23:ARG:HH11	1.60	0.67
1:AA:160:A:N6	1:AA:345:C:OP2	2.27	0.67
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.29	0.67
1:AA:67:C:H2'	1:AA:68:G:C8	2.30	0.67
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.27	0.67
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.76	0.67
26:DA:1783:A:N7	61:DA:4510:HOH:O	2.26	0.67
51:D4:38:LYS:O	51:D4:40:HIS:N	2.21	0.67
1:AA:1022:G:H2'	1:AA:1023:G:H8	1.60	0.67
46:BZ:108:PRO:HB3	46:BZ:117:LEU:HD13	1.75	0.67
1:CA:560:U:O2'	1:CA:561:U:OP2	2.13	0.67
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.58	0.67
26:DA:131:G:OP1	61:DA:3791:HOH:O	2.11	0.67
26:DA:2126:A:H61	26:DA:2172:U:H3'	1.60	0.67
26:DA:2287:A:H62	26:DA:2344:U:H3	1.40	0.67
34:DN:115:ARG:HA	34:DN:118:LYS:HE3	1.75	0.67
25:CY:9:A:OP2	25:CY:13:C:N4	2.26	0.67
26:DA:7:G:N2	26:DA:2896:C:O2	2.23	0.67
26:DA:2127:G:N1	26:DA:2161:C:N4	2.42	0.67
26:DA:2148:G:H2'	26:DA:2149:G:H8	1.58	0.67
31:DG:13:GLU:O	31:DG:15:VAL:N	2.27	0.67
1:CA:673:G:H2'	1:CA:674:G:C8	2.30	0.66
25:CY:62:C:H2'	25:CY:63:G:C8	2.30	0.66
3:AC:70:VAL:HG22	3:AC:72:LYS:H	1.59	0.66
26:BA:971:C:OP2	61:BA:5252:HOH:O	2.11	0.66
1:CA:951:G:OP2	13:CM:102:ARG:NH1	2.29	0.66
2:CB:87:ARG:HH21	2:CB:233:SER:HB3	1.60	0.66
19:CS:49:ILE:HG13	19:CS:62:ILE:HD11	1.76	0.66
27:DB:50:G:OP1	39:DS:63:THR:N	2.27	0.66
1:CA:1155:G:H2'	1:CA:1156:G:C8	2.29	0.66
1:CA:1191:A:OP1	3:CC:3:ASN:ND2	2.28	0.66
3:CC:22:TRP:CD2	3:CC:59:ARG:HD2	2.30	0.66
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.60	0.66
37:BQ:54:MET:HG3	37:BQ:117:ALA:HB1	1.76	0.66
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.27	0.66
7:CG:59:LEU:HG	7:CG:63:LYS:HE2	1.77	0.66
26:DA:2400:G:O3'	53:D6:18:ARG:NH1	2.27	0.66
27:DB:76:G:N2	27:DB:101:G:O6	2.25	0.66
1:AA:1245:A:H61	1:AA:1292:U:H3	1.44	0.66
2:AB:93:VAL:HG21	2:AB:97:TRP:CD1	2.30	0.66
13:AM:34:LEU:HD13	13:AM:41:PRO:HA	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:6:G:O6	25:AY:7:A:N6	2.29	0.66
26:BA:123:G:OP2	61:BA:3977:HOH:O	2.14	0.66
26:BA:2277:G:OP2	47:B0:10:THR:HG21	1.96	0.66
26:BA:2759:G:N7	61:BA:4108:HOH:O	2.27	0.66
42:BV:34:GLU:HB3	42:BV:56:SER:HB2	1.75	0.66
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.13	0.66
20:AT:15:ARG:O	20:AT:19:SER:OG	2.13	0.66
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.28	0.66
1:CA:1316:G:H4'	14:CN:18:VAL:HG13	1.77	0.66
26:DA:1278:A:OP1	38:DR:36:THR:HG23	1.96	0.66
1:CA:1348:U:H4'	9:CI:120:ARG:HD3	1.78	0.66
3:CC:150:LYS:HB2	3:CC:173:VAL:HG21	1.77	0.66
26:BA:248:G:OP1	61:BA:4977:HOH:O	2.13	0.66
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.43	0.66
17:CQ:53:LEU:HD23	17:CQ:82:MET:HE1	1.77	0.66
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.29	0.66
26:BA:880:G:H2'	26:BA:881:G:C8	2.30	0.66
1:CA:660:G:H1	1:CA:745:C:H42	1.43	0.66
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.29	0.66
26:BA:607:U:OP1	30:BF:102:PRO:HA	1.96	0.66
26:BA:739:G:OP1	61:BA:5169:HOH:O	2.13	0.66
26:BA:998:C:OP1	61:BA:4644:HOH:O	2.14	0.66
26:BA:1405:U:H2'	26:BA:1406:U:C6	2.31	0.66
26:BA:2080:G:O6	61:BA:4418:HOH:O	2.12	0.66
26:BA:2140:C:C2	26:BA:2151:G:N2	2.64	0.66
35:BO:64:ARG:NH1	35:BO:81:ASP:OD1	2.29	0.66
1:AA:193:C:H2'	1:AA:194:C:H6	1.59	0.65
1:CA:649:G:H2'	1:CA:650:G:H5"	1.78	0.65
24:CX:9:G:O2'	24:CX:10:G:N7	2.20	0.65
31:DG:16:ARG:O	31:DG:20:ILE:HG13	1.95	0.65
50:D3:7:LYS:NZ	50:D3:32:GLN:O	2.29	0.65
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.78	0.65
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.77	0.65
23:AW:5:G:H2'	23:AW:6:G:H8	1.60	0.65
26:BA:1174:A:H4'	26:BA:1175:U:OP1	1.95	0.65
26:BA:1754:C:H5"	40:BT:113:LYS:HE3	1.77	0.65
26:BA:2722:G:OP2	61:BA:4098:HOH:O	2.14	0.65
29:BE:105:THR:OG1	29:BE:199:ARG:NH2	2.30	0.65
1:CA:1026:G:O6	1:CA:1036:G:N2	2.28	0.65
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.30	0.65
1:AA:1239:A:H62	1:AA:1299:A:N6	1.94	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:977:A:O2'	1:CA:981:U:N3	2.29	0.65
1:CA:1320:C:N3	19:CS:36:ARG:NH2	2.44	0.65
1:CA:573:A:N3	1:CA:883:C:O2'	2.29	0.65
1:CA:1022:G:H2'	1:CA:1023:G:H8	1.60	0.65
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.76	0.65
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.70	0.65
15:CO:55:GLY:HA2	15:CO:58:MET:HE2	1.77	0.65
25:CY:4:C:N4	25:CY:69:G:H1	1.94	0.65
30:DF:184:TYR:CE2	30:DF:188:ARG:HD2	2.32	0.65
36:DP:44:GLY:O	61:DP:301:HOH:O	2.14	0.65
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.32	0.65
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.12	0.65
25:AY:29:G:N2	25:AY:41:C:N3	2.36	0.65
26:BA:880:G:H2'	26:BA:881:G:H8	1.61	0.65
26:DA:323:G:HO2'	26:DA:1205:U:H3	1.43	0.65
26:DA:857:C:OP2	47:D0:77:ARG:NH2	2.29	0.65
2:AB:93:VAL:HG21	2:AB:97:TRP:HD1	1.59	0.65
26:BA:278:A:H2'	26:BA:279:C:C6	2.31	0.65
1:CA:954:G:H21	1:CA:1227:A:H62	1.44	0.65
26:BA:1342:A:OP2	61:BA:4209:HOH:O	2.13	0.65
1:CA:501:C:H2'	1:CA:502:G:C8	2.31	0.65
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.62	0.65
1:CA:1359:C:H1'	1:CA:1362:C:H41	1.61	0.65
23:CW:3:C:N3	23:CW:70:G:O6	2.29	0.65
26:DA:500:G:N1	26:DA:503:A:OP2	2.30	0.65
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.32	0.65
27:BB:106:G:H5'	46:BZ:31:ARG:HG2	1.79	0.65
26:DA:1693:U:O2'	28:DD:14:ARG:NH2	2.29	0.65
31:DG:44:GLY:O	31:DG:47:LYS:HB2	1.95	0.65
46:DZ:130:PRO:HA	46:DZ:133:ILE:HD11	1.77	0.65
1:AA:1030(D):A:N6	1:AA:1031:G:H21	1.95	0.65
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.32	0.65
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	1.78	0.65
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.79	0.65
26:BA:1204:A:H2	26:BA:1241:A:H62	1.43	0.65
26:BA:131:G:OP1	61:BA:4045:HOH:O	2.13	0.65
26:BA:2478:A:OP2	56:B9:2:LYS:NZ	2.29	0.65
38:BR:67:LEU:HD13	38:BR:76:VAL:HG21	1.79	0.65
4:CD:157:LEU:O	4:CD:161:ASN:ND2	2.29	0.65
7:CG:72:ARG:HH22	7:CG:138:LYS:HZ1	1.44	0.65
8:CH:49:GLU:OE2	8:CH:62:TYR:OH	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:150:LYS:HG3	3:AC:169:ALA:HB2	1.79	0.64
20:CT:56:MET:HE2	20:CT:84:LEU:HD22	1.79	0.64
26:DA:1803:A:O2'	28:DD:259:THR:HG21	1.97	0.64
1:AA:942:G:H21	9:AI:124:GLN:NE2	1.95	0.64
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.30	0.64
25:AY:51:U:H2'	25:AY:52:G:C8	2.32	0.64
26:BA:882:G:N2	26:BA:895:U:O2	2.27	0.64
26:BA:1796:U:H2'	26:BA:1797:C:C6	2.32	0.64
27:BB:23:G:O6	61:BB:3133:HOH:O	2.10	0.64
51:B4:59:PHE:HA	51:B4:61:ARG:H	1.63	0.64
53:B6:6:ARG:NH1	53:B6:26:ASN:HB2	2.12	0.64
26:DA:2794:C:N4	26:DA:2802:G:O6	2.30	0.64
47:D0:10:THR:HG22	47:D0:12:ASN:H	1.61	0.64
40:BT:112:ARG:HG3	40:BT:115:ARG:HH21	1.62	0.64
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.15	0.64
39:DS:28:VAL:HG13	39:DS:35:ILE:HD11	1.79	0.64
51:D4:1:MET:HG2	51:D4:6:HIS:CD2	2.32	0.64
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.32	0.64
26:BA:1315:C:OP2	61:BA:4634:HOH:O	2.14	0.64
26:BA:2162:G:C2'	26:BA:2163:C:H5"	2.28	0.64
1:CA:599:C:H2'	1:CA:600:C:H5"	1.80	0.64
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.33	0.64
2:CB:218:ALA:O	2:CB:222:ILE:HG23	1.97	0.64
26:DA:1648:C:OP1	61:DA:4201:HOH:O	2.14	0.64
27:DB:24:G:N7	27:DB:56:G:H2'	2.12	0.64
30:DF:116:ASP:OD2	36:DP:1:MET:N	2.30	0.64
2:AB:13:ALA:HB2	2:AB:44:LEU:HG	1.80	0.64
26:BA:744:G:OP1	61:BA:4683:HOH:O	2.15	0.64
26:BA:2124:G:H1	26:BA:2174:C:H42	1.45	0.64
1:CA:664:G:P	18:CR:64:ARG:HH22	2.19	0.64
11:CK:98:LEU:O	11:CK:101:SER:OG	2.14	0.64
26:DA:528:A:O2'	26:DA:529:A:H5"	1.96	0.64
39:DS:10:ARG:NH2	39:DS:91:PRO:O	2.27	0.64
26:BA:1993:U:OP2	61:BA:5277:HOH:O	2.15	0.64
1:CA:1323:G:H4'	1:CA:1363:C:C2	2.32	0.64
26:DA:236:C:H2'	26:DA:237:C:H6	1.63	0.64
27:DB:66:A:H61	27:DB:109:C:H5"	1.63	0.64
33:DI:12:LEU:HD22	33:DI:19:VAL:HG21	1.78	0.64
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.77	0.64
48:B1:23:LYS:HB3	48:B1:29:GLY:HA3	1.78	0.64
1:CA:1002:G:C4	1:CA:1003:G:H8	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1792:G:O2'	26:DA:1830:C:OP1	2.15	0.64
30:DF:101:LEU:HD12	30:DF:102:PRO:HD2	1.80	0.64
1:AA:195:A:OP1	20:AT:68:LYS:NZ	2.30	0.64
23:AW:5:G:H2'	23:AW:6:G:C8	2.33	0.64
45:BY:54:LYS:HA	45:BY:56:PRO:HD3	1.80	0.64
1:CA:1309:G:OP2	13:CM:99:ARG:NH2	2.28	0.64
5:CE:20:GLN:NE2	5:CE:21:ALA:O	2.31	0.64
26:DA:2323:G:O6	26:DA:2332:U:N3	2.18	0.64
33:DI:102:SER:O	33:DI:106:GLY:N	2.30	0.64
12:AL:33:ARG:HH11	12:AL:62:SER:HB3	1.62	0.64
26:BA:2849:U:OP2	40:BT:95:ARG:NH1	2.30	0.64
1:CA:444:C:H2'	1:CA:445:G:H8	1.62	0.64
1:CA:1004:A:H2'	1:CA:1038:C:H1'	1.80	0.64
1:CA:1133:G:H1	1:CA:1141:C:N4	1.95	0.64
1:CA:1507:A:N6	1:CA:1528:U:O4	2.16	0.64
1:AA:56:U:H2'	1:AA:57:G:C8	2.33	0.64
3:AC:37:GLN:NE2	14:AN:52:GLN:OE1	2.31	0.64
24:AX:19:G:H4'	24:AX:20:U:OP2	1.97	0.64
32:BH:86:GLU:OE2	32:BH:132:ARG:NH2	2.30	0.64
32:BH:149:ARG:NH1	32:BH:167:GLU:OE2	2.30	0.64
43:BW:88:ARG:HG3	43:BW:92:ARG:HH21	1.61	0.64
1:AA:405:U:OP2	4:AD:3:ARG:NH2	2.32	0.63
1:AA:1464:G:OP2	40:BT:111:ARG:NH2	2.30	0.63
26:BA:441:U:O2	30:BF:46:ARG:NH2	2.26	0.63
44:BX:31:HIS:CD2	44:BX:33:LYS:H	2.14	0.63
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.11	0.63
1:CA:1165:C:N4	1:CA:1171:G:H1	1.93	0.63
2:CB:178:ARG:NH2	8:CH:68:ARG:HH22	1.95	0.63
29:DE:101:ARG:CZ	29:DE:171:GLU:HB2	2.28	0.63
1:AA:894:G:N7	61:AA:4110:HOH:O	2.30	0.63
1:AA:1027:C:C2	1:AA:1034:G:C6	2.86	0.63
23:AW:55:PSU:O3'	26:BA:897:C:H4'	1.98	0.63
25:AY:25:C:O2'	25:AY:26:A:H8	1.82	0.63
26:BA:1165:U:H2'	26:BA:1166:C:C6	2.33	0.63
26:BA:1418:G:OP2	61:BA:4561:HOH:O	2.16	0.63
46:BZ:7:ALA:HB2	46:BZ:59:LEU:HD22	1.78	0.63
1:CA:562:C:H1'	12:CL:15:ARG:HB3	1.80	0.63
1:CA:1216:G:H5"	14:CN:5:ALA:HB2	1.79	0.63
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.31	0.63
1:CA:1318:A:OP1	19:CS:3:ARG:NH1	2.32	0.63
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1521:G:N3	61:CA:3217:HOH:O	2.30	0.63
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.79	0.63
25:CY:31:A:N1	25:CY:39:PSU:C2	2.65	0.63
26:DA:971:C:OP2	61:DA:4615:HOH:O	2.15	0.63
35:DO:115:VAL:HG13	35:DO:121:VAL:HG21	1.79	0.63
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.31	0.63
3:AC:181:ASN:ND2	3:AC:204:LEU:HD12	2.13	0.63
26:BA:363(A):A:H2'	26:BA:363(B):G:C8	2.34	0.63
1:CA:533:A:O2'	1:CA:535:A:OP2	2.17	0.63
1:CA:1013:G:N2	1:CA:1016:A:OP2	2.25	0.63
26:DA:2127:G:C2	26:DA:2161:C:C4	2.87	0.63
26:DA:2805:G:H2'	26:DA:2807:G:C8	2.34	0.63
26:DA:2880:C:O3'	38:DR:90:ARG:NH1	2.30	0.63
27:DB:19:G:H2'	27:DB:20:C:O4'	1.99	0.63
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	1.79	0.63
25:AY:15:G:H22	25:AY:48:C:N4	1.96	0.63
26:BA:2312:U:H5'	31:BG:88:ILE:HD11	1.81	0.63
7:CG:113:GLU:HB2	7:CG:119:ARG:HG2	1.81	0.63
16:CP:23:ASP:OD2	16:CP:25:ARG:NH1	2.32	0.63
26:DA:2632:A:O2'	26:DA:2811:G:O2'	2.13	0.63
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	1.81	0.63
20:AT:87:LYS:O	20:AT:91:LEU:HG	1.98	0.63
26:BA:2683:C:OP1	40:BT:53:ARG:NH2	2.31	0.63
26:DA:2206:G:H3'	26:DA:2207:G:N7	2.13	0.63
28:DD:206:LEU:HD22	28:DD:211:ARG:HG2	1.80	0.63
32:DH:3:ARG:HH22	32:DH:5:GLY:H	1.47	0.63
46:DZ:157:LEU:HD13	46:DZ:161:VAL:HG13	1.80	0.63
8:AH:34:GLU:OE2	8:AH:37:ARG:NH1	2.31	0.63
19:AS:64:GLU:O	19:AS:67:VAL:HG23	1.98	0.63
25:AY:5:G:N1	25:AY:68:C:N4	2.31	0.63
33:BI:93:THR:OG1	33:BI:96:ASP:OD1	2.17	0.63
26:DA:1038:C:N4	26:DA:1117:G:H1	1.97	0.63
1:AA:1036:G:H3'	1:AA:1037:C:H6	1.63	0.63
1:CA:539:A:H2'	1:CA:540:G:C8	2.33	0.63
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.30	0.63
23:CW:76:F3N:OP2	61:CW:3102:HOH:O	2.15	0.63
1:AA:1321:C:H5"	1:AA:1322:C:H2'	1.78	0.63
1:CA:1002:G:H1	1:CA:1038:C:H42	1.44	0.63
1:CA:1402:C:N4	22:CV:18:G:OP2	2.31	0.63
26:DA:1021:A:H62	26:DA:1141:U:H3	1.44	0.63
26:DA:1637:A:OP2	61:DA:4544:HOH:O	2.16	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1939:U:OP1	26:DA:2604:U:O2'	2.17	0.63
26:DA:2173:A:H2'	26:DA:2174:C:O4'	1.99	0.63
1:CA:1150:U:O4	1:CA:1151:A:N6	2.32	0.63
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.31	0.63
8:CH:37:ARG:HH21	8:CH:38:ILE:HD11	1.63	0.63
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.31	0.63
26:DA:1602:U:O4	61:DA:3879:HOH:O	2.11	0.63
31:DG:145:THR:HG22	31:DG:148:MET:SD	2.38	0.63
1:AA:1025:U:O2	1:AA:1036:G:O6	2.16	0.62
23:AW:47:U:H6	23:AW:47:U:H5'	1.64	0.62
26:BA:1566:A:OP1	28:BD:211:ARG:NH1	2.32	0.62
1:CA:1120:G:C6	1:CA:1154:G:N2	2.67	0.62
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.33	0.62
2:CB:216:SER:O	2:CB:220:ASP:N	2.21	0.62
29:DE:14:ILE:HG13	29:DE:21:VAL:HG13	1.80	0.62
1:AA:673:G:H2'	1:AA:674:G:C8	2.34	0.62
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.82	0.62
26:BA:1155:A:OP1	41:BU:55:ARG:HD3	1.99	0.62
26:BA:2532:G:O2'	26:BA:2657:A:N1	2.31	0.62
3:CC:125:GLU:OE2	3:CC:125:GLU:N	2.26	0.62
11:CK:93:GLN:HA	11:CK:93:GLN:HE21	1.64	0.62
13:CM:32:GLU:OE1	13:CM:59:TYR:OH	2.16	0.62
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.62	0.62
26:DA:601:C:OP1	30:DF:108:LYS:NZ	2.23	0.62
37:DQ:67:ARG:O	37:DQ:101:ARG:NH2	2.30	0.62
47:B0:27:GLU:HG3	47:B0:68:GLU:HA	1.81	0.62
1:CA:981:U:H5'	14:CN:21:TYR:CZ	2.35	0.62
3:CC:16:ARG:NH1	3:CC:181:ASN:OD1	2.31	0.62
5:CE:36:ASP:O	5:CE:38:GLN:N	2.27	0.62
25:CY:76:A:O2'	26:DA:2394:C:N3	2.31	0.62
26:DA:1300:U:H4'	26:DA:1301:A:C5'	2.29	0.62
1:CA:1023:G:H3'	1:CA:1024:G:H8	1.63	0.62
25:CY:31:A:C6	25:CY:39:PSU:O2	2.52	0.62
26:DA:322:A:OP2	30:DF:169:ASN:HB2	1.98	0.62
26:DA:902:C:H2'	26:DA:903:C:C6	2.35	0.62
42:DV:72:VAL:HG13	42:DV:85:LYS:HB3	1.80	0.62
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.80	0.62
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.81	0.62
36:BP:65:ARG:HG3	55:B8:25:MET:HG3	1.80	0.62
1:CA:694:A:O2'	25:CY:38:A:O2'	2.13	0.62
1:CA:946:A:H2'	1:CA:947:G:C8	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:951:G:N3	1:CA:970:C:O2'	2.29	0.62
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.33	0.62
13:CM:20:THR:HA	13:CM:25:ILE:HG22	1.81	0.62
26:DA:1890:A:OP2	61:DA:4438:HOH:O	2.16	0.62
37:DQ:85:LYS:HB2	47:D0:7:LEU:HD12	1.82	0.62
24:AX:21:A:H61	24:AX:46:G:H2'	1.64	0.62
1:CA:56:U:H2'	1:CA:57:G:C8	2.35	0.62
1:CA:975:A:N1	10:CJ:48:THR:HB	2.13	0.62
16:CP:28:ARG:NH1	16:CP:29:ASP:OD1	2.31	0.62
30:DF:122:LYS:NZ	30:DF:152:GLU:OE2	2.30	0.62
43:DW:88:ARG:NH1	43:DW:94:ASP:OD2	2.32	0.62
45:DY:102:CYS:SG	45:DY:103:GLY:N	2.72	0.62
1:AA:1187:G:H4'	9:AI:111:ARG:HH11	1.64	0.62
1:AA:1414:U:H3	1:AA:1486:G:H1	1.46	0.62
46:BZ:28:MET:HE1	46:BZ:61:LEU:HD21	1.80	0.62
51:B4:63:TYR:N	51:B4:64:GLY:HA2	2.15	0.62
1:CA:661:G:H1	1:CA:744:C:H42	1.46	0.62
1:CA:957:U:H2'	1:CA:959:A:OP2	2.00	0.62
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.23	0.62
26:DA:577:G:O2'	26:DA:1254:A:OP1	2.18	0.62
26:DA:658:C:H2'	26:DA:659:C:C6	2.34	0.62
31:DG:101:ILE:HD13	51:D4:25:TYR:HB2	1.82	0.62
1:AA:97:G:O2'	1:AA:98:G:H5"	2.00	0.62
1:CA:54:C:N4	1:CA:353:A:OP2	2.32	0.62
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.81	0.62
26:DA:2096:U:H3	26:DA:2193:G:H1	1.48	0.62
1:AA:984:C:H42	1:AA:1221:G:H1	1.48	0.62
3:AC:39:ILE:HG23	3:AC:91:LEU:HD11	1.82	0.62
3:AC:82:GLU:HG2	3:AC:85:ARG:HH21	1.63	0.62
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.82	0.62
1:CA:1404:C:O2	1:CA:1519:A:O2'	2.14	0.62
10:CJ:6:ILE:HG23	10:CJ:98:ILE:HG13	1.82	0.62
26:DA:2379:G:O2'	39:DS:17:ARG:NH2	2.30	0.62
30:DF:28:ILE:HG23	30:DF:112:MET:HE3	1.81	0.62
26:BA:271(L):U:OP1	33:BI:50:ARG:NH2	2.29	0.62
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.33	0.62
26:DA:1149:G:H2'	26:DA:1150:C:C6	2.35	0.62
26:DA:2816:C:O3'	38:DR:99:LYS:NZ	2.32	0.62
33:DI:38:LEU:HD12	33:DI:38:LEU:H	1.64	0.62
36:DP:39:LYS:HB2	36:DP:45:LEU:HG	1.81	0.62
55:D8:33:ASN:HA	55:D8:36:LYS:HD2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:76:F3N:N	24:AX:76:31H:O2'	2.33	0.61
26:BA:1859:A:N6	26:BA:1883:G:O2'	2.32	0.61
30:DF:18:ARG:NH2	30:DF:127:GLU:OE1	2.31	0.61
31:DG:5:VAL:HG22	31:DG:8:LYS:H	1.64	0.61
37:BQ:21:THR:HG21	37:BQ:101:ARG:HB2	1.82	0.61
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.81	0.61
26:DA:881:G:H1	26:DA:895:U:H3	1.48	0.61
1:AA:62:U:OP1	1:AA:385:C:O2'	2.17	0.61
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.15	0.61
26:BA:646:A:H2'	26:BA:647:G:O4'	2.01	0.61
30:BF:184:TYR:O	30:BF:188:ARG:HG3	2.00	0.61
34:BN:1:MET:HE3	42:BV:13:ARG:HB3	1.81	0.61
51:B4:53:GLU:HB3	51:B4:54:GLY:HA2	1.82	0.61
1:CA:662:G:H2'	1:CA:663:A:C8	2.34	0.61
1:CA:1376:U:H3'	7:CG:94:ARG:HH21	1.65	0.61
2:CB:101:MET:HA	2:CB:108:ILE:HG13	1.82	0.61
10:CJ:49:VAL:HG12	10:CJ:61:GLU:O	2.00	0.61
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.26	0.61
26:BA:1447:G:N7	61:BA:4947:HOH:O	2.31	0.61
29:BE:29:GLY:HA3	61:BE:408:HOH:O	1.99	0.61
31:BG:43:LEU:HD11	31:BG:153:ARG:HG2	1.83	0.61
45:BY:102:CYS:SG	45:BY:103:GLY:N	2.73	0.61
1:CA:1397:C:OP2	5:CE:24:ARG:NH2	2.33	0.61
26:DA:796:C:H2'	26:DA:797:C:C6	2.34	0.61
26:DA:1028:A:N6	26:DA:1125:G:H2'	2.15	0.61
26:DA:1031:G:H5"	56:D9:8:LYS:HE3	1.80	0.61
27:DB:45:A:O4'	31:DG:95:ARG:NH1	2.33	0.61
41:DU:83:LEU:HD12	41:DU:88:ILE:HD12	1.81	0.61
1:AA:139:G:N2	1:AA:224:C:O2	2.28	0.61
1:AA:1036:G:H3'	1:AA:1037:C:C6	2.34	0.61
42:BV:40:LEU:HB2	42:BV:46:VAL:HG13	1.81	0.61
46:BZ:24:LEU:HB2	46:BZ:41:LEU:HD23	1.81	0.61
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.82	0.61
1:CA:1297:C:OP1	13:CM:44:ARG:NH2	2.27	0.61
26:DA:1371:G:O6	61:DA:3964:HOH:O	2.12	0.61
23:AW:26:A:N1	23:AW:44:G:N2	2.44	0.61
26:BA:2430:A:H2'	26:BA:2430:A:N3	2.15	0.61
30:BF:101:LEU:O	30:BF:106:ARG:NH1	2.32	0.61
1:CA:1193:G:O2'	5:CE:25:ARG:NH2	2.34	0.61
2:CB:16:HIS:CD2	2:CB:17:PHE:H	2.18	0.61
6:CF:61:LEU:HB3	6:CF:63:TYR:HE1	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.36	0.61
12:CL:113:ARG:NH2	61:CL:201:HOH:O	2.33	0.61
13:CM:91:ARG:HB2	13:CM:98:VAL:HG13	1.82	0.61
26:DA:958:U:OP2	37:DQ:14:ARG:NH1	2.33	0.61
27:DB:106:G:H5'	46:DZ:31:ARG:HG2	1.83	0.61
26:BA:1113:U:H2'	26:BA:1114:G:C8	2.36	0.61
26:BA:1843:C:H5'	28:BD:253:GLN:NE2	2.15	0.61
27:BB:105:A:OP1	46:BZ:72:ARG:NH1	2.34	0.61
8:CH:45:ILE:HG22	8:CH:63:LEU:HA	1.83	0.61
44:DX:60:ARG:HH12	54:D7:47:ARG:NH2	1.98	0.61
26:BA:2305:A:H5"	31:BG:134:GLY:HA3	1.83	0.61
36:BP:59:LEU:HD21	55:B8:10:ALA:HA	1.82	0.61
4:CD:154:ASN:HA	4:CD:159:ARG:HH21	1.65	0.61
10:CJ:29:ARG:HB2	10:CJ:84:GLN:HE22	1.65	0.61
26:DA:2114:A:N6	26:DA:2119:A:N7	2.48	0.61
35:DO:71:ARG:NE	35:DO:105:GLU:OE2	2.32	0.61
56:D9:25:VAL:HB	56:D9:34:GLN:HB2	1.81	0.61
25:AY:15:G:N2	25:AY:48:C:H42	1.99	0.61
30:BF:8:GLN:HA	30:BF:8:GLN:HE21	1.65	0.61
1:CA:735:C:H2'	1:CA:736:C:H6	1.64	0.61
1:CA:1240:U:OP2	7:CG:116:ALA:N	2.34	0.61
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.11	0.61
2:CB:113:HIS:O	2:CB:117:GLU:N	2.32	0.61
26:DA:2169:A:H2'	26:DA:2170:A:C8	2.35	0.61
1:AA:69:G:H2'	1:AA:70:G:C8	2.36	0.61
11:AK:51:LYS:HD3	11:AK:55:LYS:HE2	1.83	0.61
2:CB:13:ALA:N	2:CB:14:GLY:HA3	2.16	0.61
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.19	0.61
9:CI:3:GLN:OE1	9:CI:20:ARG:NH2	2.34	0.61
26:DA:1140:C:O3'	34:DN:25:ARG:NH1	2.34	0.61
26:DA:1557:C:OP2	26:DA:1558:A:O2'	2.17	0.61
26:DA:2022:U:O2'	26:DA:2617:C:H5'	2.01	0.61
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.20	0.60
1:AA:1502:A:H2	1:AA:1505:G:N1	1.95	0.60
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.82	0.60
13:AM:23:TYR:HB3	13:AM:67:GLU:HA	1.83	0.60
18:AR:26:LEU:HD21	18:AR:39:VAL:HG13	1.82	0.60
26:BA:1913:A:H4'	26:BA:1914:C:H5"	1.83	0.60
27:BB:41:U:H5	31:BG:70:VAL:H	1.49	0.60
54:B7:34:ARG:NH1	54:B7:41:ARG:O	2.34	0.60
1:CA:728:A:H2'	1:CA:729:A:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.19	0.60
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.82	0.60
26:DA:93:G:H2'	26:DA:94:C:C6	2.36	0.60
26:DA:821:A:N1	61:DA:4084:HOH:O	2.31	0.60
12:AL:32:PHE:HB3	12:AL:84:LEU:HD11	1.82	0.60
14:AN:21:TYR:OH	14:AN:23:ARG:NH2	2.33	0.60
1:CA:1329:A:H5'	13:CM:29:ARG:HD2	1.82	0.60
26:DA:83:G:OP1	45:DY:95:LYS:NZ	2.32	0.60
26:DA:1231:G:H2'	26:DA:1232:G:C8	2.36	0.60
26:DA:1250:G:N7	36:DP:18:ARG:NH2	2.49	0.60
26:DA:2312:U:H5'	31:DG:88:ILE:HD11	1.83	0.60
15:AO:55:GLY:HA2	15:AO:58:MET:HE2	1.83	0.60
26:BA:1179:C:H2'	26:BA:1180:C:H6	1.66	0.60
26:BA:2096:U:H3	26:BA:2193:G:H1	1.49	0.60
26:BA:2822:G:N7	61:BA:5279:HOH:O	2.32	0.60
1:CA:222:U:H2'	1:CA:223:U:C6	2.35	0.60
1:CA:289:G:OP2	61:CA:3236:HOH:O	2.16	0.60
1:CA:1297:C:O3'	7:CG:114:ARG:NH2	2.34	0.60
4:CD:100:ARG:NH1	4:CD:137:SER:OG	2.34	0.60
19:AS:31:ILE:HB	19:AS:49:ILE:HG23	1.83	0.60
25:AY:62:C:H2'	25:AY:63:G:H8	1.66	0.60
26:BA:288:C:H2'	26:BA:289:A:H8	1.66	0.60
26:BA:568:U:H5'	26:BA:945:A:N1	2.16	0.60
30:BF:116:ASP:OD1	30:BF:119:ARG:NH2	2.34	0.60
54:D7:34:ARG:NH1	54:D7:41:ARG:O	2.34	0.60
1:AA:26:A:O2'	4:AD:209:ARG:NH2	2.34	0.60
1:AA:243:A:H4'	1:AA:244:U:H5"	1.82	0.60
2:AB:60:ASP:HA	2:AB:63:MET:HE2	1.82	0.60
19:AS:63:THR:HG23	19:AS:66:MET:HE2	1.84	0.60
26:BA:1278:A:OP1	38:BR:36:THR:HG23	2.02	0.60
1:CA:1135:U:H2'	1:CA:1137:C:C2	2.36	0.60
17:CQ:81:ARG:HB3	17:CQ:84:LEU:HD12	1.83	0.60
26:DA:2130:U:H4'	26:DA:2133:G:H4'	1.82	0.60
1:AA:1106:G:H5"	3:AC:172:ARG:HG2	1.82	0.60
1:AA:1183:A:H3'	1:AA:1184:G:H5"	1.84	0.60
31:BG:66:GLN:HG3	51:B4:1:MET:HE1	1.82	0.60
1:CA:501:C:H2'	1:CA:502:G:H8	1.67	0.60
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.37	0.60
9:CI:14:VAL:HG23	9:CI:66:ARG:HB3	1.83	0.60
25:CY:15:G:N1	25:CY:48:C:N3	2.46	0.60
46:DZ:111:VAL:HG21	46:DZ:117:LEU:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1025:G:C4	26:BA:1135:C:H1'	2.37	0.60
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.00	0.60
1:AA:1241:G:OP1	7:AG:35:LYS:NZ	2.35	0.60
1:AA:1351:U:O4	9:AI:118:LYS:NZ	2.35	0.60
13:CM:14:ARG:HB2	13:CM:17:VAL:HG23	1.83	0.60
26:DA:483:A:O2'	45:DY:49:VAL:O	2.10	0.60
26:DA:2185:C:H2'	26:DA:2186:G:O4'	2.01	0.60
35:DO:53:LYS:NZ	35:DO:56:ASP:OD1	2.34	0.60
46:DZ:93:ASP:HA	46:DZ:131:ARG:NH2	2.17	0.60
49:D2:29:LYS:HG2	49:D2:57:ILE:HD13	1.84	0.60
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.83	0.60
26:BA:636:G:OP1	36:BP:132:LYS:HE2	2.02	0.60
33:BI:104:GLN:HB3	33:BI:105:HIS:HD2	1.67	0.60
1:CA:148:G:H2'	1:CA:149:A:H8	1.66	0.60
18:AR:70:ILE:HG23	18:AR:79:LEU:HD12	1.84	0.60
23:AW:7:A:N6	23:AW:66:U:H3	2.00	0.60
26:BA:71:A:OP2	26:BA:71:A:H3'	2.02	0.60
26:BA:1507:A:O2'	26:BA:1508:A:O4'	2.20	0.60
28:BD:108:PRO:HB3	28:BD:143:HIS:CE1	2.37	0.60
38:BR:97:VAL:HG22	38:BR:114:VAL:HG13	1.84	0.60
46:BZ:117:LEU:HD21	46:BZ:144:LEU:HD13	1.84	0.60
46:BZ:138:GLU:N	46:BZ:156:LYS:HD3	2.13	0.60
1:CA:19:C:H5"	5:CE:86:ALA:HB3	1.83	0.60
1:CA:1456:G:N1	20:CT:51:GLU:OE2	2.30	0.60
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.67	0.60
26:DA:2836:U:H2'	26:DA:2837:G:C8	2.37	0.60
51:D4:16:CYS:HA	51:D4:33:VAL:HB	1.83	0.60
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.34	0.59
36:BP:91:PHE:O	36:BP:121:LYS:NZ	2.35	0.59
1:CA:662:G:H2'	1:CA:663:A:H8	1.67	0.59
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.37	0.59
3:CC:70:VAL:HG22	3:CC:72:LYS:H	1.66	0.59
26:DA:307:G:N1	26:DA:310:A:OP2	2.33	0.59
31:DG:41:GLN:HB3	31:DG:43:LEU:HD22	1.83	0.59
33:DI:4:ILE:HG12	33:DI:18:VAL:HG22	1.84	0.59
46:DZ:59:LEU:HD11	46:DZ:69:THR:HG21	1.81	0.59
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.59
1:AA:1125:U:H4'	10:AJ:5:ARG:HH22	1.67	0.59
7:AG:37:ASN:ND2	9:AI:39:GLY:O	2.33	0.59
9:AI:49:PRO:HG3	9:AI:101:PHE:HD2	1.65	0.59
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:92:TYR:N	2:CB:151:GLY:O	2.32	0.59
9:CI:96:LEU:HD22	9:CI:101:PHE:HB2	1.84	0.59
26:DA:144:C:H2'	26:DA:145:G:H8	1.67	0.59
26:DA:2815:C:H5'	52:D5:29:THR:HG21	1.83	0.59
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.25	0.59
23:AW:9:A:OP2	23:AW:13:C:N4	2.30	0.59
26:BA:1359:A:H61	26:BA:1372:U:H3	1.49	0.59
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.37	0.59
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.36	0.59
25:CY:50:U:O2	25:CY:64:A:N1	2.35	0.59
26:DA:1310:G:OP2	54:D7:9:ARG:NH1	2.35	0.59
26:DA:2127:G:N2	26:DA:2161:C:N3	2.50	0.59
40:DT:30:VAL:HG22	40:DT:86:ILE:HG12	1.83	0.59
46:DZ:5:LEU:HD22	46:DZ:6:LYS:H	1.68	0.59
1:AA:262:A:H2'	1:AA:263:A:C8	2.38	0.59
9:AI:117:HIS:HB2	9:AI:121:ARG:HG3	1.84	0.59
11:CK:54:ARG:NH1	25:CY:39:PSU:O2'	2.35	0.59
12:CL:117:ARG:CZ	12:CL:117:ARG:HB2	2.32	0.59
26:DA:2336:A:H61	47:D0:43:THR:HG22	1.67	0.59
3:AC:50:ALA:HB1	3:AC:70:VAL:HG21	1.84	0.59
4:AD:173:TRP:CZ3	4:AD:174:LEU:HG	2.38	0.59
26:BA:1359:A:N6	26:BA:1372:U:H3	2.00	0.59
28:BD:68:LYS:HD2	28:BD:70:TRP:CZ2	2.38	0.59
1:CA:646:U:H2'	1:CA:647:C:C6	2.37	0.59
24:CX:31:G:H3'	24:CX:32:5MC:HM53	1.83	0.59
26:DA:668:G:H5'	26:DA:669:G:OP2	2.01	0.59
26:BA:2136:C:N4	26:BA:2155:G:N1	2.30	0.59
1:CA:986:A:N3	19:CS:52:TYR:OH	2.33	0.59
1:CA:1070:U:H2'	1:CA:1071:C:H6	1.67	0.59
2:CB:15:VAL:HG12	2:CB:209:ARG:HB3	1.85	0.59
2:CB:133:LYS:O	2:CB:137:ARG:N	2.32	0.59
39:DS:5:THR:OG1	39:DS:8:GLU:OE2	2.13	0.59
39:DS:43:GLU:HB3	39:DS:44:LYS:HE2	1.82	0.59
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	1.84	0.59
11:AK:91:ARG:HG3	11:AK:92:GLU:N	2.15	0.59
36:BP:52:GLU:OE1	36:BP:55:ARG:NH1	2.31	0.59
46:BZ:111:VAL:HG12	46:BZ:112:ARG:H	1.68	0.59
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.17	0.59
2:CB:91:PRO:HB3	2:CB:154:LEU:HB3	1.83	0.59
26:DA:2140:C:H2'	26:DA:2141:G:H5'	1.85	0.59
26:DA:2745:C:O2'	32:DH:139:GLN:O	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1025:U:O2'	1:AA:1026:G:H8	1.86	0.59
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.35	0.59
9:AI:17:VAL:HG23	9:AI:63:ILE:HG12	1.83	0.59
50:B3:3:ARG:NH1	50:B3:60:GLU:OE2	2.35	0.59
1:CA:1298:C:P	7:CG:114:ARG:HH22	2.26	0.59
10:CJ:46:ARG:HG2	10:CJ:64:GLU:HB3	1.83	0.59
16:CP:52:ASP:O	16:CP:54:GLU:N	2.36	0.59
26:DA:481:G:O5'	45:DY:47:LYS:NZ	2.35	0.59
26:DA:2315:G:H2'	26:DA:2316:C:C6	2.37	0.59
26:DA:2646:C:OP2	26:DA:2732:G:O2'	2.20	0.59
30:DF:185:ASP:HA	30:DF:188:ARG:HD3	1.84	0.59
37:DQ:34:LEU:HB2	37:DQ:118:LEU:HD22	1.84	0.59
40:DT:56:GLY:O	40:DT:59:THR:HG23	2.02	0.59
1:AA:750:G:O2'	15:AO:22:THR:O	2.14	0.59
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.36	0.59
17:AQ:9:VAL:HG21	17:AQ:84:LEU:HD13	1.84	0.59
26:BA:307:G:H21	26:BA:330:A:H62	1.49	0.59
26:BA:2141:G:H22	26:BA:2149:G:H22	1.51	0.59
35:BO:63:VAL:HG12	35:BO:106:LEU:HD11	1.84	0.59
1:CA:375:U:OP1	16:CP:69:THR:HG21	2.02	0.59
7:CG:72:ARG:N	7:CG:142:GLU:OE2	2.30	0.59
8:CH:4:ASP:OD1	8:CH:7:ALA:N	2.25	0.59
26:DA:2273:A:H2'	26:DA:2274:A:C8	2.38	0.59
29:DE:1:MET:HE1	29:DE:199:ARG:HD2	1.84	0.59
34:DN:38:HIS:CE1	34:DN:39:ARG:HG3	2.37	0.59
1:AA:1320:C:H5"	19:AS:70:LYS:HG3	1.84	0.59
26:BA:1019:U:H3	26:BA:1142(A):A:H62	1.51	0.59
26:BA:1478:G:O2'	26:BA:1558:A:N1	2.35	0.59
1:CA:1104:G:O5'	2:CB:111:ARG:HD2	2.02	0.59
2:CB:121:LEU:H	2:CB:125:PRO:HG2	1.68	0.59
26:DA:1025:G:C4	26:DA:1135:C:H1'	2.38	0.59
36:DP:86:LYS:HB3	36:DP:118:GLY:HA3	1.83	0.59
1:AA:46:G:O2'	1:AA:365:U:O2	2.21	0.58
26:BA:1170:G:C2	26:BA:1171:G:H1'	2.38	0.58
39:BS:15:ARG:O	39:BS:19:LYS:HG2	2.02	0.58
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.38	0.58
1:CA:1049:U:C5	1:CA:1201:A:H5'	2.37	0.58
1:CA:1120:G:C6	1:CA:1121:U:C4	2.91	0.58
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.84	0.58
2:CB:57:PHE:HE2	2:CB:185:ILE:HD12	1.67	0.58
2:CB:73:THR:HA	2:CB:94:ASN:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CS:38:SER:HB2	19:CS:71:LEU:HD22	1.84	0.58
49:D2:22:GLU:OE2	49:D2:68:ARG:NH2	2.35	0.58
13:AM:3:ARG:HG3	13:AM:4:ILE:N	2.18	0.58
2:CB:55:PHE:O	2:CB:59:GLU:N	2.25	0.58
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.51	0.58
13:CM:121:LYS:HZ3	23:CW:40:C:H4'	1.68	0.58
27:DB:11:C:OP2	27:DB:12:C:N4	2.30	0.58
2:AB:19:HIS:HE1	2:AB:189:ASP:HB3	1.69	0.58
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.86	0.58
26:DA:888:C:H2'	26:DA:889:C:C4	2.38	0.58
33:DI:141:LYS:HZ2	33:DI:141:LYS:HB2	1.69	0.58
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.68	0.58
26:BA:1045:A:H1'	26:BA:1047:G:N3	2.18	0.58
26:BA:2173:A:H3'	26:BA:2174:C:H6	1.69	0.58
26:BA:2206:G:H5'	26:BA:2207:G:N7	2.18	0.58
28:BD:79:VAL:HG21	28:BD:111:LEU:HD11	1.85	0.58
40:BT:65:LYS:HE2	40:BT:67:SER:HB2	1.85	0.58
46:BZ:110:GLY:N	46:BZ:144:LEU:O	2.32	0.58
1:CA:396:G:O2'	1:CA:398:C:OP1	2.11	0.58
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.18	0.58
2:CB:87:ARG:NH2	2:CB:233:SER:HB3	2.18	0.58
6:CF:67:MET:HE1	6:CF:75:LEU:HD12	1.85	0.58
13:CM:121:LYS:NZ	13:CM:121:LYS:H	2.01	0.58
18:CR:60:ALA:O	18:CR:64:ARG:HG3	2.02	0.58
25:CY:8:4SU:H1'	25:CY:48:C:O2	2.04	0.58
26:DA:1639:U:H2'	26:DA:1640:C:H5"	1.85	0.58
47:D0:11:ARG:O	47:D0:14:ARG:NH2	2.36	0.58
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.18	0.58
1:AA:1309:G:OP2	13:AM:99:ARG:NH2	2.33	0.58
3:AC:29:TYR:OH	14:AN:54:PRO:O	2.20	0.58
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.03	0.58
25:AY:60:U:H5"	25:AY:61:C:H5	1.69	0.58
45:BY:90:LEU:HD21	45:BY:96:ILE:HG12	1.85	0.58
6:CF:69:GLU:CD	6:CF:69:GLU:H	2.09	0.58
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.84	0.58
26:DA:1371:G:H2'	26:DA:1372:U:H5	1.69	0.58
26:DA:2680:C:OP2	29:DE:111:ARG:NH2	2.36	0.58
35:DO:24:VAL:HA	35:DO:39:ILE:HG22	1.86	0.58
1:AA:473:G:H2'	1:AA:474:G:H8	1.68	0.58
1:AA:731:G:H5'	1:AA:766:A:H4'	1.85	0.58
13:AM:11:ARG:HB2	13:AM:46:LYS:HB3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:880:G:N2	26:BA:898:C:N3	2.44	0.58
26:BA:1021:A:H62	26:BA:1141:U:H3	1.49	0.58
42:BV:72:VAL:HG13	42:BV:85:LYS:HB3	1.85	0.58
1:CA:1028:C:C2	1:CA:1033:G:N1	2.72	0.58
1:CA:1122:U:C4	1:CA:1123:A:N7	2.72	0.58
1:CA:1298:C:H4'	1:CA:1299:A:H5'	1.85	0.58
13:CM:92:HIS:CD2	13:CM:98:VAL:HG21	2.39	0.58
26:DA:362:U:O2'	26:DA:363:G:H5"	2.03	0.58
1:AA:1026:G:C2	1:AA:1027:C:H4'	2.38	0.58
5:AE:53:LEU:HD12	5:AE:53:LEU:H	1.68	0.58
11:AK:98:LEU:O	11:AK:101:SER:OG	2.16	0.58
19:AS:62:ILE:HA	19:AS:66:MET:HE3	1.83	0.58
26:BA:301:G:OP2	45:BY:84:ARG:NH2	2.37	0.58
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.20	0.58
32:DH:58:GLU:OE2	32:DH:60:ARG:NH1	2.37	0.58
36:DP:63:PRO:HG2	55:D8:25:MET:HB2	1.86	0.58
1:AA:78:G:N2	1:AA:92:C:N3	2.51	0.58
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.38	0.58
1:AA:998:G:H1	1:AA:1043:C:N4	1.98	0.58
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.36	0.58
26:BA:882:G:H1	26:BA:894:C:H42	1.50	0.58
1:CA:148:G:H2'	1:CA:149:A:C8	2.39	0.58
1:CA:328:C:H4'	1:CA:329:A:H5'	1.86	0.58
3:CC:54:ARG:HH11	3:CC:54:ARG:HB3	1.68	0.58
10:CJ:89:ASP:O	10:CJ:91:PRO:HD3	2.04	0.58
26:DA:1412:A:H2'	26:DA:1413:G:H8	1.68	0.58
26:DA:2127:G:C5	26:DA:2161:C:N4	2.71	0.58
31:DG:15:VAL:HG22	31:DG:175:LEU:HB3	1.85	0.58
46:DZ:150:LEU:H	46:DZ:172:ALA:HB3	1.68	0.58
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.18	0.58
26:BA:1815:A:OP2	28:BD:54:ARG:NH2	2.35	0.58
26:BA:2404:C:O3'	36:BP:77:ARG:NH2	2.37	0.58
30:BF:192:LEU:HD13	30:BF:194:MET:HE2	1.85	0.58
1:CA:407:G:OP1	4:CD:115:ARG:NH2	2.35	0.58
26:DA:858:U:H1'	26:DA:2268:A:H2'	1.84	0.58
26:DA:903:C:H2'	26:DA:904:C:C6	2.38	0.58
26:DA:1166:C:H2'	26:DA:1167:U:C6	2.39	0.58
1:AA:72:C:H2'	1:AA:73:G:O4'	2.03	0.58
2:AB:158:LEU:HD21	2:AB:180:LEU:HD13	1.86	0.58
28:BD:180:GLY:HA3	28:BD:275:LYS:HB2	1.86	0.58
30:BF:116:ASP:OD2	36:BP:1:MET:N	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BY:92:ASN:N	45:BY:93:GLY:HA2	2.18	0.58
1:CA:964:A:N3	1:CA:969:A:O2'	2.33	0.58
1:CA:978:A:O2'	1:CA:1321:C:N4	2.36	0.58
3:CC:65:ALA:HA	3:CC:100:ALA:HB3	1.86	0.58
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.85	0.58
24:CX:16:C:H5'	24:CX:59:A:N1	2.19	0.58
25:CY:56:C:O4'	26:DA:2169:A:H1'	2.04	0.58
28:DD:28:GLU:OE2	61:DD:416:HOH:O	2.17	0.58
31:DG:43:LEU:HD12	31:DG:45:GLU:HG3	1.86	0.58
43:DW:57:ASN:HA	43:DW:61:ASN:HD22	1.69	0.58
1:AA:21:G:OP1	61:AA:4104:HOH:O	2.17	0.57
1:AA:1456:G:O6	20:AT:54:LYS:NZ	2.30	0.57
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	1.86	0.57
26:BA:2113:U:N3	26:BA:2114:A:N7	2.52	0.57
56:B9:25:VAL:HB	56:B9:34:GLN:HB2	1.86	0.57
1:CA:998:G:H1	1:CA:1043:C:H42	0.74	0.57
2:CB:52:GLU:O	2:CB:56:ARG:HG2	2.04	0.57
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.04	0.57
42:DV:6:LYS:HG2	42:DV:11:GLN:HG2	1.85	0.57
2:AB:95:GLN:HG3	2:AB:147:LYS:HD3	1.85	0.57
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HB3	1.86	0.57
35:BO:80:ASP:OD1	40:BT:64:ARG:NH2	2.36	0.57
1:CA:114:U:H2'	1:CA:115:G:C8	2.39	0.57
2:CB:25:ASN:OD1	2:CB:27:LYS:HG2	2.04	0.57
23:CW:21:A:N6	23:CW:46:7MG:C4	2.72	0.57
25:CY:49:C:N3	25:CY:65:G:N2	2.46	0.57
26:DA:848:G:H2'	26:DA:849:A:C8	2.39	0.57
26:DA:1857:G:O2'	26:DA:1885:A:N6	2.32	0.57
26:DA:2144:U:N3	26:DA:2146:C:N3	2.52	0.57
1:AA:1392:G:H21	1:AA:1502:A:H8	1.53	0.57
2:AB:71:VAL:HG11	2:AB:170:GLU:HG2	1.86	0.57
26:BA:630:G:OP2	55:B8:15:LYS:NZ	2.30	0.57
26:BA:831:G:O2'	36:BP:38:GLN:NE2	2.38	0.57
35:BO:64:ARG:NH2	35:BO:99:PHE:O	2.37	0.57
43:BW:68:ARG:HH11	43:BW:111:HIS:HA	1.67	0.57
54:B7:34:ARG:NH2	61:B7:202:HOH:O	2.36	0.57
1:CA:45:U:H2'	1:CA:46:G:C8	2.39	0.57
1:CA:1119:C:N3	1:CA:1154:G:O6	2.36	0.57
3:CC:47:LEU:O	3:CC:51:GLY:N	2.34	0.57
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.86	0.57
7:CG:27:ILE:HD13	7:CG:40:ALA:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:4:C:N3	23:CW:69:G:C2	2.72	0.57
26:DA:1022:G:H22	26:DA:1142(A):A:H2	1.50	0.57
23:AW:52:G:H4'	37:BQ:56:ARG:NH2	2.20	0.57
26:BA:668:G:H5'	26:BA:669:G:OP2	2.05	0.57
26:BA:1267:U:OP1	61:BA:5075:HOH:O	2.17	0.57
1:CA:1097:C:H1'	1:CA:1170:A:H1'	1.86	0.57
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.36	0.57
7:CG:111:ARG:NH1	7:CG:113:GLU:OE1	2.37	0.57
23:CW:30:G:H1	23:CW:40:C:N4	2.03	0.57
26:DA:643:A:N1	26:DA:2369:A:O2'	2.36	0.57
26:DA:2070:G:OP2	61:DA:4461:HOH:O	2.17	0.57
28:DD:108:PRO:HG2	28:DD:111:LEU:HB2	1.87	0.57
35:DO:92:GLU:OE2	35:DO:113:LYS:HD3	2.05	0.57
42:DV:60:GLU:HB2	42:DV:97:LYS:HE2	1.85	0.57
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.43	0.57
2:AB:137:ARG:NH1	2:AB:137:ARG:HB3	2.19	0.57
12:AL:34:ARG:NH2	61:AL:301:HOH:O	2.36	0.57
15:AO:4:THR:OG1	15:AO:7:GLU:OE1	2.22	0.57
26:BA:2123:G:H1	26:BA:2175:C:N4	2.02	0.57
1:CA:998:G:H2'	1:CA:999:C:O4'	2.04	0.57
1:CA:1051:C:H2'	1:CA:1052:U:C6	2.40	0.57
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.04	0.57
1:CA:1168:A:H2'	1:CA:1169:A:C8	2.39	0.57
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.20	0.57
4:CD:61:LYS:NZ	4:CD:72:GLU:OE1	2.35	0.57
13:CM:93:ARG:NH1	26:DA:888:C:O5'	2.37	0.57
23:CW:3:C:O2	23:CW:70:G:N1	2.29	0.57
24:CX:55:PSU:N3	24:CX:58:A:OP2	2.26	0.57
29:DE:30:PRO:HB3	29:DE:92:THR:HG22	1.86	0.57
37:DQ:111:GLU:O	37:DQ:115:MET:HG2	2.05	0.57
1:AA:1000:U:O2	1:AA:1042:G:N2	2.37	0.57
38:BR:28:LEU:HD12	38:BR:48:VAL:HG21	1.86	0.57
1:CA:444:C:H2'	1:CA:445:G:C8	2.39	0.57
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.38	0.57
16:CP:57:ARG:NH2	16:CP:79:VAL:O	2.38	0.57
30:DF:195:ASP:OD1	30:DF:196:LEU:N	2.38	0.57
1:AA:184:G:H2'	1:AA:185:A:H8	1.70	0.57
6:AF:81:ILE:HD11	28:BD:125:ILE:HB	1.87	0.57
25:AY:33:U:H2'	25:AY:34:G:H3'	1.86	0.57
45:BY:86:ARG:HD2	45:BY:100:ALA:HA	1.87	0.57
54:B7:33:ARG:NH2	61:B7:201:HOH:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:652:U:O4	1:CA:752:G:O2'	2.21	0.57
1:CA:1154:G:N7	1:CA:1155:G:C4	2.72	0.57
2:CB:16:HIS:O	2:CB:18:GLY:N	2.37	0.57
26:DA:674:G:H1'	30:DF:74:ARG:HD3	1.85	0.57
26:DA:686:G:N2	26:DA:788:A:H61	2.02	0.57
26:DA:1188:U:H4'	42:DV:79:VAL:HG22	1.86	0.57
28:DD:3:VAL:HG13	28:DD:17:THR:HB	1.86	0.57
30:DF:13:SER:OG	30:DF:16:GLY:O	2.21	0.57
30:DF:192:LEU:HD13	30:DF:194:MET:HE2	1.86	0.57
1:AA:159:G:H2'	1:AA:161:A:OP2	2.05	0.57
1:AA:1057:G:OP2	61:AA:4024:HOH:O	2.16	0.57
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.05	0.57
26:BA:892:G:H3'	26:BA:893:C:C6	2.39	0.57
31:BG:5:VAL:HG22	31:BG:8:LYS:H	1.69	0.57
1:CA:619:U:N3	4:CD:134:ASP:OD1	2.32	0.57
1:CA:1001:A:H2'	1:CA:1001(A):G:C8	2.39	0.57
1:CA:1012:U:O2	1:CA:1017:G:O6	2.23	0.57
3:CC:18:TRP:HE3	3:CC:18:TRP:H	1.52	0.57
26:DA:479:A:N3	26:DA:481:G:H5"	2.19	0.57
27:DB:3:C:H2'	27:DB:4:C:C6	2.39	0.57
6:AF:69:GLU:CD	6:AF:69:GLU:H	2.12	0.57
13:AM:40:ASN:O	13:AM:43:THR:OG1	2.23	0.57
25:AY:15:G:O6	25:AY:48:C:O2	2.23	0.57
1:CA:130:A:N3	1:CA:263:A:O2'	2.32	0.57
1:CA:297:G:N2	1:CA:300:A:OP2	2.38	0.57
31:DG:151:ALA:HB3	31:DG:153:ARG:HH11	1.70	0.57
46:DZ:159:PRO:HA	46:DZ:161:VAL:N	2.20	0.57
1:AA:375:U:OP1	16:AP:69:THR:HG21	2.05	0.57
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.34	0.57
26:BA:1173:G:O2'	26:BA:1174:A:O4'	2.17	0.57
26:BA:2357:U:OP1	47:B0:20:ARG:NH1	2.38	0.57
26:BA:2522:U:O2'	26:BA:2647:U:OP1	2.20	0.57
1:CA:588:G:O6	1:CA:651:C:N4	2.33	0.57
1:CA:1204:A:OP1	14:CN:3:ARG:NH1	2.37	0.57
3:CC:3:ASN:HD22	3:CC:4:LYS:HG3	1.69	0.57
24:CX:21:A:N6	24:CX:46:G:H2'	2.19	0.57
26:DA:614(C):A:C4	30:DF:180:GLY:HA2	2.40	0.57
26:DA:1169:G:H1	26:DA:1180:C:N4	2.01	0.57
45:DY:28:LYS:HD2	45:DY:40:GLU:HG3	1.87	0.57
46:DZ:92:SER:O	46:DZ:130:PRO:HG2	2.05	0.57
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AL:52:LEU:O	12:AL:54:LYS:NZ	2.34	0.56
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.86	0.56
49:B2:65:ASN:OD1	49:B2:69:ARG:NH1	2.38	0.56
26:DA:247:G:H4'	26:DA:386:G:C5	2.40	0.56
26:DA:2137:C:H2'	26:DA:2138:C:C6	2.40	0.56
35:DO:1:MET:HG3	35:DO:67:LYS:HG2	1.86	0.56
36:DP:96:THR:H	36:DP:99:LEU:CD2	2.17	0.56
45:DY:6:HIS:CD2	45:DY:7:VAL:HG23	2.40	0.56
26:BA:222:A:H5"	26:BA:421:U:OP1	2.05	0.56
1:CA:1183:A:H5'	1:CA:1183:A:H8	1.69	0.56
8:CH:41:ARG:NH2	8:CH:123:GLU:OE2	2.38	0.56
13:CM:16:ASP:HB3	13:CM:34:LEU:HD11	1.87	0.56
26:DA:422:A:OP2	61:DA:3787:HOH:O	2.17	0.56
26:DA:740:U:H2'	26:DA:741:G:C8	2.39	0.56
26:DA:2062:A:OP1	61:DA:3826:HOH:O	2.17	0.56
26:DA:2522:U:O2'	26:DA:2647:U:OP1	2.18	0.56
26:DA:2532:G:O2'	26:DA:2657:A:N1	2.36	0.56
31:DG:101:ILE:HG22	31:DG:105:LYS:HE2	1.86	0.56
36:DP:99:LEU:O	36:DP:103:ALA:N	2.37	0.56
44:DX:35:THR:HG22	44:DX:38:GLU:H	1.70	0.56
47:D0:27:GLU:HG3	47:D0:68:GLU:HA	1.86	0.56
1:AA:93:G:H2'	1:AA:96:U:O4'	2.06	0.56
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.27	0.56
1:AA:1392:G:N2	1:AA:1502:A:H8	2.03	0.56
9:AI:23:ASN:ND2	9:AI:60:ASP:OD2	2.38	0.56
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.70	0.56
13:AM:88:ARG:HG3	13:AM:98:VAL:HG12	1.87	0.56
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.70	0.56
26:BA:9:U:H3	26:BA:2629:A:H2	1.54	0.56
26:BA:800:A:H8	26:BA:800:A:OP1	1.88	0.56
26:BA:1300:U:H4'	26:BA:1301:A:C5'	2.36	0.56
26:BA:2127:G:H21	26:BA:2173:A:H1'	1.71	0.56
26:BA:2138:C:N3	26:BA:2153:G:N2	2.52	0.56
40:BT:1:MET:HE2	40:BT:3:ARG:HG2	1.86	0.56
42:BV:76:LYS:HB2	42:BV:81:TYR:HB3	1.87	0.56
51:B4:59:PHE:C	51:B4:61:ARG:H	2.13	0.56
1:CA:1247:U:H1'	1:CA:1291:G:N2	2.20	0.56
2:CB:134:GLU:HA	2:CB:137:ARG:HB2	1.87	0.56
10:CJ:55:LYS:HE3	10:CJ:56:HIS:NE2	2.20	0.56
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.86	0.56
13:CM:29:ARG:HG3	13:CM:64:TRP:CZ3	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:71:ARG:HH11	13:CM:71:ARG:CG	2.18	0.56
17:CQ:78:GLU:OE2	17:CQ:81:ARG:NH1	2.37	0.56
18:CR:43:PHE:HD1	18:CR:56:THR:HG22	1.69	0.56
21:CU:12:LYS:HZ2	21:CU:19:GLY:HA3	1.71	0.56
26:DA:236:C:H2'	26:DA:237:C:C6	2.41	0.56
26:DA:614(A):U:H4'	26:DA:614(B):G:H5'	1.86	0.56
26:DA:1412:A:H2'	26:DA:1413:G:C8	2.41	0.56
26:DA:2184:G:H2'	26:DA:2185:C:C6	2.39	0.56
27:DB:28:C:H2'	27:DB:29:A:C8	2.39	0.56
46:DZ:150:LEU:N	46:DZ:172:ALA:HB3	2.20	0.56
1:AA:198:G:O6	1:AA:219:C:N4	2.39	0.56
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.22	0.56
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.88	0.56
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.41	0.56
1:AA:1328:C:OP1	21:AU:21:TYR:OH	2.23	0.56
2:AB:54:THR:HG23	2:AB:199:TYR:HB3	1.87	0.56
26:BA:363(A):A:H2'	26:BA:363(B):G:H8	1.71	0.56
26:BA:1796:U:H2'	26:BA:1797:C:H6	1.68	0.56
26:BA:2279:G:N7	47:B0:14:ARG:NH1	2.53	0.56
26:BA:2646:C:OP2	26:BA:2732:G:O2'	2.20	0.56
26:BA:2839:G:H5'	38:BR:46:GLY:HA2	1.87	0.56
31:BG:28:VAL:O	31:BG:31:VAL:HG12	2.05	0.56
43:BW:14:PRO:HG2	43:BW:78:GLU:HG2	1.86	0.56
7:CG:15:ASP:HB3	7:CG:24:THR:HG23	1.86	0.56
26:DA:518:G:H2'	26:DA:519:U:C6	2.41	0.56
26:DA:2112:G:C5	26:DA:2113:U:H1'	2.40	0.56
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.87	0.56
26:BA:1173:G:O2'	26:BA:1174:A:O5'	2.23	0.56
26:BA:1187:G:H5"	42:BV:81:TYR:CE1	2.39	0.56
26:BA:2243:U:H2'	26:BA:2244:U:C6	2.40	0.56
26:BA:2719:G:OP2	61:BA:4851:HOH:O	2.18	0.56
40:BT:24:PRO:HD3	40:BT:52:ILE:HD12	1.88	0.56
1:CA:532:A:H61	3:CC:193:TYR:CB	2.16	0.56
23:CW:18:G:O2'	23:CW:57:G:N2	2.26	0.56
26:DA:84:A:H5'	45:DY:8:LYS:HG2	1.86	0.56
26:DA:1231:G:H2'	26:DA:1232:G:H8	1.69	0.56
26:DA:2867:G:OP2	40:DT:119:LYS:NZ	2.39	0.56
27:DB:42:C:O2'	31:DG:67:LYS:O	2.16	0.56
1:AA:45:U:H2'	1:AA:46:G:C8	2.40	0.56
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.88	0.56
10:AJ:35:SER:N	10:AJ:73:ASP:O	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:33:U:C3'	25:AY:34:G:H5"	2.35	0.56
26:BA:1045:A:OP1	26:BA:1046:A:H3'	2.05	0.56
29:BE:55:ASN:HB3	29:BE:58:ARG:HG3	1.87	0.56
26:DA:2061:G:H5"	26:DA:2503:A:C2	2.40	0.56
26:DA:2142:C:N3	26:DA:2149:G:O6	2.39	0.56
1:AA:976:G:H5'	1:AA:1358:U:O2'	2.06	0.56
1:AA:1278:U:H5'	1:AA:1279:A:O4'	2.06	0.56
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.06	0.56
13:AM:122:LYS:HD3	13:AM:123:ALA:N	2.18	0.56
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.38	0.56
26:BA:2130:U:O2	26:BA:2131:G:N2	2.38	0.56
44:BX:53:LYS:HB3	44:BX:82:GLN:HB3	1.88	0.56
1:CA:587:G:N2	1:CA:754:C:OP2	2.37	0.56
4:CD:191:ARG:NH1	4:CD:191:ARG:O	2.38	0.56
15:CO:17:ARG:HH11	15:CO:17:ARG:HG3	1.69	0.56
26:DA:1579:A:H2'	26:DA:1580:A:C8	2.41	0.56
26:DA:2533:A:OP1	26:DA:2665:A:O2'	2.20	0.56
51:D4:59:PHE:HA	51:D4:60:GLN:C	2.29	0.56
1:AA:1003:G:C2	1:AA:1004:A:N3	2.73	0.56
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.05	0.56
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.30	0.56
25:AY:38:A:C2'	25:AY:39:PSU:H5"	2.35	0.56
26:BA:1171:G:H3'	26:BA:1173:G:H5'	1.88	0.56
1:CA:1154:G:N7	1:CA:1155:G:N9	2.54	0.56
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.39	0.56
6:CF:50:TYR:CE2	18:CR:77:GLY:HA2	2.41	0.56
9:CI:8:GLY:O	9:CI:15:ALA:N	2.35	0.56
1:AA:78:G:C2	1:AA:91:C:C4	2.94	0.56
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.86	0.56
9:AI:29:ASN:OD1	9:AI:65:VAL:N	2.37	0.56
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.06	0.56
25:AY:25:C:O2'	25:AY:26:A:O5'	2.18	0.56
39:BS:14:VAL:O	39:BS:18:ILE:HG12	2.06	0.56
2:CB:8:LYS:HD2	2:CB:9:GLU:H	1.71	0.56
5:CE:84:PHE:N	5:CE:87:SER:O	2.33	0.56
13:CM:71:ARG:HH11	13:CM:71:ARG:HG3	1.69	0.56
37:DQ:77:LYS:NZ	37:DQ:86:GLY:O	2.39	0.56
1:AA:193:C:H2'	1:AA:194:C:C6	2.41	0.56
24:AX:21:A:H5'	24:AX:22:G:OP1	2.05	0.56
26:BA:64:A:O3'	44:BX:71:GLY:HA3	2.05	0.56
26:BA:456:C:H4'	61:BA:3937:HOH:O	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1588:C:H2'	26:BA:1589:C:C6	2.40	0.56
35:BO:1:MET:HG3	35:BO:67:LYS:HG2	1.87	0.56
49:B2:23:LYS:O	49:B2:27:GLU:HG3	2.06	0.56
1:CA:1057:G:H2'	1:CA:1058:G:O4'	2.05	0.56
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.06	0.56
1:CA:1095:U:H5"	1:CA:1109:C:O2	2.05	0.56
25:CY:19:G:N1	25:CY:56:C:N4	2.41	0.56
26:DA:1316:U:H2'	26:DA:1317:A:H8	1.71	0.56
26:DA:2327:A:H2'	26:DA:2328:A:C8	2.41	0.56
46:DZ:100:VAL:HG21	46:DZ:134:PRO:HG2	1.88	0.56
1:AA:946:A:H2'	1:AA:947:G:C8	2.40	0.55
10:AJ:8:LEU:HB2	10:AJ:70:ARG:HB2	1.88	0.55
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.32	0.55
26:BA:278:A:O2'	26:BA:279:C:OP1	2.16	0.55
26:BA:911:A:H2'	37:BQ:9:TYR:OH	2.05	0.55
26:BA:1033:U:OP1	56:B9:9:ARG:NH2	2.39	0.55
26:BA:2023:G:H5'	26:BA:2617:C:H4'	1.87	0.55
1:CA:757:U:H2'	1:CA:758:G:O4'	2.06	0.55
4:CD:43:HIS:ND1	4:CD:46:LYS:HE2	2.20	0.55
23:CW:51:U:H3	23:CW:63:G:H1	1.54	0.55
26:DA:299:A:N1	26:DA:322:A:O2'	2.30	0.55
26:DA:478:A:N1	26:DA:500:G:H4'	2.21	0.55
41:DU:76:TYR:CZ	41:DU:80:ILE:HG13	2.42	0.55
44:DX:60:ARG:NH1	54:D7:47:ARG:HH22	2.01	0.55
1:AA:68:G:C2	1:AA:69:G:H1'	2.42	0.55
26:BA:389:G:N1	36:BP:70:GLN:HG3	2.22	0.55
1:CA:1028:C:C4	1:CA:1033:G:O6	2.59	0.55
20:CT:10:LEU:HD23	20:CT:12:ALA:HB2	1.88	0.55
23:CW:44:G:H2'	23:CW:45:U:H5'	1.88	0.55
26:DA:586:A:N1	26:DA:809:G:O2'	2.31	0.55
26:DA:2776:A:H4'	26:DA:2777:G:H5"	1.87	0.55
1:AA:167:G:H2'	1:AA:168:G:H8	1.72	0.55
1:AA:181:G:O2'	1:AA:183:G:O6	2.18	0.55
1:AA:652:U:O4	1:AA:752:G:O2'	2.13	0.55
1:AA:674:G:H2'	1:AA:675:A:H8	1.69	0.55
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.73	0.55
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.06	0.55
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.39	0.55
26:BA:588:U:H2'	26:BA:589:C:C6	2.40	0.55
26:BA:2848:G:C8	40:BT:97:ALA:HB2	2.41	0.55
36:BP:63:PRO:HG2	55:B8:25:MET:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:56:ASP:HB2	3:CC:67:THR:HB	1.88	0.55
27:DB:55:U:H1'	31:DG:29:TRP:CD1	2.42	0.55
29:DE:116:VAL:HG13	29:DE:122:PHE:HB2	1.88	0.55
29:DE:163:GLU:HG2	29:DE:164:ARG:N	2.20	0.55
1:AA:222:U:H2'	1:AA:223:U:C6	2.42	0.55
10:AJ:30:SER:O	10:AJ:81:THR:HG21	2.07	0.55
26:BA:535:C:O3'	41:BU:53:ARG:NH1	2.39	0.55
33:BI:114:LEU:HD12	33:BI:130:TYR:HA	1.87	0.55
1:CA:420:U:O2'	1:CA:423:G:O6	2.13	0.55
1:CA:521:G:H4'	12:CL:73:GLU:HG2	1.87	0.55
1:CA:527:G:O2'	1:CA:535:A:N1	2.34	0.55
1:CA:957:U:O2'	1:CA:959:A:N7	2.30	0.55
1:CA:1023:G:H3'	1:CA:1024:G:C8	2.41	0.55
18:CR:43:PHE:CD1	18:CR:56:THR:HG22	2.41	0.55
26:DA:888:C:H5"	26:DA:889:C:OP2	2.07	0.55
26:DA:1446:C:H42	26:DA:1465:G:H1	1.52	0.55
26:DA:2674:G:H2'	26:DA:2675:A:C8	2.41	0.55
26:DA:2753:A:N3	56:D9:15:LYS:NZ	2.43	0.55
28:DD:71:ASP:HB3	28:DD:103:ARG:HH22	1.71	0.55
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.89	0.55
26:BA:1540:U:H2'	26:BA:1541:G:O4'	2.07	0.55
26:BA:2207:G:O2'	26:BA:2208:A:OP1	2.24	0.55
26:BA:2567:G:H2'	26:BA:2568:C:C6	2.41	0.55
32:BH:41:MET:HE2	32:BH:65:HIS:HA	1.87	0.55
1:CA:811:C:O2'	1:CA:901:A:N1	2.40	0.55
1:CA:984:C:O5'	1:CA:984:C:H6	1.88	0.55
1:CA:1223:C:H5"	1:CA:1224:G:H5"	1.88	0.55
2:CB:162:ILE:O	2:CB:185:ILE:HG12	2.06	0.55
5:CE:137:GLU:HG2	5:CE:140:ARG:HH11	1.71	0.55
6:CF:97:PHE:HE1	18:CR:62:GLU:HG2	1.71	0.55
26:DA:39:C:H2'	26:DA:40:C:C6	2.42	0.55
26:DA:848:G:C4	26:DA:933:A:H8	2.24	0.55
26:DA:2787:C:H1'	29:DE:62:PRO:HG3	1.88	0.55
38:DR:55:ALA:HB2	38:DR:79:LEU:HD13	1.88	0.55
40:DT:50:ILE:HA	40:DT:99:LEU:HD12	1.89	0.55
48:D1:59:THR:O	48:D1:91:LYS:NZ	2.26	0.55
2:AB:167:PRO:HG3	2:AB:186:ALA:HB1	1.88	0.55
26:BA:330:A:H2	26:BA:1210:A:H2'	1.71	0.55
26:BA:1021:A:H8	26:BA:1022:G:H5"	1.71	0.55
26:BA:2108:C:H2'	26:BA:2109:U:H6	1.71	0.55
33:BI:93:THR:HG22	33:BI:119:PRO:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1028:C:N3	1:CA:1033:G:O6	2.40	0.55
1:CA:1316:G:H22	1:CA:1319:A:H5"	1.72	0.55
23:CW:19:G:H1	23:CW:56:C:N4	2.03	0.55
26:DA:1434:A:H61	26:DA:1558:A:H62	1.54	0.55
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.07	0.55
23:AW:50:U:H3	23:AW:64:A:N6	2.05	0.55
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.21	0.55
1:CA:1299:A:H2'	1:CA:1299:A:N3	2.21	0.55
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.41	0.55
2:CB:87:ARG:NH1	2:CB:220:ASP:OD1	2.39	0.55
2:CB:122:PHE:CE2	2:CB:139:LYS:HG2	2.42	0.55
5:CE:6:PHE:HB2	5:CE:34:VAL:HG22	1.89	0.55
26:DA:84:A:H5"	45:DY:8:LYS:HE3	1.89	0.55
26:DA:2126:A:N6	26:DA:2162:G:O2'	2.39	0.55
26:DA:2630:G:H2'	26:DA:2631:G:C8	2.42	0.55
48:D1:76:ARG:HH11	48:D1:97:LEU:HD22	1.71	0.55
3:AC:58:GLU:HB2	3:AC:65:ALA:HB3	1.88	0.55
27:BB:66:A:H61	27:BB:108:U:H2'	1.72	0.55
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.47	0.55
26:DA:528:A:C2	26:DA:2042:A:H2'	2.42	0.55
26:DA:566:U:H5"	36:DP:29:LYS:HE3	1.87	0.55
26:DA:1528:A:OP2	61:DA:3982:HOH:O	2.18	0.55
26:DA:2098:U:H3	26:DA:2191:G:H1	1.53	0.55
26:DA:2303:G:O2'	31:DG:132:ASN:HB2	2.07	0.55
1:AA:814:A:H2'	1:AA:816:A:H5"	1.89	0.55
18:CR:25:THR:O	18:CR:25:THR:OG1	2.19	0.55
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.06	0.55
26:DA:900:A:H2'	26:DA:901:A:C8	2.41	0.55
26:DA:1889:A:H2'	26:DA:1890:A:C8	2.42	0.55
38:DR:36:THR:HG22	38:DR:37:THR:H	1.72	0.55
44:DX:4:ALA:HB1	44:DX:42:ALA:HA	1.89	0.55
48:D1:83:GLU:OE1	48:D1:83:GLU:N	2.39	0.55
50:D3:7:LYS:HB2	50:D3:34:GLU:HG3	1.89	0.55
55:D8:6:THR:HG22	55:D8:63:PRO:HD2	1.88	0.55
1:AA:79:G:C2	1:AA:90:U:O2	2.60	0.55
1:AA:954:G:H21	1:AA:1227:A:H62	1.55	0.55
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.21	0.55
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.38	0.55
26:BA:1420:U:O2'	26:BA:1421:G:OP1	2.22	0.55
26:BA:2190:G:C2'	26:BA:2191:G:H5"	2.34	0.55
37:BQ:14:ARG:HG2	37:BQ:41:TRP:HH2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.42	0.55
23:CW:11:C:H42	23:CW:24:G:H1	1.54	0.55
26:DA:1292:U:H2'	26:DA:1293:C:C6	2.42	0.55
26:DA:1466:G:O2'	26:DA:1546:C:O2'	2.16	0.55
26:DA:2298:A:H1'	26:DA:2321:G:H21	1.72	0.55
26:DA:2848:G:C8	40:DT:97:ALA:HB2	2.42	0.55
28:DD:10:THR:OG1	28:DD:13:ARG:HG2	2.07	0.55
36:DP:48:PRO:O	55:D8:57:ARG:NH2	2.37	0.55
37:DQ:36:ALA:HA	37:DQ:129:THR:HG22	1.89	0.55
47:D0:32:ARG:H	47:D0:35:ASN:ND2	2.05	0.55
14:AN:33:VAL:HA	14:AN:40:CYS:HA	1.89	0.54
32:BH:154:PRO:HB3	32:BH:163:TYR:CZ	2.42	0.54
33:BI:72:LEU:C	33:BI:74:ASN:H	2.14	0.54
33:BI:116:LEU:HD21	33:BI:119:PRO:HA	1.89	0.54
51:B4:53:GLU:HB3	51:B4:54:GLY:CA	2.37	0.54
1:CA:1004:A:H62	1:CA:1037:C:H2'	1.71	0.54
1:CA:1262:C:H42	1:CA:1273:G:H1	1.53	0.54
1:CA:1359:C:H3'	14:CN:35:ARG:HH21	1.72	0.54
26:DA:297:C:H2'	26:DA:298:G:O4'	2.07	0.54
26:DA:1011:G:OP2	41:DU:66:ASN:ND2	2.39	0.54
26:DA:2592:G:OP1	61:DA:4233:HOH:O	2.18	0.54
26:DA:2595:G:N7	61:DA:4305:HOH:O	2.34	0.54
1:AA:757:U:H2'	1:AA:758:G:O4'	2.08	0.54
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.75	0.54
19:AS:67:VAL:HG21	51:B4:59:PHE:CD1	2.42	0.54
26:BA:2687:U:H2'	26:BA:2688:U:O4'	2.07	0.54
36:BP:50:ARG:HD3	55:B8:7:HIS:CD2	2.42	0.54
1:CA:1055:A:N3	3:CC:156:ARG:NH1	2.51	0.54
1:CA:1118:C:C2	1:CA:1119:C:H5	2.26	0.54
1:CA:1376:U:O5'	7:CG:94:ARG:NH2	2.40	0.54
2:CB:63:MET:HG2	2:CB:225:ALA:HB1	1.89	0.54
19:CS:19:VAL:O	19:CS:23:ASN:ND2	2.40	0.54
24:CX:19:G:H4'	24:CX:20:U:OP2	2.07	0.54
26:DA:1796:U:H2'	26:DA:1797:C:C6	2.42	0.54
28:DD:36:PRO:HA	28:DD:61:LEU:HD12	1.88	0.54
30:DF:34:TRP:CE2	36:DP:8:PRO:HG3	2.43	0.54
37:DQ:18:LYS:O	37:DQ:98:LYS:NZ	2.33	0.54
5:AE:68:GLU:HG2	5:AE:70:PRO:HD3	1.87	0.54
46:BZ:111:VAL:C	46:BZ:113:ALA:H	2.15	0.54
1:CA:920:U:H2'	1:CA:921:U:C6	2.41	0.54
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1165:C:N3	1:CA:1171:G:N2	2.56	0.54
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.89	0.54
26:DA:2113:U:H3	26:DA:2170:A:N6	2.03	0.54
31:DG:18:GLU:HG2	31:DG:175:LEU:HD21	1.89	0.54
31:DG:41:GLN:HE22	31:DG:153:ARG:HB3	1.71	0.54
33:DI:61:ARG:NE	33:DI:61:ARG:HA	2.22	0.54
36:DP:44:GLY:CA	36:DP:45:LEU:HB2	2.37	0.54
38:DR:95:THR:HG22	38:DR:116:LEU:HD23	1.90	0.54
1:AA:456:C:C2'	1:AA:457:C:H5'	2.37	0.54
1:AA:1026:G:C6	1:AA:1027:C:H1'	2.42	0.54
12:AL:97:ARG:HB2	12:AL:98:TYR:CE1	2.42	0.54
26:BA:620:G:N3	26:BA:620:G:H5'	2.23	0.54
26:BA:671:C:N4	61:BA:4880:HOH:O	2.39	0.54
26:BA:1786:A:H1'	26:BA:1938:A:N6	2.22	0.54
26:BA:2327:A:H2'	26:BA:2328:A:C8	2.42	0.54
26:BA:2336:A:H61	47:B0:43:THR:CG2	2.21	0.54
46:BZ:75:ASN:O	46:BZ:84:GLU:HG2	2.08	0.54
1:CA:674:G:H2'	1:CA:675:A:H8	1.72	0.54
4:CD:70:ILE:HG12	4:CD:74:GLN:HB3	1.88	0.54
26:DA:1005:C:H2'	26:DA:1006:C:C6	2.43	0.54
26:DA:1805:U:O2	28:DD:50:THR:HB	2.08	0.54
26:DA:2748:A:O2'	32:DH:63:SER:O	2.18	0.54
26:BA:323:G:C8	30:BF:171:PRO:HG3	2.43	0.54
26:BA:614(C):A:C4	30:BF:180:GLY:HA2	2.42	0.54
26:BA:729:G:C6	28:BD:208:LYS:HB2	2.42	0.54
26:BA:886:C:OP1	26:BA:886:C:H4'	2.08	0.54
30:BF:18:ARG:NH2	30:BF:127:GLU:OE1	2.37	0.54
36:BP:97:PRO:HD3	36:BP:126:VAL:O	2.08	0.54
42:BV:98:GLU:OE2	42:BV:100:ARG:NH1	2.41	0.54
1:CA:991:U:C4	1:CA:1212:U:H1'	2.42	0.54
1:CA:1132:C:H42	1:CA:1142:G:H1	1.55	0.54
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.73	0.54
2:CB:16:HIS:HB2	2:CB:204:ASN:CB	2.30	0.54
4:CD:150:GLU:OE2	4:CD:151:LYS:N	2.41	0.54
26:DA:590:A:OP1	30:DF:95:ARG:NH1	2.41	0.54
30:DF:165:ARG:HG2	30:DF:168:ARG:HH21	1.73	0.54
37:DQ:1:MET:HB2	37:DQ:44:ALA:HB1	1.89	0.54
50:D3:3:ARG:HH21	50:D3:36:VAL:HG11	1.73	0.54
51:D4:59:PHE:HA	51:D4:61:ARG:N	2.23	0.54
52:D5:49:CYS:O	52:D5:56:LYS:NZ	2.40	0.54
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:178:VAL:HG12	4:AD:179:GLU:H	1.72	0.54
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.07	0.54
10:AJ:5:ARG:NH2	10:AJ:73:ASP:OD2	2.24	0.54
26:BA:100:G:O2'	49:B2:7:ARG:NH2	2.40	0.54
1:CA:266:G:H5"	1:CA:268:C:H41	1.73	0.54
1:CA:1348:U:OP2	1:CA:1373:G:N2	2.32	0.54
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.88	0.54
23:CW:7:A:H5'	23:CW:8:4SU:H5	1.88	0.54
24:CX:23:C:H2'	24:CX:24:U:C6	2.43	0.54
26:DA:954:G:H5"	37:DQ:13:GLN:HB3	1.89	0.54
26:DA:1639:U:OP1	61:DA:4007:HOH:O	2.19	0.54
31:DG:44:GLY:N	31:DG:88:ILE:O	2.40	0.54
37:DQ:32:TYR:HB2	37:DQ:106:VAL:HG23	1.88	0.54
1:AA:1399:C:C2	1:AA:1502:A:N6	2.76	0.54
5:AE:78:HIS:HD1	8:AH:104:ARG:HD2	1.72	0.54
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.08	0.54
25:AY:63:G:H2'	25:AY:64:A:O4'	2.08	0.54
26:BA:1779:U:H2'	61:BA:5029:HOH:O	2.07	0.54
26:BA:2445:G:OP1	30:BF:74:ARG:NH2	2.41	0.54
26:BA:2815:C:H5'	52:B5:29:THR:HG21	1.88	0.54
34:BN:75:TYR:CE2	34:BN:77:GLY:HA2	2.43	0.54
1:CA:296:U:O2'	1:CA:556:C:O2	2.25	0.54
1:CA:1153:C:H42	1:CA:1154:G:N2	2.04	0.54
2:CB:12:GLU:O	2:CB:15:VAL:N	2.34	0.54
11:CK:48:ILE:HD11	11:CK:64:ALA:HA	1.89	0.54
26:DA:370:G:OP2	61:DA:3787:HOH:O	2.18	0.54
26:DA:2139:C:C4	26:DA:2153:G:C2	2.96	0.54
26:DA:2285:C:OP2	53:D6:6:ARG:NH1	2.38	0.54
33:DI:27:ARG:HD2	48:D1:71:TYR:CE2	2.43	0.54
38:DR:21:TYR:OH	38:DR:43:GLU:HG2	2.08	0.54
1:AA:79:G:N1	1:AA:90:U:N3	2.56	0.54
1:AA:1298:C:H4'	1:AA:1299:A:H5"	1.89	0.54
19:AS:65:ASN:HD22	19:AS:65:ASN:N	2.05	0.54
26:BA:1799:G:H4'	26:BA:1800:C:H5"	1.89	0.54
37:BQ:85:LYS:HB2	47:B0:7:LEU:HD12	1.90	0.54
1:CA:1003:G:H2'	1:CA:1004:A:H1'	1.89	0.54
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.07	0.54
26:DA:305:U:H2'	26:DA:306:U:C6	2.42	0.54
26:DA:1803:A:HO2'	28:DD:259:THR:HG21	1.71	0.54
26:DA:1859:A:N6	26:DA:1883:G:O2'	2.41	0.54
26:DA:2552:U:OP2	61:DA:4518:HOH:O	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DO:80:ASP:OD1	40:DT:64:ARG:NH2	2.41	0.54
1:AA:560:U:O2'	1:AA:561:U:OP2	2.21	0.54
1:AA:1258:G:O2'	1:AA:1259:C:H5'	2.08	0.54
13:AM:57:ARG:O	13:AM:61:GLU:HG2	2.08	0.54
2:CB:105:PHE:CE1	2:CB:155:LEU:HD12	2.42	0.54
3:CC:130:VAL:O	3:CC:134:ILE:HG12	2.07	0.54
4:CD:108:LEU:HD13	4:CD:174:LEU:HD13	1.88	0.54
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.89	0.54
26:DA:289:A:H2'	26:DA:290:G:O4'	2.08	0.54
26:DA:1010:A:OP2	61:DA:4178:HOH:O	2.18	0.54
26:DA:1514:U:H2'	26:DA:1515:G:H8	1.73	0.54
26:DA:2153:G:C6	26:DA:2154:G:C6	2.96	0.54
30:DF:101:LEU:O	30:DF:106:ARG:NH1	2.34	0.54
32:DH:3:ARG:NH2	32:DH:5:GLY:H	2.05	0.54
46:DZ:69:THR:HG22	46:DZ:90:VAL:HA	1.90	0.54
1:AA:950:U:H2'	1:AA:951:G:H8	1.73	0.54
1:AA:1316:G:N2	1:AA:1319:A:H5"	2.17	0.54
2:AB:69:LEU:HD12	2:AB:91:PRO:HB2	1.90	0.54
12:AL:53:ARG:HG3	12:AL:93:LEU:HD21	1.90	0.54
25:AY:58:A:HO2'	25:AY:60:U:H5	1.55	0.54
26:BA:910:A:H62	37:BQ:12:GLN:HA	1.73	0.54
26:BA:2101:G:H2'	26:BA:2102:U:C6	2.43	0.54
26:BA:2141:G:N7	26:BA:2151:G:N2	2.56	0.54
26:BA:2690:C:OP1	38:BR:17:ARG:NH1	2.38	0.54
34:BN:21:LYS:HE3	34:BN:140:VAL:OXT	2.08	0.54
1:CA:1120:G:O6	1:CA:1154:G:N2	2.41	0.54
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.42	0.54
2:CB:115:LEU:HD11	2:CB:153:ARG:HD2	1.90	0.54
9:CI:23:ASN:HD22	9:CI:23:ASN:N	2.06	0.54
19:CS:48:THR:HG22	19:CS:61:TYR:HA	1.88	0.54
25:CY:5:G:H1	25:CY:68:C:N4	2.06	0.54
31:DG:39:ILE:HB	31:DG:92:VAL:HG13	1.90	0.54
1:AA:78:G:N1	1:AA:91:C:C4	2.76	0.53
4:AD:173:TRP:NE1	4:AD:193:ASP:OD2	2.38	0.53
5:AE:80:ILE:HG22	5:AE:91:LEU:HB2	1.89	0.53
23:AW:47:U:O2'	23:AW:48:C:OP1	2.23	0.53
25:AY:19:G:H4'	25:AY:20:U:OP2	2.06	0.53
26:BA:226:G:H21	26:BA:228:A:H62	1.56	0.53
26:BA:1230:C:H2'	26:BA:1231:G:C8	2.43	0.53
31:BG:170:ARG:NH2	31:BG:182:LYS:O	2.41	0.53
51:B4:57:GLU:CB	51:B4:58:ARG:HA	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1033:G:C2'	1:CA:1034:G:H5'	2.38	0.53
10:CJ:81:THR:HA	10:CJ:84:GLN:HB2	1.89	0.53
13:CM:121:LYS:H	13:CM:121:LYS:HZ2	1.56	0.53
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.19	0.53
23:CW:58:A:O2'	23:CW:60:U:OP2	2.20	0.53
26:DA:2144:U:H1'	26:DA:2148:G:N2	2.23	0.53
1:AA:202:U:O2'	1:AA:203:U:O5'	2.13	0.53
19:AS:65:ASN:HA	51:B4:58:ARG:HG3	1.89	0.53
26:BA:614(B):G:OP1	61:BA:5228:HOH:O	2.19	0.53
26:BA:1378:A:OP1	54:B7:10:ARG:NH2	2.42	0.53
26:BA:2142:C:O2'	26:BA:2143:C:H5'	2.08	0.53
26:BA:2151:G:H2'	26:BA:2152:G:C8	2.42	0.53
44:BX:94:GLY:N	44:BX:95:LEU:HA	2.23	0.53
1:CA:890:G:O2'	1:CA:906:G:O6	2.21	0.53
1:CA:952:U:H2'	1:CA:953:G:C8	2.43	0.53
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.08	0.53
2:CB:186:ALA:O	2:CB:201:ILE:N	2.40	0.53
7:CG:72:ARG:NH1	7:CG:142:GLU:OE2	2.41	0.53
8:CH:51:VAL:HG11	8:CH:60:ARG:HH11	1.73	0.53
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.09	0.53
23:CW:50:U:H3	23:CW:64:A:H2	1.54	0.53
61:CW:3102:HOH:O	47:D0:2:ALA:N	2.41	0.53
26:DA:144:C:H2'	26:DA:145:G:C8	2.44	0.53
26:DA:973:A:H8	26:DA:973:A:OP1	1.92	0.53
27:DB:28:C:OP1	39:DS:36:TYR:OH	2.16	0.53
49:D2:1:MET:HE2	49:D2:6:VAL:HG22	1.88	0.53
26:BA:141:A:H8	26:BA:1408:C:HO2'	1.55	0.53
5:CE:6:PHE:HD1	5:CE:36:ASP:HB3	1.72	0.53
26:DA:526:A:O2'	26:DA:2043:C:O2	2.24	0.53
26:DA:2261:C:O2'	26:DA:2262:U:H5'	2.08	0.53
39:DS:67:ARG:O	39:DS:71:ARG:HG3	2.08	0.53
1:AA:646:U:H2'	1:AA:647:C:C6	2.43	0.53
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.08	0.53
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.89	0.53
26:BA:197:A:N6	26:BA:2430:A:O2'	2.40	0.53
26:BA:642:G:H21	26:BA:646:A:H2	1.56	0.53
26:BA:667:U:O2	55:B8:2:PRO:HD2	2.08	0.53
26:BA:2659:G:O2'	32:BH:175:LYS:NZ	2.41	0.53
31:BG:161:THR:HG22	31:BG:163:ALA:H	1.73	0.53
1:CA:1250:A:N3	1:CA:1370:G:O2'	2.35	0.53
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CT:36:LEU:HD12	20:CT:55:ILE:HG23	1.90	0.53
26:DA:2590:A:OP2	28:DD:238:GLY:HA2	2.08	0.53
1:AA:1028:C:H2'	1:AA:1029:C:C4'	2.37	0.53
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.43	0.53
1:AA:1270:C:OP2	21:AU:24:ARG:NH2	2.42	0.53
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	1.89	0.53
20:AT:27:LYS:O	20:AT:31:SER:OG	2.27	0.53
26:BA:71:A:N7	44:BX:31:HIS:HE1	2.05	0.53
33:BI:27:ARG:HD2	48:B1:71:TYR:CE1	2.44	0.53
1:CA:243:A:H4'	1:CA:244:U:H5"	1.90	0.53
1:CA:1057:G:O3'	3:CC:197:GLY:HA3	2.09	0.53
1:CA:1152:A:H2'	1:CA:1153:C:H6	1.73	0.53
3:CC:52:LEU:HD13	3:CC:118:GLN:HE22	1.73	0.53
9:CI:17:VAL:HG23	9:CI:63:ILE:HG12	1.89	0.53
25:CY:70:G:H2'	25:CY:71:G:H5'	1.91	0.53
26:DA:2128:C:H5'	26:DA:2173:A:N3	2.23	0.53
26:DA:2364:C:OP1	47:D0:55:ARG:NH1	2.41	0.53
35:DO:120:GLU:HB2	40:DT:68:TYR:HE2	1.74	0.53
39:DS:77:ALA:HB1	39:DS:82:ILE:HB	1.89	0.53
46:DZ:50:GLN:OE1	46:DZ:50:GLN:N	2.34	0.53
1:AA:1239:A:H62	1:AA:1299:A:H62	1.57	0.53
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.44	0.53
26:BA:1047:G:H2'	26:BA:1110:G:H22	1.74	0.53
26:BA:1107:G:H2'	26:BA:1107:G:N3	2.23	0.53
30:BF:20:LEU:HD22	30:BF:21:ALA:H	1.73	0.53
1:CA:97:G:O2'	1:CA:98:G:H5"	2.08	0.53
1:CA:316:G:OP2	1:CA:351:G:O2'	2.24	0.53
1:CA:1166:G:H5'	1:CA:1168:A:OP2	2.08	0.53
25:CY:68:C:C2'	25:CY:69:G:H5'	2.38	0.53
26:DA:1593:G:H2'	26:DA:1594:G:H8	1.73	0.53
26:DA:2302:G:H2'	26:DA:2303:G:H5'	1.91	0.53
31:DG:97:ASP:HA	31:DG:100:TRP:HD1	1.73	0.53
40:DT:28:VAL:HG13	40:DT:86:ILE:HG23	1.89	0.53
41:DU:92:ARG:HA	41:DU:95:LEU:HB2	1.91	0.53
53:D6:35:GLU:OE2	53:D6:50:ARG:NH1	2.42	0.53
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.91	0.53
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.37	0.53
25:AY:60:U:H5"	25:AY:61:C:C5	2.43	0.53
26:BA:624:C:O2'	26:BA:657:U:OP1	2.24	0.53
26:BA:1688:U:O2	26:BA:1700:A:H5'	2.09	0.53
26:BA:2887:U:H2'	26:BA:2888:C:C6	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BF:197:ASP:N	30:BF:197:ASP:OD1	2.41	0.53
31:BG:179:PRO:HB2	51:B4:42:PHE:HE1	1.73	0.53
41:BU:66:ASN:O	41:BU:70:ARG:HG3	2.09	0.53
1:CA:142:G:H2'	1:CA:143:A:C8	2.44	0.53
1:CA:430:A:P	4:CD:22:LYS:HZ1	2.32	0.53
1:CA:876:G:O5'	8:CH:14:ARG:NH1	2.41	0.53
1:CA:1173:G:H2'	1:CA:1174:G:H8	1.73	0.53
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.43	0.53
12:CL:32:PHE:HB3	12:CL:84:LEU:HD11	1.89	0.53
18:CR:53:ARG:HA	18:CR:56:THR:OG1	2.08	0.53
26:DA:1309:G:H3'	54:D7:9:ARG:HH12	1.73	0.53
26:DA:1645:G:H5"	26:DA:1646:C:H5'	1.89	0.53
26:DA:2430:A:N3	26:DA:2430:A:H2'	2.23	0.53
27:DB:110:G:H2'	27:DB:111:G:H5'	1.90	0.53
32:DH:154:PRO:HB3	32:DH:163:TYR:CE2	2.43	0.53
34:DN:67:LEU:O	34:DN:88:GLU:HG2	2.08	0.53
35:DO:77:ILE:HB	40:DT:74:ARG:HD3	1.91	0.53
40:DT:60:THR:HG22	40:DT:77:PRO:HA	1.90	0.53
1:AA:1238:A:OP2	61:AA:4136:HOH:O	2.18	0.53
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.91	0.53
23:AW:47:U:H5'	23:AW:47:U:C6	2.44	0.53
26:BA:242:G:C8	55:B8:5:LYS:HG2	2.44	0.53
26:BA:969:U:H2'	26:BA:970:C:C6	2.44	0.53
1:CA:522:C:H41	12:CL:53:ARG:NH2	2.07	0.53
1:CA:1119:C:C4	1:CA:1154:G:O6	2.62	0.53
2:CB:70:PHE:HE1	2:CB:163:PHE:HD2	1.56	0.53
4:CD:78:LEU:HD22	4:CD:96:LEU:HB3	1.90	0.53
4:CD:159:ARG:O	4:CD:163:GLU:N	2.40	0.53
23:CW:76:F3N:O2'	26:DA:2585:U:O4	2.15	0.53
26:DA:8:A:H2'	26:DA:9:U:H6	1.74	0.53
26:DA:852:G:H2'	26:DA:853:G:C8	2.44	0.53
26:DA:1405:U:H2'	26:DA:1406:U:C6	2.43	0.53
26:DA:1839:G:C8	26:DA:1927:A:H1'	2.44	0.53
26:DA:2127:G:N2	26:DA:2161:C:C2	2.77	0.53
26:DA:2206:G:H5'	26:DA:2207:G:N7	2.24	0.53
27:DB:66:A:N6	27:DB:109:C:H5"	2.24	0.53
31:DG:7:LEU:HD13	31:DG:104:GLU:HA	1.91	0.53
46:DZ:145:GLU:H	46:DZ:148:ASP:HB2	1.73	0.53
1:AA:877:C:H5"	8:AH:88:LYS:HD3	1.90	0.53
26:BA:1176:G:H1'	26:BA:1177:A:C5'	2.33	0.53
26:BA:2334:G:O6	47:B0:74:ARG:NH2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BI:104:GLN:HB3	33:BI:105:HIS:CD2	2.43	0.53
39:BS:46:VAL:HG12	39:BS:48:LEU:HD12	1.91	0.53
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.49	0.53
1:CA:1023:G:C4	1:CA:1024:G:C8	2.97	0.53
1:CA:1133:G:C4	1:CA:1134:G:C8	2.97	0.53
26:DA:90:U:H1'	26:DA:92:A:C8	2.44	0.53
26:DA:1688:U:O2	26:DA:1700:A:H5'	2.09	0.53
26:DA:2023:G:H5'	26:DA:2617:C:H4'	1.91	0.53
1:AA:79:G:C6	1:AA:90:U:N3	2.77	0.53
1:AA:841:U:H6	1:AA:841:U:P	2.32	0.53
1:AA:1241:G:C2'	1:AA:1242:C:H5'	2.38	0.53
4:AD:165:MET:C	4:AD:168:ARG:HH12	2.17	0.53
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.44	0.53
27:BB:2:C:H2'	27:BB:3:C:C6	2.43	0.53
32:BH:88:LEU:HD13	32:BH:130:ARG:HG2	1.91	0.53
42:BV:14:VAL:HB	42:BV:96:ILE:HG13	1.90	0.53
1:CA:309:G:O2'	1:CA:607:A:N1	2.42	0.53
1:CA:1330:U:H4'	13:CM:23:TYR:CE1	2.43	0.53
2:CB:33:TYR:HB2	2:CB:43:ASP:HA	1.91	0.53
8:CH:103:VAL:HG11	8:CH:136:GLU:HB2	1.91	0.53
9:CI:29:ASN:OD1	9:CI:64:THR:HA	2.09	0.53
32:DH:26:VAL:HG21	32:DH:75:ALA:HB1	1.90	0.53
34:DN:4:TYR:HB2	41:DU:101:ARG:HH12	1.74	0.53
41:DU:79:PHE:CZ	41:DU:83:LEU:HD21	2.43	0.53
51:D4:58:ARG:HB3	51:D4:59:PHE:HD1	1.74	0.53
1:AA:539:A:H2'	1:AA:540:G:C8	2.42	0.52
8:AH:51:VAL:HG12	8:AH:52:ASP:H	1.74	0.52
26:BA:1223:G:N2	26:BA:1226:A:OP2	2.35	0.52
26:BA:2611:U:C4	52:B5:3:LYS:HG2	2.44	0.52
51:B4:64:GLY:C	51:B4:66:SER:H	2.16	0.52
1:CA:263:A:OP1	20:CT:79:ARG:NH1	2.41	0.52
1:CA:714:G:H2'	1:CA:715:A:C8	2.44	0.52
1:CA:952:U:H2'	1:CA:953:G:H8	1.73	0.52
7:CG:78:ARG:NH1	7:CG:154:TYR:O	2.41	0.52
20:CT:13:LEU:O	20:CT:17:ARG:HG3	2.09	0.52
27:DB:56:G:OP1	31:DG:27:ASN:ND2	2.42	0.52
46:DZ:111:VAL:HA	46:DZ:115:GLY:HA3	1.91	0.52
1:AA:714:G:H2'	1:AA:715:A:C8	2.44	0.52
1:AA:1035:A:H8	1:AA:1035:A:O5'	1.92	0.52
26:BA:271(E):U:H2'	26:BA:271(F):C:C6	2.44	0.52
26:BA:2168:G:C6	26:BA:2171:A:H8	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BZ:144:LEU:HD21	46:BZ:148:ASP:O	2.08	0.52
53:B6:35:GLU:OE2	53:B6:50:ARG:NH1	2.43	0.52
1:CA:952:U:O2'	1:CA:965:A:N6	2.41	0.52
1:CA:975:A:H4'	1:CA:976:G:C5'	2.35	0.52
1:CA:1066:C:H2'	1:CA:1067:A:C8	2.45	0.52
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.45	0.52
3:CC:43:LEU:HD11	3:CC:91:LEU:HD11	1.91	0.52
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.09	0.52
25:CY:27:G:O6	25:CY:43:C:N3	2.42	0.52
26:DA:589:C:H2'	26:DA:590:A:C8	2.44	0.52
26:DA:1019:U:OP1	26:DA:1035:U:O2'	2.26	0.52
45:DY:49:VAL:HG21	45:DY:61:ILE:HG23	1.91	0.52
46:DZ:33:LEU:HD21	46:DZ:90:VAL:HG21	1.90	0.52
55:D8:26:LYS:HB2	55:D8:44:LYS:O	2.10	0.52
1:AA:662:G:H2'	1:AA:663:A:C8	2.44	0.52
4:AD:49:ARG:H	4:AD:49:ARG:NE	2.07	0.52
5:AE:79:GLU:HG3	5:AE:93:PRO:HD2	1.92	0.52
19:AS:48:THR:HG22	19:AS:61:TYR:HA	1.91	0.52
26:BA:2126:A:N3	26:BA:2127:G:H1'	2.24	0.52
26:BA:2870:C:H2'	26:BA:2871:C:O4'	2.09	0.52
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.09	0.52
1:CA:1095:U:C4	1:CA:1096:C:C4	2.98	0.52
1:CA:1264:C:O2	1:CA:1272:G:N2	2.41	0.52
26:DA:646:A:H2'	26:DA:647:G:O4'	2.09	0.52
26:DA:885:C:H1'	26:DA:892:G:H22	1.75	0.52
40:DT:51:ARG:HG3	40:DT:98:LYS:HZ3	1.74	0.52
46:DZ:6:LYS:HD2	46:DZ:8:TYR:OH	2.10	0.52
3:AC:40:ARG:O	3:AC:44:GLU:HB2	2.10	0.52
26:BA:2110:G:C2	26:BA:2120:G:H1'	2.44	0.52
35:BO:104:ARG:CZ	40:BT:34:VAL:HG21	2.39	0.52
1:CA:56:U:H2'	1:CA:57:G:H8	1.74	0.52
1:CA:302:G:N3	1:CA:556:C:H4'	2.24	0.52
1:CA:1039:C:H2'	1:CA:1040:U:O4'	2.09	0.52
1:CA:1318:A:H5"	19:CS:3:ARG:NH2	2.20	0.52
27:DB:66:A:N6	27:DB:108:U:H3'	2.25	0.52
29:DE:111:ARG:HA	38:DR:1:MET:SD	2.50	0.52
39:DS:14:VAL:O	39:DS:18:ILE:HG12	2.10	0.52
46:DZ:105:VAL:N	46:DZ:139:VAL:O	2.39	0.52
1:AA:626:U:H2'	1:AA:627:G:C8	2.45	0.52
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.41	0.52
16:AP:58:TYR:O	16:AP:62:VAL:HG23	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BG:48:GLU:HA	31:BG:51:ARG:HG2	1.91	0.52
1:CA:1004:A:N6	1:CA:1037:C:C2	2.77	0.52
1:CA:1286:A:N1	21:CU:18:TYR:OH	2.42	0.52
3:CC:119:ARG:HG2	3:CC:123:GLN:HE21	1.75	0.52
13:CM:29:ARG:HG3	13:CM:64:TRP:CH2	2.45	0.52
25:CY:9:A:H5'	25:CY:46:7MG:H1'	1.91	0.52
26:DA:729:G:H5'	26:DA:730:C:H5"	1.91	0.52
26:DA:859:G:O2'	26:DA:916:G:O6	2.24	0.52
26:DA:2117:A:O2'	26:DA:2118:U:H5"	2.09	0.52
26:DA:2126:A:N6	26:DA:2172:U:H3'	2.24	0.52
26:DA:2128:C:H2'	26:DA:2129:C:O4'	2.10	0.52
26:DA:2350:C:H2'	26:DA:2351:G:O4'	2.10	0.52
26:DA:2815:C:C5'	52:D5:29:THR:HG21	2.39	0.52
27:DB:110:G:C2'	27:DB:111:G:H5'	2.39	0.52
28:DD:175:LEU:HD12	28:DD:185:VAL:HG21	1.92	0.52
35:DO:73:ASP:HB2	40:DT:82:LEU:HD13	1.92	0.52
36:DP:37:GLY:O	36:DP:40:SER:OG	2.22	0.52
1:AA:946:A:O2'	1:AA:1333:A:N3	2.35	0.52
1:AA:1279:A:H4'	1:AA:1281:U:H5	1.75	0.52
26:BA:848:G:C4	26:BA:933:A:H8	2.26	0.52
26:BA:1028:A:H61	26:BA:1125:G:H2'	1.75	0.52
26:BA:1153:C:OP1	41:BU:92:ARG:NH1	2.43	0.52
26:BA:2173:A:H3'	26:BA:2174:C:C6	2.45	0.52
37:BQ:30:GLY:HA2	37:BQ:107:ALA:HB2	1.92	0.52
45:BY:35:TYR:CE2	45:BY:69:ALA:HB3	2.44	0.52
53:B6:6:ARG:NE	53:B6:24:GLU:OE1	2.32	0.52
53:B6:13:CYS:SG	53:B6:47:THR:HG21	2.49	0.52
2:CB:100:GLY:O	2:CB:108:ILE:HD11	2.10	0.52
2:CB:158:LEU:HD23	2:CB:182:ILE:HD11	1.91	0.52
3:CC:125:GLU:HG3	3:CC:190:ARG:O	2.10	0.52
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.09	0.52
25:CY:33:U:C3'	25:CY:34:G:H5"	2.40	0.52
26:DA:200:U:O4	26:DA:250:G:N2	2.43	0.52
34:DN:38:HIS:ND1	34:DN:39:ARG:HG3	2.25	0.52
1:AA:353:A:H8	1:AA:353:A:H5'	1.74	0.52
1:AA:950:U:H2'	1:AA:951:G:C8	2.45	0.52
1:AA:1144:G:N2	1:AA:1146:A:H62	2.08	0.52
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.43	0.52
30:BF:53:THR:CG2	30:BF:55:GLY:H	2.22	0.52
35:BO:73:ASP:HB2	40:BT:82:LEU:HD13	1.91	0.52
1:CA:171:A:H2'	1:CA:172:A:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:448:A:P	1:CA:485:G:H22	2.33	0.52
1:CA:1353:G:OP1	21:CU:10:ARG:NH1	2.43	0.52
18:CR:70:ILE:HG23	18:CR:79:LEU:HD12	1.92	0.52
26:DA:77:C:H42	26:DA:109:G:H1	1.57	0.52
26:DA:79:G:H1	26:DA:107:C:H42	1.58	0.52
26:DA:992:C:OP1	41:DU:47:TYR:OH	2.26	0.52
26:DA:2155:G:H2'	26:DA:2156:G:O4'	2.10	0.52
27:DB:17:C:O2	27:DB:67:G:N2	2.35	0.52
30:DF:184:TYR:O	30:DF:188:ARG:HG3	2.09	0.52
1:AA:677:U:H3	1:AA:713:G:H22	1.58	0.52
1:AA:1125:U:H4'	10:AJ:5:ARG:NH2	2.24	0.52
6:AF:10:LEU:HB2	6:AF:59:TYR:HB3	1.92	0.52
23:AW:52:G:H4'	37:BQ:56:ARG:CZ	2.39	0.52
24:AX:21:A:N6	24:AX:46:G:H2'	2.24	0.52
26:BA:892:G:H3'	26:BA:893:C:H6	1.74	0.52
26:BA:1653:G:H3'	38:BR:2:ARG:HD3	1.90	0.52
29:BE:111:ARG:HG3	29:BE:160:TYR:CD2	2.44	0.52
1:CA:142:G:H2'	1:CA:143:A:H8	1.74	0.52
1:CA:457:C:H2'	1:CA:458:C:H6	1.75	0.52
26:DA:263:C:H2'	26:DA:264:C:O4'	2.10	0.52
26:DA:528:A:OP2	34:DN:114:ARG:NH1	2.43	0.52
26:DA:1341:U:OP1	26:DA:1397:U:N3	2.35	0.52
26:DA:1608:A:H1'	26:DA:1610:A:OP2	2.10	0.52
26:DA:1827:C:OP2	28:DD:222:ARG:NH1	2.43	0.52
39:DS:34:HIS:ND1	39:DS:53:SER:OG	2.35	0.52
1:AA:69:G:H2'	1:AA:70:G:H8	1.74	0.52
1:AA:619:U:N3	4:AD:134:ASP:OD2	2.38	0.52
1:AA:1024:G:H2'	1:AA:1025:U:H5"	1.92	0.52
4:AD:128:VAL:HG12	4:AD:129:ASN:ND2	2.25	0.52
9:AI:9:ARG:H	9:AI:79:LEU:HD23	1.75	0.52
19:AS:23:ASN:HA	19:AS:27:GLU:CD	2.35	0.52
26:BA:639:U:H2'	26:BA:640:C:C6	2.45	0.52
26:BA:1406:U:H2'	26:BA:1407:C:C6	2.45	0.52
1:CA:346:G:OP1	40:DT:41:ARG:NH2	2.42	0.52
1:CA:1030(A):G:N2	1:CA:1030(C):G:H3'	2.25	0.52
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.45	0.52
3:CC:22:TRP:CB	3:CC:59:ARG:HB2	2.40	0.52
12:CL:34:ARG:HG3	12:CL:105:TYR:CE2	2.44	0.52
19:CS:17:GLU:O	19:CS:21:GLU:N	2.36	0.52
25:CY:18:G:N2	25:CY:55:PSU:C4	2.77	0.52
26:DA:637:A:H8	36:DP:117:GLU:HG3	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2114:A:N6	26:DA:2115:G:H21	2.08	0.52
56:D9:17:ILE:HG22	56:D9:24:TYR:HB2	1.92	0.52
1:AA:582:U:OP1	15:AO:64:ARG:NH1	2.43	0.52
12:AL:77:LEU:HD21	12:AL:107:ALA:HA	1.92	0.52
13:AM:15:VAL:HB	13:AM:34:LEU:HD11	1.92	0.52
16:AP:1:MET:N	16:AP:1:MET:SD	2.62	0.52
28:BD:101:GLU:OE1	28:BD:103:ARG:NH1	2.42	0.52
29:BE:77:ILE:HD13	29:BE:195:LEU:HD12	1.92	0.52
52:B5:55:ARG:NH1	52:B5:57:VAL:HG22	2.25	0.52
1:CA:545:C:O2'	1:CA:549:C:OP1	2.22	0.52
6:CF:3:ARG:HD3	6:CF:64:GLN:NE2	2.25	0.52
12:CL:69:TYR:HE2	12:CL:71:PRO:HA	1.73	0.52
22:CV:14:A:C2	22:CV:15:A:C4	2.98	0.52
26:DA:93:G:H2'	26:DA:94:C:H6	1.74	0.52
30:DF:32:LEU:O	30:DF:36:VAL:HG23	2.09	0.52
38:DR:74:LYS:HG2	38:DR:77:ARG:HH21	1.74	0.52
42:DV:21:ARG:HG2	42:DV:91:TYR:CD2	2.45	0.52
43:DW:60:ASN:HD22	43:DW:60:ASN:N	2.07	0.52
1:AA:1022:G:H2'	1:AA:1023:G:C8	2.44	0.51
8:AH:112:LEU:HA	8:AH:134:ILE:HG12	1.92	0.51
25:AY:13:C:H2'	25:AY:14:A:C8	2.45	0.51
26:BA:971:C:O2'	26:BA:983:A:N3	2.40	0.51
26:BA:1028:A:N6	26:BA:1125:G:H2'	2.25	0.51
26:BA:1345:C:OP2	61:BA:4016:HOH:O	2.18	0.51
26:BA:2875:C:OP1	40:BT:3:ARG:NH1	2.42	0.51
46:BZ:29:TYR:HB3	46:BZ:34:ASN:HD22	1.75	0.51
46:BZ:92:SER:O	46:BZ:130:PRO:HG2	2.10	0.51
1:CA:1250:A:H4'	9:CI:68:GLY:N	2.25	0.51
2:CB:135:GLN:O	2:CB:139:LYS:HB2	2.10	0.51
23:CW:76:F3N:N	24:CX:76:31H:O2'	2.43	0.51
24:CX:67:C:C2'	24:CX:68:C:H5'	2.40	0.51
26:DA:323:G:O2'	26:DA:1205:U:N3	2.35	0.51
26:DA:956:G:H5"	37:DQ:77:LYS:HD2	1.92	0.51
26:DA:1032:A:H2	26:DA:1122:G:H22	1.59	0.51
26:DA:2124:G:H1	26:DA:2174:C:H42	1.58	0.51
26:DA:2400:G:H2'	26:DA:2401:U:H6	1.74	0.51
31:DG:48:GLU:HA	31:DG:51:ARG:HG2	1.90	0.51
31:DG:106:LEU:O	31:DG:111:LEU:HD22	2.10	0.51
1:AA:524:G:H2'	1:AA:525:C:C6	2.46	0.51
1:AA:606:G:N2	1:AA:631:G:N7	2.58	0.51
23:AW:19:G:C5	26:BA:882:G:H4'	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AX:61:C:H2'	24:AX:62:C:H6	1.76	0.51
24:AX:66:C:H2'	24:AX:67:C:O4'	2.10	0.51
26:BA:86:C:H4'	26:BA:104:U:H1'	1.92	0.51
26:BA:2191:G:H5'	26:BA:2191:G:H8	1.74	0.51
39:BS:11:LYS:O	39:BS:15:ARG:HG3	2.10	0.51
43:BW:2:GLU:OE2	43:BW:72:LYS:HE2	2.10	0.51
53:B6:14:THR:HG21	53:B6:48:VAL:HG22	1.92	0.51
1:CA:1028:C:H2'	1:CA:1029:C:C6	2.45	0.51
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.45	0.51
1:CA:1359:C:H3'	14:CN:35:ARG:NH2	2.25	0.51
2:CB:219:VAL:O	2:CB:222:ILE:HG12	2.11	0.51
4:CD:18:LYS:NZ	4:CD:31:CYS:SG	2.84	0.51
8:CH:15:ASN:O	8:CH:19:VAL:HG23	2.10	0.51
19:CS:33:THR:HG21	19:CS:71:LEU:HD21	1.91	0.51
26:DA:1721:G:N1	26:DA:1739:U:OP2	2.43	0.51
26:DA:2537:U:H2'	26:DA:2538:C:C6	2.45	0.51
26:DA:2645:G:N2	26:DA:2767:C:OP2	2.43	0.51
27:DB:48:A:P	39:DS:30:ARG:HH12	2.33	0.51
29:DE:115:GLY:O	29:DE:119:ARG:HB2	2.11	0.51
44:DX:11:PRO:HB3	44:DX:92:LEU:HD11	1.91	0.51
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.58	0.51
11:AK:16:SER:O	11:AK:35:PRO:HD3	2.11	0.51
13:AM:14:ARG:HB2	13:AM:17:VAL:HG23	1.91	0.51
26:BA:41:C:H2'	26:BA:42:G:O4'	2.10	0.51
26:BA:2110:G:OP1	26:BA:2118:U:N3	2.27	0.51
26:BA:2751:G:C2	32:BH:2:SER:HB3	2.45	0.51
35:BO:120:GLU:OE1	40:BT:67:SER:OG	2.24	0.51
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.45	0.51
24:CX:48:C:C2	24:CX:59:A:H1'	2.45	0.51
26:DA:1366:A:OP1	48:D1:3:LYS:NZ	2.30	0.51
27:DB:7:G:N1	27:DB:114:C:N3	2.48	0.51
27:DB:94:C:H2'	27:DB:95:C:H6	1.75	0.51
1:AA:265:G:H2'	1:AA:267:C:H5	1.74	0.51
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.46	0.51
24:AX:8:4SU:O5'	24:AX:8:4SU:H6	2.11	0.51
26:BA:330:A:H2	26:BA:1210:A:HO2'	1.58	0.51
26:BA:687:C:H5"	54:B7:2:LYS:HE2	1.91	0.51
46:BZ:59:LEU:HD12	46:BZ:69:THR:HG21	1.92	0.51
48:B1:51:VAL:HG11	48:B1:74:VAL:HG21	1.92	0.51
1:CA:1134:G:N2	1:CA:1140:C:N3	2.54	0.51
14:CN:6:LEU:HB3	14:CN:23:ARG:HH22	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:31:A:C2	25:CY:39:PSU:N3	2.79	0.51
26:DA:708:C:H42	26:DA:723:G:H1	1.57	0.51
26:DA:1325:G:OP1	26:DA:1647:G:O2'	2.15	0.51
46:DZ:108:PRO:HG3	46:DZ:141:VAL:HB	1.91	0.51
20:AT:9:ASN:O	20:AT:10:LEU:HB2	2.10	0.51
26:BA:271(M):G:H4'	26:BA:271(N):U:OP1	2.10	0.51
26:BA:601:C:OP1	30:BF:108:LYS:HE3	2.11	0.51
1:CA:1011:G:N2	1:CA:1018:C:N3	2.53	0.51
1:CA:1028:C:O2	1:CA:1033:G:N1	2.44	0.51
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.10	0.51
26:DA:392:C:H5"	26:DA:409:C:H5"	1.93	0.51
26:DA:528:A:C2'	26:DA:529:A:H5"	2.40	0.51
26:DA:1187:G:H5'	42:DV:81:TYR:CE1	2.45	0.51
26:DA:2394:C:OP2	55:D8:30:ARG:NH1	2.43	0.51
31:DG:105:LYS:NZ	31:DG:143:GLU:OE1	2.43	0.51
34:DN:58:ASP:OD1	34:DN:58:ASP:N	2.41	0.51
46:DZ:59:LEU:HD21	46:DZ:69:THR:OG1	2.10	0.51
1:AA:309:G:O2'	1:AA:607:A:N1	2.44	0.51
2:AB:10:LEU:C	2:AB:12:GLU:H	2.17	0.51
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.46	0.51
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.26	0.51
25:AY:38:A:H2'	25:AY:39:PSU:H5"	1.91	0.51
43:BW:25:ARG:NH2	43:BW:74:ALA:O	2.40	0.51
1:CA:419:C:OP1	1:CA:513:C:O2'	2.25	0.51
1:CA:1120:G:C6	1:CA:1154:G:C2	2.99	0.51
9:CI:85:LEU:HB3	9:CI:92:TYR:CD2	2.40	0.51
9:CI:125:TYR:HD1	9:CI:126:SER:N	2.09	0.51
13:CM:71:ARG:HG3	13:CM:71:ARG:NH1	2.25	0.51
26:DA:184:C:H2'	26:DA:185:U:C6	2.45	0.51
26:DA:667:U:O2	55:D8:2:PRO:HD2	2.10	0.51
26:DA:2724:C:OP1	29:DE:118:LYS:NZ	2.33	0.51
27:DB:95:C:H2'	27:DB:96:U:C6	2.46	0.51
28:DD:20:ASP:OD1	28:DD:20:ASP:N	2.44	0.51
42:DV:35:LEU:HB2	42:DV:57:VAL:HG23	1.93	0.51
1:AA:625:G:H4'	16:AP:16:HIS:CD2	2.45	0.51
26:BA:457:A:H5"	61:BA:3937:HOH:O	2.10	0.51
26:BA:2183:C:H2'	26:BA:2184:G:H8	1.76	0.51
36:BP:39:LYS:NZ	61:BP:3108:HOH:O	2.29	0.51
36:BP:59:LEU:HD11	55:B8:10:ALA:HB2	1.91	0.51
45:BY:86:ARG:HH11	45:BY:100:ALA:HB1	1.76	0.51
1:CA:1347:G:HO2'	1:CA:1373:G:H1	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.92	0.51
24:CX:23:C:H2'	24:CX:24:U:H6	1.75	0.51
25:CY:33:U:H3'	25:CY:34:G:H5"	1.92	0.51
26:DA:872:A:H2'	26:DA:873:G:C8	2.45	0.51
26:DA:1246:A:OP1	30:DF:38:ARG:NH1	2.43	0.51
26:DA:1378:A:OP1	54:D7:10:ARG:NH2	2.44	0.51
26:DA:2126:A:N3	26:DA:2127:G:H1'	2.26	0.51
27:DB:80:U:H2'	27:DB:81:G:C8	2.44	0.51
32:DH:30:LYS:HG3	32:DH:80:SER:O	2.10	0.51
41:DU:49:HIS:HA	41:DU:52:ARG:HB3	1.91	0.51
43:DW:18:ARG:NH1	43:DW:76:VAL:O	2.44	0.51
1:AA:78:G:N2	1:AA:91:C:C2	2.79	0.51
1:AA:328:C:H4'	1:AA:329:A:H5'	1.93	0.51
1:AA:841:U:C4	1:AA:848:C:H1'	2.45	0.51
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.32	0.51
2:AB:137:ARG:HB3	2:AB:137:ARG:CZ	2.41	0.51
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.92	0.51
9:AI:99:LEU:HB3	9:AI:101:PHE:CD1	2.44	0.51
13:AM:19:LEU:HD21	13:AM:56:LEU:HD11	1.92	0.51
25:AY:68:C:C2'	25:AY:69:G:H5'	2.40	0.51
33:BI:140:LEU:HD22	33:BI:142:VAL:HG22	1.92	0.51
1:CA:1517:G:H1'	26:DA:1919:A:O3'	2.11	0.51
3:CC:63:ASN:HB2	3:CC:98:ASN:HB2	1.93	0.51
6:CF:87:ARG:HB2	6:CF:87:ARG:HH11	1.75	0.51
11:CK:101:SER:HB2	11:CK:103:LEU:HD23	1.92	0.51
13:CM:25:ILE:HG23	13:CM:29:ARG:HB3	1.92	0.51
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.92	0.51
26:DA:71:A:N7	44:DX:31:HIS:HE1	2.08	0.51
1:AA:1001:A:H2'	1:AA:1001(A):G:C8	2.46	0.51
1:AA:1022:G:H4'	1:AA:1022:G:OP1	2.11	0.51
1:AA:1068:G:N2	1:AA:1191:A:N3	2.47	0.51
1:AA:1226:C:O2'	13:AM:111:LYS:NZ	2.41	0.51
13:AM:123:ALA:HB2	23:AW:39:PSU:H1'	1.93	0.51
20:AT:76:ALA:HA	20:AT:79:ARG:NH1	2.26	0.51
26:BA:887:A:O2'	26:BA:888:C:OP2	2.28	0.51
29:BE:47:VAL:HG22	29:BE:84:PHE:O	2.11	0.51
51:B4:63:TYR:N	51:B4:63:TYR:CD1	2.77	0.51
1:CA:1038:C:H2'	1:CA:1039:C:H5"	1.91	0.51
1:CA:1264:C:H42	1:CA:1271:G:H1	1.58	0.51
8:CH:69:ARG:HG3	8:CH:76:PRO:HA	1.93	0.51
26:DA:218:A:C2	26:DA:235:U:H4'	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1410:G:H2'	26:DA:1411:C:C6	2.46	0.51
27:DB:3:C:H2'	27:DB:4:C:H6	1.76	0.51
27:DB:42:C:O2'	31:DG:66:GLN:HG2	2.11	0.51
34:DN:30:ILE:HG22	34:DN:34:LEU:HD22	1.93	0.51
46:DZ:145:GLU:HG2	46:DZ:146:ILE:HD12	1.93	0.51
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.27	0.51
1:AA:1288:A:N3	1:AA:1352:C:O2'	2.42	0.51
2:AB:16:HIS:C	2:AB:18:GLY:H	2.14	0.51
9:AI:48:GLU:HB3	9:AI:101:PHE:HE2	1.76	0.51
18:AR:56:THR:HB	18:AR:58:LEU:HD22	1.93	0.51
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.92	0.51
24:AX:19:G:H3'	24:AX:20:U:H6	1.76	0.51
26:BA:880:G:N2	26:BA:898:C:C2	2.79	0.51
26:BA:893:C:O2'	26:BA:894:C:H5'	2.10	0.51
26:BA:1048:A:P	26:BA:1109:C:H42	2.32	0.51
26:BA:2319:G:N2	39:BS:3:ARG:HA	2.26	0.51
33:BI:96:ASP:OD1	33:BI:96:ASP:N	2.44	0.51
1:CA:160:A:H61	1:CA:347:G:H1'	1.76	0.51
1:CA:839:U:O2'	1:CA:840:C:OP1	2.27	0.51
1:CA:982:U:O2	1:CA:1222:G:N1	2.43	0.51
2:CB:19:HIS:CE1	2:CB:206:ASP:HB2	2.44	0.51
3:CC:125:GLU:O	3:CC:127:ARG:NH1	2.41	0.51
8:CH:73:ASP:OD1	8:CH:75:ARG:HD3	2.10	0.51
26:DA:997:G:OP1	41:DU:92:ARG:HG2	2.10	0.51
26:DA:2376:A:H3'	26:DA:2377:A:H8	1.76	0.51
26:DA:2769:C:H2'	26:DA:2770:G:O4'	2.11	0.51
28:DD:79:VAL:HG21	28:DD:111:LEU:HD11	1.93	0.51
30:DF:24:LEU:HD23	30:DF:115:ALA:HA	1.93	0.51
30:DF:150:GLY:HA2	30:DF:172:TRP:CE3	2.46	0.51
32:DH:20:ALA:HB3	32:DH:23:ARG:HG3	1.93	0.51
32:DH:154:PRO:HB3	32:DH:163:TYR:CZ	2.46	0.51
40:DT:24:PRO:HD3	40:DT:52:ILE:HD12	1.93	0.51
1:AA:46:G:O6	61:AA:4164:HOH:O	2.16	0.50
1:AA:96:U:O2'	1:AA:97:G:H5'	2.11	0.50
1:AA:735:C:H2'	1:AA:736:C:H6	1.76	0.50
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.21	0.50
25:AY:28:G:H2'	25:AY:29:G:C8	2.46	0.50
40:BT:118:ARG:HG3	40:BT:118:ARG:NH1	2.14	0.50
52:B5:16:ARG:NH1	52:B5:17:ASP:OD1	2.44	0.50
1:CA:344:A:H4'	1:CA:345:C:OP2	2.11	0.50
1:CA:707:C:H2'	1:CA:708:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:735:C:H2'	1:CA:736:C:C6	2.45	0.50
4:CD:12:CYS:SG	4:CD:19:LEU:HB2	2.51	0.50
5:CE:18:ARG:HG2	5:CE:19:MET:N	2.27	0.50
8:CH:20:TYR:CE2	8:CH:76:PRO:HG2	2.46	0.50
18:CR:38:GLU:O	18:CR:41:LYS:NZ	2.45	0.50
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.11	0.50
21:CU:7:ARG:NH1	21:CU:21:TYR:OH	2.43	0.50
23:CW:21:A:H1'	23:CW:48:C:N4	2.26	0.50
26:DA:656:G:H2'	26:DA:657:U:O4'	2.10	0.50
26:DA:662:G:H5"	36:DP:16:ARG:HG2	1.92	0.50
26:DA:1299:G:OP1	61:DA:4540:HOH:O	2.19	0.50
26:DA:2103:C:C2'	26:DA:2104:G:H5'	2.40	0.50
1:AA:523:A:H61	12:AL:92:ASP:HB2	1.76	0.50
1:AA:1302:U:OP2	13:AM:21:TYR:OH	2.27	0.50
26:BA:184:C:H2'	26:BA:185:U:C6	2.47	0.50
26:BA:848:G:H2'	26:BA:849:A:C8	2.46	0.50
26:BA:1803:A:O2'	28:BD:259:THR:HG21	2.11	0.50
26:BA:1996:C:H4'	26:BA:1997:G:OP1	2.11	0.50
26:BA:2176:A:H2'	26:BA:2177:C:C6	2.46	0.50
26:BA:2748:A:H5'	32:BH:4:ILE:HD12	1.93	0.50
38:BR:38:VAL:HG12	38:BR:42:LYS:HE3	1.92	0.50
1:CA:580:U:H5"	15:CO:58:MET:HG2	1.92	0.50
1:CA:1164:G:C2'	1:CA:1165:C:H5'	2.40	0.50
2:CB:120:ALA:O	2:CB:121:LEU:HB3	2.11	0.50
20:CT:86:ARG:NH1	20:CT:90:GLN:HE22	2.10	0.50
26:DA:2139:C:N4	26:DA:2152:G:C6	2.79	0.50
26:DA:2611:U:C4	52:D5:3:LYS:HG2	2.46	0.50
28:DD:148:GLU:HB2	28:DD:151:LYS:HD2	1.91	0.50
31:DG:5:VAL:HG22	31:DG:8:LYS:HB2	1.93	0.50
33:DI:43:ASN:HD22	33:DI:43:ASN:C	2.19	0.50
44:DX:31:HIS:CD2	44:DX:33:LYS:H	2.29	0.50
26:BA:657:U:H2'	26:BA:658:C:C6	2.45	0.50
26:BA:2133:G:O2'	26:BA:2156:G:N2	2.43	0.50
26:BA:2816:C:O3'	38:BR:99:LYS:NZ	2.40	0.50
26:BA:2869:G:H2'	26:BA:2870:C:O4'	2.11	0.50
31:BG:143:GLU:O	51:B4:28:LYS:NZ	2.32	0.50
1:CA:1007:C:H2'	1:CA:1008:C:H6	1.75	0.50
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.46	0.50
26:DA:272(A):U:H5	26:DA:272(C):G:OP1	1.95	0.50
26:DA:571:A:H5'	26:DA:2030:A:N7	2.27	0.50
26:DA:2046:G:H5'	52:D5:19:ARG:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:27:C:H5”	39:DS:54:LEU:HD21	1.94	0.50
1:AA:551:U:H2’	1:AA:552:U:C6	2.47	0.50
1:AA:752:G:H4’	15:AO:69:TYR:OH	2.12	0.50
1:AA:1034:G:H3’	1:AA:1035:A:C8	2.46	0.50
26:BA:652(C):G:H1	26:BA:652(V):C:H42	1.59	0.50
26:BA:907:U:HO2’	37:BQ:101:ARG:HH22	1.58	0.50
26:BA:2893:G:H4’	26:BA:2894:G:O5’	2.11	0.50
51:B4:46:GLN:O	51:B4:48:ARG:N	2.44	0.50
53:B6:9:LEU:HD13	53:B6:51:GLU:HG3	1.92	0.50
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.30	0.50
1:CA:429:U:O3’	4:CD:22:LYS:NZ	2.45	0.50
1:CA:473:G:H2’	1:CA:474:G:H8	1.76	0.50
1:CA:1119:C:H2’	1:CA:1120:G:C8	2.46	0.50
1:CA:1154:G:N7	1:CA:1155:G:C8	2.80	0.50
4:CD:155:LEU:O	4:CD:159:ARG:HG3	2.11	0.50
8:CH:103:VAL:HG21	8:CH:109:ILE:C	2.35	0.50
25:CY:59:U:H3’	25:CY:60:U:O2	2.12	0.50
26:DA:271(R):G:H5”	48:D1:97:LEU:HD21	1.93	0.50
26:DA:361:G:O2’	26:DA:362:U:H5’	2.12	0.50
26:DA:866:A:H2	26:DA:867:C:C4	2.29	0.50
26:DA:873:G:N2	26:DA:905:U:C2	2.80	0.50
41:DU:61:TRP:CH2	41:DU:93:LYS:HB2	2.47	0.50
50:D3:18:ASP:OD1	50:D3:18:ASP:N	2.44	0.50
1:AA:186:C:H2’	1:AA:187:C:C6	2.47	0.50
1:AA:1346:A:N1	1:AA:1374:A:H5”	2.26	0.50
4:AD:65:ARG:HG2	4:AD:75:PHE:CD1	2.47	0.50
20:AT:45:GLN:HA	20:AT:91:LEU:HB3	1.94	0.50
26:BA:566:U:H5”	36:BP:29:LYS:HE3	1.93	0.50
26:BA:1113:U:H2’	26:BA:1114:G:H8	1.75	0.50
26:BA:1177:A:O2’	26:BA:1178:C:O4’	2.24	0.50
26:BA:2238:G:H2’	26:BA:2238:G:N3	2.25	0.50
45:BY:16:ALA:HB2	45:BY:73:ARG:HD3	1.94	0.50
1:CA:344:A:H5”	1:CA:345:C:C5	2.43	0.50
1:CA:376:G:H5”	16:CP:5:ARG:HB2	1.93	0.50
1:CA:1033:G:H2’	1:CA:1034:G:H5’	1.93	0.50
1:CA:1119:C:OP2	9:CI:9:ARG:NH1	2.35	0.50
1:CA:1492:A:H2’	1:CA:1493:A:C8	2.46	0.50
3:CC:22:TRP:HB3	3:CC:59:ARG:HB2	1.93	0.50
25:CY:1:G:H1	25:CY:72:C:H42	1.60	0.50
25:CY:26:A:N1	25:CY:44:G:C6	2.80	0.50
26:DA:289:A:H62	26:DA:351:G:H21	1.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1166:C:H1'	26:DA:1184:G:N2	2.27	0.50
26:DA:2252:G:H2'	26:DA:2253:G:C8	2.47	0.50
26:DA:2364:C:H2'	26:DA:2365:G:O4'	2.12	0.50
26:DA:2528:U:O2'	26:DA:2529:G:H3'	2.12	0.50
29:DE:174:ASP:OD1	29:DE:175:VAL:N	2.44	0.50
32:DH:73:ALA:O	32:DH:76:VAL:HG12	2.11	0.50
35:DO:78:ARG:HG2	40:DT:73:GLU:HB2	1.93	0.50
7:AG:78:ARG:NH2	7:AG:154:TYR:O	2.43	0.50
25:AY:25:C:C2	25:AY:26:A:C8	3.00	0.50
25:AY:44:G:H8	25:AY:44:G:OP2	1.95	0.50
26:BA:2150:U:C2'	26:BA:2151:G:H5'	2.41	0.50
26:BA:2564:A:C2	26:BA:2647:U:H4'	2.46	0.50
1:CA:1342:C:H2'	1:CA:1343:G:C8	2.46	0.50
6:CF:15:ASP:OD1	6:CF:18:GLN:N	2.24	0.50
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.39	0.50
13:CM:57:ARG:NH1	51:D4:34:GLU:HA	2.27	0.50
23:CW:61:C:O2'	23:CW:62:C:H6	1.95	0.50
26:DA:601:C:O2	26:DA:605:C:H4'	2.11	0.50
26:DA:1379:A:H4'	26:DA:1380:G:OP2	2.11	0.50
27:DB:66:A:H61	27:DB:108:U:H3'	1.76	0.50
31:DG:144:ILE:HG23	31:DG:148:MET:HE1	1.93	0.50
26:BA:222:A:H3'	26:BA:421:U:H5'	1.94	0.50
26:BA:662:G:H5"	36:BP:16:ARG:HG2	1.94	0.50
26:BA:857:C:N4	26:BA:858:U:O4	2.45	0.50
34:BN:73:THR:OG1	34:BN:82:LEU:HD11	2.11	0.50
38:BR:21:TYR:OH	38:BR:43:GLU:HG2	2.11	0.50
1:CA:109:A:C6	1:CA:326:G:C6	3.00	0.50
2:CB:134:GLU:O	2:CB:138:LEU:HG	2.11	0.50
4:CD:38:TYR:CZ	4:CD:45:GLN:HG3	2.47	0.50
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.94	0.50
10:CJ:27:ALA:HA	10:CJ:81:THR:CG2	2.41	0.50
12:CL:71:PRO:O	12:CL:102:ARG:HD2	2.12	0.50
26:DA:304:G:O6	61:DA:4181:HOH:O	2.18	0.50
26:DA:570:G:H5"	61:DA:3844:HOH:O	2.11	0.50
26:DA:1038:C:N3	26:DA:1117:G:N2	2.50	0.50
26:DA:2001:A:H2'	26:DA:2002:G:C8	2.46	0.50
33:DI:14:ASP:N	33:DI:17:GLN:OE1	2.44	0.50
37:DQ:38:GLU:HG3	37:DQ:127:ILE:HB	1.94	0.50
1:AA:977:A:H1'	1:AA:982:U:O4	2.12	0.50
1:AA:1064:G:N2	1:AA:1191:A:OP2	2.41	0.50
2:AB:185:ILE:HG23	2:AB:199:TYR:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:67:MET:HE1	6:AF:75:LEU:HD12	1.94	0.50
26:BA:84:A:H5"	45:BY:8:LYS:HG3	1.93	0.50
26:BA:271(H):G:HO2'	26:BA:271(I):G:H8	1.60	0.50
26:BA:2689:U:H4'	26:BA:2690:C:H5'	1.93	0.50
1:CA:67:C:O2'	1:CA:171:A:N3	2.37	0.50
1:CA:457:C:H2'	1:CA:458:C:C6	2.46	0.50
1:CA:1035:A:H2'	1:CA:1036:G:C8	2.46	0.50
1:CA:1049:U:C6	1:CA:1201:A:H5'	2.47	0.50
1:CA:1137:C:H5"	1:CA:1138:G:OP1	2.12	0.50
24:CX:8:4SU:O2'	24:CX:21:A:N1	2.28	0.50
25:CY:34:G:C6	25:CY:35:A:C6	3.00	0.50
26:DA:2240:C:OP2	61:DA:3953:HOH:O	2.19	0.50
29:DE:89:ASP:OD1	29:DE:89:ASP:N	2.43	0.50
30:DF:137:LYS:HA	30:DF:140:LEU:HD23	1.93	0.50
31:DG:125:PHE:CZ	31:DG:170:ARG:HA	2.47	0.50
39:DS:50:SER:O	39:DS:76:LYS:NZ	2.45	0.50
1:AA:250:A:H4'	1:AA:251:G:O5'	2.10	0.50
1:AA:1002:G:C4	1:AA:1003:G:H1'	2.47	0.50
2:AB:30:ARG:HH21	2:AB:194:PRO:HB2	1.76	0.50
26:BA:2612:C:OP2	52:B5:2:ALA:N	2.45	0.50
26:BA:2846:G:H2'	26:BA:2847:U:O4'	2.11	0.50
27:BB:87:G:N2	27:BB:90:A:OP2	2.30	0.50
41:BU:58:ARG:HA	41:BU:61:TRP:CE3	2.46	0.50
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.26	0.50
1:CA:1342:C:O2'	9:CI:124:GLN:HG2	2.12	0.50
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.12	0.50
5:CE:137:GLU:HA	5:CE:140:ARG:HB3	1.94	0.50
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.92	0.50
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.94	0.50
23:CW:66:U:H2'	23:CW:67:C:O4'	2.12	0.50
26:DA:686:G:H21	26:DA:788:A:H61	1.58	0.50
26:DA:1184:G:H5'	50:D3:29:ARG:HH11	1.77	0.50
26:DA:2305:A:H5"	31:DG:134:GLY:HA3	1.94	0.50
26:DA:2750:A:H8	26:DA:2750:A:OP1	1.95	0.50
28:DD:17:THR:O	28:DD:211:ARG:NH2	2.43	0.50
30:DF:110:LEU:HD12	30:DF:202:PHE:CE1	2.47	0.50
31:DG:37:VAL:O	31:DG:94:LEU:N	2.41	0.50
35:DO:24:VAL:HB	35:DO:33:ALA:HB2	1.92	0.50
1:AA:79:G:N1	1:AA:90:U:C2	2.80	0.49
1:AA:92:C:H2'	1:AA:93:G:C8	2.47	0.49
1:AA:1027:C:C4	1:AA:1034:G:O6	2.64	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:47:LEU:HD13	3:AC:68:VAL:HG11	1.94	0.49
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.75	0.49
17:AQ:28:PRO:HA	17:AQ:35:VAL:HA	1.94	0.49
26:BA:271(V):G:O6	61:BA:4929:HOH:O	2.19	0.49
26:BA:614(A):U:H5"	61:BA:5227:HOH:O	2.12	0.49
26:BA:1274:A:N3	26:BA:1297:C:H1'	2.27	0.49
26:BA:1507:A:O2'	26:BA:1508:A:O5'	2.26	0.49
26:BA:2646:C:H2'	26:BA:2647:U:O4'	2.12	0.49
26:BA:2691:C:O3'	26:BA:2871:C:H4'	2.12	0.49
36:BP:82:GLY:HA2	36:BP:113:LYS:O	2.11	0.49
51:B4:59:PHE:CA	51:B4:61:ARG:H	2.24	0.49
1:CA:54:C:H2'	1:CA:352:C:H41	1.77	0.49
1:CA:404:U:H5'	4:CD:122:ARG:HD3	1.94	0.49
1:CA:1016:A:C5	1:CA:1017:G:H1'	2.47	0.49
1:CA:1128:C:H4'	1:CA:1148:U:O2	2.12	0.49
1:CA:1316:G:O2'	1:CA:1318:A:N7	2.37	0.49
25:CY:4:C:H2'	25:CY:5:G:H5'	1.92	0.49
26:DA:1357:U:H2'	26:DA:1358:G:O4'	2.12	0.49
26:DA:2025:C:N4	61:DA:4191:HOH:O	2.45	0.49
27:DB:44:G:OP1	31:DG:98:ARG:NH2	2.45	0.49
27:DB:98:G:H2'	27:DB:99:G:O4'	2.12	0.49
34:DN:4:TYR:CD2	41:DU:100:VAL:HG11	2.47	0.49
1:AA:1007:C:O2	1:AA:1022:G:N1	2.31	0.49
1:AA:1366:C:O2'	10:AJ:60:ARG:NH2	2.44	0.49
4:AD:53:ASP:O	4:AD:57:ARG:HG3	2.12	0.49
5:AE:18:ARG:HE	5:AE:27:ARG:HH21	1.60	0.49
26:BA:247:G:H4'	26:BA:386:G:C5	2.47	0.49
26:BA:1866:C:H2'	26:BA:1876:A:O4'	2.12	0.49
26:BA:2187:G:O2'	26:BA:2188:C:OP1	2.20	0.49
50:B3:18:ASP:OD1	50:B3:18:ASP:N	2.40	0.49
1:CA:65:U:C6	1:CA:65:U:H5'	2.47	0.49
1:CA:195:A:OP1	20:CT:68:LYS:NZ	2.44	0.49
1:CA:441:A:H3'	1:CA:442:C:C6	2.48	0.49
1:CA:716:A:N3	11:CK:118:GLY:HA2	2.27	0.49
1:CA:954:G:H21	1:CA:1227:A:N6	2.10	0.49
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.94	0.49
1:CA:992:U:H5"	1:CA:992:U:C6	2.41	0.49
1:CA:1028:C:C2	1:CA:1033:G:C6	3.00	0.49
1:CA:1152:A:H2'	1:CA:1153:C:C6	2.46	0.49
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.26	0.49
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1452:C:O5'	1:CA:1452:C:H6	1.95	0.49
13:CM:3:ARG:HB2	51:D4:34:GLU:HG2	1.94	0.49
26:DA:141:A:C8	26:DA:1408:C:O2'	2.64	0.49
26:DA:443:A:H5"	26:DA:444:C:OP1	2.13	0.49
26:DA:900:A:O2'	26:DA:901:A:OP1	2.29	0.49
26:DA:2153:G:H3'	26:DA:2154:G:H8	1.77	0.49
30:DF:178:PRO:HB2	30:DF:201:VAL:HG21	1.94	0.49
32:DH:69:ARG:HG3	32:DH:70:THR:N	2.27	0.49
34:DN:30:ILE:HG23	34:DN:52:VAL:HG11	1.94	0.49
1:AA:279:A:C4	17:AQ:98:LEU:HD23	2.47	0.49
1:AA:576:G:O6	1:AA:880:C:O2'	2.29	0.49
2:AB:112:VAL:O	2:AB:116:GLU:HG3	2.11	0.49
26:BA:645:C:H5'	26:BA:646:A:OP2	2.12	0.49
29:BE:52:LEU:HD12	29:BE:77:ILE:HD11	1.94	0.49
31:BG:139:LEU:HD12	31:BG:139:LEU:H	1.75	0.49
33:BI:6:LEU:HD11	33:BI:37:VAL:HG23	1.93	0.49
51:B4:53:GLU:HG2	51:B4:56:VAL:HG22	1.94	0.49
1:CA:1249:C:O2'	9:CI:73:GLN:NE2	2.44	0.49
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.47	0.49
1:CA:1324:A:H4'	1:CA:1362:C:O3'	2.12	0.49
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.47	0.49
3:CC:6:HIS:ND1	14:CN:49:HIS:HB3	2.27	0.49
13:CM:19:LEU:HD21	13:CM:56:LEU:HD11	1.94	0.49
25:CY:61:C:H2'	25:CY:62:C:C6	2.48	0.49
26:DA:1991:U:H2'	26:DA:1992:G:H5"	1.93	0.49
26:DA:2557:G:H2'	26:DA:2558:C:C6	2.47	0.49
28:DD:108:PRO:HB3	28:DD:143:HIS:CE1	2.47	0.49
35:DO:64:ARG:NH1	35:DO:81:ASP:OD1	2.45	0.49
1:AA:131:C:O2'	1:AA:262:A:N3	2.41	0.49
26:BA:272:G:N7	26:BA:421:U:H2'	2.27	0.49
46:BZ:45:ASP:OD2	46:BZ:49:ARG:NH1	2.45	0.49
1:CA:254:G:OP1	17:CQ:66:SER:OG	2.23	0.49
1:CA:814:A:H2'	1:CA:816:A:H5"	1.94	0.49
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.42	0.49
5:CE:6:PHE:HB3	5:CE:35:GLY:C	2.37	0.49
13:CM:60:VAL:HA	13:CM:63:THR:OG1	2.11	0.49
23:CW:70:G:H2'	23:CW:71:G:H8	1.76	0.49
26:DA:624:C:OP1	61:DA:3854:HOH:O	2.20	0.49
26:DA:1264:G:H2'	26:DA:2014:A:N6	2.28	0.49
26:DA:1296:G:OP1	26:DA:2709:G:O2'	2.28	0.49
26:DA:1509(B):A:H2'	26:DA:1510:G:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2135:A:H2'	26:DA:2136:C:C5	2.47	0.49
26:DA:2314:C:H2'	26:DA:2315:G:C8	2.47	0.49
28:DD:182:LEU:HB2	28:DD:272:ALA:HB3	1.95	0.49
29:DE:73:GLU:N	29:DE:73:GLU:OE2	2.41	0.49
30:DF:29:ASN:O	30:DF:112:MET:HE1	2.12	0.49
39:DS:58:LEU:HD21	39:DS:65:VAL:HG13	1.94	0.49
44:DX:31:HIS:HD2	44:DX:33:LYS:H	1.59	0.49
46:DZ:108:PRO:HB2	46:DZ:111:VAL:HG23	1.94	0.49
55:D8:15:LYS:HG2	55:D8:16:ILE:N	2.26	0.49
1:AA:335:C:O2'	1:AA:1433:A:N3	2.41	0.49
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.43	0.49
26:BA:443:A:H1'	26:BA:1201:C:O4'	2.12	0.49
26:BA:625:G:O6	36:BP:107:LYS:NZ	2.46	0.49
26:BA:1044:G:H5'	26:BA:1045:A:OP2	2.12	0.49
26:BA:1713:U:H2'	26:BA:1714:G:H8	1.77	0.49
26:BA:2533:A:H2'	26:BA:2534:A:O4'	2.13	0.49
33:BI:66:GLU:HA	33:BI:69:LYS:HB3	1.93	0.49
34:BN:4:TYR:HB2	41:BU:101:ARG:NH1	2.28	0.49
36:BP:121:LYS:HB3	36:BP:123:LEU:HG	1.95	0.49
36:BP:138:LEU:HD23	36:BP:145:PRO:HB3	1.94	0.49
46:BZ:152:ALA:HA	46:BZ:155:LEU:HD22	1.93	0.49
3:CC:110:ASN:O	3:CC:141:VAL:HG22	2.12	0.49
3:CC:157:ILE:HD12	3:CC:164:ARG:HB3	1.94	0.49
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.48	0.49
10:CJ:51:ARG:O	14:CN:45:ARG:NH1	2.45	0.49
13:CM:34:LEU:HD13	13:CM:41:PRO:HB3	1.94	0.49
15:CO:8:LYS:O	15:CO:12:ILE:HG13	2.12	0.49
23:CW:68:C:H2'	23:CW:69:G:H8	1.76	0.49
25:CY:74:C:H4'	48:D1:23:LYS:HE3	1.93	0.49
26:DA:335:C:H4'	45:DY:73:ARG:NE	2.27	0.49
26:DA:2343:C:O2'	26:DA:2373:G:O2'	2.22	0.49
26:DA:2602:A:H4'	26:DA:2603:G:O5'	2.12	0.49
27:DB:45:A:H2'	27:DB:46:A:C8	2.47	0.49
30:DF:64:ILE:HG21	30:DF:78:ILE:HG23	1.95	0.49
1:AA:110:C:O2'	16:AP:25:ARG:O	2.26	0.49
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.47	0.49
5:AE:144:THR:OG1	5:AE:147:ASP:OD1	2.25	0.49
8:AH:64:LYS:HG2	8:AH:79:VAL:HG21	1.94	0.49
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.48	0.49
23:AW:69:G:H2'	23:AW:69:G:N3	2.28	0.49
24:AX:7:G:O2'	24:AX:49:G:H5'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:657:U:H2'	26:BA:658:C:H6	1.77	0.49
41:BU:29:SER:OG	41:BU:30:LYS:NZ	2.40	0.49
1:CA:585:G:OP1	17:CQ:37:LYS:NZ	2.45	0.49
1:CA:978:A:O2'	1:CA:1322:C:N3	2.43	0.49
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.27	0.49
2:CB:105:PHE:HE1	2:CB:155:LEU:HD12	1.78	0.49
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.12	0.49
5:CE:80:ILE:HD11	8:CH:104:ARG:HH21	1.77	0.49
25:CY:19:G:C2	25:CY:57:G:C6	3.01	0.49
26:DA:692:C:O2'	28:DD:38:LYS:NZ	2.44	0.49
26:DA:1514:U:H2'	26:DA:1515:G:C8	2.48	0.49
26:DA:2164:C:H5	26:DA:2165:G:N3	2.11	0.49
44:DX:52:VAL:HG12	44:DX:82:GLN:O	2.13	0.49
1:AA:256:U:H2'	1:AA:257:G:H8	1.77	0.49
1:AA:266:G:O3'	17:AQ:67:LYS:HB2	2.13	0.49
1:AA:1014:A:H4'	19:AS:14:HIS:CE1	2.46	0.49
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.43	0.49
2:AB:42:ILE:HD12	2:AB:203:GLY:HA2	1.93	0.49
3:AC:181:ASN:HD21	3:AC:204:LEU:HD12	1.77	0.49
16:AP:22:THR:HA	16:AP:33:ILE:HG12	1.93	0.49
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.45	0.49
25:AY:50:U:H2'	25:AY:51:U:C6	2.46	0.49
26:BA:400:G:N7	61:BA:4974:HOH:O	2.34	0.49
26:BA:579:G:H2'	26:BA:580:C:C6	2.48	0.49
26:BA:1045:A:OP1	26:BA:1045:A:H4'	2.12	0.49
26:BA:2439:A:H5'	26:BA:2439:A:C8	2.48	0.49
45:BY:28:LYS:HD2	45:BY:40:GLU:HG3	1.94	0.49
48:B1:86:SER:HG	48:B1:89:GLU:CD	2.17	0.49
1:CA:343:U:H2'	1:CA:345:C:C5	2.47	0.49
1:CA:1324:A:O4'	1:CA:1362:C:H4'	2.13	0.49
2:CB:140:HIS:O	2:CB:143:GLU:HB2	2.12	0.49
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.11	0.49
26:DA:854:G:H2'	26:DA:855:G:H8	1.77	0.49
26:DA:1508:A:H4'	26:DA:1509(A):A:C5	2.47	0.49
26:DA:2528:U:H5"	56:D9:31:LYS:HE2	1.94	0.49
26:DA:2602:A:H4'	26:DA:2603:G:C5'	2.42	0.49
33:DI:130:TYR:HB3	33:DI:138:ILE:HB	1.94	0.49
37:DQ:85:LYS:HG2	47:D0:7:LEU:HB3	1.94	0.49
39:DS:31:SER:OG	39:DS:32:LEU:N	2.46	0.49
40:DT:24:PRO:HA	40:DT:49:VAL:HG23	1.95	0.49
1:AA:346:G:C4	1:AA:347:G:H1'	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:115:LEU:HD13	2:AB:145:LEU:HB3	1.93	0.49
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.77	0.49
8:AH:6:ILE:HD11	8:AH:31:PHE:HD2	1.78	0.49
33:BI:109:ILE:HG23	33:BI:130:TYR:CZ	2.48	0.49
44:BX:5:TYR:CZ	49:B2:30:ARG:HB2	2.48	0.49
53:B6:6:ARG:HH12	53:B6:26:ASN:HB2	1.78	0.49
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.30	0.49
1:CA:834:C:H2'	1:CA:835:U:C6	2.47	0.49
1:CA:1003:G:N2	1:CA:1025:U:O4	2.46	0.49
1:CA:1151:A:H5'	10:CJ:41:PRO:HA	1.95	0.49
20:CT:56:MET:HE1	20:CT:85:MET:HG2	1.93	0.49
26:DA:242:G:N2	26:DA:255:A:OP2	2.38	0.49
30:DF:183:VAL:O	30:DF:187:VAL:HG23	2.13	0.49
42:DV:25:LEU:H	42:DV:92:THR:HG1	1.60	0.49
1:AA:628:G:H2'	1:AA:629:G:C8	2.48	0.49
1:AA:1137:C:H5"	1:AA:1138:G:OP1	2.13	0.49
13:AM:65:LYS:NZ	51:B4:53:GLU:OE1	2.45	0.49
19:AS:27:GLU:CB	19:AS:28:LYS:HA	2.38	0.49
26:BA:700:G:O2'	26:BA:1632:A:N3	2.43	0.49
31:BG:170:ARG:HD3	31:BG:174:GLU:HG3	1.94	0.49
32:BH:154:PRO:HB3	32:BH:163:TYR:CE2	2.48	0.49
32:BH:154:PRO:HD3	32:BH:162:ILE:O	2.12	0.49
1:CA:250:A:H4'	1:CA:251:G:O5'	2.12	0.49
1:CA:392:G:H2'	1:CA:393:A:C8	2.48	0.49
1:CA:429:U:H1'	1:CA:430:A:H5"	1.95	0.49
1:CA:576:G:O6	1:CA:880:C:O2'	2.26	0.49
1:CA:589:C:N3	1:CA:650:G:N1	2.41	0.49
1:CA:976:G:C8	1:CA:1362:C:N4	2.80	0.49
1:CA:1010:G:N2	1:CA:1020:U:O2	2.46	0.49
25:CY:35:A:N6	25:CY:36:A:N1	2.61	0.49
26:DA:465:G:OP1	54:D7:12:ARG:NH2	2.41	0.49
26:DA:1300:U:H4'	26:DA:1301:A:H5'	1.94	0.49
26:DA:1313:U:H4'	26:DA:1332:G:H4'	1.95	0.49
26:DA:1652:A:OP1	38:DR:8:ARG:NH1	2.46	0.49
26:DA:1657:C:H2'	26:DA:1658:C:C6	2.48	0.49
42:DV:24:LYS:HG2	42:DV:64:HIS:CD2	2.35	0.49
1:AA:111:G:H5"	16:AP:27:LYS:HG2	1.93	0.49
1:AA:262:A:C6	1:AA:263:A:C6	3.00	0.49
1:AA:736:C:H2'	1:AA:737:A:C8	2.48	0.49
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.48	0.49
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.48	0.49
9:AI:93:ARG:HH11	9:AI:93:ARG:HB2	1.78	0.49
19:AS:38:SER:HB2	19:AS:71:LEU:HD13	1.95	0.49
24:AX:7:G:H1	24:AX:66:C:H42	1.61	0.49
26:BA:576:U:H2'	26:BA:577:G:C8	2.47	0.49
26:BA:2022:U:O2'	26:BA:2617:C:H5'	2.13	0.49
26:BA:2124:G:H1	26:BA:2174:C:N4	2.11	0.49
32:BH:11:VAL:HG21	32:BH:50:VAL:HG23	1.94	0.49
39:BS:65:VAL:O	39:BS:69:VAL:HG13	2.13	0.49
51:B4:24:THR:OG1	51:B4:25:TYR:N	2.45	0.49
1:CA:434:U:H2'	1:CA:435:C:C6	2.48	0.49
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.77	0.49
5:CE:12:LEU:O	5:CE:30:ALA:HA	2.13	0.49
9:CI:17:VAL:HG11	9:CI:80:GLY:C	2.37	0.49
20:CT:56:MET:HE2	20:CT:56:MET:HB2	1.70	0.49
23:CW:21:A:N6	23:CW:46:7MG:N3	2.61	0.49
26:DA:724:U:H2'	26:DA:725:G:O4'	2.13	0.49
26:DA:1339:G:N2	26:DA:1603:A:H1'	2.27	0.49
26:DA:1952:A:OP1	35:DO:42:SER:OG	2.29	0.49
27:DB:20:C:H2'	27:DB:21:G:H5'	1.93	0.49
27:DB:118:G:H2'	27:DB:119:G:H5'	1.95	0.49
30:DF:154:VAL:HG22	30:DF:191:ARG:HB2	1.94	0.49
36:DP:84:ASN:OD1	36:DP:117:GLU:HB2	2.13	0.49
1:AA:1027:C:C2	1:AA:1034:G:C2	3.01	0.48
1:AA:1131:G:H8	1:AA:1131:G:O5'	1.96	0.48
3:AC:81:GLY:O	3:AC:85:ARG:HG3	2.13	0.48
13:AM:80:ARG:NH2	19:AS:69:HIS:HE1	2.11	0.48
23:AW:1:G:C6	23:AW:72:C:N3	2.79	0.48
26:BA:578:A:OP2	61:BA:4085:HOH:O	2.20	0.48
26:BA:1021:A:H3'	26:BA:1021:A:C8	2.47	0.48
26:BA:1588:C:H2'	26:BA:1589:C:H6	1.78	0.48
26:BA:2763:G:OP2	61:BA:4693:HOH:O	2.20	0.48
32:BH:86:GLU:OE2	32:BH:130:ARG:NH1	2.46	0.48
34:BN:67:LEU:O	34:BN:88:GLU:HG3	2.13	0.48
36:BP:121:LYS:O	36:BP:123:LEU:N	2.42	0.48
42:BV:21:ARG:HG2	42:BV:91:TYR:CD1	2.48	0.48
49:B2:31:GLU:HB3	49:B2:53:LEU:HD11	1.94	0.48
1:CA:976:G:C8	1:CA:1358:U:C2	3.01	0.48
15:CO:25:THR:HG21	15:CO:70:LEU:HB2	1.94	0.48
15:CO:26:GLU:N	15:CO:26:GLU:OE2	2.43	0.48
26:DA:196:A:H2'	26:DA:196:A:N3	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:539:G:H2'	26:DA:540:C:H6	1.78	0.48
26:DA:918:A:N3	27:DB:80:U:O2'	2.45	0.48
26:DA:2693:A:H2'	26:DA:2694:G:H8	1.78	0.48
29:DE:9:VAL:HG13	29:DE:25:VAL:O	2.13	0.48
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.13	0.48
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.13	0.48
9:AI:77:ILE:O	9:AI:81:ILE:HG23	2.13	0.48
26:BA:1164:G:H2'	26:BA:1165:U:C6	2.49	0.48
26:BA:1587:A:H2'	26:BA:1588:C:C6	2.49	0.48
26:BA:2141:G:C2	26:BA:2142:C:C2	3.02	0.48
26:BA:2286:A:H4'	26:BA:2287:A:O4'	2.13	0.48
30:BF:64:ILE:HD11	30:BF:75:HIS:HB2	1.94	0.48
33:BI:43:ASN:HD22	33:BI:43:ASN:C	2.20	0.48
1:CA:834:C:H2'	1:CA:835:U:H6	1.78	0.48
1:CA:936:C:H2'	1:CA:937:A:O4'	2.13	0.48
1:CA:938:A:C6	1:CA:939:G:C5	3.01	0.48
2:CB:210:SER:OG	2:CB:211:ILE:N	2.46	0.48
4:CD:175:SER:OG	4:CD:184:LYS:HB2	2.12	0.48
14:CN:29:ARG:HD3	14:CN:40:CYS:HB2	1.94	0.48
23:CW:8:4SU:H1'	23:CW:48:C:H1'	1.95	0.48
26:DA:191:A:H2'	26:DA:192:C:C6	2.48	0.48
26:DA:607:U:OP1	30:DF:102:PRO:HA	2.13	0.48
26:DA:1434:A:H61	26:DA:1558:A:N6	2.11	0.48
26:DA:2552:U:H2'	26:DA:2554:U:H5"	1.96	0.48
36:DP:39:LYS:CB	36:DP:45:LEU:HG	2.43	0.48
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.35	0.48
17:AQ:58:GLU:O	17:AQ:74:LEU:N	2.41	0.48
26:BA:762:U:H5"	61:BA:4793:HOH:O	2.13	0.48
26:BA:1019:U:O2'	26:BA:1021:A:H2	1.96	0.48
26:BA:1379:A:H4'	26:BA:1380:G:OP2	2.13	0.48
35:BO:24:VAL:HB	35:BO:33:ALA:HB2	1.95	0.48
45:BY:6:HIS:H	45:BY:6:HIS:CD2	2.30	0.48
54:B7:46:VAL:HG13	54:B7:48:LYS:HE3	1.95	0.48
56:B9:2:LYS:HE2	56:B9:31:LYS:O	2.12	0.48
1:CA:979:C:H2'	1:CA:980:C:H5'	1.95	0.48
1:CA:1053:G:O5'	1:CA:1054:C:H5'	2.13	0.48
1:CA:1060:C:C5	3:CC:2:GLY:HA3	2.49	0.48
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.48	0.48
1:CA:1181:G:O2'	1:CA:1182:G:N7	2.38	0.48
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.81	0.48
2:CB:27:LYS:HG3	2:CB:194:PRO:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CG:20:ASP:OD2	7:CG:23:VAL:HG23	2.14	0.48
7:CG:76:ARG:HB3	7:CG:156:TRP:HH2	1.78	0.48
8:CH:134:ILE:HG22	8:CH:135:CYS:SG	2.54	0.48
26:DA:223:A:O2'	26:DA:420:C:O2	2.31	0.48
26:DA:277:C:O2'	26:DA:278:A:OP1	2.30	0.48
26:DA:531:C:H4'	26:DA:532:A:H5"	1.95	0.48
26:DA:858:U:OP1	47:D0:44:ARG:NH2	2.44	0.48
26:DA:1218:C:H42	26:DA:1231:G:H1	1.61	0.48
26:DA:1550:C:OP1	26:DA:1720:U:O2'	2.17	0.48
26:DA:1769:G:O2'	26:DA:1958:C:OP1	2.27	0.48
26:DA:2183:C:H2'	26:DA:2184:G:C8	2.46	0.48
35:DO:98:VAL:HG22	35:DO:118:ALA:HA	1.95	0.48
54:D7:9:ARG:HE	54:D7:47:ARG:HB2	1.78	0.48
1:AA:963:G:H5'	61:AA:4173:HOH:O	2.12	0.48
1:AA:1243:C:H2'	1:AA:1244:C:C6	2.48	0.48
1:AA:1525:G:OP1	11:AK:120:ARG:NH2	2.46	0.48
3:AC:181:ASN:HD22	3:AC:204:LEU:HB2	1.78	0.48
19:AS:19:VAL:O	19:AS:23:ASN:ND2	2.47	0.48
26:BA:234:C:H2'	26:BA:235:U:H6	1.79	0.48
26:BA:1714:G:H1	26:BA:1745(A):C:N4	2.11	0.48
26:BA:2693:A:H2'	26:BA:2694:G:H8	1.77	0.48
27:BB:22:U:H2'	27:BB:23:G:C8	2.49	0.48
48:B1:85:LEU:HB3	48:B1:89:GLU:CG	2.43	0.48
1:CA:17:U:H2'	1:CA:18:C:C6	2.49	0.48
1:CA:73:G:C6	1:CA:97:G:C6	3.01	0.48
1:CA:736:C:H2'	1:CA:737:A:C8	2.48	0.48
1:CA:988:G:H1	1:CA:1217:C:H42	1.60	0.48
1:CA:1126:U:O4	10:CJ:71:LEU:HD13	2.14	0.48
1:CA:1376:U:OP1	7:CG:98:SER:OG	2.29	0.48
1:CA:1399:C:C2	1:CA:1502:A:N6	2.81	0.48
5:CE:24:ARG:NH1	22:CV:24:A:OP2	2.46	0.48
9:CI:89:ASN:C	9:CI:89:ASN:HD22	2.22	0.48
17:CQ:40:LYS:HD2	17:CQ:42:TYR:CZ	2.49	0.48
23:CW:22:G:H2'	23:CW:23:A:C8	2.48	0.48
26:DA:250:G:C6	26:DA:251:A:C6	3.01	0.48
26:DA:894:C:H2'	26:DA:895:U:C6	2.48	0.48
26:DA:2348:U:O4	26:DA:2382:G:N1	2.47	0.48
27:DB:43:C:OP1	51:D4:6:HIS:NE2	2.42	0.48
46:DZ:103:ARG:O	46:DZ:139:VAL:N	2.45	0.48
3:AC:13:GLY:HA3	14:AN:57:ARG:NH2	2.27	0.48
10:AJ:5:ARG:HD3	10:AJ:71:LEU:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	1.95	0.48
24:AX:67:C:H2'	24:AX:68:C:H5'	1.94	0.48
26:BA:900:A:H2'	26:BA:901:A:C8	2.49	0.48
26:BA:2127:G:C6	26:BA:2128:C:C4	3.01	0.48
1:CA:203:U:H2'	1:CA:203:U:OP2	2.13	0.48
1:CA:692:U:O2'	1:CA:694:A:N7	2.34	0.48
1:CA:1030:C:N3	1:CA:1031:G:N2	2.54	0.48
10:CJ:55:LYS:O	10:CJ:57:LYS:N	2.46	0.48
12:CL:67:THR:OG1	12:CL:95:GLY:O	2.31	0.48
26:DA:455:C:N3	26:DA:472:A:H2'	2.28	0.48
26:DA:539:G:H2'	26:DA:540:C:C6	2.48	0.48
26:DA:2839:G:H5'	38:DR:46:GLY:CA	2.37	0.48
36:DP:50:ARG:HD3	55:D8:7:HIS:CD2	2.49	0.48
39:DS:11:LYS:O	39:DS:15:ARG:HG3	2.13	0.48
40:DT:109:GLU:O	40:DT:113:LYS:HB2	2.13	0.48
44:DX:12:VAL:HG22	44:DX:29:TRP:CE2	2.48	0.48
51:D4:46:GLN:C	51:D4:48:ARG:H	2.21	0.48
1:AA:36:C:OP1	12:AL:123:LYS:NZ	2.24	0.48
1:AA:584:G:H5'	17:AQ:91:ARG:HH22	1.78	0.48
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.96	0.48
4:AD:3:ARG:O	4:AD:5:ILE:HG22	2.12	0.48
4:AD:107:ARG:HH22	4:AD:194:LEU:HD11	1.78	0.48
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.46	0.48
7:AG:73:MET:HG3	7:AG:89:MET:O	2.14	0.48
8:AH:96:GLY:N	8:AH:99:GLU:OE2	2.33	0.48
25:AY:35:A:H8	25:AY:35:A:H5"	1.78	0.48
26:BA:744:G:OP1	29:BE:132:HIS:ND1	2.37	0.48
26:BA:1204:A:N6	26:BA:1240:U:H2'	2.28	0.48
26:BA:1798:U:OP2	28:BD:274:ARG:NH2	2.43	0.48
26:BA:1825:A:OP1	28:BD:249:PRO:HD3	2.14	0.48
26:BA:2165:G:H1	26:BA:2172:U:H5	1.61	0.48
26:BA:2836:U:H2'	26:BA:2837:G:C8	2.49	0.48
41:BU:49:HIS:HA	41:BU:52:ARG:HB3	1.94	0.48
1:CA:1030:C:N4	1:CA:1031:G:N1	2.58	0.48
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.49	0.48
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.94	0.48
13:CM:86:CYS:SG	13:CM:87:TYR:N	2.86	0.48
13:CM:108:ARG:HA	13:CM:108:ARG:HD3	1.74	0.48
26:DA:8:A:H2'	26:DA:9:U:C6	2.49	0.48
26:DA:597:U:H2'	26:DA:598:G:H8	1.79	0.48
33:DI:128:LEU:O	33:DI:140:LEU:N	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DY:43:ASN:CG	45:DY:65:ALA:HB3	2.39	0.48
46:DZ:40:ASP:OD2	46:DZ:42:VAL:HG12	2.14	0.48
46:DZ:144:LEU:HD21	46:DZ:172:ALA:HB1	1.95	0.48
1:AA:175:C:H2'	1:AA:176:C:C6	2.48	0.48
1:AA:390:C:H2'	1:AA:391:G:C8	2.49	0.48
1:AA:520:A:N1	1:AA:536:C:H1'	2.28	0.48
1:AA:688:G:H2'	1:AA:689:C:H6	1.79	0.48
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.43	0.48
3:AC:45:LYS:HG3	3:AC:46:GLU:N	2.28	0.48
25:AY:58:A:O2'	25:AY:60:U:H5	1.96	0.48
26:BA:2292:C:P	39:BS:17:ARG:HH12	2.35	0.48
26:BA:2820:A:OP2	38:BR:2:ARG:NH2	2.47	0.48
30:BF:157:VAL:HB	30:BF:194:MET:HG2	1.96	0.48
34:BN:58:ASP:OD1	34:BN:58:ASP:N	2.45	0.48
1:CA:524:G:H2'	1:CA:525:C:C6	2.49	0.48
1:CA:1013:G:N2	1:CA:1015:A:H3'	2.28	0.48
1:CA:1236:A:O2'	1:CA:1304:G:H4'	2.13	0.48
20:CT:16:HIS:O	20:CT:19:SER:OG	2.22	0.48
25:CY:9:A:H8	25:CY:11:C:N4	2.11	0.48
25:CY:64:A:C2'	25:CY:65:G:H5'	2.43	0.48
26:DA:752:A:P	54:D7:3:ARG:HH22	2.37	0.48
26:DA:1721:G:H2'	26:DA:1740:G:O6	2.14	0.48
26:DA:2036:C:H2'	26:DA:2037:G:C8	2.48	0.48
26:DA:2291:U:H2'	26:DA:2292:C:C6	2.49	0.48
31:DG:57:ALA:HA	31:DG:90:LEU:HD13	1.94	0.48
36:DP:121:LYS:HG2	36:DP:122:PRO:HD2	1.96	0.48
46:DZ:43:GLU:O	46:DZ:47:VAL:HG23	2.13	0.48
1:AA:1144:G:H21	1:AA:1146:A:H62	1.61	0.48
23:AW:2:C:H2'	23:AW:3:C:C6	2.48	0.48
26:BA:271(H):G:H5"	48:B1:81:LYS:HE3	1.96	0.48
26:BA:1803:A:H4'	28:BD:259:THR:HG23	1.95	0.48
32:BH:104:GLU:HG3	32:BH:114:VAL:HG22	1.95	0.48
41:BU:108:GLU:O	41:BU:112:ARG:HG2	2.13	0.48
1:CA:359:U:H2'	1:CA:360:A:C8	2.49	0.48
1:CA:421:U:O2'	1:CA:423:G:N7	2.47	0.48
1:CA:442:C:H42	1:CA:492:G:H1	1.61	0.48
1:CA:683:G:H2'	1:CA:684:A:C8	2.49	0.48
1:CA:1268:A:N3	1:CA:1326:C:O2'	2.38	0.48
2:CB:16:HIS:HD2	2:CB:204:ASN:N	2.11	0.48
14:CN:24:CYS:O	14:CN:28:GLY:N	2.33	0.48
25:CY:22:G:N7	25:CY:46:7MG:C2	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:622:G:H2'	26:DA:623:G:H8	1.78	0.48
26:DA:1899:G:N3	26:DA:1899:G:H2'	2.28	0.48
26:DA:2144:U:H1'	26:DA:2148:G:H22	1.79	0.48
26:DA:2591:C:OP1	28:DD:239:ARG:HD2	2.14	0.48
32:DH:3:ARG:NH1	32:DH:3:ARG:HB3	2.29	0.48
34:DN:34:LEU:O	34:DN:49:GLY:HA3	2.13	0.48
41:DU:108:GLU:O	41:DU:112:ARG:HG2	2.14	0.48
43:DW:33:ARG:NE	43:DW:52:GLU:OE1	2.47	0.48
1:AA:270:A:H2'	1:AA:271:C:C6	2.49	0.48
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.13	0.48
1:AA:1162:C:H42	1:AA:1174:G:H1	1.59	0.48
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.49	0.48
26:BA:1665:A:H2'	26:BA:1666:G:O4'	2.13	0.48
51:B4:16:CYS:HB3	51:B4:20:ASN:HB3	1.96	0.48
1:CA:1000:U:O2	1:CA:1041:A:N1	2.47	0.48
7:CG:12:LEU:H	7:CG:12:LEU:HD12	1.78	0.48
13:CM:50:GLU:O	13:CM:54:VAL:HG22	2.14	0.48
26:DA:340:A:H2'	26:DA:341:G:O4'	2.14	0.48
26:DA:2483:C:H2'	26:DA:2484:G:O4'	2.14	0.48
30:DF:56:GLU:OE2	30:DF:93:LYS:NZ	2.46	0.48
32:DH:69:ARG:O	32:DH:73:ALA:N	2.31	0.48
32:DH:122:THR:O	32:DH:134:SER:OG	2.29	0.48
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.47	0.48
25:AY:22:G:C8	25:AY:46:7MG:O6	2.67	0.48
26:BA:774:A:H2'	26:BA:774:A:N3	2.29	0.48
26:BA:893:C:H2'	26:BA:894:C:C6	2.49	0.48
26:BA:1007:C:OP1	34:BN:37:LYS:NZ	2.46	0.48
26:BA:1268:A:H2'	26:BA:1269:A:O4'	2.14	0.48
26:BA:2336:A:H61	47:B0:43:THR:HG21	1.79	0.48
26:BA:2364:C:H2'	26:BA:2365:G:O4'	2.14	0.48
31:BG:41:GLN:HB2	31:BG:90:LEU:HB2	1.94	0.48
1:CA:392:G:H2'	1:CA:393:A:H8	1.78	0.48
1:CA:991:U:H4'	1:CA:992:U:OP1	2.14	0.48
1:CA:1434:A:H2'	1:CA:1435:G:O4'	2.14	0.48
4:CD:53:ASP:O	4:CD:57:ARG:HG3	2.13	0.48
8:CH:119:LEU:HB3	8:CH:123:GLU:HB3	1.94	0.48
11:CK:66:LEU:HB3	11:CK:70:LYS:NZ	2.29	0.48
13:CM:4:ILE:HG22	13:CM:7:VAL:O	2.13	0.48
13:CM:91:ARG:NE	13:CM:97:PRO:O	2.43	0.48
14:CN:12:ARG:HG2	14:CN:13:THR:N	2.29	0.48
26:DA:898:C:H2'	26:DA:899:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2314:C:H2'	26:DA:2315:G:H8	1.79	0.48
30:DF:116:ASP:O	30:DF:120:GLU:HG3	2.14	0.48
35:DO:68:GLU:OE2	35:DO:78:ARG:NH1	2.47	0.48
43:DW:82:LEU:HB2	43:DW:98:LYS:HB2	1.95	0.48
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.28	0.47
17:AQ:22:LEU:HD13	17:AQ:41:LYS:HG3	1.96	0.47
23:AW:29:G:H1	23:AW:41:C:H42	1.62	0.47
26:BA:2849:U:H4'	26:BA:2868:A:C2	2.49	0.47
30:BF:101:LEU:HD12	30:BF:102:PRO:HD2	1.95	0.47
35:BO:16:ALA:HB2	35:BO:52:VAL:HG21	1.95	0.47
45:BY:45:VAL:HG23	45:BY:63:LYS:HG2	1.95	0.47
1:CA:583:A:H2'	1:CA:584:G:O4'	2.14	0.47
1:CA:1162:C:N4	1:CA:1174:G:N1	2.36	0.47
1:CA:1490:C:H2'	1:CA:1491:G:C8	2.49	0.47
2:CB:71:VAL:CG2	2:CB:164:VAL:HA	2.44	0.47
2:CB:153:ARG:HE	2:CB:153:ARG:HB2	1.53	0.47
4:CD:57:ARG:NH2	5:CE:107:ARG:HD3	2.26	0.47
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.14	0.47
10:CJ:38:ILE:HG13	10:CJ:71:LEU:HB3	1.96	0.47
26:DA:863:A:H2'	26:DA:864:G:H8	1.79	0.47
26:DA:947:G:H2'	26:DA:948:G:C8	2.49	0.47
26:DA:1242:A:N1	36:DP:4:SER:OG	2.41	0.47
26:DA:1453:U:O4	38:DR:67:LEU:HD21	2.14	0.47
26:DA:1509(B):A:H2'	26:DA:1510:G:C8	2.49	0.47
27:DB:42:C:H1'	31:DG:68:PRO:HA	1.96	0.47
43:DW:71:VAL:HA	43:DW:107:LEU:HD12	1.96	0.47
45:DY:13:VAL:HB	45:DY:72:VAL:HG13	1.95	0.47
48:D1:76:ARG:NH1	48:D1:97:LEU:O	2.46	0.47
1:AA:1104:G:O5'	2:AB:111:ARG:HD2	2.14	0.47
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.96	0.47
14:AN:14:PRO:HB2	14:AN:16:PHE:O	2.14	0.47
26:BA:218:A:C2	26:BA:235:U:H4'	2.50	0.47
26:BA:1899:G:H2'	26:BA:1899:G:N3	2.29	0.47
26:BA:2142:C:H2'	26:BA:2143:C:C6	2.49	0.47
37:BQ:21:THR:HG21	37:BQ:101:ARG:HD3	1.96	0.47
1:CA:59:A:H3'	1:CA:331:G:H22	1.79	0.47
1:CA:659:U:H2'	1:CA:660:G:O4'	2.14	0.47
1:CA:811:C:N3	61:CA:3210:HOH:O	2.35	0.47
1:CA:1017:G:H2'	1:CA:1018:C:C6	2.49	0.47
1:CA:1502:A:H2	1:CA:1505:G:N1	2.07	0.47
5:CE:6:PHE:CD1	5:CE:36:ASP:HB3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:40:ASN:HB3	13:CM:43:THR:HG23	1.95	0.47
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.14	0.47
26:DA:863:A:P	37:DQ:22:LYS:HG3	2.54	0.47
26:DA:2124:G:H1	26:DA:2174:C:N4	2.13	0.47
26:DA:2321:G:H2'	26:DA:2321:G:N3	2.28	0.47
30:DF:36:VAL:HG11	30:DF:183:VAL:HG11	1.96	0.47
32:DH:35:VAL:HG11	32:DH:71:LEU:HG	1.97	0.47
33:DI:102:SER:OG	33:DI:103:ARG:N	2.47	0.47
36:DP:21:ARG:HD3	36:DP:21:ARG:HA	1.50	0.47
39:DS:77:ALA:O	39:DS:81:GLY:N	2.46	0.47
48:D1:65:SER:OG	48:D1:66:HIS:ND1	2.41	0.47
53:D6:21:TYR:CE1	53:D6:38:LYS:HG2	2.49	0.47
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.79	0.47
1:AA:346:G:P	40:BT:41:ARG:HH22	2.36	0.47
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.50	0.47
3:AC:191:THR:OG1	3:AC:194:GLY:O	2.33	0.47
15:AO:84:LYS:O	15:AO:84:LYS:HD3	2.13	0.47
17:AQ:78:GLU:HG2	17:AQ:79:SER:N	2.29	0.47
26:BA:330:A:H2	26:BA:1210:A:C2'	2.26	0.47
26:BA:2130:U:H1'	26:BA:2158:A:N1	2.29	0.47
45:BY:11:ASP:OD1	45:BY:11:ASP:N	2.40	0.47
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.96	0.47
1:CA:664:G:N2	1:CA:741:G:H1	2.04	0.47
1:CA:1267:C:H6	1:CA:1267:C:O5'	1.97	0.47
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.95	0.47
4:CD:179:GLU:O	4:CD:181:MET:HE2	2.14	0.47
26:DA:62:C:H42	26:DA:93:G:H1	1.62	0.47
26:DA:885:C:H2'	26:DA:886:C:H4'	1.96	0.47
26:DA:1604:C:O2'	26:DA:1610:A:N1	2.38	0.47
27:DB:24:G:H4'	27:DB:25:A:C8	2.49	0.47
30:DF:33:LEU:HD13	30:DF:112:MET:HE2	1.95	0.47
31:DG:15:VAL:HG13	31:DG:175:LEU:HD23	1.97	0.47
31:DG:111:LEU:HA	31:DG:114:ILE:HD13	1.96	0.47
36:DP:82:GLY:HA2	36:DP:113:LYS:O	2.14	0.47
39:DS:30:ARG:HD3	39:DS:98:VAL:HG22	1.97	0.47
39:DS:84:GLN:H	39:DS:111:GLU:HB2	1.79	0.47
40:DT:99:LEU:O	40:DT:102:ILE:HG12	2.14	0.47
46:DZ:45:ASP:CG	46:DZ:49:ARG:HH11	2.22	0.47
49:D2:16:LEU:HB2	49:D2:21:LEU:HD23	1.97	0.47
1:AA:1033:G:H2'	1:AA:1034:G:C8	2.45	0.47
1:AA:1255:G:N7	10:AJ:43:ARG:NH2	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1479:C:H2'	1:AA:1480:G:C8	2.49	0.47
26:BA:826:U:H4'	36:BP:55:ARG:HB2	1.96	0.47
31:BG:144:ILE:HA	31:BG:148:MET:HE1	1.96	0.47
45:BY:13:VAL:HB	45:BY:72:VAL:HG13	1.95	0.47
51:B4:18:CYS:SG	51:B4:20:ASN:HB2	2.55	0.47
1:CA:353:A:H5'	1:CA:353:A:H8	1.78	0.47
1:CA:1004:A:H62	1:CA:1037:C:C2'	2.28	0.47
1:CA:1179:A:H2'	1:CA:1180:A:O4'	2.13	0.47
1:CA:1225:A:OP1	13:CM:103:THR:OG1	2.30	0.47
2:CB:178:ARG:HH21	8:CH:74:PRO:HG3	1.80	0.47
4:CD:20:TYR:HD1	4:CD:26:CYS:HB3	1.78	0.47
11:CK:24:SER:OG	11:CK:25:TYR:N	2.45	0.47
25:CY:66:U:H2'	25:CY:67:C:O4'	2.14	0.47
26:DA:212:G:H2'	26:DA:213:A:O4'	2.13	0.47
26:DA:571:A:N6	26:DA:2499:C:O3'	2.46	0.47
26:DA:1029:A:N6	26:DA:1125:G:O2'	2.44	0.47
26:DA:1639:U:C2'	26:DA:1640:C:H5"	2.42	0.47
26:DA:2646:C:H2'	26:DA:2647:U:O4'	2.15	0.47
39:DS:53:SER:O	39:DS:57:LYS:N	2.47	0.47
1:AA:167:G:H2'	1:AA:168:G:C8	2.49	0.47
1:AA:428:G:OP2	4:AD:10:ARG:NH1	2.47	0.47
1:AA:457:C:H2'	1:AA:458:C:H6	1.79	0.47
1:AA:741:G:H2'	1:AA:742:G:O4'	2.15	0.47
1:AA:952:U:H2'	1:AA:953:G:C8	2.50	0.47
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.96	0.47
5:AE:6:PHE:HB3	5:AE:35:GLY:C	2.40	0.47
8:AH:33:GLU:HG2	8:AH:48:TYR:OH	2.14	0.47
24:AX:56:C:O5'	24:AX:56:C:H6	1.97	0.47
33:BI:85:GLU:HB3	33:BI:86:THR:H	1.55	0.47
46:BZ:108:PRO:HB3	46:BZ:117:LEU:HD22	1.97	0.47
2:CB:91:PRO:HG3	2:CB:155:LEU:HD23	1.95	0.47
4:CD:163:GLU:C	4:CD:165:MET:H	2.22	0.47
5:CE:10:MET:HG3	5:CE:32:VAL:HG22	1.96	0.47
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.50	0.47
18:CR:41:LYS:NZ	18:CR:41:LYS:HB3	2.29	0.47
18:CR:73:ALA:HB3	18:CR:79:LEU:HG	1.96	0.47
26:DA:65:C:O2'	26:DA:456:C:N3	2.46	0.47
26:DA:641:C:H42	26:DA:647:G:H1	1.62	0.47
26:DA:657:U:H2'	26:DA:658:C:C6	2.49	0.47
26:DA:1220:A:OP2	41:DU:19:LYS:NZ	2.34	0.47
26:DA:1316:U:H2'	26:DA:1317:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1420:U:HO2'	26:DA:1421:G:P	2.37	0.47
26:DA:2136:C:H1'	26:DA:2137:C:H5'	1.96	0.47
28:DD:2:ALA:O	28:DD:3:VAL:HB	2.15	0.47
30:DF:178:PRO:HB3	30:DF:198:ALA:HA	1.97	0.47
44:DX:35:THR:HB	44:DX:38:GLU:HB2	1.97	0.47
4:AD:12:CYS:SG	4:AD:19:LEU:HB2	2.54	0.47
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.96	0.47
16:AP:20:VAL:HG23	16:AP:35:LYS:HA	1.96	0.47
16:AP:28:ARG:NE	16:AP:29:ASP:OD1	2.29	0.47
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.13	0.47
25:AY:2:C:H42	25:AY:71:G:H1	1.63	0.47
25:AY:15:G:C6	25:AY:48:C:O2	2.68	0.47
26:BA:534:U:H2'	26:BA:535:C:C6	2.49	0.47
26:BA:1930:G:O2'	26:BA:1968:G:O6	2.32	0.47
26:BA:2207:G:H2'	26:BA:2208:A:C2	2.50	0.47
33:BI:48:GLU:O	33:BI:52:ARG:HB3	2.14	0.47
1:CA:601:C:H42	1:CA:637:G:H1	1.63	0.47
1:CA:1362:C:C2'	1:CA:1363:C:H5"	2.45	0.47
2:CB:17:PHE:CD2	2:CB:44:LEU:HD11	2.49	0.47
8:CH:84:ARG:O	8:CH:84:ARG:HG3	2.14	0.47
23:CW:50:U:H2'	23:CW:51:U:O4'	2.15	0.47
24:CX:12:G:H4'	26:DA:1908:C:O2	2.14	0.47
24:CX:37:A:H2'	24:CX:38:A:O4'	2.14	0.47
26:DA:1019:U:O2'	26:DA:1021:A:H2	1.97	0.47
28:DD:164:GLN:NE2	28:DD:176:ARG:HH22	2.12	0.47
35:DO:120:GLU:HG2	35:DO:122:LEU:HG	1.97	0.47
45:DY:28:LYS:HB3	45:DY:28:LYS:HE2	1.67	0.47
50:D3:50:VAL:O	50:D3:54:VAL:HB	2.15	0.47
1:AA:162:A:H3'	1:AA:163:C:C4'	2.45	0.47
1:AA:564:C:O2'	8:AH:91:ARG:NH2	2.38	0.47
1:AA:620:C:H2'	1:AA:621:A:O4'	2.15	0.47
1:AA:1007:C:N3	1:AA:1022:G:C6	2.83	0.47
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.50	0.47
1:AA:1285:A:H4'	1:AA:1286:A:O5'	2.15	0.47
1:AA:1392:G:N2	1:AA:1502:A:C8	2.83	0.47
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.50	0.47
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.15	0.47
3:AC:62:ASP:HA	3:AC:97:LYS:HD3	1.96	0.47
16:AP:48:TRP:HH2	16:AP:76:GLN:NE2	2.12	0.47
24:AX:2:G:N3	24:AX:2:G:H2'	2.29	0.47
26:BA:271(X):G:C2	26:BA:271(Y):U:O4	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2140:C:C4	26:BA:2151:G:N1	2.83	0.47
26:BA:2345:G:H4'	26:BA:2346:A:H5"	1.97	0.47
26:BA:2557:G:H2'	26:BA:2558:C:C6	2.50	0.47
30:BF:39:TRP:O	30:BF:43:LYS:HD3	2.14	0.47
31:BG:19:LEU:HG	31:BG:175:LEU:HD23	1.97	0.47
1:CA:22:G:H4'	1:CA:885:G:C8	2.50	0.47
1:CA:24:U:OP1	12:CL:23:LYS:NZ	2.47	0.47
1:CA:643:C:H2'	1:CA:644:G:H8	1.79	0.47
1:CA:1256:A:N1	1:CA:1278:U:H1'	2.29	0.47
1:CA:1392:G:H21	1:CA:1502:A:H8	1.63	0.47
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.78	0.47
4:CD:22:LYS:HG3	58:CD:501:SF4:S4	2.55	0.47
7:CG:72:ARG:NH2	7:CG:138:LYS:HZ1	2.12	0.47
13:CM:39:ILE:HG12	13:CM:52:GLU:HG2	1.96	0.47
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.55	0.47
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.14	0.47
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	1.96	0.47
19:CS:41:VAL:O	19:CS:44:MET:HB2	2.14	0.47
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.96	0.47
20:CT:93:GLU:C	20:CT:95:ALA:H	2.23	0.47
22:CV:14:A:C4	25:CY:34:G:C6	3.02	0.47
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	2.15	0.47
26:DA:1239:G:H2'	26:DA:1240:U:O4'	2.14	0.47
26:DA:1270:C:H5"	26:DA:1271:G:O5'	2.15	0.47
26:DA:1528(A):A:H2'	26:DA:1529:G:O4'	2.15	0.47
26:DA:1592:C:H2'	26:DA:1593:G:H8	1.79	0.47
26:DA:2128:C:N4	26:DA:2160:G:H1	2.09	0.47
26:DA:2331:G:O2'	26:DA:2336:A:N1	2.43	0.47
26:DA:2547:U:O2	35:DO:23:ARG:NH2	2.47	0.47
27:DB:70:C:H42	27:DB:107:G:H1	1.61	0.47
27:DB:94:C:H2'	27:DB:95:C:C6	2.50	0.47
28:DD:26:LYS:HE2	28:DD:28:GLU:O	2.15	0.47
28:DD:134:ARG:NH1	28:DD:188:GLU:OE2	2.47	0.47
32:DH:98:LEU:HD13	32:DH:102:ALA:O	2.13	0.47
36:DP:16:ARG:HG3	61:DP:305:HOH:O	2.13	0.47
50:D3:8:LEU:HD13	50:D3:31:LEU:HD23	1.97	0.47
1:AA:346:G:OP1	40:BT:41:ARG:NH1	2.42	0.47
1:AA:1122:U:C4	1:AA:1123:A:N7	2.83	0.47
1:AA:1250:A:H4'	9:AI:68:GLY:N	2.30	0.47
9:AI:4:TYR:CE2	9:AI:88:TYR:HD1	2.33	0.47
26:BA:34:C:H5"	26:BA:35:G:OP2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:784:A:N6	28:BD:229:VAL:HG11	2.30	0.47
26:BA:1416:G:O2'	26:BA:1417:C:OP2	2.24	0.47
26:BA:1482:G:O6	26:BA:1507:A:N6	2.48	0.47
26:BA:1686:C:H2'	26:BA:1687:G:O4'	2.15	0.47
26:BA:2137:C:N3	26:BA:2154:G:O6	2.48	0.47
26:BA:2168:G:C6	26:BA:2171:A:C8	3.02	0.47
30:BF:53:THR:HG23	30:BF:55:GLY:H	1.80	0.47
1:CA:1360:A:O5'	1:CA:1360:A:H8	1.97	0.47
5:CE:145:LYS:HE3	5:CE:149:GLU:OE2	2.15	0.47
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.30	0.47
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.97	0.47
11:CK:65:ALA:HB3	11:CK:97:ALA:HB3	1.97	0.47
26:DA:251:A:C5	26:DA:252:G:H1'	2.50	0.47
26:DA:602:G:O2'	26:DA:655:A:N6	2.48	0.47
26:DA:782:A:H5'	26:DA:783:A:N7	2.30	0.47
26:DA:1127:A:H2'	26:DA:1128:A:H5"	1.97	0.47
26:DA:2059:A:O2'	30:DF:69:HIS:HD2	1.98	0.47
26:DA:2820:A:O2'	26:DA:2821:A:OP1	2.29	0.47
27:DB:8:U:O2'	39:DS:40:ILE:HD13	2.15	0.47
51:D4:16:CYS:SG	51:D4:17:GLY:N	2.87	0.47
1:AA:256:U:H2'	1:AA:257:G:C8	2.49	0.47
1:AA:413:G:N2	1:AA:428:G:H1'	2.30	0.47
1:AA:626:U:H2'	1:AA:627:G:H8	1.78	0.47
1:AA:743:U:H2'	1:AA:744:C:C6	2.50	0.47
1:AA:1095:U:H5"	1:AA:1109:C:O2	2.14	0.47
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.42	0.47
1:AA:1525:G:P	11:AK:120:ARG:HH22	2.37	0.47
2:AB:59:GLU:O	2:AB:63:MET:HG3	2.14	0.47
4:AD:98:GLU:HG2	4:AD:189:PRO:HG2	1.96	0.47
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.15	0.47
18:AR:26:LEU:HD23	18:AR:29:PHE:CE2	2.50	0.47
26:BA:904:C:H4'	46:BZ:169:GLU:OE2	2.15	0.47
33:BI:12:LEU:HD23	33:BI:12:LEU:HA	1.79	0.47
33:BI:47:LEU:HD23	33:BI:47:LEU:HA	1.75	0.47
46:BZ:7:ALA:HB3	46:BZ:61:LEU:HD12	1.97	0.47
1:CA:258:G:OP1	20:CT:86:ARG:NH1	2.48	0.47
1:CA:1314:C:OP1	19:CS:6:LYS:NZ	2.24	0.47
25:CY:35:A:H2'	25:CY:36:A:O4'	2.15	0.47
25:CY:50:U:H2'	25:CY:51:U:C6	2.50	0.47
26:DA:272:G:H4'	26:DA:272(A):U:H5"	1.97	0.47
26:DA:1600:C:OP1	44:DX:58:HIS:NE2	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1794:U:H2'	26:DA:1795:C:C6	2.50	0.47
26:DA:2136:C:N4	26:DA:2155:G:C6	2.82	0.47
26:DA:2391:G:O6	26:DA:2425:A:H8	1.98	0.47
30:DF:20:LEU:HD12	30:DF:125:LEU:HD13	1.97	0.47
1:AA:502:G:H2'	1:AA:503:C:O4'	2.14	0.47
2:AB:80:ILE:O	2:AB:84:GLU:HB2	2.15	0.47
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.45	0.47
19:AS:41:VAL:HG12	19:AS:43:GLU:H	1.80	0.47
26:BA:848:G:N9	26:BA:933:A:H8	2.11	0.47
26:BA:875:G:H2'	26:BA:876:C:O4'	2.15	0.47
26:BA:1124:C:H1'	56:B9:36:GLN:NE2	2.30	0.47
26:BA:1745(A):C:H5'	26:BA:1746:G:OP2	2.15	0.47
26:BA:1778:U:H2'	26:BA:1784:A:N6	2.29	0.47
26:BA:2163:C:C6	26:BA:2163:C:H5'	2.49	0.47
32:BH:25:LYS:HG2	32:BH:34:GLU:HG2	1.97	0.47
35:BO:34:THR:OG1	35:BO:35:VAL:N	2.43	0.47
1:CA:107:G:H2'	1:CA:108:G:O4'	2.15	0.47
1:CA:827:U:H5"	1:CA:828:A:OP2	2.15	0.47
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	1.96	0.47
2:CB:219:VAL:HA	2:CB:222:ILE:HG12	1.96	0.47
3:CC:54:ARG:H	3:CC:69:HIS:HB2	1.79	0.47
3:CC:127:ARG:NH2	3:CC:192:THR:HG23	2.29	0.47
4:CD:103:ASN:OD1	4:CD:114:ARG:NE	2.39	0.47
6:CF:97:PHE:CE1	18:CR:62:GLU:HG2	2.50	0.47
26:DA:613:G:O2'	26:DA:614(C):A:N1	2.40	0.47
26:DA:900:A:C8	26:DA:901:A:N7	2.83	0.47
26:DA:955:C:OP1	37:DQ:87:LYS:HE3	2.15	0.47
26:DA:1027:A:C6	26:DA:1126:A:C4	3.03	0.47
26:DA:2153:G:C2	26:DA:2154:G:C4	3.03	0.47
26:DA:2841:C:H2'	26:DA:2842:G:C8	2.51	0.47
34:DN:108:PRO:O	34:DN:113:GLY:HA3	2.15	0.47
49:D2:29:LYS:HE2	49:D2:57:ILE:HG21	1.96	0.47
1:AA:116:A:O5'	1:AA:116:A:H8	1.97	0.46
1:AA:664:G:N2	1:AA:741:G:H1	2.03	0.46
1:AA:890:G:O2'	1:AA:906:G:O6	2.19	0.46
1:AA:992:U:H4'	1:AA:993:G:H5"	1.97	0.46
1:AA:1367:C:H4'	10:AJ:48:THR:HG21	1.96	0.46
1:AA:1458:G:H5"	20:AT:31:SER:HB2	1.96	0.46
2:AB:60:ASP:OD1	2:AB:64:ARG:NH2	2.49	0.46
3:AC:122:GLU:O	3:AC:126:ARG:NH1	2.41	0.46
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:86:ARG:O	6:AF:87:ARG:HG2	2.14	0.46
9:AI:79:LEU:O	9:AI:83:ARG:HG3	2.15	0.46
25:AY:57:G:H2'	25:AY:58:A:H5'	1.97	0.46
25:AY:58:A:N6	25:AY:61:C:C2	2.83	0.46
26:BA:1470:G:N2	26:BA:1520:G:OP2	2.36	0.46
52:B5:11:THR:HG23	52:B5:15:ARG:HB3	1.96	0.46
1:CA:447:G:O6	1:CA:485:G:O2'	2.23	0.46
1:CA:1129:C:H2'	1:CA:1139:G:C5	2.49	0.46
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.50	0.46
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.14	0.46
3:CC:121:ALA:HB1	3:CC:189:ALA:HB2	1.96	0.46
20:CT:87:LYS:O	20:CT:91:LEU:HG	2.15	0.46
26:DA:908:C:OP2	37:DQ:22:LYS:NZ	2.48	0.46
26:DA:1628:G:H2'	26:DA:1629:U:C6	2.50	0.46
26:DA:2136:C:O2'	26:DA:2137:C:O5'	2.22	0.46
26:DA:2577:A:OP2	52:D5:3:LYS:NZ	2.43	0.46
31:DG:41:GLN:NE2	31:DG:153:ARG:HB3	2.30	0.46
31:DG:43:LEU:C	31:DG:45:GLU:H	2.21	0.46
31:DG:66:GLN:HG3	51:D4:1:MET:HE3	1.97	0.46
31:DG:107:LEU:HD21	31:DG:178:PHE:CE1	2.50	0.46
31:DG:122:PRO:HG3	31:DG:180:PHE:HB3	1.96	0.46
34:DN:104:LYS:HA	34:DN:107:LEU:HD12	1.97	0.46
36:DP:54:GLY:O	61:DP:308:HOH:O	2.20	0.46
39:DS:106:ARG:HG3	39:DS:112:PHE:CZ	2.50	0.46
1:AA:405:U:H5"	1:AA:495:A:H2	1.80	0.46
1:AA:955:U:O2'	19:AS:83:HIS:HD2	1.98	0.46
4:AD:107:ARG:NH2	4:AD:194:LEU:HD21	2.31	0.46
5:AE:110:LEU:HD13	5:AE:118:ILE:HD13	1.97	0.46
12:AL:88:GLY:O	12:AL:99:HIS:HD2	1.99	0.46
15:AO:82:ILE:HB	15:AO:87:ILE:HB	1.96	0.46
17:AQ:53:LEU:HD23	17:AQ:82:MET:HE1	1.97	0.46
23:AW:50:U:H2'	23:AW:51:U:O4'	2.14	0.46
26:BA:363(B):G:H2'	26:BA:363(C):G:H5'	1.97	0.46
26:BA:839:U:H2'	26:BA:840:C:C6	2.51	0.46
26:BA:1952:A:C6	26:BA:1953:A:N1	2.83	0.46
26:BA:2159:G:H2'	26:BA:2160:G:C8	2.50	0.46
27:BB:77:U:OP1	46:BZ:19:ARG:NH2	2.39	0.46
36:BP:135:LEU:HA	36:BP:135:LEU:HD23	1.71	0.46
38:BR:44:LEU:HD22	38:BR:48:VAL:HG23	1.97	0.46
38:BR:55:ALA:HB2	38:BR:79:LEU:HD13	1.97	0.46
39:BS:10:ARG:O	39:BS:14:VAL:HG13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BW:71:VAL:HA	43:BW:107:LEU:HD12	1.96	0.46
44:BX:60:ARG:HA	44:BX:75:ASP:OD2	2.16	0.46
1:CA:59:A:H5"	1:CA:60:A:H5"	1.96	0.46
1:CA:1256:A:C6	1:CA:1278:U:H1'	2.51	0.46
1:CA:1279:A:O2'	1:CA:1282:C:N4	2.49	0.46
1:CA:1291:G:O2'	9:CI:38:GLN:HG3	2.14	0.46
1:CA:1320:C:C1'	19:CS:73:GLU:HG2	2.46	0.46
25:CY:35:A:C6	25:CY:36:A:C2	3.03	0.46
26:DA:293:U:H5"	26:DA:294:A:OP2	2.15	0.46
26:DA:1430:C:H2'	26:DA:1431:U:C6	2.50	0.46
26:DA:1916:A:H2'	26:DA:1917:U:O4'	2.16	0.46
47:D0:14:ARG:NH1	47:D0:14:ARG:HB2	2.30	0.46
1:AA:65:U:H5'	1:AA:65:U:H6	1.80	0.46
1:AA:154:C:C2'	1:AA:155:C:H5'	2.45	0.46
4:AD:18:LYS:HG2	58:AD:501:SF4:S1	2.55	0.46
10:AJ:8:LEU:N	10:AJ:70:ARG:O	2.33	0.46
26:BA:784:A:C6	28:BD:229:VAL:HG11	2.50	0.46
32:BH:69:ARG:HG3	32:BH:70:THR:N	2.29	0.46
45:BY:28:LYS:HE2	45:BY:28:LYS:HB3	1.75	0.46
2:CB:71:VAL:HG12	2:CB:93:VAL:CG2	2.45	0.46
13:CM:25:ILE:HG13	13:CM:29:ARG:HG2	1.97	0.46
26:DA:857:C:H4'	47:D0:23:VAL:HG21	1.98	0.46
26:DA:1006:C:C2	26:DA:1138:G:N2	2.84	0.46
26:DA:2127:G:H4'	26:DA:2127:G:OP1	2.15	0.46
1:AA:316:G:OP2	1:AA:351:G:O2'	2.30	0.46
1:AA:448:A:OP2	1:AA:485:G:N1	2.33	0.46
1:AA:1002:G:N3	1:AA:1003:G:H1'	2.30	0.46
1:AA:1090:U:H2'	1:AA:1091:U:C6	2.50	0.46
1:AA:1296:C:H5"	13:AM:14:ARG:HD2	1.96	0.46
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.80	0.46
4:AD:187:ARG:HG2	4:AD:188:LEU:N	2.31	0.46
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.68	0.46
25:AY:5:G:H2'	25:AY:6:G:C8	2.51	0.46
26:BA:414:C:H2'	26:BA:415:A:C8	2.51	0.46
26:BA:1166:C:H2'	26:BA:1167:U:C6	2.51	0.46
26:BA:2101:G:H2'	26:BA:2102:U:H6	1.80	0.46
26:BA:2126:A:H4'	26:BA:2127:G:OP1	2.16	0.46
26:BA:2162:G:C3'	26:BA:2163:C:H5"	2.46	0.46
26:BA:2562:U:O2'	35:BO:23:ARG:HD3	2.15	0.46
31:BG:66:GLN:HG3	51:B4:1:MET:CE	2.46	0.46
31:BG:66:GLN:OE1	31:BG:98:ARG:NE	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.50	0.46
1:CA:1164:G:O2'	1:CA:1165:C:H5'	2.15	0.46
9:CI:18:PHE:HD2	9:CI:62:TYR:HD2	1.63	0.46
24:CX:47:U:N3	24:CX:50:U:OP1	2.49	0.46
26:DA:242:G:C8	55:D8:5:LYS:HG2	2.51	0.46
26:DA:1199:U:H2'	26:DA:1200:C:C6	2.51	0.46
26:DA:1789:A:H2'	26:DA:1790:C:C6	2.50	0.46
26:DA:1998:G:O2'	26:DA:2724:C:O2'	2.25	0.46
26:DA:2296:U:OP2	39:DS:9:ARG:NH2	2.46	0.46
26:DA:2689:U:P	26:DA:2719:G:H22	2.39	0.46
31:DG:96:ARG:O	31:DG:99:MET:HB3	2.15	0.46
36:DP:121:LYS:O	36:DP:123:LEU:N	2.44	0.46
1:AA:8:A:N6	4:AD:205:GLU:O	2.49	0.46
1:AA:601:C:H2'	1:AA:602:A:C8	2.50	0.46
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.51	0.46
26:BA:234:C:H2'	26:BA:235:U:C6	2.51	0.46
26:BA:1766:U:H2'	26:BA:1767:C:C6	2.51	0.46
26:BA:1963:U:H4'	26:BA:1964:G:OP1	2.15	0.46
26:BA:2848:G:H8	40:BT:97:ALA:HB2	1.79	0.46
26:BA:2871:C:N3	61:BA:4761:HOH:O	2.35	0.46
30:BF:33:LEU:HB3	36:BP:6:LEU:HD21	1.98	0.46
30:BF:183:VAL:O	30:BF:187:VAL:HG23	2.15	0.46
39:BS:110:LEU:HD12	39:BS:110:LEU:HA	1.74	0.46
1:CA:390:C:H2'	1:CA:391:G:C8	2.50	0.46
1:CA:1241:G:C2'	1:CA:1242:C:H5'	2.45	0.46
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.47	0.46
1:CA:1390:U:H2'	1:CA:1391:U:C6	2.51	0.46
2:CB:87:ARG:HD3	2:CB:219:VAL:HG11	1.98	0.46
2:CB:137:ARG:HB3	2:CB:137:ARG:CZ	2.45	0.46
13:CM:47:ASP:C	13:CM:48:LEU:HD23	2.41	0.46
23:CW:31:A:H2'	23:CW:32:PSU:O4'	2.16	0.46
24:CX:33:U:N3	24:CX:36:U:OP2	2.48	0.46
26:DA:852:G:H2'	26:DA:853:G:H8	1.80	0.46
26:DA:1449:A:HO2'	26:DA:1529:G:H21	1.52	0.46
26:DA:2712:U:OP1	26:DA:2714:G:H4'	2.16	0.46
1:AA:627:G:H2'	1:AA:628:G:H8	1.81	0.46
1:AA:1245:A:N6	1:AA:1292:U:H3	2.11	0.46
1:AA:1286:A:H8	1:AA:1286:A:H3'	1.81	0.46
2:AB:67:THR:N	2:AB:160:ASP:OD1	2.47	0.46
2:AB:80:ILE:HD11	2:AB:212:GLN:CA	2.44	0.46
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:22:LEU:HD11	7:AG:101:LEU:HD21	1.96	0.46
11:AK:91:ARG:NH1	11:AK:110:ASP:OD2	2.48	0.46
25:AY:25:C:HO2'	25:AY:26:A:P	2.38	0.46
26:BA:2086:U:H2'	26:BA:2087:G:C8	2.51	0.46
26:BA:2850:A:OP2	26:BA:2866:U:H5	1.98	0.46
36:BP:86:LYS:HB3	36:BP:118:GLY:HA3	1.96	0.46
45:BY:6:HIS:HE1	45:BY:72:VAL:O	1.99	0.46
1:CA:841:U:OP1	1:CA:841:U:H6	1.98	0.46
2:CB:76:GLN:H	2:CB:76:GLN:HG2	1.49	0.46
10:CJ:12:ASP:OD1	10:CJ:13:HIS:N	2.48	0.46
15:CO:11:VAL:HG21	15:CO:34:LEU:HD22	1.97	0.46
16:CP:53:VAL:O	16:CP:57:ARG:HB2	2.15	0.46
20:CT:26:ASN:HA	20:CT:71:THR:HG23	1.97	0.46
26:DA:2648:C:H2'	26:DA:2649:U:C6	2.50	0.46
27:DB:90:A:C5	27:DB:91:C:H1'	2.51	0.46
46:DZ:5:LEU:O	46:DZ:59:LEU:HA	2.16	0.46
46:DZ:141:VAL:HG12	46:DZ:144:LEU:HD13	1.98	0.46
7:AG:138:LYS:NZ	7:AG:142:GLU:OE2	2.48	0.46
24:AX:23:C:H2'	24:AX:24:U:C6	2.51	0.46
25:AY:19:G:N2	25:AY:56:C:N3	2.64	0.46
26:BA:1047:G:H2'	26:BA:1110:G:H1	1.81	0.46
26:BA:2359:C:H2'	26:BA:2360:A:O4'	2.15	0.46
26:BA:2470:G:O6	26:BA:2476:A:O2'	2.26	0.46
30:BF:172:TRP:H	30:BF:172:TRP:CD1	2.34	0.46
36:BP:6:LEU:HA	36:BP:6:LEU:HD23	1.71	0.46
41:BU:76:TYR:CZ	41:BU:80:ILE:HG13	2.51	0.46
1:CA:773:G:O3'	28:DD:202:LYS:NZ	2.43	0.46
4:CD:157:LEU:HD22	4:CD:161:ASN:HD21	1.80	0.46
5:CE:39:GLY:HA2	5:CE:71:LEU:HD13	1.98	0.46
5:CE:53:LEU:H	5:CE:53:LEU:HD12	1.80	0.46
8:CH:111:ILE:HD11	8:CH:118:VAL:HG12	1.98	0.46
9:CI:116:LYS:HA	9:CI:123:PRO:HD3	1.97	0.46
11:CK:79:SER:OG	11:CK:106:LYS:HE3	2.15	0.46
13:CM:23:TYR:CE2	13:CM:70:LEU:HB3	2.50	0.46
13:CM:65:LYS:N	51:D4:50:VAL:HG21	2.31	0.46
26:DA:82:G:H5"	26:DA:296:C:H5'	1.96	0.46
26:DA:699:A:H4'	26:DA:1554:A:N6	2.29	0.46
26:DA:848:G:N9	26:DA:933:A:H8	2.13	0.46
26:DA:1027:A:C2	26:DA:2488:A:H5'	2.51	0.46
26:DA:1790:C:H5"	26:DA:1791:A:OP1	2.15	0.46
26:DA:1833:U:O2'	26:DA:1969:A:N1	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2302:G:C2'	26:DA:2303:G:H5'	2.46	0.46
27:DB:20:C:C2'	27:DB:21:G:H5'	2.45	0.46
31:DG:8:LYS:HG3	31:DG:100:TRP:CE2	2.51	0.46
32:DH:98:LEU:HD23	32:DH:125:VAL:HG23	1.97	0.46
36:DP:38:GLN:O	36:DP:39:LYS:HB3	2.15	0.46
37:DQ:108:GLY:HA3	46:DZ:116:VAL:HG13	1.96	0.46
46:DZ:67:LEU:HA	46:DZ:68:PRO:HD3	1.83	0.46
47:D0:82:ARG:HA	47:D0:83:PRO:HD3	1.67	0.46
1:AA:473:G:H2'	1:AA:474:G:C8	2.50	0.46
1:AA:532:A:H2	1:AA:1206:G:H21	1.63	0.46
1:AA:1036:G:H2'	1:AA:1036:G:N3	2.31	0.46
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	1.98	0.46
26:BA:45:C:OP2	26:BA:215:G:H2'	2.16	0.46
26:BA:1683:C:H2'	26:BA:1684:C:C6	2.51	0.46
26:BA:2001:A:H2'	26:BA:2002:G:C8	2.51	0.46
38:BR:118:GLU:CD	38:BR:118:GLU:H	2.23	0.46
1:CA:276:G:O3'	17:CQ:68:ARG:NH1	2.48	0.46
1:CA:472:A:H5"	16:CP:80:PHE:HB3	1.98	0.46
1:CA:1135:U:H2'	1:CA:1137:C:N3	2.31	0.46
1:CA:1251:A:N1	1:CA:1354:C:O2'	2.47	0.46
1:CA:1392:G:N2	1:CA:1502:A:H8	2.14	0.46
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.30	0.46
13:CM:24:GLY:C	13:CM:25:ILE:HD12	2.41	0.46
16:CP:3:LYS:O	16:CP:21:VAL:HA	2.15	0.46
23:CW:4:C:C4	23:CW:69:G:N1	2.84	0.46
26:DA:375:C:H2'	26:DA:376:C:C6	2.51	0.46
33:DI:66:GLU:HA	33:DI:69:LYS:HB3	1.97	0.46
36:DP:124:LYS:HA	36:DP:144:GLU:O	2.16	0.46
1:AA:715:A:H2'	1:AA:716:A:C8	2.51	0.46
2:AB:119:GLU:OE1	2:AB:153:ARG:NH2	2.49	0.46
4:AD:168:ARG:H	4:AD:168:ARG:NH1	2.13	0.46
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	1.97	0.46
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.16	0.46
26:BA:330:A:H2	26:BA:1210:A:O2'	1.99	0.46
26:BA:1939:U:OP1	26:BA:2604:U:O2'	2.33	0.46
28:BD:10:THR:OG1	28:BD:13:ARG:HG2	2.16	0.46
37:BQ:1:MET:HB2	37:BQ:44:ALA:HB1	1.96	0.46
39:BS:41:ASP:OD2	39:BS:44:LYS:NZ	2.42	0.46
1:CA:991:U:H3'	1:CA:1212:U:C4	2.51	0.46
1:CA:1064:G:H4'	1:CA:1065:U:O5'	2.16	0.46
1:CA:1321:C:H4'	13:CM:87:TYR:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1368:G:C2'	1:CA:1369:C:H5'	2.46	0.46
2:CB:23:ARG:H	2:CB:23:ARG:HG2	1.53	0.46
20:CT:63:ILE:HD13	20:CT:80:ARG:HB3	1.98	0.46
24:CX:40:C:H2'	24:CX:41:C:H6	1.81	0.46
26:DA:476:G:H4'	26:DA:502:A:N1	2.31	0.46
26:DA:1015:G:O2'	26:DA:1016:G:H5'	2.15	0.46
26:DA:1418:G:H8	26:DA:1418:G:O5'	1.99	0.46
26:DA:1467:C:C5	26:DA:1546:C:H2'	2.51	0.46
26:DA:2114:A:N1	26:DA:2117:A:N6	2.64	0.46
28:DD:5:LYS:HB3	28:DD:5:LYS:HE3	1.66	0.46
28:DD:242:ARG:N	28:DD:242:ARG:HD3	2.31	0.46
36:DP:121:LYS:HD2	36:DP:123:LEU:HG	1.97	0.46
39:DS:62:LYS:HA	39:DS:65:VAL:HB	1.98	0.46
55:D8:8:LYS:HB3	55:D8:12:LYS:HE3	1.98	0.46
1:AA:99:U:H2'	1:AA:100:C:C6	2.50	0.46
18:AR:32:ARG:HA	18:AR:69:THR:HG21	1.97	0.46
23:AW:2:C:H2'	23:AW:3:C:H6	1.81	0.46
26:BA:879:G:H8	26:BA:879:G:O5'	1.98	0.46
26:BA:1021:A:H8	26:BA:1021:A:H3'	1.79	0.46
26:BA:1420:U:HO2'	26:BA:1421:G:P	2.38	0.46
31:BG:163:ALA:HB1	31:BG:168:GLU:HB2	1.98	0.46
38:BR:36:THR:HG22	38:BR:37:THR:H	1.81	0.46
46:BZ:70:LEU:HG	46:BZ:91:LEU:HD21	1.98	0.46
48:B1:3:LYS:HB2	48:B1:61:ARG:HH12	1.81	0.46
1:CA:337:C:H2'	1:CA:338:A:H8	1.81	0.46
1:CA:983:A:O2'	1:CA:1050:G:OP2	2.26	0.46
1:CA:1310:G:P	13:CM:88:ARG:HH22	2.39	0.46
2:CB:122:PHE:HA	2:CB:127:ILE:HD12	1.98	0.46
5:CE:41:VAL:O	5:CE:66:MET:HA	2.15	0.46
10:CJ:7:LYS:HA	10:CJ:71:LEU:HD12	1.98	0.46
26:DA:27:G:N2	26:DA:512:G:H1'	2.31	0.46
26:DA:330:A:H2	26:DA:1210:A:H2'	1.80	0.46
26:DA:332:A:O2'	26:DA:334:C:OP2	2.33	0.46
26:DA:855:G:H2'	26:DA:856:C:C6	2.51	0.46
26:DA:863:A:H2'	26:DA:864:G:C8	2.51	0.46
26:DA:1366:A:H2'	26:DA:1367:A:O4'	2.16	0.46
26:DA:2191:G:H2'	26:DA:2192:G:O4'	2.16	0.46
26:DA:2846:G:H2'	26:DA:2847:U:O4'	2.15	0.46
27:DB:14:U:O3'	27:DB:108:U:O2'	2.33	0.46
29:DE:143:ASN:HD22	29:DE:147:PRO:HD3	1.80	0.46
32:DH:86:GLU:CD	32:DH:130:ARG:HD3	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:DS:35:ILE:HD12	39:DS:101:LEU:HD12	1.98	0.46
40:DT:6:LEU:HD12	40:DT:6:LEU:HA	1.80	0.46
44:DX:94:GLY:N	44:DX:95:LEU:HA	2.30	0.46
46:DZ:50:GLN:N	46:DZ:50:GLN:CD	2.73	0.46
1:AA:134:A:N1	16:AP:25:ARG:NH1	2.65	0.45
1:AA:198:G:H2'	1:AA:199:G:H8	1.81	0.45
1:AA:373:A:H2'	1:AA:374:A:H8	1.80	0.45
1:AA:864:A:H2'	1:AA:865:A:C8	2.51	0.45
21:AU:18:TYR:CD1	21:AU:24:ARG:HG2	2.51	0.45
26:BA:956:G:OP2	37:BQ:87:LYS:NZ	2.42	0.45
26:BA:1814:G:H4'	28:BD:51:VAL:HG21	1.99	0.45
26:BA:2074:U:H2'	26:BA:2075:U:C6	2.51	0.45
26:BA:2114:A:H2'	26:BA:2115:G:O4'	2.16	0.45
28:BD:68:LYS:O	28:BD:69:ARG:HB2	2.16	0.45
33:BI:61:ARG:N	33:BI:61:ARG:HD2	2.31	0.45
34:BN:4:TYR:HB2	41:BU:101:ARG:HH12	1.81	0.45
1:CA:427:U:P	4:CD:13:ARG:HH22	2.39	0.45
1:CA:532:A:N6	3:CC:193:TYR:HB3	2.25	0.45
1:CA:1126:U:C4'	1:CA:1281:U:H1'	2.45	0.45
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.15	0.45
2:CB:112:VAL:O	2:CB:115:LEU:HD23	2.17	0.45
3:CC:50:ALA:HB1	3:CC:70:VAL:HG21	1.98	0.45
5:CE:110:LEU:HD13	5:CE:118:ILE:HD13	1.97	0.45
10:CJ:5:ARG:N	10:CJ:72:VAL:O	2.48	0.45
11:CK:20:TYR:CZ	11:CK:83:ILE:HD12	2.51	0.45
19:CS:22:LEU:O	19:CS:27:GLU:HG3	2.16	0.45
19:CS:23:ASN:HA	19:CS:27:GLU:CD	2.41	0.45
25:CY:33:U:H2'	25:CY:35:A:OP2	2.16	0.45
26:DA:648:G:O2'	26:DA:2351:G:OP1	2.23	0.45
26:DA:992:C:OP1	42:DV:74:LYS:NZ	2.33	0.45
26:DA:1913:A:H4'	26:DA:1914:C:C5'	2.45	0.45
26:DA:2378:A:H8	26:DA:2378:A:O5'	1.98	0.45
26:DA:2507:C:H5"	26:DA:2573:C:N4	2.31	0.45
29:DE:47:VAL:HG11	29:DE:86:PRO:HD2	1.98	0.45
40:DT:42:ILE:HG12	40:DT:84:GLN:NE2	2.31	0.45
50:D3:5:LYS:HB3	50:D3:57:GLU:HG2	1.98	0.45
1:AA:166:G:H2'	1:AA:167:G:H8	1.79	0.45
1:AA:236:G:H5"	17:AQ:42:TYR:OH	2.16	0.45
1:AA:323:U:H5'	20:AT:23:ARG:HB2	1.98	0.45
1:AA:1039:C:H2'	1:AA:1040:U:C6	2.51	0.45
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1505:G:O2'	22:AV:13:A:O2'	2.33	0.45
2:AB:212:GLN:O	2:AB:216:SER:OG	2.27	0.45
13:AM:3:ARG:HG2	13:AM:8:GLU:HA	1.98	0.45
13:AM:68:GLY:HA3	31:BG:116:ASP:OD1	2.16	0.45
25:AY:48:C:OP1	25:AY:48:C:H2'	2.16	0.45
26:BA:740:U:H2'	26:BA:741:G:C8	2.51	0.45
26:BA:885:C:H3'	26:BA:886:C:C5'	2.44	0.45
26:BA:2732:G:H3'	26:BA:2733:A:O4'	2.17	0.45
26:BA:2791:C:H2'	26:BA:2792:G:H8	1.81	0.45
33:BI:130:TYR:HB3	33:BI:138:ILE:HB	1.98	0.45
55:B8:6:THR:HG22	55:B8:62:LEU:HA	1.98	0.45
1:CA:696:A:H8	1:CA:696:A:O5'	1.99	0.45
1:CA:727:G:P	1:CA:742:G:H21	2.39	0.45
1:CA:1008:C:H2'	1:CA:1009:G:O4'	2.16	0.45
1:CA:1096:C:H2'	1:CA:1097:C:H6	1.81	0.45
1:CA:1315:U:H2'	1:CA:1316:G:O4'	2.16	0.45
6:CF:87:ARG:HH11	6:CF:87:ARG:CB	2.29	0.45
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.98	0.45
26:DA:288:C:H2'	26:DA:289:A:H8	1.80	0.45
26:DA:597:U:H2'	26:DA:598:G:C8	2.51	0.45
26:DA:921:G:C6	26:DA:922:U:C4	3.04	0.45
26:DA:2167:U:O2	26:DA:2167:U:H2'	2.15	0.45
29:DE:27:LEU:HD22	40:DT:1:MET:CE	2.46	0.45
34:DN:39:ARG:HA	34:DN:40:PRO:HD3	1.88	0.45
35:DO:20:MET:HE3	35:DO:44:LYS:HE3	1.98	0.45
35:DO:103:ALA:HB1	35:DO:105:GLU:OE1	2.16	0.45
37:DQ:79:LEU:C	37:DQ:80:GLU:HG2	2.42	0.45
1:AA:11:G:O2'	1:AA:506:G:N2	2.46	0.45
1:AA:1038:C:O2'	1:AA:1039:C:H5'	2.17	0.45
2:AB:20:GLU:HA	2:AB:21:ARG:NH2	2.30	0.45
2:AB:222:ILE:O	2:AB:226:ARG:HG2	2.16	0.45
4:AD:187:ARG:HE	4:AD:187:ARG:HB3	1.53	0.45
8:AH:51:VAL:HG21	8:AH:60:ARG:HB2	1.98	0.45
25:AY:2:C:N4	25:AY:71:G:H1	2.14	0.45
26:BA:141:A:H8	26:BA:1408:C:O2'	1.99	0.45
26:BA:1266:G:O5'	43:BW:15:ARG:NH2	2.49	0.45
26:BA:2010:G:H5"	43:BW:42:ARG:HB2	1.97	0.45
26:BA:2180:U:H2'	26:BA:2181:G:O4'	2.17	0.45
26:BA:2747:G:O6	26:BA:2755:C:H5"	2.16	0.45
30:BF:64:ILE:HG21	30:BF:78:ILE:HG23	1.96	0.45
1:CA:456:C:C2'	1:CA:457:C:H5'	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:620:C:H2'	1:CA:621:A:O4'	2.17	0.45
9:CI:45:ALA:O	9:CI:48:GLU:HB2	2.16	0.45
13:CM:3:ARG:HA	51:D4:34:GLU:HG2	1.99	0.45
19:CS:63:THR:O	19:CS:66:MET:HG3	2.16	0.45
23:CW:9:A:O2'	23:CW:10:G:N7	2.47	0.45
23:CW:22:G:C2	23:CW:23:A:C5	3.04	0.45
25:CY:10:G:N2	25:CY:25:C:N3	2.54	0.45
25:CY:35:A:O5'	25:CY:35:A:H8	1.98	0.45
26:DA:271(H):G:O2'	26:DA:271(I):G:H8	2.00	0.45
26:DA:1213:A:N3	26:DA:1238:G:O2'	2.46	0.45
26:DA:1417:C:H3'	61:DA:4108:HOH:O	2.16	0.45
26:DA:2149:G:H5"	26:DA:2150:U:OP2	2.17	0.45
26:DA:2543:G:H2'	26:DA:2544:G:C8	2.51	0.45
29:DE:144:ARG:HB3	29:DE:145:LYS:H	1.53	0.45
1:AA:163:C:H2'	1:AA:164:U:C6	2.51	0.45
1:AA:189(D):C:O2	1:AA:189(H):G:C6	2.69	0.45
1:AA:735:C:H2'	1:AA:736:C:C6	2.52	0.45
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.80	0.45
1:AA:1055:A:H2'	3:AC:156:ARG:HD2	1.99	0.45
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.85	0.45
3:AC:71:ALA:HB2	3:AC:115:LEU:HD21	1.97	0.45
8:AH:49:GLU:OE2	8:AH:62:TYR:OH	2.26	0.45
10:AJ:8:LEU:HD21	10:AJ:96:ILE:HG23	1.98	0.45
13:AM:113:PRO:O	13:AM:115:LYS:NZ	2.50	0.45
24:AX:9:G:O2'	24:AX:10:G:N7	2.49	0.45
26:BA:2099:U:H2'	26:BA:2100:G:C8	2.51	0.45
26:BA:2340:G:H2'	26:BA:2341:G:H8	1.81	0.45
35:BO:98:VAL:HG13	35:BO:117:LEU:HB3	1.97	0.45
41:BU:76:TYR:CE1	41:BU:80:ILE:HG13	2.52	0.45
43:BW:88:ARG:HA	43:BW:88:ARG:HD2	1.76	0.45
51:B4:41:PRO:HA	51:B4:47:GLN:HB3	1.98	0.45
53:B6:40:CYS:HA	53:B6:41:PRO:HD3	1.80	0.45
1:CA:110:C:O2'	16:CP:25:ARG:O	2.27	0.45
1:CA:859:A:H2'	1:CA:860:A:O4'	2.16	0.45
1:CA:1009:G:C2	1:CA:1010:G:C4	3.04	0.45
1:CA:1062:U:H2'	1:CA:1063:C:C5	2.51	0.45
11:CK:34:ASP:OD2	11:CK:38:ASN:HB2	2.16	0.45
12:CL:37:CYS:SG	12:CL:81:SER:HB2	2.56	0.45
26:DA:536:A:H2'	26:DA:537:C:C6	2.51	0.45
26:DA:996:A:H4'	41:DU:91:ASP:OD2	2.16	0.45
26:DA:1654:A:OP1	38:DR:1:MET:HA	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2659:G:O2'	26:DA:2661:G:N7	2.38	0.45
28:DD:218:ARG:HB3	28:DD:219:PRO:HD2	1.99	0.45
31:DG:66:GLN:HE21	31:DG:92:VAL:HG23	1.82	0.45
40:DT:51:ARG:HG3	40:DT:98:LYS:NZ	2.32	0.45
46:DZ:23:LYS:NZ	46:DZ:40:ASP:OD1	2.48	0.45
46:DZ:43:GLU:O	46:DZ:47:VAL:N	2.50	0.45
49:D2:62:THR:O	49:D2:66:GLU:HG3	2.16	0.45
51:D4:62:ARG:HB2	51:D4:63:TYR:CE1	2.51	0.45
56:D9:3:VAL:HA	56:D9:35:ARG:O	2.17	0.45
1:AA:161:A:H2'	1:AA:162:A:C8	2.52	0.45
1:AA:811:C:O2'	1:AA:901:A:N1	2.43	0.45
8:AH:29:SER:OG	8:AH:32:LYS:HG3	2.17	0.45
17:AQ:78:GLU:HG2	17:AQ:79:SER:H	1.81	0.45
24:AX:4:G:H1	24:AX:69:C:H42	1.64	0.45
26:BA:582:G:H2'	26:BA:583:G:C8	2.52	0.45
26:BA:1045:A:H1'	26:BA:1047:G:C2	2.51	0.45
26:BA:2191:G:H5'	26:BA:2191:G:C8	2.50	0.45
28:BD:24:ILE:HD13	28:BD:84:TYR:HB2	1.99	0.45
43:BW:18:ARG:NH1	43:BW:76:VAL:O	2.50	0.45
1:CA:399:G:H2'	1:CA:400:C:C6	2.51	0.45
1:CA:920:U:H2'	1:CA:921:U:H6	1.80	0.45
1:CA:959:A:O2'	1:CA:984:C:O2'	2.06	0.45
1:CA:1347:G:O2'	1:CA:1373:G:N1	2.47	0.45
12:CL:8:ASN:O	12:CL:12:ARG:HG3	2.16	0.45
24:CX:22:G:OP2	24:CX:22:G:H8	2.00	0.45
25:CY:36:A:H2'	25:CY:37:MIA:O4'	2.16	0.45
26:DA:71:A:H5"	26:DA:73:A:C8	2.51	0.45
26:DA:527:C:H4'	26:DA:528:A:O5'	2.15	0.45
26:DA:652:C:C2'	26:DA:652(A):A:H5'	2.46	0.45
26:DA:2153:G:H3'	26:DA:2154:G:C8	2.51	0.45
30:DF:12:LEU:HB2	30:DF:124:LEU:HD11	1.97	0.45
31:DG:106:LEU:HA	31:DG:110:ALA:CB	2.45	0.45
33:DI:69:LYS:HG3	33:DI:73:GLU:OE1	2.16	0.45
38:DR:70:LEU:HD13	38:DR:75:LEU:HD13	1.98	0.45
42:DV:89:GLN:HA	42:DV:90:PRO:HD3	1.83	0.45
1:AA:17:U:H2'	1:AA:18:C:C6	2.52	0.45
1:AA:175:C:H2'	1:AA:176:C:H6	1.80	0.45
1:AA:850:U:H2'	1:AA:851:G:H5"	1.98	0.45
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.97	0.45
23:AW:9:A:O2'	23:AW:10:G:N7	2.49	0.45
26:BA:8:A:H2'	26:BA:9:U:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:27:G:N2	26:BA:512:G:H1'	2.32	0.45
26:BA:95:G:O2'	49:B2:48:HIS:ND1	2.38	0.45
26:BA:747:U:O2	26:BA:2014:A:H1'	2.17	0.45
26:BA:2803:C:H2'	26:BA:2804:C:C6	2.51	0.45
46:BZ:146:ILE:HA	46:BZ:147:GLY:HA2	1.70	0.45
1:CA:1121:U:C4	1:CA:1122:U:C5	3.05	0.45
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.80	0.45
1:CA:1320:C:H2'	1:CA:1321:C:O4'	2.17	0.45
1:CA:1385:G:H2'	1:CA:1386:G:C8	2.51	0.45
9:CI:9:ARG:HA	9:CI:13:ALA:O	2.17	0.45
13:CM:57:ARG:O	13:CM:61:GLU:HB2	2.17	0.45
26:DA:784:A:N6	28:DD:229:VAL:HG11	2.31	0.45
26:DA:1527:G:H5"	26:DA:1528:A:OP1	2.16	0.45
26:DA:1876:A:H2'	26:DA:1877:A:C8	2.52	0.45
26:DA:2120:G:O6	26:DA:2178:C:N3	2.49	0.45
26:DA:2207:G:P	26:DA:2207:G:H8	2.40	0.45
26:DA:2468:G:C4	26:DA:2481:G:C2	3.05	0.45
26:DA:2494:G:O2'	37:DQ:80:GLU:HA	2.16	0.45
28:DD:141:VAL:HG12	28:DD:164:GLN:HG3	1.99	0.45
29:DE:54:GLN:HB2	29:DE:76:ARG:HG2	1.98	0.45
40:DT:11:GLU:O	40:DT:15:VAL:HG23	2.16	0.45
42:DV:12:TYR:CG	42:DV:20:LEU:HD21	2.52	0.45
44:DX:44:GLU:OE2	44:DX:51:VAL:N	2.45	0.45
52:D5:40:LYS:NZ	52:D5:44:THR:O	2.34	0.45
52:D5:49:CYS:SG	52:D5:51:TYR:HB2	2.57	0.45
54:D7:5:TRP:CD1	54:D7:7:PRO:HD3	2.50	0.45
1:AA:375:U:O2'	16:AP:6:LEU:O	2.32	0.45
1:AA:407:G:O2'	4:AD:116:GLN:HG3	2.17	0.45
1:AA:445:G:H2'	1:AA:446:G:C8	2.52	0.45
1:AA:688:G:H2'	1:AA:689:C:C6	2.52	0.45
1:AA:881:G:P	12:AL:12:ARG:HH22	2.40	0.45
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.17	0.45
2:AB:19:HIS:CD2	2:AB:206:ASP:HB2	2.52	0.45
2:AB:48:MET:HA	2:AB:51:LEU:HD12	1.97	0.45
4:AD:144:ASP:OD1	4:AD:144:ASP:N	2.49	0.45
13:AM:33:ALA:O	13:AM:37:THR:OG1	2.29	0.45
24:AX:4:G:H2'	24:AX:5:G:C8	2.52	0.45
26:BA:405:U:O5'	26:BA:405:U:H6	1.99	0.45
26:BA:592:G:O6	61:BA:4916:HOH:O	2.15	0.45
26:BA:1364:G:OP2	48:B1:3:LYS:HG3	2.17	0.45
26:BA:1430:C:H2'	26:BA:1431:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1593:G:H2'	26:BA:1594:G:C8	2.52	0.45
30:BF:125:LEU:HD12	30:BF:194:MET:HB2	1.98	0.45
33:BI:135:GLU:C	33:BI:137:PRO:HD3	2.42	0.45
1:CA:411:A:OP1	4:CD:30:LYS:HD3	2.16	0.45
1:CA:660:G:H1	1:CA:745:C:N4	2.12	0.45
1:CA:742:G:H5'	15:CO:58:MET:HE1	1.97	0.45
1:CA:985:C:N4	1:CA:1220:G:N1	2.29	0.45
1:CA:1036:G:N7	1:CA:1037:C:C2	2.85	0.45
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.99	0.45
23:CW:10:G:N2	23:CW:11:C:C2	2.84	0.45
24:CX:5:G:H2'	24:CX:6:G:H5'	1.99	0.45
25:CY:71:G:H4'	26:DA:1851:U:H4'	1.99	0.45
26:DA:620:G:N3	26:DA:620:G:H5'	2.31	0.45
26:DA:783:A:O2'	26:DA:785:G:OP1	2.29	0.45
26:DA:848:G:C2	26:DA:933:A:H1'	2.52	0.45
32:DH:95:ARG:HG2	32:DH:96:ALA:N	2.32	0.45
44:DX:31:HIS:CD2	44:DX:33:LYS:HB2	2.52	0.45
45:DY:90:LEU:HD11	45:DY:96:ILE:HG23	1.98	0.45
46:DZ:158:PRO:HA	46:DZ:159:PRO:HD3	1.71	0.45
1:AA:217:C:C2'	1:AA:218:C:H5'	2.46	0.45
1:AA:1290:G:H2'	1:AA:1291:G:H8	1.82	0.45
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.45	0.45
3:AC:8:ILE:HG23	3:AC:16:ARG:HG2	1.98	0.45
26:BA:675:A:C8	26:BA:804:A:C6	3.05	0.45
26:BA:2011:U:OP1	43:BW:42:ARG:HD3	2.17	0.45
26:BA:2168:G:O6	26:BA:2171:A:H2'	2.16	0.45
26:BA:2199:A:OP2	26:BA:2200:C:H5	1.99	0.45
26:BA:2312:U:OP1	31:BG:73:ALA:HA	2.17	0.45
26:BA:2640:G:OP1	34:BN:97:ARG:NH2	2.49	0.45
28:BD:70:TRP:CE2	28:BD:150:LYS:HD3	2.52	0.45
28:BD:232:PRO:O	61:BD:3103:HOH:O	2.21	0.45
29:BE:31:CYS:HA	29:BE:32:PRO:HD2	1.89	0.45
30:BF:150:GLY:HA2	30:BF:172:TRP:CE3	2.52	0.45
34:BN:68:GLU:H	34:BN:68:GLU:HG2	1.46	0.45
48:B1:3:LYS:HB3	48:B1:4:VAL:H	1.50	0.45
55:B8:33:ASN:HA	55:B8:36:LYS:HD2	1.99	0.45
1:CA:826:C:H2'	1:CA:827:U:C6	2.51	0.45
1:CA:1035:A:H2'	1:CA:1036:G:H8	1.82	0.45
1:CA:1205:U:H4'	3:CC:195:VAL:HG23	1.98	0.45
1:CA:1490:C:H2'	1:CA:1491:G:O4'	2.17	0.45
2:CB:12:GLU:C	2:CB:14:GLY:HA3	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:70:PHE:HB2	2:CB:92:TYR:CB	2.47	0.45
4:CD:8:VAL:O	4:CD:11:LEU:HB2	2.17	0.45
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.17	0.45
26:DA:271(K):U:O2	33:DI:50:ARG:HG3	2.17	0.45
26:DA:2138:C:N4	26:DA:2153:G:N1	2.32	0.45
26:DA:2328:A:H2'	26:DA:2329:G:C8	2.52	0.45
26:DA:2461:C:H2'	26:DA:2462:U:C6	2.52	0.45
27:DB:34:U:O4	27:DB:44:G:O2'	2.29	0.45
28:DD:171:ASP:O	28:DD:187:GLY:N	2.49	0.45
32:DH:148:ILE:H	32:DH:148:ILE:HG12	1.54	0.45
48:D1:83:GLU:HA	48:D1:84:GLY:HA2	1.70	0.45
51:D4:40:HIS:O	51:D4:44:THR:N	2.24	0.45
52:D5:33:CYS:HA	52:D5:34:PRO:HD3	1.85	0.45
1:AA:678:U:H2'	1:AA:679:C:C6	2.52	0.45
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.52	0.45
3:AC:108:ASN:HB3	3:AC:111:LEU:HD12	1.99	0.45
3:AC:121:ALA:HB1	3:AC:189:ALA:HB2	1.99	0.45
3:AC:156:ARG:HE	3:AC:156:ARG:HB3	1.50	0.45
26:BA:127:A:H5"	26:BA:128:C:C6	2.52	0.45
26:BA:245:G:O5'	36:BP:73:GLY:HA2	2.16	0.45
26:BA:1501:C:O4'	28:BD:100:GLY:HA2	2.17	0.45
28:BD:52:ARG:NH2	61:BD:3112:HOH:O	2.42	0.45
29:BE:1:MET:HE1	29:BE:199:ARG:HD2	1.99	0.45
46:BZ:157:LEU:C	46:BZ:161:VAL:HG11	2.42	0.45
1:CA:6:G:H4'	1:CA:298:A:H4'	1.98	0.45
1:CA:376:G:O2'	16:CP:5:ARG:NH2	2.50	0.45
1:CA:982:U:H4'	1:CA:983:A:O5'	2.17	0.45
1:CA:1253:G:H2'	1:CA:1254:C:C6	2.52	0.45
3:CC:40:ARG:NH1	3:CC:57:ILE:HD13	2.32	0.45
9:CI:81:ILE:O	9:CI:85:LEU:HG	2.17	0.45
19:CS:30:LEU:HA	19:CS:48:THR:O	2.16	0.45
24:CX:10:G:N2	24:CX:26:G:H1'	2.31	0.45
26:DA:34:C:H2'	26:DA:34:C:O2	2.17	0.45
26:DA:297:C:OP1	45:DY:87:LYS:HG3	2.17	0.45
26:DA:862:G:H2'	26:DA:863:A:O4'	2.16	0.45
26:DA:1165:U:H2'	26:DA:1166:C:C6	2.51	0.45
26:DA:1287:A:C5	26:DA:1288:U:C4	3.05	0.45
26:DA:2263:C:H2'	26:DA:2264:C:O4'	2.17	0.45
26:DA:2365:G:P	47:D0:55:ARG:HG2	2.57	0.45
26:DA:2683:C:O2	35:DO:70:LYS:NZ	2.44	0.45
26:DA:2872:G:C2	26:DA:2873:A:N6	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DE:24:THR:HG22	29:DE:184:VAL:HG12	1.98	0.45
30:DF:156:LEU:HD21	30:DF:163:VAL:HG12	1.98	0.45
31:DG:171:ALA:O	31:DG:175:LEU:N	2.37	0.45
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.99	0.45
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.05	0.45
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.17	0.45
13:AM:15:VAL:O	13:AM:19:LEU:HD22	2.17	0.45
13:AM:108:ARG:HA	13:AM:108:ARG:HD3	1.66	0.45
20:AT:9:ASN:ND2	20:AT:10:LEU:H	2.15	0.45
25:AY:13:C:H2'	25:AY:14:A:H8	1.82	0.45
26:BA:11:G:H2'	26:BA:12:U:H5"	1.98	0.45
26:BA:574:C:N3	29:BE:145:LYS:NZ	2.51	0.45
26:BA:587:C:P	36:BP:21:ARG:HH22	2.40	0.45
26:BA:2080:G:OP1	48:B1:35:THR:HG21	2.17	0.45
26:BA:2246:G:H2'	26:BA:2247:A:C8	2.52	0.45
28:BD:20:ASP:OD2	28:BD:22:SER:HB2	2.17	0.45
30:BF:184:TYR:CE2	30:BF:188:ARG:HD2	2.52	0.45
37:BQ:85:LYS:HG2	47:B0:7:LEU:HB3	1.99	0.45
48:B1:67:ILE:N	48:B1:68:PRO:HD2	2.31	0.45
1:CA:25:C:H5'	1:CA:524:G:H1'	1.98	0.45
1:CA:65:U:H5'	1:CA:65:U:H6	1.81	0.45
1:CA:502:G:C2	1:CA:503:C:C2	3.05	0.45
1:CA:1206:G:C6	1:CA:1207:G:C5	3.05	0.45
2:CB:71:VAL:O	2:CB:71:VAL:HG23	2.17	0.45
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.52	0.45
7:CG:144:MET:HE2	7:CG:144:MET:HB3	1.90	0.45
17:CQ:63:ARG:HG2	17:CQ:64:PRO:HD2	1.99	0.45
23:CW:38:A:H5'	26:DA:1913:A:N6	2.32	0.45
26:DA:1031:G:H21	56:D9:36:GLN:HE22	1.63	0.45
26:DA:1131:G:O6	26:DA:2040:C:H1'	2.17	0.45
26:DA:1427:A:H4'	26:DA:1428:C:O5'	2.17	0.45
26:DA:1588:C:H2'	26:DA:1589:C:H6	1.82	0.45
27:DB:73:A:C4	27:DB:105:A:C2	3.04	0.45
31:DG:166:ASP:O	31:DG:170:ARG:N	2.46	0.45
41:DU:85:LYS:HB2	41:DU:116:ALA:HB1	1.99	0.45
43:DW:2:GLU:OE2	43:DW:72:LYS:HE2	2.17	0.45
44:DX:31:HIS:HA	44:DX:32:PRO:HD3	1.87	0.45
51:D4:62:ARG:O	51:D4:63:TYR:C	2.61	0.45
53:D6:23:THR:OG1	53:D6:24:GLU:N	2.48	0.45
1:AA:345:C:H6	1:AA:345:C:O5'	2.00	0.44
1:AA:750:G:H1'	15:AO:22:THR:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1161:C:O2'	1:AA:1162:C:H5'	2.18	0.44
6:AF:55:ASP:HA	6:AF:56:PRO:HD3	1.84	0.44
14:AN:14:PRO:HG2	14:AN:20:ALA:HB2	1.98	0.44
18:AR:59:SER:OG	18:AR:62:GLU:HG2	2.18	0.44
19:AS:36:ARG:NH1	19:AS:52:TYR:O	2.48	0.44
23:AW:4:C:N3	23:AW:69:G:O6	2.50	0.44
23:AW:61:C:H2'	23:AW:62:C:H6	1.82	0.44
26:BA:817:C:H4'	26:BA:932:G:C5	2.52	0.44
36:BP:65:ARG:HG3	55:B8:25:MET:CG	2.46	0.44
38:BR:53:HIS:O	38:BR:56:LYS:HB2	2.18	0.44
51:B4:48:ARG:HB3	51:B4:51:ASP:O	2.17	0.44
1:CA:154:C:H2'	1:CA:155:C:C6	2.52	0.44
1:CA:382:A:H2'	1:CA:383:A:C8	2.52	0.44
1:CA:606:G:H5"	1:CA:607:A:H5'	1.99	0.44
1:CA:986:A:H2'	1:CA:987:G:O4'	2.17	0.44
1:CA:1015:A:H4'	14:CN:15:LYS:NZ	2.33	0.44
1:CA:1084:G:C5	1:CA:1085:U:C4	3.05	0.44
1:CA:1120:G:N1	1:CA:1154:G:N3	2.65	0.44
1:CA:1258:G:O2'	1:CA:1259:C:H5'	2.17	0.44
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.51	0.44
7:CG:155:ARG:HG2	7:CG:156:TRP:N	2.32	0.44
12:CL:110:VAL:O	12:CL:122:THR:OG1	2.30	0.44
23:CW:47:U:O2'	23:CW:48:C:OP1	2.29	0.44
26:DA:751:A:H5'	43:DW:90:ARG:HA	1.98	0.44
26:DA:971:C:H2'	26:DA:972:G:O4'	2.17	0.44
26:DA:1913:A:H4'	26:DA:1914:C:H5"	1.98	0.44
26:DA:2356:C:O3'	47:D0:20:ARG:HD3	2.17	0.44
26:DA:2727:G:O2'	35:DO:70:LYS:NZ	2.51	0.44
31:DG:152:LEU:H	31:DG:152:LEU:HD12	1.82	0.44
32:DH:13:LYS:HA	32:DH:14:GLY:HA2	1.55	0.44
36:DP:95:VAL:HG13	36:DP:125:VAL:HG12	1.98	0.44
43:DW:17:VAL:HG11	43:DW:103:ILE:HD11	1.98	0.44
45:DY:3:VAL:HB	45:DY:32:PRO:HB3	2.00	0.44
1:AA:100:C:H2'	1:AA:101:A:C8	2.52	0.44
1:AA:114:U:H1'	1:AA:353:A:H1'	1.99	0.44
1:AA:431:A:H2'	1:AA:432:A:O4'	2.18	0.44
1:AA:1027:C:H2'	1:AA:1028:C:C6	2.52	0.44
4:AD:112:VAL:HG23	4:AD:116:GLN:OE1	2.16	0.44
8:AH:56:LYS:HB2	8:AH:58:TYR:HE1	1.81	0.44
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.51	0.44
9:AI:102:LEU:HD22	9:AI:102:LEU:HA	1.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AQ:92:ARG:HD2	17:AQ:92:ARG:HA	1.92	0.44
19:AS:9:VAL:HG21	51:B4:61:ARG:HH12	1.82	0.44
25:AY:6:G:C6	25:AY:7:A:C5	3.05	0.44
26:BA:372:G:H8	48:B1:65:SER:O	2.00	0.44
26:BA:686:G:H8	54:B7:6:GLN:O	2.00	0.44
26:BA:1794:U:H2'	26:BA:1795:C:H6	1.81	0.44
26:BA:2130:U:H2'	26:BA:2131:G:H21	1.82	0.44
26:BA:2260:C:H2'	26:BA:2261:C:H6	1.82	0.44
27:BB:91:C:OP1	37:BQ:16:ARG:HG3	2.18	0.44
29:BE:149:ARG:O	61:BE:406:HOH:O	2.21	0.44
30:BF:8:GLN:HA	30:BF:8:GLN:NE2	2.32	0.44
32:BH:13:LYS:HA	32:BH:14:GLY:HA2	1.58	0.44
39:BS:27:SER:HA	39:BS:88:ASP:HB3	1.98	0.44
1:CA:683:G:H2'	1:CA:684:A:H8	1.81	0.44
1:CA:848:C:O5'	1:CA:848:C:H6	2.00	0.44
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.98	0.44
2:CB:162:ILE:O	2:CB:162:ILE:HG13	2.15	0.44
2:CB:167:PRO:HG3	2:CB:188:ALA:HB2	1.98	0.44
3:CC:85:ARG:O	3:CC:89:GLU:HG3	2.17	0.44
6:CF:100:ASN:HD21	18:CR:23:LYS:HG2	1.83	0.44
9:CI:16:ARG:HB2	9:CI:64:THR:HG23	1.99	0.44
12:CL:6:THR:HG23	12:CL:9:GLN:OE1	2.17	0.44
16:CP:40:ASP:O	16:CP:48:TRP:HB2	2.18	0.44
26:DA:774:A:N3	26:DA:774:A:H2'	2.33	0.44
26:DA:776:G:H4'	26:DA:777:A:O5'	2.17	0.44
26:DA:921:G:H4'	26:DA:2269:A:C5	2.51	0.44
26:DA:1021:A:C8	26:DA:1021:A:H3'	2.52	0.44
26:DA:1127:A:N7	26:DA:2488:A:O2'	2.50	0.44
26:DA:1583:A:H4'	26:DA:1586:A:C4	2.52	0.44
26:DA:2723:C:O3'	38:DR:1:MET:HE2	2.17	0.44
27:DB:75:G:O2'	46:DZ:85:HIS:NE2	2.42	0.44
33:DI:77:LEU:HD11	33:DI:97:ILE:HG23	1.99	0.44
34:DN:73:THR:OG1	34:DN:82:LEU:HD11	2.16	0.44
35:DO:76:ALA:HB3	40:DT:75:ILE:HB	1.99	0.44
46:DZ:79:ARG:HD2	46:DZ:80:ARG:NH2	2.32	0.44
1:AA:110:C:H2'	1:AA:111:G:O4'	2.18	0.44
2:AB:219:VAL:O	2:AB:223:ILE:HG12	2.16	0.44
2:AB:223:ILE:HD12	2:AB:230:VAL:HG12	2.00	0.44
4:AD:18:LYS:HD2	4:AD:31:CYS:SG	2.57	0.44
24:AX:46:G:H5"	24:AX:47:U:OP2	2.16	0.44
26:BA:226:G:N2	26:BA:228:A:H62	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:796:C:H2'	26:BA:797:C:C6	2.52	0.44
26:BA:2790:A:N3	26:BA:2790:A:H2'	2.31	0.44
30:BF:165:ARG:HG2	30:BF:168:ARG:HH21	1.82	0.44
31:BG:43:LEU:HD12	31:BG:43:LEU:HA	1.81	0.44
32:BH:124:GLU:OE1	32:BH:132:ARG:HD2	2.18	0.44
33:BI:75:LEU:HD22	33:BI:105:HIS:ND1	2.31	0.44
39:BS:6:ALA:O	39:BS:10:ARG:HB2	2.17	0.44
1:CA:437:U:O2'	4:CD:125:HIS:HE1	1.99	0.44
1:CA:543:C:O2'	1:CA:544:G:H5'	2.17	0.44
1:CA:715:A:H5"	1:CA:805:C:H1'	1.99	0.44
1:CA:743:U:H2'	1:CA:744:C:C6	2.52	0.44
1:CA:1001(A):G:H5"	1:CA:1002:G:OP2	2.17	0.44
1:CA:1131:G:H2'	1:CA:1132:C:H6	1.82	0.44
1:CA:1132:C:H2'	1:CA:1133:G:H8	1.83	0.44
1:CA:1239:A:H4'	1:CA:1240:U:H5"	1.98	0.44
11:CK:66:LEU:O	11:CK:70:LYS:HD2	2.18	0.44
14:CN:40:CYS:O	14:CN:44:LEU:HB3	2.18	0.44
14:CN:45:ARG:O	14:CN:49:HIS:HD2	1.99	0.44
19:CS:33:THR:HG22	19:CS:50:ALA:O	2.17	0.44
25:CY:51:U:N3	25:CY:63:G:N1	2.41	0.44
25:CY:67:C:H2'	25:CY:68:C:C6	2.52	0.44
26:DA:752:A:H4'	26:DA:753:C:H5'	1.99	0.44
26:DA:902:C:H2'	26:DA:903:C:H6	1.82	0.44
26:DA:1030:G:OP2	37:DQ:128:LYS:HD3	2.17	0.44
26:DA:2169:A:O2'	26:DA:2170:A:O5'	2.32	0.44
26:DA:2355:C:H4'	47:D0:24:LYS:HD3	1.99	0.44
26:DA:2441:C:OP2	26:DA:2586:C:O2'	2.31	0.44
26:DA:2849:U:H4'	26:DA:2868:A:C2	2.51	0.44
27:DB:45:A:H2'	27:DB:46:A:H8	1.82	0.44
28:DD:96:HIS:CD2	28:DD:102:LYS:HG2	2.53	0.44
31:DG:3:LEU:HD23	31:DG:3:LEU:H	1.81	0.44
37:DQ:29:PHE:HB2	37:DQ:105:GLU:OE2	2.18	0.44
37:DQ:134:ARG:CZ	46:DZ:122:ARG:HE	2.30	0.44
38:DR:118:GLU:H	38:DR:118:GLU:CD	2.25	0.44
40:DT:97:ALA:C	40:DT:98:LYS:HD2	2.42	0.44
46:DZ:50:GLN:CD	46:DZ:50:GLN:H	2.23	0.44
1:AA:21:G:H2'	1:AA:22:G:C8	2.53	0.44
1:AA:217:C:O2'	1:AA:218:C:H5'	2.17	0.44
1:AA:435:C:H6	1:AA:435:C:O5'	2.01	0.44
1:AA:1057:G:H2'	1:AA:1058:G:O4'	2.17	0.44
1:AA:1131:G:H2'	1:AA:1132:C:H6	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:27:ARG:HE	5:AE:27:ARG:HB2	1.53	0.44
10:AJ:33:GLN:O	10:AJ:75:ILE:N	2.44	0.44
17:AQ:60:ILE:O	17:AQ:62:SER:OG	2.34	0.44
26:BA:1009:A:OP2	34:BN:37:LYS:NZ	2.50	0.44
26:BA:1178:C:O5'	26:BA:1178:C:H6	2.00	0.44
27:BB:91:C:OP2	37:BQ:16:ARG:NH1	2.51	0.44
33:BI:38:LEU:H	33:BI:38:LEU:CD1	2.23	0.44
1:CA:90:U:O2'	1:CA:91:C:H5'	2.18	0.44
1:CA:814:A:N7	1:CA:816:A:C4	2.85	0.44
1:CA:994:A:C5	1:CA:1216:G:H4'	2.53	0.44
1:CA:1004:A:C2	1:CA:1038:C:C4	3.05	0.44
1:CA:1016:A:O2'	1:CA:1217:C:O2'	2.14	0.44
1:CA:1085:U:H3'	1:CA:1086:U:C5	2.52	0.44
1:CA:1134:G:C6	1:CA:1135:U:C2	3.05	0.44
4:CD:173:TRP:CE2	4:CD:189:PRO:HG3	2.53	0.44
7:CG:78:ARG:CZ	7:CG:79:ARG:HH22	2.30	0.44
8:CH:125:ARG:HE	8:CH:125:ARG:HB2	1.49	0.44
9:CI:24:GLY:HA2	9:CI:59:PHE:O	2.17	0.44
13:CM:13:LYS:HA	13:CM:44:ARG:NH1	2.33	0.44
26:DA:87:C:H5"	26:DA:88:G:H5'	1.99	0.44
26:DA:1129:A:N6	26:DA:2491:U:OP1	2.50	0.44
26:DA:1406:U:H2'	26:DA:1407:C:C6	2.52	0.44
26:DA:1999:C:H4'	26:DA:2723:C:O2	2.17	0.44
26:DA:2192:G:H5'	26:DA:2193:G:OP2	2.17	0.44
26:DA:2611:U:H3'	26:DA:2611:U:OP2	2.18	0.44
27:DB:33:G:N3	27:DB:50:G:N2	2.66	0.44
30:DF:24:LEU:HD21	30:DF:114:VAL:HG12	1.99	0.44
30:DF:187:VAL:HG12	36:DP:3:LEU:HD12	1.99	0.44
34:DN:103:VAL:O	34:DN:107:LEU:HG	2.17	0.44
47:D0:14:ARG:HB2	47:D0:14:ARG:HH11	1.83	0.44
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.63	0.44
1:AA:1152:A:H2'	1:AA:1153:C:H6	1.82	0.44
2:AB:107:THR:O	2:AB:110:GLN:HB2	2.18	0.44
3:AC:156:ARG:NH2	3:AC:159:GLY:O	2.48	0.44
11:AK:34:ASP:HB3	11:AK:40:ILE:HD11	1.99	0.44
16:AP:19:ILE:HG22	16:AP:37:GLY:C	2.43	0.44
25:AY:57:G:H2'	25:AY:58:A:C5'	2.48	0.44
26:BA:187:G:OP2	61:BA:4447:HOH:O	2.21	0.44
26:BA:637:A:H8	36:BP:117:GLU:HG3	1.82	0.44
26:BA:2028:U:H2'	26:BA:2029:G:O4'	2.18	0.44
26:BA:2191:G:H2'	26:BA:2192:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2405:G:O2'	26:BA:2411:A:N6	2.50	0.44
32:BH:125:VAL:HG12	32:BH:127:GLU:O	2.18	0.44
33:BI:62:LYS:HE3	33:BI:133:HIS:CE1	2.53	0.44
49:B2:2:LYS:O	49:B2:6:VAL:HG23	2.17	0.44
52:B5:16:ARG:HD2	52:B5:20:ARG:NH1	2.31	0.44
1:CA:878:G:OP1	8:CH:88:LYS:HB3	2.17	0.44
1:CA:947:G:C6	1:CA:948:C:C4	3.06	0.44
1:CA:1113:C:H42	1:CA:1187:G:H1	1.65	0.44
1:CA:1132:C:H2'	1:CA:1133:G:C8	2.52	0.44
1:CA:1360:A:H2'	1:CA:1361:G:O4'	2.18	0.44
1:CA:1371:G:OP1	9:CI:12:GLU:HB2	2.18	0.44
2:CB:36:ARG:O	2:CB:37:ASN:HB2	2.17	0.44
3:CC:83:ARG:O	3:CC:87:LEU:HG	2.18	0.44
5:CE:57:LYS:O	5:CE:61:TYR:HD2	2.00	0.44
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.16	0.44
26:DA:1235:G:C6	26:DA:1236:G:N1	2.85	0.44
26:DA:2131:G:H5"	26:DA:2131:G:N3	2.32	0.44
26:DA:2274:A:C5	26:DA:2276:G:C8	3.05	0.44
26:DA:2286:A:H4'	26:DA:2287:A:O4'	2.17	0.44
26:DA:2748:A:H5'	32:DH:4:ILE:HD12	1.99	0.44
30:DF:140:LEU:HD13	30:DF:170:LEU:HD21	1.99	0.44
31:DG:161:THR:HG22	31:DG:163:ALA:H	1.83	0.44
32:DH:137:ASP:HB3	32:DH:140:LYS:HB3	1.98	0.44
44:DX:8:ILE:O	49:D2:36:ARG:NH2	2.51	0.44
1:AA:1479:C:H2'	1:AA:1480:G:H8	1.82	0.44
3:AC:36:ASP:C	3:AC:40:ARG:HG3	2.43	0.44
8:AH:119:LEU:HB3	8:AH:123:GLU:HB3	1.99	0.44
13:AM:49:THR:OG1	13:AM:52:GLU:HG3	2.18	0.44
13:AM:79:LYS:HA	13:AM:82:MET:HE2	2.00	0.44
25:AY:71:G:H2'	25:AY:72:C:C6	2.53	0.44
26:BA:281:G:O2'	26:BA:359:A:N6	2.47	0.44
26:BA:528:A:N1	26:BA:2042:A:H2'	2.32	0.44
26:BA:614:U:H5'	26:BA:614(C):A:N6	2.33	0.44
26:BA:764:A:H5'	28:BD:210:GLY:HA2	1.99	0.44
26:BA:952:G:P	37:BQ:16:ARG:HH21	2.40	0.44
26:BA:1377:G:H2'	61:BA:3925:HOH:O	2.18	0.44
26:BA:1405:U:H2'	26:BA:1406:U:H6	1.78	0.44
26:BA:2134:A:OP2	26:BA:2157:G:N2	2.50	0.44
26:BA:2820:A:P	38:BR:2:ARG:HH22	2.41	0.44
29:BE:174:ASP:OD1	29:BE:175:VAL:N	2.50	0.44
30:BF:24:LEU:HD23	30:BF:115:ALA:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BG:43:LEU:HB3	31:BG:44:GLY:H	1.50	0.44
33:BI:4:ILE:HD13	33:BI:47:LEU:HG	2.00	0.44
43:BW:14:PRO:HG2	43:BW:78:GLU:CD	2.42	0.44
1:CA:727:G:OP1	1:CA:742:G:N2	2.43	0.44
1:CA:1002:G:C2	1:CA:1003:G:C8	3.06	0.44
1:CA:1286:A:H2'	1:CA:1287:A:H5'	1.99	0.44
1:CA:1432:G:OP2	40:DT:108:ARG:HD2	2.18	0.44
3:CC:98:ASN:N	3:CC:98:ASN:OD1	2.49	0.44
5:CE:90:VAL:O	5:CE:120:THR:HA	2.17	0.44
7:CG:72:ARG:HH22	7:CG:138:LYS:NZ	2.15	0.44
10:CJ:69:ASN:O	10:CJ:70:ARG:HD3	2.18	0.44
13:CM:93:ARG:HD3	26:DA:888:C:OP1	2.18	0.44
23:CW:61:C:HO2'	23:CW:62:C:P	2.37	0.44
25:CY:8:4SU:S4	25:CY:14:A:N7	2.90	0.44
26:DA:492:A:H2'	26:DA:493:G:O4'	2.18	0.44
26:DA:2165:G:H2'	26:DA:2166:G:O4'	2.17	0.44
27:DB:33:G:C6	27:DB:34:U:C4	3.06	0.44
46:DZ:120:ILE:HD13	46:DZ:171:ILE:HA	1.99	0.44
1:AA:35:G:O2'	12:AL:118:SER:O	2.29	0.44
1:AA:589:C:H5"	8:AH:29:SER:HB3	1.99	0.44
1:AA:834:C:H2'	1:AA:835:U:C6	2.53	0.44
1:AA:1223:C:H5"	1:AA:1224:G:H5"	2.00	0.44
1:AA:1469:G:H2'	1:AA:1470:G:C8	2.53	0.44
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.53	0.44
7:AG:72:ARG:HG3	7:AG:142:GLU:OE2	2.18	0.44
9:AI:17:VAL:HG11	9:AI:80:GLY:C	2.43	0.44
13:AM:31:LYS:O	13:AM:35:GLU:HG3	2.18	0.44
13:AM:60:VAL:HG12	13:AM:66:LEU:HD11	2.00	0.44
16:AP:56:ALA:O	16:AP:60:LEU:HB2	2.18	0.44
17:AQ:74:LEU:HD13	17:AQ:75:ARG:HG2	2.00	0.44
23:AW:56:C:H5	26:BA:897:C:O4'	2.00	0.44
25:AY:54:5MU:H72	25:AY:55:PSU:O2	2.18	0.44
26:BA:768:G:O2'	26:BA:1379:A:N1	2.44	0.44
26:BA:1142(A):A:C4	26:BA:1144:G:C8	3.06	0.44
26:BA:1453:U:OP1	38:BR:77:ARG:NH1	2.39	0.44
31:BG:97:ASP:O	31:BG:101:ILE:HG13	2.17	0.44
46:BZ:108:PRO:HB2	46:BZ:111:VAL:HG23	1.99	0.44
51:B4:40:HIS:HB3	51:B4:43:TYR:HB2	2.00	0.44
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.33	0.44
2:CB:16:HIS:CD2	2:CB:17:PHE:N	2.85	0.44
7:CG:16:LEU:HD23	9:CI:41:VAL:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:483:A:H1'	45:DY:59:GLY:O	2.18	0.44
26:DA:784:A:C8	26:DA:792:G:C5	3.06	0.44
26:DA:994:C:H1'	42:DV:10:LYS:HE3	1.98	0.44
26:DA:1410:G:H2'	26:DA:1411:C:H6	1.82	0.44
26:DA:2104:G:H2'	26:DA:2105:C:C6	2.53	0.44
26:DA:2136:C:HO2'	26:DA:2137:C:C5'	2.27	0.44
26:DA:2302:G:C2	26:DA:2303:G:C8	3.06	0.44
26:DA:2344:U:H3'	53:D6:37:ARG:O	2.18	0.44
31:DG:129:GLY:O	31:DG:161:THR:HB	2.18	0.44
36:DP:6:LEU:HA	36:DP:6:LEU:HD23	1.73	0.44
36:DP:83:VAL:HG11	36:DP:100:LEU:HD13	1.99	0.44
38:DR:28:LEU:HD12	38:DR:48:VAL:HG21	2.00	0.44
40:DT:50:ILE:HG22	40:DT:102:ILE:HD11	1.99	0.44
45:DY:5:MET:HE2	45:DY:5:MET:HB2	1.74	0.44
46:DZ:99:TYR:HA	46:DZ:124:ILE:O	2.17	0.44
1:AA:15:G:H1'	5:AE:19:MET:HE2	2.00	0.44
1:AA:1025:U:O2'	1:AA:1026:G:C8	2.67	0.44
1:AA:1130:A:H5'	9:AI:18:PHE:CE2	2.52	0.44
1:AA:1261:A:H3'	1:AA:1262:C:C6	2.52	0.44
2:AB:158:LEU:HG	2:AB:182:ILE:HD11	2.00	0.44
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.87	0.44
10:AJ:69:ASN:O	10:AJ:70:ARG:HD3	2.17	0.44
25:AY:4:C:H3'	25:AY:5:G:H5"	2.00	0.44
26:BA:892:G:H2'	26:BA:892:G:N3	2.32	0.44
26:BA:893:C:H2'	26:BA:894:C:H6	1.81	0.44
26:BA:1766:U:H2'	26:BA:1767:C:H6	1.83	0.44
26:BA:2271:G:OP1	47:B0:18:ALA:HB1	2.18	0.44
26:BA:2377:A:H2'	26:BA:2378:A:C8	2.53	0.44
26:BA:2693:A:H2'	26:BA:2694:G:C8	2.53	0.44
26:BA:2849:U:P	40:BT:95:ARG:HH12	2.40	0.44
31:BG:150:ASP:OD1	31:BG:150:ASP:N	2.46	0.44
33:BI:103:ARG:HG3	33:BI:104:GLN:H	1.82	0.44
51:B4:61:ARG:O	51:B4:62:ARG:C	2.60	0.44
1:CA:6:G:O2'	1:CA:7:G:H5'	2.17	0.44
1:CA:570:G:H1'	1:CA:820:U:C4	2.53	0.44
1:CA:1000:U:H2'	1:CA:1001:A:H8	1.83	0.44
1:CA:1014:A:O2'	1:CA:1219:U:H4'	2.17	0.44
1:CA:1245:A:N1	1:CA:1292:U:O2	2.51	0.44
1:CA:1291:G:C6	1:CA:1292:U:C4	3.05	0.44
2:CB:15:VAL:HG21	2:CB:213:LEU:HD13	1.99	0.44
2:CB:109:SER:O	2:CB:112:VAL:HB	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:111:ALA:HB1	4:CD:116:GLN:HB3	2.00	0.44
6:CF:37:VAL:HA	6:CF:65:VAL:HG12	2.00	0.44
9:CI:16:ARG:CB	9:CI:64:THR:HG23	2.47	0.44
10:CJ:43:ARG:HB2	10:CJ:67:THR:HG23	2.00	0.44
19:CS:67:VAL:H	51:D4:58:ARG:HD3	1.82	0.44
22:CV:14:A:C2	25:CY:34:G:C2	3.06	0.44
25:CY:40:C:H2'	25:CY:41:C:C6	2.53	0.44
26:DA:1268:A:H2'	26:DA:1269:A:O4'	2.17	0.44
26:DA:1983:C:H4'	26:DA:2606:C:H4'	1.99	0.44
26:DA:2127:G:N1	26:DA:2128:C:C4	2.85	0.44
26:DA:2313:C:H4'	31:DG:91:ARG:HG3	2.00	0.44
26:DA:2617:C:H2'	26:DA:2618:G:O4'	2.17	0.44
26:DA:2805:G:H2'	26:DA:2807:G:H8	1.79	0.44
32:DH:18:GLU:HB3	32:DH:25:LYS:HB2	2.00	0.44
40:DT:117:ASP:O	40:DT:121:ILE:HG13	2.18	0.44
41:DU:66:ASN:O	41:DU:70:ARG:HG3	2.18	0.44
1:AA:166:G:H2'	1:AA:167:G:C8	2.53	0.44
1:AA:419:C:OP1	1:AA:513:C:O2'	2.21	0.44
1:AA:1153:C:H2'	1:AA:1154:G:O4'	2.18	0.44
1:AA:1179:A:H4'	9:AI:103:THR:HA	2.00	0.44
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	2.00	0.44
7:AG:16:LEU:HD23	9:AI:41:VAL:O	2.18	0.44
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.33	0.44
26:BA:141:A:C8	26:BA:1408:C:O2'	2.68	0.44
26:BA:1297:C:OP1	26:BA:2710:C:H4'	2.18	0.44
26:BA:2104:G:H2'	26:BA:2105:C:C6	2.53	0.44
28:BD:35:LYS:HB2	28:BD:36:PRO:HD2	1.99	0.44
32:BH:26:VAL:HG12	32:BH:79:VAL:HG21	1.99	0.44
42:BV:65:GLY:HA3	42:BV:91:TYR:CZ	2.53	0.44
52:B5:35:GLU:HG3	52:B5:51:TYR:CD2	2.53	0.44
1:CA:44:G:H2'	1:CA:45:U:O4'	2.18	0.44
1:CA:1154:G:O6	1:CA:1155:G:N1	2.51	0.44
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.18	0.44
2:CB:71:VAL:HG22	2:CB:163:PHE:O	2.18	0.44
5:CE:96:PRO:HA	5:CE:117:ASP:OD2	2.18	0.44
24:CX:13:C:O2'	26:DA:1924:C:H4'	2.17	0.44
26:DA:172:C:H2'	26:DA:173:G:H8	1.83	0.44
26:DA:764:A:H5'	28:DD:210:GLY:HA2	2.00	0.44
26:DA:861:A:N3	27:DB:79:C:O2'	2.43	0.44
26:DA:1185:C:H5"	26:DA:1186:G:OP1	2.18	0.44
26:DA:1308:A:H2'	26:DA:1309:G:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1826:G:H4'	28:DD:242:ARG:CZ	2.47	0.44
26:DA:2439:A:H5'	26:DA:2439:A:C8	2.52	0.44
26:DA:2567:G:H2'	26:DA:2568:C:C6	2.53	0.44
27:DB:42:C:C2	31:DG:92:VAL:HA	2.53	0.44
30:DF:39:TRP:CZ2	30:DF:43:LYS:HE2	2.52	0.44
53:D6:14:THR:HG22	53:D6:15:GLU:HG3	2.00	0.44
1:AA:973:G:OP1	10:AJ:57:LYS:HE3	2.18	0.43
1:AA:1014:A:C2	1:AA:1219:U:H1'	2.53	0.43
2:AB:21:ARG:H	2:AB:21:ARG:HD2	1.83	0.43
4:AD:19:LEU:HB3	4:AD:21:LEU:HD21	2.00	0.43
4:AD:107:ARG:HA	4:AD:107:ARG:HD2	1.78	0.43
4:AD:163:GLU:O	4:AD:166:LYS:HG2	2.18	0.43
5:AE:131:ILE:HD13	5:AE:131:ILE:HA	1.79	0.43
7:AG:146:GLU:OE2	7:AG:149:ARG:NE	2.51	0.43
11:AK:81:ASP:OD1	11:AK:81:ASP:N	2.50	0.43
12:AL:24:VAL:HG13	12:AL:98:TYR:HE2	1.84	0.43
23:AW:19:G:N1	23:AW:56:C:N4	2.53	0.43
25:AY:36:A:H2'	25:AY:37:MIA:O4'	2.18	0.43
26:BA:144:C:H5'	44:BX:2:LYS:HE2	2.00	0.43
26:BA:1817:G:OP1	28:BD:88:ARG:NH2	2.43	0.43
26:BA:2141:G:N1	26:BA:2142:C:C2	2.86	0.43
26:BA:2345:G:OP2	53:B6:38:LYS:NZ	2.46	0.43
26:BA:2561:A:H2'	26:BA:2562:U:O4'	2.17	0.43
26:BA:2749:A:P	32:BH:3:ARG:HH21	2.41	0.43
27:BB:13:A:N1	27:BB:69:G:O2'	2.51	0.43
56:B9:32:HIS:O	56:B9:34:GLN:HG3	2.18	0.43
1:CA:685:G:C2	1:CA:686:U:C4	3.06	0.43
1:CA:954:G:H2'	1:CA:955:U:O4'	2.17	0.43
1:CA:1177:G:H3'	1:CA:1178:G:H8	1.83	0.43
1:CA:1226:C:C5	13:CM:104:ARG:HA	2.52	0.43
1:CA:1278:U:H5'	1:CA:1279:A:O4'	2.18	0.43
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.18	0.43
3:CC:111:LEU:HD11	3:CC:144:SER:O	2.17	0.43
4:CD:20:TYR:CD1	4:CD:26:CYS:HB3	2.52	0.43
7:CG:22:LEU:HD13	7:CG:97:GLN:OE1	2.17	0.43
9:CI:4:TYR:CD2	9:CI:88:TYR:HB2	2.53	0.43
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.36	0.43
12:CL:34:ARG:O	12:CL:61:THR:HG23	2.18	0.43
13:CM:16:ASP:O	13:CM:20:THR:HG23	2.17	0.43
13:CM:54:VAL:HA	13:CM:57:ARG:HB3	2.00	0.43
15:CO:58:MET:O	15:CO:62:GLN:N	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:63:G:H5"	37:DQ:1:MET:HE1	1.99	0.43
23:CW:69:G:N2	23:CW:70:G:C4	2.86	0.43
26:DA:298:G:H5"	26:DA:299:A:OP1	2.18	0.43
26:DA:1274:A:N3	26:DA:1297:C:H1'	2.33	0.43
26:DA:2318:G:H21	39:DS:3:ARG:HD2	1.83	0.43
29:DE:21:VAL:HG23	29:DE:185:LYS:HD2	1.99	0.43
29:DE:77:ILE:CD1	29:DE:195:LEU:HD13	2.49	0.43
31:DG:115:ARG:NH1	31:DG:137:GLU:OE2	2.51	0.43
33:DI:44:LEU:HD13	33:DI:44:LEU:HA	1.77	0.43
34:DN:88:GLU:HG2	34:DN:88:GLU:H	1.56	0.43
45:DY:19:LYS:HB3	45:DY:19:LYS:HE2	1.74	0.43
45:DY:86:ARG:HB2	45:DY:98:VAL:HG23	1.99	0.43
48:D1:91:LYS:HG2	48:D1:95:LEU:HD22	2.00	0.43
50:D3:10:LYS:HB3	50:D3:53:LEU:HA	2.00	0.43
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.84	0.43
1:AA:737:A:H2'	1:AA:738:C:C6	2.53	0.43
1:AA:1131:G:H22	1:AA:1143:G:H21	1.65	0.43
2:AB:208:ILE:H	2:AB:208:ILE:HG13	1.43	0.43
2:AB:219:VAL:HA	2:AB:222:ILE:HD12	2.00	0.43
12:AL:92:ASP:O	12:AL:94:PRO:HD3	2.18	0.43
20:AT:56:MET:HE3	20:AT:88:VAL:HG21	2.00	0.43
21:AU:3:LYS:HB3	21:AU:14:TRP:CG	2.54	0.43
26:BA:228:A:H8	26:BA:229:A:H5'	1.83	0.43
45:BY:52:SER:HB2	45:BY:53:PRO:HD2	2.00	0.43
1:CA:448:A:O5'	1:CA:485:G:N2	2.45	0.43
1:CA:999:C:N4	1:CA:1042:G:N1	2.30	0.43
1:CA:1005:A:O2'	1:CA:1006:C:OP1	2.32	0.43
1:CA:1446:U:O2'	1:CA:1447:A:O5'	2.25	0.43
2:CB:53:ARG:HB3	2:CB:53:ARG:NH1	2.33	0.43
2:CB:97:TRP:HH2	2:CB:102:LEU:HD13	1.83	0.43
7:CG:113:GLU:O	7:CG:119:ARG:HD3	2.19	0.43
15:CO:3:ILE:O	15:CO:3:ILE:HG12	2.18	0.43
15:CO:26:GLU:HB3	15:CO:81:LEU:HD13	1.99	0.43
25:CY:71:G:H2'	25:CY:72:C:C6	2.53	0.43
26:DA:122:G:OP1	26:DA:149:A:O2'	2.29	0.43
26:DA:1805:U:C2	26:DA:1813:G:N2	2.86	0.43
26:DA:2112:G:C4	26:DA:2113:U:H1'	2.53	0.43
26:DA:2115:G:O2'	26:DA:2167:U:O4	2.35	0.43
26:DA:2119:A:C2	26:DA:2171:A:H5'	2.46	0.43
35:DO:34:THR:OG1	35:DO:35:VAL:N	2.50	0.43
36:DP:1:MET:HG2	36:DP:5:ASP:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DP:44:GLY:HA3	36:DP:45:LEU:HB2	2.00	0.43
1:AA:1320:C:H2'	1:AA:1321:C:O4'	2.19	0.43
2:AB:96:ARG:HD2	2:AB:98:LEU:HD23	2.00	0.43
2:AB:189:ASP:O	2:AB:192:SER:OG	2.35	0.43
4:AD:105:VAL:HG21	4:AD:126:ILE:HG13	2.00	0.43
26:BA:563:G:H22	26:BA:578:A:H2	1.65	0.43
26:BA:1047:G:H2'	26:BA:1110:G:N2	2.33	0.43
26:BA:1371:G:H2'	26:BA:1372:U:H5	1.82	0.43
26:BA:1449:A:H5'	26:BA:1450:G:OP2	2.18	0.43
26:BA:1557:C:OP2	26:BA:1558:A:O2'	2.28	0.43
27:BB:29:A:H2'	27:BB:30:C:O4'	2.18	0.43
30:BF:135:LYS:HB2	30:BF:138:GLU:CD	2.43	0.43
33:BI:68:LEU:HD23	33:BI:68:LEU:HA	1.77	0.43
38:BR:54:LEU:HD12	38:BR:54:LEU:HA	1.88	0.43
49:B2:53:LEU:HD23	49:B2:53:LEU:HA	1.83	0.43
55:B8:6:THR:HG23	55:B8:63:PRO:HD2	2.00	0.43
1:CA:1106:G:C6	1:CA:1107:C:C4	3.07	0.43
1:CA:1106:G:OP1	3:CC:172:ARG:HD3	2.18	0.43
1:CA:1172:C:H2'	1:CA:1173:G:C8	2.53	0.43
1:CA:1442:G:H3'	1:CA:1442:G:H8	1.84	0.43
2:CB:16:HIS:HB3	2:CB:210:SER:HB3	1.99	0.43
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.54	0.43
9:CI:23:ASN:HD22	9:CI:23:ASN:H	1.66	0.43
10:CJ:42:THR:HG21	10:CJ:66:ARG:HB3	1.99	0.43
26:DA:493:G:H2'	26:DA:494:G:O4'	2.17	0.43
26:DA:522:G:H2'	26:DA:523:C:C6	2.54	0.43
26:DA:868:U:C4	26:DA:869:G:N7	2.87	0.43
26:DA:875:G:O2'	46:DZ:151:HIS:HE1	2.00	0.43
26:DA:1607:C:N4	26:DA:1622:G:OP2	2.45	0.43
26:DA:2512:C:H2'	26:DA:2513:G:O4'	2.17	0.43
34:DN:37:LYS:HG3	34:DN:42:TRP:NE1	2.33	0.43
1:AA:44:G:H2'	1:AA:45:U:O4'	2.18	0.43
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.53	0.43
2:AB:87:ARG:NE	2:AB:233:SER:HB3	2.33	0.43
9:AI:4:TYR:CD1	9:AI:88:TYR:HA	2.53	0.43
20:AT:60:GLU:HG2	20:AT:81:LYS:HD3	2.00	0.43
26:BA:484:C:H2'	26:BA:485:C:C6	2.53	0.43
26:BA:528:A:C2	26:BA:2043:C:H4'	2.53	0.43
26:BA:813:U:H2'	26:BA:814:C:C6	2.53	0.43
26:BA:954:G:H5"	37:BQ:13:GLN:HB3	2.00	0.43
26:BA:956:G:P	37:BQ:14:ARG:HH22	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1001:A:H2'	26:BA:1002:G:O4'	2.19	0.43
28:BD:13:ARG:HA	28:BD:13:ARG:HD2	1.82	0.43
46:BZ:104:PHE:HB3	46:BZ:141:VAL:HG21	1.99	0.43
1:CA:404:U:H2'	1:CA:405:U:C6	2.53	0.43
1:CA:881:G:OP2	12:CL:12:ARG:NH2	2.51	0.43
1:CA:934:C:H5	1:CA:1344:C:H2'	1.84	0.43
1:CA:1011:G:C6	1:CA:1012:U:C2	3.06	0.43
1:CA:1304:G:C6	1:CA:1305:G:N1	2.86	0.43
1:CA:1342:C:H2'	1:CA:1343:G:H8	1.83	0.43
7:CG:23:VAL:HG13	7:CG:43:PHE:CE2	2.54	0.43
23:CW:2:C:N3	23:CW:71:G:O6	2.52	0.43
25:CY:58:A:H4'	25:CY:59:U:OP1	2.18	0.43
26:DA:862:G:O2'	27:DB:78:A:N3	2.51	0.43
26:DA:880:G:N2	26:DA:898:C:H1'	2.21	0.43
26:DA:2156:G:H8	26:DA:2156:G:O5'	2.01	0.43
26:DA:2393:A:H2'	26:DA:2394:C:O4'	2.19	0.43
26:DA:2485:G:C2	26:DA:2486:G:C8	3.06	0.43
26:DA:2519:U:O4'	26:DA:2542:A:N6	2.51	0.43
26:DA:2821:A:H2'	26:DA:2822:G:C8	2.54	0.43
29:DE:60:ASN:OD1	29:DE:62:PRO:HD2	2.18	0.43
37:DQ:66:ILE:HG12	37:DQ:104:PHE:CE1	2.53	0.43
1:AA:841:U:H6	1:AA:841:U:OP2	2.02	0.43
1:AA:1049:U:OP1	14:AN:3:ARG:HB2	2.19	0.43
2:AB:211:ILE:O	2:AB:215:LEU:HB2	2.19	0.43
9:AI:18:PHE:O	9:AI:61:ALA:HA	2.19	0.43
9:AI:55:ALA:HA	9:AI:58:HIS:CD2	2.54	0.43
11:AK:34:ASP:OD2	11:AK:38:ASN:HB2	2.19	0.43
11:AK:41:THR:OG1	11:AK:42:TRP:N	2.52	0.43
26:BA:196:A:N3	26:BA:196:A:H2'	2.34	0.43
26:BA:586:A:N1	26:BA:809:G:O2'	2.44	0.43
26:BA:662:G:H5'	36:BP:14:LYS:O	2.18	0.43
26:BA:1709:U:H2'	26:BA:1710:C:C6	2.54	0.43
26:BA:1769:G:O2'	26:BA:1958:C:OP1	2.24	0.43
26:BA:2121:G:N2	26:BA:2177:C:N3	2.50	0.43
32:BH:164:TYR:HB2	32:BH:167:GLU:HB2	2.00	0.43
39:BS:34:HIS:ND1	39:BS:53:SER:OG	2.42	0.43
46:BZ:79:ARG:HB3	46:BZ:80:ARG:NH1	2.33	0.43
1:CA:731:G:H5'	1:CA:766:A:H4'	2.00	0.43
1:CA:988:G:H1'	1:CA:1014:A:N1	2.32	0.43
1:CA:1240:U:N3	7:CG:30:ILE:O	2.44	0.43
5:CE:41:VAL:HG23	5:CE:67:VAL:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CT:47:GLY:HA2	20:CT:48:LYS:C	2.44	0.43
26:DA:373:U:H2'	26:DA:374:A:H8	1.83	0.43
26:DA:647:G:H8	26:DA:647:G:O5'	2.02	0.43
26:DA:949:C:H2'	26:DA:950:G:C8	2.54	0.43
26:DA:1652:A:O2'	26:DA:1653:G:H5'	2.17	0.43
26:DA:1778:U:H2'	26:DA:1784:A:N6	2.34	0.43
26:DA:1847:A:H4'	26:DA:1848:A:OP2	2.18	0.43
26:DA:2036:C:H2'	26:DA:2037:G:H8	1.83	0.43
26:DA:2639:A:C2	26:DA:2778:A:C8	3.07	0.43
30:DF:129:PHE:HA	30:DF:142:TRP:NE1	2.33	0.43
31:DG:43:LEU:HB3	31:DG:44:GLY:H	1.48	0.43
41:DU:43:GLY:HA3	42:DV:73:SER:HB3	2.01	0.43
41:DU:58:ARG:HA	41:DU:61:TRP:CE3	2.53	0.43
51:D4:64:GLY:C	51:D4:66:SER:H	2.26	0.43
1:AA:71:C:N3	1:AA:98:G:O6	2.51	0.43
1:AA:164:U:H2'	1:AA:165:C:C6	2.54	0.43
1:AA:202:U:HO2'	1:AA:203:U:P	2.39	0.43
1:AA:658:G:H2'	1:AA:659:U:C6	2.54	0.43
1:AA:1217:C:OP1	14:AN:9:LYS:HE2	2.18	0.43
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.19	0.43
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	2.00	0.43
6:AF:35:ALA:HB2	6:AF:67:MET:HE2	2.00	0.43
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.19	0.43
7:AG:144:MET:HE2	7:AG:144:MET:HB3	1.82	0.43
14:AN:13:THR:HA	14:AN:14:PRO:HD3	1.81	0.43
26:BA:422:A:H2'	26:BA:423:A:C8	2.53	0.43
26:BA:543:C:N3	26:BA:549:G:N1	2.49	0.43
26:BA:1654:A:OP1	38:BR:1:MET:HA	2.19	0.43
26:BA:1669:A:H5"	26:BA:2550:G:OP1	2.18	0.43
26:BA:1712:C:H2'	26:BA:1713:U:O4'	2.18	0.43
46:BZ:111:VAL:CG2	46:BZ:117:LEU:HB2	2.48	0.43
1:CA:396:G:H2'	1:CA:397:A:H5"	1.99	0.43
1:CA:553:A:H2'	1:CA:554:C:C6	2.53	0.43
1:CA:953:G:N7	13:CM:104:ARG:NH2	2.67	0.43
1:CA:1187:G:H5"	9:CI:113:LYS:HE3	1.99	0.43
19:CS:13:ASP:HA	19:CS:16:LEU:HB2	2.01	0.43
20:CT:59:ALA:O	20:CT:63:ILE:HG13	2.19	0.43
26:DA:286:C:H2'	26:DA:287:C:C6	2.54	0.43
26:DA:910:A:C6	26:DA:911:A:C6	3.06	0.43
26:DA:1588:C:H2'	26:DA:1589:C:C6	2.53	0.43
26:DA:1853:A:H2'	26:DA:1854:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2172:U:O2'	26:DA:2173:A:OP1	2.36	0.43
26:DA:2180:U:H2'	26:DA:2181:G:O4'	2.17	0.43
26:DA:2526:G:H2'	26:DA:2527:C:H6	1.83	0.43
27:DB:15:A:C8	27:DB:110:G:C4	3.07	0.43
31:DG:150:ASP:OD1	31:DG:150:ASP:N	2.44	0.43
37:DQ:20:ALA:HB2	46:DZ:79:ARG:HG2	2.00	0.43
38:DR:88:ARG:NH2	38:DR:89:ASP:OD1	2.50	0.43
44:DX:35:THR:HG22	44:DX:37:THR:N	2.34	0.43
44:DX:55:ASN:O	44:DX:79:ALA:HA	2.19	0.43
1:AA:434:U:H2'	1:AA:435:C:C6	2.54	0.43
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.18	0.43
2:AB:21:ARG:H	2:AB:21:ARG:HH21	1.65	0.43
3:AC:78:GLY:HA3	3:AC:83:ARG:H	1.84	0.43
11:AK:67:ASP:OD1	11:AK:71:LYS:HE3	2.18	0.43
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.80	0.43
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.99	0.43
26:BA:1429:G:H2'	26:BA:1430:C:C6	2.53	0.43
28:BD:20:ASP:OD1	28:BD:20:ASP:N	2.39	0.43
31:BG:179:PRO:HG3	51:B4:43:TYR:OH	2.19	0.43
36:BP:64:LYS:HE3	55:B8:12:LYS:HD3	2.01	0.43
41:BU:86:ALA:O	42:BV:49:THR:HG23	2.19	0.43
51:B4:46:GLN:O	51:B4:46:GLN:HG2	2.19	0.43
1:CA:20:U:H2'	1:CA:21:G:O4'	2.18	0.43
1:CA:21:G:H2'	1:CA:22:G:C8	2.54	0.43
1:CA:62:U:H2'	1:CA:63:C:C6	2.54	0.43
1:CA:299:G:H2'	1:CA:300:A:C8	2.53	0.43
1:CA:427:U:H3'	1:CA:428:G:H2'	2.01	0.43
1:CA:707:C:H2'	1:CA:708:C:H6	1.83	0.43
1:CA:719:C:N4	18:CR:71:LYS:NZ	2.66	0.43
1:CA:1321:C:H3'	1:CA:1322:C:H6	1.82	0.43
3:CC:19:GLU:HB3	3:CC:55:VAL:O	2.18	0.43
3:CC:104:GLN:NE2	3:CC:105:GLU:HG3	2.34	0.43
4:CD:53:ASP:HB3	4:CD:57:ARG:NH1	2.34	0.43
4:CD:181:MET:HE3	4:CD:181:MET:HB2	1.84	0.43
8:CH:56:LYS:HB2	8:CH:58:TYR:HE1	1.83	0.43
8:CH:124:ALA:O	8:CH:128:GLY:N	2.52	0.43
9:CI:22:GLY:N	9:CI:58:HIS:O	2.30	0.43
16:CP:74:LEU:O	16:CP:79:VAL:HG23	2.19	0.43
25:CY:19:G:C4'	25:CY:57:G:H22	2.32	0.43
26:DA:272(D):G:C2	26:DA:272(E):G:C8	3.07	0.43
26:DA:839:U:H2'	26:DA:840:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1836:C:H2'	26:DA:1837:C:H6	1.84	0.43
26:DA:2125:G:H1	26:DA:2172:U:P	2.41	0.43
26:DA:2406:U:H2'	26:DA:2406:U:OP2	2.19	0.43
34:DN:71:ILE:HG21	34:DN:84:LYS:HB3	2.01	0.43
40:DT:92:GLY:O	40:DT:120:ARG:NH2	2.51	0.43
41:DU:8:VAL:O	41:DU:12:ARG:HG3	2.18	0.43
41:DU:81:HIS:HB3	41:DU:117:GLN:HE22	1.83	0.43
42:DV:5:VAL:HG11	42:DV:57:VAL:HG21	2.00	0.43
46:DZ:4:ARG:HG3	46:DZ:58:VAL:HB	2.01	0.43
1:AA:339:C:H2'	1:AA:340:U:C6	2.54	0.43
1:AA:942:G:C2	1:AA:1342:C:C2	3.06	0.43
1:AA:984:C:N4	1:AA:1221:G:H1	2.13	0.43
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.83	0.43
1:AA:1362:C:H2'	1:AA:1363:C:H5"	2.01	0.43
11:AK:62:GLN:O	11:AK:66:LEU:HG	2.19	0.43
18:AR:31:LEU:HD23	18:AR:31:LEU:H	1.83	0.43
25:AY:3:C:H2'	25:AY:4:C:O4'	2.18	0.43
25:AY:23:A:H2'	25:AY:24:G:C8	2.54	0.43
26:BA:476:G:H4'	26:BA:502:A:N1	2.34	0.43
26:BA:1019:U:OP1	26:BA:1035:U:O2'	2.35	0.43
26:BA:1441:G:H2'	26:BA:1442:G:H8	1.83	0.43
26:BA:2037:G:H2'	26:BA:2038:G:C8	2.54	0.43
26:BA:2335:A:C8	26:BA:2337:G:C5	3.07	0.43
26:BA:2611:U:H2'	52:B5:2:ALA:O	2.19	0.43
26:BA:2627:G:O2'	26:BA:2781:A:N1	2.44	0.43
30:BF:106:ARG:H	30:BF:106:ARG:HG2	1.67	0.43
43:BW:67:ASP:OD1	43:BW:67:ASP:N	2.50	0.43
45:BY:19:LYS:HB3	45:BY:19:LYS:HE2	1.60	0.43
46:BZ:151:HIS:HA	46:BZ:169:GLU:O	2.19	0.43
51:B4:68:ARG:HA	51:B4:68:ARG:HD2	1.84	0.43
1:CA:988:G:O2'	1:CA:1014:A:N6	2.52	0.43
1:CA:1051:C:H2'	1:CA:1052:U:H6	1.82	0.43
1:CA:1119:C:C2	1:CA:1154:G:O6	2.71	0.43
1:CA:1368:G:OP2	9:CI:112:LYS:HG3	2.19	0.43
2:CB:73:THR:HG22	2:CB:95:GLN:O	2.18	0.43
2:CB:178:ARG:NH1	2:CB:196:LEU:O	2.52	0.43
3:CC:20:SER:OG	3:CC:22:TRP:NE1	2.52	0.43
7:CG:72:ARG:HH12	7:CG:138:LYS:NZ	2.17	0.43
10:CJ:99:LYS:O	10:CJ:100:THR:OG1	2.32	0.43
13:CM:123:ALA:HB2	23:CW:39:PSU:H1'	2.00	0.43
14:CN:37:PHE:HB2	14:CN:39:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:289:A:H62	26:DA:351:G:N2	2.15	0.43
26:DA:1364:G:OP2	48:D1:3:LYS:HG3	2.19	0.43
26:DA:1652:A:C2'	26:DA:1653:G:H5'	2.48	0.43
26:DA:1720:U:H2'	26:DA:1721:G:O4'	2.19	0.43
26:DA:1999:C:H5"	26:DA:2723:C:O2'	2.19	0.43
26:DA:2031:A:C6	26:DA:2498:C:H1'	2.54	0.43
26:DA:2152:G:H2'	26:DA:2153:G:O4'	2.18	0.43
26:DA:2526:G:H2'	26:DA:2527:C:C6	2.53	0.43
26:DA:2682:U:H5'	29:DE:11:MET:O	2.19	0.43
26:DA:2732:G:H3'	26:DA:2733:A:O4'	2.19	0.43
26:DA:2741:A:H2'	26:DA:2742:C:O4'	2.18	0.43
35:DO:69:ILE:H	35:DO:69:ILE:HG12	1.61	0.43
36:DP:59:LEU:HD21	55:D8:10:ALA:HA	2.01	0.43
37:DQ:16:ARG:NH2	37:DQ:18:LYS:HD3	2.33	0.43
37:DQ:26:TYR:O	37:DQ:67:ARG:NH1	2.42	0.43
46:DZ:159:PRO:HA	46:DZ:161:VAL:HG12	2.01	0.43
49:D2:32:LEU:HD12	49:D2:57:ILE:HD12	2.00	0.43
1:AA:438:G:H4'	4:AD:123:HIS:CE1	2.54	0.43
1:AA:671:G:H5'	6:AF:77:ARG:HH12	1.83	0.43
1:AA:909:A:H2'	1:AA:910:C:O4'	2.19	0.43
4:AD:33:MET:O	4:AD:37:PRO:HB3	2.19	0.43
12:AL:117:ARG:HB3	12:AL:122:THR:HB	2.00	0.43
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.18	0.43
26:BA:1394:U:H2'	26:BA:1395:A:O4'	2.18	0.43
26:BA:1783:A:H5'	26:BA:2608:G:H4'	2.00	0.43
26:BA:2100:G:H1	26:BA:2189:U:H3	1.66	0.43
29:BE:121:ASN:ND2	61:BE:411:HOH:O	2.40	0.43
32:BH:117:PRO:HG3	32:BH:123:PHE:CD2	2.54	0.43
34:BN:9:VAL:HG11	34:BN:39:ARG:HH22	1.83	0.43
45:BY:54:LYS:CA	45:BY:56:PRO:HD3	2.48	0.43
1:CA:664:G:H5"	18:CR:64:ARG:NH2	2.34	0.43
1:CA:955:U:H2'	1:CA:956:U:O4'	2.19	0.43
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.34	0.43
1:CA:1261:A:C6	1:CA:1262:C:C2	3.07	0.43
1:CA:1317:C:O2	19:CS:37:ARG:NH1	2.52	0.43
4:CD:13:ARG:HD2	4:CD:38:TYR:O	2.18	0.43
5:CE:83:GLU:HA	5:CE:88:LYS:HA	2.00	0.43
6:CF:91:VAL:HG11	18:CR:72:ARG:NH1	2.34	0.43
20:CT:56:MET:HE1	20:CT:85:MET:HA	2.00	0.43
25:CY:76:A:H62	26:DA:2422:A:C5'	2.31	0.43
26:DA:322:A:C5	26:DA:340:A:C2	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:770:G:OP2	61:DA:4255:HOH:O	2.21	0.43
26:DA:1636:C:H2'	26:DA:1637:A:C8	2.54	0.43
26:DA:2171:A:C4	26:DA:2172:U:C4	3.06	0.43
26:DA:2173:A:H3'	26:DA:2173:A:OP2	2.18	0.43
26:DA:2193:G:H2'	26:DA:2194:G:H8	1.84	0.43
26:DA:2439:A:H5'	26:DA:2439:A:H8	1.84	0.43
26:DA:2516:G:C6	26:DA:2517:C:C4	3.07	0.43
26:DA:2557:G:H2'	26:DA:2558:C:H6	1.83	0.43
26:DA:2693:A:H2'	26:DA:2694:G:C8	2.54	0.43
27:DB:15:A:OP2	27:DB:69:G:N2	2.49	0.43
30:DF:172:TRP:CD1	30:DF:172:TRP:H	2.37	0.43
30:DF:195:ASP:HB3	30:DF:197:ASP:OD1	2.18	0.43
31:DG:64:THR:OG1	31:DG:66:GLN:O	2.37	0.43
31:DG:145:THR:HG23	31:DG:147:ASP:N	2.23	0.43
1:AA:936:C:H2'	1:AA:937:A:O4'	2.19	0.43
3:AC:6:HIS:CD2	3:AC:8:ILE:HB	2.54	0.43
3:AC:116:VAL:O	3:AC:120:VAL:HG23	2.19	0.43
9:AI:20:ARG:HA	9:AI:21:PRO:HD3	1.92	0.43
12:AL:110:VAL:O	12:AL:122:THR:OG1	2.32	0.43
14:AN:23:ARG:HH11	14:AN:30:ALA:HB2	1.83	0.43
20:AT:29:LYS:O	20:AT:33:ILE:HG13	2.18	0.43
26:BA:1005:C:O2'	34:BN:28:THR:HG21	2.19	0.43
26:BA:2154:G:C2'	26:BA:2155:G:H5'	2.49	0.43
26:BA:2712:U:OP1	26:BA:2714:G:H4'	2.19	0.43
32:BH:11:VAL:HG13	32:BH:15:VAL:HG22	2.00	0.43
35:BO:98:VAL:HG22	35:BO:118:ALA:HA	2.01	0.43
37:BQ:7:MET:HB2	37:BQ:7:MET:HE2	1.71	0.43
37:BQ:56:ARG:HA	37:BQ:56:ARG:HD2	1.72	0.43
51:B4:46:GLN:C	51:B4:48:ARG:HE	2.27	0.43
52:B5:59:GLU:HG2	52:B5:60:VAL:H	1.83	0.43
1:CA:1112:C:N3	3:CC:177:THR:HA	2.34	0.43
1:CA:1176:A:H2'	1:CA:1177:G:H8	1.84	0.43
1:CA:1216:G:H5"	14:CN:5:ALA:CB	2.47	0.43
2:CB:115:LEU:HD21	2:CB:153:ARG:NE	2.34	0.43
3:CC:42:LEU:HA	3:CC:45:LYS:NZ	2.33	0.43
5:CE:110:LEU:HD13	5:CE:118:ILE:HG21	2.00	0.43
13:CM:66:LEU:O	13:CM:68:GLY:N	2.52	0.43
19:CS:71:LEU:HD12	19:CS:71:LEU:HA	1.91	0.43
25:CY:1:G:H2'	25:CY:2:C:C6	2.54	0.43
25:CY:51:U:H2'	25:CY:52:G:O4'	2.18	0.43
26:DA:714:U:O2'	26:DA:716:A:N7	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1010:A:H1'	26:DA:1153:C:H1'	2.00	0.43
26:DA:1394:U:C4	26:DA:1395:A:C5	3.07	0.43
26:DA:1899:G:O2'	26:DA:1900:A:OP2	2.35	0.43
26:DA:2019:A:H4'	41:DU:34:LYS:HD2	2.01	0.43
26:DA:2265:U:C4	26:DA:2266:A:C5	3.07	0.43
26:DA:2461:C:H2'	26:DA:2462:U:H6	1.84	0.43
26:DA:2740:A:H2'	26:DA:2741:A:C8	2.54	0.43
26:DA:2747:G:O6	26:DA:2755:C:H5"	2.19	0.43
27:DB:24:G:O4'	27:DB:26:A:N6	2.47	0.43
29:DE:27:LEU:HD22	40:DT:1:MET:HE1	2.00	0.43
32:DH:124:GLU:OE1	32:DH:132:ARG:HD2	2.19	0.43
34:DN:96:GLU:H	34:DN:96:GLU:CD	2.26	0.43
36:DP:99:LEU:HD23	36:DP:99:LEU:H	1.83	0.43
37:DQ:36:ALA:HB2	37:DQ:103:MET:SD	2.59	0.43
38:DR:2:ARG:NH1	38:DR:5:LYS:O	2.52	0.43
50:D3:46:ASN:O	50:D3:50:VAL:HG22	2.19	0.43
1:AA:294:U:OP1	1:AA:610:G:O2'	2.30	0.42
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.48	0.42
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.53	0.42
2:AB:224:GLN:HA	2:AB:228:GLY:O	2.19	0.42
3:AC:77:ILE:HG22	3:AC:81:GLY:HA2	2.01	0.42
3:AC:82:GLU:HA	3:AC:85:ARG:NE	2.34	0.42
4:AD:170:VAL:HG12	4:AD:171:GLY:N	2.34	0.42
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.34	0.42
23:AW:51:U:H2'	23:AW:52:G:C8	2.54	0.42
26:BA:1354:A:H2'	26:BA:1355:G:O4'	2.19	0.42
26:BA:1504:C:H2'	26:BA:1505:C:C6	2.54	0.42
26:BA:1794:U:H2'	26:BA:1795:C:C6	2.54	0.42
26:BA:1882:C:H2'	26:BA:1883:G:O4'	2.19	0.42
26:BA:1913:A:H4'	26:BA:1914:C:C5'	2.49	0.42
26:BA:2199:A:H5"	26:BA:2200:C:OP2	2.19	0.42
33:BI:40:THR:O	33:BI:44:LEU:HB2	2.19	0.42
36:BP:100:LEU:HD12	36:BP:112:LEU:HD11	2.01	0.42
43:BW:14:PRO:HG2	43:BW:78:GLU:CG	2.48	0.42
45:BY:1:MET:HB2	45:BY:2:ARG:H	1.53	0.42
48:B1:62:VAL:HG22	48:B1:63:ALA:O	2.18	0.42
1:CA:103:C:P	20:CT:17:ARG:HH21	2.42	0.42
1:CA:228:A:H5'	16:CP:62:VAL:HG21	2.01	0.42
1:CA:495:A:H4'	1:CA:496:A:OP1	2.18	0.42
1:CA:993:G:N3	1:CA:993:G:H2'	2.33	0.42
1:CA:1025:U:H1'	1:CA:1026:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:115:LEU:HG	2:CB:119:GLU:OE2	2.19	0.42
2:CB:122:PHE:HE2	2:CB:139:LYS:HG2	1.84	0.42
10:CJ:30:SER:OG	10:CJ:84:GLN:OE1	2.29	0.42
13:CM:4:ILE:HG23	13:CM:22:ILE:HD11	2.01	0.42
18:CR:76:LEU:HD12	18:CR:76:LEU:HA	1.81	0.42
26:DA:150:C:H2'	26:DA:151:C:C6	2.54	0.42
26:DA:272(E):G:C2	26:DA:364:C:C2	3.07	0.42
26:DA:524:U:H2'	26:DA:525:U:C6	2.54	0.42
26:DA:563:G:OP2	61:DA:4169:HOH:O	2.21	0.42
26:DA:660:G:H5'	30:DF:99:TYR:CE2	2.53	0.42
26:DA:1463:C:H2'	26:DA:1464:C:C6	2.54	0.42
26:DA:2302:G:C6	26:DA:2303:G:N7	2.88	0.42
26:DA:2302:G:H1	26:DA:2314:C:H42	1.67	0.42
26:DA:2316:C:O2'	31:DG:128:ARG:NH1	2.52	0.42
26:DA:2529:G:O6	56:D9:31:LYS:NZ	2.51	0.42
26:DA:2591:C:H2'	26:DA:2592:G:C8	2.54	0.42
26:DA:2723:C:OP2	29:DE:109:LYS:NZ	2.52	0.42
28:DD:75:ILE:HA	28:DD:76:PRO:HD3	1.93	0.42
29:DE:181:LEU:HD12	29:DE:181:LEU:HA	1.76	0.42
30:DF:31:HIS:HB2	36:DP:9:ASN:OD1	2.19	0.42
31:DG:23:PHE:HB2	31:DG:25:TYR:CE1	2.54	0.42
31:DG:135:LEU:HD13	31:DG:135:LEU:HA	1.89	0.42
32:DH:2:SER:O	32:DH:3:ARG:HG2	2.19	0.42
32:DH:56:SER:HB3	32:DH:61:HIS:ND1	2.33	0.42
32:DH:164:TYR:HB2	32:DH:167:GLU:HB2	2.00	0.42
35:DO:17:ARG:HA	35:DO:17:ARG:HD3	1.69	0.42
38:DR:12:ARG:HG2	38:DR:16:HIS:ND1	2.34	0.42
39:DS:8:GLU:H	39:DS:8:GLU:CD	2.27	0.42
41:DU:107:ALA:O	41:DU:111:GLU:HG2	2.18	0.42
42:DV:31:ALA:O	42:DV:61:VAL:HG12	2.18	0.42
1:AA:54:C:H2'	1:AA:352:C:H41	1.84	0.42
1:AA:373:A:H1'	1:AA:481:G:N3	2.34	0.42
1:AA:405:U:O4	4:AD:2:GLY:N	2.53	0.42
1:AA:1286:A:H3'	1:AA:1286:A:C8	2.54	0.42
4:AD:170:VAL:HG11	4:AD:174:LEU:HD12	2.01	0.42
7:AG:28:ASN:HD22	7:AG:31:MET:HE2	1.84	0.42
8:AH:78:GLN:HE21	8:AH:78:GLN:HB2	1.47	0.42
26:BA:2291:U:H2'	26:BA:2292:C:C6	2.54	0.42
32:BH:24:VAL:HG22	32:BH:35:VAL:HB	2.01	0.42
44:BX:64:LYS:HD3	44:BX:64:LYS:HA	1.83	0.42
1:CA:850:U:H2'	1:CA:851:G:H5"	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1154:G:C8	1:CA:1155:G:C8	3.07	0.42
5:CE:60:TYR:CD1	5:CE:60:TYR:C	2.98	0.42
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	2.01	0.42
19:CS:41:VAL:HG13	19:CS:42:PRO:HD2	2.01	0.42
26:DA:39:C:H2'	26:DA:40:C:H6	1.84	0.42
26:DA:1204:A:N6	26:DA:1240:U:H2'	2.34	0.42
26:DA:1556:C:H2'	26:DA:1557:C:H6	1.84	0.42
26:DA:1877:A:H5'	26:DA:1878:G:OP2	2.19	0.42
31:DG:47:LYS:HE2	31:DG:47:LYS:HB3	1.56	0.42
45:DY:5:MET:HG2	45:DY:30:VAL:HG11	2.00	0.42
1:AA:59:A:H3'	1:AA:331:G:H22	1.84	0.42
1:AA:78:G:C2	1:AA:91:C:N4	2.87	0.42
1:AA:530:G:O6	22:AV:21:C:H1'	2.19	0.42
1:AA:539:A:H2'	1:AA:540:G:H8	1.84	0.42
1:AA:688:G:H5'	11:AK:46:GLY:C	2.43	0.42
1:AA:1002:G:C6	1:AA:1003:G:N3	2.88	0.42
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.34	0.42
2:AB:12:GLU:HA	2:AB:213:LEU:HD11	2.01	0.42
5:AE:103:GLY:O	5:AE:106:PRO:HD2	2.19	0.42
6:AF:10:LEU:HD23	6:AF:61:LEU:HD23	2.02	0.42
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.34	0.42
13:AM:84:ILE:HG13	13:AM:85:GLY:CA	2.44	0.42
25:AY:5:G:C2	25:AY:6:G:C4	3.07	0.42
25:AY:7:A:C6	25:AY:49:C:C4	3.07	0.42
26:BA:529:A:H62	26:BA:2041:U:H3	1.67	0.42
26:BA:971:C:H2'	26:BA:972:G:O4'	2.19	0.42
26:BA:1177:A:H3'	26:BA:1178:C:C6	2.54	0.42
26:BA:1252:G:OP1	41:BU:36:ARG:NH2	2.52	0.42
26:BA:1268:A:C2	26:BA:2013:A:C4	3.08	0.42
27:BB:32:C:C2	27:BB:51:G:N2	2.86	0.42
31:BG:53:LEU:HD23	31:BG:53:LEU:HA	1.84	0.42
1:CA:1122:U:H2'	1:CA:1123:A:O4'	2.19	0.42
1:CA:1124:G:H5'	10:CJ:36:GLY:H	1.84	0.42
3:CC:39:ILE:O	3:CC:43:LEU:HG	2.19	0.42
5:CE:116:THR:HG23	5:CE:117:ASP:CG	2.44	0.42
13:CM:47:ASP:O	13:CM:48:LEU:HD23	2.18	0.42
18:CR:44:LEU:HD23	18:CR:50:ILE:HA	2.02	0.42
23:CW:4:C:N4	23:CW:5:G:C6	2.87	0.42
24:CX:9:G:H21	24:CX:45:G:H3'	1.84	0.42
26:DA:735:A:N7	26:DA:761:A:H2	2.17	0.42
26:DA:1021:A:H3'	26:DA:1021:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1188:U:C4'	42:DV:79:VAL:HG22	2.50	0.42
26:DA:2386:C:H2'	26:DA:2387:U:C6	2.54	0.42
26:DA:2705:A:H2'	26:DA:2706:G:O4'	2.20	0.42
27:DB:11:C:H3'	27:DB:12:C:C6	2.55	0.42
29:DE:96:PHE:O	29:DE:175:VAL:HG11	2.19	0.42
42:DV:5:VAL:CG1	42:DV:57:VAL:HG21	2.49	0.42
45:DY:7:VAL:HG21	45:DY:72:VAL:HG12	2.00	0.42
45:DY:83:THR:HG21	45:DY:99:CYS:HB2	2.01	0.42
46:DZ:28:MET:HA	46:DZ:88:PHE:O	2.18	0.42
46:DZ:100:VAL:HA	46:DZ:101:PRO:HD3	1.91	0.42
1:AA:658:G:H2'	1:AA:659:U:H6	1.85	0.42
1:AA:1004:A:N7	1:AA:1036:G:C2	2.87	0.42
1:AA:1187:G:N3	14:AN:60:SER:OG	2.53	0.42
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.55	0.42
4:AD:176:LEU:HD12	4:AD:182:LYS:O	2.19	0.42
9:AI:127:LYS:O	9:AI:128:ARG:HG2	2.19	0.42
11:AK:20:TYR:CZ	11:AK:83:ILE:HD12	2.52	0.42
17:AQ:76:LEU:HD12	17:AQ:77:VAL:H	1.84	0.42
20:AT:13:LEU:O	20:AT:17:ARG:HG3	2.19	0.42
26:BA:171:G:O2'	26:BA:172:C:H5'	2.19	0.42
26:BA:489:G:N7	43:BW:49:LYS:NZ	2.68	0.42
26:BA:784:A:C8	26:BA:792:G:C5	3.07	0.42
26:BA:841:A:H2'	26:BA:842:G:C8	2.54	0.42
26:BA:918:A:H5"	27:BB:98:G:O2'	2.19	0.42
26:BA:1292:U:H2'	26:BA:1293:C:C6	2.54	0.42
26:BA:2439:A:H5'	26:BA:2439:A:H8	1.85	0.42
26:BA:2709:G:H2'	26:BA:2710:C:C6	2.54	0.42
29:BE:18:ASP:HB3	40:BT:82:LEU:HD21	2.01	0.42
34:BN:20:GLY:HA2	34:BN:61:ARG:HD2	2.01	0.42
49:B2:3:LEU:O	49:B2:7:ARG:HG3	2.19	0.42
52:B5:20:ARG:C	52:B5:22:HIS:H	2.27	0.42
1:CA:156:G:H1	1:CA:165:C:H42	1.67	0.42
1:CA:933:G:C6	1:CA:1385:G:C6	3.07	0.42
1:CA:985:C:C2	1:CA:1220:G:N2	2.80	0.42
1:CA:1009:G:C4	1:CA:1021:G:C2	3.08	0.42
1:CA:1320:C:H5'	1:CA:1320:C:H6	1.85	0.42
2:CB:51:LEU:HA	2:CB:54:THR:HB	2.01	0.42
3:CC:134:ILE:HG22	3:CC:168:ALA:HB3	2.01	0.42
5:CE:57:LYS:HG2	5:CE:61:TYR:HE2	1.84	0.42
7:CG:114:ARG:HB2	7:CG:115:ARG:NH2	2.35	0.42
7:CG:155:ARG:CZ	7:CG:155:ARG:HB3	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CX:21:A:H61	24:CX:46:G:H2'	1.84	0.42
26:DA:2203:U:H2'	26:DA:2205:C:C6	2.54	0.42
26:DA:2510:C:C4	26:DA:2511:U:C4	3.07	0.42
27:DB:117:G:C2	27:DB:118:G:C5	3.07	0.42
30:DF:179:GLU:CD	30:DF:179:GLU:H	2.27	0.42
31:DG:43:LEU:HD11	31:DG:153:ARG:HG2	2.01	0.42
32:DH:89:ILE:O	32:DH:129:THR:HG23	2.18	0.42
34:DN:123:TYR:CZ	34:DN:129:PRO:HD2	2.54	0.42
37:DQ:73:PRO:HA	37:DQ:93:TYR:CD1	2.54	0.42
1:AA:79:G:C2	1:AA:90:U:C2	3.07	0.42
1:AA:580:U:H5"	15:AO:58:MET:HG2	2.01	0.42
1:AA:1004:A:C5	1:AA:1037:C:N3	2.87	0.42
1:AA:1029:C:N4	1:AA:1030(A):G:C2	2.88	0.42
1:AA:1191:A:OP1	3:AC:4:LYS:NZ	2.53	0.42
2:AB:18:GLY:O	2:AB:19:HIS:HB3	2.19	0.42
2:AB:204:ASN:OD1	2:AB:204:ASN:C	2.63	0.42
3:AC:136:GLN:O	3:AC:140:ARG:HG3	2.18	0.42
9:AI:4:TYR:CE1	9:AI:88:TYR:HA	2.55	0.42
26:BA:1721:G:H3'	26:BA:1722:A:H5"	2.01	0.42
26:BA:2029:G:H2'	26:BA:2031:A:OP1	2.19	0.42
26:BA:2233:U:H2'	26:BA:2234:G:C8	2.55	0.42
26:BA:2396:G:OP1	48:B1:25:LYS:NZ	2.30	0.42
31:BG:28:VAL:HG23	31:BG:29:TRP:CD1	2.54	0.42
32:BH:170:ARG:O	32:BH:171:LEU:HD23	2.19	0.42
36:BP:112:LEU:HD23	36:BP:112:LEU:HA	1.85	0.42
51:B4:28:LYS:HA	51:B4:29:PRO:HD3	1.84	0.42
53:B6:50:ARG:HE	53:B6:50:ARG:HB2	1.67	0.42
1:CA:357:G:O2'	1:CA:358:U:H5'	2.18	0.42
1:CA:560:U:OP2	61:CA:3313:HOH:O	2.21	0.42
1:CA:911:U:O2'	1:CA:912:C:H5'	2.20	0.42
1:CA:1067:A:N3	1:CA:1068:G:H1'	2.33	0.42
1:CA:1388:C:H2'	1:CA:1389:C:C6	2.54	0.42
1:CA:1422:G:H5'	35:DO:48:PRO:HB3	2.01	0.42
3:CC:69:HIS:HB3	3:CC:106:VAL:CG2	2.50	0.42
4:CD:150:GLU:H	4:CD:150:GLU:HG3	1.68	0.42
12:CL:62:SER:HB2	12:CL:64:TYR:HD1	1.85	0.42
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.55	0.42
17:CQ:62:SER:CB	17:CQ:72:ARG:HD3	2.49	0.42
26:DA:64:A:O3'	44:DX:71:GLY:HA3	2.19	0.42
26:DA:117:G:C6	26:DA:119:A:C6	3.07	0.42
26:DA:764:A:H5'	28:DD:210:GLY:CA	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:829:A:N7	26:DA:2248:C:H5'	2.34	0.42
26:DA:1127:A:C2'	26:DA:1128:A:H5"	2.50	0.42
26:DA:1317:A:H2'	26:DA:1318:C:C6	2.55	0.42
26:DA:1341:U:O4	44:DX:16:LYS:HE2	2.19	0.42
26:DA:2130:U:H3	26:DA:2159:G:N2	2.17	0.42
26:DA:2408:U:H2'	26:DA:2409:G:C8	2.55	0.42
27:DB:62:C:H2'	27:DB:63:G:C8	2.55	0.42
27:DB:91:C:OP1	37:DQ:16:ARG:HG3	2.19	0.42
31:DG:53:LEU:HD23	31:DG:53:LEU:HA	1.88	0.42
39:DS:15:ARG:C	39:DS:19:LYS:HD3	2.45	0.42
41:DU:92:ARG:HG2	41:DU:92:ARG:H	1.44	0.42
48:D1:89:GLU:O	48:D1:93:GLU:HG2	2.19	0.42
50:D3:6:VAL:HG13	50:D3:56:VAL:HG22	2.02	0.42
1:AA:162:A:N7	1:AA:163:C:H1'	2.35	0.42
1:AA:299:G:H2'	1:AA:300:A:C8	2.55	0.42
1:AA:765:G:N1	1:AA:812:C:O2'	2.42	0.42
7:AG:120:ILE:O	7:AG:124:LEU:HB2	2.20	0.42
9:AI:20:ARG:O	9:AI:60:ASP:N	2.30	0.42
15:AO:85:LEU:HD23	15:AO:85:LEU:HA	1.75	0.42
26:BA:652(C):G:H1	26:BA:652(V):C:N4	2.18	0.42
26:BA:775:G:C4	26:BA:794:G:C8	3.07	0.42
26:BA:881:G:N1	26:BA:897:C:N4	2.67	0.42
26:BA:2093:G:C6	26:BA:2225:A:C8	3.08	0.42
26:BA:2529:G:H5"	26:BA:2530:A:H5"	2.01	0.42
29:BE:12:THR:HG22	29:BE:13:ARG:H	1.85	0.42
32:BH:98:LEU:HD12	32:BH:98:LEU:HA	1.91	0.42
33:BI:73:GLU:HG3	33:BI:139:GLN:O	2.19	0.42
1:CA:336:C:H2'	1:CA:337:C:C6	2.55	0.42
1:CA:815:A:N7	1:CA:1509:C:O2'	2.46	0.42
1:CA:921:U:O2	5:CE:19:MET:HB2	2.19	0.42
1:CA:1118:C:C2	1:CA:1119:C:C5	3.06	0.42
2:CB:82:ARG:HG3	2:CB:92:TYR:OH	2.18	0.42
2:CB:107:THR:O	2:CB:110:GLN:HB3	2.19	0.42
3:CC:52:LEU:HD23	3:CC:55:VAL:HG23	2.01	0.42
3:CC:56:ASP:C	3:CC:57:ILE:HD12	2.44	0.42
9:CI:28:VAL:HA	9:CI:63:ILE:O	2.20	0.42
11:CK:59:TYR:O	11:CK:63:LEU:HG	2.20	0.42
26:DA:925:C:H2'	26:DA:926:A:H8	1.85	0.42
26:DA:935:C:C2'	26:DA:936:C:H5'	2.50	0.42
26:DA:2006:C:O5'	26:DA:2006:C:H6	2.02	0.42
26:DA:2228:G:OP1	28:DD:261:LYS:HE3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2320:A:H2'	26:DA:2320:A:N3	2.33	0.42
27:DB:31:C:H4'	31:DG:29:TRP:CZ2	2.54	0.42
27:DB:55:U:H1'	31:DG:29:TRP:HD1	1.81	0.42
27:DB:57:A:N3	31:DG:29:TRP:HB3	2.33	0.42
28:DD:245:PRO:HA	28:DD:246:PRO:HD3	1.91	0.42
31:DG:121:ASN:HA	31:DG:181:ARG:HH21	1.84	0.42
32:DH:84:SER:HB3	32:DH:132:ARG:HH11	1.85	0.42
53:D6:13:CYS:SG	53:D6:47:THR:HG21	2.60	0.42
53:D6:18:ARG:HD2	53:D6:42:TRP:CG	2.55	0.42
1:AA:171:A:H2'	1:AA:172:A:C8	2.54	0.42
1:AA:396:G:O2'	1:AA:398:C:OP1	2.23	0.42
2:AB:111:ARG:HG2	2:AB:111:ARG:HH11	1.84	0.42
5:AE:85:GLY:C	5:AE:87:SER:H	2.27	0.42
8:AH:13:ILE:O	8:AH:17:THR:HG23	2.20	0.42
20:AT:13:LEU:HD12	20:AT:14:LYS:N	2.35	0.42
25:AY:18:G:N2	25:AY:58:A:C8	2.88	0.42
26:BA:601:C:O2'	26:BA:605:C:H5"	2.19	0.42
26:BA:1359:A:H2'	26:BA:1360:A:H5'	2.02	0.42
26:BA:2139:C:H2'	26:BA:2140:C:H4'	2.01	0.42
26:BA:2706:G:N7	61:BA:4712:HOH:O	2.37	0.42
34:BN:4:TYR:CE2	41:BU:100:VAL:HG11	2.55	0.42
34:BN:96:GLU:CD	34:BN:96:GLU:H	2.27	0.42
36:BP:63:PRO:HD3	55:B8:27:THR:HG22	2.00	0.42
39:BS:58:LEU:HD23	39:BS:58:LEU:HA	1.71	0.42
46:BZ:108:PRO:CB	46:BZ:117:LEU:HD13	2.46	0.42
1:CA:695:A:H2'	1:CA:696:A:C8	2.55	0.42
1:CA:779:C:O2'	11:CK:120:ARG:HD3	2.20	0.42
1:CA:1002:G:N2	1:CA:1038:C:N3	2.55	0.42
1:CA:1065:U:H1'	1:CA:1066:C:OP2	2.20	0.42
1:CA:1126:U:H4'	1:CA:1281:U:H1'	2.01	0.42
1:CA:1279:A:OP2	10:CJ:9:ARG:NH1	2.53	0.42
1:CA:1357:A:N7	1:CA:1358:U:C4	2.88	0.42
1:CA:1368:G:H2'	1:CA:1369:C:H5'	2.01	0.42
5:CE:98:THR:HB	5:CE:117:ASP:HB3	2.01	0.42
8:CH:51:VAL:HG12	8:CH:52:ASP:H	1.84	0.42
19:CS:52:TYR:HB2	19:CS:57:HIS:CE1	2.55	0.42
19:CS:65:ASN:OD1	19:CS:65:ASN:N	2.51	0.42
26:DA:108:U:H2'	26:DA:109:G:H8	1.83	0.42
26:DA:296:C:O3'	45:DY:95:LYS:NZ	2.52	0.42
26:DA:1019:U:H3	26:DA:1142(A):A:N6	2.06	0.42
26:DA:1248:G:C5	41:DU:3:ARG:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1449:A:OP2	26:DA:1449:A:H8	2.02	0.42
26:DA:2055:C:H1'	29:DE:145:LYS:HE2	2.01	0.42
26:DA:2187:G:C6	26:DA:2188:C:N3	2.87	0.42
26:DA:2262:U:H4'	26:DA:2328:A:C2	2.54	0.42
27:DB:57:A:H1'	31:DG:29:TRP:C	2.44	0.42
33:DI:77:LEU:HG	33:DI:101:LEU:HD12	2.02	0.42
34:DN:128:HIS:HA	34:DN:129:PRO:HD3	1.81	0.42
46:DZ:71:VAL:HG13	46:DZ:88:PHE:CD1	2.54	0.42
46:DZ:121:HIS:HB3	46:DZ:123:ASP:O	2.20	0.42
1:AA:457:C:H2'	1:AA:458:C:C6	2.54	0.42
1:AA:636:U:H2'	1:AA:637:G:H8	1.84	0.42
1:AA:1304:G:C6	1:AA:1305:G:N1	2.88	0.42
1:AA:1493:A:H5"	1:AA:1494:G:OP2	2.20	0.42
4:AD:36:ARG:HB3	4:AD:38:TYR:CZ	2.55	0.42
7:AG:73:MET:HE2	7:AG:90:GLU:HA	2.02	0.42
8:AH:73:ASP:OD1	8:AH:75:ARG:NH1	2.49	0.42
10:AJ:8:LEU:CD2	10:AJ:96:ILE:HG23	2.50	0.42
16:AP:4:ILE:C	16:AP:5:ARG:HG3	2.45	0.42
16:AP:18:ARG:NH1	16:AP:32:TYR:OH	2.52	0.42
26:BA:895:U:H5'	26:BA:896:A:OP1	2.20	0.42
26:BA:957:A:H5'	37:BQ:76:LYS:HG2	2.02	0.42
26:BA:1300:U:H4'	26:BA:1301:A:H5"	2.01	0.42
26:BA:1470:G:H5"	26:BA:1471:A:OP1	2.20	0.42
26:BA:1651:G:OP1	38:BR:40:LYS:HE3	2.20	0.42
26:BA:1652:A:C2'	26:BA:1653:G:H5'	2.49	0.42
26:BA:2218:U:O4'	48:B1:52:ARG:NH2	2.53	0.42
26:BA:2319:G:C2	39:BS:3:ARG:HA	2.54	0.42
26:BA:2328:A:H2'	26:BA:2329:G:H8	1.80	0.42
42:BV:55:ALA:HB2	42:BV:101:GLY:HA2	2.02	0.42
46:BZ:19:ARG:HD3	46:BZ:25:PRO:CD	2.50	0.42
51:B4:49:PHE:HD1	51:B4:49:PHE:HA	1.72	0.42
53:B6:8:LYS:HD3	55:B8:34:TRP:CD2	2.55	0.42
1:CA:1268:A:H2	1:CA:1326:C:O2	2.02	0.42
1:CA:1362:C:H2'	1:CA:1363:C:H5"	2.00	0.42
2:CB:70:PHE:HE1	2:CB:163:PHE:CD2	2.36	0.42
2:CB:95:GLN:HB2	2:CB:148:TYR:CD1	2.44	0.42
5:CE:79:GLU:O	5:CE:79:GLU:HG2	2.18	0.42
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.20	0.42
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HA	2.01	0.42
18:CR:73:ALA:CB	18:CR:79:LEU:HG	2.49	0.42
24:CX:21:A:H3'	24:CX:46:G:O6	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:11:G:H2'	26:DA:12:U:H5"	2.02	0.42
26:DA:271(K):U:H4'	26:DA:271(L):U:OP1	2.20	0.42
26:DA:479:A:H4'	26:DA:480:A:OP1	2.19	0.42
26:DA:740:U:H2'	26:DA:741:G:H8	1.81	0.42
26:DA:807:U:OP2	36:DP:41:ARG:NH2	2.53	0.42
26:DA:820:A:N3	26:DA:943:U:H4'	2.35	0.42
26:DA:1262:A:H2	52:D5:10:LYS:HD2	1.84	0.42
26:DA:1266:G:O5'	43:DW:15:ARG:NH2	2.52	0.42
26:DA:1445(A):C:H2'	26:DA:1446:C:H6	1.83	0.42
28:DD:29:PRO:HA	28:DD:83:GLU:OE1	2.19	0.42
30:DF:117:ARG:HH12	36:DP:1:MET:N	2.18	0.42
37:DQ:141:GLN:NE2	46:DZ:74:VAL:O	2.39	0.42
1:AA:377:G:OP1	16:AP:3:LYS:HD3	2.20	0.42
1:AA:393:A:OP1	61:AA:4195:HOH:O	2.21	0.42
1:AA:627:G:O2'	1:AA:628:G:H5'	2.20	0.42
1:AA:1262:C:H2'	1:AA:1263:C:C6	2.55	0.42
1:AA:1267:C:O5'	1:AA:1267:C:H6	2.02	0.42
2:AB:71:VAL:CG1	2:AB:170:GLU:HG2	2.49	0.42
5:AE:116:THR:HG23	5:AE:117:ASP:OD2	2.19	0.42
25:AY:24:G:C6	25:AY:25:C:C4	3.08	0.42
25:AY:53:G:N1	25:AY:61:C:N4	2.38	0.42
26:BA:171:G:C2'	26:BA:172:C:H5'	2.49	0.42
26:BA:185:U:H4'	26:BA:218:A:H4'	2.02	0.42
26:BA:2260:C:H2'	26:BA:2261:C:C6	2.55	0.42
26:BA:2810:A:N6	26:BA:2891:G:O2'	2.39	0.42
29:BE:141:ILE:HA	29:BE:154:LYS:HE2	2.02	0.42
32:BH:56:SER:HB3	32:BH:61:HIS:ND1	2.35	0.42
34:BN:4:TYR:CD2	41:BU:100:VAL:HG11	2.54	0.42
34:BN:42:TRP:HD1	34:BN:48:MET:HE1	1.85	0.42
37:BQ:37:LEU:HD21	37:BQ:130:LYS:HD3	2.01	0.42
46:BZ:24:LEU:HD21	46:BZ:86:VAL:HG13	2.01	0.42
1:CA:255:G:C6	1:CA:256:U:C4	3.08	0.42
1:CA:456:C:H2'	1:CA:457:C:H5'	2.00	0.42
1:CA:586:C:O2'	1:CA:878:G:H4'	2.19	0.42
1:CA:865:A:N3	1:CA:918:A:O2'	2.47	0.42
1:CA:1048:G:OP1	14:CN:3:ARG:HD2	2.19	0.42
1:CA:1118:C:N1	1:CA:1119:C:H5	2.18	0.42
5:CE:80:ILE:HD12	5:CE:80:ILE:HA	1.87	0.42
6:CF:2:ARG:HG3	6:CF:69:GLU:HG3	2.02	0.42
6:CF:89:MET:HE1	18:CR:72:ARG:HB3	2.02	0.42
6:CF:100:ASN:ND2	18:CR:23:LYS:HE3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:3:ARG:HG2	13:CM:8:GLU:HA	2.01	0.42
17:CQ:76:LEU:HD12	17:CQ:77:VAL:H	1.84	0.42
25:CY:19:G:N3	25:CY:57:G:N1	2.68	0.42
25:CY:37:MIA:H2'	25:CY:38:A:O4'	2.20	0.42
25:CY:76:A:N6	26:DA:2422:A:H5'	2.35	0.42
26:DA:192:C:O2'	26:DA:802:A:N3	2.48	0.42
26:DA:211:A:H2'	26:DA:212:G:O4'	2.20	0.42
26:DA:644:A:C2	26:DA:2369:A:H1'	2.55	0.42
26:DA:708:C:N4	26:DA:723:G:H1	2.18	0.42
26:DA:848:G:C4	26:DA:933:A:C8	3.06	0.42
26:DA:1237:A:OP1	61:DA:4484:HOH:O	2.21	0.42
26:DA:1371:G:H2'	26:DA:1372:U:C5	2.51	0.42
26:DA:1748:G:H2'	26:DA:1749:A:O4'	2.20	0.42
26:DA:2140:C:C2	26:DA:2152:G:C2	3.07	0.42
26:DA:2150:U:H2'	26:DA:2151:G:C8	2.55	0.42
27:DB:40:U:N3	27:DB:44:G:OP2	2.48	0.42
28:DD:68:LYS:O	28:DD:69:ARG:HB2	2.20	0.42
30:DF:196:LEU:HD23	30:DF:196:LEU:HA	1.86	0.42
35:DO:73:ASP:OD2	40:DT:32:TYR:OH	2.35	0.42
41:DU:90:VAL:HG12	41:DU:95:LEU:HD12	2.02	0.42
46:DZ:97:GLU:HB2	46:DZ:125:LEU:HD11	2.02	0.42
51:D4:38:LYS:C	51:D4:40:HIS:H	2.22	0.42
51:D4:47:GLN:C	51:D4:49:PHE:H	2.27	0.42
53:D6:35:GLU:HA	53:D6:49:HIS:O	2.20	0.42
1:AA:16:A:O2'	5:AE:16:THR:HB	2.20	0.42
1:AA:56:U:H2'	1:AA:57:G:H8	1.79	0.42
1:AA:342:C:C2	1:AA:348:G:N2	2.88	0.42
1:AA:584:G:H5'	17:AQ:91:ARG:NH2	2.35	0.42
1:AA:674:G:H2'	1:AA:675:A:C8	2.53	0.42
1:AA:729:A:H2'	1:AA:730:G:H8	1.84	0.42
1:AA:820:U:H4'	1:AA:821:G:OP2	2.20	0.42
1:AA:1210:C:C2'	1:AA:1211:U:H5'	2.50	0.42
8:AH:49:GLU:HG2	8:AH:62:TYR:HE1	1.84	0.42
12:AL:34:ARG:HG3	12:AL:105:TYR:CE2	2.55	0.42
26:BA:1881:C:H2'	26:BA:1882:C:C6	2.55	0.42
26:BA:2097:C:H2'	26:BA:2098:U:O4'	2.19	0.42
28:BD:242:ARG:N	28:BD:242:ARG:HD3	2.34	0.42
29:BE:14:ILE:HD11	29:BE:173:VAL:HG11	2.01	0.42
31:BG:18:GLU:OE1	31:BG:22:ARG:HD3	2.20	0.42
32:BH:54:ARG:HD3	32:BH:65:HIS:ND1	2.35	0.42
32:BH:98:LEU:HD13	32:BH:125:VAL:HG23	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BO:4:PRO:O	35:BO:5:GLN:HB2	2.20	0.42
42:BV:5:VAL:HG21	42:BV:35:LEU:HD23	2.02	0.42
1:CA:452:A:O2'	1:CA:453:A:OP2	2.34	0.42
1:CA:1011:G:H21	1:CA:1019:C:H1'	1.84	0.42
1:CA:1151:A:O2'	1:CA:1152:A:H8	2.00	0.42
1:CA:1162:C:H2'	1:CA:1163:C:O4'	2.20	0.42
1:CA:1203:C:H2'	1:CA:1204:A:O4'	2.20	0.42
1:CA:1323:G:O2'	1:CA:1362:C:O2'	2.23	0.42
2:CB:57:PHE:CE2	2:CB:185:ILE:HD12	2.50	0.42
2:CB:193:ASP:HA	2:CB:194:PRO:HD2	1.89	0.42
9:CI:20:ARG:HA	9:CI:21:PRO:HD3	1.92	0.42
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.46	0.42
14:CN:24:CYS:HA	14:CN:38:GLY:O	2.20	0.42
14:CN:26:ARG:HD2	14:CN:43:CYS:HB3	2.01	0.42
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.20	0.42
17:CQ:78:GLU:OE1	17:CQ:81:ARG:HD3	2.19	0.42
26:DA:30:G:H2'	26:DA:31:C:O4'	2.19	0.42
26:DA:271(D):G:C6	26:DA:271(E):U:C4	3.08	0.42
26:DA:847:U:OP2	61:DA:4017:HOH:O	2.22	0.42
26:DA:1221(A):C:C2	26:DA:1229:G:C2	3.08	0.42
26:DA:1927:A:H8	26:DA:1927:A:OP1	2.03	0.42
26:DA:2110:G:H4'	26:DA:2111:C:OP2	2.20	0.42
31:DG:49:ASP:N	31:DG:49:ASP:OD1	2.53	0.42
31:DG:72:ARG:HA	31:DG:86:MET:O	2.20	0.42
38:DR:65:LEU:HD12	38:DR:65:LEU:HA	1.87	0.42
42:DV:21:ARG:HG2	42:DV:91:TYR:CE2	2.55	0.42
48:D1:72:GLU:OE1	48:D1:76:ARG:NH2	2.53	0.42
1:AA:571:U:H5"	1:AA:819:A:C5	2.55	0.41
1:AA:841:U:C5	1:AA:848:C:H1'	2.54	0.41
1:AA:1362:C:C2'	1:AA:1363:C:H5"	2.49	0.41
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.34	0.41
15:AO:53:HIS:O	15:AO:56:LEU:HB3	2.20	0.41
19:AS:63:THR:H	19:AS:66:MET:CE	2.33	0.41
21:AU:15:ARG:HB2	21:AU:15:ARG:HH11	1.85	0.41
25:AY:5:G:H2'	25:AY:6:G:H8	1.85	0.41
25:AY:7:A:HO2'	25:AY:49:C:H5'	1.79	0.41
26:BA:26:G:H1'	26:BA:515:A:H61	1.85	0.41
26:BA:288:C:H2'	26:BA:289:A:C8	2.49	0.41
26:BA:2181:G:O2'	26:BA:2182:G:OP1	2.31	0.41
27:BB:40:U:H1'	27:BB:45:A:H61	1.84	0.41
28:BD:61:LEU:O	28:BD:63:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BZ:5:LEU:O	46:BZ:59:LEU:HA	2.20	0.41
46:BZ:104:PHE:CZ	46:BZ:119:GLU:HG2	2.55	0.41
49:B2:1:MET:HE1	49:B2:9:GLN:OE1	2.20	0.41
1:CA:337:C:H2'	1:CA:338:A:C8	2.54	0.41
1:CA:583:A:N6	1:CA:758:G:O2'	2.53	0.41
1:CA:804:U:OP1	61:CA:3206:HOH:O	2.21	0.41
1:CA:981:U:O5'	1:CA:981:U:H6	2.03	0.41
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.55	0.41
10:CJ:16:LEU:O	10:CJ:20:ALA:N	2.34	0.41
26:DA:245:G:O6	55:D8:8:LYS:NZ	2.38	0.41
26:DA:460:A:C2	26:DA:470:A:C4	3.08	0.41
26:DA:812:C:H2'	26:DA:813:U:H6	1.85	0.41
26:DA:2093:G:C6	26:DA:2225:A:C8	3.08	0.41
26:DA:2100:G:C6	26:DA:2190:G:C6	3.08	0.41
26:DA:2135:A:OP1	26:DA:2160:G:H1'	2.20	0.41
26:DA:2147:G:C4	26:DA:2148:G:H1'	2.55	0.41
26:DA:2370:G:C6	26:DA:2371:G:C6	3.07	0.41
26:DA:2483:C:O2	37:DQ:124:LYS:NZ	2.52	0.41
26:DA:2833:G:H4'	26:DA:2834:G:OP2	2.20	0.41
27:DB:19:G:H1	27:DB:64:C:H42	1.67	0.41
27:DB:80:U:H2'	27:DB:81:G:H8	1.85	0.41
28:DD:276:LYS:H	28:DD:276:LYS:CD	2.15	0.41
29:DE:146:THR:HA	29:DE:147:PRO:HA	1.90	0.41
31:DG:33:ARG:O	31:DG:34:LEU:HD23	2.19	0.41
31:DG:137:GLU:HB3	31:DG:139:LEU:HG	2.02	0.41
45:DY:2:ARG:NH1	45:DY:4:LYS:HA	2.35	0.41
45:DY:9:LYS:HA	45:DY:10:GLY:HA2	1.49	0.41
45:DY:38:ILE:HD11	45:DY:66:PRO:HG3	2.01	0.41
47:D0:52:GLY:O	47:D0:59:LEU:HA	2.20	0.41
1:AA:78:G:O2'	1:AA:79:G:H8	2.03	0.41
1:AA:454:C:OP1	16:AP:75:ARG:NH2	2.53	0.41
1:AA:690:G:C6	1:AA:691:G:C6	3.08	0.41
13:AM:5:ALA:HA	13:AM:61:GLU:OE2	2.18	0.41
17:AQ:87:LYS:HD3	17:AQ:87:LYS:HA	1.73	0.41
19:AS:12:ASP:OD1	19:AS:35:SER:HB3	2.19	0.41
19:AS:65:ASN:N	19:AS:65:ASN:ND2	2.66	0.41
19:AS:69:HIS:HD2	19:AS:73:GLU:OE1	2.03	0.41
25:AY:20:U:C4'	25:AY:21:A:H5'	2.50	0.41
25:AY:21:A:OP2	25:AY:21:A:H8	2.03	0.41
26:BA:7:G:H2'	26:BA:8:A:O4'	2.20	0.41
26:BA:1038:C:H42	26:BA:1117:G:H1	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1515:G:H2'	26:BA:1516:C:C6	2.55	0.41
26:BA:1903:G:OP1	28:BD:241:PRO:HB2	2.20	0.41
26:BA:2135:A:N6	26:BA:2156:G:O2'	2.53	0.41
26:BA:2150:U:O2	26:BA:2150:U:H2'	2.19	0.41
26:BA:2418:A:H2'	26:BA:2419:U:C6	2.54	0.41
26:BA:2784:C:H1'	29:BE:37:ARG:NH1	2.36	0.41
30:BF:140:LEU:HD13	30:BF:140:LEU:HA	1.86	0.41
32:BH:54:ARG:HA	32:BH:55:PRO:HD3	1.87	0.41
40:BT:27:THR:HB	40:BT:90:GLN:HB3	2.01	0.41
51:B4:46:GLN:N	51:B4:46:GLN:HE21	2.18	0.41
1:CA:60:A:H4'	1:CA:61:G:O5'	2.21	0.41
1:CA:266:G:H8	1:CA:266:G:H2'	1.68	0.41
1:CA:1030(A):G:H2'	1:CA:1030(B):C:H5"	2.02	0.41
1:CA:1133:G:N2	1:CA:1141:C:N3	2.61	0.41
1:CA:1274:G:N2	1:CA:1275:A:H62	2.17	0.41
1:CA:1279:A:H5"	1:CA:1280:A:OP1	2.20	0.41
2:CB:16:HIS:HD2	2:CB:204:ASN:H	1.67	0.41
13:CM:72:ALA:O	13:CM:76:ALA:N	2.48	0.41
20:CT:64:ASP:OD2	20:CT:81:LYS:NZ	2.44	0.41
24:CX:30:G:C6	24:CX:31:G:N7	2.89	0.41
25:CY:56:C:H2'	25:CY:57:G:O4'	2.20	0.41
26:DA:373:U:H2'	26:DA:374:A:C8	2.55	0.41
26:DA:382:G:OP2	61:DA:4359:HOH:O	2.22	0.41
26:DA:732:C:H2'	26:DA:733:G:O4'	2.20	0.41
26:DA:2297:C:N3	26:DA:2321:G:N2	2.66	0.41
26:DA:2875:C:H2'	26:DA:2876:G:O4'	2.20	0.41
36:DP:47:ASP:HA	36:DP:48:PRO:HD3	1.84	0.41
46:DZ:96:VAL:O	46:DZ:127:LYS:HA	2.20	0.41
49:D2:23:LYS:O	49:D2:27:GLU:HG3	2.20	0.41
1:AA:6:G:O2'	1:AA:7:G:H5'	2.20	0.41
1:AA:114:U:H2'	1:AA:115:G:C8	2.54	0.41
1:AA:160:A:H61	1:AA:345:C:H5'	1.86	0.41
1:AA:456:C:H2'	1:AA:457:C:H5'	2.02	0.41
1:AA:624:C:O3'	16:AP:10:GLY:HA2	2.20	0.41
1:AA:812:C:OP1	1:AA:903:G:H1'	2.19	0.41
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.56	0.41
4:AD:194:LEU:HD12	4:AD:195:ALA:N	2.36	0.41
10:AJ:11:PHE:CE1	10:AJ:67:THR:HG22	2.51	0.41
13:AM:56:LEU:O	13:AM:60:VAL:HG23	2.19	0.41
20:AT:48:LYS:HA	20:AT:48:LYS:HD3	1.77	0.41
23:AW:52:G:H4'	37:BQ:56:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:22:G:N7	25:AY:46:7MG:C6	2.87	0.41
26:BA:652(C):G:N2	26:BA:652(V):C:N3	2.64	0.41
26:BA:762:U:OP1	61:BA:4794:HOH:O	2.21	0.41
26:BA:2135:A:N1	26:BA:2156:G:O2'	2.44	0.41
26:BA:2142:C:C2	26:BA:2143:C:C5	3.08	0.41
30:BF:120:GLU:HB2	30:BF:122:LYS:HG2	2.01	0.41
34:BN:67:LEU:HD12	34:BN:67:LEU:HA	1.82	0.41
39:BS:59:LYS:HE3	39:BS:59:LYS:HB2	1.64	0.41
45:BY:9:LYS:HA	45:BY:10:GLY:HA2	1.68	0.41
46:BZ:150:LEU:O	46:BZ:171:ILE:HG13	2.19	0.41
1:CA:51:A:N7	1:CA:114:U:O2'	2.53	0.41
1:CA:617:G:H4'	16:CP:44:THR:O	2.19	0.41
1:CA:1044:A:C5	1:CA:1045:C:H1'	2.55	0.41
1:CA:1096:C:H2'	1:CA:1097:C:C6	2.55	0.41
1:CA:1366:C:HO2'	10:CJ:60:ARG:NH2	2.18	0.41
2:CB:70:PHE:CD1	2:CB:163:PHE:HB3	2.55	0.41
3:CC:71:ALA:C	3:CC:73:PRO:HD3	2.44	0.41
7:CG:65:ALA:O	7:CG:69:VAL:HG23	2.20	0.41
8:CH:58:TYR:O	8:CH:59:LEU:HD23	2.19	0.41
23:CW:18:G:O6	23:CW:55:PSU:H1'	2.20	0.41
25:CY:18:G:N2	25:CY:55:PSU:N3	2.68	0.41
25:CY:35:A:H3'	25:CY:36:A:C8	2.55	0.41
26:DA:38:A:H2'	26:DA:39:C:C6	2.55	0.41
26:DA:565:C:H4'	26:DA:1253:A:N6	2.35	0.41
26:DA:956:G:OP2	37:DQ:14:ARG:NH2	2.53	0.41
26:DA:980:A:C4	26:DA:1136:G:O4'	2.73	0.41
26:DA:1291:C:H2'	26:DA:1292:U:C6	2.55	0.41
26:DA:1463:C:H2'	26:DA:1464:C:H6	1.86	0.41
26:DA:1860:G:C6	26:DA:1883:G:N2	2.88	0.41
26:DA:2137:C:C2	26:DA:2138:C:C5	3.09	0.41
26:DA:2366:A:H2'	26:DA:2367:G:O4'	2.20	0.41
27:DB:32:C:H2'	27:DB:33:G:O4'	2.20	0.41
29:DE:7:VAL:HG12	29:DE:27:LEU:HB3	2.01	0.41
30:DF:20:LEU:HD23	30:DF:20:LEU:HA	1.90	0.41
46:DZ:98:MET:SD	46:DZ:100:VAL:HG23	2.60	0.41
46:DZ:124:ILE:HD11	46:DZ:163:LEU:HD11	2.02	0.41
46:DZ:159:PRO:HA	46:DZ:161:VAL:H	1.84	0.41
48:D1:86:SER:OG	48:D1:89:GLU:OE2	2.19	0.41
49:D2:41:ILE:HG13	49:D2:43:GLN:HB2	2.02	0.41
23:AW:66:U:H2'	23:AW:67:C:C6	2.55	0.41
25:AY:68:C:C4	25:AY:69:G:N7	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BE:96:PHE:O	29:BE:175:VAL:HG11	2.20	0.41
34:BN:61:ARG:HE	34:BN:61:ARG:HA	1.85	0.41
1:CA:237:C:H5"	17:CQ:25:ARG:CZ	2.49	0.41
1:CA:445:G:H2'	1:CA:446:G:C8	2.55	0.41
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.68	0.41
1:CA:607:A:H2'	1:CA:608:A:O4'	2.20	0.41
1:CA:719:C:N4	18:CR:71:LYS:HZ3	2.18	0.41
1:CA:839:U:H5"	1:CA:840:C:C5	2.56	0.41
1:CA:922:G:N3	1:CA:1398:A:H2	2.19	0.41
1:CA:1050:G:C6	1:CA:1051:C:C4	3.09	0.41
1:CA:1070:U:H2'	1:CA:1071:C:C6	2.52	0.41
1:CA:1183:A:H5'	1:CA:1183:A:C8	2.53	0.41
1:CA:1272:G:H2'	1:CA:1273:G:O4'	2.20	0.41
1:CA:1290:G:C4	1:CA:1291:G:C8	3.08	0.41
1:CA:1412:C:H2'	1:CA:1413:A:H8	1.81	0.41
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.21	0.41
1:CA:1496:C:H2'	1:CA:1497:G:O4'	2.21	0.41
2:CB:32:ILE:HD13	2:CB:40:HIS:CG	2.55	0.41
3:CC:66:VAL:HB	3:CC:101:LEU:HA	2.02	0.41
3:CC:116:VAL:O	3:CC:120:VAL:HG23	2.21	0.41
8:CH:28:ALA:HB3	8:CH:57:PRO:HB2	2.03	0.41
9:CI:96:LEU:O	9:CI:100:GLY:N	2.54	0.41
13:CM:91:ARG:HH22	13:CM:103:THR:CG2	2.33	0.41
19:CS:5:LEU:H	19:CS:5:LEU:HG	1.48	0.41
26:DA:96:G:H4'	49:D2:48:HIS:CD2	2.55	0.41
26:DA:108:U:H2'	26:DA:109:G:C8	2.56	0.41
26:DA:1638:C:H5"	26:DA:2710:C:O2'	2.21	0.41
26:DA:2318:G:N3	26:DA:2318:G:O2'	2.51	0.41
26:DA:2431:U:O2'	26:DA:2433:A:N7	2.49	0.41
30:DF:178:PRO:HB2	30:DF:201:VAL:CG2	2.49	0.41
31:DG:38:VAL:HG22	31:DG:93:THR:HG23	2.02	0.41
32:DH:90:LYS:HD2	32:DH:163:TYR:CD1	2.54	0.41
32:DH:117:PRO:HG3	32:DH:123:PHE:CD2	2.55	0.41
34:DN:4:TYR:HB2	41:DU:101:ARG:NH1	2.35	0.41
36:DP:97:PRO:HD3	36:DP:126:VAL:O	2.19	0.41
37:DQ:18:LYS:HB2	37:DQ:18:LYS:HE3	1.68	0.41
37:DQ:81:VAL:HB	47:D0:7:LEU:HD21	2.01	0.41
40:DT:65:LYS:HE2	40:DT:67:SER:HB2	2.02	0.41
1:AA:266:G:H4'	1:AA:267:C:C5	2.55	0.41
1:AA:374:A:C6	1:AA:375:U:C4	3.08	0.41
1:AA:971:G:N2	1:AA:1363(A):A:OP2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:975:A:H4'	1:AA:976:G:C5'	2.46	0.41
1:AA:1152:A:H2'	1:AA:1153:C:C6	2.55	0.41
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	2.03	0.41
4:AD:111:ALA:HB1	4:AD:116:GLN:HB3	2.03	0.41
5:AE:136:MET:HE3	5:AE:136:MET:HB3	1.84	0.41
11:AK:81:ASP:HB3	11:AK:107:SER:OG	2.21	0.41
13:AM:40:ASN:HA	13:AM:41:PRO:HD3	1.84	0.41
13:AM:54:VAL:HA	13:AM:57:ARG:HB3	2.03	0.41
24:AX:27:U:H2'	24:AX:28:C:C6	2.56	0.41
25:AY:6:G:C6	25:AY:7:A:C6	3.08	0.41
25:AY:62:C:H2'	25:AY:63:G:C8	2.51	0.41
26:BA:27:G:C2	26:BA:512:G:N3	2.88	0.41
26:BA:493:G:H2'	26:BA:494:G:O4'	2.20	0.41
26:BA:1359:A:N1	26:BA:1372:U:O4	2.54	0.41
26:BA:2698:U:H2'	26:BA:2699:C:C6	2.55	0.41
30:BF:143:ALA:HB1	30:BF:148:LEU:HB2	2.02	0.41
44:BX:12:VAL:HG21	44:BX:27:THR:HG22	2.03	0.41
44:BX:31:HIS:HA	44:BX:32:PRO:HD3	1.96	0.41
46:BZ:8:TYR:HB2	46:BZ:38:TYR:CE2	2.56	0.41
1:CA:411:A:C8	1:CA:413:G:C8	3.09	0.41
1:CA:932:C:H4'	7:CG:4:ARG:NH2	2.35	0.41
1:CA:1030(A):G:N3	1:CA:1030(C):G:C8	2.88	0.41
1:CA:1128:C:H1'	1:CA:1147:C:N4	2.31	0.41
1:CA:1373:G:H5"	7:CG:36:LYS:HD2	2.03	0.41
3:CC:11:ARG:HD3	3:CC:15:THR:HG21	2.01	0.41
8:CH:6:ILE:O	8:CH:10:LEU:HG	2.19	0.41
9:CI:125:TYR:C	9:CI:125:TYR:CD1	2.98	0.41
10:CJ:6:ILE:O	10:CJ:71:LEU:HD12	2.21	0.41
12:CL:33:ARG:O	12:CL:85:ILE:HG12	2.21	0.41
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.53	0.41
25:CY:38:A:C2'	25:CY:39:PSU:H5'	2.50	0.41
25:CY:76:A:H62	26:DA:2422:A:H5'	1.86	0.41
26:DA:120:U:H5"	26:DA:122:G:OP2	2.20	0.41
26:DA:266:G:N2	26:DA:427:U:H1'	2.35	0.41
26:DA:328:U:H4'	45:DY:68:HIS:CG	2.56	0.41
26:DA:443:A:H1'	26:DA:1201:C:O4'	2.19	0.41
26:DA:1857:G:C6	26:DA:1858:G:C6	3.08	0.41
31:DG:136:ARG:HD2	31:DG:137:GLU:HG3	2.03	0.41
36:DP:126:VAL:HG12	36:DP:148:LEU:HD22	2.03	0.41
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.36	0.41
1:AA:992:U:H4'	1:AA:993:G:C5'	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1002:G:H3'	1:AA:1003:G:O4'	2.20	0.41
1:AA:1241:G:O2'	1:AA:1242:C:H5'	2.20	0.41
1:AA:1368:G:OP2	9:AI:112:LYS:HG3	2.20	0.41
2:AB:20:GLU:HA	2:AB:21:ARG:HH21	1.86	0.41
2:AB:92:TYR:CE1	2:AB:151:GLY:HA3	2.55	0.41
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.20	0.41
3:AC:179:ARG:NH1	3:AC:206:GLU:OE1	2.54	0.41
5:AE:77:PRO:HG2	5:AE:78:HIS:HD2	1.85	0.41
11:AK:98:LEU:C	11:AK:101:SER:HG	2.19	0.41
20:AT:59:ALA:O	20:AT:63:ILE:HG13	2.21	0.41
26:BA:109:G:H2'	26:BA:110:G:O4'	2.20	0.41
26:BA:1518:U:H2'	26:BA:1519:G:O4'	2.20	0.41
29:BE:59:VAL:HG21	29:BE:74:PRO:HB3	2.02	0.41
30:BF:196:LEU:HD23	30:BF:196:LEU:HA	1.91	0.41
31:BG:33:ARG:N	31:BG:162:THR:OG1	2.52	0.41
32:BH:33:LEU:HD21	32:BH:136:ILE:HG13	2.02	0.41
39:BS:83:LYS:HE2	39:BS:83:LYS:HB2	1.88	0.41
40:BT:42:ILE:HG12	40:BT:84:GLN:NE2	2.36	0.41
45:BY:55:TYR:CD1	45:BY:55:TYR:N	2.88	0.41
48:B1:85:LEU:HB3	48:B1:89:GLU:HG3	2.03	0.41
1:CA:615:C:H2'	1:CA:616:G:O4'	2.20	0.41
1:CA:918:A:H2'	1:CA:919:A:O4'	2.21	0.41
1:CA:1179:A:C2	1:CA:1180:A:H1'	2.55	0.41
1:CA:1401:G:C2	1:CA:1402:C:H1'	2.55	0.41
2:CB:16:HIS:C	2:CB:18:GLY:H	2.27	0.41
13:CM:50:GLU:O	13:CM:50:GLU:HG3	2.20	0.41
21:CU:6:ARG:HG2	21:CU:15:ARG:HD2	2.02	0.41
26:DA:79:G:H1	26:DA:107:C:N4	2.19	0.41
26:DA:431:U:H6	26:DA:431:U:O5'	2.02	0.41
26:DA:1153:C:H2'	26:DA:1154:G:O4'	2.20	0.41
26:DA:1446:C:N4	26:DA:1465:G:H1	2.19	0.41
26:DA:1567:A:H2'	28:DD:84:TYR:HE2	1.86	0.41
26:DA:1754:C:OP2	40:DT:113:LYS:HE2	2.21	0.41
26:DA:1968:G:OP1	61:DA:4233:HOH:O	2.22	0.41
26:DA:2238:G:H2'	26:DA:2238:G:N3	2.35	0.41
26:DA:2507:C:H2'	26:DA:2508:G:O4'	2.21	0.41
26:DA:2751:G:C8	32:DH:2:SER:HA	2.56	0.41
31:DG:68:PRO:HB3	31:DG:92:VAL:HB	2.02	0.41
34:DN:97:ARG:HA	34:DN:100:GLU:HB2	2.03	0.41
40:DT:127:ALA:C	40:DT:129:ARG:H	2.29	0.41
51:D4:60:GLN:O	51:D4:63:TYR:HE2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:4:U:O4	8:AH:105:ARG:HD3	2.20	0.41
1:AA:190:U:H6	1:AA:190:U:H3'	1.85	0.41
1:AA:1317:C:OP1	14:AN:17:LYS:HG2	2.19	0.41
2:AB:47:THR:HA	2:AB:202:PRO:HG2	2.02	0.41
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.30	0.41
4:AD:57:ARG:HB3	4:AD:206:PHE:HB2	2.01	0.41
8:AH:87:SER:HB2	8:AH:93:VAL:H	1.85	0.41
26:BA:143:G:H2'	26:BA:143(A):C:C6	2.55	0.41
26:BA:855:G:O2'	47:B0:27:GLU:OE2	2.29	0.41
26:BA:2334:G:H4'	26:BA:2335:A:OP2	2.20	0.41
26:BA:2366:A:H2'	26:BA:2367:G:O4'	2.21	0.41
26:BA:2712:U:O2'	26:BA:2713:A:H5'	2.21	0.41
26:BA:2875:C:O2'	40:BT:4:GLY:HA3	2.21	0.41
27:BB:75:G:H5"	27:BB:75:G:H8	1.85	0.41
32:BH:11:VAL:CG2	32:BH:50:VAL:HG23	2.50	0.41
33:BI:93:THR:H	33:BI:96:ASP:CG	2.29	0.41
1:CA:278:G:OP2	17:CQ:41:LYS:NZ	2.36	0.41
1:CA:340:U:H2'	1:CA:341:C:C6	2.56	0.41
1:CA:418:C:H2'	1:CA:419:C:C6	2.56	0.41
1:CA:1070:U:O2'	1:CA:1071:C:H5'	2.21	0.41
3:CC:70:VAL:HG13	3:CC:73:PRO:HA	2.02	0.41
6:CF:55:ASP:HA	6:CF:56:PRO:HD3	1.83	0.41
9:CI:17:VAL:HG11	9:CI:81:ILE:N	2.36	0.41
11:CK:82:VAL:HB	11:CK:108:ILE:HG12	2.02	0.41
13:CM:3:ARG:CB	51:D4:34:GLU:HG2	2.50	0.41
23:CW:11:C:N4	23:CW:24:G:H1	2.17	0.41
25:CY:27:G:N1	25:CY:43:C:O2	2.49	0.41
26:DA:624:C:O2'	26:DA:657:U:OP1	2.36	0.41
26:DA:1012:U:C4	34:DN:25:ARG:HG2	2.56	0.41
26:DA:1470:G:N2	26:DA:1523:U:C4	2.88	0.41
26:DA:2161:C:H2'	26:DA:2162:G:O4'	2.20	0.41
27:DB:57:A:C4	31:DG:29:TRP:HB3	2.55	0.41
27:DB:118:G:C2'	27:DB:119:G:H5'	2.51	0.41
28:DD:61:LEU:HD12	28:DD:61:LEU:HA	1.93	0.41
32:DH:15:VAL:HG23	32:DH:27:LYS:O	2.21	0.41
34:DN:26:LEU:O	34:DN:30:ILE:HG13	2.21	0.41
44:DX:32:PRO:O	44:DX:77:LYS:NZ	2.51	0.41
46:DZ:4:ARG:HD3	46:DZ:60:GLU:OE1	2.21	0.41
55:D8:34:TRP:CG	55:D8:35:GLN:N	2.89	0.41
1:AA:154:C:N3	1:AA:168:G:C2	2.88	0.41
1:AA:920:U:H2'	1:AA:921:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:938:A:C6	1:AA:939:G:C5	3.09	0.41
1:AA:958:A:C6	1:AA:959:A:N1	2.88	0.41
1:AA:995:C:H5'	14:AN:8:GLU:HG2	2.02	0.41
1:AA:1418:A:H2	26:BA:1948:G:N3	2.19	0.41
1:AA:1469:G:H2'	1:AA:1470:G:H8	1.86	0.41
3:AC:32:LEU:HD13	3:AC:59:ARG:HD3	2.02	0.41
8:AH:75:ARG:HA	8:AH:76:PRO:HD2	1.87	0.41
14:AN:25:VAL:HG22	14:AN:38:GLY:O	2.20	0.41
24:AX:61:C:H2'	24:AX:62:C:C6	2.56	0.41
26:BA:558:G:OP1	34:BN:111:PRO:HD2	2.21	0.41
26:BA:881:G:H1	26:BA:897:C:N4	2.19	0.41
26:BA:1179:C:H2'	26:BA:1180:C:C6	2.52	0.41
26:BA:2070:G:C2	26:BA:2442:C:C2	3.09	0.41
26:BA:2131:G:H5'	26:BA:2133:G:O4'	2.21	0.41
26:BA:2287:A:H2	26:BA:2346:A:H62	1.64	0.41
29:BE:119:ARG:HD2	29:BE:120:TRP:CE2	2.55	0.41
45:BY:91:GLU:N	45:BY:91:GLU:OE2	2.54	0.41
50:B3:16:PRO:HB2	50:B3:18:ASP:OD1	2.20	0.41
51:B4:34:GLU:H	51:B4:34:GLU:HG3	1.56	0.41
51:B4:53:GLU:HB3	51:B4:54:GLY:O	2.21	0.41
1:CA:255:G:P	17:CQ:69:LYS:HZ1	2.41	0.41
1:CA:265:G:H5'	17:CQ:64:PRO:O	2.20	0.41
1:CA:443:C:H2'	1:CA:444:C:H6	1.85	0.41
1:CA:972:C:O2'	10:CJ:55:LYS:O	2.39	0.41
1:CA:1084:G:OP1	1:CA:1086:U:C2	2.73	0.41
1:CA:1134:G:C2	1:CA:1135:U:H1'	2.56	0.41
1:CA:1427:U:H2'	1:CA:1428:A:C8	2.55	0.41
5:CE:60:TYR:C	5:CE:60:TYR:HD1	2.29	0.41
8:CH:35:ILE:HG22	8:CH:39:LEU:HD23	2.03	0.41
13:CM:37:THR:HG21	13:CM:56:LEU:HA	2.03	0.41
14:CN:22:THR:HB	14:CN:33:VAL:HG21	2.03	0.41
14:CN:45:ARG:O	14:CN:49:HIS:CD2	2.74	0.41
26:DA:637:A:C8	36:DP:117:GLU:HG3	2.55	0.41
26:DA:889:C:O2'	26:DA:890:A:O5'	2.36	0.41
26:DA:899:A:C2'	26:DA:900:A:H5"	2.51	0.41
26:DA:1165:U:O5'	26:DA:1165:U:H6	2.04	0.41
26:DA:1445(A):C:H2'	26:DA:1446:C:C6	2.56	0.41
28:DD:72:LYS:HE3	28:DD:72:LYS:HB3	1.85	0.41
29:DE:5:LEU:HD21	29:DE:79:ARG:HB2	2.03	0.41
30:DF:64:ILE:HG13	30:DF:65:TRP:N	2.36	0.41
31:DG:33:ARG:NH2	31:DG:162:THR:HG21	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DG:122:PRO:HG2	31:DG:182:LYS:O	2.20	0.41
46:DZ:70:LEU:O	46:DZ:89:PHE:N	2.44	0.41
1:AA:34:C:H2'	1:AA:35:G:C8	2.56	0.41
1:AA:571:U:H5"	1:AA:819:A:C4	2.56	0.41
1:AA:925:G:H1'	1:AA:1502:A:C4	2.55	0.41
1:AA:953:G:H5'	1:AA:965:A:N6	2.31	0.41
1:AA:981:U:O5'	1:AA:981:U:H6	2.04	0.41
1:AA:1026:G:N3	1:AA:1026:G:H2'	2.35	0.41
1:AA:1060:C:C4	3:AC:2:GLY:HA3	2.56	0.41
1:AA:1305:G:OP2	21:AU:2:GLY:N	2.53	0.41
1:AA:1427:U:H2'	1:AA:1428:A:C8	2.55	0.41
1:AA:1457:G:P	20:AT:39:LYS:NZ	2.94	0.41
6:AF:9:VAL:HA	6:AF:59:TYR:O	2.20	0.41
8:AH:118:VAL:O	8:AH:119:LEU:HD23	2.21	0.41
13:AM:84:ILE:CG1	13:AM:85:GLY:HA2	2.44	0.41
13:AM:94:ARG:CZ	19:AS:80:TYR:HD2	2.34	0.41
15:AO:56:LEU:HD21	26:BA:715:G:C2	2.56	0.41
16:AP:72:ARG:O	16:AP:76:GLN:N	2.30	0.41
17:AQ:9:VAL:CG2	17:AQ:84:LEU:HD13	2.50	0.41
23:AW:9:A:H1'	23:AW:45:U:H2'	2.03	0.41
26:BA:391:G:H1'	26:BA:411:G:O4'	2.20	0.41
26:BA:947:G:H2'	26:BA:948:G:C8	2.56	0.41
26:BA:1352:U:OP2	61:BA:4017:HOH:O	2.22	0.41
26:BA:1800:C:OP1	28:BD:264:LYS:NZ	2.51	0.41
26:BA:2129:C:C2	26:BA:2130:U:H5	2.39	0.41
26:BA:2138:C:C2	26:BA:2154:G:C2	3.08	0.41
26:BA:2156:G:H21	26:BA:2157:G:H22	1.69	0.41
26:BA:2641:G:H5'	34:BN:83:LYS:HE2	2.03	0.41
26:BA:2788:C:OP1	29:BE:61:ARG:NH2	2.48	0.41
28:BD:108:PRO:HB3	28:BD:143:HIS:HE1	1.84	0.41
31:BG:137:GLU:HG2	31:BG:152:LEU:HD22	2.03	0.41
33:BI:106:GLY:N	33:BI:107:VAL:HG23	2.36	0.41
34:BN:39:ARG:HA	34:BN:40:PRO:HD3	1.84	0.41
35:BO:9:GLU:H	35:BO:9:GLU:HG2	1.72	0.41
35:BO:10:VAL:HG21	35:BO:16:ALA:HB3	2.03	0.41
44:BX:61:GLY:HA3	44:BX:73:ARG:O	2.21	0.41
49:B2:1:MET:HE2	49:B2:6:VAL:HG22	2.03	0.41
49:B2:13:ALA:HA	49:B2:16:LEU:HD12	2.03	0.41
50:B3:31:LEU:HD23	50:B3:31:LEU:HA	1.87	0.41
50:B3:31:LEU:O	50:B3:32:GLN:HB2	2.21	0.41
52:B5:35:GLU:HG3	52:B5:51:TYR:CG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:131:C:H2'	1:CA:132:C:C6	2.55	0.41
1:CA:784:C:H4'	26:DA:1837:C:OP1	2.20	0.41
1:CA:875:C:O2'	8:CH:14:ARG:HD2	2.21	0.41
1:CA:974:A:P	14:CN:29:ARG:HH21	2.44	0.41
1:CA:974:A:O4'	14:CN:31:ARG:HD3	2.21	0.41
1:CA:1011:G:C2	1:CA:1019:C:C2	3.09	0.41
1:CA:1097:C:O2'	1:CA:1169:A:N3	2.53	0.41
1:CA:1252:A:H2'	1:CA:1253:G:O4'	2.21	0.41
1:CA:1321:C:H3'	1:CA:1322:C:C6	2.56	0.41
1:CA:1401:G:OP1	22:CV:18:G:O2'	2.28	0.41
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.21	0.41
1:CA:1529:G:H4'	1:CA:1530:G:OP2	2.21	0.41
2:CB:48:MET:HA	2:CB:51:LEU:CD2	2.51	0.41
3:CC:122:GLU:HA	3:CC:125:GLU:OE1	2.21	0.41
4:CD:163:GLU:O	4:CD:166:LYS:HG2	2.20	0.41
4:CD:191:ARG:HA	4:CD:191:ARG:HD2	1.94	0.41
7:CG:91:VAL:HB	7:CG:96:GLN:HG2	2.02	0.41
9:CI:7:THR:OG1	9:CI:83:ARG:NH1	2.54	0.41
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.54	0.41
15:CO:85:LEU:HA	15:CO:85:LEU:HD23	1.82	0.41
26:DA:25:U:H5'	43:DW:78:GLU:O	2.21	0.41
26:DA:116:C:H2'	26:DA:117:G:O4'	2.21	0.41
26:DA:793:A:OP2	26:DA:2072:G:H5'	2.20	0.41
26:DA:819:A:C4	26:DA:1189:A:C2	3.09	0.41
26:DA:854:G:H2'	26:DA:855:G:C8	2.54	0.41
26:DA:899:A:O2'	26:DA:900:A:H5"	2.21	0.41
26:DA:923:C:H2'	26:DA:924:C:H6	1.84	0.41
26:DA:1116:C:H2'	26:DA:1117:G:C8	2.55	0.41
26:DA:1257:C:H2'	26:DA:1258:C:C6	2.56	0.41
26:DA:1270:C:O2'	26:DA:1648:C:OP2	2.37	0.41
26:DA:2009:G:OP1	43:DW:41:LYS:HE2	2.20	0.41
26:DA:2193:G:H2'	26:DA:2194:G:C8	2.56	0.41
28:DD:213:ARG:HA	28:DD:213:ARG:HD2	1.86	0.41
29:DE:2:LYS:NZ	29:DE:95:ILE:O	2.40	0.41
31:DG:105:LYS:NZ	51:D4:25:TYR:O	2.53	0.41
32:DH:35:VAL:HA	32:DH:36:PRO:HD2	1.94	0.41
32:DH:84:SER:CB	32:DH:132:ARG:HH11	2.33	0.41
33:DI:79:ILE:HA	33:DI:80:PRO:HD2	1.90	0.41
39:DS:15:ARG:HB3	39:DS:19:LYS:NZ	2.36	0.41
39:DS:16:ASN:O	39:DS:19:LYS:HG2	2.21	0.41
44:DX:1:MET:N	49:D2:29:LYS:HE3	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DZ:70:LEU:HA	46:DZ:70:LEU:HD23	1.80	0.41
49:D2:31:GLU:O	49:D2:35:LEU:HG	2.21	0.41
50:D3:4:LEU:O	50:D3:36:VAL:HA	2.21	0.41
51:D4:24:THR:OG1	51:D4:25:TYR:N	2.54	0.41
53:D6:43:CYS:O	53:D6:45:LYS:HG2	2.21	0.41
54:D7:8:ASN:HB3	54:D7:11:LYS:HB3	2.02	0.41
1:AA:439:A:C8	1:AA:496:A:C6	3.09	0.41
1:AA:976:G:N2	1:AA:1363:C:OP2	2.45	0.41
3:AC:8:ILE:HD12	3:AC:8:ILE:HA	1.94	0.41
4:AD:105:VAL:HG13	4:AD:110:PHE:HB2	2.02	0.41
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.21	0.41
6:AF:61:LEU:HA	6:AF:61:LEU:HD13	1.86	0.41
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.53	0.41
22:AV:16:A:H2'	22:AV:17:U:O4'	2.21	0.41
25:AY:5:G:C6	25:AY:6:G:C6	3.08	0.41
26:BA:481:G:C4	26:BA:507:A:C2	3.09	0.41
26:BA:606:U:H4'	26:BA:658:C:H4'	2.03	0.41
26:BA:1021:A:C8	26:BA:1022:G:H5"	2.55	0.41
26:BA:1408:C:H2'	26:BA:1409:C:C6	2.56	0.41
26:BA:1477:A:C2	26:BA:1515:G:C2	3.09	0.41
26:BA:1649:G:O2'	38:BR:107:ASP:OD2	2.32	0.41
26:BA:2154:G:H2'	26:BA:2155:G:H5'	2.03	0.41
26:BA:2273:A:H2'	26:BA:2274:A:C8	2.55	0.41
26:BA:2296:U:OP2	39:BS:9:ARG:NH2	2.49	0.41
27:BB:92:C:OP1	46:BZ:79:ARG:NH1	2.54	0.41
30:BF:165:ARG:HG2	30:BF:168:ARG:NH2	2.36	0.41
31:BG:56:ALA:HA	31:BG:153:ARG:HH21	1.86	0.41
33:BI:47:LEU:O	33:BI:51:ILE:HG13	2.21	0.41
37:BQ:45:GLN:CD	37:BQ:45:GLN:H	2.29	0.41
37:BQ:48:GLU:O	37:BQ:52:VAL:HG23	2.20	0.41
45:BY:1:MET:HB2	45:BY:1:MET:HE3	1.73	0.41
51:B4:53:GLU:O	51:B4:56:VAL:HG13	2.21	0.41
1:CA:61:G:C5	1:CA:107:G:C2	3.08	0.41
1:CA:423:G:H3'	1:CA:423:G:N3	2.35	0.41
1:CA:757:U:O2'	1:CA:879:C:O2	2.38	0.41
1:CA:1163:C:C2	1:CA:1174:G:C2	3.09	0.41
1:CA:1267:C:N4	1:CA:1268:A:C6	2.89	0.41
8:CH:64:LYS:HB3	8:CH:79:VAL:HG21	2.02	0.41
12:CL:89:ARG:HG2	12:CL:90:VAL:N	2.36	0.41
20:CT:36:LEU:HD13	20:CT:36:LEU:HA	1.90	0.41
24:CX:3:C:H2'	24:CX:4:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:25:U:C4	26:DA:26:G:C6	3.09	0.41
26:DA:77:C:O2'	49:D2:14:ARG:NH2	2.52	0.41
26:DA:590:A:P	30:DF:95:ARG:HH11	2.44	0.41
26:DA:642:G:H21	26:DA:646:A:H2	1.68	0.41
26:DA:706:A:H2'	26:DA:707:G:O4'	2.21	0.41
26:DA:1005:C:H2'	26:DA:1006:C:H6	1.83	0.41
26:DA:1518:U:H2'	26:DA:1519:G:O4'	2.20	0.41
26:DA:1575:C:H2'	26:DA:1576:U:O4'	2.21	0.41
26:DA:2135:A:H61	26:DA:2157:G:N2	2.19	0.41
26:DA:2669:G:C2	26:DA:2670:A:C8	3.09	0.41
28:DD:237:GLU:OE2	61:DD:401:HOH:O	2.22	0.41
31:DG:56:ALA:HA	31:DG:153:ARG:HH21	1.85	0.41
32:DH:54:ARG:HB3	32:DH:65:HIS:CD2	2.56	0.41
36:DP:37:GLY:C	36:DP:38:GLN:O	2.62	0.41
41:DU:86:ALA:O	42:DV:49:THR:HG23	2.20	0.41
1:AA:44:G:N7	61:AA:4044:HOH:O	2.37	0.40
1:AA:165:C:H2'	1:AA:166:G:C8	2.56	0.40
1:AA:183:G:H1	1:AA:194:C:H42	1.69	0.40
1:AA:964:A:N3	1:AA:969:A:O2'	2.50	0.40
1:AA:1028:C:C2	1:AA:1029:C:H1'	2.56	0.40
1:AA:1047:G:C2'	1:AA:1048:G:H5'	2.51	0.40
2:AB:161:ALA:HB1	2:AB:185:ILE:HD11	2.02	0.40
2:AB:183:PRO:HA	2:AB:198:ASP:OD2	2.21	0.40
3:AC:110:ASN:O	3:AC:141:VAL:HG22	2.21	0.40
4:AD:178:VAL:HG12	4:AD:179:GLU:N	2.35	0.40
8:AH:138:TRP:CD1	8:AH:138:TRP:C	2.99	0.40
14:AN:50:LYS:HB2	14:AN:50:LYS:HE2	1.76	0.40
19:AS:42:PRO:HD2	51:B4:61:ARG:HH21	1.86	0.40
26:BA:242:G:H5"	55:B8:64:TYR:CZ	2.57	0.40
26:BA:274:G:H2'	26:BA:275:G:C8	2.56	0.40
26:BA:470:A:OP1	30:BF:59:TYR:HE1	2.03	0.40
26:BA:994:C:OP1	41:BU:53:ARG:NH2	2.54	0.40
26:BA:1107:G:N2	26:BA:1108:U:O4	2.54	0.40
26:BA:1171:G:N7	26:BA:1173:G:C8	2.89	0.40
26:BA:1860:G:N2	26:BA:1882:C:O2	2.49	0.40
26:BA:2137:C:H2'	26:BA:2138:C:C6	2.56	0.40
26:BA:2191:G:H8	26:BA:2191:G:C5'	2.33	0.40
26:BA:2447:G:N2	26:BA:2450:A:OP2	2.53	0.40
29:BE:51:PHE:CD2	29:BE:52:LEU:HG	2.56	0.40
29:BE:144:ARG:HB3	29:BE:145:LYS:H	1.53	0.40
30:BF:177:ALA:O	30:BF:180:GLY:N	2.45	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BG:64:THR:HB	31:BG:94:LEU:HD21	2.03	0.40
32:BH:94:TYR:HA	32:BH:106:THR:O	2.21	0.40
46:BZ:7:ALA:O	46:BZ:62:PRO:HD3	2.21	0.40
46:BZ:76:LEU:HD12	46:BZ:76:LEU:HA	1.87	0.40
46:BZ:158:PRO:HA	46:BZ:159:PRO:HD3	1.90	0.40
1:CA:9:G:H2'	1:CA:10:A:C8	2.56	0.40
1:CA:130:A:H1'	1:CA:263:A:O2'	2.20	0.40
1:CA:629:G:H2'	1:CA:630:G:O4'	2.21	0.40
1:CA:895:G:N7	61:CA:3246:HOH:O	2.37	0.40
1:CA:1325:C:H4'	21:CU:17:THR:HG21	2.02	0.40
1:CA:1350:A:OP1	9:CI:121:ARG:HD3	2.22	0.40
2:CB:48:MET:HA	2:CB:51:LEU:HD21	2.02	0.40
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.46	0.40
10:CJ:42:THR:HG23	10:CJ:68:HIS:HD2	1.86	0.40
12:CL:119:LYS:O	12:CL:120:TYR:HB2	2.21	0.40
15:CO:3:ILE:H	15:CO:3:ILE:HD13	1.86	0.40
15:CO:31:LEU:HD23	15:CO:31:LEU:HA	1.89	0.40
16:CP:68:ASP:O	16:CP:71:ARG:HG2	2.21	0.40
19:CS:3:ARG:NH2	19:CS:10:PHE:HB2	2.36	0.40
25:CY:36:A:C2	25:CY:37:MIA:C4	3.04	0.40
26:DA:195:A:H2'	26:DA:198:C:N4	2.36	0.40
26:DA:528:A:C2	26:DA:2043:C:H4'	2.57	0.40
26:DA:531:C:OP1	26:DA:561:G:N1	2.50	0.40
26:DA:911:A:H2'	37:DQ:9:TYR:OH	2.22	0.40
26:DA:953:A:OP2	37:DQ:16:ARG:NE	2.50	0.40
26:DA:1479:G:C2	26:DA:1480:G:C4	3.09	0.40
26:DA:2037:G:O2'	26:DA:2038:G:H5'	2.22	0.40
26:DA:2058:A:N7	61:DA:3874:HOH:O	2.37	0.40
26:DA:2142:C:H2'	26:DA:2143:C:C6	2.56	0.40
26:DA:2694:G:C6	26:DA:2695:C:C4	3.08	0.40
26:DA:2848:G:H8	40:DT:97:ALA:HB2	1.85	0.40
29:DE:72:VAL:HG12	29:DE:73:GLU:O	2.21	0.40
30:DF:30:PRO:HB3	36:DP:1:MET:HE1	2.03	0.40
36:DP:135:LEU:HD23	36:DP:135:LEU:HA	1.79	0.40
42:DV:58:VAL:O	42:DV:97:LYS:N	2.45	0.40
45:DY:74:PRO:O	45:DY:82:PRO:HA	2.20	0.40
1:AA:993:G:N3	1:AA:993:G:H2'	2.35	0.40
2:AB:17:PHE:HD2	2:AB:44:LEU:HD21	1.86	0.40
2:AB:47:THR:HG22	2:AB:51:LEU:HD11	2.03	0.40
3:AC:134:ILE:HD11	3:AC:153:VAL:HG23	2.04	0.40
3:AC:150:LYS:HB2	3:AC:173:VAL:HG21	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:123:GLU:O	8:AH:127:LEU:HD13	2.22	0.40
10:AJ:30:SER:C	10:AJ:81:THR:HG21	2.46	0.40
23:AW:19:G:H4'	23:AW:20:U:OP1	2.20	0.40
25:AY:18:G:O6	25:AY:55:PSU:H1'	2.21	0.40
26:BA:1022:G:C6	26:BA:1141:U:C5	3.09	0.40
26:BA:1421:G:C2	26:BA:1422:G:C8	3.10	0.40
26:BA:2138:C:C4	26:BA:2154:G:C6	3.10	0.40
26:BA:2181:G:HO2'	26:BA:2182:G:P	2.43	0.40
27:BB:78:A:H2'	27:BB:79:C:O4'	2.21	0.40
36:BP:88:LEU:HD22	36:BP:95:VAL:HG21	2.03	0.40
52:B5:40:LYS:HE2	52:B5:46:CYS:HA	2.04	0.40
1:CA:981:U:H5'	14:CN:21:TYR:CE2	2.56	0.40
1:CA:1118:C:N4	1:CA:1119:C:H41	2.19	0.40
1:CA:1350:A:C2	1:CA:1351:U:C2	3.09	0.40
2:CB:77:ALA:HB2	2:CB:165:VAL:HG11	2.03	0.40
2:CB:80:ILE:HD13	2:CB:211:ILE:HB	2.02	0.40
2:CB:201:ILE:HA	2:CB:202:PRO:HD2	1.97	0.40
3:CC:70:VAL:HG22	3:CC:72:LYS:N	2.35	0.40
3:CC:105:GLU:OE1	3:CC:107:GLN:N	2.55	0.40
4:CD:76:ARG:NE	4:CD:80:GLU:OE1	2.50	0.40
4:CD:108:LEU:HA	4:CD:108:LEU:HD12	1.74	0.40
11:CK:18:ARG:NH2	11:CK:35:PRO:O	2.49	0.40
11:CK:87:THR:O	11:CK:87:THR:OG1	2.37	0.40
13:CM:10:PRO:HD2	13:CM:18:ALA:HB1	2.03	0.40
16:CP:69:THR:O	16:CP:72:ARG:HB2	2.22	0.40
19:CS:36:ARG:HD2	19:CS:52:TYR:O	2.21	0.40
23:CW:23:A:H2'	23:CW:24:G:C8	2.56	0.40
25:CY:9:A:H5'	25:CY:46:7MG:C1'	2.52	0.40
26:DA:511:U:H4'	26:DA:1235:G:H4'	2.03	0.40
26:DA:581:C:H2'	26:DA:582:G:C8	2.56	0.40
26:DA:885:C:H2'	26:DA:886:C:C4'	2.51	0.40
26:DA:1359:A:N1	26:DA:1372:U:C4	2.89	0.40
26:DA:1482:G:C6	26:DA:1507:A:C2	3.08	0.40
26:DA:1539:G:H2'	26:DA:1540:U:O4'	2.20	0.40
26:DA:2074:U:H2'	26:DA:2075:U:C6	2.56	0.40
26:DA:2137:C:N3	26:DA:2138:C:N4	2.68	0.40
26:DA:2542:A:H4'	26:DA:2543:G:C8	2.56	0.40
26:DA:2542:A:H4'	26:DA:2543:G:H8	1.87	0.40
27:DB:50:G:OP1	39:DS:63:THR:HG22	2.21	0.40
29:DE:52:LEU:O	29:DE:76:ARG:N	2.33	0.40
31:DG:25:TYR:C	31:DG:27:ASN:H	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DH:9:ILE:HG12	32:DH:69:ARG:HD2	2.04	0.40
32:DH:144:VAL:O	32:DH:148:ILE:HG12	2.21	0.40
48:D1:50:ARG:NH1	48:D1:57:GLU:OE2	2.54	0.40
1:AA:1003:G:N3	1:AA:1004:A:H1'	2.36	0.40
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.21	0.40
1:AA:1358:U:OP2	1:AA:1359:C:N4	2.54	0.40
2:AB:77:ALA:O	2:AB:81:VAL:HG22	2.20	0.40
2:AB:192:SER:O	2:AB:194:PRO:HD3	2.22	0.40
6:AF:95:GLU:HA	6:AF:96:PRO:HD3	1.98	0.40
7:AG:29:LYS:HD3	7:AG:29:LYS:HA	1.92	0.40
13:AM:117:VAL:HG12	13:AM:118:ALA:O	2.21	0.40
17:AQ:75:ARG:HH12	17:AQ:77:VAL:HA	1.86	0.40
26:BA:1851:U:H2'	26:BA:1852:C:O4'	2.21	0.40
26:BA:2331:G:O2'	47:B0:43:THR:HG22	2.21	0.40
26:BA:2506:U:C2	26:BA:2585:U:O4	2.75	0.40
35:BO:10:VAL:HG11	35:BO:16:ALA:HB1	2.04	0.40
36:BP:47:ASP:HA	36:BP:48:PRO:HD3	1.92	0.40
42:BV:6:LYS:HG2	42:BV:11:GLN:HG2	2.03	0.40
49:B2:64:LEU:CD2	49:B2:68:ARG:HE	2.34	0.40
1:CA:9:G:H2'	1:CA:10:A:H8	1.85	0.40
1:CA:300:A:H1'	1:CA:565:U:O2	2.20	0.40
1:CA:426:G:OP1	4:CD:36:ARG:NH1	2.42	0.40
1:CA:1347:G:H5"	9:CI:107:ARG:HB3	2.02	0.40
2:CB:197:VAL:HB	2:CB:200:ILE:HG12	2.03	0.40
2:CB:213:LEU:HD23	2:CB:213:LEU:C	2.45	0.40
3:CC:70:VAL:N	3:CC:106:VAL:HG23	2.37	0.40
3:CC:109:PRO:HB3	3:CC:115:LEU:HD23	2.03	0.40
4:CD:3:ARG:O	4:CD:5:ILE:HG22	2.21	0.40
13:CM:95:GLY:HA2	13:CM:110:ARG:NH1	2.36	0.40
24:CX:47:U:H3'	24:CX:48:C:C5'	2.51	0.40
24:CX:58:A:O2'	24:CX:60:U:OP2	2.34	0.40
26:DA:565:C:H2'	26:DA:566:U:O4'	2.21	0.40
26:DA:587:C:OP2	36:DP:21:ARG:NH2	2.55	0.40
26:DA:1487:G:H2'	26:DA:1488:G:H5"	2.04	0.40
26:DA:1777:U:O2'	26:DA:1778:U:H5'	2.20	0.40
26:DA:2136:C:O2'	26:DA:2137:C:H6	2.05	0.40
26:DA:2447:G:N2	26:DA:2450:A:OP2	2.54	0.40
26:DA:2689:U:C4'	26:DA:2690:C:H5'	2.48	0.40
27:DB:57:A:O4'	31:DG:30:GLU:HG3	2.21	0.40
38:DR:78:LYS:HE2	38:DR:83:ILE:HD11	2.04	0.40
39:DS:36:TYR:CD2	39:DS:52:SER:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:DU:103:PRO:O	41:DU:107:ALA:N	2.50	0.40
46:DZ:7:ALA:HB3	46:DZ:61:LEU:HD12	2.03	0.40
46:DZ:79:ARG:HD2	46:DZ:80:ARG:CZ	2.51	0.40
46:DZ:97:GLU:HA	46:DZ:126:VAL:O	2.21	0.40
54:D7:10:ARG:O	54:D7:14:LYS:HB2	2.22	0.40
56:D9:29:ASN:HA	56:D9:30:PRO:HD3	1.88	0.40
1:AA:7:G:H5"	1:AA:298:A:O4'	2.22	0.40
1:AA:49:U:O4	1:AA:365:U:H5	2.05	0.40
1:AA:57:G:H2'	1:AA:58:C:C6	2.57	0.40
1:AA:201:C:H2'	1:AA:202:U:H2'	2.03	0.40
1:AA:376:G:O2'	16:AP:5:ARG:NH2	2.54	0.40
1:AA:737:A:OP1	6:AF:92:LYS:HG3	2.21	0.40
1:AA:784:C:H2'	1:AA:785:G:O4'	2.22	0.40
1:AA:1001:A:N1	1:AA:1040:U:O4	2.54	0.40
1:AA:1006:C:H2'	1:AA:1007:C:C6	2.56	0.40
1:AA:1118:C:OP1	9:AI:9:ARG:NH1	2.53	0.40
1:AA:1166:G:H5'	1:AA:1168:A:OP2	2.21	0.40
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.17	0.40
1:AA:1457:G:H2'	1:AA:1458:G:C8	2.57	0.40
4:AD:147:ALA:HB2	4:AD:182:LYS:HA	2.04	0.40
7:AG:144:MET:HE3	25:AY:40:C:O2'	2.21	0.40
14:AN:27:CYS:SG	14:AN:29:ARG:HB2	2.61	0.40
19:AS:41:VAL:O	19:AS:44:MET:HB2	2.21	0.40
26:BA:286:C:H2'	26:BA:287:C:C6	2.57	0.40
26:BA:303:U:O4	61:BA:4656:HOH:O	2.22	0.40
26:BA:335:C:H5'	45:BY:73:ARG:NH2	2.36	0.40
26:BA:526:A:H5"	26:BA:527:C:OP1	2.21	0.40
26:BA:536:A:H2'	26:BA:537:C:C6	2.56	0.40
26:BA:1636:C:H2'	26:BA:1637:A:C8	2.56	0.40
26:BA:2262:U:H4'	26:BA:2328:A:C2	2.56	0.40
28:BD:38:LYS:HA	28:BD:38:LYS:HD2	1.98	0.40
30:BF:93:LYS:HD3	30:BF:93:LYS:HA	1.91	0.40
31:BG:79:ASN:OD1	31:BG:79:ASN:N	2.52	0.40
35:BO:23:ARG:HG3	35:BO:24:VAL:N	2.36	0.40
40:BT:80:SER:HA	40:BT:81:PRO:HD3	1.89	0.40
51:B4:40:HIS:HA	51:B4:41:PRO:HD2	1.88	0.40
1:CA:1442:G:H3'	1:CA:1442:G:C8	2.56	0.40
2:CB:15:VAL:CG1	2:CB:209:ARG:HB3	2.49	0.40
2:CB:42:ILE:HG21	2:CB:202:PRO:HB2	2.03	0.40
2:CB:168:THR:OG1	2:CB:192:SER:HA	2.22	0.40
4:CD:61:LYS:HZ1	4:CD:72:GLU:CD	2.27	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CQ:46:ASP:CG	17:CQ:49:GLU:HA	2.46	0.40
24:CX:28:C:H2'	24:CX:29:G:C8	2.56	0.40
24:CX:28:C:H2'	24:CX:29:G:H8	1.85	0.40
24:CX:50:U:H3	24:CX:64:G:H1	1.68	0.40
26:DA:19:C:H2'	26:DA:20:C:H6	1.86	0.40
26:DA:469:G:H2'	26:DA:470:A:H5"	2.02	0.40
26:DA:478:A:H62	26:DA:502:A:N6	2.19	0.40
26:DA:1501:C:O4'	28:DD:100:GLY:HA2	2.21	0.40
26:DA:1653:G:H3'	38:DR:2:ARG:HD3	2.04	0.40
26:DA:1773:A:H5"	61:DA:4357:HOH:O	2.21	0.40
26:DA:2224:G:H4'	26:DA:2226:C:C2	2.56	0.40
26:DA:2273:A:H2'	26:DA:2274:A:H8	1.85	0.40
29:DE:24:THR:CG2	29:DE:184:VAL:HG12	2.52	0.40
32:DH:77:LYS:HG3	32:DH:81:GLU:OE2	2.21	0.40
35:DO:9:GLU:OE2	35:DO:18:LYS:HE3	2.21	0.40
42:DV:39:LEU:HG	42:DV:46:VAL:O	2.21	0.40
44:DX:64:LYS:HA	44:DX:64:LYS:HD2	1.88	0.40
44:DX:84:ALA:HB3	44:DX:87:GLN:NE2	2.37	0.40
48:D1:23:LYS:HE3	48:D1:23:LYS:HB2	1.79	0.40
52:D5:11:THR:HG22	52:D5:12:SER:O	2.21	0.40
1:AA:22:G:H4'	1:AA:885:G:C8	2.57	0.40
1:AA:38:G:O2'	1:AA:39:G:H5"	2.21	0.40
1:AA:719:C:H1'	18:AR:49:LYS:HB3	2.03	0.40
1:AA:881:G:H2'	1:AA:882:C:O4'	2.21	0.40
1:AA:1121:U:C2'	1:AA:1122:U:H5'	2.52	0.40
1:AA:1261:A:H3'	1:AA:1262:C:H6	1.87	0.40
1:AA:1410:G:H2'	1:AA:1411:C:C6	2.57	0.40
1:AA:1529:G:H4'	1:AA:1530:G:OP2	2.22	0.40
2:AB:10:LEU:C	2:AB:12:GLU:N	2.79	0.40
7:AG:97:GLN:HE21	7:AG:97:GLN:HB2	1.66	0.40
12:AL:7:ILE:O	12:AL:11:VAL:HG23	2.21	0.40
12:AL:24:VAL:HG13	12:AL:98:TYR:CE2	2.57	0.40
24:AX:55:PSU:O2'	24:AX:57:A:N7	2.51	0.40
26:BA:125:G:N2	54:B7:48:LYS:HA	2.36	0.40
26:BA:303:U:H2'	26:BA:304:G:C8	2.56	0.40
26:BA:484:C:H2'	26:BA:485:C:H6	1.87	0.40
26:BA:1022:G:N2	26:BA:1142(A):A:C2	2.80	0.40
26:BA:1230:C:H2'	26:BA:1231:G:H8	1.86	0.40
26:BA:1753:G:N1	26:BA:1756:G:OP2	2.53	0.40
26:BA:1817:G:C6	26:BA:1818:U:C4	3.10	0.40
26:BA:2147:G:H2'	26:BA:2148:G:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BD:258:LYS:HE2	28:BD:273:ARG:CZ	2.51	0.40
31:BG:38:VAL:HG22	31:BG:93:THR:HG23	2.03	0.40
35:BO:79:PHE:CD2	40:BT:72:VAL:HG22	2.56	0.40
43:BW:13:SER:HA	43:BW:14:PRO:HD3	1.82	0.40
1:CA:179:A:C2'	1:CA:180:U:H5'	2.52	0.40
1:CA:377:G:H5'	16:CP:5:ARG:NH2	2.37	0.40
1:CA:407:G:H5"	4:CD:115:ARG:HB3	2.03	0.40
1:CA:408:A:H2'	1:CA:409:G:O4'	2.21	0.40
1:CA:643:C:H2'	1:CA:644:G:C8	2.57	0.40
1:CA:785:G:C2'	1:CA:786:G:H5'	2.51	0.40
1:CA:1014:A:H4'	19:CS:14:HIS:CE1	2.57	0.40
1:CA:1028:C:O2	1:CA:1034:G:H1'	2.21	0.40
1:CA:1065:U:P	1:CA:1190:G:H22	2.45	0.40
1:CA:1100:C:H2'	1:CA:1102:A:O5'	2.22	0.40
1:CA:1133:G:H2'	1:CA:1134:G:O4'	2.22	0.40
2:CB:189:ASP:O	2:CB:192:SER:OG	2.40	0.40
6:CF:82:ARG:HD2	6:CF:82:ARG:HA	1.71	0.40
6:CF:95:GLU:HA	6:CF:96:PRO:HD3	1.85	0.40
8:CH:27:PRO:O	8:CH:32:LYS:HD2	2.22	0.40
20:CT:24:LEU:HD13	20:CT:24:LEU:HA	1.71	0.40
26:DA:195:A:H2'	26:DA:198:C:H41	1.86	0.40
26:DA:463:G:N2	26:DA:466:A:OP2	2.49	0.40
26:DA:661:C:H2'	26:DA:662:G:C8	2.56	0.40
26:DA:729:G:C6	28:DD:208:LYS:HB2	2.56	0.40
26:DA:1011:G:C2	26:DA:1151:G:N3	2.90	0.40
26:DA:1935:G:H1'	26:DA:1964:G:N2	2.37	0.40
26:DA:2625:G:H2'	26:DA:2626:C:O4'	2.22	0.40
26:DA:2734:A:H2'	26:DA:2735:G:O4'	2.21	0.40
26:DA:2849:U:P	40:DT:95:ARG:HH12	2.44	0.40
27:DB:5:C:N4	27:DB:116:G:H1	2.13	0.40
29:DE:201:THR:OG1	29:DE:202:LYS:N	2.55	0.40
31:DG:51:ARG:H	31:DG:51:ARG:HG3	1.69	0.40
31:DG:97:ASP:O	31:DG:101:ILE:HG13	2.21	0.40
33:DI:57:ARG:O	33:DI:61:ARG:HG2	2.21	0.40
35:DO:2:ILE:HB	35:DO:33:ALA:HB3	2.03	0.40
38:DR:1:MET:HB2	38:DR:2:ARG:H	1.71	0.40
38:DR:96:ARG:HD3	38:DR:98:LEU:HD11	2.04	0.40
51:D4:13:ARG:O	51:D4:30:GLU:HA	2.20	0.40
53:D6:8:LYS:HD3	55:D8:34:TRP:CD2	2.56	0.40
56:D9:12:ASP:OD1	56:D9:13:LYS:HG2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	AB	229/256 (90%)	208 (91%)	13 (6%)	8 (4%)	3 4
2	CB	229/256 (90%)	208 (91%)	14 (6%)	7 (3%)	3 5
3	AC	204/239 (85%)	193 (95%)	10 (5%)	1 (0%)	24 46
3	CC	204/239 (85%)	191 (94%)	13 (6%)	0	100 100
4	AD	206/209 (99%)	197 (96%)	9 (4%)	0	100 100
4	CD	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	24 46
5	AE	146/162 (90%)	142 (97%)	4 (3%)	0	100 100
5	CE	146/162 (90%)	142 (97%)	3 (2%)	1 (1%)	18 38
6	AF	98/101 (97%)	95 (97%)	3 (3%)	0	100 100
6	CF	98/101 (97%)	95 (97%)	3 (3%)	0	100 100
7	AG	153/156 (98%)	149 (97%)	3 (2%)	1 (1%)	18 38
7	CG	153/156 (98%)	149 (97%)	3 (2%)	1 (1%)	18 38
8	AH	135/138 (98%)	133 (98%)	2 (2%)	0	100 100
8	CH	135/138 (98%)	131 (97%)	4 (3%)	0	100 100
9	AI	125/128 (98%)	119 (95%)	5 (4%)	1 (1%)	16 34
9	CI	125/128 (98%)	120 (96%)	4 (3%)	1 (1%)	16 34
10	AJ	95/105 (90%)	85 (90%)	8 (8%)	2 (2%)	5 11
10	CJ	94/105 (90%)	84 (89%)	6 (6%)	4 (4%)	2 2
11	AK	112/129 (87%)	107 (96%)	4 (4%)	1 (1%)	14 30
11	CK	112/129 (87%)	107 (96%)	4 (4%)	1 (1%)	14 30
12	AL	120/132 (91%)	118 (98%)	2 (2%)	0	100 100
12	CL	120/132 (91%)	117 (98%)	2 (2%)	1 (1%)	16 34
13	AM	121/126 (96%)	116 (96%)	4 (3%)	1 (1%)	16 34
13	CM	120/126 (95%)	113 (94%)	4 (3%)	3 (2%)	4 8
14	AN	58/61 (95%)	57 (98%)	1 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
14	CN	58/61 (95%)	57 (98%)	1 (2%)	0	100 100
15	AO	86/89 (97%)	84 (98%)	2 (2%)	0	100 100
15	CO	86/89 (97%)	83 (96%)	3 (4%)	0	100 100
16	AP	80/88 (91%)	78 (98%)	2 (2%)	0	100 100
16	CP	80/88 (91%)	78 (98%)	1 (1%)	1 (1%)	9 21
17	AQ	97/105 (92%)	94 (97%)	3 (3%)	0	100 100
17	CQ	97/105 (92%)	94 (97%)	3 (3%)	0	100 100
18	AR	66/88 (75%)	64 (97%)	2 (3%)	0	100 100
18	CR	66/88 (75%)	64 (97%)	2 (3%)	0	100 100
19	AS	82/93 (88%)	76 (93%)	5 (6%)	1 (1%)	10 23
19	CS	81/93 (87%)	75 (93%)	6 (7%)	0	100 100
20	AT	94/106 (89%)	85 (90%)	4 (4%)	5 (5%)	1 1
20	CT	94/106 (89%)	85 (90%)	4 (4%)	5 (5%)	1 1
21	AU	21/27 (78%)	20 (95%)	1 (5%)	0	100 100
21	CU	21/27 (78%)	21 (100%)	0	0	100 100
28	BD	273/276 (99%)	263 (96%)	9 (3%)	1 (0%)	30 51
28	DD	273/276 (99%)	261 (96%)	10 (4%)	2 (1%)	18 38
29	BE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	24 46
29	DE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	24 46
30	BF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	24 46
30	DF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	24 46
31	BG	179/182 (98%)	171 (96%)	7 (4%)	1 (1%)	21 42
31	DG	179/182 (98%)	168 (94%)	8 (4%)	3 (2%)	7 15
32	BH	172/180 (96%)	166 (96%)	6 (4%)	0	100 100
32	DH	172/180 (96%)	166 (96%)	6 (4%)	0	100 100
33	BI	144/148 (97%)	132 (92%)	7 (5%)	5 (4%)	3 4
33	DI	144/148 (97%)	135 (94%)	8 (6%)	1 (1%)	18 38
34	BN	138/140 (99%)	136 (99%)	2 (1%)	0	100 100
34	DN	138/140 (99%)	135 (98%)	3 (2%)	0	100 100
35	BO	120/122 (98%)	114 (95%)	6 (5%)	0	100 100
35	DO	120/122 (98%)	115 (96%)	5 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
36	BP	147/150 (98%)	142 (97%)	4 (3%)	1 (1%)	18 38
36	DP	147/150 (98%)	139 (95%)	6 (4%)	2 (1%)	9 19
37	BQ	139/141 (99%)	135 (97%)	4 (3%)	0	100 100
37	DQ	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18 38
38	BR	116/118 (98%)	115 (99%)	1 (1%)	0	100 100
38	DR	116/118 (98%)	114 (98%)	2 (2%)	0	100 100
39	BS	108/112 (96%)	106 (98%)	2 (2%)	0	100 100
39	DS	108/112 (96%)	107 (99%)	0	1 (1%)	14 30
40	BT	129/146 (88%)	123 (95%)	6 (5%)	0	100 100
40	DT	129/146 (88%)	126 (98%)	3 (2%)	0	100 100
41	BU	114/118 (97%)	114 (100%)	0	0	100 100
41	DU	114/118 (97%)	114 (100%)	0	0	100 100
42	BV	99/101 (98%)	93 (94%)	5 (5%)	1 (1%)	12 28
42	DV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	12 28
43	BW	110/113 (97%)	110 (100%)	0	0	100 100
43	DW	110/113 (97%)	110 (100%)	0	0	100 100
44	BX	93/96 (97%)	91 (98%)	2 (2%)	0	100 100
44	DX	93/96 (97%)	91 (98%)	1 (1%)	1 (1%)	11 25
45	BY	105/110 (96%)	98 (93%)	7 (7%)	0	100 100
45	DY	105/110 (96%)	101 (96%)	4 (4%)	0	100 100
46	BZ	169/206 (82%)	153 (90%)	15 (9%)	1 (1%)	21 42
46	DZ	172/206 (84%)	159 (92%)	13 (8%)	0	100 100
47	B0	81/85 (95%)	81 (100%)	0	0	100 100
47	D0	81/85 (95%)	79 (98%)	1 (1%)	1 (1%)	10 23
48	B1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11 25
48	D1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11 25
49	B2	68/72 (94%)	68 (100%)	0	0	100 100
49	D2	68/72 (94%)	68 (100%)	0	0	100 100
50	B3	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
50	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
51	B4	67/71 (94%)	54 (81%)	9 (13%)	4 (6%)	1 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
51	D4	67/71 (94%)	53 (79%)	11 (16%)	3 (4%)	2 2
52	B5	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
52	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
53	B6	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
53	D6	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
54	B7	46/49 (94%)	45 (98%)	1 (2%)	0	100 100
54	D7	46/49 (94%)	45 (98%)	0	1 (2%)	5 10
55	B8	62/65 (95%)	62 (100%)	0	0	100 100
55	D8	62/65 (95%)	62 (100%)	0	0	100 100
56	B9	35/37 (95%)	35 (100%)	0	0	100 100
56	D9	35/37 (95%)	35 (100%)	0	0	100 100
All	All	11410/12128 (94%)	10945 (96%)	381 (3%)	84 (1%)	18 38

All (84) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	17	PHE
2	AB	19	HIS
2	AB	231	GLU
9	AI	54	ASP
10	AJ	56	HIS
28	BD	275	LYS
30	BF	130	ALA
33	BI	106	GLY
33	BI	107	VAL
48	B1	3	LYS
51	B4	53	GLU
51	B4	62	ARG
2	CB	8	LYS
2	CB	16	HIS
2	CB	17	PHE
2	CB	123	ALA
2	CB	126	GLU
2	CB	231	GLU
9	CI	54	ASP
10	CJ	56	HIS
10	CJ	75	ILE
13	CM	67	GLU

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Mol	Chain	Res	Type
13	CM	85	GLY
31	DG	14	GLU
51	D4	39	CYS
51	D4	45	GLY
51	D4	62	ARG
54	D7	46	VAL
2	AB	10	LEU
2	AB	16	HIS
3	AC	66	VAL
7	AG	55	GLY
10	AJ	31	GLY
19	AS	84	GLY
20	AT	10	LEU
20	AT	47	GLY
20	AT	96	GLY
20	AT	100	ILE
33	BI	105	HIS
42	BV	79	VAL
51	B4	47	GLN
2	CB	20	GLU
4	CD	46	LYS
5	CE	37	ARG
7	CG	55	GLY
10	CJ	78	ASN
20	CT	47	GLY
31	DG	81	LYS
42	DV	79	VAL
48	D1	3	LYS
13	AM	67	GLU
29	BE	52	LEU
33	BI	10	GLU
10	CJ	55	LYS
20	CT	102	GLY
28	DD	239	ARG
31	DG	47	LYS
33	DI	10	GLU
39	DS	84	GLN
2	AB	125	PRO
11	AK	105	VAL
20	CT	10	LEU
28	DD	3	VAL
29	DE	52	LEU

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Mol	Chain	Res	Type
36	DP	45	LEU
47	D0	4	LYS
2	AB	11	LEU
31	BG	47	LYS
46	BZ	159	PRO
51	B4	59	PHE
11	CK	105	VAL
30	DF	130	ALA
44	DX	2	LYS
33	BI	73	GLU
36	BP	29	LYS
36	DP	29	LYS
37	DQ	27	VAL
20	AT	102	GLY
16	CP	53	VAL
20	CT	100	ILE
13	CM	4	ILE
12	CL	30	ALA
20	CT	96	GLY
2	AB	234	PRO

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	AB	192/220 (87%)	153 (80%)	39 (20%)	1 2
2	CB	187/220 (85%)	151 (81%)	36 (19%)	1 2
3	AC	143/188 (76%)	126 (88%)	17 (12%)	5 10
3	CC	141/188 (75%)	116 (82%)	25 (18%)	2 3
4	AD	170/181 (94%)	147 (86%)	23 (14%)	4 7
4	CD	174/181 (96%)	146 (84%)	28 (16%)	2 4
5	AE	113/123 (92%)	99 (88%)	14 (12%)	4 9
5	CE	114/123 (93%)	98 (86%)	16 (14%)	3 6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
6	AF	84/90 (93%)	74 (88%)	10 (12%)	5 10
6	CF	86/90 (96%)	71 (83%)	15 (17%)	2 3
7	AG	119/127 (94%)	97 (82%)	22 (18%)	1 3
7	CG	120/127 (94%)	103 (86%)	17 (14%)	3 6
8	AH	114/119 (96%)	100 (88%)	14 (12%)	4 9
8	CH	114/119 (96%)	92 (81%)	22 (19%)	1 2
9	AI	91/99 (92%)	69 (76%)	22 (24%)	1 1
9	CI	89/99 (90%)	69 (78%)	20 (22%)	1 1
10	AJ	66/92 (72%)	58 (88%)	8 (12%)	5 10
10	CJ	69/92 (75%)	59 (86%)	10 (14%)	3 6
11	AK	83/99 (84%)	74 (89%)	9 (11%)	6 13
11	CK	83/99 (84%)	71 (86%)	12 (14%)	3 6
12	AL	97/109 (89%)	88 (91%)	9 (9%)	8 18
12	CL	97/109 (89%)	84 (87%)	13 (13%)	4 7
13	AM	95/101 (94%)	78 (82%)	17 (18%)	2 3
13	CM	92/101 (91%)	75 (82%)	17 (18%)	1 3
14	AN	49/50 (98%)	40 (82%)	9 (18%)	1 3
14	CN	49/50 (98%)	37 (76%)	12 (24%)	1 1
15	AO	78/80 (98%)	69 (88%)	9 (12%)	5 11
15	CO	78/80 (98%)	67 (86%)	11 (14%)	3 6
16	AP	69/74 (93%)	54 (78%)	15 (22%)	1 2
16	CP	68/74 (92%)	60 (88%)	8 (12%)	5 10
17	AQ	94/97 (97%)	84 (89%)	10 (11%)	6 14
17	CQ	94/97 (97%)	83 (88%)	11 (12%)	5 11
18	AR	59/77 (77%)	49 (83%)	10 (17%)	2 4
18	CR	59/77 (77%)	45 (76%)	14 (24%)	1 1
19	AS	70/80 (88%)	58 (83%)	12 (17%)	2 3
19	CS	67/80 (84%)	53 (79%)	14 (21%)	1 2
20	AT	70/82 (85%)	57 (81%)	13 (19%)	1 3
20	CT	71/82 (87%)	58 (82%)	13 (18%)	2 3
21	AU	18/22 (82%)	13 (72%)	5 (28%)	0 1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
21	CU	18/22 (82%)	15 (83%)	3 (17%)	2 4
28	BD	215/218 (99%)	193 (90%)	22 (10%)	7 15
28	DD	216/218 (99%)	195 (90%)	21 (10%)	8 17
29	BE	164/166 (99%)	141 (86%)	23 (14%)	3 6
29	DE	164/166 (99%)	137 (84%)	27 (16%)	2 4
30	BF	160/166 (96%)	141 (88%)	19 (12%)	5 10
30	DF	159/166 (96%)	139 (87%)	20 (13%)	4 9
31	BG	143/156 (92%)	126 (88%)	17 (12%)	5 10
31	DG	142/156 (91%)	112 (79%)	30 (21%)	1 2
32	BH	144/148 (97%)	128 (89%)	16 (11%)	6 12
32	DH	144/148 (97%)	122 (85%)	22 (15%)	3 5
33	BI	110/124 (89%)	85 (77%)	25 (23%)	1 1
33	DI	107/124 (86%)	79 (74%)	28 (26%)	0 1
34	BN	118/119 (99%)	97 (82%)	21 (18%)	2 3
34	DN	118/119 (99%)	99 (84%)	19 (16%)	2 4
35	BO	100/100 (100%)	91 (91%)	9 (9%)	9 20
35	DO	100/100 (100%)	86 (86%)	14 (14%)	3 6
36	BP	116/116 (100%)	100 (86%)	16 (14%)	3 7
36	DP	115/116 (99%)	101 (88%)	14 (12%)	5 10
37	BQ	111/111 (100%)	95 (86%)	16 (14%)	3 6
37	DQ	111/111 (100%)	95 (86%)	16 (14%)	3 6
38	BR	101/101 (100%)	83 (82%)	18 (18%)	2 3
38	DR	101/101 (100%)	86 (85%)	15 (15%)	3 5
39	BS	87/88 (99%)	75 (86%)	12 (14%)	3 7
39	DS	85/88 (97%)	66 (78%)	19 (22%)	1 1
40	BT	115/127 (91%)	101 (88%)	14 (12%)	5 10
40	DT	113/127 (89%)	100 (88%)	13 (12%)	5 11
41	BU	93/94 (99%)	83 (89%)	10 (11%)	6 13
41	DU	93/94 (99%)	84 (90%)	9 (10%)	8 17
42	BV	80/82 (98%)	68 (85%)	12 (15%)	3 5
42	DV	80/82 (98%)	67 (84%)	13 (16%)	2 4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
43	BW	90/92 (98%)	80 (89%)	10 (11%)	6 12
43	DW	90/92 (98%)	82 (91%)	8 (9%)	9 20
44	BX	77/78 (99%)	70 (91%)	7 (9%)	9 19
44	DX	77/78 (99%)	70 (91%)	7 (9%)	9 19
45	BY	85/91 (93%)	75 (88%)	10 (12%)	5 10
45	DY	85/91 (93%)	80 (94%)	5 (6%)	18 38
46	BZ	145/179 (81%)	121 (83%)	24 (17%)	2 4
46	DZ	145/179 (81%)	123 (85%)	22 (15%)	3 5
47	B0	65/67 (97%)	61 (94%)	4 (6%)	16 36
47	D0	65/67 (97%)	61 (94%)	4 (6%)	16 36
48	B1	80/83 (96%)	75 (94%)	5 (6%)	16 36
48	D1	80/83 (96%)	71 (89%)	9 (11%)	5 12
49	B2	65/67 (97%)	59 (91%)	6 (9%)	8 19
49	D2	65/67 (97%)	60 (92%)	5 (8%)	12 27
50	B3	51/52 (98%)	46 (90%)	5 (10%)	7 17
50	D3	50/52 (96%)	44 (88%)	6 (12%)	5 10
51	B4	60/63 (95%)	50 (83%)	10 (17%)	2 4
51	D4	53/63 (84%)	38 (72%)	15 (28%)	0 1
52	B5	50/52 (96%)	47 (94%)	3 (6%)	17 37
52	D5	50/52 (96%)	48 (96%)	2 (4%)	28 55
53	B6	51/52 (98%)	44 (86%)	7 (14%)	3 7
53	D6	50/52 (96%)	46 (92%)	4 (8%)	11 25
54	B7	41/42 (98%)	37 (90%)	4 (10%)	7 17
54	D7	41/42 (98%)	37 (90%)	4 (10%)	7 17
55	B8	54/55 (98%)	51 (94%)	3 (6%)	19 40
55	D8	54/55 (98%)	50 (93%)	4 (7%)	13 29
56	B9	34/34 (100%)	32 (94%)	2 (6%)	18 38
56	D9	34/34 (100%)	31 (91%)	3 (9%)	9 21
All	All	9336/10066 (93%)	8004 (86%)	1332 (14%)	3 6

All (1332) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	7	VAL
2	AB	11	LEU
2	AB	15	VAL
2	AB	17	PHE
2	AB	19	HIS
2	AB	20	GLU
2	AB	21	ARG
2	AB	35	GLU
2	AB	42	ILE
2	AB	48	MET
2	AB	60	ASP
2	AB	64	ARG
2	AB	67	THR
2	AB	76	GLN
2	AB	83	MET
2	AB	84	GLU
2	AB	90	MET
2	AB	101	MET
2	AB	121	LEU
2	AB	126	GLU
2	AB	127	ILE
2	AB	137	ARG
2	AB	144	ARG
2	AB	145	LEU
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	160	ASP
2	AB	170	GLU
2	AB	185	ILE
2	AB	187	LEU
2	AB	196	LEU
2	AB	200	ILE
2	AB	208	ILE
2	AB	209	ARG
2	AB	217	ARG
2	AB	221	LEU
2	AB	223	ILE
2	AB	230	VAL
3	AC	3	ASN
3	AC	8	ILE
3	AC	15	THR
3	AC	27	LYS

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Mol	Chain	Res	Type
3	AC	45	LYS
3	AC	52	LEU
3	AC	64	VAL
3	AC	77	ILE
3	AC	101	LEU
3	AC	115	LEU
3	AC	118	GLN
3	AC	131	ARG
3	AC	136	GLN
3	AC	178	LEU
3	AC	179	ARG
3	AC	190	ARG
3	AC	195	VAL
4	AD	3	ARG
4	AD	5	ILE
4	AD	15	GLU
4	AD	19	LEU
4	AD	28	SER
4	AD	31	CYS
4	AD	49	ARG
4	AD	50	ARG
4	AD	58	LEU
4	AD	65	ARG
4	AD	86	LYS
4	AD	91	SER
4	AD	108	LEU
4	AD	112	VAL
4	AD	127	THR
4	AD	135	LEU
4	AD	144	ASP
4	AD	155	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	194	LEU
4	AD	196	LEU
4	AD	200	GLU
5	AE	6	PHE
5	AE	10	MET
5	AE	12	LEU
5	AE	31	LEU
5	AE	41	VAL
5	AE	47	LYS

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Mol	Chain	Res	Type
5	AE	51	VAL
5	AE	57	LYS
5	AE	67	VAL
5	AE	68	GLU
5	AE	91	LEU
5	AE	111	GLU
5	AE	131	ILE
5	AE	151	LEU
6	AF	10	LEU
6	AF	17	SER
6	AF	40	VAL
6	AF	45	LEU
6	AF	55	ASP
6	AF	61	LEU
6	AF	69	GLU
6	AF	70	ASP
6	AF	75	LEU
6	AF	82	ARG
7	AG	8	GLU
7	AG	12	LEU
7	AG	16	LEU
7	AG	24	THR
7	AG	31	MET
7	AG	38	LEU
7	AG	53	LYS
7	AG	56	GLN
7	AG	61	VAL
7	AG	72	ARG
7	AG	73	MET
7	AG	76	ARG
7	AG	78	ARG
7	AG	79	ARG
7	AG	91	VAL
7	AG	97	GLN
7	AG	104	LEU
7	AG	113	GLU
7	AG	120	ILE
7	AG	135	VAL
7	AG	138	LYS
7	AG	155	ARG
8	AH	10	LEU
8	AH	21	LYS

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Mol	Chain	Res	Type
8	AH	33	GLU
8	AH	37	ARG
8	AH	39	LEU
8	AH	51	VAL
8	AH	52	ASP
8	AH	63	LEU
8	AH	78	GLN
8	AH	84	ARG
8	AH	91	ARG
8	AH	107	LEU
8	AH	122	ARG
8	AH	137	VAL
9	AI	9	ARG
9	AI	11	LYS
9	AI	23	ASN
9	AI	27	THR
9	AI	42	ARG
9	AI	53	VAL
9	AI	56	LEU
9	AI	64	THR
9	AI	65	VAL
9	AI	71	SER
9	AI	75	ASP
9	AI	78	LYS
9	AI	81	ILE
9	AI	89	ASN
9	AI	93	ARG
9	AI	97	LYS
9	AI	102	LEU
9	AI	103	THR
9	AI	108	VAL
9	AI	121	ARG
9	AI	127	LYS
9	AI	128	ARG
10	AJ	5	ARG
10	AJ	7	LYS
10	AJ	9	ARG
10	AJ	16	LEU
10	AJ	38	ILE
10	AJ	43	ARG
10	AJ	84	GLN
10	AJ	92	THR

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Mol	Chain	Res	Type
11	AK	31	THR
11	AK	48	ILE
11	AK	51	LYS
11	AK	81	ASP
11	AK	87	THR
11	AK	91	ARG
11	AK	96	ARG
11	AK	106	LYS
11	AK	114	VAL
12	AL	16	GLU
12	AL	23	LYS
12	AL	33	ARG
12	AL	47	LYS
12	AL	52	LEU
12	AL	60	LEU
12	AL	67	THR
12	AL	83	VAL
12	AL	89	ARG
13	AM	3	ARG
13	AM	4	ILE
13	AM	13	LYS
13	AM	15	VAL
13	AM	17	VAL
13	AM	19	LEU
13	AM	43	THR
13	AM	46	LYS
13	AM	56	LEU
13	AM	70	LEU
13	AM	73	GLU
13	AM	94	ARG
13	AM	98	VAL
13	AM	110	ARG
13	AM	115	LYS
13	AM	121	LYS
13	AM	122	LYS
14	AN	3	ARG
14	AN	6	LEU
14	AN	7	ILE
14	AN	9	LYS
14	AN	12	ARG
14	AN	13	THR
14	AN	18	VAL

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Mol	Chain	Res	Type
14	AN	32	SER
14	AN	50	LYS
15	AO	7	GLU
15	AO	22	THR
15	AO	26	GLU
15	AO	38	ARG
15	AO	39	LEU
15	AO	72	ARG
15	AO	76	GLU
15	AO	83	GLU
15	AO	87	ILE
16	AP	1	MET
16	AP	2	VAL
16	AP	5	ARG
16	AP	8	ARG
16	AP	19	ILE
16	AP	20	VAL
16	AP	27	LYS
16	AP	50	LYS
16	AP	53	VAL
16	AP	54	GLU
16	AP	60	LEU
16	AP	62	VAL
16	AP	67	THR
16	AP	69	THR
16	AP	71	ARG
17	AQ	9	VAL
17	AQ	53	LEU
17	AQ	60	ILE
17	AQ	63	ARG
17	AQ	72	ARG
17	AQ	74	LEU
17	AQ	76	LEU
17	AQ	91	ARG
17	AQ	92	ARG
17	AQ	97	SER
18	AR	31	LEU
18	AR	35	ARG
18	AR	37	VAL
18	AR	38	GLU
18	AR	46	GLU
18	AR	55	ARG

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Mol	Chain	Res	Type
18	AR	58	LEU
18	AR	68	LYS
18	AR	76	LEU
18	AR	85	LEU
19	AS	5	LEU
19	AS	12	ASP
19	AS	17	GLU
19	AS	36	ARG
19	AS	37	ARG
19	AS	62	ILE
19	AS	63	THR
19	AS	65	ASN
19	AS	70	LYS
19	AS	78	ARG
19	AS	83	HIS
19	AS	85	LYS
20	AT	10	LEU
20	AT	13	LEU
20	AT	19	SER
20	AT	24	LEU
20	AT	31	SER
20	AT	41	ILE
20	AT	45	GLN
20	AT	58	LYS
20	AT	60	GLU
20	AT	62	LEU
20	AT	71	THR
20	AT	72	LEU
20	AT	84	LEU
21	AU	9	ARG
21	AU	10	ARG
21	AU	12	LYS
21	AU	20	LYS
21	AU	24	ARG
28	BD	3	VAL
28	BD	22	SER
28	BD	38	LYS
28	BD	61	LEU
28	BD	68	LYS
28	BD	71	ASP
28	BD	94	LEU
28	BD	99	ASP

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Mol	Chain	Res	Type
28	BD	106	ILE
28	BD	113	VAL
28	BD	116	GLN
28	BD	126	GLN
28	BD	142	VAL
28	BD	173	VAL
28	BD	193	VAL
28	BD	211	ARG
28	BD	217	ARG
28	BD	221	VAL
28	BD	229	VAL
28	BD	257	LEU
28	BD	259	THR
28	BD	260	ARG
29	BE	8	LYS
29	BE	9	VAL
29	BE	12	THR
29	BE	21	VAL
29	BE	33	VAL
29	BE	34	VAL
29	BE	47	VAL
29	BE	75	VAL
29	BE	77	ILE
29	BE	78	LEU
29	BE	82	ARG
29	BE	97	LYS
29	BE	116	VAL
29	BE	119	ARG
29	BE	127	ASP
29	BE	144	ARG
29	BE	154	LYS
29	BE	163	GLU
29	BE	170	LEU
29	BE	175	VAL
29	BE	181	LEU
29	BE	184	VAL
29	BE	202	LYS
30	BF	12	LEU
30	BF	19	GLU
30	BF	33	LEU
30	BF	35	GLU
30	BF	53	THR

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Mol	Chain	Res	Type
30	BF	57	VAL
30	BF	74	ARG
30	BF	88	VAL
30	BF	106	ARG
30	BF	110	LEU
30	BF	125	LEU
30	BF	132	VAL
30	BF	140	LEU
30	BF	162	LEU
30	BF	183	VAL
30	BF	192	LEU
30	BF	197	ASP
30	BF	200	GLU
30	BF	201	VAL
31	BG	3	LEU
31	BG	5	VAL
31	BG	7	LEU
31	BG	22	ARG
31	BG	43	LEU
31	BG	45	GLU
31	BG	49	ASP
31	BG	70	VAL
31	BG	81	LYS
31	BG	82	LEU
31	BG	86	MET
31	BG	139	LEU
31	BG	140	ILE
31	BG	143	GLU
31	BG	159	VAL
31	BG	175	LEU
31	BG	181	ARG
32	BH	2	SER
32	BH	6	ARG
32	BH	13	LYS
32	BH	15	VAL
32	BH	44	VAL
32	BH	45	VAL
32	BH	51	ARG
32	BH	69	ARG
32	BH	71	LEU
32	BH	76	VAL
32	BH	92	ILE

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Mol	Chain	Res	Type
32	BH	98	LEU
32	BH	105	LEU
32	BH	119	GLU
32	BH	122	THR
32	BH	124	GLU
33	BI	5	LEU
33	BI	9	LEU
33	BI	15	VAL
33	BI	20	ASP
33	BI	38	LEU
33	BI	41	GLU
33	BI	43	ASN
33	BI	44	LEU
33	BI	47	LEU
33	BI	52	ARG
33	BI	58	LEU
33	BI	61	ARG
33	BI	62	LYS
33	BI	64	GLU
33	BI	66	GLU
33	BI	77	LEU
33	BI	78	THR
33	BI	86	THR
33	BI	87	LYS
33	BI	92	VAL
33	BI	96	ASP
33	BI	101	LEU
33	BI	107	VAL
33	BI	117	GLU
33	BI	122	GLU
34	BN	1	MET
34	BN	5	VAL
34	BN	8	GLN
34	BN	9	VAL
34	BN	12	ARG
34	BN	14	VAL
34	BN	15	LEU
34	BN	28	THR
34	BN	33	LEU
34	BN	34	LEU
34	BN	48	MET
34	BN	61	ARG

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Mol	Chain	Res	Type
34	BN	65	LYS
34	BN	67	LEU
34	BN	68	GLU
34	BN	87	LEU
34	BN	97	ARG
34	BN	99	LEU
34	BN	120	LEU
34	BN	138	LEU
34	BN	140	VAL
35	BO	8	LEU
35	BO	10	VAL
35	BO	18	LYS
35	BO	24	VAL
35	BO	66	LYS
35	BO	92	GLU
35	BO	98	VAL
35	BO	105	GLU
35	BO	108	GLU
36	BP	1	MET
36	BP	21	ARG
36	BP	55	ARG
36	BP	59	LEU
36	BP	65	ARG
36	BP	68	GLN
36	BP	83	VAL
36	BP	95	VAL
36	BP	98	GLU
36	BP	101	VAL
36	BP	106	LEU
36	BP	112	LEU
36	BP	121	LYS
36	BP	144	GLU
36	BP	147	LEU
36	BP	149	GLU
37	BQ	1	MET
37	BQ	8	LYS
37	BQ	21	THR
37	BQ	22	LYS
37	BQ	35	VAL
37	BQ	42	ILE
37	BQ	45	GLN
37	BQ	54	MET

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Mol	Chain	Res	Type
37	BQ	55	VAL
37	BQ	60	ARG
37	BQ	63	LYS
37	BQ	75	THR
37	BQ	80	GLU
37	BQ	109	VAL
37	BQ	110	THR
37	BQ	113	GLN
38	BR	1	MET
38	BR	18	LEU
38	BR	28	LEU
38	BR	29	LEU
38	BR	33	ARG
38	BR	36	THR
38	BR	44	LEU
38	BR	54	LEU
38	BR	60	LEU
38	BR	65	LEU
38	BR	67	LEU
38	BR	75	LEU
38	BR	79	LEU
38	BR	86	ARG
38	BR	100	LEU
38	BR	102	GLU
38	BR	111	LEU
38	BR	114	VAL
39	BS	3	ARG
39	BS	4	LEU
39	BS	10	ARG
39	BS	14	VAL
39	BS	20	ARG
39	BS	49	VAL
39	BS	52	SER
39	BS	59	LYS
39	BS	69	VAL
39	BS	73	LEU
39	BS	83	LYS
39	BS	103	GLU
40	BT	16	ARG
40	BT	28	VAL
40	BT	36	GLU
40	BT	49	VAL

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Mol	Chain	Res	Type
40	BT	53	ARG
40	BT	65	LYS
40	BT	74	ARG
40	BT	78	LEU
40	BT	89	VAL
40	BT	96	ARG
40	BT	113	LYS
40	BT	118	ARG
40	BT	119	LYS
40	BT	128	GLU
41	BU	8	VAL
41	BU	17	ILE
41	BU	27	LEU
41	BU	31	SER
41	BU	36	ARG
41	BU	60	LEU
41	BU	74	LEU
41	BU	92	ARG
41	BU	95	LEU
41	BU	104	GLN
42	BV	6	LYS
42	BV	21	ARG
42	BV	43	GLU
42	BV	46	VAL
42	BV	51	VAL
42	BV	52	VAL
42	BV	61	VAL
42	BV	62	LEU
42	BV	72	VAL
42	BV	79	VAL
42	BV	95	LEU
42	BV	100	ARG
43	BW	4	LYS
43	BW	11	ARG
43	BW	15	ARG
43	BW	17	VAL
43	BW	19	LEU
43	BW	23	LEU
43	BW	51	LEU
43	BW	67	ASP
43	BW	96	ILE
43	BW	107	LEU

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Mol	Chain	Res	Type
44	BX	2	LYS
44	BX	35	THR
44	BX	52	VAL
44	BX	57	LEU
44	BX	65	ARG
44	BX	76	ARG
44	BX	88	LYS
45	BY	1	MET
45	BY	7	VAL
45	BY	11	ASP
45	BY	23	ARG
45	BY	43	ASN
45	BY	72	VAL
45	BY	73	ARG
45	BY	85	VAL
45	BY	90	LEU
45	BY	99	CYS
46	BZ	5	LEU
46	BZ	14	LYS
46	BZ	18	LEU
46	BZ	19	ARG
46	BZ	33	LEU
46	BZ	46	LYS
46	BZ	50	GLN
46	BZ	58	VAL
46	BZ	61	LEU
46	BZ	72	ARG
46	BZ	76	LEU
46	BZ	91	LEU
46	BZ	102	LEU
46	BZ	107	THR
46	BZ	117	LEU
46	BZ	120	ILE
46	BZ	129	SER
46	BZ	136	PHE
46	BZ	138	GLU
46	BZ	146	ILE
46	BZ	153	SER
46	BZ	154	ASP
46	BZ	155	LEU
46	BZ	169	GLU
47	B0	10	THR

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Mol	Chain	Res	Type
47	B0	20	ARG
47	B0	55	ARG
47	B0	74	ARG
48	B1	3	LYS
48	B1	21	ARG
48	B1	35	THR
48	B1	59	THR
48	B1	95	LEU
49	B2	19	VAL
49	B2	30	ARG
49	B2	32	LEU
49	B2	40	SER
49	B2	55	ARG
49	B2	70	GLN
50	B3	3	ARG
50	B3	8	LEU
50	B3	23	LEU
50	B3	54	VAL
50	B3	60	GLU
51	B4	3	GLU
51	B4	34	GLU
51	B4	46	GLN
51	B4	49	PHE
51	B4	50	VAL
51	B4	56	VAL
51	B4	58	ARG
51	B4	63	TYR
51	B4	66	SER
51	B4	68	ARG
52	B5	6	VAL
52	B5	29	THR
52	B5	40	LYS
53	B6	4	GLU
53	B6	6	ARG
53	B6	9	LEU
53	B6	14	THR
53	B6	28	ARG
53	B6	38	LYS
53	B6	48	VAL
54	B7	9	ARG
54	B7	23	ARG
54	B7	24	THR

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Mol	Chain	Res	Type
54	B7	43	THR
55	B8	6	THR
55	B8	14	VAL
55	B8	59	LYS
56	B9	4	ARG
56	B9	17	ILE
2	CB	8	LYS
2	CB	15	VAL
2	CB	19	HIS
2	CB	23	ARG
2	CB	35	GLU
2	CB	42	ILE
2	CB	50	GLU
2	CB	51	LEU
2	CB	67	THR
2	CB	73	THR
2	CB	74	LYS
2	CB	76	GLN
2	CB	83	MET
2	CB	87	ARG
2	CB	94	ASN
2	CB	95	GLN
2	CB	101	MET
2	CB	108	ILE
2	CB	115	LEU
2	CB	117	GLU
2	CB	119	GLU
2	CB	124	SER
2	CB	126	GLU
2	CB	127	ILE
2	CB	128	GLU
2	CB	139	LYS
2	CB	154	LEU
2	CB	155	LEU
2	CB	157	ARG
2	CB	158	LEU
2	CB	185	ILE
2	CB	187	LEU
2	CB	200	ILE
2	CB	208	ILE
2	CB	224	GLN
2	CB	235	SER

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Mol	Chain	Res	Type
3	CC	3	ASN
3	CC	15	THR
3	CC	17	ASP
3	CC	21	ARG
3	CC	32	LEU
3	CC	33	LEU
3	CC	45	LYS
3	CC	47	LEU
3	CC	52	LEU
3	CC	54	ARG
3	CC	85	ARG
3	CC	91	LEU
3	CC	98	ASN
3	CC	101	LEU
3	CC	104	GLN
3	CC	105	GLU
3	CC	115	LEU
3	CC	128	PHE
3	CC	131	ARG
3	CC	140	ARG
3	CC	151	VAL
3	CC	152	ILE
3	CC	164	ARG
3	CC	190	ARG
3	CC	195	VAL
4	CD	10	ARG
4	CD	15	GLU
4	CD	30	LYS
4	CD	31	CYS
4	CD	34	GLU
4	CD	50	ARG
4	CD	58	LEU
4	CD	61	LYS
4	CD	65	ARG
4	CD	85	LYS
4	CD	86	LYS
4	CD	96	LEU
4	CD	108	LEU
4	CD	122	ARG
4	CD	127	THR
4	CD	135	LEU
4	CD	145	GLU

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Mol	Chain	Res	Type
4	CD	150	GLU
4	CD	155	LEU
4	CD	156	GLU
4	CD	157	LEU
4	CD	169	LYS
4	CD	170	VAL
4	CD	181	MET
4	CD	184	LYS
4	CD	187	ARG
4	CD	194	LEU
4	CD	208	SER
5	CE	10	MET
5	CE	12	LEU
5	CE	18	ARG
5	CE	31	LEU
5	CE	41	VAL
5	CE	51	VAL
5	CE	57	LYS
5	CE	64	ARG
5	CE	67	VAL
5	CE	68	GLU
5	CE	75	THR
5	CE	79	GLU
5	CE	91	LEU
5	CE	117	ASP
5	CE	147	ASP
5	CE	150	ARG
6	CF	17	SER
6	CF	21	LEU
6	CF	27	GLN
6	CF	28	ARG
6	CF	40	VAL
6	CF	41	GLU
6	CF	45	LEU
6	CF	61	LEU
6	CF	69	GLU
6	CF	72	VAL
6	CF	75	LEU
6	CF	82	ARG
6	CF	87	ARG
6	CF	92	LYS
6	CF	94	GLN

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Mol	Chain	Res	Type
7	CG	6	ARG
7	CG	12	LEU
7	CG	16	LEU
7	CG	24	THR
7	CG	32	ARG
7	CG	41	ARG
7	CG	49	ILE
7	CG	51	GLN
7	CG	56	GLN
7	CG	72	ARG
7	CG	73	MET
7	CG	97	GLN
7	CG	104	LEU
7	CG	120	ILE
7	CG	135	VAL
7	CG	138	LYS
7	CG	155	ARG
8	CH	3	THR
8	CH	10	LEU
8	CH	13	ILE
8	CH	29	SER
8	CH	33	GLU
8	CH	34	GLU
8	CH	45	ILE
8	CH	51	VAL
8	CH	52	ASP
8	CH	63	LEU
8	CH	78	GLN
8	CH	85	ARG
8	CH	91	ARG
8	CH	98	LYS
8	CH	103	VAL
8	CH	107	LEU
8	CH	111	ILE
8	CH	112	LEU
8	CH	125	ARG
8	CH	127	LEU
8	CH	135	CYS
8	CH	137	VAL
9	CI	7	THR
9	CI	14	VAL
9	CI	23	ASN

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Mol	Chain	Res	Type
9	CI	27	THR
9	CI	40	LEU
9	CI	50	LEU
9	CI	51	ARG
9	CI	56	LEU
9	CI	64	THR
9	CI	65	VAL
9	CI	75	ASP
9	CI	81	ILE
9	CI	83	ARG
9	CI	102	LEU
9	CI	103	THR
9	CI	104	ARG
9	CI	108	VAL
9	CI	121	ARG
9	CI	124	GLN
9	CI	128	ARG
10	CJ	6	ILE
10	CJ	9	ARG
10	CJ	21	GLN
10	CJ	34	VAL
10	CJ	59	SER
10	CJ	67	THR
10	CJ	74	ILE
10	CJ	81	THR
10	CJ	97	GLU
10	CJ	98	ILE
11	CK	31	THR
11	CK	32	ILE
11	CK	41	THR
11	CK	48	ILE
11	CK	73	MET
11	CK	92	GLU
11	CK	93	GLN
11	CK	96	ARG
11	CK	104	GLN
11	CK	114	VAL
11	CK	123	LYS
11	CK	126	ARG
12	CL	23	LYS
12	CL	33	ARG
12	CL	34	ARG

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Mol	Chain	Res	Type
12	CL	36	VAL
12	CL	39	VAL
12	CL	47	LYS
12	CL	60	LEU
12	CL	62	SER
12	CL	75	HIS
12	CL	83	VAL
12	CL	104	VAL
12	CL	117	ARG
12	CL	124	LYS
13	CM	15	VAL
13	CM	19	LEU
13	CM	27	LYS
13	CM	29	ARG
13	CM	32	GLU
13	CM	52	GLU
13	CM	56	LEU
13	CM	63	THR
13	CM	66	LEU
13	CM	70	LEU
13	CM	71	ARG
13	CM	73	GLU
13	CM	84	ILE
13	CM	98	VAL
13	CM	99	ARG
13	CM	105	THR
13	CM	121	LYS
14	CN	3	ARG
14	CN	6	LEU
14	CN	7	ILE
14	CN	11	LYS
14	CN	13	THR
14	CN	17	LYS
14	CN	18	VAL
14	CN	22	THR
14	CN	23	ARG
14	CN	32	SER
14	CN	44	LEU
14	CN	46	GLU
15	CO	3	ILE
15	CO	4	THR
15	CO	5	LYS

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Mol	Chain	Res	Type
15	CO	22	THR
15	CO	26	GLU
15	CO	38	ARG
15	CO	39	LEU
15	CO	48	LYS
15	CO	68	ARG
15	CO	83	GLU
15	CO	87	ILE
16	CP	2	VAL
16	CP	5	ARG
16	CP	20	VAL
16	CP	21	VAL
16	CP	60	LEU
16	CP	67	THR
16	CP	69	THR
16	CP	71	ARG
17	CQ	36	ILE
17	CQ	37	LYS
17	CQ	53	LEU
17	CQ	60	ILE
17	CQ	63	ARG
17	CQ	69	LYS
17	CQ	74	LEU
17	CQ	75	ARG
17	CQ	76	LEU
17	CQ	83	ASP
17	CQ	91	ARG
18	CR	25	THR
18	CR	26	LEU
18	CR	28	GLU
18	CR	31	LEU
18	CR	32	ARG
18	CR	37	VAL
18	CR	41	LYS
18	CR	42	ARG
18	CR	56	THR
18	CR	58	LEU
18	CR	76	LEU
18	CR	84	LYS
18	CR	85	LEU
18	CR	87	ARG
19	CS	5	LEU

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Mol	Chain	Res	Type
19	CS	7	LYS
19	CS	15	LEU
19	CS	22	LEU
19	CS	30	LEU
19	CS	56	GLN
19	CS	63	THR
19	CS	64	GLU
19	CS	65	ASN
19	CS	66	MET
19	CS	77	THR
19	CS	78	ARG
19	CS	81	ARG
19	CS	83	HIS
20	CT	8	ARG
20	CT	10	LEU
20	CT	24	LEU
20	CT	36	LEU
20	CT	41	ILE
20	CT	45	GLN
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	72	LEU
20	CT	80	ARG
20	CT	84	LEU
20	CT	93	GLU
21	CU	9	ARG
21	CU	10	ARG
21	CU	12	LYS
28	DD	3	VAL
28	DD	61	LEU
28	DD	68	LYS
28	DD	94	LEU
28	DD	99	ASP
28	DD	106	ILE
28	DD	113	VAL
28	DD	126	GLN
28	DD	134	ARG
28	DD	142	VAL
28	DD	173	VAL
28	DD	193	VAL
28	DD	211	ARG

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Mol	Chain	Res	Type
28	DD	217	ARG
28	DD	221	VAL
28	DD	229	VAL
28	DD	253	GLN
28	DD	257	LEU
28	DD	259	THR
28	DD	260	ARG
28	DD	276	LYS
29	DE	7	VAL
29	DE	9	VAL
29	DE	12	THR
29	DE	14	ILE
29	DE	21	VAL
29	DE	33	VAL
29	DE	34	VAL
29	DE	38	THR
29	DE	40	GLU
29	DE	47	VAL
29	DE	52	LEU
29	DE	61	ARG
29	DE	73	GLU
29	DE	75	VAL
29	DE	78	LEU
29	DE	82	ARG
29	DE	89	ASP
29	DE	116	VAL
29	DE	119	ARG
29	DE	134	ILE
29	DE	144	ARG
29	DE	154	LYS
29	DE	163	GLU
29	DE	170	LEU
29	DE	175	VAL
29	DE	181	LEU
29	DE	184	VAL
30	DF	12	LEU
30	DF	17	ARG
30	DF	19	GLU
30	DF	33	LEU
30	DF	38	ARG
30	DF	53	THR
30	DF	57	VAL

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Mol	Chain	Res	Type
30	DF	70	THR
30	DF	88	VAL
30	DF	106	ARG
30	DF	110	LEU
30	DF	132	VAL
30	DF	135	LYS
30	DF	140	LEU
30	DF	152	GLU
30	DF	157	VAL
30	DF	183	VAL
30	DF	192	LEU
30	DF	200	GLU
30	DF	201	VAL
31	DG	5	VAL
31	DG	7	LEU
31	DG	9	ARG
31	DG	16	ARG
31	DG	19	LEU
31	DG	22	ARG
31	DG	31	VAL
31	DG	35	GLU
31	DG	43	LEU
31	DG	45	GLU
31	DG	47	LYS
31	DG	49	ASP
31	DG	58	GLN
31	DG	70	VAL
31	DG	84	LYS
31	DG	92	VAL
31	DG	97	ASP
31	DG	98	ARG
31	DG	111	LEU
31	DG	113	ARG
31	DG	114	ILE
31	DG	115	ARG
31	DG	135	LEU
31	DG	136	ARG
31	DG	140	ILE
31	DG	143	GLU
31	DG	148	MET
31	DG	152	LEU
31	DG	159	VAL

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Mol	Chain	Res	Type
31	DG	164	GLU
32	DH	3	ARG
32	DH	6	ARG
32	DH	33	LEU
32	DH	34	GLU
32	DH	40	GLU
32	DH	41	MET
32	DH	42	ARG
32	DH	44	VAL
32	DH	45	VAL
32	DH	47	GLU
32	DH	49	VAL
32	DH	65	HIS
32	DH	69	ARG
32	DH	72	ILE
32	DH	95	ARG
32	DH	98	LEU
32	DH	124	GLU
32	DH	136	ILE
32	DH	139	GLN
32	DH	148	ILE
32	DH	171	LEU
32	DH	172	LYS
33	DI	5	LEU
33	DI	9	LEU
33	DI	14	ASP
33	DI	15	VAL
33	DI	20	ASP
33	DI	38	LEU
33	DI	40	THR
33	DI	41	GLU
33	DI	43	ASN
33	DI	44	LEU
33	DI	47	LEU
33	DI	57	ARG
33	DI	58	LEU
33	DI	68	LEU
33	DI	75	LEU
33	DI	77	LEU
33	DI	78	THR
33	DI	85	GLU
33	DI	86	THR

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Mol	Chain	Res	Type
33	DI	101	LEU
33	DI	102	SER
33	DI	114	LEU
33	DI	116	LEU
33	DI	121	LYS
33	DI	127	VAL
33	DI	135	GLU
33	DI	140	LEU
33	DI	141	LYS
34	DN	5	VAL
34	DN	12	ARG
34	DN	14	VAL
34	DN	15	LEU
34	DN	28	THR
34	DN	33	LEU
34	DN	34	LEU
34	DN	38	HIS
34	DN	46	VAL
34	DN	48	MET
34	DN	62	VAL
34	DN	85	ILE
34	DN	87	LEU
34	DN	88	GLU
34	DN	97	ARG
34	DN	120	LEU
34	DN	137	LYS
34	DN	138	LEU
34	DN	140	VAL
35	DO	8	LEU
35	DO	9	GLU
35	DO	10	VAL
35	DO	23	ARG
35	DO	24	VAL
35	DO	47	ILE
35	DO	53	LYS
35	DO	66	LYS
35	DO	69	ILE
35	DO	70	LYS
35	DO	78	ARG
35	DO	92	GLU
35	DO	98	VAL
35	DO	108	GLU

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Mol	Chain	Res	Type
36	DP	15	ARG
36	DP	45	LEU
36	DP	55	ARG
36	DP	56	SER
36	DP	65	ARG
36	DP	83	VAL
36	DP	95	VAL
36	DP	98	GLU
36	DP	106	LEU
36	DP	112	LEU
36	DP	121	LYS
36	DP	136	GLU
36	DP	144	GLU
36	DP	147	LEU
37	DQ	1	MET
37	DQ	16	ARG
37	DQ	21	THR
37	DQ	22	LYS
37	DQ	35	VAL
37	DQ	42	ILE
37	DQ	45	GLN
37	DQ	48	GLU
37	DQ	55	VAL
37	DQ	56	ARG
37	DQ	60	ARG
37	DQ	75	THR
37	DQ	80	GLU
37	DQ	85	LYS
37	DQ	109	VAL
37	DQ	110	THR
38	DR	1	MET
38	DR	18	LEU
38	DR	28	LEU
38	DR	29	LEU
38	DR	33	ARG
38	DR	36	THR
38	DR	44	LEU
38	DR	54	LEU
38	DR	60	LEU
38	DR	65	LEU
38	DR	75	LEU
38	DR	79	LEU

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Mol	Chain	Res	Type
38	DR	86	ARG
38	DR	100	LEU
38	DR	111	LEU
39	DS	3	ARG
39	DS	4	LEU
39	DS	10	ARG
39	DS	14	VAL
39	DS	19	LYS
39	DS	20	ARG
39	DS	28	VAL
39	DS	35	ILE
39	DS	44	LYS
39	DS	49	VAL
39	DS	52	SER
39	DS	58	LEU
39	DS	67	ARG
39	DS	68	GLN
39	DS	73	LEU
39	DS	78	LEU
39	DS	82	ILE
39	DS	83	LYS
39	DS	103	GLU
40	DT	8	LYS
40	DT	13	ARG
40	DT	31	SER
40	DT	36	GLU
40	DT	49	VAL
40	DT	59	THR
40	DT	78	LEU
40	DT	85	LYS
40	DT	89	VAL
40	DT	96	ARG
40	DT	98	LYS
40	DT	113	LYS
40	DT	118	ARG
41	DU	31	SER
41	DU	36	ARG
41	DU	60	LEU
41	DU	74	LEU
41	DU	83	LEU
41	DU	89	GLU
41	DU	92	ARG

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Mol	Chain	Res	Type
41	DU	93	LYS
41	DU	104	GLN
42	DV	6	LYS
42	DV	15	GLU
42	DV	18	LEU
42	DV	21	ARG
42	DV	24	LYS
42	DV	38	LEU
42	DV	46	VAL
42	DV	52	VAL
42	DV	57	VAL
42	DV	62	LEU
42	DV	72	VAL
42	DV	79	VAL
42	DV	95	LEU
43	DW	4	LYS
43	DW	11	ARG
43	DW	17	VAL
43	DW	23	LEU
43	DW	51	LEU
43	DW	96	ILE
43	DW	100	THR
43	DW	107	LEU
44	DX	35	THR
44	DX	44	GLU
44	DX	52	VAL
44	DX	57	LEU
44	DX	66	LEU
44	DX	76	ARG
44	DX	92	LEU
45	DY	43	ASN
45	DY	49	VAL
45	DY	72	VAL
45	DY	91	GLU
45	DY	99	CYS
46	DZ	4	ARG
46	DZ	5	LEU
46	DZ	18	LEU
46	DZ	33	LEU
46	DZ	35	ARG
46	DZ	59	LEU
46	DZ	61	LEU

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Mol	Chain	Res	Type
46	DZ	71	VAL
46	DZ	92	SER
46	DZ	97	GLU
46	DZ	100	VAL
46	DZ	102	LEU
46	DZ	107	THR
46	DZ	120	ILE
46	DZ	131	ARG
46	DZ	136	PHE
46	DZ	138	GLU
46	DZ	144	LEU
46	DZ	146	ILE
46	DZ	153	SER
46	DZ	154	ASP
46	DZ	157	LEU
47	D0	20	ARG
47	D0	24	LYS
47	D0	68	GLU
47	D0	74	ARG
48	D1	3	LYS
48	D1	4	VAL
48	D1	21	ARG
48	D1	40	ARG
48	D1	59	THR
48	D1	85	LEU
48	D1	89	GLU
48	D1	95	LEU
48	D1	97	LEU
49	D2	21	LEU
49	D2	30	ARG
49	D2	32	LEU
49	D2	64	LEU
49	D2	70	GLN
50	D3	3	ARG
50	D3	8	LEU
50	D3	30	ARG
50	D3	31	LEU
50	D3	54	VAL
50	D3	55	ARG
51	D4	1	MET
51	D4	3	GLU
51	D4	5	ILE

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Mol	Chain	Res	Type
51	D4	8	LYS
51	D4	10	VAL
51	D4	13	ARG
51	D4	14	ILE
51	D4	23	GLU
51	D4	31	ILE
51	D4	50	VAL
51	D4	56	VAL
51	D4	61	ARG
51	D4	63	TYR
51	D4	68	ARG
51	D4	69	LYS
52	D5	6	VAL
52	D5	40	LYS
53	D6	9	LEU
53	D6	14	THR
53	D6	38	LYS
53	D6	48	VAL
54	D7	1	MET
54	D7	14	LYS
54	D7	43	THR
54	D7	48	LYS
55	D8	26	LYS
55	D8	32	LEU
55	D8	50	LEU
55	D8	59	LYS
56	D9	4	ARG
56	D9	17	ILE
56	D9	35	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (160) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	19	HIS
2	AB	76	GLN
2	AB	94	ASN
3	AC	6	HIS
3	AC	28	GLN
3	AC	37	GLN
3	AC	108	ASN
3	AC	118	GLN
3	AC	162	GLN

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Mol	Chain	Res	Type
3	AC	170	GLN
3	AC	181	ASN
4	AD	42	GLN
4	AD	45	GLN
4	AD	77	ASN
4	AD	123	HIS
5	AE	20	GLN
5	AE	38	GLN
5	AE	73	ASN
6	AF	73	ASN
6	AF	94	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	51	GLN
7	AG	64	GLN
7	AG	86	GLN
7	AG	97	GLN
7	AG	106	GLN
9	AI	23	ASN
9	AI	31	GLN
9	AI	58	HIS
9	AI	73	GLN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	93	GLN
11	AK	104	GLN
11	AK	116	HIS
12	AL	78	GLN
13	AM	92	HIS
15	AO	13	GLN
15	AO	28	GLN
16	AP	13	HIS
17	AQ	16	GLN
19	AS	23	ASN
19	AS	65	ASN
19	AS	69	HIS
20	AT	9	ASN
20	AT	26	ASN
20	AT	45	GLN
20	AT	73	HIS
28	BD	164	GLN
28	BD	201	HIS

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Mol	Chain	Res	Type
28	BD	253	GLN
29	BE	143	ASN
30	BF	8	GLN
30	BF	69	HIS
30	BF	133	ASN
30	BF	169	ASN
30	BF	203	GLN
31	BG	41	GLN
31	BG	132	ASN
33	BI	43	ASN
33	BI	105	HIS
34	BN	8	GLN
34	BN	133	GLN
36	BP	38	GLN
38	BR	71	GLN
40	BT	58	ASN
40	BT	123	GLN
41	BU	72	HIS
41	BU	81	HIS
41	BU	117	GLN
44	BX	31	HIS
44	BX	82	GLN
45	BY	6	HIS
45	BY	43	ASN
45	BY	92	ASN
46	BZ	34	ASN
46	BZ	118	GLN
46	BZ	151	HIS
51	B4	46	GLN
53	B6	20	ASN
56	B9	36	GLN
2	CB	16	HIS
2	CB	40	HIS
2	CB	76	GLN
2	CB	94	ASN
2	CB	140	HIS
3	CC	3	ASN
3	CC	6	HIS
3	CC	28	GLN
3	CC	104	GLN
3	CC	118	GLN
3	CC	123	GLN

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Mol	Chain	Res	Type
4	CD	74	GLN
4	CD	77	ASN
4	CD	119	GLN
4	CD	123	HIS
4	CD	125	HIS
4	CD	160	GLN
4	CD	161	ASN
5	CE	127	ASN
5	CE	130	ASN
6	CF	27	GLN
6	CF	73	ASN
6	CF	100	ASN
7	CG	28	ASN
7	CG	51	GLN
8	CH	78	GLN
9	CI	23	ASN
9	CI	58	HIS
9	CI	73	GLN
9	CI	89	ASN
9	CI	124	GLN
10	CJ	21	GLN
10	CJ	62	HIS
10	CJ	68	HIS
11	CK	22	HIS
11	CK	93	GLN
12	CL	99	HIS
13	CM	62	ASN
13	CM	92	HIS
14	CN	49	HIS
15	CO	28	GLN
16	CP	16	HIS
17	CQ	16	GLN
17	CQ	45	HIS
19	CS	69	HIS
20	CT	73	HIS
20	CT	90	GLN
28	DD	164	GLN
28	DD	253	GLN
30	DF	69	HIS
30	DF	75	HIS
30	DF	169	ASN
30	DF	203	GLN

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Mol	Chain	Res	Type
31	DG	40	ASN
31	DG	41	GLN
33	DI	43	ASN
34	DN	8	GLN
36	DP	38	GLN
37	DQ	45	GLN
38	DR	31	HIS
38	DR	50	HIS
39	DS	68	GLN
40	DT	123	GLN
41	DU	72	HIS
41	DU	94	ASN
44	DX	31	HIS
45	DY	43	ASN
46	DZ	55	HIS
46	DZ	75	ASN
46	DZ	118	GLN
46	DZ	121	HIS
46	DZ	151	HIS
47	D0	35	ASN
48	D1	56	GLN
49	D2	38	GLN
50	D3	32	GLN
53	D6	20	ASN
56	D9	36	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1494/1521 (98%)	361 (24%)	19 (1%)
1	CA	1501/1521 (98%)	371 (24%)	25 (1%)
22	AV	12/24 (50%)	3 (25%)	0
22	CV	11/24 (45%)	3 (27%)	0
23	AW	71/76 (93%)	27 (38%)	2 (2%)
23	CW	68/76 (89%)	26 (38%)	3 (4%)
24	AX	74/77 (96%)	16 (21%)	0
24	CX	74/77 (96%)	23 (31%)	0
25	AY	72/76 (94%)	38 (52%)	3 (4%)
25	CY	70/76 (92%)	37 (52%)	1 (1%)
26	BA	2812/2915 (96%)	449 (15%)	36 (1%)
26	DA	2791/2915 (95%)	564 (20%)	24 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	BB	119/121 (98%)	13 (10%)	0
27	DB	119/121 (98%)	38 (31%)	0
All	All	9288/9620 (96%)	1969 (21%)	113 (1%)

All (1969) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	7	G
1	AA	9	G
1	AA	22	G
1	AA	29	G
1	AA	32	A
1	AA	39	G
1	AA	41	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	55	A
1	AA	59	A
1	AA	61	G
1	AA	65	U
1	AA	77	G
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	96	U
1	AA	97	G
1	AA	98	G
1	AA	100	C
1	AA	101	A
1	AA	112	G
1	AA	115	G
1	AA	116	A
1	AA	121	C
1	AA	131	C
1	AA	140	A
1	AA	143	A
1	AA	154	C
1	AA	155	C
1	AA	163	C
1	AA	166	G

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Mol	Chain	Res	Type
1	AA	169	C
1	AA	170	U
1	AA	172	A
1	AA	174	C
1	AA	180	U
1	AA	182	U
1	AA	189(C)	C
1	AA	189(D)	C
1	AA	189(F)	U
1	AA	189(G)	G
1	AA	189(H)	G
1	AA	189(I)	G
1	AA	189(K)	U
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	243	A
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C
1	AA	270	A
1	AA	277	C
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	342	C
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U

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Mol	Chain	Res	Type
1	AA	372	C
1	AA	373	A
1	AA	396	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	409	G
1	AA	412	A
1	AA	413	G
1	AA	421	U
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	439	A
1	AA	442	C
1	AA	443	C
1	AA	452	A
1	AA	457	C
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	477	A
1	AA	485	G
1	AA	496	A
1	AA	498	U
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	521	G
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	544	G
1	AA	547	A
1	AA	559	A
1	AA	561	U
1	AA	564	C
1	AA	572	A

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Mol	Chain	Res	Type
1	AA	573	A
1	AA	576	G
1	AA	581	G
1	AA	592	G
1	AA	593	G
1	AA	596	C
1	AA	617	G
1	AA	630	G
1	AA	631	G
1	AA	633	G
1	AA	647	C
1	AA	653	A
1	AA	661	G
1	AA	665	A
1	AA	671	G
1	AA	673	G
1	AA	683	G
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	695	A
1	AA	705	U
1	AA	717	C
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	752	G
1	AA	753	A
1	AA	755	G
1	AA	761	G
1	AA	774	G
1	AA	777	A
1	AA	786	G
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	798	G
1	AA	815	A
1	AA	816	A
1	AA	817	C

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Mol	Chain	Res	Type
1	AA	827	U
1	AA	828	A
1	AA	829	G
1	AA	832	C
1	AA	834	C
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	851	G
1	AA	853	G
1	AA	855	G
1	AA	859	A
1	AA	874	G
1	AA	875	C
1	AA	885	G
1	AA	902	G
1	AA	914	A
1	AA	916	G
1	AA	922	G
1	AA	926	G
1	AA	927	G
1	AA	932	C
1	AA	934	C
1	AA	943	U
1	AA	957	U
1	AA	960	U
1	AA	961	U
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	973	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	979	C
1	AA	981	U
1	AA	989	C
1	AA	992	U
1	AA	993	G
1	AA	997	U
1	AA	1000	U

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Mol	Chain	Res	Type
1	AA	1001	A
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1009	G
1	AA	1010	G
1	AA	1016	A
1	AA	1019	C
1	AA	1022	G
1	AA	1023	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1033	G
1	AA	1034	G
1	AA	1037	C
1	AA	1043	C
1	AA	1045	C
1	AA	1046	A
1	AA	1048	G
1	AA	1052	U
1	AA	1054	C
1	AA	1055	A
1	AA	1060	C
1	AA	1065	U
1	AA	1066	C
1	AA	1067	A
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1087	G
1	AA	1092	A
1	AA	1093	A
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C

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Mol	Chain	Res	Type
1	AA	1101	A
1	AA	1108	G
1	AA	1109	C
1	AA	1111	A
1	AA	1113	C
1	AA	1116	C
1	AA	1122	U
1	AA	1123	A
1	AA	1124	G
1	AA	1125	U
1	AA	1130	A
1	AA	1132	C
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1142	G
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1159	U
1	AA	1163	C
1	AA	1165	C
1	AA	1166	G
1	AA	1168	A
1	AA	1169	A
1	AA	1170	A
1	AA	1173	G
1	AA	1174	G
1	AA	1181	G
1	AA	1182	G
1	AA	1183	A
1	AA	1184	G
1	AA	1193	G
1	AA	1196	U
1	AA	1197	G
1	AA	1201	A
1	AA	1202	G
1	AA	1206	G
1	AA	1212	U
1	AA	1213	A

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Mol	Chain	Res	Type
1	AA	1218	C
1	AA	1227	A
1	AA	1228	C
1	AA	1235	U
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1242	C
1	AA	1246	C
1	AA	1253	G
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1270	C
1	AA	1273	G
1	AA	1275	A
1	AA	1276	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1282	C
1	AA	1286	A
1	AA	1287	A
1	AA	1289	A
1	AA	1290	G
1	AA	1294	G
1	AA	1296	C
1	AA	1297	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1309	G
1	AA	1317	C
1	AA	1319	A
1	AA	1320	C
1	AA	1322	C
1	AA	1327	C
1	AA	1331	G
1	AA	1338	G
1	AA	1346	A
1	AA	1347	G

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Mol	Chain	Res	Type
1	AA	1353	G
1	AA	1358	U
1	AA	1360	A
1	AA	1363	C
1	AA	1368	G
1	AA	1370	G
1	AA	1397	C
1	AA	1406	U
1	AA	1411	C
1	AA	1419	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1456	G
1	AA	1475	G
1	AA	1487	G
1	AA	1491	G
1	AA	1492	A
1	AA	1494	G
1	AA	1497	G
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
22	AV	13	A
22	AV	19	U
22	AV	24	A
23	AW	3	C
23	AW	8	4SU
23	AW	12	U
23	AW	13	C
23	AW	14	A
23	AW	15	G
23	AW	19	G

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Mol	Chain	Res	Type
23	AW	20	U
23	AW	21	A
23	AW	23	A
23	AW	24	G
23	AW	35	A
23	AW	45	U
23	AW	46	7MG
23	AW	47	U
23	AW	48	C
23	AW	49	C
23	AW	50	U
23	AW	52	G
23	AW	61	C
23	AW	63	G
23	AW	64	A
23	AW	66	U
23	AW	68	C
23	AW	70	G
23	AW	73	A
23	AW	74	C
24	AX	6	G
24	AX	9	G
24	AX	14	A
24	AX	18	G
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	22	G
24	AX	42	G
24	AX	46	G
24	AX	47	U
24	AX	58	A
24	AX	59	A
24	AX	61	C
24	AX	67	C
24	AX	68	C
25	AY	2	C
25	AY	4	C
25	AY	5	G
25	AY	7	A
25	AY	9	A
25	AY	10	G

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Mol	Chain	Res	Type
25	AY	11	C
25	AY	14	A
25	AY	19	G
25	AY	20	U
25	AY	21	A
25	AY	23	A
25	AY	25	C
25	AY	26	A
25	AY	32	PSU
25	AY	34	G
25	AY	37	MIA
25	AY	39	PSU
25	AY	41	C
25	AY	42	C
25	AY	44	G
25	AY	45	U
25	AY	46	7MG
25	AY	47	U
25	AY	48	C
25	AY	49	C
25	AY	54	5MU
25	AY	56	C
25	AY	57	G
25	AY	58	A
25	AY	59	U
25	AY	60	U
25	AY	61	C
25	AY	62	C
25	AY	67	C
25	AY	68	C
25	AY	69	G
25	AY	73	A
26	BA	10	G
26	BA	12	U
26	BA	13	A
26	BA	34	C
26	BA	45	C
26	BA	55	G
26	BA	64	A
26	BA	71	A
26	BA	72	U
26	BA	74	A

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Mol	Chain	Res	Type
26	BA	75	G
26	BA	84	A
26	BA	100	G
26	BA	118	A
26	BA	119	A
26	BA	120	U
26	BA	149	A
26	BA	154	G
26	BA	154(A)	C
26	BA	172	C
26	BA	182	A
26	BA	196	A
26	BA	197	A
26	BA	199	A
26	BA	200	U
26	BA	205	G
26	BA	215	G
26	BA	216	A
26	BA	221	A
26	BA	222	A
26	BA	229	A
26	BA	232	G
26	BA	233	A
26	BA	248	G
26	BA	271(E)	U
26	BA	271(I)	G
26	BA	271(K)	U
26	BA	271(L)	U
26	BA	271(M)	G
26	BA	271(N)	U
26	BA	271(O)	C
26	BA	271(S)	G
26	BA	271(U)	G
26	BA	272(B)	G
26	BA	272(H)	C
26	BA	272(I)	U
26	BA	275	G
26	BA	279	C
26	BA	283	A
26	BA	294	A
26	BA	311	A
26	BA	329	G

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Mol	Chain	Res	Type
26	BA	330	A
26	BA	352	G
26	BA	363	G
26	BA	363(B)	G
26	BA	370	G
26	BA	372	G
26	BA	380	U
26	BA	386	G
26	BA	396	G
26	BA	407	G
26	BA	411	G
26	BA	421	U
26	BA	428	A
26	BA	443	A
26	BA	444	C
26	BA	448	U
26	BA	451	C
26	BA	456	C
26	BA	457	A
26	BA	470	A
26	BA	481	G
26	BA	504	U
26	BA	505	A
26	BA	509	C
26	BA	512	G
26	BA	528	A
26	BA	530	G
26	BA	531	C
26	BA	532	A
26	BA	533	G
26	BA	545	G
26	BA	549	G
26	BA	563	G
26	BA	568	U
26	BA	573	G
26	BA	575	A
26	BA	586	A
26	BA	592	G
26	BA	603	A
26	BA	604	G
26	BA	607	U
26	BA	614(B)	G

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Mol	Chain	Res	Type
26	BA	615	G
26	BA	637	A
26	BA	645	C
26	BA	646	A
26	BA	652(D)	C
26	BA	652(E)	G
26	BA	652(T)	C
26	BA	652(U)	G
26	BA	669	G
26	BA	686	G
26	BA	730	C
26	BA	740	U
26	BA	746	A
26	BA	747	U
26	BA	764	A
26	BA	775	G
26	BA	776	G
26	BA	782	A
26	BA	783	A
26	BA	784	A
26	BA	785	G
26	BA	792	G
26	BA	805	G
26	BA	812	C
26	BA	819	A
26	BA	827	U
26	BA	828	U
26	BA	830	G
26	BA	859	G
26	BA	866	A
26	BA	877	U
26	BA	880	G
26	BA	884	C
26	BA	885	C
26	BA	886	C
26	BA	887	A
26	BA	888	C
26	BA	889	C
26	BA	890	A
26	BA	892	G
26	BA	893	C
26	BA	894	C

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Mol	Chain	Res	Type
26	BA	896	A
26	BA	897	C
26	BA	899	A
26	BA	900	A
26	BA	907	U
26	BA	910	A
26	BA	926	A
26	BA	932	G
26	BA	941	A
26	BA	945	A
26	BA	946	G
26	BA	958	U
26	BA	959	A
26	BA	961	C
26	BA	974	G
26	BA	975	C
26	BA	983	A
26	BA	990	A
26	BA	996	A
26	BA	1012	U
26	BA	1013	C
26	BA	1022	G
26	BA	1025	G
26	BA	1026	U
26	BA	1033	U
26	BA	1038	C
26	BA	1045	A
26	BA	1046	A
26	BA	1047	G
26	BA	1048	A
26	BA	1051	G
26	BA	1107	G
26	BA	1110	G
26	BA	1112	G
26	BA	1128	A
26	BA	1130	U
26	BA	1135	C
26	BA	1136	G
26	BA	1139	G
26	BA	1170	G
26	BA	1171	G
26	BA	1173	G

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Mol	Chain	Res	Type
26	BA	1174	A
26	BA	1175	U
26	BA	1176	G
26	BA	1177	A
26	BA	1210	A
26	BA	1211	U
26	BA	1220	A
26	BA	1244	G
26	BA	1253	A
26	BA	1256	G
26	BA	1271	G
26	BA	1272	A
26	BA	1273	U
26	BA	1300	U
26	BA	1301	A
26	BA	1303	G
26	BA	1314	C
26	BA	1352	U
26	BA	1359	A
26	BA	1360	A
26	BA	1365	A
26	BA	1380	G
26	BA	1384	A
26	BA	1385	G
26	BA	1395	A
26	BA	1416	G
26	BA	1417	C
26	BA	1421	G
26	BA	1422	G
26	BA	1428	C
26	BA	1445	A
26	BA	1449	A
26	BA	1450	G
26	BA	1455	G
26	BA	1467	C
26	BA	1471	A
26	BA	1478	G
26	BA	1482	G
26	BA	1490	A
26	BA	1493	C
26	BA	1504	C
26	BA	1508	A

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Mol	Chain	Res	Type
26	BA	1509	C
26	BA	1509(A)	A
26	BA	1531	C
26	BA	1539	G
26	BA	1540	U
26	BA	1542	A
26	BA	1543	C
26	BA	1554	A
26	BA	1558	A
26	BA	1566	A
26	BA	1569	A
26	BA	1578	U
26	BA	1580	A
26	BA	1581	G
26	BA	1584	C
26	BA	1586	A
26	BA	1608	A
26	BA	1610	A
26	BA	1648	C
26	BA	1654	A
26	BA	1674	G
26	BA	1696	G
26	BA	1700	A
26	BA	1701	A
26	BA	1703	G
26	BA	1722	A
26	BA	1739	U
26	BA	1746	G
26	BA	1756	G
26	BA	1762	A
26	BA	1763	G
26	BA	1764	G
26	BA	1773	A
26	BA	1780	A
26	BA	1791	A
26	BA	1800	C
26	BA	1816	G
26	BA	1828	G
26	BA	1839	G
26	BA	1847	A
26	BA	1858	G
26	BA	1861	G

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Mol	Chain	Res	Type
26	BA	1878	G
26	BA	1889	A
26	BA	1900	A
26	BA	1906	G
26	BA	1919	A
26	BA	1927	A
26	BA	1929	G
26	BA	1930	G
26	BA	1937	A
26	BA	1938	A
26	BA	1955	U
26	BA	1963	U
26	BA	1967	C
26	BA	1970	A
26	BA	1971	A
26	BA	1972	A
26	BA	1992	G
26	BA	1993	U
26	BA	1997	G
26	BA	2020	A
26	BA	2023	G
26	BA	2031	A
26	BA	2032	G
26	BA	2033	A
26	BA	2043	C
26	BA	2049	G
26	BA	2055	C
26	BA	2056	G
26	BA	2060	A
26	BA	2061	G
26	BA	2062	A
26	BA	2067	G
26	BA	2069	G
26	BA	2093	G
26	BA	2098	U
26	BA	2100	G
26	BA	2101	G
26	BA	2104	G
26	BA	2111	C
26	BA	2116	G
26	BA	2119	A
26	BA	2122	U

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Mol	Chain	Res	Type
26	BA	2125	G
26	BA	2127	G
26	BA	2129	C
26	BA	2130	U
26	BA	2131	G
26	BA	2132	U
26	BA	2133	G
26	BA	2134	A
26	BA	2135	A
26	BA	2136	C
26	BA	2137	C
26	BA	2138	C
26	BA	2140	C
26	BA	2141	G
26	BA	2142	C
26	BA	2143	C
26	BA	2145	C
26	BA	2147	G
26	BA	2151	G
26	BA	2152	G
26	BA	2153	G
26	BA	2155	G
26	BA	2157	G
26	BA	2158	A
26	BA	2159	G
26	BA	2160	G
26	BA	2161	C
26	BA	2163	C
26	BA	2164	C
26	BA	2165	G
26	BA	2166	G
26	BA	2167	U
26	BA	2168	G
26	BA	2169	A
26	BA	2171	A
26	BA	2172	U
26	BA	2174	C
26	BA	2175	C
26	BA	2178	C
26	BA	2181	G
26	BA	2182	G
26	BA	2183	C

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Mol	Chain	Res	Type
26	BA	2184	G
26	BA	2188	C
26	BA	2189	U
26	BA	2191	G
26	BA	2198	A
26	BA	2199	A
26	BA	2206	G
26	BA	2207	G
26	BA	2208	A
26	BA	2218	U
26	BA	2225	A
26	BA	2238	G
26	BA	2239	G
26	BA	2268	A
26	BA	2273	A
26	BA	2275	C
26	BA	2280	G
26	BA	2283	C
26	BA	2286	A
26	BA	2287	A
26	BA	2289	G
26	BA	2298	A
26	BA	2305	A
26	BA	2308	G
26	BA	2313	C
26	BA	2320	A
26	BA	2325	G
26	BA	2334	G
26	BA	2336	A
26	BA	2343	C
26	BA	2347	C
26	BA	2350	C
26	BA	2361	A
26	BA	2383	G
26	BA	2385	C
26	BA	2393	A
26	BA	2396	G
26	BA	2406	U
26	BA	2407	G
26	BA	2414	G
26	BA	2425	A
26	BA	2429	G

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Mol	Chain	Res	Type
26	BA	2430	A
26	BA	2431	U
26	BA	2435	A
26	BA	2439	A
26	BA	2441	C
26	BA	2448	A
26	BA	2468	G
26	BA	2469	A
26	BA	2474	C
26	BA	2476	A
26	BA	2478	A
26	BA	2502	G
26	BA	2505	G
26	BA	2518	A
26	BA	2529	G
26	BA	2554	U
26	BA	2566	A
26	BA	2567	G
26	BA	2573	C
26	BA	2582	G
26	BA	2602	A
26	BA	2609	U
26	BA	2611	U
26	BA	2612	C
26	BA	2629	A
26	BA	2630	G
26	BA	2654	A
26	BA	2689	U
26	BA	2690	C
26	BA	2691	C
26	BA	2703	C
26	BA	2712(A)	A
26	BA	2713	A
26	BA	2714	G
26	BA	2726	U
26	BA	2733	A
26	BA	2757	A
26	BA	2758	A
26	BA	2764	A
26	BA	2765	A
26	BA	2766	G
26	BA	2778	A

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Mol	Chain	Res	Type
26	BA	2790	A
26	BA	2791	C
26	BA	2793	G
26	BA	2802	G
26	BA	2808	U
26	BA	2818	G
26	BA	2820	A
26	BA	2821	A
26	BA	2824	C
26	BA	2833	G
26	BA	2835	A
26	BA	2872	G
26	BA	2873	A
26	BA	2874	C
26	BA	2875	C
26	BA	2880	C
26	BA	2892	A
26	BA	2893	G
26	BA	2894	G
27	BB	2	C
27	BB	45	A
27	BB	52	A
27	BB	56	G
27	BB	73	A
27	BB	75	G
27	BB	85	G
27	BB	89	G
27	BB	106	G
27	BB	109	C
27	BB	110	G
27	BB	119	G
27	BB	120	A
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	41	G
1	CA	47	C

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Mol	Chain	Res	Type
1	CA	48	C
1	CA	51	A
1	CA	55	A
1	CA	59	A
1	CA	61	G
1	CA	65	U
1	CA	66	G
1	CA	70	G
1	CA	78	G
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	96	U
1	CA	97	G
1	CA	98	G
1	CA	100	C
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	140	A
1	CA	142	G
1	CA	154	C
1	CA	155	C
1	CA	163	C
1	CA	166	G
1	CA	169	C
1	CA	170	U
1	CA	172	A
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(D)	C
1	CA	189(F)	U
1	CA	189(G)	G
1	CA	189(H)	G
1	CA	189(I)	G
1	CA	189(K)	U
1	CA	190	U

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Mol	Chain	Res	Type
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	243	A
1	CA	247	G
1	CA	251	G
1	CA	258	G
1	CA	266	G
1	CA	267	C
1	CA	270	A
1	CA	277	C
1	CA	289	G
1	CA	301	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	342	C
1	CA	344	A
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	396	G
1	CA	398	C
1	CA	406	G
1	CA	409	G
1	CA	412	A
1	CA	413	G
1	CA	421	U
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	439	A
1	CA	442	C
1	CA	443	C
1	CA	452	A

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Mol	Chain	Res	Type
1	CA	455	C
1	CA	457	C
1	CA	461	A
1	CA	471	G
1	CA	477	A
1	CA	485	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	521	G
1	CA	527	G
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	544	G
1	CA	547	A
1	CA	559	A
1	CA	561	U
1	CA	564	C
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	581	G
1	CA	592	G
1	CA	593	G
1	CA	596	C
1	CA	600	C
1	CA	617	G
1	CA	630	G
1	CA	631	G
1	CA	633	G
1	CA	647	C
1	CA	650	G
1	CA	653	A
1	CA	657	G
1	CA	661	G
1	CA	665	A

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Mol	Chain	Res	Type
1	CA	671	G
1	CA	673	G
1	CA	683	G
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	695	A
1	CA	705	U
1	CA	717	C
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	749	C
1	CA	752	G
1	CA	753	A
1	CA	755	G
1	CA	761	G
1	CA	774	G
1	CA	777	A
1	CA	786	G
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	798	G
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	827	U
1	CA	828	A
1	CA	829	G
1	CA	833	U
1	CA	834	C
1	CA	840	C
1	CA	841	U
1	CA	848	C
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	874	G
1	CA	875	C
1	CA	885	G
1	CA	902	G

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Mol	Chain	Res	Type
1	CA	914	A
1	CA	916	G
1	CA	922	G
1	CA	926	G
1	CA	927	G
1	CA	932	C
1	CA	934	C
1	CA	943	U
1	CA	957	U
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	973	G
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	978	A
1	CA	979	C
1	CA	981	U
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	997	U
1	CA	999	C
1	CA	1001	A
1	CA	1002	G
1	CA	1003	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1009	G
1	CA	1010	G
1	CA	1016	A
1	CA	1019	C
1	CA	1022	G
1	CA	1023	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G

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Mol	Chain	Res	Type
1	CA	1027	C
1	CA	1028	C
1	CA	1029	C
1	CA	1030	C
1	CA	1030(A)	G
1	CA	1030(B)	C
1	CA	1030(C)	G
1	CA	1031	G
1	CA	1033	G
1	CA	1034	G
1	CA	1037	C
1	CA	1038	C
1	CA	1039	C
1	CA	1041	A
1	CA	1043	C
1	CA	1045	C
1	CA	1046	A
1	CA	1050	G
1	CA	1052	U
1	CA	1053	G
1	CA	1054	C
1	CA	1060	C
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1087	G
1	CA	1092	A
1	CA	1093	A
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1100	C
1	CA	1101	A
1	CA	1108	G
1	CA	1109	C
1	CA	1111	A
1	CA	1116	C
1	CA	1122	U
1	CA	1124	G
1	CA	1125	U

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Mol	Chain	Res	Type
1	CA	1127	G
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1142	G
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1159	U
1	CA	1163	C
1	CA	1165	C
1	CA	1166	G
1	CA	1168	A
1	CA	1169	A
1	CA	1170	A
1	CA	1174	G
1	CA	1176	A
1	CA	1182	G
1	CA	1183	A
1	CA	1184	G
1	CA	1193	G
1	CA	1196	U
1	CA	1197	G
1	CA	1202	G
1	CA	1206	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1218	C
1	CA	1227	A
1	CA	1228	C
1	CA	1235	U
1	CA	1236	A
1	CA	1238	A
1	CA	1240	U
1	CA	1242	C

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Mol	Chain	Res	Type
1	CA	1246	C
1	CA	1253	G
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1262	C
1	CA	1273	G
1	CA	1275	A
1	CA	1276	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1286	A
1	CA	1287	A
1	CA	1289	A
1	CA	1290	G
1	CA	1294	G
1	CA	1296	C
1	CA	1297	C
1	CA	1299	A
1	CA	1300	G
1	CA	1305	G
1	CA	1309	G
1	CA	1317	C
1	CA	1319	A
1	CA	1320	C
1	CA	1322	C
1	CA	1327	C
1	CA	1331	G
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1358	U
1	CA	1360	A
1	CA	1363	C
1	CA	1368	G
1	CA	1370	G
1	CA	1397	C
1	CA	1406	U

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Mol	Chain	Res	Type
1	CA	1411	C
1	CA	1419	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1446	U
1	CA	1447	A
1	CA	1456	G
1	CA	1475	G
1	CA	1487	G
1	CA	1491	G
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G
1	CA	1497	G
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1517	G
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	14	A
22	CV	19	U
22	CV	24	A
23	CW	3	C
23	CW	8	4SU
23	CW	9	A
23	CW	12	U
23	CW	13	C
23	CW	14	A
23	CW	15	G
23	CW	19	G
23	CW	22	G
23	CW	23	A
23	CW	35	A
23	CW	46	7MG
23	CW	47	U
23	CW	48	C

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Mol	Chain	Res	Type
23	CW	49	C
23	CW	50	U
23	CW	52	G
23	CW	61	C
23	CW	62	C
23	CW	63	G
23	CW	64	A
23	CW	66	U
23	CW	67	C
23	CW	68	C
23	CW	73	A
23	CW	74	C
24	CX	5	G
24	CX	6	G
24	CX	9	G
24	CX	13	C
24	CX	15	G
24	CX	16	C
24	CX	18	G
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	22	G
24	CX	31	G
24	CX	47	U
24	CX	48	C
24	CX	52	G
24	CX	58	A
24	CX	59	A
24	CX	60	U
24	CX	62	C
24	CX	63	G
24	CX	64	G
24	CX	65	C
24	CX	68	C
25	CY	2	C
25	CY	7	A
25	CY	9	A
25	CY	10	G
25	CY	11	C
25	CY	14	A
25	CY	15	G

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Mol	Chain	Res	Type
25	CY	19	G
25	CY	23	A
25	CY	25	C
25	CY	26	A
25	CY	32	PSU
25	CY	33	U
25	CY	34	G
25	CY	37	MIA
25	CY	39	PSU
25	CY	41	C
25	CY	42	C
25	CY	45	U
25	CY	46	7MG
25	CY	47	U
25	CY	49	C
25	CY	52	G
25	CY	54	5MU
25	CY	55	PSU
25	CY	56	C
25	CY	57	G
25	CY	58	A
25	CY	59	U
25	CY	61	C
25	CY	62	C
25	CY	65	G
25	CY	67	C
25	CY	68	C
25	CY	69	G
25	CY	70	G
25	CY	73	A
26	DA	10	G
26	DA	12	U
26	DA	13	A
26	DA	15	G
26	DA	34	C
26	DA	35	G
26	DA	45	C
26	DA	59	U
26	DA	71	A
26	DA	74	A
26	DA	75	G
26	DA	79	G

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Mol	Chain	Res	Type
26	DA	83	G
26	DA	84	A
26	DA	90	U
26	DA	94	C
26	DA	100	G
26	DA	102	G
26	DA	118	A
26	DA	119	A
26	DA	120	U
26	DA	125	G
26	DA	140	G
26	DA	141	A
26	DA	154(A)	C
26	DA	157	U
26	DA	173	G
26	DA	181	A
26	DA	182	A
26	DA	196	A
26	DA	199	A
26	DA	205	G
26	DA	214	G
26	DA	215	G
26	DA	216	A
26	DA	221	A
26	DA	222	A
26	DA	228	A
26	DA	229	A
26	DA	232	G
26	DA	233	A
26	DA	248	G
26	DA	266	G
26	DA	271	A
26	DA	271(D)	G
26	DA	271(I)	G
26	DA	271(J)	C
26	DA	271(L)	U
26	DA	271(M)	G
26	DA	271(N)	U
26	DA	271(O)	C
26	DA	272(A)	U
26	DA	272(B)	G
26	DA	274	G

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Mol	Chain	Res	Type
26	DA	277	C
26	DA	278	A
26	DA	292	C
26	DA	293	U
26	DA	294	A
26	DA	311	A
26	DA	324	A
26	DA	327	G
26	DA	329	G
26	DA	330	A
26	DA	333	G
26	DA	338	G
26	DA	342	G
26	DA	352	G
26	DA	353	G
26	DA	354	G
26	DA	362	U
26	DA	363	G
26	DA	363(A)	A
26	DA	363(C)	G
26	DA	364	C
26	DA	372	G
26	DA	380	U
26	DA	386	G
26	DA	389	G
26	DA	396	G
26	DA	405	U
26	DA	406	G
26	DA	411	G
26	DA	412	A
26	DA	428	A
26	DA	442	G
26	DA	443	A
26	DA	444	C
26	DA	454	A
26	DA	455	C
26	DA	457	A
26	DA	470	A
26	DA	479	A
26	DA	481	G
26	DA	504	U
26	DA	505	A

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Mol	Chain	Res	Type
26	DA	508	G
26	DA	509	C
26	DA	512	G
26	DA	521	G
26	DA	528	A
26	DA	529	A
26	DA	530	G
26	DA	531	C
26	DA	532	A
26	DA	533	G
26	DA	545	G
26	DA	563	G
26	DA	568	U
26	DA	573	G
26	DA	575	A
26	DA	586	A
26	DA	588	U
26	DA	592	G
26	DA	599	G
26	DA	603	A
26	DA	604	G
26	DA	607	U
26	DA	614(B)	G
26	DA	614(C)	A
26	DA	615	G
26	DA	616	G
26	DA	627	A
26	DA	637	A
26	DA	645	C
26	DA	646	A
26	DA	651	G
26	DA	652(A)	A
26	DA	652(B)	A
26	DA	652(C)	G
26	DA	652(U)	G
26	DA	669	G
26	DA	686	G
26	DA	715	G
26	DA	717	G
26	DA	726	G
26	DA	730	C
26	DA	752	A

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Mol	Chain	Res	Type
26	DA	753	C
26	DA	765	G
26	DA	774	A
26	DA	775	G
26	DA	776	G
26	DA	782	A
26	DA	783	A
26	DA	784	A
26	DA	785	G
26	DA	792	G
26	DA	805	G
26	DA	812	C
26	DA	819	A
26	DA	827	U
26	DA	828	U
26	DA	847	U
26	DA	854	G
26	DA	857	C
26	DA	859	G
26	DA	866	A
26	DA	867	C
26	DA	872	A
26	DA	874	G
26	DA	879	G
26	DA	880	G
26	DA	882	G
26	DA	884	C
26	DA	886	C
26	DA	887	A
26	DA	889	C
26	DA	890	A
26	DA	893	C
26	DA	896	A
26	DA	897	C
26	DA	898	C
26	DA	900	A
26	DA	901	A
26	DA	902	C
26	DA	903	C
26	DA	910	A
26	DA	911	A
26	DA	917	A

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Mol	Chain	Res	Type
26	DA	923	C
26	DA	932	G
26	DA	933	A
26	DA	936	C
26	DA	938	G
26	DA	941	A
26	DA	943	U
26	DA	945	A
26	DA	946	G
26	DA	953	A
26	DA	958	U
26	DA	959	A
26	DA	961	C
26	DA	974	G
26	DA	975	C
26	DA	980	A
26	DA	983	A
26	DA	996	A
26	DA	1005	C
26	DA	1006	C
26	DA	1012	U
26	DA	1013	C
26	DA	1018	C
26	DA	1020	A
26	DA	1021	A
26	DA	1022	G
26	DA	1025	G
26	DA	1026	U
26	DA	1033	U
26	DA	1034	G
26	DA	1038	C
26	DA	1039	G
26	DA	1042	G
26	DA	1043	C
26	DA	1113	U
26	DA	1114	G
26	DA	1116	C
26	DA	1121	C
26	DA	1126	A
26	DA	1128	A
26	DA	1129	A
26	DA	1130	U

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Mol	Chain	Res	Type
26	DA	1135	C
26	DA	1136	G
26	DA	1137	G
26	DA	1139	G
26	DA	1144	G
26	DA	1159	U
26	DA	1171	G
26	DA	1204	A
26	DA	1210	A
26	DA	1211	U
26	DA	1212	G
26	DA	1220	A
26	DA	1244	G
26	DA	1247	A
26	DA	1253	A
26	DA	1256	G
26	DA	1271	G
26	DA	1272	A
26	DA	1273	U
26	DA	1292	U
26	DA	1300	U
26	DA	1301	A
26	DA	1303	G
26	DA	1314	C
26	DA	1332	G
26	DA	1352	U
26	DA	1359	A
26	DA	1360	A
26	DA	1365	A
26	DA	1368	G
26	DA	1370	C
26	DA	1380	G
26	DA	1384	A
26	DA	1385	G
26	DA	1386	C
26	DA	1413	G
26	DA	1416	G
26	DA	1417	C
26	DA	1419	A
26	DA	1420	U
26	DA	1421	G
26	DA	1428	C

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Mol	Chain	Res	Type
26	DA	1435	G
26	DA	1437	C
26	DA	1445	A
26	DA	1445(A)	C
26	DA	1449	A
26	DA	1450	G
26	DA	1459	G
26	DA	1461	G
26	DA	1467	C
26	DA	1471	A
26	DA	1474	C
26	DA	1482	G
26	DA	1488	G
26	DA	1489	U
26	DA	1490	A
26	DA	1493	C
26	DA	1496	A
26	DA	1497	U
26	DA	1508	A
26	DA	1509	C
26	DA	1509(A)	A
26	DA	1525	G
26	DA	1531	C
26	DA	1533	G
26	DA	1539	G
26	DA	1541	G
26	DA	1542	A
26	DA	1543	C
26	DA	1545	A
26	DA	1547	C
26	DA	1558	A
26	DA	1559	G
26	DA	1566	A
26	DA	1569	A
26	DA	1578	U
26	DA	1582	C
26	DA	1584	C
26	DA	1586	A
26	DA	1608	A
26	DA	1609	A
26	DA	1610	A
26	DA	1616	A

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Mol	Chain	Res	Type
26	DA	1640	C
26	DA	1648	C
26	DA	1653	G
26	DA	1654	A
26	DA	1669	A
26	DA	1674	G
26	DA	1695	G
26	DA	1696	G
26	DA	1700	A
26	DA	1701	A
26	DA	1721	G
26	DA	1722	A
26	DA	1739	U
26	DA	1740	G
26	DA	1741	A
26	DA	1743	C
26	DA	1746	G
26	DA	1750	G
26	DA	1756	G
26	DA	1758	G
26	DA	1762	A
26	DA	1763	G
26	DA	1764	G
26	DA	1773	A
26	DA	1780	A
26	DA	1782	C
26	DA	1791	A
26	DA	1800	C
26	DA	1801	G
26	DA	1812	A
26	DA	1816	G
26	DA	1828	G
26	DA	1829	A
26	DA	1835	G
26	DA	1847	A
26	DA	1848	A
26	DA	1877	A
26	DA	1878	G
26	DA	1889	A
26	DA	1900	A
26	DA	1906	G
26	DA	1913	A

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Mol	Chain	Res	Type
26	DA	1914	C
26	DA	1927	A
26	DA	1929	G
26	DA	1930	G
26	DA	1931	U
26	DA	1937	A
26	DA	1938	A
26	DA	1955	U
26	DA	1963	U
26	DA	1967	C
26	DA	1970	A
26	DA	1971	A
26	DA	1972	A
26	DA	1984	G
26	DA	1993	U
26	DA	1997	G
26	DA	2020	A
26	DA	2023	G
26	DA	2027	G
26	DA	2031	A
26	DA	2032	G
26	DA	2033	A
26	DA	2043	C
26	DA	2046	G
26	DA	2055	C
26	DA	2056	G
26	DA	2060	A
26	DA	2061	G
26	DA	2062	A
26	DA	2069	G
26	DA	2096	U
26	DA	2099	U
26	DA	2102	U
26	DA	2104	G
26	DA	2105	C
26	DA	2106	G
26	DA	2110	G
26	DA	2111	C
26	DA	2112	G
26	DA	2113	U
26	DA	2115	G
26	DA	2116	G

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Mol	Chain	Res	Type
26	DA	2119	A
26	DA	2122	U
26	DA	2124	G
26	DA	2126	A
26	DA	2127	G
26	DA	2129	C
26	DA	2130	U
26	DA	2131	G
26	DA	2132	U
26	DA	2133	G
26	DA	2134	A
26	DA	2135	A
26	DA	2136	C
26	DA	2137	C
26	DA	2138	C
26	DA	2139	C
26	DA	2142	C
26	DA	2144	U
26	DA	2146	C
26	DA	2148	G
26	DA	2150	U
26	DA	2151	G
26	DA	2154	G
26	DA	2155	G
26	DA	2158	A
26	DA	2159	G
26	DA	2160	G
26	DA	2161	C
26	DA	2162	G
26	DA	2164	C
26	DA	2165	G
26	DA	2166	G
26	DA	2167	U
26	DA	2168	G
26	DA	2169	A
26	DA	2170	A
26	DA	2171	A
26	DA	2172	U
26	DA	2173	A
26	DA	2177	C
26	DA	2178	C
26	DA	2181	G

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Mol	Chain	Res	Type
26	DA	2185	C
26	DA	2186	G
26	DA	2187	G
26	DA	2188	C
26	DA	2189	U
26	DA	2192	G
26	DA	2198	A
26	DA	2206	G
26	DA	2207	G
26	DA	2208	A
26	DA	2218	U
26	DA	2225	A
26	DA	2232	U
26	DA	2238	G
26	DA	2239	G
26	DA	2243	U
26	DA	2269	A
26	DA	2275	C
26	DA	2279	G
26	DA	2283	C
26	DA	2287	A
26	DA	2289	G
26	DA	2294	C
26	DA	2297	C
26	DA	2299	G
26	DA	2301	C
26	DA	2303	G
26	DA	2305	A
26	DA	2308	G
26	DA	2312	U
26	DA	2318	G
26	DA	2319	G
26	DA	2320	A
26	DA	2321	G
26	DA	2322	A
26	DA	2325	G
26	DA	2327	A
26	DA	2334	G
26	DA	2336	A
26	DA	2343	C
26	DA	2347	C
26	DA	2354	G

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Mol	Chain	Res	Type
26	DA	2372	G
26	DA	2376	A
26	DA	2377	A
26	DA	2383	G
26	DA	2385	C
26	DA	2387	U
26	DA	2402	C
26	DA	2406	U
26	DA	2410	G
26	DA	2422	A
26	DA	2423	U
26	DA	2425	A
26	DA	2429	G
26	DA	2430	A
26	DA	2431	U
26	DA	2434	A
26	DA	2435	A
26	DA	2439	A
26	DA	2441	C
26	DA	2445	G
26	DA	2448	A
26	DA	2465	C
26	DA	2474	C
26	DA	2476	A
26	DA	2490	G
26	DA	2494	G
26	DA	2502	G
26	DA	2505	G
26	DA	2506	U
26	DA	2518	A
26	DA	2520	C
26	DA	2525	G
26	DA	2532	G
26	DA	2549	G
26	DA	2554	U
26	DA	2555	U
26	DA	2566	A
26	DA	2567	G
26	DA	2569	G
26	DA	2573	C
26	DA	2578	G
26	DA	2602	A

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Mol	Chain	Res	Type
26	DA	2603	G
26	DA	2609	U
26	DA	2611	U
26	DA	2612	C
26	DA	2629	A
26	DA	2630	G
26	DA	2634	G
26	DA	2652	C
26	DA	2654	A
26	DA	2663	G
26	DA	2673	G
26	DA	2689	U
26	DA	2690	C
26	DA	2691	C
26	DA	2703	C
26	DA	2712(A)	A
26	DA	2713	A
26	DA	2714	G
26	DA	2726	U
26	DA	2732	G
26	DA	2733	A
26	DA	2744	G
26	DA	2751	G
26	DA	2758	A
26	DA	2764	A
26	DA	2765	A
26	DA	2766	G
26	DA	2778	A
26	DA	2780	G
26	DA	2793	G
26	DA	2794	C
26	DA	2802	G
26	DA	2807	G
26	DA	2808	U
26	DA	2818	G
26	DA	2820	A
26	DA	2821	A
26	DA	2833	G
26	DA	2834	G
26	DA	2835	A
26	DA	2839	G
26	DA	2872	G

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Mol	Chain	Res	Type
26	DA	2873	A
26	DA	2880	C
26	DA	2886	G
26	DA	2892	A
26	DA	2894	G
26	DA	2897	U
27	DB	2	C
27	DB	7	G
27	DB	8	U
27	DB	9	G
27	DB	10	C
27	DB	13	A
27	DB	15	A
27	DB	20	C
27	DB	21	G
27	DB	25	A
27	DB	28	C
27	DB	30	C
27	DB	32	C
27	DB	34	U
27	DB	38	C
27	DB	41	U
27	DB	42	C
27	DB	44	G
27	DB	52	A
27	DB	53	A
27	DB	56	G
27	DB	58	A
27	DB	59	A
27	DB	63	G
27	DB	64	C
27	DB	65	C
27	DB	66	A
27	DB	73	A
27	DB	85	G
27	DB	93	G
27	DB	94	C
27	DB	106	G
27	DB	108	U
27	DB	110	G
27	DB	111	G
27	DB	112	U

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Mol	Chain	Res	Type
27	DB	119	G
27	DB	120	A

All (113) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	793	U
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1065	U
1	AA	1067	A
1	AA	1165	C
1	AA	1201	A
1	AA	1256	A
1	AA	1285	A
1	AA	1442	G
23	AW	13	C
23	AW	45	U
25	AY	19	G
25	AY	44	G
25	AY	58	A
26	BA	71	A
26	BA	196	A
26	BA	271(M)	G
26	BA	278	A
26	BA	548	A
26	BA	746	A
26	BA	774	A
26	BA	827	U
26	BA	899	A
26	BA	958	U
26	BA	960	A
26	BA	974	G

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Mol	Chain	Res	Type
26	BA	1047	G
26	BA	1174	A
26	BA	1175	U
26	BA	1176	G
26	BA	1210	A
26	BA	1300	U
26	BA	1301	A
26	BA	1420	U
26	BA	1530	C
26	BA	1608	A
26	BA	1653	G
26	BA	1992	G
26	BA	2126	A
26	BA	2134	A
26	BA	2163	C
26	BA	2181	G
26	BA	2183	C
26	BA	2187	G
26	BA	2238	G
26	BA	2406	U
26	BA	2430	A
26	BA	2689	U
26	BA	2756	U
26	BA	2893	G
1	CA	60	A
1	CA	65	U
1	CA	115	G
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	560	U
1	CA	687	A
1	CA	748	C
1	CA	793	U
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1005	A
1	CA	1027	C
1	CA	1064	G
1	CA	1065	U
1	CA	1129	C

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Mol	Chain	Res	Type
1	CA	1183	A
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1331	G
1	CA	1442	G
1	CA	1492	A
23	CW	13	C
23	CW	14	A
23	CW	66	U
25	CY	46	7MG
26	DA	196	A
26	DA	271(M)	G
26	DA	277	C
26	DA	614(B)	G
26	DA	752	A
26	DA	774	A
26	DA	856	C
26	DA	888	C
26	DA	900	A
26	DA	1210	A
26	DA	1300	U
26	DA	1379	A
26	DA	1420	U
26	DA	1427	A
26	DA	1558	A
26	DA	1653	G
26	DA	1913	A
26	DA	1992	G
26	DA	2110	G
26	DA	2126	A
26	DA	2318	G
26	DA	2422	A
26	DA	2430	A
26	DA	2689	U

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
23	7MG	AW	46	23	23,26,27	1.38	4 (17%)	27,39,42	2.51	6 (22%)
23	PSU	CW	55	23	18,21,22	1.32	2 (11%)	21,30,33	2.11	4 (19%)
23	MIA	CW	37	23	21,24,32	1.60	4 (19%)	30,35,47	2.04	7 (23%)
24	31H	CX	76	57,24	31,34,35	1.35	5 (16%)	35,47,50	2.32	11 (31%)
23	MIA	AW	37	23	28,31,32	2.32	6 (21%)	38,44,47	2.67	12 (31%)
25	5MU	AY	54	25	19,22,23	1.57	6 (31%)	27,32,35	2.03	6 (22%)
25	PSU	CY	55	25	18,21,22	1.34	2 (11%)	21,30,33	2.01	4 (19%)
24	4SU	AX	8	24	18,21,22	2.26	5 (27%)	25,30,33	1.60	4 (16%)
25	4SU	CY	8	25	18,21,22	1.89	4 (22%)	25,30,33	2.48	5 (20%)
25	7MG	AY	46	25	23,26,27	1.26	2 (8%)	27,39,42	3.06	9 (33%)
24	5MU	AX	54	57,24	19,22,23	1.38	5 (26%)	27,32,35	2.05	6 (22%)
24	5MC	AX	32	24	19,22,23	1.66	3 (15%)	26,32,35	1.23	4 (15%)
25	PSU	AY	55	25	18,21,22	1.32	2 (11%)	21,30,33	2.11	5 (23%)
25	PSU	CY	39	25	18,21,22	1.55	5 (27%)	21,30,33	2.65	4 (19%)
23	F3N	CW	76	23	33,36,37	1.49	5 (15%)	41,51,54	1.73	9 (21%)
25	MIA	AY	37	25	21,24,32	1.63	4 (19%)	30,35,47	2.00	7 (23%)
24	31H	AX	76	57,24	31,34,35	1.40	5 (16%)	35,47,50	2.00	11 (31%)
23	F3N	AW	76	23	33,36,37	1.50	4 (12%)	41,51,54	1.70	8 (19%)
23	4SU	CW	8	23	18,21,22	1.73	4 (22%)	25,30,33	2.40	5 (20%)
23	PSU	CW	32	23	18,21,22	1.32	2 (11%)	21,30,33	1.99	4 (19%)
25	5MU	CY	54	25	19,22,23	1.35	4 (21%)	27,32,35	2.27	6 (22%)
25	PSU	AY	39	25	18,21,22	1.43	2 (11%)	21,30,33	1.83	4 (19%)
23	PSU	AW	55	23	18,21,22	1.43	2 (11%)	21,30,33	2.03	3 (14%)
23	PSU	CW	39	23	18,21,22	1.39	2 (11%)	21,30,33	1.70	3 (14%)
24	PSU	CX	55	24	18,21,22	1.37	2 (11%)	21,30,33	2.02	4 (19%)
25	7MG	CY	46	25	23,26,27	1.42	4 (17%)	27,39,42	2.65	9 (33%)
23	4SU	AW	8	23	18,21,22	1.87	4 (22%)	25,30,33	2.06	5 (20%)
25	PSU	AY	32	25	18,21,22	1.39	2 (11%)	21,30,33	1.93	4 (19%)
25	PSU	CY	32	25	18,21,22	1.37	2 (11%)	21,30,33	1.96	4 (19%)
23	PSU	AW	39	23	18,21,22	1.37	2 (11%)	21,30,33	1.95	3 (14%)
24	PSU	AX	55	24	18,21,22	1.35	2 (11%)	21,30,33	2.11	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
25	MIA	CY	37	25	21,24,32	1.66	4 (19%)	30,35,47	2.03	8 (26%)
24	5MC	CX	32	24	19,22,23	1.55	3 (15%)	26,32,35	1.23	4 (15%)
25	4SU	AY	8	25	18,21,22	1.76	3 (16%)	25,30,33	2.33	6 (24%)
23	5MU	AW	54	23	19,22,23	1.41	4 (21%)	27,32,35	1.90	5 (18%)
23	7MG	CW	46	23	23,26,27	1.36	4 (17%)	27,39,42	2.59	9 (33%)
23	PSU	AW	32	23,57	18,21,22	1.33	2 (11%)	21,30,33	2.04	3 (14%)
24	4SU	CX	8	24	18,21,22	2.00	6 (33%)	25,30,33	1.36	3 (12%)
24	5MU	CX	54	24	19,22,23	1.37	5 (26%)	27,32,35	2.17	6 (22%)
23	5MU	CW	54	23	19,22,23	1.41	5 (26%)	27,32,35	1.82	7 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	7MG	AW	46	23	-	4/7/37/38	0/3/3/3
23	PSU	CW	55	23	-	0/7/25/26	0/2/2/2
23	MIA	CW	37	23	-	0/7/25/34	0/3/3/3
24	31H	CX	76	57,24	-	12/22/40/41	0/3/3/3
23	MIA	AW	37	23	-	1/15/33/34	0/3/3/3
25	5MU	AY	54	25	-	4/7/25/26	0/2/2/2
25	PSU	CY	55	25	-	3/7/25/26	0/2/2/2
24	4SU	AX	8	24	-	0/7/25/26	0/2/2/2
25	4SU	CY	8	25	-	1/7/25/26	0/2/2/2
25	7MG	AY	46	25	-	4/7/37/38	0/3/3/3
24	5MU	AX	54	57,24	-	0/7/25/26	0/2/2/2
24	5MC	AX	32	24	-	0/7/25/26	0/2/2/2
25	PSU	AY	55	25	-	1/7/25/26	0/2/2/2
25	PSU	CY	39	25	-	1/7/25/26	0/2/2/2
23	F3N	CW	76	23	-	5/19/37/38	0/4/4/4
25	MIA	AY	37	25	-	3/7/25/34	0/3/3/3
24	31H	AX	76	57,24	-	7/22/40/41	0/3/3/3
23	F3N	AW	76	23	-	0/19/37/38	0/4/4/4
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
25	5MU	CY	54	25	-	2/7/25/26	0/2/2/2
25	PSU	AY	39	25	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	PSU	AW	55	23	-	0/7/25/26	0/2/2/2
23	PSU	CW	39	23	-	0/7/25/26	0/2/2/2
24	PSU	CX	55	24	-	0/7/25/26	0/2/2/2
25	7MG	CY	46	25	-	2/7/37/38	0/3/3/3
23	4SU	AW	8	23	-	0/7/25/26	0/2/2/2
25	PSU	AY	32	25	-	2/7/25/26	0/2/2/2
25	PSU	CY	32	25	-	2/7/25/26	0/2/2/2
23	PSU	AW	39	23	-	0/7/25/26	0/2/2/2
24	PSU	AX	55	24	-	0/7/25/26	0/2/2/2
25	MIA	CY	37	25	-	3/7/25/34	0/3/3/3
24	5MC	CX	32	24	-	0/7/25/26	0/2/2/2
25	4SU	AY	8	25	-	0/7/25/26	0/2/2/2
23	5MU	AW	54	23	-	0/7/25/26	0/2/2/2
23	7MG	CW	46	23	-	3/7/37/38	0/3/3/3
23	PSU	AW	32	23,57	-	0/7/25/26	0/2/2/2
24	4SU	CX	8	24	-	0/7/25/26	0/2/2/2
24	5MU	CX	54	24	-	0/7/25/26	0/2/2/2
23	5MU	CW	54	23	-	0/7/25/26	0/2/2/2

All (143) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C13-C14	7.04	1.53	1.32
23	AW	37	MIA	C2-S10	-6.41	1.70	1.75
24	AX	32	5MC	C5-C4	6.00	1.48	1.44
24	AX	8	4SU	C4-N3	-5.40	1.32	1.37
24	CX	32	5MC	C5-C4	5.37	1.48	1.44
25	CY	37	MIA	C5-C4	5.25	1.48	1.39
25	AY	37	MIA	C5-C4	5.19	1.48	1.39
23	AW	76	F3N	CB-CG	-5.09	1.39	1.51
25	CY	8	4SU	C4-S4	-5.06	1.59	1.68
23	CW	37	MIA	C5-C4	5.01	1.48	1.39
23	AW	8	4SU	C4-S4	-4.99	1.59	1.68
25	AY	8	4SU	C4-S4	-4.90	1.60	1.68
23	AW	37	MIA	C5-C4	4.81	1.47	1.39
24	AX	8	4SU	C4-S4	-4.71	1.60	1.68
23	CW	8	4SU	C4-S4	-4.68	1.60	1.68
23	CW	76	F3N	CB-CG	-4.63	1.40	1.51
24	CX	8	4SU	C4-S4	-4.60	1.60	1.68
24	AX	76	31H	C5-N7	-4.45	1.31	1.39
24	CX	8	4SU	C4-N3	-4.29	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	76	F3N	C5-N7	-4.14	1.31	1.39
25	AY	39	PSU	C6-C5	4.00	1.39	1.35
23	AW	55	PSU	C6-C5	3.95	1.39	1.35
25	CY	32	PSU	C6-C5	3.81	1.39	1.35
24	CX	76	31H	C5-C4	-3.81	1.32	1.39
25	AY	32	PSU	C6-C5	3.79	1.39	1.35
23	CW	39	PSU	C6-C5	3.77	1.39	1.35
24	AX	8	4SU	C2-N3	-3.75	1.31	1.38
25	CY	39	PSU	C6-C5	3.69	1.39	1.35
23	CW	76	F3N	C5-N7	-3.63	1.32	1.39
23	CW	55	PSU	C6-C5	3.63	1.39	1.35
23	CW	76	F3N	C5-C4	-3.59	1.32	1.39
24	CX	55	PSU	C6-C5	3.57	1.39	1.35
23	CW	32	PSU	C6-C5	3.52	1.39	1.35
24	CX	76	31H	C5-N7	-3.49	1.32	1.39
23	AW	39	PSU	C6-C5	3.46	1.39	1.35
25	CY	46	7MG	C5-C4	3.44	1.48	1.37
23	AW	32	PSU	C6-C5	3.43	1.39	1.35
23	AW	46	7MG	C5-C4	3.40	1.48	1.37
25	CY	46	7MG	C4-N9	-3.37	1.33	1.37
23	AW	46	7MG	C4-N9	-3.35	1.33	1.37
25	AY	46	7MG	C5-C4	3.35	1.47	1.37
23	CW	46	7MG	C4-N9	-3.31	1.33	1.37
25	AY	55	PSU	C6-C5	3.27	1.38	1.35
24	AX	8	4SU	C5-C4	-3.26	1.38	1.42
24	AX	55	PSU	C6-C5	3.23	1.38	1.35
25	AY	54	5MU	C2-N1	3.22	1.43	1.38
24	CX	8	4SU	C5-C4	-3.21	1.38	1.42
23	AW	76	F3N	C5-C4	-3.18	1.33	1.39
24	AX	76	31H	C5-C4	-3.16	1.33	1.39
25	AY	54	5MU	C6-C5	3.13	1.39	1.34
25	CY	55	PSU	C6-C5	3.10	1.38	1.35
23	AW	8	4SU	C4-N3	-3.09	1.34	1.37
25	CY	8	4SU	C5-C4	-3.04	1.38	1.42
25	CY	37	MIA	C5-C6	3.03	1.49	1.41
23	CW	46	7MG	C5-C4	3.03	1.47	1.37
25	AY	8	4SU	C4-N3	-3.02	1.34	1.37
23	AW	37	MIA	C5-C6	3.01	1.49	1.41
25	CY	8	4SU	C2-N1	2.99	1.43	1.38
25	AY	37	MIA	C5-C6	2.95	1.49	1.41
25	CY	54	5MU	C6-C5	2.90	1.39	1.34
24	CX	32	5MC	C6-C5	2.90	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CW	37	MIA	C5-C6	2.87	1.49	1.41
23	CW	54	5MU	C6-C5	2.85	1.39	1.34
24	AX	54	5MU	C6-C5	2.82	1.39	1.34
23	AW	54	5MU	C6-C5	2.80	1.39	1.34
24	CX	54	5MU	C6-C5	2.78	1.39	1.34
25	CY	8	4SU	C4-N3	-2.77	1.34	1.37
23	AW	8	4SU	C2-N1	2.77	1.42	1.38
25	AY	8	4SU	C5-C4	-2.77	1.39	1.42
24	AX	54	5MU	C4-N3	-2.74	1.33	1.38
23	AW	8	4SU	C5-C4	-2.72	1.39	1.42
23	CW	8	4SU	C2-N1	2.72	1.42	1.38
24	AX	76	31H	C8-N9	-2.69	1.33	1.37
23	CW	8	4SU	C4-N3	-2.66	1.34	1.37
25	AY	39	PSU	C4-N3	-2.65	1.33	1.38
25	AY	54	5MU	C4-N3	-2.63	1.33	1.38
24	AX	32	5MC	C6-C5	2.63	1.38	1.34
25	CY	55	PSU	C4-N3	-2.62	1.33	1.38
23	CW	39	PSU	C4-N3	-2.61	1.34	1.38
23	AW	39	PSU	C4-N3	-2.57	1.34	1.38
24	AX	8	4SU	O2-C2	2.57	1.27	1.23
23	CW	76	F3N	C5-C6	-2.56	1.33	1.41
23	AW	54	5MU	C4-N3	-2.56	1.34	1.38
24	AX	32	5MC	C6-N1	-2.55	1.33	1.38
23	CW	54	5MU	C4-N3	-2.55	1.34	1.38
24	CX	55	PSU	C4-N3	-2.54	1.34	1.38
23	AW	76	F3N	C5-C6	-2.53	1.33	1.41
25	AY	55	PSU	C4-N3	-2.53	1.34	1.38
24	CX	54	5MU	C4-C5	2.53	1.48	1.44
25	AY	32	PSU	C4-N3	-2.52	1.34	1.38
24	CX	54	5MU	C4-N3	-2.51	1.34	1.38
23	CW	54	5MU	C4-C5	2.49	1.48	1.44
25	AY	54	5MU	C4-C5	2.49	1.48	1.44
23	AW	32	PSU	C4-N3	-2.49	1.34	1.38
25	CY	39	PSU	C4-N3	-2.46	1.34	1.38
23	AW	54	5MU	C4-C5	2.44	1.48	1.44
23	CW	8	4SU	C5-C4	-2.44	1.39	1.42
25	CY	37	MIA	C8-N7	2.43	1.36	1.31
25	AY	46	7MG	C6-N1	-2.43	1.34	1.38
23	AW	37	MIA	C8-N7	2.42	1.36	1.31
24	CX	8	4SU	C2-N3	-2.42	1.33	1.38
23	CW	32	PSU	C4-N3	-2.42	1.34	1.38
24	CX	76	31H	C3'-N3'	2.40	1.49	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	CY	46	7MG	C8-N9	2.39	1.47	1.45
23	AW	55	PSU	C4-N3	-2.39	1.34	1.38
23	CW	55	PSU	C4-N3	-2.39	1.34	1.38
24	CX	76	31H	C5-C6	-2.39	1.34	1.41
25	CY	46	7MG	C6-N1	-2.38	1.34	1.38
25	CY	54	5MU	C4-N3	-2.36	1.34	1.38
24	AX	76	31H	C5-C6	-2.35	1.34	1.41
24	CX	8	4SU	O2-C2	2.34	1.27	1.23
25	AY	37	MIA	C8-N7	2.33	1.36	1.31
23	AW	54	5MU	C2-N1	2.32	1.42	1.38
24	AX	54	5MU	C4-C5	2.31	1.48	1.44
23	CW	46	7MG	C5-C6	2.30	1.49	1.43
25	CY	39	PSU	C6-N1	-2.30	1.32	1.36
23	CW	37	MIA	C8-N7	2.29	1.36	1.31
23	AW	37	MIA	C5-N7	-2.29	1.34	1.39
25	CY	54	5MU	C4-C5	2.28	1.48	1.44
24	CX	8	4SU	C2-N1	2.27	1.42	1.38
24	AX	55	PSU	C4-N3	-2.27	1.34	1.38
23	AW	46	7MG	C6-N1	-2.22	1.34	1.38
25	CY	32	PSU	C4-N3	-2.19	1.34	1.38
24	CX	76	31H	C8-N9	-2.19	1.33	1.37
25	CY	39	PSU	O4'-C1'	-2.16	1.40	1.43
24	AX	54	5MU	C2-N3	-2.16	1.34	1.38
23	CW	37	MIA	C5-N7	-2.15	1.35	1.39
25	CY	39	PSU	C2-N1	-2.14	1.33	1.36
24	CX	54	5MU	C6-N1	-2.14	1.34	1.38
23	CW	46	7MG	C8-N9	2.13	1.47	1.45
23	CW	76	F3N	C3'-N3'	2.13	1.49	1.45
24	AX	76	31H	C3'-N3'	2.12	1.49	1.45
23	CW	54	5MU	C2-N1	2.10	1.41	1.38
24	CX	32	5MC	C6-N1	-2.09	1.34	1.38
24	AX	54	5MU	C6-N1	-2.08	1.34	1.38
25	AY	54	5MU	C6-N1	-2.07	1.34	1.38
25	AY	54	5MU	C2-N3	-2.07	1.34	1.38
25	AY	37	MIA	C5-N7	-2.07	1.35	1.39
23	CW	54	5MU	C2-N3	-2.06	1.34	1.38
25	CY	54	5MU	C2-N1	2.04	1.41	1.38
24	CX	54	5MU	C2-N3	-2.01	1.34	1.38
25	CY	37	MIA	C5-N7	-2.01	1.35	1.39
23	AW	46	7MG	C8-N9	2.00	1.47	1.45

All (231) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	AY	46	7MG	N9-C4-N3	10.89	141.42	125.46
23	AW	46	7MG	N9-C4-N3	8.54	137.97	125.46
25	CY	39	PSU	N1-C2-N3	8.34	123.97	115.17
25	CY	46	7MG	N9-C4-N3	8.33	137.66	125.46
23	AW	37	MIA	C5-C4-N3	-8.22	118.53	127.18
24	CX	76	31H	O4'-C1'-N9	7.60	122.69	108.09
23	AW	37	MIA	C12-C13-C14	-7.57	113.42	127.01
23	CW	8	4SU	C4-N3-C2	-7.26	120.35	127.31
23	CW	46	7MG	N9-C4-N3	7.23	136.05	125.46
25	AY	8	4SU	C4-N3-C2	-6.90	120.70	127.31
25	CY	8	4SU	C4-N3-C2	-6.75	120.85	127.31
25	AY	55	PSU	N1-C2-N3	6.64	122.18	115.17
24	AX	55	PSU	N1-C2-N3	6.43	121.95	115.17
23	AW	55	PSU	N1-C2-N3	6.39	121.91	115.17
24	CX	55	PSU	N1-C2-N3	6.36	121.88	115.17
25	AY	46	7MG	C5-C4-N3	-6.34	116.23	128.13
23	CW	55	PSU	N1-C2-N3	6.26	121.77	115.17
25	CY	8	4SU	C5-C4-N3	6.20	120.52	114.75
23	AW	32	PSU	N1-C2-N3	6.20	121.70	115.17
23	AW	39	PSU	N1-C2-N3	6.18	121.68	115.17
25	CY	39	PSU	O2-C2-N1	-6.10	116.50	122.79
23	CW	32	PSU	N1-C2-N3	6.06	121.56	115.17
25	CY	32	PSU	N1-C2-N3	5.95	121.44	115.17
25	AY	32	PSU	N1-C2-N3	5.92	121.42	115.17
23	AW	37	MIA	N3-C4-N9	5.92	134.50	126.99
23	CW	37	MIA	C5-C4-N3	-5.87	118.64	126.72
25	AY	37	MIA	C5-C4-N3	-5.78	118.75	126.72
23	AW	8	4SU	C5-C4-N3	5.78	120.13	114.75
25	CY	37	MIA	C5-C4-N3	-5.73	118.82	126.72
25	AY	39	PSU	N1-C2-N3	5.73	121.21	115.17
25	AY	8	4SU	C5-C4-N3	5.69	120.05	114.75
23	CW	8	4SU	C5-C4-N3	5.65	120.01	114.75
24	CX	76	31H	N1-C2-N3	-5.64	120.04	128.58
23	CW	76	F3N	N1-C2-N3	-5.63	120.06	128.58
25	CY	55	PSU	N1-C2-N3	5.58	121.06	115.17
23	AW	76	F3N	N1-C2-N3	-5.55	120.18	128.58
24	AX	76	31H	N1-C2-N3	-5.53	120.20	128.58
24	CX	54	5MU	N3-C2-N1	5.53	122.09	114.89
23	CW	46	7MG	N9-C8-N7	-5.52	95.56	103.37
25	CY	54	5MU	C4-N3-C2	-5.45	120.19	127.34
23	AW	46	7MG	N9-C8-N7	-5.44	95.67	103.37
23	AW	8	4SU	C4-N3-C2	-5.42	122.12	127.31
25	CY	46	7MG	N9-C8-N7	-5.34	95.81	103.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CW	46	7MG	C5-C4-N3	-5.32	118.15	128.13
25	CY	8	4SU	C5-C4-S4	-5.30	118.25	124.31
23	CW	39	PSU	N1-C2-N3	5.29	120.75	115.17
24	CX	54	5MU	C4-N3-C2	-5.28	120.41	127.34
25	AY	54	5MU	N3-C2-N1	5.26	121.74	114.89
23	CW	46	7MG	C2-N3-C4	5.20	121.25	112.30
25	CY	54	5MU	N3-C2-N1	5.09	121.52	114.89
24	AX	54	5MU	N3-C2-N1	5.03	121.44	114.89
25	AY	46	7MG	N9-C8-N7	-4.96	96.35	103.37
25	CY	54	5MU	O4-C4-C5	-4.91	119.30	124.92
24	AX	54	5MU	C4-N3-C2	-4.91	120.90	127.34
23	CW	76	F3N	C5-C4-N3	-4.89	119.98	126.72
25	CY	39	PSU	C4-N3-C2	-4.84	119.70	126.37
25	AY	46	7MG	C2-N3-C4	4.84	120.64	112.30
23	AW	46	7MG	C5-C4-N3	-4.75	119.21	128.13
25	CY	46	7MG	C5-C4-N3	-4.75	119.22	128.13
23	CW	37	MIA	N3-C4-N9	4.73	135.21	127.17
25	AY	54	5MU	C4-N3-C2	-4.71	121.17	127.34
25	CY	54	5MU	C5-C4-N3	4.69	119.40	115.32
23	AW	54	5MU	N3-C2-N1	4.64	120.93	114.89
25	CY	37	MIA	N3-C4-N9	4.61	135.00	127.17
25	AY	37	MIA	N3-C4-N9	4.61	135.00	127.17
23	AW	76	F3N	C5-C4-N3	-4.53	120.48	126.72
23	AW	54	5MU	C4-N3-C2	-4.50	121.44	127.34
23	CW	8	4SU	C5-C4-S4	-4.41	119.27	124.31
25	CY	46	7MG	C2-N3-C4	4.40	119.87	112.30
24	CX	76	31H	C5-C4-N3	-4.39	120.68	126.72
23	CW	8	4SU	N3-C2-N1	4.38	120.59	114.89
23	CW	55	PSU	C4-N3-C2	-4.37	120.36	126.37
25	AY	8	4SU	C5-C4-S4	-4.36	119.33	124.31
23	CW	54	5MU	N3-C2-N1	4.30	120.50	114.89
24	AX	54	5MU	C5-C4-N3	4.29	119.06	115.32
23	AW	55	PSU	O2-C2-N1	-4.26	118.40	122.79
23	CW	32	PSU	C4-N3-C2	-4.25	120.51	126.37
23	CW	54	5MU	C4-N3-C2	-4.20	121.84	127.34
24	AX	55	PSU	O2-C2-N1	-4.15	118.51	122.79
25	AY	8	4SU	N3-C2-N1	4.12	120.26	114.89
24	AX	8	4SU	C6-C5-C4	-4.11	116.39	119.95
23	AW	32	PSU	O2-C2-N1	-4.11	118.55	122.79
25	AY	55	PSU	C4-N3-C2	-4.09	120.74	126.37
25	AY	32	PSU	C4-N3-C2	-4.08	120.75	126.37
24	CX	55	PSU	C4-N3-C2	-4.06	120.78	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	CX	54	5MU	C5-C4-N3	4.05	118.85	115.32
23	AW	37	MIA	C15-C14-C13	-4.03	110.58	122.66
23	AW	46	7MG	C2-N3-C4	4.02	119.22	112.30
24	AX	55	PSU	C4-N3-C2	-4.01	120.85	126.37
23	AW	32	PSU	C4-N3-C2	-4.00	120.86	126.37
23	AW	54	5MU	C5-C4-N3	3.98	118.78	115.32
25	CY	54	5MU	C5-C6-N1	-3.98	118.99	123.31
25	AY	55	PSU	O2-C2-N1	-3.97	118.69	122.79
23	AW	37	MIA	C4-C5-N7	-3.93	106.08	110.58
23	CW	54	5MU	C5-C4-N3	3.93	118.74	115.32
23	AW	39	PSU	C4-N3-C2	-3.88	121.03	126.37
25	CY	32	PSU	O2-C2-N1	-3.87	118.80	122.79
23	AW	8	4SU	C5-C4-S4	-3.86	119.90	124.31
24	CX	54	5MU	O4-C4-C5	-3.84	120.53	124.92
24	AX	76	31H	C5-C4-N3	-3.80	121.49	126.72
24	AX	32	5MC	C5-C6-N1	-3.78	119.20	123.31
24	AX	54	5MU	O4-C4-C5	-3.75	120.62	124.92
25	CY	55	PSU	C4-N3-C2	-3.75	121.20	126.37
25	CY	55	PSU	C6-C5-C4	-3.75	115.64	118.17
25	CY	37	MIA	C4-C5-N7	-3.71	106.34	110.58
25	AY	39	PSU	C4-N3-C2	-3.69	121.28	126.37
23	CW	37	MIA	C2-N3-C4	3.69	120.84	111.83
24	AX	8	4SU	C5-C4-N3	3.65	118.14	114.75
25	AY	54	5MU	C5-C4-N3	3.64	118.48	115.32
24	CX	8	4SU	C5-C4-N3	3.62	118.12	114.75
25	CY	8	4SU	N3-C2-N1	3.62	119.60	114.89
23	AW	37	MIA	C2-N3-C4	3.60	121.73	112.29
25	AY	37	MIA	C4-C5-N7	-3.60	106.47	110.58
24	AX	76	31H	O4'-C1'-N9	3.59	114.99	108.09
24	AX	76	31H	C5-N7-C8	3.59	109.09	103.45
25	CY	32	PSU	C4-N3-C2	-3.59	121.43	126.37
23	AW	37	MIA	C6-C5-N7	3.58	136.34	132.43
24	CX	54	5MU	O2-C2-N1	-3.57	118.15	122.80
25	AY	37	MIA	C2-N3-C4	3.57	120.55	111.83
23	AW	54	5MU	O4-C4-C5	-3.57	120.84	124.92
24	AX	76	31H	N9-C8-N7	-3.54	108.91	113.94
23	CW	37	MIA	C4-C5-N7	-3.54	106.54	110.58
25	CY	37	MIA	C2-N3-C4	3.53	120.46	111.83
25	CY	54	5MU	O2-C2-N1	-3.53	118.20	122.80
23	AW	55	PSU	C4-N3-C2	-3.51	121.53	126.37
23	CW	55	PSU	O2-C2-N1	-3.51	119.17	122.79
25	AY	54	5MU	O4-C4-C5	-3.49	120.93	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CW	37	MIA	N3-C2-N1	-3.43	123.39	128.58
24	CX	76	31H	N9-C8-N7	-3.43	109.08	113.94
23	AW	76	F3N	N9-C8-N7	-3.41	109.10	113.94
24	AX	54	5MU	C5-C6-N1	-3.41	119.61	123.31
23	AW	37	MIA	C16-C14-C13	-3.41	112.43	122.66
24	CX	54	5MU	C5-C6-N1	-3.40	119.62	123.31
25	CY	55	PSU	O2-C2-N1	-3.35	119.34	122.79
24	CX	55	PSU	O2-C2-N1	-3.33	119.35	122.79
23	CW	54	5MU	O4-C4-C5	-3.30	121.14	124.92
25	AY	54	5MU	C5-C6-N1	-3.30	119.73	123.31
25	AY	46	7MG	O6-C6-C5	-3.29	119.54	127.62
25	AY	37	MIA	N3-C2-N1	-3.29	123.60	128.58
23	CW	76	F3N	N9-C8-N7	-3.28	109.28	113.94
24	CX	8	4SU	C1'-N1-C2	3.28	123.49	117.59
23	CW	76	F3N	C2-N3-C4	3.24	119.75	111.83
24	AX	8	4SU	O2-C2-N1	3.24	127.01	122.80
23	CW	39	PSU	C4-N3-C2	-3.23	121.92	126.37
23	CW	32	PSU	O2-C2-N1	-3.21	119.48	122.79
25	CY	37	MIA	N3-C2-N1	-3.20	123.73	128.58
25	AY	46	7MG	C5-C6-N1	3.18	116.54	110.94
24	CX	76	31H	C5-N7-C8	3.16	108.42	103.45
25	CY	8	4SU	C1'-N1-C2	3.16	123.27	117.59
23	AW	76	F3N	C5-N7-C8	3.15	108.40	103.45
23	AW	8	4SU	N3-C2-N1	3.15	119.00	114.89
23	AW	39	PSU	O2-C2-N1	-3.14	119.55	122.79
25	AY	46	7MG	C5-C4-N9	-3.11	102.35	106.33
24	CX	76	31H	C2-N3-C4	3.10	119.40	111.83
23	AW	76	F3N	C2-N3-C4	3.09	119.38	111.83
24	AX	54	5MU	O2-C2-N1	-3.05	118.83	122.80
23	CW	46	7MG	C5-C6-N1	3.03	116.28	110.94
23	CW	76	F3N	C5-C4-N9	3.01	109.09	105.81
23	AW	54	5MU	C5-C6-N1	-3.00	120.05	123.31
23	CW	54	5MU	C5-C6-N1	-2.97	120.08	123.31
24	AX	76	31H	C2-N3-C4	2.97	119.09	111.83
24	CX	32	5MC	C5-C6-N1	-2.97	120.09	123.31
24	AX	8	4SU	S4-C4-N3	-2.96	117.10	120.20
23	CW	76	F3N	C5-N7-C8	2.95	108.09	103.45
24	CX	76	31H	C4'-O4'-C1'	-2.93	102.99	109.47
25	AY	54	5MU	O2-C2-N3	-2.85	116.22	121.49
24	AX	32	5MC	C5-C4-N3	-2.85	118.84	121.75
23	CW	8	4SU	C1'-N1-C2	2.83	122.68	117.59
25	CY	37	MIA	C4-N9-C8	2.80	108.68	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	AY	32	PSU	O2-C2-N1	-2.78	119.92	122.79
23	AW	46	7MG	C5-C4-N9	-2.75	102.81	106.33
25	CY	37	MIA	C5-N7-C8	2.72	107.73	103.45
23	AW	76	F3N	C5-C4-N9	2.67	108.72	105.81
23	AW	37	MIA	C5-N7-C8	2.66	107.63	103.45
23	CW	37	MIA	C5-N7-C8	2.64	107.60	103.45
24	CX	32	5MC	C5-C4-N3	-2.63	119.06	121.75
24	CX	32	5MC	O2-C2-N3	-2.61	118.21	122.33
25	AY	37	MIA	C5-N7-C8	2.60	107.54	103.45
23	AW	8	4SU	C1'-N1-C2	2.59	122.25	117.59
23	CW	37	MIA	C4-N9-C8	2.59	108.46	105.74
23	CW	46	7MG	C6-C5-N7	2.55	135.88	131.93
23	AW	37	MIA	N3-C2-N1	-2.53	122.37	127.00
23	CW	55	PSU	C5-C6-N1	-2.53	118.63	122.14
25	CY	46	7MG	C5-C4-N9	-2.52	103.10	106.33
25	CY	46	7MG	C5-C6-N1	2.50	115.33	110.94
23	CW	76	F3N	C6-C5-C4	2.49	120.57	117.18
24	CX	76	31H	C5-C4-N9	2.48	108.52	105.81
25	AY	37	MIA	C4-N9-C8	2.47	108.33	105.74
23	AW	37	MIA	C2-N1-C6	2.47	122.22	117.54
24	CX	8	4SU	C6-C5-C4	-2.40	117.87	119.95
24	AX	76	31H	C4'-O4'-C1'	-2.40	104.17	109.47
23	CW	32	PSU	C5-C6-N1	-2.40	118.81	122.14
25	AY	8	4SU	O2-C2-N1	-2.34	119.75	122.80
23	AW	46	7MG	C5-C6-N1	2.32	115.03	110.94
24	CX	55	PSU	C5-C6-N1	-2.29	118.96	122.14
25	CY	46	7MG	O4'-C1'-N9	-2.29	106.17	109.30
24	AX	55	PSU	C5-C6-N1	-2.26	119.00	122.14
25	AY	8	4SU	C1'-N1-C2	2.25	121.63	117.59
24	AX	76	31H	N3-C4-N9	2.24	130.98	127.17
23	CW	54	5MU	C5M-C5-C4	2.22	121.16	118.78
23	CW	76	F3N	C4-C5-N7	-2.22	108.05	110.58
23	CW	76	F3N	N3-C4-N9	2.21	130.93	127.17
24	CX	76	31H	C4-C5-N7	-2.21	108.05	110.58
25	CY	39	PSU	C6-N1-C2	-2.21	120.64	122.69
25	AY	39	PSU	O2-C2-N3	-2.20	117.95	121.86
25	AY	39	PSU	C5-C6-N1	-2.17	119.12	122.14
25	AY	55	PSU	C5-C6-N1	-2.17	119.13	122.14
24	AX	76	31H	O2'-C2'-C3'	2.16	116.46	111.16
24	CX	76	31H	C6-C5-C4	2.14	120.10	117.18
25	AY	46	7MG	C4-C5-N7	2.13	107.90	105.38
24	CX	76	31H	N3-C4-N9	2.13	130.80	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	AW	76	F3N	N3-C4-N9	2.13	130.79	127.17
25	CY	46	7MG	C6-C5-C4	-2.13	118.66	122.40
23	CW	46	7MG	O4'-C1'-N9	2.12	112.19	109.30
23	AW	76	F3N	C4-C5-N7	-2.12	108.16	110.58
25	CY	32	PSU	O4'-C1'-C2'	2.11	108.08	105.15
25	AY	32	PSU	C5-C6-N1	-2.11	119.21	122.14
24	CX	32	5MC	C1'-N1-C6	-2.11	117.68	121.15
24	AX	76	31H	C4-C5-N7	-2.10	108.19	110.58
24	AX	76	31H	CA-N-CN	-2.08	119.62	122.82
24	AX	32	5MC	O2-C2-N3	-2.08	119.05	122.33
23	CW	46	7MG	O6-C6-C5	-2.08	122.52	127.62
24	AX	32	5MC	CM5-C5-C6	-2.07	120.04	122.85
23	CW	46	7MG	C6-C5-C4	-2.07	118.76	122.40
23	CW	54	5MU	O2-C2-N1	-2.03	120.15	122.80
25	CY	46	7MG	N2-C2-N1	2.03	121.04	116.76
25	AY	46	7MG	O6-C6-N1	2.03	123.92	120.11
23	AW	37	MIA	C4-N9-C8	2.02	107.86	105.74
25	CY	37	MIA	N9-C8-N7	-2.02	111.08	113.94
25	AY	55	PSU	O4'-C1'-C2'	2.01	107.94	105.15
23	CW	39	PSU	O2-C2-N3	-2.01	118.29	121.86

There are no chirality outliers.

All (62) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	AW	37	MIA	C12-C13-C14-C16
24	AX	76	31H	OCN-CN-N-CA
25	AY	32	PSU	O4'-C4'-C5'-O5'
25	AY	46	7MG	C4'-C5'-O5'-P
24	CX	76	31H	C4'-C5'-O5'-P
24	CX	76	31H	CB-CA-N-CN
24	CX	76	31H	OCN-CN-N-CA
25	CY	46	7MG	O4'-C4'-C5'-O5'
25	CY	54	5MU	O4'-C4'-C5'-O5'
24	CX	76	31H	O-C-N3'-C3'
25	AY	37	MIA	C3'-C4'-C5'-O5'
25	AY	54	5MU	C3'-C4'-C5'-O5'
25	AY	54	5MU	O4'-C4'-C5'-O5'
25	CY	32	PSU	O4'-C4'-C5'-O5'
25	CY	37	MIA	C3'-C4'-C5'-O5'
25	CY	54	5MU	C3'-C4'-C5'-O5'
23	AW	46	7MG	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
24	AX	76	31H	C3'-C4'-C5'-O5'
23	CW	76	F3N	C3'-C4'-C5'-O5'
25	CY	46	7MG	C3'-C4'-C5'-O5'
25	CY	55	PSU	O4'-C4'-C5'-O5'
24	AX	76	31H	C4'-C5'-O5'-P
24	CX	76	31H	C3'-C4'-C5'-O5'
23	AW	46	7MG	C3'-C4'-C5'-O5'
25	AY	32	PSU	C3'-C4'-C5'-O5'
25	AY	39	PSU	C3'-C4'-C5'-O5'
25	CY	32	PSU	C3'-C4'-C5'-O5'
25	AY	37	MIA	O4'-C4'-C5'-O5'
25	AY	39	PSU	O4'-C4'-C5'-O5'
25	CY	37	MIA	O4'-C4'-C5'-O5'
24	CX	76	31H	CB-CG-SD-CE
24	AX	76	31H	O4'-C4'-C5'-O5'
24	CX	76	31H	O4'-C4'-C5'-O5'
24	CX	76	31H	N3'-C-CA-N
23	CW	76	F3N	C-CA-CB-CG
25	AY	46	7MG	C2'-C1'-N9-C8
23	CW	46	7MG	C2'-C1'-N9-C8
23	CW	76	F3N	O4'-C4'-C5'-O5'
25	CY	55	PSU	C3'-C4'-C5'-O5'
23	CW	76	F3N	N-CA-CB-CG
25	CY	37	MIA	C4'-C5'-O5'-P
25	AY	55	PSU	O4'-C1'-C5-C4
23	CW	76	F3N	C4'-C5'-O5'-P
23	AW	46	7MG	C4'-C5'-O5'-P
24	CX	76	31H	O-C-CA-N
24	AX	76	31H	N3'-C-CA-N
24	CX	76	31H	N-CA-CB-CG
23	CW	46	7MG	C4'-C5'-O5'-P
24	CX	76	31H	C-CA-CB-CG
25	CY	39	PSU	C4'-C5'-O5'-P
24	AX	76	31H	O-C-CA-N
25	AY	46	7MG	O4'-C1'-N9-C8
23	CW	46	7MG	O4'-C1'-N9-C8
25	AY	46	7MG	C3'-C4'-C5'-O5'
24	AX	76	31H	CB-CA-N-CN
25	CY	55	PSU	C2'-C1'-C5-C6
25	AY	37	MIA	C4'-C5'-O5'-P
23	AW	46	7MG	C2'-C1'-N9-C8
25	AY	54	5MU	C2'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
24	CX	76	31H	N3'-C-CA-CB
25	AY	54	5MU	C2'-C1'-N1-C2
25	CY	8	4SU	C2'-C1'-N1-C2

There are no ring outliers.

27 monomers are involved in 48 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	CW	55	PSU	1	0
24	CX	76	31H	1	0
25	AY	54	5MU	1	0
25	CY	55	PSU	2	0
24	AX	8	4SU	1	0
25	CY	8	4SU	2	0
25	AY	46	7MG	3	0
25	AY	55	PSU	2	0
25	CY	39	PSU	8	0
23	CW	76	F3N	3	0
25	AY	37	MIA	1	0
24	AX	76	31H	1	0
23	AW	76	F3N	1	0
23	CW	8	4SU	2	0
23	CW	32	PSU	1	0
25	AY	39	PSU	2	0
23	AW	55	PSU	1	0
23	CW	39	PSU	1	0
24	CX	55	PSU	1	0
25	CY	46	7MG	4	0
23	AW	39	PSU	1	0
24	AX	55	PSU	1	0
25	CY	37	MIA	3	0
24	CX	32	5MC	1	0
25	AY	8	4SU	1	0
23	CW	46	7MG	2	0
24	CX	8	4SU	3	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2063 ligands modelled in this entry, 2061 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
58	SF4	AD	501	4	0,12,12	-	-	-		
58	SF4	CD	501	4	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	SF4	AD	501	4	-	-	0/6/5/5
58	SF4	CD	501	4	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

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

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AA	1497/1521 (98%)	0.49	47 (3%) 51 45	41, 72, 93, 106	0
1	CA	1503/1521 (98%)	0.74	152 (10%) 12 9	43, 75, 94, 106	0
2	AB	231/256 (90%)	1.33	43 (18%) 3 3	68, 82, 89, 95	0
2	CB	231/256 (90%)	1.55	57 (24%) 2 1	68, 83, 90, 96	0
3	AC	206/239 (86%)	1.10	20 (9%) 13 10	69, 79, 87, 94	0
3	CC	206/239 (86%)	1.86	84 (40%) 0 0	70, 82, 90, 94	0
4	AD	208/209 (99%)	1.05	24 (11%) 9 7	57, 72, 81, 87	0
4	CD	208/209 (99%)	1.05	18 (8%) 16 12	60, 72, 81, 89	0
5	AE	148/162 (91%)	1.05	16 (10%) 11 8	58, 71, 81, 85	0
5	CE	148/162 (91%)	1.28	14 (9%) 14 10	60, 74, 83, 86	0
6	AF	100/101 (99%)	0.61	0 100 100	52, 67, 75, 85	0
6	CF	100/101 (99%)	0.95	4 (4%) 42 37	57, 71, 81, 85	0
7	AG	155/156 (99%)	1.15	24 (15%) 5 4	66, 76, 85, 96	0
7	CG	155/156 (99%)	1.27	22 (14%) 6 5	68, 77, 86, 97	0
8	AH	137/138 (99%)	0.97	15 (10%) 10 8	62, 72, 79, 83	0
8	CH	137/138 (99%)	1.23	19 (13%) 6 5	64, 74, 80, 85	0
9	AI	127/128 (99%)	1.38	27 (21%) 2 2	62, 80, 87, 89	0
9	CI	127/128 (99%)	2.32	74 (58%) 0 0	69, 82, 89, 91	0
10	AJ	97/105 (92%)	1.68	35 (36%) 1 0	66, 83, 91, 92	0
10	CJ	96/105 (91%)	1.74	36 (37%) 1 0	68, 84, 91, 93	0
11	AK	114/129 (88%)	0.89	6 (5%) 32 26	51, 70, 80, 84	0
11	CK	114/129 (88%)	1.09	10 (8%) 15 12	52, 72, 81, 85	0
12	AL	122/132 (92%)	0.54	8 (6%) 24 19	41, 56, 71, 75	0
12	CL	122/132 (92%)	1.40	35 (28%) 1 1	58, 73, 82, 87	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	AM	123/126 (97%)	0.83	10 (8%) 18 14	57, 72, 83, 88	0
13	CM	122/126 (96%)	1.95	52 (42%) 0 0	69, 85, 92, 97	0
14	AN	60/61 (98%)	1.06	4 (6%) 24 19	70, 76, 83, 84	0
14	CN	60/61 (98%)	2.59	40 (66%) 0 0	73, 79, 85, 87	0
15	AO	88/89 (98%)	0.73	4 (4%) 38 32	54, 68, 79, 83	0
15	CO	88/89 (98%)	0.78	3 (3%) 48 42	56, 70, 81, 84	0
16	AP	82/88 (93%)	1.30	15 (18%) 3 3	59, 71, 79, 84	0
16	CP	82/88 (93%)	1.07	7 (8%) 16 13	59, 70, 79, 83	0
17	AQ	99/105 (94%)	0.69	3 (3%) 52 47	57, 70, 79, 84	0
17	CQ	99/105 (94%)	1.06	9 (9%) 15 11	60, 71, 79, 84	0
18	AR	68/88 (77%)	0.79	3 (4%) 39 33	59, 69, 81, 84	0
18	CR	68/88 (77%)	1.06	6 (8%) 15 12	58, 70, 81, 85	0
19	AS	84/93 (90%)	0.86	4 (4%) 35 30	70, 81, 87, 92	0
19	CS	83/93 (89%)	2.30	54 (65%) 0 0	74, 83, 90, 94	0
20	AT	96/106 (90%)	1.33	20 (20%) 2 2	59, 71, 80, 83	0
20	CT	96/106 (90%)	1.00	14 (14%) 6 4	59, 71, 80, 83	0
21	AU	23/27 (85%)	1.24	1 (4%) 40 34	70, 75, 78, 82	0
21	CU	23/27 (85%)	2.28	14 (60%) 0 0	71, 78, 81, 82	0
22	AV	13/24 (54%)	1.34	4 (30%) 1 1	58, 77, 95, 100	0
22	CV	12/24 (50%)	1.97	6 (50%) 0 0	64, 81, 93, 95	0
23	AW	66/76 (86%)	1.50	15 (22%) 2 1	66, 95, 102, 105	0
23	CW	64/76 (84%)	1.82	22 (34%) 1 1	70, 96, 101, 106	0
24	AX	71/77 (92%)	0.69	7 (9%) 13 10	42, 73, 90, 96	0
24	CX	71/77 (92%)	0.84	3 (4%) 40 35	55, 86, 95, 98	0
25	AY	67/76 (88%)	1.37	11 (16%) 4 3	44, 97, 101, 105	0
25	CY	66/76 (86%)	1.71	16 (24%) 2 1	48, 98, 102, 103	0
26	BA	2819/2915 (96%)	-0.25	86 (3%) 51 45	23, 43, 87, 106	0
26	DA	2800/2915 (96%)	-0.19	72 (2%) 57 51	27, 48, 90, 108	0
27	BB	120/121 (99%)	0.39	1 (0%) 82 80	41, 64, 76, 88	0
27	DB	120/121 (99%)	1.16	19 (15%) 5 4	48, 70, 80, 91	0
28	BD	275/276 (99%)	0.12	6 (2%) 62 57	24, 41, 58, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	DD	275/276 (99%)	0.04	4 (1%) 72 68	28, 44, 61, 79	0
29	BE	204/206 (99%)	0.13	1 (0%) 87 85	23, 46, 65, 83	0
29	DE	204/206 (99%)	0.22	3 (1%) 72 68	26, 50, 67, 84	0
30	BF	203/210 (96%)	0.33	1 (0%) 87 85	25, 51, 76, 86	0
30	DF	203/210 (96%)	0.37	5 (2%) 58 52	28, 56, 78, 88	0
31	BG	181/182 (99%)	1.18	23 (12%) 8 6	55, 72, 83, 93	0
31	DG	181/182 (99%)	1.69	55 (30%) 1 1	64, 76, 85, 93	0
32	BH	174/180 (96%)	0.90	12 (6%) 23 18	50, 66, 75, 82	0
32	DH	174/180 (96%)	1.20	29 (16%) 4 3	56, 71, 79, 83	0
33	BI	146/148 (98%)	0.82	6 (4%) 41 36	49, 74, 83, 87	0
33	DI	146/148 (98%)	1.14	14 (9%) 13 10	50, 74, 83, 87	0
34	BN	140/140 (100%)	0.41	1 (0%) 84 82	29, 48, 67, 79	0
34	DN	140/140 (100%)	0.59	3 (2%) 63 58	35, 53, 70, 82	0
35	BO	122/122 (100%)	-0.24	1 (0%) 82 80	25, 40, 57, 67	0
35	DO	122/122 (100%)	0.43	1 (0%) 82 80	44, 58, 74, 79	0
36	BP	149/150 (99%)	0.40	4 (2%) 56 50	25, 55, 75, 80	0
36	DP	149/150 (99%)	0.68	4 (2%) 56 50	28, 58, 78, 83	0
37	BQ	141/141 (100%)	0.49	2 (1%) 73 69	37, 52, 68, 77	0
37	DQ	141/141 (100%)	0.79	8 (5%) 29 24	41, 58, 72, 79	0
38	BR	118/118 (100%)	-0.35	0 100 100	22, 34, 50, 59	0
38	DR	118/118 (100%)	0.19	1 (0%) 82 80	38, 53, 64, 75	0
39	BS	110/112 (98%)	0.04	0 100 100	34, 50, 64, 70	0
39	DS	110/112 (98%)	1.68	31 (28%) 1 1	70, 79, 87, 91	0
40	BT	131/146 (89%)	0.31	4 (3%) 51 45	38, 51, 73, 82	0
40	DT	131/146 (89%)	0.30	4 (3%) 51 45	40, 54, 75, 81	0
41	BU	116/118 (98%)	-0.41	0 100 100	17, 30, 50, 63	0
41	DU	116/118 (98%)	0.49	2 (1%) 69 64	40, 59, 79, 85	0
42	BV	101/101 (100%)	-0.38	0 100 100	16, 38, 58, 68	0
42	DV	101/101 (100%)	0.88	7 (6%) 23 18	44, 73, 81, 92	0
43	BW	112/113 (99%)	-0.31	1 (0%) 81 78	22, 30, 49, 83	0
43	DW	112/113 (99%)	0.24	2 (1%) 67 63	35, 50, 66, 86	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	BX	95/96 (98%)	0.32	1 (1%) 78 74	31, 46, 67, 83	0
44	DX	95/96 (98%)	0.54	6 (6%) 26 20	36, 50, 68, 83	0
45	BY	107/110 (97%)	0.81	5 (4%) 36 30	42, 58, 73, 84	0
45	DY	107/110 (97%)	0.86	8 (7%) 20 16	47, 61, 75, 84	0
46	BZ	171/206 (83%)	0.80	31 (18%) 3 3	40, 66, 91, 95	0
46	DZ	174/206 (84%)	1.32	30 (17%) 4 3	69, 85, 94, 101	0
47	B0	83/85 (97%)	0.75	7 (8%) 17 13	34, 50, 67, 75	0
47	D0	83/85 (97%)	1.03	10 (12%) 9 7	40, 56, 71, 76	0
48	B1	97/98 (98%)	0.35	4 (4%) 41 36	31, 49, 72, 76	0
48	D1	97/98 (98%)	0.44	2 (2%) 63 58	34, 53, 73, 78	0
49	B2	70/72 (97%)	0.11	2 (2%) 53 48	33, 49, 64, 82	0
49	D2	70/72 (97%)	0.76	1 (1%) 73 69	58, 69, 78, 82	0
50	B3	59/60 (98%)	-0.26	0 100 100	24, 37, 63, 74	0
50	D3	59/60 (98%)	0.45	1 (1%) 69 64	52, 65, 79, 87	0
51	B4	69/71 (97%)	0.96	10 (14%) 6 4	49, 76, 89, 91	0
51	D4	69/71 (97%)	1.73	26 (37%) 1 0	74, 89, 95, 99	0
52	B5	59/60 (98%)	-0.48	1 (1%) 69 64	16, 30, 46, 68	0
52	D5	59/60 (98%)	0.12	1 (1%) 69 64	35, 49, 65, 77	0
53	B6	53/54 (98%)	-0.26	0 100 100	32, 44, 57, 72	0
53	D6	53/54 (98%)	0.64	0 100 100	49, 64, 74, 79	0
54	B7	48/49 (97%)	0.03	5 (10%) 11 9	23, 32, 58, 70	0
54	D7	48/49 (97%)	-0.04	2 (4%) 40 35	26, 35, 61, 70	0
55	B8	64/65 (98%)	0.26	2 (3%) 51 45	34, 42, 50, 65	0
55	D8	64/65 (98%)	0.40	1 (1%) 70 66	37, 46, 54, 65	0
56	B9	37/37 (100%)	0.48	1 (2%) 56 50	36, 51, 65, 73	0
56	D9	37/37 (100%)	0.75	1 (2%) 56 50	43, 55, 68, 76	0
All	All	20895/21748 (96%)	0.51	1708 (8%) 17 14	16, 64, 89, 108	0

All (1708) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	AG	82	GLY	7.8
32	BH	2	SER	7.6

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Mol	Chain	Res	Type	RSRZ
13	CM	124	PRO	7.5
13	CM	102	ARG	7.5
13	CM	123	ALA	6.7
19	CS	9	VAL	6.3
28	BD	276	LYS	6.1
3	CC	13	GLY	6.0
20	AT	103	GLY	6.0
26	BA	2145	C	5.9
2	CB	165	VAL	5.6
13	AM	124	PRO	5.5
9	CI	105	ASP	5.5
31	BG	146	TYR	5.5
1	CA	1224	G	5.4
13	CM	122	LYS	5.4
9	CI	102	LEU	5.4
9	CI	9	ARG	5.3
13	AM	122	LYS	5.3
14	CN	2	ALA	5.2
9	CI	126	SER	5.2
23	AW	1	G	5.1
9	CI	14	VAL	5.1
14	CN	3	ARG	5.1
48	D1	2	SER	5.1
19	CS	84	GLY	5.0
1	CA	1030(B)	C	5.0
7	CG	81	GLY	5.0
1	AA	1257	U	5.0
3	AC	207	VAL	4.9
9	CI	106	ALA	4.9
47	B0	6	GLY	4.9
1	CA	1116	C	4.8
1	CA	1219	U	4.8
5	CE	94	ALA	4.8
23	CW	73	A	4.8
14	AN	2	ALA	4.7
5	AE	85	GLY	4.7
3	CC	128	PHE	4.7
13	CM	121	LYS	4.7
26	BA	1026	U	4.7
2	AB	12	GLU	4.6
26	BA	2143	C	4.6
39	DS	3	ARG	4.6

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Mol	Chain	Res	Type	RSRZ
46	DZ	114	GLY	4.6
7	CG	83	ALA	4.6
2	CB	237	ALA	4.5
9	CI	11	LYS	4.5
7	AG	153	HIS	4.5
7	AG	85	TYR	4.5
14	CN	7	ILE	4.5
47	B0	7	LEU	4.4
26	DA	2112	G	4.4
1	CA	1114	C	4.4
1	CA	1115	C	4.4
13	AM	2	ALA	4.3
1	CA	1030(A)	G	4.3
23	AW	70	G	4.3
25	CY	18	G	4.3
46	BZ	144	LEU	4.3
31	BG	50	ALA	4.3
27	DB	23	G	4.3
3	CC	192	THR	4.3
31	DG	19	LEU	4.3
16	CP	82	GLN	4.2
31	DG	20	ILE	4.2
26	BA	2113	U	4.2
9	AI	106	ALA	4.2
1	CA	1034	G	4.2
8	CH	2	LEU	4.2
19	CS	52	TYR	4.2
14	CN	5	ALA	4.2
22	CV	13	A	4.2
1	CA	1220	G	4.2
3	CC	189	ALA	4.1
7	CG	12	LEU	4.1
26	BA	2161	C	4.1
1	CA	973	G	4.1
21	CU	14	TRP	4.1
10	CJ	63	PHE	4.1
31	DG	53	LEU	4.1
39	DS	32	LEU	4.1
10	AJ	76	ASN	4.1
1	CA	1002	G	4.1
13	AM	121	LYS	4.1
2	CB	187	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
14	CN	33	VAL	4.1
26	BA	2112	G	4.0
26	DA	2127	G	4.0
3	CC	129	ALA	4.0
40	BT	130	ALA	4.0
1	CA	1223	C	4.0
19	CS	35	SER	4.0
23	AW	72	C	4.0
1	CA	1033	G	4.0
46	BZ	113	ALA	4.0
10	AJ	4	ILE	4.0
46	BZ	109	ALA	4.0
10	CJ	47	PHE	4.0
7	CG	82	GLY	4.0
2	CB	152	PHE	4.0
1	AA	1002	G	3.9
46	DZ	113	ALA	3.9
3	CC	161	GLU	3.9
21	CU	6	ARG	3.9
2	AB	165	VAL	3.9
23	AW	73	A	3.9
54	B7	48	LYS	3.9
23	CW	3	C	3.9
10	CJ	32	ALA	3.9
1	CA	1040	U	3.9
8	AH	4	ASP	3.9
26	DA	1171	G	3.8
26	DA	2158	A	3.8
7	AG	83	ALA	3.8
25	AY	20	U	3.8
51	B4	50	VAL	3.8
1	CA	1117	G	3.8
19	CS	11	VAL	3.8
13	CM	60	VAL	3.8
23	AW	71	G	3.8
9	CI	2	GLU	3.8
55	B8	65	GLU	3.8
26	DA	2144	U	3.8
1	CA	1322	C	3.8
44	DX	92	LEU	3.8
13	AM	123	ALA	3.8
9	CI	101	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
2	CB	71	VAL	3.8
31	DG	142	PRO	3.8
7	AG	84	ASN	3.7
7	CG	37	ASN	3.7
26	BA	2162	G	3.7
26	DA	2156	G	3.7
26	BA	885	C	3.7
46	DZ	108	PRO	3.7
26	DA	2318	G	3.7
26	BA	34	C	3.7
26	BA	2108	C	3.7
10	AJ	100	THR	3.7
14	CN	10	ALA	3.7
26	DA	2155	G	3.7
13	CM	104	ARG	3.7
31	DG	28	VAL	3.7
46	DZ	111	VAL	3.7
10	CJ	40	LEU	3.6
7	AG	79	ARG	3.6
26	BA	2115	G	3.6
1	CA	980	C	3.6
26	BA	2146	C	3.6
7	AG	81	GLY	3.6
51	D4	66	SER	3.6
14	CN	6	LEU	3.6
8	AH	3	THR	3.6
19	CS	13	ASP	3.6
3	CC	155	GLY	3.6
20	CT	103	GLY	3.6
31	DG	146	TYR	3.6
1	AA	1030(A)	G	3.6
24	CX	70	G	3.6
14	CN	25	VAL	3.6
16	AP	82	GLN	3.6
4	AD	2	GLY	3.6
9	AI	126	SER	3.6
32	DH	45	VAL	3.6
46	DZ	144	LEU	3.6
1	CA	1354	C	3.6
26	BA	2794	C	3.6
1	AA	1036	G	3.6
1	CA	1001(A)	G	3.6

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Mol	Chain	Res	Type	RSRZ
3	CC	8	ILE	3.5
1	CA	1038	C	3.5
26	BA	1106	G	3.5
14	CN	30	ALA	3.5
14	CN	4	LYS	3.5
1	CA	1150	U	3.5
1	CA	1363(A)	A	3.5
14	CN	13	THR	3.5
1	CA	1321	C	3.5
10	AJ	77	PRO	3.5
26	DA	1536	C	3.5
26	DA	2145	C	3.5
51	D4	49	PHE	3.5
20	AT	9	ASN	3.5
9	CI	67	GLY	3.5
19	CS	82	GLY	3.5
31	DG	32	PRO	3.5
12	CL	32	PHE	3.5
39	DS	56	LEU	3.5
14	CN	21	TYR	3.5
26	DA	2146	C	3.5
15	AO	87	ILE	3.5
19	CS	49	ILE	3.5
13	CM	103	THR	3.5
46	BZ	107	THR	3.5
9	AI	15	ALA	3.5
14	CN	59	ALA	3.5
37	DQ	61	GLY	3.5
14	CN	16	PHE	3.5
7	AG	80	VAL	3.5
9	CI	66	ARG	3.5
1	CA	1397	C	3.4
27	DB	119	G	3.4
31	DG	147	ASP	3.4
1	CA	1001	A	3.4
19	CS	80	TYR	3.4
10	CJ	59	SER	3.4
1	AA	163	C	3.4
9	CI	123	PRO	3.4
46	DZ	172	ALA	3.4
23	CW	70	G	3.4
26	BA	2166	G	3.4

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Mol	Chain	Res	Type	RSRZ
46	DZ	171	ILE	3.4
2	CB	236	TYR	3.4
9	AI	113	LYS	3.4
9	CI	92	TYR	3.4
19	CS	79	THR	3.4
20	AT	101	GLY	3.4
47	B0	3	HIS	3.4
9	CI	17	VAL	3.4
14	CN	18	VAL	3.4
31	DG	102	PHE	3.4
39	DS	12	PHE	3.4
46	DZ	107	THR	3.4
2	CB	91	PRO	3.4
3	CC	12	LEU	3.4
9	CI	10	ARG	3.4
12	AL	19	ARG	3.4
13	CM	72	ALA	3.4
20	CT	97	ALA	3.4
40	BT	131	ALA	3.4
44	BX	95	LEU	3.4
19	CS	53	ASN	3.4
51	D4	65	ASP	3.4
46	BZ	116	VAL	3.4
10	AJ	74	ILE	3.3
28	BD	38	LYS	3.3
1	CA	1149	C	3.3
23	AW	2	C	3.3
24	AX	69	C	3.3
3	AC	15	THR	3.3
14	CN	22	THR	3.3
9	CI	96	LEU	3.3
31	BG	53	LEU	3.3
31	DG	2	PRO	3.3
1	AA	1531	A	3.3
3	CC	187	ALA	3.3
47	D0	6	GLY	3.3
22	CV	24	A	3.3
26	BA	896	A	3.3
26	DA	2119	A	3.3
1	AA	1001(A)	G	3.3
26	BA	2125	G	3.3
27	DB	118	G	3.3

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Mol	Chain	Res	Type	RSRZ
31	DG	4	ASP	3.3
3	CC	195	VAL	3.3
28	BD	275	LYS	3.3
9	CI	4	TYR	3.3
9	CI	110	GLU	3.3
31	DG	172	LEU	3.3
9	CI	86	VAL	3.3
22	AV	12	A	3.3
26	BA	1046	A	3.3
26	BA	2119	A	3.3
26	DA	896	A	3.3
2	CB	196	LEU	3.3
9	CI	36	TYR	3.3
10	AJ	64	GLU	3.3
12	CL	94	PRO	3.3
1	CA	961	U	3.3
31	BG	73	ALA	3.3
51	D4	50	VAL	3.3
1	CA	1286	A	3.3
25	AY	36	A	3.3
10	AJ	29	ARG	3.3
2	CB	234	PRO	3.3
9	AI	19	LEU	3.3
9	CI	99	LEU	3.3
2	AB	19	HIS	3.3
31	DG	74	LYS	3.3
46	DZ	115	GLY	3.3
12	AL	18	VAL	3.3
26	BA	2111	C	3.2
26	DA	2140	C	3.2
14	CN	29	ARG	3.2
49	B2	69	ARG	3.2
14	CN	14	PRO	3.2
26	BA	548	A	3.2
19	CS	38	SER	3.2
3	CC	194	GLY	3.2
9	CI	115	GLY	3.2
12	CL	56	ALA	3.2
31	BG	80	PHE	3.2
46	BZ	171	ILE	3.2
19	CS	15	LEU	3.2
10	AJ	81	THR	3.2

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Mol	Chain	Res	Type	RSRZ
13	CM	92	HIS	3.2
15	CO	75	PRO	3.2
32	DH	2	SER	3.2
47	B0	8	GLY	3.2
48	B1	2	SER	3.2
2	AB	237	ALA	3.2
13	CM	118	ALA	3.2
26	BA	2173	A	3.2
7	CG	84	ASN	3.2
20	CT	9	ASN	3.2
16	AP	68	ASP	3.2
1	CA	1202	G	3.2
26	BA	2141	G	3.2
9	CI	127	LYS	3.2
7	CG	16	LEU	3.2
45	BY	91	GLU	3.2
3	CC	6	HIS	3.2
47	D0	3	HIS	3.2
20	AT	18	GLN	3.2
8	AH	90	GLY	3.2
1	CA	1054	C	3.2
23	CW	2	C	3.2
31	DG	50	ALA	3.2
2	AB	214	ILE	3.2
39	DS	98	VAL	3.2
46	DZ	116	VAL	3.2
51	D4	10	VAL	3.2
27	DB	26	A	3.2
2	AB	126	GLU	3.2
3	CC	196	LEU	3.2
9	CI	19	LEU	3.2
18	AR	79	LEU	3.2
1	CA	951	G	3.2
11	CK	31	THR	3.2
25	AY	18	G	3.2
51	D4	24	THR	3.2
2	AB	29	ALA	3.2
9	AI	114	TYR	3.2
26	BA	888	C	3.1
3	CC	190	ARG	3.1
1	CA	975	A	3.1
14	CN	38	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
21	CU	2	GLY	3.1
26	BA	2144	U	3.1
27	DB	1	U	3.1
8	CH	29	SER	3.1
56	B9	17	ILE	3.1
14	AN	16	PHE	3.1
1	AA	1023	G	3.1
26	DA	2154	G	3.1
5	CE	10	MET	3.1
9	AI	75	ASP	3.1
1	CA	1030	C	3.1
12	CL	27	LEU	3.1
9	CI	124	GLN	3.1
46	DZ	118	GLN	3.1
13	CM	105	THR	3.1
39	DS	104	GLY	3.1
13	CM	64	TRP	3.1
2	AB	136	VAL	3.1
2	AB	163	PHE	3.1
19	CS	4	SER	3.1
31	DG	15	VAL	3.1
1	AA	1025	U	3.1
7	AG	5	ARG	3.1
10	AJ	79	ARG	3.1
27	DB	22	U	3.1
54	D7	48	LYS	3.1
2	CB	142	LEU	3.1
1	CA	1221	G	3.1
23	CW	72	C	3.1
26	BA	884	C	3.1
26	DA	2111	C	3.1
46	BZ	143	GLY	3.1
3	CC	77	ILE	3.1
26	DA	2173	A	3.1
7	CG	80	VAL	3.1
19	CS	10	PHE	3.1
9	CI	79	LEU	3.1
39	DS	54	LEU	3.1
9	CI	91	ASP	3.1
3	CC	191	THR	3.1
10	AJ	31	GLY	3.1
26	BA	1176	G	3.1

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Mol	Chain	Res	Type	RSRZ
26	DA	1533	G	3.1
26	DA	2131	G	3.1
44	DX	94	GLY	3.1
51	D4	54	GLY	3.1
9	CI	76	ALA	3.1
14	CN	15	LYS	3.1
15	CO	3	ILE	3.1
47	D0	5	LYS	3.1
32	BH	3	ARG	3.1
1	CA	979	C	3.1
46	BZ	104	PHE	3.1
1	CA	1030(D)	A	3.0
8	CH	94	TYR	3.0
20	CT	24	LEU	3.0
19	AS	85	LYS	3.0
2	AB	127	ILE	3.0
3	CC	124	ILE	3.0
5	CE	109	ILE	3.0
13	CM	78	ILE	3.0
4	AD	195	ALA	3.0
2	CB	7	VAL	3.0
3	CC	55	VAL	3.0
9	CI	44	VAL	3.0
39	DS	29	PHE	3.0
51	D4	56	VAL	3.0
8	CH	135	CYS	3.0
1	CA	1003	G	3.0
26	DA	2319	G	3.0
4	AD	194	LEU	3.0
7	AG	12	LEU	3.0
10	CJ	88	LEU	3.0
1	CA	962	C	3.0
3	CC	193	TYR	3.0
26	BA	897	C	3.0
51	D4	32	TYR	3.0
1	CA	978	A	3.0
1	CA	1049	U	3.0
1	CA	1532	U	3.0
26	DA	1026	U	3.0
10	AJ	75	ILE	3.0
10	CJ	87	THR	3.0
13	CM	100	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
32	BH	166	GLY	3.0
45	BY	1	MET	3.0
46	BZ	111	VAL	3.0
2	CB	97	TRP	3.0
31	DG	3	LEU	3.0
3	CC	48	TYR	3.0
31	DG	12	TYR	3.0
46	BZ	108	PRO	3.0
25	AY	15	G	3.0
25	CY	19	G	3.0
26	BA	2142	C	3.0
21	CU	4	GLY	3.0
31	BG	88	ILE	3.0
5	AE	134	ALA	3.0
10	AJ	27	ALA	3.0
26	BA	12	U	3.0
2	CB	93	VAL	3.0
10	CJ	54	PHE	3.0
4	AD	21	LEU	3.0
46	DZ	166	SER	3.0
7	AG	151	TYR	3.0
12	CL	69	TYR	3.0
31	BG	51	ARG	3.0
1	CA	1036	G	3.0
3	CC	160	ALA	3.0
25	AY	19	G	3.0
26	BA	614(B)	G	3.0
26	DA	883	G	3.0
26	DA	2110	G	3.0
26	DA	2159	G	3.0
31	DG	73	ALA	3.0
26	BA	2135	A	3.0
26	BA	2167	U	2.9
15	AO	19	PRO	2.9
51	D4	7	PRO	2.9
10	AJ	78	ASN	2.9
2	AB	130	ARG	2.9
10	AJ	26	ALA	2.9
12	CL	18	VAL	2.9
48	B1	98	LEU	2.9
2	AB	97	TRP	2.9
26	BA	1045	A	2.9

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Mol	Chain	Res	Type	RSRZ
26	BA	2114	A	2.9
1	CA	950	U	2.9
9	CI	125	TYR	2.9
14	CN	34	TYR	2.9
3	CC	134	ILE	2.9
3	CC	157	ILE	2.9
3	CC	145	GLY	2.9
3	CC	158	GLY	2.9
9	CI	7	THR	2.9
13	CM	5	ALA	2.9
2	AB	7	VAL	2.9
1	AA	1503	A	2.9
26	BA	2138	C	2.9
1	CA	1216	G	2.9
10	CJ	76	ASN	2.9
25	CY	57	G	2.9
26	DA	2132	U	2.9
2	CB	200	ILE	2.9
7	AG	154	TYR	2.9
13	CM	21	TYR	2.9
31	BG	49	ASP	2.9
51	D4	25	TYR	2.9
39	DS	60	GLY	2.9
7	CG	7	ALA	2.9
13	CM	18	ALA	2.9
20	AT	94	ALA	2.9
2	AB	15	VAL	2.9
2	CB	70	PHE	2.9
3	CC	207	VAL	2.9
14	CN	44	LEU	2.9
17	AQ	27	PHE	2.9
39	DS	33	LYS	2.9
21	CU	24	ARG	2.9
20	AT	75	ASN	2.9
1	AA	1286	A	2.9
9	CI	100	GLY	2.9
23	CW	31	A	2.9
26	BA	2150	U	2.9
26	DA	2128	C	2.9
9	CI	27	THR	2.9
1	CA	1048	G	2.9
1	CA	1190	G	2.9

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Mol	Chain	Res	Type	RSRZ
1	CA	1222	G	2.9
2	CB	207	ALA	2.9
9	AI	56	LEU	2.9
25	CY	1	G	2.9
39	DS	34	HIS	2.9
5	AE	10	MET	2.8
7	CG	4	ARG	2.8
32	BH	56	SER	2.8
46	DZ	149	SER	2.8
7	CG	33	ASP	2.8
9	CI	69	GLY	2.8
31	BG	182	LYS	2.8
3	CC	42	LEU	2.8
4	AD	176	LEU	2.8
4	CD	188	LEU	2.8
14	AN	59	ALA	2.8
19	CS	16	LEU	2.8
19	CS	75	ALA	2.8
32	DH	102	ALA	2.8
39	DS	80	LEU	2.8
46	DZ	170	THR	2.8
2	CB	81	VAL	2.8
19	CS	41	VAL	2.8
1	CA	959	A	2.8
22	CV	22	U	2.8
1	CA	1019	C	2.8
1	CA	1039	C	2.8
32	BH	58	GLU	2.8
26	BA	2160	G	2.8
31	DG	129	GLY	2.8
51	B4	54	GLY	2.8
9	CI	5	TYR	2.8
13	AM	87	TYR	2.8
46	BZ	117	LEU	2.8
4	AD	170	VAL	2.8
51	B4	56	VAL	2.8
9	AI	10	ARG	2.8
1	CA	1251	A	2.8
10	AJ	33	GLN	2.8
1	CA	985	C	2.8
25	CY	4	C	2.8
3	CC	202	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
7	AG	156	TRP	2.8
51	D4	31	ILE	2.8
1	AA	1024	G	2.8
26	BA	2151	G	2.8
2	CB	154	LEU	2.8
20	AT	69	GLY	2.8
4	AD	102	ASP	2.8
17	CQ	7	THR	2.8
3	CC	184	TYR	2.8
5	CE	41	VAL	2.8
10	CJ	86	MET	2.8
51	B4	49	PHE	2.8
51	B4	60	GLN	2.8
1	CA	1041	A	2.8
2	CB	211	ILE	2.8
12	AL	7	ILE	2.8
26	BA	2170	A	2.8
1	CA	1066	C	2.8
12	CL	62	SER	2.8
31	DG	76	SER	2.8
21	CU	16	GLY	2.8
2	CB	164	VAL	2.8
13	CM	117	VAL	2.8
21	CU	17	THR	2.8
31	DG	160	VAL	2.8
1	CA	993	G	2.8
10	AJ	60	ARG	2.8
23	CW	15	G	2.8
26	BA	2168	G	2.8
39	DS	36	TYR	2.8
8	AH	89	PRO	2.7
20	CT	98	PRO	2.7
14	CN	50	LYS	2.7
14	CN	42	ILE	2.7
13	CM	66	LEU	2.7
47	D0	7	LEU	2.7
1	AA	532	A	2.7
1	CA	974	A	2.7
1	CA	977	A	2.7
1	CA	994	A	2.7
2	AB	18	GLY	2.7
26	BA	2169	A	2.7

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Mol	Chain	Res	Type	RSRZ
26	DA	1445	A	2.7
27	DB	120	A	2.7
43	BW	112	GLY	2.7
1	CA	1362	C	2.7
7	AG	2	ALA	2.7
3	CC	79	ARG	2.7
8	CH	102	ARG	2.7
9	AI	108	VAL	2.7
9	CI	108	VAL	2.7
20	CT	94	ALA	2.7
13	CM	94	ARG	2.7
21	AU	24	ARG	2.7
26	BA	886	C	2.7
31	DG	5	VAL	2.7
2	AB	33	TYR	2.7
4	AD	138	TYR	2.7
8	CH	101	PRO	2.7
15	AO	69	TYR	2.7
1	CA	1017	G	2.7
26	BA	2133	G	2.7
3	AC	39	ILE	2.7
20	AT	55	ILE	2.7
8	AH	112	LEU	2.7
14	CN	53	LEU	2.7
19	CS	71	LEU	2.7
3	CC	167	TRP	2.7
4	CD	87	GLY	2.7
13	CM	112	GLY	2.7
31	DG	24	GLY	2.7
46	DZ	1	MET	2.7
1	CA	992	U	2.7
3	CC	168	ALA	2.7
7	CG	2	ALA	2.7
9	CI	104	ARG	2.7
3	CC	10	PHE	2.7
9	CI	18	PHE	2.7
10	CJ	34	VAL	2.7
11	AK	14	VAL	2.7
31	DG	145	THR	2.7
36	DP	15	ARG	2.7
1	CA	1363	C	2.7
26	BA	1509	C	2.7

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Mol	Chain	Res	Type	RSRZ
26	DA	2789	C	2.7
2	CB	201	ILE	2.7
14	CN	47	LEU	2.7
36	BP	105	LEU	2.7
1	CA	631	G	2.7
1	CA	1030(C)	G	2.7
1	CA	1233	G	2.7
23	CW	71	G	2.7
24	AX	70	G	2.7
26	DA	2133	G	2.7
39	DS	95	HIS	2.7
7	AG	90	GLU	2.7
9	CI	128	ARG	2.7
31	BG	48	GLU	2.7
36	BP	79	ARG	2.7
9	CI	13	ALA	2.7
9	CI	109	VAL	2.7
39	DS	5	THR	2.7
47	D0	2	ALA	2.7
46	BZ	154	ASP	2.7
1	CA	1020	U	2.7
19	CS	2	PRO	2.7
19	CS	70	LYS	2.7
23	CW	66	U	2.7
33	DI	112	LYS	2.7
46	BZ	118	GLN	2.7
22	AV	14	A	2.7
26	DA	2310	A	2.7
14	AN	7	ILE	2.7
23	AW	13	C	2.7
26	DA	2174	C	2.7
27	DB	5	C	2.7
27	DB	6	C	2.7
27	DB	27	C	2.7
2	AB	215	LEU	2.7
2	AB	221	LEU	2.7
2	CB	69	LEU	2.7
33	BI	38	LEU	2.7
21	CU	11	GLY	2.7
2	AB	231	GLU	2.7
9	AI	2	GLU	2.7
20	CT	26	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
31	BG	137	GLU	2.7
31	DG	29	TRP	2.7
3	CC	149	ALA	2.7
8	AH	88	LYS	2.7
9	CI	28	VAL	2.7
12	CL	51	ALA	2.7
14	CN	17	LYS	2.7
30	DF	6	VAL	2.7
31	DG	151	ALA	2.7
32	DH	49	VAL	2.7
16	AP	69	THR	2.7
31	DG	71	THR	2.7
37	DQ	104	PHE	2.7
10	CJ	41	PRO	2.7
31	DG	17	PRO	2.7
31	DG	87	PRO	2.7
1	AA	346	G	2.6
1	AA	1026	G	2.6
26	BA	2121	G	2.6
26	DA	2166	G	2.6
2	CB	92	TYR	2.6
23	CW	47	U	2.6
51	D4	67	TYR	2.6
3	CC	5	ILE	2.6
2	AB	48	MET	2.6
3	CC	52	LEU	2.6
13	CM	90	LEU	2.6
14	CN	39	LEU	2.6
26	BA	2117	A	2.6
26	DA	652(B)	A	2.6
31	DG	34	LEU	2.6
39	DS	58	LEU	2.6
4	CD	49	ARG	2.6
10	CJ	60	ARG	2.6
20	AT	86	ARG	2.6
19	CS	26	GLY	2.6
32	BH	14	GLY	2.6
1	CA	1028	C	2.6
1	CA	1325	C	2.6
14	CN	9	LYS	2.6
2	CB	131	PRO	2.6
19	CS	74	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
37	DQ	58	PHE	2.6
3	CC	123	GLN	2.6
46	DZ	120	ILE	2.6
1	CA	976	G	2.6
26	DA	2153	G	2.6
3	AC	52	LEU	2.6
3	CC	94	LEU	2.6
10	AJ	88	LEU	2.6
9	CI	107	ARG	2.6
13	AM	24	GLY	2.6
21	CU	3	LYS	2.6
28	BD	28	GLU	2.6
28	DD	276	LYS	2.6
56	D9	37	GLY	2.6
1	CA	532	A	2.6
1	CA	1004	A	2.6
1	CA	1213	A	2.6
1	CA	1357	A	2.6
1	CA	1531	A	2.6
40	DT	131	ALA	2.6
46	DZ	141	VAL	2.6
13	CM	41	PRO	2.6
8	CH	70	GLN	2.6
1	CA	984	C	2.6
1	CA	1118	C	2.6
45	DY	107	ASP	2.6
2	CB	83	MET	2.6
13	CM	4	ILE	2.6
19	CS	40	ILE	2.6
20	AT	100	ILE	2.6
46	BZ	146	ILE	2.6
51	D4	5	ILE	2.6
2	CB	11	LEU	2.6
2	CB	31	TYR	2.6
9	AI	102	LEU	2.6
31	DG	11	TYR	2.6
19	CS	14	HIS	2.6
8	CH	90	GLY	2.6
8	CH	128	GLY	2.6
19	CS	8	GLY	2.6
20	CT	96	GLY	2.6
3	CC	86	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
9	CI	94	ALA	2.6
13	CM	97	PRO	2.6
19	CS	67	VAL	2.6
46	BZ	141	VAL	2.6
7	AG	86	GLN	2.6
11	CK	24	SER	2.6
46	BZ	149	SER	2.6
1	CA	965	A	2.6
24	AX	72	A	2.6
26	DA	2126	A	2.6
31	DG	156	ASP	2.6
2	AB	201	ILE	2.6
16	CP	33	ILE	2.6
18	CR	65	ILE	2.6
1	AA	1030	C	2.6
26	BA	2140	C	2.6
8	AH	91	ARG	2.6
8	AH	92	ARG	2.6
8	AH	94	TYR	2.6
12	CL	64	TYR	2.6
32	BH	59	ARG	2.6
9	AI	69	GLY	2.6
19	CS	72	GLY	2.6
45	DY	58	GLY	2.6
46	BZ	114	GLY	2.6
1	CA	1196	U	2.6
11	CK	89	ALA	2.6
12	CL	43	VAL	2.6
13	CM	7	VAL	2.6
13	CM	33	ALA	2.6
33	DI	92	VAL	2.6
14	CN	61	TRP	2.5
46	BZ	166	SER	2.5
1	CA	1353	G	2.5
23	CW	34	G	2.5
26	BA	2131	G	2.5
26	BA	2152	G	2.5
26	DA	2149	G	2.5
27	DB	24	G	2.5
35	BO	81	ASP	2.5
31	DG	77	ILE	2.5
39	DS	35	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	CA	1005	A	2.5
3	CC	188	LEU	2.5
26	DA	2135	A	2.5
31	DG	175	LEU	2.5
9	CI	113	LYS	2.5
21	CU	15	ARG	2.5
10	CJ	56	HIS	2.5
5	CE	8	GLU	2.5
51	D4	57	GLU	2.5
25	AY	56	C	2.5
10	CJ	72	VAL	2.5
32	DH	8	PRO	2.5
50	D3	2	PRO	2.5
54	D7	46	VAL	2.5
2	CB	122	PHE	2.5
3	CC	53	ALA	2.5
3	CC	71	ALA	2.5
11	CK	119	CYS	2.5
20	AT	95	ALA	2.5
28	DD	2	ALA	2.5
33	BI	146	ALA	2.5
46	DZ	173	ALA	2.5
10	CJ	78	ASN	2.5
47	D0	43	THR	2.5
51	B4	52	THR	2.5
17	CQ	99	SER	2.5
23	AW	20	U	2.5
45	DY	1	MET	2.5
2	CB	10	LEU	2.5
3	CC	91	LEU	2.5
4	CD	21	LEU	2.5
14	CN	12	ARG	2.5
14	CN	57	ARG	2.5
39	DS	4	LEU	2.5
19	CS	47	HIS	2.5
1	CA	630	G	2.5
1	CA	1207	G	2.5
23	CW	18	G	2.5
25	CY	15	G	2.5
25	CY	34	G	2.5
1	AA	162	A	2.5
1	AA	1035	A	2.5

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Mol	Chain	Res	Type	RSRZ
1	CA	1188	A	2.5
5	AE	122	GLU	2.5
25	CY	35	A	2.5
26	BA	2158	A	2.5
10	CJ	52	GLY	2.5
13	CM	95	GLY	2.5
37	BQ	61	GLY	2.5
42	DV	63	GLY	2.5
46	BZ	106	GLY	2.5
21	CU	23	PRO	2.5
32	DH	112	PRO	2.5
3	CC	75	VAL	2.5
3	CC	138	VAL	2.5
9	CI	65	VAL	2.5
31	DG	149	VAL	2.5
32	DH	17	VAL	2.5
33	BI	37	VAL	2.5
42	DV	22	VAL	2.5
46	DZ	139	VAL	2.5
51	D4	35	VAL	2.5
3	CC	163	ALA	2.5
33	DI	146	ALA	2.5
46	BZ	164	ALA	2.5
49	B2	70	GLN	2.5
1	CA	972	C	2.5
1	CA	1214	C	2.5
26	BA	2136	C	2.5
18	CR	47	THR	2.5
19	CS	33	THR	2.5
19	CS	48	THR	2.5
19	CS	77	THR	2.5
51	D4	44	THR	2.5
9	CI	71	SER	2.5
14	CN	60	SER	2.5
2	AB	200	ILE	2.5
2	CB	214	ILE	2.5
3	CC	45	LYS	2.5
1	CA	982	U	2.5
4	AD	188	LEU	2.5
7	AG	78	ARG	2.5
9	CI	85	LEU	2.5
10	CJ	46	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
12	CL	41	ARG	2.5
31	BG	152	LEU	2.5
31	DG	97	ASP	2.5
33	DI	138	ILE	2.5
12	CL	84	LEU	2.5
26	BA	2132	U	2.5
37	DQ	60	ARG	2.5
46	BZ	150	LEU	2.5
3	AC	201	TYR	2.5
31	BG	25	TYR	2.5
8	CH	131	GLY	2.5
12	CL	29	GLY	2.5
1	AA	1224	G	2.5
1	CA	953	G	2.5
1	CA	1092	A	2.5
1	CA	1186	G	2.5
23	CW	14	A	2.5
26	BA	229	A	2.5
26	BA	2165	G	2.5
26	BA	2805	G	2.5
3	AC	10	PHE	2.5
9	AI	59	PHE	2.5
11	CK	13	GLN	2.5
32	DH	44	VAL	2.5
16	AP	80	PHE	2.5
36	DP	89	ALA	2.5
2	CB	67	THR	2.5
10	AJ	87	THR	2.5
20	CT	74	LYS	2.5
2	CB	185	ILE	2.5
9	CI	42	ARG	2.5
39	DS	97	ARG	2.5
1	AA	1008	C	2.5
1	CA	1119	C	2.5
26	BA	2163	C	2.5
1	CA	981	U	2.5
1	CA	1205	U	2.5
10	AJ	83	GLU	2.5
2	CB	66	GLY	2.5
4	CD	44	GLY	2.5
9	AI	8	GLY	2.5
16	AP	38	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
28	BD	114	GLY	2.5
39	DS	45	GLY	2.5
51	B4	63	TYR	2.5
4	AD	105	VAL	2.5
31	DG	31	VAL	2.5
34	BN	140	VAL	2.5
2	AB	17	PHE	2.5
5	AE	138	ALA	2.5
2	AB	22	LYS	2.4
20	CT	30	LYS	2.4
47	D0	4	LYS	2.4
13	AM	49	THR	2.4
1	AA	1005	A	2.4
1	CA	949	A	2.4
13	CM	106	ASN	2.4
16	AP	42	ARG	2.4
13	CM	34	LEU	2.4
44	DX	95	LEU	2.4
1	CA	988	G	2.4
26	DA	2160	G	2.4
27	DB	61	G	2.4
9	AI	117	HIS	2.4
19	CS	83	HIS	2.4
4	CD	34	GLU	2.4
31	BG	35	GLU	2.4
1	CA	1112	C	2.4
24	AX	71	C	2.4
26	DA	2297	C	2.4
27	BB	88	C	2.4
27	DB	88	C	2.4
4	CD	51	PRO	2.4
30	DF	131	GLY	2.4
32	DH	36	PRO	2.4
9	CI	62	TYR	2.4
11	CK	50	TYR	2.4
45	DY	55	TYR	2.4
34	DN	9	VAL	2.4
9	CI	15	ALA	2.4
32	DH	96	ALA	2.4
51	D4	42	PHE	2.4
5	AE	135	THR	2.4
9	CI	64	THR	2.4

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Mol	Chain	Res	Type	RSRZ
20	AT	8	ARG	2.4
31	BG	83	ARG	2.4
52	D5	29	THR	2.4
2	AB	213	LEU	2.4
6	CF	61	LEU	2.4
9	CI	40	LEU	2.4
12	CL	52	LEU	2.4
13	CM	19	LEU	2.4
16	AP	19	ILE	2.4
20	AT	24	LEU	2.4
20	CT	99	LEU	2.4
10	AJ	35	SER	2.4
1	AA	1001	A	2.4
1	AA	1447	A	2.4
1	CA	1035	A	2.4
19	CS	12	ASP	2.4
22	CV	23	A	2.4
25	CY	36	A	2.4
2	CB	126	GLU	2.4
33	DI	85	GLU	2.4
1	AA	625	G	2.4
1	CA	1022	G	2.4
1	CA	1053	G	2.4
1	CA	1187	G	2.4
25	AY	34	G	2.4
26	BA	2159	G	2.4
26	DA	2125	G	2.4
4	CD	165	MET	2.4
10	AJ	86	MET	2.4
3	CC	9	GLY	2.4
13	CM	119	GLY	2.4
51	B4	64	GLY	2.4
9	AI	127	LYS	2.4
12	CL	28	LYS	2.4
4	AD	140	VAL	2.4
5	CE	100	VAL	2.4
18	CR	86	VAL	2.4
26	BA	2178	C	2.4
26	DA	645	C	2.4
26	DA	2138	C	2.4
36	BP	70	GLN	2.4
46	DZ	174	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
2	CB	123	ALA	2.4
4	AD	48	ALA	2.4
4	CD	195	ALA	2.4
8	CH	31	PHE	2.4
7	AG	4	ARG	2.4
10	AJ	43	ARG	2.4
15	CO	79	ARG	2.4
19	AS	81	ARG	2.4
19	CS	29	ARG	2.4
3	AC	204	LEU	2.4
31	BG	133	LEU	2.4
31	DG	140	ILE	2.4
39	DS	61	ASN	2.4
3	CC	20	SER	2.4
39	DS	52	SER	2.4
5	AE	81	GLU	2.4
33	DI	10	GLU	2.4
4	AD	33	MET	2.4
1	AA	607	A	2.4
1	CA	983	A	2.4
1	CA	1016	A	2.4
16	AP	35	LYS	2.4
19	CS	18	LYS	2.4
22	AV	13	A	2.4
27	DB	25	A	2.4
3	AC	155	GLY	2.4
3	CC	2	GLY	2.4
5	CE	22	GLY	2.4
42	DV	9	GLY	2.4
6	CF	16	GLN	2.4
13	CM	101	GLN	2.4
2	AB	230	VAL	2.4
2	CB	112	VAL	2.4
3	CC	198	VAL	2.4
19	CS	19	VAL	2.4
32	DH	52	VAL	2.4
1	CA	1323	G	2.4
7	AG	155	ARG	2.4
7	CG	39	ALA	2.4
9	AI	66	ARG	2.4
11	AK	25	TYR	2.4
31	DG	171	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
39	DS	7	TYR	2.4
44	DX	68	ARG	2.4
46	DZ	164	ALA	2.4
1	AA	1030(B)	C	2.4
1	CA	952	U	2.4
2	CB	208	ILE	2.4
3	AC	182	ILE	2.4
10	AJ	8	LEU	2.4
10	CJ	90	LEU	2.4
10	CJ	48	THR	2.4
10	CJ	50	ILE	2.4
1	CA	995	C	2.4
26	DA	2139	C	2.4
4	CD	161	ASN	2.4
31	BG	76	SER	2.4
21	CU	5	ASP	2.4
4	CD	33	MET	2.4
7	CG	156	TRP	2.4
8	CH	116	LYS	2.4
28	DD	275	LYS	2.4
37	DQ	18	LYS	2.4
30	BF	14	PRO	2.4
46	DZ	167	PRO	2.4
51	D4	29	PRO	2.4
9	CI	80	GLY	2.4
12	CL	14	GLY	2.4
8	AH	93	VAL	2.4
12	AL	89	ARG	2.4
14	CN	19	ARG	2.4
19	CS	37	ARG	2.4
39	DS	28	VAL	2.4
1	AA	134	A	2.4
1	CA	996	A	2.4
7	CG	26	PHE	2.4
26	BA	278	A	2.4
9	CI	61	ALA	2.4
12	CL	68	ALA	2.4
13	CM	75	ALA	2.4
16	AP	7	ALA	2.4
51	B4	59	PHE	2.4
5	AE	119	LEU	2.3
7	CG	151	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
9	CI	114	TYR	2.3
12	CL	10	LEU	2.3
32	DH	64	LEU	2.3
44	DX	69	TYR	2.3
4	AD	5	ILE	2.3
21	CU	13	ILE	2.3
21	CU	8	THR	2.3
1	CA	971	G	2.3
1	CA	1310	G	2.3
1	CA	1368	G	2.3
23	AW	15	G	2.3
24	AX	4	G	2.3
2	AB	134	GLU	2.3
45	DY	29	GLU	2.3
8	CH	9	MET	2.3
1	AA	984	C	2.3
1	CA	948	C	2.3
1	CA	1027	C	2.3
1	CA	1218	C	2.3
9	AI	105	ASP	2.3
10	CJ	55	LYS	2.3
12	AL	20	LYS	2.3
26	BA	2164	C	2.3
9	CI	49	PRO	2.3
14	CN	40	CYS	2.3
31	BG	87	PRO	2.3
2	AB	45	GLN	2.3
9	CI	6	GLY	2.3
12	CL	63	GLY	2.3
7	AG	3	ARG	2.3
13	CM	29	ARG	2.3
12	CL	39	VAL	2.3
13	CM	15	VAL	2.3
31	BG	31	VAL	2.3
2	AB	11	LEU	2.3
2	CB	138	LEU	2.3
14	CN	20	ALA	2.3
29	DE	204	ALA	2.3
47	D0	84	LEU	2.3
19	CS	31	ILE	2.3
2	CB	148	TYR	2.3
3	AC	184	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
3	CC	69	HIS	2.3
25	CY	73	A	2.3
26	DA	2320	A	2.3
6	CF	89	MET	2.3
12	AL	126	LYS	2.3
14	CN	46	GLU	2.3
20	AT	74	LYS	2.3
32	DH	40	GLU	2.3
47	B0	5	LYS	2.3
51	D4	2	LYS	2.3
11	AK	36	ASP	2.3
1	CA	1338	G	2.3
12	CL	31	PRO	2.3
25	CY	22	G	2.3
51	D4	41	PRO	2.3
1	CA	1113	C	2.3
3	CC	78	GLY	2.3
10	CJ	93	GLY	2.3
16	CP	25	ARG	2.3
23	AW	4	C	2.3
24	AX	67	C	2.3
28	DD	217	ARG	2.3
32	BH	66	GLY	2.3
32	DH	166	GLY	2.3
45	DY	57	GLN	2.3
46	DZ	147	GLY	2.3
54	B7	23	ARG	2.3
55	B8	46	ARG	2.3
3	CC	76	VAL	2.3
5	CE	33	VAL	2.3
17	CQ	9	VAL	2.3
2	AB	120	ALA	2.3
3	CC	47	LEU	2.3
3	CC	178	LEU	2.3
8	CH	110	ALA	2.3
18	AR	78	LEU	2.3
2	CB	162	ILE	2.3
3	AC	14	ILE	2.3
9	CI	81	ILE	2.3
10	AJ	6	ILE	2.3
31	DG	39	ILE	2.3
31	DG	52	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
7	CG	154	TYR	2.3
12	CL	44	THR	2.3
19	CS	66	MET	2.3
29	BE	1	MET	2.3
1	CA	1225	A	2.3
1	CA	1324	A	2.3
22	AV	24	A	2.3
22	CV	15	A	2.3
25	CY	21	A	2.3
26	BA	899	A	2.3
26	DA	2134	A	2.3
26	DA	2602	A	2.3
12	CL	50	SER	2.3
32	BH	60	ARG	2.3
46	DZ	95	PRO	2.3
4	CD	2	GLY	2.3
46	BZ	110	GLY	2.3
1	AA	173	U	2.3
1	CA	1358	U	2.3
26	BA	271(K)	U	2.3
26	BA	1175	U	2.3
10	CJ	49	VAL	2.3
14	CN	27	CYS	2.3
19	CS	58	VAL	2.3
32	DH	37	VAL	2.3
10	CJ	65	LEU	2.3
19	AS	71	LEU	2.3
31	DG	23	PHE	2.3
40	DT	6	LEU	2.3
1	AA	219	C	2.3
1	AA	1368	G	2.3
1	CA	963	G	2.3
1	CA	1021	G	2.3
1	CA	1032	G	2.3
2	CB	80	ILE	2.3
3	CC	84	ILE	2.3
3	CC	152	ILE	2.3
5	AE	129	ILE	2.3
5	CE	21	ALA	2.3
8	AH	86	ILE	2.3
8	CH	111	ILE	2.3
9	CI	122	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
54	B7	45	ALA	2.3
23	CW	19	G	2.3
25	CY	2	C	2.3
26	BA	530	G	2.3
26	BA	880	G	2.3
26	BA	1047	G	2.3
26	BA	2156	G	2.3
26	BA	2174	C	2.3
26	DA	2147	G	2.3
26	DA	2157	G	2.3
26	DA	2168	G	2.3
5	AE	88	LYS	2.3
20	AT	14	LYS	2.3
33	DI	108	THR	2.3
4	CD	73	ARG	2.3
12	CL	92	ASP	2.3
32	BH	57	ASP	2.3
38	DR	68	ARG	2.3
42	DV	73	SER	2.3
46	BZ	112	ARG	2.3
10	AJ	84	GLN	2.3
33	DI	54	GLN	2.3
12	AL	29	GLY	2.3
19	CS	68	GLY	2.3
31	BG	42	GLY	2.3
2	CB	121	LEU	2.3
2	CB	215	LEU	2.3
3	CC	33	LEU	2.3
3	CC	141	VAL	2.3
4	AD	155	LEU	2.3
4	CD	78	LEU	2.3
5	CE	142	LEU	2.3
9	AI	41	VAL	2.3
9	CI	56	LEU	2.3
19	CS	60	VAL	2.3
32	DH	79	VAL	2.3
39	DS	14	VAL	2.3
45	BY	45	VAL	2.3
2	CB	163	PHE	2.3
3	CC	186	PHE	2.3
1	CA	1000	U	2.2
3	CC	65	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
9	AI	13	ALA	2.2
9	CI	52	ALA	2.2
13	CM	30	ALA	2.2
26	DA	895	U	2.2
51	D4	40	HIS	2.2
3	CC	135	LYS	2.2
11	CK	124	LYS	2.2
45	DY	34	LYS	2.2
9	AI	64	THR	2.2
51	D4	52	THR	2.2
3	CC	46	GLU	2.2
10	CJ	64	GLU	2.2
13	CM	67	GLU	2.2
13	CM	73	GLU	2.2
33	DI	99	GLU	2.2
1	AA	174	C	2.2
1	AA	1354	C	2.2
1	CA	1029	C	2.2
1	CA	1320	C	2.2
23	CW	25	C	2.2
23	CW	56	C	2.2
1	CA	998	G	2.2
1	CA	1031	G	2.2
1	CA	1373	G	2.2
2	AB	37	ASN	2.2
23	AW	44	G	2.2
23	CW	44	G	2.2
26	BA	271(M)	G	2.2
26	DA	11	G	2.2
26	DA	2116	G	2.2
8	CH	92	ARG	2.2
9	AI	121	ARG	2.2
31	DG	21	ARG	2.2
40	BT	125	ARG	2.2
45	BY	2	ARG	2.2
33	DI	132	PRO	2.2
11	CK	42	TRP	2.2
2	CB	136	VAL	2.2
3	CC	151	VAL	2.2
7	CG	21	VAL	2.2
8	AH	133	LEU	2.2
11	CK	14	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
46	DZ	105	VAL	2.2
48	D1	62	VAL	2.2
54	B7	46	VAL	2.2
2	AB	34	ALA	2.2
2	AB	172	ILE	2.2
3	AC	135	LYS	2.2
9	CI	37	PHE	2.2
9	CI	45	ALA	2.2
9	CI	63	ILE	2.2
13	CM	120	LYS	2.2
17	AQ	36	ILE	2.2
18	CR	20	ALA	2.2
23	AW	14	A	2.2
26	BA	2126	A	2.2
47	B0	4	LYS	2.2
13	CM	50	GLU	2.2
46	BZ	169	GLU	2.2
11	CK	25	TYR	2.2
12	CL	120	TYR	2.2
13	CM	23	TYR	2.2
3	CC	164	ARG	2.2
4	CD	47	ARG	2.2
55	D8	46	ARG	2.2
32	DH	55	PRO	2.2
1	AA	754	C	2.2
25	CY	48	C	2.2
26	BA	2803	C	2.2
9	AI	30	GLY	2.2
10	AJ	59	SER	2.2
1	CA	1184	G	2.2
20	AT	102	GLY	2.2
17	CQ	76	LEU	2.2
19	CS	22	LEU	2.2
20	AT	62	LEU	2.2
23	CW	5	G	2.2
26	BA	2833	G	2.2
48	B1	84	GLY	2.2
3	CC	204	LEU	2.2
30	DF	12	LEU	2.2
46	DZ	102	LEU	2.2
2	CB	132	LYS	2.2
3	CC	173	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
8	CH	103	VAL	2.2
9	AI	112	LYS	2.2
12	CL	13	LYS	2.2
12	CL	24	VAL	2.2
16	CP	48	TRP	2.2
45	BY	34	LYS	2.2
45	DY	45	VAL	2.2
2	CB	48	MET	2.2
16	AP	33	ILE	2.2
32	DH	61	HIS	2.2
7	AG	7	ALA	2.2
10	AJ	32	ALA	2.2
11	AK	23	ALA	2.2
33	DI	115	ALA	2.2
46	BZ	152	ALA	2.2
9	AI	12	GLU	2.2
10	AJ	25	GLU	2.2
12	CL	65	GLU	2.2
22	CV	14	A	2.2
7	CG	32	ARG	2.2
24	AX	47	U	2.2
47	B0	74	ARG	2.2
3	AC	23	TYR	2.2
19	CS	59	PRO	2.2
3	AC	188	LEU	2.2
4	AD	11	LEU	2.2
6	CF	21	LEU	2.2
8	AH	131	GLY	2.2
9	AI	47	LEU	2.2
11	AK	81	ASP	2.2
33	BI	12	LEU	2.2
36	BP	99	LEU	2.2
37	DQ	37	LEU	2.2
32	DH	43	VAL	2.2
1	AA	217	C	2.2
1	AA	1027	C	2.2
3	AC	84	ILE	2.2
5	AE	6	PHE	2.2
10	CJ	75	ILE	2.2
14	CN	49	HIS	2.2
24	CX	71	C	2.2
25	CY	72	C	2.2

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Mol	Chain	Res	Type	RSRZ
27	DB	65	C	2.2
51	D4	22	ILE	2.2
2	AB	186	ALA	2.2
39	DS	105	ALA	2.2
46	DZ	152	ALA	2.2
1	AA	1034	G	2.2
1	CA	987	G	2.2
8	CH	99	GLU	2.2
23	CW	10	G	2.2
26	DA	2162	G	2.2
31	DG	18	GLU	2.2
31	DG	35	GLU	2.2
54	B7	47	ARG	2.2
1	CA	1183	A	2.2
2	CB	125	PRO	2.2
3	AC	193	TYR	2.2
10	CJ	37	PRO	2.2
19	AS	80	TYR	2.2
26	DA	229	A	2.2
33	DI	137	PRO	2.2
4	CD	30	LYS	2.2
9	CI	25	LYS	2.2
23	AW	66	U	2.2
31	BG	75	LYS	2.2
3	CC	159	GLY	2.2
4	AD	180	GLY	2.2
5	AE	22	GLY	2.2
29	DE	195	LEU	2.2
31	DG	139	LEU	2.2
32	DH	5	GLY	2.2
42	DV	20	LEU	2.2
46	BZ	155	LEU	2.2
8	AH	100	ILE	2.2
10	AJ	34	VAL	2.2
10	CJ	23	ILE	2.2
10	CJ	38	ILE	2.2
31	DG	101	ILE	2.2
46	BZ	120	ILE	2.2
10	AJ	20	ALA	2.1
31	DG	158	ALA	2.1
46	DZ	21	ALA	2.1
2	AB	129	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
3	CC	19	GLU	2.1
1	CA	1018	C	2.1
1	CA	1260	C	2.1
7	CG	3	ARG	2.1
10	AJ	48	THR	2.1
13	CM	91	ARG	2.1
14	CN	31	ARG	2.1
17	AQ	68	ARG	2.1
23	AW	3	C	2.1
26	BA	652(S)	C	2.1
26	DA	897	C	2.1
27	DB	28	C	2.1
1	CA	587	G	2.1
26	BA	883	G	2.1
26	BA	2793	G	2.1
11	AK	51	LYS	2.1
12	CL	17	LYS	2.1
13	CM	87	TYR	2.1
17	CQ	32	TYR	2.1
49	D2	46	GLN	2.1
5	CE	119	LEU	2.1
13	CM	48	LEU	2.1
19	CS	5	LEU	2.1
32	BH	41	MET	2.1
32	DH	41	MET	2.1
46	DZ	41	LEU	2.1
1	CA	986	A	2.1
4	AD	90	GLY	2.1
16	AP	30	GLY	2.1
25	AY	35	A	2.1
26	DA	2170	A	2.1
27	DB	90	A	2.1
32	DH	22	GLY	2.1
42	DV	30	GLY	2.1
1	AA	343	U	2.1
2	AB	112	VAL	2.1
10	CJ	89	ASP	2.1
19	CS	62	ILE	2.1
26	DA	2113	U	2.1
26	DA	2897	U	2.1
33	BI	91	SER	2.1
46	BZ	161	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
52	B5	60	VAL	2.1
2	AB	70	PHE	2.1
3	CC	121	ALA	2.1
20	CT	12	ALA	2.1
32	BH	86	GLU	2.1
3	CC	88	ARG	2.1
10	AJ	28	ARG	2.1
39	DS	63	THR	2.1
12	AL	91	LYS	2.1
19	CS	76	PRO	2.1
46	DZ	15	PRO	2.1
1	CA	1045	C	2.1
8	AH	70	GLN	2.1
26	BA	898	C	2.1
26	BA	2137	C	2.1
26	DA	34	C	2.1
26	DA	2108	C	2.1
10	CJ	8	LEU	2.1
10	CJ	69	ASN	2.1
19	CS	61	TYR	2.1
31	DG	7	LEU	2.1
2	CB	72	GLY	2.1
3	CC	197	GLY	2.1
12	CL	95	GLY	2.1
1	AA	606	G	2.1
1	CA	1024	G	2.1
2	AB	32	ILE	2.1
2	AB	41	ILE	2.1
2	AB	229	VAL	2.1
3	CC	153	VAL	2.1
23	CW	65	G	2.1
25	CY	30	G	2.1
26	BA	275	G	2.1
26	BA	881	G	2.1
26	BA	2116	G	2.1
26	DA	2148	G	2.1
32	DH	11	VAL	2.1
1	CA	1056	U	2.1
1	CA	1232	U	2.1
5	AE	21	ALA	2.1
5	CE	138	ALA	2.1
26	BA	887	A	2.1

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Mol	Chain	Res	Type	RSRZ
26	DA	12	U	2.1
26	DA	899	A	2.1
27	DB	52	A	2.1
7	AG	8	GLU	2.1
12	CL	16	GLU	2.1
36	DP	18	ARG	2.1
2	AB	131	PRO	2.1
20	AT	98	PRO	2.1
40	DT	1	MET	2.1
5	AE	31	LEU	2.1
5	AE	71	LEU	2.1
9	CI	39	GLY	2.1
36	DP	104	GLY	2.1
43	DW	111	HIS	2.1
46	BZ	115	GLY	2.1
1	CA	1254	C	2.1
1	CA	1317	C	2.1
2	CB	230	VAL	2.1
3	AC	106	VAL	2.1
3	AC	124	ILE	2.1
4	AD	8	VAL	2.1
12	CL	40	VAL	2.1
19	CS	51	VAL	2.1
20	CT	100	ILE	2.1
24	CX	3	C	2.1
26	DA	2136	C	2.1
37	DQ	106	VAL	2.1
18	CR	29	PHE	2.1
31	DG	80	PHE	2.1
3	AC	79	ARG	2.1
3	CC	92	ALA	2.1
4	AD	168	ARG	2.1
9	CI	120	ARG	2.1
19	CS	78	ARG	2.1
28	BD	262	ARG	2.1
31	DG	57	ALA	2.1
31	DG	143	GLU	2.1
40	BT	109	GLU	2.1
44	DX	91	ALA	2.1
47	D0	74	ARG	2.1
48	B1	75	GLU	2.1
1	CA	966	G	2.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1108	G	2.1
1	AA	161	A	2.1
1	AA	960	U	2.1
1	CA	964	A	2.1
1	CA	1025	U	2.1
1	CA	1289	A	2.1
13	CM	65	LYS	2.1
19	CS	32	LYS	2.1
23	CW	24	G	2.1
26	BA	1107	G	2.1
26	BA	2147	G	2.1
13	AM	105	THR	2.1
13	CM	63	THR	2.1
23	CW	7	A	2.1
26	BA	614(A)	U	2.1
26	DA	2169	A	2.1
2	AB	167	PRO	2.1
41	DU	2	PRO	2.1
2	CB	90	MET	2.1
43	DW	1	MET	2.1
13	CM	81	LEU	2.1
31	DG	173	LEU	2.1
4	AD	69	GLY	2.1
29	DE	10	GLY	2.1
2	CB	172	ILE	2.1
4	CD	20	TYR	2.1
10	AJ	82	ILE	2.1
17	CQ	95	TYR	2.1
39	DS	92	TYR	2.1
51	D4	14	ILE	2.1
3	CC	64	VAL	2.1
5	AE	34	VAL	2.1
5	CE	67	VAL	2.1
7	AG	17	VAL	2.1
12	CL	101	VAL	2.1
31	DG	38	VAL	2.1
34	DN	140	VAL	2.1
37	DQ	65	PHE	2.1
39	DS	17	ARG	2.0
40	DT	115	ARG	2.0
2	CB	62	ALA	2.0
2	CB	186	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
7	CG	77	SER	2.0
39	DS	100	ALA	2.0
1	AA	1029	C	2.0
1	CA	1037	C	2.0
1	CA	1217	C	2.0
25	AY	13	C	2.0
26	DA	2175	C	2.0
27	DB	60	C	2.0
19	CS	34	TRP	2.0
10	CJ	100	THR	2.0
15	AO	22	THR	2.0
16	AP	22	THR	2.0
16	AP	45	THR	2.0
19	CS	39	THR	2.0
37	BQ	21	THR	2.0
1	CA	1364	U	2.0
2	CB	213	LEU	2.0
3	CC	87	LEU	2.0
18	AR	76	LEU	2.0
18	CR	31	LEU	2.0
32	DH	171	LEU	2.0
1	AA	1003	G	2.0
1	CA	1287	A	2.0
1	CA	1305	G	2.0
23	AW	19	G	2.0
25	AY	1	G	2.0
26	BA	655	A	2.0
26	DA	2114	A	2.0
26	DA	2207	G	2.0
9	CI	29	ASN	2.0
33	BI	11	ASN	2.0
34	DN	45	ASN	2.0
46	BZ	121	HIS	2.0
3	AC	2	GLY	2.0
7	AG	133	GLY	2.0
9	CI	72	GLY	2.0
12	CL	7	ILE	2.0
12	CL	100	ILE	2.0
13	CM	6	GLY	2.0
17	CQ	54	GLY	2.0
17	CQ	80	GLY	2.0
51	D4	4	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
4	AD	88	VAL	2.0
4	CD	88	VAL	2.0
5	CE	105	VAL	2.0
10	AJ	72	VAL	2.0
16	CP	20	VAL	2.0
17	CQ	5	VAL	2.0
32	DH	76	VAL	2.0
32	DH	115	VAL	2.0
41	DU	90	VAL	2.0
13	AM	102	ARG	2.0
31	BG	21	ARG	2.0
31	BG	136	ARG	2.0
2	AB	128	GLU	2.0
4	AD	192	GLU	2.0
9	CI	75	ASP	2.0
10	CJ	83	GLU	2.0
33	DI	64	GLU	2.0
47	D0	69	PHE	2.0
16	AP	29	ASP	2.0
51	B4	57	GLU	2.0
2	CB	188	ALA	2.0
3	CC	93	LYS	2.0
3	CC	137	ALA	2.0
9	CI	95	LYS	2.0
10	AJ	80	LYS	2.0
13	CM	51	ALA	2.0
20	AT	12	ALA	2.0
20	CT	95	ALA	2.0
30	DF	130	ALA	2.0
30	DF	166	ALA	2.0
3	CC	73	PRO	2.0
9	CI	103	THR	2.0
31	DG	100	TRP	2.0
10	CJ	77	PRO	2.0
32	DH	39	PRO	2.0
32	DH	173	PRO	2.0
1	AA	221	C	2.0
1	AA	1007	C	2.0
1	CA	1007	C	2.0
1	CA	1059	C	2.0
1	CA	1384	C	2.0
2	CB	155	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
3	CC	37	GLN	2.0
20	AT	13	LEU	2.0
26	DA	1745(A)	C	2.0
26	DA	2142	C	2.0
26	DA	2143	C	2.0
39	DS	101	LEU	2.0
32	DH	111	HIS	2.0
1	AA	202	U	2.0
1	AA	1313	U	2.0
3	CC	3	ASN	2.0
7	CG	42	ILE	2.0
9	CI	68	GLY	2.0
16	AP	37	GLY	2.0
16	CP	4	ILE	2.0
16	CP	19	ILE	2.0
33	DI	11	ASN	2.0
42	DV	67	GLY	2.0
46	BZ	12	GLY	2.0
1	CA	1179	A	2.0
3	CC	106	VAL	2.0
4	AD	191	ARG	2.0
8	CH	61	VAL	2.0
13	CM	74	VAL	2.0
25	AY	21	A	2.0
26	DA	2117	A	2.0
35	DO	57	VAL	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	7MG	CY	46	24/25	0.52	0.17	87,101,108,135	0
23	7MG	AW	46	24/25	0.54	0.16	80,97,112,135	0
25	4SU	CY	8	20/21	0.58	0.15	88,102,112,128	0
23	7MG	CW	46	24/25	0.59	0.15	81,97,101,125	0
25	MIA	CY	37	22/30	0.61	0.16	79,95,102,124	0
25	7MG	AY	46	24/25	0.63	0.16	80,99,107,116	0
25	PSU	CY	55	20/21	0.65	0.21	86,100,107,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	5MU	CY	54	21/22	0.67	0.20	89,99,105,136	0
23	4SU	CW	8	20/21	0.67	0.14	85,96,117,121	0
25	PSU	CY	39	20/21	0.69	0.15	86,91,104,110	0
25	4SU	AY	8	20/21	0.69	0.14	83,95,104,129	0
23	PSU	CW	55	20/21	0.72	0.13	76,90,103,106	0
23	4SU	AW	8	20/21	0.76	0.14	83,89,107,110	0
24	4SU	CX	8	20/21	0.76	0.15	84,92,105,111	0
23	5MU	CW	54	21/22	0.77	0.13	76,87,97,99	0
25	PSU	AY	55	20/21	0.78	0.12	85,96,106,117	0
25	MIA	AY	37	22/30	0.79	0.13	79,89,101,116	0
25	5MU	AY	54	21/22	0.80	0.12	81,89,99,128	0
25	PSU	CY	32	20/21	0.81	0.12	77,91,109,114	0
23	MIA	CW	37	22/30	0.81	0.14	72,86,92,96	0
25	PSU	AY	32	20/21	0.81	0.14	76,92,107,110	0
25	PSU	AY	39	20/21	0.82	0.13	84,90,102,107	0
23	PSU	CW	39	20/21	0.83	0.13	76,85,92,95	0
23	PSU	AW	55	20/21	0.83	0.10	76,88,103,105	0
24	PSU	CX	55	20/21	0.85	0.10	81,87,92,97	0
23	PSU	AW	32	20/21	0.87	0.16	77,84,98,106	0
24	5MU	CX	54	21/22	0.88	0.11	71,85,94,104	0
23	PSU	CW	32	20/21	0.89	0.15	77,86,95,106	0
24	4SU	AX	8	20/21	0.90	0.11	59,69,79,85	0
24	31H	CX	76	32/33	0.91	0.17	48,68,88,99	0
24	5MC	CX	32	21/22	0.91	0.12	63,77,85,87	0
24	5MU	AX	54	21/22	0.91	0.11	46,72,77,86	0
23	5MU	AW	54	21/22	0.91	0.10	66,80,87,93	0
24	PSU	AX	55	20/21	0.92	0.10	52,69,77,77	0
23	F3N	CW	76	33/34	0.92	0.14	53,69,79,80	0
23	PSU	AW	39	20/21	0.93	0.10	71,82,92,93	0
23	MIA	AW	37	29/30	0.93	0.13	56,65,80,82	0
24	31H	AX	76	32/33	0.94	0.14	31,57,76,77	10
23	F3N	AW	76	33/34	0.94	0.14	44,58,72,77	0
24	5MC	AX	32	21/22	0.95	0.12	50,57,69,76	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CA	3086	1/1	0.39	0.29	93,93,93,93	0
57	MG	DA	3254	1/1	0.52	0.20	68,68,68,68	0
57	MG	DA	3626	1/1	0.57	0.20	81,81,81,81	0
57	MG	AA	1784	1/1	0.60	0.26	72,72,72,72	0
57	MG	DA	3079	1/1	0.60	0.42	72,72,72,72	0
57	MG	DA	3606	1/1	0.62	0.17	74,74,74,74	0
57	MG	AA	1741	1/1	0.63	0.28	86,86,86,86	0
57	MG	DA	3628	1/1	0.63	0.26	77,77,77,77	0
57	MG	CA	3153	1/1	0.64	0.19	69,69,69,69	0
57	MG	CA	3115	1/1	0.64	0.23	82,82,82,82	0
57	MG	AA	1810	1/1	0.65	0.16	86,86,86,86	0
57	MG	BA	3693	1/1	0.65	0.20	77,77,77,77	0
57	MG	CA	3108	1/1	0.68	0.25	72,72,72,72	0
57	MG	BA	3569	1/1	0.68	0.19	56,56,56,56	0
57	MG	BA	3710	1/1	0.69	0.38	65,65,65,65	0
57	MG	DA	3617	1/1	0.69	0.32	51,51,51,51	0
57	MG	AA	1755	1/1	0.70	0.16	80,80,80,80	0
57	MG	BA	3655	1/1	0.71	0.15	55,55,55,55	0
57	MG	BA	3477	1/1	0.71	0.17	68,68,68,68	0
57	MG	BA	3369	1/1	0.71	0.25	62,62,62,62	0
57	MG	DA	3545	1/1	0.71	0.13	62,62,62,62	0
57	MG	DB	3010	1/1	0.71	0.19	75,75,75,75	0
57	MG	DA	3417	1/1	0.72	0.16	52,52,52,52	0
57	MG	CA	3112	1/1	0.73	0.27	72,72,72,72	0
57	MG	BA	3442	1/1	0.73	0.27	65,65,65,65	0
57	MG	DA	3286	1/1	0.74	0.14	55,55,55,55	0
57	MG	DA	3351	1/1	0.74	0.12	56,56,56,56	0
57	MG	DA	3616	1/1	0.74	0.20	63,63,63,63	0
57	MG	CA	3143	1/1	0.74	0.18	74,74,74,74	0
57	MG	DA	3618	1/1	0.74	0.18	46,46,46,46	0
57	MG	DA	3462	1/1	0.74	0.23	50,50,50,50	0
57	MG	DA	3478	1/1	0.74	0.22	58,58,58,58	0
57	MG	DA	3486	1/1	0.74	0.12	57,57,57,57	0
57	MG	BA	3644	1/1	0.75	0.26	64,64,64,64	0
57	MG	DA	3332	1/1	0.75	0.20	46,46,46,46	0
57	MG	CA	3144	1/1	0.75	0.23	82,82,82,82	0
57	MG	AA	1601	1/1	0.75	0.22	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CE	202	1/1	0.75	0.14	95,95,95,95	0
57	MG	BA	3491	1/1	0.75	0.21	56,56,56,56	0
57	MG	AA	1610	1/1	0.75	0.26	81,81,81,81	0
57	MG	DA	3508	1/1	0.75	0.17	57,57,57,57	0
57	MG	DA	3516	1/1	0.76	0.18	67,67,67,67	0
57	MG	BA	3717	1/1	0.76	0.20	72,72,72,72	0
57	MG	DA	3596	1/1	0.76	0.17	69,69,69,69	0
57	MG	DA	3456	1/1	0.76	0.18	38,38,38,38	0
57	MG	CA	3089	1/1	0.76	0.22	74,74,74,74	0
57	MG	BA	3688	1/1	0.77	0.21	61,61,61,61	0
57	MG	CA	3019	1/1	0.77	0.22	68,68,68,68	0
57	MG	DA	3112	1/1	0.77	0.15	56,56,56,56	0
57	MG	DA	3135	1/1	0.77	0.18	63,63,63,63	0
57	MG	BA	3016	1/1	0.77	0.21	67,67,67,67	0
57	MG	DA	3257	1/1	0.77	0.19	44,44,44,44	0
57	MG	BA	3676	1/1	0.77	0.19	70,70,70,70	0
57	MG	BA	3712	1/1	0.77	0.18	51,51,51,51	0
57	MG	DA	3542	1/1	0.77	0.16	60,60,60,60	0
57	MG	DA	3122	1/1	0.78	0.14	60,60,60,60	0
57	MG	BA	3727	1/1	0.78	0.18	53,53,53,53	0
57	MG	BA	3747	1/1	0.78	0.20	55,55,55,55	0
57	MG	BA	3805	1/1	0.78	0.17	48,48,48,48	0
57	MG	BA	3018	1/1	0.78	0.14	39,39,39,39	0
57	MG	AA	1757	1/1	0.78	0.29	68,68,68,68	0
57	MG	AX	3007	1/1	0.79	0.30	68,68,68,68	0
57	MG	CA	3095	1/1	0.79	0.26	71,71,71,71	0
57	MG	AA	1790	1/1	0.79	0.17	81,81,81,81	0
57	MG	AA	1613	1/1	0.79	0.11	75,75,75,75	0
57	MG	BA	3204	1/1	0.79	0.32	67,67,67,67	0
57	MG	CA	3117	1/1	0.79	0.11	63,63,63,63	0
57	MG	BB	3017	1/1	0.79	0.23	81,81,81,81	0
57	MG	BA	3298	1/1	0.79	0.11	27,27,27,27	0
57	MG	DA	3645	1/1	0.79	0.12	64,64,64,64	0
57	MG	DA	3649	1/1	0.79	0.15	71,71,71,71	0
57	MG	BA	3352	1/1	0.79	0.19	68,68,68,68	0
57	MG	CA	3148	1/1	0.80	0.22	68,68,68,68	0
57	MG	BA	3041	1/1	0.80	0.21	63,63,63,63	0
57	MG	DA	3400	1/1	0.80	0.16	62,62,62,62	0
57	MG	CA	3090	1/1	0.80	0.19	76,76,76,76	0
57	MG	BA	3449	1/1	0.80	0.17	62,62,62,62	0
57	MG	BA	3680	1/1	0.80	0.18	42,42,42,42	0
57	MG	AX	3013	1/1	0.80	0.23	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AY	3003	1/1	0.80	0.16	79,79,79,79	0
57	MG	AW	3002	1/1	0.80	0.36	79,79,79,79	0
57	MG	CA	3070	1/1	0.80	0.27	69,69,69,69	0
57	MG	AA	1771	1/1	0.80	0.17	75,75,75,75	0
57	MG	BA	3640	1/1	0.81	0.21	57,57,57,57	0
57	MG	AA	1618	1/1	0.81	0.16	68,68,68,68	0
57	MG	CA	3125	1/1	0.81	0.22	64,64,64,64	0
57	MG	DA	3410	1/1	0.81	0.17	40,40,40,40	0
57	MG	BA	3700	1/1	0.81	0.19	36,36,36,36	0
57	MG	DA	3442	1/1	0.81	0.26	64,64,64,64	0
57	MG	DA	3444	1/1	0.81	0.13	44,44,44,44	0
57	MG	AX	3012	1/1	0.81	0.24	52,52,52,52	0
57	MG	BA	3374	1/1	0.81	0.12	50,50,50,50	0
57	MG	AA	1650	1/1	0.81	0.33	74,74,74,74	0
57	MG	CA	3160	1/1	0.81	0.21	73,73,73,73	0
57	MG	DA	3491	1/1	0.81	0.17	43,43,43,43	0
57	MG	DA	3306	1/1	0.81	0.23	65,65,65,65	0
57	MG	DA	3001	1/1	0.82	0.11	57,57,57,57	0
57	MG	DA	3016	1/1	0.82	0.23	66,66,66,66	0
57	MG	CA	3102	1/1	0.82	0.25	71,71,71,71	0
57	MG	CA	3103	1/1	0.82	0.18	73,73,73,73	0
57	MG	DA	3487	1/1	0.82	0.17	55,55,55,55	0
57	MG	BA	3561	1/1	0.82	0.16	34,34,34,34	0
57	MG	AA	1712	1/1	0.82	0.30	69,69,69,69	0
57	MG	DA	3248	1/1	0.82	0.16	58,58,58,58	0
57	MG	BA	3274	1/1	0.82	0.33	66,66,66,66	0
57	MG	BB	3019	1/1	0.82	0.17	70,70,70,70	0
57	MG	BB	3020	1/1	0.82	0.15	65,65,65,65	0
57	MG	CA	3130	1/1	0.82	0.30	64,64,64,64	0
57	MG	DA	3328	1/1	0.82	0.18	42,42,42,42	0
57	MG	CA	3131	1/1	0.82	0.24	69,69,69,69	0
57	MG	BA	3642	1/1	0.82	0.18	64,64,64,64	0
57	MG	AA	1787	1/1	0.82	0.16	49,49,49,49	0
57	MG	BA	3404	1/1	0.82	0.27	59,59,59,59	0
57	MG	DA	3630	1/1	0.82	0.20	69,69,69,69	0
57	MG	BA	3667	1/1	0.82	0.17	58,58,58,58	0
57	MG	BA	3723	1/1	0.82	0.15	30,30,30,30	0
57	MG	BA	3518	1/1	0.82	0.16	46,46,46,46	0
57	MG	DU	201	1/1	0.82	0.27	58,58,58,58	0
57	MG	AA	1705	1/1	0.83	0.30	70,70,70,70	0
57	MG	BA	3730	1/1	0.83	0.18	68,68,68,68	0
57	MG	DA	3502	1/1	0.83	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
57	MG	AA	1711	1/1	0.83	0.12	51,51,51,51	0
57	MG	DA	3305	1/1	0.83	0.10	53,53,53,53	0
57	MG	BA	3765	1/1	0.83	0.17	49,49,49,49	0
57	MG	BA	3653	1/1	0.83	0.26	57,57,57,57	0
57	MG	DA	3557	1/1	0.83	0.20	57,57,57,57	0
57	MG	DA	3572	1/1	0.83	0.19	65,65,65,65	0
57	MG	CA	3105	1/1	0.83	0.22	75,75,75,75	0
57	MG	BA	3705	1/1	0.83	0.10	59,59,59,59	0
57	MG	DA	3611	1/1	0.83	0.14	53,53,53,53	0
57	MG	BA	3563	1/1	0.83	0.14	50,50,50,50	0
57	MG	DA	3070	1/1	0.83	0.16	65,65,65,65	0
57	MG	BA	3323	1/1	0.83	0.15	57,57,57,57	0
57	MG	DA	3107	1/1	0.83	0.12	61,61,61,61	0
57	MG	CA	3009	1/1	0.83	0.16	73,73,73,73	0
57	MG	DA	3448	1/1	0.83	0.16	55,55,55,55	0
57	MG	DA	3637	1/1	0.83	0.21	72,72,72,72	0
57	MG	BA	3715	1/1	0.83	0.16	52,52,52,52	0
57	MG	BA	3632	1/1	0.83	0.23	55,55,55,55	0
57	MG	DB	3003	1/1	0.83	0.11	78,78,78,78	0
57	MG	DA	3222	1/1	0.83	0.10	58,58,58,58	0
57	MG	BA	3340	1/1	0.83	0.12	27,27,27,27	0
57	MG	BA	3769	1/1	0.84	0.15	47,47,47,47	0
57	MG	BA	3571	1/1	0.84	0.13	28,28,28,28	0
57	MG	BB	3014	1/1	0.84	0.18	67,67,67,67	0
57	MG	BA	3575	1/1	0.84	0.09	50,50,50,50	0
57	MG	DA	3488	1/1	0.84	0.10	53,53,53,53	0
57	MG	BA	3660	1/1	0.84	0.18	60,60,60,60	0
57	MG	DA	3146	1/1	0.84	0.10	54,54,54,54	0
57	MG	DA	3204	1/1	0.84	0.21	68,68,68,68	0
57	MG	BA	3593	1/1	0.84	0.17	55,55,55,55	0
57	MG	DA	3530	1/1	0.84	0.18	55,55,55,55	0
57	MG	DA	3539	1/1	0.84	0.13	55,55,55,55	0
57	MG	BA	3611	1/1	0.84	0.21	59,59,59,59	0
57	MG	DA	3543	1/1	0.84	0.18	64,64,64,64	0
57	MG	AX	3016	1/1	0.84	0.25	86,86,86,86	0
57	MG	CA	3036	1/1	0.84	0.22	73,73,73,73	0
57	MG	CA	3049	1/1	0.84	0.35	65,65,65,65	0
57	MG	CA	3059	1/1	0.84	0.15	75,75,75,75	0
57	MG	DA	3601	1/1	0.84	0.15	55,55,55,55	0
57	MG	BA	3074	1/1	0.84	0.24	69,69,69,69	0
57	MG	DA	3308	1/1	0.84	0.23	62,62,62,62	0
57	MG	DA	3314	1/1	0.84	0.13	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3728	1/1	0.84	0.12	52,52,52,52	0
57	MG	AA	1688	1/1	0.84	0.26	66,66,66,66	0
57	MG	DA	3624	1/1	0.84	0.18	59,59,59,59	0
57	MG	BA	3743	1/1	0.84	0.33	47,47,47,47	0
57	MG	DA	3356	1/1	0.84	0.12	39,39,39,39	0
57	MG	CJ	5001	1/1	0.84	0.20	77,77,77,77	0
57	MG	CA	3091	1/1	0.84	0.18	69,69,69,69	0
57	MG	DA	3002	1/1	0.84	0.19	64,64,64,64	0
57	MG	BA	3694	1/1	0.84	0.19	53,53,53,53	0
57	MG	DA	3663	1/1	0.84	0.25	73,73,73,73	0
57	MG	DB	3001	1/1	0.84	0.24	63,63,63,63	0
57	MG	DA	3033	1/1	0.84	0.14	68,68,68,68	0
57	MG	DB	3004	1/1	0.84	0.23	63,63,63,63	0
57	MG	DA	3065	1/1	0.84	0.13	56,56,56,56	0
57	MG	BA	3517	1/1	0.84	0.16	33,33,33,33	0
57	MG	AA	1679	1/1	0.85	0.20	51,51,51,51	0
57	MG	BA	3734	1/1	0.85	0.14	65,65,65,65	0
57	MG	BA	3121	1/1	0.85	0.14	42,42,42,42	0
57	MG	DA	3130	1/1	0.85	0.17	52,52,52,52	0
57	MG	BA	3666	1/1	0.85	0.23	74,74,74,74	0
57	MG	CA	3107	1/1	0.85	0.14	68,68,68,68	0
57	MG	BA	3164	1/1	0.85	0.12	46,46,46,46	0
57	MG	DA	3524	1/1	0.85	0.23	52,52,52,52	0
57	MG	CA	3110	1/1	0.85	0.18	63,63,63,63	0
57	MG	DA	3538	1/1	0.85	0.16	60,60,60,60	0
57	MG	BA	3673	1/1	0.85	0.24	61,61,61,61	0
57	MG	DA	3250	1/1	0.85	0.10	50,50,50,50	0
57	MG	CA	3113	1/1	0.85	0.19	47,47,47,47	0
57	MG	BA	3377	1/1	0.85	0.18	51,51,51,51	0
57	MG	DA	3284	1/1	0.85	0.17	58,58,58,58	0
57	MG	BA	3678	1/1	0.85	0.19	67,67,67,67	0
57	MG	DA	3591	1/1	0.85	0.15	66,66,66,66	0
57	MG	BA	3572	1/1	0.85	0.15	39,39,39,39	0
57	MG	BA	3573	1/1	0.85	0.11	41,41,41,41	0
57	MG	AB	3001	1/1	0.85	0.15	77,77,77,77	0
57	MG	B0	3002	1/1	0.85	0.18	63,63,63,63	0
57	MG	CA	3002	1/1	0.85	0.22	77,77,77,77	0
57	MG	BA	3581	1/1	0.85	0.12	59,59,59,59	0
57	MG	BA	3439	1/1	0.85	0.14	36,36,36,36	0
57	MG	DA	3619	1/1	0.85	0.10	40,40,40,40	0
57	MG	CA	3030	1/1	0.85	0.25	74,74,74,74	0
57	MG	DA	3368	1/1	0.85	0.20	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3246	1/1	0.85	0.27	55,55,55,55	0
57	MG	BA	3615	1/1	0.85	0.12	71,71,71,71	0
57	MG	DA	3415	1/1	0.85	0.16	43,43,43,43	0
57	MG	CA	3051	1/1	0.85	0.22	77,77,77,77	0
57	MG	DA	3647	1/1	0.85	0.14	52,52,52,52	0
57	MG	DA	3441	1/1	0.85	0.25	58,58,58,58	0
57	MG	AA	1717	1/1	0.85	0.24	75,75,75,75	0
57	MG	BA	3636	1/1	0.85	0.26	66,66,66,66	0
57	MG	BA	3275	1/1	0.85	0.15	66,66,66,66	0
57	MG	AA	1788	1/1	0.85	0.32	75,75,75,75	0
57	MG	AX	3008	1/1	0.85	0.28	76,76,76,76	0
57	MG	DB	3011	1/1	0.85	0.31	67,67,67,67	0
57	MG	AA	1669	1/1	0.85	0.23	69,69,69,69	0
57	MG	BA	3713	1/1	0.86	0.24	33,33,33,33	0
57	MG	CA	3146	1/1	0.86	0.20	72,72,72,72	0
57	MG	DA	3226	1/1	0.86	0.13	57,57,57,57	0
57	MG	BA	3746	1/1	0.86	0.29	78,78,78,78	0
57	MG	B6	103	1/1	0.86	0.15	52,52,52,52	0
57	MG	AL	201	1/1	0.86	0.18	63,63,63,63	0
57	MG	DA	3518	1/1	0.86	0.12	56,56,56,56	0
57	MG	CA	3164	1/1	0.86	0.18	76,76,76,76	0
57	MG	CA	3167	1/1	0.86	0.26	57,57,57,57	0
57	MG	BA	3755	1/1	0.86	0.14	43,43,43,43	0
57	MG	DA	3293	1/1	0.86	0.12	61,61,61,61	0
57	MG	DA	3295	1/1	0.86	0.22	67,67,67,67	0
57	MG	CA	3013	1/1	0.86	0.29	67,67,67,67	0
57	MG	CA	3018	1/1	0.86	0.19	63,63,63,63	0
57	MG	AX	3015	1/1	0.86	0.17	51,51,51,51	0
57	MG	DA	3560	1/1	0.86	0.25	60,60,60,60	0
57	MG	CA	3022	1/1	0.86	0.22	76,76,76,76	0
57	MG	DA	3017	1/1	0.86	0.14	59,59,59,59	0
57	MG	DA	3024	1/1	0.86	0.16	61,61,61,61	0
57	MG	DA	3342	1/1	0.86	0.09	53,53,53,53	0
57	MG	DA	3344	1/1	0.86	0.13	38,38,38,38	0
57	MG	DA	3032	1/1	0.86	0.13	57,57,57,57	0
57	MG	AA	1743	1/1	0.86	0.13	66,66,66,66	0
57	MG	DA	3358	1/1	0.86	0.11	50,50,50,50	0
57	MG	DA	3366	1/1	0.86	0.12	44,44,44,44	0
57	MG	AA	1781	1/1	0.86	0.12	59,59,59,59	0
57	MG	DA	3066	1/1	0.86	0.15	58,58,58,58	0
57	MG	BA	3809	1/1	0.86	0.17	61,61,61,61	0
57	MG	BB	3009	1/1	0.86	0.10	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3089	1/1	0.86	0.18	52,52,52,52	0
57	MG	DA	3433	1/1	0.86	0.19	59,59,59,59	0
57	MG	AA	1674	1/1	0.86	0.22	58,58,58,58	0
57	MG	CA	3124	1/1	0.86	0.19	69,69,69,69	0
57	MG	BA	3228	1/1	0.86	0.26	65,65,65,65	0
57	MG	DA	3445	1/1	0.86	0.11	52,52,52,52	0
57	MG	CA	3076	1/1	0.86	0.24	77,77,77,77	0
57	MG	CA	3082	1/1	0.86	0.34	66,66,66,66	0
57	MG	DA	3143	1/1	0.86	0.21	62,62,62,62	0
57	MG	DA	3463	1/1	0.86	0.13	44,44,44,44	0
57	MG	AA	1623	1/1	0.86	0.30	65,65,65,65	0
57	MG	DA	3190	1/1	0.86	0.21	63,63,63,63	0
57	MG	CA	3094	1/1	0.87	0.18	61,61,61,61	0
57	MG	DA	3435	1/1	0.87	0.12	44,44,44,44	0
57	MG	AA	1766	1/1	0.87	0.19	71,71,71,71	0
57	MG	BA	3796	1/1	0.87	0.14	47,47,47,47	0
57	MG	DA	3081	1/1	0.87	0.11	51,51,51,51	0
57	MG	BA	3498	1/1	0.87	0.10	45,45,45,45	0
57	MG	DA	3097	1/1	0.87	0.10	47,47,47,47	0
57	MG	DA	3098	1/1	0.87	0.14	66,66,66,66	0
57	MG	AK	3101	1/1	0.87	0.24	69,69,69,69	0
57	MG	BA	3111	1/1	0.87	0.29	53,53,53,53	0
57	MG	BA	3329	1/1	0.87	0.13	60,60,60,60	0
57	MG	CA	3109	1/1	0.87	0.12	74,74,74,74	0
57	MG	BA	3338	1/1	0.87	0.14	55,55,55,55	0
57	MG	AA	1748	1/1	0.87	0.22	64,64,64,64	0
57	MG	AA	1662	1/1	0.87	0.14	58,58,58,58	0
57	MG	BZ	301	1/1	0.87	0.09	49,49,49,49	0
57	MG	DA	3202	1/1	0.87	0.21	62,62,62,62	0
57	MG	DA	3510	1/1	0.87	0.19	64,64,64,64	0
57	MG	BA	3200	1/1	0.87	0.18	48,48,48,48	0
57	MG	CA	3121	1/1	0.87	0.21	67,67,67,67	0
57	MG	CA	3122	1/1	0.87	0.15	69,69,69,69	0
57	MG	AX	3005	1/1	0.87	0.13	65,65,65,65	0
57	MG	BA	3224	1/1	0.87	0.21	59,59,59,59	0
57	MG	BA	3394	1/1	0.87	0.19	40,40,40,40	0
57	MG	CA	3012	1/1	0.87	0.26	64,64,64,64	0
57	MG	DA	3261	1/1	0.87	0.12	39,39,39,39	0
57	MG	DA	3275	1/1	0.87	0.18	65,65,65,65	0
57	MG	DA	3553	1/1	0.87	0.18	72,72,72,72	0
57	MG	DA	3282	1/1	0.87	0.15	55,55,55,55	0
57	MG	BA	3225	1/1	0.87	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
57	MG	DA	3571	1/1	0.87	0.11	45,45,45,45	0
57	MG	BA	3604	1/1	0.87	0.14	43,43,43,43	0
57	MG	DA	3289	1/1	0.87	0.13	52,52,52,52	0
57	MG	BA	3609	1/1	0.87	0.22	56,56,56,56	0
57	MG	BA	3429	1/1	0.87	0.14	50,50,50,50	0
57	MG	CA	3152	1/1	0.87	0.18	71,71,71,71	0
57	MG	CA	3029	1/1	0.87	0.09	50,50,50,50	0
57	MG	DA	3612	1/1	0.87	0.09	58,58,58,58	0
57	MG	BA	3431	1/1	0.87	0.19	57,57,57,57	0
57	MG	BA	3722	1/1	0.87	0.24	64,64,64,64	0
57	MG	BA	3629	1/1	0.87	0.17	58,58,58,58	0
57	MG	CE	201	1/1	0.87	0.19	65,65,65,65	0
57	MG	DA	3620	1/1	0.87	0.11	53,53,53,53	0
57	MG	DA	3623	1/1	0.87	0.10	45,45,45,45	0
57	MG	DA	3334	1/1	0.87	0.23	57,57,57,57	0
57	MG	DA	3625	1/1	0.87	0.10	60,60,60,60	0
57	MG	BA	3435	1/1	0.87	0.15	53,53,53,53	0
57	MG	CA	3058	1/1	0.87	0.15	66,66,66,66	0
57	MG	BA	3006	1/1	0.87	0.14	54,54,54,54	0
57	MG	AA	1801	1/1	0.87	0.13	71,71,71,71	0
57	MG	BA	3641	1/1	0.87	0.22	68,68,68,68	0
57	MG	BA	3443	1/1	0.87	0.11	59,59,59,59	0
57	MG	BA	3272	1/1	0.87	0.25	64,64,64,64	0
57	MG	DA	3393	1/1	0.87	0.12	37,37,37,37	0
57	MG	BA	3647	1/1	0.87	0.10	53,53,53,53	0
57	MG	BA	3462	1/1	0.87	0.13	53,53,53,53	0
57	MG	DA	3414	1/1	0.87	0.13	42,42,42,42	0
57	MG	DA	3035	1/1	0.87	0.09	37,37,37,37	0
57	MG	AA	1664	1/1	0.87	0.17	62,62,62,62	0
57	MG	DA	3421	1/1	0.87	0.14	56,56,56,56	0
59	ZN	D4	501	1/1	0.87	0.10	162,162,162,162	0
57	MG	DA	3396	1/1	0.88	0.16	46,46,46,46	0
57	MG	BA	3327	1/1	0.88	0.10	39,39,39,39	0
57	MG	BA	3702	1/1	0.88	0.08	39,39,39,39	0
57	MG	BA	3068	1/1	0.88	0.09	49,49,49,49	0
57	MG	CA	3057	1/1	0.88	0.19	84,84,84,84	0
57	MG	AA	1775	1/1	0.88	0.14	73,73,73,73	0
57	MG	DA	3418	1/1	0.88	0.10	47,47,47,47	0
57	MG	DA	3419	1/1	0.88	0.20	50,50,50,50	0
57	MG	DA	3056	1/1	0.88	0.12	49,49,49,49	0
57	MG	DA	3061	1/1	0.88	0.12	60,60,60,60	0
57	MG	DA	3434	1/1	0.88	0.12	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3079	1/1	0.88	0.22	58,58,58,58	0
57	MG	BA	3351	1/1	0.88	0.13	45,45,45,45	0
57	MG	BA	3099	1/1	0.88	0.23	61,61,61,61	0
57	MG	AX	3002	1/1	0.88	0.24	71,71,71,71	0
57	MG	BA	3579	1/1	0.88	0.09	63,63,63,63	0
57	MG	DA	3087	1/1	0.88	0.15	55,55,55,55	0
57	MG	BA	3372	1/1	0.88	0.08	40,40,40,40	0
57	MG	DA	3096	1/1	0.88	0.13	68,68,68,68	0
57	MG	AA	1656	1/1	0.88	0.20	63,63,63,63	0
57	MG	BA	3594	1/1	0.88	0.15	45,45,45,45	0
57	MG	DA	3099	1/1	0.88	0.19	63,63,63,63	0
57	MG	DA	3101	1/1	0.88	0.16	56,56,56,56	0
57	MG	BA	3600	1/1	0.88	0.16	44,44,44,44	0
57	MG	BA	3375	1/1	0.88	0.12	39,39,39,39	0
57	MG	BA	3608	1/1	0.88	0.16	58,58,58,58	0
57	MG	DA	3504	1/1	0.88	0.12	52,52,52,52	0
57	MG	BA	3139	1/1	0.88	0.12	44,44,44,44	0
57	MG	AA	1625	1/1	0.88	0.27	73,73,73,73	0
57	MG	DA	3515	1/1	0.88	0.13	55,55,55,55	0
57	MG	AA	1701	1/1	0.88	0.38	73,73,73,73	0
57	MG	BA	3616	1/1	0.88	0.22	59,59,59,59	0
57	MG	DA	3523	1/1	0.88	0.09	39,39,39,39	0
57	MG	DA	3159	1/1	0.88	0.15	62,62,62,62	0
57	MG	DA	3172	1/1	0.88	0.26	61,61,61,61	0
57	MG	DA	3533	1/1	0.88	0.14	56,56,56,56	0
57	MG	DA	3535	1/1	0.88	0.12	44,44,44,44	0
57	MG	BA	3416	1/1	0.88	0.13	60,60,60,60	0
57	MG	DA	3201	1/1	0.88	0.11	52,52,52,52	0
57	MG	BA	3775	1/1	0.88	0.29	39,39,39,39	0
57	MG	BA	3423	1/1	0.88	0.17	69,69,69,69	0
57	MG	DA	3219	1/1	0.88	0.15	50,50,50,50	0
57	MG	AA	1631	1/1	0.88	0.16	64,64,64,64	0
57	MG	AA	1708	1/1	0.88	0.11	60,60,60,60	0
57	MG	AA	1794	1/1	0.88	0.21	58,58,58,58	0
57	MG	DA	3570	1/1	0.88	0.10	43,43,43,43	0
57	MG	CA	3120	1/1	0.88	0.23	68,68,68,68	0
57	MG	DA	3253	1/1	0.88	0.12	54,54,54,54	0
57	MG	AA	1756	1/1	0.88	0.24	45,45,45,45	0
57	MG	DA	3594	1/1	0.88	0.15	58,58,58,58	0
57	MG	AA	1614	1/1	0.88	0.23	75,75,75,75	0
57	MG	BA	3265	1/1	0.88	0.31	72,72,72,72	0
57	MG	DA	3602	1/1	0.88	0.22	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	1655	1/1	0.88	0.09	53,53,53,53	0
57	MG	CA	3127	1/1	0.88	0.10	59,59,59,59	0
57	MG	CA	3129	1/1	0.88	0.18	69,69,69,69	0
57	MG	BO	5001	1/1	0.88	0.15	61,61,61,61	0
57	MG	DA	3287	1/1	0.88	0.18	52,52,52,52	0
57	MG	BA	3458	1/1	0.88	0.15	59,59,59,59	0
57	MG	DA	3291	1/1	0.88	0.16	36,36,36,36	0
57	MG	AA	1714	1/1	0.88	0.12	56,56,56,56	0
57	MG	B2	3001	1/1	0.88	0.11	53,53,53,53	0
57	MG	AA	1773	1/1	0.88	0.14	61,61,61,61	0
57	MG	BA	3484	1/1	0.88	0.15	40,40,40,40	0
57	MG	BA	3669	1/1	0.88	0.10	28,28,28,28	0
57	MG	DA	3311	1/1	0.88	0.09	46,46,46,46	0
57	MG	AT	3001	1/1	0.88	0.27	63,63,63,63	0
57	MG	DA	3633	1/1	0.88	0.12	58,58,58,58	0
57	MG	CA	3154	1/1	0.88	0.15	68,68,68,68	0
57	MG	BA	3497	1/1	0.88	0.12	50,50,50,50	0
57	MG	BA	3318	1/1	0.88	0.12	54,54,54,54	0
57	MG	BA	3504	1/1	0.88	0.15	56,56,56,56	0
57	MG	DA	3650	1/1	0.88	0.15	61,61,61,61	0
57	MG	DA	3657	1/1	0.88	0.21	54,54,54,54	0
57	MG	BA	3512	1/1	0.88	0.11	23,23,23,23	0
57	MG	CA	3024	1/1	0.88	0.23	67,67,67,67	0
57	MG	CA	3027	1/1	0.88	0.32	65,65,65,65	0
57	MG	CX	3001	1/1	0.88	0.22	57,57,57,57	0
57	MG	DA	3362	1/1	0.88	0.14	42,42,42,42	0
57	MG	BA	3320	1/1	0.88	0.17	55,55,55,55	0
57	MG	DF	302	1/1	0.88	0.10	53,53,53,53	0
57	MG	BA	3062	1/1	0.88	0.42	59,59,59,59	0
57	MG	CA	3032	1/1	0.88	0.19	53,53,53,53	0
57	MG	AM	3002	1/1	0.89	0.10	68,68,68,68	0
57	MG	DA	3345	1/1	0.89	0.15	58,58,58,58	0
57	MG	DA	3348	1/1	0.89	0.10	53,53,53,53	0
57	MG	B7	104	1/1	0.89	0.17	62,62,62,62	0
57	MG	BA	3507	1/1	0.89	0.18	43,43,43,43	0
57	MG	CA	3004	1/1	0.89	0.08	69,69,69,69	0
57	MG	CA	3005	1/1	0.89	0.13	73,73,73,73	0
57	MG	BA	3334	1/1	0.89	0.15	56,56,56,56	0
57	MG	BA	3199	1/1	0.89	0.30	64,64,64,64	0
57	MG	DA	3377	1/1	0.89	0.11	50,50,50,50	0
57	MG	AA	1644	1/1	0.89	0.12	56,56,56,56	0
57	MG	DA	3395	1/1	0.89	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
57	MG	CA	3014	1/1	0.89	0.16	62,62,62,62	0
57	MG	BA	3522	1/1	0.89	0.12	44,44,44,44	0
57	MG	BA	3525	1/1	0.89	0.08	43,43,43,43	0
57	MG	DA	3411	1/1	0.89	0.13	37,37,37,37	0
57	MG	DA	3413	1/1	0.89	0.15	62,62,62,62	0
57	MG	BA	3684	1/1	0.89	0.17	51,51,51,51	0
57	MG	BA	3530	1/1	0.89	0.15	33,33,33,33	0
57	MG	CA	3025	1/1	0.89	0.23	53,53,53,53	0
57	MG	DA	3041	1/1	0.89	0.14	60,60,60,60	0
57	MG	DA	3044	1/1	0.89	0.18	53,53,53,53	0
57	MG	DA	3420	1/1	0.89	0.09	49,49,49,49	0
57	MG	DA	3048	1/1	0.89	0.10	59,59,59,59	0
57	MG	DA	3431	1/1	0.89	0.18	42,42,42,42	0
57	MG	DA	3055	1/1	0.89	0.13	53,53,53,53	0
57	MG	CA	3026	1/1	0.89	0.21	66,66,66,66	0
57	MG	DA	3060	1/1	0.89	0.23	60,60,60,60	0
57	MG	BA	3538	1/1	0.89	0.10	68,68,68,68	0
57	MG	BA	3542	1/1	0.89	0.10	44,44,44,44	0
57	MG	BA	3696	1/1	0.89	0.10	46,46,46,46	0
57	MG	BA	3557	1/1	0.89	0.17	53,53,53,53	0
57	MG	DA	3072	1/1	0.89	0.10	47,47,47,47	0
57	MG	BA	3558	1/1	0.89	0.10	51,51,51,51	0
57	MG	CA	3046	1/1	0.89	0.23	61,61,61,61	0
57	MG	BA	3342	1/1	0.89	0.16	67,67,67,67	0
57	MG	BA	3343	1/1	0.89	0.13	54,54,54,54	0
57	MG	BA	3202	1/1	0.89	0.10	62,62,62,62	0
57	MG	BA	3017	1/1	0.89	0.18	65,65,65,65	0
57	MG	BA	3364	1/1	0.89	0.09	47,47,47,47	0
57	MG	BA	3209	1/1	0.89	0.18	48,48,48,48	0
57	MG	DA	3497	1/1	0.89	0.19	58,58,58,58	0
57	MG	BA	3219	1/1	0.89	0.15	58,58,58,58	0
57	MG	DA	3102	1/1	0.89	0.11	40,40,40,40	0
57	MG	DA	3106	1/1	0.89	0.11	50,50,50,50	0
57	MG	AA	1620	1/1	0.89	0.19	59,59,59,59	0
57	MG	DA	3111	1/1	0.89	0.17	56,56,56,56	0
57	MG	BA	3726	1/1	0.89	0.12	31,31,31,31	0
57	MG	AA	1738	1/1	0.89	0.13	68,68,68,68	0
57	MG	AA	1651	1/1	0.89	0.25	58,58,58,58	0
57	MG	BA	3240	1/1	0.89	0.14	53,53,53,53	0
57	MG	DA	3527	1/1	0.89	0.17	52,52,52,52	0
57	MG	DA	3139	1/1	0.89	0.08	44,44,44,44	0
57	MG	BA	3245	1/1	0.89	0.10	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3738	1/1	0.89	0.13	41,41,41,41	0
57	MG	BA	3741	1/1	0.89	0.11	57,57,57,57	0
57	MG	BA	3411	1/1	0.89	0.17	50,50,50,50	0
57	MG	DA	3541	1/1	0.89	0.20	59,59,59,59	0
57	MG	DA	3173	1/1	0.89	0.17	62,62,62,62	0
57	MG	DA	3177	1/1	0.89	0.25	58,58,58,58	0
57	MG	AA	1798	1/1	0.89	0.10	62,62,62,62	0
57	MG	DA	3196	1/1	0.89	0.19	54,54,54,54	0
57	MG	DA	3556	1/1	0.89	0.11	55,55,55,55	0
57	MG	DA	3200	1/1	0.89	0.12	41,41,41,41	0
57	MG	DA	3559	1/1	0.89	0.12	67,67,67,67	0
57	MG	BA	3248	1/1	0.89	0.21	67,67,67,67	0
57	MG	DA	3567	1/1	0.89	0.23	44,44,44,44	0
57	MG	BA	3252	1/1	0.89	0.18	36,36,36,36	0
57	MG	BA	3763	1/1	0.89	0.14	44,44,44,44	0
57	MG	DA	3212	1/1	0.89	0.29	62,62,62,62	0
57	MG	DA	3573	1/1	0.89	0.13	61,61,61,61	0
57	MG	BA	3614	1/1	0.89	0.15	53,53,53,53	0
57	MG	DA	3592	1/1	0.89	0.17	67,67,67,67	0
57	MG	CA	3111	1/1	0.89	0.10	72,72,72,72	0
57	MG	BA	3255	1/1	0.89	0.17	55,55,55,55	0
57	MG	DA	3227	1/1	0.89	0.14	56,56,56,56	0
57	MG	DA	3232	1/1	0.89	0.32	56,56,56,56	0
57	MG	DA	3234	1/1	0.89	0.21	54,54,54,54	0
57	MG	DA	3236	1/1	0.89	0.20	55,55,55,55	0
57	MG	AA	1629	1/1	0.89	0.45	68,68,68,68	0
57	MG	BA	3786	1/1	0.89	0.15	51,51,51,51	0
57	MG	BA	3794	1/1	0.89	0.10	37,37,37,37	0
57	MG	CA	3119	1/1	0.89	0.19	59,59,59,59	0
57	MG	BA	3625	1/1	0.89	0.08	33,33,33,33	0
57	MG	BA	3798	1/1	0.89	0.14	22,22,22,22	0
57	MG	DA	3265	1/1	0.89	0.19	57,57,57,57	0
57	MG	DA	3269	1/1	0.89	0.14	50,50,50,50	0
57	MG	AA	1747	1/1	0.89	0.13	55,55,55,55	0
57	MG	BA	3087	1/1	0.89	0.22	43,43,43,43	0
57	MG	BB	3001	1/1	0.89	0.22	68,68,68,68	0
57	MG	BB	3004	1/1	0.89	0.24	69,69,69,69	0
57	MG	AA	1624	1/1	0.89	0.35	66,66,66,66	0
57	MG	BA	3277	1/1	0.89	0.18	52,52,52,52	0
57	MG	DA	3644	1/1	0.89	0.29	58,58,58,58	0
57	MG	BA	3282	1/1	0.89	0.23	57,57,57,57	0
57	MG	DA	3646	1/1	0.89	0.13	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CA	3139	1/1	0.89	0.15	81,81,81,81	0
57	MG	CA	3142	1/1	0.89	0.15	50,50,50,50	0
57	MG	DA	3302	1/1	0.89	0.18	53,53,53,53	0
57	MG	BA	3286	1/1	0.89	0.14	44,44,44,44	0
57	MG	BA	3100	1/1	0.89	0.19	61,61,61,61	0
57	MG	BF	306	1/1	0.89	0.28	49,49,49,49	0
57	MG	BG	202	1/1	0.89	0.09	52,52,52,52	0
57	MG	BA	3103	1/1	0.89	0.29	63,63,63,63	0
57	MG	DA	3315	1/1	0.89	0.08	44,44,44,44	0
57	MG	AF	3001	1/1	0.89	0.13	50,50,50,50	0
57	MG	DB	3012	1/1	0.89	0.26	66,66,66,66	0
57	MG	AA	1685	1/1	0.89	0.19	62,62,62,62	0
57	MG	DG	3001	1/1	0.89	0.22	66,66,66,66	0
57	MG	DP	201	1/1	0.89	0.23	69,69,69,69	0
57	MG	DQ	3003	1/1	0.89	0.18	62,62,62,62	0
57	MG	AA	1785	1/1	0.89	0.17	72,72,72,72	0
57	MG	CA	3161	1/1	0.89	0.09	76,76,76,76	0
57	MG	AA	1713	1/1	0.90	0.20	67,67,67,67	0
57	MG	DA	3422	1/1	0.90	0.16	62,62,62,62	0
57	MG	DA	3430	1/1	0.90	0.14	47,47,47,47	0
57	MG	BA	3570	1/1	0.90	0.15	31,31,31,31	0
57	MG	DA	3153	1/1	0.90	0.08	44,44,44,44	0
57	MG	DA	3154	1/1	0.90	0.11	51,51,51,51	0
57	MG	DA	3158	1/1	0.90	0.17	56,56,56,56	0
57	MG	AX	3011	1/1	0.90	0.14	60,60,60,60	0
57	MG	BA	3419	1/1	0.90	0.13	25,25,25,25	0
57	MG	BA	3699	1/1	0.90	0.17	67,67,67,67	0
57	MG	CA	3137	1/1	0.90	0.23	78,78,78,78	0
57	MG	BA	3117	1/1	0.90	0.28	38,38,38,38	0
57	MG	CA	3141	1/1	0.90	0.11	62,62,62,62	0
57	MG	DA	3459	1/1	0.90	0.14	49,49,49,49	0
57	MG	DA	3199	1/1	0.90	0.35	62,62,62,62	0
57	MG	AA	1663	1/1	0.90	0.07	50,50,50,50	0
57	MG	DA	3470	1/1	0.90	0.10	61,61,61,61	0
57	MG	AA	1692	1/1	0.90	0.25	65,65,65,65	0
57	MG	DA	3481	1/1	0.90	0.12	40,40,40,40	0
57	MG	BA	3296	1/1	0.90	0.14	55,55,55,55	0
57	MG	BA	3436	1/1	0.90	0.11	57,57,57,57	0
57	MG	AA	1806	1/1	0.90	0.31	74,74,74,74	0
57	MG	DA	3217	1/1	0.90	0.23	57,57,57,57	0
57	MG	AA	1767	1/1	0.90	0.16	67,67,67,67	0
57	MG	AY	3001	1/1	0.90	0.23	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	1816	1/1	0.90	0.18	59,59,59,59	0
57	MG	CA	3155	1/1	0.90	0.11	57,57,57,57	0
57	MG	BA	3452	1/1	0.90	0.10	56,56,56,56	0
57	MG	DA	3514	1/1	0.90	0.14	47,47,47,47	0
57	MG	AA	1718	1/1	0.90	0.16	66,66,66,66	0
57	MG	CA	3162	1/1	0.90	0.12	79,79,79,79	0
57	MG	DA	3238	1/1	0.90	0.14	48,48,48,48	0
57	MG	BA	3205	1/1	0.90	0.36	57,57,57,57	0
57	MG	BA	3463	1/1	0.90	0.17	56,56,56,56	0
57	MG	CA	3169	1/1	0.90	0.14	62,62,62,62	0
57	MG	AA	1723	1/1	0.90	0.10	63,63,63,63	0
57	MG	DA	3256	1/1	0.90	0.12	51,51,51,51	0
57	MG	BA	3623	1/1	0.90	0.11	43,43,43,43	0
57	MG	CF	3001	1/1	0.90	0.16	51,51,51,51	0
57	MG	BA	3337	1/1	0.90	0.15	44,44,44,44	0
57	MG	AA	1731	1/1	0.90	0.21	56,56,56,56	0
57	MG	CA	3039	1/1	0.90	0.30	64,64,64,64	0
57	MG	AA	1643	1/1	0.90	0.22	58,58,58,58	0
57	MG	DA	3005	1/1	0.90	0.21	54,54,54,54	0
57	MG	DA	3012	1/1	0.90	0.08	43,43,43,43	0
57	MG	BA	3633	1/1	0.90	0.13	57,57,57,57	0
57	MG	BA	3024	1/1	0.90	0.27	58,58,58,58	0
57	MG	CA	3052	1/1	0.90	0.13	71,71,71,71	0
57	MG	BA	3749	1/1	0.90	0.12	52,52,52,52	0
57	MG	BA	3637	1/1	0.90	0.09	38,38,38,38	0
57	MG	DA	3301	1/1	0.90	0.12	63,63,63,63	0
57	MG	AA	1654	1/1	0.90	0.31	65,65,65,65	0
57	MG	BA	3346	1/1	0.90	0.09	39,39,39,39	0
57	MG	CA	3073	1/1	0.90	0.20	55,55,55,55	0
57	MG	DA	3585	1/1	0.90	0.12	55,55,55,55	0
57	MG	BA	3239	1/1	0.90	0.16	47,47,47,47	0
57	MG	DA	3052	1/1	0.90	0.07	49,49,49,49	0
57	MG	DA	3593	1/1	0.90	0.10	60,60,60,60	0
57	MG	DA	3313	1/1	0.90	0.09	39,39,39,39	0
57	MG	CA	3077	1/1	0.90	0.23	60,60,60,60	0
57	MG	DA	3600	1/1	0.90	0.09	72,72,72,72	0
57	MG	BA	3774	1/1	0.90	0.14	27,27,27,27	0
57	MG	DA	3317	1/1	0.90	0.09	54,54,54,54	0
57	MG	DA	3605	1/1	0.90	0.14	45,45,45,45	0
57	MG	DA	3057	1/1	0.90	0.10	44,44,44,44	0
57	MG	DA	3608	1/1	0.90	0.19	57,57,57,57	0
57	MG	DA	3331	1/1	0.90	0.16	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AN	502	1/1	0.90	0.32	62,62,62,62	0
57	MG	CA	3087	1/1	0.90	0.08	57,57,57,57	0
57	MG	DA	3063	1/1	0.90	0.17	47,47,47,47	0
57	MG	BA	3646	1/1	0.90	0.15	50,50,50,50	0
57	MG	BA	3792	1/1	0.90	0.15	52,52,52,52	0
57	MG	BA	3066	1/1	0.90	0.29	58,58,58,58	0
57	MG	DA	3621	1/1	0.90	0.29	52,52,52,52	0
57	MG	AA	1603	1/1	0.90	0.10	64,64,64,64	0
57	MG	DA	3074	1/1	0.90	0.13	59,59,59,59	0
57	MG	AW	3001	1/1	0.90	0.12	59,59,59,59	0
57	MG	BA	3656	1/1	0.90	0.15	45,45,45,45	0
57	MG	BA	3527	1/1	0.90	0.11	24,24,24,24	0
57	MG	AA	1786	1/1	0.90	0.14	69,69,69,69	0
57	MG	DA	3376	1/1	0.90	0.10	51,51,51,51	0
57	MG	BA	3535	1/1	0.90	0.11	39,39,39,39	0
57	MG	DA	3641	1/1	0.90	0.12	46,46,46,46	0
57	MG	DA	3642	1/1	0.90	0.23	62,62,62,62	0
57	MG	DA	3390	1/1	0.90	0.14	58,58,58,58	0
57	MG	DA	3391	1/1	0.90	0.12	45,45,45,45	0
57	MG	DA	3392	1/1	0.90	0.20	53,53,53,53	0
57	MG	AA	1710	1/1	0.90	0.18	64,64,64,64	0
57	MG	AA	1647	1/1	0.90	0.21	44,44,44,44	0
57	MG	BA	3674	1/1	0.90	0.27	48,48,48,48	0
57	MG	BB	3018	1/1	0.90	0.09	54,54,54,54	0
57	MG	DA	3401	1/1	0.90	0.14	69,69,69,69	0
57	MG	DA	3403	1/1	0.90	0.08	49,49,49,49	0
57	MG	DB	3002	1/1	0.90	0.26	63,63,63,63	0
57	MG	DA	3406	1/1	0.90	0.19	70,70,70,70	0
57	MG	DA	3407	1/1	0.90	0.09	58,58,58,58	0
57	MG	BA	3268	1/1	0.90	0.18	54,54,54,54	0
57	MG	BA	3396	1/1	0.90	0.14	25,25,25,25	0
57	MG	BB	3022	1/1	0.90	0.14	60,60,60,60	0
57	MG	DB	3013	1/1	0.90	0.16	66,66,66,66	0
57	MG	DE	3004	1/1	0.90	0.10	31,31,31,31	0
57	MG	BE	301	1/1	0.90	0.11	31,31,31,31	0
57	MG	BA	3400	1/1	0.90	0.15	39,39,39,39	0
57	MG	BA	3682	1/1	0.90	0.10	60,60,60,60	0
57	MG	AA	1641	1/1	0.90	0.24	65,65,65,65	0
57	MG	BY	502	1/1	0.90	0.17	46,46,46,46	0
57	MG	D0	101	1/1	0.90	0.22	71,71,71,71	0
57	MG	BA	3687	1/1	0.90	0.15	64,64,64,64	0
57	MG	DA	3142	1/1	0.91	0.08	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	1732	1/1	0.91	0.19	63,63,63,63	0
57	MG	DA	3424	1/1	0.91	0.13	41,41,41,41	0
57	MG	DA	3426	1/1	0.91	0.11	49,49,49,49	0
57	MG	AA	1671	1/1	0.91	0.10	60,60,60,60	0
57	MG	BA	3102	1/1	0.91	0.24	57,57,57,57	0
57	MG	AA	1739	1/1	0.91	0.36	72,72,72,72	0
57	MG	DA	3156	1/1	0.91	0.22	52,52,52,52	0
57	MG	AA	1699	1/1	0.91	0.28	58,58,58,58	0
57	MG	AA	1605	1/1	0.91	0.13	50,50,50,50	0
57	MG	DA	3167	1/1	0.91	0.21	40,40,40,40	0
57	MG	BA	3685	1/1	0.91	0.29	61,61,61,61	0
57	MG	AY	3002	1/1	0.91	0.14	52,52,52,52	0
57	MG	AA	1782	1/1	0.91	0.14	54,54,54,54	0
57	MG	DA	3455	1/1	0.91	0.14	64,64,64,64	0
57	MG	DA	3184	1/1	0.91	0.16	52,52,52,52	0
57	MG	BA	3145	1/1	0.91	0.21	48,48,48,48	0
57	MG	DA	3194	1/1	0.91	0.14	48,48,48,48	0
57	MG	CA	3133	1/1	0.91	0.15	82,82,82,82	0
57	MG	BA	3577	1/1	0.91	0.17	58,58,58,58	0
57	MG	BA	3279	1/1	0.91	0.23	52,52,52,52	0
57	MG	BA	3147	1/1	0.91	0.22	36,36,36,36	0
57	MG	BA	3283	1/1	0.91	0.33	57,57,57,57	0
57	MG	AA	1617	1/1	0.91	0.08	58,58,58,58	0
57	MG	BA	3597	1/1	0.91	0.14	55,55,55,55	0
57	MG	DA	3214	1/1	0.91	0.08	51,51,51,51	0
57	MG	DA	3492	1/1	0.91	0.09	48,48,48,48	0
57	MG	CA	3145	1/1	0.91	0.19	65,65,65,65	0
57	MG	BA	3598	1/1	0.91	0.12	33,33,33,33	0
57	MG	BA	3175	1/1	0.91	0.23	57,57,57,57	0
57	MG	CA	3149	1/1	0.91	0.17	54,54,54,54	0
57	MG	CA	3007	1/1	0.91	0.18	51,51,51,51	0
57	MG	DA	3513	1/1	0.91	0.11	69,69,69,69	0
57	MG	BA	3601	1/1	0.91	0.18	40,40,40,40	0
57	MG	DA	3233	1/1	0.91	0.28	65,65,65,65	0
57	MG	BA	3177	1/1	0.91	0.19	46,46,46,46	0
57	MG	BA	3716	1/1	0.91	0.23	45,45,45,45	0
57	MG	BA	3315	1/1	0.91	0.10	40,40,40,40	0
57	MG	CA	3015	1/1	0.91	0.18	64,64,64,64	0
57	MG	DA	3249	1/1	0.91	0.17	65,65,65,65	0
57	MG	DA	3529	1/1	0.91	0.11	76,76,76,76	0
57	MG	CA	3016	1/1	0.91	0.09	48,48,48,48	0
57	MG	DA	3532	1/1	0.91	0.12	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CA	3017	1/1	0.91	0.14	54,54,54,54	0
57	MG	BA	3190	1/1	0.91	0.26	54,54,54,54	0
57	MG	BA	3196	1/1	0.91	0.25	56,56,56,56	0
57	MG	BA	3197	1/1	0.91	0.28	58,58,58,58	0
57	MG	AA	1684	1/1	0.91	0.08	54,54,54,54	0
57	MG	AA	1749	1/1	0.91	0.14	50,50,50,50	0
57	MG	BA	3470	1/1	0.91	0.10	57,57,57,57	0
57	MG	CT	3001	1/1	0.91	0.17	60,60,60,60	0
57	MG	DA	3552	1/1	0.91	0.11	34,34,34,34	0
57	MG	BA	3732	1/1	0.91	0.15	33,33,33,33	0
57	MG	DA	3554	1/1	0.91	0.08	50,50,50,50	0
57	MG	CX	3002	1/1	0.91	0.10	67,67,67,67	0
57	MG	BA	3733	1/1	0.91	0.10	42,42,42,42	0
57	MG	BA	3333	1/1	0.91	0.13	57,57,57,57	0
57	MG	DA	3288	1/1	0.91	0.14	39,39,39,39	0
57	MG	DA	3563	1/1	0.91	0.10	70,70,70,70	0
57	MG	DA	3004	1/1	0.91	0.26	53,53,53,53	0
57	MG	BA	3735	1/1	0.91	0.14	50,50,50,50	0
57	MG	CA	3035	1/1	0.91	0.13	53,53,53,53	0
57	MG	BA	3737	1/1	0.91	0.09	34,34,34,34	0
57	MG	BA	3626	1/1	0.91	0.14	50,50,50,50	0
57	MG	DA	3577	1/1	0.91	0.09	60,60,60,60	0
57	MG	DA	3578	1/1	0.91	0.10	43,43,43,43	0
57	MG	DA	3023	1/1	0.91	0.12	58,58,58,58	0
57	MG	CA	3040	1/1	0.91	0.16	56,56,56,56	0
57	MG	CA	3041	1/1	0.91	0.14	57,57,57,57	0
57	MG	AA	1753	1/1	0.91	0.17	55,55,55,55	0
57	MG	BA	3487	1/1	0.91	0.10	54,54,54,54	0
57	MG	DA	3595	1/1	0.91	0.09	57,57,57,57	0
57	MG	CA	3050	1/1	0.91	0.45	73,73,73,73	0
57	MG	AA	1719	1/1	0.91	0.13	63,63,63,63	0
57	MG	BA	3027	1/1	0.91	0.44	64,64,64,64	0
57	MG	CA	3055	1/1	0.91	0.26	63,63,63,63	0
57	MG	DA	3324	1/1	0.91	0.09	54,54,54,54	0
57	MG	DA	3327	1/1	0.91	0.13	45,45,45,45	0
57	MG	DA	3607	1/1	0.91	0.10	64,64,64,64	0
57	MG	AA	1789	1/1	0.91	0.19	60,60,60,60	0
57	MG	BA	3751	1/1	0.91	0.19	37,37,37,37	0
57	MG	BA	3752	1/1	0.91	0.07	34,34,34,34	0
57	MG	DA	3614	1/1	0.91	0.15	55,55,55,55	0
57	MG	DA	3059	1/1	0.91	0.13	50,50,50,50	0
57	MG	DA	3335	1/1	0.91	0.15	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3336	1/1	0.91	0.08	49,49,49,49	0
57	MG	DA	3341	1/1	0.91	0.10	55,55,55,55	0
57	MG	CA	3063	1/1	0.91	0.15	65,65,65,65	0
57	MG	BA	3058	1/1	0.91	0.11	54,54,54,54	0
57	MG	BA	3757	1/1	0.91	0.16	43,43,43,43	0
57	MG	BA	3505	1/1	0.91	0.15	53,53,53,53	0
57	MG	BA	3764	1/1	0.91	0.19	66,66,66,66	0
57	MG	DA	3067	1/1	0.91	0.19	63,63,63,63	0
57	MG	DA	3627	1/1	0.91	0.16	57,57,57,57	0
57	MG	AA	1722	1/1	0.91	0.19	57,57,57,57	0
57	MG	BA	3768	1/1	0.91	0.14	57,57,57,57	0
57	MG	DA	3363	1/1	0.91	0.13	50,50,50,50	0
57	MG	DA	3634	1/1	0.91	0.12	68,68,68,68	0
57	MG	AA	1658	1/1	0.91	0.28	64,64,64,64	0
57	MG	DA	3367	1/1	0.91	0.12	49,49,49,49	0
57	MG	BA	3348	1/1	0.91	0.09	37,37,37,37	0
57	MG	DA	3643	1/1	0.91	0.12	54,54,54,54	0
57	MG	DA	3369	1/1	0.91	0.10	55,55,55,55	0
57	MG	AA	1761	1/1	0.91	0.16	70,70,70,70	0
57	MG	DA	3086	1/1	0.91	0.10	47,47,47,47	0
57	MG	DA	3379	1/1	0.91	0.08	46,46,46,46	0
57	MG	BA	3781	1/1	0.91	0.10	56,56,56,56	0
57	MG	BA	3785	1/1	0.91	0.19	56,56,56,56	0
57	MG	DA	3653	1/1	0.91	0.10	33,33,33,33	0
57	MG	BA	3231	1/1	0.91	0.10	57,57,57,57	0
57	MG	CA	3099	1/1	0.91	0.15	64,64,64,64	0
57	MG	BA	3790	1/1	0.91	0.23	66,66,66,66	0
57	MG	BA	3358	1/1	0.91	0.11	52,52,52,52	0
57	MG	AA	1659	1/1	0.91	0.30	65,65,65,65	0
57	MG	BA	3365	1/1	0.91	0.09	51,51,51,51	0
57	MG	DB	3005	1/1	0.91	0.14	68,68,68,68	0
57	MG	DB	3007	1/1	0.91	0.16	67,67,67,67	0
57	MG	BA	3662	1/1	0.91	0.13	62,62,62,62	0
57	MG	AX	3010	1/1	0.91	0.40	68,68,68,68	0
57	MG	DA	3110	1/1	0.91	0.12	49,49,49,49	0
57	MG	BA	3242	1/1	0.91	0.50	55,55,55,55	0
57	MG	BA	3668	1/1	0.91	0.13	75,75,75,75	0
57	MG	DF	301	1/1	0.91	0.11	48,48,48,48	0
57	MG	DA	3114	1/1	0.91	0.14	51,51,51,51	0
57	MG	DA	3115	1/1	0.91	0.11	55,55,55,55	0
57	MG	DN	5001	1/1	0.91	0.08	63,63,63,63	0
57	MG	DA	3120	1/1	0.91	0.34	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	1804	1/1	0.91	0.18	70,70,70,70	0
57	MG	BB	3006	1/1	0.91	0.12	62,62,62,62	0
57	MG	BA	3672	1/1	0.91	0.18	44,44,44,44	0
57	MG	BA	3094	1/1	0.91	0.14	52,52,52,52	0
57	MG	BA	3690	1/1	0.92	0.08	39,39,39,39	0
57	MG	DA	3147	1/1	0.92	0.12	44,44,44,44	0
57	MG	BE	306	1/1	0.92	0.07	38,38,38,38	0
57	MG	BA	3410	1/1	0.92	0.08	55,55,55,55	0
57	MG	BA	3288	1/1	0.92	0.11	44,44,44,44	0
57	MG	BA	3414	1/1	0.92	0.07	54,54,54,54	0
57	MG	BA	3289	1/1	0.92	0.12	49,49,49,49	0
57	MG	DA	3160	1/1	0.92	0.13	62,62,62,62	0
57	MG	DA	3166	1/1	0.92	0.23	55,55,55,55	0
57	MG	BA	3290	1/1	0.92	0.14	57,57,57,57	0
57	MG	B0	3001	1/1	0.92	0.14	47,47,47,47	0
57	MG	DA	3446	1/1	0.92	0.15	50,50,50,50	0
57	MG	BA	3420	1/1	0.92	0.10	25,25,25,25	0
57	MG	DA	3449	1/1	0.92	0.08	34,34,34,34	0
57	MG	DA	3454	1/1	0.92	0.09	43,43,43,43	0
57	MG	BA	3704	1/1	0.92	0.16	26,26,26,26	0
57	MG	CA	3136	1/1	0.92	0.15	48,48,48,48	0
57	MG	DA	3457	1/1	0.92	0.07	44,44,44,44	0
57	MG	DA	3187	1/1	0.92	0.12	47,47,47,47	0
57	MG	AM	3001	1/1	0.92	0.06	66,66,66,66	0
57	MG	DA	3191	1/1	0.92	0.14	54,54,54,54	0
57	MG	DA	3468	1/1	0.92	0.11	62,62,62,62	0
57	MG	AA	1602	1/1	0.92	0.10	68,68,68,68	0
57	MG	CA	3140	1/1	0.92	0.13	57,57,57,57	0
57	MG	BA	3711	1/1	0.92	0.20	44,44,44,44	0
57	MG	DA	3485	1/1	0.92	0.11	56,56,56,56	0
57	MG	CA	3003	1/1	0.92	0.10	58,58,58,58	0
57	MG	BA	3584	1/1	0.92	0.08	55,55,55,55	0
57	MG	BA	3301	1/1	0.92	0.15	62,62,62,62	0
57	MG	DA	3490	1/1	0.92	0.09	33,33,33,33	0
57	MG	CA	3006	1/1	0.92	0.10	68,68,68,68	0
57	MG	BA	3433	1/1	0.92	0.10	27,27,27,27	0
57	MG	DA	3493	1/1	0.92	0.09	51,51,51,51	0
57	MG	DA	3495	1/1	0.92	0.07	50,50,50,50	0
57	MG	CA	3008	1/1	0.92	0.25	47,47,47,47	0
57	MG	BA	3081	1/1	0.92	0.24	48,48,48,48	0
57	MG	CA	3150	1/1	0.92	0.15	65,65,65,65	0
57	MG	CA	3011	1/1	0.92	0.34	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	1764	1/1	0.92	0.16	66,66,66,66	0
57	MG	BA	3438	1/1	0.92	0.11	35,35,35,35	0
57	MG	AA	1609	1/1	0.92	0.18	63,63,63,63	0
57	MG	CA	3159	1/1	0.92	0.26	62,62,62,62	0
57	MG	BA	3441	1/1	0.92	0.10	39,39,39,39	0
57	MG	BA	3215	1/1	0.92	0.19	37,37,37,37	0
57	MG	DA	3520	1/1	0.92	0.10	57,57,57,57	0
57	MG	DA	3237	1/1	0.92	0.13	59,59,59,59	0
57	MG	BA	3096	1/1	0.92	0.28	60,60,60,60	0
57	MG	DA	3241	1/1	0.92	0.14	55,55,55,55	0
57	MG	DA	3243	1/1	0.92	0.08	48,48,48,48	0
57	MG	BA	3446	1/1	0.92	0.07	59,59,59,59	0
57	MG	AU	101	1/1	0.92	0.12	56,56,56,56	0
57	MG	AA	1805	1/1	0.92	0.08	48,48,48,48	0
57	MG	BA	3014	1/1	0.92	0.10	35,35,35,35	0
57	MG	BA	3621	1/1	0.92	0.18	43,43,43,43	0
57	MG	DA	3255	1/1	0.92	0.13	47,47,47,47	0
57	MG	DA	3540	1/1	0.92	0.07	50,50,50,50	0
57	MG	BA	3460	1/1	0.92	0.08	52,52,52,52	0
57	MG	AA	1676	1/1	0.92	0.10	58,58,58,58	0
57	MG	BA	3107	1/1	0.92	0.28	57,57,57,57	0
57	MG	BA	3468	1/1	0.92	0.08	45,45,45,45	0
57	MG	DA	3549	1/1	0.92	0.10	49,49,49,49	0
57	MG	CA	3031	1/1	0.92	0.24	58,58,58,58	0
57	MG	DA	3270	1/1	0.92	0.15	42,42,42,42	0
57	MG	AA	1807	1/1	0.92	0.14	68,68,68,68	0
57	MG	DA	3281	1/1	0.92	0.08	36,36,36,36	0
57	MG	CA	3033	1/1	0.92	0.20	54,54,54,54	0
57	MG	AA	1707	1/1	0.92	0.16	57,57,57,57	0
57	MG	DA	3285	1/1	0.92	0.10	50,50,50,50	0
57	MG	BA	3019	1/1	0.92	0.20	54,54,54,54	0
57	MG	DA	3006	1/1	0.92	0.10	41,41,41,41	0
57	MG	DA	3568	1/1	0.92	0.10	43,43,43,43	0
57	MG	CA	3037	1/1	0.92	0.10	53,53,53,53	0
57	MG	BA	3129	1/1	0.92	0.12	54,54,54,54	0
57	MG	BA	3638	1/1	0.92	0.20	65,65,65,65	0
57	MG	BA	3753	1/1	0.92	0.13	68,68,68,68	0
57	MG	DA	3576	1/1	0.92	0.16	67,67,67,67	0
57	MG	CA	3042	1/1	0.92	0.10	57,57,57,57	0
57	MG	AX	3006	1/1	0.92	0.13	68,68,68,68	0
57	MG	BA	3496	1/1	0.92	0.11	51,51,51,51	0
57	MG	DA	3587	1/1	0.92	0.08	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3588	1/1	0.92	0.10	59,59,59,59	0
57	MG	DA	3590	1/1	0.92	0.11	51,51,51,51	0
57	MG	BA	3761	1/1	0.92	0.09	36,36,36,36	0
57	MG	BA	3349	1/1	0.92	0.09	34,34,34,34	0
57	MG	BA	3026	1/1	0.92	0.14	60,60,60,60	0
57	MG	DA	3045	1/1	0.92	0.12	51,51,51,51	0
57	MG	DA	3046	1/1	0.92	0.20	56,56,56,56	0
57	MG	BA	3645	1/1	0.92	0.08	47,47,47,47	0
57	MG	DA	3597	1/1	0.92	0.14	48,48,48,48	0
57	MG	BA	3500	1/1	0.92	0.11	57,57,57,57	0
57	MG	AA	1811	1/1	0.92	0.18	49,49,49,49	0
57	MG	DA	3318	1/1	0.92	0.08	45,45,45,45	0
57	MG	BA	3773	1/1	0.92	0.23	32,32,32,32	0
57	MG	DA	3325	1/1	0.92	0.24	45,45,45,45	0
57	MG	DA	3326	1/1	0.92	0.09	46,46,46,46	0
57	MG	CA	3060	1/1	0.92	0.16	71,71,71,71	0
57	MG	CA	3061	1/1	0.92	0.12	66,66,66,66	0
57	MG	CA	3062	1/1	0.92	0.15	64,64,64,64	0
57	MG	BA	3651	1/1	0.92	0.12	66,66,66,66	0
57	MG	CA	3069	1/1	0.92	0.19	58,58,58,58	0
57	MG	BA	3153	1/1	0.92	0.11	45,45,45,45	0
57	MG	BA	3267	1/1	0.92	0.18	61,61,61,61	0
57	MG	DA	3337	1/1	0.92	0.09	48,48,48,48	0
57	MG	BA	3508	1/1	0.92	0.10	20,20,20,20	0
57	MG	DA	3069	1/1	0.92	0.10	43,43,43,43	0
57	MG	BA	3154	1/1	0.92	0.09	52,52,52,52	0
57	MG	DA	3071	1/1	0.92	0.10	47,47,47,47	0
57	MG	CA	3078	1/1	0.92	0.23	65,65,65,65	0
57	MG	DA	3350	1/1	0.92	0.10	31,31,31,31	0
57	MG	BA	3789	1/1	0.92	0.12	47,47,47,47	0
57	MG	DA	3352	1/1	0.92	0.07	34,34,34,34	0
57	MG	DA	3078	1/1	0.92	0.07	47,47,47,47	0
57	MG	CA	3084	1/1	0.92	0.24	56,56,56,56	0
57	MG	BA	3366	1/1	0.92	0.10	52,52,52,52	0
57	MG	DA	3636	1/1	0.92	0.10	62,62,62,62	0
57	MG	BA	3030	1/1	0.92	0.14	39,39,39,39	0
57	MG	AA	1689	1/1	0.92	0.33	71,71,71,71	0
57	MG	BA	3057	1/1	0.92	0.09	48,48,48,48	0
57	MG	BA	3276	1/1	0.92	0.17	44,44,44,44	0
57	MG	BA	3803	1/1	0.92	0.21	55,55,55,55	0
57	MG	BA	3376	1/1	0.92	0.09	29,29,29,29	0
57	MG	BA	3185	1/1	0.92	0.08	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CA	3100	1/1	0.92	0.17	59,59,59,59	0
57	MG	DA	3385	1/1	0.92	0.10	60,60,60,60	0
57	MG	CA	3101	1/1	0.92	0.13	65,65,65,65	0
57	MG	DA	3104	1/1	0.92	0.10	57,57,57,57	0
57	MG	BA	3812	1/1	0.92	0.12	42,42,42,42	0
57	MG	BA	3379	1/1	0.92	0.07	35,35,35,35	0
57	MG	AA	1670	1/1	0.92	0.22	67,67,67,67	0
57	MG	BB	3005	1/1	0.92	0.18	51,51,51,51	0
57	MG	DA	3399	1/1	0.92	0.10	59,59,59,59	0
57	MG	AA	1779	1/1	0.92	0.14	59,59,59,59	0
57	MG	AA	1696	1/1	0.92	0.11	83,83,83,83	0
57	MG	DB	3006	1/1	0.92	0.07	55,55,55,55	0
57	MG	BA	3681	1/1	0.92	0.19	61,61,61,61	0
57	MG	DA	3116	1/1	0.92	0.18	53,53,53,53	0
57	MG	BA	3401	1/1	0.92	0.14	26,26,26,26	0
57	MG	AA	1796	1/1	0.92	0.16	64,64,64,64	0
57	MG	DA	3123	1/1	0.92	0.21	54,54,54,54	0
57	MG	DD	303	1/1	0.92	0.20	51,51,51,51	0
57	MG	DA	3126	1/1	0.92	0.19	59,59,59,59	0
57	MG	DE	3007	1/1	0.92	0.10	58,58,58,58	0
57	MG	DA	3127	1/1	0.92	0.15	52,52,52,52	0
57	MG	DA	3129	1/1	0.92	0.21	56,56,56,56	0
57	MG	BA	3565	1/1	0.92	0.13	61,61,61,61	0
57	MG	DA	3131	1/1	0.92	0.10	49,49,49,49	0
57	MG	BA	3568	1/1	0.92	0.16	24,24,24,24	0
57	MG	CA	3116	1/1	0.92	0.24	57,57,57,57	0
57	MG	BA	3407	1/1	0.92	0.08	32,32,32,32	0
57	MG	BD	3003	1/1	0.92	0.10	37,37,37,37	0
57	MG	DA	3423	1/1	0.92	0.14	37,37,37,37	0
57	MG	DA	3010	1/1	0.93	0.06	41,41,41,41	0
57	MG	BA	3618	1/1	0.93	0.09	35,35,35,35	0
57	MG	BA	3619	1/1	0.93	0.07	28,28,28,28	0
57	MG	DA	3480	1/1	0.93	0.10	58,58,58,58	0
57	MG	DA	3245	1/1	0.93	0.26	58,58,58,58	0
57	MG	DA	3482	1/1	0.93	0.17	60,60,60,60	0
57	MG	AA	1700	1/1	0.93	0.16	71,71,71,71	0
57	MG	BA	3622	1/1	0.93	0.11	43,43,43,43	0
57	MG	BA	3176	1/1	0.93	0.14	55,55,55,55	0
57	MG	DA	3252	1/1	0.93	0.07	50,50,50,50	0
57	MG	DA	3026	1/1	0.93	0.22	50,50,50,50	0
57	MG	BA	3316	1/1	0.93	0.12	54,54,54,54	0
57	MG	AA	1642	1/1	0.93	0.25	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3034	1/1	0.93	0.08	42,42,42,42	0
57	MG	BA	3627	1/1	0.93	0.15	56,56,56,56	0
57	MG	AA	1604	1/1	0.93	0.12	58,58,58,58	0
57	MG	DA	3499	1/1	0.93	0.12	52,52,52,52	0
57	MG	DA	3042	1/1	0.93	0.12	49,49,49,49	0
57	MG	AA	1657	1/1	0.93	0.14	64,64,64,64	0
57	MG	DA	3506	1/1	0.93	0.13	55,55,55,55	0
57	MG	DA	3507	1/1	0.93	0.09	59,59,59,59	0
57	MG	BA	3194	1/1	0.93	0.20	39,39,39,39	0
57	MG	DA	3273	1/1	0.93	0.15	62,62,62,62	0
57	MG	DA	3512	1/1	0.93	0.07	37,37,37,37	0
57	MG	DA	3274	1/1	0.93	0.13	40,40,40,40	0
57	MG	BA	3028	1/1	0.93	0.17	37,37,37,37	0
57	MG	BA	3332	1/1	0.93	0.12	54,54,54,54	0
57	MG	BA	3476	1/1	0.93	0.11	48,48,48,48	0
57	MG	CA	3066	1/1	0.93	0.19	48,48,48,48	0
57	MG	AA	1678	1/1	0.93	0.17	47,47,47,47	0
57	MG	BA	3481	1/1	0.93	0.11	54,54,54,54	0
57	MG	CA	3071	1/1	0.93	0.18	56,56,56,56	0
57	MG	CA	3072	1/1	0.93	0.21	62,62,62,62	0
57	MG	AA	1606	1/1	0.93	0.09	54,54,54,54	0
57	MG	BA	3045	1/1	0.93	0.17	39,39,39,39	0
57	MG	DA	3292	1/1	0.93	0.07	29,29,29,29	0
57	MG	DA	3064	1/1	0.93	0.07	46,46,46,46	0
57	MG	BA	3052	1/1	0.93	0.20	50,50,50,50	0
57	MG	BA	3055	1/1	0.93	0.17	37,37,37,37	0
57	MG	AA	1646	1/1	0.93	0.28	58,58,58,58	0
57	MG	BA	3648	1/1	0.93	0.17	58,58,58,58	0
57	MG	BA	3804	1/1	0.93	0.07	36,36,36,36	0
57	MG	AA	1634	1/1	0.93	0.17	64,64,64,64	0
57	MG	BA	3806	1/1	0.93	0.17	43,43,43,43	0
57	MG	BA	3213	1/1	0.93	0.13	43,43,43,43	0
57	MG	BA	3347	1/1	0.93	0.10	38,38,38,38	0
57	MG	AA	1686	1/1	0.93	0.12	61,61,61,61	0
57	MG	BA	3506	1/1	0.93	0.16	61,61,61,61	0
57	MG	BA	3064	1/1	0.93	0.09	45,45,45,45	0
57	MG	DA	3555	1/1	0.93	0.14	46,46,46,46	0
57	MG	AA	1754	1/1	0.93	0.14	58,58,58,58	0
57	MG	BA	3067	1/1	0.93	0.15	43,43,43,43	0
57	MG	BA	3513	1/1	0.93	0.22	50,50,50,50	0
57	MG	AX	3003	1/1	0.93	0.12	56,56,56,56	0
57	MG	BA	3360	1/1	0.93	0.16	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3566	1/1	0.93	0.14	37,37,37,37	0
57	MG	BA	3519	1/1	0.93	0.11	45,45,45,45	0
57	MG	AA	1648	1/1	0.93	0.20	56,56,56,56	0
57	MG	DA	3569	1/1	0.93	0.12	45,45,45,45	0
57	MG	AA	1637	1/1	0.93	0.17	61,61,61,61	0
57	MG	AA	1797	1/1	0.93	0.19	59,59,59,59	0
57	MG	AA	1665	1/1	0.93	0.16	55,55,55,55	0
57	MG	BE	303	1/1	0.93	0.10	43,43,43,43	0
57	MG	BA	3532	1/1	0.93	0.17	55,55,55,55	0
57	MG	BA	3243	1/1	0.93	0.38	44,44,44,44	0
57	MG	BF	307	1/1	0.93	0.11	34,34,34,34	0
57	MG	DA	3580	1/1	0.93	0.12	62,62,62,62	0
57	MG	BA	3093	1/1	0.93	0.19	41,41,41,41	0
57	MG	DA	3347	1/1	0.93	0.08	35,35,35,35	0
57	MG	AX	3009	1/1	0.93	0.31	65,65,65,65	0
57	MG	BP	3001	1/1	0.93	0.13	34,34,34,34	0
57	MG	DA	3117	1/1	0.93	0.13	56,56,56,56	0
57	MG	DA	3118	1/1	0.93	0.09	39,39,39,39	0
57	MG	BR	5001	1/1	0.93	0.13	50,50,50,50	0
57	MG	DA	3357	1/1	0.93	0.08	33,33,33,33	0
57	MG	AA	1693	1/1	0.93	0.30	76,76,76,76	0
57	MG	BA	3249	1/1	0.93	0.13	53,53,53,53	0
57	MG	BZ	302	1/1	0.93	0.11	60,60,60,60	0
57	MG	BA	3559	1/1	0.93	0.11	26,26,26,26	0
57	MG	DA	3128	1/1	0.93	0.33	56,56,56,56	0
57	MG	BA	3691	1/1	0.93	0.06	43,43,43,43	0
57	MG	BA	3250	1/1	0.93	0.25	68,68,68,68	0
57	MG	B4	502	1/1	0.93	0.07	70,70,70,70	0
57	MG	AA	1763	1/1	0.93	0.06	79,79,79,79	0
57	MG	BA	3564	1/1	0.93	0.06	44,44,44,44	0
57	MG	DA	3380	1/1	0.93	0.07	66,66,66,66	0
57	MG	CA	3001	1/1	0.93	0.10	59,59,59,59	0
57	MG	DA	3389	1/1	0.93	0.13	59,59,59,59	0
57	MG	AA	1720	1/1	0.93	0.21	55,55,55,55	0
57	MG	BA	3263	1/1	0.93	0.30	60,60,60,60	0
57	MG	AA	1721	1/1	0.93	0.12	57,57,57,57	0
57	MG	BA	3266	1/1	0.93	0.10	44,44,44,44	0
57	MG	AX	3014	1/1	0.93	0.24	61,61,61,61	0
57	MG	BA	3408	1/1	0.93	0.10	51,51,51,51	0
57	MG	BA	3106	1/1	0.93	0.12	52,52,52,52	0
57	MG	BA	3270	1/1	0.93	0.26	56,56,56,56	0
57	MG	CA	3147	1/1	0.93	0.14	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3161	1/1	0.93	0.21	50,50,50,50	0
57	MG	DA	3165	1/1	0.93	0.24	55,55,55,55	0
57	MG	BA	3413	1/1	0.93	0.09	37,37,37,37	0
57	MG	DA	3408	1/1	0.93	0.12	55,55,55,55	0
57	MG	AA	1695	1/1	0.93	0.11	59,59,59,59	0
57	MG	AA	1639	1/1	0.93	0.12	54,54,54,54	0
57	MG	AA	1726	1/1	0.93	0.18	58,58,58,58	0
57	MG	DA	3175	1/1	0.93	0.12	41,41,41,41	0
57	MG	DA	3639	1/1	0.93	0.23	59,59,59,59	0
57	MG	DA	3640	1/1	0.93	0.22	62,62,62,62	0
57	MG	BA	3720	1/1	0.93	0.07	38,38,38,38	0
57	MG	DA	3416	1/1	0.93	0.10	52,52,52,52	0
57	MG	BA	3591	1/1	0.93	0.38	41,41,41,41	0
57	MG	AA	1812	1/1	0.93	0.16	63,63,63,63	0
57	MG	CA	3156	1/1	0.93	0.12	59,59,59,59	0
57	MG	CA	3158	1/1	0.93	0.17	55,55,55,55	0
57	MG	DA	3192	1/1	0.93	0.23	34,34,34,34	0
57	MG	AA	1814	1/1	0.93	0.20	57,57,57,57	0
57	MG	BA	3596	1/1	0.93	0.12	59,59,59,59	0
57	MG	DA	3197	1/1	0.93	0.25	59,59,59,59	0
57	MG	AA	1815	1/1	0.93	0.14	47,47,47,47	0
57	MG	DA	3662	1/1	0.93	0.20	50,50,50,50	0
57	MG	DA	3429	1/1	0.93	0.15	36,36,36,36	0
57	MG	BA	3430	1/1	0.93	0.10	34,34,34,34	0
57	MG	BA	3599	1/1	0.93	0.10	60,60,60,60	0
57	MG	BA	3141	1/1	0.93	0.09	38,38,38,38	0
57	MG	DA	3203	1/1	0.93	0.21	53,53,53,53	0
57	MG	BA	3144	1/1	0.93	0.13	41,41,41,41	0
57	MG	DA	3211	1/1	0.93	0.12	51,51,51,51	0
57	MG	BA	3602	1/1	0.93	0.09	47,47,47,47	0
57	MG	DB	3008	1/1	0.93	0.17	56,56,56,56	0
57	MG	DA	3443	1/1	0.93	0.16	51,51,51,51	0
57	MG	AA	1774	1/1	0.93	0.18	51,51,51,51	0
57	MG	BA	3015	1/1	0.93	0.11	47,47,47,47	0
57	MG	BA	3740	1/1	0.93	0.16	65,65,65,65	0
57	MG	AA	1626	1/1	0.93	0.29	59,59,59,59	0
57	MG	AE	3001	1/1	0.93	0.07	63,63,63,63	0
57	MG	BA	3613	1/1	0.93	0.20	53,53,53,53	0
57	MG	BA	3293	1/1	0.93	0.09	58,58,58,58	0
57	MG	CA	3038	1/1	0.93	0.17	57,57,57,57	0
57	MG	DF	303	1/1	0.93	0.07	42,42,42,42	0
57	MG	BA	3161	1/1	0.93	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
57	MG	DA	3235	1/1	0.93	0.08	48,48,48,48	0
57	MG	AA	1777	1/1	0.93	0.08	71,71,71,71	0
57	MG	BA	3617	1/1	0.93	0.09	42,42,42,42	0
57	MG	DA	3465	1/1	0.93	0.11	42,42,42,42	0
57	MG	DV	201	1/1	0.93	0.19	58,58,58,58	0
57	MG	DA	3466	1/1	0.93	0.07	48,48,48,48	0
57	MG	D3	3001	1/1	0.93	0.13	63,63,63,63	0
57	MG	DA	3467	1/1	0.93	0.11	52,52,52,52	0
57	MG	AA	1675	1/1	0.94	0.23	61,61,61,61	0
57	MG	BA	3697	1/1	0.94	0.15	41,41,41,41	0
57	MG	B7	105	1/1	0.94	0.18	28,28,28,28	0
57	MG	B8	5002	1/1	0.94	0.21	53,53,53,53	0
57	MG	BA	3405	1/1	0.94	0.12	52,52,52,52	0
57	MG	DA	3451	1/1	0.94	0.06	55,55,55,55	0
57	MG	DA	3193	1/1	0.94	0.10	47,47,47,47	0
57	MG	BA	3165	1/1	0.94	0.14	52,52,52,52	0
57	MG	BA	3170	1/1	0.94	0.11	38,38,38,38	0
57	MG	BA	3056	1/1	0.94	0.14	46,46,46,46	0
57	MG	DA	3198	1/1	0.94	0.24	52,52,52,52	0
57	MG	DA	3461	1/1	0.94	0.08	51,51,51,51	0
57	MG	CA	3151	1/1	0.94	0.14	64,64,64,64	0
57	MG	AA	1640	1/1	0.94	0.19	54,54,54,54	0
57	MG	DA	3464	1/1	0.94	0.11	54,54,54,54	0
57	MG	AA	1698	1/1	0.94	0.12	58,58,58,58	0
57	MG	BA	3179	1/1	0.94	0.18	43,43,43,43	0
57	MG	BA	3415	1/1	0.94	0.09	35,35,35,35	0
57	MG	AA	1760	1/1	0.94	0.14	65,65,65,65	0
57	MG	DA	3208	1/1	0.94	0.23	54,54,54,54	0
57	MG	DA	3474	1/1	0.94	0.06	53,53,53,53	0
57	MG	AA	1660	1/1	0.94	0.26	51,51,51,51	0
57	MG	BA	3291	1/1	0.94	0.14	53,53,53,53	0
57	MG	BA	3422	1/1	0.94	0.09	36,36,36,36	0
57	MG	BA	3065	1/1	0.94	0.08	50,50,50,50	0
57	MG	DA	3484	1/1	0.94	0.10	46,46,46,46	0
57	MG	BA	3426	1/1	0.94	0.10	46,46,46,46	0
57	MG	DA	3220	1/1	0.94	0.27	50,50,50,50	0
57	MG	CA	3163	1/1	0.94	0.17	62,62,62,62	0
57	MG	BA	3295	1/1	0.94	0.10	23,23,23,23	0
57	MG	AA	1803	1/1	0.94	0.09	46,46,46,46	0
57	MG	DA	3230	1/1	0.94	0.09	46,46,46,46	0
57	MG	DA	3231	1/1	0.94	0.23	61,61,61,61	0
57	MG	BA	3297	1/1	0.94	0.07	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CD	502	1/1	0.94	0.28	53,53,53,53	0
57	MG	AA	1762	1/1	0.94	0.21	66,66,66,66	0
57	MG	CA	3020	1/1	0.94	0.10	45,45,45,45	0
57	MG	DA	3500	1/1	0.94	0.16	55,55,55,55	0
57	MG	BA	3300	1/1	0.94	0.12	53,53,53,53	0
57	MG	AA	1628	1/1	0.94	0.11	65,65,65,65	0
57	MG	BA	3437	1/1	0.94	0.18	62,62,62,62	0
57	MG	DA	3239	1/1	0.94	0.10	49,49,49,49	0
57	MG	CW	3001	1/1	0.94	0.10	66,66,66,66	0
57	MG	BA	3603	1/1	0.94	0.21	42,42,42,42	0
57	MG	BA	3306	1/1	0.94	0.10	15,15,15,15	0
57	MG	CA	3028	1/1	0.94	0.17	48,48,48,48	0
57	MG	BA	3606	1/1	0.94	0.07	36,36,36,36	0
57	MG	BA	3309	1/1	0.94	0.14	65,65,65,65	0
57	MG	BA	3313	1/1	0.94	0.12	38,38,38,38	0
57	MG	AA	1725	1/1	0.94	0.15	51,51,51,51	0
57	MG	DA	3009	1/1	0.94	0.16	61,61,61,61	0
57	MG	DA	3522	1/1	0.94	0.09	51,51,51,51	0
57	MG	BA	3078	1/1	0.94	0.26	54,54,54,54	0
57	MG	CA	3034	1/1	0.94	0.32	66,66,66,66	0
57	MG	AA	1765	1/1	0.94	0.21	65,65,65,65	0
57	MG	BA	3448	1/1	0.94	0.06	17,17,17,17	0
57	MG	BA	3748	1/1	0.94	0.27	61,61,61,61	0
57	MG	DA	3267	1/1	0.94	0.07	44,44,44,44	0
57	MG	AA	1680	1/1	0.94	0.19	51,51,51,51	0
57	MG	AA	1727	1/1	0.94	0.11	50,50,50,50	0
57	MG	AA	1769	1/1	0.94	0.11	50,50,50,50	0
57	MG	AA	1770	1/1	0.94	0.07	51,51,51,51	0
57	MG	BA	3754	1/1	0.94	0.08	42,42,42,42	0
57	MG	BA	3218	1/1	0.94	0.07	45,45,45,45	0
57	MG	CA	3047	1/1	0.94	0.10	50,50,50,50	0
57	MG	CA	3048	1/1	0.94	0.08	58,58,58,58	0
57	MG	BA	3095	1/1	0.94	0.17	53,53,53,53	0
57	MG	BA	3222	1/1	0.94	0.08	42,42,42,42	0
57	MG	BA	3762	1/1	0.94	0.09	20,20,20,20	0
57	MG	AA	1702	1/1	0.94	0.20	47,47,47,47	0
57	MG	CA	3054	1/1	0.94	0.33	69,69,69,69	0
57	MG	BA	3001	1/1	0.94	0.09	43,43,43,43	0
57	MG	AA	1682	1/1	0.94	0.30	59,59,59,59	0
57	MG	BA	3767	1/1	0.94	0.11	45,45,45,45	0
57	MG	BA	3628	1/1	0.94	0.20	52,52,52,52	0
57	MG	DA	3296	1/1	0.94	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
57	MG	DA	3561	1/1	0.94	0.10	52,52,52,52	0
57	MG	BA	3010	1/1	0.94	0.20	53,53,53,53	0
57	MG	BA	3630	1/1	0.94	0.17	39,39,39,39	0
57	MG	BA	3631	1/1	0.94	0.16	46,46,46,46	0
57	MG	BA	3482	1/1	0.94	0.07	51,51,51,51	0
57	MG	CA	3064	1/1	0.94	0.31	55,55,55,55	0
57	MG	DA	3310	1/1	0.94	0.07	35,35,35,35	0
57	MG	BA	3237	1/1	0.94	0.08	44,44,44,44	0
57	MG	CA	3068	1/1	0.94	0.13	58,58,58,58	0
57	MG	BA	3485	1/1	0.94	0.11	26,26,26,26	0
57	MG	DA	3575	1/1	0.94	0.09	56,56,56,56	0
57	MG	BA	3345	1/1	0.94	0.12	51,51,51,51	0
57	MG	BA	3787	1/1	0.94	0.07	45,45,45,45	0
57	MG	AA	1737	1/1	0.94	0.11	60,60,60,60	0
57	MG	DA	3579	1/1	0.94	0.11	62,62,62,62	0
57	MG	DA	3319	1/1	0.94	0.09	33,33,33,33	0
57	MG	DA	3583	1/1	0.94	0.10	52,52,52,52	0
57	MG	BA	3492	1/1	0.94	0.06	38,38,38,38	0
57	MG	DA	3077	1/1	0.94	0.07	38,38,38,38	0
57	MG	CA	3074	1/1	0.94	0.17	60,60,60,60	0
57	MG	CA	3075	1/1	0.94	0.20	65,65,65,65	0
57	MG	AA	1622	1/1	0.94	0.15	69,69,69,69	0
57	MG	DA	3085	1/1	0.94	0.14	28,28,28,28	0
57	MG	AA	1653	1/1	0.94	0.16	54,54,54,54	0
57	MG	DA	3333	1/1	0.94	0.11	47,47,47,47	0
57	MG	BA	3110	1/1	0.94	0.08	36,36,36,36	0
57	MG	DA	3088	1/1	0.94	0.13	50,50,50,50	0
57	MG	CA	3081	1/1	0.94	0.12	44,44,44,44	0
57	MG	AA	1616	1/1	0.94	0.07	73,73,73,73	0
57	MG	BA	3801	1/1	0.94	0.10	71,71,71,71	0
57	MG	AA	1742	1/1	0.94	0.10	52,52,52,52	0
57	MG	DA	3604	1/1	0.94	0.11	61,61,61,61	0
57	MG	BA	3353	1/1	0.94	0.10	55,55,55,55	0
57	MG	AA	1687	1/1	0.94	0.22	46,46,46,46	0
57	MG	AA	1619	1/1	0.94	0.15	64,64,64,64	0
57	MG	BA	3130	1/1	0.94	0.26	48,48,48,48	0
57	MG	DA	3610	1/1	0.94	0.09	47,47,47,47	0
57	MG	DA	3349	1/1	0.94	0.10	34,34,34,34	0
57	MG	BA	3654	1/1	0.94	0.10	59,59,59,59	0
57	MG	BA	3135	1/1	0.94	0.34	56,56,56,56	0
57	MG	DA	3109	1/1	0.94	0.10	49,49,49,49	0
57	MG	CA	3097	1/1	0.94	0.21	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3137	1/1	0.94	0.19	52,52,52,52	0
57	MG	BA	3516	1/1	0.94	0.12	46,46,46,46	0
57	MG	DA	3361	1/1	0.94	0.06	33,33,33,33	0
57	MG	AA	1645	1/1	0.94	0.21	61,61,61,61	0
57	MG	DA	3622	1/1	0.94	0.14	49,49,49,49	0
57	MG	BA	3664	1/1	0.94	0.18	69,69,69,69	0
57	MG	BA	3264	1/1	0.94	0.18	51,51,51,51	0
57	MG	AA	1691	1/1	0.94	0.27	62,62,62,62	0
57	MG	AA	1750	1/1	0.94	0.08	49,49,49,49	0
57	MG	AA	1751	1/1	0.94	0.20	53,53,53,53	0
57	MG	DA	3371	1/1	0.94	0.08	34,34,34,34	0
57	MG	DA	3375	1/1	0.94	0.15	57,57,57,57	0
57	MG	BA	3526	1/1	0.94	0.18	41,41,41,41	0
57	MG	AA	1612	1/1	0.94	0.07	63,63,63,63	0
57	MG	DA	3125	1/1	0.94	0.17	56,56,56,56	0
57	MG	BD	3002	1/1	0.94	0.10	28,28,28,28	0
57	MG	DA	3638	1/1	0.94	0.06	47,47,47,47	0
57	MG	AA	1621	1/1	0.94	0.08	44,44,44,44	0
57	MG	BA	3381	1/1	0.94	0.07	49,49,49,49	0
57	MG	BA	3383	1/1	0.94	0.07	37,37,37,37	0
57	MG	BE	304	1/1	0.94	0.11	23,23,23,23	0
57	MG	BA	3536	1/1	0.94	0.06	32,32,32,32	0
57	MG	DA	3133	1/1	0.94	0.09	60,60,60,60	0
57	MG	DA	3134	1/1	0.94	0.11	52,52,52,52	0
57	MG	BA	3385	1/1	0.94	0.13	30,30,30,30	0
57	MG	DA	3397	1/1	0.94	0.09	42,42,42,42	0
57	MG	DA	3648	1/1	0.94	0.12	62,62,62,62	0
57	MG	DA	3136	1/1	0.94	0.15	48,48,48,48	0
57	MG	DA	3138	1/1	0.94	0.12	54,54,54,54	0
57	MG	BA	3386	1/1	0.94	0.06	28,28,28,28	0
57	MG	DA	3402	1/1	0.94	0.09	48,48,48,48	0
57	MG	DA	3140	1/1	0.94	0.10	64,64,64,64	0
57	MG	DA	3405	1/1	0.94	0.08	47,47,47,47	0
57	MG	BA	3549	1/1	0.94	0.11	66,66,66,66	0
57	MG	BA	3389	1/1	0.94	0.15	37,37,37,37	0
57	MG	DA	3145	1/1	0.94	0.30	48,48,48,48	0
57	MG	CA	3123	1/1	0.94	0.26	61,61,61,61	0
57	MG	BA	3686	1/1	0.94	0.08	27,27,27,27	0
57	MG	DA	3149	1/1	0.94	0.11	46,46,46,46	0
57	MG	DA	3150	1/1	0.94	0.16	50,50,50,50	0
57	MG	BP	3002	1/1	0.94	0.09	60,60,60,60	0
57	MG	CA	3126	1/1	0.94	0.09	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3155	1/1	0.94	0.26	53,53,53,53	0
57	MG	BA	3390	1/1	0.94	0.06	31,31,31,31	0
57	MG	DA	3157	1/1	0.94	0.12	34,34,34,34	0
57	MG	DD	301	1/1	0.94	0.08	44,44,44,44	0
57	MG	BV	204	1/1	0.94	0.09	39,39,39,39	0
57	MG	BW	3004	1/1	0.94	0.10	45,45,45,45	0
57	MG	BA	3271	1/1	0.94	0.13	60,60,60,60	0
57	MG	BA	3560	1/1	0.94	0.12	63,63,63,63	0
57	MG	BA	3051	1/1	0.94	0.17	37,37,37,37	0
57	MG	BA	3692	1/1	0.94	0.08	58,58,58,58	0
57	MG	CA	3138	1/1	0.94	0.11	65,65,65,65	0
57	MG	BA	3160	1/1	0.94	0.09	49,49,49,49	0
57	MG	DO	202	1/1	0.94	0.15	60,60,60,60	0
57	MG	AA	1791	1/1	0.94	0.06	54,54,54,54	0
57	MG	DA	3174	1/1	0.94	0.17	52,52,52,52	0
57	MG	DR	3001	1/1	0.94	0.09	49,49,49,49	0
57	MG	BA	3695	1/1	0.94	0.06	40,40,40,40	0
57	MG	DA	3176	1/1	0.94	0.18	38,38,38,38	0
57	MG	B6	101	1/1	0.94	0.21	60,60,60,60	0
57	MG	DA	3179	1/1	0.94	0.10	59,59,59,59	0
57	MG	D8	5001	1/1	0.94	0.12	44,44,44,44	0
57	MG	DA	3181	1/1	0.94	0.09	49,49,49,49	0
60	K	AX	3001	1/1	0.94	0.11	77,77,77,77	0
57	MG	BA	3663	1/1	0.95	0.14	50,50,50,50	0
57	MG	AA	1778	1/1	0.95	0.09	51,51,51,51	0
57	MG	DA	3425	1/1	0.95	0.14	51,51,51,51	0
57	MG	BA	3665	1/1	0.95	0.11	42,42,42,42	0
57	MG	BD	3005	1/1	0.95	0.09	44,44,44,44	0
57	MG	CA	3128	1/1	0.95	0.13	52,52,52,52	0
57	MG	BA	3524	1/1	0.95	0.12	33,33,33,33	0
57	MG	DA	3432	1/1	0.95	0.17	52,52,52,52	0
57	MG	BA	3025	1/1	0.95	0.06	43,43,43,43	0
57	MG	AA	1733	1/1	0.95	0.10	50,50,50,50	0
57	MG	BE	305	1/1	0.95	0.08	48,48,48,48	0
57	MG	DA	3437	1/1	0.95	0.14	48,48,48,48	0
57	MG	DA	3438	1/1	0.95	0.05	42,42,42,42	0
57	MG	CA	3135	1/1	0.95	0.09	59,59,59,59	0
57	MG	AA	1759	1/1	0.95	0.09	55,55,55,55	0
57	MG	BA	3670	1/1	0.95	0.16	54,54,54,54	0
57	MG	BA	3387	1/1	0.95	0.10	29,29,29,29	0
57	MG	BG	201	1/1	0.95	0.09	39,39,39,39	0
57	MG	BA	3280	1/1	0.95	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
57	MG	BN	3002	1/1	0.95	0.08	51,51,51,51	0
57	MG	DA	3183	1/1	0.95	0.17	41,41,41,41	0
57	MG	BA	3533	1/1	0.95	0.11	23,23,23,23	0
57	MG	DA	3185	1/1	0.95	0.07	51,51,51,51	0
57	MG	BA	3675	1/1	0.95	0.17	56,56,56,56	0
57	MG	DA	3189	1/1	0.95	0.12	47,47,47,47	0
57	MG	BA	3281	1/1	0.95	0.25	50,50,50,50	0
57	MG	BA	3391	1/1	0.95	0.07	41,41,41,41	0
57	MG	DA	3460	1/1	0.95	0.17	37,37,37,37	0
57	MG	BU	201	1/1	0.95	0.21	43,43,43,43	0
57	MG	BU	204	1/1	0.95	0.19	47,47,47,47	0
57	MG	AA	1636	1/1	0.95	0.18	52,52,52,52	0
57	MG	BW	3002	1/1	0.95	0.23	58,58,58,58	0
57	MG	BA	3187	1/1	0.95	0.23	38,38,38,38	0
57	MG	BA	3545	1/1	0.95	0.08	28,28,28,28	0
57	MG	BA	3683	1/1	0.95	0.07	62,62,62,62	0
57	MG	BA	3546	1/1	0.95	0.06	68,68,68,68	0
57	MG	BA	3284	1/1	0.95	0.13	57,57,57,57	0
57	MG	DA	3473	1/1	0.95	0.19	50,50,50,50	0
57	MG	BA	3552	1/1	0.95	0.15	55,55,55,55	0
57	MG	DA	3477	1/1	0.95	0.08	53,53,53,53	0
57	MG	BA	3554	1/1	0.95	0.07	51,51,51,51	0
57	MG	CA	3157	1/1	0.95	0.13	60,60,60,60	0
57	MG	DA	3205	1/1	0.95	0.09	62,62,62,62	0
57	MG	BA	3285	1/1	0.95	0.10	58,58,58,58	0
57	MG	BA	3689	1/1	0.95	0.11	59,59,59,59	0
57	MG	BA	3403	1/1	0.95	0.12	33,33,33,33	0
57	MG	B7	103	1/1	0.95	0.13	40,40,40,40	0
57	MG	BA	3189	1/1	0.95	0.06	39,39,39,39	0
57	MG	AA	1783	1/1	0.95	0.10	35,35,35,35	0
57	MG	BA	3193	1/1	0.95	0.06	37,37,37,37	0
57	MG	CA	3166	1/1	0.95	0.07	55,55,55,55	0
57	MG	DA	3224	1/1	0.95	0.08	39,39,39,39	0
57	MG	BA	3562	1/1	0.95	0.09	55,55,55,55	0
57	MG	DA	3494	1/1	0.95	0.07	45,45,45,45	0
57	MG	BA	3101	1/1	0.95	0.17	37,37,37,37	0
57	MG	DA	3496	1/1	0.95	0.17	56,56,56,56	0
57	MG	BA	3036	1/1	0.95	0.09	56,56,56,56	0
57	MG	DA	3498	1/1	0.95	0.13	35,35,35,35	0
57	MG	AA	1615	1/1	0.95	0.12	51,51,51,51	0
57	MG	BA	3566	1/1	0.95	0.10	31,31,31,31	0
57	MG	BA	3105	1/1	0.95	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
57	MG	AA	1666	1/1	0.95	0.26	63,63,63,63	0
57	MG	DA	3505	1/1	0.95	0.07	51,51,51,51	0
57	MG	CK	5001	1/1	0.95	0.10	61,61,61,61	0
57	MG	BA	3049	1/1	0.95	0.12	46,46,46,46	0
57	MG	BA	3203	1/1	0.95	0.30	61,61,61,61	0
57	MG	BA	3706	1/1	0.95	0.09	47,47,47,47	0
57	MG	BA	3707	1/1	0.95	0.20	39,39,39,39	0
57	MG	BA	3709	1/1	0.95	0.31	48,48,48,48	0
57	MG	DA	3242	1/1	0.95	0.10	52,52,52,52	0
57	MG	BA	3108	1/1	0.95	0.07	42,42,42,42	0
57	MG	DA	3244	1/1	0.95	0.21	55,55,55,55	0
57	MG	DA	3003	1/1	0.95	0.15	36,36,36,36	0
57	MG	DA	3519	1/1	0.95	0.19	58,58,58,58	0
57	MG	DA	3247	1/1	0.95	0.15	49,49,49,49	0
57	MG	DA	3521	1/1	0.95	0.07	57,57,57,57	0
57	MG	BA	3109	1/1	0.95	0.11	56,56,56,56	0
57	MG	BA	3421	1/1	0.95	0.16	62,62,62,62	0
57	MG	AA	1638	1/1	0.95	0.07	60,60,60,60	0
57	MG	BA	3578	1/1	0.95	0.25	39,39,39,39	0
57	MG	DA	3528	1/1	0.95	0.10	36,36,36,36	0
57	MG	AA	1703	1/1	0.95	0.23	43,43,43,43	0
57	MG	BA	3310	1/1	0.95	0.08	26,26,26,26	0
57	MG	DA	3015	1/1	0.95	0.11	60,60,60,60	0
57	MG	CA	3021	1/1	0.95	0.24	61,61,61,61	0
57	MG	DA	3534	1/1	0.95	0.07	46,46,46,46	0
57	MG	BA	3582	1/1	0.95	0.07	31,31,31,31	0
57	MG	DA	3020	1/1	0.95	0.04	26,26,26,26	0
57	MG	DA	3262	1/1	0.95	0.10	20,20,20,20	0
57	MG	DA	3263	1/1	0.95	0.07	65,65,65,65	0
57	MG	DA	3264	1/1	0.95	0.10	51,51,51,51	0
57	MG	DA	3021	1/1	0.95	0.09	50,50,50,50	0
57	MG	DA	3022	1/1	0.95	0.27	60,60,60,60	0
57	MG	DA	3544	1/1	0.95	0.09	53,53,53,53	0
57	MG	BA	3721	1/1	0.95	0.08	47,47,47,47	0
57	MG	DA	3546	1/1	0.95	0.07	47,47,47,47	0
57	MG	BA	3112	1/1	0.95	0.17	41,41,41,41	0
57	MG	BA	3588	1/1	0.95	0.07	43,43,43,43	0
57	MG	DA	3027	1/1	0.95	0.30	43,43,43,43	0
57	MG	BA	3724	1/1	0.95	0.05	20,20,20,20	0
57	MG	DA	3279	1/1	0.95	0.07	36,36,36,36	0
57	MG	BA	3314	1/1	0.95	0.10	39,39,39,39	0
57	MG	BA	3592	1/1	0.95	0.09	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3558	1/1	0.95	0.09	48,48,48,48	0
57	MG	DA	3283	1/1	0.95	0.06	27,27,27,27	0
57	MG	BA	3113	1/1	0.95	0.09	50,50,50,50	0
57	MG	DA	3038	1/1	0.95	0.07	56,56,56,56	0
57	MG	AA	1704	1/1	0.95	0.20	57,57,57,57	0
57	MG	BA	3595	1/1	0.95	0.12	61,61,61,61	0
57	MG	AA	1652	1/1	0.95	0.19	62,62,62,62	0
57	MG	BA	3122	1/1	0.95	0.09	35,35,35,35	0
57	MG	BA	3321	1/1	0.95	0.08	53,53,53,53	0
57	MG	BA	3736	1/1	0.95	0.07	22,22,22,22	0
57	MG	DA	3050	1/1	0.95	0.23	44,44,44,44	0
57	MG	DA	3294	1/1	0.95	0.06	40,40,40,40	0
57	MG	BA	3123	1/1	0.95	0.07	43,43,43,43	0
57	MG	BA	3325	1/1	0.95	0.09	45,45,45,45	0
57	MG	DA	3298	1/1	0.95	0.14	55,55,55,55	0
57	MG	BA	3739	1/1	0.95	0.07	21,21,21,21	0
57	MG	AA	1706	1/1	0.95	0.18	60,60,60,60	0
57	MG	DA	3303	1/1	0.95	0.11	43,43,43,43	0
57	MG	BA	3229	1/1	0.95	0.10	52,52,52,52	0
57	MG	BA	3230	1/1	0.95	0.13	58,58,58,58	0
57	MG	CA	3043	1/1	0.95	0.16	44,44,44,44	0
57	MG	CA	3045	1/1	0.95	0.24	62,62,62,62	0
57	MG	BA	3745	1/1	0.95	0.13	61,61,61,61	0
57	MG	BA	3444	1/1	0.95	0.09	48,48,48,48	0
57	MG	AA	1683	1/1	0.95	0.20	62,62,62,62	0
57	MG	BA	3607	1/1	0.95	0.07	36,36,36,36	0
57	MG	DA	3068	1/1	0.95	0.18	53,53,53,53	0
57	MG	BA	3236	1/1	0.95	0.16	52,52,52,52	0
57	MG	BA	3750	1/1	0.95	0.10	46,46,46,46	0
57	MG	DA	3320	1/1	0.95	0.09	49,49,49,49	0
57	MG	BA	3132	1/1	0.95	0.09	50,50,50,50	0
57	MG	BA	3610	1/1	0.95	0.06	61,61,61,61	0
57	MG	DA	3073	1/1	0.95	0.06	33,33,33,33	0
57	MG	BA	3060	1/1	0.95	0.18	51,51,51,51	0
57	MG	DA	3076	1/1	0.95	0.20	52,52,52,52	0
57	MG	DA	3330	1/1	0.95	0.10	36,36,36,36	0
57	MG	BA	3453	1/1	0.95	0.07	50,50,50,50	0
57	MG	BA	3455	1/1	0.95	0.07	52,52,52,52	0
57	MG	BA	3136	1/1	0.95	0.28	49,49,49,49	0
57	MG	BA	3759	1/1	0.95	0.09	70,70,70,70	0
57	MG	DA	3084	1/1	0.95	0.08	44,44,44,44	0
57	MG	BA	3341	1/1	0.95	0.11	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3613	1/1	0.95	0.11	56,56,56,56	0
57	MG	BA	3241	1/1	0.95	0.15	56,56,56,56	0
57	MG	DA	3339	1/1	0.95	0.12	52,52,52,52	0
57	MG	AA	1633	1/1	0.95	0.26	59,59,59,59	0
57	MG	BA	3466	1/1	0.95	0.12	51,51,51,51	0
57	MG	CA	3065	1/1	0.95	0.14	59,59,59,59	0
57	MG	DA	3090	1/1	0.95	0.15	50,50,50,50	0
57	MG	DA	3092	1/1	0.95	0.15	57,57,57,57	0
57	MG	DA	3094	1/1	0.95	0.05	39,39,39,39	0
57	MG	BA	3620	1/1	0.95	0.07	29,29,29,29	0
57	MG	BA	3467	1/1	0.95	0.05	46,46,46,46	0
57	MG	BA	3063	1/1	0.95	0.17	47,47,47,47	0
57	MG	AA	1795	1/1	0.95	0.08	55,55,55,55	0
57	MG	DA	3354	1/1	0.95	0.07	41,41,41,41	0
57	MG	BA	3770	1/1	0.95	0.14	49,49,49,49	0
57	MG	AA	1709	1/1	0.95	0.19	55,55,55,55	0
57	MG	DA	3103	1/1	0.95	0.10	56,56,56,56	0
57	MG	DA	3359	1/1	0.95	0.11	40,40,40,40	0
57	MG	DA	3360	1/1	0.95	0.06	31,31,31,31	0
57	MG	AA	1627	1/1	0.95	0.06	54,54,54,54	0
57	MG	AN	503	1/1	0.95	0.11	52,52,52,52	0
57	MG	BA	3152	1/1	0.95	0.13	23,23,23,23	0
57	MG	DA	3365	1/1	0.95	0.06	19,19,19,19	0
57	MG	DA	3108	1/1	0.95	0.08	50,50,50,50	0
57	MG	BA	3784	1/1	0.95	0.07	52,52,52,52	0
57	MG	AA	1728	1/1	0.95	0.18	49,49,49,49	0
57	MG	AA	1799	1/1	0.95	0.10	78,78,78,78	0
57	MG	BA	3486	1/1	0.95	0.08	41,41,41,41	0
57	MG	DA	3372	1/1	0.95	0.13	53,53,53,53	0
57	MG	DA	3374	1/1	0.95	0.25	62,62,62,62	0
57	MG	BA	3788	1/1	0.95	0.09	44,44,44,44	0
57	MG	CA	3083	1/1	0.95	0.11	50,50,50,50	0
57	MG	BA	3355	1/1	0.95	0.08	35,35,35,35	0
57	MG	DA	3651	1/1	0.95	0.07	48,48,48,48	0
57	MG	AA	1800	1/1	0.95	0.12	59,59,59,59	0
57	MG	DA	3654	1/1	0.95	0.14	35,35,35,35	0
57	MG	BA	3791	1/1	0.95	0.21	49,49,49,49	0
57	MG	DA	3658	1/1	0.95	0.23	62,62,62,62	0
57	MG	DA	3660	1/1	0.95	0.27	46,46,46,46	0
57	MG	DA	3382	1/1	0.95	0.06	41,41,41,41	0
57	MG	BA	3634	1/1	0.95	0.07	55,55,55,55	0
57	MG	DA	3387	1/1	0.95	0.13	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3388	1/1	0.95	0.10	47,47,47,47	0
57	MG	BA	3359	1/1	0.95	0.07	60,60,60,60	0
57	MG	AA	1697	1/1	0.95	0.18	65,65,65,65	0
57	MG	BA	3363	1/1	0.95	0.12	52,52,52,52	0
57	MG	BA	3799	1/1	0.95	0.10	42,42,42,42	0
57	MG	AA	1776	1/1	0.95	0.16	73,73,73,73	0
57	MG	BA	3083	1/1	0.95	0.21	60,60,60,60	0
57	MG	DB	3009	1/1	0.95	0.08	58,58,58,58	0
57	MG	BA	3167	1/1	0.95	0.17	45,45,45,45	0
57	MG	BA	3367	1/1	0.95	0.09	52,52,52,52	0
57	MG	BA	3169	1/1	0.95	0.12	50,50,50,50	0
57	MG	BA	3807	1/1	0.95	0.11	66,66,66,66	0
57	MG	BA	3370	1/1	0.95	0.17	50,50,50,50	0
57	MG	BA	3269	1/1	0.95	0.11	45,45,45,45	0
57	MG	BA	3509	1/1	0.95	0.15	50,50,50,50	0
57	MG	DE	3005	1/1	0.95	0.08	35,35,35,35	0
57	MG	DE	3006	1/1	0.95	0.12	38,38,38,38	0
57	MG	BB	3002	1/1	0.95	0.17	55,55,55,55	0
57	MG	BA	3650	1/1	0.95	0.13	45,45,45,45	0
57	MG	BA	3373	1/1	0.95	0.07	34,34,34,34	0
57	MG	DA	3141	1/1	0.95	0.10	51,51,51,51	0
57	MG	DF	304	1/1	0.95	0.05	51,51,51,51	0
57	MG	DF	305	1/1	0.95	0.23	45,45,45,45	0
57	MG	DA	3409	1/1	0.95	0.10	54,54,54,54	0
57	MG	BA	3652	1/1	0.95	0.07	58,58,58,58	0
57	MG	BB	3008	1/1	0.95	0.28	59,59,59,59	0
57	MG	DA	3144	1/1	0.95	0.18	41,41,41,41	0
57	MG	CA	3114	1/1	0.95	0.17	71,71,71,71	0
57	MG	AA	1635	1/1	0.95	0.22	65,65,65,65	0
57	MG	BA	3515	1/1	0.95	0.07	27,27,27,27	0
57	MG	BB	3015	1/1	0.95	0.11	45,45,45,45	0
57	MG	DY	502	1/1	0.95	0.12	55,55,55,55	0
57	MG	BA	3171	1/1	0.95	0.20	35,35,35,35	0
57	MG	BA	3172	1/1	0.95	0.14	40,40,40,40	0
57	MG	BA	3273	1/1	0.95	0.08	45,45,45,45	0
57	MG	BA	3174	1/1	0.95	0.38	38,38,38,38	0
57	MG	BB	3021	1/1	0.95	0.07	41,41,41,41	0
57	MG	BA	3362	1/1	0.96	0.09	47,47,47,47	0
57	MG	DA	3271	1/1	0.96	0.07	30,30,30,30	0
57	MG	BA	3212	1/1	0.96	0.19	57,57,57,57	0
57	MG	CA	3096	1/1	0.96	0.12	43,43,43,43	0
57	MG	DA	3082	1/1	0.96	0.08	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3083	1/1	0.96	0.07	41,41,41,41	0
57	MG	DA	3280	1/1	0.96	0.07	48,48,48,48	0
57	MG	BE	302	1/1	0.96	0.06	35,35,35,35	0
57	MG	CA	3098	1/1	0.96	0.09	54,54,54,54	0
57	MG	BA	3461	1/1	0.96	0.07	45,45,45,45	0
57	MG	BA	3703	1/1	0.96	0.25	28,28,28,28	0
57	MG	AA	1632	1/1	0.96	0.06	48,48,48,48	0
57	MG	AA	1694	1/1	0.96	0.06	47,47,47,47	0
57	MG	BF	301	1/1	0.96	0.19	40,40,40,40	0
57	MG	DA	3091	1/1	0.96	0.08	54,54,54,54	0
57	MG	BF	303	1/1	0.96	0.07	33,33,33,33	0
57	MG	BA	3216	1/1	0.96	0.28	39,39,39,39	0
57	MG	DA	3503	1/1	0.96	0.14	38,38,38,38	0
57	MG	BA	3155	1/1	0.96	0.09	40,40,40,40	0
57	MG	BA	3159	1/1	0.96	0.12	27,27,27,27	0
57	MG	BA	3287	1/1	0.96	0.09	27,27,27,27	0
57	MG	BH	201	1/1	0.96	0.07	56,56,56,56	0
57	MG	DA	3100	1/1	0.96	0.10	47,47,47,47	0
57	MG	BN	3001	1/1	0.96	0.09	48,48,48,48	0
57	MG	DA	3511	1/1	0.96	0.06	44,44,44,44	0
57	MG	BA	3475	1/1	0.96	0.07	49,49,49,49	0
57	MG	AA	1715	1/1	0.96	0.16	45,45,45,45	0
57	MG	BA	3223	1/1	0.96	0.07	41,41,41,41	0
57	MG	BA	3714	1/1	0.96	0.06	46,46,46,46	0
57	MG	BQ	3002	1/1	0.96	0.23	46,46,46,46	0
57	MG	DA	3517	1/1	0.96	0.09	48,48,48,48	0
57	MG	BA	3480	1/1	0.96	0.07	47,47,47,47	0
57	MG	DA	3309	1/1	0.96	0.06	48,48,48,48	0
57	MG	AA	1802	1/1	0.96	0.09	54,54,54,54	0
57	MG	BA	3605	1/1	0.96	0.12	47,47,47,47	0
57	MG	BA	3719	1/1	0.96	0.08	41,41,41,41	0
57	MG	BW	3001	1/1	0.96	0.21	44,44,44,44	0
57	MG	BA	3162	1/1	0.96	0.24	41,41,41,41	0
57	MG	AA	1780	1/1	0.96	0.10	69,69,69,69	0
57	MG	BX	3001	1/1	0.96	0.09	44,44,44,44	0
57	MG	BA	3029	1/1	0.96	0.07	36,36,36,36	0
57	MG	BA	3166	1/1	0.96	0.14	33,33,33,33	0
57	MG	DA	3531	1/1	0.96	0.07	48,48,48,48	0
57	MG	DA	3323	1/1	0.96	0.10	49,49,49,49	0
57	MG	DA	3119	1/1	0.96	0.13	50,50,50,50	0
57	MG	AX	3004	1/1	0.96	0.16	61,61,61,61	0
57	MG	BA	3232	1/1	0.96	0.11	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3612	1/1	0.96	0.10	60,60,60,60	0
57	MG	BA	3299	1/1	0.96	0.10	60,60,60,60	0
57	MG	DA	3329	1/1	0.96	0.07	47,47,47,47	0
57	MG	BA	3494	1/1	0.96	0.07	38,38,38,38	0
57	MG	B5	102	1/1	0.96	0.15	43,43,43,43	0
57	MG	BA	3034	1/1	0.96	0.19	35,35,35,35	0
57	MG	BA	3069	1/1	0.96	0.28	48,48,48,48	0
57	MG	B7	102	1/1	0.96	0.07	41,41,41,41	0
57	MG	BA	3388	1/1	0.96	0.07	25,25,25,25	0
57	MG	DA	3132	1/1	0.96	0.10	43,43,43,43	0
57	MG	DA	3551	1/1	0.96	0.13	49,49,49,49	0
57	MG	BA	3303	1/1	0.96	0.14	26,26,26,26	0
57	MG	DA	3338	1/1	0.96	0.06	44,44,44,44	0
57	MG	BA	3238	1/1	0.96	0.33	44,44,44,44	0
57	MG	AA	1630	1/1	0.96	0.11	53,53,53,53	0
57	MG	B9	502	1/1	0.96	0.07	46,46,46,46	0
57	MG	DA	3137	1/1	0.96	0.12	52,52,52,52	0
57	MG	BA	3392	1/1	0.96	0.11	26,26,26,26	0
57	MG	BA	3116	1/1	0.96	0.15	46,46,46,46	0
57	MG	BA	3395	1/1	0.96	0.10	30,30,30,30	0
57	MG	BA	3624	1/1	0.96	0.05	38,38,38,38	0
57	MG	BA	3311	1/1	0.96	0.12	56,56,56,56	0
57	MG	DA	3564	1/1	0.96	0.11	53,53,53,53	0
57	MG	BA	3399	1/1	0.96	0.09	41,41,41,41	0
57	MG	BA	3312	1/1	0.96	0.07	31,31,31,31	0
57	MG	DA	3353	1/1	0.96	0.09	47,47,47,47	0
57	MG	BA	3514	1/1	0.96	0.11	43,43,43,43	0
57	MG	BA	3173	1/1	0.96	0.12	32,32,32,32	0
57	MG	BA	3076	1/1	0.96	0.12	42,42,42,42	0
57	MG	BA	3037	1/1	0.96	0.09	42,42,42,42	0
57	MG	BA	3038	1/1	0.96	0.13	20,20,20,20	0
57	MG	DA	3151	1/1	0.96	0.04	37,37,37,37	0
57	MG	BA	3406	1/1	0.96	0.09	56,56,56,56	0
57	MG	BA	3520	1/1	0.96	0.12	29,29,29,29	0
57	MG	BA	3521	1/1	0.96	0.10	40,40,40,40	0
57	MG	DA	3364	1/1	0.96	0.07	45,45,45,45	0
57	MG	BA	3317	1/1	0.96	0.07	43,43,43,43	0
57	MG	DA	3581	1/1	0.96	0.09	44,44,44,44	0
57	MG	BA	3523	1/1	0.96	0.11	41,41,41,41	0
57	MG	AA	1793	1/1	0.96	0.16	63,63,63,63	0
57	MG	DA	3586	1/1	0.96	0.06	50,50,50,50	0
57	MG	BA	3178	1/1	0.96	0.07	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3124	1/1	0.96	0.10	57,57,57,57	0
57	MG	DA	3370	1/1	0.96	0.14	59,59,59,59	0
57	MG	BA	3643	1/1	0.96	0.11	52,52,52,52	0
57	MG	DA	3162	1/1	0.96	0.16	57,57,57,57	0
57	MG	BA	3180	1/1	0.96	0.18	46,46,46,46	0
57	MG	BA	3528	1/1	0.96	0.10	36,36,36,36	0
57	MG	BA	3766	1/1	0.96	0.08	47,47,47,47	0
57	MG	DA	3169	1/1	0.96	0.22	41,41,41,41	0
57	MG	BA	3529	1/1	0.96	0.12	24,24,24,24	0
57	MG	DA	3599	1/1	0.96	0.09	48,48,48,48	0
57	MG	BA	3324	1/1	0.96	0.10	60,60,60,60	0
57	MG	BA	3184	1/1	0.96	0.08	42,42,42,42	0
57	MG	BA	3253	1/1	0.96	0.16	31,31,31,31	0
57	MG	DA	3603	1/1	0.96	0.06	65,65,65,65	0
57	MG	BA	3771	1/1	0.96	0.08	41,41,41,41	0
57	MG	BA	3328	1/1	0.96	0.07	27,27,27,27	0
57	MG	BA	3254	1/1	0.96	0.07	33,33,33,33	0
57	MG	BA	3331	1/1	0.96	0.13	53,53,53,53	0
57	MG	BA	3776	1/1	0.96	0.16	60,60,60,60	0
57	MG	DA	3609	1/1	0.96	0.09	61,61,61,61	0
57	MG	BA	3777	1/1	0.96	0.06	41,41,41,41	0
57	MG	BA	3778	1/1	0.96	0.05	40,40,40,40	0
57	MG	BA	3541	1/1	0.96	0.11	38,38,38,38	0
57	MG	DA	3188	1/1	0.96	0.09	35,35,35,35	0
57	MG	BA	3782	1/1	0.96	0.09	38,38,38,38	0
57	MG	BA	3044	1/1	0.96	0.32	43,43,43,43	0
57	MG	BA	3257	1/1	0.96	0.10	43,43,43,43	0
57	MG	DA	3008	1/1	0.96	0.10	45,45,45,45	0
57	MG	BA	3659	1/1	0.96	0.08	47,47,47,47	0
57	MG	BA	3425	1/1	0.96	0.15	48,48,48,48	0
57	MG	BA	3548	1/1	0.96	0.06	35,35,35,35	0
57	MG	BA	3261	1/1	0.96	0.04	18,18,18,18	0
57	MG	BA	3427	1/1	0.96	0.09	33,33,33,33	0
57	MG	BA	3553	1/1	0.96	0.09	45,45,45,45	0
57	MG	BA	3428	1/1	0.96	0.09	51,51,51,51	0
57	MG	AA	1772	1/1	0.96	0.13	47,47,47,47	0
57	MG	BA	3088	1/1	0.96	0.13	43,43,43,43	0
57	MG	DA	3412	1/1	0.96	0.09	41,41,41,41	0
57	MG	DA	3629	1/1	0.96	0.09	57,57,57,57	0
57	MG	BA	3092	1/1	0.96	0.17	40,40,40,40	0
57	MG	DA	3631	1/1	0.96	0.07	49,49,49,49	0
57	MG	DA	3632	1/1	0.96	0.12	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3432	1/1	0.96	0.09	32,32,32,32	0
57	MG	BA	3671	1/1	0.96	0.07	24,24,24,24	0
57	MG	DA	3635	1/1	0.96	0.07	43,43,43,43	0
57	MG	DA	3206	1/1	0.96	0.11	50,50,50,50	0
57	MG	DA	3207	1/1	0.96	0.14	48,48,48,48	0
57	MG	CA	3056	1/1	0.96	0.11	64,64,64,64	0
57	MG	DA	3210	1/1	0.96	0.06	52,52,52,52	0
57	MG	DA	3029	1/1	0.96	0.22	45,45,45,45	0
57	MG	DA	3030	1/1	0.96	0.10	44,44,44,44	0
57	MG	DA	3031	1/1	0.96	0.13	42,42,42,42	0
57	MG	BA	3802	1/1	0.96	0.10	46,46,46,46	0
57	MG	DA	3218	1/1	0.96	0.08	52,52,52,52	0
57	MG	BA	3047	1/1	0.96	0.10	43,43,43,43	0
57	MG	AL	202	1/1	0.96	0.23	56,56,56,56	0
57	MG	DA	3427	1/1	0.96	0.15	47,47,47,47	0
57	MG	DA	3428	1/1	0.96	0.06	38,38,38,38	0
57	MG	DA	3221	1/1	0.96	0.07	41,41,41,41	0
57	MG	BA	3138	1/1	0.96	0.10	43,43,43,43	0
57	MG	DA	3223	1/1	0.96	0.08	39,39,39,39	0
57	MG	AA	1608	1/1	0.96	0.18	43,43,43,43	0
57	MG	DA	3225	1/1	0.96	0.10	55,55,55,55	0
57	MG	DA	3040	1/1	0.96	0.09	28,28,28,28	0
57	MG	BA	3140	1/1	0.96	0.05	58,58,58,58	0
57	MG	DA	3436	1/1	0.96	0.06	35,35,35,35	0
57	MG	AA	1808	1/1	0.96	0.09	49,49,49,49	0
57	MG	DA	3043	1/1	0.96	0.21	53,53,53,53	0
57	MG	BA	3811	1/1	0.96	0.15	48,48,48,48	0
57	MG	BA	3201	1/1	0.96	0.13	48,48,48,48	0
57	MG	BA	3814	1/1	0.96	0.11	39,39,39,39	0
57	MG	CA	3067	1/1	0.96	0.23	46,46,46,46	0
57	MG	AA	1746	1/1	0.96	0.14	56,56,56,56	0
57	MG	DA	3051	1/1	0.96	0.09	44,44,44,44	0
57	MG	DA	3447	1/1	0.96	0.18	59,59,59,59	0
57	MG	AA	1736	1/1	0.96	0.07	49,49,49,49	0
57	MG	DA	3053	1/1	0.96	0.13	47,47,47,47	0
57	MG	BB	3003	1/1	0.96	0.04	30,30,30,30	0
57	MG	AA	1673	1/1	0.96	0.08	48,48,48,48	0
57	MG	BA	3445	1/1	0.96	0.09	54,54,54,54	0
57	MG	BA	3150	1/1	0.96	0.10	39,39,39,39	0
57	MG	BA	3574	1/1	0.96	0.08	42,42,42,42	0
57	MG	DD	302	1/1	0.96	0.08	49,49,49,49	0
57	MG	BA	3447	1/1	0.96	0.13	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3062	1/1	0.96	0.15	53,53,53,53	0
57	MG	BB	3013	1/1	0.96	0.08	39,39,39,39	0
57	MG	BA	3576	1/1	0.96	0.16	30,30,30,30	0
57	MG	BA	3354	1/1	0.96	0.08	47,47,47,47	0
57	MG	CA	3080	1/1	0.96	0.07	49,49,49,49	0
57	MG	BA	3207	1/1	0.96	0.09	36,36,36,36	0
57	MG	BA	3451	1/1	0.96	0.10	44,44,44,44	0
57	MG	BA	3278	1/1	0.96	0.42	54,54,54,54	0
57	MG	BA	3208	1/1	0.96	0.07	43,43,43,43	0
57	MG	DA	3258	1/1	0.96	0.09	45,45,45,45	0
57	MG	DA	3471	1/1	0.96	0.15	54,54,54,54	0
57	MG	DA	3472	1/1	0.96	0.07	25,25,25,25	0
57	MG	BA	3023	1/1	0.96	0.10	41,41,41,41	0
57	MG	BA	3586	1/1	0.96	0.07	55,55,55,55	0
57	MG	DA	3475	1/1	0.96	0.20	56,56,56,56	0
57	MG	DA	3476	1/1	0.96	0.07	45,45,45,45	0
57	MG	BB	3023	1/1	0.96	0.13	47,47,47,47	0
57	MG	BA	3456	1/1	0.96	0.13	37,37,37,37	0
57	MG	DA	3479	1/1	0.96	0.07	42,42,42,42	0
57	MG	DA	3075	1/1	0.96	0.12	55,55,55,55	0
57	MG	BA	3589	1/1	0.96	0.19	59,59,59,59	0
59	ZN	CN	501	1/1	0.96	0.08	100,100,100,100	0
57	MG	CA	3093	1/1	0.96	0.09	55,55,55,55	0
57	MG	DA	3483	1/1	0.96	0.10	53,53,53,53	0
57	MG	BA	3585	1/1	0.97	0.08	29,29,29,29	0
57	MG	BA	3163	1/1	0.97	0.20	55,55,55,55	0
57	MG	BA	3031	1/1	0.97	0.16	36,36,36,36	0
57	MG	BA	3226	1/1	0.97	0.10	25,25,25,25	0
57	MG	DA	3509	1/1	0.97	0.06	49,49,49,49	0
57	MG	BA	3032	1/1	0.97	0.17	33,33,33,33	0
57	MG	BA	3380	1/1	0.97	0.09	40,40,40,40	0
57	MG	AA	1758	1/1	0.97	0.07	37,37,37,37	0
57	MG	DA	3148	1/1	0.97	0.09	49,49,49,49	0
57	MG	BA	3382	1/1	0.97	0.08	55,55,55,55	0
57	MG	BA	3008	1/1	0.97	0.05	28,28,28,28	0
57	MG	BA	3168	1/1	0.97	0.16	45,45,45,45	0
57	MG	DA	3152	1/1	0.97	0.05	45,45,45,45	0
57	MG	AA	1809	1/1	0.97	0.12	42,42,42,42	0
57	MG	BA	3302	1/1	0.97	0.09	49,49,49,49	0
57	MG	BA	3701	1/1	0.97	0.12	39,39,39,39	0
57	MG	BA	3488	1/1	0.97	0.04	20,20,20,20	0
57	MG	BA	3233	1/1	0.97	0.15	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	CA	3053	1/1	0.97	0.09	41,41,41,41	0
57	MG	BB	3010	1/1	0.97	0.06	53,53,53,53	0
57	MG	BB	3011	1/1	0.97	0.08	47,47,47,47	0
57	MG	DA	3011	1/1	0.97	0.10	35,35,35,35	0
57	MG	DA	3340	1/1	0.97	0.07	27,27,27,27	0
57	MG	BB	3012	1/1	0.97	0.13	56,56,56,56	0
57	MG	DA	3164	1/1	0.97	0.16	44,44,44,44	0
57	MG	BA	3304	1/1	0.97	0.11	39,39,39,39	0
57	MG	BA	3493	1/1	0.97	0.12	38,38,38,38	0
57	MG	DA	3346	1/1	0.97	0.06	49,49,49,49	0
57	MG	BA	3305	1/1	0.97	0.06	46,46,46,46	0
57	MG	DA	3536	1/1	0.97	0.05	52,52,52,52	0
57	MG	DA	3168	1/1	0.97	0.08	44,44,44,44	0
57	MG	DA	3018	1/1	0.97	0.04	31,31,31,31	0
57	MG	DA	3019	1/1	0.97	0.06	42,42,42,42	0
57	MG	BA	3234	1/1	0.97	0.12	52,52,52,52	0
57	MG	BA	3708	1/1	0.97	0.24	33,33,33,33	0
57	MG	BA	3308	1/1	0.97	0.16	39,39,39,39	0
57	MG	BA	3235	1/1	0.97	0.11	44,44,44,44	0
57	MG	DA	3355	1/1	0.97	0.06	43,43,43,43	0
57	MG	BA	3070	1/1	0.97	0.10	41,41,41,41	0
57	MG	DA	3547	1/1	0.97	0.06	48,48,48,48	0
57	MG	DA	3548	1/1	0.97	0.07	66,66,66,66	0
57	MG	DA	3025	1/1	0.97	0.18	47,47,47,47	0
57	MG	DA	3180	1/1	0.97	0.18	48,48,48,48	0
57	MG	BA	3071	1/1	0.97	0.24	59,59,59,59	0
57	MG	DA	3182	1/1	0.97	0.24	52,52,52,52	0
57	MG	BA	3398	1/1	0.97	0.12	32,32,32,32	0
57	MG	DA	3028	1/1	0.97	0.04	39,39,39,39	0
57	MG	BA	3115	1/1	0.97	0.06	33,33,33,33	0
57	MG	DA	3186	1/1	0.97	0.18	49,49,49,49	0
57	MG	BA	3072	1/1	0.97	0.13	49,49,49,49	0
57	MG	BA	3012	1/1	0.97	0.11	25,25,25,25	0
57	MG	BD	3008	1/1	0.97	0.07	45,45,45,45	0
57	MG	BD	3009	1/1	0.97	0.05	37,37,37,37	0
57	MG	BA	3119	1/1	0.97	0.08	46,46,46,46	0
57	MG	BA	3510	1/1	0.97	0.06	45,45,45,45	0
57	MG	DA	3565	1/1	0.97	0.05	52,52,52,52	0
57	MG	BA	3511	1/1	0.97	0.13	50,50,50,50	0
57	MG	BA	3120	1/1	0.97	0.12	45,45,45,45	0
57	MG	DA	3195	1/1	0.97	0.08	42,42,42,42	0
57	MG	AA	1672	1/1	0.97	0.15	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3244	1/1	0.97	0.16	31,31,31,31	0
57	MG	BA	3319	1/1	0.97	0.08	23,23,23,23	0
57	MG	BA	3077	1/1	0.97	0.07	15,15,15,15	0
57	MG	BF	304	1/1	0.97	0.18	41,41,41,41	0
57	MG	DA	3381	1/1	0.97	0.10	40,40,40,40	0
57	MG	BF	305	1/1	0.97	0.10	36,36,36,36	0
57	MG	DA	3384	1/1	0.97	0.04	38,38,38,38	0
57	MG	BA	3042	1/1	0.97	0.05	37,37,37,37	0
57	MG	DA	3386	1/1	0.97	0.05	44,44,44,44	0
57	MG	DA	3049	1/1	0.97	0.10	47,47,47,47	0
57	MG	BA	3043	1/1	0.97	0.12	31,31,31,31	0
57	MG	BF	309	1/1	0.97	0.13	31,31,31,31	0
57	MG	BF	310	1/1	0.97	0.14	56,56,56,56	0
57	MG	BA	3181	1/1	0.97	0.04	40,40,40,40	0
57	MG	BA	3182	1/1	0.97	0.20	52,52,52,52	0
57	MG	DA	3209	1/1	0.97	0.06	49,49,49,49	0
57	MG	DA	3394	1/1	0.97	0.04	60,60,60,60	0
57	MG	BA	3326	1/1	0.97	0.05	24,24,24,24	0
57	MG	CA	3092	1/1	0.97	0.14	51,51,51,51	0
57	MG	DA	3058	1/1	0.97	0.14	61,61,61,61	0
57	MG	BA	3251	1/1	0.97	0.15	43,43,43,43	0
57	MG	DA	3215	1/1	0.97	0.16	40,40,40,40	0
57	MG	DA	3216	1/1	0.97	0.11	35,35,35,35	0
57	MG	BA	3418	1/1	0.97	0.10	38,38,38,38	0
57	MG	BN	3003	1/1	0.97	0.07	38,38,38,38	0
57	MG	BA	3125	1/1	0.97	0.11	38,38,38,38	0
57	MG	BA	3126	1/1	0.97	0.22	36,36,36,36	0
57	MG	BA	3127	1/1	0.97	0.11	45,45,45,45	0
57	MG	BQ	3001	1/1	0.97	0.14	37,37,37,37	0
57	MG	BA	3188	1/1	0.97	0.16	32,32,32,32	0
57	MG	AA	1668	1/1	0.97	0.06	63,63,63,63	0
57	MG	BA	3424	1/1	0.97	0.13	31,31,31,31	0
57	MG	BA	3258	1/1	0.97	0.21	44,44,44,44	0
57	MG	CA	3104	1/1	0.97	0.14	37,37,37,37	0
57	MG	DA	3228	1/1	0.97	0.12	44,44,44,44	0
57	MG	DA	3229	1/1	0.97	0.08	38,38,38,38	0
57	MG	BV	201	1/1	0.97	0.22	31,31,31,31	0
57	MG	CA	3106	1/1	0.97	0.10	58,58,58,58	0
57	MG	BA	3744	1/1	0.97	0.07	55,55,55,55	0
57	MG	BA	3531	1/1	0.97	0.06	60,60,60,60	0
57	MG	DA	3615	1/1	0.97	0.14	62,62,62,62	0
57	MG	BA	3335	1/1	0.97	0.06	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	1661	1/1	0.97	0.27	54,54,54,54	0
57	MG	BA	3534	1/1	0.97	0.12	26,26,26,26	0
57	MG	BA	3191	1/1	0.97	0.12	40,40,40,40	0
57	MG	BA	3339	1/1	0.97	0.09	43,43,43,43	0
57	MG	DA	3080	1/1	0.97	0.04	49,49,49,49	0
57	MG	DA	3240	1/1	0.97	0.10	52,52,52,52	0
57	MG	BA	3086	1/1	0.97	0.14	42,42,42,42	0
57	MG	BA	3539	1/1	0.97	0.06	42,42,42,42	0
57	MG	BA	3540	1/1	0.97	0.07	31,31,31,31	0
57	MG	BA	3133	1/1	0.97	0.14	37,37,37,37	0
57	MG	BA	3195	1/1	0.97	0.12	36,36,36,36	0
57	MG	DA	3246	1/1	0.97	0.04	46,46,46,46	0
57	MG	B5	101	1/1	0.97	0.28	30,30,30,30	0
57	MG	BA	3543	1/1	0.97	0.11	52,52,52,52	0
57	MG	B5	104	1/1	0.97	0.08	58,58,58,58	0
57	MG	BA	3649	1/1	0.97	0.08	55,55,55,55	0
57	MG	BA	3760	1/1	0.97	0.08	50,50,50,50	0
57	MG	AA	1813	1/1	0.97	0.14	38,38,38,38	0
57	MG	DA	3439	1/1	0.97	0.07	40,40,40,40	0
57	MG	BA	3434	1/1	0.97	0.04	19,19,19,19	0
57	MG	DA	3093	1/1	0.97	0.06	47,47,47,47	0
57	MG	BA	3344	1/1	0.97	0.07	71,71,71,71	0
57	MG	BA	3048	1/1	0.97	0.08	29,29,29,29	0
57	MG	B8	5001	1/1	0.97	0.08	42,42,42,42	0
57	MG	DA	3260	1/1	0.97	0.10	39,39,39,39	0
57	MG	BA	3198	1/1	0.97	0.11	44,44,44,44	0
57	MG	BA	3089	1/1	0.97	0.10	36,36,36,36	0
57	MG	CA	3132	1/1	0.97	0.10	64,64,64,64	0
57	MG	DA	3450	1/1	0.97	0.05	50,50,50,50	0
57	MG	BA	3090	1/1	0.97	0.12	38,38,38,38	0
57	MG	DA	3452	1/1	0.97	0.05	45,45,45,45	0
57	MG	CA	3134	1/1	0.97	0.15	64,64,64,64	0
57	MG	DA	3266	1/1	0.97	0.07	37,37,37,37	0
57	MG	BA	3658	1/1	0.97	0.09	61,61,61,61	0
57	MG	DA	3268	1/1	0.97	0.07	41,41,41,41	0
57	MG	DA	3652	1/1	0.97	0.12	31,31,31,31	0
57	MG	DA	3458	1/1	0.97	0.06	41,41,41,41	0
57	MG	BA	3091	1/1	0.97	0.11	42,42,42,42	0
57	MG	DA	3656	1/1	0.97	0.15	41,41,41,41	0
57	MG	DA	3105	1/1	0.97	0.07	45,45,45,45	0
57	MG	AA	1724	1/1	0.97	0.07	39,39,39,39	0
57	MG	DA	3659	1/1	0.97	0.10	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3272	1/1	0.97	0.11	49,49,49,49	0
57	MG	DA	3661	1/1	0.97	0.06	62,62,62,62	0
57	MG	BA	3661	1/1	0.97	0.09	25,25,25,25	0
57	MG	AA	1716	1/1	0.97	0.12	50,50,50,50	0
57	MG	DA	3664	1/1	0.97	0.10	51,51,51,51	0
57	MG	BA	3022	1/1	0.97	0.04	25,25,25,25	0
57	MG	DA	3276	1/1	0.97	0.08	28,28,28,28	0
57	MG	DA	3278	1/1	0.97	0.04	39,39,39,39	0
57	MG	AA	1752	1/1	0.97	0.06	48,48,48,48	0
57	MG	DA	3469	1/1	0.97	0.05	50,50,50,50	0
57	MG	BA	3206	1/1	0.97	0.04	34,34,34,34	0
57	MG	BA	3146	1/1	0.97	0.12	41,41,41,41	0
57	MG	DA	3113	1/1	0.97	0.12	35,35,35,35	0
57	MG	AA	1607	1/1	0.97	0.10	55,55,55,55	0
57	MG	BA	3780	1/1	0.97	0.04	42,42,42,42	0
57	MG	BA	3097	1/1	0.97	0.06	41,41,41,41	0
57	MG	BA	3361	1/1	0.97	0.07	56,56,56,56	0
57	MG	BA	3210	1/1	0.97	0.12	41,41,41,41	0
57	MG	BA	3098	1/1	0.97	0.09	23,23,23,23	0
57	MG	BA	3454	1/1	0.97	0.09	46,46,46,46	0
57	MG	AA	1667	1/1	0.97	0.20	55,55,55,55	0
57	MG	DD	304	1/1	0.97	0.08	36,36,36,36	0
57	MG	BA	3214	1/1	0.97	0.30	43,43,43,43	0
57	MG	DA	3124	1/1	0.97	0.11	43,43,43,43	0
57	MG	AA	1690	1/1	0.97	0.37	52,52,52,52	0
57	MG	AA	1729	1/1	0.97	0.05	35,35,35,35	0
57	MG	CA	3023	1/1	0.97	0.04	39,39,39,39	0
57	MG	BA	3677	1/1	0.97	0.07	44,44,44,44	0
57	MG	DA	3299	1/1	0.97	0.05	46,46,46,46	0
57	MG	BA	3217	1/1	0.97	0.05	50,50,50,50	0
57	MG	DA	3489	1/1	0.97	0.07	48,48,48,48	0
57	MG	BA	3793	1/1	0.97	0.10	11,11,11,11	0
57	MG	BA	3061	1/1	0.97	0.18	25,25,25,25	0
57	MG	DO	201	1/1	0.97	0.14	49,49,49,49	0
57	MG	DA	3304	1/1	0.97	0.05	42,42,42,42	0
57	MG	BA	3795	1/1	0.97	0.11	19,19,19,19	0
57	MG	DP	202	1/1	0.97	0.09	49,49,49,49	0
57	MG	DQ	3002	1/1	0.97	0.12	47,47,47,47	0
57	MG	BA	3371	1/1	0.97	0.06	49,49,49,49	0
57	MG	DA	3307	1/1	0.97	0.06	51,51,51,51	0
57	MG	BA	3797	1/1	0.97	0.24	51,51,51,51	0
57	MG	BA	3465	1/1	0.97	0.04	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	AA	1677	1/1	0.97	0.13	43,43,43,43	0
57	MG	BA	3580	1/1	0.97	0.04	48,48,48,48	0
57	MG	BA	3002	1/1	0.97	0.12	53,53,53,53	0
57	MG	DA	3501	1/1	0.97	0.09	49,49,49,49	0
57	MG	BA	3005	1/1	0.97	0.12	44,44,44,44	0
57	MG	BA	3469	1/1	0.97	0.11	61,61,61,61	0
57	MG	DA	3316	1/1	0.97	0.18	57,57,57,57	0
57	MG	BA	3556	1/1	0.98	0.04	46,46,46,46	0
57	MG	BA	3075	1/1	0.98	0.13	24,24,24,24	0
57	MG	BA	3783	1/1	0.98	0.11	37,37,37,37	0
57	MG	AA	1649	1/1	0.98	0.07	28,28,28,28	0
57	MG	DA	3453	1/1	0.98	0.10	54,54,54,54	0
57	MG	BR	5002	1/1	0.98	0.12	50,50,50,50	0
57	MG	BA	3059	1/1	0.98	0.06	36,36,36,36	0
57	MG	DA	3095	1/1	0.98	0.18	60,60,60,60	0
57	MG	CA	3165	1/1	0.98	0.05	42,42,42,42	0
57	MG	BU	202	1/1	0.98	0.11	40,40,40,40	0
57	MG	BU	203	1/1	0.98	0.13	34,34,34,34	0
57	MG	CA	3168	1/1	0.98	0.08	41,41,41,41	0
57	MG	DA	3213	1/1	0.98	0.10	37,37,37,37	0
57	MG	BA	3368	1/1	0.98	0.12	32,32,32,32	0
57	MG	BA	3489	1/1	0.98	0.11	50,50,50,50	0
57	MG	BV	202	1/1	0.98	0.18	32,32,32,32	0
57	MG	BV	203	1/1	0.98	0.07	23,23,23,23	0
57	MG	BA	3490	1/1	0.98	0.04	43,43,43,43	0
57	MG	DA	3598	1/1	0.98	0.04	55,55,55,55	0
57	MG	BV	205	1/1	0.98	0.08	34,34,34,34	0
57	MG	BA	3156	1/1	0.98	0.11	35,35,35,35	0
57	MG	DA	3343	1/1	0.98	0.06	34,34,34,34	0
57	MG	BA	3157	1/1	0.98	0.07	46,46,46,46	0
57	MG	BW	3003	1/1	0.98	0.07	35,35,35,35	0
57	MG	BA	3158	1/1	0.98	0.06	41,41,41,41	0
57	MG	BA	3322	1/1	0.98	0.04	38,38,38,38	0
57	MG	BA	3639	1/1	0.98	0.13	49,49,49,49	0
57	MG	CA	3079	1/1	0.98	0.08	49,49,49,49	0
57	MG	BA	3495	1/1	0.98	0.07	43,43,43,43	0
57	MG	BA	3021	1/1	0.98	0.04	43,43,43,43	0
57	MG	BA	3011	1/1	0.98	0.05	30,30,30,30	0
57	MG	AA	1735	1/1	0.98	0.07	45,45,45,45	0
57	MG	DA	3007	1/1	0.98	0.04	30,30,30,30	0
57	MG	BA	3082	1/1	0.98	0.06	28,28,28,28	0
57	MG	CA	3085	1/1	0.98	0.08	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3503	1/1	0.98	0.05	51,51,51,51	0
57	MG	BA	3718	1/1	0.98	0.07	47,47,47,47	0
57	MG	CA	3088	1/1	0.98	0.10	43,43,43,43	0
57	MG	DA	3014	1/1	0.98	0.06	44,44,44,44	0
57	MG	BA	3128	1/1	0.98	0.05	42,42,42,42	0
57	MG	BA	3378	1/1	0.98	0.09	39,39,39,39	0
57	MG	BA	3104	1/1	0.98	0.11	24,24,24,24	0
57	MG	BA	3046	1/1	0.98	0.04	43,43,43,43	0
57	MG	B7	101	1/1	0.98	0.04	41,41,41,41	0
57	MG	BA	3330	1/1	0.98	0.07	27,27,27,27	0
57	MG	BA	3131	1/1	0.98	0.12	44,44,44,44	0
57	MG	BA	3808	1/1	0.98	0.12	38,38,38,38	0
57	MG	BA	3084	1/1	0.98	0.06	42,42,42,42	0
57	MG	BA	3384	1/1	0.98	0.04	45,45,45,45	0
57	MG	BA	3085	1/1	0.98	0.13	31,31,31,31	0
57	MG	BA	3583	1/1	0.98	0.05	33,33,33,33	0
57	MG	BA	3134	1/1	0.98	0.16	40,40,40,40	0
57	MG	BA	3657	1/1	0.98	0.07	38,38,38,38	0
57	MG	BA	3033	1/1	0.98	0.43	31,31,31,31	0
57	MG	BA	3247	1/1	0.98	0.13	29,29,29,29	0
57	MG	DA	3378	1/1	0.98	0.06	52,52,52,52	0
57	MG	AA	1611	1/1	0.98	0.04	20,20,20,20	0
57	MG	BA	3292	1/1	0.98	0.12	26,26,26,26	0
57	MG	BB	3007	1/1	0.98	0.03	41,41,41,41	0
57	MG	BA	3035	1/1	0.98	0.11	49,49,49,49	0
57	MG	BA	3294	1/1	0.98	0.09	43,43,43,43	0
57	MG	DA	3036	1/1	0.98	0.07	35,35,35,35	0
57	MG	DA	3037	1/1	0.98	0.04	26,26,26,26	0
57	MG	CA	3010	1/1	0.98	0.05	49,49,49,49	0
57	MG	BA	3450	1/1	0.98	0.07	54,54,54,54	0
57	MG	BA	3004	1/1	0.98	0.14	36,36,36,36	0
57	MG	BA	3742	1/1	0.98	0.05	48,48,48,48	0
57	MG	AA	1745	1/1	0.98	0.07	36,36,36,36	0
57	MG	BA	3053	1/1	0.98	0.16	23,23,23,23	0
57	MG	BA	3114	1/1	0.98	0.06	39,39,39,39	0
57	MG	BB	3016	1/1	0.98	0.04	34,34,34,34	0
57	MG	DA	3047	1/1	0.98	0.14	45,45,45,45	0
57	MG	BA	3142	1/1	0.98	0.19	46,46,46,46	0
57	MG	BA	3054	1/1	0.98	0.14	30,30,30,30	0
57	MG	BA	3457	1/1	0.98	0.12	48,48,48,48	0
57	MG	DA	3655	1/1	0.98	0.05	38,38,38,38	0
57	MG	BA	3256	1/1	0.98	0.30	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3459	1/1	0.98	0.07	31,31,31,31	0
57	MG	DA	3525	1/1	0.98	0.08	28,28,28,28	0
57	MG	DA	3526	1/1	0.98	0.06	52,52,52,52	0
57	MG	DA	3277	1/1	0.98	0.05	50,50,50,50	0
57	MG	BA	3402	1/1	0.98	0.05	27,27,27,27	0
57	MG	DA	3163	1/1	0.98	0.14	34,34,34,34	0
57	MG	DA	3054	1/1	0.98	0.07	27,27,27,27	0
57	MG	AA	1792	1/1	0.98	0.06	47,47,47,47	0
57	MG	BA	3350	1/1	0.98	0.04	34,34,34,34	0
57	MG	BA	3039	1/1	0.98	0.14	36,36,36,36	0
57	MG	BD	3004	1/1	0.98	0.17	28,28,28,28	0
57	MG	BA	3464	1/1	0.98	0.03	44,44,44,44	0
57	MG	DA	3170	1/1	0.98	0.08	35,35,35,35	0
57	MG	DA	3537	1/1	0.98	0.06	45,45,45,45	0
57	MG	DA	3171	1/1	0.98	0.09	40,40,40,40	0
57	MG	BD	3007	1/1	0.98	0.11	46,46,46,46	0
57	MG	BA	3756	1/1	0.98	0.05	18,18,18,18	0
57	MG	DA	3290	1/1	0.98	0.07	33,33,33,33	0
57	MG	BA	3679	1/1	0.98	0.11	52,52,52,52	0
57	MG	BD	3010	1/1	0.98	0.07	46,46,46,46	0
57	MG	BA	3260	1/1	0.98	0.08	19,19,19,19	0
57	MG	BA	3118	1/1	0.98	0.12	35,35,35,35	0
57	MG	DA	3178	1/1	0.98	0.08	40,40,40,40	0
57	MG	BA	3537	1/1	0.98	0.05	43,43,43,43	0
57	MG	DA	3297	1/1	0.98	0.15	51,51,51,51	0
57	MG	DE	3001	1/1	0.98	0.26	31,31,31,31	0
57	MG	DE	3002	1/1	0.98	0.12	33,33,33,33	0
57	MG	DE	3003	1/1	0.98	0.12	43,43,43,43	0
57	MG	BA	3220	1/1	0.98	0.07	35,35,35,35	0
57	MG	DA	3550	1/1	0.98	0.04	60,60,60,60	0
57	MG	BA	3409	1/1	0.98	0.09	22,22,22,22	0
57	MG	DA	3300	1/1	0.98	0.11	38,38,38,38	0
57	MG	BA	3221	1/1	0.98	0.14	29,29,29,29	0
57	MG	BA	3357	1/1	0.98	0.04	34,34,34,34	0
57	MG	BF	302	1/1	0.98	0.17	30,30,30,30	0
57	MG	BA	3474	1/1	0.98	0.13	33,33,33,33	0
57	MG	BA	3148	1/1	0.98	0.21	38,38,38,38	0
57	MG	BA	3544	1/1	0.98	0.05	52,52,52,52	0
57	MG	BA	3183	1/1	0.98	0.18	49,49,49,49	0
57	MG	BA	3149	1/1	0.98	0.04	42,42,42,42	0
57	MG	BF	308	1/1	0.98	0.06	43,43,43,43	0
57	MG	BA	3478	1/1	0.98	0.07	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3772	1/1	0.98	0.14	36,36,36,36	0
57	MG	BF	311	1/1	0.98	0.07	52,52,52,52	0
57	MG	BA	3073	1/1	0.98	0.04	32,32,32,32	0
57	MG	DA	3440	1/1	0.98	0.06	36,36,36,36	0
57	MG	BA	3550	1/1	0.98	0.06	50,50,50,50	0
57	MG	BA	3551	1/1	0.98	0.05	44,44,44,44	0
57	MG	DW	3001	1/1	0.98	0.07	41,41,41,41	0
57	MG	BA	3151	1/1	0.98	0.07	36,36,36,36	0
57	MG	BA	3227	1/1	0.98	0.05	33,33,33,33	0
57	MG	BA	3698	1/1	0.98	0.05	47,47,47,47	0
57	MG	BA	3779	1/1	0.98	0.03	17,17,17,17	0
58	SF4	AD	501	8/8	0.98	0.06	59,68,73,79	0
58	SF4	CD	501	8/8	0.98	0.04	64,67,74,91	0
57	MG	DA	3574	1/1	0.98	0.04	61,61,61,61	0
57	MG	DA	3322	1/1	0.98	0.09	42,42,42,42	0
57	MG	AA	1740	1/1	0.98	0.08	41,41,41,41	0
57	MG	DA	3251	1/1	0.99	0.04	40,40,40,40	0
57	MG	BA	3050	1/1	0.99	0.11	32,32,32,32	0
57	MG	BA	3040	1/1	0.99	0.20	33,33,33,33	0
57	MG	CA	3044	1/1	0.99	0.09	47,47,47,47	0
57	MG	BA	3587	1/1	0.99	0.05	46,46,46,46	0
57	MG	BA	3186	1/1	0.99	0.09	41,41,41,41	0
57	MG	BA	3013	1/1	0.99	0.04	28,28,28,28	0
57	MG	BA	3590	1/1	0.99	0.07	33,33,33,33	0
57	MG	DA	3259	1/1	0.99	0.06	42,42,42,42	0
57	MG	DA	3312	1/1	0.99	0.03	42,42,42,42	0
57	MG	AA	1734	1/1	0.99	0.05	43,43,43,43	0
57	MG	BA	3555	1/1	0.99	0.08	50,50,50,50	0
57	MG	AA	1768	1/1	0.99	0.06	53,53,53,53	0
57	MG	DA	3013	1/1	0.99	0.03	39,39,39,39	0
57	MG	BA	3307	1/1	0.99	0.05	28,28,28,28	0
57	MG	BA	3412	1/1	0.99	0.03	30,30,30,30	0
57	MG	DA	3373	1/1	0.99	0.03	31,31,31,31	0
57	MG	AA	1744	1/1	0.99	0.06	44,44,44,44	0
57	MG	BA	3009	1/1	0.99	0.06	31,31,31,31	0
57	MG	DA	3321	1/1	0.99	0.09	29,29,29,29	0
57	MG	BA	3192	1/1	0.99	0.06	19,19,19,19	0
57	MG	BA	3635	1/1	0.99	0.04	42,42,42,42	0
57	MG	BA	3440	1/1	0.99	0.04	35,35,35,35	0
57	MG	AA	1730	1/1	0.99	0.10	27,27,27,27	0
57	MG	BA	3417	1/1	0.99	0.09	24,24,24,24	0
57	MG	DA	3121	1/1	0.99	0.10	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	DA	3383	1/1	0.99	0.02	28,28,28,28	0
57	MG	BA	3393	1/1	0.99	0.06	23,23,23,23	0
57	MG	BA	3499	1/1	0.99	0.03	39,39,39,39	0
57	MG	BD	3001	1/1	0.99	0.04	34,34,34,34	0
57	MG	BA	3080	1/1	0.99	0.07	31,31,31,31	0
57	MG	DA	3562	1/1	0.99	0.03	31,31,31,31	0
57	MG	BA	3501	1/1	0.99	0.03	42,42,42,42	0
57	MG	BA	3003	1/1	0.99	0.05	33,33,33,33	0
57	MG	BA	3758	1/1	0.99	0.05	41,41,41,41	0
57	MG	BD	3006	1/1	0.99	0.06	34,34,34,34	0
57	MG	BA	3471	1/1	0.99	0.07	27,27,27,27	0
57	MG	BA	3800	1/1	0.99	0.06	29,29,29,29	0
57	MG	BA	3472	1/1	0.99	0.05	24,24,24,24	0
57	MG	CA	3118	1/1	0.99	0.11	60,60,60,60	0
57	MG	BA	3473	1/1	0.99	0.07	28,28,28,28	0
57	MG	BA	3259	1/1	0.99	0.08	25,25,25,25	0
57	MG	DA	3398	1/1	0.99	0.02	40,40,40,40	0
57	MG	BA	3211	1/1	0.99	0.09	43,43,43,43	0
57	MG	BA	3020	1/1	0.99	0.04	25,25,25,25	0
57	MG	DA	3039	1/1	0.99	0.07	38,38,38,38	0
57	MG	DQ	3001	1/1	0.99	0.05	50,50,50,50	0
57	MG	BA	3356	1/1	0.99	0.09	31,31,31,31	0
57	MG	BA	3336	1/1	0.99	0.04	20,20,20,20	0
57	MG	DA	3404	1/1	0.99	0.03	43,43,43,43	0
57	MG	BA	3479	1/1	0.99	0.05	53,53,53,53	0
57	MG	BA	3262	1/1	0.99	0.26	31,31,31,31	0
57	MG	DA	3582	1/1	0.99	0.05	53,53,53,53	0
57	MG	BA	3810	1/1	0.99	0.04	35,35,35,35	0
57	MG	DA	3584	1/1	0.99	0.03	31,31,31,31	0
57	MG	BA	3729	1/1	0.99	0.04	46,46,46,46	0
57	MG	BA	3143	1/1	0.99	0.08	41,41,41,41	0
57	MG	BA	3813	1/1	0.99	0.12	29,29,29,29	0
57	MG	BA	3731	1/1	0.99	0.04	32,32,32,32	0
59	ZN	AN	501	1/1	0.99	0.04	77,77,77,77	0
59	ZN	BY	501	1/1	0.99	0.04	68,68,68,68	0
59	ZN	B4	501	1/1	0.99	0.03	118,118,118,118	0
57	MG	BA	3547	1/1	0.99	0.06	45,45,45,45	0
59	ZN	DY	501	1/1	0.99	0.03	90,90,90,90	0
57	MG	AA	1681	1/1	0.99	0.03	38,38,38,38	0
59	ZN	D5	501	1/1	0.99	0.04	57,57,57,57	0
59	ZN	D6	501	1/1	0.99	0.04	65,65,65,65	0
59	ZN	D9	501	1/1	0.99	0.03	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	BA	3483	1/1	0.99	0.06	44,44,44,44	0
59	ZN	B6	102	1/1	1.00	0.07	50,50,50,50	0
59	ZN	B9	501	1/1	1.00	0.07	49,49,49,49	0
57	MG	BA	3397	1/1	1.00	0.04	28,28,28,28	0
57	MG	BA	3725	1/1	1.00	0.05	31,31,31,31	0
57	MG	BA	3502	1/1	1.00	0.11	30,30,30,30	0
57	MG	BA	3007	1/1	1.00	0.09	21,21,21,21	0
57	MG	BA	3567	1/1	1.00	0.11	32,32,32,32	0
57	MG	DA	3589	1/1	1.00	0.02	29,29,29,29	0
59	ZN	B5	103	1/1	1.00	0.03	40,40,40,40	0

6.5 Other polymers (i)

There are no such residues in this entry.