



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:11 PM GMT

PDB ID : 4U1U
Title : Crystal structure of the E. coli ribosome bound to quinupristin.
Authors : Noeske, J.; Huang, J.; Olivier, N.B.; Giacobbe, R.A.; Zambrowski, M.; Cate, J.H.D.
Deposited on : 2014-04-23
Resolution : 2.95 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

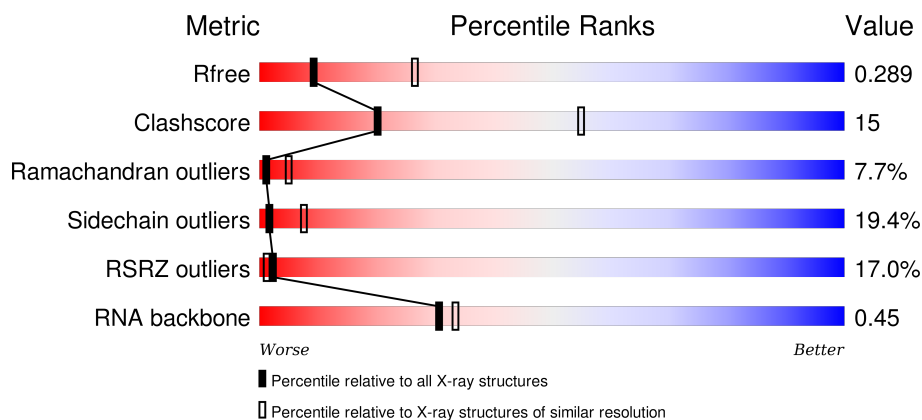
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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}	91344	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)
RNA backbone	2183	1010 (3.36-2.56)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. 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	1539	<div> <div>3%</div> <div>42%</div> <div>44%</div> <div>12%</div> <div>.</div> </div>
1	CA	1539	<div> <div>7%</div> <div>43%</div> <div>44%</div> <div>12%</div> <div>.</div> </div>
2	AB	218	<div> <div>19%</div> <div>20%</div> <div>47%</div> <div>28%</div> <div>6%</div> </div>
2	CB	218	<div> <div>36%</div> <div>30%</div> <div>47%</div> <div>20%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
3	AC	206	
3	CC	206	
4	AD	205	
4	CD	205	
5	AE	150	
5	CE	150	
6	AF	100	
6	CF	100	
7	AG	151	
7	CG	151	
8	AH	129	
8	CH	129	
9	AI	127	
9	CI	127	
10	AJ	98	
10	CJ	98	
11	AK	117	
11	CK	117	
12	AL	123	
12	CL	123	
13	AM	114	
13	CM	114	
14	AN	100	
14	CN	100	
15	AO	88	

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Mol	Chain	Length	Quality of chain
15	CO	88	
16	AP	82	
16	CP	82	
17	AQ	80	
17	CQ	80	
18	AR	55	
18	CR	55	
19	AS	79	
19	CS	79	
20	AT	85	
20	CT	85	
21	AU	51	
21	CU	51	
22	BA	2903	
22	DA	2903	
23	BB	119	
23	DB	119	
24	BC	271	
24	DC	271	
25	BD	209	
25	DD	209	
26	BE	201	
26	DE	201	
27	BF	177	
27	DF	177	

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Mol	Chain	Length	Quality of chain
28	BG	176	
28	DG	176	
29	BH	149	
29	DH	149	
30	BI	141	
30	DI	141	
31	BJ	142	
31	DJ	142	
32	BK	122	
32	DK	122	
33	BL	143	
33	DL	143	
34	BM	136	
34	DM	136	
35	BN	120	
35	DN	120	
36	BO	116	
36	DO	116	
37	BP	114	
37	DP	114	
38	BQ	117	
38	DQ	117	
39	BR	103	
39	DR	103	
40	BS	110	

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Mol	Chain	Length	Quality of chain
40	DS	110	
41	BT	93	
41	DT	93	
42	BU	102	
42	DU	102	
43	BV	94	
43	DV	94	
44	BW	76	
44	DW	76	
45	BX	77	
45	DX	77	
46	BY	63	
46	DY	63	
47	BZ	58	
47	DZ	58	
48	B0	56	
48	D0	56	
49	B1	50	
49	D1	50	
50	B2	46	
50	D2	46	
51	B3	64	
51	D3	64	
52	B4	38	
52	D4	38	

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Mol	Chain	Length	Quality of chain
53	B5	228	
54	B6	8	
54	D6	8	

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
54	004	D6	7	-	-	X	-
55	MG	AA	1622	-	-	-	X
55	MG	AA	1669	-	-	-	X
55	MG	BA	3040	-	-	-	X
55	MG	BA	3070	-	-	-	X
55	MG	BA	3108	-	-	-	X
55	MG	BA	3113	-	-	-	X
55	MG	BA	3116	-	-	-	X
55	MG	BA	3130	-	-	-	X
55	MG	BA	3152	-	-	-	X
55	MG	BA	3153	-	-	-	X
55	MG	BA	3161	-	-	-	X
55	MG	BA	3163	-	-	-	X
55	MG	BA	3168	-	-	-	X
55	MG	BA	3170	-	-	-	X
55	MG	BA	3178	-	-	-	X
55	MG	BA	3186	-	-	-	X
55	MG	BA	3188	-	-	-	X
55	MG	DA	3002	-	-	-	X
55	MG	DA	3005	-	-	-	X
55	MG	DA	3008	-	-	-	X
55	MG	DA	3013	-	-	-	X
55	MG	DA	3027	-	-	-	X
55	MG	DA	3057	-	-	-	X
55	MG	DA	3070	-	-	-	X
55	MG	DA	3071	-	-	-	X
55	MG	DA	3109	-	-	-	X
55	MG	DA	3124	-	-	-	X
55	MG	DA	3153	-	-	-	X
55	MG	DA	3157	-	-	-	X
55	MG	DA	3162	-	-	-	X
55	MG	DA	3165	-	-	-	X

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 288328 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 rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1538	Total	C	N	O	P	0	0	0
			32995	14716	6050	10691	1538			
1	CA	1539	Total	C	N	O	P	0	0	0
			33015	14725	6052	10699	1539			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	218	Total	C	N	O	S	0	0	0
			1705	1081	305	312	7			
2	CB	218	Total	C	N	O	S	0	0	0
			1705	1081	305	312	7			

- 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
			1625	1028	305	289	3			
3	CC	206	Total	C	N	O	S	0	0	0
			1625	1028	305	289	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			
4	CD	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0	0
			1106	687	211	202	6			
5	CE	150	Total	C	N	O	S	0	0	0
			1106	687	211	202	6			

- 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
			818	515	148	149	6			
6	CF	100	Total	C	N	O	S	0	0	0
			818	515	148	149	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	151	Total	C	N	O	S	0	0	0
			1182	735	227	216	4			
7	CG	151	Total	C	N	O	S	0	0	0
			1182	735	227	216	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			
8	CH	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			
9	CI	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0	0
			787	493	150	143	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	CJ	98	Total	C	N	O	S	0	0	0
			787	493	150	143	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AK	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			
11	CK	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			
12	CL	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	114	Total	C	N	O	S	0	0	0
			884	546	178	157	3			
13	CM	114	Total	C	N	O	S	0	0	0
			884	546	178	157	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			
14	CN	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			

- 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
			710	437	143	129	1			
15	CO	88	Total	C	N	O	S	0	0	0
			710	437	143	129	1			

- 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
			649	406	128	114	1			
16	CP	82	Total	C	N	O	S	0	0	0
			649	406	128	114	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	80	Total	C	N	O	S	0	0	0
			649	411	121	114	3			
17	CQ	80	Total	C	N	O	S	0	0	0
			649	411	121	114	3			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	55	Total	C	N	O	0	0	0
			456	288	86	82			
18	CR	55	Total	C	N	O	0	0	0
			456	288	86	82			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	79	Total	C	N	O	S	0	0	0
			638	408	120	108	2			
19	CS	79	Total	C	N	O	S	0	0	0
			638	408	120	108	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			
20	CT	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AU	51	Total	C	N	O	S	0	0	0
			426	265	86	74	1			
21	CU	51	Total	C	N	O	S	0	0	0
			426	265	86	74	1			

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	BA	2897	Total	C	N	O	P	0	0	0
			62195	27745	11446	20107	2897			
22	DA	2897	Total	C	N	O	P	0	0	0
			62195	27745	11446	20107	2897			

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	BB	119	Total	C	N	O	P	0	0	0
			2549	1135	466	829	119			
23	DB	118	Total	C	N	O	P	0	0	0
			2529	1126	464	821	118			

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	BC	271	Total	C	N	O	S	0	0	0
			2083	1288	423	365	7			
24	DC	271	Total	C	N	O	S	0	0	0
			2083	1288	423	365	7			

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BD	209	Total	C	N	O	S	0	0	0
			1565	979	288	294	4			
25	DD	209	Total	C	N	O	S	0	0	0
			1565	979	288	294	4			

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BE	201	Total	C	N	O	S	0	0	0
			1552	974	283	290	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	DE	201	Total	C	N	O	S	0	0	0
			1552	974	283	290	5			

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BF	177	Total	C	N	O	S	0	0	0
			1411	899	249	257	6			
27	DF	177	Total	C	N	O	S	0	0	0
			1411	899	249	257	6			

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BG	176	Total	C	N	O	S	0	0	0
			1323	832	243	246	2			
28	DG	176	Total	C	N	O	S	0	0	0
			1323	832	243	246	2			

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BH	149	Total	C	N	O	S	0	0	0
			1110	699	197	213	1			
29	DH	149	Total	C	N	O	S	0	0	0
			1110	699	197	213	1			

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BI	141	Total	C	N	O	S	0	0	0
			1032	651	179	196	6			
30	DI	141	Total	C	N	O	S	0	0	0
			1032	651	179	196	6			

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BJ	142	Total	C	N	O	S	0	0	0
			1129	714	212	199	4			
31	DJ	142	Total	C	N	O	S	0	0	0
			1129	714	212	199	4			

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BK	122	Total	C	N	O	S	0	0	0
			939	587	180	166	6			
32	DK	122	Total	C	N	O	S	0	0	0
			939	587	180	166	6			

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BL	143	Total	C	N	O	S	0	0	0
			1045	649	206	189	1			
33	DL	143	Total	C	N	O	S	0	0	0
			1045	649	206	189	1			

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BM	136	Total	C	N	O	S	0	0	0
			1074	686	205	177	6			
34	DM	136	Total	C	N	O	S	0	0	0
			1074	686	205	177	6			

- Molecule 35 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BN	120	Total	C	N	O	S	0	0	0
			961	593	196	167	5			
35	DN	120	Total	C	N	O	S	0	0	0
			961	593	196	167	5			

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
36	BO	116	Total	C	N	O	0	0	0
			892	552	178	162			
36	DO	116	Total	C	N	O	0	0	0
			892	552	178	162			

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BP	114	Total	C	N	O	S	0	0	0
			917	574	179	163	1			
37	DP	114	Total	C	N	O	S	0	0	0
			917	574	179	163	1			

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BQ	117	Total	C	N	O	S	0	0	0
			947	604	192	151				
38	DQ	117	Total	C	N	O	S	0	0	0
			947	604	192	151				

- Molecule 39 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BR	103	Total	C	N	O	S	0	0	0
			816	516	153	145	2			
39	DR	103	Total	C	N	O	S	0	0	0
			816	516	153	145	2			

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BS	110	Total	C	N	O	S	0	0	0
			857	532	166	156	3			
40	DS	110	Total	C	N	O	S	0	0	0
			857	532	166	156	3			

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BT	93	Total	C	N	O	S	0	0	0
			739	466	139	132	2			
41	DT	93	Total	C	N	O	S	0	0	0
			739	466	139	132	2			

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BU	102	Total	C	N	O	S	0	0	0
			780	492	146	142				

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
42	DU	102	Total	C	N	O			
			780	492	146	142	0	0	0

- Molecule 43 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
43	BV	94	Total	C	N	O	S		
			753	479	137	134	3	0	0
43	DV	94	Total	C	N	O	S		
			753	479	137	134	3	0	0

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
44	BW	76	Total	C	N	O	S		
			580	359	117	103	1	0	0
44	DW	75	Total	C	N	O	S		
			569	353	113	102	1	0	0

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
45	BX	77	Total	C	N	O	S		
			625	388	129	106	2	0	0
45	DX	77	Total	C	N	O	S		
			625	388	129	106	2	0	0

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
46	BY	63	Total	C	N	O	S		
			509	313	99	95	2	0	0
46	DY	63	Total	C	N	O	S		
			509	313	99	95	2	0	0

- Molecule 47 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
47	BZ	58	Total	C	N	O	S		
			449	281	87	79	2	0	0
47	DZ	58	Total	C	N	O	S		
			449	281	87	79	2	0	0

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B0	56	Total	C	N	O	S	0	0	0
			444	269	94	80	1			
48	D0	56	Total	C	N	O	S	0	0	0
			444	269	94	80	1			

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	B1	50	Total	C	N	O	0	0	0
			410	263	75	72			
49	D1	50	Total	C	N	O	0	0	0
			410	263	75	72			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B2	46	Total	C	N	O	S	0	0	0
			377	228	90	57	2			
50	D2	46	Total	C	N	O	S	0	0	0
			377	228	90	57	2			

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B3	64	Total	C	N	O	S	0	0	0
			504	323	105	74	2			
51	D3	64	Total	C	N	O	S	0	0	0
			504	323	105	74	2			

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B4	38	Total	C	N	O	S	0	0	0
			302	185	65	48	4			
52	D4	38	Total	C	N	O	S	0	0	0
			302	185	65	48	4			

- Molecule 53 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
53	B5	191	Total	C	N	O	0	0	1
			1142	691	221	230			

- Molecule 54 is a protein called Quinupristin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	B6	8	Total	C	N	O	S	0	0	0
			73	53	9	10	1			
54	D6	8	Total	C	N	O	S	0	0	0
			73	53	9	10	1			

- Molecule 55 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
55	BB	4	Total	Mg	0	0
			4	4		
55	BA	195	Total	Mg	0	0
			195	195		
55	CA	55	Total	Mg	0	0
			55	55		
55	DQ	1	Total	Mg	0	0
			1	1		
55	CM	1	Total	Mg	0	0
			1	1		
55	AA	71	Total	Mg	0	0
			71	71		
55	DA	167	Total	Mg	0	0
			167	167		
55	DB	3	Total	Mg	0	0
			3	3		
55	AM	1	Total	Mg	0	0
			1	1		

- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	B4	1	Total	Zn	0	0
			1	1		
56	D4	1	Total	Zn	0	0
			1	1		

- Molecule 57 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	AA	194	Total O 194 194	0	0
57	AL	1	Total O 1 1	0	0
57	AN	5	Total O 5 5	0	0
57	AT	2	Total O 2 2	0	0
57	AU	1	Total O 1 1	0	0
57	BA	619	Total O 619 619	0	0
57	BB	13	Total O 13 13	0	0
57	BC	8	Total O 8 8	0	0
57	BD	3	Total O 3 3	0	0
57	BE	3	Total O 3 3	0	0
57	BF	1	Total O 1 1	0	0
57	BG	1	Total O 1 1	0	0
57	BL	5	Total O 5 5	0	0
57	BN	5	Total O 5 5	0	0
57	BS	1	Total O 1 1	0	0
57	BV	1	Total O 1 1	0	0
57	B2	1	Total O 1 1	0	0
57	B3	3	Total O 3 3	0	0
57	B4	2	Total O 2 2	0	0
57	CA	189	Total O 189 189	0	0
57	CL	1	Total O 1 1	0	0
57	CN	3	Total O 3 3	0	0

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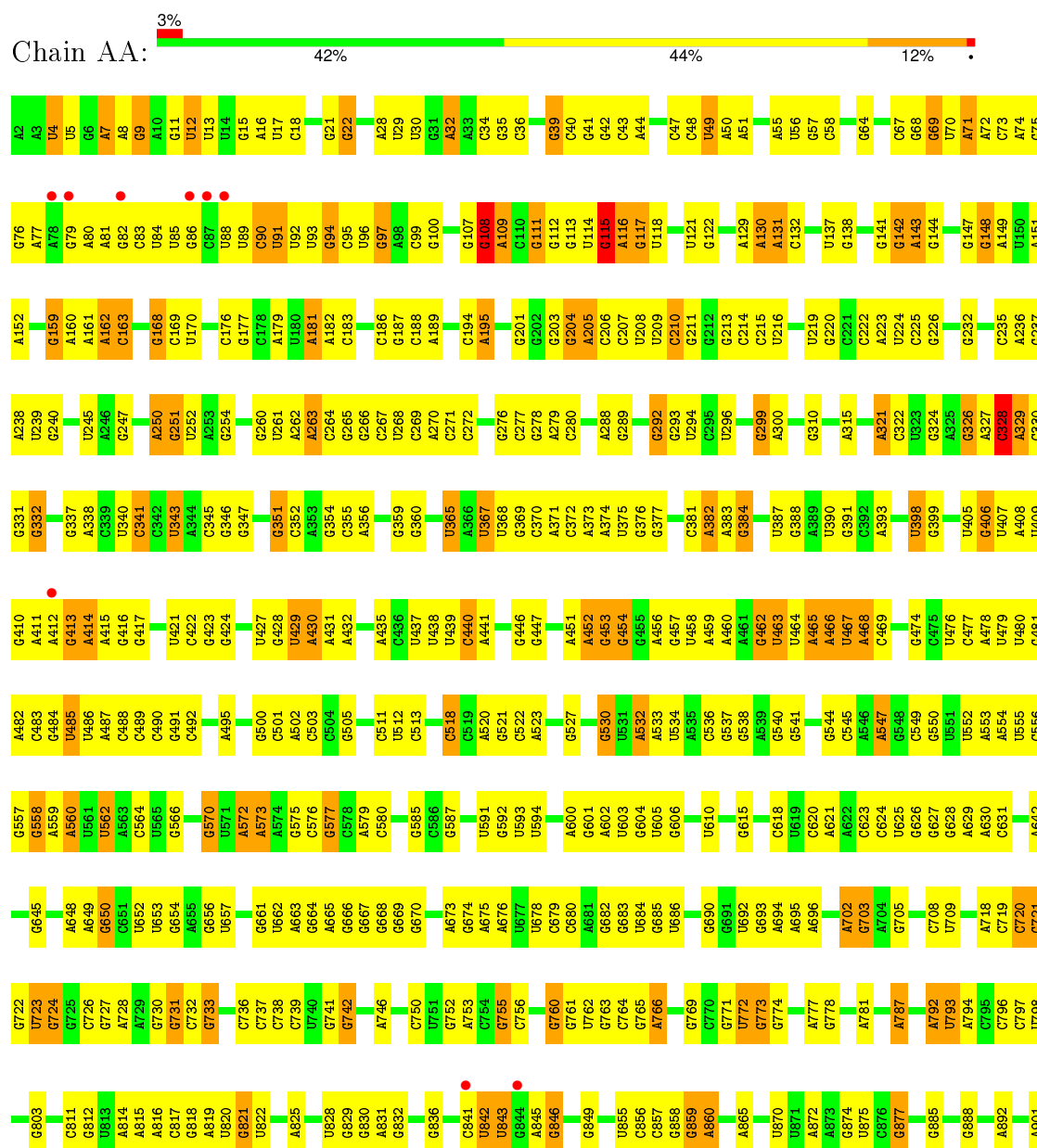
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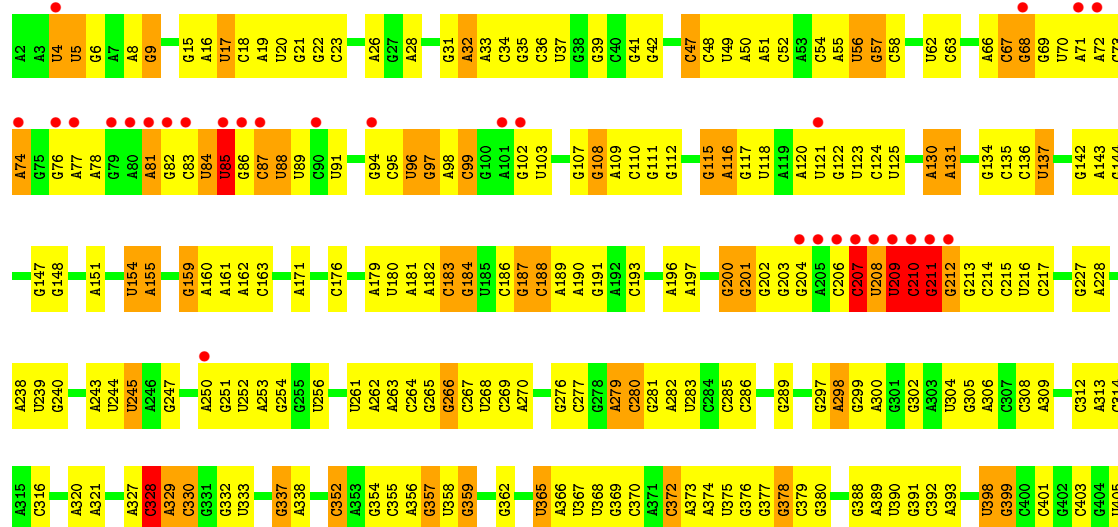
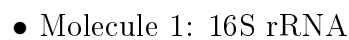
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57	DB	13	Total 13	O 13	0	0
57	DC	7	Total 7	O 7	0	0
57	DD	4	Total 4	O 4	0	0
57	DE	4	Total 4	O 4	0	0
57	DL	4	Total 4	O 4	0	0
57	DN	1	Total 1	O 1	0	0
57	DQ	2	Total 2	O 2	0	0
57	DT	3	Total 3	O 3	0	0
57	DV	1	Total 1	O 1	0	0
57	D0	1	Total 1	O 1	0	0
57	D2	2	Total 2	O 2	0	0
57	D3	1	Total 1	O 1	0	0
57	D4	1	Total 1	O 1	0	0

3 Residue-property plots

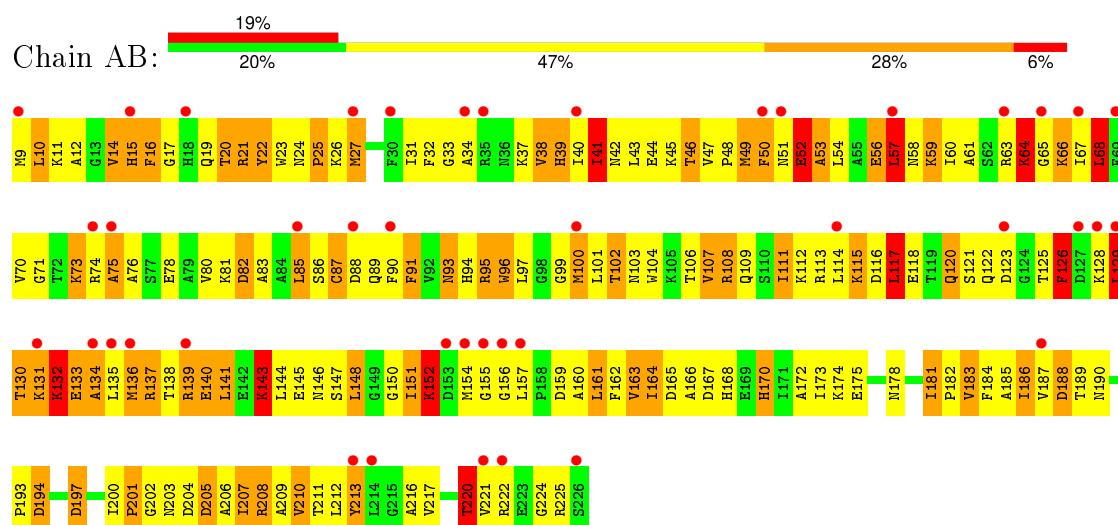
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

• Molecule 1: 16S rRNA

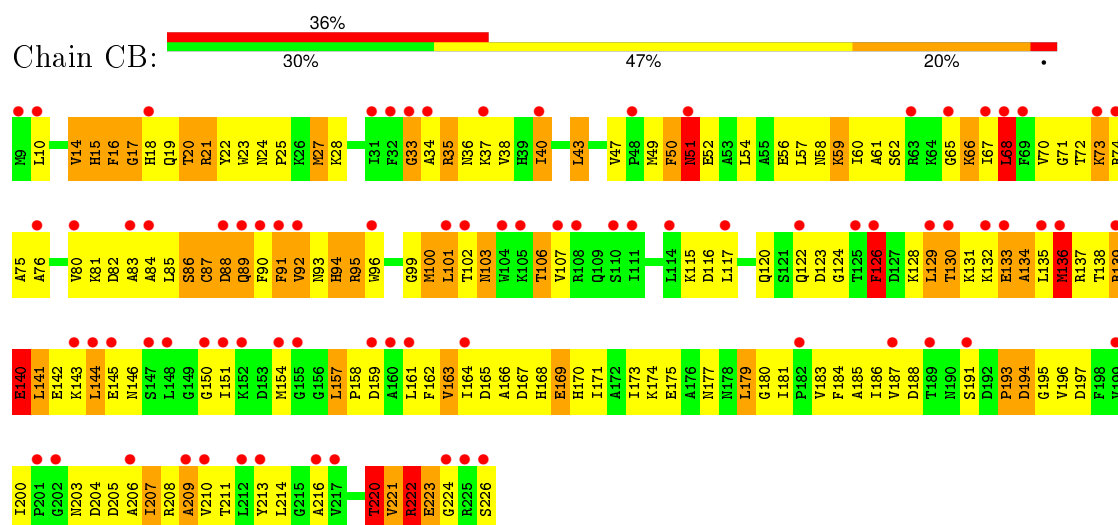




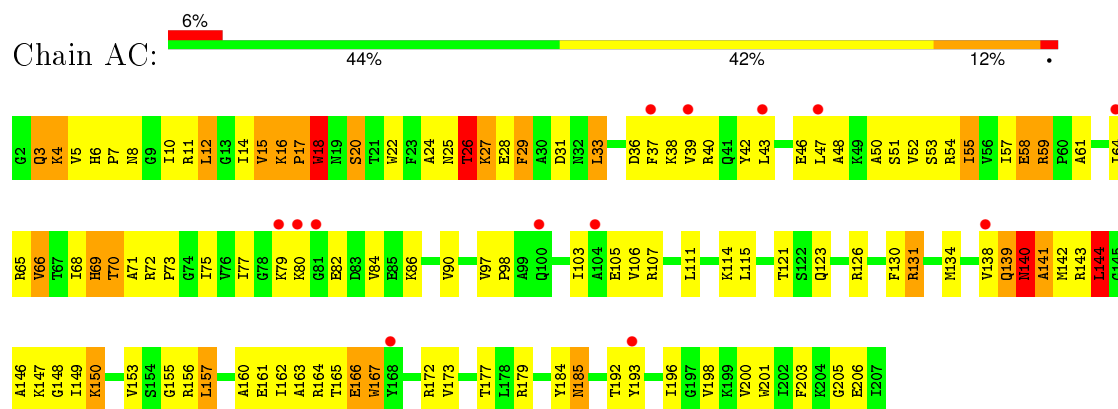
C1509	A1433	C1284	G1218	U062	U997	U921	U820	G733	A649	C549	G484	G406
A1513	A1350	A1285	A1219	C1063	C998	G922	G821	G734	G650	G950	U485	U407
G1514	U1351	U1286	G1220	G1064	C999	G926	U822	C735	G651	U551	U486	A408
G1515	C1352	A1287	G1221	U1065	A1000	G926	C823	C736	U652	U552	A487	U409
G1516	G1353	A1288	G1222	U1066	C1001	G929	U827	C737	U653	A553	C488	G410
A1441	U1354	A1289	G1223	A1067	G1002	G930	U828	C738	G654	U555	C489	A411
G1442	G1355	U1291	A1225	U1068	G1003	C931	G833	C739	A663	C556	C490	A412
G1356	A1357	G1292	C1226	G1069	A1004	C932	U834	U740	A664	G557	C491	G413
A1446	U1358	A1227	A1227	U1070	A1005	C933	G835	U741	G665	U558	C492	C418
A1447	C1359	A1228	C1228	C1071	U1006	G934	U836	G745	A666	A559	G493	U421
C1448	U1295	A1229	A1229	G1072	U1007	A935	U835	U746	A667	U560	A495	U422
A1449	G1360	G1296	G1230	U1073	U1008	A938	C840	A747	G668	U562	A496	G423
G1361	A1231	U1231	G1231	G1074	U1009	G939	C841	G748	U672	U563	A498	G424
A1362	U1232	U1232	U1232	G1077	U1010	C940	U842	G749	A673	C564	A499	G425
A1363	A1299	G1233	G1233	G1077	A1012	G942	U843	U751	G674	U565	G500	U426
U1451	U1301	G1234	A1238	A1080	G1013	G942	U844	U752	A675	C566	C501	U427
G1453	U1302	G1235	A1239	A1081	A1014	G942	U845	U753	A676	C567	A502	G428
G1365	U1303	G1236	A1240	U1082	U1015	G942	U846	A754	U677	G568	C503	U429
C1366	G1304	G1237	G1241	U1083	U1016	G942	U847	C754	U677	G568	C504	A430
G1370	G1305	G1238	G1242	U1084	U1017	G942	U848	U757	G682	A572	G505	C436
G1371	G1306	G1239	G1243	U1085	U1018	G942	U849	U758	A687	A574	A509	U437
G1372	U1308	A1243	G1244	U1086	U1019	G942	U850	U759	G688	A575	A510	U438
A1374	G1309	A1244	G1245	U1087	U1020	G942	U851	A766	G689	C576	C511	U439
A1377	G1310	A1246	A1246	G1088	A1021	G942	U852	A767	G690	C579	C512	U440
A1378	A1311	U1247	U1247	U1089	A1022	G942	U853	A768	G691	C580	C513	A441
G1379	G1312	A1248	A1248	U1090	U1023	G942	U854	A769	G692	C581	C514	G445
G1379	G1313	C1249	C1249	U1091	U1024	G942	U855	A770	A695	C582	C515	G445
U1380	C1314	A1250	A1250	U1092	U1025	G942	U856	A771	A696	C583	C516	G445
U1381	U1315	A1251	A1251	C1096	U1026	G942	U857	A772	A697	C584	C517	A451
U1387	G1316	A1252	A1252	C1097	U1027	G942	U858	A773	A698	C585	C518	A452
G1387	C1317	A1253	A1253	C1098	U1028	G942	U859	A774	A699	C586	C519	G454
G1388	A1318	A1254	A1254	U1099	U1029	G942	U860	A775	A699	C587	C520	U458
U1391	A1319	G1255	G1255	A1101	U1030	G942	U861	A776	A699	C588	C521	A459
U1393	G1320	A1256	A1256	G1108	U1031	G942	U862	A777	A699	C589	C522	U458
A1394	U1321	A1257	A1257	G1108	U1032	G942	U863	A778	A699	C590	C523	U459
C1397	G1322	A1258	A1258	G1108	U1033	G942	U864	A779	A699	C591	C524	U459
A1398	G1323	A1259	A1259	G1108	U1034	G942	U865	A780	A699	C592	C525	U459
C1403	A1324	A1260	A1260	G1108	U1035	G942	U866	A781	A699	C593	C526	U459
C1404	C1325	A1261	A1261	G1108	U1036	G942	U867	A782	A699	C594	C527	U459
A1408	U1326	C1262	C1262	G1108	U1037	G942	U868	A783	A699	C595	C528	U459
A1410	C1327	U1264	U1264	G1108	U1038	G942	U869	A784	A699	C596	C529	U459
C1412	U1328	G1265	G1265	G1108	U1039	G942	U870	A785	A699	C597	C530	U459
A1413	A1329	G1266	G1266	G1108	U1040	G942	U871	A786	A699	C598	C531	U459
A1404	U1331	A1269	A1269	G1108	U1041	G942	U872	A787	A699	C599	C532	U459
A1408	G1332	G1270	G1270	G1108	U1042	G942	U873	A788	A699	C600	C533	U459
A1411	A1333	A1271	A1271	G1108	U1043	G942	U874	A789	A699	C601	C534	U459
C1414	G1334	C1272	C1272	G1108	U1044	G942	U875	A790	A699	C602	C535	U459
A1414	U1337	A1273	A1273	G1108	U1045	G942	U876	A791	A699	C603	C536	U459
A1500	G1338	A1274	A1274	G1108	U1046	G942	U877	A792	A699	C604	C537	U459
C1501	U1342	G1276	G1276	G1108	U1047	G942	U878	A793	A699	C605	C538	U459
A1502	G1343	C1277	C1277	G1108	U1048	G942	U879	A794	A699	C606	C539	U459
A1503	G1344	G1278	G1278	G1108	U1049	G942	U880	A795	A699	C607	C540	U459
A1418	C1345	U1279	U1279	G1108	U1050	G942	U881	A796	A699	C608	C541	U459
G1419	U1346	A1280	A1280	G1108	U1051	G942	U882	A797	A699	C609	C542	U459
A1431	G1347	C1281	C1281	G1108	U1052	G942	U883	A798	A699	C610	C543	U459
A1508	U1348	U1283	U1283	G1108	U1053	G942	U884	A799	A699	C611	C544	U459
				G1108	U1054	G942	U885	A800	A699	C612	C545	U459
				G1108	U1055	G942	U886	A801	A699	C613	C546	U459
				G1108	U1056	G942	U887	A802	A699	C614	C547	U459
				G1108	U1057	G942	U888	A803	A699	C615	C548	U459
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				G1108	U1059	G942	U890	A805	A699	C617	C550	U459
				G1108	U1060	G942	U891	A806	A699	C618	C551	U459
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				G1108	U1062	G942	U893	A808	A699	C620	C553	U459
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				G1108	U1064	G942	U895	A810	A699	C622	C555	U459
				G1108	U1065	G942	U896	A811	A699	C623	C556	U459
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				G1108	U1068	G942	U899	A814	A699	C626	C559	U459
				G1108	U1069	G942	U900	A815	A699	C627	C560	U459
				G1108	U1070	G942	U901	A816	A699	C628	C561	U459
				G1108	U1071	G942	U902	A817	A699	C629	C562	U459
				G1108	U1072	G942	U903	A818	A699	C630	C563	U459
				G1108	U1073	G942	U904	A819	A699	C631	C564	U459
				G1108	U1074	G942	U905	A820	A699	C632	C565	U459
				G1108	U1075	G942	U906	A821	A699	C633	C566	U459
				G1108	U1076	G942	U907	A822	A699	C634	C567	U459
				G1108	U1077	G942	U908	A823	A699	C635	C568	U459
				G1108	U1078	G942	U909	A824	A699	C636	C569	U459
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				G1108	U1080	G942	U911	A826	A699	C638	C571	U459
				G1108	U1081	G942	U912	A827	A699	C639	C572	U459
				G1108	U1082	G942	U913	A828	A699	C640	C573	U459
				G1108	U1083	G942	U914	A829	A699	C641	C574	U459
				G1108	U1084	G942	U915	A830	A699	C642	C575	U459
				G1108	U1085	G942	U916	A831	A699	C643	C576	U459
				G1108	U1086	G942	U917	A832	A699	C644	C577	U459
				G1108	U1087	G942	U918	A833	A699	C645	C578	U459
				G1108	U1088	G942	U919	A834	A699	C646	C579	U459
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				G1108	U1090	G942	U921	A836	A699	C648	C581	U459
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				G1108	U1105	G942	U936	A851	A699	C663	C596	U459
				G1108	U1106	G942	U937	A852	A699	C664	C597	U459
				G1108	U1107	G942	U938	A853	A699	C665	C598	U459
				G1108	U1108	G942	U939	A854	A699	C666	C599	U459
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• Molecule 2: 30S ribosomal protein S2

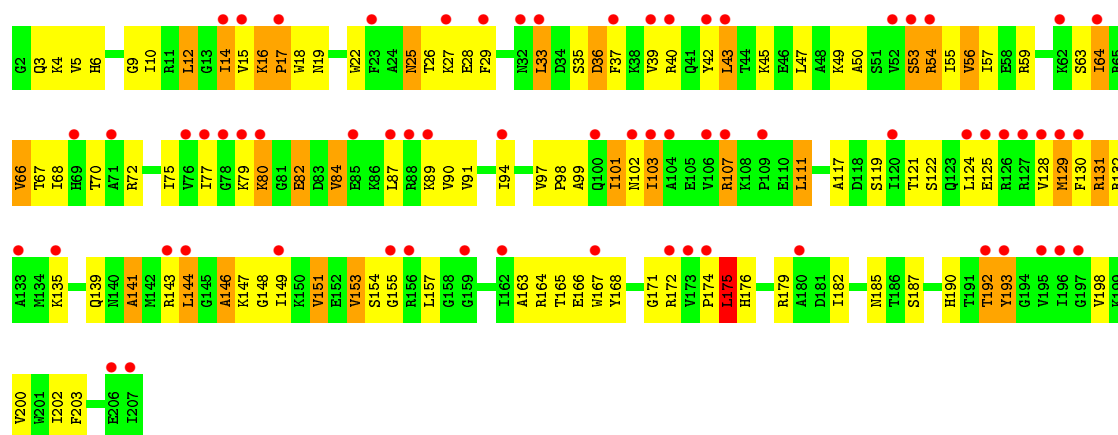


• Molecule 3: 30S ribosomal protein S3

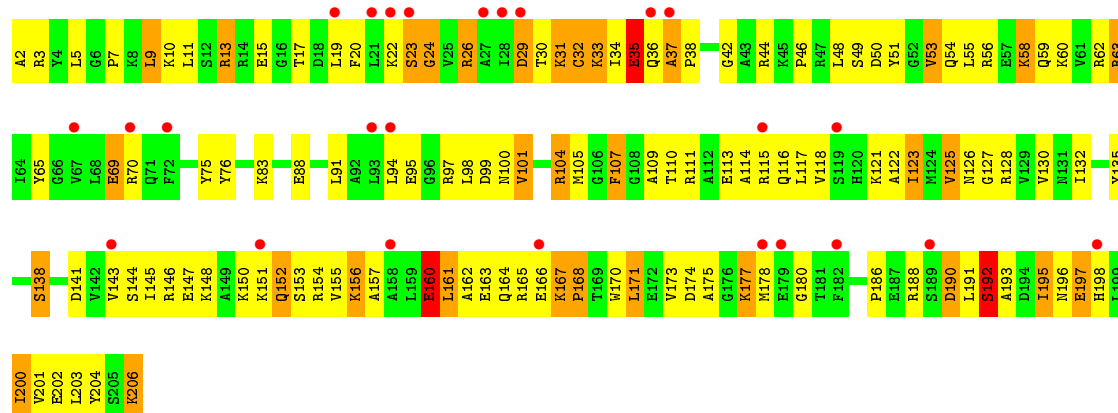
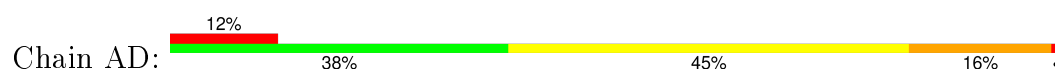


• Molecule 3: 30S ribosomal protein S3

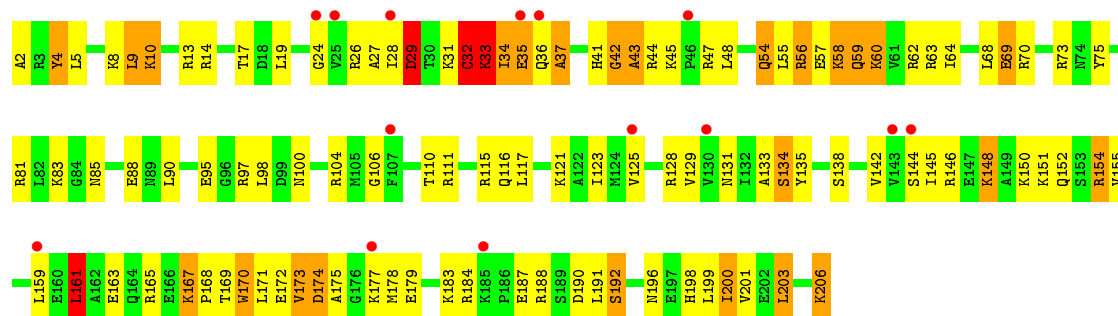




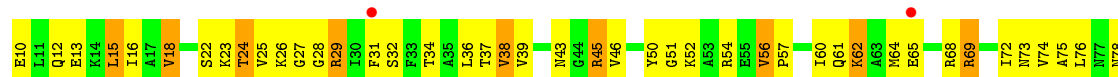
• Molecule 4: 30S ribosomal protein S4

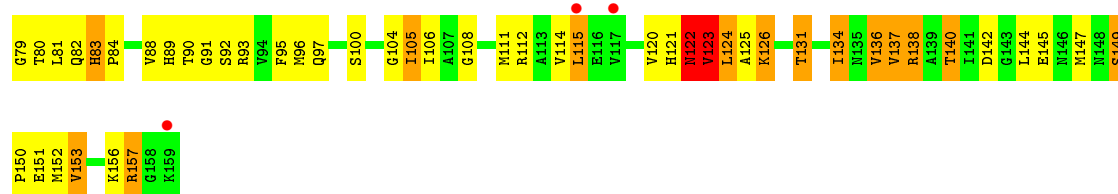


• Molecule 4: 30S ribosomal protein S4

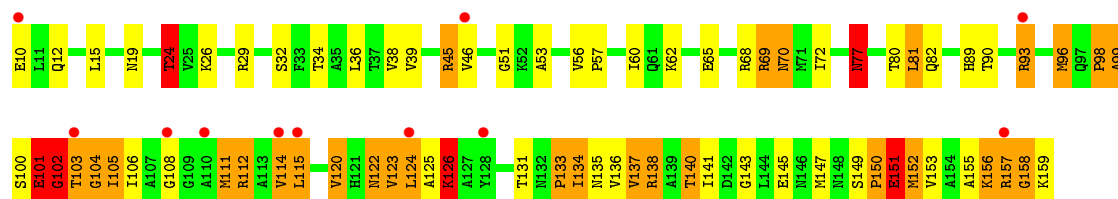


• Molecule 5: 30S ribosomal protein S5

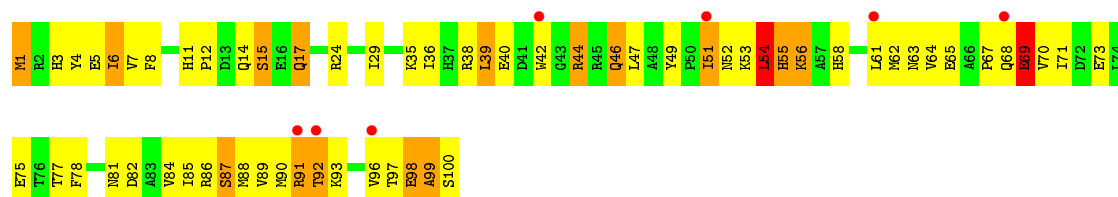




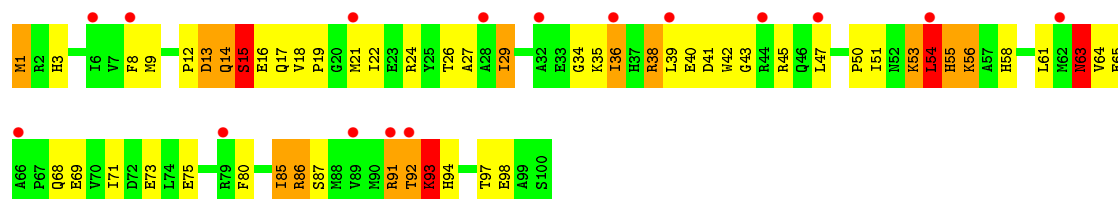
• Molecule 5: 30S ribosomal protein S5



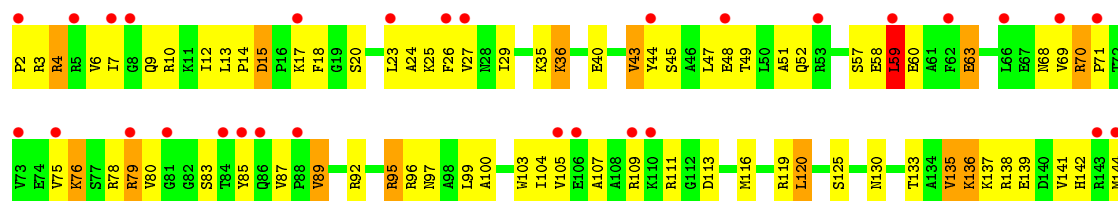
• Molecule 6: 30S ribosomal protein S6

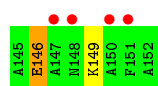


• Molecule 6: 30S ribosomal protein S6

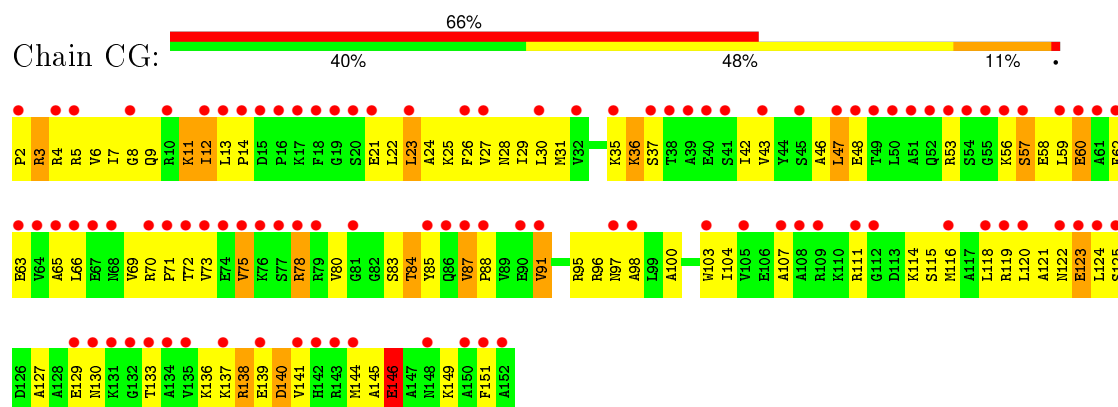


• Molecule 7: 30S ribosomal protein S7

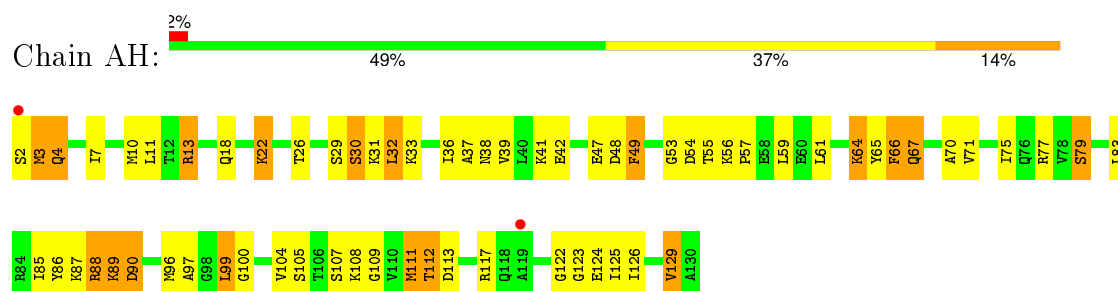




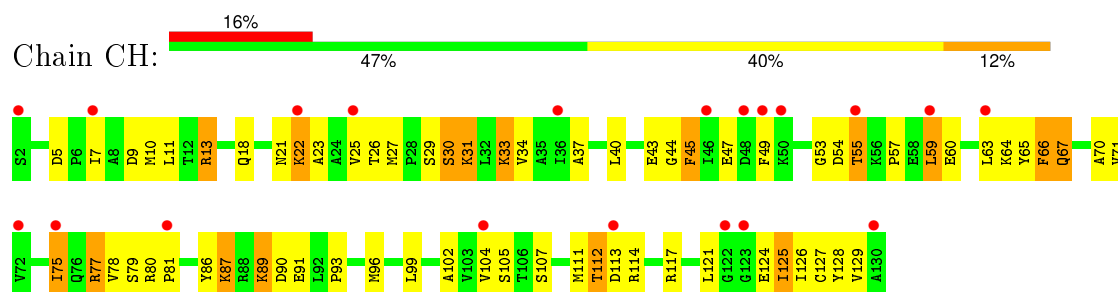
• Molecule 7: 30S ribosomal protein S7



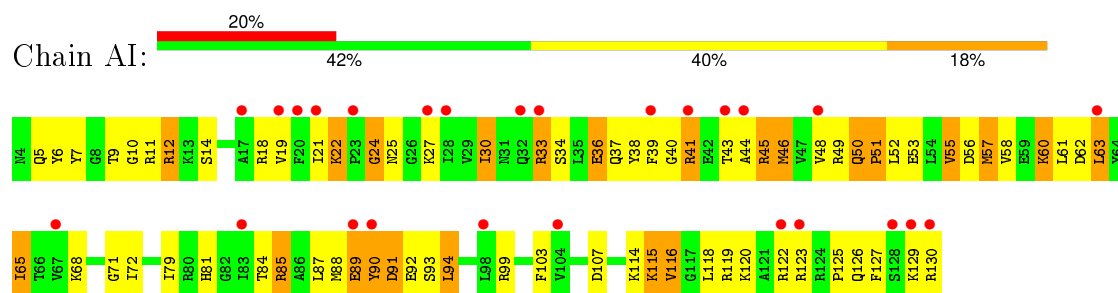
• Molecule 8: 30S ribosomal protein S8



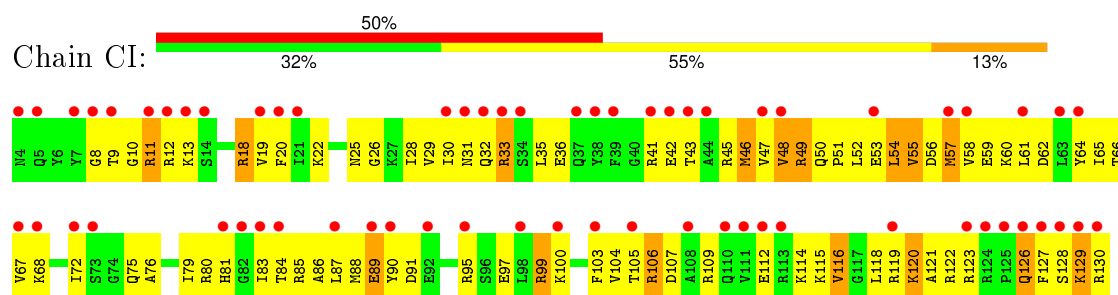
• Molecule 8: 30S ribosomal protein S8



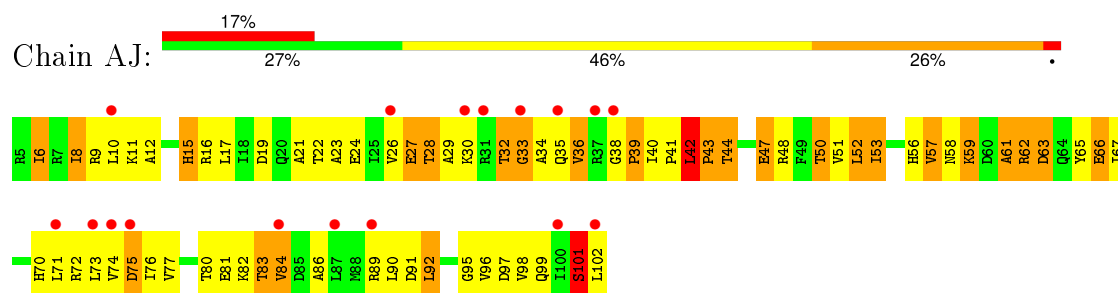
• Molecule 9: 30S ribosomal protein S9



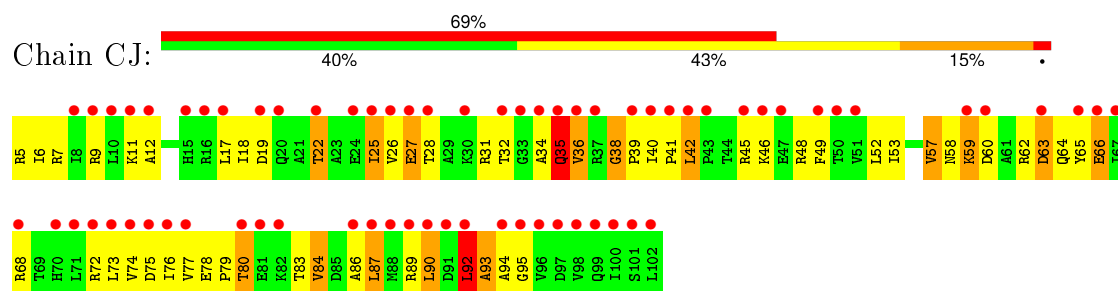
• Molecule 9: 30S ribosomal protein S9



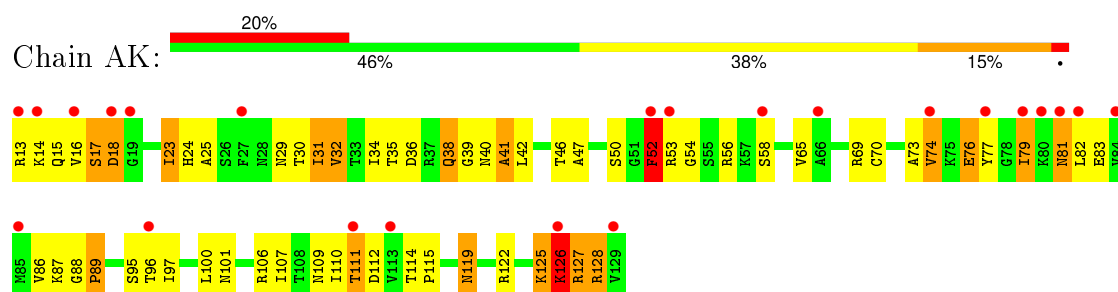
- Molecule 10: 30S ribosomal protein S10



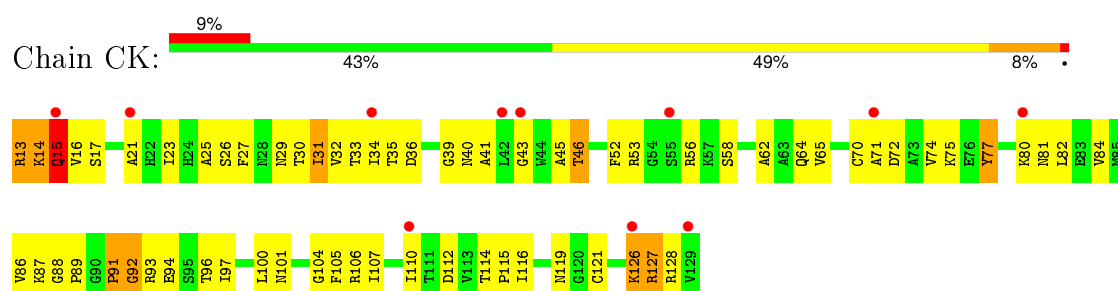
- Molecule 10: 30S ribosomal protein S10



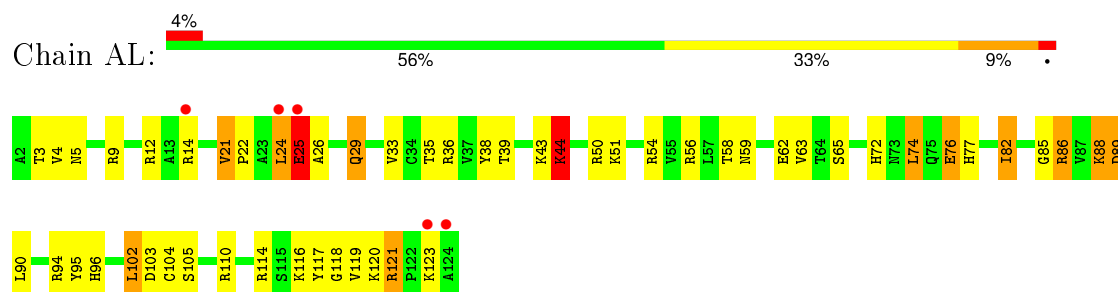
- Molecule 11: 30S ribosomal protein S11

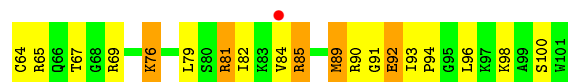


- Molecule 11: 30S ribosomal protein S11

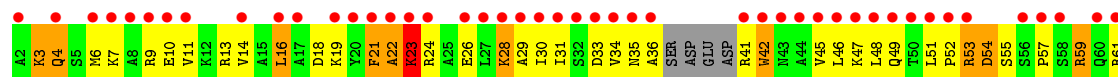


- Molecule 12: 30S ribosomal protein S12

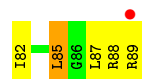




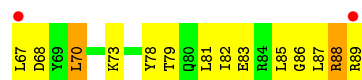
- Molecule 14: 30S ribosomal protein S14



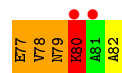
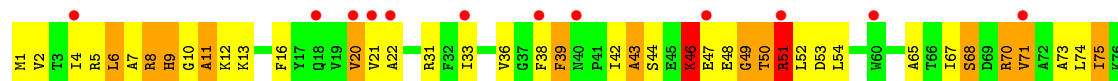
- Molecule 15: 30S ribosomal protein S15



- Molecule 15: 30S ribosomal protein S15

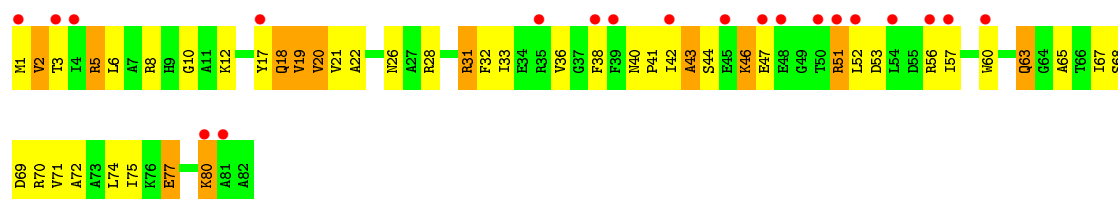


- Molecule 16: 30S ribosomal protein S16

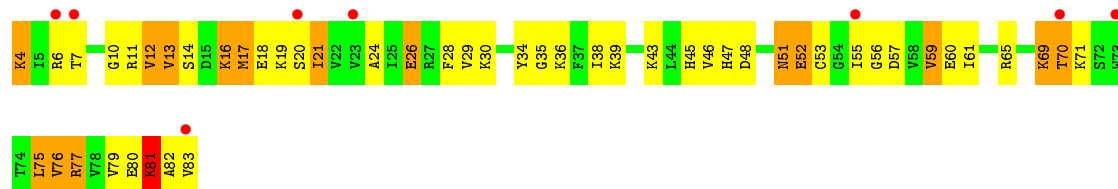


- Molecule 16: 30S ribosomal protein S16

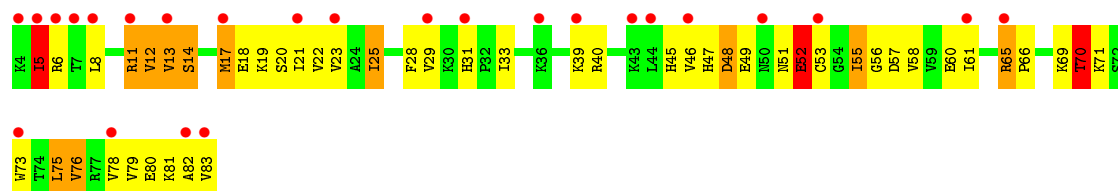




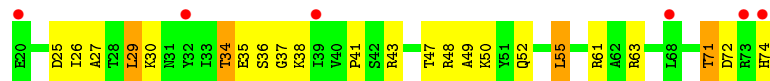
- Molecule 17: 30S ribosomal protein S17



- Molecule 17: 30S ribosomal protein S17



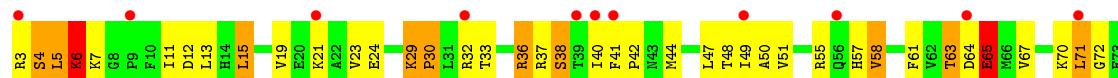
- Molecule 18: 30S ribosomal protein S18

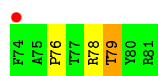


- Molecule 18: 30S ribosomal protein S18

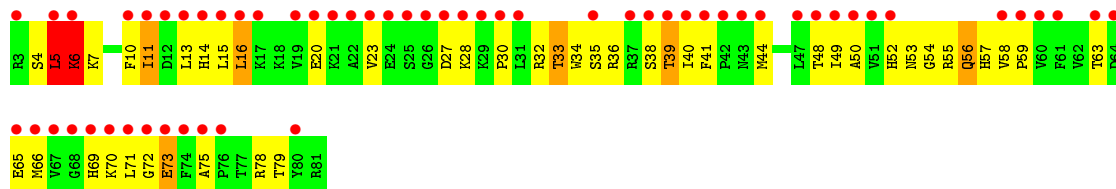
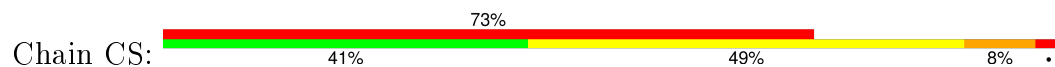


- Molecule 19: 30S ribosomal protein S19

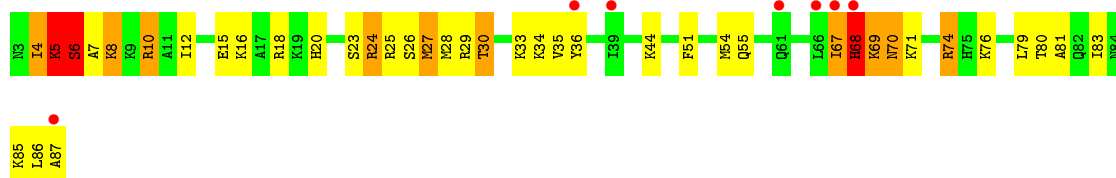




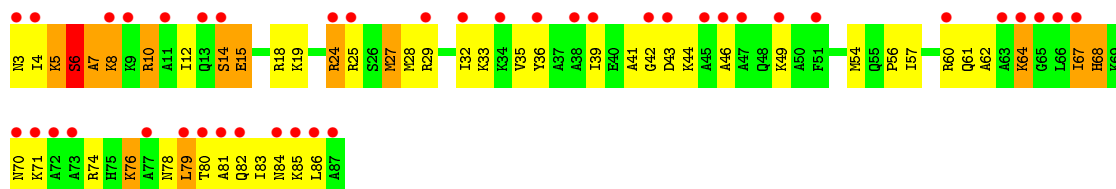
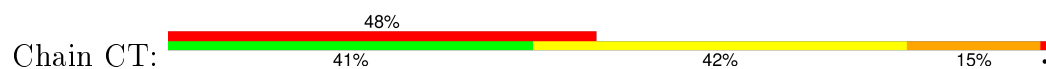
- Molecule 19: 30S ribosomal protein S19



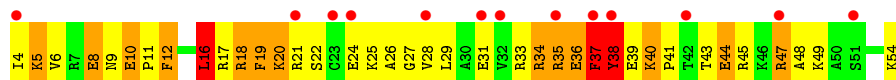
- Molecule 20: 30S ribosomal protein S20



- Molecule 20: 30S ribosomal protein S20



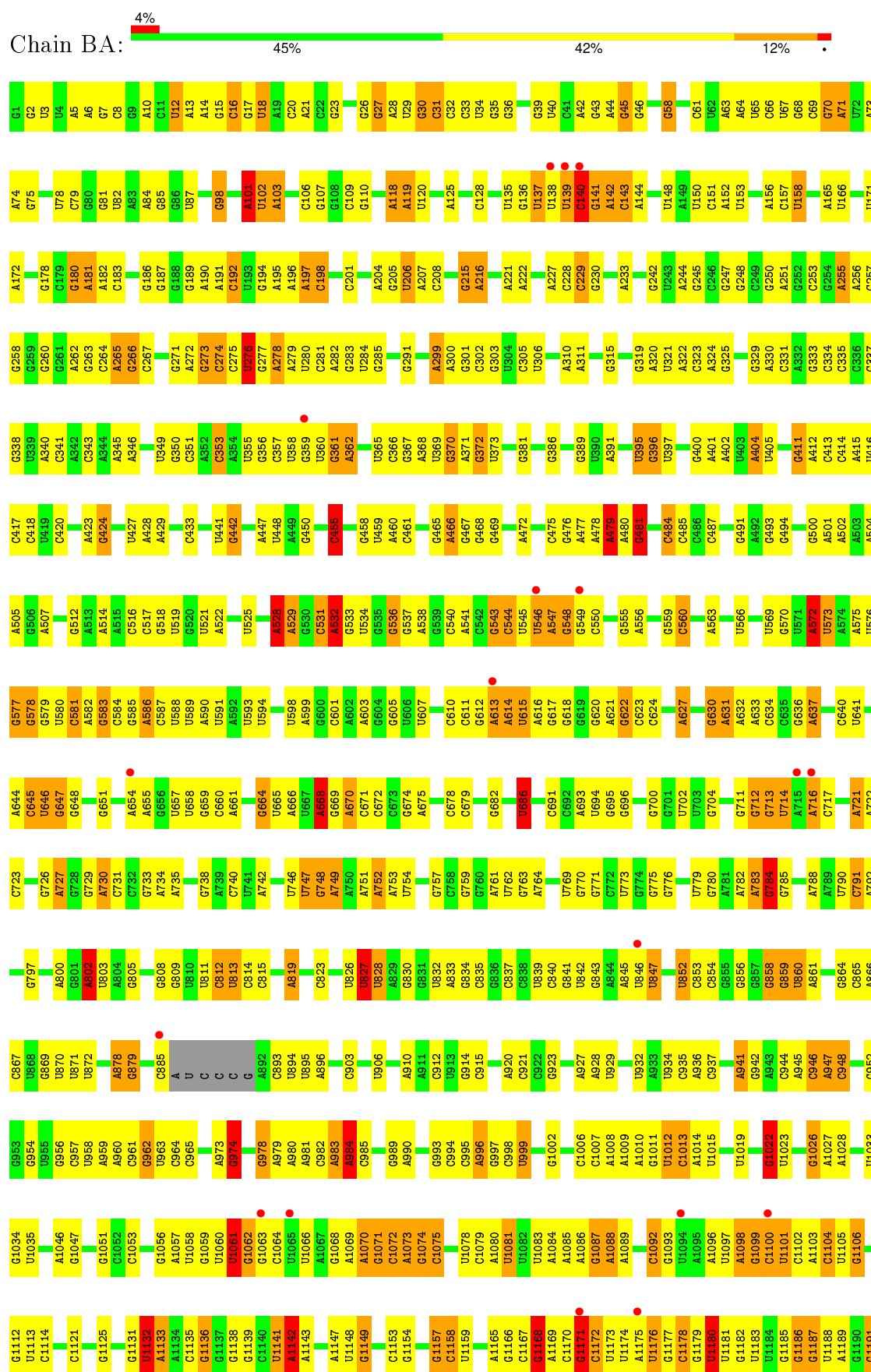
- Molecule 21: 30S ribosomal protein S21



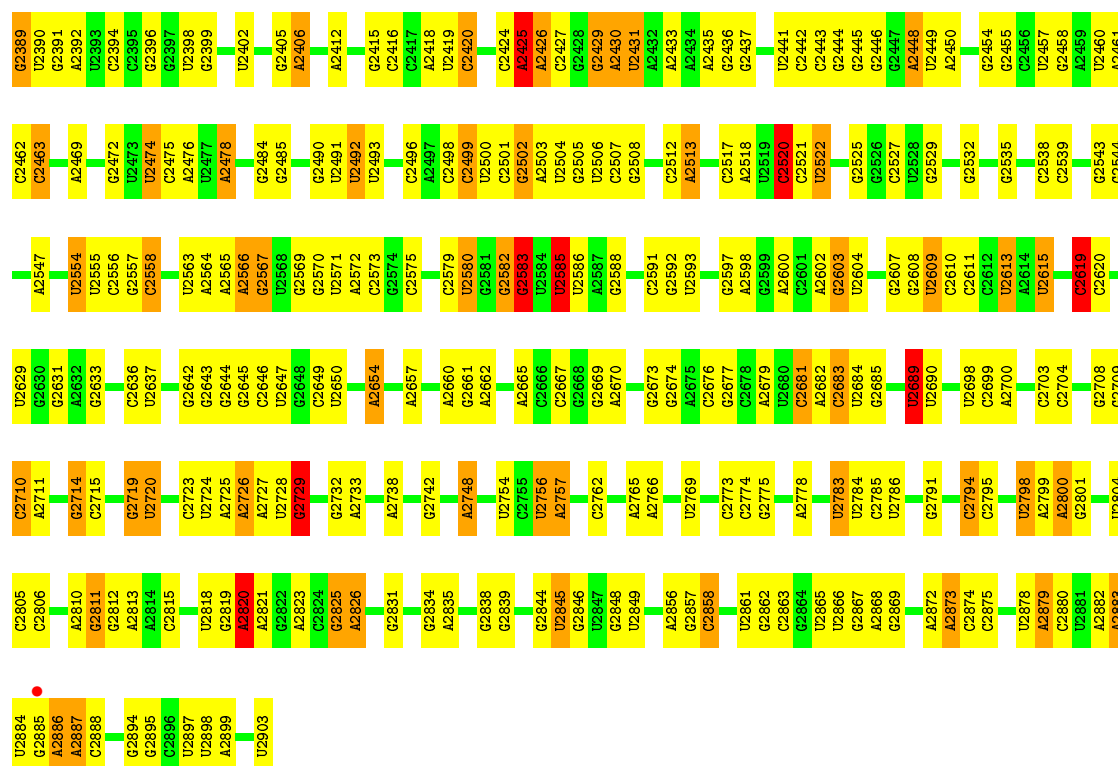
- Molecule 21: 30S ribosomal protein S21



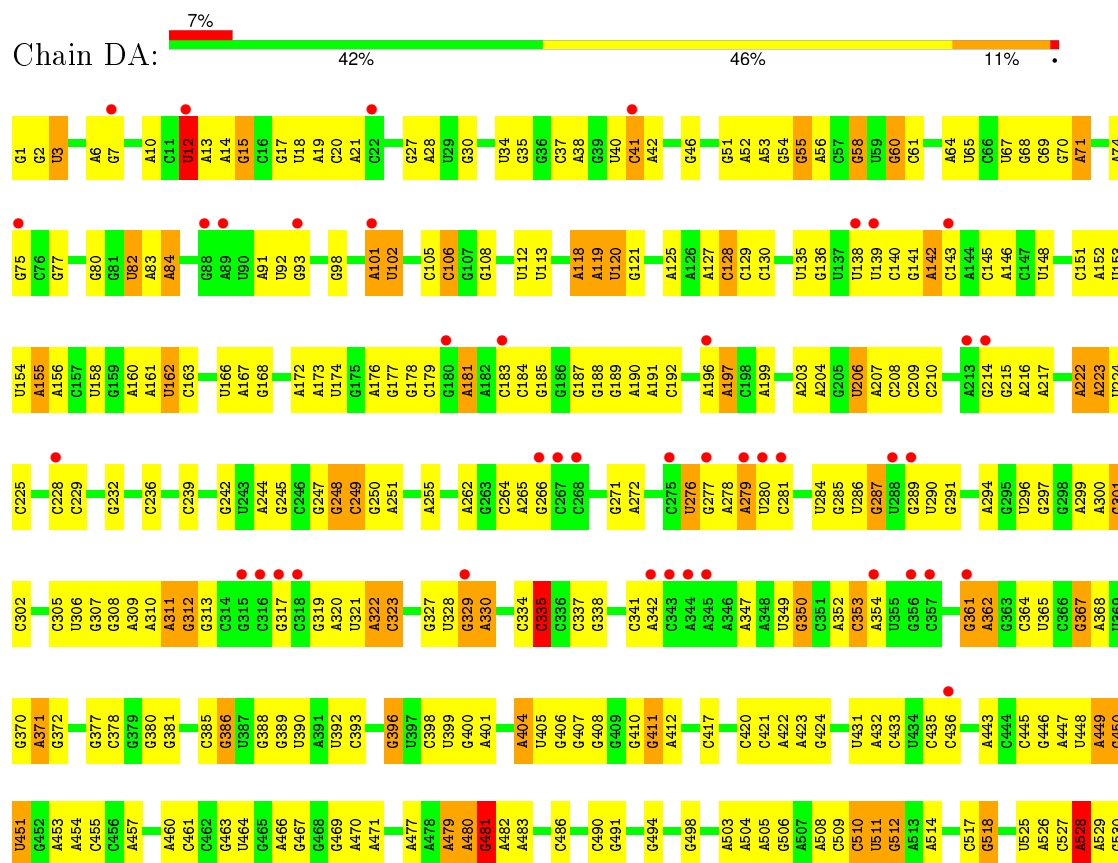
- Molecule 22: 23S rRNA





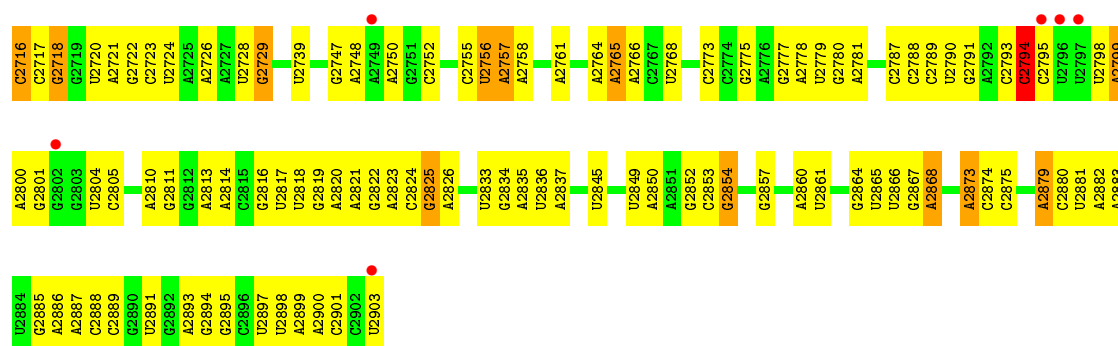


• Molecule 22: 23S rRNA

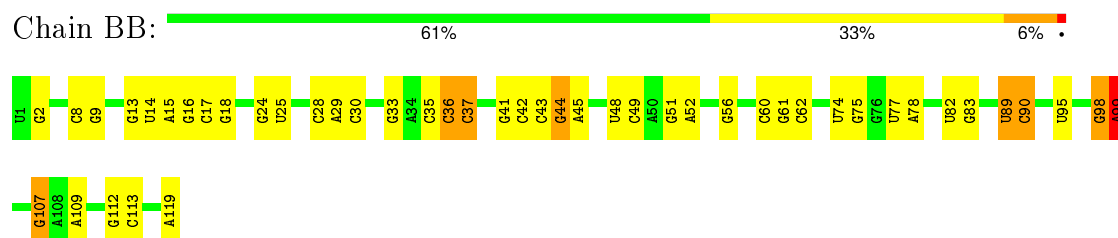




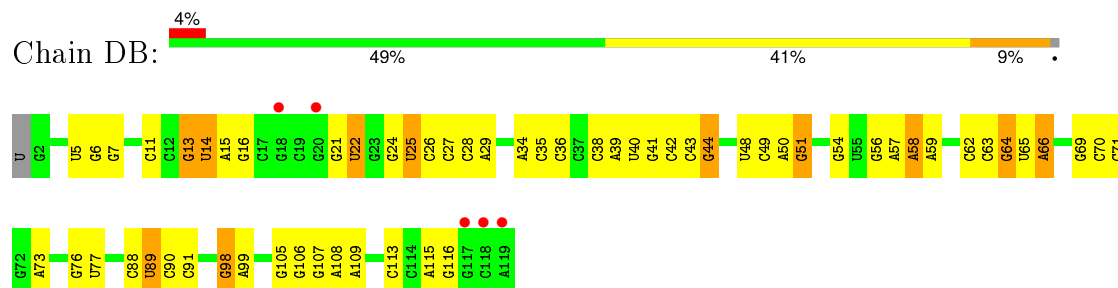
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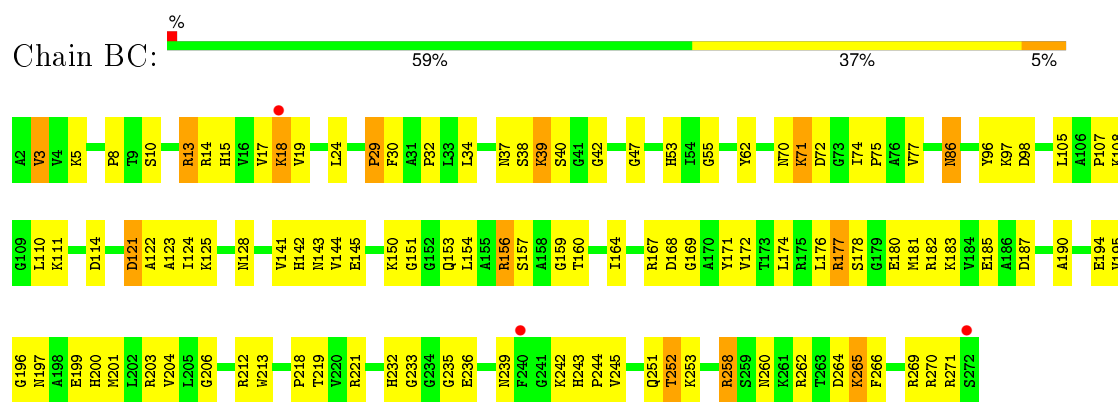
• Molecule 23: 5S rRNA



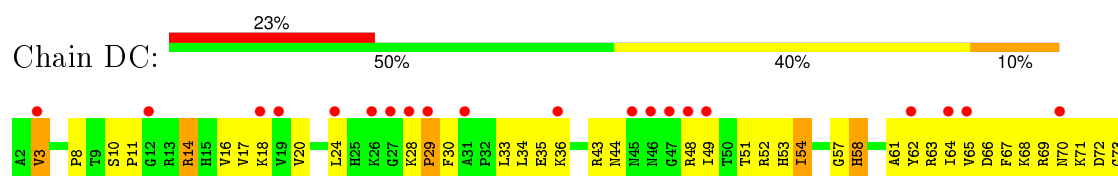
• Molecule 23: 5S rRNA

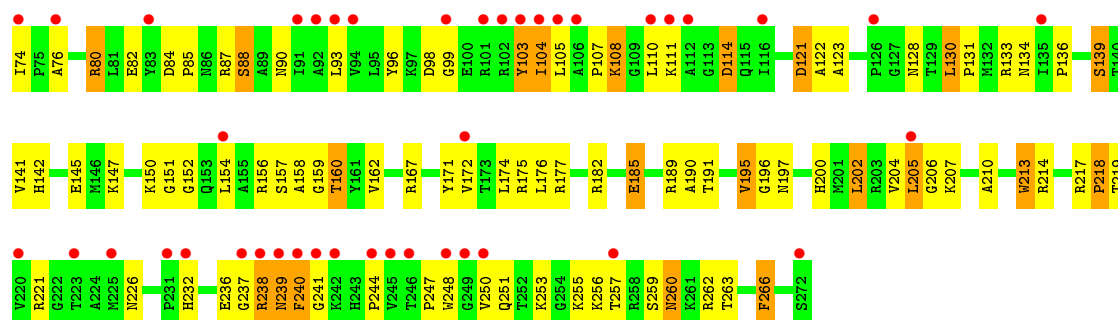


• Molecule 24: 50S ribosomal protein L2



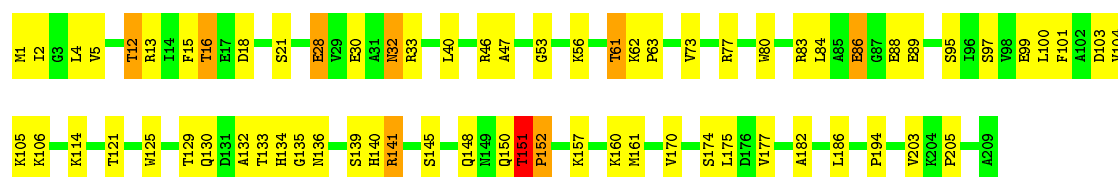
• Molecule 24: 50S ribosomal protein L2





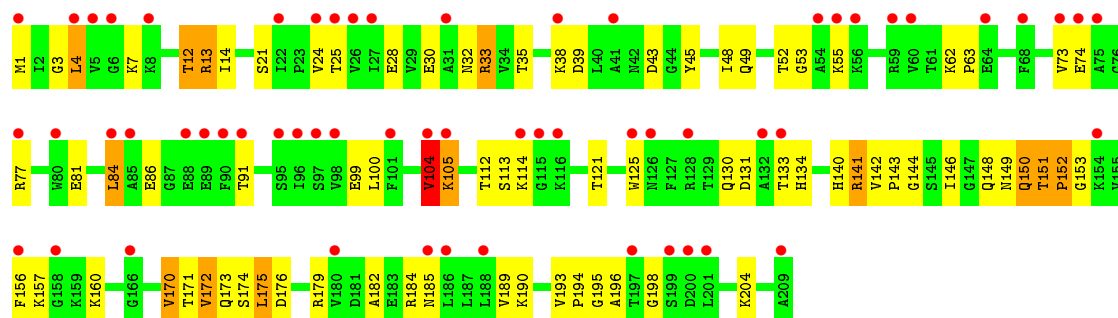
• Molecule 25: 50S ribosomal protein L3

Chain BD: 67% 29% .



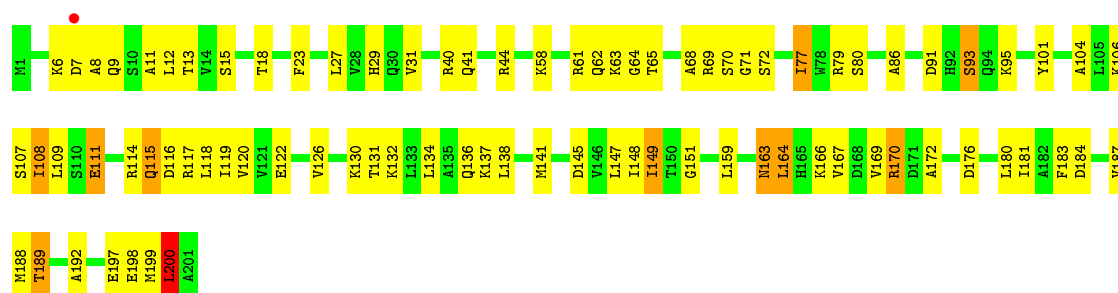
• Molecule 25: 50S ribosomal protein L3

Chain DD: 28% 62% 32% 6%



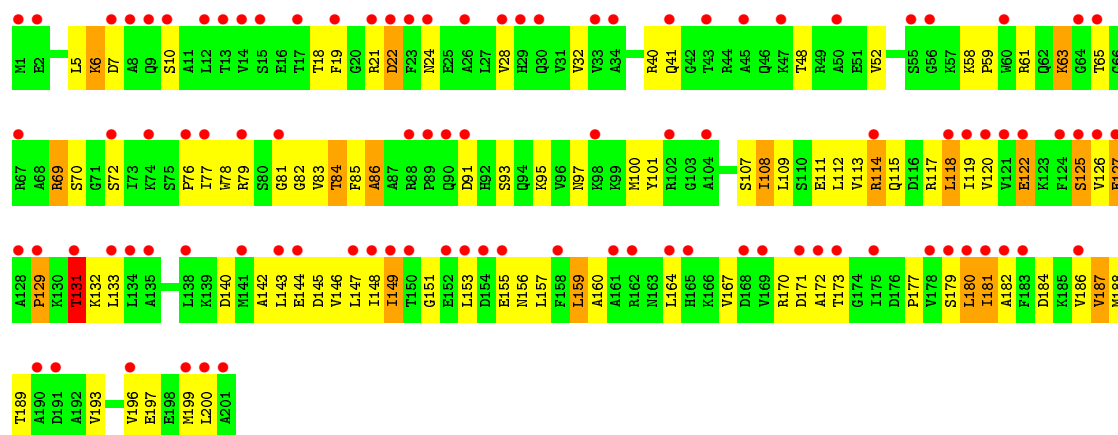
• Molecule 26: 50S ribosomal protein L4

Chain BE: 58% 36% 6%

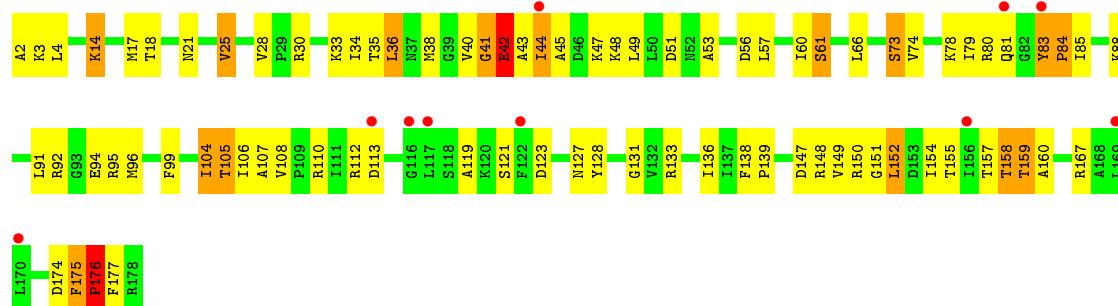


• Molecule 26: 50S ribosomal protein L4

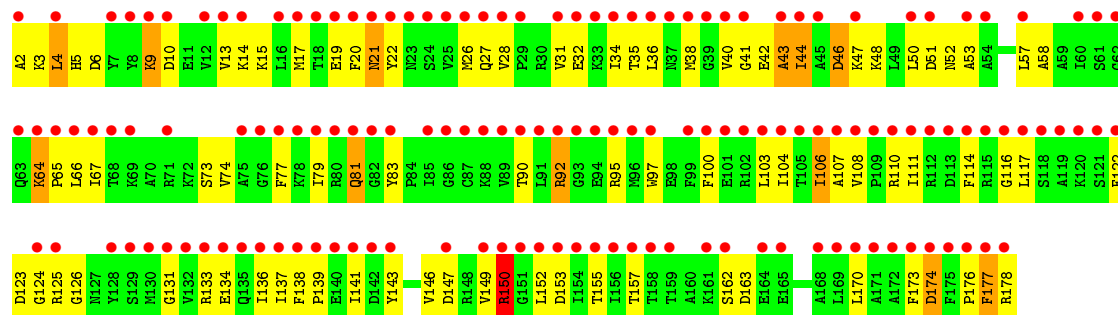
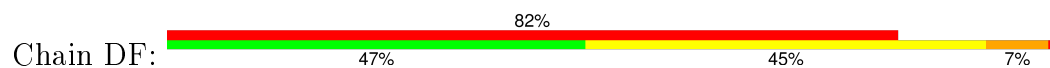
Chain DE: 49% 52% 38% 9%



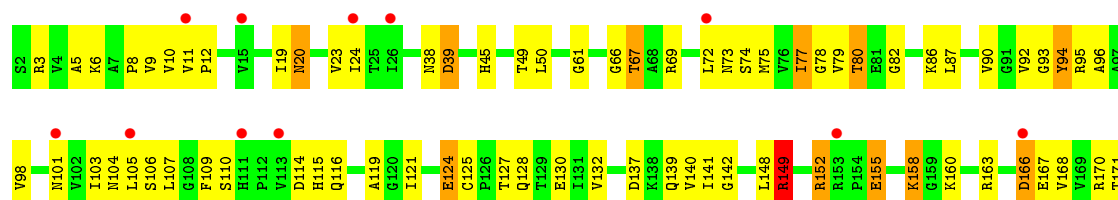
• Molecule 27: 50S ribosomal protein L5

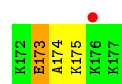


• Molecule 27: 50S ribosomal protein L5

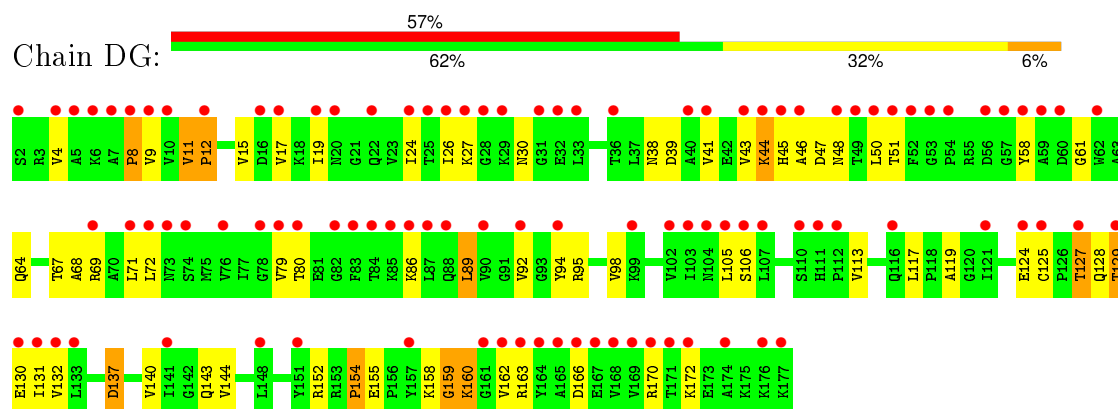


• Molecule 28: 50S ribosomal protein L6

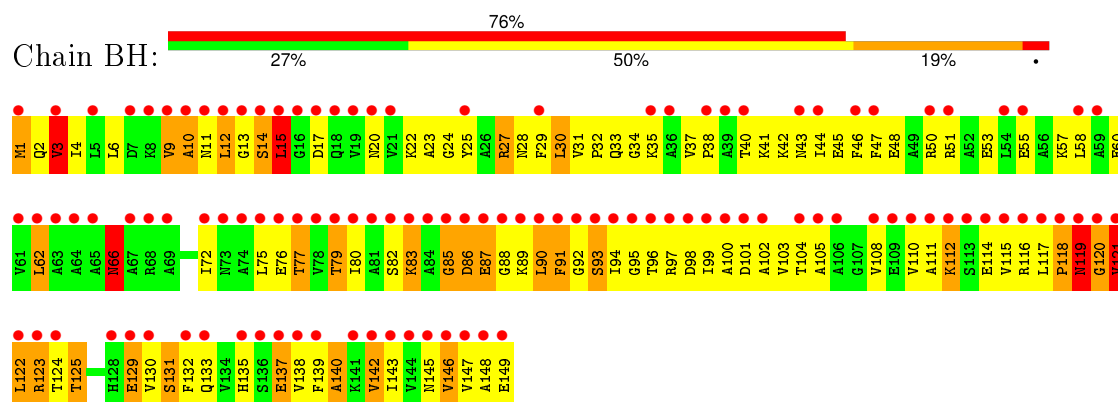




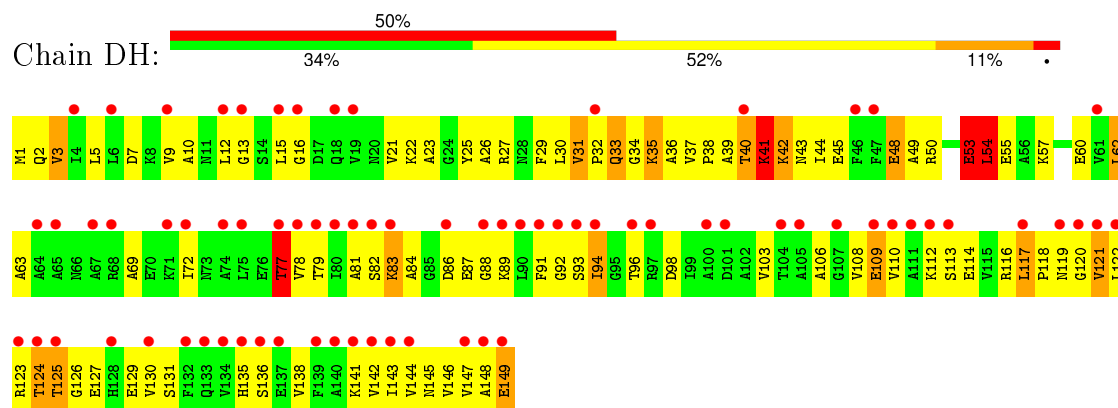
• Molecule 28: 50S ribosomal protein L6



• Molecule 29: 50S ribosomal protein L9

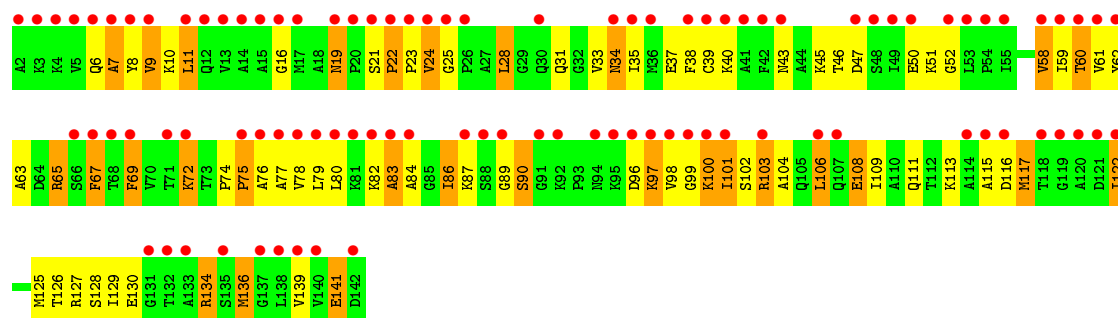


• Molecule 29: 50S ribosomal protein L9

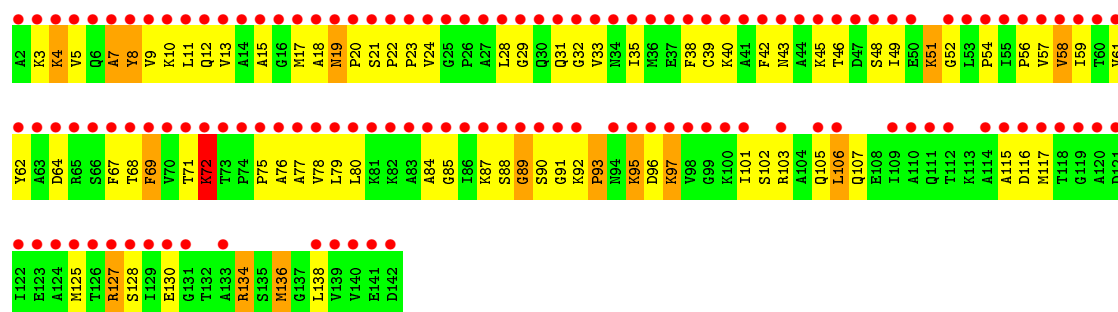
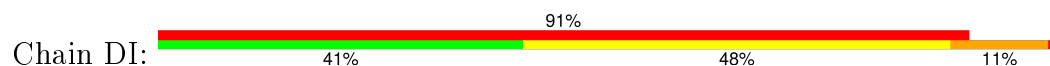


• Molecule 30: 50S ribosomal protein L11

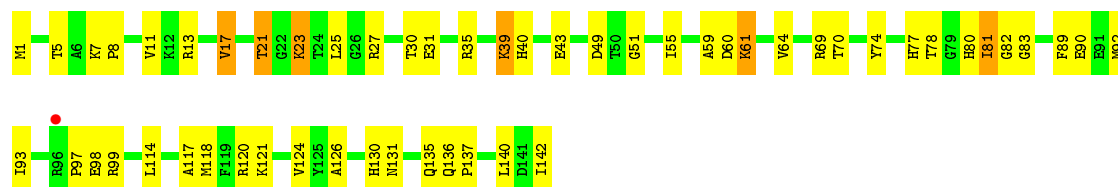




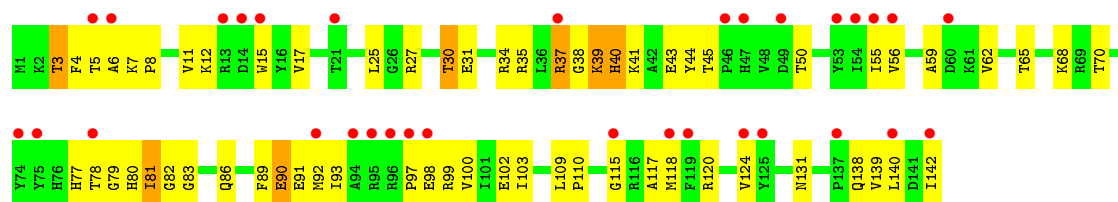
- Molecule 30: 50S ribosomal protein L11



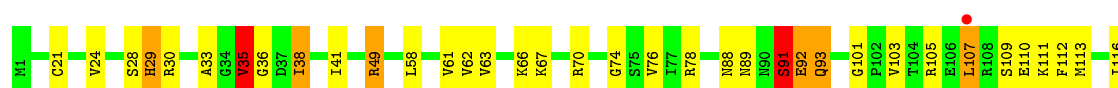
- Molecule 31: 50S ribosomal protein L13



- Molecule 31: 50S ribosomal protein L13



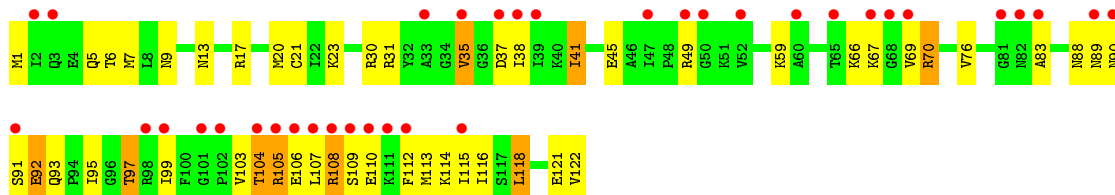
- Molecule 32: 50S ribosomal protein L14



S117
L118
A119
P120
E121
V122

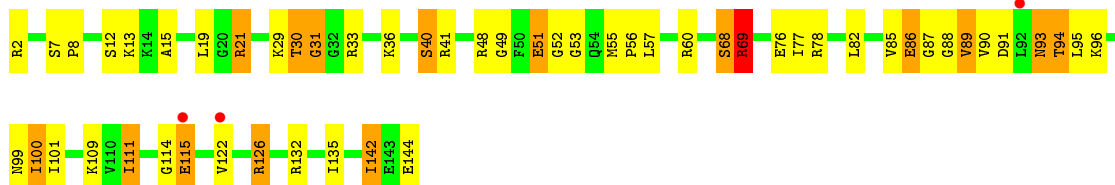
• Molecule 32: 50S ribosomal protein L14

Chain DK: 



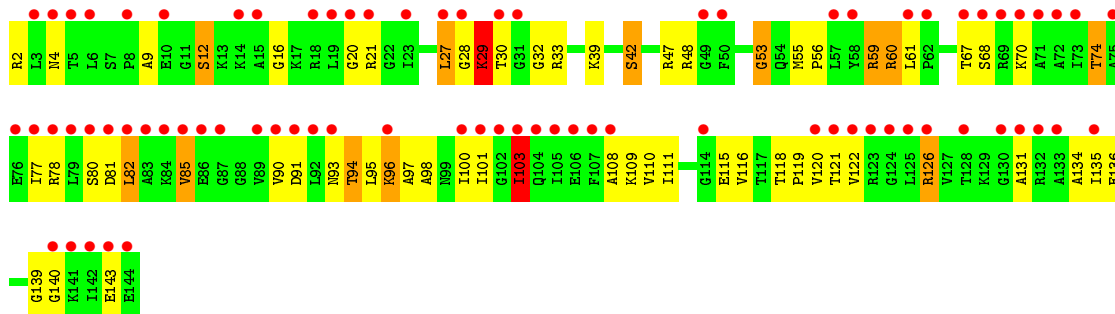
• Molecule 33: 50S ribosomal protein L15

Chain BL: 



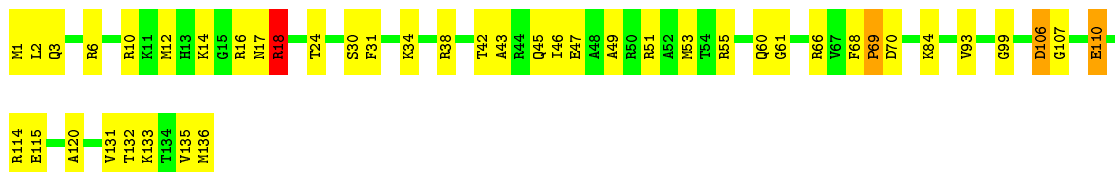
• Molecule 33: 50S ribosomal protein L15

Chain DL: 



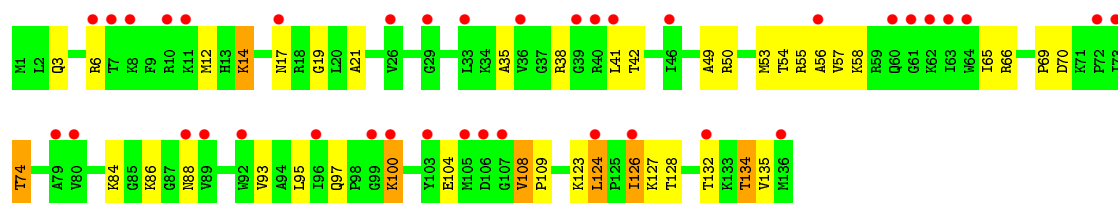
• Molecule 34: 50S ribosomal protein L16

Chain BM: 



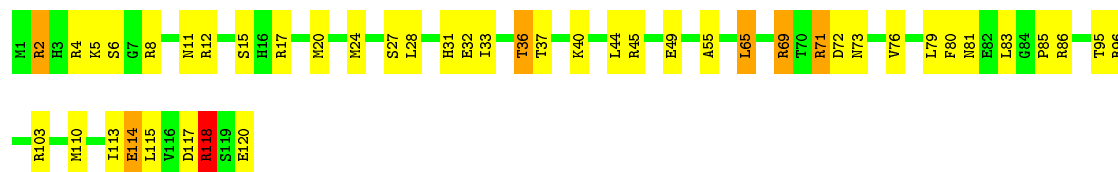
• Molecule 34: 50S ribosomal protein L16

Chain DM: 



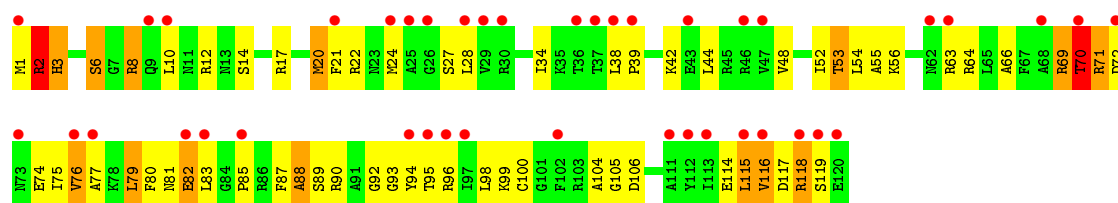
• Molecule 35: 50S ribosomal protein L17

Chain BN: 63% 32% 5% •



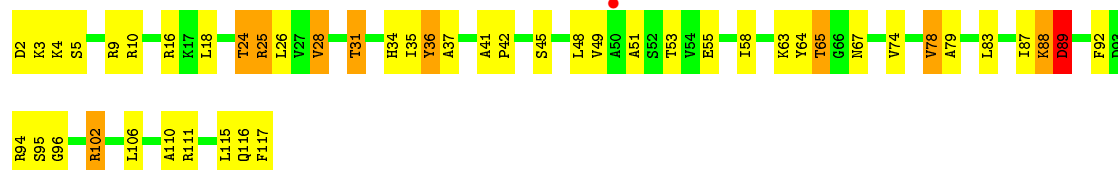
• Molecule 35: 50S ribosomal protein L17

Chain DN: 47% 40% 12% •



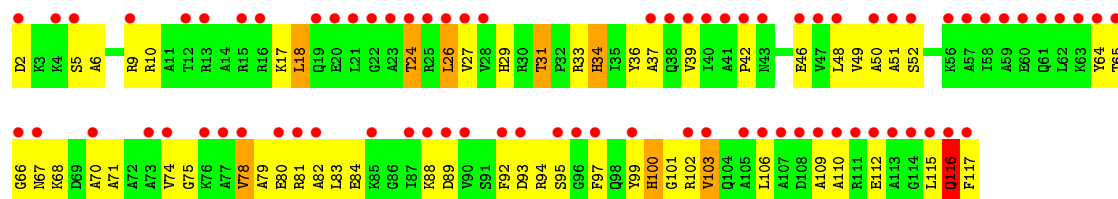
• Molecule 36: 50S ribosomal protein L18

Chain BO: 59% 33% 8% •



• Molecule 36: 50S ribosomal protein L18

Chain DO: 49% 43% 7% •

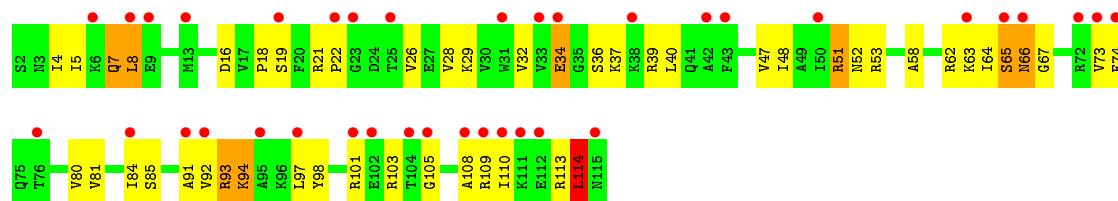


• Molecule 37: 50S ribosomal protein L19

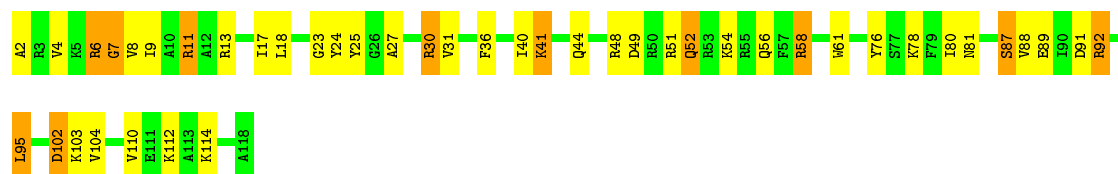
Chain BP: 58% 36% 5% •



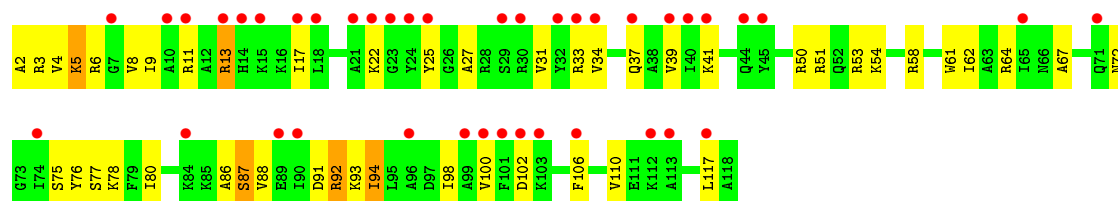
• Molecule 37: 50S ribosomal protein L19



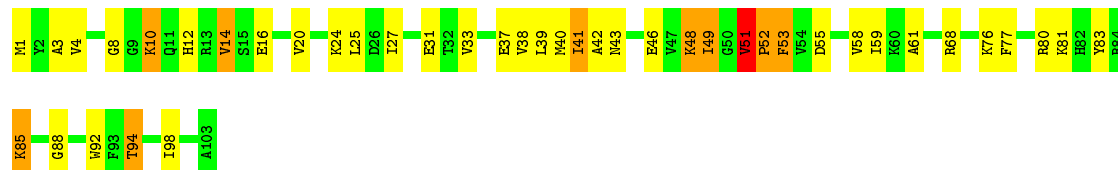
• Molecule 38: 50S ribosomal protein L20



• Molecule 38: 50S ribosomal protein L20

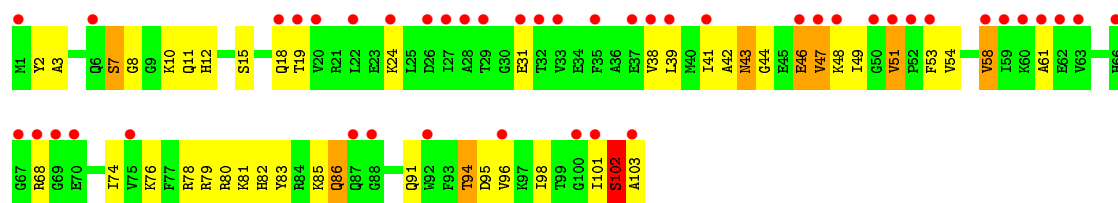


• Molecule 39: 50S ribosomal protein L21

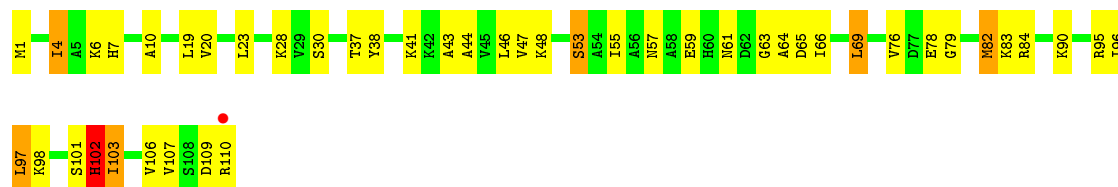


• Molecule 39: 50S ribosomal protein L21

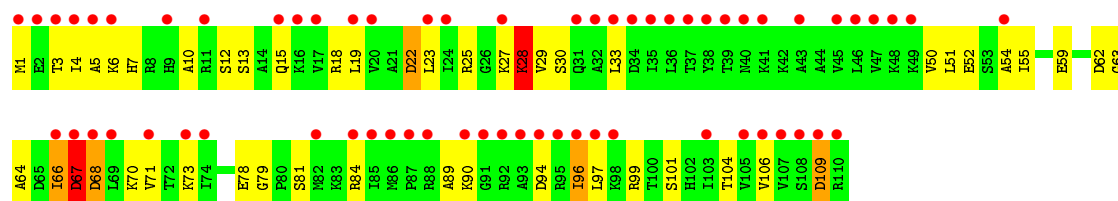




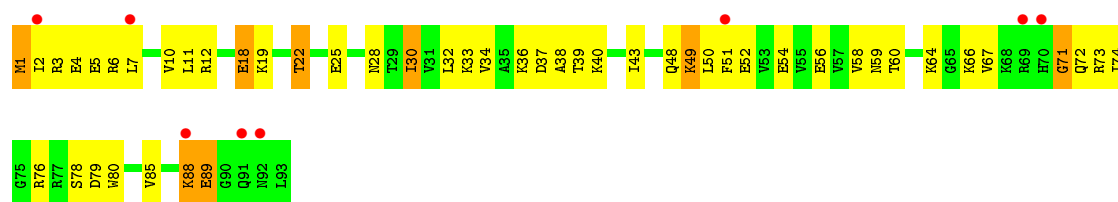
• Molecule 40: 50S ribosomal protein L22



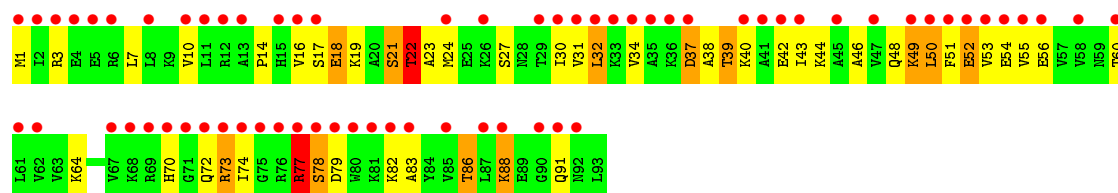
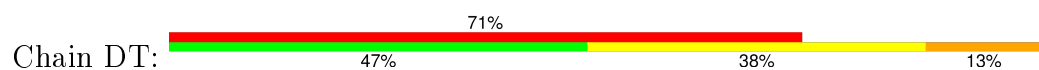
• Molecule 40: 50S ribosomal protein L22



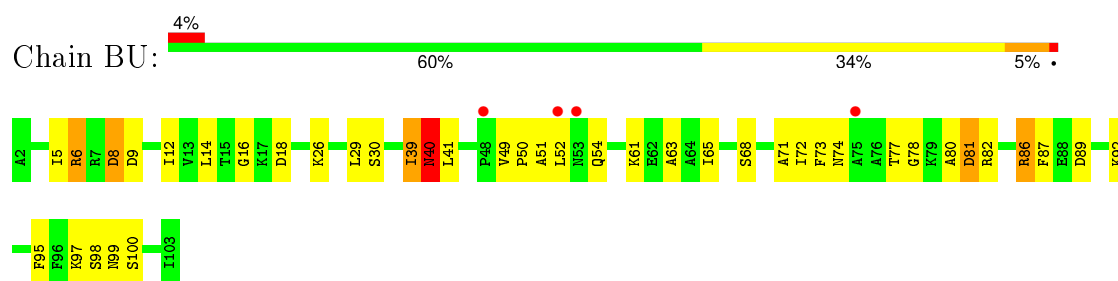
• Molecule 41: 50S ribosomal protein L23



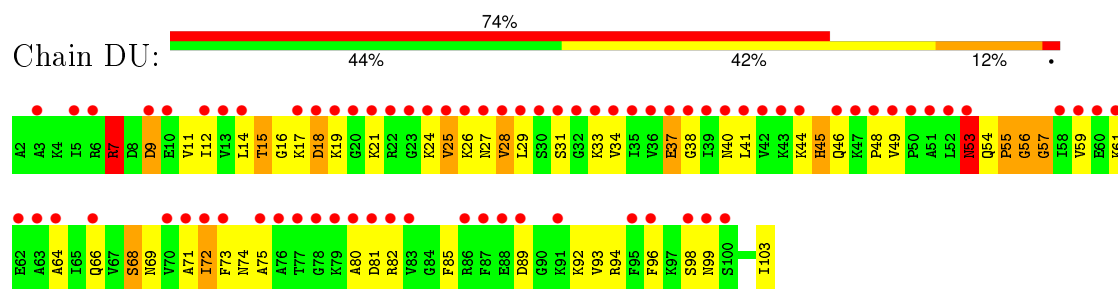
• Molecule 41: 50S ribosomal protein L23



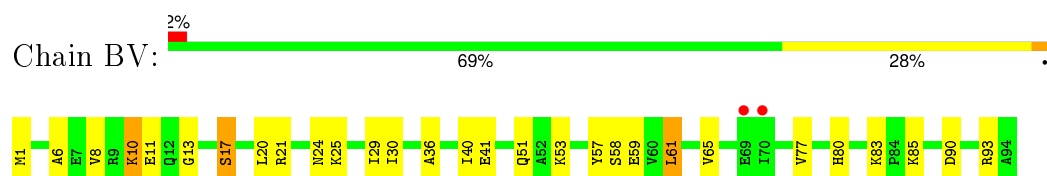
• Molecule 42: 50S ribosomal protein L24



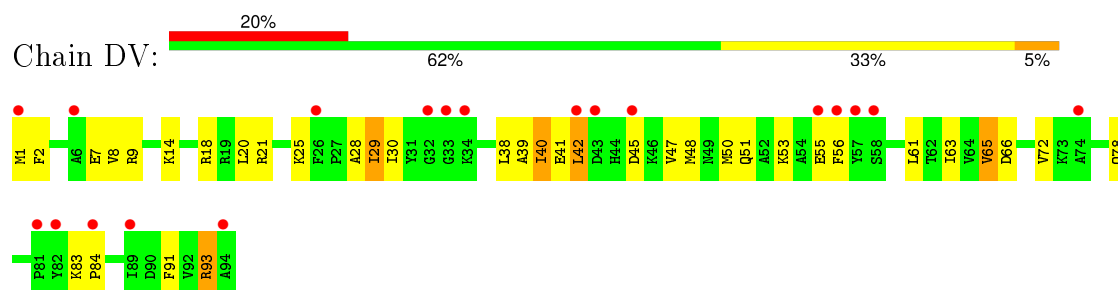
- Molecule 42: 50S ribosomal protein L24



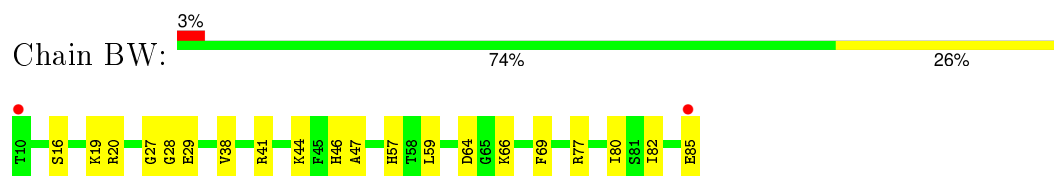
- Molecule 43: 50S ribosomal protein L25



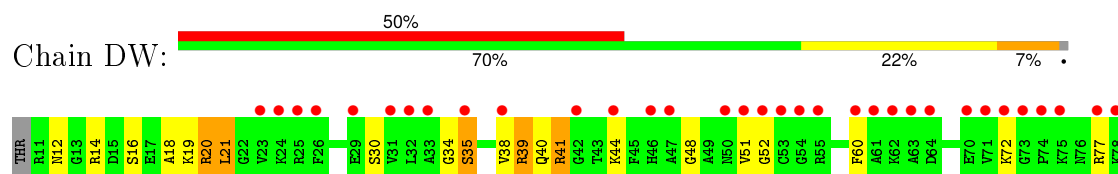
- Molecule 43: 50S ribosomal protein L25

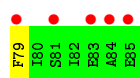


- Molecule 44: 50S ribosomal protein L27

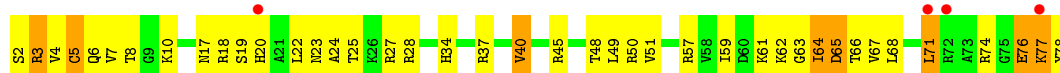


- Molecule 44: 50S ribosomal protein L27

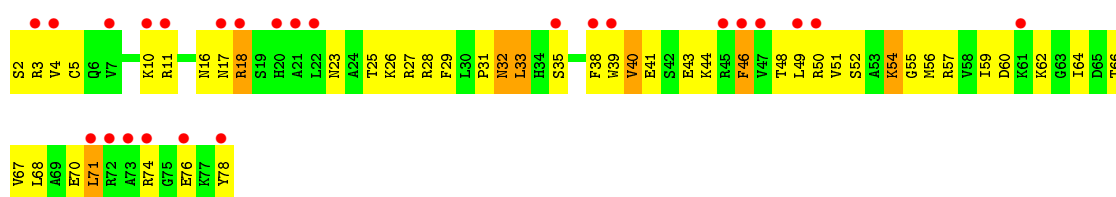




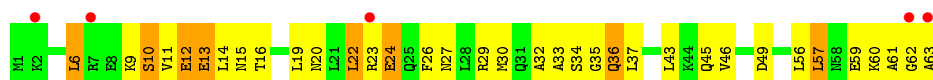
- Molecule 45: 50S ribosomal protein L28



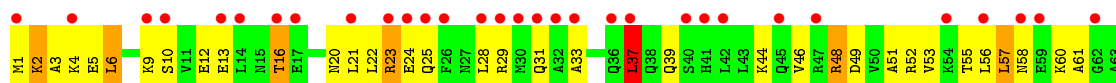
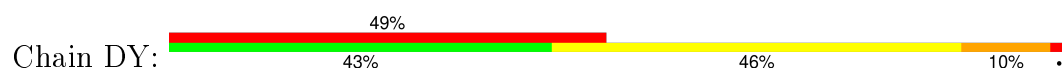
- Molecule 45: 50S ribosomal protein L28



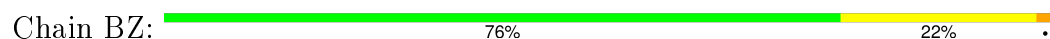
- Molecule 46: 50S ribosomal protein L29



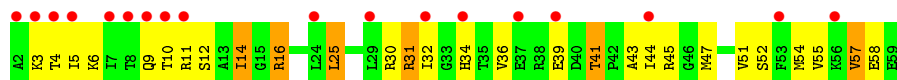
- Molecule 46: 50S ribosomal protein L29



- Molecule 47: 50S ribosomal protein L30

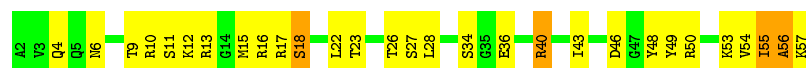


- Molecule 47: 50S ribosomal protein L30



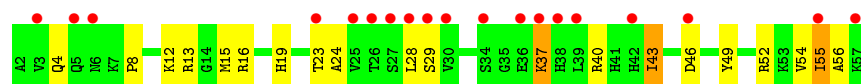
- Molecule 48: 50S ribosomal protein L32

Chain B0: 



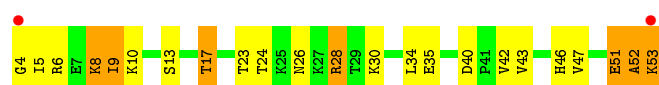
- Molecule 48: 50S ribosomal protein L32

Chain D0: 



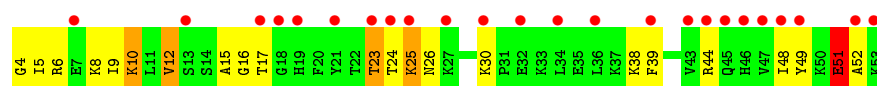
- Molecule 49: 50S ribosomal protein L33

Chain B1: 



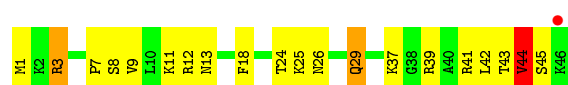
- Molecule 49: 50S ribosomal protein L33

Chain D1: 



- Molecule 50: 50S ribosomal protein L34

Chain B2: 



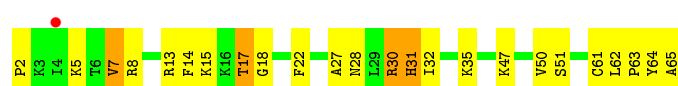
- Molecule 50: 50S ribosomal protein L34

Chain D2: 

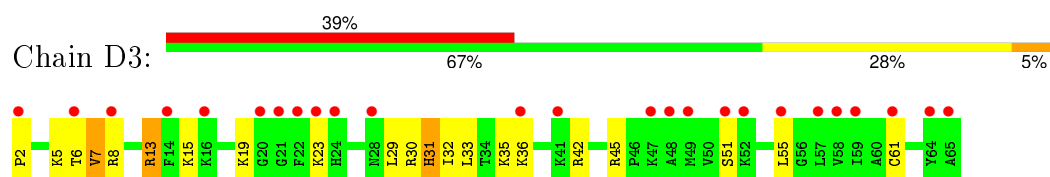


- Molecule 51: 50S ribosomal protein L35

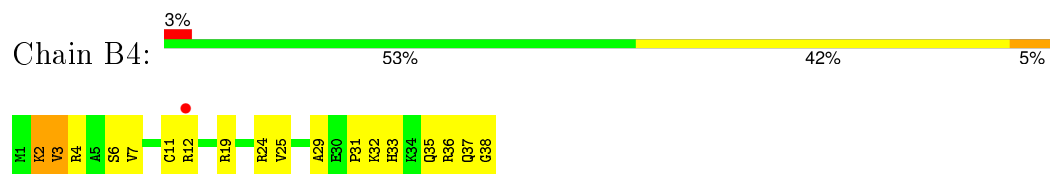
Chain B3: 



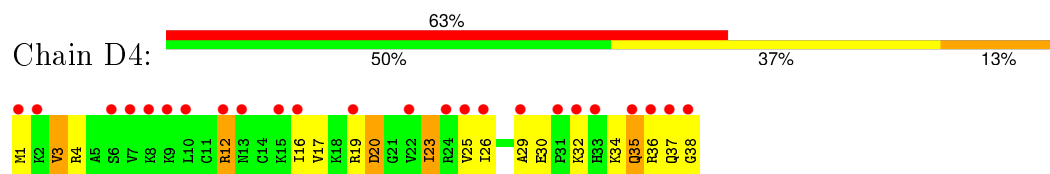
- Molecule 51: 50S ribosomal protein L35



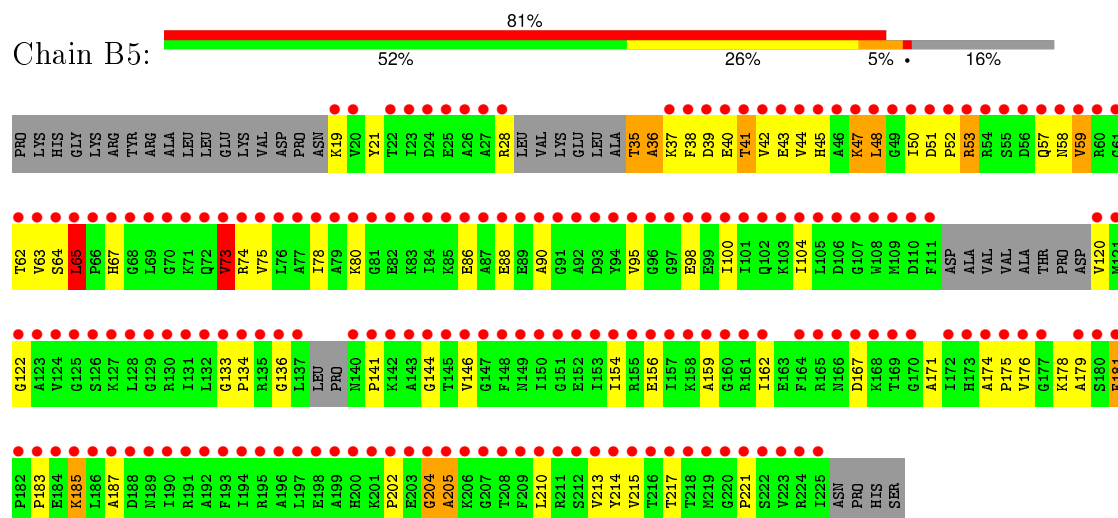
- Molecule 52: 50S ribosomal protein L36



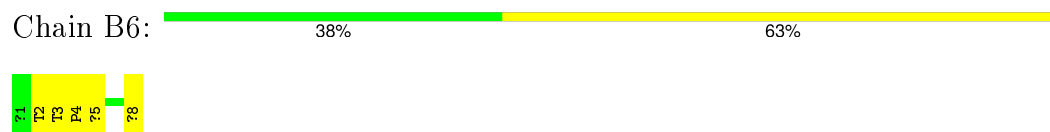
- Molecule 52: 50S ribosomal protein L36



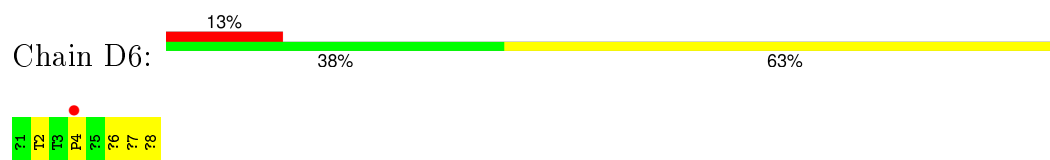
- Molecule 53: 50S ribosomal protein L1



- Molecule 54: Quinupristin



- Molecule 54: Quinupristin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	211.08Å 432.73Å 631.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	68.68 – 2.95 68.68 – 2.95	Depositor EDS
% Data completeness (in resolution range)	93.2 (68.68-2.95) 93.2 (68.68-2.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 2.96Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.248 , 0.282 0.255 , 0.289	Depositor DCC
R_{free} test set	4515 reflections (0.41%)	DCC
Wilson B-factor (Å ²)	54.4	Xtriage
Anisotropy	0.520	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 52.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 1118451 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	288328	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, DBB, MG, 004, MHV, MHW, MHT, MHU

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	0.44	0/36944	1.04	74/57632 (0.1%)
1	CA	0.39	0/36966	0.99	74/57666 (0.1%)
2	AB	0.36	0/1736	0.72	1/2338 (0.0%)
2	CB	0.33	0/1736	0.70	0/2338
3	AC	0.35	0/1652	0.65	2/2225 (0.1%)
3	CC	0.32	0/1652	0.58	1/2225 (0.0%)
4	AD	0.35	0/1665	0.68	0/2227
4	CD	0.38	0/1665	0.71	1/2227 (0.0%)
5	AE	0.38	0/1119	0.74	0/1504
5	CE	0.37	0/1119	0.73	0/1504
6	AF	0.39	0/836	0.71	2/1128 (0.2%)
6	CF	0.34	0/836	0.68	0/1128
7	AG	0.32	0/1196	0.59	0/1602
7	CG	0.31	0/1196	0.56	0/1602
8	AH	0.36	0/989	0.67	0/1326
8	CH	0.30	0/989	0.59	0/1326
9	AI	0.32	0/1034	0.65	1/1375 (0.1%)
9	CI	0.32	0/1034	0.64	0/1375
10	AJ	0.35	0/797	0.65	0/1077
10	CJ	0.30	0/797	0.66	2/1077 (0.2%)
11	AK	0.35	0/893	0.63	0/1205
11	CK	0.32	0/893	0.63	0/1205
12	AL	0.39	0/969	0.69	0/1300
12	CL	0.35	0/969	0.72	0/1300
13	AM	0.33	0/893	0.69	0/1193
13	CM	0.33	0/893	0.65	0/1193
14	AN	0.31	0/785	0.66	0/1043
14	CN	0.29	0/785	0.57	0/1043
15	AO	0.31	0/718	0.61	0/959
15	CO	0.30	0/718	0.61	0/959
16	AP	0.39	0/659	0.72	1/884 (0.1%)
16	CP	0.33	0/659	0.59	0/884

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.37	0/658	0.72	1/881 (0.1%)
17	CQ	0.38	0/658	0.63	0/881
18	AR	0.31	0/463	0.60	0/621
18	CR	0.30	0/463	0.57	0/621
19	AS	0.32	0/653	0.63	0/877
19	CS	0.33	0/653	0.59	0/877
20	AT	0.36	0/671	0.64	0/888
20	CT	0.32	0/671	0.62	0/888
21	AU	0.43	0/431	0.75	0/570
21	CU	0.45	0/431	0.78	0/570
22	BA	0.68	6/69659 (0.0%)	1.32	534/108672 (0.5%)
22	DA	0.38	0/69659	0.99	76/108672 (0.1%)
23	BB	0.62	1/2850 (0.0%)	1.22	7/4444 (0.2%)
23	DB	0.32	0/2828	0.92	2/4410 (0.0%)
24	BC	0.45	0/2122	0.71	0/2852
24	DC	0.34	0/2122	0.62	0/2852
25	BD	0.50	0/1586	0.74	1/2134 (0.0%)
25	DD	0.32	0/1586	0.59	0/2134
26	BE	0.42	0/1571	0.70	0/2113
26	DE	0.34	0/1571	0.62	1/2113 (0.0%)
27	BF	0.37	0/1435	0.63	0/1926
27	DF	0.30	0/1435	0.56	0/1926
28	BG	0.39	0/1343	0.69	1/1816 (0.1%)
28	DG	0.31	0/1343	0.55	0/1816
29	BH	0.36	0/1121	0.66	1/1515 (0.1%)
29	DH	0.35	0/1121	0.56	0/1515
30	BI	0.38	0/1046	0.69	0/1410
30	DI	0.35	0/1046	0.67	0/1410
31	BJ	0.49	0/1152	0.70	0/1551
31	DJ	0.31	0/1152	0.59	0/1551
32	BK	0.51	0/948	0.73	0/1268
32	DK	0.34	0/948	0.58	0/1268
33	BL	0.45	0/1054	0.80	2/1403 (0.1%)
33	DL	0.32	0/1054	0.62	0/1403
34	BM	0.48	0/1093	0.73	1/1460 (0.1%)
34	DM	0.30	0/1093	0.57	0/1460
35	BN	0.47	0/974	0.77	0/1301
35	DN	0.33	0/974	0.59	0/1301
36	BO	0.43	0/902	0.66	0/1209
36	DO	0.29	0/902	0.53	0/1209
37	BP	0.47	0/929	0.72	1/1242 (0.1%)
37	DP	0.32	0/929	0.59	1/1242 (0.1%)
38	BQ	0.56	0/960	0.73	0/1278

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DQ	0.32	0/960	0.53	0/1278
39	BR	0.53	0/829	0.82	1/1107 (0.1%)
39	DR	0.34	0/829	0.66	0/1107
40	BS	0.71	2/864 (0.2%)	0.89	2/1156 (0.2%)
40	DS	0.33	0/864	0.63	0/1156
41	BT	0.45	0/745	0.70	0/994
41	DT	0.33	0/745	0.61	0/994
42	BU	0.43	0/788	0.72	0/1051
42	DU	0.37	0/788	0.61	0/1051
43	BV	0.40	0/766	0.67	1/1025 (0.1%)
43	DV	0.28	0/766	0.54	0/1025
44	BW	0.52	0/587	0.69	0/776
44	DW	0.29	0/576	0.54	0/762
45	BX	0.39	0/635	0.67	0/848
45	DX	0.32	0/635	0.61	0/848
46	BY	0.39	0/510	0.76	0/677
46	DY	0.32	0/510	0.64	0/677
47	BZ	0.52	0/453	0.74	0/605
47	DZ	0.30	0/453	0.56	0/605
48	B0	0.52	0/450	0.75	0/599
48	D0	0.31	0/450	0.61	0/599
49	B1	0.44	0/417	0.69	0/554
49	D1	0.32	0/417	0.56	0/554
50	B2	0.48	0/380	0.80	0/498
50	D2	0.30	0/380	0.58	0/498
51	B3	0.43	0/513	0.71	0/676
51	D3	0.29	0/513	0.49	0/676
52	B4	0.52	0/303	0.66	0/397
52	D4	0.37	0/303	0.58	0/397
53	B5	0.32	0/1145	0.69	1/1556 (0.1%)
54	B6	1.71	0/13	2.43	1/15 (6.7%)
54	D6	1.45	0/13	2.67	2/15 (13.3%)
All	All	0.47	9/310652 (0.0%)	1.01	796/464396 (0.2%)

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	CB	0	1
5	AE	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	CE	0	2
6	CF	0	1
11	AK	0	1
11	CK	0	1
12	CL	0	2
21	AU	0	2
21	CU	0	1
25	BD	0	1
25	DD	0	1
26	BE	0	1
40	BS	0	1
All	All	0	16

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	BA	984	A	N9-C4	-9.06	1.32	1.37
22	BA	1142	A	N9-C4	-8.98	1.32	1.37
40	BS	102	HIS	CB-CG	-6.45	1.38	1.50
22	BA	1936	A	N9-C4	-5.92	1.34	1.37
23	BB	99	A	N9-C4	-5.46	1.34	1.37
40	BS	103	ILE	CA-CB	-5.43	1.42	1.54
22	BA	984	A	N3-C4	-5.26	1.31	1.34
22	BA	974	G	N9-C8	5.08	1.41	1.37
22	BA	1977	A	N9-C4	-5.00	1.34	1.37

All (796) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	984	A	C2-N3-C4	-12.57	104.31	110.60
1	AA	1054	C	O5'-P-OP2	-12.23	94.69	105.70
22	BA	1936	A	C2-N3-C4	-10.65	105.28	110.60
25	BD	151	THR	C-N-CD	-10.63	97.20	120.60
22	BA	1142	A	C2-N3-C4	-10.48	105.36	110.60
22	BA	984	A	N3-C4-N9	-10.31	119.15	127.40
22	BA	2499	C	N1-C2-O2	-10.29	112.72	118.90
1	CA	558	G	O5'-P-OP1	-9.62	97.04	105.70
22	BA	1658	C	O5'-P-OP1	-9.50	97.15	105.70
22	BA	1926	U	N1-C2-O2	9.48	129.44	122.80
22	BA	1779	U	C5-C6-N1	-9.48	117.96	122.70
22	BA	1648	U	O5'-P-OP1	-9.17	97.44	105.70
22	BA	2076	U	C5-C4-O4	9.15	131.39	125.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	759	G	C8-N9-C4	8.92	109.97	106.40
1	AA	1286	U	C2-N1-C1'	8.90	128.38	117.70
22	BA	2076	U	N3-C2-O2	-8.87	115.99	122.20
22	BA	965	C	N1-C2-O2	-8.86	113.59	118.90
22	BA	577	G	O5'-P-OP2	8.80	121.26	110.70
22	BA	572	A	O5'-P-OP1	-8.78	97.80	105.70
22	BA	974	G	C4-C5-N7	8.78	114.31	110.80
22	BA	1926	U	N3-C2-O2	-8.61	116.17	122.20
22	BA	1415	U	N3-C2-O2	-8.59	116.18	122.20
22	BA	823	C	C2-N3-C4	-8.58	115.61	119.90
1	CA	1286	U	C2-N1-C1'	8.57	127.98	117.70
22	BA	528	A	C2-N3-C4	-8.56	106.32	110.60
1	AA	108	G	C8-N9-C4	-8.53	102.99	106.40
22	BA	984	A	N3-C4-C5	8.53	132.77	126.80
22	BA	2035	G	N1-C6-O6	-8.44	114.84	119.90
1	CA	632	U	N1-C2-O2	8.44	128.71	122.80
22	BA	2076	U	N3-C4-O4	-8.43	113.50	119.40
22	BA	665	U	C5-C6-N1	-8.43	118.49	122.70
1	CA	207	C	C2-N1-C1'	8.42	128.06	118.80
1	CA	328	C	C2-N1-C1'	8.37	128.00	118.80
22	BA	947	A	O5'-P-OP1	-8.35	98.19	105.70
22	BA	974	G	C5-N7-C8	-8.34	100.13	104.30
22	BA	1977	A	C2-N3-C4	-8.22	106.49	110.60
1	CA	207	C	N1-C2-O2	8.16	123.79	118.90
22	BA	528	A	C8-N9-C4	-8.14	102.54	105.80
22	BA	1271	G	OP1-P-OP2	-8.13	107.40	119.60
1	AA	299	G	N9-C4-C5	-8.12	102.15	105.40
1	CA	1298	U	N1-C2-O2	8.10	128.47	122.80
22	BA	1790	C	C2-N3-C4	-8.08	115.86	119.90
22	BA	1964	G	O5'-P-OP1	-8.02	98.48	105.70
1	CA	1029	U	N1-C2-O2	8.02	128.41	122.80
22	BA	2825	G	C8-N9-C4	-8.02	103.19	106.40
22	BA	528	A	N7-C8-N9	8.01	117.81	113.80
1	AA	4	U	N1-C2-O2	7.99	128.39	122.80
1	CA	209	U	C2-N1-C1'	7.98	127.27	117.70
22	BA	2825	G	C4-N9-C1'	7.96	136.85	126.50
22	BA	1415	U	C2-N1-C1'	7.95	127.24	117.70
22	BA	2610	C	C5-C6-N1	-7.93	117.03	121.00
22	BA	1614	A	O5'-P-OP1	-7.93	98.56	105.70
1	AA	1279	G	N7-C8-N9	7.91	117.06	113.10
22	BA	276	U	N1-C2-O2	7.91	128.34	122.80
1	AA	4	U	C2-N1-C1'	7.86	127.13	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	DA	2430	A	O5'-P-OP2	-7.81	98.67	105.70
22	BA	2034	U	N3-C2-O2	-7.75	116.77	122.20
22	BA	2825	G	N3-C4-C5	-7.75	124.72	128.60
22	BA	784	G	N3-C4-N9	7.75	130.65	126.00
22	DA	12	U	N3-C2-O2	-7.74	116.78	122.20
22	BA	784	G	C8-N9-C1'	-7.71	116.98	127.00
1	CA	632	U	N3-C2-O2	-7.71	116.81	122.20
22	BA	823	C	C5-C6-N1	-7.70	117.15	121.00
22	BA	1909	C	C2-N1-C1'	7.68	127.25	118.80
1	AA	1279	G	C8-N9-C4	-7.66	103.34	106.40
22	DA	12	U	N1-C2-O2	7.64	128.15	122.80
22	DA	2165	C	C6-N1-C2	-7.64	117.24	120.30
22	BA	837	C	N1-C2-O2	-7.63	114.32	118.90
22	BA	752	A	C6-C5-N7	-7.63	126.96	132.30
39	BR	51	VAL	C-N-CD	7.61	144.38	128.40
22	BA	2250	G	C5-N7-C8	-7.58	100.51	104.30
22	BA	2039	U	C5-C6-N1	-7.58	118.91	122.70
22	BA	2429	G	O5'-P-OP1	7.56	119.77	110.70
22	BA	1656	C	N3-C4-C5	7.55	124.92	121.90
22	BA	192	C	O5'-P-OP1	-7.51	98.94	105.70
22	BA	2499	C	O5'-P-OP2	-7.51	98.94	105.70
22	BA	1584	U	N3-C2-O2	-7.51	116.94	122.20
22	BA	1584	U	N1-C2-O2	7.51	128.06	122.80
22	BA	536	G	C8-N9-C4	7.51	109.40	106.40
22	BA	1584	U	C2-N1-C1'	7.49	126.68	117.70
22	BA	516	C	C2-N3-C4	-7.48	116.16	119.90
22	BA	198	C	O5'-P-OP2	-7.46	98.98	105.70
22	BA	948	C	C4-C5-C6	7.41	121.11	117.40
22	BA	1142	A	N3-C4-C5	7.40	131.98	126.80
1	AA	1286	U	N1-C2-O2	7.37	127.96	122.80
22	BA	784	G	O4'-C1'-N9	-7.36	102.31	108.20
22	BA	948	C	N1-C2-O2	-7.34	114.49	118.90
22	BA	1395	A	O5'-P-OP1	-7.33	99.10	105.70
22	BA	1677	A	N1-C6-N6	7.32	122.99	118.60
1	CA	1028	C	N1-C2-O2	7.30	123.28	118.90
22	BA	1790	C	C5-C6-N1	-7.29	117.36	121.00
22	BA	2260	C	C5-C6-N1	-7.27	117.36	121.00
1	CA	1029	U	C2-N1-C1'	7.27	126.42	117.70
1	CA	207	C	N3-C2-O2	-7.27	116.81	121.90
22	BA	581	C	N3-C2-O2	-7.26	116.82	121.90
22	BA	516	C	C5-C6-N1	-7.25	117.38	121.00
1	CA	1364	U	C2-N1-C1'	7.22	126.36	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1029	U	N3-C2-O2	-7.18	117.17	122.20
22	BA	847	U	N3-C2-O2	-7.18	117.17	122.20
22	DA	784	G	N3-C4-N9	7.15	130.29	126.00
22	BA	516	C	C4-C5-C6	7.13	120.97	117.40
22	BA	1681	G	N1-C6-O6	7.13	124.18	119.90
22	BA	1064	C	N1-C2-O2	7.13	123.18	118.90
22	BA	2077	A	O5'-P-OP2	-7.13	99.29	105.70
22	BA	528	A	C6-C5-N7	-7.11	127.32	132.30
22	BA	2006	C	O5'-P-OP1	-7.10	99.31	105.70
22	BA	783	A	N7-C8-N9	7.10	117.35	113.80
1	AA	4	U	N3-C2-O2	-7.10	117.23	122.20
22	BA	1920	C	C6-N1-C2	-7.09	117.46	120.30
22	BA	581	C	N1-C2-O2	7.08	123.15	118.90
22	BA	528	A	C5-N7-C8	-7.07	100.37	103.90
1	CA	328	C	N1-C2-O2	7.06	123.13	118.90
22	BA	2825	G	C6-C5-N7	-7.03	126.18	130.40
22	BA	752	A	N7-C8-N9	7.01	117.30	113.80
22	BA	2682	A	O5'-P-OP1	-7.00	99.40	105.70
22	BA	1415	U	N1-C2-O2	6.99	127.69	122.80
22	BA	784	G	N9-C4-C5	-6.98	102.61	105.40
22	BA	2211	A	P-O3'-C3'	6.98	128.08	119.70
1	AA	1168	U	N1-C2-O2	6.98	127.69	122.80
22	BA	1658	C	C6-N1-C2	6.98	123.09	120.30
1	AA	299	G	C4-C5-N7	6.96	113.58	110.80
22	BA	276	U	C2-N1-C1'	6.96	126.05	117.70
1	AA	1168	U	C2-N1-C1'	6.95	126.04	117.70
22	BA	1188	U	N1-C2-N3	6.94	119.06	114.90
22	BA	1681	G	C5-C6-O6	-6.93	124.44	128.60
22	BA	752	A	N1-C6-N6	6.92	122.75	118.60
1	AA	365	U	C5-C6-N1	-6.92	119.24	122.70
22	BA	2492	U	O5'-P-OP2	-6.91	99.48	105.70
22	DA	827	U	O5'-P-OP1	-6.91	99.48	105.70
1	CA	485	U	N3-C2-O2	-6.90	117.37	122.20
22	BA	2825	G	N7-C8-N9	6.89	116.54	113.10
22	BA	811	U	C5-C4-O4	6.88	130.03	125.90
1	CA	632	U	C2-N1-C1'	6.88	125.95	117.70
22	BA	984	A	C8-N9-C1'	6.87	140.07	127.70
22	BA	808	G	C5-C6-N1	6.86	114.93	111.50
22	BA	2610	C	C2-N3-C4	-6.85	116.47	119.90
1	CA	1298	U	N3-C2-O2	-6.85	117.41	122.20
54	B6	2	THR	N-CA-CB	-6.83	97.31	110.30
1	AA	1001	C	C5-C6-N1	6.82	124.41	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	984	A	O4'-C1'-N9	6.80	113.64	108.20
22	BA	1779	U	N3-C4-O4	-6.79	114.65	119.40
22	BA	2506	U	N3-C2-O2	-6.79	117.45	122.20
22	BA	1694	C	C6-N1-C2	6.79	123.01	120.30
22	BA	1656	C	C2-N3-C4	-6.78	116.51	119.90
22	BA	783	A	C5-N7-C8	-6.76	100.52	103.90
22	BA	2260	C	N3-C2-O2	-6.76	117.17	121.90
22	BA	1406	U	O4'-C1'-N1	6.75	113.60	108.20
1	CA	96	U	P-O3'-C3'	6.74	127.79	119.70
22	BA	965	C	N3-C2-O2	6.73	126.61	121.90
1	CA	207	C	C6-N1-C2	-6.73	117.61	120.30
22	BA	276	U	N3-C2-O2	-6.72	117.50	122.20
1	CA	328	C	N3-C2-O2	-6.71	117.21	121.90
22	BA	528	A	N1-C6-N6	6.70	122.62	118.60
22	BA	1332	G	O5'-P-OP1	6.70	118.74	110.70
1	CA	412	A	O4'-C1'-N9	6.70	113.56	108.20
22	DA	2425	A	P-O3'-C3'	6.69	127.72	119.70
1	CA	1298	U	C2-N1-C1'	6.68	125.72	117.70
1	CA	21	G	O5'-P-OP1	-6.68	99.69	105.70
22	BA	1142	A	N3-C4-N9	-6.68	122.06	127.40
1	AA	108	G	C2-N3-C4	6.67	115.24	111.90
22	BA	1909	C	C5-C6-N1	6.67	124.33	121.00
1	CA	108	G	C2-N3-C4	6.65	115.23	111.90
22	BA	1064	C	C2-N1-C1'	6.65	126.11	118.80
22	BA	2825	G	N3-C4-N9	6.65	129.99	126.00
22	BA	740	C	OP1-P-OP2	-6.63	109.66	119.60
1	CA	1364	U	N1-C2-O2	6.62	127.44	122.80
22	BA	528	A	N1-C2-N3	6.62	132.61	129.30
22	BA	1692	U	N3-C2-O2	6.59	126.81	122.20
22	BA	852	U	C5-C6-N1	-6.59	119.41	122.70
1	AA	188	C	N1-C2-O2	6.58	122.85	118.90
22	BA	31	C	O5'-P-OP1	-6.58	99.78	105.70
22	DA	776	G	C4-N9-C1'	6.57	135.05	126.50
22	BA	33	C	N1-C2-O2	-6.57	114.96	118.90
22	BA	808	G	N1-C6-O6	-6.57	115.96	119.90
1	CA	1028	C	C2-N1-C1'	6.57	126.03	118.80
22	BA	516	C	N1-C2-N3	6.56	123.79	119.20
22	BA	999	U	OP1-P-OP2	-6.56	109.76	119.60
22	BA	686	U	C2-N1-C1'	-6.55	109.84	117.70
22	DA	1313	U	C2-N1-C1'	6.55	125.56	117.70
22	BA	665	U	C2-N3-C4	-6.52	123.09	127.00
1	AA	560	A	O5'-P-OP2	-6.52	99.83	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	752	A	C5-N7-C8	-6.52	100.64	103.90
22	BA	1677	A	C6-C5-N7	-6.51	127.74	132.30
22	BA	1406	U	C2-N1-C1'	-6.50	109.90	117.70
22	BA	532	A	O5'-P-OP1	-6.47	99.88	105.70
22	BA	984	A	C5-C6-N1	-6.47	114.47	117.70
22	DA	1648	U	O5'-P-OP1	-6.47	99.88	105.70
22	BA	578	G	N3-C4-C5	-6.46	125.37	128.60
22	BA	1909	C	N1-C2-O2	6.45	122.77	118.90
4	CD	161	LEU	CA-CB-CG	6.44	130.12	115.30
22	BA	2499	C	N3-C2-O2	6.44	126.41	121.90
1	AA	326	G	N3-C4-C5	-6.43	125.38	128.60
22	BA	578	G	N3-C4-N9	6.43	129.86	126.00
22	BA	752	A	O4'-C1'-N9	6.43	113.34	108.20
22	BA	759	G	N7-C8-N9	-6.41	109.89	113.10
22	BA	808	G	N3-C4-N9	6.40	129.84	126.00
23	BB	83	G	O5'-P-OP1	6.39	118.37	110.70
40	BS	102	HIS	ND1-CG-CD2	-6.39	97.06	106.00
1	AA	1168	U	N3-C2-O2	-6.38	117.73	122.20
54	D6	2	THR	N-CA-CB	-6.38	98.19	110.30
22	BA	1121	C	C2-N3-C4	-6.37	116.71	119.90
1	AA	1279	G	C6-C5-N7	-6.37	126.58	130.40
1	AA	188	C	C2-N1-C1'	6.36	125.80	118.80
22	BA	1617	C	C5-C6-N1	-6.36	117.82	121.00
22	BA	2034	U	C5-C6-N1	-6.36	119.52	122.70
1	CA	754	C	C2-N1-C1'	6.35	125.79	118.80
22	DA	2447	G	C4-N9-C1'	-6.35	118.25	126.50
22	BA	2274	A	C8-N9-C4	6.34	108.34	105.80
22	BA	984	A	C4-N9-C1'	-6.33	114.90	126.30
22	BA	1188	U	N3-C2-O2	-6.32	117.78	122.20
22	DA	1614	A	O5'-P-OP1	-6.32	100.01	105.70
40	BS	102	HIS	CG-ND1-CE1	6.32	117.04	108.20
22	DA	1820	U	O5'-P-OP1	-6.30	100.03	105.70
22	BA	229	C	C5-C6-N1	6.29	124.15	121.00
1	AA	1286	U	N3-C2-O2	-6.28	117.81	122.20
22	BA	528	A	C5-C6-N1	-6.27	114.56	117.70
22	BA	1775	U	C5-C6-N1	-6.27	119.56	122.70
22	BA	2035	G	C4-C5-N7	-6.27	108.29	110.80
22	BA	2076	U	N1-C2-N3	6.27	118.66	114.90
22	BA	1649	G	C8-N9-C4	-6.26	103.89	106.40
1	AA	892	A	C2-N3-C4	-6.25	107.48	110.60
22	DA	1584	U	C2-N1-C1'	6.25	125.19	117.70
22	DA	12	U	C2-N1-C1'	6.24	125.19	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	664	G	O5'-P-OP2	-6.24	100.08	105.70
22	BA	783	A	C8-N9-C4	-6.23	103.31	105.80
22	BA	1615	C	N1-C2-O2	-6.23	115.16	118.90
23	BB	99	A	C2-N3-C4	-6.22	107.49	110.60
22	BA	2019	A	O5'-P-OP2	-6.22	100.10	105.70
22	BA	2538	C	C5-C6-N1	-6.21	117.89	121.00
22	BA	1695	G	O5'-P-OP1	-6.21	100.11	105.70
1	CA	1364	U	C5-C6-N1	6.21	125.81	122.70
22	BA	2633	G	C2-N3-C4	-6.21	108.80	111.90
1	AA	631	C	N1-C2-O2	-6.20	115.18	118.90
22	BA	1784	A	C4-C5-C6	6.20	120.10	117.00
22	BA	1787	A	N1-C6-N6	6.20	122.32	118.60
22	DA	2473	U	C2-N1-C1'	6.20	125.13	117.70
1	CA	1286	U	N1-C2-O2	6.18	127.13	122.80
6	AF	54	LEU	CA-CB-CG	6.18	129.52	115.30
22	DA	729	G	O4'-C1'-N9	6.18	113.14	108.20
22	BA	1121	C	C5-C6-N1	-6.18	117.91	121.00
22	BA	1936	A	N1-C2-N3	6.18	132.39	129.30
22	BA	957	C	C6-N1-C2	6.16	122.76	120.30
22	BA	1210	G	C6-C5-N7	-6.15	126.71	130.40
1	CA	209	U	C5-C6-N1	6.15	125.78	122.70
22	BA	2250	G	N7-C8-N9	6.14	116.17	113.10
22	BA	1948	G	C8-N9-C4	6.14	108.86	106.40
1	AA	1498	U	N1-C2-N3	6.13	118.58	114.90
22	BA	1255	U	OP1-P-OP2	6.13	128.79	119.60
1	AA	328	C	N3-C2-O2	-6.13	117.61	121.90
1	AA	365	U	C2-N1-C1'	-6.12	110.36	117.70
22	BA	2260	C	C2-N3-C4	-6.12	116.84	119.90
22	BA	2047	C	C6-N1-C2	6.10	122.74	120.30
1	AA	1286	U	C6-N1-C1'	-6.10	112.66	121.20
22	BA	2056	G	OP1-P-O3'	6.10	118.61	105.20
1	CA	1137	C	N1-C2-O2	6.09	122.55	118.90
22	BA	2773	C	C6-N1-C2	6.08	122.73	120.30
1	CA	1322	C	C2-N1-C1'	6.08	125.49	118.80
22	BA	1758	U	N1-C2-N3	6.08	118.55	114.90
22	BA	529	A	C8-N9-C4	6.07	108.23	105.80
22	BA	827	U	O5'-P-OP1	-6.07	100.24	105.70
1	CA	467	U	C2-N1-C1'	6.06	124.98	117.70
1	CA	1286	U	C6-N1-C1'	-6.06	112.71	121.20
1	AA	328	C	N1-C2-O2	6.05	122.53	118.90
22	BA	2006	C	C5-C4-N4	-6.05	115.97	120.20
22	BA	584	C	N1-C2-O2	-6.05	115.27	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	811	U	N3-C4-O4	-6.04	115.17	119.40
1	CA	328	C	C6-N1-C2	-6.04	117.88	120.30
22	BA	206	U	C5-C6-N1	-6.04	119.68	122.70
22	DA	847	U	C5-C6-N1	6.03	125.72	122.70
1	AA	299	G	C5-C6-O6	-6.03	124.98	128.60
23	BB	95	U	N1-C2-O2	6.03	127.02	122.80
22	BA	197	A	O5'-P-OP2	6.02	117.93	110.70
22	BA	752	A	C8-N9-C4	-6.02	103.39	105.80
22	BA	1147	A	O5'-P-OP2	-6.02	100.29	105.70
22	DA	748	G	O4'-C1'-N9	6.02	113.01	108.20
22	BA	1328	A	OP1-P-OP2	-6.01	110.58	119.60
1	AA	452	A	C8-N9-C4	-6.00	103.40	105.80
1	AA	1001	C	C6-N1-C2	-6.00	117.90	120.30
22	BA	2615	U	N3-C2-O2	-6.00	118.00	122.20
22	DA	776	G	C8-N9-C1'	-6.00	119.20	127.00
22	BA	783	A	C2-N3-C4	-6.00	107.60	110.60
22	BA	2260	C	C4-C5-C6	6.00	120.40	117.40
22	BA	2631	G	N7-C8-N9	-5.99	110.10	113.10
22	BA	23	G	O5'-P-OP1	-5.97	100.32	105.70
22	BA	461	C	C2-N3-C4	-5.97	116.91	119.90
1	CA	496	A	O4'-C1'-N9	5.97	112.97	108.20
1	AA	351	G	C4-C5-N7	5.96	113.19	110.80
22	BA	2034	U	C4-C5-C6	5.95	123.27	119.70
22	BA	2773	C	N3-C4-C5	5.95	124.28	121.90
22	BA	2450	A	C8-N9-C4	5.95	108.18	105.80
1	AA	888	G	O5'-P-OP2	-5.95	100.34	105.70
22	BA	1758	U	C2-N3-C4	-5.95	123.43	127.00
22	DA	2055	C	C2-N3-C4	5.95	122.88	119.90
22	BA	1267	U	C5-C4-O4	5.95	129.47	125.90
22	DA	106	C	N1-C2-O2	5.94	122.47	118.90
22	BA	1132	U	N1-C2-O2	-5.93	118.65	122.80
22	BA	1800	C	N1-C2-O2	-5.93	115.34	118.90
22	BA	1965	C	C6-N1-C2	-5.93	117.93	120.30
43	BV	61	LEU	CA-CB-CG	5.93	128.94	115.30
22	DA	2501	C	C2-N1-C1'	-5.93	112.28	118.80
22	BA	942	G	OP1-P-OP2	-5.92	110.71	119.60
22	DA	335	C	C5-C6-N1	5.92	123.96	121.00
1	CA	733	G	P-O3'-C3'	5.92	126.80	119.70
22	DA	2794	C	C6-N1-C2	-5.92	117.93	120.30
22	BA	353	C	N1-C2-O2	5.92	122.45	118.90
22	BA	993	G	N1-C6-O6	-5.91	116.35	119.90
22	BA	1012	U	N1-C2-O2	5.91	126.94	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	1682	G	N3-C4-N9	5.91	129.55	126.00
22	DA	481	G	O4'-C1'-N9	5.91	112.93	108.20
22	BA	1681	G	C6-C5-N7	-5.91	126.86	130.40
22	BA	1775	U	C2-N3-C4	-5.90	123.46	127.00
22	BA	1993	U	N3-C2-O2	-5.90	118.07	122.20
22	BA	2615	U	C5-C6-N1	-5.90	119.75	122.70
22	BA	2075	U	C5-C6-N1	-5.90	119.75	122.70
22	BA	1142	A	C5-C6-N1	-5.89	114.75	117.70
22	BA	1022	G	N9-C4-C5	5.89	107.76	105.40
22	BA	1428	C	N1-C2-O2	-5.89	115.36	118.90
37	BP	103	ARG	NE-CZ-NH1	5.89	123.25	120.30
22	BA	2250	G	C4-C5-N7	5.89	113.16	110.80
22	DA	1584	U	N1-C2-O2	5.88	126.92	122.80
22	BA	1322	A	C8-N9-C4	-5.88	103.45	105.80
22	BA	2429	G	C5-C6-N1	5.88	114.44	111.50
22	BA	2429	G	C6-N1-C2	-5.87	121.58	125.10
22	DA	450	G	N1-C6-O6	-5.87	116.38	119.90
1	AA	299	G	N3-C4-N9	5.87	129.52	126.00
22	BA	830	G	C2-N3-C4	-5.87	108.97	111.90
22	BA	1656	C	C5-C6-N1	-5.87	118.07	121.00
22	BA	1382	G	C8-N9-C4	5.86	108.75	106.40
22	BA	984	A	O5'-P-OP1	-5.86	100.43	105.70
22	BA	2463	C	N1-C2-O2	-5.86	115.39	118.90
22	BA	2588	G	O5'-P-OP2	-5.86	100.43	105.70
22	BA	1252	G	OP1-P-OP2	-5.85	110.83	119.60
22	BA	2619	C	C2-N3-C4	-5.84	116.98	119.90
22	BA	534	U	C5-C6-N1	-5.84	119.78	122.70
22	BA	2506	U	N1-C2-O2	5.84	126.89	122.80
22	BA	630	G	C8-N9-C4	5.83	108.73	106.40
22	DA	323	C	N1-C2-O2	5.83	122.40	118.90
22	BA	974	G	N7-C8-N9	5.83	116.01	113.10
23	BB	75	G	O5'-P-OP2	5.83	117.69	110.70
22	DA	2311	A	P-O3'-C3'	5.82	126.68	119.70
1	CA	575	G	N3-C4-C5	5.82	131.51	128.60
22	DA	1022	G	N3-C4-N9	-5.82	122.51	126.00
22	BA	1223	G	C5-C6-O6	5.80	132.08	128.60
22	BA	1682	G	C8-N9-C1'	-5.80	119.46	127.00
22	BA	2679	A	N1-C6-N6	5.80	122.08	118.60
22	BA	1283	G	N1-C6-O6	-5.79	116.42	119.90
22	BA	2035	G	C5-C6-O6	5.79	132.07	128.60
22	BA	18	U	C2-N3-C4	-5.79	123.53	127.00
22	DA	847	U	C2-N1-C1'	5.78	124.64	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	DA	2196	C	N1-C2-O2	5.78	122.37	118.90
1	CA	1028	C	N3-C2-O2	-5.78	117.86	121.90
1	CA	1286	U	C5-C6-N1	5.77	125.58	122.70
22	BA	1663	G	C2-N3-C4	-5.76	109.02	111.90
22	BA	2065	C	N1-C2-O2	5.76	122.36	118.90
3	AC	144	LEU	CA-CB-CG	5.75	128.53	115.30
22	BA	2738	A	C8-N9-C4	5.75	108.10	105.80
22	BA	125	A	N1-C6-N6	-5.75	115.15	118.60
22	BA	648	G	OP1-P-OP2	5.75	128.22	119.60
1	AA	299	G	C8-N9-C4	5.75	108.70	106.40
22	BA	912	C	OP1-P-OP2	5.75	128.22	119.60
22	BA	1430	G	OP1-P-OP2	-5.75	110.98	119.60
17	AQ	75	LEU	CA-CB-CG	5.74	128.49	115.30
22	BA	1494	A	P-O3'-C3'	5.74	126.58	119.70
22	BA	752	A	C4-C5-N7	5.73	113.56	110.70
22	DA	546	U	N3-C2-O2	-5.73	118.19	122.20
22	BA	1936	A	C5-C6-N1	-5.73	114.84	117.70
23	BB	98	G	O5'-P-OP2	-5.72	100.55	105.70
22	BA	1426	G	N3-C4-C5	-5.72	125.74	128.60
33	BL	41	ARG	NE-CZ-NH2	-5.71	117.44	120.30
22	BA	1919	A	N9-C1'-C2'	-5.71	105.72	112.00
1	CA	209	U	N1-C2-O2	5.71	126.80	122.80
1	AA	1031	C	P-O3'-C3'	5.71	126.55	119.70
1	CA	1397	C	C2-N1-C1'	5.71	125.08	118.80
22	BA	984	A	N1-C2-N3	5.71	132.15	129.30
1	CA	428	G	C4-N9-C1'	-5.70	119.09	126.50
22	BA	984	A	N9-C4-C5	5.70	108.08	105.80
22	BA	1762	A	C8-N9-C4	5.70	108.08	105.80
22	BA	2619	C	C5-C6-N1	-5.70	118.15	121.00
22	BA	1276	A	N1-C6-N6	5.69	122.02	118.60
1	CA	1397	C	N1-C2-O2	5.69	122.31	118.90
22	BA	404	A	P-O3'-C3'	5.69	126.53	119.70
1	AA	326	G	N3-C4-N9	5.68	129.41	126.00
22	BA	1790	C	OP1-P-O3'	5.68	117.70	105.20
22	BA	784	G	P-O3'-C3'	5.68	126.51	119.70
22	BA	1330	C	OP2-P-O3'	5.68	117.69	105.20
22	BA	2710	C	C2-N3-C4	-5.68	117.06	119.90
22	BA	2571	U	N3-C2-O2	-5.68	118.23	122.20
22	BA	1938	A	O5'-P-OP2	-5.67	100.59	105.70
22	BA	2825	G	C8-N9-C1'	-5.67	119.62	127.00
22	DA	2501	C	C6-N1-C1'	5.67	127.61	120.80
22	BA	867	C	N1-C2-O2	-5.67	115.50	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	1300	G	O5'-P-OP2	-5.66	100.60	105.70
22	BA	1787	A	N9-C4-C5	-5.66	103.54	105.80
22	BA	2631	G	C8-N9-C4	5.66	108.66	106.40
1	AA	115	G	P-O3'-C3'	5.66	126.49	119.70
1	AA	49	U	C5-C6-N1	-5.65	119.88	122.70
22	DA	528	A	C5-C6-N1	-5.65	114.88	117.70
22	BA	1976	U	C5-C6-N1	-5.65	119.88	122.70
22	BA	2446	G	O5'-P-OP2	-5.65	100.62	105.70
22	BA	461	C	C5-C6-N1	-5.65	118.18	121.00
22	BA	860	U	N3-C2-O2	-5.64	118.25	122.20
22	BA	2715	C	N3-C2-O2	-5.64	117.95	121.90
22	DA	781	A	OP2-P-O3'	5.64	117.61	105.20
22	BA	2030	A	C5-C6-N6	5.64	128.21	123.70
1	AA	1136	C	C6-N1-C2	-5.63	118.05	120.30
22	BA	1779	U	C2-N3-C4	-5.63	123.62	127.00
22	BA	2689	U	C5-C4-O4	5.63	129.28	125.90
22	BA	2820	A	N1-C6-N6	5.63	121.98	118.60
1	CA	328	C	C6-N1-C1'	-5.63	114.05	120.80
22	BA	2506	U	O4'-C1'-N1	5.62	112.69	108.20
22	BA	36	G	C8-N9-C4	-5.62	104.15	106.40
22	BA	941	A	C8-N9-C4	5.62	108.05	105.80
22	BA	1015	U	C5-C6-N1	-5.61	119.89	122.70
22	DA	784	G	C8-N9-C1'	-5.61	119.70	127.00
22	BA	2039	U	C4-C5-C6	5.61	123.06	119.70
22	BA	2715	C	O5'-P-OP2	-5.61	100.65	105.70
22	DA	1314	C	N1-C2-O2	5.61	122.26	118.90
22	BA	993	G	C4-C5-N7	-5.60	108.56	110.80
1	CA	485	U	N1-C2-O2	5.60	126.72	122.80
22	BA	140	C	N1-C2-O2	5.60	122.26	118.90
22	BA	2260	C	OP1-P-OP2	5.60	128.00	119.60
22	BA	128	C	N1-C2-O2	-5.59	115.55	118.90
22	BA	752	A	C4-N9-C1'	5.59	136.35	126.30
22	BA	2642	G	N1-C6-O6	-5.58	116.55	119.90
1	CA	1028	C	C6-N1-C2	-5.58	118.07	120.30
22	BA	2501	C	C2-N1-C1'	-5.57	112.67	118.80
22	BA	2681	C	O5'-P-OP2	-5.57	100.69	105.70
22	DA	2447	G	O4'-C1'-N9	5.57	112.65	108.20
22	BA	1191	G	C4-C5-N7	-5.57	108.57	110.80
22	BA	704	G	O4'-C1'-N9	5.56	112.65	108.20
1	CA	428	G	C8-N9-C1'	5.56	134.23	127.00
22	BA	802	A	O5'-P-OP1	-5.56	100.70	105.70
22	BA	2277	G	C6-N1-C2	-5.56	121.77	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	557	G	N3-C4-C5	-5.55	125.82	128.60
22	BA	455	C	N1-C2-O2	5.55	122.23	118.90
22	BA	1617	C	C4-C5-C6	5.55	120.18	117.40
22	BA	2286	G	C4-C5-N7	5.54	113.02	110.80
22	BA	2127	G	OP1-P-O3'	5.54	117.39	105.20
22	BA	1618	A	C5-C6-N6	5.54	128.13	123.70
22	BA	948	C	O5'-P-OP1	-5.54	100.72	105.70
22	BA	2034	U	N1-C2-N3	5.54	118.22	114.90
22	DA	2055	C	C5-C6-N1	5.53	123.77	121.00
22	BA	1936	A	N3-C4-C5	5.53	130.67	126.80
22	DA	60	G	OP1-P-O3'	5.53	117.37	105.20
22	BA	2385	C	C6-N1-C2	5.53	122.51	120.30
1	AA	12	U	C5-C6-N1	-5.53	119.94	122.70
1	AA	452	A	N7-C8-N9	5.53	116.56	113.80
22	BA	993	G	C5-N7-C8	5.53	107.06	104.30
22	BA	2683	C	N1-C2-O2	-5.53	115.58	118.90
22	BA	560	C	C6-N1-C2	5.53	122.51	120.30
34	BM	18	ARG	NE-CZ-NH2	5.53	123.06	120.30
22	BA	1158	C	C2-N3-C4	-5.52	117.14	119.90
22	BA	395	U	O4'-C1'-N1	5.52	112.62	108.20
22	BA	2520	C	C6-N1-C2	-5.52	118.09	120.30
22	DA	2196	C	N3-C2-O2	-5.52	118.04	121.90
22	BA	247	G	C8-N9-C4	-5.52	104.19	106.40
22	BA	763	G	N1-C6-O6	5.51	123.21	119.90
22	BA	1930	G	C4-C5-N7	-5.51	108.60	110.80
22	BA	1677	A	N9-C4-C5	-5.50	103.60	105.80
22	BA	2059	A	OP1-P-OP2	5.50	127.85	119.60
22	BA	2677	G	C8-N9-C4	5.50	108.60	106.40
1	AA	188	C	N3-C2-O2	-5.49	118.06	121.90
1	CA	575	G	N3-C4-N9	-5.49	122.71	126.00
22	DA	2501	C	O4'-C1'-N1	5.49	112.59	108.20
22	BA	852	U	C2-N3-C4	-5.48	123.71	127.00
2	AB	57	LEU	CA-CB-CG	5.48	127.91	115.30
22	BA	784	G	N1-C2-N2	-5.48	111.27	116.20
22	BA	1002	G	C5-C6-O6	5.48	131.89	128.60
22	BA	2257	U	N3-C2-O2	-5.48	118.36	122.20
22	BA	12	U	N3-C2-O2	-5.48	118.36	122.20
1	CA	429	U	C2-N1-C1'	-5.48	111.13	117.70
22	BA	1612	C	C6-N1-C2	5.47	122.49	120.30
22	DA	60	G	P-O3'-C3'	5.47	126.26	119.70
22	BA	484	C	C6-N1-C2	-5.46	118.11	120.30
22	BA	1556	C	N1-C2-O2	-5.46	115.62	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1158	C	C2-N1-C1'	5.46	124.81	118.80
22	BA	1019	U	C5-C6-N1	-5.46	119.97	122.70
22	BA	2615	U	C2-N3-C4	-5.46	123.72	127.00
22	BA	1614	A	C2-N3-C4	-5.46	107.87	110.60
22	BA	481	G	O4'-C1'-N9	5.46	112.56	108.20
16	AP	51	ARG	NE-CZ-NH1	5.45	123.03	120.30
22	DA	2473	U	C5-C6-N1	5.45	125.43	122.70
22	BA	1617	C	C2-N3-C4	-5.45	117.18	119.90
22	BA	1142	A	C5-N7-C8	-5.44	101.18	103.90
22	BA	1282	U	N1-C2-O2	-5.44	118.99	122.80
22	BA	1909	C	C6-N1-C2	-5.44	118.12	120.30
22	BA	672	C	C6-N1-C2	5.44	122.47	120.30
22	BA	784	G	C4-N9-C1'	5.44	133.57	126.50
1	CA	1137	C	N3-C2-O2	-5.44	118.09	121.90
22	DA	546	U	N1-C2-O2	5.44	126.61	122.80
22	DA	2240	U	N3-C2-O2	-5.43	118.39	122.20
22	BA	854	C	N1-C2-O2	-5.43	115.64	118.90
22	BA	1216	G	C5-C6-N1	5.43	114.22	111.50
22	BA	2588	G	N1-C6-O6	-5.43	116.64	119.90
1	AA	557	G	OP1-P-O3'	5.43	117.14	105.20
22	BA	1475	G	O4'-C1'-N9	5.43	112.54	108.20
22	DA	323	C	C2-N1-C1'	5.42	124.77	118.80
22	BA	783	A	C5-C6-N1	-5.42	114.99	117.70
22	BA	952	G	O5'-P-OP2	5.42	117.21	110.70
22	BA	528	A	C4-C5-C6	5.42	119.71	117.00
22	BA	759	G	N9-C4-C5	-5.41	103.23	105.40
22	BA	962	G	C8-N9-C1'	5.41	134.04	127.00
1	AA	1279	G	C5-N7-C8	-5.41	101.59	104.30
22	BA	101	A	C2-N3-C4	-5.41	107.90	110.60
22	BA	1930	G	C6-C5-N7	5.41	133.64	130.40
22	BA	1415	U	C6-N1-C2	-5.40	117.76	121.00
22	BA	2633	G	C8-N9-C4	5.40	108.56	106.40
22	BA	999	U	O5'-P-OP2	5.40	117.18	110.70
1	CA	563	A	C4-N9-C1'	5.40	136.02	126.30
1	CA	207	C	C6-N1-C1'	-5.40	114.33	120.80
22	BA	1258	U	C4-C5-C6	5.39	122.94	119.70
22	BA	682	G	C6-C5-N7	-5.39	127.17	130.40
22	BA	579	G	O5'-P-OP1	-5.39	100.85	105.70
23	BB	74	U	N3-C2-O2	-5.39	118.43	122.20
22	BA	583	G	OP1-P-O3'	5.39	117.05	105.20
22	DA	546	U	C2-N1-C1'	5.38	124.16	117.70
1	CA	210	C	C2-N1-C1'	5.38	124.72	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	DP	114	LEU	CA-CB-CG	5.38	127.67	115.30
22	BA	2878	U	C5-C6-N1	-5.38	120.01	122.70
22	DA	1606	C	P-O3'-C3'	5.38	126.15	119.70
22	BA	861	A	OP1-P-O3'	5.37	117.02	105.20
22	DA	974	G	C4-N9-C1'	5.37	133.49	126.50
22	BA	2848	G	O4'-C1'-N9	5.37	112.50	108.20
23	BB	82	U	C5-C4-O4	5.37	129.12	125.90
28	BG	149	ARG	NE-CZ-NH1	5.37	122.98	120.30
3	AC	18	TRP	N-CA-C	-5.37	96.52	111.00
22	BA	1251	C	N3-C4-N4	5.37	121.76	118.00
1	AA	365	U	C4-C5-C6	5.36	122.92	119.70
1	AA	1322	C	C2-N1-C1'	5.36	124.70	118.80
22	BA	1977	A	C8-N9-C4	5.36	107.94	105.80
22	BA	1358	G	N1-C6-O6	5.36	123.11	119.90
22	BA	1428	C	C2-N3-C4	-5.36	117.22	119.90
22	BA	1639	C	N1-C2-O2	-5.36	115.69	118.90
22	BA	1791	A	OP1-P-OP2	-5.36	111.57	119.60
22	DA	784	G	C6-C5-N7	-5.34	127.19	130.40
22	BA	942	G	C8-N9-C4	5.34	108.54	106.40
22	BA	2894	G	N7-C8-N9	-5.34	110.43	113.10
1	CA	428	G	O4'-C1'-N9	5.34	112.47	108.20
3	CC	175	LEU	CA-CB-CG	5.34	127.58	115.30
22	DA	106	C	C5-C6-N1	5.34	123.67	121.00
22	BA	1390	U	C2-N3-C4	-5.34	123.80	127.00
1	AA	452	A	N1-C2-N3	5.33	131.97	129.30
22	DA	2794	C	C5-C6-N1	5.33	123.67	121.00
22	BA	229	C	C6-N1-C2	-5.33	118.17	120.30
22	BA	962	G	O4'-C1'-N9	5.33	112.47	108.20
22	BA	2710	C	C5-C6-N1	-5.33	118.33	121.00
22	BA	2211	A	OP1-P-O3'	5.33	116.93	105.20
1	AA	971	G	O4'-C1'-N9	5.33	112.46	108.20
22	BA	1132	U	C4-C5-C6	5.33	122.90	119.70
22	BA	2826	A	N7-C8-N9	-5.32	111.14	113.80
22	BA	830	G	N1-C2-N3	5.32	127.09	123.90
22	BA	1993	U	OP1-P-OP2	-5.32	111.62	119.60
22	BA	740	C	C6-N1-C2	5.32	122.43	120.30
22	BA	1132	U	N1-C2-N3	5.31	118.09	114.90
22	BA	2715	C	C6-N1-C2	-5.31	118.17	120.30
22	BA	140	C	C2-N1-C1'	5.31	124.64	118.80
22	BA	1188	U	C5-C6-N1	-5.31	120.04	122.70
22	BA	2558	C	N1-C2-O2	5.31	122.09	118.90
22	BA	813	U	C5-C6-N1	-5.31	120.04	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	948	C	C5-C6-N1	-5.31	118.34	121.00
22	BA	912	C	O5'-P-OP1	-5.31	100.92	105.70
22	DA	784	G	N9-C4-C5	-5.31	103.28	105.40
33	BL	52	GLY	N-CA-C	-5.31	99.83	113.10
22	DA	1843	C	C5-C6-N1	5.30	123.65	121.00
22	BA	536	G	N7-C8-N9	-5.30	110.45	113.10
22	BA	2583	G	OP1-P-OP2	-5.30	111.65	119.60
22	BA	2040	G	C5-C6-N1	5.30	114.15	111.50
22	DA	1096	A	C8-N9-C4	-5.30	103.68	105.80
22	BA	1681	G	C4-C5-N7	5.29	112.92	110.80
1	CA	754	C	N1-C2-O2	5.29	122.08	118.90
22	BA	1784	A	C5-C6-N1	-5.29	115.06	117.70
22	BA	2724	U	C4-C5-C6	5.29	122.88	119.70
1	AA	365	U	N1-C2-N3	5.29	118.07	114.90
22	BA	1168	G	N3-C4-N9	5.29	129.17	126.00
22	BA	1683	U	C5-C6-N1	-5.29	120.06	122.70
22	DA	1313	U	C5-C6-N1	5.29	125.34	122.70
1	AA	742	G	C8-N9-C4	5.29	108.52	106.40
22	BA	1012	U	N3-C2-O2	-5.29	118.50	122.20
22	BA	1251	C	C5-C4-N4	-5.29	116.50	120.20
22	DA	2473	U	N1-C2-O2	5.29	126.50	122.80
22	BA	1219	U	C5-C6-N1	-5.28	120.06	122.70
22	BA	2858	C	N3-C4-C5	5.28	124.01	121.90
22	BA	1168	G	C8-N9-C1'	-5.28	120.13	127.00
22	BA	1784	A	C2-N3-C4	-5.28	107.96	110.60
22	BA	1533	C	N1-C2-O2	5.28	122.07	118.90
22	BA	742	A	C2-N3-C4	-5.28	107.96	110.60
22	BA	808	G	C8-N9-C4	5.28	108.51	106.40
1	AA	1136	C	N1-C2-O2	5.27	122.06	118.90
6	AF	39	LEU	CA-CB-CG	5.27	127.43	115.30
1	CA	792	A	O4'-C1'-N9	5.27	112.41	108.20
22	BA	1132	U	N3-C4-C5	-5.27	111.44	114.60
22	BA	742	A	C5-C6-N1	-5.26	115.07	117.70
22	BA	101	A	C5-C6-N1	-5.26	115.07	117.70
22	BA	1758	U	C5-C6-N1	-5.26	120.07	122.70
22	BA	1157	G	O5'-P-OP2	-5.26	100.97	105.70
22	BA	2429	G	OP1-P-OP2	-5.26	111.72	119.60
22	DA	404	A	OP2-P-O3'	5.25	116.76	105.20
1	AA	558	G	O5'-P-OP1	-5.25	100.98	105.70
22	BA	740	C	N3-C4-C5	5.25	124.00	121.90
22	BA	2724	U	C5-C6-N1	-5.25	120.08	122.70
22	DA	2447	G	C8-N9-C1'	5.25	133.82	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	1818	U	C5-C6-N1	-5.24	120.08	122.70
22	BA	1965	C	N3-C4-N4	5.24	121.67	118.00
22	BA	192	C	OP1-P-OP2	5.24	127.46	119.60
22	BA	2006	C	O5'-P-OP2	5.24	116.99	110.70
22	BA	974	G	C6-C5-N7	-5.24	127.26	130.40
1	CA	463	U	C2-N1-C1'	5.24	123.99	117.70
22	BA	956	G	C2-N3-C4	-5.24	109.28	111.90
22	BA	1670	C	OP1-P-O3'	5.24	116.72	105.20
22	BA	2019	A	N1-C6-N6	-5.23	115.46	118.60
22	BA	771	G	C6-C5-N7	-5.23	127.26	130.40
22	BA	1223	G	N3-C4-N9	-5.23	122.86	126.00
22	BA	2517	C	N3-C4-C5	5.23	123.99	121.90
22	BA	2676	C	C6-N1-C2	5.23	122.39	120.30
22	DA	1834	U	C2-N1-C1'	5.23	123.97	117.70
22	BA	2496	C	O5'-P-OP2	-5.23	101.00	105.70
22	DA	1584	U	N3-C2-O2	-5.22	118.55	122.20
22	BA	370	G	O4'-C1'-N9	-5.22	104.03	108.20
1	CA	209	U	C6-N1-C1'	-5.22	113.89	121.20
22	BA	1672	A	C5-N7-C8	5.22	106.51	103.90
10	CJ	92	LEU	CA-CB-CG	5.21	127.29	115.30
22	DA	2165	C	N3-C2-O2	-5.21	118.25	121.90
22	BA	671	C	C5-C6-N1	-5.21	118.40	121.00
22	BA	2248	C	N3-C4-N4	-5.21	114.36	118.00
9	AI	63	LEU	CA-CB-CG	5.20	127.27	115.30
22	BA	2715	C	C4-C5-C6	5.20	120.00	117.40
10	CJ	87	LEU	CA-CB-CG	5.20	127.26	115.30
1	CA	561	U	C5-C6-N1	-5.20	120.10	122.70
22	BA	1669	A	C5-C6-N1	5.20	120.30	117.70
22	BA	2264	C	C6-N1-C2	5.19	122.38	120.30
22	DA	2447	G	C6-C5-N7	5.19	133.51	130.40
22	BA	1964	G	OP1-P-OP2	5.19	127.38	119.60
22	DA	1788	C	C5-C6-N1	5.18	123.59	121.00
22	BA	1288	G	N3-C2-N2	5.18	123.53	119.90
22	BA	2032	G	O4'-C1'-N9	5.18	112.35	108.20
1	AA	727	G	C6-C5-N7	-5.18	127.29	130.40
22	BA	835	C	C2-N3-C4	-5.18	117.31	119.90
22	BA	1909	C	C6-N1-C1'	-5.18	114.58	120.80
22	BA	2645	G	O4'-C1'-N9	5.18	112.34	108.20
1	AA	557	G	N3-C4-N9	5.18	129.11	126.00
22	BA	1007	C	O5'-P-OP1	-5.18	101.04	105.70
1	AA	1505	G	C4-C5-N7	-5.17	108.73	110.80
22	BA	823	C	C6-N1-C2	5.17	122.37	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	85	U	C2-N1-C1'	5.17	123.91	117.70
22	BA	1178	C	C6-N1-C2	-5.17	118.23	120.30
22	BA	1273	U	C5-C6-N1	-5.17	120.11	122.70
22	BA	1977	A	C5-C6-N1	-5.17	115.11	117.70
29	BH	121	VAL	C-N-CA	5.17	134.62	121.70
22	BA	1779	U	C5-C4-O4	5.17	129.00	125.90
22	BA	746	U	C2-N1-C1'	-5.16	111.50	117.70
22	BA	2754	U	N1-C2-O2	5.16	126.41	122.80
22	BA	466	A	N1-C6-N6	-5.16	115.50	118.60
22	BA	2039	U	N3-C2-O2	-5.16	118.59	122.20
1	CA	575	G	C4-N9-C1'	-5.16	119.79	126.50
22	BA	723	C	N3-C2-O2	-5.16	118.29	121.90
22	BA	1406	U	C6-N1-C1'	5.16	128.42	121.20
22	BA	2773	C	OP1-P-OP2	-5.16	111.87	119.60
23	DB	14	U	C2-N1-C1'	5.16	123.89	117.70
1	CA	844	G	N3-C4-C5	-5.15	126.02	128.60
22	BA	1305	C	N1-C2-O2	5.15	121.99	118.90
22	BA	2719	G	C2-N3-C4	-5.15	109.32	111.90
53	B5	122	GLY	N-CA-C	5.15	125.96	113.10
1	CA	188	C	C6-N1-C2	-5.15	118.24	120.30
22	DA	2211	A	P-O3'-C3'	5.14	125.87	119.70
22	BA	2263	C	N3-C4-C5	5.14	123.96	121.90
22	BA	2585	U	C2-N1-C1'	-5.14	111.53	117.70
22	BA	686	U	C6-N1-C1'	5.14	128.39	121.20
22	BA	1936	A	N3-C4-N9	-5.14	123.29	127.40
1	AA	4	U	C5-C6-N1	5.14	125.27	122.70
1	CA	210	C	C5-C6-N1	5.14	123.57	121.00
1	AA	1158	C	C2-N1-C1'	5.13	124.45	118.80
22	BA	18	U	C5-C6-N1	-5.13	120.13	122.70
22	BA	479	A	P-O3'-C3'	5.13	125.86	119.70
22	BA	1550	C	N1-C2-O2	-5.13	115.82	118.90
22	BA	2449	U	O5'-P-OP2	-5.13	101.08	105.70
22	BA	1917	U	C2-N1-C1'	5.13	123.86	117.70
22	BA	2460	U	C5-C4-O4	-5.13	122.82	125.90
22	BA	536	G	N9-C4-C5	-5.13	103.35	105.40
22	BA	714	U	O4'-C1'-N1	5.13	112.31	108.20
22	BA	1266	G	N1-C6-O6	-5.13	116.82	119.90
22	BA	2063	C	N1-C2-O2	5.13	121.98	118.90
22	BA	1779	U	O4'-C1'-N1	5.13	112.30	108.20
22	BA	1258	U	N1-C2-N3	5.13	117.98	114.90
1	CA	211	G	N3-C4-N9	5.13	129.08	126.00
1	CA	1230	C	C5-C6-N1	5.13	123.56	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	1658	C	N3-C4-C5	5.13	123.95	121.90
1	AA	1108	G	C5-C6-O6	-5.12	125.53	128.60
1	CA	1364	U	N3-C2-O2	-5.12	118.61	122.20
1	AA	1136	C	C2-N1-C1'	5.12	124.44	118.80
1	AA	1031	C	OP2-P-O3'	5.12	116.47	105.20
1	AA	1168	U	C5-C6-N1	5.12	125.26	122.70
22	BA	1759	A	C2-N3-C4	5.12	113.16	110.60
22	BA	1769	U	N3-C2-O2	-5.12	118.62	122.20
22	BA	1168	G	C4-N9-C1'	5.12	133.15	126.50
22	BA	2580	U	C5-C6-N1	5.12	125.26	122.70
22	BA	1332	G	C6-C5-N7	-5.11	127.33	130.40
22	DA	512	G	O4'-C1'-N9	5.11	112.29	108.20
22	BA	1061	U	O4'-C1'-N1	5.11	112.29	108.20
22	BA	752	A	N9-C1'-C2'	5.11	120.64	114.00
22	BA	903	C	N1-C2-O2	-5.11	115.84	118.90
22	BA	1428	C	C4-C5-C6	5.11	119.95	117.40
22	BA	180	G	N3-C4-C5	5.10	131.15	128.60
22	BA	1287	A	C4-C5-C6	5.10	119.55	117.00
22	BA	668	A	OP1-P-O3'	5.10	116.42	105.20
22	BA	2325	G	O5'-P-OP2	-5.10	101.11	105.70
1	AA	108	G	N3-C4-C5	-5.10	126.05	128.60
22	BA	1171	G	C4-N9-C1'	5.10	133.13	126.50
22	BA	1695	G	OP1-P-OP2	5.10	127.25	119.60
22	BA	2039	U	C2-N3-C4	-5.10	123.94	127.00
54	D6	4	PRO	N-CA-CB	5.10	109.42	103.30
22	BA	1682	G	C4-N9-C1'	5.10	133.12	126.50
22	BA	2501	C	C6-N1-C1'	5.09	126.92	120.80
22	DA	1774	C	C6-N1-C2	-5.09	118.26	120.30
22	BA	691	C	OP1-P-OP2	-5.09	111.96	119.60
22	BA	2127	G	P-O3'-C3'	5.09	125.81	119.70
22	BA	2633	G	N1-C2-N3	5.09	126.95	123.90
1	CA	429	U	C5-C6-N1	-5.09	120.16	122.70
22	BA	2826	A	C5-N7-C8	5.09	106.44	103.90
22	BA	1651	G	C6-N1-C2	-5.09	122.05	125.10
22	BA	2075	U	C2-N3-C4	-5.08	123.95	127.00
1	AA	365	U	C6-N1-C1'	5.08	128.32	121.20
22	BA	1666	G	C5-C6-N1	5.08	114.04	111.50
22	BA	1990	C	C5-C6-N1	-5.08	118.46	121.00
22	BA	45	G	OP1-P-O3'	5.08	116.38	105.20
22	BA	2002	G	C6-C5-N7	-5.08	127.35	130.40
22	BA	102	U	C2-N1-C1'	5.08	123.79	117.70
22	BA	1149	G	OP2-P-O3'	5.08	116.37	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	2270	A	C8-N9-C4	5.08	107.83	105.80
22	BA	2522	U	N1-C2-O2	-5.08	119.25	122.80
22	BA	16	C	OP1-P-O3'	5.07	116.36	105.20
22	BA	2513	A	N1-C6-N6	-5.07	115.56	118.60
22	BA	2729	G	C6-C5-N7	-5.07	127.36	130.40
22	BA	2794	C	N1-C2-O2	-5.07	115.86	118.90
22	BA	2720	U	N1-C2-O2	-5.07	119.25	122.80
22	BA	2845	U	C5-C6-N1	-5.07	120.17	122.70
22	BA	1064	C	C5-C6-N1	5.07	123.53	121.00
1	AA	618	C	C2-N1-C1'	5.06	124.37	118.80
22	BA	2248	C	N1-C2-O2	5.06	121.94	118.90
26	DE	180	LEU	CA-CB-CG	5.06	126.94	115.30
1	AA	1479	C	N1-C2-O2	-5.06	115.86	118.90
22	BA	1341	G	C8-N9-C4	5.06	108.42	106.40
22	BA	1660	G	N3-C4-C5	-5.06	126.07	128.60
22	BA	1210	G	C4-C5-N7	5.06	112.82	110.80
22	BA	1985	C	C6-N1-C2	5.05	122.32	120.30
22	DA	1834	U	C5-C6-N1	5.05	125.22	122.70
1	AA	1317	C	C6-N1-C2	-5.05	118.28	120.30
22	BA	748	G	C4-N9-C1'	-5.05	119.94	126.50
22	BA	808	G	C6-N1-C2	-5.05	122.07	125.10
22	BA	837	C	C2-N3-C4	-5.05	117.38	119.90
22	BA	1957	C	O5'-P-OP2	5.05	116.76	110.70
22	BA	1992	G	C6-N1-C2	-5.05	122.07	125.10
22	BA	32	C	C2-N1-C1'	-5.05	113.25	118.80
22	BA	578	G	C6-C5-N7	-5.05	127.37	130.40
22	BA	978	G	N1-C2-N3	5.04	126.93	123.90
22	BA	30	G	OP1-P-O3'	5.04	116.30	105.20
22	BA	1282	U	N3-C2-O2	5.04	125.73	122.20
22	BA	1658	C	O5'-P-OP2	5.04	116.75	110.70
22	BA	1838	C	N1-C2-O2	-5.04	115.88	118.90
22	BA	2331	G	N3-C4-C5	5.04	131.12	128.60
22	BA	993	G	N3-C4-C5	-5.04	126.08	128.60
22	BA	2047	C	N3-C4-C5	5.04	123.92	121.90
22	BA	1061	U	C2-N1-C1'	5.03	123.74	117.70
22	BA	1679	A	C4-C5-C6	5.03	119.52	117.00
22	DA	2146	C	P-O3'-C3'	5.03	125.74	119.70
1	AA	476	U	N3-C2-O2	-5.03	118.68	122.20
22	BA	2059	A	C2-N3-C4	-5.03	108.08	110.60
22	DA	528	A	C2-N3-C4	-5.03	108.08	110.60
22	DA	1198	U	C5-C6-N1	5.03	125.22	122.70
22	BA	665	U	N1-C2-N3	5.03	117.92	114.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	1651	G	N3-C4-C5	-5.03	126.09	128.60
22	BA	2724	U	N1-C2-N3	5.03	117.92	114.90
1	CA	365	U	C5-C6-N1	-5.03	120.19	122.70
22	BA	2018	G	OP2-P-O3'	5.03	116.26	105.20
1	AA	877	G	N1-C2-N2	-5.02	111.68	116.20
1	AA	1505	G	N9-C4-C5	5.02	107.41	105.40
22	BA	1180	U	C2-N1-C1'	5.02	123.73	117.70
22	BA	1771	C	C5-C6-N1	-5.02	118.49	121.00
22	BA	2061	G	C5-C6-O6	5.02	131.61	128.60
22	BA	276	U	C5-C6-N1	5.02	125.21	122.70
22	BA	974	G	O5'-P-OP2	-5.02	101.18	105.70
22	BA	260	G	N1-C6-O6	-5.02	116.89	119.90
22	BA	1313	U	C2-N1-C1'	5.02	123.72	117.70
22	BA	1219	U	C2-N3-C4	-5.01	123.99	127.00
22	BA	1694	C	C5-C6-N1	-5.01	118.49	121.00
22	DA	784	G	C4-N9-C1'	5.01	133.02	126.50
1	CA	1477	U	C5-C6-N1	5.01	125.21	122.70
22	BA	783	A	C6-C5-N7	-5.01	128.79	132.30
22	BA	1142	A	N1-C6-N6	5.01	121.61	118.60
22	BA	2011	U	N1-C2-O2	-5.01	119.29	122.80
22	BA	2425	A	P-O3'-C3'	5.01	125.71	119.70
22	DA	2165	C	C5-C6-N1	5.01	123.50	121.00
22	BA	1961	C	O5'-P-OP2	5.01	116.71	110.70
23	DB	89	U	N1-C2-O2	5.00	126.30	122.80
22	BA	420	C	N1-C2-O2	5.00	121.90	118.90
1	AA	1049	U	P-O3'-C3'	5.00	125.70	119.70
22	BA	1034	G	C6-C5-N7	-5.00	127.40	130.40

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	AE	123	VAL	Peptide
11	AK	126	LYS	Peptide
21	AU	39	GLU	Peptide
21	AU	8	GLU	Peptide
25	BD	151	THR	Peptide
26	BE	40	ARG	Peptide
40	BS	102	HIS	Sidechain
2	CB	84	ALA	Peptide
5	CE	102	GLY	Peptide
5	CE	104	GLY	Peptide

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Mol	Chain	Res	Type	Group
6	CF	54	LEU	Peptide
11	CK	126	LYS	Peptide
12	CL	23	ALA	Peptide
12	CL	38	TYR	Peptide
21	CU	35	ARG	Peptide
25	DD	151	THR	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	32995	0	16607	608	14
1	CA	33015	0	16616	645	0
2	AB	1705	0	1732	135	0
2	CB	1705	0	1732	109	0
3	AC	1625	0	1696	75	0
3	CC	1625	0	1696	67	0
4	AD	1643	0	1707	93	0
4	CD	1643	0	1707	74	0
5	AE	1106	0	1148	60	0
5	CE	1106	0	1148	72	0
6	AF	818	0	808	37	0
6	CF	818	0	808	35	0
7	AG	1182	0	1238	47	0
7	CG	1182	0	1238	49	0
8	AH	979	0	1031	38	0
8	CH	979	0	1031	43	0
9	AI	1022	0	1070	51	0
9	CI	1022	0	1070	64	0
10	AJ	787	0	828	60	0
10	CJ	787	0	828	44	0
11	AK	877	0	887	54	0
11	CK	877	0	887	39	0
12	AL	955	0	1016	38	0
12	CL	955	0	1016	48	0
13	AM	884	0	941	49	0
13	CM	884	0	941	40	0
14	AN	774	0	824	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	CN	774	0	824	44	0
15	AO	710	0	728	20	0
15	CO	710	0	728	38	0
16	AP	649	0	666	34	0
16	CP	649	0	666	30	0
17	AQ	649	0	691	30	0
17	CQ	649	0	691	33	0
18	AR	456	0	478	12	0
18	CR	456	0	478	25	0
19	AS	638	0	665	32	0
19	CS	638	0	665	31	0
20	AT	665	0	714	31	0
20	CT	665	0	714	34	0
21	AU	426	0	449	39	0
21	CU	426	0	449	29	0
22	BA	62195	0	31280	1058	0
22	DA	62195	0	31280	1193	1
23	BB	2549	0	1291	19	0
23	DB	2529	0	1281	44	0
24	BC	2083	0	2154	76	0
24	DC	2083	0	2154	94	0
25	BD	1565	0	1616	48	0
25	DD	1565	0	1616	55	0
26	BE	1552	0	1619	47	0
26	DE	1552	0	1619	63	0
27	BF	1411	0	1444	51	0
27	DF	1411	0	1444	50	0
28	BG	1323	0	1371	44	0
28	DG	1323	0	1371	39	0
29	BH	1110	0	1145	196	0
29	DH	1110	0	1148	91	13
30	BI	1032	0	1085	52	0
30	DI	1032	0	1085	54	0
31	BJ	1129	0	1162	28	0
31	DJ	1129	0	1162	48	0
32	BK	939	0	1012	30	0
32	DK	939	0	1012	29	0
33	BL	1045	0	1117	38	0
33	DL	1045	0	1117	46	0
34	BM	1074	0	1157	30	0
34	DM	1074	0	1157	20	0
35	BN	961	0	1000	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	DN	961	0	1000	47	0
36	BO	892	0	923	25	0
36	DO	892	0	923	42	0
37	BP	917	0	962	39	0
37	DP	917	0	962	34	0
38	BQ	947	0	1019	35	0
38	DQ	947	0	1019	44	0
39	BR	816	0	839	37	0
39	DR	816	0	839	34	0
40	BS	857	0	922	34	0
40	DS	857	0	922	25	0
41	BT	739	0	807	27	0
41	DT	739	0	807	27	0
42	BU	780	0	831	18	0
42	DU	780	0	831	44	0
43	BV	753	0	780	14	0
43	DV	753	0	780	27	0
44	BW	580	0	594	14	0
44	DW	569	0	581	18	0
45	BX	625	0	652	29	0
45	DX	625	0	652	46	0
46	BY	509	0	543	25	0
46	DY	509	0	543	24	0
47	BZ	449	0	488	7	0
47	DZ	449	0	488	15	0
48	B0	444	0	458	20	0
48	D0	444	0	458	16	0
49	B1	410	0	440	15	0
49	D1	410	0	440	14	0
50	B2	377	0	418	13	0
50	D2	377	0	418	14	0
51	B3	504	0	572	18	0
51	D3	504	0	572	17	0
52	B4	302	0	341	15	0
52	D4	302	0	340	12	0
53	B5	1142	0	865	27	0
54	B6	73	0	64	5	0
54	D6	73	0	64	7	0
55	AA	71	0	0	0	0
55	AM	1	0	0	0	0
55	BA	195	0	0	0	0
55	BB	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	CA	55	0	0	0	0
55	CM	1	0	0	0	0
55	DA	167	0	0	0	0
55	DB	3	0	0	0	0
55	DQ	1	0	0	0	0
56	B4	1	0	0	0	0
56	D4	1	0	0	0	0
57	AA	194	0	0	6	0
57	AL	1	0	0	0	0
57	AN	5	0	0	1	0
57	AT	2	0	0	0	0
57	AU	1	0	0	1	0
57	B2	1	0	0	0	0
57	B3	3	0	0	0	0
57	B4	2	0	0	0	0
57	BA	619	0	0	59	0
57	BB	13	0	0	1	0
57	BC	8	0	0	1	0
57	BD	3	0	0	2	0
57	BE	3	0	0	0	0
57	BF	1	0	0	1	0
57	BG	1	0	0	0	0
57	BL	5	0	0	1	0
57	BN	5	0	0	1	0
57	BS	1	0	0	0	0
57	BV	1	0	0	0	0
57	CA	189	0	0	10	0
57	CL	1	0	0	0	0
57	CN	3	0	0	0	0
57	CT	4	0	0	0	0
57	CU	1	0	0	1	0
57	D0	1	0	0	0	0
57	D2	2	0	0	1	0
57	D3	1	0	0	0	0
57	D4	1	0	0	0	0
57	DA	612	0	0	63	0
57	DB	13	0	0	0	0
57	DC	7	0	0	1	0
57	DD	4	0	0	1	0
57	DE	4	0	0	0	0
57	DL	4	0	0	0	0
57	DN	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	DQ	2	0	0	0	0
57	DT	3	0	0	0	0
57	DV	1	0	0	0	0
All	All	288328	0	192913	6784	14

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 15.

All (6784) 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)
29:BH:83:LYS:HD2	1:CA:55:A:O2'	1.21	1.29
29:BH:117:LEU:O	29:BH:121:VAL:HG23	1.34	1.22
29:BH:117:LEU:O	29:BH:121:VAL:CG2	1.95	1.14
29:BH:123:ARG:O	29:BH:124:THR:CG2	2.01	1.09
29:BH:97:ARG:HD2	1:CA:369:G:O2'	1.51	1.09
29:BH:83:LYS:HG3	1:CA:55:A:N3	1.69	1.08
29:BH:90:LEU:O	1:CA:358:U:H4'	1.54	1.07
22:BA:2092:U:OP2	29:BH:27:ARG:NE	1.92	1.03
29:BH:83:LYS:HE2	1:CA:55:A:H2'	1.40	1.03
29:BH:117:LEU:HD21	29:BH:121:VAL:H	1.23	1.00
29:BH:89:LYS:HB3	1:CA:359:G:H5''	1.43	1.00
22:BA:730:A:OP2	57:BA:3697:HOH:O	1.76	1.00
29:BH:123:ARG:O	29:BH:124:THR:HG23	1.61	0.99
1:CA:978:A:HO2'	1:CA:1322:C:H5	1.06	0.99
29:BH:83:LYS:CD	1:CA:55:A:O2'	2.12	0.97
29:DH:40:THR:O	29:DH:42:LYS:N	1.98	0.96
22:BA:731:C:OP2	57:BA:3697:HOH:O	1.83	0.96
29:BH:120:GLY:C	29:BH:122:LEU:HA	1.85	0.95
1:CA:1101:A:H61	2:CB:102:THR:HG21	1.29	0.94
15:AO:89:ARG:NH1	22:BA:716:A:OP2	1.99	0.94
29:BH:83:LYS:HD2	1:CA:55:A:HO2'	1.15	0.93
22:BA:2199:A:C1'	29:BH:28:ASN:ND2	2.33	0.92
22:DA:1060:U:H4'	22:DA:1061:U:H5'	1.51	0.92
22:BA:2499:C:OP2	57:BA:3689:HOH:O	1.85	0.92
22:DA:2711:A:OP2	57:DA:3545:HOH:O	1.88	0.91
17:CQ:46:VAL:HG21	17:CQ:61:ILE:HD11	1.50	0.90
22:BA:2819:G:OP1	57:BA:3807:HOH:O	1.88	0.90
22:DA:1936:A:H2	22:DA:1943:U:H3	1.13	0.90
22:DA:2588:G:OP1	57:DA:3312:HOH:O	1.89	0.90
29:DH:83:LYS:HG3	29:DH:149:GLU:CG	2.02	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2720:U:OP1	37:BP:53:ARG:NH2	2.04	0.90
1:CA:1097:C:OP1	2:CB:139:ARG:NH2	2.05	0.90
22:BA:978:G:N7	57:BA:3592:HOH:O	2.04	0.90
22:BA:1073:A:H3'	22:BA:1074:G:H5''	1.54	0.90
22:BA:1478:G:H1	22:BA:1513:U:H3	1.17	0.89
22:BA:1153:C:OP2	57:BA:3360:HOH:O	1.91	0.89
29:BH:89:LYS:HB3	1:CA:359:G:C5'	2.03	0.88
22:BA:2199:A:O4'	29:BH:28:ASN:ND2	2.06	0.88
26:DE:108:ILE:HD13	26:DE:181:ILE:HG12	1.52	0.88
29:BH:123:ARG:O	29:BH:124:THR:HG22	1.74	0.88
29:BH:93:SER:OG	1:CA:357:G:H4'	1.73	0.88
9:CI:13:LYS:H	9:CI:106:ARG:HH12	1.19	0.88
21:CU:10:GLU:HG3	21:CU:11:PRO:HD3	1.56	0.87
29:BH:117:LEU:C	29:BH:121:VAL:HG23	1.93	0.87
29:BH:86:ASP:H	1:CA:359:G:H4'	1.38	0.87
29:BH:83:LYS:CE	1:CA:55:A:H2'	2.04	0.87
29:DH:83:LYS:HG3	29:DH:149:GLU:HG2	1.56	0.87
22:DA:1847:A:HO2'	22:DA:1848:A:H8	1.18	0.86
35:BN:2:ARG:HA	35:BN:5:LYS:HD2	1.57	0.86
4:AD:147:GLU:HA	4:AD:150:LYS:HD2	1.58	0.86
10:AJ:9:ARG:HB2	10:AJ:99:GLN:HB2	1.55	0.86
33:BL:29:LYS:O	33:BL:31:GLY:N	2.07	0.86
1:AA:973:G:H1'	10:AJ:56:HIS:HD2	1.40	0.86
30:BI:16:GLY:HA2	30:BI:51:LYS:HB3	1.57	0.86
22:BA:733:G:OP2	57:BA:3297:HOH:O	1.93	0.86
22:BA:2448:A:OP2	57:BA:3689:HOH:O	1.93	0.86
4:AD:26:ARG:HD2	4:AD:31:LYS:HE3	1.56	0.86
29:BH:147:VAL:HG12	29:BH:149:GLU:HG3	1.57	0.85
22:DA:1006:C:OP2	57:DA:3779:HOH:O	1.95	0.85
22:DA:2624:G:H1'	48:D0:19:HIS:HE1	1.40	0.85
22:BA:999:U:OP2	57:BA:3362:HOH:O	1.95	0.85
11:AK:34:ILE:HB	11:AK:74:VAL:HG11	1.58	0.85
2:AB:21:ARG:O	2:AB:23:TRP:N	2.08	0.84
1:AA:702:A:N6	22:BA:1846:G:O2'	2.10	0.84
22:BA:2478:A:H5'	52:B4:32:LYS:HD3	1.59	0.84
25:DD:140:HIS:NE2	57:DD:302:HOH:O	2.10	0.84
22:BA:397:U:OP2	45:BX:10:LYS:NZ	2.09	0.84
29:BH:117:LEU:HD21	29:BH:121:VAL:N	1.93	0.84
22:DA:192:C:OP1	57:DA:3736:HOH:O	1.94	0.84
1:AA:684:U:O2'	11:AK:40:ASN:O	1.95	0.84
29:BH:117:LEU:O	29:BH:119:ASN:N	2.07	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DH:82:SER:O	29:DH:84:ALA:N	2.10	0.83
22:BA:1056:G:HO2'	22:BA:1086:A:H8	1.23	0.83
29:BH:86:ASP:H	1:CA:359:G:C4'	1.91	0.83
25:DD:3:GLY:HA3	25:DD:204:LYS:HG2	1.58	0.83
5:CE:99:ALA:O	5:CE:122:ASN:ND2	2.11	0.83
41:BT:1:MET:HB2	41:BT:2:ILE:HD12	1.60	0.83
7:AG:27:VAL:HG12	7:AG:43:VAL:HG21	1.61	0.83
12:CL:34:CYS:HA	12:CL:55:VAL:HA	1.60	0.83
22:DA:1154:G:OP2	38:DQ:58:ARG:NH1	2.12	0.83
4:AD:37:ALA:HA	4:AD:42:GLY:HA3	1.58	0.83
26:DE:108:ILE:HD11	26:DE:180:LEU:HB2	1.60	0.83
22:BA:1936:A:H2	22:BA:1943:U:H3	1.23	0.83
22:DA:1937:A:OP1	57:DA:3453:HOH:O	1.97	0.83
47:DZ:41:THR:HG23	47:DZ:44:ILE:HG12	1.61	0.83
22:DA:1371:G:N7	57:DA:3396:HOH:O	2.11	0.82
36:BO:31:THR:O	36:BO:102:ARG:NH1	2.11	0.82
29:BH:93:SER:HG	1:CA:357:G:H4'	1.44	0.82
6:AF:3:HIS:H	6:AF:92:THR:HG23	1.42	0.82
22:BA:1482:G:H1'	22:BA:1509:A:H61	1.45	0.82
10:AJ:11:LYS:HG3	10:AJ:97:ASP:HB3	1.62	0.82
29:DH:94:ILE:HB	29:DH:122:LEU:HD12	1.60	0.82
29:BH:120:GLY:C	29:BH:122:LEU:CA	2.47	0.82
22:BA:84:A:H62	22:BA:101:A:H2	1.25	0.82
22:DA:370:G:N7	57:DA:3557:HOH:O	2.13	0.82
1:AA:1228:C:OP2	13:AM:107:ARG:NH2	2.13	0.82
1:CA:1266:G:N2	1:CA:1269:A:OP2	2.13	0.81
22:DA:1427:A:N6	22:DA:1571:A:OP2	2.13	0.81
4:CD:100:ASN:OD1	4:CD:111:ARG:NH1	2.12	0.81
5:CE:24:THR:HA	5:CE:29:ARG:HA	1.61	0.81
22:DA:2164:C:H2'	22:DA:2165:C:C6	2.16	0.81
49:B1:34:LEU:H	49:B1:52:ALA:HB3	1.43	0.81
45:DX:71:LEU:HA	45:DX:74:ARG:HG2	1.62	0.81
11:AK:17:SER:HA	11:AK:79:ILE:HA	1.61	0.81
26:BE:108:ILE:HD11	26:BE:180:LEU:HB3	1.62	0.81
12:AL:24:LEU:HG	12:AL:25:GLU:H	1.46	0.81
10:CJ:5:ARG:HG3	10:CJ:6:ILE:HG13	1.62	0.81
22:DA:136:G:H1	22:DA:143:C:H42	1.26	0.81
26:DE:76:PRO:HA	26:DE:82:GLY:HA2	1.61	0.81
26:DE:145:ASP:HB3	26:DE:184:ASP:HB2	1.63	0.80
22:BA:1746:A:H2'	22:BA:1747:U:C6	2.17	0.80
22:DA:2279:G:N7	44:DW:14:ARG:NH2	2.30	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:59:ASN:H	12:CL:59:ASN:HD22	1.29	0.80
2:AB:15:HIS:HB2	2:AB:209:ALA:HB2	1.64	0.80
22:DA:2343:U:HO2'	22:DA:2373:G:HO2'	1.28	0.80
22:BA:2199:A:H1'	29:BH:28:ASN:ND2	1.96	0.80
33:BL:99:ASN:ND2	57:BL:302:HOH:O	2.14	0.80
3:CC:40:ARG:HG2	3:CC:55:ILE:HD11	1.64	0.80
25:DD:33:ARG:NH2	25:DD:74:GLU:O	2.15	0.80
20:AT:67:ILE:HG13	20:AT:71:LYS:HG2	1.64	0.79
50:D2:9:VAL:O	50:D2:13:ASN:ND2	2.15	0.79
22:DA:514:A:N3	22:DA:581:C:O2'	2.14	0.79
22:BA:797:G:O6	57:BA:3323:HOH:O	2.01	0.79
24:DC:226:ASN:ND2	57:DC:303:HOH:O	2.15	0.79
22:BA:2029:G:N1	22:BA:2033:A:OP2	2.13	0.79
22:BA:842:U:O4	57:BA:3590:HOH:O	2.00	0.79
1:CA:537:G:OP1	12:CL:110:ARG:NH2	2.16	0.79
24:DC:157:SER:O	24:DC:160:THR:OG1	2.00	0.79
10:AJ:28:THR:HG22	10:AJ:86:ALA:HB1	1.64	0.79
21:CU:34:ARG:HE	21:CU:35:ARG:HB2	1.48	0.79
22:DA:1840:G:O6	22:DA:1902:C:N4	2.16	0.79
22:DA:1258:U:H2'	22:DA:1259:G:C8	2.18	0.78
2:AB:95:ARG:HH12	2:AB:97:LEU:HA	1.47	0.78
26:DE:52:VAL:HG21	26:DE:81:GLY:HA2	1.64	0.78
22:BA:1907:G:N1	22:BA:1923:U:O2	2.12	0.78
22:BA:1179:G:C5	22:BA:1180:U:H1'	2.18	0.78
22:DA:2627:G:O2'	22:DA:2781:A:N1	2.17	0.78
22:BA:1434:A:HO2'	22:BA:1435:G:H8	1.30	0.78
22:DA:783:A:O2'	22:DA:1779:U:O2	2.01	0.78
1:CA:1379:G:N2	1:CA:1381:U:O4	2.17	0.78
1:AA:142:G:H3'	1:AA:143:A:H8	1.48	0.78
29:BH:95:GLY:N	1:CA:368:U:OP1	2.16	0.78
29:BH:83:LYS:HD2	1:CA:55:A:C2'	2.14	0.78
22:BA:1287:A:H5'	35:BN:103:ARG:HD2	1.65	0.78
2:CB:221:VAL:O	2:CB:223:GLU:N	2.17	0.78
22:BA:761:A:OP1	57:BA:3697:HOH:O	2.03	0.77
38:BQ:49:ASP:HA	38:BQ:52:GLN:HB2	1.65	0.77
2:AB:41:ILE:HG21	2:AB:202:GLY:HA2	1.66	0.77
31:BJ:81:ILE:HG23	31:BJ:82:GLY:H	1.49	0.77
9:AI:24:GLY:H	9:AI:61:LEU:HA	1.49	0.77
2:CB:99:GLY:O	2:CB:103:ASN:N	2.16	0.77
6:CF:12:PRO:O	6:CF:15:SER:OG	2.03	0.77
18:CR:22:ASP:OD2	18:CR:24:LYS:NZ	2.17	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DH:124:THR:OG1	29:DH:125:THR:N	2.17	0.77
1:AA:278:G:OP2	17:AQ:43:LYS:NZ	2.14	0.77
30:DI:20:PRO:HB2	30:DI:23:PRO:HD2	1.66	0.77
30:DI:77:ALA:HA	30:DI:80:LEU:HD12	1.66	0.77
1:AA:405:U:O4	4:AD:2:ALA:N	2.18	0.77
39:DR:8:GLY:O	39:DR:10:LYS:NZ	2.16	0.77
22:BA:2198:A:C4	29:BH:29:PHE:HB2	2.19	0.77
28:BG:104:ASN:ND2	28:BG:114:ASP:OD1	2.17	0.77
22:BA:2131:U:H5'	22:BA:2132:U:H5''	1.67	0.77
4:CD:173:VAL:HG13	4:CD:174:ASP:H	1.49	0.77
1:CA:1074:G:H4'	2:CB:103:ASN:HB3	1.66	0.77
22:DA:197:A:H62	22:DA:2430:A:H2'	1.50	0.77
22:BA:2714:G:OP2	57:BA:3552:HOH:O	2.03	0.76
22:BA:2268:A:OP1	57:BA:3513:HOH:O	2.01	0.76
22:BA:674:G:H1'	26:BE:69:ARG:HD3	1.66	0.76
6:CF:9:MET:HG3	6:CF:86:ARG:HB2	1.66	0.76
22:BA:228:C:H4'	22:BA:229:C:H5''	1.65	0.76
17:CQ:21:ILE:N	17:CQ:48:ASP:OD1	2.19	0.76
22:BA:812:C:H4'	38:BQ:13:ARG:HH22	1.50	0.76
29:DH:1:MET:SD	29:DH:27:ARG:NH1	2.58	0.76
36:BO:31:THR:HG22	36:BO:34:HIS:H	1.50	0.76
22:DA:756:A:N7	57:DA:3298:HOH:O	2.18	0.76
20:AT:68:HIS:HB3	20:AT:69:LYS:HE3	1.67	0.76
29:DH:53:GLU:O	29:DH:55:GLU:N	2.19	0.76
53:B5:42:VAL:HG12	53:B5:214:TYR:HA	1.66	0.76
29:BH:86:ASP:N	1:CA:359:G:H4'	2.00	0.76
10:AJ:10:LEU:HB2	10:AJ:72:ARG:HB2	1.65	0.76
22:BA:2005:A:OP1	57:BA:3386:HOH:O	2.02	0.76
22:DA:2271:G:O6	57:DA:3506:HOH:O	2.02	0.76
22:DA:15:G:OP2	57:DA:3546:HOH:O	2.03	0.76
29:DH:45:GLU:O	29:DH:49:ALA:N	2.19	0.76
1:AA:1123:U:H4'	10:AJ:39:PRO:HD2	1.68	0.76
10:CJ:65:TYR:HB3	14:CN:96:LEU:HD11	1.69	0.75
4:AD:58:LYS:HG2	4:AD:203:LEU:HD22	1.69	0.75
29:DH:32:PRO:HB3	45:DX:39:TRP:HB3	1.69	0.75
22:BA:2507:C:OP1	57:BA:3716:HOH:O	2.03	0.75
35:DN:87:PHE:O	35:DN:89:SER:N	2.18	0.75
28:DG:170:ARG:NH1	52:D4:29:ALA:O	2.19	0.75
22:DA:602:A:HO2'	22:DA:604:G:HO2'	1.34	0.75
22:BA:946:C:OP2	57:BA:3350:HOH:O	2.04	0.75
22:DA:1064:C:H4'	30:DI:91:GLY:H	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2838:G:OP1	57:BA:3810:HOH:O	2.03	0.75
39:BR:49:ILE:HG22	39:BR:53:PHE:N	2.01	0.75
22:BA:194:G:N7	57:BA:3764:HOH:O	2.19	0.75
11:AK:34:ILE:HG13	11:AK:74:VAL:HG21	1.68	0.75
3:AC:77:ILE:HA	3:AC:84:VAL:HG23	1.69	0.75
22:DA:2438:U:O2'	22:DA:2440:C:OP1	2.05	0.75
5:CE:106:ILE:HD11	5:CE:124:LEU:HD23	1.67	0.75
21:AU:37:PHE:HB3	21:AU:41:PRO:HG3	1.66	0.75
22:BA:2305:U:C2	27:BF:151:GLY:HA3	2.22	0.75
42:DU:38:GLY:HA2	42:DU:41:LEU:HD21	1.68	0.75
22:DA:1378:A:O2'	57:DA:3751:HOH:O	2.03	0.75
22:DA:2507:C:OP1	57:DA:3708:HOH:O	2.04	0.75
1:AA:536:C:OP1	57:AA:1884:HOH:O	2.05	0.75
27:DF:111:ILE:HB	27:DF:114:PHE:HB2	1.67	0.74
54:D6:6:MHV:HE1	54:D6:7:004:HNA	1.50	0.74
1:CA:1513:A:H2'	1:CA:1514:G:H8	1.51	0.74
2:CB:163:VAL:HG23	2:CB:185:ALA:HB2	1.68	0.74
26:BE:106:LYS:HG3	26:BE:200:LEU:HG	1.68	0.74
26:DE:21:ARG:O	26:DE:114:ARG:NH2	2.19	0.74
22:BA:1439:A:OP2	57:BA:3636:HOH:O	2.05	0.74
29:BH:117:LEU:HD11	29:BH:122:LEU:HD12	1.69	0.74
35:BN:45:ARG:HG2	35:BN:95:THR:HG21	1.70	0.74
27:DF:58:ALA:HB2	27:DF:65:PRO:HD3	1.69	0.74
29:BH:88:GLY:O	29:BH:125:THR:OG1	2.04	0.74
22:DA:2164:C:H2'	22:DA:2165:C:H6	1.51	0.74
22:DA:297:G:H5''	42:DU:85:PHE:HB2	1.70	0.74
8:CH:64:LYS:HE2	8:CH:71:VAL:HG21	1.68	0.74
22:DA:1050:A:N6	22:DA:1109:C:O2	2.20	0.74
22:DA:1667:G:O2'	22:DA:1991:U:O4	2.04	0.74
22:DA:2010:G:N7	57:DA:3368:HOH:O	2.20	0.74
36:DO:51:ALA:HB3	36:DO:78:VAL:HG22	1.68	0.74
2:AB:99:GLY:O	2:AB:103:ASN:N	2.13	0.74
29:BH:123:ARG:C	29:BH:124:THR:HG23	2.06	0.74
22:BA:1179:G:H3'	22:BA:1180:U:H4'	1.70	0.74
22:BA:2611:C:OP2	57:BA:3546:HOH:O	2.06	0.74
44:DW:18:ALA:HB3	44:DW:20:ARG:HH21	1.50	0.74
22:DA:483:A:H1'	42:DU:45:HIS:HB2	1.69	0.74
37:DP:39:ARG:HG3	37:DP:40:LEU:H	1.52	0.74
1:AA:675:A:OP1	18:AR:74:HIS:NE2	2.20	0.74
1:CA:1001:C:H2'	1:CA:1002:G:C8	2.22	0.74
27:BF:4:LEU:HD11	27:BF:104:ILE:HD11	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BL:111:ILE:H	33:BL:111:ILE:HD12	1.51	0.74
22:BA:455:C:N3	22:BA:472:A:H2'	2.02	0.74
22:DA:450:G:O6	57:DA:3239:HOH:O	2.05	0.73
36:DO:49:VAL:HG21	36:DO:82:ALA:HA	1.70	0.73
35:DN:55:ALA:HB1	35:DN:80:PHE:H	1.53	0.73
22:BA:301:G:OP2	42:BU:82:ARG:NH1	2.22	0.73
22:BA:622:G:OP2	57:BA:3294:HOH:O	2.07	0.73
18:CR:25:ASP:O	18:CR:27:ALA:N	2.21	0.73
10:CJ:19:ASP:HA	10:CJ:22:THR:HB	1.70	0.73
1:AA:1166:G:N1	1:AA:1169:A:OP2	2.19	0.73
13:AM:14:HIS:HB2	13:AM:17:ILE:HD12	1.70	0.73
30:DI:32:GLY:HA3	30:DI:61:VAL:HG11	1.70	0.73
22:DA:1200:C:O2	22:DA:1245:G:N2	2.17	0.73
22:DA:1429:G:N7	24:DC:28:LYS:NZ	2.36	0.73
1:CA:1499:A:OP2	57:CA:1880:HOH:O	2.06	0.73
2:CB:54:LEU:HD12	2:CB:220:THR:HG21	1.69	0.73
27:DF:122:PHE:O	27:DF:124:GLY:N	2.22	0.73
5:CE:101:GLU:O	5:CE:103:THR:N	2.22	0.73
22:BA:1565:C:H3'	24:BC:18:LYS:NZ	2.03	0.73
22:BA:135:U:H3	22:BA:144:A:H61	1.37	0.73
22:BA:587:C:N3	33:BL:33:ARG:NH2	2.37	0.73
22:DA:618:G:O6	57:DA:3289:HOH:O	2.06	0.73
1:CA:1198:G:OP1	57:CA:1835:HOH:O	2.07	0.73
22:BA:2897:U:H2'	22:BA:2898:U:H6	1.54	0.73
26:BE:149:ILE:HD11	26:BE:172:ALA:HA	1.69	0.73
14:CN:41:ARG:NH1	14:CN:42:TRP:O	2.21	0.73
29:DH:27:ARG:HE	45:DX:60:ASP:CG	1.93	0.72
1:AA:1491:G:H5''	12:AL:43:LYS:HG3	1.71	0.72
22:BA:780:G:H21	22:BA:783:A:H62	1.37	0.72
22:BA:948:C:O2	22:BA:984:A:O2'	2.08	0.72
3:AC:36:ASP:OD1	3:AC:59:ARG:NH1	2.22	0.72
24:BC:107:PRO:HD2	24:BC:110:LEU:HD22	1.69	0.72
33:BL:29:LYS:HG2	33:BL:30:THR:HG23	1.70	0.72
1:CA:1198:G:N7	57:CA:1849:HOH:O	2.22	0.72
22:DA:1265:A:OP1	57:DA:3745:HOH:O	2.07	0.72
22:DA:668:A:N6	22:DA:670:A:O2'	2.22	0.72
22:BA:370:G:O2'	22:BA:424:G:OP1	2.06	0.72
33:BL:132:ARG:HG3	33:BL:142:ILE:HD13	1.71	0.72
27:DF:64:LYS:H	27:DF:64:LYS:HE2	1.54	0.72
22:DA:247:G:H4'	22:DA:386:G:C5	2.25	0.72
22:DA:2250:G:OP1	34:DM:84:LYS:NZ	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:7:A:N6	5:AE:97:GLN:OE1	2.22	0.72
30:BI:80:LEU:HA	30:BI:84:ALA:HB3	1.70	0.72
4:CD:54:GLN:HG2	4:CD:203:LEU:HB2	1.70	0.72
1:AA:1064:G:O2'	1:AA:1190:G:N2	2.22	0.72
22:DA:151:C:H2'	22:DA:152:A:C8	2.25	0.72
22:DA:471:A:OP1	26:DE:79:ARG:NH1	2.22	0.72
22:DA:206:U:H2'	22:DA:207:A:H8	1.54	0.72
25:BD:1:MET:HG3	25:BD:205:PRO:HG2	1.72	0.72
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.22	0.72
17:CQ:12:VAL:HG12	17:CQ:13:VAL:H	1.51	0.72
16:CP:42:ILE:O	16:CP:44:SER:N	2.21	0.72
17:CQ:52:GLU:HG2	17:CQ:53:CYS:H	1.53	0.72
22:BA:2066:C:OP1	57:BA:3512:HOH:O	2.07	0.72
1:CA:484:G:H4'	1:CA:485:U:O5'	1.90	0.72
7:CG:75:VAL:HG21	7:CG:144:MET:HG2	1.71	0.72
22:DA:2624:G:H1'	48:D0:19:HIS:CE1	2.24	0.72
29:DH:31:VAL:HB	29:DH:32:PRO:CD	2.20	0.72
32:BK:121:GLU:OE2	37:BP:65:SER:OG	2.07	0.72
4:AD:125:VAL:O	4:AD:127:GLY:N	2.21	0.72
1:CA:1124:G:O2'	1:CA:1145:A:N6	2.23	0.72
6:CF:1:MET:HG2	6:CF:65:GLU:HG2	1.71	0.72
13:AM:4:ILE:O	13:AM:6:GLY:N	2.23	0.72
3:CC:117:ALA:HB1	3:CC:187:SER:HB2	1.72	0.72
22:BA:1266:G:OP1	48:B0:16:ARG:NE	2.19	0.71
3:AC:54:ARG:HB3	3:AC:69:HIS:HB2	1.72	0.71
8:CH:75:ILE:HD13	8:CH:129:VAL:HG22	1.71	0.71
1:CA:683:G:N2	11:CK:39:GLY:O	2.22	0.71
4:CD:32:CYS:SG	4:CD:33:LYS:N	2.63	0.71
5:CE:89:HIS:CE1	5:CE:138:ARG:HD3	2.25	0.71
22:BA:1993:U:H4'	25:BD:133:THR:HG21	1.71	0.71
22:DA:1153:C:H5'	38:DQ:62:ILE:HD13	1.72	0.71
22:BA:447:A:OP2	57:BA:3210:HOH:O	2.08	0.71
22:BA:265:A:N1	22:BA:427:U:O2'	2.21	0.71
1:AA:1441:A:H62	1:AA:1461:G:H21	1.38	0.71
27:DF:131:GLY:HA2	27:DF:153:ASP:HA	1.71	0.71
22:BA:1869:G:H3'	22:BA:1870:C:H5'	1.70	0.71
12:AL:24:LEU:HB2	12:AL:59:ASN:HD22	1.55	0.71
1:AA:376:G:H1	1:AA:387:U:H3	1.38	0.71
22:DA:1251:C:OP2	38:DQ:6:ARG:NH2	2.22	0.71
22:BA:2430:A:H5'	22:BA:2431:U:OP2	1.90	0.71
13:CM:6:GLY:O	13:CM:8:ASN:N	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DP:29:LYS:HB3	37:DP:40:LEU:HD21	1.72	0.71
22:BA:2897:U:H2'	22:BA:2898:U:C6	2.25	0.71
8:AH:49:PHE:HB3	8:AH:61:LEU:HD23	1.73	0.71
19:AS:40:ILE:HG12	19:AS:71:LEU:HD23	1.73	0.71
26:DE:58:LYS:NZ	26:DE:70:SER:O	2.22	0.71
1:CA:728:A:H2'	1:CA:729:A:C8	2.24	0.71
22:DA:249:C:O5'	22:DA:2394:C:O2'	2.09	0.71
1:CA:8:A:C6	4:CD:206:LYS:HB3	2.26	0.71
22:DA:732:C:OP2	57:DA:3295:HOH:O	2.07	0.71
1:AA:537:G:OP1	12:AL:110:ARG:NH2	2.23	0.71
25:DD:121:THR:HG21	25:DD:143:PRO:HB3	1.72	0.71
22:BA:136:G:H1	22:BA:143:C:H42	1.36	0.71
22:DA:1378:A:O2'	22:DA:1380:G:N7	2.20	0.71
22:DA:733:G:OP2	57:DA:3293:HOH:O	2.09	0.71
25:BD:140:HIS:NE2	57:BD:302:HOH:O	1.98	0.71
22:DA:161:A:H3'	22:DA:162:U:H5''	1.73	0.71
1:CA:1458:G:H5'	20:CT:27:MET:HB3	1.73	0.71
22:BA:2278:A:OP1	34:BM:10:ARG:NH2	2.24	0.71
22:DA:449:A:OP2	57:DA:3240:HOH:O	2.08	0.71
48:B0:15:MET:O	48:B0:18:SER:HB3	1.91	0.71
42:DU:33:LYS:HB3	42:DU:64:ALA:HB1	1.71	0.71
7:AG:146:GLU:HA	7:AG:149:LYS:HB2	1.72	0.71
2:CB:193:PRO:O	2:CB:195:GLY:N	2.24	0.71
15:CO:25:THR:HG23	15:CO:66:LEU:HD12	1.73	0.71
29:BH:97:ARG:HH12	1:CA:369:G:H21	1.39	0.71
22:BA:2742:G:OP2	52:B4:24:ARG:NH1	2.24	0.71
1:CA:619:U:H3	4:CD:131:ASN:HB3	1.56	0.71
22:DA:1255:U:O2'	57:DA:3269:HOH:O	2.07	0.71
38:BQ:89:GLU:H	39:BR:49:ILE:HD12	1.56	0.70
22:BA:1265:A:OP1	57:BA:3753:HOH:O	2.07	0.70
19:CS:53:ASN:HB3	19:CS:75:ALA:HB1	1.73	0.70
1:AA:877:G:H21	8:AH:2:SER:N	1.89	0.70
22:BA:2151:U:H2'	22:BA:2152:G:C8	2.25	0.70
23:DB:34:A:N6	23:DB:44:G:O2'	2.24	0.70
37:BP:103:ARG:HG3	37:BP:103:ARG:HH11	1.56	0.70
1:CA:369:G:OP2	1:CA:388:G:N1	2.24	0.70
22:DA:822:G:OP2	57:DA:3345:HOH:O	2.09	0.70
28:DG:89:LEU:HB2	28:DG:129:THR:HG22	1.71	0.70
23:DB:57:A:H1'	27:DF:27:GLN:HA	1.71	0.70
1:AA:562:U:OP2	12:AL:14:ARG:NH1	2.24	0.70
22:DA:2046:G:OP1	48:D0:12:LYS:NZ	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CE:38:VAL:HG11	5:CE:114:VAL:HA	1.73	0.70
12:CL:68:GLY:O	12:CL:99:ARG:NH1	2.23	0.70
1:AA:131:A:H2'	1:AA:132:C:C6	2.27	0.70
1:CA:1500:A:OP2	57:CA:1880:HOH:O	2.09	0.70
6:AF:46:GLN:HB2	6:AF:56:LYS:HE2	1.73	0.70
29:BH:83:LYS:CD	1:CA:55:A:C2'	2.69	0.70
29:BH:123:ARG:HH12	1:CA:366:A:H5''	1.56	0.70
22:DA:740:C:H5'	22:DA:1784:A:H3'	1.72	0.70
22:BA:1808:A:O2'	45:BX:3:ARG:NH1	2.25	0.70
51:B3:17:THR:OG1	51:B3:18:GLY:N	2.19	0.70
22:DA:1010:A:OP2	57:DA:3778:HOH:O	2.10	0.70
22:BA:273:G:N2	22:BA:365:U:O2	2.23	0.70
22:DA:833:A:H2'	22:DA:834:G:C8	2.26	0.70
35:DN:83:LEU:HD21	35:DN:115:LEU:HD13	1.74	0.70
1:CA:736:C:OP1	18:CR:61:ARG:NH1	2.24	0.70
20:AT:67:ILE:HD11	20:AT:71:LYS:HE3	1.72	0.70
2:CB:103:ASN:ND2	2:CB:106:THR:OG1	2.25	0.70
1:CA:811:C:O2'	1:CA:901:A:N1	2.24	0.70
22:DA:1709:U:H2'	22:DA:1710:G:H8	1.54	0.70
1:CA:858:G:N7	57:CA:1817:HOH:O	2.25	0.70
1:AA:1161:C:H2'	1:AA:1162:C:H6	1.55	0.70
22:DA:1010:A:N7	57:DA:3776:HOH:O	2.23	0.70
34:DM:66:ARG:NH1	34:DM:104:GLU:OE1	2.25	0.70
2:CB:33:GLY:HA2	2:CB:40:ILE:H	1.55	0.70
32:DK:30:ARG:NH2	32:DK:37:ASP:OD1	2.23	0.70
33:DL:20:GLY:HA2	33:DL:28:GLY:HA2	1.74	0.70
22:DA:381:G:OP1	45:DX:18:ARG:NH2	2.25	0.70
29:BH:94:ILE:HG22	29:BH:99:ILE:HG13	1.72	0.70
17:CQ:48:ASP:N	17:CQ:48:ASP:OD2	2.20	0.70
22:DA:1709:U:H2'	22:DA:1710:G:C8	2.26	0.70
22:DA:1248:G:C4	38:DQ:3:ARG:HG3	2.26	0.70
22:DA:2899:A:H2'	22:DA:2900:A:C8	2.27	0.70
1:CA:1047:G:H1	1:CA:1210:C:H42	1.37	0.70
22:BA:2199:A:H4'	29:BH:28:ASN:OD1	1.91	0.69
22:DA:1380:G:OP2	57:DA:3751:HOH:O	2.08	0.69
22:DA:1325:U:OP1	22:DA:1647:U:O2'	2.08	0.69
1:AA:989:U:H2'	1:AA:990:C:H6	1.57	0.69
22:DA:228:C:H4'	22:DA:229:C:H5''	1.74	0.69
15:CO:19:ALA:O	15:CO:20:ASN:HB2	1.92	0.69
14:AN:31:ILE:HG23	14:AN:45:VAL:HB	1.74	0.69
22:BA:686:U:H2'	22:BA:788:A:N1	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CJ:46:LYS:HG2	10:CJ:68:ARG:HG2	1.74	0.69
22:BA:1799:G:OP2	24:BC:270:ARG:NH2	2.21	0.69
22:BA:2199:A:C1'	29:BH:28:ASN:HD21	2.05	0.69
1:CA:933:G:N7	7:CG:3:ARG:NH2	2.39	0.69
30:BI:83:ALA:HB1	30:BI:109:ILE:HD13	1.73	0.69
23:DB:28:C:OP1	36:DO:36:TYR:OH	2.07	0.69
2:AB:96:TRP:HZ2	2:AB:101:LEU:HD23	1.57	0.69
22:DA:833:A:H2'	22:DA:834:G:H8	1.57	0.69
22:DA:587:C:OP2	33:DL:21:ARG:NH1	2.24	0.69
1:CA:1513:A:H2'	1:CA:1514:G:C8	2.27	0.69
46:BY:9:LYS:HB3	46:BY:12:GLU:HG3	1.73	0.69
16:AP:4:ILE:HG12	16:AP:21:VAL:HG22	1.75	0.69
33:DL:56:PRO:HD2	33:DL:59:ARG:HB2	1.73	0.69
43:DV:48:MET:O	43:DV:51:GLN:NE2	2.25	0.69
10:AJ:57:VAL:HG22	10:AJ:58:ASN:H	1.57	0.69
8:CH:53:GLY:HA3	8:CH:57:PRO:HA	1.75	0.69
2:CB:203:ASN:OD1	2:CB:204:ASP:N	2.26	0.69
22:DA:2262:U:OP1	44:DW:41:ARG:NH2	2.26	0.69
22:DA:2243:U:OP1	57:DA:3736:HOH:O	2.11	0.69
22:BA:1171:G:N2	22:BA:1178:C:O2	2.25	0.69
24:BC:107:PRO:HB3	24:BC:142:HIS:CE1	2.28	0.69
1:CA:738:C:H2'	1:CA:739:C:H6	1.58	0.69
13:CM:33:ILE:HD13	13:CM:59:GLU:HB3	1.75	0.69
23:DB:48:U:H4'	36:DO:100:HIS:CD2	2.28	0.69
22:BA:2455:G:O6	57:BA:3532:HOH:O	2.09	0.69
1:CA:1049:U:OP1	57:CA:1843:HOH:O	2.11	0.69
6:CF:9:MET:HB2	6:CF:85:ILE:HG13	1.73	0.69
22:DA:1619:G:N7	57:DA:3641:HOH:O	2.25	0.69
1:CA:890:G:O2'	1:CA:906:A:N6	2.25	0.69
1:AA:532:A:N6	3:AC:192:THR:OG1	2.25	0.69
29:BH:91:PHE:CD1	1:CA:358:U:H1'	2.28	0.69
22:BA:2093:G:H4'	29:BH:25:TYR:N	2.08	0.69
1:CA:978:A:OP2	1:CA:1362:A:N6	2.26	0.69
22:DA:587:C:N3	33:DL:33:ARG:NH2	2.40	0.69
4:AD:32:CYS:SG	4:AD:33:LYS:N	2.66	0.69
10:CJ:6:ILE:HD12	10:CJ:76:ILE:HB	1.75	0.68
22:BA:1563:U:H2'	22:BA:1564:C:C6	2.28	0.68
22:DA:1395:A:OP2	57:DA:3400:HOH:O	2.10	0.68
22:BA:192:C:OP1	57:BA:3745:HOH:O	2.11	0.68
26:BE:31:VAL:HG21	26:BE:104:ALA:HB2	1.75	0.68
22:BA:1070:A:O2'	22:BA:1097:U:OP1	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CE:150:PRO:HD2	5:CE:151:GLU:HG2	1.74	0.68
35:DN:90:ARG:CZ	35:DN:116:VAL:HG11	2.23	0.68
22:DA:2720:U:OP1	37:DP:53:ARG:NH2	2.27	0.68
17:AQ:12:VAL:HB	17:AQ:56:GLY:H	1.57	0.68
25:DD:12:THR:OG1	25:DD:13:ARG:N	2.25	0.68
10:AJ:10:LEU:HG	10:AJ:98:VAL:HG12	1.75	0.68
22:DA:602:A:O2'	22:DA:604:G:O2'	2.07	0.68
22:BA:349:U:H2'	22:BA:350:G:H8	1.58	0.68
53:B5:64:SER:O	53:B5:65:LEU:HB2	1.92	0.68
22:BA:997:G:OP1	38:BQ:92:ARG:HG3	1.94	0.68
31:DJ:40:HIS:HE1	31:DJ:41:LYS:HE3	1.58	0.68
48:D0:43:ILE:HG22	48:D0:49:TYR:HB2	1.75	0.68
1:AA:620:C:H1'	4:AD:132:ILE:HD11	1.74	0.68
22:BA:2579:C:OP1	57:BA:3544:HOH:O	2.11	0.68
19:CS:11:ILE:HG22	19:CS:39:THR:H	1.57	0.68
22:DA:1602:U:O4	57:DA:3710:HOH:O	2.09	0.68
45:DX:27:ARG:NE	45:DX:28:ARG:O	2.26	0.68
6:AF:98:GLU:HG3	6:AF:99:ALA:H	1.57	0.68
1:CA:1305:G:N7	57:CA:1866:HOH:O	2.25	0.68
23:BB:8:C:O3'	36:BO:25:ARG:NH1	2.23	0.68
2:AB:136:MET:N	2:AB:136:MET:SD	2.67	0.68
27:BF:108:VAL:HG11	27:BF:176:PRO:HG2	1.75	0.68
22:BA:2286:G:OP2	49:B1:6:ARG:NH2	2.27	0.68
53:B5:43:GLU:HA	53:B5:178:LYS:HA	1.75	0.68
4:AD:22:LYS:O	4:AD:24:GLY:N	2.27	0.68
18:AR:34:THR:OG1	18:AR:35:GLU:N	2.27	0.68
22:DA:2162:G:H4'	22:DA:2163:A:OP1	1.94	0.68
4:AD:59:GLN:O	4:AD:63:ARG:HG2	1.94	0.68
2:AB:138:THR:HA	2:AB:141:LEU:HB2	1.74	0.68
22:DA:2469:A:H4'	34:DM:55:ARG:HD3	1.75	0.68
42:DU:11:VAL:HG12	42:DU:72:ILE:HA	1.74	0.68
22:BA:2575:C:OP2	57:BA:3715:HOH:O	2.10	0.68
1:CA:216:U:H4'	1:CA:464:U:H4'	1.74	0.68
10:CJ:36:VAL:HG12	10:CJ:38:GLY:H	1.59	0.68
30:BI:77:ALA:HA	30:BI:80:LEU:HD12	1.76	0.68
23:BB:30:C:OP1	36:BO:3:LYS:NZ	2.26	0.68
22:DA:1469:A:H2'	22:DA:1470:A:C8	2.29	0.68
1:CA:337:G:H2'	1:CA:338:A:C8	2.28	0.68
1:CA:405:U:O4	4:CD:2:ALA:N	2.27	0.68
22:BA:14:A:OP2	57:BA:3555:HOH:O	2.11	0.68
15:AO:30:ALA:HA	15:AO:85:LEU:HD21	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BG:124:GLU:CD	28:BG:125:CYS:H	1.97	0.67
1:AA:1015:G:H21	1:AA:1218:C:H1'	1.59	0.67
1:CA:532:A:N6	3:CC:192:THR:OG1	2.26	0.67
21:CU:37:PHE:HA	21:CU:40:LYS:HE3	1.77	0.67
25:BD:129:THR:HG22	25:BD:130:GLN:O	1.94	0.67
39:BR:24:LYS:HA	39:BR:94:THR:HG23	1.75	0.67
1:AA:973:G:H1'	10:AJ:56:HIS:CD2	2.27	0.67
7:AG:135:VAL:HB	7:AG:138:ARG:HH21	1.59	0.67
30:BI:108:GLU:HA	30:BI:111:GLN:HB3	1.76	0.67
22:BA:487:C:O2	40:BS:53:SER:OG	2.13	0.67
2:CB:35:ARG:O	2:CB:38:VAL:N	2.26	0.67
37:DP:91:ALA:HB2	37:DP:113:ARG:HA	1.74	0.67
29:BH:122:LEU:HD23	29:BH:123:ARG:N	2.10	0.67
26:BE:108:ILE:HD13	26:BE:181:ILE:HG12	1.76	0.67
22:DA:1638:C:H4'	22:DA:2710:C:O2	1.94	0.67
1:CA:439:U:H4'	4:CD:121:LYS:HG3	1.74	0.67
3:AC:25:ASN:O	3:AC:27:LYS:N	2.27	0.67
30:DI:90:SER:HB3	30:DI:93:PRO:HG3	1.77	0.67
1:AA:1161:C:H2'	1:AA:1162:C:C6	2.29	0.67
22:BA:1260:A:N6	57:BA:3278:HOH:O	2.27	0.67
5:AE:142:ASP:HA	5:AE:145:GLU:HB3	1.75	0.67
22:BA:2800:A:H3'	22:BA:2801:G:H5'	1.76	0.67
3:AC:53:SER:HB3	3:AC:115:LEU:HG	1.76	0.67
26:BE:189:THR:HG22	26:BE:192:ALA:H	1.60	0.67
35:BN:55:ALA:HB1	35:BN:80:PHE:H	1.59	0.67
22:BA:617:G:N7	57:BA:3289:HOH:O	2.27	0.67
22:DA:2291:U:H2'	22:DA:2292:U:C6	2.30	0.67
16:AP:22:ALA:HA	16:AP:33:ILE:HG13	1.76	0.67
24:BC:123:ALA:O	24:BC:128:ASN:ND2	2.25	0.67
22:DA:784:G:OP1	57:DA:3312:HOH:O	2.12	0.67
22:DA:1817:G:OP1	24:DC:62:TYR:OH	2.05	0.67
2:CB:141:LEU:O	2:CB:145:GLU:N	2.26	0.67
11:CK:87:LYS:HA	11:CK:114:THR:HG22	1.76	0.67
22:BA:1794:A:H2'	22:BA:1795:C:H6	1.60	0.67
5:CE:156:LYS:HD2	8:CH:71:VAL:HG13	1.76	0.67
24:DC:147:LYS:HB2	24:DC:150:LYS:HB2	1.77	0.67
6:CF:91:ARG:O	6:CF:92:THR:OG1	2.13	0.67
39:DR:58:VAL:HG13	39:DR:102:SER:HB2	1.75	0.67
22:DA:2058:A:N7	57:DA:3484:HOH:O	2.27	0.67
6:AF:1:MET:HG2	6:AF:65:GLU:HG2	1.75	0.67
5:CE:157:ARG:O	5:CE:159:LYS:N	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DN:76:VAL:HA	35:DN:79:LEU:HD12	1.77	0.67
13:CM:54:ASP:HA	13:CM:57:ARG:HB3	1.77	0.67
25:BD:103:ASP:O	25:BD:105:LYS:N	2.27	0.67
22:BA:1131:G:OP1	31:BJ:82:GLY:HA2	1.94	0.67
16:AP:75:ILE:HG22	16:AP:80:LYS:HE2	1.77	0.67
1:AA:965:U:OP2	57:AA:1832:HOH:O	2.12	0.67
22:DA:761:A:OP2	57:DA:3292:HOH:O	2.12	0.67
12:CL:65:SER:HB2	12:CL:82:ILE:HD11	1.75	0.67
22:DA:684:G:OP1	50:D2:16:HIS:ND1	2.19	0.67
29:BH:27:ARG:O	29:BH:28:ASN:HB2	1.95	0.67
22:DA:1269:A:OP2	57:DA:3381:HOH:O	2.12	0.67
22:BA:1667:G:O2'	22:BA:1991:U:O4	2.12	0.67
22:DA:310:A:H5''	42:DU:15:THR:HG22	1.76	0.67
41:BT:67:VAL:HG22	41:BT:76:ARG:HG3	1.76	0.66
22:DA:1607:C:N4	22:DA:1622:G:N7	2.42	0.66
2:AB:82:ASP:O	2:AB:85:LEU:N	2.29	0.66
12:AL:24:LEU:O	12:AL:26:ALA:N	2.28	0.66
1:AA:601:G:H2'	1:AA:602:A:C8	2.30	0.66
22:DA:84:A:H62	22:DA:101:A:H2	1.40	0.66
22:BA:752:A:H62	22:BA:2609:U:H3	1.43	0.66
12:CL:7:LEU:HD22	12:CL:12:ARG:HD2	1.77	0.66
36:DO:110:ALA:HB3	36:DO:117:PHE:HE2	1.60	0.66
1:AA:263:A:P	20:AT:74:ARG:HH12	2.19	0.66
22:DA:2171:A:O2'	22:DA:2173:A:OP1	2.13	0.66
1:AA:1348:U:H4'	9:AI:122:ARG:HG3	1.77	0.66
1:AA:1040:U:H2'	1:AA:1041:G:C8	2.31	0.66
9:CI:52:LEU:HD13	9:CI:57:MET:HG2	1.77	0.66
22:BA:1909:C:O2	22:BA:1921:G:N2	2.27	0.66
1:CA:86:G:H1'	1:CA:87:C:O4'	1.94	0.66
13:CM:107:ARG:HH22	13:CM:110:LYS:HE2	1.60	0.66
8:AH:10:MET:HE1	8:AH:33:LYS:HA	1.77	0.66
29:BH:94:ILE:CG2	29:BH:99:ILE:HG13	2.26	0.66
22:BA:2267:A:H5''	22:BA:2268:A:H5'	1.78	0.66
22:BA:2291:U:H2'	22:BA:2292:U:C6	2.30	0.66
9:AI:57:MET:SD	9:AI:58:VAL:N	2.67	0.66
24:BC:39:LYS:HE3	24:BC:55:GLY:HA2	1.78	0.66
9:AI:90:TYR:HB3	9:AI:94:LEU:HD21	1.76	0.66
2:AB:213:TYR:O	2:AB:217:VAL:HG23	1.94	0.66
9:AI:25:ASN:HB2	9:AI:27:LYS:HG2	1.77	0.66
46:DY:9:LYS:H	46:DY:12:GLU:HG3	1.61	0.66
22:BA:587:C:OP2	33:BL:21:ARG:NH1	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:729:G:OP2	24:DC:207:LYS:NZ	2.24	0.66
22:BA:2485:G:OP1	34:BM:45:GLN:NE2	2.28	0.66
41:DT:14:PRO:HD2	46:DY:33:ALA:HB1	1.78	0.66
2:AB:73:LYS:O	2:AB:75:ALA:N	2.27	0.66
4:CD:59:GLN:O	4:CD:63:ARG:HG3	1.95	0.66
22:BA:197:A:H62	22:BA:2430:A:H2'	1.60	0.66
35:BN:24:MET:HE3	35:BN:44:LEU:HD13	1.78	0.66
21:AU:4:ILE:HA	21:AU:20:LYS:HE3	1.76	0.66
1:AA:1358:U:H3	1:AA:1363:A:H62	1.43	0.66
9:AI:45:ARG:HG2	9:AI:46:MET:SD	2.36	0.66
1:AA:1182:G:H4'	1:AA:1183:U:H5'	1.78	0.66
16:AP:77:GLU:C	16:AP:79:ASN:H	1.99	0.66
22:BA:517:C:OP2	48:B0:10:ARG:NH2	2.29	0.66
22:DA:2788:C:H2'	22:DA:2789:C:C6	2.31	0.66
37:BP:93:ARG:O	37:BP:94:LYS:HB2	1.95	0.66
22:BA:2327:A:H2'	22:BA:2328:A:C8	2.30	0.66
29:BH:14:SER:O	29:BH:15:LEU:HB2	1.95	0.66
2:CB:73:LYS:O	2:CB:75:ALA:N	2.29	0.66
33:BL:87:GLY:O	33:BL:89:VAL:N	2.29	0.66
22:BA:612:G:H4'	22:BA:613:A:C2	2.31	0.66
6:AF:29:ILE:HD13	6:AF:64:VAL:HG11	1.77	0.66
22:BA:181:A:H2'	22:BA:182:A:C8	2.31	0.66
2:CB:10:LEU:HD12	2:CB:43:LEU:HD22	1.76	0.66
43:BV:13:GLY:O	43:BV:17:SER:OG	2.14	0.66
22:BA:2128:G:H2'	22:BA:2129:C:O4'	1.96	0.66
5:AE:15:LEU:HB3	5:AE:37:THR:HG22	1.78	0.65
40:DS:73:LYS:HB2	40:DS:106:VAL:HB	1.78	0.65
20:CT:25:ARG:O	20:CT:29:ARG:HG2	1.96	0.65
50:D2:43:THR:O	50:D2:44:VAL:HB	1.96	0.65
1:CA:1323:G:O2'	1:CA:1362:A:N3	2.27	0.65
11:AK:74:VAL:C	11:AK:76:GLU:H	1.99	0.65
22:DA:2609:U:H6	54:D6:7:004:HA	1.61	0.65
1:AA:376:G:H5''	16:AP:5:ARG:HB3	1.79	0.65
19:AS:51:VAL:HG22	19:AS:71:LEU:HD13	1.76	0.65
22:BA:627:A:OP1	33:BL:78:ARG:NH1	2.28	0.65
22:DA:1789:A:H5''	24:DC:219:THR:O	1.96	0.65
33:DL:136:GLU:HA	33:DL:140:GLY:HA3	1.77	0.65
22:BA:281:C:H2'	22:BA:282:A:C8	2.30	0.65
22:DA:2498:C:OP2	57:DA:3681:HOH:O	2.13	0.65
1:AA:1238:A:H5'	1:AA:1336:C:H41	1.60	0.65
3:CC:143:ARG:HG2	3:CC:144:LEU:HD13	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:194:G:OP2	57:BA:3765:HOH:O	2.14	0.65
30:BI:86:ILE:HD13	30:BI:89:GLY:HA2	1.78	0.65
22:BA:1073:A:H3'	22:BA:1074:G:C5'	2.25	0.65
12:AL:24:LEU:HB2	12:AL:59:ASN:ND2	2.11	0.65
15:CO:89:ARG:NH1	22:DA:716:A:OP1	2.29	0.65
3:AC:58:GLU:HG3	3:AC:65:ARG:HB3	1.78	0.65
22:BA:1056:G:H5''	22:BA:1057:A:H5'	1.77	0.65
15:CO:64:ARG:NH1	15:CO:68:ASP:OD2	2.26	0.65
1:CA:1273:C:H2'	1:CA:1274:A:O4'	1.97	0.65
11:AK:69:ARG:HH11	22:BA:2146:C:H42	1.45	0.65
34:DM:49:ALA:HB2	34:DM:123:LYS:HB2	1.79	0.65
24:BC:107:PRO:HB3	24:BC:142:HIS:HE1	1.62	0.65
1:CA:403:C:OP1	4:CD:134:SER:HB3	1.97	0.65
29:BH:114:GLU:HB3	29:BH:133:GLN:O	1.97	0.65
1:AA:1077:G:N7	57:AA:1789:HOH:O	2.28	0.65
22:DA:2134:A:H62	22:DA:2157:G:H1'	1.60	0.65
29:BH:122:LEU:C	29:BH:123:ARG:HG2	2.17	0.65
29:BH:89:LYS:CB	1:CA:359:G:H5''	2.21	0.65
22:BA:2820:A:OP1	57:BA:3811:HOH:O	2.15	0.65
22:DA:1992:G:N2	22:DA:1996:C:O2'	2.30	0.65
40:DS:4:ILE:HG12	40:DS:106:VAL:HG22	1.77	0.65
26:DE:131:THR:HA	26:DE:160:ALA:HB1	1.78	0.65
39:DR:61:ALA:HB2	39:DR:98:ILE:HD13	1.78	0.65
35:BN:79:LEU:O	35:BN:81:ASN:N	2.30	0.65
12:AL:21:VAL:HG23	12:AL:95:TYR:CE1	2.31	0.65
2:CB:21:ARG:O	2:CB:23:TRP:N	2.27	0.65
1:AA:79:G:H2'	1:AA:80:A:H8	1.61	0.65
4:CD:35:GLU:O	4:CD:37:ALA:N	2.24	0.65
29:BH:139:PHE:O	29:BH:140:ALA:CB	2.44	0.65
22:BA:2243:U:OP1	57:BA:3748:HOH:O	2.14	0.65
1:CA:801:U:H2'	1:CA:802:A:H8	1.59	0.65
1:AA:1422:G:O3'	32:BK:49:ARG:NH2	2.29	0.65
51:B3:31:HIS:CD2	51:B3:32:ILE:HG13	2.31	0.65
38:BQ:88:VAL:HG13	39:BR:49:ILE:HD11	1.79	0.65
6:AF:46:GLN:HA	6:AF:56:LYS:HG2	1.79	0.65
22:DA:1035:U:H2'	22:DA:1036:G:H8	1.62	0.65
1:CA:1296:C:H4'	1:CA:1302:C:N4	2.12	0.65
22:BA:1796:U:H2'	22:BA:1797:G:H8	1.62	0.65
3:AC:140:ASN:HA	3:AC:143:ARG:HB3	1.78	0.65
14:AN:91:GLY:O	14:AN:93:ILE:N	2.30	0.65
3:AC:16:LYS:HG3	3:AC:17:PRO:HD2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:398:C:OP1	45:DX:32:ASN:ND2	2.30	0.65
1:CA:1540:U:O3'	21:CU:18:ARG:NE	2.30	0.65
43:BV:36:ALA:O	43:BV:93:ARG:NH2	2.28	0.65
28:BG:90:VAL:HG21	28:BG:163:ARG:HE	1.61	0.65
22:BA:1364:G:OP2	45:BX:2:SER:N	2.29	0.65
4:CD:201:VAL:HG11	5:CE:103:THR:HB	1.78	0.64
22:BA:1936:A:H2	22:BA:1943:U:N3	1.94	0.64
22:BA:1916:A:H2'	22:BA:1917:U:O4'	1.96	0.64
22:DA:1094:U:H2'	22:DA:1096:A:OP2	1.96	0.64
27:BF:158:THR:HG22	27:BF:160:ALA:H	1.62	0.64
13:AM:11:ASP:OD1	13:AM:12:HIS:N	2.30	0.64
33:BL:68:SER:OG	33:BL:69:ARG:N	2.29	0.64
9:AI:38:TYR:HD2	9:AI:39:PHE:HD2	1.45	0.64
21:AU:37:PHE:HA	21:AU:40:LYS:HE3	1.79	0.64
22:DA:777:G:N7	22:DA:793:A:H2	1.96	0.64
24:DC:123:ALA:O	24:DC:128:ASN:ND2	2.29	0.64
22:DA:2054:A:OP1	22:DA:2055:C:O2'	2.14	0.64
22:DA:1476:U:H1'	22:DA:1732:C:C2	2.31	0.64
1:CA:651:C:N4	1:CA:753:A:OP2	2.29	0.64
34:BM:42:THR:HG22	34:BM:93:VAL:HG12	1.79	0.64
4:CD:88:GLU:HG2	4:CD:188:ARG:HD3	1.79	0.64
22:BA:245:G:O6	51:B3:8:ARG:HD3	1.98	0.64
22:BA:2461:A:H2'	22:BA:2462:C:C6	2.32	0.64
22:DA:2328:A:H2'	22:DA:2329:U:C6	2.33	0.64
4:AD:32:CYS:O	4:AD:33:LYS:HB2	1.97	0.64
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.79	0.64
24:DC:145:GLU:HG2	24:DC:152:GLY:N	2.12	0.64
25:BD:13:ARG:HD3	25:BD:21:SER:OG	1.96	0.64
21:CU:25:LYS:HD3	21:CU:26:ALA:H	1.62	0.64
7:CG:27:VAL:HG12	7:CG:43:VAL:HG21	1.79	0.64
1:CA:464:U:N3	1:CA:467:U:OP2	2.27	0.64
22:DA:1097:U:C5	22:DA:1098:A:H1'	2.33	0.64
22:DA:17:G:H4'	38:DQ:25:TYR:CE1	2.33	0.64
22:DA:1344:U:O2'	22:DA:1345:C:OP2	2.15	0.64
22:DA:2852:G:H5'	35:DN:64:ARG:HH22	1.63	0.64
22:DA:1808:A:N1	45:DX:28:ARG:HD2	2.12	0.64
22:DA:2136:G:N1	22:DA:2156:G:H1'	2.12	0.64
1:CA:757:U:OP1	1:CA:822:U:O2'	2.15	0.64
22:BA:580:U:H2'	22:BA:581:C:H6	1.61	0.64
20:CT:43:ASP:HB3	20:CT:46:ALA:HB3	1.78	0.64
51:D3:15:LYS:HD3	51:D3:23:LYS:HE2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:11:LEU:HD22	4:AD:63:ARG:HD3	1.80	0.64
38:BQ:76:TYR:OH	38:BQ:92:ARG:NH1	2.30	0.64
11:CK:25:ALA:HA	11:CK:30:THR:HG22	1.80	0.64
22:BA:465:G:H2'	22:BA:466:A:C8	2.32	0.64
11:CK:17:SER:O	11:CK:80:LYS:N	2.30	0.64
22:BA:2311:A:N3	27:BF:85:ILE:HD11	2.13	0.64
22:DA:2210:U:H4'	22:DA:2211:A:H5'	1.79	0.64
22:BA:2243:U:OP1	57:BA:3745:HOH:O	2.15	0.64
24:DC:72:ASP:O	24:DC:74:ILE:N	2.25	0.64
2:AB:163:VAL:HG13	2:AB:185:ALA:HB2	1.80	0.64
28:DG:38:ASN:HB3	28:DG:41:VAL:HG23	1.79	0.64
12:CL:74:LEU:HD11	12:CL:80:ILE:HG21	1.80	0.64
22:DA:1342:A:OP2	57:DA:3710:HOH:O	2.15	0.64
1:AA:1031:C:H4'	1:AA:1032:G:H5''	1.80	0.64
48:B0:10:ARG:HB2	48:B0:13:ARG:HH21	1.61	0.64
1:CA:451:A:H61	1:CA:481:G:H5'	1.62	0.64
1:CA:929:G:H5''	1:CA:1535:C:H5''	1.78	0.64
41:DT:73:ARG:NH1	41:DT:74:ILE:O	2.30	0.64
24:DC:70:ASN:O	24:DC:72:ASP:N	2.31	0.64
22:BA:361:G:OP2	22:BA:361:G:H8	1.81	0.64
22:DA:2817:U:O2	22:DA:2836:U:H1'	1.98	0.64
22:DA:341:C:H2'	22:DA:342:A:C8	2.31	0.64
22:DA:2004:G:OP2	57:DA:3802:HOH:O	2.15	0.64
1:CA:1291:U:OP1	7:CG:37:SER:HB3	1.97	0.64
29:DH:117:LEU:CD1	29:DH:130:VAL:HG22	2.28	0.64
14:CN:51:LEU:O	14:CN:53:ARG:N	2.31	0.64
22:DA:1809:A:H2'	22:DA:1810:A:C8	2.33	0.64
4:AD:58:LYS:HB3	4:AD:200:ILE:HB	1.80	0.64
1:CA:1279:G:OP2	10:CJ:11:LYS:NZ	2.31	0.64
22:DA:2750:A:O2'	22:DA:2752:C:N4	2.32	0.64
1:CA:748:G:H2'	1:CA:749:A:C8	2.33	0.64
28:DG:98:VAL:HG21	28:DG:124:GLU:HA	1.78	0.64
1:CA:1391:U:H2'	1:CA:1392:G:C8	2.33	0.64
1:CA:798:U:O4	57:CA:1805:HOH:O	2.11	0.64
22:BA:1250:G:OP2	33:BL:21:ARG:NH2	2.31	0.63
22:BA:1746:A:H2'	22:BA:1747:U:H6	1.59	0.63
22:DA:197:A:N6	22:DA:2430:A:H2'	2.13	0.63
27:BF:73:SER:HB2	27:BF:81:GLN:H	1.63	0.63
20:CT:70:ASN:O	20:CT:74:ARG:N	2.25	0.63
1:CA:214:C:H2'	1:CA:215:C:C6	2.33	0.63
28:BG:149:ARG:NH2	28:BG:167:GLU:OE2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DN:96:ARG:HH11	35:DN:116:VAL:HG22	1.63	0.63
22:BA:197:A:N6	22:BA:2430:A:H2'	2.13	0.63
22:BA:39:G:H2'	22:BA:40:U:C6	2.33	0.63
9:AI:118:LEU:HA	9:AI:125:PRO:HD3	1.78	0.63
34:BM:18:ARG:HH21	34:BM:18:ARG:HG2	1.64	0.63
7:CG:145:ALA:O	7:CG:146:GLU:HB2	1.97	0.63
16:AP:7:ALA:O	16:AP:9:HIS:N	2.30	0.63
29:BH:83:LYS:CG	1:CA:55:A:N3	2.55	0.63
5:CE:81:LEU:HA	5:CE:147:MET:HE3	1.80	0.63
19:AS:32:ARG:HA	19:AS:50:ALA:HB3	1.81	0.63
22:DA:411:G:OP2	22:DA:2406:A:O2'	2.13	0.63
1:AA:1004:A:H2'	1:AA:1005:A:O4'	1.98	0.63
20:AT:6:SER:OG	20:AT:7:ALA:N	2.31	0.63
3:CC:9:GLY:HA2	3:CC:12:LEU:HG	1.81	0.63
30:DI:39:CYS:HA	30:DI:42:PHE:HB3	1.80	0.63
11:AK:83:GLU:HG3	11:AK:109:ASN:HD22	1.63	0.63
2:AB:148:LEU:HD22	2:AB:151:ILE:HG21	1.81	0.63
22:DA:1847:A:O2'	22:DA:1848:A:H8	1.78	0.63
13:CM:11:ASP:OD1	13:CM:12:HIS:N	2.32	0.63
2:AB:27:MET:HG2	2:AB:189:THR:HA	1.80	0.63
25:BD:33:ARG:NH1	25:BD:53:GLY:O	2.32	0.63
3:CC:72:ARG:HB3	3:CC:75:ILE:HG22	1.80	0.63
22:DA:848:C:H2'	22:DA:849:A:H8	1.64	0.63
32:DK:7:MET:HE1	32:DK:20:MET:HB2	1.79	0.63
50:D2:34:ARG:HB2	50:D2:42:LEU:HD13	1.80	0.63
1:AA:600:A:H2'	1:AA:601:G:C8	2.34	0.63
29:DH:117:LEU:HG	29:DH:120:GLY:O	1.98	0.63
22:DA:2638:G:O2'	22:DA:2775:G:N2	2.26	0.63
45:DX:41:GLU:O	45:DX:44:LYS:HD2	1.98	0.63
36:BO:88:LYS:O	36:BO:89:ASP:HB2	1.99	0.63
14:AN:33:ASP:O	14:AN:35:ASN:N	2.30	0.63
20:CT:6:SER:OG	20:CT:7:ALA:N	2.32	0.63
6:AF:91:ARG:O	6:AF:92:THR:OG1	2.14	0.63
21:AU:36:GLU:O	21:AU:37:PHE:HB2	1.99	0.63
35:BN:49:GLU:OE2	35:BN:95:THR:HG22	1.98	0.63
22:DA:2125:G:N1	22:DA:2171:A:OP1	2.31	0.63
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.16	0.63
22:DA:2131:U:H1'	22:DA:2158:A:H61	1.64	0.63
22:BA:721:A:H2'	22:BA:722:A:C8	2.32	0.63
22:DA:2189:U:H2'	22:DA:2190:G:H5''	1.80	0.63
8:CH:18:GLN:HG2	8:CH:63:LEU:HD13	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:14:VAL:H	2:AB:208:ARG:HH12	1.46	0.63
22:BA:945:A:N7	57:BA:3261:HOH:O	2.31	0.63
24:DC:16:VAL:HG22	24:DC:206:GLY:HA3	1.80	0.63
22:BA:141:G:H3'	22:BA:142:A:C8	2.34	0.63
22:DA:2349:G:OP1	51:D3:45:ARG:NH2	2.26	0.63
38:DQ:27:ALA:HB1	38:DQ:31:VAL:HB	1.80	0.63
16:CP:38:PHE:HE2	16:CP:51:ARG:HD3	1.64	0.63
1:CA:211:G:H21	1:CA:212:G:H1'	1.63	0.63
22:BA:1428:C:N4	22:BA:1570:A:OP2	2.28	0.63
13:CM:27:LYS:HA	13:CM:30:SER:HB2	1.81	0.63
29:BH:83:LYS:CE	1:CA:55:A:C2'	2.77	0.63
9:AI:22:LYS:O	9:AI:62:ASP:N	2.27	0.63
8:AH:79:SER:HA	8:AH:85:ILE:HG12	1.80	0.63
22:DA:1315:C:O2'	22:DA:1392:A:N3	2.31	0.63
9:AI:91:ASP:OD2	9:AI:93:SER:N	2.31	0.63
1:AA:315:A:O2'	1:AA:330:C:H4'	1.99	0.63
13:AM:29:ARG:CZ	13:AM:63:PHE:HB2	2.29	0.63
13:AM:73:ILE:O	13:AM:76:SER:OG	2.17	0.63
32:DK:38:ILE:HD11	32:DK:112:PHE:HZ	1.64	0.63
5:AE:97:GLN:HB2	5:AE:124:LEU:HD12	1.81	0.62
1:CA:748:G:H2'	1:CA:749:A:H8	1.64	0.62
20:CT:7:ALA:HB1	20:CT:10:ARG:HB2	1.81	0.62
7:AG:70:ARG:HG3	7:AG:96:ARG:HG2	1.81	0.62
5:AE:25:VAL:O	5:AE:28:GLY:N	2.31	0.62
30:DI:29:GLY:HA2	30:DI:33:VAL:HB	1.81	0.62
22:DA:1793:C:N4	57:DA:3780:HOH:O	2.31	0.62
22:DA:2787:C:H1'	25:DD:63:PRO:HG3	1.81	0.62
3:AC:130:PHE:CZ	3:AC:131:ARG:HD2	2.33	0.62
1:CA:374:A:H5''	1:CA:452:A:N1	2.13	0.62
1:CA:49:U:O4	1:CA:362:G:N2	2.33	0.62
36:DO:79:ALA:HA	36:DO:115:LEU:HD22	1.81	0.62
1:AA:951:G:OP2	13:AM:101:ARG:NH2	2.31	0.62
22:DA:2857:G:N2	22:DA:2860:A:OP2	2.20	0.62
53:B5:45:HIS:CD2	53:B5:176:VAL:HA	2.34	0.62
17:CQ:11:ARG:HA	17:CQ:58:VAL:HA	1.80	0.62
22:BA:2198:A:N3	29:BH:29:PHE:HB2	2.15	0.62
7:CG:146:GLU:HA	7:CG:149:LYS:HB2	1.80	0.62
22:DA:948:C:O2	22:DA:984:A:O2'	2.17	0.62
22:DA:2502:G:H5'	22:DA:2503:A:H5''	1.80	0.62
1:CA:1040:U:H2'	1:CA:1041:G:C8	2.33	0.62
20:CT:80:THR:O	20:CT:83:ILE:HG13	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:D4:16:ILE:HD13	52:D4:25:VAL:HG22	1.80	0.62
22:BA:1434:A:O2'	22:BA:1435:G:H8	1.82	0.62
40:BS:37:THR:OG1	40:BS:48:LYS:NZ	2.30	0.62
35:DN:20:MET:HG3	35:DN:21:PHE:N	2.15	0.62
1:CA:1233:G:OP1	9:CI:119:ARG:NH2	2.32	0.62
1:CA:1225:A:H2'	1:CA:1226:C:C5	2.34	0.62
46:BY:32:ALA:HB2	46:BY:37:LEU:HD23	1.80	0.62
6:AF:67:PRO:O	6:AF:69:GLU:N	2.32	0.62
16:AP:51:ARG:HH11	16:AP:51:ARG:HG2	1.64	0.62
5:CE:105:ILE:N	5:CE:122:ASN:O	2.27	0.62
16:AP:68:SER:HB2	16:AP:71:VAL:HB	1.81	0.62
22:BA:1444:G:H2'	22:BA:1445:G:C8	2.35	0.62
22:DA:2121:G:N2	22:DA:2177:C:O2	2.25	0.62
22:BA:1824:G:N3	24:BC:252:THR:HG21	2.15	0.62
32:BK:24:VAL:HG13	32:BK:33:ALA:HB2	1.81	0.62
1:AA:1377:A:N3	7:AG:2:PRO:HG3	2.15	0.62
1:CA:407:U:H2'	1:CA:408:A:H8	1.62	0.62
4:CD:62:ARG:HH21	4:CD:68:LEU:HA	1.65	0.62
9:CI:84:THR:HG21	9:CI:103:PHE:HB3	1.81	0.62
22:DA:1570:A:H2'	22:DA:1571:A:C8	2.34	0.62
50:B2:12:ARG:HD2	50:B2:44:VAL:HG11	1.81	0.62
22:DA:1096:A:H2'	22:DA:1097:U:O4'	1.99	0.62
24:BC:168:ASP:OD2	24:BC:169:GLY:N	2.32	0.62
40:BS:79:GLY:HA2	40:BS:102:HIS:CE1	2.35	0.62
1:AA:1232:U:OP1	9:AI:126:GLN:NE2	2.33	0.62
22:DA:527:C:OP2	22:DA:2779:U:N3	2.29	0.62
4:CD:188:ARG:HH12	4:CD:192:SER:HB3	1.65	0.62
22:BA:576:U:H2'	22:BA:577:G:C8	2.34	0.62
1:AA:913:A:OP1	12:AL:88:LYS:NZ	2.27	0.62
1:AA:269:C:H2'	1:AA:270:A:C8	2.34	0.62
24:DC:69:ARG:HD3	24:DC:104:ILE:HG21	1.82	0.62
35:BN:73:ASN:HA	35:BN:76:VAL:HG12	1.80	0.62
22:DA:1667:G:N2	22:DA:1992:G:OP2	2.21	0.62
22:DA:2232:C:OP1	45:DX:27:ARG:NH1	2.28	0.62
22:DA:2757:A:N1	28:DG:67:THR:HG21	2.14	0.62
1:AA:1226:C:O2'	13:AM:110:LYS:NZ	2.33	0.62
24:DC:260:ASN:OD1	24:DC:263:THR:N	2.23	0.62
22:BA:1508:A:O2'	22:BA:1509:A:O4'	2.17	0.62
1:CA:374:A:H5''	1:CA:452:A:C2	2.35	0.62
12:AL:86:ARG:NE	12:AL:88:LYS:HB3	2.15	0.62
35:BN:32:GLU:CD	35:BN:86:ARG:HH22	2.02	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:798:G:H2'	22:DA:799:G:H8	1.65	0.62
22:BA:2585:U:H2'	54:B6:3:DBB:HG1	1.82	0.62
22:DA:973:A:OP2	39:DR:81:LYS:NZ	2.29	0.62
17:AQ:46:VAL:HG11	17:AQ:61:ILE:HG13	1.82	0.62
22:BA:1062:G:OP1	22:BA:1070:A:H4'	2.00	0.62
1:CA:398:U:H2'	1:CA:399:G:H8	1.64	0.62
22:BA:2182:U:H2'	22:BA:2183:A:C8	2.35	0.62
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.35	0.61
26:DE:196:VAL:HA	26:DE:199:MET:HE2	1.80	0.61
35:DN:69:ARG:O	35:DN:71:ARG:N	2.25	0.61
22:DA:608:A:H2'	22:DA:609:A:C8	2.35	0.61
14:AN:61:ARG:O	14:AN:62:ASN:HB2	1.99	0.61
30:DI:69:PHE:N	30:DI:69:PHE:HD1	1.98	0.61
1:AA:512:U:H2'	1:AA:513:C:C6	2.34	0.61
22:DA:118:A:N3	22:DA:178:G:H1'	2.14	0.61
1:CA:1326:U:H2'	1:CA:1327:C:C6	2.35	0.61
4:AD:118:VAL:HA	4:AD:123:ILE:HD12	1.81	0.61
28:DG:159:GLY:O	28:DG:163:ARG:NH1	2.33	0.61
22:BA:1170:C:H2'	22:BA:1171:G:C8	2.34	0.61
22:DA:247:G:H4'	22:DA:386:G:C4	2.35	0.61
17:CQ:31:HIS:HD2	17:CQ:33:ILE:H	1.48	0.61
22:DA:2184:A:H2'	22:DA:2185:U:C6	2.35	0.61
1:CA:724:G:OP2	1:CA:833:G:O2'	2.16	0.61
3:CC:16:LYS:HG3	3:CC:17:PRO:HD2	1.82	0.61
10:AJ:42:LEU:HD23	10:AJ:43:PRO:HD2	1.81	0.61
7:AG:15:ASP:HB3	7:AG:20:SER:H	1.64	0.61
1:AA:988:G:N2	1:AA:1217:C:O2	2.33	0.61
16:AP:42:ILE:O	16:AP:44:SER:N	2.32	0.61
34:BM:110:GLU:OE2	34:BM:114:ARG:NH2	2.34	0.61
29:BH:85:GLY:HA3	1:CA:359:G:O4'	2.00	0.61
29:BH:95:GLY:CA	1:CA:368:U:OP1	2.46	0.61
10:CJ:36:VAL:HA	10:CJ:76:ILE:HA	1.82	0.61
29:DH:32:PRO:O	29:DH:33:GLN:CB	2.48	0.61
22:DA:250:G:OP2	51:D3:13:ARG:NH1	2.33	0.61
22:BA:1794:A:H2'	22:BA:1795:C:C6	2.34	0.61
1:CA:983:A:OP1	14:CN:9:ARG:NH2	2.32	0.61
22:BA:1925:C:H4'	22:BA:1926:U:C5	2.34	0.61
22:BA:1417:C:H2'	22:BA:1418:G:O4'	1.99	0.61
1:CA:1147:C:O2'	9:CI:18:ARG:NH1	2.32	0.61
22:DA:1738:G:O2'	22:DA:1739:A:O5'	2.18	0.61
5:CE:134:ILE:HD12	5:CE:134:ILE:H	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:91:PHE:H	2:AB:150:GLY:HA3	1.65	0.61
22:DA:1679:A:N6	57:DA:3436:HOH:O	2.33	0.61
22:DA:594:U:H2'	22:DA:595:C:C6	2.35	0.61
1:AA:1031:C:O2'	1:AA:1032:G:OP2	2.17	0.61
22:BA:2390:U:OP2	51:B3:35:LYS:NZ	2.33	0.61
22:DA:1336:A:H2'	22:DA:1337:G:C8	2.35	0.61
11:AK:81:ASN:HB3	11:AK:106:ARG:HB3	1.82	0.61
1:CA:642:A:C5	8:CH:107:SER:HA	2.36	0.61
2:CB:86:SER:OG	2:CB:87:CYS:N	2.32	0.61
22:DA:1195:G:O2'	22:DA:1226:A:N1	2.31	0.61
22:DA:192:C:O2'	22:DA:802:A:N3	2.33	0.61
1:AA:1441:A:H2	37:BP:114:LEU:HD22	1.65	0.61
50:D2:43:THR:OG1	50:D2:44:VAL:N	2.32	0.61
2:AB:64:LYS:HB3	2:AB:66:LYS:HE2	1.83	0.61
47:DZ:6:LYS:HB2	47:DZ:58:GLU:HG3	1.83	0.61
2:AB:88:ASP:HB2	2:AB:221:VAL:HG12	1.83	0.61
9:CI:31:ASN:HA	9:CI:66:THR:HG22	1.83	0.61
25:BD:16:THR:OG1	25:BD:18:ASP:OD1	2.18	0.61
1:AA:109:A:H2'	1:AA:326:G:N2	2.15	0.61
22:BA:1730:C:OP1	22:BA:1730:C:H4'	1.99	0.61
1:AA:1425:U:O2'	1:AA:1426:G:H5'	2.01	0.61
5:CE:77:ASN:HB2	5:CE:82:GLN:HG2	1.81	0.61
22:DA:250:G:H2'	22:DA:251:A:C8	2.36	0.61
22:DA:58:G:OP1	41:DT:78:SER:OG	2.17	0.61
25:DD:7:LYS:HD3	25:DD:198:GLY:HA2	1.82	0.61
22:BA:2887:A:H5'	22:BA:2888:C:OP2	2.00	0.61
24:BC:86:ASN:N	24:BC:86:ASN:OD1	2.32	0.61
1:AA:721:G:H4'	1:AA:722:G:O4'	2.00	0.61
29:DH:83:LYS:H	29:DH:149:GLU:HG2	1.64	0.61
22:BA:1086:A:O2'	22:BA:1087:G:N7	2.34	0.61
21:CU:40:LYS:H	21:CU:41:PRO:CD	2.14	0.61
22:DA:2031:A:C6	22:DA:2498:C:H1'	2.36	0.61
22:BA:560:C:O2	38:BQ:48:ARG:NH1	2.34	0.61
45:DX:52:SER:OG	45:DX:55:GLY:N	2.32	0.61
1:CA:1182:G:H5'	1:CA:1184:G:H5''	1.83	0.61
1:CA:477:C:H2'	1:CA:478:A:C8	2.34	0.61
1:AA:1313:U:OP2	19:AS:6:LYS:HB3	2.01	0.61
31:BJ:140:LEU:HD11	31:BJ:142:ILE:HD13	1.82	0.61
25:BD:125:TRP:CD2	25:BD:160:LYS:HD3	2.36	0.61
22:BA:1563:U:H2'	22:BA:1564:C:H6	1.65	0.61
2:AB:115:LYS:O	2:AB:117:LEU:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1592:C:H2'	22:DA:1593:A:C8	2.36	0.61
2:AB:46:THR:HG23	2:AB:201:PRO:HB2	1.82	0.61
22:DA:7:G:H4'	31:DJ:15:TRP:CZ2	2.35	0.61
1:CA:1006:G:H2'	1:CA:1007:U:C6	2.35	0.61
1:AA:1129:C:O2	1:AA:1130:A:N6	2.34	0.61
28:DG:12:PRO:HD2	28:DG:15:VAL:HG21	1.83	0.61
29:BH:117:LEU:O	29:BH:121:VAL:HG22	1.93	0.61
22:BA:265:A:H4'	22:BA:266:G:OP1	2.01	0.61
1:CA:890:G:HO2'	1:CA:891:U:P	2.23	0.61
22:DA:2134:A:OP2	22:DA:2157:G:N2	2.33	0.61
20:AT:29:ARG:O	20:AT:33:LYS:HG2	2.01	0.61
22:BA:20:C:H2'	22:BA:21:A:H8	1.64	0.61
22:DA:306:U:O2	22:DA:312:G:N2	2.34	0.61
53:B5:42:VAL:O	53:B5:179:ALA:N	2.34	0.60
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.01	0.60
7:AG:135:VAL:O	7:AG:139:GLU:HG2	2.01	0.60
1:AA:1407:C:O2'	22:BA:1912:A:N6	2.33	0.60
2:AB:89:GLN:HE21	2:AB:221:VAL:HB	1.66	0.60
22:DA:2134:A:N6	22:DA:2157:G:O2'	2.33	0.60
22:BA:2831:G:OP1	25:BD:56:LYS:NZ	2.30	0.60
24:BC:17:VAL:H	24:BC:204:VAL:HG22	1.67	0.60
7:CG:42:ILE:HD13	7:CG:116:MET:HB3	1.83	0.60
27:DF:134:GLU:HG3	27:DF:136:ILE:HD12	1.83	0.60
22:BA:1379:U:C6	22:BA:1379:U:OP1	2.54	0.60
22:BA:2520:C:C6	22:BA:2567:G:H1'	2.36	0.60
19:AS:11:ILE:HG13	19:AS:38:SER:HB3	1.83	0.60
29:BH:100:ALA:HB1	29:BH:112:LYS:HA	1.83	0.60
9:AI:46:MET:N	9:AI:46:MET:SD	2.74	0.60
24:DC:237:GLY:O	24:DC:239:ASN:N	2.34	0.60
1:CA:909:A:H2'	1:CA:910:C:O4'	2.01	0.60
35:BN:12:ARG:O	35:BN:17:ARG:NH2	2.34	0.60
22:BA:1342:A:OP2	57:BA:3719:HOH:O	2.17	0.60
29:BH:121:VAL:N	29:BH:122:LEU:HB2	2.16	0.60
2:AB:20:THR:OG1	2:AB:21:ARG:N	2.30	0.60
5:CE:104:GLY:O	5:CE:105:ILE:HG22	2.01	0.60
1:CA:728:A:H2'	1:CA:729:A:H8	1.66	0.60
22:DA:1177:G:H2'	22:DA:1178:C:O4'	2.00	0.60
22:DA:848:C:H2'	22:DA:849:A:C8	2.36	0.60
52:D4:23:ILE:HB	52:D4:38:GLY:HA3	1.84	0.60
21:AU:8:GLU:HB3	21:AU:12:PHE:HZ	1.65	0.60
22:DA:661:A:H1'	33:DL:12:SER:O	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:219:U:H2'	1:AA:220:G:H8	1.65	0.60
22:DA:2421:G:O6	51:D3:31:HIS:HD2	1.83	0.60
24:DC:121:ASP:N	24:DC:121:ASP:OD1	2.33	0.60
22:DA:2346:A:H3'	22:DA:2347:C:H5''	1.84	0.60
22:BA:1070:A:C2	22:BA:1097:U:H4'	2.36	0.60
22:BA:580:U:H2'	22:BA:581:C:C6	2.36	0.60
53:B5:50:ILE:O	53:B5:52:PRO:HD3	2.02	0.60
1:CA:709:U:H2'	1:CA:710:G:H8	1.66	0.60
22:BA:2667:C:N3	28:BG:110:SER:OG	2.32	0.60
3:AC:20:SER:HB3	14:AN:94:PRO:HG3	1.82	0.60
22:BA:1026:G:H2'	22:BA:1027:A:C8	2.36	0.60
43:DV:30:ILE:HG12	43:DV:91:PHE:HB2	1.83	0.60
22:BA:2539:C:H5'	52:B4:3:VAL:HG21	1.83	0.60
22:BA:528:A:C8	22:BA:528:A:H3'	2.36	0.60
29:BH:117:LEU:CD2	29:BH:121:VAL:HA	2.31	0.60
22:DA:2043:C:OP1	22:DA:2777:G:O2'	2.18	0.60
22:DA:1178:C:H2'	22:DA:1179:G:C8	2.36	0.60
1:AA:532:A:O3'	57:AA:1847:HOH:O	2.16	0.60
1:AA:407:U:H2'	1:AA:408:A:H8	1.66	0.60
1:CA:475:C:H2'	1:CA:476:U:C6	2.36	0.60
22:DA:2428:G:H5''	22:DA:2429:G:OP1	2.02	0.60
46:DY:31:GLN:HG2	46:DY:37:LEU:HB2	1.84	0.60
1:CA:159:G:N2	1:CA:162:A:OP2	2.34	0.60
22:BA:726:G:O2'	22:BA:727:A:OP2	2.17	0.60
22:DA:1394:U:H4'	22:DA:1603:A:H4'	1.83	0.60
22:DA:2286:G:H4'	22:DA:2287:A:O5'	2.01	0.60
22:DA:2215:C:H2'	22:DA:2216:G:C8	2.37	0.60
2:CB:15:HIS:O	2:CB:17:GLY:N	2.35	0.60
33:BL:100:ILE:HG13	33:BL:101:ILE:HG23	1.84	0.60
16:AP:46:LYS:HD3	16:AP:47:GLU:N	2.17	0.60
23:DB:7:G:H5'	36:DO:29:HIS:CE1	2.36	0.60
23:DB:62:C:H2'	23:DB:63:C:C6	2.37	0.60
24:DC:108:LYS:HA	24:DC:196:GLY:HA2	1.83	0.60
6:CF:64:VAL:HG12	6:CF:65:GLU:H	1.65	0.60
22:BA:1342:A:OP2	57:BA:3721:HOH:O	2.16	0.60
1:CA:1346:A:H5''	9:CI:122:ARG:HH12	1.67	0.60
26:DE:113:VAL:HG23	26:DE:118:LEU:HD23	1.83	0.60
22:DA:2226:C:H2'	22:DA:2227:A:O4'	2.01	0.60
30:BI:99:GLY:O	30:BI:139:VAL:HG23	2.02	0.60
22:BA:585:G:O2'	26:BE:77:ILE:HG22	2.01	0.60
35:BN:32:GLU:OE2	35:BN:86:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2874:C:H2'	22:DA:2875:C:C6	2.37	0.60
1:AA:32:A:OP1	1:AA:398:U:H1'	2.02	0.60
22:DA:208:C:H2'	22:DA:209:C:C6	2.35	0.60
10:CJ:53:ILE:HG13	14:CN:85:ARG:HD2	1.84	0.60
22:DA:2885:G:N7	48:D0:40:ARG:NH2	2.50	0.60
22:BA:1565:C:H3'	24:BC:18:LYS:HZ2	1.67	0.60
22:DA:2143:C:H2'	22:DA:2144:G:O4'	2.01	0.60
19:CS:36:ARG:NH2	19:CS:75:ALA:O	2.34	0.60
19:CS:15:LEU:HD13	19:CS:33:THR:HG21	1.82	0.60
36:DO:92:PHE:HB2	36:DO:117:PHE:CD1	2.36	0.60
3:CC:49:LYS:O	3:CC:72:ARG:NH1	2.34	0.60
1:CA:1181:G:O2'	1:CA:1182:G:N7	2.35	0.60
22:DA:18:U:O4	57:DA:3205:HOH:O	2.11	0.60
22:DA:1377:G:OP2	57:DA:3391:HOH:O	2.15	0.60
22:DA:724:U:H2'	22:DA:725:G:O4'	2.02	0.60
22:BA:2703:C:H2'	22:BA:2704:C:H6	1.66	0.60
8:CH:96:MET:HB2	8:CH:99:LEU:O	2.01	0.60
39:BR:37:GLU:HB3	39:BR:53:PHE:CE1	2.36	0.60
1:AA:91:U:H2'	1:AA:92:U:O4'	2.02	0.60
2:AB:111:ILE:HD11	2:AB:151:ILE:HG12	1.84	0.60
9:AI:12:ARG:NH2	9:AI:107:ASP:OD1	2.34	0.60
25:BD:99:GLU:HG2	25:BD:182:ALA:HB2	1.84	0.60
22:DA:2873:A:H4'	57:DA:3806:HOH:O	2.01	0.60
25:DD:151:THR:O	25:DD:153:GLY:N	2.34	0.60
22:BA:591:U:HO2'	51:B3:2:PRO:N	1.99	0.60
1:CA:1203:C:H4'	14:CN:67:THR:HB	1.83	0.60
20:CT:57:ILE:O	20:CT:61:GLN:HG2	2.01	0.60
53:B5:35:THR:O	53:B5:35:THR:OG1	2.15	0.60
40:DS:66:ILE:O	40:DS:68:ASP:N	2.35	0.60
10:AJ:19:ASP:HA	10:AJ:22:THR:HB	1.84	0.60
2:CB:210:VAL:O	2:CB:214:LEU:HB2	2.02	0.60
29:DH:126:GLY:O	29:DH:146:VAL:HG23	2.00	0.60
29:BH:93:SER:HG	1:CA:357:G:C4'	2.14	0.60
1:AA:427:U:OP2	1:AA:428:G:O2'	2.15	0.60
4:CD:104:ARG:HH11	4:CD:111:ARG:HH12	1.50	0.60
22:DA:2290:G:H4'	22:DA:2381:A:O2'	2.02	0.60
2:AB:33:GLY:HA3	2:AB:40:ILE:H	1.66	0.60
30:DI:42:PHE:O	30:DI:46:THR:OG1	2.20	0.60
30:DI:69:PHE:N	30:DI:69:PHE:CD1	2.70	0.60
29:DH:126:GLY:O	29:DH:146:VAL:N	2.35	0.60
1:CA:518:C:H2'	1:CA:530:G:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:90:LEU:HB2	12:CL:93:VAL:HG21	1.84	0.60
3:CC:149:ILE:HG13	3:CC:202:ILE:HG12	1.83	0.60
22:DA:13:A:N1	22:DA:525:U:H2'	2.17	0.60
1:CA:268:U:H2'	1:CA:269:C:C6	2.36	0.60
22:BA:1403:A:H2'	22:BA:1404:C:C6	2.37	0.60
9:CI:29:VAL:HB	9:CI:64:TYR:HD2	1.66	0.60
22:DA:2111:U:H5	22:DA:2145:C:H2'	1.67	0.60
13:AM:68:ASP:OD2	13:AM:68:ASP:N	2.34	0.60
1:CA:1087:G:N2	1:CA:1099:G:H1'	2.17	0.59
22:BA:636:G:OP2	33:BL:109:LYS:NZ	2.28	0.59
35:DN:79:LEU:O	35:DN:81:ASN:N	2.30	0.59
18:CR:35:GLU:HB2	21:CU:19:PHE:CZ	2.37	0.59
22:DA:730:A:OP1	22:DA:1775:U:O2'	2.10	0.59
1:AA:79:G:H2'	1:AA:80:A:C8	2.37	0.59
22:BA:588:U:H2'	22:BA:589:U:C6	2.36	0.59
1:CA:308:C:H2'	1:CA:309:A:C8	2.37	0.59
22:BA:2502:G:H5'	22:BA:2503:A:H5''	1.82	0.59
22:DA:990:A:N1	39:DR:78:ARG:NH1	2.50	0.59
22:DA:910:A:N3	22:DA:2264:C:O2'	2.33	0.59
1:AA:1525:G:OP1	11:AK:122:ARG:NH2	2.33	0.59
22:BA:321:U:H5''	26:BE:131:THR:HG23	1.84	0.59
31:BJ:130:HIS:HE1	31:BJ:137:PRO:HG3	1.65	0.59
1:CA:228:A:H4'	16:CP:63:GLN:HG2	1.84	0.59
30:DI:106:LEU:HD13	30:DI:130:GLU:HG3	1.84	0.59
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.37	0.59
1:AA:972:C:H4'	10:AJ:59:LYS:HE3	1.83	0.59
24:BC:8:PRO:HB3	24:BC:14:ARG:HB2	1.84	0.59
2:CB:54:LEU:HA	2:CB:57:LEU:HB3	1.84	0.59
35:DN:54:LEU:HD23	35:DN:66:ALA:HB2	1.83	0.59
30:DI:18:ALA:HB1	30:DI:43:ASN:HD21	1.67	0.59
36:DO:80:GLU:HA	36:DO:83:LEU:HD12	1.83	0.59
1:AA:673:A:H2'	1:AA:674:G:C8	2.37	0.59
34:BM:51:ARG:O	34:BM:55:ARG:HG2	2.03	0.59
22:DA:1345:C:H5'	22:DA:1396:U:C5	2.38	0.59
22:DA:2853:C:H2'	22:DA:2854:G:C8	2.38	0.59
33:BL:77:ILE:HD12	33:BL:100:ILE:HD11	1.85	0.59
1:AA:673:A:H5''	6:AF:86:ARG:NH1	2.16	0.59
33:DL:82:LEU:HA	33:DL:85:VAL:HG13	1.84	0.59
14:CN:47:LYS:HE3	19:CS:16:LEU:HD23	1.83	0.59
30:BI:74:PRO:HB2	30:BI:78:VAL:HG21	1.83	0.59
1:AA:9:G:OP2	5:AE:126:LYS:NZ	2.26	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:39:ILE:HG13	13:CM:56:LEU:HD11	1.83	0.59
22:DA:309:A:H5'	42:DU:17:LYS:HG2	1.83	0.59
29:BH:99:ILE:HB	29:BH:115:VAL:HG11	1.84	0.59
28:BG:125:CYS:HA	28:BG:130:GLU:O	2.02	0.59
22:DA:2001:C:H4'	22:DA:2689:U:H2'	1.85	0.59
41:DT:39:THR:HG23	41:DT:42:GLU:H	1.67	0.59
1:CA:1175:G:H2'	1:CA:1176:A:H8	1.65	0.59
1:CA:252:U:O4	1:CA:253:A:N6	2.36	0.59
10:CJ:57:VAL:HG22	10:CJ:58:ASN:H	1.67	0.59
49:D1:4:GLY:O	49:D1:6:ARG:N	2.31	0.59
19:AS:29:LYS:HB3	19:AS:30:PRO:HD2	1.82	0.59
22:BA:614:A:O2'	22:BA:615:U:OP2	2.21	0.59
29:BH:94:ILE:HG22	29:BH:99:ILE:CG1	2.32	0.59
22:BA:2846:G:OP2	37:BP:52:ASN:HB2	2.02	0.59
1:AA:1225:A:H2'	1:AA:1226:C:C5	2.38	0.59
10:CJ:12:ALA:HB3	10:CJ:18:ILE:HB	1.83	0.59
2:CB:59:LYS:HA	2:CB:62:SER:HB2	1.84	0.59
22:DA:420:C:H2'	22:DA:421:C:H6	1.67	0.59
24:DC:136:PRO:O	24:DC:139:SER:OG	2.21	0.59
10:AJ:36:VAL:HG22	10:AJ:76:ILE:HG12	1.84	0.59
12:AL:3:THR:HG22	12:AL:5:ASN:H	1.68	0.59
4:CD:29:ASP:C	4:CD:31:LYS:H	2.05	0.59
1:AA:796:C:OP1	11:AK:126:LYS:HB2	2.03	0.59
22:DA:2591:C:H2'	22:DA:2592:G:C8	2.38	0.59
22:BA:2615:U:C2	48:B0:4:GLN:HA	2.38	0.59
33:BL:122:VAL:HG21	33:BL:135:ILE:HD13	1.84	0.59
10:AJ:12:ALA:HB2	10:AJ:96:VAL:HA	1.83	0.59
22:BA:1911:U:H2'	22:BA:1918:A:N1	2.17	0.59
26:BE:91:ASP:OD1	26:BE:93:SER:OG	2.19	0.59
32:BK:78:ARG:NH1	37:BP:71:GLU:OE2	2.35	0.59
31:DJ:80:HIS:O	31:DJ:82:GLY:N	2.36	0.59
22:DA:400:G:N7	45:DX:57:ARG:NH1	2.50	0.59
22:BA:2794:C:H2'	22:BA:2795:C:H6	1.67	0.59
22:DA:2039:U:H2'	22:DA:2040:G:C8	2.37	0.59
23:DB:98:G:H1	43:DV:14:LYS:HB3	1.67	0.59
22:BA:2287:A:OP1	49:B1:30:LYS:NZ	2.31	0.59
22:BA:2092:U:H4'	29:BH:24:GLY:HA3	1.85	0.59
1:CA:1372:U:OP2	9:CI:13:LYS:NZ	2.35	0.59
22:DA:143:C:O2	41:DT:1:MET:N	2.35	0.59
21:AU:34:ARG:CZ	21:AU:35:ARG:HB2	2.32	0.59
39:BR:25:LEU:H	39:BR:94:THR:CG2	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1003:G:H21	1:AA:1005:A:H5'	1.67	0.59
22:DA:1869:G:N2	22:DA:1871:A:O2'	2.36	0.59
29:BH:1:MET:O	29:BH:20:ASN:ND2	2.35	0.59
41:DT:18:GLU:O	41:DT:22:THR:OG1	2.18	0.59
10:CJ:27:GLU:O	10:CJ:31:ARG:HB3	2.02	0.59
1:AA:129:A:H2	1:AA:232:G:H22	1.51	0.59
22:DA:2311:A:O2'	22:DA:2312:U:O4'	2.20	0.59
4:CD:169:THR:O	4:CD:171:LEU:N	2.35	0.59
17:AQ:19:LYS:O	17:AQ:71:LYS:NZ	2.35	0.59
41:DT:54:GLU:HB3	41:DT:88:LYS:HG3	1.84	0.59
1:AA:1033:G:H2'	1:AA:1034:G:H5'	1.84	0.59
1:AA:398:U:H2'	1:AA:399:G:C8	2.38	0.59
1:AA:34:C:H2'	1:AA:35:G:H8	1.68	0.59
22:DA:1309:G:H4'	50:D2:7:PRO:HB2	1.84	0.59
5:CE:65:GLU:OE2	5:CE:69:ARG:NH1	2.35	0.59
22:DA:1425:G:H2'	22:DA:1426:G:C8	2.38	0.59
31:DJ:99:ARG:HB3	31:DJ:103:ILE:HD12	1.85	0.59
20:CT:62:ALA:HA	20:CT:68:HIS:H	1.68	0.59
3:AC:57:ILE:HG12	3:AC:66:VAL:HG22	1.85	0.59
22:DA:1993:U:H4'	25:DD:133:THR:HG21	1.84	0.59
22:DA:2425:A:H4'	22:DA:2426:A:O5'	2.02	0.59
2:CB:82:ASP:N	2:CB:82:ASP:OD1	2.36	0.59
43:DV:42:LEU:HD12	43:DV:47:VAL:HG21	1.85	0.59
6:AF:3:HIS:N	6:AF:92:THR:HG23	2.17	0.59
22:BA:1910:G:H2'	22:BA:1911:U:O4'	2.03	0.59
22:DA:1721:G:HO2'	22:DA:1722:A:H8	1.50	0.59
1:CA:1348:U:H4'	9:CI:122:ARG:HG3	1.83	0.59
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.67	0.59
22:BA:2882:A:OP1	35:BN:96:ARG:HD3	2.03	0.59
47:DZ:31:ARG:HG2	47:DZ:34:HIS:HB2	1.84	0.59
1:CA:509:A:N3	1:CA:543:U:O2'	2.36	0.59
22:BA:414:C:H2'	22:BA:415:A:C8	2.37	0.59
38:DQ:72:ASN:HB3	38:DQ:110:VAL:HG11	1.85	0.59
10:CJ:80:THR:O	10:CJ:84:VAL:HB	2.02	0.59
22:DA:2573:C:OP1	22:DA:2574:G:H5''	2.03	0.59
30:BI:75:PRO:HB2	30:BI:78:VAL:HG13	1.85	0.59
1:AA:8:A:C6	4:AD:206:LYS:HB3	2.37	0.59
5:CE:69:ARG:O	5:CE:70:ASN:HB2	2.02	0.59
6:CF:19:PRO:HA	6:CF:22:ILE:HB	1.85	0.59
20:AT:81:ALA:O	20:AT:85:LYS:HG2	2.02	0.59
26:BE:119:ILE:HB	26:BE:187:VAL:HG22	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:999:C:H2'	1:AA:1000:A:C8	2.38	0.59
45:DX:71:LEU:HB2	45:DX:76:GLU:HB2	1.83	0.58
22:DA:1064:C:N3	22:DA:1074:G:N2	2.51	0.58
26:BE:118:LEU:HD11	26:BE:188:MET:HG3	1.84	0.58
45:BX:2:SER:O	45:BX:4:VAL:N	2.36	0.58
22:BA:528:A:H3'	22:BA:528:A:H8	1.67	0.58
1:CA:1522:U:H2'	1:CA:1523:G:H8	1.67	0.58
29:DH:34:GLY:O	29:DH:35:LYS:CB	2.51	0.58
1:CA:41:G:H2'	1:CA:42:G:C8	2.38	0.58
10:CJ:52:LEU:HB2	14:CN:81:ARG:HD2	1.84	0.58
22:DA:1774:C:O2	24:DC:11:PRO:HB2	2.02	0.58
1:CA:147:G:H2'	1:CA:148:G:C8	2.37	0.58
22:DA:2074:U:H2'	22:DA:2075:U:C6	2.38	0.58
22:BA:1059:G:H5''	22:BA:1060:U:H3'	1.85	0.58
22:BA:139:U:C4	41:BT:2:ILE:HD13	2.38	0.58
22:BA:84:A:N1	22:BA:98:G:O2'	2.28	0.58
2:CB:21:ARG:C	2:CB:23:TRP:H	2.06	0.58
1:CA:407:U:H2'	1:CA:408:A:C8	2.38	0.58
40:DS:84:ARG:HB2	40:DS:96:ILE:HG12	1.84	0.58
1:CA:1071:C:H2'	1:CA:1072:G:H8	1.67	0.58
5:AE:153:VAL:HG11	8:AH:99:LEU:HD13	1.84	0.58
22:DA:2096:C:H2'	22:DA:2097:A:C8	2.38	0.58
22:BA:668:A:H2'	22:BA:670:A:H62	1.67	0.58
3:AC:155:GLY:HA2	3:AC:163:ALA:HB1	1.84	0.58
11:AK:125:LYS:O	21:AU:34:ARG:NE	2.32	0.58
15:CO:59:MET:O	15:CO:63:ARG:N	2.33	0.58
42:BU:16:GLY:O	42:BU:18:ASP:N	2.30	0.58
25:DD:179:ARG:NH1	37:DP:8:LEU:HD21	2.18	0.58
9:AI:10:GLY:HA2	9:AI:81:HIS:ND1	2.19	0.58
22:BA:395:U:O2'	22:BA:396:G:N7	2.34	0.58
1:CA:1220:G:H21	19:CS:54:GLY:HA2	1.68	0.58
1:AA:429:U:H3'	4:AD:9:LEU:HD23	1.84	0.58
22:BA:1403:A:H2'	22:BA:1404:C:H6	1.68	0.58
1:AA:645:G:N7	57:AA:1749:HOH:O	2.32	0.58
52:B4:25:VAL:HB	52:B4:35:GLN:HB2	1.84	0.58
2:CB:100:MET:HA	2:CB:107:VAL:HG21	1.85	0.58
5:AE:82:GLN:H	5:AE:147:MET:CE	2.16	0.58
22:BA:660:C:H2'	22:BA:661:A:H8	1.68	0.58
15:AO:46:HIS:O	15:AO:48:LYS:N	2.29	0.58
1:CA:355:C:H2'	1:CA:356:A:O4'	2.03	0.58
22:DA:2111:U:C5	22:DA:2145:C:H2'	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2813:A:H2'	22:DA:2814:A:C8	2.38	0.58
22:DA:2819:G:H5''	57:DA:3807:HOH:O	2.03	0.58
22:BA:1736:U:H2'	22:BA:1737:G:O4'	2.04	0.58
22:DA:679:C:H2'	22:DA:680:C:H6	1.69	0.58
29:BH:31:VAL:N	29:BH:32:PRO:HD2	2.18	0.58
21:CU:34:ARG:NE	21:CU:35:ARG:HB2	2.16	0.58
22:BA:1818:U:OP2	24:BC:156:ARG:NH1	2.36	0.58
1:AA:1081:A:H5'	5:AE:23:LYS:HG3	1.85	0.58
2:AB:114:LEU:O	2:AB:118:GLU:HG2	2.03	0.58
22:DA:1272:A:C5	22:DA:1618:A:H1'	2.38	0.58
1:CA:841:C:H3'	1:CA:843:U:H5''	1.84	0.58
49:D1:23:THR:OG1	49:D1:24:THR:N	2.34	0.58
1:CA:1231:G:H4'	9:CI:128:SER:HB2	1.85	0.58
17:CQ:19:LYS:HD3	17:CQ:49:GLU:HA	1.84	0.58
22:BA:572:A:OP2	39:BR:80:ARG:NH2	2.29	0.58
22:DA:616:A:H4'	26:DE:101:TYR:CZ	2.38	0.58
28:BG:24:ILE:HD12	28:BG:72:LEU:HD21	1.85	0.58
24:BC:182:ARG:NH2	24:BC:183:LYS:O	2.36	0.58
1:AA:1307:U:H2'	1:AA:1308:U:C6	2.38	0.58
24:DC:232:HIS:NE2	24:DC:244:PRO:HA	2.18	0.58
31:BJ:21:THR:HA	31:BJ:61:LYS:HB3	1.86	0.58
4:CD:41:HIS:O	4:CD:43:ALA:N	2.37	0.58
31:DJ:4:PHE:HB3	38:DQ:64:ARG:NH1	2.19	0.58
4:AD:88:GLU:HG2	4:AD:188:ARG:HD3	1.86	0.58
17:CQ:31:HIS:CD2	17:CQ:33:ILE:H	2.21	0.58
1:CA:161:A:H2'	1:CA:162:A:C8	2.39	0.58
22:DA:1993:U:H4'	25:DD:133:THR:CG2	2.34	0.58
9:CI:116:VAL:HG21	10:CJ:62:ARG:HB2	1.85	0.58
22:BA:1651:G:OP1	35:BN:40:LYS:HE3	2.04	0.58
5:AE:149:SER:HB2	5:AE:152:MET:HB2	1.86	0.58
22:DA:276:U:O2'	22:DA:278:A:N7	2.37	0.58
27:DF:73:SER:HB2	27:DF:81:GLN:HB3	1.85	0.58
22:BA:819:A:OP2	22:BA:1187:G:N2	2.27	0.58
24:BC:70:ASN:O	24:BC:72:ASP:N	2.37	0.58
24:DC:61:ALA:O	24:DC:63:ARG:NH2	2.36	0.58
24:DC:8:PRO:HB3	24:DC:14:ARG:HB2	1.86	0.58
29:BH:97:ARG:HD2	1:CA:369:G:C2'	2.33	0.58
22:BA:1073:A:C3'	22:BA:1074:G:H5''	2.29	0.58
22:BA:2326:C:HO2'	22:BA:2327:A:H8	1.51	0.58
42:BU:14:LEU:HD11	42:BU:71:ALA:HB2	1.85	0.58
33:DL:96:LYS:HD3	33:DL:103:ILE:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:64:ILE:HG12	3:CC:66:VAL:HG23	1.85	0.58
4:AD:11:LEU:HD13	4:AD:63:ARG:HB3	1.86	0.58
14:AN:46:LEU:O	14:AN:48:LEU:N	2.37	0.58
33:DL:109:LYS:HG2	33:DL:126:ARG:HB3	1.86	0.58
24:DC:67:PHE:HB3	24:DC:151:GLY:O	2.04	0.58
22:BA:906:U:O2'	34:BM:66:ARG:NH2	2.28	0.58
4:CD:90:LEU:HD21	4:CD:200:ILE:HD11	1.85	0.58
22:DA:20:C:H2'	22:DA:21:A:H8	1.69	0.58
22:BA:64:A:H2'	22:BA:65:U:C6	2.39	0.58
22:BA:2117:A:N6	22:BA:2170:A:N1	2.51	0.58
43:DV:55:GLU:H	43:DV:55:GLU:CD	2.07	0.58
32:DK:70:ARG:HD3	32:DK:76:VAL:HB	1.86	0.58
10:AJ:44:THR:HG22	10:AJ:70:HIS:HA	1.86	0.57
10:AJ:32:THR:HG21	10:AJ:86:ALA:HB2	1.86	0.57
22:BA:627:A:C6	22:BA:637:A:C8	2.92	0.57
22:DA:155:A:H2'	22:DA:156:A:C8	2.39	0.57
22:BA:1141:U:H4'	22:BA:1142:A:O4'	2.04	0.57
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.85	0.57
22:DA:2793:C:H2'	22:DA:2794:C:H6	1.68	0.57
32:DK:35:VAL:HG22	32:DK:69:VAL:HG12	1.86	0.57
22:BA:585:G:N7	38:BQ:6:ARG:NH1	2.51	0.57
22:DA:1019:U:OP1	22:DA:1035:U:O2'	2.17	0.57
3:AC:143:ARG:HG3	3:AC:144:LEU:HD13	1.86	0.57
51:D3:31:HIS:ND1	51:D3:32:ILE:HG13	2.20	0.57
1:AA:181:A:N6	1:AA:195:A:OP2	2.37	0.57
22:DA:328:U:H4'	42:DU:66:GLN:HE21	1.69	0.57
3:CC:10:ILE:HD12	14:CN:98:LYS:HG3	1.85	0.57
3:AC:73:PRO:HG2	3:AC:105:GLU:OE1	2.04	0.57
9:CI:67:VAL:HG11	9:CI:79:ILE:HD11	1.85	0.57
44:DW:21:LEU:HA	44:DW:39:ARG:HB2	1.86	0.57
40:DS:52:GLU:HA	40:DS:55:ILE:HD12	1.86	0.57
27:BF:80:ARG:NE	27:BF:81:GLN:O	2.35	0.57
1:CA:1041:G:H2'	1:CA:1042:A:C8	2.39	0.57
1:AA:960:U:H2'	1:AA:1225:A:H62	1.69	0.57
22:DA:788:A:OP1	22:DA:791:C:N4	2.33	0.57
22:BA:1536:C:H4'	22:BA:1537:G:H5''	1.86	0.57
22:BA:1182:G:H2'	22:BA:1183:U:O4'	2.04	0.57
22:BA:2204:G:H4'	24:BC:150:LYS:HG3	1.87	0.57
40:BS:43:ALA:HA	40:BS:46:LEU:HD12	1.86	0.57
22:BA:481:G:C4	22:BA:507:A:C2	2.93	0.57
1:AA:669:G:H2'	1:AA:670:G:H8	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DY:1:MET:HA	46:DY:4:LYS:HD3	1.86	0.57
32:BK:93:GLN:NE2	32:BK:111:LYS:HB2	2.19	0.57
1:AA:345:C:N3	32:BK:117:SER:OG	2.37	0.57
1:AA:995:C:N3	1:AA:1046:A:O2'	2.37	0.57
27:BF:40:VAL:O	27:BF:42:GLU:N	2.37	0.57
22:BA:2186:G:H2'	22:BA:2187:U:C6	2.39	0.57
5:AE:104:GLY:O	5:AE:105:ILE:HG22	2.04	0.57
22:DA:2391:G:OP2	51:D3:35:LYS:NZ	2.23	0.57
22:DA:1799:G:C8	24:DC:176:LEU:HD13	2.39	0.57
5:CE:89:HIS:CE1	5:CE:90:THR:HG1	2.23	0.57
1:AA:989:U:H2'	1:AA:990:C:C6	2.38	0.57
8:AH:30:SER:HB3	8:AH:33:LYS:HG3	1.85	0.57
2:AB:73:LYS:HE3	2:AB:205:ASP:HB2	1.87	0.57
22:DA:466:A:OP1	50:D2:34:ARG:NE	2.38	0.57
22:DA:798:G:H2'	22:DA:799:G:C8	2.39	0.57
22:DA:826:U:O2'	33:DL:53:GLY:HA3	2.04	0.57
1:CA:519:C:H2'	1:CA:520:A:O4'	2.04	0.57
22:DA:2641:G:H5''	31:DJ:78:THR:HB	1.87	0.57
17:AQ:69:LYS:O	17:AQ:70:THR:HB	2.04	0.57
1:CA:67:C:O2'	1:CA:171:A:N3	2.37	0.57
42:DU:24:LYS:H	42:DU:37:GLU:CD	2.08	0.57
50:B2:18:PHE:HA	50:B2:43:THR:HG21	1.85	0.57
22:DA:1827:U:H2'	22:DA:1828:G:O4'	2.05	0.57
29:DH:108:VAL:O	29:DH:110:VAL:N	2.36	0.57
22:BA:974:G:H8	22:BA:990:A:H62	1.53	0.57
14:CN:45:VAL:HG23	14:CN:46:LEU:H	1.67	0.57
28:DG:17:VAL:HG12	28:DG:19:ILE:HD11	1.86	0.57
29:BH:117:LEU:CD2	29:BH:121:VAL:H	2.08	0.57
9:AI:21:ILE:HG21	9:AI:61:LEU:HD12	1.86	0.57
22:BA:569:U:O2'	22:BA:983:A:N1	2.34	0.57
22:DA:450:G:N1	22:DA:454:A:OP2	2.30	0.57
24:DC:210:ALA:HA	24:DC:213:TRP:CE2	2.39	0.57
2:AB:160:ALA:O	2:AB:161:LEU:HB2	2.03	0.57
22:DA:2591:C:H2'	22:DA:2592:G:H8	1.69	0.57
22:DA:2096:C:H2'	22:DA:2097:A:H8	1.69	0.57
5:AE:82:GLN:NE2	5:AE:150:PRO:HD3	2.19	0.57
22:DA:2793:C:H2'	22:DA:2794:C:C6	2.38	0.57
19:CS:69:HIS:ND1	19:CS:73:GLU:OE2	2.37	0.57
45:BX:17:ASN:OD1	45:BX:27:ARG:HD2	2.05	0.57
30:DI:7:ALA:O	30:DI:59:ILE:HB	2.03	0.57
1:AA:322:C:O2'	20:AT:18:ARG:HG3	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:899:C:O2'	22:DA:1832:C:OP1	2.22	0.57
46:BY:6:LEU:HD13	46:BY:56:LEU:HD22	1.86	0.57
7:CG:13:LEU:HD13	7:CG:14:PRO:HD2	1.85	0.57
41:BT:71:GLY:O	41:BT:73:ARG:N	2.37	0.57
29:BH:95:GLY:HA2	29:BH:117:LEU:HD22	1.87	0.57
5:CE:105:ILE:H	5:CE:122:ASN:C	2.08	0.57
1:CA:1348:U:OP1	9:CI:112:GLU:N	2.30	0.57
1:AA:8:A:N6	4:AD:202:GLU:O	2.38	0.57
22:DA:674:G:N2	22:DA:2445:G:OP1	2.38	0.57
30:BI:34:ASN:OD1	30:BI:65:ARG:NH2	2.36	0.57
24:BC:260:ASN:O	24:BC:262:ARG:N	2.35	0.57
22:BA:323:C:O2	26:BE:163:ASN:ND2	2.38	0.57
20:CT:35:VAL:HG21	20:CT:54:MET:HG2	1.86	0.57
29:DH:62:LEU:C	29:DH:62:LEU:HD13	2.25	0.57
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.39	0.57
22:DA:1009:A:N3	22:DA:1153:C:O2'	2.36	0.57
33:BL:109:LYS:HG2	33:BL:126:ARG:HB2	1.85	0.57
2:CB:33:GLY:HA2	2:CB:40:ILE:N	2.19	0.57
22:BA:582:A:H2'	22:BA:583:G:C8	2.39	0.57
46:BY:61:ALA:O	46:BY:63:ALA:N	2.38	0.57
9:AI:19:VAL:HA	9:AI:65:ILE:HG22	1.86	0.57
3:CC:47:LEU:HB3	3:CC:50:ALA:HB3	1.86	0.57
22:BA:381:G:OP1	45:BX:18:ARG:NH2	2.32	0.57
23:DB:29:A:O2'	23:DB:58:A:N1	2.28	0.57
1:CA:1239:A:H2'	1:CA:1298:U:O4	2.05	0.57
1:AA:570:G:O6	1:AA:865:A:N6	2.38	0.57
29:BH:117:LEU:HD21	29:BH:121:VAL:CA	2.35	0.57
29:BH:132:PHE:CE2	29:BH:142:VAL:HG21	2.40	0.57
2:AB:17:GLY:HA3	2:AB:40:ILE:HA	1.86	0.57
4:AD:188:ARG:HH12	4:AD:192:SER:CB	2.18	0.57
2:CB:50:PHE:HD1	2:CB:54:LEU:HD23	1.69	0.57
29:DH:117:LEU:HB3	29:DH:120:GLY:O	2.05	0.57
28:BG:149:ARG:HH21	28:BG:167:GLU:CD	2.07	0.57
1:CA:32:A:OP1	1:CA:398:U:H1'	2.03	0.57
10:AJ:53:ILE:HG22	10:AJ:61:ALA:HB1	1.87	0.57
22:BA:1063:G:N2	30:BI:90:SER:HG	2.02	0.57
1:CA:1070:U:H2'	1:CA:1071:C:C6	2.40	0.57
22:BA:2532:G:O2'	22:BA:2657:A:N6	2.36	0.57
22:DA:92:U:H2'	22:DA:93:G:O4'	2.04	0.57
30:DI:15:ALA:HB3	30:DI:52:GLY:H	1.68	0.57
1:CA:304:U:H2'	1:CA:305:G:C8	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2636:C:H2'	22:DA:2637:U:C6	2.39	0.57
37:DP:65:SER:O	37:DP:67:GLY:N	2.37	0.57
13:CM:40:ALA:O	13:CM:42:ASP:N	2.38	0.57
33:DL:29:LYS:HG3	33:DL:30:THR:HG23	1.86	0.57
1:CA:689:C:HO2'	1:CA:705:G:HO2'	1.52	0.57
14:AN:54:ASP:OD1	14:AN:59:ARG:NH1	2.37	0.57
17:AQ:21:ILE:HB	17:AQ:48:ASP:OD2	2.05	0.57
25:BD:5:VAL:HG21	25:BD:80:TRP:CD2	2.40	0.57
1:AA:337:G:H2'	1:AA:338:A:C8	2.40	0.57
30:BI:101:ILE:O	30:BI:141:GLU:HB2	2.05	0.57
22:DA:2346:A:H3'	22:DA:2347:C:C5'	2.35	0.57
1:CA:689:C:OP1	11:CK:46:THR:OG1	2.15	0.57
37:DP:22:PRO:HA	37:DP:47:VAL:HG12	1.87	0.57
24:BC:10:SER:O	24:BC:13:ARG:HB3	2.05	0.57
22:DA:631:A:N3	22:DA:2415:G:O2'	2.34	0.57
23:DB:41:G:H8	27:DF:66:LEU:HD11	1.69	0.57
1:AA:1278:G:H4'	1:AA:1279:G:C8	2.40	0.57
38:BQ:87:SER:HB3	39:BR:51:VAL:HA	1.86	0.57
39:BR:39:LEU:O	39:BR:49:ILE:HG23	2.04	0.57
2:AB:103:ASN:O	2:AB:106:THR:N	2.25	0.57
22:DA:2674:G:H4'	32:DK:30:ARG:HD2	1.85	0.57
22:DA:1035:U:H2'	22:DA:1036:G:C8	2.40	0.57
22:DA:1827:U:O2'	22:DA:1970:A:N3	2.32	0.57
52:D4:36:ARG:HG2	52:D4:37:GLN:H	1.69	0.57
31:DJ:17:VAL:HG22	31:DJ:55:ILE:HB	1.87	0.57
19:CS:4:SER:O	19:CS:5:LEU:HB2	2.05	0.57
22:BA:1028:A:N6	22:BA:1125:G:H2'	2.20	0.57
51:D3:33:LEU:HA	51:D3:36:LYS:HD2	1.87	0.57
1:CA:54:C:H2'	1:CA:352:C:H41	1.70	0.56
31:BJ:130:HIS:CE1	31:BJ:137:PRO:HG3	2.40	0.56
12:AL:5:ASN:HB3	12:AL:9:ARG:HH12	1.70	0.56
3:AC:40:ARG:NH1	3:AC:55:ILE:O	2.37	0.56
6:CF:45:ARG:O	6:CF:56:LYS:HA	2.05	0.56
1:CA:687:A:N3	1:CA:688:G:H1'	2.19	0.56
1:AA:68:G:C5	1:AA:69:G:H1'	2.40	0.56
1:AA:203:G:O2'	1:AA:465:A:N1	2.38	0.56
1:CA:1108:G:H5''	3:CC:176:HIS:CD2	2.40	0.56
22:BA:1584:U:O2	22:BA:1585:C:H5'	2.04	0.56
38:DQ:87:SER:HB3	39:DR:51:VAL:HA	1.85	0.56
1:AA:1144:G:N2	1:AA:1146:A:H62	2.02	0.56
2:AB:23:TRP:CH2	2:AB:25:PRO:HA	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BQ:88:VAL:HG22	39:BR:49:ILE:HG13	1.87	0.56
22:DA:729:G:H2'	22:DA:1775:U:H1'	1.87	0.56
22:DA:813:U:H1'	22:DA:1226:A:N3	2.20	0.56
33:BL:85:VAL:HG11	33:BL:95:LEU:HD23	1.85	0.56
22:DA:1187:G:N7	57:DA:3575:HOH:O	2.32	0.56
22:DA:328:U:O3'	42:DU:66:GLN:HG3	2.05	0.56
1:CA:1166:G:C6	1:CA:1168:U:H5''	2.41	0.56
22:DA:1181:U:H2'	22:DA:1182:G:C8	2.40	0.56
24:DC:17:VAL:H	24:DC:204:VAL:HG22	1.69	0.56
11:AK:88:GLY:H	11:AK:114:THR:HG22	1.69	0.56
28:DG:44:LYS:H	28:DG:44:LYS:HE3	1.70	0.56
2:CB:94:HIS:CD2	2:CB:146:ASN:HB2	2.39	0.56
11:CK:45:ALA:HB3	11:CK:70:CYS:HB2	1.87	0.56
14:CN:3:LYS:HB3	14:CN:6:MET:HG2	1.86	0.56
29:BH:83:LYS:CD	1:CA:55:A:HO2'	2.03	0.56
1:CA:56:U:H2'	1:CA:57:G:C8	2.40	0.56
22:BA:2198:A:C2	29:BH:29:PHE:HB2	2.40	0.56
22:BA:1056:G:O2'	22:BA:1086:A:H8	1.87	0.56
22:DA:1076:C:H1'	30:DI:93:PRO:HG2	1.86	0.56
22:BA:979:A:H2'	22:BA:982:C:H42	1.68	0.56
13:CM:8:ASN:ND2	13:CM:10:PRO:HG3	2.20	0.56
1:AA:587:G:H4'	8:AH:4:GLN:HA	1.88	0.56
2:AB:85:LEU:HG	2:AB:86:SER:N	2.20	0.56
22:BA:2683:C:O2	32:BK:70:ARG:NH2	2.35	0.56
20:CT:10:ARG:O	20:CT:14:SER:OG	2.21	0.56
1:CA:1226:C:H2'	13:CM:102:THR:HB	1.87	0.56
1:AA:1129:C:H5'	9:AI:18:ARG:HH22	1.70	0.56
20:AT:25:ARG:HG2	20:AT:29:ARG:HH11	1.71	0.56
24:BC:15:HIS:O	24:BC:204:VAL:HG21	2.05	0.56
24:BC:17:VAL:HB	24:BC:204:VAL:HG13	1.87	0.56
22:BA:1187:G:H5'	39:BR:83:TYR:CE2	2.39	0.56
22:BA:1624:U:H2'	22:BA:1625:C:H6	1.69	0.56
37:DP:92:VAL:HG21	37:DP:97:LEU:HD11	1.87	0.56
22:BA:2674:G:H4'	32:BK:30:ARG:HD2	1.85	0.56
22:BA:2591:C:H2'	22:BA:2592:G:C8	2.39	0.56
22:DA:2849:U:OP2	37:DP:93:ARG:NH2	2.35	0.56
1:AA:215:C:H2'	1:AA:216:U:O4'	2.04	0.56
1:CA:1036:A:H3'	1:CA:1037:C:C6	2.40	0.56
11:AK:23:ILE:HD11	11:AK:86:VAL:HG13	1.86	0.56
1:CA:718:A:H5'	11:CK:119:ASN:ND2	2.21	0.56
44:BW:66:LYS:HD2	44:BW:85:GLU:HB3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1342:C:H2'	1:CA:1343:G:C8	2.39	0.56
22:BA:450:G:O6	57:BA:3243:HOH:O	2.16	0.56
22:DA:750:A:H5''	22:DA:751:A:OP2	2.05	0.56
4:AD:168:PRO:HG2	4:AD:171:LEU:HD11	1.88	0.56
22:DA:2461:A:H1'	22:DA:2492:U:C2	2.41	0.56
43:DV:21:ARG:HA	43:DV:25:LYS:O	2.06	0.56
22:DA:279:A:H61	22:DA:361:G:H1'	1.70	0.56
22:DA:1823:G:N7	57:DA:3651:HOH:O	2.32	0.56
43:BV:6:ALA:HB1	43:BV:40:ILE:HG23	1.87	0.56
4:AD:107:PHE:CG	4:AD:145:ILE:HD11	2.41	0.56
15:CO:39:LEU:HG	15:CO:43:PHE:CE1	2.40	0.56
22:DA:1259:G:H2'	22:DA:1260:A:H8	1.69	0.56
29:DH:21:VAL:HG22	29:DH:22:LYS:N	2.19	0.56
22:DA:1197:G:H2'	22:DA:1198:U:C6	2.40	0.56
18:AR:36:SER:HA	18:AR:72:ASP:HB3	1.87	0.56
23:DB:27:C:OP1	36:DO:34:HIS:NE2	2.38	0.56
22:BA:30:G:H2'	22:BA:31:C:C6	2.40	0.56
24:DC:88:SER:HB2	24:DC:158:ALA:H	1.70	0.56
22:DA:1267:U:OP2	22:DA:2012:G:N1	2.24	0.56
1:CA:955:U:H2'	1:CA:956:U:O4'	2.06	0.56
39:BR:76:LYS:HD3	39:BR:85:LYS:HD2	1.87	0.56
22:BA:2339:C:H2'	22:BA:2340:A:C8	2.41	0.56
22:DA:2341:G:H2'	22:DA:2342:C:C6	2.40	0.56
22:DA:538:A:H5''	31:DJ:7:LYS:HE3	1.88	0.56
22:DA:1060:U:O4'	22:DA:1062:G:H5'	2.06	0.56
29:DH:83:LYS:N	29:DH:149:GLU:HG2	2.20	0.56
22:DA:2032:G:H1'	25:DD:150:GLN:NE2	2.21	0.56
22:DA:2720:U:H5''	37:DP:53:ARG:NH2	2.20	0.56
22:DA:222:A:H3'	22:DA:421:C:H5'	1.87	0.56
1:CA:1219:A:H2'	1:CA:1220:G:C8	2.39	0.56
22:DA:223:A:N1	22:DA:407:G:O2'	2.29	0.56
22:BA:1441:G:H2'	22:BA:1442:U:C6	2.41	0.56
22:DA:27:G:N2	22:DA:512:G:H1'	2.20	0.56
22:DA:536:G:N2	22:DA:557:C:O2	2.39	0.56
2:AB:49:MET:O	2:AB:53:ALA:HB2	2.06	0.56
18:AR:37:GLY:O	18:AR:63:ARG:NH2	2.37	0.56
22:BA:1073:A:N7	22:BA:1074:G:H8	2.04	0.56
1:AA:702:A:H61	22:BA:1846:G:H4'	1.71	0.56
24:DC:159:GLY:N	24:DC:195:VAL:HG22	2.20	0.56
6:CF:13:ASP:O	6:CF:15:SER:N	2.36	0.56
12:AL:21:VAL:HG23	12:AL:95:TYR:HE1	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:80:LEU:HD21	13:AM:87:ARG:HE	1.69	0.56
22:DA:120:U:OP2	22:DA:120:U:H3'	2.06	0.56
38:DQ:72:ASN:CB	38:DQ:110:VAL:HG11	2.36	0.56
27:DF:43:ALA:O	27:DF:47:LYS:HD2	2.05	0.56
3:AC:114:LYS:HD3	3:AC:185:ASN:OD1	2.06	0.56
22:BA:2032:G:H1'	25:BD:150:GLN:OE1	2.06	0.56
36:DO:109:ALA:HA	36:DO:112:GLU:HB2	1.88	0.56
22:DA:1501:G:H2'	22:DA:1502:A:H8	1.69	0.56
22:BA:70:G:H4'	22:BA:71:A:OP1	2.05	0.56
1:AA:983:A:H2	1:AA:1222:G:H22	1.53	0.56
22:BA:2275:C:O2	34:BM:84:LYS:HD3	2.06	0.56
5:CE:155:ALA:HB3	5:CE:156:LYS:HE3	1.87	0.56
4:AD:10:LYS:HA	4:AD:13:ARG:HG3	1.88	0.56
22:BA:1179:G:N7	22:BA:1180:U:H1'	2.20	0.56
1:CA:1320:C:N3	19:CS:36:ARG:NH1	2.54	0.56
30:BI:78:VAL:HG23	30:BI:79:LEU:HG	1.87	0.56
27:BF:36:LEU:HD21	27:BF:99:PHE:CE1	2.40	0.56
22:BA:441:U:H2'	22:BA:442:G:C8	2.41	0.56
22:DA:1515:A:HO2'	22:DA:1556:C:HO2'	1.54	0.56
43:BV:21:ARG:HA	43:BV:25:LYS:O	2.06	0.56
1:CA:920:U:H2'	1:CA:921:U:C6	2.41	0.56
22:BA:1783:A:H5'	22:BA:2608:G:H4'	1.87	0.56
14:CN:21:PHE:O	14:CN:23:LYS:N	2.39	0.56
22:DA:591:U:HO2'	51:D3:2:PRO:N	2.03	0.56
6:AF:70:VAL:HA	6:AF:73:GLU:HG2	1.86	0.56
22:DA:1258:U:H2'	22:DA:1259:G:H8	1.66	0.56
39:BR:49:ILE:HB	39:BR:51:VAL:O	2.06	0.56
2:AB:160:ALA:HA	2:AB:182:PRO:HD2	1.87	0.56
12:CL:50:ARG:HB2	12:CL:90:LEU:HD11	1.88	0.56
22:DA:1231:U:H2'	22:DA:1232:G:C8	2.41	0.56
1:CA:703:G:H4'	1:CA:704:A:H5'	1.87	0.56
1:AA:41:G:H2'	1:AA:42:G:C8	2.41	0.56
4:AD:97:ARG:HB3	4:AD:99:ASP:OD1	2.05	0.56
11:AK:112:ASP:HB2	21:AU:17:ARG:HH12	1.70	0.56
8:CH:77:ARG:NE	8:CH:79:SER:O	2.38	0.56
35:DN:98:LEU:HD13	48:D0:54:VAL:HG21	1.87	0.56
1:CA:663:A:O3'	18:CR:53:ARG:NH2	2.38	0.56
22:DA:214:G:H1'	22:DA:217:A:H5'	1.88	0.56
1:AA:91:U:C2	1:AA:92:U:H1'	2.41	0.56
1:CA:1540:U:H4'	21:CU:18:ARG:HG2	1.88	0.56
22:DA:1187:G:H5"	39:DR:83:TYR:CE2	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:65:U:H2'	22:BA:66:C:H6	1.69	0.56
1:CA:620:C:H2'	1:CA:621:A:O4'	2.06	0.56
5:CE:115:LEU:O	5:CE:120:VAL:HG23	2.06	0.56
49:B1:26:ASN:OD1	49:B1:28:ARG:HB2	2.06	0.56
22:BA:118:A:N3	22:BA:178:G:H1'	2.21	0.56
22:DA:352:A:H2'	22:DA:353:C:O4'	2.06	0.56
22:DA:286:U:H2'	22:DA:287:G:C8	2.40	0.56
42:BU:49:VAL:O	42:BU:51:ALA:N	2.39	0.56
22:BA:151:C:H2'	22:BA:152:A:C8	2.41	0.56
22:DA:2114:A:C5	22:DA:2167:U:H4'	2.41	0.56
22:BA:2198:A:N1	29:BH:25:TYR:HD1	2.04	0.56
4:CD:167:LYS:HE2	4:CD:173:VAL:HG11	1.88	0.56
22:BA:2128:G:H5'	53:B5:36:ALA:HA	1.88	0.56
22:BA:360:U:H3'	22:BA:361:G:C8	2.40	0.56
2:AB:58:ASN:HA	2:AB:61:ALA:HB3	1.88	0.56
33:BL:93:ASN:HA	33:BL:96:LYS:HB2	1.87	0.56
39:DR:78:ARG:HB3	39:DR:83:TYR:HB3	1.88	0.56
1:CA:1330:U:H4'	13:CM:23:TYR:CE1	2.41	0.56
29:BH:40:THR:OG1	29:BH:43:ASN:OD1	2.24	0.56
14:CN:64:CYS:SG	14:CN:83:LYS:HG3	2.46	0.56
22:DA:1605:C:H2'	22:DA:1606:C:H5'	1.87	0.56
25:DD:25:THR:HG21	25:DD:193:VAL:HG22	1.87	0.56
7:CG:65:ALA:O	7:CG:127:ALA:HB1	2.06	0.56
1:CA:123:U:H2'	1:CA:124:C:H6	1.70	0.56
1:CA:840:C:N3	1:CA:842:U:H4'	2.21	0.56
22:DA:2773:C:OP1	25:DD:171:THR:OG1	2.22	0.56
22:DA:1297:C:O2'	22:DA:1302:A:N1	2.31	0.56
22:DA:1947:C:H2'	22:DA:1948:G:H8	1.70	0.56
11:CK:15:GLN:HA	11:CK:77:TYR:HA	1.88	0.56
1:AA:1351:U:H2'	1:AA:1352:C:C6	2.41	0.56
46:BY:46:VAL:HA	46:BY:49:ASP:HB2	1.86	0.56
22:DA:1652:A:OP1	35:DN:8:ARG:NH2	2.35	0.56
1:AA:1094:G:O2'	1:AA:1095:U:OP2	2.23	0.56
11:AK:76:GLU:O	22:BA:2141:G:H5''	2.06	0.55
22:BA:1168:G:H2'	22:BA:1169:A:O4'	2.06	0.55
54:D6:6:MHV:CE	54:D6:7:004:HNA	2.19	0.55
7:AG:146:GLU:HG3	7:AG:149:LYS:HE2	1.87	0.55
16:AP:71:VAL:O	16:AP:75:ILE:HG13	2.06	0.55
22:BA:282:A:H2'	22:BA:283:G:C8	2.41	0.55
1:CA:1277:C:O2'	1:CA:1279:G:H1'	2.06	0.55
1:AA:723:U:H5'	1:AA:724:G:OP1	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DN:38:LEU:HD11	35:DN:42:LYS:HE3	1.88	0.55
22:DA:648:G:H2'	22:DA:649:G:H8	1.71	0.55
22:BA:26:G:H1'	22:BA:514:A:H61	1.71	0.55
8:AH:22:LYS:N	8:AH:65:TYR:OH	2.39	0.55
22:DA:1794:A:H2'	22:DA:1795:C:H6	1.70	0.55
37:BP:91:ALA:HB2	37:BP:113:ARG:HA	1.86	0.55
22:BA:2313:C:H5''	27:BF:88:LYS:HD3	1.88	0.55
1:CA:1356:G:H2'	1:CA:1357:A:C8	2.41	0.55
22:DA:753:A:H2'	22:DA:754:U:C6	2.41	0.55
35:BN:11:ASN:ND2	57:BN:203:HOH:O	2.39	0.55
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.87	0.55
10:AJ:81:GLU:HA	10:AJ:84:VAL:HG12	1.87	0.55
1:AA:376:G:H2'	1:AA:377:G:H8	1.71	0.55
2:AB:117:LEU:HB3	2:AB:141:LEU:HD11	1.87	0.55
46:BY:9:LYS:HG2	46:BY:11:VAL:H	1.71	0.55
1:CA:216:U:H2'	1:CA:217:C:C6	2.40	0.55
15:AO:33:THR:HG21	15:AO:85:LEU:HG	1.88	0.55
2:AB:83:ALA:HA	2:AB:86:SER:OG	2.06	0.55
22:DA:764:A:N1	22:DA:1789:A:O2'	2.38	0.55
1:CA:1070:U:H2'	1:CA:1071:C:H6	1.71	0.55
1:CA:1219:A:H2'	1:CA:1220:G:H8	1.70	0.55
22:BA:151:C:H2'	22:BA:152:A:H8	1.71	0.55
2:AB:57:LEU:O	2:AB:60:ILE:HG13	2.06	0.55
22:BA:5:A:H2'	22:BA:6:A:C8	2.41	0.55
5:AE:24:THR:HA	5:AE:29:ARG:HA	1.87	0.55
40:BS:66:ILE:HA	40:BS:69:LEU:HD22	1.88	0.55
2:CB:187:VAL:HB	2:CB:191:SER:HB2	1.89	0.55
6:AF:42:TRP:HZ2	6:AF:61:LEU:HD22	1.70	0.55
3:CC:67:THR:HA	3:CC:102:ASN:HB2	1.88	0.55
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.88	0.55
22:BA:1178:C:H2'	22:BA:1179:G:N7	2.21	0.55
3:AC:140:ASN:HA	3:AC:143:ARG:CB	2.36	0.55
2:CB:80:VAL:HG13	2:CB:214:LEU:HD11	1.86	0.55
1:CA:1343:G:O2'	9:CI:123:ARG:HD2	2.05	0.55
22:BA:2321:U:H5'	22:BA:2322:A:OP2	2.06	0.55
27:BF:119:ALA:HB1	27:BF:167:ARG:HD2	1.88	0.55
2:AB:186:ILE:HA	2:AB:200:ILE:HB	1.89	0.55
2:CB:157:LEU:HD12	2:CB:181:ILE:HD11	1.89	0.55
28:BG:121:ILE:HD12	28:BG:141:ILE:HG23	1.88	0.55
24:DC:247:PRO:HG2	24:DC:248:TRP:CZ3	2.42	0.55
22:BA:58:G:OP1	41:BT:78:SER:HB2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:159:G:H8	1:AA:159:G:H5''	1.71	0.55
24:BC:232:HIS:NE2	24:BC:244:PRO:HA	2.22	0.55
29:BH:86:ASP:O	29:BH:87:GLU:CB	2.53	0.55
29:BH:83:LYS:CD	1:CA:55:A:H2'	2.36	0.55
22:BA:2094:A:H5'	29:BH:25:TYR:CG	2.41	0.55
5:CE:102:GLY:O	5:CE:104:GLY:N	2.39	0.55
22:BA:2683:C:H4'	25:BD:13:ARG:NH1	2.22	0.55
20:CT:67:ILE:HD11	20:CT:71:LYS:HD3	1.88	0.55
1:AA:998:C:H2'	1:AA:999:C:C6	2.41	0.55
22:DA:674:G:H1'	26:DE:69:ARG:NE	2.21	0.55
31:DJ:4:PHE:HB3	38:DQ:64:ARG:HH12	1.71	0.55
1:AA:1277:C:H2'	1:AA:1279:G:H8	1.72	0.55
22:BA:646:U:H5'	22:BA:647:G:H5''	1.88	0.55
22:DA:2564:A:H5'	22:DA:2648:G:H4'	1.88	0.55
22:DA:704:G:H1'	22:DA:726:G:H22	1.72	0.55
22:BA:2315:G:H2'	22:BA:2316:G:H8	1.72	0.55
23:BB:48:U:H2'	23:BB:49:C:C6	2.42	0.55
1:AA:694:A:N1	1:AA:787:A:O2'	2.39	0.55
31:DJ:65:THR:O	31:DJ:68:LYS:HB2	2.06	0.55
22:DA:2780:G:N1	31:DJ:102:GLU:OE2	2.32	0.55
29:BH:98:ASP:O	29:BH:102:ALA:HB3	2.07	0.55
22:BA:2498:C:OP2	57:BA:3689:HOH:O	2.18	0.55
41:BT:3:ARG:HB3	41:BT:6:ARG:HB3	1.89	0.55
22:DA:2372:U:H2'	22:DA:2373:G:C8	2.42	0.55
45:DX:41:GLU:OE1	45:DX:44:LYS:NZ	2.31	0.55
1:CA:33:A:H2'	1:CA:34:C:C6	2.42	0.55
1:CA:1203:C:H2'	1:CA:1204:A:C8	2.42	0.55
2:CB:211:THR:HA	2:CB:214:LEU:HB3	1.89	0.55
33:DL:77:ILE:HG23	33:DL:81:ASP:OD2	2.07	0.55
41:DT:34:VAL:HG21	41:DT:43:ILE:HD11	1.87	0.55
30:BI:39:CYS:O	30:BI:43:ASN:HB2	2.07	0.55
8:AH:36:ILE:HD11	8:AH:126:ILE:HG21	1.87	0.55
36:DO:97:PHE:HB2	36:DO:103:VAL:HG11	1.88	0.55
22:BA:1006:C:P	57:BA:3787:HOH:O	2.64	0.55
1:AA:593:U:H2'	1:AA:594:U:C6	2.42	0.55
1:CA:866:C:C4	1:CA:867:G:H1'	2.42	0.55
34:BM:17:ASN:O	34:BM:38:ARG:HD3	2.07	0.55
22:BA:994:C:H1'	39:BR:10:LYS:HE3	1.89	0.55
31:DJ:77:HIS:HA	31:DJ:83:GLY:O	2.07	0.55
25:BD:47:ALA:HA	25:BD:84:LEU:H	1.71	0.55
24:BC:235:GLY:HA2	24:BC:239:ASN:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:121:VAL:N	29:BH:122:LEU:CA	2.69	0.55
29:BH:90:LEU:O	1:CA:358:U:C4'	2.43	0.55
22:BA:2093:G:O2'	29:BH:25:TYR:CB	2.55	0.55
22:BA:2199:A:H1'	29:BH:28:ASN:HD21	1.67	0.55
4:AD:150:LYS:NZ	4:AD:177:LYS:O	2.25	0.55
22:DA:1153:C:OP1	38:DQ:92:ARG:NH1	2.40	0.55
42:BU:81:ASP:OD1	42:BU:82:ARG:N	2.40	0.55
2:AB:206:ALA:O	2:AB:208:ARG:N	2.40	0.55
16:CP:19:VAL:HG22	16:CP:36:VAL:HG12	1.87	0.55
22:DA:981:A:N1	22:DA:2027:G:O2'	2.29	0.55
22:DA:153:U:H2'	22:DA:154:U:C6	2.42	0.55
3:AC:153:VAL:HG12	3:AC:198:VAL:HG22	1.88	0.55
1:CA:1113:C:H4'	3:CC:14:ILE:HD12	1.88	0.55
22:DA:2115:G:O2'	22:DA:2117:A:N6	2.40	0.55
5:AE:45:ARG:HG2	5:AE:73:ASN:HB3	1.87	0.55
11:CK:97:ILE:HD13	11:CK:110:ILE:HD11	1.89	0.55
11:CK:23:ILE:HD11	11:CK:86:VAL:HG13	1.87	0.55
1:CA:1492:A:H3'	1:CA:1493:A:C8	2.41	0.55
29:BH:121:VAL:N	29:BH:122:LEU:CB	2.70	0.55
29:BH:120:GLY:CA	29:BH:122:LEU:HA	2.37	0.55
22:DA:1779:U:H5	22:DA:1784:A:N7	2.05	0.55
22:BA:660:C:H2'	22:BA:661:A:C8	2.42	0.55
22:BA:1582:C:O2'	22:BA:1585:C:N3	2.38	0.55
22:DA:1230:A:H2'	22:DA:1231:U:C6	2.42	0.55
30:DI:28:LEU:HD13	30:DI:38:PHE:CD2	2.42	0.55
4:AD:198:HIS:HA	4:AD:201:VAL:HB	1.88	0.55
1:AA:1053:G:O5'	1:AA:1054:C:H5'	2.06	0.55
38:DQ:78:LYS:HE2	38:DQ:117:LEU:HD21	1.88	0.55
26:DE:108:ILE:HB	33:DL:2:ARG:HH22	1.72	0.55
39:BR:49:ILE:HB	39:BR:52:PRO:HA	1.88	0.55
22:DA:2185:U:H2'	22:DA:2186:G:C8	2.42	0.55
32:BK:93:GLN:HE22	32:BK:111:LYS:HB2	1.72	0.55
22:BA:2757:A:N1	28:BG:67:THR:HG21	2.22	0.55
22:BA:1358:G:H1'	22:BA:1374:G:N2	2.22	0.55
1:AA:108:G:N3	1:AA:108:G:H5'	2.22	0.55
1:AA:666:G:H5'	1:AA:726:C:H1'	1.88	0.55
22:BA:927:A:H2'	22:BA:928:A:C8	2.42	0.55
1:CA:466:A:H2'	1:CA:468:A:H2	1.71	0.55
40:DS:22:ASP:CG	40:DS:25:ARG:HH22	2.10	0.55
22:BA:250:G:OP2	51:B3:13:ARG:NH1	2.39	0.55
19:CS:41:PHE:HB2	19:CS:44:MET:HG3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CG:136:LYS:O	7:CG:140:ASP:HB2	2.07	0.55
31:DJ:11:VAL:HG11	31:DJ:50:THR:HA	1.87	0.55
22:BA:610:C:O2	22:BA:618:G:N2	2.28	0.55
22:DA:494:G:H4'	40:DS:6:LYS:HG3	1.89	0.55
2:CB:142:GLU:HA	2:CB:145:GLU:HB2	1.88	0.55
7:AG:18:PHE:HZ	7:AG:58:GLU:HG2	1.72	0.55
22:BA:528:A:C2	22:BA:2043:C:H4'	2.42	0.55
1:AA:34:C:H2'	1:AA:35:G:C8	2.42	0.55
22:DA:679:C:H2'	22:DA:680:C:C6	2.42	0.55
1:AA:41:G:H2'	1:AA:42:G:H8	1.72	0.55
35:DN:1:MET:O	35:DN:3:HIS:N	2.40	0.55
1:CA:805:C:H2'	1:CA:806:C:H6	1.72	0.55
22:DA:335:C:O5'	22:DA:335:C:H6	1.90	0.55
22:DA:448:U:H5''	57:DA:3241:HOH:O	2.07	0.55
3:AC:6:HIS:HB3	14:AN:89:MET:HG3	1.89	0.55
29:BH:10:ALA:O	29:BH:12:LEU:N	2.40	0.55
4:AD:50:ASP:O	4:AD:54:GLN:HB2	2.07	0.55
41:BT:51:PHE:HE1	46:BY:26:PHE:HZ	1.55	0.55
8:CH:93:PRO:HG3	8:CH:125:ILE:HD12	1.88	0.55
22:DA:1951:U:H2'	22:DA:1953:A:OP2	2.07	0.55
25:BD:4:LEU:HD12	25:BD:32:ASN:CG	2.27	0.55
22:BA:2127:G:H4'	22:BA:2128:G:OP1	2.06	0.55
22:BA:1926:U:O2	22:BA:1926:U:H2'	2.06	0.55
22:BA:1386:C:H2'	22:BA:1387:A:C8	2.42	0.55
33:DL:82:LEU:HD12	33:DL:90:VAL:HG21	1.89	0.55
41:DT:44:LYS:O	41:DT:48:GLN:HG2	2.07	0.55
22:DA:883:G:N2	22:DA:894:U:O2	2.40	0.55
13:AM:75:MET:SD	27:BF:112:ARG:HB2	2.46	0.55
48:B0:34:SER:OG	48:B0:36:GLU:HG2	2.06	0.55
22:BA:1965:C:OP1	22:BA:1966:A:O2'	2.13	0.55
1:AA:1234:C:H2'	1:AA:1235:U:H6	1.70	0.55
28:DG:140:VAL:O	28:DG:144:VAL:HG23	2.06	0.55
20:CT:81:ALA:O	20:CT:85:LYS:HG2	2.07	0.55
22:DA:2267:A:H5''	22:DA:2268:A:H5'	1.88	0.54
10:CJ:49:PHE:N	10:CJ:65:TYR:O	2.31	0.54
22:DA:446:G:H5''	38:DQ:5:LYS:NZ	2.21	0.54
22:BA:1322:A:O3'	40:BS:84:ARG:NH1	2.36	0.54
22:BA:20:C:H2'	22:BA:21:A:C8	2.41	0.54
22:DA:893:C:H2'	22:DA:894:U:O4'	2.08	0.54
22:DA:1935:G:H1'	22:DA:1964:G:N2	2.22	0.54
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DN:72:ASP:HB3	35:DN:75:ILE:HB	1.90	0.54
22:DA:1358:G:H1'	22:DA:1374:G:N2	2.22	0.54
22:DA:532:A:N1	22:DA:2020:A:H1'	2.21	0.54
22:BA:417:C:H2'	22:BA:418:C:H6	1.72	0.54
22:DA:2790:U:H5'	22:DA:2893:A:N7	2.22	0.54
22:BA:878:A:H5'	22:BA:879:G:OP2	2.07	0.54
32:DK:99:ILE:HD13	32:DK:118:LEU:HD12	1.89	0.54
1:AA:903:G:H2'	1:AA:904:U:H6	1.72	0.54
24:BC:71:LYS:HD2	24:BC:74:ILE:HD12	1.89	0.54
1:CA:736:C:H2'	1:CA:737:C:C6	2.41	0.54
22:BA:1799:G:O6	24:BC:178:SER:HB3	2.06	0.54
22:DA:2057:G:H2'	22:DA:2058:A:O4'	2.07	0.54
3:CC:111:LEU:HD13	3:CC:146:ALA:HB2	1.88	0.54
2:AB:173:ILE:HG23	2:AB:183:VAL:HG11	1.89	0.54
22:BA:1442:U:H2'	22:BA:1443:U:C6	2.43	0.54
33:DL:116:VAL:HG11	33:DL:134:ALA:HB1	1.89	0.54
1:CA:1252:A:H2'	1:CA:1253:G:O4'	2.08	0.54
34:DM:41:LEU:HD21	34:DM:124:LEU:HD13	1.89	0.54
22:BA:1927:A:H2'	22:BA:1928:A:C8	2.42	0.54
42:DU:96:PHE:CE1	42:DU:103:ILE:HG12	2.42	0.54
42:DU:74:ASN:HA	42:DU:96:PHE:CZ	2.41	0.54
1:AA:772:U:O2'	1:AA:773:G:OP1	2.23	0.54
6:AF:8:PHE:HA	6:AF:87:SER:HA	1.88	0.54
26:DE:24:ASN:O	26:DE:28:VAL:HG23	2.07	0.54
1:AA:1442:G:H2'	1:AA:1443:C:H6	1.71	0.54
22:BA:1430:G:H2'	22:BA:1431:A:C8	2.42	0.54
22:BA:1796:U:H2'	22:BA:1797:G:C8	2.40	0.54
22:BA:2845:U:H5''	37:BP:52:ASN:O	2.08	0.54
7:AG:57:SER:OG	7:AG:58:GLU:N	2.40	0.54
2:AB:63:ARG:O	2:AB:64:LYS:HB2	2.07	0.54
1:CA:1492:A:H3'	1:CA:1493:A:H8	1.72	0.54
22:DA:1045:C:H41	22:DA:1111:A:H2'	1.72	0.54
3:CC:130:PHE:CE2	3:CC:131:ARG:HD3	2.43	0.54
6:AF:90:MET:HG2	18:AR:61:ARG:HH21	1.72	0.54
26:DE:97:ASN:HB2	26:DE:100:MET:HB2	1.89	0.54
22:BA:2547:A:H5''	32:BK:29:HIS:NE2	2.23	0.54
46:DY:3:ALA:HA	46:DY:6:LEU:HB2	1.88	0.54
11:CK:35:THR:OG1	11:CK:40:ASN:N	2.38	0.54
22:BA:2153:C:H2'	22:BA:2154:A:O4'	2.07	0.54
22:DA:1299:G:O6	22:DA:1639:C:H5''	2.07	0.54
29:BH:90:LEU:HA	29:BH:125:THR:HG23	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:13:ARG:HG3	11:AK:77:TYR:HE1	1.73	0.54
29:BH:14:SER:OG	29:BH:17:ASP:CG	2.46	0.54
4:CD:26:ARG:HG3	4:CD:27:ALA:N	2.23	0.54
11:AK:88:GLY:N	11:AK:114:THR:HG22	2.23	0.54
22:DA:2849:U:H4'	22:DA:2868:A:C2	2.41	0.54
28:DG:24:ILE:HG21	28:DG:72:LEU:HD21	1.88	0.54
22:DA:2540:C:H2'	22:DA:2541:A:H8	1.71	0.54
11:AK:24:HIS:HB3	11:AK:31:ILE:HG23	1.89	0.54
8:AH:88:ARG:O	8:AH:122:GLY:HA3	2.08	0.54
22:DA:999:U:OP2	57:DA:3357:HOH:O	2.18	0.54
7:CG:91:VAL:HG23	7:CG:95:ARG:HB3	1.89	0.54
22:DA:1747:U:H2'	22:DA:1748:C:C6	2.43	0.54
1:AA:1152:A:H5'	10:AJ:15:HIS:CD2	2.43	0.54
1:AA:545:C:H5'	4:AD:69:GLU:HB2	1.89	0.54
4:AD:62:ARG:NH1	4:AD:69:GLU:HG2	2.22	0.54
29:BH:90:LEU:CD2	29:BH:93:SER:HA	2.37	0.54
22:BA:423:A:H5''	22:BA:424:G:H5'	1.90	0.54
36:DO:26:LEU:HB3	36:DO:92:PHE:HD1	1.72	0.54
22:DA:17:G:H4'	38:DQ:25:TYR:HE1	1.72	0.54
20:CT:5:LYS:O	20:CT:7:ALA:N	2.40	0.54
22:DA:119:A:H4'	22:DA:120:U:O5'	2.07	0.54
22:BA:588:U:H2'	22:BA:589:U:H6	1.70	0.54
14:AN:81:ARG:HA	14:AN:84:VAL:HB	1.90	0.54
33:DL:77:ILE:HD11	33:DL:101:ILE:HG21	1.89	0.54
27:DF:44:ILE:HG21	27:DF:79:ILE:HG22	1.89	0.54
14:CN:91:GLY:O	14:CN:93:ILE:N	2.40	0.54
1:CA:689:C:OP2	11:CK:53:ARG:NH2	2.40	0.54
22:BA:2572:A:N7	25:BD:150:GLN:HB2	2.23	0.54
22:BA:1672:A:C2	22:BA:2582:G:H5'	2.43	0.54
36:BO:94:ARG:O	36:BO:96:GLY:N	2.40	0.54
29:BH:77:THR:O	29:BH:77:THR:CG2	2.56	0.54
1:AA:1142:G:C2	1:AA:1143:G:H1'	2.42	0.54
37:DP:18:PRO:HG3	37:DP:84:ILE:O	2.07	0.54
22:BA:2140:G:N3	22:BA:2140:G:H2'	2.23	0.54
22:DA:858:G:N2	22:DA:919:U:O4	2.38	0.54
2:AB:167:ASP:OD1	2:AB:168:HIS:N	2.40	0.54
29:BH:103:VAL:HG21	29:BH:132:PHE:CE1	2.42	0.54
22:DA:447:A:H5'	22:DA:449:A:C5	2.42	0.54
40:BS:83:LYS:O	40:BS:84:ARG:HD3	2.07	0.54
14:AN:43:ASN:HA	14:AN:45:VAL:HG22	1.90	0.54
1:AA:93:U:H2'	1:AA:94:G:H5''	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BC:62:TYR:HD2	24:BC:86:ASN:HD22	1.54	0.54
23:DB:62:C:H2'	23:DB:63:C:H6	1.71	0.54
45:DX:54:LYS:HA	45:DX:57:ARG:HB2	1.88	0.54
2:AB:71:GLY:HA2	2:AB:164:ILE:HG22	1.90	0.54
34:DM:54:THR:HA	34:DM:57:VAL:HG22	1.89	0.54
38:BQ:44:GLN:NE2	39:BR:77:PHE:HB3	2.22	0.54
22:DA:2544:G:H2'	22:DA:2545:G:H8	1.73	0.54
33:DL:93:ASN:OD1	33:DL:94:THR:N	2.40	0.54
1:AA:859:G:H2'	1:AA:860:A:C8	2.42	0.54
37:DP:51:ARG:O	37:DP:58:ALA:N	2.34	0.54
22:DA:1439:A:N7	22:DA:1552:A:H2	2.04	0.54
1:AA:1239:A:H62	1:AA:1299:A:N6	2.05	0.54
1:AA:522:C:H2'	1:AA:523:A:O4'	2.06	0.54
38:DQ:94:ILE:HD13	39:DR:11:GLN:HB2	1.89	0.54
22:DA:2615:U:C2	48:D0:4:GLN:HA	2.41	0.54
15:CO:45:GLU:HG2	15:CO:46:HIS:H	1.73	0.54
22:DA:740:C:H5'	22:DA:1784:A:C3'	2.37	0.54
7:AG:40:GLU:HB2	7:AG:44:TYR:CE2	2.43	0.54
22:BA:1266:G:O2'	22:BA:2012:G:O6	2.18	0.54
22:DA:2899:A:H2'	22:DA:2900:A:H8	1.71	0.54
20:CT:29:ARG:O	20:CT:33:LYS:HG2	2.08	0.54
22:BA:2683:C:OP1	37:BP:51:ARG:NH2	2.41	0.54
16:AP:38:PHE:CZ	16:AP:51:ARG:HB2	2.43	0.54
6:AF:47:LEU:HB3	6:AF:49:TYR:O	2.08	0.54
22:BA:65:U:H2'	22:BA:66:C:C6	2.42	0.54
44:DW:21:LEU:HD22	44:DW:39:ARG:HB3	1.90	0.54
2:AB:54:LEU:HD22	2:AB:54:LEU:H	1.72	0.54
22:BA:1006:C:OP2	57:BA:3787:HOH:O	2.18	0.54
25:DD:104:VAL:O	25:DD:105:LYS:HB3	2.07	0.54
1:AA:381:C:H2'	1:AA:382:A:O4'	2.08	0.54
1:AA:116:A:H2'	1:AA:117:G:H8	1.73	0.54
22:DA:82:U:H5'	22:DA:296:U:H5''	1.89	0.54
22:DA:135:U:H2'	22:DA:136:G:C8	2.43	0.54
37:BP:103:ARG:CG	37:BP:103:ARG:HH11	2.21	0.54
22:DA:1270:C:O2'	22:DA:1648:U:OP2	2.25	0.54
9:AI:114:LYS:HG2	9:AI:120:LYS:HA	1.90	0.54
30:DI:5:VAL:HA	30:DI:8:TYR:CE1	2.43	0.54
11:CK:16:VAL:HG12	11:CK:77:TYR:HB3	1.90	0.54
7:CG:69:VAL:HG21	7:CG:104:ILE:HD11	1.88	0.54
1:CA:1308:U:H2'	1:CA:1309:G:C8	2.43	0.54
1:CA:644:U:H2'	1:CA:645:G:O4'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1726:C:H2'	22:DA:1727:C:H6	1.73	0.54
22:BA:1590:A:H2'	22:BA:1591:A:C8	2.43	0.54
22:DA:2291:U:H2'	22:DA:2292:U:H6	1.72	0.54
22:DA:1411:U:H2'	22:DA:1412:U:O4'	2.07	0.54
25:BD:13:ARG:HD2	25:BD:15:PHE:CZ	2.43	0.54
10:AJ:36:VAL:HA	10:AJ:75:ASP:O	2.08	0.54
1:AA:668:G:H2'	1:AA:669:G:H8	1.73	0.54
1:AA:669:G:H2'	1:AA:670:G:C8	2.42	0.54
37:DP:62:ARG:CZ	37:DP:101:ARG:HA	2.38	0.54
27:DF:32:GLU:OE1	27:DF:92:ARG:NH1	2.40	0.54
1:CA:131:A:O2'	1:CA:262:A:N3	2.36	0.54
25:BD:170:VAL:O	25:BD:194:PRO:HG2	2.08	0.54
13:CM:13:LYS:O	13:CM:44:LYS:HG2	2.08	0.54
22:DA:51:G:H4'	22:DA:52:A:H5'	1.89	0.54
31:DJ:109:LEU:HD22	31:DJ:118:MET:HG3	1.88	0.54
22:BA:18:U:OP1	38:BQ:30:ARG:NH2	2.41	0.54
29:BH:97:ARG:CD	1:CA:369:G:O2'	2.42	0.54
1:CA:1362:A:H4'	1:CA:1362:A:OP1	2.06	0.54
22:BA:1509:A:O2'	22:BA:1510:G:OP2	2.21	0.54
1:CA:673:A:O3'	6:CF:86:ARG:NH2	2.41	0.54
40:BS:84:ARG:HB2	40:BS:96:ILE:HG13	1.90	0.54
33:DL:59:ARG:CZ	33:DL:59:ARG:HB3	2.38	0.54
22:DA:1141:U:H4'	22:DA:1142:A:O4'	2.08	0.54
1:AA:398:U:H2'	1:AA:399:G:H8	1.72	0.54
30:DI:5:VAL:HG22	30:DI:8:TYR:HE1	1.72	0.54
1:CA:1491:G:H2'	1:CA:1492:A:C8	2.43	0.54
22:BA:250:G:OP1	57:BA:3818:HOH:O	2.19	0.54
1:CA:1067:A:H4'	1:CA:1068:G:O5'	2.07	0.54
13:AM:16:VAL:HG22	13:AM:41:GLU:O	2.08	0.54
22:DA:1432:G:H2'	22:DA:1433:A:C8	2.42	0.54
2:CB:173:ILE:O	2:CB:177:ASN:ND2	2.40	0.54
28:BG:155:GLU:OE2	28:BG:158:LYS:N	2.41	0.54
29:DH:79:THR:HA	29:DH:145:ASN:HB2	1.89	0.54
1:CA:778:G:O2'	11:CK:121:CYS:HB3	2.08	0.54
29:DH:32:PRO:O	29:DH:33:GLN:HB2	2.08	0.53
22:DA:2572:A:OP1	22:DA:2574:G:O2'	2.18	0.53
17:CQ:52:GLU:CG	17:CQ:53:CYS:H	2.20	0.53
1:AA:1157:A:H5'	1:AA:1158:C:C6	2.43	0.53
1:CA:1206:G:H4'	3:CC:192:THR:O	2.07	0.53
22:DA:2215:C:H2'	22:DA:2216:G:H8	1.73	0.53
1:AA:487:A:H3'	1:AA:488:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BR:8:GLY:O	39:BR:10:LYS:NZ	2.41	0.53
22:BA:2376:A:N3	36:BO:111:ARG:NH1	2.56	0.53
46:DY:51:ALA:O	46:DY:55:THR:OG1	2.24	0.53
22:DA:37:C:H2'	22:DA:38:A:C8	2.42	0.53
22:BA:858:G:H3'	22:BA:859:G:C8	2.43	0.53
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.43	0.53
1:CA:1317:C:OP1	14:CN:57:PRO:HD2	2.08	0.53
23:DB:48:U:H2'	23:DB:49:C:C6	2.43	0.53
22:DA:320:A:HO2'	22:DA:322:A:H8	1.54	0.53
9:CI:114:LYS:HG3	9:CI:120:LYS:HA	1.88	0.53
22:BA:68:G:H2'	22:BA:69:C:O4'	2.08	0.53
27:BF:107:ALA:O	27:BF:110:ARG:N	2.41	0.53
11:AK:25:ALA:HA	11:AK:30:THR:HG22	1.89	0.53
22:BA:559:G:H1'	38:BQ:56:GLN:NE2	2.23	0.53
22:BA:1668:A:H4'	22:BA:1669:A:O5'	2.08	0.53
1:CA:1053:G:N7	1:CA:1200:C:H5''	2.23	0.53
22:DA:1551:A:N6	57:DA:3629:HOH:O	2.40	0.53
22:BA:2394:C:OP1	51:B3:30:ARG:NH2	2.41	0.53
5:AE:79:GLY:O	5:AE:121:HIS:N	2.34	0.53
22:BA:1515:A:H3'	22:BA:1516:G:H8	1.73	0.53
42:DU:7:ARG:O	42:DU:25:VAL:HB	2.08	0.53
22:DA:1317:G:H2'	22:DA:1318:U:O4'	2.07	0.53
1:CA:1096:C:H2'	1:CA:1097:C:H6	1.73	0.53
22:BA:1936:A:N6	22:BA:1963:U:H3	2.05	0.53
22:BA:1169:A:H2'	22:BA:1170:C:O4'	2.08	0.53
6:CF:86:ARG:HH11	6:CF:86:ARG:CG	2.21	0.53
1:CA:33:A:H2'	1:CA:34:C:H6	1.73	0.53
1:AA:254:G:OP1	17:AQ:70:THR:HB	2.09	0.53
15:CO:35:GLN:NE2	15:CO:39:LEU:HD22	2.22	0.53
4:AD:3:ARG:CZ	4:AD:115:ARG:HD3	2.38	0.53
1:AA:667:G:H4'	15:AO:51:HIS:ND1	2.23	0.53
22:BA:630:G:H5''	22:BA:631:A:OP2	2.08	0.53
22:DA:2811:G:OP1	25:DD:62:LYS:N	2.40	0.53
22:BA:2118:U:O4	22:BA:2148:G:O2'	2.24	0.53
22:BA:372:G:OP2	45:BX:61:LYS:HD3	2.07	0.53
20:CT:15:GLU:OE2	20:CT:18:ARG:NH2	2.24	0.53
1:AA:206:C:H2'	1:AA:207:C:O4'	2.07	0.53
15:AO:24:SER:HB3	15:AO:27:VAL:HG23	1.89	0.53
19:CS:6:LYS:HB2	19:CS:7:LYS:HG2	1.90	0.53
1:CA:102:G:H2'	1:CA:103:U:H6	1.73	0.53
7:CG:12:ILE:HD12	7:CG:24:ALA:HB1	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1369:C:H2'	1:AA:1370:G:C8	2.43	0.53
1:CA:1088:G:H21	1:CA:1167:A:N6	2.07	0.53
5:CE:156:LYS:HG2	8:CH:71:VAL:HG22	1.91	0.53
22:DA:1799:G:N2	22:DA:1818:U:O2'	2.38	0.53
4:AD:91:LEU:HD11	4:AD:195:ILE:HD11	1.90	0.53
22:BA:947:A:HO2'	22:BA:984:A:H2	1.55	0.53
22:DA:2609:U:C6	54:D6:7:004:HA	2.41	0.53
1:CA:483:C:H2'	1:CA:484:G:C8	2.44	0.53
22:DA:2898:U:H2'	22:DA:2899:A:C8	2.43	0.53
16:AP:6:LEU:HD13	16:AP:71:VAL:HG23	1.91	0.53
1:AA:1032:G:H3'	1:AA:1033:G:O4'	2.09	0.53
1:AA:1377:A:O2'	7:AG:2:PRO:HB3	2.08	0.53
1:CA:1182:G:H4'	1:CA:1183:U:H5''	1.89	0.53
1:AA:558:G:H8	1:AA:558:G:O5'	1.90	0.53
2:CB:62:SER:HA	2:CB:224:GLY:HA2	1.90	0.53
24:DC:68:LYS:HG2	24:DC:151:GLY:HA2	1.88	0.53
3:CC:5:VAL:HG21	3:CC:10:ILE:HD13	1.90	0.53
22:DA:1266:G:OP1	48:D0:16:ARG:NE	2.40	0.53
22:DA:1231:U:H2'	22:DA:1232:G:H8	1.71	0.53
22:BA:994:C:OP2	38:BQ:54:LYS:NZ	2.41	0.53
1:CA:9:G:H5'	5:CE:108:GLY:HA3	1.89	0.53
53:B5:73:VAL:HG12	53:B5:74:ARG:H	1.72	0.53
22:BA:832:U:H2'	22:BA:833:A:C8	2.44	0.53
1:CA:1463:U:H2'	1:CA:1464:U:C6	2.44	0.53
1:CA:1467:C:H2'	1:CA:1468:A:C8	2.43	0.53
22:DA:2886:A:C2	48:D0:29:SER:HB3	2.43	0.53
20:AT:80:THR:O	20:AT:83:ILE:HG13	2.09	0.53
8:AH:41:LYS:HD2	8:AH:48:ASP:HA	1.89	0.53
22:BA:1097:U:H1'	30:BI:9:VAL:HG12	1.90	0.53
2:AB:16:PHE:HD1	2:AB:17:GLY:H	1.56	0.53
22:DA:2250:G:H8	22:DA:2250:G:O5'	1.90	0.53
22:BA:141:G:H5''	22:BA:142:A:C5	2.44	0.53
9:AI:57:MET:HA	9:AI:60:LYS:HB2	1.90	0.53
33:BL:90:VAL:HG13	33:BL:95:LEU:HD21	1.91	0.53
23:DB:41:G:C8	27:DF:66:LEU:HD11	2.44	0.53
14:CN:66:GLN:HG3	14:CN:79:LEU:HD21	1.89	0.53
41:DT:40:LYS:HG3	41:DT:60:THR:HG23	1.91	0.53
22:DA:2716:C:H2'	22:DA:2717:C:H6	1.74	0.53
30:BI:69:PHE:H	30:BI:69:PHE:HD1	1.55	0.53
28:BG:98:VAL:HG22	28:BG:103:ILE:HG12	1.90	0.53
29:DH:37:VAL:CG2	29:DH:38:PRO:HD2	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CH:29:SER:HB2	8:CH:59:LEU:HB2	1.90	0.53
29:DH:103:VAL:HA	29:DH:106:ALA:HB3	1.89	0.53
12:AL:76:GLU:O	12:AL:77:HIS:HB2	2.09	0.53
22:DA:125:A:H3'	50:D2:19:ARG:HG3	1.90	0.53
5:AE:89:HIS:CE1	5:AE:138:ARG:HD3	2.43	0.53
29:BH:93:SER:OG	1:CA:357:G:C4'	2.51	0.53
22:BA:2142:A:H2'	22:BA:2143:C:C6	2.44	0.53
12:AL:86:ARG:CZ	12:AL:88:LYS:HB3	2.38	0.53
1:CA:501:C:H1'	1:CA:549:C:H1'	1.91	0.53
21:AU:8:GLU:HB3	21:AU:12:PHE:CZ	2.44	0.53
22:DA:1938:A:C6	22:DA:2590:A:H1'	2.43	0.53
8:AH:96:MET:HB2	8:AH:99:LEU:O	2.08	0.53
32:DK:76:VAL:HG12	37:DP:73:VAL:HG22	1.90	0.53
46:BY:13:GLU:HG2	46:BY:57:LEU:HD13	1.90	0.53
1:AA:337:G:H2'	1:AA:338:A:H8	1.74	0.53
1:CA:123:U:H2'	1:CA:124:C:C6	2.44	0.53
1:CA:1308:U:H2'	1:CA:1309:G:H8	1.74	0.53
26:BE:15:SER:N	26:BE:197:GLU:OE2	2.30	0.53
22:BA:1078:U:H1'	22:BA:1088:A:C2	2.43	0.53
28:BG:86:LYS:HG2	28:BG:132:VAL:HG13	1.91	0.53
11:CK:26:SER:HG	11:CK:29:ASN:H	1.55	0.53
1:AA:591:U:H2'	1:AA:592:G:C8	2.44	0.53
22:DA:2578:G:H21	25:DD:130:GLN:NE2	2.07	0.53
22:DA:548:G:H4'	22:DA:549:G:C2	2.43	0.53
7:CG:88:PRO:HD2	7:CG:151:PHE:O	2.08	0.53
34:BM:30:SER:N	34:BM:106:ASP:HB2	2.24	0.53
32:BK:101:GLY:O	32:BK:120:PRO:HD2	2.08	0.53
22:DA:1289:C:O2'	22:DA:1330:C:H4'	2.09	0.53
49:D1:9:ILE:HG21	49:D1:25:LYS:HD2	1.89	0.53
24:DC:24:LEU:HD11	24:DC:90:ASN:HD21	1.73	0.53
2:AB:94:HIS:ND1	2:AB:146:ASN:HB2	2.24	0.53
36:BO:31:THR:HG22	36:BO:34:HIS:N	2.20	0.53
24:DC:160:THR:H	24:DC:195:VAL:HG13	1.73	0.53
22:BA:2305:U:H2'	22:BA:2306:C:C6	2.44	0.53
17:CQ:12:VAL:HG23	17:CQ:57:ASP:O	2.09	0.53
13:CM:33:ILE:HG23	13:CM:59:GLU:HB3	1.90	0.53
21:CU:40:LYS:H	21:CU:41:PRO:HD2	1.73	0.53
7:AG:135:VAL:HB	7:AG:138:ARG:NH2	2.22	0.53
1:CA:642:A:N3	8:CH:105:SER:OG	2.32	0.53
22:DA:1338:G:H4'	41:DT:18:GLU:OE2	2.09	0.53
23:DB:43:C:H1'	27:DF:90:THR:HB	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2756:U:H1'	22:BA:2757:A:H5''	1.91	0.53
22:DA:2540:C:H2'	22:DA:2541:A:C8	2.44	0.53
22:DA:1745:A:H2'	22:DA:1746:A:H8	1.73	0.53
13:AM:34:LEU:HD22	13:AM:41:GLU:HA	1.90	0.53
24:BC:144:VAL:HG12	24:BC:145:GLU:O	2.09	0.53
22:DA:1969:A:O2'	22:DA:1972:G:N3	2.29	0.53
27:DF:2:ALA:O	27:DF:5:HIS:HB3	2.07	0.53
27:DF:5:HIS:O	27:DF:9:LYS:HG3	2.09	0.53
22:BA:2698:U:H2'	22:BA:2699:C:C6	2.44	0.53
26:BE:164:LEU:HB3	26:BE:167:VAL:HB	1.91	0.53
29:DH:2:GLN:O	29:DH:3:VAL:HG22	2.09	0.53
1:AA:825:A:O2'	8:AH:13:ARG:NH1	2.42	0.53
39:DR:41:ILE:HD13	39:DR:103:ALA:HA	1.91	0.53
24:DC:114:ASP:N	24:DC:114:ASP:OD2	2.40	0.53
22:BA:2366:A:H2'	22:BA:2367:G:O4'	2.08	0.53
1:CA:581:G:OP2	1:CA:581:G:H8	1.91	0.53
22:BA:893:C:H2'	22:BA:894:U:O4'	2.09	0.53
1:CA:505:G:H5'	1:CA:534:U:C2	2.44	0.53
29:BH:147:VAL:CG1	29:BH:149:GLU:HG3	2.36	0.53
22:BA:1072:C:OP2	22:BA:1075:C:N4	2.41	0.53
22:DA:1063:G:O2'	30:DI:89:GLY:HA3	2.09	0.53
29:DH:31:VAL:HB	29:DH:32:PRO:HD3	1.89	0.53
22:DA:1199:U:H2'	22:DA:1200:C:C6	2.44	0.53
13:CM:106:ALA:O	13:CM:110:LYS:HB3	2.09	0.53
1:AA:219:U:H2'	1:AA:220:G:C8	2.43	0.53
22:DA:1568:G:O4'	24:DC:58:HIS:HE1	1.90	0.53
53:B5:53:ARG:HD3	53:B5:204:GLY:HA3	1.90	0.53
22:BA:458:G:N2	22:BA:459:U:O4	2.36	0.53
1:CA:499:A:C6	1:CA:547:A:C8	2.96	0.53
28:BG:93:GLY:O	28:BG:95:ARG:HG2	2.09	0.53
22:DA:329:G:O4'	22:DA:477:A:H1'	2.09	0.53
28:BG:20:ASN:ND2	28:BG:20:ASN:O	2.40	0.53
1:AA:1539:C:H5''	21:AU:18:ARG:HG3	1.91	0.53
29:DH:40:THR:O	29:DH:41:LYS:C	2.48	0.53
5:CE:155:ALA:HB1	8:CH:66:PHE:CD2	2.44	0.53
31:BJ:80:HIS:HB3	31:BJ:81:ILE:HG22	1.91	0.53
29:DH:31:VAL:CB	29:DH:32:PRO:CD	2.86	0.53
22:BA:752:A:H3'	50:B2:1:MET:SD	2.48	0.53
22:DA:463:G:N2	22:DA:466:A:OP2	2.36	0.53
22:BA:1385:A:H1'	22:BA:1386:C:C6	2.44	0.53
22:BA:2794:C:H2'	22:BA:2795:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:27:G:O2'	22:DA:28:A:OP2	2.20	0.53
1:CA:102:G:O2'	1:CA:151:A:N3	2.31	0.53
10:AJ:48:ARG:NH1	10:AJ:66:GLU:OE1	2.42	0.53
22:DA:622:G:H2'	22:DA:623:C:C6	2.44	0.53
26:DE:127:GLU:O	26:DE:156:ASN:ND2	2.42	0.53
1:CA:1191:A:H5''	3:CC:4:LYS:HE3	1.91	0.53
22:BA:1410:G:H2'	22:BA:1411:U:C6	2.44	0.53
30:DI:45:LYS:HA	30:DI:48:SER:HB3	1.90	0.53
21:CU:51:SER:O	21:CU:53:VAL:N	2.42	0.53
22:DA:2612:C:H5''	22:DA:2613:U:OP1	2.08	0.53
2:CB:175:GLU:O	2:CB:179:LEU:N	2.39	0.53
22:BA:1061:U:O4	30:BI:11:LEU:HA	2.09	0.53
22:DA:142:A:H2'	22:DA:143:C:C6	2.44	0.53
22:BA:572:A:H5''	22:BA:573:U:OP2	2.09	0.53
24:DC:159:GLY:H	24:DC:195:VAL:HG22	1.74	0.53
16:CP:40:ASN:HB3	16:CP:43:ALA:HB2	1.91	0.53
9:CI:57:MET:O	9:CI:59:GLU:N	2.41	0.53
21:AU:6:VAL:HB	21:AU:8:GLU:HG2	1.90	0.53
52:B4:36:ARG:HG2	52:B4:37:GLN:H	1.74	0.53
33:DL:81:ASP:O	33:DL:82:LEU:HB3	2.08	0.53
29:DH:34:GLY:O	29:DH:35:LYS:HB2	2.08	0.53
3:CC:68:ILE:HD12	3:CC:101:ILE:HD11	1.91	0.53
22:DA:2537:U:H2'	22:DA:2538:C:C6	2.43	0.53
8:AH:64:LYS:HB2	8:AH:71:VAL:HG21	1.90	0.53
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.44	0.53
28:DG:45:HIS:HA	28:DG:50:LEU:HD23	1.91	0.53
22:DA:1656:C:H5''	25:DD:141:ARG:HB2	1.90	0.53
1:AA:205:A:H4'	1:AA:205:A:OP1	2.07	0.53
12:CL:38:TYR:HB2	12:CL:52:VAL:HG13	1.89	0.53
22:BA:1848:A:H2'	22:BA:1849:G:O4'	2.08	0.53
27:BF:49:LEU:HG	27:BF:150:ARG:HH12	1.74	0.53
14:CN:54:ASP:OD1	14:CN:59:ARG:NH1	2.42	0.53
4:AD:190:ASP:OD2	4:AD:190:ASP:N	2.32	0.53
29:BH:97:ARG:HB2	1:CA:369:G:O2'	2.09	0.52
1:CA:369:G:OP2	1:CA:388:G:N2	2.39	0.52
1:AA:1441:A:C2	37:BP:114:LEU:HD22	2.44	0.52
28:DG:89:LEU:HD12	28:DG:162:VAL:HG22	1.91	0.52
11:CK:25:ALA:N	11:CK:87:LYS:O	2.41	0.52
22:DA:2345:G:H5'	22:DA:2347:C:O4'	2.09	0.52
53:B5:50:ILE:C	53:B5:52:PRO:HD3	2.29	0.52
1:CA:1202:U:H2'	1:CA:1203:C:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1695:G:H1'	24:BC:8:PRO:O	2.08	0.52
33:DL:90:VAL:HB	33:DL:122:VAL:HA	1.91	0.52
28:BG:19:ILE:HG12	28:BG:24:ILE:HD13	1.90	0.52
22:DA:1651:G:H4'	35:DN:39:PRO:HG2	1.91	0.52
4:AD:151:LYS:HB2	4:AD:156:LYS:HE3	1.90	0.52
22:DA:183:C:H1'	22:DA:433:C:H1'	1.90	0.52
1:AA:762:U:H2'	1:AA:763:G:H8	1.73	0.52
27:BF:14:LYS:O	27:BF:18:THR:HG23	2.08	0.52
22:DA:482:A:N6	22:DA:506:G:O2'	2.41	0.52
5:AE:96:MET:HB3	5:AE:125:ALA:HB2	1.91	0.52
1:CA:1074:G:H4'	2:CB:103:ASN:CB	2.36	0.52
53:B5:43:GLU:O	53:B5:213:VAL:HA	2.09	0.52
22:DA:27:G:H22	22:DA:512:G:H1'	1.73	0.52
27:BF:60:ILE:HG22	27:BF:99:PHE:HE1	1.74	0.52
2:AB:168:HIS:ND1	2:AB:168:HIS:O	2.42	0.52
39:DR:41:ILE:O	39:DR:47:VAL:N	2.42	0.52
22:DA:482:A:H1'	22:DA:498:G:N2	2.23	0.52
22:DA:1881:C:H2'	22:DA:1882:U:O4'	2.09	0.52
2:CB:169:GLU:O	2:CB:171:ILE:N	2.43	0.52
22:DA:1999:C:O2	22:DA:2687:U:O2'	2.27	0.52
40:BS:90:LYS:NZ	54:B6:8:MHT:H7	2.24	0.52
17:CQ:70:THR:HG22	17:CQ:71:LYS:H	1.73	0.52
27:DF:126:GLY:HA2	27:DF:163:ASP:HA	1.92	0.52
22:DA:2765:A:H5'	22:DA:2766:A:OP2	2.09	0.52
50:D2:11:LYS:NZ	57:D2:102:HOH:O	2.41	0.52
22:DA:1152:C:H4'	38:DQ:77:SER:HA	1.91	0.52
22:DA:1681:G:O2'	22:DA:1762:A:N3	2.39	0.52
2:AB:95:ARG:NH1	2:AB:97:LEU:HA	2.23	0.52
22:DA:2344:U:H4'	22:DA:2345:G:OP1	2.09	0.52
1:CA:1203:C:H2'	1:CA:1204:A:H8	1.73	0.52
22:BA:2298:A:H61	22:BA:2318:G:H1'	1.74	0.52
22:BA:7:G:H2'	22:BA:8:C:C6	2.45	0.52
3:CC:148:GLY:HA2	3:CC:171:GLY:HA3	1.91	0.52
22:DA:1636:U:H2'	22:DA:1637:A:C8	2.45	0.52
41:DT:21:SER:O	41:DT:24:MET:N	2.42	0.52
39:DR:76:LYS:HB2	39:DR:85:LYS:HB2	1.91	0.52
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.08	0.52
22:DA:204:A:H5'	22:DA:206:U:O4'	2.10	0.52
22:DA:834:G:H1'	22:DA:2358:A:N3	2.24	0.52
33:BL:89:VAL:O	33:BL:94:THR:HG21	2.09	0.52
40:BS:78:GLU:C	40:BS:102:HIS:HE1	2.13	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:723:U:H5''	21:AU:49:LYS:HG2	1.92	0.52
29:DH:34:GLY:O	29:DH:35:LYS:HD2	2.10	0.52
22:BA:1818:U:O2'	24:BC:153:GLN:O	2.22	0.52
3:CC:59:ARG:HB2	3:CC:63:SER:O	2.10	0.52
22:BA:479:A:N3	22:BA:481:G:H5''	2.24	0.52
22:BA:2315:G:H2'	22:BA:2316:G:C8	2.44	0.52
1:AA:593:U:H2'	1:AA:594:U:H6	1.75	0.52
29:BH:77:THR:HA	29:BH:143:ILE:O	2.10	0.52
1:AA:731:G:OP1	1:AA:766:A:H1'	2.09	0.52
22:DA:846:U:H1'	22:DA:847:U:H5	1.74	0.52
1:AA:1112:C:O2	3:AC:179:ARG:HG3	2.10	0.52
35:DN:28:LEU:HD23	35:DN:48:VAL:HG21	1.90	0.52
22:DA:1597:A:O3'	22:DA:1598:A:H8	1.91	0.52
22:DA:102:U:C2	46:DY:2:LYS:HE2	2.43	0.52
12:AL:72:HIS:ND1	12:AL:74:LEU:HB2	2.25	0.52
22:DA:987:C:H2'	22:DA:988:A:O4'	2.09	0.52
22:BA:1877:A:H2'	22:BA:1878:G:O4'	2.10	0.52
23:DB:66:A:N6	23:DB:107:G:H2'	2.25	0.52
23:DB:113:C:H1'	36:DO:46:GLU:HA	1.92	0.52
2:CB:131:LYS:O	2:CB:135:LEU:N	2.42	0.52
6:CF:40:GLU:HB2	6:CF:42:TRP:HE1	1.75	0.52
1:CA:1361:G:C2	1:CA:1362:A:N7	2.77	0.52
5:CE:105:ILE:HG13	5:CE:112:ARG:HG3	1.90	0.52
1:AA:600:A:H2'	1:AA:601:G:H8	1.70	0.52
9:AI:52:LEU:HD13	9:AI:57:MET:HG2	1.90	0.52
1:AA:92:U:H2'	1:AA:93:U:C6	2.45	0.52
22:DA:2053:G:H2'	22:DA:2054:A:O4'	2.10	0.52
1:AA:1227:A:O2'	13:AM:115:PRO:HD2	2.10	0.52
2:CB:206:ALA:O	2:CB:208:ARG:N	2.43	0.52
1:CA:518:C:H4'	1:CA:519:C:O5'	2.10	0.52
23:BB:77:U:P	43:BV:21:ARG:HH22	2.33	0.52
13:CM:14:HIS:HB2	13:CM:17:ILE:HD12	1.90	0.52
29:BH:51:ARG:NH1	29:BH:55:GLU:OE1	2.43	0.52
22:DA:2557:G:H2'	22:DA:2558:C:C6	2.45	0.52
1:AA:390:U:H2'	1:AA:391:G:H8	1.74	0.52
26:DE:146:VAL:HG22	26:DE:167:VAL:HG22	1.91	0.52
22:DA:1911:U:H2'	22:DA:1918:A:C2	2.44	0.52
26:DE:22:ASP:OD2	26:DE:22:ASP:N	2.37	0.52
18:AR:26:ILE:HA	18:AR:29:LEU:HB2	1.91	0.52
5:AE:111:MET:O	5:AE:115:LEU:HB2	2.08	0.52
22:DA:1783:A:H5'	22:DA:2608:G:H4'	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:412:A:O2'	1:CA:413:G:H4'	2.09	0.52
1:CA:463:U:H5'	1:CA:464:U:OP2	2.09	0.52
15:AO:81:LEU:HD11	15:AO:85:LEU:HD22	1.92	0.52
3:AC:55:ILE:HG13	3:AC:55:ILE:O	2.09	0.52
5:AE:83:HIS:CE1	5:AE:147:MET:HG3	2.43	0.52
1:AA:1277:C:HO2'	1:AA:1279:G:H8	1.57	0.52
5:CE:80:THR:HA	5:CE:120:VAL:HG12	1.92	0.52
24:BC:3:VAL:HG12	24:BC:19:VAL:HG22	1.92	0.52
22:BA:2689:U:OP2	22:BA:2719:G:N2	2.29	0.52
7:CG:71:PRO:HD2	7:CG:96:ARG:O	2.10	0.52
26:BE:12:LEU:HD23	26:BE:13:THR:N	2.25	0.52
1:CA:957:U:O2	1:CA:959:A:H8	1.93	0.52
4:CD:196:ASN:HB3	4:CD:198:HIS:CE1	2.44	0.52
22:DA:2850:A:OP2	22:DA:2866:U:N3	2.31	0.52
15:AO:4:SER:O	15:AO:8:THR:HG23	2.09	0.52
14:CN:16:LEU:HB3	14:CN:55:SER:HA	1.92	0.52
1:CA:690:G:H2'	1:CA:691:G:O4'	2.09	0.52
29:DH:72:ILE:O	29:DH:72:ILE:HG22	2.09	0.52
23:DB:64:G:H2'	23:DB:65:U:C6	2.45	0.52
31:DJ:56:VAL:HB	31:DJ:124:VAL:HG12	1.91	0.52
8:CH:9:ASP:OD2	8:CH:13:ARG:NH1	2.41	0.52
1:CA:545:C:H5'	4:CD:69:GLU:CG	2.40	0.52
29:BH:94:ILE:CG2	29:BH:99:ILE:CG1	2.88	0.52
5:CE:149:SER:HB2	5:CE:152:MET:HG2	1.92	0.52
22:BA:1287:A:C5'	35:BN:103:ARG:HD2	2.38	0.52
17:CQ:12:VAL:HG12	17:CQ:13:VAL:N	2.22	0.52
28:DG:127:THR:HG22	28:DG:128:GLN:H	1.74	0.52
22:BA:583:G:OP1	38:BQ:7:GLY:HA2	2.09	0.52
9:AI:120:LYS:HG3	9:AI:123:ARG:HB3	1.92	0.52
1:AA:1313:U:P	19:AS:6:LYS:HB3	2.50	0.52
1:CA:1201:A:H4'	1:CA:1202:U:O5'	2.09	0.52
3:CC:22:TRP:CD1	3:CC:57:ILE:HG22	2.45	0.52
15:CO:3:LEU:HD22	15:CO:35:GLN:HG2	1.91	0.52
22:DA:934:U:H2'	22:DA:935:C:C6	2.45	0.52
19:AS:15:LEU:HD13	19:AS:33:THR:HG21	1.92	0.52
1:CA:425:G:H2'	1:CA:426:U:O4'	2.10	0.52
20:AT:24:ARG:O	20:AT:27:MET:HG3	2.10	0.52
22:DA:1973:G:OP1	57:DA:3460:HOH:O	2.19	0.52
13:AM:18:ALA:O	13:AM:21:SER:HB2	2.10	0.52
22:DA:2094:A:H2'	22:DA:2095:A:H8	1.75	0.52
35:DN:85:PRO:HA	35:DN:88:ALA:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1450:G:C6	22:DA:1451:C:N4	2.77	0.52
7:CG:137:LYS:O	7:CG:141:VAL:HG23	2.10	0.52
2:AB:197:ASP:N	2:AB:197:ASP:OD1	2.41	0.52
22:DA:1773:A:N7	22:DA:1829:A:H1'	2.24	0.52
1:AA:1338:G:H2'	1:AA:1339:A:C8	2.45	0.52
29:BH:94:ILE:HD12	29:BH:98:ASP:HB3	1.92	0.52
9:AI:22:LYS:HZ2	9:AI:24:GLY:HA3	1.75	0.52
29:DH:23:ALA:O	29:DH:27:ARG:N	2.38	0.52
33:DL:56:PRO:O	33:DL:60:ARG:HB3	2.09	0.52
22:DA:320:A:H4'	22:DA:322:A:N7	2.25	0.52
1:CA:200:G:H2'	1:CA:201:G:H5''	1.92	0.52
34:BM:18:ARG:CG	34:BM:18:ARG:HH21	2.22	0.52
6:AF:51:ILE:HD12	6:AF:86:ARG:CZ	2.39	0.52
31:DJ:78:THR:OG1	31:DJ:80:HIS:HB2	2.10	0.52
22:DA:224:U:OP2	22:DA:408:G:N2	2.41	0.52
8:CH:7:ILE:HB	8:CH:77:ARG:NH1	2.25	0.52
1:CA:940:C:H2'	1:CA:941:G:C8	2.45	0.52
22:BA:372:G:OP1	45:BX:62:LYS:NZ	2.43	0.52
22:BA:2649:C:H2'	22:BA:2650:U:H6	1.75	0.52
2:AB:166:ALA:HB2	2:AB:187:VAL:HG12	1.92	0.52
42:DU:14:LEU:HD11	42:DU:71:ALA:HB2	1.91	0.52
28:BG:74:SER:HA	28:BG:77:ILE:HG13	1.92	0.52
29:DH:25:TYR:CZ	29:DH:30:LEU:HD21	2.45	0.52
22:DA:2567:G:H2'	22:DA:2568:U:C6	2.44	0.52
3:AC:205:GLY:O	3:AC:206:GLU:HG2	2.10	0.52
22:BA:1779:U:H5	22:BA:1784:A:N7	2.07	0.52
13:AM:95:LEU:HB3	13:AM:96:PRO:HD2	1.92	0.52
1:CA:791:G:C6	1:CA:792:A:N7	2.78	0.52
29:BH:117:LEU:CD2	29:BH:121:VAL:N	2.70	0.52
22:BA:1070:A:C2	30:BI:10:LYS:HG3	2.45	0.52
4:AD:147:GLU:O	4:AD:150:LYS:HB2	2.10	0.52
5:CE:82:GLN:H	5:CE:147:MET:HE3	1.73	0.52
22:DA:1259:G:H2'	22:DA:1260:A:C8	2.45	0.52
22:BA:780:G:N2	22:BA:783:A:H62	2.04	0.52
1:AA:452:A:C8	1:AA:452:A:H3'	2.45	0.52
1:CA:858:G:O6	1:CA:869:G:H3'	2.10	0.52
46:DY:9:LYS:N	46:DY:12:GLU:HG3	2.24	0.52
1:CA:821:G:H2'	1:CA:822:U:C6	2.45	0.52
13:AM:29:ARG:NH2	13:AM:63:PHE:HB2	2.25	0.52
11:AK:110:ILE:HB	21:AU:6:VAL:HG22	1.91	0.52
10:AJ:6:ILE:HD12	10:AJ:76:ILE:HB	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1567:G:H2'	24:DC:85:PRO:HG3	1.90	0.52
1:CA:1053:G:O5'	1:CA:1054:C:H5'	2.10	0.52
29:BH:2:GLN:O	29:BH:3:VAL:HG22	2.10	0.52
36:DO:2:ASP:O	36:DO:6:ALA:HB2	2.10	0.52
27:BF:136:ILE:HD11	27:BF:149:VAL:HG12	1.92	0.52
1:CA:950:U:H2'	1:CA:951:G:C8	2.45	0.52
22:BA:2636:C:H2'	22:BA:2637:U:C6	2.45	0.52
25:DD:172:VAL:HG23	25:DD:194:PRO:HD3	1.91	0.52
30:BI:117:MET:SD	30:BI:129:ILE:HD11	2.50	0.52
2:AB:67:ILE:HB	2:AB:89:GLN:HB3	1.92	0.52
1:AA:1217:C:P	14:AN:9:ARG:HH21	2.33	0.52
1:CA:708:C:H2'	1:CA:709:U:C6	2.45	0.52
2:CB:14:VAL:HG23	2:CB:208:ARG:HH12	1.74	0.52
23:DB:29:A:OP2	36:DO:31:THR:HG23	2.10	0.52
1:CA:266:G:H3'	17:CQ:69:LYS:HB2	1.92	0.52
22:DA:845:A:H5'	22:DA:846:U:OP2	2.10	0.52
12:AL:29:GLN:HB2	12:AL:82:ILE:O	2.10	0.52
8:AH:18:GLN:NE2	8:AH:70:ALA:HB1	2.25	0.52
53:B5:75:VAL:HA	53:B5:120:VAL:O	2.10	0.52
1:AA:946:A:H2'	1:AA:947:G:C8	2.45	0.52
40:BS:57:ASN:O	40:BS:61:ASN:HB2	2.10	0.52
9:CI:8:GLY:N	9:CI:86:ALA:HB2	2.25	0.52
13:AM:46:SER:O	13:AM:47:GLU:HB3	2.10	0.52
38:DQ:50:ARG:NH2	39:DR:74:ILE:HG13	2.25	0.52
42:DU:12:ILE:HG13	42:DU:21:LYS:O	2.10	0.52
22:BA:253:C:OP2	51:B3:5:LYS:NZ	2.28	0.52
32:DK:107:LEU:O	32:DK:109:SER:N	2.43	0.52
25:DD:48:ILE:HG23	25:DD:84:LEU:HD21	1.90	0.52
1:AA:686:U:O4	1:AA:703:G:O2'	2.18	0.51
22:BA:84:A:H4'	22:BA:85:G:O5'	2.09	0.51
22:BA:1435:G:O2'	22:BA:1436:G:H5'	2.09	0.51
1:AA:142:G:H3'	1:AA:143:A:C8	2.38	0.51
1:AA:452:A:N6	1:AA:480:U:H3	2.08	0.51
6:AF:38:ARG:HB3	6:AF:63:ASN:HB2	1.92	0.51
22:DA:2127:G:H4'	22:DA:2128:G:OP1	2.10	0.51
1:CA:136:C:H2'	1:CA:137:U:H6	1.75	0.51
1:CA:1410:A:H2'	1:CA:1411:C:C6	2.46	0.51
6:CF:14:GLN:C	6:CF:16:GLU:H	2.14	0.51
22:DA:328:U:H4'	42:DU:66:GLN:NE2	2.25	0.51
46:DY:1:MET:O	46:DY:5:GLU:HG3	2.10	0.51
32:BK:92:GLU:HG3	32:BK:111:LYS:NZ	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DI:8:TYR:HB2	30:DI:59:ILE:H	1.75	0.51
1:AA:1321:U:O3'	19:AS:78:ARG:NH2	2.43	0.51
6:CF:39:LEU:HD12	6:CF:40:GLU:N	2.25	0.51
22:BA:2563:U:H2'	22:BA:2565:A:OP2	2.10	0.51
1:AA:466:A:H5'	1:AA:467:U:OP2	2.10	0.51
22:DA:1323:C:N4	22:DA:1324:G:O6	2.43	0.51
22:BA:543:G:C2	22:BA:544:C:H1'	2.45	0.51
1:AA:1001:C:H2'	1:AA:1002:G:C8	2.45	0.51
19:AS:5:LEU:O	19:AS:7:LYS:N	2.42	0.51
22:BA:605:G:N3	22:BA:657:U:O2'	2.37	0.51
22:DA:1719:G:N2	22:DA:1742:U:H1'	2.25	0.51
22:DA:2761:A:H1'	28:DG:143:GLN:NE2	2.25	0.51
22:BA:593:U:H2'	22:BA:594:U:C6	2.45	0.51
24:DC:141:VAL:O	24:DC:162:VAL:N	2.41	0.51
22:DA:671:C:H2'	22:DA:672:C:C6	2.45	0.51
50:B2:8:SER:OG	50:B2:11:LYS:HG3	2.10	0.51
22:BA:1340:U:OP1	41:BT:19:LYS:NZ	2.39	0.51
5:CE:56:VAL:N	5:CE:57:PRO:HD2	2.24	0.51
2:CB:222:ARG:HE	2:CB:223:GLU:H	1.57	0.51
20:AT:69:LYS:HB2	20:AT:70:ASN:OD1	2.10	0.51
5:AE:95:PHE:CZ	5:AE:97:GLN:HG3	2.45	0.51
22:BA:282:A:H2'	22:BA:283:G:H8	1.75	0.51
38:BQ:27:ALA:HB1	38:BQ:31:VAL:HB	1.91	0.51
32:DK:38:ILE:HD11	32:DK:112:PHE:CZ	2.46	0.51
13:AM:114:LYS:HB2	13:AM:115:PRO:HD3	1.91	0.51
22:DA:511:U:O4	22:DA:512:G:N1	2.43	0.51
22:DA:847:U:O2	22:DA:934:U:H1'	2.10	0.51
15:AO:8:THR:O	15:AO:12:VAL:HG23	2.10	0.51
1:AA:152:A:N6	1:AA:170:U:C2	2.78	0.51
14:CN:61:ARG:O	14:CN:62:ASN:HB2	2.10	0.51
1:CA:952:U:H2'	1:CA:953:G:C8	2.45	0.51
22:DA:851:C:O2'	47:DZ:43:ALA:O	2.28	0.51
8:CH:78:VAL:N	8:CH:126:ILE:O	2.42	0.51
22:BA:856:G:H1'	44:BW:27:GLY:H	1.75	0.51
1:AA:1317:C:H4'	14:AN:49:GLN:HE21	1.75	0.51
32:BK:76:VAL:HB	37:BP:73:VAL:HG13	1.92	0.51
19:AS:79:THR:O	19:AS:79:THR:OG1	2.26	0.51
1:AA:340:U:H2'	1:AA:341:C:H6	1.75	0.51
22:DA:765:C:H2'	22:DA:766:U:C6	2.46	0.51
27:DF:15:LYS:O	27:DF:19:GLU:HG3	2.09	0.51
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1063:G:H2'	22:DA:1064:C:O4'	2.09	0.51
22:BA:2305:U:N3	27:BF:151:GLY:HA3	2.25	0.51
22:BA:1869:G:C3'	22:BA:1870:C:H5'	2.40	0.51
1:AA:601:G:H2'	1:AA:602:A:H8	1.74	0.51
24:DC:145:GLU:HA	24:DC:152:GLY:HA2	1.92	0.51
1:CA:261:U:OP2	20:CT:71:LYS:HD2	2.11	0.51
2:AB:104:TRP:CZ2	2:AB:154:MET:HG2	2.45	0.51
22:DA:420:C:H2'	22:DA:421:C:C6	2.46	0.51
33:DL:94:THR:HA	33:DL:97:ALA:HB3	1.92	0.51
22:BA:1538:G:OP2	22:BA:1538:G:H8	1.93	0.51
24:DC:171:TYR:HD2	24:DC:185:GLU:HA	1.75	0.51
1:AA:118:U:O4	1:AA:288:A:H2'	2.09	0.51
22:BA:1277:G:H5'	35:BN:20:MET:HE2	1.92	0.51
22:BA:276:U:O2	22:BA:276:U:H2'	2.11	0.51
22:DA:1572:A:H2'	22:DA:1573:G:H8	1.74	0.51
20:AT:4:ILE:HG12	20:AT:8:LYS:HZ1	1.74	0.51
22:DA:172:A:H2'	22:DA:173:A:C8	2.46	0.51
28:BG:109:PHE:HE2	28:BG:152:ARG:CZ	2.23	0.51
36:BO:41:ALA:HB2	36:BO:48:LEU:HD21	1.93	0.51
22:DA:1682:G:H2'	22:DA:1683:U:C6	2.45	0.51
29:BH:99:ILE:O	29:BH:103:VAL:CG2	2.58	0.51
29:DH:121:VAL:O	29:DH:122:LEU:HB2	2.11	0.51
30:DI:61:VAL:HG22	30:DI:67:PHE:HB3	1.91	0.51
29:BH:110:VAL:HG22	29:BH:114:GLU:HB2	1.90	0.51
22:DA:1594:U:H2'	22:DA:1595:C:C6	2.45	0.51
22:DA:118:A:H1'	22:DA:178:G:O4'	2.09	0.51
6:AF:47:LEU:HD12	6:AF:55:HIS:HA	1.93	0.51
1:CA:1071:C:H2'	1:CA:1072:G:C8	2.45	0.51
22:BA:1442:U:H2'	22:BA:1443:U:H6	1.75	0.51
27:DF:40:VAL:O	27:DF:42:GLU:N	2.42	0.51
45:DX:31:PRO:HB2	45:DX:33:LEU:HD13	1.92	0.51
38:DQ:17:ILE:HG23	38:DQ:39:VAL:HG21	1.92	0.51
14:AN:64:CYS:SG	14:AN:67:THR:OG1	2.69	0.51
22:BA:1100:C:H2'	22:BA:1101:U:C6	2.46	0.51
22:DA:727:A:H2'	22:DA:728:G:C8	2.45	0.51
5:AE:50:TYR:CE2	5:AE:134:ILE:HD11	2.45	0.51
18:CR:62:ALA:HB3	18:CR:68:LEU:HD12	1.92	0.51
1:CA:1329:A:H5''	13:CM:25:VAL:HA	1.91	0.51
22:DA:469:G:O6	50:D2:37:LYS:HE2	2.11	0.51
1:CA:328:C:H4'	1:CA:329:A:H5''	1.92	0.51
29:BH:100:ALA:CB	29:BH:112:LYS:HA	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:132:PHE:O	29:BH:139:PHE:HB3	2.11	0.51
1:CA:562:U:OP2	12:CL:14:ARG:NH2	2.44	0.51
22:BA:1917:U:C4	22:BA:1918:A:C5	2.99	0.51
9:AI:30:ILE:HD11	9:AI:38:TYR:CD2	2.46	0.51
20:AT:25:ARG:O	20:AT:29:ARG:HG3	2.10	0.51
23:DB:58:A:H2'	23:DB:59:A:O4'	2.11	0.51
22:BA:645:C:O2'	22:BA:646:U:H5''	2.11	0.51
3:CC:130:PHE:CE1	3:CC:157:LEU:HB3	2.46	0.51
11:CK:35:THR:OG1	11:CK:36:ASP:N	2.44	0.51
38:BQ:40:ILE:O	38:BQ:44:GLN:HG3	2.11	0.51
7:CG:114:LYS:HB2	7:CG:118:LEU:HD12	1.93	0.51
15:CO:26:GLU:HG2	15:CO:81:LEU:HD13	1.92	0.51
40:BS:4:ILE:HG23	40:BS:106:VAL:HG22	1.92	0.51
1:AA:73:C:O2'	1:AA:74:A:H5''	2.10	0.51
1:AA:1128:C:H4'	1:AA:1148:U:O2	2.10	0.51
22:DA:451:U:H2'	22:DA:453:A:N7	2.25	0.51
24:DC:167:ARG:HG3	24:DC:172:VAL:HG12	1.91	0.51
1:CA:847:G:H2'	1:CA:848:C:O4'	2.10	0.51
22:BA:2086:U:H2'	22:BA:2087:G:C8	2.45	0.51
22:BA:2093:G:O2'	29:BH:25:TYR:HB2	2.11	0.51
22:DA:1009:A:O2'	22:DA:1153:C:H4'	2.10	0.51
26:DE:117:ARG:HH21	26:DE:184:ASP:HA	1.74	0.51
12:CL:59:ASN:ND2	12:CL:59:ASN:H	2.05	0.51
22:BA:1131:G:O2'	22:BA:2026:U:H5'	2.10	0.51
39:BR:25:LEU:H	39:BR:94:THR:HG21	1.75	0.51
46:DY:9:LYS:HG2	46:DY:10:SER:N	2.26	0.51
22:BA:1364:G:P	45:BX:50:ARG:HH22	2.33	0.51
27:BF:80:ARG:HG2	27:BF:81:GLN:N	2.26	0.51
46:BY:34:SER:O	46:BY:36:GLN:N	2.42	0.51
7:AG:15:ASP:H	7:AG:24:ALA:HB2	1.75	0.51
46:DY:28:LEU:HD11	46:DY:46:VAL:HG21	1.92	0.51
5:AE:153:VAL:O	5:AE:156:LYS:HB2	2.11	0.51
22:DA:674:G:H1'	26:DE:69:ARG:HE	1.76	0.51
22:DA:1515:A:H5'	22:DA:1516:G:OP2	2.11	0.51
30:DI:28:LEU:HD11	30:DI:35:ILE:HG23	1.91	0.51
22:DA:919:U:H2'	22:DA:920:A:O4'	2.11	0.51
22:BA:1837:C:H2'	22:BA:1899:A:H61	1.76	0.51
27:DF:5:HIS:HB2	27:DF:97:TRP:CG	2.45	0.51
15:CO:62:GLN:HA	15:CO:65:LYS:HE3	1.92	0.51
22:DA:987:C:O2'	22:DA:1000:A:N3	2.39	0.51
1:CA:790:A:C6	1:CA:791:G:C6	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1853:A:N1	22:BA:2087:G:H1'	2.25	0.51
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.11	0.51
22:BA:171:U:H2'	22:BA:172:A:C8	2.45	0.51
22:BA:2804:U:H2'	22:BA:2805:C:H6	1.75	0.51
1:CA:1377:A:N3	7:CG:2:PRO:HG3	2.26	0.51
22:BA:934:U:H2'	22:BA:935:C:C6	2.45	0.51
22:DA:1090:A:N6	22:DA:1091:G:O6	2.43	0.51
1:AA:974:A:P	14:AN:69:ARG:HH22	2.34	0.51
13:CM:48:LEU:HD22	13:CM:53:ILE:HG13	1.92	0.51
22:DA:2112:G:N3	22:DA:2112:G:H2'	2.26	0.51
41:DT:56:GLU:HB3	41:DT:86:THR:HB	1.92	0.51
1:AA:264:C:H2'	1:AA:265:G:O4'	2.11	0.51
45:BX:49:LEU:HB3	45:BX:51:VAL:HG13	1.91	0.51
42:DU:57:GLY:O	42:DU:59:VAL:HG23	2.10	0.51
34:BM:2:LEU:O	34:BM:3:GLN:HB3	2.10	0.51
46:DY:16:THR:O	46:DY:20:ASN:ND2	2.32	0.51
1:CA:50:A:H1'	1:CA:52:C:O4'	2.10	0.51
17:CQ:46:VAL:HG22	17:CQ:73:TRP:HB2	1.93	0.51
29:DH:53:GLU:O	29:DH:54:LEU:C	2.49	0.51
21:AU:35:ARG:O	21:AU:37:PHE:N	2.44	0.51
6:CF:64:VAL:HG12	6:CF:65:GLU:N	2.24	0.51
1:AA:374:A:H5''	1:AA:452:A:H2	1.75	0.51
22:BA:1753:G:H5''	37:BP:93:ARG:HH11	1.75	0.51
5:CE:111:MET:HG3	5:CE:140:THR:HG21	1.92	0.51
22:DA:1947:C:H2'	22:DA:1948:G:C8	2.46	0.51
22:DA:2047:C:N4	57:DA:3672:HOH:O	2.44	0.51
22:DA:2822:G:H2'	22:DA:2823:A:H5''	1.92	0.51
5:AE:13:GLU:HB3	5:AE:39:VAL:HG12	1.92	0.51
22:DA:2382:G:OP1	22:DA:2382:G:H3'	2.10	0.51
35:DN:117:ASP:O	35:DN:118:ARG:HB2	2.10	0.51
2:AB:51:ASN:O	2:AB:52:GLU:HB2	2.11	0.51
22:DA:1802:A:H2'	22:DA:1803:A:C8	2.46	0.51
44:BW:19:LYS:HG3	44:BW:41:ARG:HH21	1.75	0.51
22:DA:1820:U:OP1	24:DC:177:ARG:HG2	2.10	0.51
1:AA:797:C:H2'	1:AA:798:U:C6	2.45	0.51
22:BA:973:A:H5''	39:BR:81:LYS:HG3	1.93	0.51
22:DA:388:G:N7	22:DA:390:U:H2'	2.25	0.51
2:AB:9:MET:SD	2:AB:9:MET:N	2.84	0.51
1:CA:313:A:H2'	1:CA:314:C:C6	2.46	0.51
44:DW:52:GLY:HA3	44:DW:60:PHE:CZ	2.45	0.51
29:BH:85:GLY:HA2	29:BH:91:PHE:CE2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2199:A:C4'	29:BH:28:ASN:CG	2.79	0.51
38:DQ:76:TYR:CZ	38:DQ:80:ILE:HG13	2.46	0.51
2:CB:15:HIS:ND1	2:CB:15:HIS:C	2.63	0.51
22:DA:1131:G:OP1	31:DJ:82:GLY:HA2	2.11	0.51
41:DT:44:LYS:HE3	41:DT:55:VAL:HB	1.92	0.51
32:DK:99:ILE:HG12	32:DK:115:ILE:HG23	1.92	0.51
22:BA:2345:G:N3	22:BA:2381:A:H2'	2.26	0.51
22:DA:796:C:H2'	22:DA:797:G:C8	2.45	0.51
22:BA:1539:U:H2'	22:BA:1540:G:C8	2.45	0.51
2:CB:81:LYS:HG3	2:CB:91:PHE:CZ	2.46	0.51
22:DA:1477:A:N6	22:DA:1514:G:O2'	2.44	0.51
1:CA:1363:A:O2'	1:CA:1365:G:N7	2.28	0.51
1:CA:1373:G:H5''	7:CG:36:LYS:HB2	1.93	0.51
17:CQ:60:GLU:HB3	17:CQ:76:VAL:HG23	1.93	0.51
22:BA:1754:A:C6	22:BA:1755:A:C6	2.99	0.51
1:CA:1031:C:H4'	1:CA:1032:G:C2	2.45	0.51
22:BA:1414:C:N3	22:BA:1415:U:H5	2.08	0.51
1:AA:501:C:H1'	1:AA:549:C:H1'	1.91	0.51
22:BA:2346:A:H4'	22:BA:2347:C:OP2	2.09	0.51
29:BH:117:LEU:CD2	29:BH:121:VAL:CA	2.89	0.51
10:AJ:10:LEU:HD23	10:AJ:96:VAL:HG11	1.93	0.51
22:BA:1288:G:C4	22:BA:1327:A:C2	2.98	0.51
22:DA:832:U:OP1	33:DL:39:LYS:N	2.36	0.51
22:BA:1753:G:OP1	37:BP:93:ARG:HD3	2.11	0.51
22:DA:2852:G:H2'	22:DA:2853:C:O4'	2.11	0.51
1:CA:214:C:H2'	1:CA:215:C:H6	1.76	0.51
30:DI:46:THR:HG22	30:DI:51:LYS:HG3	1.93	0.51
20:CT:3:ASN:O	20:CT:5:LYS:N	2.43	0.51
22:DA:1364:G:H5''	45:DX:3:ARG:NH1	2.26	0.51
34:BM:47:GLU:OE2	34:BM:51:ARG:NE	2.44	0.51
1:AA:9:G:H5'	5:AE:108:GLY:HA3	1.92	0.51
17:AQ:47:HIS:HB2	17:AQ:71:LYS:HE3	1.93	0.51
4:CD:44:ARG:NE	4:CD:44:ARG:HA	2.25	0.51
22:BA:1186:G:H5'	57:BA:3603:HOH:O	2.10	0.51
11:AK:87:LYS:HA	11:AK:114:THR:HG22	1.92	0.51
30:BI:59:ILE:HG22	30:BI:61:VAL:HG23	1.93	0.51
22:BA:894:U:H2'	22:BA:895:U:C6	2.46	0.51
22:BA:357:C:H2'	22:BA:358:U:C6	2.45	0.51
22:BA:2856:A:N6	22:BA:2857:G:C6	2.79	0.51
22:BA:1376:C:H3'	57:BA:3399:HOH:O	2.10	0.51
22:DA:1468:U:H2'	22:DA:1522:A:N6	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:636:U:H2'	1:CA:637:C:C6	2.46	0.51
22:DA:720:U:H2'	22:DA:721:A:C8	2.46	0.51
3:CC:172:ARG:O	3:CC:174:PRO:HD3	2.09	0.51
23:DB:25:U:H2'	23:DB:26:C:O4'	2.10	0.51
22:BA:137:U:H2'	22:BA:140:C:C2	2.46	0.51
28:BG:9:VAL:HG13	28:BG:50:LEU:HB2	1.93	0.51
22:BA:1999:C:OP1	22:BA:2723:C:O2'	2.26	0.51
1:AA:1450:U:H2'	1:AA:1452:C:C5	2.46	0.51
29:BH:83:LYS:HA	29:BH:148:ALA:HA	1.93	0.51
22:DA:1846:G:H5''	22:DA:1847:A:OP2	2.11	0.51
1:AA:452:A:H8	1:AA:452:A:H3'	1.76	0.51
1:AA:981:U:O2'	14:AN:61:ARG:NE	2.44	0.51
1:CA:280:C:H4'	1:CA:281:G:OP2	2.11	0.51
1:CA:1493:A:H8	1:CA:1493:A:OP2	1.94	0.51
1:CA:805:C:H2'	1:CA:806:C:C6	2.46	0.51
29:DH:26:ALA:HA	29:DH:30:LEU:HB2	1.92	0.51
5:CE:57:PRO:O	5:CE:60:ILE:HG13	2.11	0.51
1:AA:1202:U:H1'	14:AN:69:ARG:HD2	1.93	0.51
7:AG:116:MET:O	7:AG:120:LEU:HB2	2.11	0.51
16:CP:67:ILE:HG22	16:CP:68:SER:O	2.11	0.51
22:BA:1759:A:H2'	22:BA:1760:C:C6	2.46	0.51
1:CA:568:G:O6	12:CL:2:ALA:HB2	2.11	0.51
22:DA:1296:G:OP1	22:DA:2709:G:O2'	2.27	0.51
2:AB:126:PHE:N	2:AB:126:PHE:CD2	2.79	0.51
1:AA:994:A:N1	1:AA:1047:G:H4'	2.26	0.51
25:DD:38:LYS:HD2	25:DD:45:TYR:OH	2.11	0.51
33:BL:30:THR:O	33:BL:33:ARG:HG2	2.11	0.50
22:BA:2064:C:H2'	22:BA:2065:C:C6	2.46	0.50
29:BH:14:SER:OG	29:BH:17:ASP:OD1	2.29	0.50
22:DA:1345:C:H5'	22:DA:1396:U:H5	1.75	0.50
28:BG:149:ARG:HH11	28:BG:149:ARG:CG	2.24	0.50
39:DR:81:LYS:N	39:DR:81:LYS:HD3	2.27	0.50
22:DA:2216:G:H2'	22:DA:2217:G:C8	2.46	0.50
9:AI:84:THR:HG21	9:AI:103:PHE:CB	2.41	0.50
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.40	0.50
1:AA:1352:C:H2'	1:AA:1353:G:C8	2.46	0.50
19:CS:55:ARG:HG3	19:CS:56:GLN:H	1.77	0.50
1:AA:591:U:H2'	1:AA:592:G:H8	1.76	0.50
22:DA:1895:C:H2'	22:DA:1896:G:H8	1.75	0.50
23:DB:106:G:H2'	23:DB:107:G:O4'	2.11	0.50
22:BA:2261:C:OP1	44:BW:19:LYS:NZ	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:121:G:H4'	22:DA:148:U:H2'	1.92	0.50
22:BA:1812:U:H2'	22:BA:1813:G:H8	1.76	0.50
27:BF:74:VAL:HG22	27:BF:79:ILE:HD11	1.94	0.50
27:BF:123:ASP:OD2	27:BF:127:ASN:HB2	2.11	0.50
24:BC:160:THR:O	24:BC:195:VAL:HG12	2.10	0.50
1:CA:677:U:H3	1:CA:713:G:H22	1.57	0.50
29:BH:66:ASN:OD1	29:BH:138:VAL:HG21	2.11	0.50
24:BC:40:SER:C	24:BC:42:GLY:H	2.14	0.50
1:CA:931:C:H2'	1:CA:932:C:H6	1.76	0.50
34:BM:49:ALA:HB1	34:BM:120:ALA:HB1	1.92	0.50
25:DD:14:ILE:HG12	25:DD:24:VAL:HG21	1.93	0.50
22:DA:1676:A:H2'	22:DA:1677:A:O4'	2.12	0.50
22:BA:2557:G:H2'	22:BA:2558:C:C6	2.46	0.50
1:CA:1086:U:OP1	1:CA:1086:U:H4'	2.10	0.50
22:BA:1846:G:H2'	22:BA:1847:A:C8	2.45	0.50
10:CJ:49:PHE:O	10:CJ:65:TYR:N	2.35	0.50
22:BA:136:G:H1	22:BA:143:C:N4	2.08	0.50
14:AN:45:VAL:HG23	14:AN:46:LEU:H	1.76	0.50
1:AA:1032:G:H5'	1:AA:1033:G:OP2	2.11	0.50
20:CT:79:LEU:O	20:CT:83:ILE:HG23	2.12	0.50
1:CA:227:G:H2'	1:CA:228:A:O4'	2.10	0.50
19:CS:16:LEU:O	19:CS:20:GLU:HG2	2.10	0.50
31:DJ:4:PHE:O	38:DQ:64:ARG:NH2	2.33	0.50
9:CI:76:ALA:HA	9:CI:79:ILE:HD12	1.92	0.50
1:AA:468:A:C2	1:AA:469:C:C4	2.99	0.50
22:BA:1721:G:O2'	22:BA:1739:A:N6	2.44	0.50
36:BO:51:ALA:HB3	36:BO:78:VAL:HG13	1.93	0.50
4:CD:98:LEU:HB2	4:CD:135:TYR:HB3	1.93	0.50
25:DD:125:TRP:CG	25:DD:160:LYS:HB3	2.46	0.50
22:DA:236:C:O2'	22:DA:431:U:H4'	2.11	0.50
22:BA:1946:U:H2'	22:BA:1947:C:C6	2.46	0.50
16:CP:17:TYR:HE1	16:CP:41:PRO:HG3	1.76	0.50
22:DA:1779:U:C5	22:DA:1784:A:N7	2.80	0.50
12:AL:24:LEU:CG	12:AL:25:GLU:H	2.13	0.50
22:DA:1075:C:H2'	22:DA:1076:C:C6	2.45	0.50
22:BA:2128:G:OP2	53:B5:37:LYS:HE3	2.11	0.50
33:DL:135:ILE:HG22	33:DL:140:GLY:HA2	1.94	0.50
1:CA:32:A:H3'	1:CA:33:A:H8	1.74	0.50
22:BA:1585:C:H2'	22:BA:1586:A:O4'	2.11	0.50
7:CG:136:LYS:HE2	7:CG:140:ASP:OD1	2.11	0.50
22:DA:933:A:H5'	22:DA:934:U:OP2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1973:G:C6	22:DA:1974:C:C4	2.99	0.50
1:AA:340:U:H2'	1:AA:341:C:C6	2.46	0.50
22:DA:236:C:H4'	22:DA:431:U:O2'	2.10	0.50
1:CA:605:U:H2'	1:CA:606:G:C8	2.46	0.50
1:AA:1060:U:H2'	1:AA:1061:G:H8	1.76	0.50
29:DH:5:LEU:HA	29:DH:36:ALA:HA	1.93	0.50
22:BA:1734:G:H2'	22:BA:1735:A:H8	1.76	0.50
1:AA:1397:C:O2'	1:AA:1398:A:OP1	2.24	0.50
14:AN:28:LYS:HG3	14:AN:29:ALA:N	2.26	0.50
22:BA:2040:G:H2'	22:BA:2041:U:O4'	2.11	0.50
38:DQ:102:ASP:OD1	39:DR:2:TYR:OH	2.17	0.50
22:BA:305:C:H2'	22:BA:306:U:C6	2.45	0.50
22:BA:869:G:H2'	22:BA:870:U:O4'	2.10	0.50
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.46	0.50
14:AN:47:LYS:HD3	19:AS:13:LEU:HD21	1.93	0.50
22:BA:337:C:H2'	22:BA:338:G:O4'	2.11	0.50
1:AA:71:A:H3'	1:AA:71:A:OP2	2.11	0.50
8:CH:75:ILE:HA	8:CH:128:TYR:O	2.12	0.50
27:BF:158:THR:CG2	27:BF:160:ALA:H	2.25	0.50
22:BA:2683:C:H5''	37:BP:56:HIS:HB3	1.92	0.50
21:CU:25:LYS:O	21:CU:29:LEU:HB2	2.11	0.50
35:BN:28:LEU:O	35:BN:32:GLU:N	2.44	0.50
22:DA:1871:A:O2'	22:DA:1872:A:N7	2.44	0.50
1:CA:1232:U:H5''	9:CI:126:GLN:O	2.11	0.50
2:AB:164:ILE:HG23	2:AB:165:ASP:H	1.75	0.50
29:DH:127:GLU:HG3	29:DH:145:ASN:HA	1.93	0.50
52:D4:30:GLU:HG3	52:D4:32:LYS:H	1.74	0.50
1:CA:667:G:OP1	1:CA:732:C:O2'	2.27	0.50
7:AG:100:ALA:O	7:AG:104:ILE:HG13	2.11	0.50
1:AA:579:A:H2'	1:AA:580:C:H6	1.76	0.50
36:DO:71:ALA:O	36:DO:75:GLY:N	2.39	0.50
11:AK:52:PHE:HB3	11:AK:56:ARG:HB3	1.93	0.50
37:DP:103:ARG:HB3	37:DP:108:ALA:HB2	1.92	0.50
39:DR:39:LEU:HA	39:DR:49:ILE:HG21	1.93	0.50
1:CA:299:G:N2	1:CA:565:U:O2	2.44	0.50
22:BA:493:G:H2'	22:BA:494:G:O4'	2.11	0.50
1:AA:1504:G:OP2	1:AA:1507:A:O2'	2.24	0.50
1:AA:237:G:H2'	1:AA:238:A:O4'	2.12	0.50
1:AA:792:A:H4'	1:AA:793:U:O5'	2.11	0.50
22:BA:1425:G:O2'	22:BA:1426:G:H5'	2.11	0.50
2:CB:213:TYR:HA	2:CB:216:ALA:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.46	0.50
22:BA:1059:G:H3'	22:BA:1060:U:H2'	1.93	0.50
22:BA:812:C:H4'	38:BQ:13:ARG:NH2	2.22	0.50
38:DQ:76:TYR:OH	38:DQ:92:ARG:NH1	2.43	0.50
22:BA:1327:A:H2'	22:BA:1328:A:O4'	2.12	0.50
9:AI:52:LEU:HA	9:AI:55:VAL:HG23	1.93	0.50
27:BF:158:THR:O	57:BF:201:HOH:O	2.18	0.50
13:AM:85:CYS:SG	13:AM:87:ARG:HG3	2.52	0.50
27:BF:60:ILE:HD13	27:BF:152:LEU:HD21	1.93	0.50
22:DA:1604:C:O2'	22:DA:1610:A:N1	2.41	0.50
22:BA:2297:A:N1	22:BA:2321:U:H5	2.09	0.50
1:AA:108:G:C6	20:AT:10:ARG:HG2	2.46	0.50
22:DA:2544:G:H2'	22:DA:2545:G:C8	2.45	0.50
1:CA:581:G:OP1	15:CO:65:LYS:NZ	2.45	0.50
22:DA:323:C:H6	22:DA:1205:A:N1	2.09	0.50
1:AA:39:G:N7	1:AA:547:A:H8	2.10	0.50
1:AA:642:A:N3	8:AH:105:SER:OG	2.38	0.50
40:DS:79:GLY:H	40:DS:101:SER:HA	1.75	0.50
31:BJ:49:ASP:OD1	31:BJ:121:LYS:NZ	2.43	0.50
4:CD:145:ILE:HD13	4:CD:178:MET:HB3	1.94	0.50
22:BA:1296:G:OP1	22:BA:2709:G:O2'	2.26	0.50
1:CA:558:G:H8	1:CA:558:G:O5'	1.94	0.50
39:DR:42:ALA:HA	39:DR:46:GLU:HA	1.93	0.50
1:CA:4:U:H5''	1:CA:5:U:OP1	2.11	0.50
1:AA:1048:G:O6	1:AA:1210:C:N4	2.44	0.50
1:AA:1508:A:H2'	1:AA:1509:C:O4'	2.11	0.50
22:DA:2597:G:H2'	22:DA:2598:A:C8	2.47	0.50
41:BT:12:ARG:HG3	41:BT:12:ARG:HH11	1.77	0.50
3:CC:77:ILE:HA	3:CC:84:VAL:HG23	1.92	0.50
1:AA:1243:C:H2'	1:AA:1244:G:C8	2.46	0.50
5:AE:136:VAL:O	5:AE:140:THR:OG1	2.29	0.50
29:BH:80:ILE:O	29:BH:147:VAL:N	2.44	0.50
1:CA:1097:C:H2'	1:CA:1098:C:C6	2.46	0.50
2:AB:19:GLN:HG2	2:AB:190:ASN:OD1	2.11	0.50
26:DE:48:THR:O	26:DE:52:VAL:HG23	2.12	0.50
1:AA:374:A:H5''	1:AA:452:A:C2	2.47	0.50
2:AB:217:VAL:O	2:AB:221:VAL:HG23	2.11	0.50
22:DA:1721:G:H2'	22:DA:1738:G:H22	1.76	0.50
37:BP:62:ARG:HH21	37:BP:71:GLU:HG3	1.77	0.50
22:BA:381:G:OP1	45:BX:18:ARG:HD3	2.12	0.50
17:AQ:21:ILE:HD13	17:AQ:48:ASP:OD1	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1299:A:H2'	1:AA:1299:A:N3	2.27	0.50
1:CA:1317:C:H2'	1:CA:1318:A:O4'	2.12	0.50
2:CB:134:ALA:O	2:CB:138:THR:N	2.35	0.50
24:DC:141:VAL:HG11	24:DC:190:ALA:HB1	1.92	0.50
3:CC:87:LEU:O	3:CC:91:VAL:HG23	2.11	0.50
43:BV:51:GLN:OE1	43:BV:57:TYR:OH	2.29	0.50
22:BA:366:C:H2'	22:BA:367:G:O4'	2.12	0.50
49:B1:17:THR:HG21	49:B1:43:VAL:HG12	1.93	0.50
1:CA:1084:G:C5	1:CA:1085:U:C4	3.00	0.50
22:DA:607:U:O4	22:DA:619:G:H2'	2.11	0.50
22:DA:1434:A:H2'	22:DA:1435:G:C8	2.47	0.50
1:CA:186:C:O4'	20:CT:76:LYS:HD2	2.11	0.50
1:AA:855:U:H2'	1:AA:856:C:C6	2.45	0.50
1:CA:302:G:O2'	1:CA:556:C:H5''	2.11	0.50
27:BF:33:LYS:HG2	27:BF:157:THR:HB	1.93	0.50
22:BA:1613:G:H4'	50:B2:3:ARG:HD3	1.93	0.50
22:DA:655:A:O3'	22:DA:656:G:H8	1.95	0.50
17:AQ:52:GLU:H	17:AQ:52:GLU:CD	2.13	0.50
5:CE:138:ARG:H	5:CE:141:ILE:HD13	1.77	0.50
22:BA:2461:A:H2'	22:BA:2462:C:H6	1.77	0.50
22:BA:2405:G:O2'	22:BA:2406:A:OP1	2.28	0.50
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.46	0.50
22:DA:2747:G:O2'	28:DG:67:THR:HG22	2.11	0.50
22:DA:2818:U:H2'	22:DA:2819:G:C8	2.47	0.50
28:BG:9:VAL:HG21	28:BG:73:ASN:HA	1.94	0.50
22:DA:422:A:OP2	57:DA:3558:HOH:O	2.20	0.50
22:DA:242:G:N7	51:D3:5:LYS:HG2	2.27	0.50
8:CH:89:LYS:HG3	8:CH:90:ASP:N	2.27	0.50
34:DM:17:ASN:OD1	34:DM:95:LEU:HB3	2.11	0.50
23:DB:13:G:H1	23:DB:69:G:HO2'	1.58	0.50
1:AA:693:G:P	11:AK:127:ARG:HH22	2.33	0.50
23:BB:60:C:N4	57:BB:303:HOH:O	2.44	0.50
22:DA:457:A:N1	22:DA:470:A:H5''	2.27	0.50
22:DA:289:G:H2'	22:DA:290:U:O4'	2.12	0.50
25:BD:61:THR:OG1	25:BD:63:PRO:HD2	2.12	0.50
1:CA:750:C:H4'	15:CO:21:ASP:HA	1.94	0.50
1:CA:495:A:C2	1:CA:496:A:C6	2.99	0.50
51:B3:63:PRO:HG2	51:B3:64:TYR:CD2	2.47	0.50
7:AG:137:LYS:O	7:AG:141:VAL:HG23	2.11	0.50
2:AB:20:THR:HB	2:AB:37:LYS:O	2.12	0.50
1:AA:702:A:N6	22:BA:1846:G:H4'	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:636:G:C6	33:BL:111:ILE:HD11	2.47	0.50
13:CM:11:ASP:HA	13:CM:45:ILE:HD13	1.94	0.50
22:BA:165:A:H2'	22:BA:166:U:O4'	2.12	0.50
6:CF:91:ARG:HG2	6:CF:93:LYS:NZ	2.27	0.50
1:CA:821:G:H2'	1:CA:822:U:H6	1.76	0.50
1:CA:73:C:H1'	1:CA:74:A:H5'	1.94	0.50
16:CP:38:PHE:CZ	16:CP:51:ARG:HB3	2.46	0.50
24:BC:251:GLN:HG3	24:BC:252:THR:O	2.10	0.50
33:DL:90:VAL:N	33:DL:121:THR:O	2.45	0.50
24:DC:29:PRO:HG3	24:DC:63:ARG:CZ	2.42	0.50
1:AA:668:G:H2'	1:AA:669:G:C8	2.47	0.50
22:DA:631:A:OP1	22:DA:631:A:H8	1.94	0.50
22:BA:1440:U:H2'	22:BA:1441:G:H8	1.77	0.50
40:BS:69:LEU:HG	40:BS:107:VAL:HG22	1.93	0.50
1:AA:1442:G:H2'	1:AA:1443:C:C6	2.47	0.50
1:AA:1236:A:H2'	1:AA:1237:C:C6	2.46	0.50
1:AA:1202:U:C2	14:AN:82:ILE:HG21	2.47	0.50
22:DA:1877:A:H2'	22:DA:1878:G:C8	2.47	0.50
1:CA:28:A:OP1	4:CD:73:ARG:NH2	2.44	0.50
34:DM:21:ALA:HB1	34:DM:100:LYS:HG2	1.93	0.50
22:BA:2070:A:H2'	22:BA:2071:A:O4'	2.12	0.50
42:DU:28:VAL:HA	42:DU:34:VAL:HG12	1.93	0.50
22:BA:2056:G:H2'	22:BA:2056:G:N3	2.26	0.50
1:CA:1478:U:H2'	1:CA:1479:C:H6	1.77	0.50
8:CH:87:LYS:HG3	8:CH:91:GLU:HB3	1.93	0.50
22:BA:157:C:H2'	22:BA:158:U:O4'	2.12	0.50
51:B3:62:LEU:HB3	51:B3:65:ALA:HB2	1.94	0.50
26:DE:149:ILE:HG23	26:DE:188:MET:HG2	1.93	0.50
29:DH:44:ILE:O	29:DH:48:GLU:HB2	2.12	0.50
22:BA:1069:A:H4'	22:BA:1070:A:H8	1.76	0.50
22:BA:1327:A:N6	22:BA:1647:U:O2	2.44	0.50
24:DC:154:LEU:HD13	24:DC:176:LEU:HD21	1.93	0.50
48:B0:11:SER:O	48:B0:15:MET:HG3	2.11	0.50
22:BA:198:C:H4'	22:BA:2243:U:O2'	2.12	0.50
22:DA:311:A:C2	22:DA:330:A:H3'	2.46	0.50
9:AI:40:GLY:HA2	9:AI:45:ARG:HB2	1.94	0.50
40:BS:79:GLY:CA	40:BS:102:HIS:CE1	2.94	0.50
1:AA:1314:C:H41	19:AS:4:SER:HA	1.77	0.50
22:DA:189:G:P	45:DX:26:LYS:HE2	2.51	0.50
10:CJ:28:THR:HG21	10:CJ:90:LEU:HD12	1.93	0.50
4:CD:14:ARG:HG2	4:CD:56:ARG:HH21	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CJ:52:LEU:HD22	10:CJ:59:LYS:HA	1.94	0.50
2:CB:72:THR:HA	2:CB:93:ASN:O	2.12	0.50
22:BA:30:G:H2'	22:BA:31:C:H6	1.76	0.50
14:CN:23:LYS:HG3	14:CN:24:ARG:HG3	1.94	0.50
22:DA:2780:G:P	31:DJ:120:ARG:HE	2.35	0.50
22:BA:18:U:O4	57:BA:3205:HOH:O	2.19	0.50
22:DA:846:U:O2'	22:DA:847:U:O5'	2.29	0.50
12:AL:74:LEU:HD21	12:AL:104:CYS:HA	1.93	0.50
5:AE:34:THR:HG22	5:AE:52:LYS:HB3	1.94	0.50
22:BA:2014:A:H2'	22:BA:2015:A:C8	2.47	0.50
22:BA:545:U:H2'	22:BA:546:U:O3'	2.11	0.50
31:DJ:89:PHE:CE2	31:DJ:100:VAL:HG11	2.47	0.50
22:DA:624:C:O2'	22:DA:657:U:H5''	2.12	0.50
16:CP:72:ALA:HA	16:CP:75:ILE:HD12	1.94	0.50
19:AS:37:ARG:O	19:AS:70:LYS:HD2	2.11	0.50
22:DA:632:A:H5''	33:DL:68:SER:HB2	1.92	0.50
1:AA:130:A:N7	17:AQ:65:ARG:HB2	2.26	0.50
27:BF:25:VAL:O	27:BF:28:VAL:HG12	2.12	0.50
38:DQ:98:ILE:HG22	38:DQ:106:PHE:HB2	1.94	0.50
32:DK:113:MET:SD	32:DK:116:ILE:HD11	2.52	0.50
29:BH:91:PHE:HB3	1:CA:55:A:C4	2.47	0.49
29:BH:94:ILE:C	1:CA:368:U:OP1	2.50	0.49
22:BA:2092:U:OP2	29:BH:27:ARG:CD	2.60	0.49
29:DH:81:ALA:C	29:DH:149:GLU:HB3	2.33	0.49
5:CE:82:GLN:OE1	5:CE:149:SER:HA	2.12	0.49
2:CB:223:GLU:OE2	2:CB:226:SER:HA	2.12	0.49
33:BL:111:ILE:CD1	33:BL:111:ILE:H	2.24	0.49
33:DL:20:GLY:N	33:DL:27:LEU:O	2.44	0.49
41:DT:14:PRO:HA	41:DT:32:LEU:HB3	1.94	0.49
1:CA:502:A:H2'	1:CA:503:C:O4'	2.12	0.49
22:DA:118:A:C8	22:DA:119:A:C8	3.00	0.49
41:DT:37:ASP:OD2	41:DT:38:ALA:N	2.42	0.49
52:B4:11:CYS:HB3	52:B4:33:HIS:HE1	1.76	0.49
30:BI:34:ASN:HB3	30:BI:37:GLU:H	1.77	0.49
1:AA:500:G:H2'	1:AA:501:C:C6	2.47	0.49
1:AA:1452:C:H4'	1:AA:1453:G:H5''	1.94	0.49
42:DU:28:VAL:HB	42:DU:34:VAL:HG12	1.94	0.49
15:CO:6:GLU:O	15:CO:10:LYS:N	2.43	0.49
22:DA:1240:U:O2'	22:DA:1241:A:O5'	2.28	0.49
10:AJ:67:ILE:HG13	14:AN:96:LEU:HD13	1.94	0.49
12:CL:22:PRO:C	12:CL:24:LEU:H	2.14	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:B3:27:ALA:O	51:B3:28:ASN:HB2	2.11	0.49
1:AA:147:G:H2'	1:AA:148:G:C8	2.47	0.49
24:BC:53:HIS:NE2	24:BC:219:THR:HG23	2.27	0.49
10:AJ:21:ALA:HA	10:AJ:24:GLU:HB3	1.94	0.49
42:BU:86:ARG:HG2	42:BU:95:PHE:CD2	2.47	0.49
29:BH:99:ILE:O	29:BH:99:ILE:HG22	2.12	0.49
22:BA:2199:A:O4'	29:BH:28:ASN:CG	2.49	0.49
22:BA:1098:A:H5'	22:BA:1099:G:OP2	2.12	0.49
2:AB:17:GLY:HA2	2:AB:41:ILE:HG23	1.93	0.49
22:DA:1097:U:H3'	22:DA:1098:A:O4'	2.12	0.49
27:DF:136:ILE:HG23	27:DF:141:ILE:HG22	1.94	0.49
43:DV:30:ILE:HG13	43:DV:40:ILE:HG13	1.94	0.49
52:B4:36:ARG:HG2	52:B4:37:GLN:N	2.27	0.49
5:AE:80:THR:HA	5:AE:122:ASN:HD21	1.77	0.49
29:BH:43:ASN:O	29:BH:46:PHE:HB3	2.12	0.49
45:BX:7:VAL:HG23	45:BX:51:VAL:HG12	1.93	0.49
11:AK:52:PHE:CB	11:AK:56:ARG:HB3	2.43	0.49
15:CO:10:LYS:O	15:CO:14:GLU:HG3	2.12	0.49
3:CC:90:VAL:O	3:CC:94:ILE:HG13	2.11	0.49
27:BF:34:ILE:HG13	27:BF:96:MET:HG3	1.94	0.49
1:CA:624:C:H2'	1:CA:625:U:O4'	2.13	0.49
22:BA:1820:U:OP1	24:BC:177:ARG:NH2	2.46	0.49
22:DA:1665:A:H5''	32:DK:66:LYS:HG3	1.93	0.49
22:DA:747:U:O2	22:DA:2014:A:H1'	2.12	0.49
3:AC:138:VAL:HA	3:AC:149:ILE:HD13	1.93	0.49
22:DA:1130:U:C2	22:DA:2025:C:H5''	2.47	0.49
22:BA:78:U:H2'	22:BA:79:C:C6	2.47	0.49
46:BY:15:ASN:O	46:BY:19:LEU:HG	2.12	0.49
1:AA:1071:C:H2'	1:AA:1072:G:H8	1.76	0.49
14:AN:48:LEU:O	14:AN:50:THR:N	2.45	0.49
22:BA:280:U:H2'	22:BA:281:C:C6	2.47	0.49
22:DA:239:C:HO2'	22:DA:621:A:H2	1.60	0.49
22:DA:931:U:O4	22:DA:1166:G:N2	2.45	0.49
29:DH:5:LEU:HD11	29:DH:13:GLY:HA2	1.93	0.49
22:DA:2718:G:H5'	37:DP:98:TYR:CD1	2.47	0.49
22:DA:1058:U:H2'	22:DA:1059:G:C8	2.47	0.49
16:CP:8:ARG:HB3	16:CP:28:ARG:NH1	2.27	0.49
22:BA:1731:G:C6	22:BA:1733:G:C5	3.00	0.49
22:DA:1184:U:OP1	47:DZ:30:ARG:HD3	2.12	0.49
11:CK:43:GLY:HA3	11:CK:74:VAL:HG12	1.93	0.49
22:BA:2079:U:H4'	22:BA:2433:A:H2	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DP:16:ASP:OD2	37:DP:16:ASP:N	2.44	0.49
22:BA:1789:A:P	24:BC:221:ARG:HH11	2.35	0.49
22:BA:521:U:H2'	22:BA:522:A:C8	2.47	0.49
29:BH:86:ASP:O	29:BH:87:GLU:HB2	2.11	0.49
17:CQ:8:LEU:HD22	17:CQ:73:TRP:CH2	2.47	0.49
5:CE:150:PRO:O	5:CE:153:VAL:HG22	2.12	0.49
22:DA:1810:A:H2'	22:DA:1811:G:O4'	2.13	0.49
6:AF:91:ARG:HG2	6:AF:93:LYS:HD3	1.94	0.49
22:DA:370:G:O2'	22:DA:423:A:H3'	2.12	0.49
10:AJ:80:THR:HB	10:AJ:83:THR:H	1.77	0.49
22:DA:2267:A:H5''	22:DA:2268:A:C5'	2.43	0.49
22:BA:622:G:H2'	22:BA:623:C:C6	2.47	0.49
14:CN:36:ALA:HB2	14:CN:41:ARG:HG3	1.95	0.49
5:CE:36:LEU:HD21	5:CE:137:VAL:HG11	1.93	0.49
1:AA:532:A:N7	3:AC:193:TYR:HB3	2.26	0.49
2:AB:50:PHE:HA	2:AB:213:TYR:OH	2.12	0.49
22:DA:320:A:H2'	26:DE:131:THR:HG21	1.94	0.49
1:AA:22:G:H4'	1:AA:885:G:C8	2.47	0.49
22:DA:813:U:H2'	22:DA:814:C:C6	2.48	0.49
22:DA:20:C:H2'	22:DA:21:A:C8	2.47	0.49
1:AA:1435:G:H2'	1:AA:1436:U:H6	1.75	0.49
1:AA:1277:C:C2'	1:AA:1279:G:H8	2.25	0.49
37:DP:48:ILE:HD13	37:DP:62:ARG:HB2	1.94	0.49
28:DG:24:ILE:HD11	28:DG:43:VAL:HG11	1.93	0.49
33:DL:94:THR:O	33:DL:98:ALA:N	2.45	0.49
1:AA:763:G:H2'	1:AA:764:C:H6	1.77	0.49
22:BA:813:U:H2'	22:BA:814:C:C6	2.46	0.49
22:BA:1826:G:O2'	22:BA:1971:U:OP2	2.30	0.49
22:DA:2376:A:H2'	22:DA:2377:A:O4'	2.11	0.49
28:DG:8:PRO:HG3	28:DG:51:THR:HG22	1.94	0.49
11:AK:111:THR:HG23	21:AU:5:LYS:HB3	1.95	0.49
27:DF:38:MET:HB2	27:DF:57:LEU:HD11	1.95	0.49
26:DE:147:LEU:HB3	26:DE:186:VAL:HG13	1.94	0.49
1:CA:392:C:H2'	1:CA:393:A:C8	2.46	0.49
23:BB:112:G:H2'	23:BB:113:C:C6	2.47	0.49
18:CR:71:THR:OG1	18:CR:72:ASP:N	2.45	0.49
4:AD:109:ALA:N	4:AD:113:GLU:OE2	2.41	0.49
22:DA:1011:G:OP1	38:DQ:75:SER:HB2	2.12	0.49
22:DA:562:U:H2'	22:DA:572:A:O4'	2.12	0.49
1:AA:1258:G:H2'	1:AA:1259:C:C6	2.48	0.49
9:CI:99:ARG:HG2	9:CI:104:VAL:HG21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2643:G:H2'	22:BA:2644:G:O4'	2.13	0.49
22:BA:400:G:N7	45:BX:57:ARG:NH1	2.59	0.49
22:BA:714:U:H2'	22:BA:716:A:N7	2.27	0.49
1:CA:532:A:N6	3:CC:193:TYR:HD2	2.10	0.49
22:DA:2293:G:H2'	22:DA:2294:G:O4'	2.12	0.49
46:DY:9:LYS:HB3	46:DY:12:GLU:HG2	1.95	0.49
13:AM:76:SER:O	13:AM:80:LEU:HD12	2.12	0.49
14:AN:92:GLU:O	14:AN:94:PRO:HD3	2.13	0.49
2:CB:72:THR:HG22	2:CB:95:ARG:NH1	2.28	0.49
22:BA:1357:C:H2'	22:BA:1358:G:O4'	2.12	0.49
20:AT:20:HIS:O	20:AT:24:ARG:HG2	2.12	0.49
22:BA:2649:C:H2'	22:BA:2650:U:C6	2.48	0.49
1:CA:312:C:H2'	1:CA:313:A:C8	2.47	0.49
39:DR:49:ILE:HG22	39:DR:54:VAL:N	2.28	0.49
22:DA:2718:G:H5'	37:DP:98:TYR:HD1	1.78	0.49
9:CI:10:GLY:HA2	9:CI:81:HIS:ND1	2.28	0.49
1:CA:401:C:OP2	4:CD:70:ARG:HD3	2.13	0.49
22:DA:2834:G:H2'	22:DA:2879:A:N6	2.28	0.49
22:BA:749:A:H4'	22:BA:1271:G:N3	2.28	0.49
22:DA:1751:U:H2'	22:DA:1752:C:C6	2.47	0.49
22:BA:659:G:H4'	26:BE:95:LYS:HD3	1.93	0.49
7:CG:57:SER:HB3	7:CG:60:GLU:HG3	1.93	0.49
24:BC:154:LEU:HD13	24:BC:176:LEU:HD21	1.94	0.49
41:BT:48:GLN:OE1	41:BT:54:GLU:HA	2.11	0.49
22:BA:300:A:OP2	42:BU:97:LYS:NZ	2.45	0.49
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.48	0.49
1:AA:1417:G:H22	1:AA:1482:G:H2'	1.78	0.49
22:BA:1234:U:H2'	22:BA:1235:G:O4'	2.13	0.49
22:DA:1563:U:H2'	22:DA:1564:C:H6	1.77	0.49
1:CA:949:A:N7	13:CM:105:ASN:ND2	2.60	0.49
20:CT:44:LYS:NZ	20:CT:86:LEU:O	2.36	0.49
1:CA:1096:C:H2'	1:CA:1097:C:C6	2.47	0.49
30:DI:89:GLY:HA2	30:DI:136:MET:HE3	1.95	0.49
22:DA:1269:A:C6	22:DA:1270:C:N4	2.81	0.49
19:AS:4:SER:O	19:AS:6:LYS:N	2.46	0.49
30:DI:4:LYS:HD2	30:DI:5:VAL:H	1.77	0.49
1:AA:1141:C:O2'	1:AA:1142:G:H8	1.96	0.49
13:CM:14:HIS:HB2	13:CM:17:ILE:CD1	2.43	0.49
22:DA:1599:U:P	41:DT:40:LYS:HD2	2.53	0.49
22:DA:2369:A:H2'	22:DA:2370:G:O4'	2.13	0.49
22:BA:1717:A:H2'	22:BA:1718:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1060:U:H2'	1:CA:1061:G:C8	2.48	0.49
1:CA:1263:C:H2'	1:CA:1264:U:C6	2.47	0.49
39:BR:3:ALA:HB3	39:BR:59:ILE:HD11	1.93	0.49
26:DE:125:SER:OG	26:DE:126:VAL:N	2.44	0.49
31:BJ:7:LYS:O	31:BJ:11:VAL:HG23	2.13	0.49
1:AA:1118:U:O3'	9:AI:85:ARG:NH2	2.45	0.49
1:AA:1219:A:H2'	1:AA:1220:G:C8	2.47	0.49
8:CH:113:ASP:OD1	8:CH:114:ARG:N	2.44	0.49
32:BK:63:VAL:HG12	32:BK:107:LEU:HD21	1.94	0.49
22:DA:1916:A:H2'	22:DA:1917:U:O4'	2.13	0.49
1:CA:206:C:H2'	1:CA:207:C:H4'	1.94	0.49
41:BT:56:GLU:HB2	41:BT:88:LYS:HA	1.95	0.49
13:CM:114:LYS:HB2	13:CM:115:PRO:HD3	1.93	0.49
1:CA:1087:G:H2'	1:CA:1088:G:H8	1.78	0.49
1:CA:1288:A:N1	1:CA:1371:G:H1'	2.27	0.49
31:BJ:78:THR:OG1	31:BJ:80:HIS:HB2	2.13	0.49
37:DP:37:LYS:NZ	37:DP:39:ARG:HD2	2.28	0.49
19:CS:36:ARG:HA	19:CS:71:LEU:HB2	1.93	0.49
22:DA:1628:G:H21	22:DA:2699:C:P	2.35	0.49
1:CA:81:A:H2'	1:CA:82:G:C8	2.47	0.49
22:DA:1019:U:O2'	22:DA:1021:A:N7	2.37	0.49
22:BA:2462:C:H2'	22:BA:2463:C:H6	1.78	0.49
22:DA:2747:G:O6	22:DA:2755:C:H5''	2.11	0.49
22:DA:973:A:H5''	39:DR:81:LYS:HG3	1.95	0.49
1:CA:34:C:H2'	1:CA:35:G:C8	2.48	0.49
27:BF:36:LEU:HD22	27:BF:91:LEU:HD11	1.95	0.49
1:AA:1053:G:N7	1:AA:1199:U:H3'	2.27	0.49
24:BC:145:GLU:HG2	24:BC:151:GLY:H	1.77	0.49
22:BA:2748:A:N1	57:BA:3815:HOH:O	2.35	0.49
51:D3:7:VAL:HB	51:D3:61:CYS:HB3	1.93	0.49
1:AA:921:U:H2'	1:AA:922:G:O4'	2.13	0.49
1:CA:714:G:H21	1:CA:777:A:H1'	1.77	0.49
47:DZ:9:GLN:HB3	47:DZ:32:ILE:HA	1.95	0.49
1:AA:1253:G:H2'	1:AA:1254:A:H8	1.77	0.49
22:BA:1747:U:H2'	22:BA:1748:C:C6	2.47	0.49
22:BA:2033:A:H4'	22:BA:2034:U:OP1	2.13	0.49
35:DN:90:ARG:HG2	35:DN:92:GLY:O	2.12	0.49
2:CB:57:LEU:O	2:CB:60:ILE:HG13	2.13	0.49
12:CL:66:TYR:O	12:CL:97:THR:OG1	2.24	0.49
1:CA:929:G:H5''	1:CA:1535:C:C5'	2.43	0.49
33:BL:95:LEU:O	33:BL:100:ILE:HG23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DD:133:THR:HG23	25:DD:134:HIS:N	2.27	0.49
22:BA:66:C:H2'	22:BA:67:U:C6	2.47	0.49
1:AA:203:G:H5'	1:AA:468:A:H8	1.77	0.49
37:DP:93:ARG:O	37:DP:94:LYS:HB2	2.12	0.49
35:DN:2:ARG:HG3	35:DN:3:HIS:N	2.28	0.49
22:BA:417:C:H2'	22:BA:418:C:C6	2.47	0.49
1:AA:1538:C:C2'	1:AA:1539:C:H5'	2.43	0.49
22:DA:1861:G:N2	22:DA:1882:U:H1'	2.27	0.49
22:BA:1779:U:C5	22:BA:1784:A:N7	2.80	0.49
24:DC:141:VAL:CG1	24:DC:190:ALA:HB1	2.43	0.49
16:CP:6:LEU:HD12	16:CP:71:VAL:HG23	1.95	0.49
22:BA:305:C:H2'	22:BA:306:U:H6	1.78	0.49
22:BA:538:A:O2'	31:BJ:8:PRO:HD2	2.13	0.49
23:BB:14:U:O2	23:BB:107:G:H4'	2.13	0.49
22:DA:790:U:N3	22:DA:794:A:O2'	2.45	0.49
1:AA:1380:U:C4	7:AG:3:ARG:HD3	2.47	0.49
24:DC:131:PRO:HB2	24:DC:133:ARG:HG2	1.95	0.49
4:AD:170:TRP:CG	4:AD:186:PRO:HG3	2.47	0.49
22:BA:1199:U:H2'	22:BA:1200:C:C6	2.47	0.49
22:DA:1264:A:H5'	48:D0:8:PRO:HG2	1.93	0.49
1:AA:624:C:H4'	16:AP:11:ALA:HB2	1.94	0.49
29:DH:112:LYS:CG	29:DH:113:SER:N	2.76	0.49
2:AB:122:GLN:H	2:AB:122:GLN:CD	2.16	0.49
27:BF:44:ILE:HG22	27:BF:83:TYR:CZ	2.48	0.49
36:BO:24:THR:HG22	36:BO:42:PRO:HD3	1.95	0.49
1:AA:718:A:H5'	11:AK:119:ASN:HB2	1.94	0.49
22:DA:1688:U:O2	22:DA:1700:A:H8	1.95	0.49
29:DH:21:VAL:CG2	29:DH:22:LYS:N	2.76	0.49
22:BA:946:C:H2'	22:BA:947:A:H8	1.78	0.49
22:BA:623:C:H2'	22:BA:624:C:C6	2.48	0.49
10:CJ:19:ASP:OD2	10:CJ:72:ARG:NH2	2.46	0.49
22:BA:998:C:P	38:BQ:92:ARG:HH21	2.35	0.49
2:AB:87:CYS:HB2	2:AB:89:GLN:NE2	2.27	0.49
22:BA:637:A:N1	22:BA:651:G:O2'	2.34	0.49
22:DA:971:G:H2'	22:DA:972:A:O4'	2.12	0.49
10:CJ:63:ASP:OD1	14:CN:85:ARG:NH1	2.41	0.49
1:CA:972:C:H4'	10:CJ:59:LYS:CG	2.43	0.49
22:DA:680:C:H2'	22:DA:681:G:C8	2.48	0.49
4:CD:42:GLY:C	4:CD:44:ARG:H	2.16	0.49
2:AB:126:PHE:N	2:AB:126:PHE:HD2	2.10	0.49
12:CL:22:PRO:O	12:CL:24:LEU:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2079:U:H4'	22:BA:2433:A:C2	2.48	0.49
22:DA:697:G:H2'	22:DA:698:C:C6	2.48	0.49
22:BA:2619:C:H2'	22:BA:2620:C:H6	1.78	0.49
1:AA:483:C:O2	16:AP:13:LYS:NZ	2.45	0.49
22:BA:484:C:H2'	22:BA:485:C:H6	1.78	0.49
23:DB:38:C:H2'	23:DB:39:A:O4'	2.12	0.49
30:DI:103:ARG:O	30:DI:107:GLN:HB2	2.12	0.49
3:CC:151:VAL:HG12	3:CC:200:VAL:HB	1.94	0.49
20:CT:78:ASN:O	20:CT:82:GLN:HG2	2.13	0.49
29:BH:121:VAL:H	29:BH:122:LEU:HB2	1.77	0.49
17:CQ:8:LEU:HD23	17:CQ:25:ILE:HD12	1.95	0.49
20:AT:71:LYS:HA	20:AT:74:ARG:NH2	2.27	0.49
2:AB:33:GLY:HA3	2:AB:40:ILE:N	2.27	0.49
25:BD:133:THR:HG23	25:BD:134:HIS:CD2	2.47	0.49
2:CB:23:TRP:O	2:CB:23:TRP:CG	2.66	0.49
2:AB:151:ILE:HG23	2:AB:152:LYS:H	1.78	0.49
24:BC:17:VAL:N	24:BC:204:VAL:HG22	2.28	0.49
1:CA:136:C:H2'	1:CA:137:U:C6	2.48	0.49
22:DA:309:A:H4'	42:DU:16:GLY:HA2	1.95	0.49
22:DA:232:G:N1	22:DA:420:C:OP1	2.35	0.49
5:AE:105:ILE:O	5:AE:112:ARG:NH1	2.46	0.49
11:AK:23:ILE:HG22	11:AK:32:VAL:HG22	1.95	0.49
2:AB:164:ILE:O	2:AB:186:ILE:HG12	2.12	0.49
22:BA:751:A:H5'	40:BS:90:LYS:HA	1.95	0.49
1:AA:73:C:O2'	1:AA:74:A:H8	1.96	0.49
22:DA:1926:U:H2'	22:DA:1928:A:N7	2.28	0.49
22:BA:1802:A:N1	22:BA:1822:C:H1'	2.28	0.49
22:BA:2654:A:N1	22:BA:2665:A:H5''	2.28	0.49
28:BG:6:LYS:O	28:BG:8:PRO:HD3	2.13	0.49
9:CI:19:VAL:HG11	9:CI:83:ILE:HA	1.94	0.49
1:AA:554:A:H2'	1:AA:555:U:C6	2.48	0.49
1:AA:1191:A:OP1	3:AC:4:LYS:HD3	2.11	0.49
21:AU:19:PHE:O	21:AU:22:SER:HB3	2.13	0.49
22:BA:2330:G:O3'	44:BW:44:LYS:HE3	2.12	0.49
39:DR:19:THR:HA	39:DR:96:VAL:O	2.13	0.49
1:CA:19:A:H2'	1:CA:20:U:H6	1.78	0.49
28:DG:4:VAL:HG12	28:DG:69:ARG:HG2	1.95	0.49
1:CA:552:U:O2'	12:CL:83:ARG:O	2.29	0.49
30:DI:97:LYS:HD2	30:DI:97:LYS:N	2.27	0.49
32:DK:103:VAL:O	32:DK:122:VAL:HB	2.13	0.49
22:DA:996:A:OP2	38:DQ:93:LYS:NZ	2.34	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DG:158:LYS:O	28:DG:160:LYS:N	2.46	0.49
11:AK:74:VAL:C	11:AK:76:GLU:N	2.65	0.48
5:CE:99:ALA:O	5:CE:101:GLU:N	2.46	0.48
1:AA:131:A:O2'	1:AA:262:A:N3	2.38	0.48
10:AJ:32:THR:OG1	10:AJ:33:GLY:N	2.46	0.48
2:CB:99:GLY:O	2:CB:101:LEU:N	2.46	0.48
26:BE:18:THR:HA	26:BE:106:LYS:HG2	1.95	0.48
1:AA:71:A:N6	1:AA:100:G:N7	2.61	0.48
38:BQ:76:TYR:CZ	38:BQ:80:ILE:HG13	2.48	0.48
12:AL:63:VAL:HG21	12:AL:95:TYR:CE2	2.48	0.48
13:AM:11:ASP:CG	13:AM:12:HIS:N	2.66	0.48
22:DA:2131:U:H5'	22:DA:2132:U:H5''	1.94	0.48
7:AG:68:ASN:C	7:AG:70:ARG:H	2.16	0.48
22:BA:528:A:C8	22:BA:528:A:C3'	2.96	0.48
22:DA:2038:G:H2'	22:DA:2039:U:O4'	2.13	0.48
3:CC:57:ILE:HG13	3:CC:66:VAL:HG22	1.94	0.48
29:DH:72:ILE:O	29:DH:141:LYS:O	2.30	0.48
22:DA:2241:A:H2'	22:DA:2242:G:C8	2.48	0.48
3:CC:155:GLY:HA2	3:CC:163:ALA:HB1	1.94	0.48
22:DA:1668:A:H4'	22:DA:1669:A:O5'	2.13	0.48
48:B0:46:ASP:O	48:B0:53:LYS:HE3	2.13	0.48
34:DM:42:THR:HA	34:DM:93:VAL:HG12	1.95	0.48
46:BY:20:ASN:O	46:BY:24:GLU:HB2	2.12	0.48
45:DX:49:LEU:HD11	45:DX:68:LEU:HD21	1.95	0.48
31:DJ:34:ARG:O	31:DJ:39:LYS:HB2	2.11	0.48
16:AP:52:LEU:O	16:AP:54:LEU:N	2.46	0.48
1:AA:1086:U:O2'	1:AA:1087:G:H5'	2.13	0.48
29:BH:139:PHE:O	29:BH:140:ALA:HB2	2.14	0.48
1:CA:1101:A:N6	2:CB:102:THR:HG21	2.12	0.48
22:BA:1074:G:H2'	22:BA:1075:C:H5'	1.95	0.48
2:AB:23:TRP:CZ3	2:AB:25:PRO:HA	2.48	0.48
1:AA:682:G:H2'	1:AA:683:G:H8	1.78	0.48
22:BA:1508:A:OP1	22:BA:1508:A:H4'	2.13	0.48
1:AA:1063:C:H2'	1:AA:1064:G:C8	2.48	0.48
8:CH:40:LEU:O	8:CH:45:PHE:HB2	2.12	0.48
1:AA:537:G:H2'	1:AA:538:G:C8	2.48	0.48
22:BA:616:A:H4'	26:BE:101:TYR:CE2	2.48	0.48
18:CR:35:GLU:HB2	21:CU:19:PHE:HZ	1.76	0.48
22:DA:760:G:H2'	22:DA:761:A:O4'	2.12	0.48
22:BA:2462:C:H2'	22:BA:2463:C:C6	2.48	0.48
2:CB:87:CYS:O	2:CB:89:GLN:N	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:154:MET:O	2:AB:156:GLY:N	2.37	0.48
1:CA:1181:G:O2'	1:CA:1182:G:C8	2.65	0.48
25:BD:125:TRP:CE3	25:BD:160:LYS:HD3	2.48	0.48
26:DE:19:PHE:HB3	26:DE:113:VAL:HG21	1.94	0.48
3:AC:40:ARG:CZ	3:AC:57:ILE:HD12	2.43	0.48
4:AD:3:ARG:NE	4:AD:115:ARG:HD3	2.28	0.48
4:AD:99:ASP:OD1	4:AD:99:ASP:N	2.44	0.48
1:CA:1490:U:H2'	1:CA:1491:G:C8	2.49	0.48
22:BA:1410:G:N7	57:BA:3628:HOH:O	2.35	0.48
1:CA:605:U:H2'	1:CA:606:G:H8	1.78	0.48
8:CH:113:ASP:OD2	8:CH:117:ARG:NH2	2.46	0.48
22:DA:1874:C:H3'	22:DA:1875:G:C8	2.47	0.48
1:CA:243:A:H4'	1:CA:244:U:H5''	1.95	0.48
7:CG:121:ALA:HA	7:CG:124:LEU:HB2	1.95	0.48
24:DC:76:ALA:HB2	24:DC:96:TYR:CD2	2.49	0.48
57:BA:3785:HOH:O	31:BJ:39:LYS:HE3	2.12	0.48
22:DA:1246:A:O2'	26:DE:40:ARG:NH2	2.46	0.48
14:AN:13:ARG:O	14:AN:17:ALA:HB2	2.13	0.48
22:DA:184:C:H2'	22:DA:185:G:C8	2.47	0.48
6:AF:53:LYS:O	6:AF:54:LEU:HB3	2.12	0.48
30:BI:122:ILE:HG23	30:BI:125:MET:SD	2.53	0.48
10:AJ:80:THR:HB	10:AJ:83:THR:HB	1.95	0.48
18:CR:20:GLU:O	18:CR:22:ASP:N	2.46	0.48
22:BA:2267:A:H5''	22:BA:2268:A:C5'	2.43	0.48
13:CM:8:ASN:HD21	13:CM:10:PRO:HG3	1.79	0.48
15:CO:54:ARG:HA	15:CO:57:LEU:HD12	1.94	0.48
22:DA:1638:C:O2	22:DA:2698:U:O2'	2.22	0.48
1:CA:211:G:N3	1:CA:211:G:H2'	2.29	0.48
22:BA:1444:G:H2'	22:BA:1445:G:H8	1.75	0.48
1:CA:476:U:O2'	1:CA:477:C:H5'	2.13	0.48
10:AJ:52:LEU:HD22	10:AJ:62:ARG:HG2	1.94	0.48
22:DA:232:G:H22	22:DA:420:C:H5'	1.78	0.48
22:DA:279:A:C2	22:DA:362:A:H4'	2.48	0.48
22:BA:712:G:C2'	22:BA:713:G:H5'	2.44	0.48
5:AE:137:VAL:O	5:AE:138:ARG:HB2	2.13	0.48
49:D1:9:ILE:HB	49:D1:52:ALA:HA	1.95	0.48
22:DA:622:G:H2'	22:DA:623:C:H6	1.77	0.48
23:DB:70:C:H2'	23:DB:71:C:C6	2.48	0.48
45:DX:33:LEU:HD23	45:DX:50:ARG:CZ	2.43	0.48
16:CP:6:LEU:HD23	16:CP:17:TYR:CG	2.48	0.48
42:BU:97:LYS:O	42:BU:98:SER:OG	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CP:21:VAL:HG21	16:CP:60:TRP:CD1	2.49	0.48
1:CA:515:G:H2'	1:CA:516:U:O4'	2.13	0.48
22:DA:244:A:H2'	22:DA:245:G:O4'	2.13	0.48
22:BA:2474:U:H5''	22:BA:2475:C:OP2	2.14	0.48
1:AA:552:U:H2'	1:AA:553:A:H8	1.79	0.48
22:DA:108:G:O2'	22:DA:347:A:N3	2.41	0.48
5:CE:45:ARG:HA	5:CE:72:ILE:O	2.13	0.48
31:BJ:74:TYR:CD1	31:BJ:92:MET:HG3	2.49	0.48
52:D4:12:ARG:NH1	52:D4:12:ARG:HB2	2.28	0.48
12:AL:51:LYS:N	12:AL:51:LYS:HD3	2.28	0.48
22:BA:790:U:O2'	22:BA:791:C:O5'	2.28	0.48
30:DI:62:TYR:HB3	30:DI:64:ASP:H	1.78	0.48
1:AA:992:U:H4'	1:AA:993:G:O5'	2.12	0.48
40:DS:5:ALA:HB3	40:DS:54:ALA:HB2	1.96	0.48
33:BL:21:ARG:HA	33:BL:21:ARG:HD3	1.56	0.48
22:BA:1087:G:N2	22:BA:1102:C:O2	2.45	0.48
5:CE:101:GLU:HA	5:CE:122:ASN:HB2	1.94	0.48
22:DA:2271:G:H2'	22:DA:2272:U:C6	2.48	0.48
22:DA:2845:U:O3'	37:DP:53:ARG:NH1	2.45	0.48
9:CI:26:GLY:H	9:CI:59:GLU:HA	1.76	0.48
9:AI:40:GLY:O	9:AI:41:ARG:HB2	2.14	0.48
30:DI:71:THR:OG1	30:DI:72:LYS:N	2.46	0.48
22:DA:2207:C:H2'	22:DA:2208:C:H6	1.77	0.48
11:AK:126:LYS:HD3	11:AK:126:LYS:H	1.79	0.48
1:CA:1366:C:O2'	10:CJ:62:ARG:NH2	2.45	0.48
1:CA:582:C:N3	1:CA:760:G:C6	2.81	0.48
11:AK:31:ILE:HB	11:AK:46:THR:HG22	1.94	0.48
22:DA:1746:A:H2'	22:DA:1747:U:C6	2.49	0.48
22:BA:858:G:H8	22:BA:858:G:H5''	1.78	0.48
4:CD:129:VAL:HG23	4:CD:146:ARG:HD3	1.94	0.48
22:DA:1435:G:C2'	22:DA:1436:G:H5'	2.42	0.48
48:B0:48:TYR:CE2	48:B0:53:LYS:HB2	2.49	0.48
8:CH:30:SER:O	8:CH:34:VAL:HG23	2.12	0.48
19:AS:44:MET:HA	19:AS:47:LEU:HD12	1.95	0.48
2:CB:66:LYS:NZ	2:CB:154:MET:O	2.46	0.48
1:CA:1118:U:H2'	1:CA:1119:C:C6	2.47	0.48
22:BA:839:U:H2'	22:BA:840:C:C6	2.49	0.48
22:BA:1474:U:O4	22:BA:1475:G:N2	2.46	0.48
19:CS:30:PRO:HA	19:CS:48:THR:O	2.12	0.48
22:DA:1273:U:H4'	22:DA:1275:A:P	2.53	0.48
7:AG:12:ILE:HD11	7:AG:25:LYS:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.49	0.48
22:DA:659:G:H4'	26:DE:95:LYS:HD3	1.94	0.48
26:DE:148:ILE:HG21	26:DE:157:LEU:HD21	1.95	0.48
22:DA:748:G:C8	40:DS:89:ALA:HB1	2.48	0.48
22:BA:1058:U:H1'	22:BA:1081:U:O2	2.13	0.48
22:DA:70:G:H5''	22:DA:112:U:O2	2.13	0.48
2:AB:10:LEU:HG	2:AB:11:LYS:N	2.29	0.48
22:BA:257:C:H2'	22:BA:258:G:O4'	2.12	0.48
22:DA:783:A:C8	22:DA:784:G:H4'	2.48	0.48
5:CE:150:PRO:C	5:CE:152:MET:H	2.16	0.48
22:BA:1435:G:H2'	22:BA:1436:G:C8	2.49	0.48
46:DY:9:LYS:HG2	46:DY:10:SER:H	1.78	0.48
7:AG:71:PRO:O	7:AG:96:ARG:HG3	2.14	0.48
31:DJ:4:PHE:CG	38:DQ:100:VAL:HG11	2.48	0.48
1:CA:663:A:H2'	1:CA:664:G:O4'	2.13	0.48
14:CN:64:CYS:HB3	14:CN:69:ARG:H	1.79	0.48
1:AA:1096:C:HO2'	1:AA:1170:A:HO2'	1.57	0.48
3:CC:129:MET:CG	3:CC:131:ARG:HH11	2.27	0.48
1:AA:763:G:H2'	1:AA:764:C:C6	2.48	0.48
22:DA:1343:G:H1'	22:DA:1597:A:C4	2.48	0.48
25:DD:172:VAL:CG2	25:DD:194:PRO:HD3	2.43	0.48
36:DO:37:ALA:HB2	36:DO:106:LEU:HD11	1.95	0.48
22:DA:1874:C:H3'	22:DA:1875:G:H8	1.78	0.48
4:AD:152:GLN:O	4:AD:155:VAL:HG12	2.13	0.48
9:CI:25:ASN:O	9:CI:62:ASP:HA	2.14	0.48
1:AA:652:U:O4	1:AA:752:G:O2'	2.24	0.48
41:BT:30:ILE:HD11	41:BT:32:LEU:HD21	1.95	0.48
37:BP:27:GLU:HG2	37:BP:87:LYS:HE2	1.95	0.48
22:DA:2480:C:H2'	22:DA:2481:G:O4'	2.13	0.48
37:BP:25:THR:HB	37:BP:88:ARG:HB3	1.94	0.48
53:B5:59:VAL:HG21	53:B5:167:ASP:C	2.33	0.48
39:BR:14:VAL:HG13	39:BR:98:ILE:HG13	1.94	0.48
26:DE:179:SER:HA	26:DE:182:ALA:HB3	1.94	0.48
22:DA:301:G:H1'	22:DA:302:C:C6	2.48	0.48
23:DB:115:A:H2'	23:DB:116:G:C8	2.48	0.48
17:CQ:47:HIS:N	17:CQ:73:TRP:O	2.30	0.48
22:BA:1092:C:H2'	22:BA:1093:G:O4'	2.13	0.48
3:CC:36:ASP:O	3:CC:40:ARG:HG3	2.14	0.48
22:BA:674:G:H5''	26:BE:71:GLY:HA3	1.94	0.48
6:CF:86:ARG:HH11	6:CF:86:ARG:HG2	1.77	0.48
22:DA:2440:C:N3	22:DA:2441:U:H1'	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:898:G:N2	1:CA:901:A:OP2	2.41	0.48
1:AA:1181:G:C2	1:AA:1182:G:N2	2.82	0.48
22:DA:734:A:OP2	22:DA:761:A:N6	2.42	0.48
22:BA:1919:A:H2'	22:BA:1919:A:N3	2.27	0.48
22:BA:2127:G:N1	22:BA:2161:C:O2	2.47	0.48
13:AM:45:ILE:HG13	13:AM:48:LEU:HD13	1.94	0.48
29:DH:117:LEU:HD11	29:DH:130:VAL:HG22	1.95	0.48
1:CA:1277:C:H2'	1:CA:1278:G:H5''	1.96	0.48
27:DF:134:GLU:HB3	27:DF:137:ILE:HG23	1.94	0.48
2:CB:208:ARG:O	2:CB:211:THR:N	2.47	0.48
22:BA:2502:G:C5'	22:BA:2503:A:H5''	2.44	0.48
10:AJ:51:VAL:HB	14:AN:81:ARG:HB2	1.96	0.48
1:CA:1175:G:H2'	1:CA:1176:A:C8	2.47	0.48
15:CO:33:THR:HA	15:CO:63:ARG:NH1	2.29	0.48
22:BA:441:U:O2'	26:BE:41:GLN:NE2	2.46	0.48
22:BA:1490:A:O2'	24:BC:98:ASP:OD2	2.31	0.48
1:AA:771:G:H2'	1:AA:772:U:C6	2.49	0.48
22:BA:833:A:H2'	22:BA:834:G:C8	2.49	0.48
1:CA:957:U:O2	1:CA:959:A:C8	2.67	0.48
36:DO:2:ASP:OD1	36:DO:5:SER:OG	2.28	0.48
23:BB:28:C:H2'	23:BB:29:A:O4'	2.14	0.48
22:DA:2834:G:H2'	22:DA:2879:A:H61	1.77	0.48
45:DX:38:PHE:HZ	45:DX:56:MET:HG2	1.77	0.48
22:DA:1933:G:H2'	22:DA:1934:C:O4'	2.14	0.48
20:AT:26:SER:O	20:AT:30:THR:OG1	2.31	0.48
22:BA:1275:A:N1	22:BA:1295:C:O2'	2.32	0.48
22:DA:897:C:H2'	22:DA:898:C:C6	2.48	0.48
22:BA:477:A:H2'	22:BA:478:A:C8	2.48	0.48
39:BR:68:ARG:HD3	39:BR:92:TRP:CZ2	2.48	0.48
22:DA:635:C:H2'	22:DA:636:G:H8	1.78	0.48
9:CI:115:LYS:HD2	9:CI:118:LEU:HD22	1.96	0.48
22:DA:1379:U:OP1	22:DA:1379:U:C6	2.66	0.48
1:AA:355:C:H2'	1:AA:356:A:O4'	2.13	0.48
25:DD:35:THR:OG1	25:DD:49:GLN:OE1	2.24	0.48
29:BH:103:VAL:HG21	29:BH:132:PHE:CZ	2.49	0.48
22:DA:1062:G:C5	22:DA:1088:A:H2'	2.49	0.48
1:AA:375:U:OP1	16:AP:70:ARG:NH1	2.47	0.48
2:AB:132:LYS:O	2:AB:134:ALA:N	2.47	0.48
22:BA:2325:G:C6	22:BA:2326:C:N4	2.82	0.48
28:BG:149:ARG:HH11	28:BG:149:ARG:HG3	1.79	0.48
22:DA:2039:U:H2'	22:DA:2040:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CE:65:GLU:HG2	5:CE:69:ARG:NH2	2.29	0.48
22:DA:2391:G:H1'	22:DA:2424:C:H41	1.79	0.48
1:AA:1144:G:N1	1:AA:1145:A:H2	2.11	0.48
22:DA:1953:A:HO2'	22:DA:2559:C:HO2'	1.60	0.48
1:CA:1467:C:H2'	1:CA:1468:A:H8	1.78	0.48
2:CB:66:LYS:HB2	2:CB:158:PRO:HA	1.96	0.48
10:AJ:26:VAL:HG12	10:AJ:30:LYS:HD3	1.95	0.48
2:AB:172:ALA:O	2:AB:175:GLU:HB2	2.13	0.48
26:DE:189:THR:O	26:DE:193:VAL:HG23	2.12	0.48
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.44	0.48
22:BA:2207:C:H2'	22:BA:2208:C:C6	2.49	0.48
2:CB:65:GLY:HA3	2:CB:159:ASP:HB2	1.95	0.48
25:DD:52:THR:O	25:DD:77:ARG:HG2	2.14	0.48
12:AL:35:THR:O	12:AL:36:ARG:HG3	2.13	0.48
18:CR:33:ILE:HA	18:CR:40:VAL:HG23	1.95	0.48
1:CA:130:A:OP1	17:CQ:65:ARG:HD2	2.14	0.48
3:AC:72:ARG:O	3:AC:75:ILE:HG22	2.14	0.48
13:AM:56:LEU:O	13:AM:60:VAL:HG12	2.13	0.48
12:AL:39:THR:OG1	12:AL:39:THR:O	2.32	0.48
4:AD:138:SER:N	4:AD:141:ASP:OD2	2.43	0.48
11:AK:70:CYS:O	11:AK:74:VAL:HG22	2.13	0.48
2:CB:222:ARG:HE	2:CB:223:GLU:N	2.12	0.48
29:DH:32:PRO:HB3	45:DX:39:TRP:CB	2.42	0.48
1:AA:413:G:N1	4:AD:32:CYS:O	2.43	0.48
22:BA:43:G:H2'	22:BA:44:A:O4'	2.12	0.48
9:AI:50:GLN:C	9:AI:52:LEU:H	2.17	0.48
1:CA:72:A:N6	1:CA:99:C:H1'	2.29	0.48
14:AN:79:LEU:HB2	14:AN:84:VAL:HG23	1.96	0.48
8:AH:66:PHE:CD2	8:AH:67:GLN:HG2	2.49	0.48
1:CA:66:A:C6	1:CA:67:C:C5	3.02	0.48
1:AA:1145:A:O2'	1:AA:1146:A:O5'	2.31	0.48
30:BI:43:ASN:OD1	30:BI:46:THR:HB	2.13	0.48
22:DA:1747:U:H2'	22:DA:1748:C:H6	1.78	0.48
29:DH:127:GLU:HG3	29:DH:144:VAL:O	2.14	0.48
7:CG:57:SER:CB	7:CG:60:GLU:HG3	2.43	0.48
36:BO:53:THR:HB	36:BO:65:THR:HG22	1.96	0.48
22:BA:1447:C:H2'	22:BA:1448:G:C8	2.49	0.48
22:DA:1415:U:H2'	22:DA:1416:G:H4'	1.95	0.48
22:DA:2109:U:H1'	22:DA:2181:U:O2	2.14	0.48
1:AA:575:G:O2'	1:AA:821:G:H5'	2.14	0.48
24:DC:80:ARG:NE	24:DC:82:GLU:OE2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:BS:109:ASP:OD1	40:BS:110:ARG:N	2.44	0.48
26:BE:148:ILE:HB	26:BE:169:VAL:HG22	1.95	0.48
29:BH:135:HIS:CD2	29:BH:137:GLU:HG3	2.48	0.48
1:CA:834:U:H2'	1:CA:835:U:C6	2.49	0.48
22:DA:1565:C:H5'	24:DC:18:LYS:NZ	2.29	0.48
12:CL:37:VAL:HG21	12:CL:75:GLN:HA	1.95	0.48
35:DN:27:SER:HB3	35:DN:34:ILE:HG21	1.95	0.48
42:DU:53:ASN:C	42:DU:55:PRO:HD3	2.33	0.48
22:DA:690:G:H1'	22:DA:779:U:O3'	2.14	0.48
4:CD:33:LYS:O	4:CD:33:LYS:HG3	2.14	0.48
25:BD:132:ALA:HA	25:BD:140:HIS:ND1	2.29	0.48
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.13	0.48
16:AP:77:GLU:C	16:AP:79:ASN:N	2.66	0.48
48:B0:13:ARG:O	48:B0:17:ARG:HG3	2.14	0.48
22:DA:1789:A:OP2	24:DC:221:ARG:NH1	2.46	0.48
15:CO:40:GLN:HE22	22:DA:716:A:H1'	1.79	0.48
22:BA:2391:G:H3'	51:B3:32:ILE:HD12	1.96	0.48
22:DA:1410:G:H2'	22:DA:1411:U:C6	2.49	0.48
27:DF:106:ILE:HD11	27:DF:139:PRO:HG2	1.96	0.48
1:CA:309:A:H1'	1:CA:608:A:C2	2.48	0.48
22:BA:614:A:H8	22:BA:614:A:H5'	1.78	0.48
5:CE:111:MET:HE2	5:CE:125:ALA:HB1	1.95	0.48
22:DA:704:G:H1'	22:DA:726:G:N2	2.29	0.48
22:BA:1430:G:H2'	22:BA:1431:A:H8	1.79	0.48
28:DG:26:ILE:HD11	28:DG:72:LEU:HD23	1.95	0.48
22:BA:2261:C:C6	44:BW:16:SER:HB3	2.49	0.48
25:DD:125:TRP:HB3	25:DD:160:LYS:HD3	1.95	0.48
9:CI:99:ARG:HA	9:CI:104:VAL:CG2	2.44	0.48
37:BP:27:GLU:HG3	37:BP:27:GLU:O	2.14	0.48
10:AJ:23:ALA:O	10:AJ:27:GLU:HB2	2.14	0.48
22:DA:1693:U:O4	22:DA:1976:U:O2'	2.26	0.48
22:BA:753:A:H2'	22:BA:754:U:H6	1.79	0.48
1:CA:285:C:H2'	1:CA:286:C:C6	2.49	0.48
22:DA:392:U:H2'	22:DA:393:C:H6	1.79	0.48
4:AD:46:PRO:O	4:AD:48:LEU:HD22	2.13	0.48
25:DD:157:LYS:HD2	31:DJ:79:GLY:O	2.13	0.48
1:CA:632:U:H2'	1:CA:632:U:O2	2.14	0.48
13:AM:79:ARG:O	13:AM:83:LEU:HG	2.13	0.48
49:D1:10:LYS:O	49:D1:51:GLU:HG2	2.14	0.48
22:DA:2244:U:H2'	22:DA:2245:U:O4'	2.14	0.48
22:DA:1800:C:O2'	22:DA:1818:U:N3	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:982:C:H5''	22:BA:983:A:OP1	2.14	0.48
18:CR:25:ASP:C	18:CR:27:ALA:H	2.17	0.48
28:DG:67:THR:O	28:DG:71:LEU:N	2.47	0.48
22:DA:609:A:H2'	22:DA:610:C:O4'	2.14	0.48
22:BA:590:A:H2'	22:BA:591:U:C6	2.49	0.48
9:CI:20:PHE:HB2	9:CI:64:TYR:HB3	1.96	0.48
10:AJ:52:LEU:HD11	10:AJ:59:LYS:HA	1.96	0.48
22:DA:2023:C:H2'	22:DA:2024:G:H8	1.79	0.48
15:CO:33:THR:HA	15:CO:63:ARG:HH11	1.79	0.48
36:DO:34:HIS:N	36:DO:65:THR:O	2.45	0.48
22:BA:186:G:O2'	22:BA:187:G:H5'	2.14	0.48
1:AA:39:G:H2'	1:AA:40:C:H6	1.78	0.48
22:DA:996:A:O3'	38:DQ:91:ASP:HB2	2.14	0.48
4:CD:75:TYR:OH	4:CD:97:ARG:NH1	2.46	0.48
1:CA:31:G:N7	1:CA:306:A:H1'	2.29	0.48
3:AC:46:GLU:C	3:AC:48:ALA:H	2.17	0.48
22:BA:1010:A:OP2	57:BA:3786:HOH:O	2.20	0.48
22:BA:944:C:H2'	57:BA:3354:HOH:O	2.13	0.48
12:CL:3:THR:HB	12:CL:6:GLN:HG3	1.96	0.48
22:BA:1143:A:OP1	31:BJ:27:ARG:NH2	2.42	0.48
22:BA:2341:G:H2'	22:BA:2342:C:C6	2.49	0.48
5:AE:131:THR:OG1	5:AE:131:THR:O	2.29	0.48
7:CG:138:ARG:HE	7:CG:138:ARG:HB3	1.43	0.48
17:CQ:61:ILE:HA	17:CQ:75:LEU:HA	1.95	0.47
22:BA:1074:G:C2'	22:BA:1075:C:H5'	2.44	0.47
37:DP:39:ARG:CG	37:DP:40:LEU:H	2.22	0.47
1:AA:374:A:C6	1:AA:375:U:C4	3.02	0.47
1:CA:619:U:H3	4:CD:131:ASN:CB	2.26	0.47
42:DU:72:ILE:HG13	42:DU:72:ILE:H	1.37	0.47
22:BA:2800:A:C2	22:BA:2895:G:H1'	2.49	0.47
24:DC:147:LYS:HG3	24:DC:150:LYS:HD2	1.96	0.47
1:CA:1534:A:H4'	1:CA:1535:C:H2'	1.96	0.47
4:CD:31:LYS:HD3	4:CD:31:LYS:N	2.28	0.47
43:DV:14:LYS:HD3	43:DV:18:ARG:NH2	2.29	0.47
32:BK:113:MET:O	32:BK:116:ILE:HG13	2.13	0.47
22:DA:1274:A:N3	22:DA:1297:C:H1'	2.29	0.47
1:AA:204:G:H2'	1:AA:205:A:O4'	2.13	0.47
44:BW:41:ARG:HH11	44:BW:41:ARG:HG3	1.78	0.47
25:DD:55:LYS:HG3	25:DD:77:ARG:HA	1.96	0.47
39:BR:40:MET:C	39:BR:41:ILE:HG12	2.34	0.47
1:AA:1386:G:H2'	1:AA:1387:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:477:C:H2'	1:AA:478:A:C8	2.49	0.47
15:CO:67:LEU:HD23	15:CO:78:TYR:CE1	2.49	0.47
7:AG:133:THR:O	7:AG:136:LYS:HB3	2.14	0.47
1:AA:57:G:H2'	1:AA:58:C:C6	2.49	0.47
22:DA:2103:C:H2'	22:DA:2104:C:C6	2.49	0.47
26:BE:117:ARG:HH12	33:BL:2:ARG:HD3	1.79	0.47
17:AQ:17:MET:HB2	17:AQ:20:SER:HB3	1.96	0.47
22:BA:2798:U:H6	22:BA:2798:U:H5'	1.79	0.47
1:AA:250:A:H4'	1:AA:251:G:O5'	2.13	0.47
22:DA:1853:A:N3	22:DA:2233:U:O2'	2.38	0.47
1:AA:17:U:H2'	1:AA:18:C:C6	2.49	0.47
15:AO:61:SER:O	15:AO:65:LYS:HG3	2.14	0.47
1:AA:1516:G:N2	1:AA:1519:A:OP2	2.45	0.47
22:DA:1243:C:H1'	33:DL:4:ASN:O	2.14	0.47
22:BA:1255:U:C5	26:BE:68:ALA:HA	2.49	0.47
22:BA:244:A:C2	22:BA:255:A:C4	3.02	0.47
8:AH:53:GLY:HA3	8:AH:57:PRO:HA	1.94	0.47
29:BH:116:ARG:O	29:BH:118:PRO:HD3	2.14	0.47
5:CE:81:LEU:O	5:CE:98:PRO:HB3	2.14	0.47
26:DE:48:THR:HG22	26:DE:86:ALA:HB3	1.97	0.47
4:AD:188:ARG:NH2	4:AD:197:GLU:OE1	2.47	0.47
22:DA:1199:U:H1'	38:DQ:4:VAL:HG22	1.97	0.47
22:DA:1708:C:H2'	22:DA:1709:U:C6	2.49	0.47
3:CC:141:ALA:O	3:CC:146:ALA:HB3	2.14	0.47
43:DV:30:ILE:HD13	43:DV:72:VAL:HG11	1.95	0.47
22:DA:2689:U:H4'	22:DA:2690:U:OP2	2.13	0.47
22:BA:27:G:O2'	22:BA:512:G:N2	2.47	0.47
22:DA:1794:A:H2'	22:DA:1795:C:C6	2.49	0.47
30:BI:58:VAL:HG12	30:BI:59:ILE:H	1.80	0.47
22:BA:242:G:C8	51:B3:5:LYS:HG2	2.49	0.47
1:AA:623:C:H2'	1:AA:624:C:H6	1.79	0.47
22:DA:2550:G:OP1	57:DA:3719:HOH:O	2.20	0.47
22:DA:301:G:C6	22:DA:317:G:C6	3.03	0.47
22:BA:536:G:C6	22:BA:537:G:C4	3.02	0.47
22:BA:1079:C:H2'	22:BA:1080:A:O4'	2.14	0.47
2:AB:139:ARG:HG3	2:AB:140:GLU:N	2.29	0.47
32:BK:21:CYS:HA	32:BK:41:ILE:HG22	1.96	0.47
22:BA:1230:A:H2'	22:BA:1231:U:O4'	2.13	0.47
22:DA:2:G:C6	22:DA:3:U:C4	3.03	0.47
29:BH:89:LYS:HD3	1:CA:359:G:OP1	2.15	0.47
22:DA:1936:A:H2	22:DA:1943:U:N3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DH:83:LYS:CG	29:DH:149:GLU:CG	2.86	0.47
2:AB:20:THR:HA	2:AB:38:VAL:HA	1.96	0.47
12:CL:59:ASN:N	12:CL:59:ASN:HD22	1.99	0.47
22:DA:2268:A:OP1	57:DA:3505:HOH:O	2.20	0.47
16:CP:44:SER:O	16:CP:46:LYS:HG3	2.15	0.47
7:CG:75:VAL:HG11	7:CG:144:MET:HG3	1.96	0.47
22:DA:1179:G:C5	22:DA:1180:U:H1'	2.49	0.47
22:BA:2485:G:H5''	34:BM:45:GLN:HE21	1.79	0.47
29:BH:111:ALA:O	29:BH:114:GLU:HB2	2.14	0.47
22:DA:948:C:H2'	22:DA:949:G:C8	2.48	0.47
9:CI:18:ARG:O	9:CI:65:ILE:HA	2.14	0.47
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.49	0.47
1:AA:194:C:O2'	1:AA:195:A:H5'	2.15	0.47
1:AA:678:U:O2	1:AA:777:A:H4'	2.13	0.47
22:DA:1373:A:H2'	22:DA:1374:G:O4'	2.14	0.47
22:DA:1906:G:C8	22:DA:1929:G:H2'	2.49	0.47
22:DA:634:C:OP2	33:DL:70:LYS:HD3	2.14	0.47
33:DL:110:VAL:HG12	33:DL:131:ALA:HB1	1.95	0.47
22:BA:773:U:H4'	24:BC:47:GLY:HA3	1.96	0.47
1:AA:235:C:H2'	1:AA:236:A:C8	2.49	0.47
1:AA:406:G:H8	1:AA:406:G:OP2	1.97	0.47
25:DD:99:GLU:HG2	25:DD:182:ALA:HB2	1.96	0.47
40:DS:28:LYS:O	40:DS:30:SER:N	2.48	0.47
4:AD:65:TYR:CG	4:AD:94:LEU:HD22	2.49	0.47
21:AU:44:GLU:OE2	21:AU:45:ARG:NH1	2.47	0.47
36:DO:70:ALA:O	36:DO:74:VAL:HB	2.15	0.47
4:AD:125:VAL:HG11	4:AD:135:TYR:CE2	2.50	0.47
22:BA:1868:C:H2'	22:BA:1869:G:O4'	2.15	0.47
19:AS:51:VAL:O	19:AS:58:VAL:HG13	2.14	0.47
1:CA:618:C:H5''	1:CA:619:U:H5''	1.96	0.47
9:CI:30:ILE:HA	9:CI:65:ILE:O	2.14	0.47
22:BA:2520:C:O2'	22:BA:2521:C:H5'	2.15	0.47
1:AA:8:A:H1'	5:AE:108:GLY:HA2	1.96	0.47
22:DA:686:U:H6	22:DA:788:A:N1	2.13	0.47
22:BA:201:C:OP1	45:BX:18:ARG:NH1	2.47	0.47
1:AA:1224:U:O2'	1:AA:1322:C:OP1	2.26	0.47
22:BA:150:U:H2'	22:BA:151:C:C6	2.50	0.47
22:DA:300:A:O5'	42:DU:82:ARG:NH1	2.47	0.47
1:AA:773:G:H2'	1:AA:774:G:O4'	2.14	0.47
22:BA:2154:A:H2'	22:BA:2155:U:C6	2.49	0.47
1:AA:1151:A:O2'	1:AA:1152:A:O5'	2.19	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:607:U:H5	22:DA:619:G:C4	2.32	0.47
1:AA:1071:C:H2'	1:AA:1072:G:C8	2.49	0.47
22:DA:563:A:OP2	39:DR:79:ARG:NH2	2.39	0.47
22:BA:2233:U:H2'	22:BA:2234:G:C8	2.50	0.47
2:CB:126:PHE:N	2:CB:126:PHE:CD2	2.82	0.47
1:CA:1230:C:O5'	1:CA:1230:C:H6	1.98	0.47
22:DA:1760:C:H2'	22:DA:1761:C:O4'	2.15	0.47
22:DA:1495:A:H2'	22:DA:1496:A:C8	2.50	0.47
29:BH:117:LEU:HD23	29:BH:121:VAL:HA	1.95	0.47
22:DA:1370:C:O4'	22:DA:1810:A:H2	1.97	0.47
13:AM:107:ARG:HH11	13:AM:107:ARG:HA	1.78	0.47
4:CD:95:GLU:OE2	4:CD:100:ASN:ND2	2.33	0.47
46:BY:9:LYS:H	46:BY:12:GLU:HG3	1.80	0.47
23:DB:49:C:OP1	36:DO:101:GLY:HA3	2.14	0.47
8:AH:29:SER:HB2	8:AH:59:LEU:HB2	1.96	0.47
22:BA:2171:A:O2'	22:BA:2172:U:H5'	2.14	0.47
5:AE:15:LEU:HA	5:AE:37:THR:HA	1.96	0.47
1:CA:107:G:O2'	1:CA:378:G:H4'	2.14	0.47
1:CA:608:A:H2'	1:CA:609:A:O4'	2.14	0.47
22:DA:2024:G:OP2	22:DA:2034:U:H4'	2.14	0.47
22:DA:1567:G:H4'	24:DC:58:HIS:CE1	2.50	0.47
29:DH:62:LEU:O	29:DH:62:LEU:HD22	2.14	0.47
3:AC:7:PRO:HG2	3:AC:184:TYR:CD1	2.49	0.47
1:AA:383:A:C5	1:AA:384:G:H1'	2.49	0.47
42:DU:9:ASP:OD1	42:DU:94:ARG:NH1	2.34	0.47
1:AA:591:U:OP1	8:AH:31:LYS:HD2	2.13	0.47
5:AE:34:THR:HB	5:AE:50:TYR:CE2	2.50	0.47
29:DH:5:LEU:HD13	29:DH:13:GLY:HA3	1.96	0.47
22:BA:1820:U:OP1	24:BC:177:ARG:HG2	2.14	0.47
22:DA:380:G:O3'	45:DX:16:ASN:HB2	2.15	0.47
22:DA:974:G:H1'	22:DA:975:A:C8	2.50	0.47
45:DX:40:VAL:CG2	45:DX:43:GLU:HB2	2.45	0.47
27:DF:100:PHE:O	27:DF:104:ILE:HG12	2.15	0.47
22:DA:586:A:H2	22:DA:809:G:N3	2.12	0.47
1:CA:372:C:H4'	1:CA:373:A:OP1	2.15	0.47
22:DA:2660:A:H2'	22:DA:2661:G:C8	2.49	0.47
1:AA:692:U:O4	11:AK:54:GLY:HA2	2.15	0.47
22:DA:731:C:OP2	57:DA:3689:HOH:O	2.20	0.47
22:BA:2334:U:C4	36:BO:16:ARG:HD3	2.48	0.47
19:CS:63:THR:HB	19:CS:66:MET:HG3	1.95	0.47
22:BA:81:G:H2'	22:BA:82:U:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1299:G:O5'	22:BA:1299:G:H8	1.97	0.47
24:DC:53:HIS:O	24:DC:217:ARG:N	2.45	0.47
7:CG:25:LYS:O	7:CG:29:ILE:HG12	2.15	0.47
6:AF:6:ILE:HG23	6:AF:89:VAL:HG12	1.96	0.47
22:BA:2189:U:H2'	22:BA:2190:G:O4'	2.15	0.47
7:AG:60:GLU:HA	7:AG:63:GLU:HB2	1.96	0.47
11:CK:127:ARG:O	21:CU:34:ARG:NH1	2.44	0.47
22:DA:2610:C:O4'	54:D6:7:004:HD2	2.13	0.47
46:BY:9:LYS:HG2	46:BY:10:SER:N	2.28	0.47
29:BH:14:SER:O	29:BH:15:LEU:CB	2.61	0.47
22:DA:2129:C:O2	22:DA:2159:G:N2	2.45	0.47
22:DA:2159:G:H2'	22:DA:2160:C:C6	2.50	0.47
25:BD:12:THR:HB	25:BD:13:ARG:H	1.41	0.47
22:DA:2707:U:O2	35:DN:71:ARG:NH1	2.47	0.47
1:AA:1280:A:H5''	10:AJ:42:LEU:HD21	1.96	0.47
34:BM:31:PHE:CZ	34:BM:110:GLU:HA	2.49	0.47
1:CA:279:A:H5''	1:CA:281:G:H5'	1.97	0.47
25:BD:84:LEU:HD22	25:BD:88:GLU:HB3	1.97	0.47
1:AA:115:G:H4'	1:AA:116:A:O5'	2.15	0.47
1:AA:116:A:H2'	1:AA:117:G:C8	2.50	0.47
8:CH:27:MET:HG2	8:CH:59:LEU:HB3	1.96	0.47
1:CA:1243:C:H2'	1:CA:1244:G:C8	2.50	0.47
22:BA:171:U:H2'	22:BA:172:A:H8	1.80	0.47
45:DX:68:LEU:HD23	45:DX:68:LEU:HA	1.81	0.47
6:AF:71:ILE:HD11	6:AF:89:VAL:HG21	1.96	0.47
22:BA:2569:G:C2	22:BA:2570:G:C8	3.03	0.47
22:DA:2804:U:H2'	22:DA:2805:C:C6	2.50	0.47
27:DF:34:ILE:HA	27:DF:155:THR:O	2.14	0.47
41:BT:18:GLU:O	41:BT:22:THR:HG23	2.14	0.47
1:AA:292:G:N7	1:AA:293:G:H1'	2.30	0.47
22:DA:699:A:H2'	22:DA:700:G:O4'	2.15	0.47
1:AA:489:C:H2'	1:AA:490:C:H6	1.80	0.47
22:DA:1352:U:H5	57:DA:3392:HOH:O	1.97	0.47
1:AA:781:A:H4'	1:AA:1522:U:O2'	2.15	0.47
7:AG:29:ILE:HG22	7:AG:105:VAL:HG21	1.96	0.47
1:AA:327:A:O3'	1:AA:328:C:H4'	2.14	0.47
13:AM:66:GLU:O	13:AM:69:LEU:N	2.48	0.47
22:DA:349:U:H2'	22:DA:350:G:H8	1.79	0.47
23:DB:11:C:O5'	23:DB:11:C:H6	1.98	0.47
13:AM:86:TYR:HA	13:AM:89:LEU:HD12	1.97	0.47
1:CA:970:C:H5''	1:CA:971:G:OP1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2199:A:H4'	29:BH:28:ASN:CG	2.34	0.47
4:AD:30:THR:HG22	4:AD:31:LYS:H	1.80	0.47
10:AJ:11:LYS:HA	10:AJ:70:HIS:O	2.15	0.47
22:BA:1167:C:H2'	22:BA:1168:G:H5''	1.97	0.47
2:AB:16:PHE:HB2	2:AB:40:ILE:HG23	1.97	0.47
22:DA:1076:C:H2'	22:DA:1077:A:O4'	2.14	0.47
1:CA:999:C:H2'	1:CA:1000:A:C8	2.50	0.47
22:BA:783:A:H8	22:BA:784:G:H4'	1.78	0.47
22:BA:783:A:C8	22:BA:784:G:H4'	2.50	0.47
6:CF:36:ILE:HB	6:CF:64:VAL:HG13	1.97	0.47
7:AG:146:GLU:HA	7:AG:149:LYS:CB	2.41	0.47
46:BY:9:LYS:HB3	46:BY:12:GLU:CG	2.41	0.47
11:CK:91:PRO:HB2	11:CK:92:GLY:H	1.48	0.47
11:CK:88:GLY:H	11:CK:114:THR:HG22	1.79	0.47
24:DC:57:GLY:HA3	24:DC:213:TRP:HA	1.96	0.47
48:B0:10:ARG:HB2	48:B0:13:ARG:NH2	2.29	0.47
28:BG:90:VAL:HG21	28:BG:163:ARG:NE	2.29	0.47
25:BD:13:ARG:HD2	25:BD:15:PHE:CE1	2.49	0.47
27:BF:73:SER:HB2	27:BF:81:GLN:N	2.29	0.47
22:BA:1570:A:C6	22:BA:1571:A:C6	3.03	0.47
22:BA:770:G:H1'	22:BA:1379:U:C4	2.49	0.47
10:CJ:28:THR:HG23	10:CJ:31:ARG:NH2	2.29	0.47
22:DA:2813:A:H2'	22:DA:2814:A:H8	1.78	0.47
40:DS:51:LEU:O	40:DS:55:ILE:HG13	2.14	0.47
22:BA:2591:C:H2'	22:BA:2592:G:H8	1.78	0.47
2:AB:162:PHE:HA	2:AB:184:PHE:O	2.14	0.47
1:CA:466:A:H2'	1:CA:468:A:C2	2.47	0.47
2:CB:165:ASP:O	2:CB:168:HIS:HB3	2.15	0.47
23:DB:66:A:H61	23:DB:107:G:H2'	1.79	0.47
28:BG:74:SER:HA	28:BG:77:ILE:CG1	2.44	0.47
22:BA:1414:C:C4	22:BA:1415:U:H5	2.33	0.47
22:BA:1683:U:H2'	22:BA:1684:G:C8	2.50	0.47
22:DA:1906:G:OP1	22:DA:1930:G:C8	2.68	0.47
22:BA:1789:A:O3'	24:BC:218:PRO:HB3	2.14	0.47
7:CG:60:GLU:HA	7:CG:63:GLU:HB3	1.97	0.47
1:AA:1192:C:OP2	3:AC:4:LYS:HE2	2.15	0.47
1:AA:251:G:H4'	1:AA:252:U:O5'	2.14	0.47
22:DA:1:G:H2'	22:DA:2:G:C8	2.50	0.47
22:DA:566:U:O4	39:DR:80:ARG:HD3	2.15	0.47
22:BA:2192:U:C2	22:BA:2193:G:C8	3.03	0.47
16:AP:39:PHE:CD2	16:AP:74:LEU:HD11	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:97:VAL:HB	3:CC:98:PRO:HD2	1.97	0.47
26:DE:5:LEU:HD23	26:DE:122:GLU:HG2	1.97	0.47
22:DA:2385:C:H2'	22:DA:2386:A:C8	2.49	0.47
42:BU:40:ASN:O	42:BU:63:ALA:N	2.47	0.47
4:AD:76:TYR:CG	4:AD:204:TYR:HD1	2.33	0.47
1:AA:1493:A:OP2	1:AA:1493:A:H8	1.96	0.47
37:DP:4:ILE:HD12	37:DP:4:ILE:H	1.80	0.47
15:AO:39:LEU:HD12	15:AO:39:LEU:HA	1.73	0.47
22:DA:2405:G:H1'	22:DA:2412:A:N6	2.29	0.47
22:BA:980:A:C6	22:BA:981:A:N1	2.83	0.47
45:BX:6:GLN:O	45:BX:74:ARG:NH1	2.48	0.47
17:AQ:60:GLU:HB3	17:AQ:76:VAL:HG23	1.96	0.47
39:BR:4:VAL:HA	39:BR:12:HIS:O	2.13	0.47
4:CD:24:GLY:O	4:CD:161:LEU:HD11	2.14	0.47
36:DO:50:ALA:O	36:DO:81:ARG:NH2	2.47	0.47
38:BQ:11:ARG:HA	38:BQ:11:ARG:HD2	1.53	0.47
30:BI:28:LEU:HD12	30:BI:28:LEU:O	2.14	0.47
12:AL:85:GLY:O	12:AL:96:HIS:ND1	2.47	0.47
25:BD:101:PHE:HZ	25:BD:203:VAL:O	1.98	0.47
14:CN:4:GLN:OE1	14:CN:7:LYS:NZ	2.42	0.47
22:BA:1073:A:N7	22:BA:1074:G:C8	2.83	0.47
22:BA:1103:A:OP2	22:BA:1104:C:N4	2.39	0.47
20:AT:71:LYS:HD2	20:AT:74:ARG:HH21	1.80	0.47
17:CQ:13:VAL:HG12	17:CQ:22:VAL:O	2.15	0.47
22:BA:686:U:O4	50:B2:12:ARG:HB2	2.15	0.47
8:CH:55:THR:C	8:CH:57:PRO:HD3	2.35	0.47
9:AI:57:MET:N	9:AI:57:MET:SD	2.86	0.47
40:BS:37:THR:HG22	40:BS:38:TYR:CD1	2.50	0.47
46:BY:30:MET:O	46:BY:34:SER:OG	2.30	0.47
2:AB:61:ALA:HA	2:AB:65:GLY:CA	2.45	0.47
1:AA:35:G:H2'	1:AA:36:C:C6	2.50	0.47
22:DA:2060:A:N6	26:DE:69:ARG:HH12	2.13	0.47
32:BK:116:ILE:HD12	32:BK:117:SER:N	2.30	0.47
22:DA:1231:U:O5'	22:DA:1231:U:H6	1.98	0.47
1:CA:974:A:OP1	14:CN:69:ARG:NH1	2.46	0.47
2:AB:71:GLY:O	2:AB:93:ASN:HA	2.14	0.47
5:AE:18:VAL:HA	5:AE:34:THR:O	2.14	0.47
33:DL:119:PRO:HB3	33:DL:139:GLY:HA3	1.97	0.47
6:CF:50:PRO:HD3	18:CR:74:HIS:HB3	1.96	0.47
22:BA:1268:A:C2	22:BA:2013:A:C4	3.03	0.47
2:AB:188:ASP:HB2	2:AB:204:ASP:OD1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1260:G:OP1	1:CA:1284:C:O2'	2.29	0.47
22:BA:1549:A:O3'	22:BA:1740:G:N2	2.47	0.47
6:AF:12:PRO:O	6:AF:15:SER:HB2	2.15	0.47
1:CA:282:A:H3'	1:CA:283:U:C6	2.50	0.47
1:CA:1034:G:H2'	1:CA:1035:A:C8	2.50	0.47
1:CA:649:A:H2'	1:CA:650:G:O4'	2.14	0.47
22:DA:1645:G:H5''	22:DA:1646:C:O4'	2.14	0.47
22:DA:737:C:H2'	22:DA:738:G:O4'	2.15	0.47
22:BA:460:A:P	50:B2:41:ARG:HH12	2.38	0.47
22:DA:1479:G:H2'	22:DA:1480:C:O4'	2.15	0.47
22:BA:2112:G:H2'	22:BA:2112:G:N3	2.30	0.47
14:CN:33:ASP:O	14:CN:35:ASN:N	2.48	0.47
15:AO:74:ASP:OD1	15:AO:77:ARG:HD3	2.14	0.47
5:CE:122:ASN:CG	5:CE:123:VAL:H	2.18	0.47
22:BA:1171:G:C2	22:BA:1172:C:C2	3.03	0.47
17:AQ:12:VAL:HG23	17:AQ:57:ASP:O	2.14	0.47
38:BQ:91:ASP:O	38:BQ:95:LEU:HD12	2.15	0.47
8:AH:29:SER:HB2	8:AH:59:LEU:H	1.79	0.47
4:AD:123:ILE:N	4:AD:123:ILE:HD13	2.30	0.47
22:BA:2812:G:H2'	22:BA:2813:A:O4'	2.15	0.47
22:DA:826:U:H5''	22:DA:2429:G:OP2	2.15	0.47
22:DA:1367:A:C5	22:DA:1368:G:H1'	2.49	0.47
22:DA:2819:G:O5'	22:DA:2819:G:H8	1.98	0.47
22:DA:830:G:P	22:DA:830:G:H8	2.38	0.47
44:DW:40:GLN:OE1	44:DW:44:LYS:N	2.48	0.47
1:AA:736:C:H5'	6:AF:88:MET:HE2	1.97	0.47
22:BA:1185:G:H5''	22:BA:1186:G:OP1	2.14	0.47
24:DC:17:VAL:N	24:DC:204:VAL:HG22	2.29	0.47
1:AA:982:U:H4'	1:AA:983:A:H5'	1.97	0.47
22:DA:1605:C:O2	22:DA:1610:A:O2'	2.29	0.47
31:DJ:11:VAL:HG12	31:DJ:12:LYS:H	1.80	0.47
31:DJ:37:ARG:HA	31:DJ:118:MET:SD	2.55	0.47
22:DA:2810:A:C8	22:DA:2811:G:C8	3.03	0.47
4:AD:151:LYS:HB3	4:AD:178:MET:HE1	1.97	0.47
22:DA:1803:A:O3'	24:DC:257:THR:HB	2.15	0.47
22:DA:607:U:O4	22:DA:620:G:H5'	2.15	0.47
1:AA:552:U:H2'	1:AA:553:A:C8	2.50	0.47
22:DA:392:U:H2'	22:DA:393:C:C6	2.50	0.47
22:DA:1645:G:OP1	22:DA:1646:C:H5'	2.15	0.47
46:DY:22:LEU:HG	46:DY:23:ARG:HE	1.80	0.47
47:BZ:47:MET:O	47:BZ:51:VAL:HG22	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:60:ILE:HG13	5:AE:61:GLN:N	2.30	0.47
12:AL:102:LEU:HB3	12:AL:103:ASP:H	1.56	0.47
22:DA:371:A:H61	22:DA:401:A:H3'	1.80	0.47
1:CA:487:A:H3'	1:CA:488:C:C6	2.50	0.47
22:BA:2081:U:H2'	22:BA:2082:A:C8	2.50	0.47
1:CA:1029:U:O2	1:CA:1029:U:H2'	2.15	0.47
48:D0:55:ILE:HG22	48:D0:56:ALA:N	2.30	0.47
12:CL:79:VAL:O	12:CL:103:ASP:HB2	2.15	0.47
22:DA:2235:G:H2'	22:DA:2236:U:O4'	2.15	0.47
22:DA:959:A:H2'	22:DA:960:A:C8	2.50	0.47
29:BH:91:PHE:HB3	1:CA:55:A:N3	2.30	0.47
22:BA:1056:G:H4'	22:BA:1086:A:C8	2.50	0.47
7:AG:47:LEU:HA	7:AG:47:LEU:HD12	1.78	0.47
22:DA:2043:C:H1'	22:DA:2779:U:O4	2.14	0.47
22:BA:674:G:H5''	26:BE:71:GLY:N	2.30	0.47
22:BA:674:G:H5''	26:BE:71:GLY:CA	2.45	0.47
39:BR:49:ILE:HG22	39:BR:52:PRO:C	2.34	0.47
1:CA:8:A:C5	4:CD:206:LYS:HB3	2.50	0.47
1:CA:935:A:N1	7:CG:3:ARG:NH1	2.63	0.47
6:AF:38:ARG:HH12	6:AF:99:ALA:HB3	1.79	0.47
1:CA:1296:C:N4	1:CA:1297:G:O6	2.48	0.47
22:BA:582:A:H2'	22:BA:583:G:H8	1.78	0.47
22:DA:2836:U:H2'	22:DA:2837:A:C8	2.50	0.47
2:CB:87:CYS:C	2:CB:89:GLN:H	2.19	0.47
20:CT:35:VAL:O	20:CT:39:ILE:HG13	2.15	0.47
2:CB:167:ASP:OD2	2:CB:191:SER:HA	2.15	0.47
22:DA:703:U:C2'	22:DA:704:G:H5'	2.46	0.47
26:DE:155:GLU:O	26:DE:159:LEU:HD12	2.15	0.47
2:CB:165:ASP:O	2:CB:169:GLU:HG2	2.15	0.47
1:AA:1449:C:H2'	1:AA:1450:U:O4'	2.15	0.47
22:DA:1434:A:H2'	22:DA:1435:G:H8	1.80	0.47
32:DK:66:LYS:HA	32:DK:66:LYS:HD2	1.79	0.47
1:CA:206:C:H2'	1:CA:207:C:C4'	2.45	0.47
1:AA:463:U:H3'	1:AA:464:U:C6	2.50	0.47
1:CA:1520:C:H2'	1:CA:1521:C:H6	1.80	0.47
27:BF:121:SER:HB2	27:BF:128:TYR:CE1	2.49	0.47
22:BA:468:G:N7	50:B2:39:ARG:NH2	2.60	0.47
3:CC:153:VAL:HB	3:CC:198:VAL:HG22	1.97	0.47
30:BI:127:ARG:HA	30:BI:130:GLU:HG3	1.97	0.47
21:AU:47:ARG:HA	21:AU:47:ARG:HE	1.80	0.47
4:CD:4:TYR:O	4:CD:5:LEU:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:B5:48:LEU:HD12	53:B5:57:GLN:HG2	1.95	0.47
47:BZ:30:ARG:HG3	47:BZ:34:HIS:CE1	2.50	0.47
1:CA:978:A:P	1:CA:1362:A:N6	2.89	0.46
22:BA:636:G:N7	33:BL:109:LYS:NZ	2.48	0.46
35:DN:55:ALA:CB	35:DN:79:LEU:HB3	2.45	0.46
30:BI:80:LEU:HD13	30:BI:136:MET:SD	2.55	0.46
40:BS:84:ARG:HB2	40:BS:96:ILE:CG1	2.44	0.46
25:DD:13:ARG:HD3	25:DD:21:SER:OG	2.15	0.46
3:AC:27:LYS:H	3:AC:27:LYS:HD2	1.79	0.46
22:DA:307:G:N1	22:DA:310:A:OP2	2.48	0.46
22:BA:1916:A:N3	22:BA:1917:U:H1'	2.31	0.46
4:AD:118:VAL:HA	4:AD:123:ILE:CD1	2.43	0.46
33:BL:95:LEU:HB3	33:BL:101:ILE:HG23	1.97	0.46
45:DX:10:LYS:HE3	45:DX:54:LYS:HD2	1.96	0.46
22:DA:406:G:H2'	22:DA:407:G:O4'	2.16	0.46
22:BA:1590:A:H2'	22:BA:1591:A:H8	1.80	0.46
30:BI:58:VAL:HG12	30:BI:59:ILE:N	2.30	0.46
8:AH:75:ILE:HD13	8:AH:129:VAL:HG13	1.97	0.46
22:DA:518:G:OP2	48:D0:13:ARG:NH2	2.48	0.46
22:BA:1380:G:OP2	57:BA:3757:HOH:O	2.19	0.46
31:BJ:70:THR:HG22	31:BJ:90:GLU:OE2	2.16	0.46
22:BA:962:G:O2'	22:BA:963:U:H5'	2.15	0.46
22:DA:2487:G:H2'	22:DA:2488:G:H8	1.79	0.46
22:DA:2487:G:H2'	22:DA:2488:G:C8	2.49	0.46
1:CA:109:A:C6	1:CA:327:A:C6	3.03	0.46
4:CD:144:SER:HB3	4:CD:179:GLU:HB2	1.97	0.46
37:BP:34:GLU:N	37:BP:37:LYS:O	2.44	0.46
27:BF:2:ALA:HB2	27:BF:94:GLU:OE1	2.15	0.46
22:DA:864:G:O2'	22:DA:914:G:O6	2.33	0.46
1:CA:1359:C:O2'	1:CA:1361:G:N7	2.48	0.46
29:DH:41:LYS:O	29:DH:44:ILE:HG12	2.15	0.46
2:AB:97:LEU:O	2:AB:100:MET:HB3	2.15	0.46
21:AU:37:PHE:HB3	21:AU:41:PRO:CG	2.41	0.46
22:BA:2579:C:H6	22:BA:2579:C:O5'	1.97	0.46
13:AM:17:ILE:O	13:AM:20:THR:OG1	2.29	0.46
31:DJ:35:ARG:HG2	31:DJ:40:HIS:HD2	1.80	0.46
45:DX:17:ASN:HB2	45:DX:25:THR:HB	1.97	0.46
11:CK:88:GLY:H	11:CK:114:THR:CG2	2.28	0.46
35:BN:44:LEU:HD23	35:BN:113:ILE:HG21	1.98	0.46
20:AT:5:LYS:O	20:AT:7:ALA:N	2.49	0.46
15:CO:29:VAL:HG13	15:CO:63:ARG:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CK:23:ILE:HG22	11:CK:32:VAL:HG13	1.97	0.46
1:CA:940:C:H2'	1:CA:941:G:H8	1.81	0.46
1:AA:1142:G:H2'	1:AA:1143:G:O4'	2.14	0.46
22:DA:2544:G:H5'	22:DA:2645:G:C2	2.50	0.46
22:DA:1930:G:N2	22:DA:1968:G:H2'	2.30	0.46
1:AA:1417:G:N2	1:AA:1482:G:H2'	2.29	0.46
1:AA:328:C:O2	1:AA:328:C:H2'	2.15	0.46
22:DA:1645:G:H4'	22:DA:1646:C:C6	2.51	0.46
1:AA:738:C:H2'	1:AA:739:C:H6	1.80	0.46
22:DA:2816:G:O3'	35:DN:99:LYS:HE2	2.15	0.46
1:AA:560:A:H5'	1:AA:566:G:N2	2.30	0.46
1:AA:1290:G:OP1	7:AG:35:LYS:NZ	2.48	0.46
22:BA:1786:A:H1'	22:BA:1938:A:N6	2.31	0.46
27:BF:30:ARG:O	27:BF:159:THR:HG23	2.16	0.46
22:BA:958:U:H2'	23:BB:89:U:C2	2.50	0.46
14:CN:10:GLU:O	14:CN:14:VAL:HG23	2.15	0.46
5:AE:69:ARG:HG2	5:AE:69:ARG:H	1.42	0.46
17:AQ:4:LYS:HE3	17:AQ:4:LYS:HB3	1.49	0.46
29:BH:132:PHE:CD2	29:BH:142:VAL:CG2	2.99	0.46
22:BA:1510:G:H2'	22:BA:1511:G:O4'	2.16	0.46
10:AJ:80:THR:HG22	10:AJ:82:LYS:H	1.80	0.46
22:DA:1265:A:N1	22:DA:2013:A:H5''	2.30	0.46
22:BA:264:C:O2'	22:BA:265:A:H2'	2.15	0.46
1:AA:537:G:H2'	1:AA:538:G:H8	1.80	0.46
1:CA:890:G:O2'	1:CA:891:U:OP2	2.30	0.46
22:DA:1269:A:O5'	22:DA:1269:A:H8	1.99	0.46
1:CA:107:G:H22	20:CT:5:LYS:NZ	2.13	0.46
16:AP:51:ARG:HH11	16:AP:51:ARG:CG	2.27	0.46
1:AA:453:G:H2'	1:AA:454:G:C8	2.50	0.46
5:AE:75:ALA:O	5:AE:82:GLN:NE2	2.49	0.46
22:DA:2461:A:H1'	22:DA:2492:U:N3	2.31	0.46
4:AD:99:ASP:OD2	4:AD:115:ARG:NH2	2.47	0.46
22:BA:26:G:H1'	22:BA:514:A:N6	2.29	0.46
3:AC:7:PRO:HG2	3:AC:184:TYR:CG	2.51	0.46
22:DA:2545:G:N3	22:DA:2565:A:H2	2.13	0.46
1:AA:207:C:H2'	1:AA:208:U:C2	2.49	0.46
22:DA:1895:C:H2'	22:DA:1896:G:C8	2.50	0.46
22:DA:1527:G:H21	22:DA:1545:A:H62	1.63	0.46
1:AA:1258:G:H2'	1:AA:1259:C:H6	1.79	0.46
32:BK:103:VAL:HB	32:BK:107:LEU:HD13	1.98	0.46
53:B5:59:VAL:HG21	53:B5:167:ASP:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2580:U:H5''	25:BD:135:GLY:O	2.15	0.46
8:AH:113:ASP:O	8:AH:117:ARG:HB2	2.16	0.46
22:BA:632:A:H2'	22:BA:633:A:C8	2.50	0.46
1:CA:15:G:C2	1:CA:16:A:C4	3.03	0.46
1:AA:294:U:OP1	1:AA:610:U:O2'	2.22	0.46
1:CA:1447:A:P	1:CA:1448:C:H41	2.39	0.46
22:BA:734:A:C5	22:BA:735:A:C8	3.04	0.46
22:DA:1666:G:O3'	32:DK:6:THR:HG23	2.15	0.46
8:CH:5:ASP:OD1	8:CH:81:PRO:HD3	2.15	0.46
22:DA:19:A:O2'	22:DA:553:G:H4'	2.16	0.46
4:AD:148:LYS:CD	4:AD:148:LYS:H	2.28	0.46
41:DT:46:ALA:O	41:DT:50:LEU:HB2	2.15	0.46
26:BE:7:ASP:O	26:BE:9:GLN:N	2.48	0.46
25:DD:30:GLU:HG2	25:DD:185:ASN:ND2	2.30	0.46
1:AA:1089:G:H2'	1:AA:1090:U:O4'	2.15	0.46
30:DI:92:LYS:HB3	30:DI:95:LYS:HE3	1.97	0.46
38:BQ:17:ILE:HG12	38:BQ:36:PHE:HD2	1.80	0.46
29:BH:80:ILE:HG21	29:BH:94:ILE:CG1	2.45	0.46
22:DA:784:G:OP1	22:DA:2588:G:H5''	2.15	0.46
22:BA:1085:A:C6	22:BA:1086:A:N6	2.83	0.46
22:DA:1073:A:H2'	22:DA:1074:G:H5'	1.97	0.46
22:BA:2012:G:OP1	40:BS:98:LYS:NZ	2.39	0.46
13:CM:4:ILE:HA	13:CM:57:ARG:CZ	2.45	0.46
22:BA:686:U:H2'	22:BA:788:A:C2	2.50	0.46
22:DA:1012:U:O4	31:DJ:30:THR:HG21	2.16	0.46
22:DA:1593:A:H2'	22:DA:1594:U:O4'	2.16	0.46
22:DA:1344:U:O5'	22:DA:1344:U:H6	1.98	0.46
23:BB:90:C:H5''	34:BM:18:ARG:HG3	1.97	0.46
35:BN:73:ASN:HA	35:BN:76:VAL:CG1	2.46	0.46
25:BD:16:THR:O	37:BP:79:PRO:HG2	2.15	0.46
24:BC:204:VAL:O	24:BC:206:GLY:N	2.48	0.46
27:DF:110:ARG:HH11	27:DF:137:ILE:C	2.19	0.46
4:CD:29:ASP:C	4:CD:31:LYS:N	2.69	0.46
25:DD:179:ARG:HH12	37:DP:8:LEU:HD21	1.79	0.46
1:CA:1342:C:H1'	9:CI:126:GLN:HG3	1.97	0.46
22:BA:26:G:C6	22:BA:27:G:N1	2.83	0.46
1:CA:313:A:H2'	1:CA:314:C:H6	1.80	0.46
1:CA:1417:G:C6	1:CA:1482:G:C6	3.04	0.46
22:DA:1:G:C2	22:DA:2:G:C4	3.03	0.46
22:BA:1176:U:H2'	22:BA:1177:G:N9	2.31	0.46
22:DA:812:C:H4'	38:DQ:13:ARG:HH12	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1657:U:P	25:BD:141:ARG:HG3	2.56	0.46
22:DA:1769:U:O2'	22:DA:1958:C:OP1	2.31	0.46
24:DC:130:LEU:HD12	24:DC:134:ASN:HB2	1.97	0.46
22:BA:555:G:O2'	22:BA:556:A:OP2	2.34	0.46
30:BI:102:SER:OG	30:BI:103:ARG:N	2.48	0.46
1:CA:458:U:H2'	1:CA:459:A:C8	2.50	0.46
9:CI:12:ARG:HD2	9:CI:107:ASP:HB3	1.98	0.46
1:CA:473:U:H2'	1:CA:474:G:H8	1.80	0.46
22:BA:2436:G:C2	22:BA:2437:G:C8	3.03	0.46
27:DF:170:LEU:HD23	27:DF:170:LEU:HA	1.78	0.46
6:AF:17:GLN:O	6:AF:17:GLN:NE2	2.49	0.46
29:BH:37:VAL:CG2	29:BH:38:PRO:HD2	2.45	0.46
30:BI:21:SER:HA	30:BI:25:GLY:HA2	1.98	0.46
8:AH:7:ILE:HD11	8:AH:32:LEU:HG	1.97	0.46
32:DK:21:CYS:HA	32:DK:41:ILE:HG22	1.97	0.46
4:CD:117:LEU:HB3	4:CD:123:ILE:HD11	1.98	0.46
29:BH:93:SER:O	1:CA:368:U:O4'	2.34	0.46
11:AK:16:VAL:HG22	11:AK:18:ASP:H	1.79	0.46
45:DX:39:TRP:HB2	45:DX:46:PHE:CE2	2.51	0.46
1:CA:1055:A:C6	1:CA:1206:G:C5	3.04	0.46
4:CD:58:LYS:HG3	4:CD:59:GLN:N	2.31	0.46
11:AK:83:GLU:HG3	11:AK:109:ASN:ND2	2.30	0.46
22:DA:1196:C:H1'	22:DA:1226:A:C4	2.51	0.46
1:CA:478:A:H8	1:CA:478:A:OP2	1.99	0.46
22:BA:2469:A:H4'	34:BM:55:ARG:HH12	1.81	0.46
4:CD:168:PRO:HB2	4:CD:171:LEU:CD1	2.45	0.46
29:DH:34:GLY:O	29:DH:35:LYS:CG	2.64	0.46
9:AI:84:THR:HG21	9:AI:103:PHE:HB3	1.97	0.46
6:CF:47:LEU:HG	6:CF:56:LYS:N	2.30	0.46
32:BK:28:SER:O	32:BK:30:ARG:N	2.48	0.46
46:BY:46:VAL:CA	46:BY:49:ASP:HB2	2.45	0.46
22:DA:2351:G:O2'	22:DA:2366:A:N6	2.43	0.46
22:BA:250:G:C6	22:BA:251:A:C6	3.04	0.46
1:AA:667:G:OP1	1:AA:732:C:O2'	2.18	0.46
1:CA:988:G:N2	1:CA:1217:C:O2	2.49	0.46
9:CI:22:LYS:O	9:CI:62:ASP:N	2.40	0.46
45:DX:40:VAL:HG21	45:DX:43:GLU:HB2	1.98	0.46
47:BZ:31:ARG:HG2	47:BZ:34:HIS:HB2	1.97	0.46
1:AA:111:G:H5''	1:AA:112:G:OP2	2.15	0.46
22:DA:1904:G:O2'	22:DA:1927:A:N6	2.40	0.46
1:AA:310:G:H5''	16:AP:31:ARG:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:852:U:H2'	22:BA:853:C:C6	2.50	0.46
1:AA:872:A:C8	1:AA:874:G:C8	3.03	0.46
10:CJ:64:GLN:HB3	14:CN:99:ALA:HB3	1.96	0.46
12:CL:44:LYS:HB2	12:CL:45:PRO:HD3	1.97	0.46
22:BA:1071:G:P	22:BA:1071:G:H8	2.39	0.46
22:BA:2114:A:H2'	22:BA:2114:A:N3	2.30	0.46
22:DA:480:A:H5''	42:DU:44:LYS:HD2	1.97	0.46
24:DC:51:THR:HG22	24:DC:54:ILE:HD11	1.97	0.46
36:DO:27:VAL:HA	36:DO:93:ASP:HB3	1.97	0.46
29:BH:94:ILE:HG23	29:BH:98:ASP:HB2	1.98	0.46
22:DA:2290:G:N2	22:DA:2343:U:H1'	2.30	0.46
29:DH:27:ARG:HE	45:DX:60:ASP:CB	2.27	0.46
14:CN:88:ALA:HB2	14:CN:96:LEU:HD23	1.97	0.46
22:BA:195:A:N7	57:BA:3764:HOH:O	2.36	0.46
22:DA:2572:A:N7	25:DD:150:GLN:HB3	2.30	0.46
1:AA:1157:A:C4	1:AA:1181:G:C6	3.04	0.46
22:BA:349:U:H2'	22:BA:350:G:C8	2.44	0.46
22:DA:814:C:OP1	39:DR:86:GLN:HG3	2.16	0.46
2:AB:64:LYS:HD3	2:AB:65:GLY:N	2.30	0.46
27:DF:106:ILE:HG12	27:DF:107:ALA:N	2.31	0.46
5:AE:81:LEU:HD21	5:AE:123:VAL:HG13	1.97	0.46
1:CA:63:C:O2'	1:CA:380:G:H4'	2.15	0.46
22:DA:327:G:N2	42:DU:68:SER:HB2	2.30	0.46
1:AA:676:A:H5''	11:AK:115:PRO:HB3	1.96	0.46
22:BA:58:G:O2'	22:BA:73:A:N1	2.45	0.46
1:AA:903:G:H2'	1:AA:904:U:C6	2.51	0.46
22:DA:1430:G:H2'	22:DA:1431:A:O4'	2.16	0.46
22:DA:1113:U:H2'	22:DA:1114:C:C6	2.51	0.46
22:BA:601:C:O2	22:BA:605:G:H4'	2.16	0.46
44:DW:34:GLY:O	44:DW:60:PHE:HB2	2.15	0.46
24:DC:66:ASP:N	24:DC:103:TYR:O	2.40	0.46
15:CO:70:LEU:HD22	15:CO:78:TYR:HB2	1.97	0.46
1:CA:1150:A:N6	1:CA:1151:A:H62	2.14	0.46
34:DM:108:VAL:HG12	34:DM:109:PRO:HD2	1.98	0.46
1:CA:77:A:H2'	1:CA:78:A:O4'	2.14	0.46
1:CA:1527:U:H2'	1:CA:1528:U:C6	2.50	0.46
25:BD:2:ILE:HG13	25:BD:100:LEU:HD21	1.97	0.46
22:BA:640:C:H2'	22:BA:641:U:C6	2.51	0.46
22:DA:53:A:C2	22:DA:179:C:H4'	2.50	0.46
1:AA:991:U:C4	1:AA:1212:U:H1'	2.50	0.46
1:AA:1216:A:OP1	14:AN:5:SER:OG	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1126:U:H3	10:CJ:42:LEU:HD21	1.80	0.46
49:D1:15:ALA:O	49:D1:17:THR:N	2.48	0.46
22:BA:2425:A:H4'	22:BA:2426:A:O5'	2.15	0.46
47:DZ:16:ARG:H	47:DZ:16:ARG:HG2	1.52	0.46
16:AP:50:THR:O	16:AP:50:THR:HG22	2.15	0.46
49:D1:38:LYS:HB2	49:D1:49:TYR:CD2	2.51	0.46
1:CA:441:A:N6	1:CA:494:G:H22	2.14	0.46
22:BA:2271:G:H2'	22:BA:2272:U:H6	1.80	0.46
1:CA:497:G:O2'	1:CA:498:A:H5'	2.15	0.46
7:CG:11:LYS:HB3	7:CG:21:GLU:OE1	2.15	0.46
7:AG:109:ARG:HH21	7:AG:119:ARG:NH1	2.14	0.46
22:DA:129:C:H2'	22:DA:130:C:H6	1.80	0.46
13:CM:66:GLU:HB3	13:CM:67:GLY:H	1.54	0.46
47:BZ:37:GLU:O	47:BZ:38:ARG:HD3	2.14	0.46
22:BA:1069:A:N1	22:BA:1073:A:N6	2.63	0.46
22:BA:1845:G:H2'	22:BA:1846:G:O4'	2.15	0.46
22:DA:1571:A:H8	22:DA:1571:A:O5'	1.98	0.46
1:AA:1166:G:O2'	1:AA:1169:A:N6	2.48	0.46
1:CA:81:A:H2'	1:CA:82:G:H8	1.80	0.46
18:AR:72:ASP:OD2	21:AU:4:ILE:HG13	2.15	0.46
1:CA:261:U:OP2	20:CT:74:ARG:NH2	2.47	0.46
1:CA:398:U:H2'	1:CA:399:G:C8	2.48	0.46
21:AU:12:PHE:CD2	21:AU:12:PHE:N	2.83	0.46
1:CA:159:G:H21	1:CA:161:A:H3'	1.81	0.46
22:DA:190:A:H2'	22:DA:191:A:O4'	2.15	0.46
12:AL:3:THR:HG22	12:AL:5:ASN:N	2.30	0.46
1:CA:1219:A:N6	1:CA:1220:G:O6	2.49	0.46
24:DC:197:ASN:OD1	24:DC:200:HIS:HB2	2.16	0.46
2:AB:216:ALA:O	2:AB:220:THR:HG22	2.16	0.46
14:CN:64:CYS:SG	14:CN:80:SER:HB2	2.56	0.46
1:AA:1351:U:H2'	1:AA:1352:C:H6	1.81	0.46
8:CH:59:LEU:HD12	8:CH:60:GLU:N	2.31	0.46
44:BW:41:ARG:O	44:BW:57:HIS:ND1	2.33	0.46
26:DE:149:ILE:CG2	26:DE:188:MET:HG2	2.46	0.46
1:AA:1417:G:C6	1:AA:1482:G:C6	3.04	0.46
5:CE:72:ILE:HD13	5:CE:145:GLU:CD	2.36	0.46
22:BA:1474:U:H2'	22:BA:1475:G:H5'	1.97	0.46
15:CO:67:LEU:HD23	15:CO:78:TYR:HE1	1.81	0.46
4:AD:148:LYS:HD3	4:AD:148:LYS:H	1.79	0.46
41:DT:64:LYS:HA	41:DT:79:ASP:OD1	2.16	0.46
36:BO:64:TYR:HB3	36:BO:67:ASN:ND2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:86:ARG:CZ	12:CL:88:LYS:HB3	2.45	0.46
22:DA:2799:A:O2'	22:DA:2800:A:H5''	2.16	0.46
31:BJ:31:GLU:OE2	31:BJ:35:ARG:NH1	2.46	0.46
17:AQ:79:VAL:HG12	17:AQ:80:GLU:HG3	1.98	0.46
44:BW:46:HIS:CE1	44:BW:77:ARG:HD3	2.51	0.46
2:AB:47:VAL:HB	2:AB:48:PRO:HD3	1.98	0.46
1:AA:572:A:H5'	1:AA:573:A:OP2	2.15	0.46
22:BA:923:G:H4'	44:BW:29:GLU:HG3	1.97	0.46
48:B0:43:ILE:HG22	48:B0:49:TYR:HB2	1.96	0.46
1:AA:1312:G:N7	19:AS:3:ARG:N	2.63	0.46
26:BE:23:PHE:HB2	26:BE:114:ARG:HH12	1.81	0.46
3:AC:22:TRP:CB	3:AC:59:ARG:HG2	2.45	0.46
19:CS:10:PHE:O	19:CS:39:THR:OG1	2.33	0.46
15:CO:89:ARG:HH12	22:DA:716:A:P	2.38	0.46
43:BV:30:ILE:HG22	43:BV:93:ARG:HG3	1.98	0.46
52:D4:25:VAL:HB	52:D4:35:GLN:HG3	1.98	0.46
22:BA:1744:A:H3'	22:BA:1745:A:H8	1.81	0.46
4:AD:122:ALA:HA	4:AD:146:ARG:HG3	1.97	0.46
1:CA:1160:G:O6	1:CA:1181:G:C6	2.69	0.46
30:DI:127:ARG:HD3	30:DI:127:ARG:H	1.81	0.46
6:CF:16:GLU:C	6:CF:18:VAL:H	2.18	0.46
9:AI:81:HIS:O	9:AI:84:THR:OG1	2.29	0.46
19:CS:70:LYS:O	19:CS:73:GLU:HB2	2.16	0.46
22:BA:2566:A:N1	32:BK:28:SER:OG	2.41	0.46
19:CS:56:GLN:CD	19:CS:57:HIS:H	2.19	0.46
8:CH:26:THR:HA	8:CH:59:LEU:O	2.16	0.46
4:AD:151:LYS:HB2	4:AD:156:LYS:CE	2.46	0.46
1:AA:390:U:H2'	1:AA:391:G:C8	2.50	0.46
27:BF:136:ILE:HD12	27:BF:136:ILE:H	1.81	0.46
3:CC:42:TYR:CE1	3:CC:90:VAL:HG21	2.50	0.46
22:BA:1789:A:OP1	24:BC:221:ARG:HD3	2.14	0.46
28:DG:9:VAL:HG23	28:DG:69:ARG:HD2	1.97	0.46
45:DX:49:LEU:O	45:DX:51:VAL:HG13	2.15	0.46
22:DA:635:C:H2'	22:DA:636:G:C8	2.50	0.46
12:AL:36:ARG:HB3	12:AL:38:TYR:HE2	1.80	0.46
22:BA:2334:U:O4	36:BO:16:ARG:NH2	2.49	0.46
22:DA:866:A:O4'	22:DA:914:G:N2	2.48	0.46
35:DN:53:THR:HA	35:DN:56:LYS:HG2	1.96	0.46
22:DA:2721:A:H2'	22:DA:2722:G:C8	2.50	0.46
9:CI:47:VAL:O	9:CI:50:GLN:HB2	2.16	0.46
22:BA:2815:C:O2'	48:B0:40:ARG:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:936:A:H2'	22:BA:937:C:C6	2.51	0.46
1:AA:1410:A:H2'	1:AA:1411:C:C6	2.50	0.46
35:BN:31:HIS:C	35:BN:33:ILE:H	2.18	0.46
1:CA:676:A:H5''	11:CK:115:PRO:HB3	1.97	0.46
38:BQ:41:LYS:HB2	38:BQ:41:LYS:HE3	1.53	0.46
1:CA:524:G:O5'	1:CA:524:G:H8	1.98	0.46
1:AA:168:G:C6	1:AA:169:C:C4	3.04	0.46
1:CA:1222:G:H5''	19:CS:78:ARG:NH1	2.30	0.46
32:DK:104:THR:O	32:DK:106:GLU:N	2.48	0.46
13:CM:3:ARG:HA	13:CM:9:ILE:HG12	1.96	0.46
45:BX:5:CYS:SG	45:BX:8:THR:HG23	2.55	0.46
22:DA:2408:U:H2'	22:DA:2409:G:C8	2.51	0.46
4:AD:31:LYS:HB2	4:AD:31:LYS:HE2	1.56	0.46
11:AK:16:VAL:HG13	11:AK:17:SER:H	1.80	0.46
22:BA:572:A:C2	22:BA:2033:A:C2	3.04	0.46
22:DA:528:A:C2	22:DA:2043:C:H4'	2.50	0.46
22:DA:1800:C:OP2	24:DC:182:ARG:NH1	2.49	0.46
1:AA:375:U:C4	1:AA:376:G:N7	2.84	0.46
2:CB:27:MET:SD	2:CB:193:PRO:HD3	2.56	0.46
1:AA:1160:G:OP1	2:AB:132:LYS:NZ	2.26	0.46
53:B5:65:LEU:HD12	53:B5:67:HIS:HB2	1.97	0.46
31:DJ:40:HIS:O	38:DQ:67:ALA:HB1	2.16	0.46
1:CA:801:U:H2'	1:CA:802:A:C8	2.46	0.46
22:DA:593:U:H2'	22:DA:594:U:C6	2.51	0.46
2:CB:83:ALA:HA	2:CB:86:SER:HB3	1.98	0.46
22:BA:2813:A:H2	22:BA:2887:A:H61	1.63	0.46
4:CD:41:HIS:O	4:CD:44:ARG:HG2	2.16	0.46
5:AE:104:GLY:HA3	5:AE:122:ASN:HA	1.97	0.46
30:DI:15:ALA:HB3	30:DI:52:GLY:N	2.31	0.46
24:BC:71:LYS:HE3	24:BC:96:TYR:CD2	2.51	0.46
22:DA:1091:G:O2'	22:DA:1092:C:OP2	2.25	0.46
39:BR:61:ALA:HB2	39:BR:98:ILE:HD13	1.98	0.46
18:CR:40:VAL:HA	18:CR:41:PRO:HD2	1.77	0.46
6:AF:11:HIS:HA	6:AF:12:PRO:HD2	1.67	0.46
47:DZ:10:THR:HG22	47:DZ:54:MET:C	2.37	0.46
1:CA:990:C:C4	1:CA:991:U:O4	2.69	0.46
22:DA:564:C:O4'	38:DQ:37:GLN:NE2	2.49	0.46
22:BA:1654:A:H1'	22:BA:2823:A:H5'	1.97	0.46
22:BA:1843:C:H2'	22:BA:1844:C:H6	1.81	0.46
27:DF:53:ALA:HB2	27:DF:150:ARG:HD2	1.96	0.46
1:AA:222:C:H2'	1:AA:223:A:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:147:LYS:HB2	3:AC:203:PHE:CD2	2.51	0.46
42:BU:5:ILE:C	42:BU:6:ARG:HG2	2.37	0.46
24:BC:212:ARG:HA	24:BC:212:ARG:HD2	1.51	0.46
29:DH:60:GLU:HA	29:DH:60:GLU:OE2	2.15	0.46
27:BF:41:GLY:O	27:BF:43:ALA:N	2.49	0.46
1:AA:720:C:H5'	18:AR:41:PRO:HA	1.98	0.46
22:DA:2704:C:H3'	22:DA:2705:A:H8	1.81	0.46
22:BA:1165:A:H2'	22:BA:1166:G:H8	1.81	0.46
29:BH:90:LEU:HD21	29:BH:93:SER:HA	1.97	0.46
29:BH:90:LEU:HD23	29:BH:93:SER:HA	1.97	0.46
22:BA:714:U:O2'	22:BA:716:A:N6	2.32	0.46
22:DA:2627:G:N2	22:DA:2777:G:OP2	2.48	0.46
22:DA:1073:A:H4'	22:DA:2474:U:H4'	1.97	0.46
2:CB:35:ARG:O	2:CB:38:VAL:HG12	2.16	0.46
1:CA:110:C:H2'	1:CA:111:G:O4'	2.16	0.46
22:DA:1592:C:H2'	22:DA:1593:A:H8	1.78	0.46
22:DA:2053:G:H5'	25:DD:149:ASN:O	2.16	0.46
22:DA:188:G:C6	22:DA:189:G:C4	3.04	0.46
22:BA:589:U:H2'	22:BA:590:A:C8	2.51	0.46
12:CL:90:LEU:HB2	12:CL:93:VAL:CG2	2.45	0.46
3:CC:39:VAL:O	3:CC:43:LEU:HB2	2.16	0.46
4:AD:165:ARG:O	4:AD:167:LYS:N	2.49	0.46
7:CG:125:SER:C	7:CG:127:ALA:H	2.18	0.46
22:DA:1998:A:H4'	22:DA:2724:U:O2'	2.16	0.46
23:DB:14:U:OP2	23:DB:70:C:O2'	2.31	0.46
22:DA:2093:G:O6	22:DA:2225:A:H5''	2.15	0.46
22:DA:1525:A:H2'	22:DA:1526:C:O4'	2.16	0.46
2:CB:90:PHE:HB3	2:CB:150:GLY:O	2.16	0.46
22:DA:635:C:O2'	22:DA:639:U:H5''	2.16	0.46
22:DA:1957:C:H5'	22:DA:1984:G:O2'	2.15	0.46
22:BA:570:G:H2'	22:BA:2030:A:N7	2.31	0.46
3:AC:47:LEU:HB3	3:AC:50:ALA:HB3	1.97	0.46
4:CD:187:GLU:N	4:CD:190:ASP:OD1	2.45	0.46
49:B1:13:SER:OG	49:B1:40:ASP:OD2	2.24	0.46
22:BA:2052:A:H4'	25:BD:148:GLN:O	2.16	0.46
22:DA:1190:G:H5''	33:DL:32:GLY:O	2.15	0.46
28:DG:105:LEU:HB2	28:DG:113:VAL:HB	1.97	0.46
32:BK:36:GLY:HA2	32:BK:62:VAL:O	2.16	0.46
22:BA:2080:A:O5'	45:BX:19:SER:OG	2.33	0.46
22:BA:954:G:OP2	34:BM:16:ARG:NH2	2.44	0.46
22:BA:864:G:C6	22:BA:865:C:N4	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:139:GLN:O	3:AC:141:ALA:N	2.49	0.46
1:AA:928:G:O2'	1:AA:1533:C:OP1	2.24	0.46
47:DZ:41:THR:HG23	47:DZ:44:ILE:CG1	2.42	0.45
10:AJ:80:THR:O	10:AJ:84:VAL:N	2.41	0.45
2:CB:70:VAL:HB	2:CB:163:VAL:HG13	1.98	0.45
5:CE:137:VAL:O	5:CE:138:ARG:HB3	2.16	0.45
12:CL:99:ARG:HB2	12:CL:117:TYR:HA	1.98	0.45
11:CK:30:THR:HG21	11:CK:92:GLY:HA3	1.99	0.45
22:DA:310:A:O2'	22:DA:311:A:OP2	2.26	0.45
1:CA:81:A:H61	1:CA:87:C:N4	2.13	0.45
1:AA:971:G:O6	1:AA:1364:U:O2'	2.34	0.45
9:AI:30:ILE:HD12	9:AI:79:ILE:HD11	1.97	0.45
32:BK:70:ARG:NH1	32:BK:74:GLY:O	2.44	0.45
22:BA:721:A:H2'	22:BA:722:A:H8	1.79	0.45
22:DA:1277:G:H5'	35:DN:20:MET:HE2	1.97	0.45
22:DA:1738:G:O2'	22:DA:1739:A:H8	1.99	0.45
1:CA:687:A:O2'	1:CA:701:U:O4	2.12	0.45
15:CO:39:LEU:HA	15:CO:39:LEU:HD12	1.85	0.45
22:DA:1266:G:O2'	22:DA:2012:G:O6	2.23	0.45
22:BA:711:G:H2'	22:BA:712:G:O4'	2.16	0.45
34:BM:136:MET:HE2	43:BV:57:TYR:CD2	2.51	0.45
1:CA:1060:U:H2'	1:CA:1061:G:H8	1.80	0.45
22:DA:67:U:H2'	22:DA:68:G:O4'	2.16	0.45
22:DA:1494:A:H2'	22:DA:1495:A:C8	2.51	0.45
34:DM:56:ALA:C	34:DM:58:LYS:H	2.19	0.45
18:AR:47:THR:HG21	18:AR:52:GLN:HB2	1.99	0.45
13:AM:26:GLY:O	13:AM:28:THR:N	2.49	0.45
22:DA:1995:U:OP1	57:DA:3809:HOH:O	2.21	0.45
22:BA:2849:U:H4'	22:BA:2868:A:C2	2.51	0.45
13:CM:19:LEU:HG	13:CM:34:LEU:HD21	1.99	0.45
39:DR:43:ASN:HB3	39:DR:44:GLY:H	1.52	0.45
29:DH:86:ASP:C	29:DH:88:GLY:H	2.19	0.45
22:DA:1736:U:H2'	22:DA:1737:G:O4'	2.17	0.45
1:CA:1010:U:H2'	1:CA:1011:C:C6	2.51	0.45
37:BP:109:ARG:HB2	37:BP:109:ARG:HH21	1.81	0.45
22:DA:2419:U:H2'	22:DA:2420:C:C6	2.50	0.45
7:CG:23:LEU:HD23	7:CG:26:PHE:HB3	1.98	0.45
29:BH:79:THR:HG23	29:BH:147:VAL:HB	1.98	0.45
29:BH:94:ILE:HG23	29:BH:98:ASP:CB	2.47	0.45
22:DA:783:A:H8	22:DA:784:G:H4'	1.81	0.45
29:DH:83:LYS:HG3	29:DH:149:GLU:HG3	1.93	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DN:87:PHE:HE1	35:DN:116:VAL:HG12	1.81	0.45
1:CA:484:G:C5	1:CA:486:U:H1'	2.51	0.45
22:DA:961:C:C2	22:DA:2031:A:C6	3.05	0.45
27:DF:106:ILE:O	27:DF:110:ARG:HD3	2.16	0.45
22:DA:825:A:H4'	22:DA:2428:G:C5	2.51	0.45
2:CB:14:VAL:H	2:CB:208:ARG:NH1	2.15	0.45
22:DA:2033:A:H4'	22:DA:2034:U:OP1	2.15	0.45
22:BA:2532:G:HO2'	22:BA:2657:A:N6	2.14	0.45
4:AD:105:MET:SD	4:AD:180:GLY:HA3	2.57	0.45
4:AD:167:LYS:HA	4:AD:168:PRO:HD3	1.63	0.45
22:DA:1998:A:OP2	25:DD:141:ARG:NH2	2.48	0.45
1:CA:1478:U:H2'	1:CA:1479:C:C6	2.50	0.45
22:BA:156:A:H2'	22:BA:157:C:O4'	2.16	0.45
9:CI:99:ARG:HA	9:CI:104:VAL:HG21	1.97	0.45
22:BA:1712:U:OP2	22:BA:1713:A:O2'	2.29	0.45
45:BX:68:LEU:HD13	45:BX:78:TYR:CE1	2.51	0.45
22:DA:2353:G:H2'	22:DA:2354:C:O4'	2.16	0.45
32:DK:59:LYS:HG3	32:DK:89:ASN:OD1	2.16	0.45
22:DA:2091:C:H3'	22:DA:2092:U:H5''	1.98	0.45
1:CA:1537:U:H5''	1:CA:1538:C:OP2	2.16	0.45
1:AA:1520:C:H2'	1:AA:1521:C:C6	2.52	0.45
30:BI:67:PHE:N	30:BI:67:PHE:CD2	2.84	0.45
22:BA:1008:A:N6	22:BA:1136:G:C6	2.84	0.45
1:AA:160:A:H2'	1:AA:161:A:O4'	2.17	0.45
1:AA:260:G:H2'	1:AA:261:U:C6	2.52	0.45
5:CE:101:GLU:HA	5:CE:122:ASN:CB	2.46	0.45
22:BA:1324:G:C4	22:BA:1328:A:N6	2.84	0.45
1:CA:673:A:H2'	1:CA:674:G:C8	2.51	0.45
1:AA:675:A:H5'	18:AR:71:THR:HG21	1.99	0.45
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.51	0.45
1:AA:451:A:H5''	16:AP:70:ARG:NH2	2.32	0.45
22:DA:2293:G:H5''	36:DO:94:ARG:HH22	1.80	0.45
33:BL:91:ASP:O	33:BL:94:THR:HB	2.17	0.45
22:DA:948:C:H6	22:DA:948:C:O5'	1.99	0.45
22:DA:1032:A:H4'	52:D4:16:ILE:HD12	1.98	0.45
22:BA:2844:G:H2'	22:BA:2845:U:O4'	2.16	0.45
2:AB:65:GLY:C	2:AB:66:LYS:HD3	2.36	0.45
21:AU:12:PHE:HD2	21:AU:12:PHE:N	2.14	0.45
35:DN:22:ARG:HG3	35:DN:70:THR:HA	1.97	0.45
1:CA:705:G:N2	11:CK:31:ILE:HD12	2.32	0.45
2:CB:72:THR:HG22	2:CB:95:ARG:HH11	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:BS:55:ILE:HG23	40:BS:66:ILE:HG12	1.97	0.45
13:AM:15:ALA:O	13:AM:19:LEU:HD23	2.16	0.45
25:DD:170:VAL:HG23	25:DD:194:PRO:HB3	1.97	0.45
1:AA:1060:U:OP1	14:AN:85:ARG:NH2	2.42	0.45
29:DH:112:LYS:HG2	29:DH:113:SER:N	2.32	0.45
42:BU:39:ILE:HG22	42:BU:40:ASN:N	2.31	0.45
22:BA:1113:U:OP1	28:BG:3:ARG:NH1	2.49	0.45
1:AA:1008:U:H2'	1:AA:1009:U:C6	2.51	0.45
1:CA:976:G:OP2	1:CA:1358:U:O2'	2.34	0.45
1:AA:843:U:OP1	1:AA:846:G:N2	2.42	0.45
30:DI:21:SER:HB3	30:DI:22:PRO:HD3	1.98	0.45
1:CA:745:G:H5''	1:CA:851:G:O2'	2.16	0.45
2:CB:183:VAL:HG12	2:CB:196:VAL:HG13	1.98	0.45
41:BT:33:LYS:HG3	41:BT:80:TRP:CE3	2.50	0.45
22:DA:40:U:H2'	22:DA:41:C:C6	2.50	0.45
22:DA:12:U:O2	22:DA:12:U:H2'	2.15	0.45
1:AA:719:C:O2'	18:AR:38:LYS:HB3	2.17	0.45
26:DE:177:PRO:O	26:DE:181:ILE:HG13	2.16	0.45
22:DA:2243:U:H2'	22:DA:2244:U:C6	2.52	0.45
12:CL:34:CYS:HB3	12:CL:55:VAL:HG22	1.98	0.45
10:CJ:36:VAL:HG22	10:CJ:76:ILE:HG12	1.99	0.45
4:AD:195:ILE:HG13	4:AD:197:GLU:OE2	2.16	0.45
22:DA:297:G:OP1	42:DU:92:LYS:HD3	2.17	0.45
22:DA:483:A:O2'	42:DU:56:GLY:HA3	2.17	0.45
18:CR:25:ASP:O	18:CR:28:THR:N	2.49	0.45
5:CE:138:ARG:H	5:CE:141:ILE:CD1	2.29	0.45
16:AP:4:ILE:HA	16:AP:20:VAL:O	2.17	0.45
2:CB:35:ARG:O	2:CB:37:LYS:N	2.50	0.45
1:AA:1363:A:C4	1:AA:1365:G:C6	3.04	0.45
1:AA:1367:C:O2'	10:AJ:50:THR:HG21	2.17	0.45
24:BC:252:THR:HG22	24:BC:253:LYS:H	1.82	0.45
4:AD:123:ILE:N	4:AD:146:ARG:HG3	2.31	0.45
22:DA:1223:G:N2	22:DA:1226:A:OP2	2.46	0.45
29:DH:34:GLY:O	29:DH:35:LYS:CD	2.65	0.45
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.52	0.45
46:BY:45:GLN:O	46:BY:46:VAL:HB	2.16	0.45
22:DA:2093:G:O2'	22:DA:2094:A:H5'	2.16	0.45
22:DA:1906:G:OP2	22:DA:1929:G:O2'	2.35	0.45
22:DA:1669:A:O4'	32:DK:5:GLN:HG3	2.16	0.45
30:DI:62:TYR:CB	30:DI:64:ASP:H	2.28	0.45
44:DW:48:GLY:H	44:DW:51:VAL:HB	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:29:ASN:OD1	11:AK:47:ALA:HB3	2.16	0.45
22:BA:284:U:H2'	22:BA:285:G:H8	1.82	0.45
23:BB:42:C:C5	27:BF:66:LEU:HD22	2.51	0.45
13:AM:54:ASP:HB3	13:AM:57:ARG:HH21	1.81	0.45
1:CA:922:G:N3	1:CA:1398:A:H2	2.15	0.45
31:BJ:98:GLU:CD	31:BJ:126:ALA:HB2	2.36	0.45
22:DA:2864:G:H2'	22:DA:2865:U:O4'	2.16	0.45
36:BO:26:LEU:HD22	36:BO:115:LEU:HD23	1.99	0.45
4:CD:9:LEU:HD12	4:CD:9:LEU:HA	1.63	0.45
22:DA:675:A:C6	22:DA:676:A:C6	3.04	0.45
36:DO:24:THR:HG23	36:DO:42:PRO:HD3	1.97	0.45
22:DA:1087:G:H2'	22:DA:1088:A:H5'	1.99	0.45
22:BA:1084:A:C2	22:BA:1106:G:H1'	2.51	0.45
22:BA:1435:G:H2'	22:BA:1436:G:H8	1.82	0.45
36:DO:39:VAL:N	36:DO:49:VAL:O	2.43	0.45
3:AC:5:VAL:HG21	3:AC:10:ILE:HD13	1.98	0.45
1:CA:857:C:H2'	1:CA:858:G:O4'	2.16	0.45
45:DX:17:ASN:OD1	45:DX:27:ARG:HB3	2.17	0.45
22:BA:1915:U:C2'	22:BA:1916:A:H5'	2.46	0.45
22:DA:1120:G:C6	22:DA:1121:C:C4	3.05	0.45
1:CA:35:G:N3	12:CL:115:SER:OG	2.48	0.45
1:CA:707:U:H2'	1:CA:708:C:C6	2.52	0.45
22:DA:708:G:N2	22:DA:724:U:H1'	2.31	0.45
3:CC:63:SER:OG	3:CC:64:ILE:N	2.48	0.45
33:DL:29:LYS:O	33:DL:30:THR:OG1	2.26	0.45
2:CB:72:THR:HG23	2:CB:94:HIS:O	2.17	0.45
1:AA:1095:U:H2'	1:AA:1096:C:O4'	2.17	0.45
2:CB:173:ILE:HG22	2:CB:177:ASN:ND2	2.31	0.45
1:AA:1538:C:H2'	1:AA:1539:C:H5'	1.99	0.45
1:AA:205:A:H2'	1:AA:205:A:N3	2.30	0.45
22:DA:1089:A:O2'	22:DA:1090:A:N7	2.42	0.45
22:BA:1424:G:H2'	22:BA:1425:G:O4'	2.16	0.45
22:DA:1926:U:H1'	22:DA:1929:G:C6	2.52	0.45
5:AE:157:ARG:NH2	8:AH:100:GLY:H	2.14	0.45
22:DA:2533:U:OP1	22:DA:2665:A:O2'	2.33	0.45
4:AD:160:GLU:O	4:AD:162:ALA:N	2.50	0.45
2:AB:42:ASN:HB3	2:AB:45:LYS:HB3	1.98	0.45
28:BG:170:ARG:HH12	52:B4:29:ALA:HA	1.82	0.45
22:DA:479:A:N3	22:DA:481:G:H5''	2.31	0.45
19:AS:36:ARG:HB3	19:AS:72:GLY:HA3	1.98	0.45
22:DA:651:G:H5'	51:D3:19:LYS:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:43:PHE:CE1	15:AO:56:LEU:HD22	2.51	0.45
24:DC:43:ARG:NH2	24:DC:49:ILE:HD11	2.31	0.45
22:DA:2888:C:H2'	22:DA:2889:C:C6	2.52	0.45
1:AA:1444:U:H2'	1:AA:1445:U:C6	2.52	0.45
29:DH:93:SER:HB3	29:DH:123:ARG:HG3	1.99	0.45
1:AA:271:C:H2'	1:AA:272:C:C6	2.52	0.45
5:CE:156:LYS:HA	5:CE:159:LYS:NZ	2.32	0.45
22:DA:1360:G:H5''	57:DA:3614:HOH:O	2.16	0.45
22:DA:1063:G:N3	30:DI:90:SER:OG	2.48	0.45
4:CD:174:ASP:OD1	4:CD:177:LYS:N	2.46	0.45
22:BA:2065:C:H2'	22:BA:2066:C:H6	1.81	0.45
49:B1:4:GLY:C	49:B1:6:ARG:H	2.20	0.45
25:BD:12:THR:HG21	37:BP:9:GLU:HG3	1.98	0.45
16:CP:38:PHE:CE2	16:CP:51:ARG:HD3	2.47	0.45
35:BN:32:GLU:HA	35:BN:115:LEU:HD12	1.98	0.45
22:DA:2311:A:H5''	27:DF:77:PHE:CE1	2.52	0.45
1:CA:972:C:H4'	10:CJ:59:LYS:HG2	1.98	0.45
22:DA:327:G:H2'	22:DA:328:U:O4'	2.17	0.45
1:AA:67:C:H2'	1:AA:68:G:C8	2.52	0.45
22:BA:118:A:C8	22:BA:119:A:C8	3.04	0.45
22:DA:334:C:OP1	22:DA:335:C:N4	2.48	0.45
22:DA:300:A:P	42:DU:82:ARG:HH12	2.39	0.45
22:DA:1045:C:H1'	22:DA:1047:G:C6	2.52	0.45
22:DA:1640:A:H2'	22:DA:1641:A:C8	2.51	0.45
22:DA:82:U:H2'	22:DA:83:A:C8	2.52	0.45
1:CA:1462:C:H2'	1:CA:1463:U:C6	2.51	0.45
1:AA:762:U:H2'	1:AA:763:G:C8	2.51	0.45
25:DD:113:SER:HB3	25:DD:170:VAL:HG21	1.97	0.45
1:AA:1001:C:H3'	1:AA:1001:C:H6	1.82	0.45
22:DA:2370:G:H4'	49:D1:44:ARG:NH1	2.31	0.45
1:CA:931:C:H2'	1:CA:932:C:C6	2.51	0.45
1:CA:206:C:N4	1:CA:213:G:H1	2.15	0.45
1:AA:1387:G:H2'	1:AA:1388:C:C6	2.51	0.45
1:CA:487:A:H3'	1:CA:488:C:H6	1.81	0.45
12:CL:79:VAL:HG12	12:CL:102:LEU:HD23	1.99	0.45
45:BX:63:GLY:O	45:BX:65:ASP:N	2.50	0.45
22:DA:2712:C:OP1	22:DA:2714:G:H4'	2.17	0.45
47:DZ:12:SER:OG	47:DZ:14:ILE:HG13	2.17	0.45
38:BQ:102:ASP:C	38:BQ:104:VAL:H	2.20	0.45
1:CA:1299:A:O2'	1:CA:1301:U:O4'	2.34	0.45
22:DA:2622:U:O2'	22:DA:2825:G:N7	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:484:G:H4'	1:AA:485:U:OP1	2.16	0.45
22:BA:2050:C:O2	25:BD:161:MET:HE1	2.17	0.45
1:AA:1052:U:O2	1:AA:1207:G:N2	2.50	0.45
22:BA:2834:G:H2'	22:BA:2879:A:H61	1.81	0.45
22:BA:500:G:N2	22:BA:502:A:H3'	2.32	0.45
8:CH:43:GLU:OE1	8:CH:112:THR:HG21	2.16	0.45
22:DA:367:G:C2	22:DA:368:A:H1'	2.52	0.45
1:AA:695:A:H2'	1:AA:696:A:O4'	2.17	0.45
22:BA:1224:U:H4'	39:BR:88:GLY:O	2.16	0.45
22:BA:1689:A:H2'	22:BA:1690:A:H8	1.81	0.45
41:BT:49:LYS:HA	41:BT:49:LYS:HD3	1.71	0.45
1:AA:540:G:H2'	1:AA:541:G:H8	1.81	0.45
22:BA:1333:G:C2	22:BA:1334:G:C8	3.04	0.45
29:DH:147:VAL:HG12	29:DH:148:ALA:N	2.32	0.45
9:AI:33:ARG:HG2	9:AI:37:GLN:HB3	1.98	0.45
6:CF:43:GLY:HA2	6:CF:58:HIS:NE2	2.32	0.45
22:DA:305:C:H1'	22:DA:313:G:N2	2.32	0.45
29:BH:72:ILE:HG23	29:BH:142:VAL:HG22	1.99	0.45
22:BA:2094:A:OP2	29:BH:22:LYS:CE	2.65	0.45
29:DH:39:ALA:O	29:DH:41:LYS:N	2.47	0.45
22:BA:2820:A:OP2	35:BN:2:ARG:NH1	2.46	0.45
49:B1:9:ILE:HD12	49:B1:52:ALA:HB1	1.97	0.45
22:BA:1287:A:C5	22:BA:1288:G:C6	3.05	0.45
22:BA:2579:C:OP1	57:BA:3546:HOH:O	2.21	0.45
16:CP:46:LYS:HD3	16:CP:47:GLU:H	1.82	0.45
1:AA:1157:A:C5	1:AA:1180:A:C6	3.05	0.45
22:DA:2172:U:H4'	22:DA:2173:A:H5'	1.99	0.45
1:CA:87:C:H2'	1:CA:88:U:C6	2.52	0.45
2:AB:68:LEU:HD22	2:AB:70:VAL:HG23	1.98	0.45
13:CM:27:LYS:HD3	13:CM:27:LYS:O	2.16	0.45
22:DA:2286:G:H5''	22:DA:2287:A:OP1	2.17	0.45
22:DA:2282:G:N3	22:DA:2425:A:N6	2.65	0.45
2:CB:82:ASP:H	2:CB:85:LEU:HB3	1.81	0.45
4:AD:97:ARG:O	4:AD:101:VAL:HG23	2.16	0.45
1:CA:1113:C:H2'	1:CA:1114:C:H6	1.82	0.45
1:AA:107:G:H2'	1:AA:108:G:H5''	1.99	0.45
1:AA:666:G:C6	1:AA:741:G:C6	3.05	0.45
13:AM:15:ALA:HB3	13:AM:34:LEU:HD21	1.99	0.45
8:AH:64:LYS:HB2	8:AH:71:VAL:CG2	2.47	0.45
22:DA:2093:G:N7	22:DA:2225:A:H2'	2.31	0.45
1:CA:568:G:N2	1:CA:883:C:C2	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:324:A:N6	22:BA:338:G:O2'	2.48	0.45
8:CH:86:TYR:C	8:CH:87:LYS:HD2	2.37	0.45
11:CK:71:ALA:O	11:CK:74:VAL:HG22	2.16	0.45
22:BA:1198:U:H2'	22:BA:1199:U:C6	2.52	0.45
26:DE:193:VAL:O	26:DE:197:GLU:HB2	2.16	0.45
1:AA:1269:A:N1	1:AA:1312:G:O2'	2.32	0.45
22:DA:1499:C:H2'	22:DA:1500:G:H8	1.82	0.45
22:DA:1482:G:H1'	22:DA:1509:A:H61	1.81	0.45
37:DP:28:VAL:HG21	37:DP:74:PHE:CE2	2.52	0.45
23:BB:17:C:H2'	23:BB:18:G:O4'	2.15	0.45
16:CP:52:LEU:HD21	16:CP:57:ILE:HD12	1.99	0.45
1:CA:490:C:H2'	1:CA:491:G:C8	2.52	0.45
1:CA:183:C:O2'	1:CA:184:G:O5'	2.34	0.45
22:DA:1717:A:H2'	22:DA:1718:G:O4'	2.16	0.45
22:BA:2872:A:O2'	22:BA:2873:A:H5'	2.17	0.45
22:BA:1013:C:O2'	22:BA:1014:A:H5'	2.17	0.45
7:CG:111:ARG:CZ	7:CG:122:ASN:HB3	2.47	0.45
47:DZ:51:VAL:O	47:DZ:55:VAL:HG22	2.16	0.45
22:BA:1206:G:C6	22:BA:1207:C:C4	3.05	0.45
23:BB:61:G:H2'	23:BB:62:C:H6	1.80	0.45
22:DA:467:G:P	50:D2:33:ARG:HH11	2.40	0.45
22:BA:729:G:H2'	22:BA:1775:U:H1'	1.99	0.45
36:BO:28:VAL:HG11	36:BO:92:PHE:CZ	2.51	0.45
22:DA:1566:A:H5'	24:DC:214:ARG:CZ	2.46	0.45
48:D0:37:LYS:HG3	48:D0:37:LYS:H	1.59	0.45
22:DA:588:U:H1'	26:DE:85:PHE:CD1	2.51	0.45
1:CA:794:A:H2'	1:CA:795:C:C6	2.50	0.45
22:DA:780:G:H21	22:DA:783:A:H62	1.63	0.45
49:B1:34:LEU:H	49:B1:52:ALA:CB	2.19	0.45
22:DA:2267:A:H2	57:DA:3506:HOH:O	1.99	0.45
29:DH:31:VAL:CG1	29:DH:32:PRO:HD3	2.47	0.45
35:DN:55:ALA:HA	35:DN:80:PHE:CE1	2.52	0.45
22:DA:1198:U:O2	38:DQ:4:VAL:HG11	2.17	0.45
1:CA:1144:G:H5''	1:CA:1145:A:OP2	2.17	0.45
40:BS:82:MET:HG3	40:BS:98:LYS:HB2	1.97	0.45
22:DA:2845:U:H5''	37:DP:52:ASN:O	2.17	0.45
1:CA:337:G:H2'	1:CA:338:A:H8	1.80	0.45
36:DO:26:LEU:HB3	36:DO:92:PHE:CD1	2.50	0.45
3:CC:66:VAL:O	3:CC:101:ILE:HG13	2.16	0.45
22:BA:323:C:H6	22:BA:1205:A:N1	2.14	0.45
9:CI:120:LYS:HG2	9:CI:123:ARG:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:664:G:P	18:CR:53:ARG:HH21	2.40	0.45
22:BA:152:A:H2'	22:BA:153:U:C6	2.52	0.45
22:BA:1903:G:H2'	22:BA:1904:G:H8	1.81	0.45
30:BI:7:ALA:HB2	30:BI:61:VAL:HB	1.99	0.45
22:DA:846:U:H1'	22:DA:847:U:C5	2.52	0.45
24:BC:157:SER:O	24:BC:195:VAL:HG11	2.17	0.45
1:CA:1119:C:OP1	9:CI:11:ARG:NH2	2.50	0.45
41:BT:18:GLU:CD	41:BT:18:GLU:H	2.18	0.45
18:CR:73:ARG:HB2	18:CR:74:HIS:HD2	1.81	0.45
8:AH:109:GLY:O	8:AH:111:MET:HG3	2.17	0.45
25:BD:151:THR:HG22	25:BD:152:PRO:CD	2.47	0.45
1:AA:1479:C:H2'	1:AA:1480:A:O4'	2.17	0.45
38:BQ:110:VAL:HG12	38:BQ:114:LYS:HE2	1.99	0.45
3:AC:39:VAL:O	3:AC:43:LEU:HB2	2.17	0.45
34:DM:134:THR:HB	34:DM:135:VAL:H	1.68	0.45
40:BS:10:ALA:N	40:BS:101:SER:O	2.47	0.45
22:DA:722:A:H2'	22:DA:723:C:O4'	2.16	0.45
3:AC:71:ALA:HB2	3:AC:106:VAL:HB	1.98	0.45
1:AA:657:U:O2	15:AO:22:THR:HG23	2.16	0.45
1:AA:690:G:O6	11:AK:53:ARG:NH2	2.50	0.45
24:BC:121:ASP:OD1	24:BC:121:ASP:N	2.48	0.45
1:CA:892:A:O2'	1:CA:1415:G:H4'	2.16	0.45
22:BA:2508:G:O2'	22:BA:2554:U:O2'	2.35	0.45
26:DE:119:ILE:HB	26:DE:187:VAL:HG23	1.99	0.45
1:CA:238:A:O2'	1:CA:239:U:H5'	2.17	0.45
29:BH:76:GLU:HA	29:BH:142:VAL:CG1	2.46	0.45
22:BA:1061:U:O2'	22:BA:1062:G:O5'	2.34	0.45
22:BA:1069:A:O2'	22:BA:1070:A:H5''	2.16	0.45
1:AA:429:U:H4'	1:AA:430:A:OP1	2.17	0.45
1:AA:1123:U:O3'	10:AJ:38:GLY:HA3	2.17	0.45
26:BE:149:ILE:HG23	26:BE:188:MET:HG2	1.99	0.45
28:DG:125:CYS:SG	28:DG:131:ILE:HG12	2.57	0.45
18:CR:34:THR:OG1	18:CR:35:GLU:N	2.49	0.45
6:CF:3:HIS:CD2	6:CF:94:HIS:HA	2.52	0.45
9:AI:114:LYS:HE2	9:AI:119:ARG:O	2.17	0.45
13:AM:114:LYS:CB	13:AM:115:PRO:HD3	2.47	0.45
1:CA:32:A:C2	1:CA:33:A:C5	3.05	0.45
30:DI:72:LYS:HG3	30:DI:116:ASP:OD2	2.17	0.45
40:DS:33:LEU:HD21	40:DS:52:GLU:CG	2.47	0.45
22:BA:2203:U:H5''	22:BA:2204:G:OP1	2.17	0.45
32:BK:91:SER:OG	32:BK:93:GLN:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:40:THR:O	29:BH:42:LYS:N	2.48	0.45
29:BH:12:LEU:HG	29:BH:13:GLY:N	2.31	0.45
1:CA:1308:U:OP1	13:CM:97:VAL:N	2.37	0.45
1:CA:1308:U:OP2	13:CM:98:ARG:HG3	2.17	0.45
1:CA:790:A:H2'	1:CA:791:G:C8	2.52	0.45
22:DA:173:A:H2'	22:DA:174:U:C6	2.52	0.45
29:DH:5:LEU:CD1	29:DH:13:GLY:CA	2.95	0.45
22:DA:1924:C:H2'	22:DA:1925:C:O4'	2.17	0.45
40:DS:59:GLU:HA	40:DS:64:ALA:HA	1.99	0.45
32:DK:17:ARG:N	32:DK:45:GLU:O	2.43	0.45
22:DA:2551:C:H2'	22:DA:2552:U:C6	2.51	0.45
3:AC:42:TYR:OH	3:AC:90:VAL:HG21	2.17	0.45
28:BG:115:HIS:CD2	28:BG:148:LEU:HD21	2.52	0.45
31:DJ:38:GLY:O	31:DJ:44:TYR:HB2	2.17	0.45
22:DA:1462:C:C1'	22:DA:2702:G:H21	2.29	0.45
49:B1:10:LYS:O	49:B1:51:GLU:HG2	2.17	0.45
22:BA:2178:C:H2'	22:BA:2179:C:C6	2.52	0.45
29:DH:15:LEU:HD22	29:DH:15:LEU:N	2.32	0.45
22:DA:2672:U:H6	22:DA:2672:U:O5'	1.99	0.45
1:AA:518:C:H5	1:AA:530:G:OP2	2.00	0.45
36:BO:37:ALA:HB2	36:BO:106:LEU:HD11	1.99	0.45
22:BA:1060:U:OP2	30:BI:76:ALA:N	2.51	0.45
4:AD:13:ARG:HH12	4:AD:37:ALA:C	2.20	0.45
22:BA:1509:A:O2'	22:BA:1510:G:P	2.74	0.45
27:BF:4:LEU:HA	27:BF:4:LEU:HD23	1.87	0.45
22:BA:142:A:C5	22:BA:143:C:C4	3.05	0.45
22:DA:2262:U:H4'	22:DA:2328:A:C2	2.52	0.45
22:DA:2125:G:H5'	22:DA:2126:A:OP2	2.16	0.45
22:BA:281:C:H2'	22:BA:282:A:H8	1.78	0.45
3:CC:111:LEU:HD21	3:CC:144:LEU:O	2.16	0.45
11:AK:69:ARG:NH1	22:BA:2146:C:H42	2.13	0.45
22:DA:947:A:O2'	22:DA:984:A:H2	2.00	0.45
22:BA:2685:G:OP1	32:BK:78:ARG:NH2	2.49	0.45
5:AE:83:HIS:HE1	5:AE:147:MET:HG3	1.82	0.45
20:AT:18:ARG:HE	20:AT:18:ARG:HB3	1.67	0.45
22:BA:1440:U:H2'	22:BA:1441:G:C8	2.50	0.45
5:CE:111:MET:O	5:CE:115:LEU:HB2	2.17	0.45
22:DA:1654:A:P	35:DN:1:MET:HA	2.56	0.45
4:AD:156:LYS:HA	4:AD:156:LYS:HD3	1.77	0.45
22:BA:1998:A:OP2	25:BD:141:ARG:NH2	2.50	0.45
22:DA:53:A:C8	22:DA:54:G:C8	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:49:GLY:O	16:AP:50:THR:OG1	2.31	0.45
1:AA:224:U:H2'	1:AA:225:C:C6	2.52	0.45
25:BD:136:ASN:HD21	25:BD:139:SER:H	1.65	0.45
40:BS:20:VAL:HA	40:BS:23:LEU:HD12	1.99	0.45
3:AC:26:THR:HG23	14:AN:76:LYS:HD3	1.99	0.45
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.52	0.45
33:BL:36:LYS:O	33:BL:40:SER:HB3	2.17	0.45
22:BA:1392:A:C6	22:BA:1393:A:C6	3.05	0.45
22:DA:2662:A:H2'	22:DA:2663:G:O4'	2.17	0.45
1:CA:1486:G:H2'	1:CA:1487:G:O4'	2.16	0.45
38:DQ:86:ALA:HB3	38:DQ:88:VAL:HG23	1.99	0.45
3:CC:124:LEU:HA	3:CC:124:LEU:HD23	1.84	0.45
1:AA:708:C:H2'	1:AA:709:U:H6	1.82	0.45
22:DA:1806:C:H1'	24:DC:44:ASN:HD21	1.82	0.45
22:DA:2514:U:H2'	22:DA:2515:C:C6	2.52	0.45
22:DA:950:G:H2'	22:DA:951:C:O4'	2.17	0.45
1:AA:629:A:H2'	1:AA:630:A:H8	1.82	0.45
22:BA:2199:A:C4'	29:BH:28:ASN:ND2	2.80	0.44
26:DE:108:ILE:HD11	26:DE:180:LEU:CB	2.40	0.44
1:CA:1350:A:H2'	1:CA:1351:U:O4'	2.17	0.44
5:CE:157:ARG:HD3	5:CE:158:GLY:H	1.82	0.44
5:CE:81:LEU:CD2	5:CE:96:MET:HG3	2.48	0.44
29:DH:32:PRO:CB	45:DX:39:TRP:HB3	2.44	0.44
1:CA:1000:A:H2'	1:CA:1001:C:O4'	2.17	0.44
12:CL:14:ARG:HA	12:CL:14:ARG:HD2	1.71	0.44
22:DA:2170:A:H1'	22:DA:2171:A:C8	2.52	0.44
9:AI:114:LYS:NZ	9:AI:118:LEU:O	2.48	0.44
22:DA:2131:U:H1'	22:DA:2158:A:N6	2.31	0.44
7:AG:92:ARG:O	7:AG:96:ARG:HB2	2.17	0.44
22:DA:1224:U:C4	22:DA:1225:G:C6	3.05	0.44
12:CL:64:THR:HG23	12:CL:93:VAL:HG13	1.99	0.44
1:CA:1130:A:H5''	9:CI:64:TYR:HE1	1.82	0.44
10:AJ:52:LEU:HD21	10:AJ:59:LYS:HA	2.00	0.44
37:BP:71:GLU:OE1	37:BP:101:ARG:NE	2.36	0.44
1:AA:818:G:HO2'	1:AA:820:U:H6	1.63	0.44
22:BA:1586:A:H8	22:BA:1586:A:O5'	2.00	0.44
1:AA:1124:G:H3'	1:AA:1145:A:N6	2.32	0.44
22:DA:1182:G:H2'	22:DA:1183:U:O4'	2.16	0.44
22:BA:815:C:OP1	39:BR:85:LYS:NZ	2.50	0.44
22:DA:2339:C:H2'	22:DA:2340:A:C8	2.52	0.44
22:DA:753:A:H2'	22:DA:754:U:H6	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:741:G:H2'	1:AA:742:G:O4'	2.16	0.44
22:BA:610:C:H2'	22:BA:611:C:H6	1.82	0.44
22:BA:18:U:O3'	38:BQ:23:GLY:HA2	2.17	0.44
1:AA:761:G:H2'	1:AA:762:U:C6	2.51	0.44
42:DU:71:ALA:HB3	42:DU:80:ALA:HB1	1.99	0.44
22:BA:1754:A:H2'	22:BA:1755:A:C8	2.51	0.44
4:CD:150:LYS:O	4:CD:151:LYS:HG2	2.17	0.44
22:DA:2594:C:N4	22:DA:2595:G:O6	2.50	0.44
22:DA:2014:A:H5'	40:DS:94:ASP:OD1	2.17	0.44
1:CA:393:A:OP2	16:CP:12:LYS:HD2	2.17	0.44
1:AA:356:A:H2	1:AA:368:U:O2	2.00	0.44
22:DA:1:G:H2'	22:DA:2:G:H8	1.81	0.44
17:AQ:4:LYS:HG3	17:AQ:7:THR:HG22	1.98	0.44
22:BA:1176:U:H2'	22:BA:1177:G:C8	2.52	0.44
1:CA:1222:G:O6	57:CA:1861:HOH:O	2.21	0.44
1:CA:1515:G:H2'	1:CA:1516:G:C8	2.52	0.44
22:DA:1056:G:N1	22:DA:1102:C:OP2	2.50	0.44
22:DA:1105:U:H2'	22:DA:1106:G:C8	2.52	0.44
22:BA:1637:A:H4'	22:BA:2711:A:O2'	2.17	0.44
21:CU:12:PHE:HD1	21:CU:13:ASP:N	2.15	0.44
22:BA:2418:A:C6	22:BA:2419:U:C4	3.06	0.44
6:AF:44:ARG:HA	6:AF:58:HIS:HA	1.99	0.44
22:DA:828:U:O2'	22:DA:829:A:H5'	2.17	0.44
42:BU:74:ASN:O	42:BU:78:GLY:N	2.47	0.44
1:AA:11:G:C6	1:AA:12:U:C4	3.05	0.44
27:BF:105:THR:HG23	27:BF:106:ILE:HG23	1.98	0.44
2:AB:21:ARG:C	2:AB:23:TRP:H	2.09	0.44
11:AK:35:THR:HA	11:AK:41:ALA:HA	1.99	0.44
5:CE:153:VAL:O	5:CE:157:ARG:N	2.39	0.44
29:DH:1:MET:CE	29:DH:27:ARG:NH1	2.80	0.44
22:DA:1200:C:H2'	22:DA:1201:U:H6	1.81	0.44
22:BA:2065:C:H2'	22:BA:2066:C:C6	2.52	0.44
5:CE:137:VAL:O	5:CE:138:ARG:CB	2.64	0.44
22:DA:732:C:H2'	22:DA:733:G:O4'	2.17	0.44
22:DA:161:A:C3'	22:DA:162:U:H5''	2.43	0.44
22:DA:2897:U:H2'	22:DA:2898:U:C6	2.52	0.44
39:BR:25:LEU:H	39:BR:94:THR:HG23	1.81	0.44
21:CU:29:LEU:O	21:CU:33:ARG:N	2.50	0.44
22:BA:580:U:O3'	38:BQ:31:VAL:HG13	2.16	0.44
7:AG:18:PHE:CZ	7:AG:58:GLU:HG2	2.50	0.44
2:AB:66:LYS:HE3	2:AB:159:ASP:OD2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2392:A:OP2	51:D3:31:HIS:CE1	2.69	0.44
14:AN:90:ARG:NH1	14:AN:92:GLU:HG3	2.32	0.44
1:CA:160:A:H2'	1:CA:161:A:O4'	2.17	0.44
22:DA:2690:U:C4	22:DA:2873:A:N1	2.85	0.44
1:CA:269:C:H2'	1:CA:270:A:C8	2.52	0.44
34:BM:43:ALA:O	34:BM:47:GLU:HB2	2.18	0.44
22:DA:327:G:H21	42:DU:68:SER:HB2	1.82	0.44
7:CG:13:LEU:CD1	7:CG:14:PRO:HD2	2.47	0.44
22:DA:1651:G:C6	22:DA:1652:A:C5	3.05	0.44
35:DN:8:ARG:HB3	35:DN:10:LEU:HG	1.98	0.44
22:BA:1374:G:H2'	22:BA:1375:U:O4'	2.17	0.44
1:AA:771:G:H2'	1:AA:772:U:H6	1.81	0.44
22:BA:2298:A:N6	22:BA:2318:G:H1'	2.32	0.44
6:CF:42:TRP:CZ2	6:CF:61:LEU:HB2	2.52	0.44
22:BA:605:G:H1'	22:BA:657:U:H1'	1.99	0.44
1:CA:206:C:H42	1:CA:213:G:H1	1.63	0.44
1:AA:555:U:H2'	1:AA:556:C:C6	2.52	0.44
22:DA:566:U:O2'	22:DA:809:G:OP2	2.26	0.44
22:DA:969:G:H2'	22:DA:970:U:C6	2.52	0.44
22:BA:1450:G:C6	22:BA:1451:C:N4	2.85	0.44
29:BH:57:LYS:CG	29:BH:58:LEU:N	2.81	0.44
7:AG:83:SER:HB2	7:AG:85:TYR:CD2	2.52	0.44
1:AA:1484:C:H2'	1:AA:1485:U:O4'	2.17	0.44
3:CC:19:ASN:HA	3:CC:56:VAL:HG13	1.99	0.44
22:DA:928:A:H5'	47:DZ:39:GLU:OE1	2.17	0.44
23:DB:5:U:H2'	23:DB:6:G:C8	2.53	0.44
22:BA:714:U:O2	22:BA:717:C:H5	1.99	0.44
22:BA:1072:C:N4	22:BA:1093:G:H1	2.15	0.44
30:BI:76:ALA:HB1	30:BI:129:ILE:HG23	2.00	0.44
22:BA:585:G:H5''	22:BA:586:A:OP1	2.17	0.44
18:CR:24:LYS:O	18:CR:26:ILE:N	2.42	0.44
22:DA:445:C:O2'	22:DA:449:A:N3	2.47	0.44
22:BA:423:A:H5''	22:BA:424:G:C5'	2.48	0.44
2:AB:113:ARG:O	2:AB:117:LEU:HB2	2.17	0.44
30:BI:106:LEU:HA	30:BI:109:ILE:HB	1.99	0.44
6:CF:3:HIS:H	6:CF:92:THR:HG23	1.82	0.44
22:DA:1408:G:H2'	22:DA:1409:U:C6	2.53	0.44
50:D2:39:ARG:HB2	50:D2:42:LEU:HD22	1.99	0.44
22:DA:7:G:H4'	31:DJ:15:TRP:CH2	2.53	0.44
53:B5:52:PRO:HB2	53:B5:205:ALA:HB3	1.99	0.44
4:CD:29:ASP:O	4:CD:31:LYS:NZ	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:543:U:P	4:CD:14:ARG:HH21	2.39	0.44
22:DA:2819:G:H2'	22:DA:2821:A:N7	2.32	0.44
2:AB:118:GLU:HA	2:AB:121:SER:HB2	1.99	0.44
1:CA:1492:A:H8	1:CA:1492:A:OP2	2.00	0.44
29:DH:37:VAL:HG22	29:DH:38:PRO:HD2	1.98	0.44
1:CA:580:C:H2'	1:CA:581:G:O4'	2.17	0.44
22:BA:7:G:H2'	22:BA:8:C:H6	1.82	0.44
14:CN:16:LEU:HA	14:CN:19:LYS:HE2	1.99	0.44
39:DR:39:LEU:HG	39:DR:49:ILE:HD13	1.99	0.44
1:AA:39:G:H2'	1:AA:40:C:C6	2.52	0.44
22:BA:2056:G:C2	22:BA:2057:G:C8	3.05	0.44
1:CA:1481:U:H2'	1:CA:1482:G:C8	2.52	0.44
4:AD:170:TRP:CD2	4:AD:186:PRO:HG3	2.52	0.44
1:AA:393:A:H5'	1:AA:483:C:O2'	2.18	0.44
1:CA:19:A:H2'	1:CA:20:U:C6	2.52	0.44
22:DA:244:A:H5''	33:DL:67:THR:HG21	1.98	0.44
22:DA:301:G:C2	22:DA:302:C:C2	3.05	0.44
1:AA:276:G:O3'	17:AQ:45:HIS:CE1	2.70	0.44
47:DZ:47:MET:O	47:DZ:51:VAL:HG22	2.17	0.44
1:CA:513:C:H2'	1:CA:514:C:C6	2.52	0.44
22:DA:787:C:OP1	57:DA:3753:HOH:O	2.21	0.44
5:AE:74:VAL:HG11	5:AE:144:LEU:HB3	2.00	0.44
5:CE:133:PRO:O	5:CE:135:ASN:N	2.49	0.44
22:BA:2774:C:H2'	22:BA:2775:G:O4'	2.16	0.44
22:DA:2297:A:N1	22:DA:2321:U:C5	2.85	0.44
22:BA:2415:G:H2'	22:BA:2416:C:C6	2.53	0.44
22:DA:187:G:C2	22:DA:210:C:C2	3.06	0.44
4:AD:51:TYR:CE2	4:AD:55:LEU:HD12	2.51	0.44
22:DA:2323:G:O2'	22:DA:2324:U:H5'	2.17	0.44
22:DA:677:A:O2'	22:DA:2071:A:H5'	2.18	0.44
35:BN:65:LEU:HD11	35:BN:69:ARG:NH2	2.33	0.44
22:BA:15:G:C6	22:BA:16:C:C4	3.04	0.44
25:DD:33:ARG:NH1	25:DD:53:GLY:O	2.50	0.44
6:CF:13:ASP:C	6:CF:15:SER:H	2.19	0.44
22:DA:1073:A:O2'	22:DA:2474:U:H5'	2.17	0.44
14:CN:41:ARG:HG2	14:CN:42:TRP:N	2.31	0.44
1:AA:374:A:C5'	1:AA:452:A:H2	2.31	0.44
13:CM:4:ILE:O	13:CM:6:GLY:N	2.50	0.44
2:AB:134:ALA:O	2:AB:138:THR:HG23	2.18	0.44
22:DA:2683:C:H4'	25:DD:13:ARG:NH1	2.33	0.44
11:CK:92:GLY:O	11:CK:94:GLU:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:203:G:N2	1:CA:215:C:C2	2.86	0.44
13:AM:29:ARG:O	13:AM:33:ILE:HG12	2.17	0.44
7:AG:68:ASN:O	7:AG:70:ARG:N	2.47	0.44
22:DA:2395:C:H42	22:DA:2421:G:H1	1.63	0.44
1:AA:36:C:OP1	12:AL:120:LYS:HE3	2.17	0.44
10:CJ:59:LYS:O	10:CJ:62:ARG:HD2	2.18	0.44
9:AI:51:PRO:HB3	9:AI:84:THR:HG23	1.98	0.44
31:BJ:59:ALA:C	31:BJ:61:LYS:H	2.21	0.44
3:CC:43:LEU:HD21	3:CC:68:ILE:HD11	1.99	0.44
22:DA:686:U:H2'	22:DA:788:A:N1	2.33	0.44
22:BA:2673:G:C2	22:BA:2674:G:C8	3.06	0.44
24:BC:71:LYS:NZ	24:BC:98:ASP:OD2	2.50	0.44
22:DA:547:A:H3'	22:DA:548:G:C5'	2.46	0.44
22:DA:432:A:H2'	22:DA:433:C:O4'	2.18	0.44
22:DA:931:U:H4'	22:DA:932:U:OP2	2.17	0.44
29:DH:25:TYR:O	29:DH:29:PHE:HB3	2.18	0.44
22:BA:1812:U:H2'	22:BA:1813:G:C8	2.52	0.44
1:CA:1133:G:C2	1:CA:1142:G:C2	3.05	0.44
22:BA:2207:C:H2'	22:BA:2208:C:H6	1.81	0.44
5:AE:57:PRO:O	5:AE:61:GLN:HB2	2.17	0.44
4:AD:157:ALA:O	4:AD:160:GLU:HB3	2.17	0.44
22:BA:1360:G:C6	22:BA:1372:U:C2	3.06	0.44
22:BA:355:U:H2'	22:BA:356:G:H8	1.82	0.44
30:BI:19:ASN:ND2	30:BI:35:ILE:O	2.47	0.44
3:CC:135:LYS:HG2	3:CC:139:GLN:OE1	2.17	0.44
1:AA:43:C:H2'	1:AA:44:A:O4'	2.18	0.44
4:AD:15:GLU:HG3	4:AD:19:LEU:HD11	1.98	0.44
16:CP:2:VAL:HG23	16:CP:65:ALA:HA	2.00	0.44
1:CA:1271:A:H2'	1:CA:1272:G:C8	2.52	0.44
22:BA:2229:U:O2	45:BX:34:HIS:HE1	1.99	0.44
1:CA:62:U:O2'	1:CA:379:C:O2	2.34	0.44
25:BD:28:GLU:OE2	25:BD:30:GLU:HG3	2.18	0.44
1:AA:414:A:H2'	1:AA:415:A:H8	1.81	0.44
28:BG:11:VAL:HA	28:BG:12:PRO:HD3	1.73	0.44
1:CA:800:G:H8	1:CA:800:G:O5'	2.00	0.44
11:CK:14:LYS:HD2	11:CK:14:LYS:C	2.38	0.44
25:DD:112:THR:O	25:DD:195:GLY:HA2	2.17	0.44
22:BA:1696:G:C6	22:BA:1697:G:C4	3.06	0.44
2:CB:130:THR:HB	2:CB:132:LYS:HB3	1.99	0.44
1:AA:49:U:O4	1:AA:365:U:H5	1.99	0.44
22:DA:1313:U:H4'	22:DA:1332:G:H4'	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:91:PHE:HE1	1:CA:54:C:O2	2.00	0.44
29:BH:97:ARG:O	29:BH:101:ASP:HB2	2.17	0.44
22:DA:1380:G:H21	22:DA:1570:A:H2	1.65	0.44
4:AD:58:LYS:HG3	4:AD:59:GLN:N	2.32	0.44
7:AG:146:GLU:CG	7:AG:149:LYS:HE2	2.46	0.44
23:DB:48:U:H4'	36:DO:100:HIS:NE2	2.32	0.44
22:DA:2292:U:H2'	22:DA:2293:G:C8	2.53	0.44
1:AA:1029:U:O2	1:AA:1032:G:N2	2.44	0.44
1:CA:982:U:H4'	1:CA:983:A:H5'	1.99	0.44
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.33	0.44
10:AJ:51:VAL:O	10:AJ:62:ARG:HA	2.18	0.44
22:BA:2607:G:H2'	22:BA:2608:G:O4'	2.16	0.44
25:BD:47:ALA:HA	25:BD:84:LEU:N	2.33	0.44
1:AA:382:A:H2'	1:AA:383:A:C8	2.53	0.44
1:AA:592:G:C6	1:AA:648:A:C6	3.05	0.44
5:AE:115:LEU:HG	5:AE:120:VAL:HG21	1.99	0.44
22:BA:1414:C:C4	22:BA:1415:U:C5	3.06	0.44
1:AA:1251:A:H2'	1:AA:1252:A:O4'	2.17	0.44
4:CD:145:ILE:HG21	4:CD:150:LYS:HA	2.00	0.44
8:CH:86:TYR:CE2	8:CH:124:GLU:HB2	2.53	0.44
22:BA:747:U:C5	22:BA:2613:U:C5	3.06	0.44
22:DA:380:G:HO2'	45:DX:29:PHE:HE1	1.65	0.44
22:DA:396:G:H1'	45:DX:29:PHE:HB3	1.99	0.44
17:AQ:4:LYS:HG3	17:AQ:7:THR:CG2	2.48	0.44
9:CI:107:ASP:OD2	9:CI:109:ARG:HG3	2.18	0.44
22:BA:570:G:H2'	22:BA:2030:A:C8	2.53	0.44
32:DK:88:ASN:HB3	32:DK:92:GLU:O	2.17	0.44
3:AC:24:ALA:HB1	3:AC:28:GLU:HG2	1.99	0.44
21:AU:25:LYS:HD2	21:AU:26:ALA:N	2.32	0.44
22:DA:1609:A:H5''	57:DA:3642:HOH:O	2.18	0.44
40:BS:41:LYS:HD2	48:B0:22:LEU:HD11	1.98	0.44
25:BD:106:LYS:HA	25:BD:175:LEU:O	2.18	0.44
1:CA:1450:U:O2'	1:CA:1451:U:H2'	2.18	0.44
40:DS:10:ALA:O	40:DS:12:SER:N	2.49	0.44
22:BA:578:G:C5	22:BA:2018:G:H5'	2.53	0.44
4:AD:114:ALA:O	4:AD:117:LEU:HB2	2.17	0.44
47:BZ:45:ARG:HD3	47:BZ:45:ARG:HA	1.65	0.44
15:CO:17:ARG:CZ	15:CO:24:SER:HB2	2.48	0.44
22:BA:2282:G:H4'	22:BA:2389:G:O2'	2.17	0.44
22:BA:340:A:H2'	22:BA:341:C:O4'	2.17	0.44
1:CA:36:C:OP1	12:CL:120:LYS:HE3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:100:ALA:HB2	29:BH:115:VAL:HG21	1.98	0.44
29:BH:89:LYS:CE	29:BH:124:THR:HG22	2.48	0.44
2:AB:23:TRP:HB3	2:AB:39:HIS:CE1	2.52	0.44
22:DA:1647:U:H3'	22:DA:1647:U:OP2	2.18	0.44
1:AA:1157:A:C6	1:AA:1180:A:C5	3.06	0.44
1:AA:1182:G:C4'	1:AA:1183:U:H5'	2.45	0.44
1:AA:1517:G:N3	22:BA:1919:A:O2'	2.26	0.44
1:AA:971:G:C8	1:AA:1365:G:H4'	2.53	0.44
1:CA:822:U:H2'	1:CA:823:C:C6	2.53	0.44
2:AB:181:ILE:O	2:AB:183:VAL:HG23	2.17	0.44
1:AA:1367:C:P	9:AI:114:LYS:HZ1	2.39	0.44
1:AA:1329:A:OP1	13:AM:29:ARG:HB2	2.18	0.44
22:BA:726:G:HO2'	22:BA:727:A:P	2.39	0.44
25:DD:151:THR:HG22	25:DD:152:PRO:CD	2.48	0.44
4:CD:168:PRO:HB3	4:CD:170:TRP:CH2	2.52	0.44
26:DE:69:ARG:HG3	26:DE:69:ARG:H	1.47	0.44
29:BH:31:VAL:N	29:BH:32:PRO:CD	2.80	0.44
38:DQ:50:ARG:HH22	39:DR:74:ILE:HA	1.83	0.44
20:AT:4:ILE:HA	20:AT:8:LYS:HZ2	1.82	0.44
17:AQ:52:GLU:N	17:AQ:52:GLU:OE1	2.34	0.44
22:BA:747:U:O2	22:BA:2014:A:H1'	2.17	0.44
22:BA:299:A:OP2	22:BA:299:A:H8	2.00	0.44
22:DA:443:A:C8	26:DE:40:ARG:HD3	2.53	0.44
53:B5:59:VAL:HG12	53:B5:63:VAL:HG21	2.00	0.44
22:BA:2077:A:H2'	22:BA:2078:C:H6	1.83	0.44
22:DA:2722:G:H2'	22:DA:2723:C:C6	2.52	0.44
8:CH:21:ASN:O	8:CH:23:ALA:N	2.51	0.44
22:BA:2710:C:OP1	57:BA:3553:HOH:O	2.21	0.44
27:DF:48:LYS:O	27:DF:51:ASP:HB2	2.18	0.44
22:DA:2283:C:H2'	22:DA:2284:A:O4'	2.18	0.44
24:BC:171:TYR:HA	24:BC:185:GLU:HA	1.99	0.44
15:AO:10:LYS:O	15:AO:14:GLU:HG3	2.18	0.44
22:DA:576:U:H2'	22:DA:577:G:C8	2.52	0.44
22:BA:2527:C:H5''	52:B4:31:PRO:HB3	2.00	0.44
31:BJ:99:ARG:HD2	31:BJ:99:ARG:HA	1.77	0.44
3:AC:157:LEU:H	3:AC:157:LEU:HG	1.60	0.44
11:CK:116:ILE:HD12	21:CU:28:VAL:HG23	2.00	0.44
15:AO:32:LEU:HA	15:AO:32:LEU:HD23	1.72	0.44
22:BA:929:U:H1'	47:BZ:26:GLY:O	2.17	0.44
22:BA:1157:G:N2	22:BA:1158:C:C2	2.86	0.44
27:BF:38:MET:SD	27:BF:53:ALA:HB1	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1333:A:C2	1:AA:1334:G:H1'	2.53	0.44
29:BH:99:ILE:CD1	29:BH:117:LEU:HD13	2.48	0.44
9:CI:13:LYS:N	9:CI:106:ARG:HH12	1.99	0.44
1:AA:831:A:OP1	2:AB:21:ARG:HG3	2.17	0.44
2:AB:19:GLN:O	2:AB:38:VAL:HG23	2.17	0.44
30:BI:84:ALA:HB1	30:BI:101:ILE:HD12	1.99	0.44
22:BA:2243:U:H2'	22:BA:2244:U:C6	2.53	0.44
22:BA:1570:A:H2'	22:BA:1571:A:C8	2.52	0.44
1:AA:937:A:N1	7:AG:2:PRO:HG2	2.32	0.44
10:AJ:42:LEU:HB3	10:AJ:71:LEU:HB3	1.99	0.44
43:DV:30:ILE:HD11	43:DV:63:ILE:HD12	1.99	0.44
43:DV:7:GLU:HB2	43:DV:41:GLU:OE2	2.18	0.44
22:DA:2060:A:H62	26:DE:69:ARG:HH12	1.64	0.44
22:DA:830:G:H22	22:DA:2446:G:C5'	2.31	0.44
2:CB:166:ALA:HB2	2:CB:187:VAL:HG12	1.99	0.44
1:AA:666:G:C5	1:AA:741:G:C6	3.05	0.44
28:DG:137:ASP:HB3	28:DG:140:VAL:HG23	2.00	0.44
3:CC:129:MET:HB2	3:CC:132:ARG:HG3	2.00	0.44
22:BA:17:G:H2'	22:BA:18:U:C6	2.53	0.44
1:CA:952:U:H2'	1:CA:953:G:H8	1.82	0.44
1:AA:1250:A:H2'	1:AA:1251:A:C8	2.53	0.44
45:DX:51:VAL:HG21	45:DX:56:MET:HG3	2.00	0.44
8:AH:75:ILE:HD13	8:AH:129:VAL:HG22	1.99	0.44
1:AA:1211:U:HO2'	1:AA:1212:U:P	2.41	0.44
22:DA:129:C:H2'	22:DA:130:C:C6	2.53	0.44
22:BA:2868:A:H2'	22:BA:2869:G:C8	2.53	0.44
21:CU:8:GLU:HB3	21:CU:12:PHE:CE2	2.53	0.44
29:BH:57:LYS:HG3	29:BH:58:LEU:N	2.33	0.44
4:AD:51:TYR:CZ	4:AD:55:LEU:HD12	2.52	0.44
3:AC:165:THR:O	3:AC:166:GLU:HB2	2.18	0.44
28:BG:5:ALA:HB2	28:BG:66:GLY:HA2	2.00	0.44
22:BA:2102:G:H5'	22:BA:2103:C:OP2	2.18	0.44
22:DA:2728:U:HO2'	22:DA:2729:G:H8	1.65	0.44
22:DA:954:G:O2'	22:DA:2274:A:N1	2.36	0.44
34:DM:35:ALA:HB1	34:DM:126:ILE:HD11	1.99	0.44
22:BA:2883:A:OP2	48:B0:50:ARG:NH1	2.51	0.44
12:CL:28:PRO:HB2	12:CL:29:GLN:OE1	2.18	0.44
22:BA:1496:A:N3	22:BA:1577:C:O2'	2.36	0.44
40:BS:97:LEU:HD12	40:BS:97:LEU:HA	1.82	0.44
5:CE:126:LYS:HE2	5:CE:126:LYS:HA	1.98	0.44
29:BH:62:LEU:O	29:BH:62:LEU:HD12	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1137:C:H1'	1:CA:1138:G:N2	2.33	0.44
5:CE:104:GLY:HA3	5:CE:122:ASN:HA	1.99	0.44
10:CJ:38:GLY:HA2	10:CJ:39:PRO:HD2	1.82	0.44
22:DA:2507:C:H5'	22:DA:2573:C:N4	2.33	0.44
22:BA:2898:U:H2'	22:BA:2899:A:C8	2.53	0.44
26:DE:59:PRO:HG2	26:DE:70:SER:HB2	1.99	0.44
31:DJ:40:HIS:CE1	31:DJ:41:LYS:HG3	2.53	0.44
28:BG:124:GLU:CD	28:BG:125:CYS:N	2.69	0.44
9:CI:57:MET:O	9:CI:60:LYS:N	2.51	0.44
29:BH:4:ILE:HG23	29:BH:17:ASP:O	2.17	0.44
22:DA:777:G:N7	22:DA:793:A:C2	2.83	0.44
22:DA:2135:A:C2	22:DA:2136:G:H1'	2.53	0.44
2:AB:108:ARG:O	2:AB:111:ILE:HB	2.18	0.44
16:CP:38:PHE:CE2	16:CP:51:ARG:HB3	2.53	0.44
28:DG:64:GLN:O	28:DG:67:THR:OG1	2.36	0.44
10:AJ:42:LEU:HA	10:AJ:43:PRO:HD2	1.73	0.44
46:DY:31:GLN:OE1	46:DY:37:LEU:HD12	2.17	0.44
22:DA:190:A:OP2	45:DX:26:LYS:NZ	2.50	0.44
2:CB:82:ASP:N	2:CB:85:LEU:HB3	2.32	0.44
3:AC:155:GLY:O	3:AC:196:ILE:HG12	2.17	0.44
22:DA:27:G:C2	22:DA:512:G:N3	2.86	0.44
29:DH:127:GLU:CG	29:DH:144:VAL:O	2.65	0.44
22:DA:1526:C:H2'	22:DA:1527:G:O4'	2.17	0.44
1:CA:298:A:H2'	1:CA:299:G:O4'	2.18	0.44
24:DC:240:PHE:HB3	24:DC:241:GLY:H	1.64	0.44
22:DA:2104:C:H2'	22:DA:2105:U:O4'	2.18	0.44
1:AA:276:G:OP1	17:AQ:17:MET:HE2	2.17	0.44
22:DA:68:G:H2'	22:DA:69:C:O4'	2.18	0.44
22:BA:255:A:C6	22:BA:256:A:C5	3.06	0.44
40:DS:28:LYS:HA	40:DS:70:LYS:HG3	1.99	0.44
22:BA:2190:G:H3'	22:BA:2191:A:H8	1.82	0.44
22:DA:291:G:H1	22:DA:349:U:H3	1.66	0.44
22:DA:2354:C:O2'	44:DW:35:SER:HA	2.18	0.44
9:AI:34:SER:HB3	9:AI:37:GLN:HB2	2.00	0.44
3:AC:26:THR:HG23	14:AN:76:LYS:HZ2	1.82	0.44
7:AG:76:LYS:HB3	7:AG:89:VAL:HG11	1.98	0.44
28:BG:94:TYR:HA	28:BG:106:SER:O	2.18	0.44
1:AA:924:C:H2'	1:AA:925:G:C8	2.53	0.44
1:AA:925:G:C2	1:AA:927:G:C8	3.06	0.44
1:CA:765:G:C6	1:CA:812:G:C4	3.06	0.44
9:CI:49:ARG:HH21	9:CI:53:GLU:HA	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2006:C:O5'	22:DA:2006:C:H6	2.01	0.44
10:AJ:35:GLN:HG2	10:AJ:77:VAL:HB	2.00	0.44
12:AL:50:ARG:HG3	12:AL:90:LEU:HD11	1.98	0.44
22:DA:839:U:H2'	22:DA:840:C:C6	2.53	0.44
1:CA:115:G:H4'	1:CA:116:A:O5'	2.18	0.44
27:DF:4:LEU:H	27:DF:4:LEU:HG	1.40	0.44
1:CA:1028:C:H2'	1:CA:1028:C:O2	2.17	0.44
1:AA:626:G:C6	1:AA:627:G:C5	3.06	0.44
22:DA:77:G:OP1	46:DY:52:ARG:HD3	2.18	0.44
4:CD:19:LEU:HD22	4:CD:64:ILE:HG13	2.00	0.44
17:AQ:59:VAL:HG23	17:AQ:77:ARG:O	2.17	0.44
22:BA:1073:A:OP1	22:BA:1073:A:C8	2.71	0.44
9:CI:13:LYS:H	9:CI:106:ARG:NH1	2.00	0.44
1:CA:1371:G:OP2	9:CI:13:LYS:HD3	2.18	0.44
22:BA:1105:U:H2'	22:BA:1106:G:H8	1.83	0.44
6:AF:92:THR:O	6:AF:93:LYS:HG2	2.17	0.44
12:AL:22:PRO:C	12:AL:24:LEU:N	2.72	0.44
1:AA:452:A:H1'	16:AP:70:ARG:NH1	2.33	0.44
28:DG:129:THR:C	28:DG:130:GLU:HG2	2.37	0.44
35:DN:115:LEU:H	35:DN:115:LEU:HG	1.67	0.44
22:DA:1171:G:N3	22:DA:1179:G:N1	2.65	0.44
10:CJ:48:ARG:HG3	10:CJ:48:ARG:HH11	1.82	0.44
23:DB:49:C:H2'	23:DB:50:A:H8	1.83	0.44
9:CI:57:MET:N	9:CI:57:MET:SD	2.91	0.44
21:AU:4:ILE:CA	21:AU:20:LYS:HE3	2.44	0.44
9:AI:36:GLU:HA	9:AI:40:GLY:HA3	2.00	0.44
1:AA:79:G:N2	1:AA:91:U:O4	2.51	0.44
22:DA:1142:A:H4'	31:DJ:27:ARG:HH22	1.82	0.44
1:CA:747:A:H2'	1:CA:748:G:O4'	2.18	0.44
1:AA:955:U:O4'	1:AA:1227:A:N6	2.51	0.44
35:BN:32:GLU:OE1	35:BN:118:ARG:HA	2.18	0.44
22:DA:1336:A:H2'	22:DA:1337:G:H8	1.80	0.44
2:AB:66:LYS:HG2	2:AB:156:GLY:HA3	2.00	0.44
43:DV:72:VAL:HG12	43:DV:93:ARG:HA	2.00	0.44
36:DO:80:GLU:O	36:DO:84:GLU:HG3	2.18	0.44
2:AB:53:ALA:HB3	2:AB:54:LEU:HD22	2.00	0.44
22:BA:69:C:H2'	22:BA:70:G:C8	2.53	0.44
27:BF:56:ASP:O	27:BF:60:ILE:HG13	2.18	0.44
24:BC:98:ASP:N	24:BC:98:ASP:OD1	2.47	0.44
37:DP:51:ARG:HD3	37:DP:58:ALA:HB3	2.00	0.44
22:BA:1854:A:H2	22:BA:2087:G:N3	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:604:G:H2'	1:CA:605:U:O4'	2.18	0.44
22:BA:2070:A:C2	22:BA:2442:C:C2	3.06	0.44
6:CF:50:PRO:HD2	18:CR:74:HIS:ND1	2.33	0.44
47:BZ:31:ARG:HG3	47:BZ:32:ILE:O	2.18	0.44
49:D1:15:ALA:C	49:D1:17:THR:H	2.20	0.44
23:BB:52:A:N7	36:BO:64:TYR:OH	2.41	0.44
6:CF:41:ASP:OD2	6:CF:43:GLY:N	2.43	0.44
22:BA:1011:G:H1'	22:BA:1013:C:O4'	2.17	0.44
15:CO:27:VAL:O	15:CO:31:LEU:HD12	2.18	0.44
1:CA:154:U:O4	1:CA:155:A:N6	2.51	0.44
52:D4:1:MET:HB2	52:D4:34:LYS:HB3	2.00	0.44
25:DD:173:GLN:O	25:DD:175:LEU:N	2.51	0.44
22:BA:1366:A:C5	22:BA:1367:A:C8	3.06	0.44
1:AA:1293:C:H5'	1:AA:1294:G:OP2	2.18	0.44
12:AL:33:VAL:HG23	12:AL:56:ARG:HB3	2.00	0.44
13:CM:91:HIS:HA	13:CM:109:ARG:NH2	2.33	0.44
1:CA:179:A:H2'	1:CA:180:U:C6	2.53	0.44
3:CC:165:THR:O	3:CC:166:GLU:HB3	2.18	0.44
33:BL:49:GLY:O	33:BL:51:GLU:HG2	2.18	0.44
1:CA:68:G:C5	1:CA:69:G:H1'	2.53	0.44
24:BC:108:LYS:HD2	24:BC:194:GLU:OE1	2.17	0.44
1:CA:117:G:H2'	1:CA:118:U:O4'	2.18	0.44
22:BA:2348:U:O4	22:BA:2382:G:N1	2.51	0.44
1:AA:437:U:C2'	1:AA:438:U:H5'	2.48	0.44
27:DF:20:PHE:HB2	27:DF:22:TYR:CE2	2.53	0.44
29:BH:89:LYS:HE3	29:BH:124:THR:HG22	1.98	0.43
5:CE:155:ALA:HB1	8:CH:66:PHE:CE2	2.53	0.43
4:CD:100:ASN:O	4:CD:104:ARG:HG2	2.17	0.43
20:AT:28:MET:HE1	20:AT:67:ILE:HG12	2.00	0.43
20:AT:71:LYS:HD2	20:AT:74:ARG:NH2	2.33	0.43
21:CU:34:ARG:HH21	21:CU:35:ARG:HD2	1.83	0.43
3:AC:36:ASP:C	3:AC:38:LYS:H	2.22	0.43
1:AA:452:A:C8	1:AA:452:A:C3'	3.01	0.43
10:CJ:46:LYS:HB3	10:CJ:66:GLU:OE1	2.18	0.43
22:BA:1800:C:OP1	24:BC:258:ARG:NH2	2.51	0.43
12:CL:12:ARG:HH11	12:CL:12:ARG:HG3	1.83	0.43
8:AH:29:SER:OG	8:AH:30:SER:N	2.51	0.43
22:BA:2125:G:N2	22:BA:2173:A:H62	2.16	0.43
40:DS:73:LYS:CB	40:DS:106:VAL:HB	2.46	0.43
3:AC:130:PHE:O	3:AC:134:MET:HG3	2.18	0.43
40:BS:78:GLU:O	40:BS:102:HIS:HE1	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BC:62:TYR:HA	24:BC:86:ASN:HD21	1.83	0.43
24:DC:84:ASP:HB3	24:DC:87:ARG:HG2	2.00	0.43
27:BF:61:SER:HB2	27:BF:91:LEU:HD21	2.00	0.43
4:AD:75:TYR:OH	4:AD:97:ARG:NH1	2.48	0.43
22:DA:1652:A:H3'	22:DA:1653:G:C8	2.53	0.43
2:CB:134:ALA:O	2:CB:138:THR:HG23	2.17	0.43
22:DA:1911:U:H2'	22:DA:1918:A:N1	2.33	0.43
22:BA:1738:G:O2'	22:BA:1739:A:H8	2.01	0.43
22:DA:2597:G:H5''	24:DC:240:PHE:O	2.18	0.43
10:AJ:27:GLU:C	10:AJ:29:ALA:H	2.21	0.43
2:AB:102:THR:HB	2:AB:175:GLU:OE1	2.18	0.43
12:CL:102:LEU:HB3	12:CL:103:ASP:H	1.67	0.43
1:AA:540:G:H2'	1:AA:541:G:C8	2.53	0.43
39:BR:27:ILE:HG21	39:BR:33:VAL:HG12	2.00	0.43
31:DJ:93:ILE:HA	31:DJ:97:PRO:HB3	1.99	0.43
34:BM:34:LYS:HE2	34:BM:99:GLY:O	2.18	0.43
22:BA:2660:A:H2'	22:BA:2661:G:O4'	2.18	0.43
19:AS:48:THR:HG22	19:AS:61:PHE:HD1	1.82	0.43
22:BA:1635:A:C6	22:BA:1636:U:C2	3.05	0.43
38:BQ:58:ARG:HA	38:BQ:61:TRP:CE3	2.52	0.43
1:CA:533:A:O2'	1:CA:535:A:OP2	2.27	0.43
24:BC:269:ARG:HG2	24:BC:269:ARG:HH11	1.83	0.43
1:AA:1044:A:C5	1:AA:1045:C:H1'	2.53	0.43
2:AB:120:GLN:N	2:AB:123:ASP:HB2	2.33	0.43
22:BA:2258:C:O2'	22:BA:2427:C:OP2	2.30	0.43
22:BA:1406:U:O2'	22:BA:1407:G:O5'	2.31	0.43
22:DA:410:G:O5'	22:DA:410:G:H8	2.01	0.43
1:AA:440:C:H2'	1:AA:441:A:H8	1.83	0.43
1:CA:55:A:N7	1:CA:56:U:C4	2.85	0.43
30:DI:54:PRO:O	30:DI:75:PRO:HD2	2.18	0.43
22:DA:997:G:OP1	38:DQ:92:ARG:HG2	2.17	0.43
22:DA:1821:A:H5'	24:DC:157:SER:OG	2.16	0.43
1:AA:520:A:N1	1:AA:536:C:H1'	2.33	0.43
23:DB:42:C:H4'	27:DF:64:LYS:HE3	1.99	0.43
31:DJ:30:THR:HG22	31:DJ:31:GLU:N	2.32	0.43
11:CK:112:ASP:HB3	21:CU:4:ILE:CG2	2.48	0.43
22:BA:871:U:H2'	22:BA:872:U:C6	2.53	0.43
2:AB:81:LYS:HG2	2:AB:85:LEU:HD22	2.00	0.43
13:AM:11:ASP:OD1	13:AM:45:ILE:HB	2.18	0.43
1:AA:1005:A:H2'	1:AA:1006:G:O4'	2.19	0.43
1:CA:408:A:OP1	4:CD:110:THR:OG1	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:15:ASP:OD1	7:AG:18:PHE:HB2	2.18	0.43
43:DV:29:ILE:HG12	43:DV:38:LEU:O	2.18	0.43
22:BA:528:A:H2'	22:BA:529:A:H5''	2.00	0.43
6:CF:16:GLU:O	6:CF:18:VAL:N	2.51	0.43
1:CA:1072:G:C6	1:CA:1073:U:C4	3.06	0.43
49:D1:8:LYS:HG3	49:D1:24:THR:HG22	1.99	0.43
22:DA:2794:C:H2'	22:DA:2795:C:O4'	2.17	0.43
25:BD:32:ASN:HD22	25:BD:32:ASN:N	2.17	0.43
22:BA:2318:G:C6	22:BA:2319:G:N1	2.86	0.43
22:DA:1092:C:H3'	22:DA:1093:G:H8	1.83	0.43
22:DA:2369:A:N6	22:DA:2382:G:O6	2.51	0.43
2:CB:91:PHE:O	2:CB:150:GLY:HA3	2.17	0.43
1:CA:667:G:H4'	15:CO:51:HIS:ND1	2.33	0.43
49:B1:17:THR:HG21	49:B1:42:VAL:HB	1.99	0.43
9:CI:87:LEU:C	9:CI:89:GLU:H	2.22	0.43
22:BA:2472:G:H2'	22:BA:2475:C:H42	1.84	0.43
7:AG:107:ALA:HB1	7:AG:133:THR:HB	2.00	0.43
2:AB:139:ARG:O	2:AB:143:LYS:HB2	2.18	0.43
22:BA:2097:A:C2	22:BA:2193:G:C6	3.06	0.43
22:BA:1113:U:H2'	22:BA:1114:C:C6	2.53	0.43
13:AM:54:ASP:HA	13:AM:57:ARG:HB2	2.00	0.43
22:DA:1491:G:C6	22:DA:1500:G:C2	3.06	0.43
45:BX:71:LEU:O	45:BX:76:GLU:HB2	2.19	0.43
22:DA:2196:C:O2'	22:DA:2197:U:H5'	2.18	0.43
41:BT:34:VAL:HG21	41:BT:43:ILE:HD11	2.00	0.43
1:CA:731:G:H5'	1:CA:766:A:H4'	1.99	0.43
28:BG:137:ASP:HB3	28:BG:140:VAL:HB	2.00	0.43
20:CT:28:MET:O	20:CT:32:ILE:HG13	2.18	0.43
48:B0:54:VAL:HG23	48:B0:55:ILE:HG12	1.99	0.43
22:BA:2420:C:H5''	49:B1:8:LYS:HE3	2.00	0.43
41:BT:64:LYS:HA	41:BT:79:ASP:OD1	2.19	0.43
30:DI:10:LYS:HB3	30:DI:56:PRO:HB2	1.99	0.43
14:AN:21:PHE:CE1	14:AN:51:LEU:HD12	2.53	0.43
1:CA:855:U:H2'	1:CA:856:C:C6	2.53	0.43
30:DI:76:ALA:HA	30:DI:79:LEU:HB2	2.00	0.43
1:AA:213:G:H8	1:AA:213:G:O5'	2.00	0.43
32:DK:9:ASN:HB2	32:DK:83:ALA:HB2	2.00	0.43
22:BA:2725:A:C4	22:BA:2727:A:C8	3.06	0.43
31:DJ:110:PRO:O	31:DJ:115:GLY:HA3	2.18	0.43
31:BJ:17:VAL:HG23	31:BJ:55:ILE:HD12	2.00	0.43
29:BH:80:ILE:HG21	29:BH:94:ILE:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:27:ARG:O	29:BH:28:ASN:CB	2.66	0.43
2:CB:102:THR:HA	2:CB:179:LEU:HD21	1.99	0.43
22:DA:1370:C:H2'	22:DA:1371:G:C8	2.53	0.43
10:CJ:77:VAL:O	10:CJ:79:PRO:HD3	2.18	0.43
22:DA:2261:C:H1'	22:DA:2388:A:N3	2.33	0.43
2:AB:41:ILE:HG21	2:AB:202:GLY:CA	2.45	0.43
29:DH:31:VAL:CB	29:DH:32:PRO:HD3	2.47	0.43
8:CH:11:LEU:HD22	8:CH:75:ILE:HD11	1.99	0.43
31:DJ:35:ARG:HG2	31:DJ:40:HIS:CD2	2.54	0.43
19:CS:15:LEU:HD22	19:CS:35:SER:HB3	2.01	0.43
11:CK:58:SER:O	11:CK:91:PRO:HG3	2.17	0.43
22:BA:1306:C:H41	22:BA:1606:C:H2'	1.83	0.43
1:CA:97:G:H2'	1:CA:98:A:O4'	2.18	0.43
1:CA:409:U:H2'	1:CA:410:G:O4'	2.18	0.43
22:DA:188:G:HO2'	22:DA:1365:A:N6	2.17	0.43
22:DA:1786:A:H1'	22:DA:1938:A:N6	2.33	0.43
28:BG:72:LEU:HA	28:BG:75:MET:HB2	1.99	0.43
1:AA:1307:U:H2'	1:AA:1308:U:H6	1.82	0.43
14:CN:79:LEU:HB3	14:CN:80:SER:H	1.62	0.43
22:DA:1795:C:C4	22:DA:1796:U:C4	3.07	0.43
22:DA:532:A:H1'	22:DA:2021:C:N4	2.33	0.43
22:DA:1552:A:N6	57:DA:3627:HOH:O	2.39	0.43
8:AH:47:GLU:HG2	8:AH:64:LYS:HG2	2.00	0.43
1:AA:238:A:H2'	1:AA:239:U:O4'	2.18	0.43
1:AA:920:U:H2'	1:AA:921:U:C6	2.53	0.43
22:BA:1850:G:C5	22:BA:1851:U:C4	3.07	0.43
24:DC:82:GLU:OE1	24:DC:103:TYR:OH	2.31	0.43
3:CC:164:ARG:NH1	3:CC:166:GLU:OE1	2.51	0.43
5:AE:90:THR:HG22	5:AE:91:GLY:N	2.34	0.43
22:BA:566:U:O2'	22:BA:809:G:OP2	2.25	0.43
1:AA:1463:U:H2'	1:AA:1464:U:C6	2.53	0.43
1:AA:649:A:H2'	1:AA:650:G:O4'	2.18	0.43
10:AJ:101:SER:HB2	10:AJ:102:LEU:H	1.61	0.43
20:CT:60:ARG:O	20:CT:64:LYS:HB2	2.18	0.43
1:AA:585:G:OP1	17:AQ:39:LYS:HE3	2.18	0.43
22:DA:2576:G:O2'	22:DA:2579:C:OP2	2.26	0.43
22:BA:1665:A:H5''	32:BK:66:LYS:HB3	2.00	0.43
22:BA:1956:U:H2'	22:BA:1957:C:H5'	2.00	0.43
22:BA:959:A:N3	22:BA:2457:U:O2'	2.42	0.43
37:BP:6:LYS:HD2	37:BP:6:LYS:HA	1.80	0.43
39:DR:82:HIS:CG	39:DR:82:HIS:O	2.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:746:A:O5'	1:AA:746:A:H8	2.00	0.43
22:BA:2360:G:OP1	51:B3:51:SER:OG	2.36	0.43
1:AA:1437:A:H2'	1:AA:1438:G:H8	1.83	0.43
22:BA:2728:U:O2'	22:BA:2729:G:OP2	2.36	0.43
37:BP:30:VAL:HG13	37:BP:80:VAL:HG12	1.99	0.43
1:CA:134:G:H2'	1:CA:135:C:O4'	2.18	0.43
22:BA:2555:U:C5	22:BA:2556:C:C2	3.06	0.43
17:CQ:14:SER:C	17:CQ:17:MET:HE1	2.38	0.43
3:CC:122:SER:HA	3:CC:125:GLU:OE2	2.17	0.43
42:BU:87:PHE:CZ	42:BU:92:LYS:HG3	2.53	0.43
24:BC:141:VAL:CG1	24:BC:190:ALA:HB1	2.48	0.43
29:BH:96:THR:O	29:BH:100:ALA:N	2.50	0.43
1:CA:702:A:C8	22:DA:1848:A:H1'	2.53	0.43
1:AA:830:G:H2'	1:AA:831:A:H8	1.84	0.43
22:DA:528:A:OP1	57:DA:3243:HOH:O	2.21	0.43
9:AI:22:LYS:HE3	9:AI:22:LYS:HB3	1.71	0.43
22:DA:167:A:C2	22:DA:168:G:H1'	2.54	0.43
1:AA:562:U:H1'	12:AL:12:ARG:HD3	2.01	0.43
3:AC:156:ARG:HD3	3:AC:193:TYR:O	2.17	0.43
22:BA:2328:A:H2'	22:BA:2329:U:C6	2.53	0.43
22:DA:2160:C:H2'	22:DA:2161:C:O4'	2.18	0.43
1:AA:268:U:H2'	1:AA:269:C:C6	2.54	0.43
22:DA:1366:A:C4	22:DA:1367:A:C8	3.06	0.43
10:AJ:59:LYS:HD2	10:AJ:59:LYS:C	2.38	0.43
1:AA:343:U:H2'	1:AA:345:C:C5	2.54	0.43
30:DI:8:TYR:HB3	30:DI:59:ILE:O	2.18	0.43
1:CA:1431:A:C6	1:CA:1432:G:C6	3.06	0.43
22:DA:1802:A:C6	22:DA:1803:A:C6	3.07	0.43
17:CQ:65:ARG:HA	17:CQ:66:PRO:HD3	1.87	0.43
27:DF:104:ILE:HA	27:DF:108:VAL:HB	1.99	0.43
22:BA:1786:A:C4	22:BA:1938:A:C6	3.06	0.43
7:CG:111:ARG:HH11	7:CG:123:GLU:HG2	1.83	0.43
37:BP:6:LYS:O	37:BP:10:GLN:HG2	2.18	0.43
37:BP:2:SER:O	37:BP:6:LYS:HG2	2.18	0.43
40:DS:7:HIS:HB2	40:DS:50:VAL:HG21	2.00	0.43
22:BA:274:C:H2'	22:BA:275:C:O4'	2.17	0.43
22:DA:980:A:C4	22:DA:1136:G:O4'	2.72	0.43
42:BU:12:ILE:HG21	42:BU:80:ALA:HB2	1.99	0.43
28:DG:39:ASP:HB3	28:DG:58:TYR:OH	2.17	0.43
1:CA:23:C:H5	1:CA:561:U:O4	2.01	0.43
47:DZ:5:ILE:HD11	47:DZ:57:VAL:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1373:G:H5''	7:AG:36:LYS:HB2	2.00	0.43
53:B5:185:LYS:C	53:B5:187:ALA:H	2.22	0.43
22:BA:1688:U:N3	22:BA:1698:A:C2	2.87	0.43
22:BA:2708:G:O2'	35:BN:71:ARG:HD3	2.18	0.43
29:BH:76:GLU:HA	29:BH:142:VAL:HG12	2.00	0.43
22:BA:1061:U:C2	30:BI:10:LYS:HB2	2.53	0.43
7:AG:40:GLU:HA	7:AG:43:VAL:HG23	2.00	0.43
22:DA:1050:A:H2'	22:DA:1051:G:C8	2.53	0.43
24:BC:258:ARG:NH1	24:BC:264:ASP:OD2	2.51	0.43
22:DA:2057:G:OP1	57:DA:3668:HOH:O	2.21	0.43
9:CI:51:PRO:HD3	9:CI:80:ARG:HG2	1.99	0.43
9:CI:51:PRO:HB3	9:CI:84:THR:HG23	1.99	0.43
22:DA:661:A:H2'	22:DA:662:G:O4'	2.18	0.43
29:BH:1:MET:HE3	29:BH:23:ALA:HA	2.00	0.43
1:AA:1308:U:O3'	13:AM:91:HIS:HE1	2.02	0.43
44:DW:21:LEU:HB3	44:DW:39:ARG:O	2.18	0.43
22:DA:810:U:C4	33:DL:30:THR:HA	2.53	0.43
22:DA:2849:U:P	37:DP:93:ARG:HH21	2.40	0.43
11:AK:23:ILE:HD13	11:AK:96:THR:HG21	2.01	0.43
22:DA:648:G:H1'	22:DA:2351:G:OP1	2.18	0.43
22:DA:1640:A:H2'	22:DA:1641:A:H8	1.84	0.43
13:CM:13:LYS:HB3	13:CM:14:HIS:H	1.58	0.43
1:AA:731:G:H2'	1:AA:732:C:H6	1.83	0.43
22:DA:2607:G:H2'	22:DA:2608:G:O4'	2.18	0.43
22:BA:78:U:H2'	22:BA:79:C:H6	1.83	0.43
24:DC:93:LEU:HD13	24:DC:103:TYR:CE1	2.54	0.43
13:AM:64:VAL:O	13:AM:69:LEU:HB2	2.18	0.43
1:AA:462:G:H3'	1:AA:463:U:H6	1.83	0.43
36:BO:35:ILE:HG12	36:BO:106:LEU:HD12	2.00	0.43
21:AU:21:ARG:NH1	21:AU:25:LYS:HG3	2.33	0.43
9:CI:46:MET:O	9:CI:49:ARG:HB3	2.19	0.43
22:BA:1627:G:C2	22:BA:1628:G:C8	3.07	0.43
22:BA:1269:A:N7	57:BA:3387:HOH:O	2.37	0.43
41:DT:82:LYS:HG2	41:DT:83:ALA:N	2.34	0.43
1:AA:936:C:O2'	1:AA:1382:C:N3	2.52	0.43
22:BA:2458:G:C2	22:BA:2490:G:N2	2.87	0.43
1:AA:299:G:C6	1:AA:300:A:C6	3.06	0.43
22:DA:1247:A:O3'	38:DQ:2:ALA:HB3	2.19	0.43
51:B3:22:PHE:O	51:B3:50:VAL:HG23	2.18	0.43
22:BA:2176:A:C6	22:BA:2177:C:N4	2.86	0.43
1:AA:162:A:H5''	1:AA:163:C:OP2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DJ:5:THR:HG23	31:DJ:45:THR:HG21	2.01	0.43
12:CL:122:PRO:O	12:CL:124:ALA:N	2.52	0.43
29:BH:103:VAL:O	29:BH:108:VAL:O	2.37	0.43
22:BA:1506:U:H2'	22:BA:1507:C:C6	2.54	0.43
26:BE:180:LEU:HD23	26:BE:180:LEU:HA	1.69	0.43
22:DA:2271:G:OP1	44:DW:18:ALA:HB1	2.19	0.43
1:AA:71:A:C6	1:AA:100:G:C8	3.07	0.43
22:BA:335:C:H5''	42:BU:82:ARG:HD3	2.00	0.43
2:CB:50:PHE:CD1	2:CB:54:LEU:HD23	2.53	0.43
3:AC:38:LYS:HE3	3:AC:38:LYS:HB2	1.86	0.43
5:AE:84:PRO:HB3	5:AE:97:GLN:HG2	2.00	0.43
6:CF:91:ARG:HG2	6:CF:93:LYS:HZ3	1.84	0.43
1:AA:109:A:C6	1:AA:326:G:C6	3.07	0.43
22:DA:2392:A:C8	22:DA:2429:G:C2	3.06	0.43
43:DV:38:LEU:HB3	43:DV:40:ILE:HD11	1.99	0.43
46:DY:28:LEU:HD23	46:DY:37:LEU:HD11	2.01	0.43
46:BY:57:LEU:HA	46:BY:60:LYS:HB3	2.01	0.43
1:AA:570:G:H1'	1:AA:820:U:C4	2.53	0.43
1:AA:201:G:HO2'	1:AA:469:C:HO2'	1.64	0.43
9:CI:120:LYS:CG	9:CI:123:ARG:HB3	2.48	0.43
43:DV:20:LEU:O	43:DV:25:LYS:HB2	2.18	0.43
1:CA:664:G:H22	1:CA:741:G:H1	1.66	0.43
14:CN:69:ARG:HA	14:CN:70:PRO:HD3	1.85	0.43
6:AF:40:GLU:HB2	6:AF:61:LEU:HB3	2.00	0.43
31:DJ:117:ALA:HA	31:DJ:120:ARG:HD2	1.99	0.43
22:DA:335:C:H5''	42:DU:82:ARG:HD3	2.00	0.43
1:CA:939:G:C6	1:CA:940:C:C4	3.07	0.43
36:BO:111:ARG:HD3	36:BO:117:PHE:OXT	2.19	0.43
26:DE:129:PRO:HB3	26:DE:159:LEU:HB2	1.99	0.43
22:DA:2094:A:H2'	22:DA:2095:A:C8	2.53	0.43
22:BA:973:A:H5''	39:BR:81:LYS:CG	2.49	0.43
7:CG:57:SER:OG	7:CG:58:GLU:N	2.50	0.43
22:DA:738:G:H2'	22:DA:739:A:C8	2.53	0.43
45:BX:64:ILE:HG13	45:BX:68:LEU:HG	2.01	0.43
1:CA:977:A:OP1	14:CN:71:HIS:HE1	2.01	0.43
22:DA:2323:G:H2'	22:DA:2324:U:O4'	2.17	0.43
1:CA:411:A:C6	1:CA:429:U:C5	3.06	0.43
29:BH:41:LYS:HA	29:BH:44:ILE:HG12	2.01	0.43
28:BG:96:ALA:HB2	28:BG:105:LEU:HD23	2.00	0.43
1:CA:17:U:H2'	1:CA:18:C:C6	2.53	0.43
22:DA:105:C:H2'	22:DA:106:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BE:145:ASP:HB3	26:BE:184:ASP:HB2	2.00	0.43
44:DW:72:LYS:HB2	44:DW:79:PHE:CD2	2.53	0.43
41:BT:40:LYS:HD3	41:BT:58:VAL:O	2.19	0.43
8:CH:65:TYR:HA	8:CH:70:ALA:HA	2.00	0.43
22:BA:1949:G:N2	22:BA:1958:C:C2	2.87	0.43
35:BN:36:THR:HG23	35:BN:37:THR:O	2.17	0.43
22:BA:1664:A:H1'	22:BA:2726:A:N1	2.33	0.43
14:CN:18:ASP:HA	14:CN:22:ALA:HB3	2.00	0.43
22:BA:695:G:C2	22:BA:696:G:C8	3.07	0.43
29:BH:94:ILE:CD1	29:BH:98:ASP:HB3	2.48	0.43
22:BA:2094:A:C2	22:BA:2196:C:C2	3.06	0.43
1:AA:684:U:H2'	1:AA:685:G:O4'	2.19	0.43
22:DA:1360:G:N1	22:DA:1361:G:H1'	2.33	0.43
5:CE:29:ARG:HG2	5:CE:29:ARG:H	1.63	0.43
10:CJ:38:GLY:O	10:CJ:40:ILE:HG13	2.18	0.43
22:DA:1109:C:H5''	22:DA:1110:G:OP2	2.19	0.43
6:AF:46:GLN:HB2	6:AF:56:LYS:CE	2.45	0.43
22:BA:2127:G:H2'	22:BA:2128:G:C8	2.54	0.43
1:CA:822:U:H2'	1:CA:823:C:H6	1.82	0.43
30:DI:58:VAL:O	30:DI:69:PHE:HB3	2.19	0.43
1:AA:722:G:C8	1:AA:724:G:H1'	2.54	0.43
28:DG:11:VAL:HG13	28:DG:48:ASN:C	2.39	0.43
22:BA:20:C:O2'	22:BA:21:A:H5'	2.18	0.43
7:CG:116:MET:HA	7:CG:119:ARG:HD3	2.00	0.43
19:AS:11:ILE:HA	19:AS:38:SER:HB3	2.00	0.43
4:AD:105:MET:HG2	4:AD:171:LEU:HD22	2.00	0.43
22:DA:754:U:H2'	22:DA:755:U:C6	2.53	0.43
29:BH:9:VAL:O	29:BH:10:ALA:O	2.36	0.43
22:BA:416:U:H2'	22:BA:417:C:C6	2.53	0.43
15:CO:45:GLU:HG2	15:CO:46:HIS:N	2.33	0.43
22:DA:1655:A:C6	22:DA:1656:C:C2	3.06	0.43
1:AA:760:G:C5	1:AA:761:G:C8	3.07	0.43
40:BS:90:LYS:NZ	54:B6:8:MHT:H6A	2.32	0.43
1:CA:1245:C:H2'	1:CA:1246:A:H8	1.84	0.43
27:DF:38:MET:HG3	27:DF:152:LEU:HB3	2.00	0.43
1:CA:552:U:C2	1:CA:553:A:C8	3.07	0.43
22:BA:2191:A:C6	22:BA:2192:U:C4	3.06	0.43
30:BI:103:ARG:HE	30:BI:104:ALA:N	2.17	0.43
45:BX:19:SER:OG	45:BX:20:HIS:N	2.52	0.43
40:BS:20:VAL:O	40:BS:23:LEU:HB2	2.18	0.43
22:DA:2005:A:OP2	22:DA:2006:C:N4	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2661:G:H2'	22:BA:2662:A:C8	2.54	0.43
1:CA:1250:A:N3	1:CA:1370:G:O2'	2.45	0.43
22:BA:1248:G:OP1	38:BQ:2:ALA:N	2.52	0.43
39:BR:1:MET:HG2	39:BR:42:ALA:O	2.19	0.43
24:BC:265:LYS:HB3	24:BC:266:PHE:CD1	2.53	0.43
9:AI:6:TYR:HB3	9:AI:89:GLU:HG2	2.01	0.43
1:AA:957:U:O2	1:AA:959:A:H8	2.01	0.43
34:DM:19:GLY:O	34:DM:38:ARG:NH1	2.37	0.43
4:CD:172:GLU:HG2	4:CD:183:LYS:HD3	2.00	0.43
44:DW:19:LYS:HD3	44:DW:19:LYS:HA	1.80	0.43
27:DF:46:ASP:N	27:DF:46:ASP:OD1	2.50	0.43
28:BG:166:ASP:OD1	28:BG:166:ASP:N	2.45	0.43
22:BA:2810:A:O3'	25:BD:62:LYS:HB2	2.17	0.43
27:DF:13:VAL:O	27:DF:17:MET:HG2	2.19	0.43
22:DA:1209:U:H2'	22:DA:1210:G:H21	1.83	0.43
29:BH:97:ARG:HH12	1:CA:369:G:N2	2.12	0.43
29:DH:82:SER:O	29:DH:83:LYS:C	2.57	0.43
1:CA:1269:A:H2	1:CA:1312:G:N3	2.16	0.43
22:BA:841:G:H2'	22:BA:842:U:C6	2.53	0.43
22:BA:946:C:H2'	22:BA:947:A:C8	2.54	0.43
22:DA:297:G:H5''	42:DU:85:PHE:CB	2.46	0.43
22:DA:35:G:N2	22:DA:450:G:H1'	2.34	0.43
23:DB:49:C:O3'	36:DO:68:LYS:HE2	2.19	0.43
31:DJ:31:GLU:HG3	31:DJ:142:ILE:HD11	2.00	0.43
49:B1:4:GLY:O	49:B1:6:ARG:N	2.48	0.43
12:CL:65:SER:OG	12:CL:97:THR:HG23	2.18	0.43
1:AA:1032:G:C2	1:AA:1033:G:H1'	2.54	0.43
22:DA:319:G:OP2	26:DE:132:LYS:HE2	2.18	0.43
1:AA:96:U:HO2'	1:AA:97:G:P	2.41	0.43
22:BA:39:G:H2'	22:BA:40:U:H6	1.79	0.43
1:CA:35:G:C2	1:CA:550:G:C2	3.07	0.43
1:CA:256:U:H3	1:CA:270:A:H61	1.66	0.43
23:DB:76:G:N3	43:DV:78:GLN:NE2	2.60	0.43
22:DA:1791:A:C8	22:DA:1792:G:C8	3.07	0.43
2:CB:71:GLY:O	2:CB:93:ASN:HA	2.19	0.43
22:DA:510:C:C4	22:DA:511:U:C4	3.07	0.43
22:DA:590:A:C6	22:DA:591:U:C4	3.06	0.43
22:BA:644:A:H2'	22:BA:645:C:O4'	2.18	0.43
22:DA:1299:G:O2'	22:DA:1640:A:N6	2.50	0.43
22:DA:1969:A:H2'	22:DA:1972:G:H21	1.84	0.43
1:AA:1537:U:H2'	1:AA:1538:C:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DF:40:VAL:HG11	27:DF:50:LEU:HD13	2.00	0.43
7:AG:103:TRP:CH2	7:AG:141:VAL:HG21	2.54	0.43
22:BA:2071:A:H2'	22:BA:2072:C:C6	2.53	0.43
26:DE:149:ILE:HD11	26:DE:172:ALA:HA	2.01	0.43
22:DA:1668:A:O4'	22:DA:1669:A:C2	2.72	0.43
22:BA:1229:C:H2'	22:BA:1230:A:C8	2.54	0.43
42:BU:39:ILE:O	42:BU:41:LEU:N	2.51	0.43
1:CA:245:U:H3	1:CA:283:U:H3	1.65	0.43
53:B5:47:LYS:HE3	53:B5:48:LEU:H	1.83	0.43
22:BA:1378:A:O2'	22:BA:1380:G:OP2	2.37	0.43
37:BP:37:LYS:HE3	37:BP:39:ARG:HE	1.84	0.43
22:BA:1457:U:H5''	22:BA:1458:U:OP1	2.18	0.43
37:BP:10:GLN:C	37:BP:12:GLN:H	2.22	0.43
1:CA:987:G:N2	1:CA:1218:C:O2	2.52	0.43
28:BG:101:ASN:ND2	28:BG:116:GLN:OE1	2.51	0.43
43:BV:58:SER:OG	43:BV:59:GLU:N	2.50	0.43
22:BA:540:C:C2	22:BA:541:A:C8	3.07	0.43
40:DS:1:MET:HB3	40:DS:109:ASP:OD2	2.18	0.43
22:BA:106:C:H2'	22:BA:107:G:C8	2.53	0.43
1:CA:1394:A:C5	1:CA:1501:C:H4'	2.53	0.43
22:BA:598:U:H2'	22:BA:599:A:H8	1.83	0.43
22:BA:401:A:H2'	22:BA:402:A:C8	2.53	0.43
36:BO:36:TYR:CD2	36:BO:36:TYR:N	2.86	0.43
40:DS:67:ASP:OD1	40:DS:67:ASP:N	2.48	0.43
3:CC:175:LEU:O	3:CC:175:LEU:HD12	2.19	0.43
22:DA:2616:C:H2'	22:DA:2617:U:H6	1.84	0.43
7:CG:28:ASN:O	7:CG:31:MET:HB3	2.19	0.43
30:DI:75:PRO:HG2	30:DI:78:VAL:HG22	2.01	0.43
22:BA:1097:U:O2'	30:BI:9:VAL:HA	2.19	0.43
1:AA:685:G:N1	1:AA:686:U:O4	2.52	0.43
3:CC:33:LEU:O	3:CC:36:ASP:HB2	2.19	0.43
10:AJ:33:GLY:HA3	10:AJ:83:THR:HB	2.01	0.43
10:AJ:86:ALA:O	10:AJ:90:LEU:HB2	2.18	0.43
22:BA:1171:G:C5	22:BA:1172:C:C4	3.07	0.43
2:AB:16:PHE:O	2:AB:41:ILE:HD12	2.19	0.43
30:DI:33:VAL:HG22	30:DI:67:PHE:CD2	2.54	0.43
17:CQ:12:VAL:CG1	17:CQ:13:VAL:H	2.28	0.43
1:AA:1181:G:O2'	1:AA:1182:G:N7	2.51	0.43
22:DA:2469:A:C4'	34:DM:55:ARG:HD3	2.46	0.43
22:DA:2056:G:C2	22:DA:2057:G:C8	3.06	0.43
22:BA:1917:U:H2'	22:BA:1918:A:H5'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2172:U:H4'	22:BA:2173:A:H5'	2.00	0.43
22:DA:1223:G:OP2	39:DR:68:ARG:NH1	2.52	0.43
1:CA:709:U:H2'	1:CA:710:G:C8	2.50	0.43
6:AF:47:LEU:HD13	6:AF:51:ILE:HG23	2.00	0.43
22:DA:2037:A:C6	22:DA:2038:G:C6	3.07	0.43
43:DV:9:ARG:HG3	43:DV:41:GLU:HB3	2.01	0.43
22:DA:830:G:H22	22:DA:2446:G:H5''	1.84	0.43
22:BA:1624:U:H2'	22:BA:1625:C:C6	2.51	0.43
37:DP:48:ILE:HA	37:DP:97:LEU:HB2	2.01	0.43
22:DA:1318:U:H2'	22:DA:1319:C:C6	2.54	0.43
23:DB:65:U:C4	23:DB:108:A:C4	3.06	0.43
22:DA:2093:G:C6	22:DA:2225:A:C8	3.07	0.43
1:CA:1216:A:H2'	1:CA:1217:C:H6	1.84	0.43
22:BA:657:U:H2'	22:BA:658:U:C6	2.54	0.43
22:DA:2047:C:H2'	22:DA:2048:G:H8	1.83	0.43
22:BA:137:U:H2'	22:BA:140:C:N1	2.33	0.43
1:AA:579:A:H2'	1:AA:580:C:C6	2.53	0.43
1:AA:855:U:H2'	1:AA:856:C:H6	1.83	0.43
22:BA:747:U:C4	22:BA:2613:U:C4	3.07	0.43
22:BA:839:U:H1'	22:BA:1191:G:H1'	2.00	0.43
5:AE:56:VAL:N	5:AE:57:PRO:HD2	2.34	0.43
22:BA:1432:G:O2'	22:BA:1433:A:H5'	2.19	0.43
1:AA:1409:C:H2'	1:AA:1410:A:C8	2.54	0.43
22:BA:319:G:H2'	22:BA:320:A:O4'	2.18	0.43
41:BT:58:VAL:HG22	41:BT:85:VAL:HG22	2.01	0.43
25:BD:186:LEU:HD21	37:BP:4:ILE:HG21	2.00	0.43
29:BH:45:GLU:HA	29:BH:48:GLU:HB2	2.01	0.43
31:DJ:70:THR:HG22	31:DJ:90:GLU:OE1	2.19	0.43
22:BA:2669:G:O2'	22:BA:2670:A:H5'	2.19	0.43
22:BA:826:U:H2'	22:BA:828:U:O4'	2.18	0.43
22:DA:2464:G:H2'	22:DA:2465:C:O4'	2.18	0.43
31:BJ:114:LEU:O	31:BJ:118:MET:HG3	2.18	0.43
22:BA:2294:G:H5''	36:BO:10:ARG:HD3	2.00	0.43
22:DA:1586:A:O5'	22:DA:1586:A:H8	2.02	0.43
1:AA:279:A:H5''	1:AA:279:A:H8	1.83	0.43
3:AC:167:TRP:HE3	3:AC:167:TRP:O	2.01	0.43
3:CC:182:ILE:HD13	3:CC:182:ILE:HA	1.86	0.43
29:BH:79:THR:CG2	29:BH:147:VAL:CG2	2.97	0.43
1:AA:683:G:H21	11:AK:40:ASN:HA	1.84	0.43
1:CA:537:G:H2'	1:CA:538:G:C8	2.54	0.43
2:CB:222:ARG:NE	2:CB:223:GLU:HB2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:54:ASP:HA	13:CM:57:ARG:CB	2.44	0.43
2:AB:129:LEU:HB3	2:AB:130:THR:H	1.60	0.43
22:BA:2800:A:H3'	22:BA:2801:G:C5'	2.47	0.43
9:AI:56:ASP:OD2	9:AI:57:MET:N	2.45	0.43
1:AA:91:U:C4	1:AA:92:U:C2	3.07	0.43
22:DA:1344:U:HO2'	22:DA:1345:C:P	2.37	0.43
30:DI:19:ASN:HB2	30:DI:39:CYS:HB3	2.00	0.43
30:DI:57:VAL:HG22	30:DI:58:VAL:N	2.34	0.43
41:DT:77:ARG:HB3	41:DT:78:SER:H	1.49	0.43
22:DA:2282:G:C4	22:DA:2425:A:N6	2.87	0.43
14:CN:72:GLY:O	14:CN:80:SER:HA	2.19	0.43
22:BA:27:G:N2	22:BA:512:G:H1'	2.33	0.43
22:BA:645:C:H2'	22:BA:647:G:C5	2.54	0.43
36:DO:97:PHE:CB	36:DO:103:VAL:HG11	2.49	0.43
22:BA:1965:C:H5''	22:BA:1966:A:H2'	2.00	0.43
25:DD:104:VAL:HG23	25:DD:105:LYS:H	1.83	0.43
1:AA:761:G:H2'	1:AA:762:U:H6	1.83	0.43
22:BA:299:A:C5	22:BA:300:A:C6	3.07	0.43
9:CI:19:VAL:HG21	9:CI:83:ILE:N	2.33	0.43
16:CP:21:VAL:HG12	16:CP:33:ILE:HB	2.00	0.43
22:DA:659:G:H4'	26:DE:95:LYS:HB3	2.00	0.43
1:AA:821:G:H2'	1:AA:822:U:C6	2.53	0.43
1:AA:56:U:H2'	1:AA:57:G:C8	2.53	0.43
22:DA:371:A:N6	22:DA:401:A:H3'	2.34	0.43
2:CB:183:VAL:N	2:CB:197:ASP:OD1	2.52	0.43
22:DA:1105:U:H2'	22:DA:1106:G:H8	1.83	0.43
22:DA:786:C:H5''	22:DA:1780:A:N7	2.34	0.43
27:BF:47:LYS:HZ1	27:BF:84:PRO:HB2	1.83	0.43
22:BA:1281:G:H2'	22:BA:1282:U:C6	2.54	0.43
49:B1:23:THR:OG1	49:B1:24:THR:N	2.51	0.43
22:BA:2862:G:H2'	22:BA:2863:C:C6	2.53	0.43
22:BA:102:U:H4'	22:BA:103:A:OP1	2.19	0.43
22:DA:1399:C:H2'	22:DA:1400:U:C6	2.53	0.43
22:BA:2602:A:H4'	22:BA:2603:G:OP2	2.18	0.43
26:DE:140:ASP:C	26:DE:142:ALA:H	2.22	0.43
12:AL:117:TYR:O	12:AL:119:VAL:HG23	2.19	0.43
1:CA:390:U:H2'	1:CA:391:G:C8	2.53	0.43
34:BM:1:MET:HE3	34:BM:1:MET:HB3	1.75	0.43
32:DK:108:ARG:HE	32:DK:108:ARG:HB2	1.67	0.43
7:AG:4:ARG:HH11	7:AG:4:ARG:HB2	1.83	0.43
22:DA:654:A:N3	22:DA:654:A:H3'	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:901:A:N7	1:AA:902:G:H1'	2.34	0.43
22:BA:2093:G:P	29:BH:24:GLY:H	2.41	0.42
4:AD:177:LYS:HD3	4:AD:177:LYS:N	2.34	0.42
30:DI:80:LEU:HD13	30:DI:136:MET:SD	2.59	0.42
22:DA:833:A:P	33:DL:39:LYS:HE2	2.59	0.42
1:CA:562:U:H1'	12:CL:12:ARG:CG	2.49	0.42
9:AI:55:VAL:HG21	9:AI:87:LEU:HD21	2.01	0.42
22:BA:1606:C:H4'	22:BA:1607:C:H5'	2.00	0.42
22:DA:764:A:H2	24:DC:218:PRO:HG3	1.84	0.42
13:AM:48:LEU:HD22	13:AM:53:ILE:HG12	2.01	0.42
14:AN:10:GLU:OE2	14:AN:61:ARG:N	2.38	0.42
10:AJ:71:LEU:HA	10:AJ:71:LEU:HD13	1.82	0.42
22:DA:814:C:H1'	22:DA:1225:G:N2	2.34	0.42
22:DA:1365:A:OP2	45:DX:3:ARG:N	2.43	0.42
1:CA:308:C:H2'	1:CA:309:A:H8	1.82	0.42
42:DU:66:GLN:O	42:DU:69:ASN:N	2.45	0.42
29:DH:62:LEU:HD13	29:DH:63:ALA:N	2.34	0.42
2:CB:95:ARG:HA	2:CB:95:ARG:HD3	1.88	0.42
7:CG:95:ARG:HA	7:CG:98:ALA:HB3	2.01	0.42
22:DA:621:A:H2'	22:DA:622:G:O4'	2.19	0.42
1:AA:764:C:H2'	1:AA:765:G:O4'	2.18	0.42
2:CB:165:ASP:HB3	2:CB:169:GLU:OE2	2.19	0.42
23:DB:70:C:H2'	23:DB:71:C:H6	1.84	0.42
1:AA:945:G:C2	1:AA:946:A:C8	3.07	0.42
22:BA:276:U:H2'	22:BA:278:A:H62	1.84	0.42
10:AJ:65:TYR:HB3	14:AN:96:LEU:HD11	2.01	0.42
45:DX:68:LEU:HD22	45:DX:78:TYR:CZ	2.53	0.42
22:BA:1223:G:OP2	39:BR:68:ARG:NH1	2.52	0.42
1:AA:1409:C:H2'	1:AA:1410:A:H8	1.84	0.42
1:CA:1537:U:H3'	1:CA:1538:C:C6	2.54	0.42
22:BA:1452:G:H2'	22:BA:1457:U:O4	2.19	0.42
12:AL:114:ARG:HB3	12:AL:119:VAL:HB	2.01	0.42
34:DM:50:ARG:HG3	34:DM:65:ILE:HD11	2.00	0.42
22:BA:2109:U:H2'	22:BA:2110:G:C8	2.54	0.42
1:AA:755:G:N2	1:AA:756:C:C2	2.87	0.42
22:DA:571:U:H1'	22:DA:573:U:C6	2.54	0.42
20:AT:51:PHE:HE1	20:AT:55:GLN:NE2	2.17	0.42
22:DA:1173:U:O2'	22:DA:1176:U:O2	2.20	0.42
1:CA:554:A:H2'	1:CA:555:U:H6	1.84	0.42
22:DA:2203:U:H5''	22:DA:2204:G:OP1	2.19	0.42
22:DA:464:U:H5'	50:D2:5:PHE:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:123:GLN:HA	3:AC:126:ARG:HB2	2.00	0.42
51:D3:29:LEU:HA	51:D3:29:LEU:HD12	1.87	0.42
46:DY:60:LYS:HE3	46:DY:60:LYS:HB2	1.91	0.42
22:DA:71:A:OP2	22:DA:113:U:H5'	2.19	0.42
50:B2:9:VAL:HG12	50:B2:13:ASN:ND2	2.33	0.42
8:CH:10:MET:HE2	8:CH:33:LYS:HD3	2.02	0.42
26:BE:111:GLU:OE1	26:BE:115:GLN:HG2	2.19	0.42
8:AH:55:THR:HG22	8:AH:56:LYS:HG3	2.00	0.42
1:AA:369:G:OP2	1:AA:388:G:N1	2.45	0.42
22:DA:1060:U:OP2	30:DI:75:PRO:HA	2.19	0.42
4:CD:173:VAL:HG13	4:CD:174:ASP:N	2.25	0.42
1:AA:64:G:C8	1:AA:99:C:N4	2.87	0.42
22:BA:1565:C:H3'	24:BC:18:LYS:HZ3	1.84	0.42
8:CH:11:LEU:HD11	8:CH:127:CYS:CB	2.49	0.42
28:BG:125:CYS:HB3	28:BG:127:THR:O	2.19	0.42
21:CU:19:PHE:HA	21:CU:22:SER:HB3	2.01	0.42
29:BH:114:GLU:CB	29:BH:133:GLN:O	2.66	0.42
22:DA:2852:G:H2'	22:DA:2853:C:C6	2.54	0.42
2:AB:181:ILE:HA	2:AB:182:PRO:HD3	1.75	0.42
2:AB:68:LEU:HD13	2:AB:161:LEU:HD21	2.00	0.42
22:BA:974:G:C8	22:BA:989:G:C2	3.07	0.42
46:BY:56:LEU:O	46:BY:57:LEU:CB	2.66	0.42
2:AB:54:LEU:HB3	2:AB:220:THR:HG21	2.02	0.42
22:BA:2297:A:N1	22:BA:2321:U:C5	2.86	0.42
2:AB:164:ILE:HG23	2:AB:165:ASP:N	2.34	0.42
22:DA:1356:G:C2	22:DA:1357:C:C2	3.08	0.42
22:BA:1899:A:O2'	22:BA:1900:A:H5''	2.19	0.42
22:BA:2262:U:OP2	44:BW:19:LYS:HE2	2.19	0.42
34:BM:49:ALA:O	34:BM:53:MET:HG2	2.18	0.42
22:DA:572:A:OP2	39:DR:79:ARG:NH1	2.52	0.42
1:AA:1119:C:P	9:AI:85:ARG:HH22	2.42	0.42
12:AL:36:ARG:HB3	12:AL:38:TYR:CE2	2.54	0.42
22:DA:1189:A:H2'	22:DA:1190:G:O4'	2.19	0.42
22:DA:2824:C:C4	22:DA:2825:G:C5	3.07	0.42
22:BA:2415:G:H2'	22:BA:2416:C:H6	1.84	0.42
1:AA:1098:C:H2'	1:AA:1099:G:O4'	2.19	0.42
1:AA:917:G:H2'	1:AA:918:A:C8	2.54	0.42
5:CE:53:ALA:HB2	5:CE:62:LYS:NZ	2.34	0.42
34:DM:74:THR:HA	34:DM:88:ASN:O	2.18	0.42
22:BA:206:U:O2'	22:BA:207:A:H5'	2.18	0.42
22:BA:531:C:C5	22:BA:2035:G:C2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:DC:107:PRO:HB3	24:DC:142:HIS:NE2	2.34	0.42
1:AA:1301:U:HO2'	1:AA:1302:C:P	2.42	0.42
1:CA:193:C:O3'	20:CT:56:PRO:HB3	2.20	0.42
40:DS:27:LYS:O	40:DS:71:VAL:HG23	2.19	0.42
41:DT:17:SER:O	41:DT:19:LYS:N	2.53	0.42
41:BT:4:GLU:HA	41:BT:7:LEU:HB2	2.00	0.42
1:CA:585:G:OP1	17:CQ:39:LYS:HE3	2.19	0.42
12:CL:35:THR:HG22	12:CL:36:ARG:HE	1.83	0.42
1:CA:209:U:H2'	1:CA:209:U:O2	2.19	0.42
17:AQ:81:LYS:HB2	17:AQ:81:LYS:HE2	1.58	0.42
22:DA:389:G:C8	22:DA:2413:G:H4'	2.53	0.42
22:DA:1856:U:O4	22:DA:1857:G:C6	2.72	0.42
44:BW:47:ALA:HB2	44:BW:59:LEU:HD22	2.01	0.42
22:BA:2454:G:O6	57:BA:3529:HOH:O	2.21	0.42
22:BA:233:A:N6	22:BA:428:A:H61	2.18	0.42
1:CA:692:U:H1'	1:CA:695:A:N7	2.34	0.42
4:CD:106:GLY:O	4:CD:159:LEU:N	2.52	0.42
16:CP:18:GLN:O	16:CP:20:VAL:HG12	2.20	0.42
22:BA:1153:C:H2'	22:BA:1154:G:O4'	2.18	0.42
11:AK:35:THR:OG1	11:AK:40:ASN:N	2.52	0.42
41:BT:2:ILE:HA	41:BT:3:ARG:C	2.39	0.42
22:DA:998:C:OP2	38:DQ:58:ARG:NH2	2.53	0.42
13:AM:107:ARG:HH21	13:AM:113:ARG:HB3	1.85	0.42
11:AK:42:LEU:HB3	11:AK:77:TYR:CD2	2.55	0.42
2:AB:95:ARG:HG2	2:AB:95:ARG:HH11	1.84	0.42
17:CQ:20:SER:N	17:CQ:48:ASP:OD1	2.53	0.42
22:DA:2272:U:H5''	22:DA:2273:A:OP1	2.19	0.42
21:AU:34:ARG:NH2	21:AU:35:ARG:HB2	2.34	0.42
22:DA:2571:U:C4	22:DA:2574:G:C8	3.06	0.42
17:CQ:52:GLU:HG2	17:CQ:53:CYS:N	2.28	0.42
1:CA:483:C:H2'	1:CA:484:G:N7	2.34	0.42
1:CA:1124:G:HO2'	1:CA:1145:A:N6	2.16	0.42
4:CD:33:LYS:O	4:CD:34:ILE:C	2.58	0.42
1:AA:1206:G:H4'	3:AC:192:THR:O	2.19	0.42
1:CA:263:A:OP1	20:CT:74:ARG:HD3	2.18	0.42
2:AB:151:ILE:HG23	2:AB:152:LYS:N	2.34	0.42
20:CT:6:SER:O	20:CT:8:LYS:N	2.53	0.42
40:BS:37:THR:HG22	40:BS:38:TYR:CE1	2.54	0.42
1:AA:21:G:H2'	1:AA:22:G:C8	2.55	0.42
22:DA:308:G:H4'	42:DU:17:LYS:NZ	2.33	0.42
22:DA:680:C:H2'	22:DA:681:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1308:U:O2'	1:AA:1309:G:H5'	2.20	0.42
22:BA:1022:G:N2	22:BA:1142:A:C2	2.82	0.42
22:DA:2391:G:H1'	22:DA:2424:C:N4	2.33	0.42
1:AA:1322:C:OP1	19:AS:78:ARG:NH2	2.53	0.42
25:BD:84:LEU:HD23	25:BD:84:LEU:HA	1.47	0.42
3:AC:7:PRO:HD2	3:AC:184:TYR:CD2	2.53	0.42
29:DH:72:ILE:O	29:DH:72:ILE:CG2	2.67	0.42
1:AA:1200:C:H4'	1:AA:1201:A:H3'	2.01	0.42
10:AJ:63:ASP:OD1	14:AN:85:ARG:HD2	2.19	0.42
1:CA:31:G:H22	1:CA:47:C:H4'	1.83	0.42
33:DL:70:LYS:O	33:DL:74:THR:HG23	2.19	0.42
22:DA:2800:A:C2	22:DA:2895:G:H1'	2.55	0.42
1:AA:629:A:H2'	1:AA:630:A:C8	2.55	0.42
22:DA:938:G:C2	22:DA:939:G:N7	2.87	0.42
3:CC:6:HIS:CD2	14:CN:89:MET:HB3	2.55	0.42
28:BG:173:GLU:HB3	28:BG:174:ALA:H	1.76	0.42
14:AN:16:LEU:HD23	14:AN:19:LYS:HE2	2.01	0.42
2:AB:56:GLU:HA	2:AB:59:LYS:HB3	2.01	0.42
40:DS:15:GLN:HA	40:DS:18:ARG:HD2	2.00	0.42
22:BA:2:G:H2'	22:BA:3:U:H6	1.84	0.42
12:CL:10:LYS:HA	12:CL:11:PRO:HD3	1.88	0.42
22:DA:176:A:H3'	22:DA:177:G:N2	2.33	0.42
22:DA:1530:G:N2	22:DA:1542:U:O2	2.53	0.42
1:AA:502:A:C2	1:AA:503:C:C2	3.07	0.42
22:DA:1490:A:N3	22:DA:1490:A:H2'	2.35	0.42
3:AC:12:LEU:HD23	3:AC:12:LEU:HA	1.79	0.42
48:B0:12:LYS:HA	48:B0:12:LYS:HD2	1.75	0.42
2:CB:161:LEU:HD12	2:CB:161:LEU:HA	1.83	0.42
1:CA:1483:A:H8	1:CA:1483:A:O5'	2.03	0.42
22:BA:1083:U:O2	22:BA:1086:A:N1	2.52	0.42
22:DA:1154:G:P	38:DQ:58:ARG:HH11	2.41	0.42
29:DH:31:VAL:HB	29:DH:32:PRO:HD2	2.00	0.42
22:BA:2305:U:H5''	27:BF:131:GLY:HA3	2.00	0.42
22:DA:35:G:H1'	22:DA:454:A:C4	2.54	0.42
1:CA:427:U:P	4:CD:13:ARG:HH22	2.42	0.42
22:BA:1870:C:H5''	22:BA:1871:A:C8	2.54	0.42
8:AH:37:ALA:HB1	8:AH:61:LEU:HD21	2.02	0.42
25:BD:140:HIS:CD2	57:BD:302:HOH:O	2.59	0.42
22:BA:2742:G:P	52:B4:24:ARG:HH12	2.42	0.42
8:AH:2:SER:C	8:AH:4:GLN:N	2.71	0.42
28:DG:127:THR:HB	28:DG:130:GLU:HG3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2189:U:C2'	22:DA:2190:G:H5''	2.49	0.42
22:DA:2349:G:OP2	51:D3:42:ARG:NH2	2.52	0.42
10:AJ:42:LEU:HD23	10:AJ:43:PRO:CD	2.48	0.42
1:AA:324:G:N2	1:AA:326:G:H3'	2.34	0.42
43:DV:38:LEU:HA	43:DV:38:LEU:HD12	1.90	0.42
22:DA:2209:G:C2	22:DA:2216:G:C2	3.07	0.42
24:DC:84:ASP:HA	24:DC:85:PRO:HD3	1.89	0.42
22:BA:1536:C:H4'	22:BA:1537:G:C5'	2.48	0.42
11:AK:114:THR:HA	11:AK:115:PRO:HD3	1.79	0.42
22:DA:703:U:H2'	22:DA:704:G:H5'	2.00	0.42
22:DA:1373:A:C5	22:DA:1374:G:H1'	2.55	0.42
22:DA:1599:U:OP2	41:DT:40:LYS:HD2	2.20	0.42
42:DU:14:LEU:HD21	42:DU:71:ALA:HB3	2.00	0.42
22:DA:2025:C:H2'	22:DA:2026:U:C6	2.54	0.42
1:CA:1180:A:P	9:CI:99:ARG:HH22	2.42	0.42
22:BA:300:A:H2'	22:BA:334:C:H1'	2.01	0.42
22:DA:1273:U:H4'	22:DA:1275:A:OP1	2.20	0.42
24:DC:65:VAL:HG22	24:DC:103:TYR:HB3	2.02	0.42
3:AC:70:THR:O	3:AC:106:VAL:N	2.52	0.42
3:AC:70:THR:OG1	3:AC:71:ALA:N	2.53	0.42
28:BG:105:LEU:HD13	28:BG:107:LEU:HD11	2.01	0.42
1:CA:554:A:H2'	1:CA:555:U:C6	2.55	0.42
24:DC:107:PRO:HD2	24:DC:110:LEU:HD22	2.00	0.42
15:AO:82:ILE:HD12	15:AO:88:ARG:HG2	2.02	0.42
46:DY:21:LEU:HA	46:DY:25:GLN:HB3	2.00	0.42
22:DA:1696:G:H21	22:DA:1978:A:H5'	1.84	0.42
52:B4:7:VAL:HG22	52:B4:38:GLY:HA3	2.02	0.42
37:BP:23:GLY:O	37:BP:110:ILE:HD11	2.18	0.42
22:BA:2492:U:H2'	22:BA:2493:U:H6	1.83	0.42
33:BL:57:LEU:HG	51:B3:14:PHE:HZ	1.84	0.42
35:DN:12:ARG:O	35:DN:17:ARG:NH2	2.51	0.42
35:DN:93:GLY:C	35:DN:95:THR:H	2.23	0.42
22:DA:2619:C:H4'	25:DD:156:PHE:O	2.19	0.42
22:DA:2676:C:OP1	32:DK:31:ARG:NH2	2.52	0.42
14:AN:58:SER:O	57:AN:201:HOH:O	2.21	0.42
45:BX:77:LYS:HD2	45:BX:77:LYS:HA	1.60	0.42
1:AA:605:U:O2'	1:AA:606:G:H5'	2.19	0.42
22:DA:1767:G:H2'	22:DA:1768:C:H6	1.82	0.42
17:AQ:10:GLY:HA3	17:AQ:24:ALA:O	2.20	0.42
1:CA:57:G:H2'	1:CA:58:C:C6	2.54	0.42
5:CE:122:ASN:CG	5:CE:123:VAL:N	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CE:150:PRO:C	5:CE:152:MET:N	2.72	0.42
29:DH:121:VAL:O	29:DH:122:LEU:CB	2.67	0.42
22:DA:537:G:C6	22:DA:555:G:C2	3.08	0.42
37:DP:39:ARG:HG3	37:DP:40:LEU:N	2.27	0.42
22:BA:1564:C:O2'	22:BA:1565:C:H5'	2.19	0.42
12:AL:43:LYS:HG2	12:AL:44:LYS:HD3	2.01	0.42
22:DA:160:A:C8	22:DA:167:A:C6	3.07	0.42
28:DG:125:CYS:HB3	28:DG:127:THR:O	2.19	0.42
45:DX:18:ARG:HD2	45:DX:18:ARG:HA	1.83	0.42
1:AA:1029:U:H2'	1:AA:1032:G:H1	1.84	0.42
1:AA:1414:U:H2'	1:AA:1415:G:C8	2.54	0.42
22:BA:2129:C:H2'	22:BA:2130:U:C6	2.55	0.42
2:AB:163:VAL:HG21	2:AB:173:ILE:HD11	1.99	0.42
20:CT:8:LYS:H	20:CT:8:LYS:HG2	1.41	0.42
3:AC:130:PHE:CE1	3:AC:131:ARG:HD2	2.54	0.42
1:CA:137:U:H1'	1:CA:227:G:N2	2.34	0.42
23:DB:76:G:OP1	43:DV:9:ARG:NH2	2.52	0.42
1:CA:718:A:H3'	1:CA:719:C:H6	1.85	0.42
3:AC:6:HIS:CB	14:AN:89:MET:HG3	2.49	0.42
22:DA:1439:A:N7	22:DA:1552:A:C2	2.85	0.42
29:DH:127:GLU:HA	29:DH:144:VAL:O	2.19	0.42
22:BA:2394:C:P	51:B3:30:ARG:HH21	2.41	0.42
22:DA:1881:C:H6	22:DA:1881:C:O5'	2.02	0.42
1:CA:1216:A:H2'	1:CA:1217:C:C6	2.54	0.42
19:AS:7:LYS:HB3	19:AS:7:LYS:HE3	1.86	0.42
22:BA:973:A:OP2	39:BR:81:LYS:HE3	2.19	0.42
22:DA:1417:C:H2'	22:DA:1418:G:O4'	2.19	0.42
30:BI:125:MET:HA	30:BI:128:SER:HB3	2.02	0.42
1:AA:321:A:N7	1:AA:328:C:O2'	2.43	0.42
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.61	0.42
1:CA:491:G:O2'	1:CA:492:C:H5'	2.20	0.42
10:AJ:47:GLU:OE2	14:AN:76:LYS:NZ	2.50	0.42
4:AD:15:GLU:OE2	4:AD:56:ARG:NH2	2.51	0.42
22:DA:2728:U:O2'	22:DA:2729:G:H5''	2.19	0.42
22:DA:176:A:C5	22:DA:177:G:C6	3.07	0.42
13:CM:79:ARG:O	13:CM:83:LEU:HD23	2.20	0.42
22:DA:2548:U:H2'	22:DA:2549:G:O4'	2.20	0.42
1:CA:1077:G:N2	1:CA:1080:A:OP2	2.49	0.42
22:BA:2865:U:C4	22:BA:2866:U:C4	3.07	0.42
29:DH:69:ALA:HB2	29:DH:138:VAL:HG12	2.02	0.42
1:CA:1416:G:N2	1:CA:1485:U:H1'	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:89:U:H6	1:CA:89:U:O5'	2.02	0.42
41:DT:51:PHE:O	41:DT:53:VAL:N	2.53	0.42
32:BK:105:ARG:NH2	37:BP:32:VAL:HG21	2.35	0.42
53:B5:40:GLU:HA	53:B5:181:PHE:HA	2.00	0.42
22:BA:2564:A:C2	22:BA:2647:U:H4'	2.54	0.42
22:DA:597:G:H2'	22:DA:598:U:O4'	2.19	0.42
22:DA:2254:C:H2'	22:DA:2255:G:O4'	2.20	0.42
1:AA:186:C:H2'	1:AA:187:G:O4'	2.19	0.42
24:BC:105:LEU:HD22	24:BC:143:ASN:HD22	1.84	0.42
29:BH:89:LYS:HB3	1:CA:359:G:H5'	1.98	0.42
5:CE:153:VAL:HG23	5:CE:157:ARG:CB	2.49	0.42
1:AA:428:G:O4'	1:AA:430:A:C8	2.72	0.42
1:AA:277:C:H2'	1:AA:278:G:H5'	2.01	0.42
29:DH:31:VAL:HG12	29:DH:32:PRO:HD3	2.02	0.42
22:DA:445:C:H2'	22:DA:446:G:C8	2.54	0.42
5:CE:36:LEU:HD12	5:CE:36:LEU:HA	1.94	0.42
19:AS:49:ILE:HG21	19:AS:71:LEU:HD11	2.01	0.42
22:DA:822:G:O6	22:DA:943:A:H2	2.02	0.42
10:CJ:48:ARG:NH1	10:CJ:66:GLU:OE1	2.52	0.42
22:BA:42:A:H2'	22:BA:43:G:O4'	2.20	0.42
22:DA:1789:A:P	24:DC:221:ARG:HH11	2.41	0.42
22:BA:581:C:H2'	22:BA:582:A:C8	2.54	0.42
22:DA:6:A:H2'	22:DA:7:G:C8	2.54	0.42
22:DA:6:A:H2'	22:DA:7:G:H8	1.83	0.42
1:CA:1022:A:C6	1:CA:1023:U:C4	3.08	0.42
27:DF:138:PHE:HA	27:DF:139:PRO:HD3	1.83	0.42
19:AS:29:LYS:HB3	19:AS:30:PRO:CD	2.48	0.42
22:DA:2436:G:C2	22:DA:2437:G:C8	3.08	0.42
14:CN:93:ILE:HA	14:CN:94:PRO:HD3	1.91	0.42
46:DY:1:MET:HG2	46:DY:5:GLU:OE2	2.19	0.42
22:DA:590:A:N6	22:DA:666:A:H61	2.18	0.42
7:CG:65:ALA:HB1	7:CG:127:ALA:HB3	2.01	0.42
22:DA:1654:A:OP2	35:DN:1:MET:HA	2.19	0.42
33:DL:93:ASN:O	33:DL:95:LEU:N	2.42	0.42
22:DA:2886:A:H2	48:D0:29:SER:HB3	1.84	0.42
9:CI:95:ARG:O	9:CI:99:ARG:N	2.41	0.42
22:DA:2233:U:H2'	22:DA:2234:G:C8	2.55	0.42
1:AA:1516:G:N1	1:AA:1519:A:OP2	2.49	0.42
22:BA:958:U:C2	23:BB:89:U:H1'	2.54	0.42
22:DA:1735:A:H2'	22:DA:1736:U:O4'	2.20	0.42
3:AC:68:ILE:O	3:AC:70:THR:HG22	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:319:G:C4	22:BA:333:G:N2	2.87	0.42
22:DA:818:G:H5'	22:DA:839:U:OP1	2.20	0.42
16:CP:31:ARG:HG3	16:CP:32:PHE:N	2.34	0.42
22:BA:532:A:H2'	22:BA:532:A:N3	2.35	0.42
6:CF:38:ARG:HG2	6:CF:63:ASN:HB3	2.02	0.42
1:CA:297:G:N2	1:CA:300:A:OP2	2.52	0.42
39:BR:48:LYS:HE2	39:BR:48:LYS:HB3	1.24	0.42
19:AS:42:PRO:HD3	19:AS:67:VAL:HG13	2.00	0.42
23:BB:43:C:H2'	23:BB:44:G:H5'	2.00	0.42
45:DX:59:ILE:HG12	45:DX:67:VAL:HG21	2.02	0.42
22:BA:2504:U:H6	22:BA:2504:U:O5'	2.02	0.42
10:CJ:7:ARG:HD3	10:CJ:75:ASP:OD1	2.20	0.42
22:BA:2600:A:N6	57:BA:3794:HOH:O	2.52	0.42
22:BA:303:G:C6	22:BA:315:G:C6	3.08	0.42
22:DA:836:G:H2'	22:DA:837:C:C6	2.54	0.42
22:DA:1068:G:N3	22:DA:1068:G:H2'	2.34	0.42
22:BA:2766:A:N3	22:BA:2766:A:H2'	2.34	0.42
1:CA:1270:G:H8	1:CA:1270:G:OP2	2.03	0.42
24:DC:266:PHE:CD1	24:DC:266:PHE:N	2.88	0.42
1:CA:84:U:O2'	1:CA:85:U:H5'	2.20	0.42
13:AM:78:LYS:HD3	13:AM:81:MET:HE3	2.02	0.42
22:BA:1317:G:C2	22:BA:1336:A:C2	3.08	0.42
26:BE:61:ARG:NH2	26:BE:64:GLY:HA3	2.35	0.42
22:BA:693:A:H2'	22:BA:694:U:O4'	2.19	0.42
29:BH:116:ARG:HB3	29:BH:131:SER:O	2.20	0.42
29:BH:89:LYS:O	29:BH:90:LEU:C	2.58	0.42
5:CE:81:LEU:CA	5:CE:147:MET:HE3	2.49	0.42
38:DQ:61:TRP:HB3	38:DQ:92:ARG:O	2.19	0.42
20:AT:70:ASN:N	20:AT:70:ASN:OD1	2.35	0.42
54:D6:7:004:O	54:D6:7:004:HG1	2.19	0.42
22:BA:622:G:H2'	22:BA:623:C:H6	1.84	0.42
18:CR:25:ASP:C	18:CR:27:ALA:N	2.72	0.42
20:CT:24:ARG:O	20:CT:27:MET:HG3	2.19	0.42
19:CS:36:ARG:HH21	19:CS:75:ALA:HB3	1.85	0.42
48:D0:12:LYS:HA	48:D0:15:MET:HB2	2.01	0.42
53:B5:65:LEU:C	53:B5:67:HIS:H	2.22	0.42
24:DC:207:LYS:HG3	24:DC:210:ALA:H	1.83	0.42
1:AA:79:G:H22	1:AA:90:C:N4	2.17	0.42
34:BM:42:THR:O	34:BM:46:ILE:HG13	2.19	0.42
3:CC:12:LEU:HD23	3:CC:12:LEU:HA	1.74	0.42
1:CA:49:U:O4	1:CA:365:U:H5	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:885:G:C2	1:AA:913:A:N1	2.87	0.42
1:CA:549:C:H2'	1:CA:550:G:O4'	2.19	0.42
10:AJ:53:ILE:CG2	10:AJ:61:ALA:HB1	2.50	0.42
43:DV:9:ARG:HB2	43:DV:39:ALA:HB1	2.01	0.42
22:DA:2074:U:C2	22:DA:2436:G:C2	3.08	0.42
52:B4:33:HIS:O	52:B4:35:GLN:HG3	2.19	0.42
22:DA:2445:G:O2'	22:DA:2446:G:H5'	2.19	0.42
46:BY:61:ALA:C	46:BY:63:ALA:H	2.22	0.42
36:DO:33:ARG:HG2	36:DO:34:HIS:CD2	2.55	0.42
30:BI:43:ASN:HA	30:BI:46:THR:HB	2.01	0.42
22:BA:2582:G:C2	22:BA:2583:G:C8	3.08	0.42
30:BI:33:VAL:HG21	30:BI:59:ILE:HG23	2.01	0.42
36:DO:6:ALA:O	36:DO:10:ARG:HB2	2.20	0.42
22:BA:2804:U:H2'	22:BA:2805:C:C6	2.54	0.42
22:BA:2786:U:O2'	25:BD:63:PRO:O	2.38	0.42
28:DG:154:PRO:HA	28:DG:160:LYS:O	2.20	0.42
22:BA:790:U:O2'	22:BA:791:C:P	2.77	0.42
42:DU:53:ASN:OD1	42:DU:53:ASN:N	2.52	0.42
22:BA:962:G:H21	22:BA:2250:G:H1	1.66	0.42
22:BA:2271:G:H2'	22:BA:2272:U:C6	2.54	0.42
1:AA:1520:C:H2'	1:AA:1521:C:H6	1.83	0.42
22:DA:676:A:H2	22:DA:2069:G:N3	2.18	0.42
15:AO:20:ASN:O	15:AO:22:THR:N	2.53	0.42
22:BA:320:A:H4'	22:BA:322:A:C8	2.54	0.42
3:CC:154:SER:HA	3:CC:165:THR:HA	2.01	0.42
29:BH:45:GLU:C	29:BH:47:PHE:N	2.72	0.42
1:CA:389:A:C6	1:CA:390:U:H1'	2.54	0.42
1:CA:209:U:H4'	1:CA:210:C:OP2	2.18	0.42
1:CA:1125:U:H4'	10:CJ:7:ARG:NH1	2.35	0.42
26:DE:111:GLU:O	26:DE:115:GLN:HG2	2.20	0.42
1:AA:1249:C:O2'	9:AI:71:GLY:HA2	2.20	0.42
22:BA:920:A:H2'	22:BA:921:C:C6	2.55	0.42
3:CC:53:SER:O	3:CC:54:ARG:HB2	2.19	0.42
22:BA:2783:U:H2'	22:BA:2784:U:C6	2.54	0.42
35:BN:8:ARG:HH21	35:BN:8:ARG:HD3	1.71	0.42
11:CK:13:ARG:HB3	11:CK:13:ARG:HE	1.57	0.42
42:DU:18:ASP:N	42:DU:18:ASP:OD2	2.52	0.42
22:DA:55:G:C2	22:DA:56:A:C8	3.08	0.42
22:BA:1309:G:H4'	50:B2:7:PRO:HG2	2.01	0.42
22:DA:1028:A:N6	22:DA:1125:G:H2'	2.35	0.42
1:CA:1505:G:H4'	1:CA:1506:U:H5''	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:118:PRO:O	29:BH:119:ASN:CB	2.68	0.42
22:BA:812:C:H5''	22:BA:1250:G:O2'	2.20	0.42
22:BA:1056:G:H21	22:BA:1103:A:H62	1.66	0.42
1:CA:6:G:H22	5:CE:102:GLY:HA2	1.85	0.42
5:CE:98:PRO:O	5:CE:122:ASN:ND2	2.52	0.42
4:AD:13:ARG:HB3	4:AD:13:ARG:HH11	1.84	0.42
26:BE:108:ILE:HD13	26:BE:181:ILE:CG1	2.48	0.42
1:CA:965:U:OP1	1:CA:1198:G:H5''	2.20	0.42
33:DL:61:LEU:O	51:D3:13:ARG:HD3	2.20	0.42
4:AD:130:VAL:HG11	4:AD:135:TYR:CD1	2.55	0.42
1:CA:728:A:C8	15:CO:54:ARG:CZ	3.03	0.42
22:BA:1808:A:H3'	22:BA:1809:A:C8	2.54	0.42
23:DB:28:C:H6	23:DB:28:C:O5'	2.03	0.42
15:AO:85:LEU:HD12	15:AO:85:LEU:HA	1.93	0.42
22:BA:1909:C:H5'	22:BA:1910:G:OP2	2.19	0.42
31:BJ:23:LYS:HE3	31:BJ:142:ILE:OXT	2.20	0.42
1:AA:1130:A:O2'	9:AI:5:GLN:HG3	2.20	0.42
2:CB:15:HIS:HD2	2:CB:209:ALA:HB2	1.85	0.42
22:DA:2873:A:O4'	35:DN:6:SER:HB2	2.19	0.42
33:DL:82:LEU:HG	33:DL:120:VAL:HG21	2.00	0.42
4:CD:56:ARG:HA	4:CD:56:ARG:NH1	2.34	0.42
24:DC:29:PRO:HB2	24:DC:30:PHE:H	1.62	0.42
44:DW:21:LEU:HD13	44:DW:40:GLN:HA	2.01	0.42
1:AA:329:A:H2'	1:AA:332:G:N7	2.35	0.42
1:AA:446:G:H2'	1:AA:447:G:O4'	2.19	0.42
42:DU:9:ASP:O	42:DU:25:VAL:HG23	2.20	0.42
5:AE:36:LEU:HD21	5:AE:137:VAL:HG11	2.02	0.42
1:CA:1244:G:C6	1:CA:1245:C:N4	2.87	0.42
26:DE:143:LEU:HB3	26:DE:146:VAL:CG1	2.50	0.42
1:AA:1201:A:H1'	1:AA:1202:U:OP2	2.20	0.42
27:DF:100:PHE:HE2	27:DF:173:PHE:CD2	2.37	0.42
21:CU:24:GLU:HA	21:CU:28:VAL:HG22	2.01	0.42
14:AN:21:PHE:HE1	14:AN:51:LEU:HD12	1.84	0.42
12:CL:84:GLY:HA2	12:CL:95:TYR:HD1	1.85	0.42
1:AA:909:A:H2'	1:AA:910:C:O4'	2.19	0.42
22:BA:2299:U:H2'	22:BA:2300:C:C6	2.55	0.42
15:CO:8:THR:O	15:CO:12:VAL:HG23	2.20	0.42
8:AH:39:VAL:HG13	8:AH:112:THR:HG22	2.02	0.42
26:BE:137:LYS:O	26:BE:141:MET:HG2	2.20	0.42
22:DA:2452:C:C4	22:DA:2453:A:C6	3.07	0.42
7:AG:95:ARG:CZ	7:AG:99:LEU:HD21	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AN:11:VAL:O	14:AN:14:VAL:HG12	2.20	0.42
34:DM:12:MET:O	34:DM:86:LYS:HE2	2.19	0.42
10:CJ:34:ALA:N	10:CJ:78:GLU:HG2	2.35	0.42
1:AA:857:C:H2'	1:AA:858:G:C8	2.55	0.42
7:CG:78:ARG:HG3	7:CG:87:VAL:HG21	2.00	0.42
22:BA:2874:C:H2'	22:BA:2875:C:H6	1.85	0.42
40:DS:23:LEU:HD22	48:D0:24:ALA:HB2	2.02	0.42
22:BA:391:A:C6	22:BA:411:G:C2	3.08	0.42
22:DA:2019:A:H4'	38:DQ:34:VAL:CG2	2.49	0.42
22:BA:413:C:H4'	22:BA:1880:U:H4'	2.02	0.42
3:AC:150:LYS:HG3	3:AC:201:TRP:CE3	2.55	0.42
12:CL:30:LYS:O	12:CL:81:LEU:HD12	2.19	0.42
1:AA:1325:C:H2'	1:AA:1326:U:H6	1.84	0.42
23:BB:78:A:C2	23:BB:99:A:C4	3.08	0.42
18:AR:55:LEU:HD22	18:AR:55:LEU:HA	1.83	0.42
52:D4:19:ARG:O	52:D4:20:ASP:HB2	2.20	0.42
52:B4:2:LYS:HE2	52:B4:4:ARG:NE	2.34	0.42
22:DA:1029:A:N7	22:DA:1030:C:C2	2.88	0.42
22:DA:127:A:H5''	22:DA:128:C:C6	2.55	0.42
22:BA:1132:U:H3'	22:BA:1133:A:H5''	2.01	0.42
1:AA:1187:G:H5'	9:AI:115:LYS:HE3	2.01	0.42
22:BA:2093:G:O3'	29:BH:25:TYR:HB2	2.20	0.42
1:CA:1361:G:H2'	1:CA:1362:A:H5''	2.01	0.42
1:CA:1098:C:H2'	1:CA:1099:G:O4'	2.20	0.42
22:BA:1098:A:C5	22:BA:1099:G:C6	3.08	0.42
30:BI:11:LEU:O	30:BI:24:VAL:HG11	2.20	0.42
22:BA:1482:G:C2	22:BA:1483:G:C8	3.08	0.42
22:BA:1482:G:H1	22:BA:1507:C:H42	1.66	0.42
1:CA:1123:U:O3'	10:CJ:38:GLY:HA3	2.20	0.42
22:DA:2278:A:H5''	44:DW:12:ASN:HD21	1.85	0.42
21:CU:35:ARG:NH2	57:CU:101:HOH:O	2.52	0.42
30:DI:80:LEU:HD22	30:DI:138:LEU:HD11	2.00	0.42
22:DA:965:C:O5'	22:DA:2273:A:H1'	2.20	0.42
27:DF:117:LEU:O	27:DF:177:PHE:HA	2.19	0.42
2:AB:106:THR:HA	2:AB:109:GLN:HE22	1.85	0.42
1:AA:1160:G:O2'	1:AA:1161:C:P	2.78	0.42
25:DD:12:THR:HG21	37:DP:5:ILE:HG23	2.02	0.42
3:AC:53:SER:CB	3:AC:115:LEU:HG	2.47	0.42
1:CA:200:G:C3'	1:CA:201:G:H5''	2.50	0.42
1:AA:407:U:H2'	1:AA:408:A:C8	2.50	0.42
1:AA:721:G:C6	1:AA:733:G:C2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:25:ARG:HG2	20:AT:29:ARG:NH1	2.33	0.42
22:DA:13:A:H4'	22:DA:14:A:OP1	2.19	0.42
11:AK:126:LYS:N	11:AK:126:LYS:HD3	2.35	0.42
22:DA:2415:G:C6	22:DA:2416:C:C4	3.08	0.42
15:CO:39:LEU:HG	15:CO:43:PHE:HE1	1.80	0.42
22:BA:441:U:H2'	22:BA:442:G:H8	1.85	0.42
1:AA:1170:A:O5'	1:AA:1170:A:H8	2.02	0.42
16:CP:5:ARG:O	16:CP:19:VAL:HA	2.20	0.42
1:AA:663:A:H5'	1:AA:836:G:OP1	2.20	0.42
19:CS:40:ILE:HA	19:CS:44:MET:SD	2.60	0.42
24:BC:74:ILE:HA	24:BC:75:PRO:HD3	1.91	0.42
1:AA:705:G:N2	11:AK:31:ILE:HD13	2.35	0.42
1:AA:208:U:C5	1:AA:210:C:C4	3.07	0.42
30:BI:58:VAL:HB	30:BI:69:PHE:HB2	2.02	0.42
22:BA:458:G:C8	50:B2:37:LYS:HG2	2.55	0.42
17:CQ:69:LYS:O	17:CQ:70:THR:OG1	2.33	0.42
44:DW:52:GLY:HA3	44:DW:60:PHE:CE1	2.55	0.42
22:BA:1946:U:H2'	22:BA:1947:C:H6	1.84	0.42
7:AG:97:ASN:HA	7:AG:100:ALA:HB3	2.01	0.42
1:CA:815:A:N7	1:CA:1509:C:O2'	2.41	0.42
25:DD:32:ASN:HA	25:DD:52:THR:HB	2.00	0.42
49:D1:12:VAL:HG23	49:D1:51:GLU:HB3	2.02	0.42
42:BU:40:ASN:HB3	42:BU:63:ALA:O	2.19	0.42
12:CL:44:LYS:HD3	12:CL:44:LYS:H	1.84	0.42
1:CA:976:G:OP1	14:CN:71:HIS:ND1	2.47	0.42
1:AA:484:G:OP1	1:AA:484:G:H8	2.01	0.42
1:CA:445:G:C2	1:CA:490:C:C2	3.08	0.42
21:AU:25:LYS:HD2	21:AU:26:ALA:H	1.84	0.42
40:BS:41:LYS:O	40:BS:44:ALA:HB3	2.20	0.42
6:AF:81:ASN:O	6:AF:84:VAL:HG12	2.19	0.42
22:DA:145:C:H2'	22:DA:146:A:C8	2.54	0.42
22:DA:337:C:H2'	22:DA:338:G:O4'	2.20	0.42
23:BB:36:C:H5''	23:BB:37:C:OP2	2.20	0.42
17:CQ:5:ILE:HB	17:CQ:6:ARG:H	1.47	0.42
35:DN:74:GLU:O	35:DN:77:ALA:HB3	2.19	0.42
22:BA:2444:G:OP2	26:BE:63:LYS:HD2	2.20	0.42
2:CB:186:ILE:HA	2:CB:200:ILE:HB	2.00	0.42
32:BK:38:ILE:HD11	32:BK:112:PHE:HZ	1.85	0.42
31:BJ:77:HIS:HA	31:BJ:83:GLY:O	2.20	0.42
22:BA:1316:U:C2	22:BA:1337:G:N2	2.88	0.42
26:BE:79:ARG:HH11	26:BE:79:ARG:HG2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:13:A:N1	22:BA:525:U:H2'	2.35	0.42
25:BD:86:GLU:O	25:BD:86:GLU:HG3	2.20	0.42
43:BV:80:HIS:CE1	43:BV:83:LYS:HE3	2.54	0.42
21:CU:10:GLU:CG	21:CU:11:PRO:HD3	2.40	0.42
5:CE:153:VAL:HG23	5:CE:157:ARG:HB2	2.02	0.42
38:DQ:58:ARG:HA	38:DQ:61:TRP:CE3	2.54	0.42
10:CJ:35:GLN:HB3	10:CJ:36:VAL:H	1.53	0.42
5:AE:106:ILE:HG13	5:AE:124:LEU:HB3	2.02	0.42
13:CM:29:ARG:NH1	13:CM:33:ILE:HD11	2.35	0.42
36:DO:100:HIS:CD2	36:DO:101:GLY:N	2.88	0.42
22:DA:2698:U:H2'	22:DA:2699:C:C6	2.55	0.42
1:AA:1034:G:H2'	1:AA:1035:A:O4'	2.19	0.42
35:BN:81:ASN:O	35:BN:85:PRO:HG2	2.20	0.42
1:CA:747:A:N6	1:CA:748:G:C6	2.88	0.42
1:CA:408:A:H2'	1:CA:409:U:O4'	2.20	0.42
1:CA:410:G:OP1	4:CD:26:ARG:NH2	2.47	0.42
35:BN:72:ASP:O	35:BN:76:VAL:HG12	2.20	0.42
1:AA:1226:C:P	13:AM:90:ARG:HH22	2.42	0.42
22:DA:262:A:H5'	22:DA:610:C:O2'	2.20	0.42
22:BA:2886:A:C5	22:BA:2887:A:C8	3.08	0.42
22:DA:662:G:O3'	33:DL:16:GLY:HA2	2.20	0.42
52:B4:3:VAL:HG12	52:B4:36:ARG:HB3	2.02	0.42
1:CA:518:C:H2'	1:CA:530:G:H8	1.81	0.42
22:DA:1567:G:O2'	24:DC:63:ARG:NH1	2.53	0.42
22:BA:476:G:N2	22:BA:479:A:O4'	2.52	0.42
46:BY:56:LEU:O	46:BY:57:LEU:HB3	2.19	0.42
23:DB:41:G:P	23:DB:43:C:H41	2.43	0.42
52:D4:3:VAL:HG12	52:D4:36:ARG:HB3	2.01	0.42
6:AF:42:TRP:CZ2	6:AF:61:LEU:HD22	2.53	0.42
22:DA:1373:A:C4	22:DA:1374:G:H1'	2.54	0.42
1:CA:938:A:O3'	7:CG:95:ARG:NH2	2.53	0.42
26:DE:129:PRO:HG3	26:DE:156:ASN:OD1	2.20	0.42
22:DA:1896:G:H2'	22:DA:1897:G:O4'	2.20	0.42
1:AA:151:A:H2'	1:AA:152:A:O4'	2.20	0.42
28:BG:49:THR:O	28:BG:50:LEU:HD23	2.20	0.42
17:AQ:17:MET:HG2	17:AQ:20:SER:HB3	2.01	0.42
22:DA:2314:A:O4'	27:DF:155:THR:HG21	2.19	0.42
22:DA:2385:C:H2'	22:DA:2386:A:H8	1.83	0.42
1:AA:223:A:H2'	1:AA:224:U:C6	2.55	0.42
34:BM:16:ARG:HA	34:BM:16:ARG:HD3	1.89	0.42
1:CA:1538:C:H2'	1:CA:1539:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2:G:H2'	22:BA:3:U:C6	2.55	0.42
41:DT:49:LYS:O	41:DT:51:PHE:N	2.53	0.42
22:DA:1132:U:O2'	22:DA:1133:A:H5'	2.20	0.42
24:DC:3:VAL:HG11	24:DC:202:LEU:HD23	2.00	0.42
13:CM:74:SER:O	13:CM:78:LYS:HG3	2.20	0.42
22:DA:2259:U:H2'	22:DA:2260:C:C6	2.55	0.42
22:BA:2392:A:O2'	33:BL:60:ARG:O	2.35	0.42
19:AS:63:THR:O	19:AS:65:GLU:N	2.43	0.42
1:CA:276:G:C6	1:CA:277:C:C4	3.08	0.42
43:BV:10:LYS:HG2	43:BV:11:GLU:HG2	2.01	0.42
1:CA:828:U:O2	2:CB:25:PRO:HG2	2.20	0.42
1:CA:1408:A:C2	1:CA:1494:G:C4	3.08	0.42
1:CA:560:A:H5'	1:CA:566:G:N2	2.34	0.42
1:AA:625:U:H4'	16:AP:16:PHE:CE2	2.54	0.42
1:CA:1293:C:H3'	1:CA:1294:G:H8	1.84	0.42
41:DT:23:ALA:O	41:DT:27:SER:N	2.43	0.42
4:AD:95:GLU:OE2	4:AD:104:ARG:NH1	2.52	0.42
2:CB:47:VAL:O	2:CB:51:ASN:ND2	2.53	0.42
22:DA:565:C:H4'	22:DA:1253:A:N6	2.35	0.42
12:CL:116:LYS:H	12:CL:116:LYS:HG3	1.68	0.42
31:DJ:59:ALA:O	31:DJ:62:VAL:HG12	2.20	0.42
26:BE:58:LYS:HZ1	26:BE:62:GLN:CA	2.33	0.42
2:CB:128:LYS:HD2	2:CB:128:LYS:HA	1.86	0.42
2:CB:128:LYS:O	2:CB:129:LEU:HB2	2.19	0.42
39:DR:24:LYS:HA	39:DR:94:THR:OG1	2.20	0.42
22:BA:2093:G:O5'	29:BH:24:GLY:HA3	2.20	0.41
26:DE:181:ILE:HG23	33:DL:2:ARG:NH1	2.35	0.41
22:DA:2163:A:C6	22:DA:2164:C:H1'	2.54	0.41
10:CJ:35:GLN:NE2	10:CJ:77:VAL:HB	2.35	0.41
6:CF:9:MET:CG	6:CF:86:ARG:HB2	2.44	0.41
29:DH:53:GLU:C	29:DH:55:GLU:N	2.72	0.41
1:AA:620:C:H2'	1:AA:621:A:O4'	2.19	0.41
19:CS:11:ILE:HB	19:CS:38:SER:CB	2.50	0.41
22:BA:2127:G:H21	22:BA:2173:A:H1'	1.85	0.41
29:BH:104:THR:CG2	29:BH:110:VAL:O	2.68	0.41
22:BA:361:G:O2'	22:BA:362:A:O5'	2.36	0.41
22:DA:971:G:C2	22:DA:972:A:H1'	2.55	0.41
1:CA:501:C:H2'	1:CA:502:A:C8	2.55	0.41
22:DA:1364:G:N2	22:DA:1367:A:OP2	2.26	0.41
1:CA:608:A:H3'	1:CA:609:A:H8	1.85	0.41
30:DI:127:ARG:HA	30:DI:130:GLU:HB2	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:308:G:C6	22:DA:309:A:C6	3.08	0.41
43:DV:41:GLU:C	43:DV:42:LEU:HD23	2.40	0.41
9:AI:51:PRO:HB3	9:AI:84:THR:CG2	2.50	0.41
22:DA:806:C:H2'	22:DA:807:U:C6	2.55	0.41
1:CA:841:C:H2'	1:CA:843:U:O4'	2.20	0.41
3:CC:22:TRP:CZ3	14:CN:94:PRO:HG2	2.54	0.41
22:BA:66:C:H2'	22:BA:67:U:H6	1.84	0.41
22:BA:1534:U:H3'	22:BA:1536:C:H41	1.84	0.41
22:DA:2340:A:H2'	22:DA:2341:G:C8	2.55	0.41
1:AA:1222:G:C6	1:AA:1223:C:C4	3.08	0.41
22:BA:58:G:OP1	41:BT:78:SER:CB	2.68	0.41
3:CC:129:MET:HG2	3:CC:131:ARG:HH11	1.84	0.41
22:DA:1726:C:H2'	22:DA:1727:C:C6	2.54	0.41
22:DA:1572:A:H2'	22:DA:1573:G:C8	2.55	0.41
20:AT:4:ILE:HG12	20:AT:8:LYS:NZ	2.35	0.41
24:BC:40:SER:O	24:BC:42:GLY:N	2.53	0.41
1:CA:1262:C:H2'	1:CA:1263:C:O4'	2.20	0.41
22:DA:1669:A:OP2	57:DA:3719:HOH:O	2.22	0.41
52:D4:12:ARG:HB2	52:D4:12:ARG:CZ	2.50	0.41
22:DA:377:G:C6	22:DA:378:C:C4	3.08	0.41
1:AA:1211:U:H1'	1:AA:1213:A:C2	2.55	0.41
1:CA:512:U:H2'	1:CA:513:C:C6	2.55	0.41
22:DA:2296:U:H4'	22:DA:2297:A:OP1	2.19	0.41
9:CI:49:ARG:NH2	9:CI:53:GLU:HA	2.34	0.41
24:BC:266:PHE:CD1	24:BC:266:PHE:N	2.86	0.41
22:BA:532:A:HO2'	22:BA:2021:C:H5	1.67	0.41
1:CA:1249:C:O3'	9:CI:75:GLN:NE2	2.50	0.41
24:BC:243:HIS:O	24:BC:245:VAL:HG13	2.20	0.41
36:DO:88:LYS:HD3	36:DO:116:GLN:NE2	2.35	0.41
22:BA:109:C:H2'	22:BA:110:G:O4'	2.19	0.41
1:AA:679:C:H2'	1:AA:680:C:C6	2.55	0.41
41:BT:37:ASP:OD1	41:BT:37:ASP:N	2.43	0.41
5:CE:93:ARG:HB3	5:CE:93:ARG:NH1	2.35	0.41
34:BM:61:GLY:HA2	34:BM:107:GLY:HA3	2.02	0.41
19:AS:19:VAL:O	19:AS:23:VAL:HG23	2.20	0.41
22:BA:607:U:O4	22:BA:620:G:H5'	2.19	0.41
6:CF:29:ILE:HG22	6:CF:34:GLY:O	2.20	0.41
22:DA:1211:C:H5''	22:DA:1212:G:C8	2.55	0.41
1:AA:907:A:C4	1:AA:908:A:C8	3.07	0.41
31:BJ:13:ARG:HB3	31:BJ:51:GLY:O	2.20	0.41
29:BH:139:PHE:O	29:BH:140:ALA:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:90:LEU:HD13	29:BH:125:THR:HA	2.03	0.41
29:DH:41:LYS:HE2	29:DH:44:ILE:CD1	2.50	0.41
22:BA:1250:G:H5'	38:BQ:6:ARG:HD3	2.02	0.41
22:DA:1069:A:N1	22:DA:1073:A:N7	2.69	0.41
21:AU:38:TYR:C	21:AU:41:PRO:HD2	2.41	0.41
27:DF:114:PHE:HE1	27:DF:117:LEU:HD22	1.85	0.41
36:DO:74:VAL:O	36:DO:78:VAL:HG23	2.20	0.41
35:DN:55:ALA:HB2	35:DN:79:LEU:HB3	2.00	0.41
22:DA:2305:U:O4'	27:DF:131:GLY:HA3	2.20	0.41
16:AP:75:ILE:HG13	16:AP:75:ILE:H	1.50	0.41
22:DA:319:G:H2'	22:DA:320:A:O4'	2.20	0.41
1:AA:93:U:C2'	1:AA:94:G:H5''	2.49	0.41
2:CB:206:ALA:O	2:CB:210:VAL:HG13	2.19	0.41
22:BA:2684:U:C4	22:BA:2685:G:N7	2.89	0.41
22:DA:223:A:H2'	22:DA:408:G:N3	2.35	0.41
28:BG:141:ILE:HD12	28:BG:142:GLY:N	2.35	0.41
22:DA:1045:C:C3'	22:DA:1046:A:H5'	2.50	0.41
1:CA:1316:G:N2	1:CA:1318:A:H3'	2.35	0.41
1:CA:1053:G:N7	1:CA:1199:U:H3'	2.35	0.41
22:DA:1596:A:C6	22:DA:1597:A:C6	3.08	0.41
36:DO:71:ALA:HB1	36:DO:106:LEU:HB2	2.02	0.41
1:CA:26:A:H61	1:CA:558:G:H1'	1.85	0.41
22:BA:747:U:C4	22:BA:2613:U:C5	3.08	0.41
22:BA:1820:U:O2	24:BC:200:HIS:HB3	2.20	0.41
39:DR:19:THR:CG2	39:DR:95:ASP:HB3	2.50	0.41
1:AA:874:G:C6	1:AA:875:U:C4	3.08	0.41
1:AA:628:G:H2'	1:AA:629:A:O4'	2.21	0.41
1:CA:765:G:N2	1:CA:813:U:H5	2.18	0.41
1:CA:115:G:H1'	1:CA:116:A:N7	2.35	0.41
2:AB:120:GLN:HG2	2:AB:125:THR:O	2.20	0.41
17:AQ:26:GLU:OE2	17:AQ:39:LYS:HB3	2.20	0.41
24:BC:141:VAL:HG11	24:BC:190:ALA:HB1	2.01	0.41
12:AL:114:ARG:NH2	12:AL:121:ARG:HA	2.34	0.41
50:B2:9:VAL:HG12	50:B2:13:ASN:HD21	1.86	0.41
22:DA:181:A:H1'	22:DA:435:C:O4'	2.20	0.41
26:BE:29:HIS:CE1	33:BL:8:PRO:HB3	2.55	0.41
22:BA:675:A:N3	22:BA:2443:C:O2'	2.50	0.41
1:AA:803:G:H8	1:AA:803:G:O5'	2.03	0.41
22:BA:2006:C:O5'	22:BA:2006:C:H6	2.03	0.41
47:DZ:25:LEU:HD23	47:DZ:25:LEU:HA	1.89	0.41
49:B1:53:LYS:H	49:B1:53:LYS:HG2	1.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BX:22:LEU:HD23	45:BX:22:LEU:HA	1.77	0.41
29:DH:135:HIS:CG	29:DH:136:SER:N	2.89	0.41
1:AA:16:A:H4'	5:AE:22:SER:H	1.85	0.41
22:DA:852:U:H2'	22:DA:853:C:C6	2.55	0.41
13:CM:63:PHE:O	13:CM:65:VAL:HG13	2.20	0.41
11:AK:16:VAL:HG12	11:AK:77:TYR:HB3	2.02	0.41
22:DA:483:A:O3'	42:DU:48:PRO:HD3	2.20	0.41
8:CH:40:LEU:HD21	8:CH:129:VAL:HG21	2.03	0.41
2:CB:193:PRO:HB2	2:CB:194:ASP:H	1.68	0.41
26:BE:27:LEU:O	26:BE:31:VAL:HG23	2.20	0.41
28:BG:127:THR:HG22	28:BG:128:GLN:N	2.34	0.41
6:AF:64:VAL:HG12	6:AF:65:GLU:N	2.34	0.41
7:AG:58:GLU:HB3	7:AG:59:LEU:H	1.59	0.41
45:DX:5:CYS:SG	45:DX:52:SER:HB3	2.60	0.41
22:DA:2347:C:O2'	49:D1:39:PHE:HB3	2.19	0.41
6:CF:18:VAL:O	6:CF:21:MET:HB2	2.21	0.41
19:CS:34:TRP:HA	19:CS:52:HIS:HB2	2.02	0.41
45:BX:18:ARG:NE	45:BX:24:ALA:HB2	2.35	0.41
1:AA:983:A:H2'	1:AA:983:A:N3	2.35	0.41
3:AC:6:HIS:CE1	3:AC:8:ASN:HB3	2.56	0.41
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.72	0.41
12:CL:38:TYR:N	12:CL:52:VAL:O	2.46	0.41
14:CN:13:ARG:HG2	14:CN:54:ASP:CG	2.40	0.41
20:AT:23:SER:OG	20:AT:24:ARG:N	2.53	0.41
28:BG:77:ILE:H	28:BG:77:ILE:HG12	1.45	0.41
27:BF:148:ARG:HG2	27:BF:149:VAL:H	1.84	0.41
22:BA:215:G:H4'	22:BA:216:A:OP1	2.21	0.41
22:DA:1819:A:H4'	22:DA:1820:U:H5''	2.02	0.41
1:AA:579:A:H4'	1:AA:728:A:H1'	2.02	0.41
1:CA:1479:C:H2'	1:CA:1480:A:H8	1.85	0.41
1:CA:1118:U:H1'	1:CA:1179:A:C5	2.55	0.41
22:DA:2824:C:N4	22:DA:2825:G:N7	2.69	0.41
22:DA:1056:G:H4'	22:DA:1086:A:C8	2.55	0.41
15:CO:24:SER:O	15:CO:27:VAL:HB	2.19	0.41
22:BA:320:A:H4'	22:BA:322:A:N7	2.35	0.41
2:CB:68:LEU:HD21	2:CB:92:VAL:HG23	2.01	0.41
22:BA:2398:U:H2'	22:BA:2399:G:H8	1.85	0.41
2:CB:58:ASN:OD1	2:CB:61:ALA:HB3	2.19	0.41
32:DK:105:ARG:NH1	37:DP:34:GLU:HG3	2.35	0.41
7:CG:103:TRP:O	7:CG:107:ALA:N	2.48	0.41
22:DA:705:A:H2'	22:DA:706:A:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:89:LYS:HG3	8:AH:90:ASP:H	1.85	0.41
9:CI:54:LEU:O	9:CI:55:VAL:HG13	2.20	0.41
1:AA:977:A:O2'	1:AA:979:C:OP2	2.35	0.41
1:AA:730:G:H2'	1:AA:730:G:N3	2.35	0.41
42:DU:26:LYS:HD2	42:DU:26:LYS:HA	1.73	0.41
3:AC:97:VAL:HB	3:AC:98:PRO:HD2	2.01	0.41
45:BX:59:ILE:HA	45:BX:67:VAL:HG21	2.02	0.41
6:AF:75:GLU:HA	6:AF:78:PHE:HB2	2.00	0.41
22:BA:1074:G:C6	22:BA:1075:C:C4	3.09	0.41
2:AB:23:TRP:HB3	2:AB:39:HIS:HE1	1.85	0.41
8:CH:64:LYS:HB3	8:CH:64:LYS:HE2	1.76	0.41
18:CR:20:GLU:HG3	18:CR:55:LEU:HD13	2.01	0.41
4:AD:197:GLU:O	4:AD:200:ILE:N	2.53	0.41
40:BS:96:ILE:HD12	40:BS:98:LYS:HG3	2.02	0.41
26:DE:58:LYS:HA	26:DE:59:PRO:HD3	1.95	0.41
1:AA:1162:C:C2	1:AA:1163:A:C8	3.08	0.41
2:CB:33:GLY:CA	2:CB:40:ILE:H	2.28	0.41
22:BA:14:A:H8	22:BA:14:A:O5'	2.03	0.41
11:CK:112:ASP:OD1	11:CK:114:THR:HG23	2.20	0.41
22:BA:182:A:H2	22:BA:433:C:O2	2.03	0.41
50:D2:31:LEU:HD21	50:D2:43:THR:HG22	2.02	0.41
1:CA:200:G:C2'	1:CA:201:G:H5''	2.51	0.41
1:AA:1217:C:OP1	14:AN:9:ARG:NE	2.38	0.41
22:DA:188:G:C2	22:DA:209:C:N3	2.88	0.41
22:DA:2033:A:H2'	22:DA:2033:A:OP1	2.20	0.41
15:CO:55:GLY:O	15:CO:59:MET:HG3	2.19	0.41
31:DJ:7:LYS:HA	31:DJ:8:PRO:HD3	1.92	0.41
1:AA:544:G:C6	1:AA:545:C:C4	3.08	0.41
22:BA:1837:C:C2	22:BA:1899:A:N6	2.89	0.41
22:DA:2886:A:C2	22:DA:2887:A:H1'	2.56	0.41
22:BA:1759:A:H2'	22:BA:1760:C:H6	1.84	0.41
1:AA:1318:A:H1'	19:AS:37:ARG:NH1	2.35	0.41
22:DA:1692:U:O2'	22:DA:1693:U:H2'	2.20	0.41
22:BA:753:A:H2'	22:BA:754:U:C6	2.56	0.41
4:AD:157:ALA:O	4:AD:161:LEU:HD13	2.21	0.41
21:CU:12:PHE:CD1	21:CU:13:ASP:N	2.87	0.41
22:DA:517:C:O2'	40:DS:18:ARG:NH2	2.48	0.41
32:BK:105:ARG:HH21	37:BP:32:VAL:HG21	1.85	0.41
43:BV:80:HIS:CE1	43:BV:83:LYS:HG3	2.56	0.41
22:BA:620:G:H4'	22:BA:621:A:O5'	2.20	0.41
22:BA:1355:G:C2	22:BA:1356:G:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:B6:4:PRO:HA	54:B6:5:MHU:HM1	1.83	0.41
22:DA:2467:C:N4	22:DA:2468:A:C6	2.89	0.41
22:DA:1346:G:H2'	22:DA:1347:A:H8	1.86	0.41
22:BA:1384:A:H1'	22:BA:1405:U:H1'	2.03	0.41
12:CL:56:ARG:NH1	12:CL:62:GLU:HB2	2.35	0.41
18:CR:59:ILE:HG22	18:CR:63:ARG:HD2	2.02	0.41
13:AM:7:ILE:HD12	13:AM:8:ASN:H	1.85	0.41
22:DA:1464:G:H2'	22:DA:1465:G:C8	2.55	0.41
21:CU:39:GLU:HA	21:CU:42:THR:OG1	2.21	0.41
39:DR:3:ALA:HB2	39:DR:101:ILE:HG23	2.03	0.41
27:BF:175:PHE:HD1	27:BF:177:PHE:CE1	2.39	0.41
28:DG:86:LYS:HG3	28:DG:132:VAL:HG22	2.02	0.41
28:DG:27:LYS:HE2	28:DG:27:LYS:HB2	1.75	0.41
1:AA:603:U:H2'	1:AA:604:G:C8	2.55	0.41
7:CG:47:LEU:HA	7:CG:47:LEU:HD12	1.88	0.41
51:B3:7:VAL:HB	51:B3:61:CYS:HB3	2.02	0.41
22:BA:1770:G:C5	22:BA:1983:G:C6	3.09	0.41
22:BA:2646:C:OP2	22:BA:2732:G:O2'	2.28	0.41
4:CD:57:GLU:O	4:CD:60:LYS:N	2.54	0.41
2:AB:24:ASN:HA	2:AB:25:PRO:HD2	1.93	0.41
5:CE:149:SER:O	5:CE:153:VAL:HG13	2.21	0.41
1:AA:430:A:OP1	4:AD:9:LEU:HB2	2.21	0.41
13:AM:20:THR:HA	13:AM:25:VAL:HG23	2.01	0.41
22:DA:248:G:H5'	22:DA:250:G:N7	2.36	0.41
1:CA:729:A:H2'	1:CA:730:G:O4'	2.20	0.41
2:AB:117:LEU:HA	2:AB:117:LEU:HD13	1.92	0.41
45:DX:17:ASN:ND2	45:DX:27:ARG:HD2	2.36	0.41
1:CA:462:G:H5''	1:CA:463:U:OP2	2.20	0.41
16:AP:75:ILE:O	16:AP:78:VAL:HG12	2.21	0.41
22:BA:2125:G:H21	22:BA:2173:A:H62	1.68	0.41
22:DA:1021:A:H8	22:DA:1122:G:O2'	2.03	0.41
22:DA:2853:C:H2'	22:DA:2854:G:H8	1.83	0.41
22:DA:2136:G:H1	22:DA:2156:G:H1'	1.83	0.41
35:BN:114:GLU:HG3	35:BN:115:LEU:O	2.20	0.41
2:AB:104:TRP:CH2	2:AB:154:MET:HG2	2.56	0.41
2:AB:66:LYS:O	2:AB:159:ASP:HB2	2.20	0.41
33:BL:96:LYS:HG3	33:BL:101:ILE:HD11	2.00	0.41
16:AP:47:GLU:HB2	16:AP:48:GLU:H	1.70	0.41
25:DD:148:GLN:HB2	25:DD:152:PRO:HG2	2.02	0.41
22:BA:321:U:OP2	26:BE:130:LYS:HD3	2.21	0.41
22:DA:222:A:H3'	22:DA:421:C:C5'	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:155:GLY:N	3:AC:164:ARG:O	2.37	0.41
22:DA:749:A:C5	22:DA:750:A:C8	3.08	0.41
1:AA:982:U:H4'	1:AA:983:A:C5'	2.51	0.41
2:AB:57:LEU:HB2	2:AB:184:PHE:CE1	2.56	0.41
1:AA:662:U:H2'	1:AA:663:A:C8	2.55	0.41
1:CA:938:A:N6	1:CA:939:G:C6	2.89	0.41
22:DA:1744:A:H3'	22:DA:1745:A:H8	1.86	0.41
22:DA:1431:A:H2'	22:DA:1432:G:O4'	2.21	0.41
1:CA:1053:G:O5'	1:CA:1054:C:H3'	2.20	0.41
22:DA:2631:G:N3	22:DA:2810:A:H2	2.18	0.41
29:DH:2:GLN:O	29:DH:3:VAL:O	2.38	0.41
21:CU:53:VAL:HG13	21:CU:54:LYS:H	1.85	0.41
40:BS:90:LYS:HZ3	54:B6:8:MHT:H5	1.85	0.41
27:BF:74:VAL:O	27:BF:79:ILE:HG13	2.20	0.41
24:BC:40:SER:C	24:BC:42:GLY:N	2.73	0.41
4:CD:146:ARG:O	4:CD:150:LYS:HB2	2.21	0.41
1:CA:1480:A:H2'	1:CA:1481:U:O4'	2.20	0.41
10:AJ:27:GLU:HA	10:AJ:30:LYS:HE2	2.02	0.41
22:DA:1485:U:H2'	22:DA:1486:U:C6	2.56	0.41
30:BI:130:GLU:HB3	30:BI:134:ARG:NH2	2.36	0.41
24:BC:180:GLU:HG3	24:BC:269:ARG:O	2.20	0.41
41:BT:10:VAL:HG12	41:BT:11:LEU:HD23	2.03	0.41
36:BO:79:ALA:HB2	36:BO:110:ALA:HA	2.03	0.41
1:CA:418:C:O2'	1:CA:540:G:H1'	2.20	0.41
43:DV:83:LYS:HA	43:DV:84:PRO:HD3	1.93	0.41
22:BA:1501:G:O2'	22:BA:1502:A:H5'	2.20	0.41
1:CA:190:A:H2'	1:CA:191:G:O4'	2.20	0.41
32:DK:13:ASN:OD1	32:DK:97:THR:N	2.38	0.41
22:BA:1394:U:H2'	22:BA:1395:A:O4'	2.19	0.41
49:D1:48:ILE:HD12	49:D1:48:ILE:H	1.84	0.41
7:AG:45:SER:HA	7:AG:48:GLU:HB2	2.01	0.41
1:AA:1074:G:C2	1:AA:1075:U:C2	3.09	0.41
1:CA:1403:C:H2'	1:CA:1404:C:C6	2.54	0.41
29:BH:33:GLN:O	29:BH:35:LYS:N	2.53	0.41
29:DH:40:THR:OG1	29:DH:43:ASN:ND2	2.53	0.41
22:BA:1060:U:H5'	22:BA:1062:G:H4'	2.03	0.41
22:BA:1061:U:H3'	22:BA:1062:G:H5'	2.01	0.41
4:AD:173:VAL:HG22	4:AD:174:ASP:N	2.36	0.41
22:DA:694:U:O2'	22:DA:1378:A:H2	2.03	0.41
22:DA:247:G:OP2	22:DA:249:C:N4	2.54	0.41
1:AA:1190:G:P	3:AC:5:VAL:H	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AN:43:ASN:C	14:AN:45:VAL:N	2.74	0.41
22:BA:1917:U:C2'	22:BA:1918:A:H5'	2.51	0.41
9:AI:50:GLN:HG2	9:AI:53:GLU:OE2	2.20	0.41
22:DA:2286:G:OP1	49:D1:30:LYS:HE3	2.21	0.41
30:DI:130:GLU:HG2	30:DI:134:ARG:HH22	1.86	0.41
33:DL:77:ILE:HB	33:DL:109:LYS:O	2.21	0.41
22:DA:2591:C:P	24:DC:238:ARG:HG3	2.60	0.41
4:CD:169:THR:C	4:CD:171:LEU:H	2.24	0.41
43:DV:9:ARG:CG	43:DV:41:GLU:HB3	2.50	0.41
31:DJ:4:PHE:CD1	38:DQ:100:VAL:HG11	2.55	0.41
46:BY:57:LEU:CA	46:BY:60:LYS:HB3	2.51	0.41
24:DC:158:ALA:HB1	24:DC:197:ASN:O	2.20	0.41
8:CH:7:ILE:HB	8:CH:77:ARG:HH12	1.86	0.41
22:DA:532:A:N3	22:DA:532:A:H2'	2.36	0.41
22:BA:1515:A:H3'	22:BA:1516:G:C8	2.53	0.41
2:AB:94:HIS:CE1	2:AB:146:ASN:HB2	2.55	0.41
34:BM:2:LEU:HD12	34:BM:68:PHE:CE1	2.56	0.41
22:DA:1923:U:H2'	22:DA:1924:C:C6	2.56	0.41
11:CK:71:ALA:O	11:CK:75:LYS:HG3	2.19	0.41
16:CP:22:ALA:HA	16:CP:33:ILE:HD12	2.01	0.41
22:DA:770:G:H1'	22:DA:1379:U:C4	2.56	0.41
2:AB:175:GLU:O	2:AB:178:ASN:HB3	2.21	0.41
7:CG:22:LEU:HA	7:CG:25:LYS:HE2	2.02	0.41
6:AF:4:TYR:CE2	6:AF:71:ILE:HG21	2.55	0.41
1:CA:1520:C:H2'	1:CA:1521:C:C6	2.55	0.41
37:BP:34:GLU:O	37:BP:36:SER:N	2.53	0.41
22:BA:1279:G:H4'	35:BN:31:HIS:CD2	2.56	0.41
48:B0:55:ILE:HG22	48:B0:56:ALA:N	2.35	0.41
22:DA:1856:U:C4	22:DA:1857:G:C6	3.08	0.41
22:BA:2069:G:C2	22:BA:2443:C:C2	3.08	0.41
22:BA:262:A:H2'	22:BA:263:G:O4'	2.20	0.41
15:CO:53:ARG:O	15:CO:56:LEU:HB3	2.21	0.41
44:BW:69:PHE:CE1	44:BW:80:ILE:HD11	2.56	0.41
1:CA:1434:A:H2'	1:CA:1435:G:O4'	2.20	0.41
20:AT:35:VAL:HG11	20:AT:79:LEU:HD13	2.01	0.41
9:CI:28:ILE:HB	9:CI:35:LEU:HB2	2.01	0.41
22:BA:547:A:C8	22:BA:548:G:N3	2.88	0.41
25:DD:114:LYS:HE2	25:DD:196:ALA:HA	2.03	0.41
7:CG:97:ASN:O	7:CG:100:ALA:HB3	2.21	0.41
20:AT:44:LYS:HD3	20:AT:87:ALA:HA	2.03	0.41
45:DX:2:SER:O	45:DX:4:VAL:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2563:U:H1'	22:DA:2566:A:N6	2.35	0.41
50:B2:26:ASN:HA	50:B2:29:GLN:HB2	2.03	0.41
19:CS:58:VAL:HA	19:CS:59:PRO:HD3	1.85	0.41
31:BJ:117:ALA:HA	31:BJ:120:ARG:HD2	2.02	0.41
1:CA:1149:C:O5'	1:CA:1149:C:H6	2.04	0.41
22:BA:1148:U:C2'	22:BA:1149:G:H5'	2.51	0.41
22:BA:204:A:OP1	22:BA:204:A:H8	2.04	0.41
22:BA:2543:G:H2'	22:BA:2544:G:C8	2.56	0.41
22:BA:1420:A:O2'	22:BA:2211:A:N6	2.52	0.41
22:BA:1421:G:C2	22:BA:1422:G:C8	3.09	0.41
22:BA:518:G:H2'	22:BA:519:U:C6	2.56	0.41
1:AA:176:C:H2'	1:AA:177:G:N3	2.36	0.41
29:BH:100:ALA:HB2	29:BH:115:VAL:CG2	2.50	0.41
29:BH:95:GLY:HA2	29:BH:117:LEU:CD2	2.51	0.41
22:DA:555:G:O2'	22:DA:556:A:OP2	2.33	0.41
1:AA:262:A:C6	1:AA:263:A:C6	3.09	0.41
22:DA:994:C:H1'	39:DR:10:LYS:HE3	2.01	0.41
22:BA:191:A:H2'	22:BA:192:C:C6	2.56	0.41
22:DA:2058:A:N6	22:DA:2059:A:N6	2.68	0.41
22:DA:2134:A:N3	22:DA:2159:G:H1'	2.36	0.41
22:DA:1070:A:H2'	22:DA:1097:U:OP1	2.20	0.41
12:CL:74:LEU:HD21	12:CL:104:CYS:SG	2.61	0.41
29:DH:130:VAL:CG1	29:DH:131:SER:N	2.82	0.41
34:BM:18:ARG:NH2	34:BM:18:ARG:HG2	2.34	0.41
1:AA:1003:G:N2	1:AA:1004:A:O2'	2.54	0.41
4:CD:68:LEU:HD23	4:CD:68:LEU:HA	1.84	0.41
1:AA:1226:C:H4'	1:AA:1227:A:OP1	2.21	0.41
22:BA:1385:A:C6	22:BA:1403:A:C5	3.09	0.41
1:AA:9:G:N7	1:AA:558:G:O2'	2.49	0.41
22:DA:2636:C:OP1	25:DD:81:GLU:HB2	2.20	0.41
31:DJ:98:GLU:O	31:DJ:102:GLU:HG3	2.21	0.41
13:AM:95:LEU:HB3	13:AM:96:PRO:CD	2.51	0.41
24:DC:177:ARG:HD2	24:DC:177:ARG:HA	1.79	0.41
21:AU:19:PHE:HD2	21:AU:19:PHE:O	2.04	0.41
45:DX:68:LEU:HB3	45:DX:78:TYR:OH	2.20	0.41
30:DI:62:TYR:C	30:DI:64:ASP:H	2.23	0.41
15:CO:78:TYR:OH	15:CO:88:ARG:NE	2.53	0.41
36:BO:115:LEU:HA	36:BO:115:LEU:HD12	1.64	0.41
38:BQ:102:ASP:O	38:BQ:104:VAL:N	2.53	0.41
22:BA:2810:A:H2'	22:BA:2811:G:O4'	2.21	0.41
31:DJ:90:GLU:HG3	31:DJ:91:GLU:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:901:A:C5	1:AA:902:G:H1'	2.56	0.41
22:DA:1346:G:H2'	22:DA:1347:A:C8	2.56	0.41
1:CA:539:A:H2'	1:CA:540:G:C8	2.56	0.41
22:DA:2444:G:OP2	26:DE:63:LYS:HD2	2.21	0.41
22:BA:700:G:O2'	22:BA:1632:A:N3	2.41	0.41
1:CA:264:C:H2'	1:CA:265:G:O4'	2.20	0.41
1:CA:966:G:O2'	9:CI:130:ARG:OXT	2.37	0.41
15:CO:82:ILE:HG13	15:CO:83:GLU:N	2.36	0.41
22:DA:1281:G:H2'	22:DA:1282:U:C6	2.55	0.41
2:CB:52:GLU:HG3	2:CB:56:GLU:HG2	2.01	0.41
3:CC:107:ARG:HD3	3:CC:107:ARG:H	1.85	0.41
9:CI:33:ARG:HD3	9:CI:33:ARG:HA	1.88	0.41
22:DA:64:A:H2'	22:DA:65:U:C6	2.56	0.41
17:AQ:16:LYS:HA	17:AQ:16:LYS:HD2	1.84	0.41
17:AQ:34:TYR:O	17:AQ:36:LYS:N	2.51	0.41
22:BA:964:C:O2'	22:BA:2273:A:N3	2.48	0.41
22:DA:2516:A:O2'	22:DA:2517:C:H5'	2.19	0.41
22:DA:2066:C:H5''	57:DA:3502:HOH:O	2.19	0.41
1:CA:1503:A:C8	1:CA:1531:A:H1'	2.56	0.41
1:CA:881:G:C6	1:CA:882:C:C4	3.09	0.41
22:DA:2220:U:H2'	22:DA:2221:G:C8	2.55	0.41
1:AA:811:C:C5	1:AA:812:G:C6	3.08	0.41
22:DA:2064:C:O3'	22:DA:2251:G:N2	2.54	0.41
26:DE:108:ILE:O	26:DE:112:LEU:HG	2.21	0.41
1:AA:683:G:N2	11:AK:39:GLY:O	2.54	0.41
1:CA:672:U:H2'	1:CA:673:A:C8	2.56	0.41
21:AU:37:PHE:HA	21:AU:37:PHE:HD1	1.73	0.41
27:BF:104:ILE:HG12	27:BF:104:ILE:H	1.71	0.41
13:CM:10:PRO:HB2	13:CM:11:ASP:H	1.66	0.41
43:DV:51:GLN:HA	43:DV:56:PHE:CB	2.50	0.41
22:DA:1638:C:O2'	22:DA:2698:U:O2	2.38	0.41
1:CA:111:G:C6	1:CA:330:C:N4	2.87	0.41
2:AB:65:GLY:O	2:AB:66:LYS:HD3	2.21	0.41
22:BA:769:U:C2	22:BA:770:G:C8	3.09	0.41
19:AS:11:ILE:HG12	19:AS:12:ASP:O	2.21	0.41
22:BA:1243:C:H2'	22:BA:1244:A:O4'	2.20	0.41
2:CB:100:MET:CA	2:CB:107:VAL:HG21	2.49	0.41
3:CC:64:ILE:HG23	3:CC:99:ALA:HB2	2.03	0.41
27:BF:138:PHE:HE2	27:BF:152:LEU:HD23	1.86	0.41
1:AA:664:G:H22	1:AA:741:G:H1	1.69	0.41
3:CC:131:ARG:HE	3:CC:131:ARG:HB2	1.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:131:LYS:HA	2:CB:134:ALA:HB3	2.03	0.41
22:DA:1436:G:C2	22:DA:1437:C:H1'	2.56	0.41
34:DM:97:GLN:O	34:DM:100:LYS:HB2	2.20	0.41
22:BA:373:U:OP2	22:BA:400:G:N1	2.30	0.41
41:BT:88:LYS:O	41:BT:89:GLU:HG2	2.21	0.41
8:CH:34:VAL:O	8:CH:37:ALA:N	2.52	0.41
4:AD:48:LEU:HD21	4:AD:53:VAL:HG12	2.02	0.41
13:CM:15:ALA:O	13:CM:19:LEU:HD23	2.21	0.41
23:BB:61:G:H2'	23:BB:62:C:C6	2.55	0.41
22:DA:1856:U:O4	22:DA:1857:G:N1	2.54	0.41
22:BA:2021:C:P	48:B0:9:THR:HG21	2.61	0.41
22:DA:2259:U:H1'	22:DA:2427:C:C2	2.56	0.41
26:BE:58:LYS:HZ1	26:BE:62:GLN:N	2.17	0.41
37:BP:8:LEU:O	37:BP:11:GLU:HG2	2.21	0.41
51:D3:51:SER:O	51:D3:55:LEU:HG	2.21	0.41
22:BA:1727:C:H2'	22:BA:1728:C:C6	2.56	0.41
22:BA:827:U:H2'	22:BA:2068:U:C2	2.56	0.41
1:CA:1082:A:C6	1:CA:1083:U:N3	2.89	0.41
24:BC:30:PHE:CD2	24:BC:32:PRO:HD2	2.56	0.41
22:DA:1082:U:H5''	22:DA:1083:U:OP2	2.21	0.41
11:CK:21:ALA:HA	11:CK:34:ILE:HD13	2.02	0.41
23:DB:21:G:H2'	23:DB:22:U:O4'	2.21	0.41
24:DC:33:LEU:HA	24:DC:33:LEU:HD23	1.88	0.41
2:AB:222:ARG:CZ	2:AB:222:ARG:HB3	2.51	0.41
35:DN:24:MET:HE3	35:DN:44:LEU:HD22	2.01	0.41
29:BH:82:SER:HB3	29:BH:146:VAL:HG12	2.03	0.41
29:BH:88:GLY:C	29:BH:125:THR:OG1	2.59	0.41
22:DA:784:G:H5''	24:DC:226:ASN:OD1	2.21	0.41
22:DA:740:C:H5'	22:DA:1784:A:C2'	2.51	0.41
10:AJ:9:ARG:O	10:AJ:98:VAL:HA	2.20	0.41
10:AJ:8:ILE:HA	10:AJ:99:GLN:O	2.21	0.41
4:AD:29:ASP:C	4:AD:30:THR:O	2.58	0.41
11:AK:38:GLN:HB2	11:AK:40:ASN:HD22	1.85	0.41
4:AD:9:LEU:HA	4:AD:9:LEU:HD13	1.74	0.41
22:BA:572:A:C6	22:BA:573:U:N3	2.89	0.41
22:BA:842:U:H2'	22:BA:843:G:O4'	2.21	0.41
24:DC:159:GLY:HA2	24:DC:195:VAL:O	2.21	0.41
4:AD:58:LYS:CB	4:AD:200:ILE:HB	2.50	0.41
18:CR:27:ALA:O	18:CR:30:LYS:HG2	2.21	0.41
3:AC:22:TRP:CG	3:AC:59:ARG:HG2	2.56	0.41
22:DA:1179:G:C6	22:DA:1180:U:H1'	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BE:101:TYR:O	26:BE:104:ALA:HB3	2.21	0.41
22:BA:997:G:C2	22:BA:1159:U:C2	3.09	0.41
22:BA:996:A:C2	22:BA:997:G:C8	3.09	0.41
22:BA:996:A:H4'	38:BQ:91:ASP:OD1	2.21	0.41
22:BA:1916:A:C2	22:BA:1917:U:H1'	2.55	0.41
22:BA:1911:U:H2'	22:BA:1918:A:C2	2.56	0.41
16:AP:79:ASN:ND2	16:AP:82:ALA:O	2.52	0.41
22:BA:2128:G:N2	22:BA:2173:A:O2'	2.52	0.41
2:CB:20:THR:OG1	2:CB:21:ARG:N	2.52	0.41
2:AB:147:SER:O	2:AB:147:SER:OG	2.35	0.41
4:AD:122:ALA:O	4:AD:123:ILE:HG23	2.20	0.41
22:DA:814:C:H1'	22:DA:1225:G:H21	1.86	0.41
43:DV:30:ILE:HG12	43:DV:91:PHE:CB	2.50	0.41
22:DA:2214:C:H2'	22:DA:2215:C:O4'	2.21	0.41
1:CA:1346:A:N6	1:CA:1374:A:C8	2.89	0.41
33:DL:77:ILE:HD13	33:DL:108:ALA:HB1	2.01	0.41
22:BA:1408:G:C6	22:BA:1409:U:C4	3.09	0.41
29:BH:30:LEU:C	29:BH:32:PRO:HD2	2.41	0.41
17:AQ:69:LYS:O	17:AQ:70:THR:CB	2.69	0.41
22:BA:29:U:H2'	22:BA:30:G:C8	2.56	0.41
31:DJ:6:ALA:O	31:DJ:7:LYS:HG3	2.20	0.41
22:DA:648:G:H2'	22:DA:649:G:C8	2.53	0.41
38:DQ:78:LYS:HB3	38:DQ:78:LYS:HE2	1.76	0.41
28:DG:24:ILE:HD13	28:DG:72:LEU:HD21	2.02	0.41
22:BA:1838:C:N4	22:BA:1899:A:C4	2.89	0.41
26:DE:155:GLU:HG3	26:DE:159:LEU:CD1	2.51	0.41
17:CQ:45:HIS:O	17:CQ:71:LYS:HA	2.21	0.41
3:CC:148:GLY:O	3:CC:203:PHE:N	2.40	0.41
22:BA:2636:C:H2'	22:BA:2637:U:H6	1.84	0.41
22:BA:657:U:O5'	22:BA:657:U:H6	2.04	0.41
22:DA:1740:G:H2'	22:DA:1741:C:C6	2.56	0.41
8:AH:105:SER:O	8:AH:123:GLY:HA3	2.21	0.41
31:BJ:7:LYS:HA	31:BJ:8:PRO:HD3	1.81	0.41
1:AA:922:G:C6	1:AA:923:A:C6	3.08	0.41
9:CI:83:ILE:O	9:CI:87:LEU:HG	2.21	0.41
22:BA:1474:U:C2'	22:BA:1475:G:H5'	2.51	0.41
22:DA:1565:C:H5'	24:DC:18:LYS:HZ2	1.86	0.41
1:AA:1386:G:H2'	1:AA:1387:G:C8	2.56	0.41
5:AE:60:ILE:O	5:AE:64:MET:HG2	2.21	0.41
22:DA:1666:G:HO2'	32:DK:6:THR:HG1	1.62	0.41
22:DA:1769:U:H1'	22:DA:1984:G:N2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1102:C:H2'	22:DA:1103:A:C8	2.56	0.41
42:BU:73:PHE:CZ	42:BU:78:GLY:HA2	2.56	0.41
1:AA:44:A:OP2	16:AP:12:LYS:HE2	2.21	0.41
22:BA:322:A:C5	22:BA:340:A:C2	3.09	0.41
22:DA:2195:U:H2'	22:DA:2196:C:H6	1.86	0.41
7:CG:31:MET:HG3	7:CG:35:LYS:O	2.21	0.41
22:BA:190:A:C4	22:BA:207:A:C2	3.08	0.41
1:AA:15:G:C4	1:AA:16:A:C8	3.08	0.41
22:DA:2443:C:H2'	22:DA:2444:G:O4'	2.21	0.41
42:DU:73:PHE:CE2	42:DU:75:ALA:HA	2.55	0.41
22:BA:1643:G:H2'	22:BA:1644:C:O4'	2.21	0.41
26:BE:147:LEU:HB2	26:BE:183:PHE:CD1	2.55	0.41
1:CA:187:G:H5''	1:CA:188:C:OP2	2.20	0.41
29:BH:129:GLU:C	29:BH:130:VAL:HG23	2.41	0.41
28:DG:94:TYR:HA	28:DG:106:SER:O	2.21	0.41
1:AA:1305:G:O2'	1:AA:1306:A:H8	2.04	0.41
7:CG:83:SER:O	7:CG:85:TYR:N	2.53	0.41
22:DA:2491:U:H5'	22:DA:2570:G:H5'	2.02	0.41
22:BA:2174:C:O2'	22:BA:2175:C:H5'	2.21	0.41
31:BJ:69:ARG:HA	31:BJ:89:PHE:CD1	2.55	0.41
43:BV:85:LYS:HB3	43:BV:85:LYS:HE3	1.82	0.41
4:CD:148:LYS:HE2	4:CD:148:LYS:HB2	1.77	0.41
38:BQ:81:ASN:HD22	38:BQ:81:ASN:HA	1.76	0.41
53:B5:19:LYS:HD3	53:B5:19:LYS:HA	1.88	0.41
45:BX:40:VAL:HG23	45:BX:45:ARG:O	2.21	0.41
22:BA:2098:U:H2'	22:BA:2099:U:C6	2.55	0.41
25:DD:176:ASP:HB2	25:DD:190:LYS:HB3	2.02	0.41
29:BH:129:GLU:C	29:BH:130:VAL:CG2	2.90	0.41
22:DA:871:U:C2	22:DA:907:G:C6	3.09	0.41
22:BA:802:A:H2'	22:BA:803:U:C6	2.56	0.41
2:CB:140:GLU:HB3	2:CB:144:LEU:HD21	2.03	0.41
1:CA:437:U:O4'	4:CD:154:ARG:NH1	2.54	0.41
8:AH:86:TYR:HD2	8:AH:124:GLU:HA	1.86	0.41
22:DA:995:C:N3	31:DJ:3:THR:N	2.56	0.41
53:B5:80:LYS:HA	53:B5:98:GLU:HG3	2.03	0.41
25:DD:142:VAL:HG23	25:DD:144:GLY:H	1.85	0.41
22:BA:666:A:H4'	33:BL:48:ARG:HD3	2.03	0.41
18:CR:23:TYR:HE1	18:CR:65:LEU:HD12	1.86	0.41
36:DO:17:LYS:HA	36:DO:17:LYS:HD3	1.89	0.41
11:AK:128:ARG:HG2	11:AK:128:ARG:HH11	1.86	0.41
22:BA:1776:G:N3	22:BA:1776:G:H2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:131:LYS:HD3	2:AB:131:LYS:HA	1.50	0.41
22:DA:2881:U:H2'	22:DA:2882:A:C8	2.56	0.41
30:BI:22:PRO:HB2	30:BI:23:PRO:HD3	2.01	0.41
22:DA:2431:U:N3	22:DA:2434:A:OP2	2.43	0.41
22:DA:2252:G:H2'	22:DA:2253:G:O4'	2.20	0.41
29:BH:90:LEU:HG	29:BH:92:GLY:C	2.42	0.41
1:CA:369:G:OP2	1:CA:388:G:C2	2.73	0.41
22:BA:1096:A:H2'	22:BA:1097:U:O4'	2.21	0.41
22:BA:1847:A:P	22:BA:1847:A:H8	2.44	0.41
21:AU:35:ARG:NH2	57:AU:101:HOH:O	2.39	0.41
1:CA:1145:A:O2'	1:CA:1146:A:H8	2.04	0.41
8:CH:11:LEU:HD11	8:CH:127:CYS:HB3	2.02	0.41
22:DA:160:A:H2'	22:DA:161:A:C8	2.56	0.41
33:DL:55:MET:SD	33:DL:59:ARG:NH2	2.94	0.41
22:BA:198:C:O5'	22:BA:198:C:H6	2.04	0.41
19:CS:15:LEU:HD23	19:CS:38:SER:HB2	2.03	0.41
39:BR:24:LYS:HE2	39:BR:24:LYS:HB3	1.91	0.41
21:CU:4:ILE:HA	21:CU:20:LYS:HZ1	1.86	0.41
22:BA:1912:A:C2	22:BA:1919:A:C4	3.09	0.41
16:AP:73:ALA:O	16:AP:77:GLU:HB2	2.21	0.41
3:AC:144:LEU:H	3:AC:144:LEU:HD22	1.85	0.41
22:DA:460:A:H2'	22:DA:461:C:O4'	2.21	0.41
1:AA:1023:U:H2'	1:AA:1024:G:O4'	2.20	0.41
1:CA:452:A:H62	1:CA:480:U:H3	1.69	0.41
1:CA:1346:A:H61	1:CA:1374:A:H3'	1.86	0.41
2:CB:76:ALA:O	2:CB:80:VAL:HG23	2.21	0.41
43:DV:28:ALA:HB3	43:DV:42:LEU:HD21	2.03	0.41
6:CF:18:VAL:O	6:CF:22:ILE:HG13	2.20	0.41
5:AE:156:LYS:HA	8:AH:66:PHE:CD2	2.56	0.41
22:DA:2446:G:OP2	22:DA:2446:G:H8	2.03	0.41
1:AA:670:G:N2	1:AA:736:C:O2	2.47	0.41
24:BC:239:ASN:ND2	57:BC:307:HOH:O	2.54	0.41
1:CA:102:G:H2'	1:CA:103:U:C6	2.55	0.41
21:AU:16:LEU:C	21:AU:18:ARG:HD2	2.42	0.41
27:BF:49:LEU:HA	27:BF:49:LEU:HD12	1.85	0.41
22:DA:1680:U:H2'	22:DA:1681:G:O4'	2.21	0.41
22:BA:2001:C:H4'	22:BA:2689:U:H2'	2.03	0.41
22:BA:1413:A:C6	22:BA:1414:C:N3	2.89	0.41
22:BA:358:U:H2'	22:BA:359:G:C8	2.56	0.41
22:BA:2785:C:H2'	22:BA:2786:U:O4'	2.20	0.41
22:DA:1418:G:H21	22:DA:1580:A:H62	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1789:A:H2'	22:BA:1790:C:O4'	2.21	0.41
22:DA:380:G:H4'	45:DX:16:ASN:O	2.20	0.41
22:BA:2190:G:C6	22:BA:2191:A:C5	3.09	0.41
1:AA:737:C:H2'	1:AA:738:C:H6	1.86	0.41
1:AA:979:C:OP2	1:AA:980:C:H5	2.04	0.41
3:AC:29:PHE:HE2	3:AC:33:LEU:HD23	1.85	0.41
1:CA:803:G:C5	1:CA:804:U:C4	3.09	0.41
5:AE:16:ILE:HD11	5:AE:38:VAL:HB	2.03	0.41
53:B5:88:GLU:HG3	53:B5:95:VAL:HG23	2.03	0.41
1:AA:750:C:O2	15:AO:23:GLY:HA3	2.21	0.41
26:BE:170:ARG:NH2	26:BE:176:ASP:OD2	2.45	0.41
23:DB:51:G:C8	36:DO:64:TYR:HE2	2.38	0.41
1:CA:37:U:O2'	1:CA:500:G:H4'	2.21	0.41
22:BA:345:A:H1'	22:BA:346:A:N7	2.36	0.41
29:BH:132:PHE:CE2	29:BH:142:VAL:CG2	3.04	0.40
22:DA:2278:A:N6	44:DW:14:ARG:O	2.55	0.40
22:DA:2474:U:H5''	22:DA:2475:C:OP2	2.21	0.40
30:DI:136:MET:HG2	30:DI:136:MET:H	1.67	0.40
29:DH:1:MET:HB3	29:DH:21:VAL:O	2.20	0.40
24:DC:34:LEU:HA	24:DC:62:TYR:O	2.21	0.40
22:BA:947:A:O2'	22:BA:984:A:H2	2.03	0.40
11:AK:125:LYS:O	21:AU:34:ARG:NH2	2.54	0.40
21:AU:40:LYS:O	21:AU:44:GLU:HB2	2.21	0.40
22:BA:2305:U:O2'	27:BF:133:ARG:NE	2.54	0.40
27:DF:64:LYS:HA	27:DF:65:PRO:HD3	1.87	0.40
35:DN:55:ALA:HB1	35:DN:80:PHE:N	2.28	0.40
22:DA:2674:G:H2'	22:DA:2675:A:C8	2.56	0.40
22:BA:1799:G:H4'	22:BA:1800:C:O5'	2.21	0.40
36:DO:36:TYR:HD2	36:DO:52:SER:HB2	1.87	0.40
35:BN:55:ALA:HA	35:BN:80:PHE:CE1	2.55	0.40
21:CU:19:PHE:HB3	21:CU:20:LYS:HZ3	1.86	0.40
1:AA:1401:G:N2	1:AA:1402:C:H1'	2.36	0.40
9:AI:50:GLN:O	9:AI:52:LEU:N	2.50	0.40
22:BA:1753:G:H5''	37:BP:93:ARG:NH1	2.36	0.40
1:CA:72:A:C6	1:CA:73:C:N4	2.89	0.40
22:DA:2131:U:C4'	22:DA:2133:G:H1'	2.50	0.40
24:DC:260:ASN:HD21	24:DC:263:THR:HG23	1.86	0.40
1:CA:981:U:H2'	1:CA:982:U:C5	2.57	0.40
1:AA:359:G:H2'	1:AA:360:G:O4'	2.21	0.40
1:AA:219:U:C2	1:AA:220:G:C8	3.08	0.40
22:BA:1027:A:O5'	22:BA:1027:A:H8	2.05	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:309:A:O3'	42:DU:16:GLY:HA2	2.21	0.40
22:DA:1695:G:C8	24:DC:8:PRO:HG2	2.56	0.40
45:BX:18:ARG:CZ	45:BX:24:ALA:HB2	2.50	0.40
9:CI:120:LYS:O	9:CI:121:ALA:HB3	2.20	0.40
22:DA:2119:A:N6	22:DA:2167:U:H1'	2.36	0.40
35:DN:38:LEU:HB3	35:DN:39:PRO:HD3	2.03	0.40
22:DA:1357:C:H2'	22:DA:1358:G:O4'	2.21	0.40
46:DY:48:ARG:O	46:DY:51:ALA:HB3	2.21	0.40
1:CA:1317:C:O2'	14:CN:49:GLN:HG2	2.22	0.40
24:DC:24:LEU:HD11	24:DC:90:ASN:ND2	2.35	0.40
22:DA:242:G:C6	51:D3:5:LYS:HE2	2.55	0.40
1:AA:1072:G:OP1	5:AE:62:LYS:NZ	2.50	0.40
22:DA:1930:G:H1'	22:DA:1968:G:N1	2.36	0.40
7:CG:46:ALA:HA	7:CG:121:ALA:HB2	2.01	0.40
32:BK:35:VAL:HB	32:BK:36:GLY:H	1.67	0.40
22:DA:2702:G:C6	22:DA:2703:C:C4	3.10	0.40
21:AU:25:LYS:O	21:AU:29:LEU:HB2	2.20	0.40
22:BA:2282:G:H5''	22:BA:2283:C:O4'	2.21	0.40
9:CI:46:MET:HA	9:CI:48:VAL:HG23	2.02	0.40
22:DA:571:U:C4	22:DA:2030:A:C6	3.09	0.40
45:DX:67:VAL:O	45:DX:70:GLU:N	2.54	0.40
13:AM:7:ILE:H	13:AM:7:ILE:HG13	1.41	0.40
22:BA:1902:C:H4'	24:BC:242:LYS:O	2.21	0.40
22:DA:2457:U:C4	22:DA:2458:G:C6	3.09	0.40
1:CA:721:G:H4'	1:CA:722:G:O5'	2.20	0.40
4:AD:35:GLU:O	4:AD:38:PRO:HD3	2.21	0.40
31:BJ:93:ILE:O	31:BJ:97:PRO:HG3	2.21	0.40
25:DD:184:ARG:CZ	37:DP:7:GLN:HE22	2.34	0.40
1:CA:375:U:OP1	16:CP:70:ARG:HD3	2.22	0.40
43:DV:2:PHE:HD1	43:DV:2:PHE:HA	1.75	0.40
30:BI:40:LYS:HD3	30:BI:40:LYS:HA	1.81	0.40
1:AA:431:A:C4	1:AA:432:A:C8	3.09	0.40
22:DA:569:U:H5'	22:DA:946:C:H1'	2.04	0.40
10:CJ:93:ALA:C	10:CJ:95:GLY:H	2.24	0.40
22:BA:1343:G:C4	22:BA:1344:U:C5	3.08	0.40
1:CA:1086:U:O2'	1:CA:1087:G:H5'	2.22	0.40
22:BA:1084:A:C5	22:BA:1085:A:C6	3.09	0.40
7:AG:43:VAL:O	7:AG:47:LEU:HB2	2.21	0.40
35:DN:94:TYR:O	35:DN:116:VAL:N	2.49	0.40
22:BA:2838:G:C6	22:BA:2839:G:C5	3.09	0.40
21:AU:41:PRO:HA	21:AU:45:ARG:NH1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1499:A:H3'	57:CA:1880:HOH:O	2.20	0.40
1:AA:1491:G:H2'	1:AA:1492:A:H8	1.86	0.40
19:CS:36:ARG:HB3	19:CS:72:GLY:CA	2.51	0.40
1:CA:469:C:H2'	1:CA:470:C:O4'	2.21	0.40
2:AB:147:SER:O	2:AB:148:LEU:HG	2.21	0.40
46:BY:36:GLN:O	46:BY:37:LEU:HB3	2.21	0.40
22:DA:2756:U:H1'	22:DA:2757:A:H5''	2.02	0.40
30:DI:57:VAL:CG2	30:DI:71:THR:HB	2.51	0.40
1:AA:109:A:H2'	1:AA:326:G:H21	1.86	0.40
28:DG:11:VAL:HA	28:DG:12:PRO:HD3	1.88	0.40
22:DA:188:G:O2'	22:DA:1365:A:N6	2.55	0.40
22:DA:308:G:H2'	22:DA:309:A:O4'	2.22	0.40
22:DA:2311:A:C2	27:DF:79:ILE:HG21	2.56	0.40
1:AA:453:G:H2'	1:AA:454:G:O4'	2.22	0.40
1:CA:1220:G:H1'	19:CS:52:HIS:CD2	2.56	0.40
5:AE:80:THR:CA	5:AE:122:ASN:HD21	2.34	0.40
1:CA:124:C:H2'	1:CA:125:U:C6	2.55	0.40
2:AB:184:PHE:CD2	2:AB:184:PHE:N	2.88	0.40
11:CK:84:VAL:HG11	11:CK:97:ILE:HG22	2.02	0.40
1:AA:663:A:H2'	1:AA:664:G:O4'	2.21	0.40
23:DB:71:C:C2	23:DB:106:G:C2	3.09	0.40
22:BA:2000:C:O2'	22:BA:2001:C:H5'	2.21	0.40
22:DA:607:U:H5	22:DA:619:G:C5	2.40	0.40
22:BA:749:A:N3	22:BA:1618:A:H2'	2.35	0.40
22:DA:585:G:H5''	22:DA:586:A:OP1	2.20	0.40
22:BA:2192:U:H2'	22:BA:2193:G:O4'	2.22	0.40
1:CA:438:U:C2	1:CA:494:G:C6	3.09	0.40
8:CH:102:ALA:O	8:CH:112:THR:HA	2.21	0.40
1:CA:490:C:H2'	1:CA:491:G:H8	1.85	0.40
5:CE:133:PRO:O	5:CE:136:VAL:N	2.54	0.40
1:AA:414:A:H2'	1:AA:415:A:C8	2.56	0.40
11:AK:89:PRO:HD3	21:AU:29:LEU:HD11	2.02	0.40
40:BS:41:LYS:HE3	48:B0:22:LEU:HD21	2.03	0.40
1:AA:437:U:H4'	4:AD:154:ARG:HH22	1.86	0.40
22:BA:2458:G:N3	22:BA:2490:G:N2	2.69	0.40
26:BE:145:ASP:HA	26:BE:166:LYS:O	2.21	0.40
22:BA:598:U:H2'	22:BA:599:A:C8	2.56	0.40
22:BA:2500:U:O2'	22:BA:2504:U:OP1	2.39	0.40
1:CA:453:G:H2'	1:CA:454:G:C8	2.56	0.40
5:AE:22:SER:HB2	5:AE:31:PHE:CD2	2.56	0.40
4:CD:148:LYS:CD	4:CD:148:LYS:H	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:26:LYS:NZ	2:AB:194:ASP:OD2	2.36	0.40
3:AC:31:ASP:HA	14:AN:65:ARG:HH22	1.86	0.40
10:CJ:25:ILE:CG2	10:CJ:74:VAL:HG21	2.51	0.40
46:DY:49:ASP:O	46:DY:53:VAL:HG23	2.21	0.40
22:BA:1292:G:H2'	22:BA:1293:C:C6	2.57	0.40
22:DA:1445:G:C6	22:DA:1446:C:C4	3.09	0.40
24:BC:29:PRO:CG	24:BC:34:LEU:HD21	2.51	0.40
22:DA:364:C:H2'	22:DA:365:U:O4'	2.21	0.40
2:AB:78:GLU:C	2:AB:80:VAL:H	2.23	0.40
40:BS:76:VAL:HG13	40:BS:103:ILE:HG12	2.03	0.40
42:DU:61:LYS:HD2	42:DU:61:LYS:HA	1.87	0.40
32:DK:23:LYS:HD3	32:DK:23:LYS:HA	1.89	0.40
29:DH:96:THR:O	29:DH:98:ASP:N	2.54	0.40
1:AA:179:A:OP2	57:AA:1880:HOH:O	2.22	0.40
1:CA:1238:A:N3	1:CA:1241:G:O2'	2.45	0.40
22:DA:2626:C:H2'	22:DA:2627:G:O4'	2.21	0.40
22:BA:983:A:C6	22:BA:984:A:C2	3.09	0.40
54:D6:6:MHV:OD1	54:D6:8:MHT:H4	2.21	0.40
26:DE:114:ARG:HE	26:DE:114:ARG:HB2	1.55	0.40
22:BA:135:U:H3	22:BA:144:A:N6	2.12	0.40
1:AA:1491:G:H2'	1:AA:1492:A:C8	2.56	0.40
16:CP:43:ALA:O	16:CP:44:SER:OG	2.29	0.40
1:CA:1380:U:C4	7:CG:3:ARG:HD3	2.56	0.40
22:BA:181:A:C2	22:BA:182:A:C4	3.09	0.40
22:DA:320:A:O3'	22:DA:321:U:H3'	2.21	0.40
35:BN:79:LEU:HA	35:BN:83:LEU:HB2	2.02	0.40
1:CA:202:G:H2'	1:CA:203:G:O4'	2.20	0.40
5:AE:25:VAL:O	5:AE:27:GLY:N	2.55	0.40
22:BA:1744:A:H2'	22:BA:1745:A:O4'	2.21	0.40
35:DN:69:ARG:C	35:DN:71:ARG:H	2.19	0.40
22:DA:2183:A:H2'	22:DA:2184:A:C8	2.57	0.40
7:AG:15:ASP:OD2	7:AG:17:LYS:N	2.49	0.40
22:DA:1335:C:H2'	22:DA:1336:A:C8	2.56	0.40
16:AP:43:ALA:O	16:AP:46:LYS:HD2	2.21	0.40
1:CA:522:C:H41	12:CL:50:ARG:NH2	2.20	0.40
12:CL:64:THR:HG23	12:CL:93:VAL:CG1	2.51	0.40
35:DN:66:ALA:O	35:DN:70:THR:HG23	2.22	0.40
22:DA:2590:A:H5''	24:DC:238:ARG:HE	1.87	0.40
22:DA:2024:G:C4	22:DA:2040:G:N2	2.90	0.40
23:DB:76:G:H2'	23:DB:77:U:O4'	2.22	0.40
5:AE:151:GLU:C	5:AE:153:VAL:H	2.25	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2186:G:C5	22:BA:2187:U:C4	3.09	0.40
5:AE:105:ILE:HD12	5:AE:105:ILE:HA	1.83	0.40
22:BA:974:G:C4	22:BA:1186:G:C2	3.09	0.40
22:BA:974:G:O2'	22:BA:989:G:N2	2.54	0.40
1:AA:468:A:H5'	1:AA:469:C:OP2	2.21	0.40
22:BA:2592:G:C6	22:BA:2593:U:C4	3.09	0.40
1:CA:1037:C:OP2	1:CA:1037:C:H6	2.05	0.40
1:AA:1223:C:OP2	19:AS:78:ARG:NH1	2.54	0.40
22:DA:2114:A:C4	22:DA:2167:U:H4'	2.56	0.40
22:BA:2756:U:OP2	52:B4:19:ARG:NE	2.54	0.40
22:BA:1927:A:C6	22:BA:1928:A:C6	3.09	0.40
11:CK:36:ASP:OD2	11:CK:40:ASN:HB2	2.21	0.40
1:AA:731:G:H2'	1:AA:732:C:C6	2.57	0.40
1:AA:577:G:C8	1:AA:816:A:C6	3.10	0.40
35:DN:48:VAL:O	35:DN:52:ILE:HG13	2.22	0.40
1:CA:950:U:H2'	1:CA:951:G:H8	1.85	0.40
24:BC:159:GLY:H	24:BC:195:VAL:HG13	1.86	0.40
26:DE:149:ILE:CD1	26:DE:172:ALA:HA	2.52	0.40
1:AA:57:G:H2'	1:AA:58:C:O4'	2.21	0.40
14:CN:30:ILE:O	14:CN:33:ASP:HB3	2.21	0.40
1:AA:842:U:H3'	1:AA:843:U:C5'	2.50	0.40
1:AA:843:U:H3	2:CB:115:LYS:HD3	1.87	0.40
3:AC:68:ILE:O	3:AC:70:THR:N	2.55	0.40
1:CA:793:U:O2	1:CA:1516:G:H4'	2.20	0.40
1:CA:1271:A:H2'	1:CA:1272:G:H8	1.86	0.40
22:BA:1688:U:H2'	22:BA:1698:A:N6	2.36	0.40
38:BQ:112:LYS:HD3	39:BR:48:LYS:HD2	2.02	0.40
22:BA:1983:G:C6	22:BA:1984:G:N7	2.89	0.40
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.56	0.40
25:DD:4:LEU:HD22	25:DD:100:LEU:HD23	2.03	0.40
1:AA:1195:C:H5''	1:AA:1196:A:OP2	2.20	0.40
15:CO:4:SER:HB2	15:CO:7:ALA:HB3	2.03	0.40
26:BE:134:LEU:O	26:BE:138:LEU:HG	2.22	0.40
22:DA:2378:A:N7	22:DA:2379:G:H1'	2.37	0.40
22:BA:1832:C:N4	22:BA:1833:C:C4	2.90	0.40
22:BA:2597:G:O2'	22:BA:2598:A:H5'	2.21	0.40
1:AA:1113:C:H2'	1:AA:1114:C:H6	1.86	0.40
1:AA:113:G:H2'	1:AA:114:U:C6	2.57	0.40
2:CB:162:PHE:HA	2:CB:184:PHE:O	2.21	0.40
22:BA:678:C:H2'	22:BA:679:C:H6	1.86	0.40
33:BL:55:MET:HA	33:BL:56:PRO:HD3	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DF:143:TYR:O	27:DF:146:VAL:HG22	2.21	0.40
36:DO:18:LEU:HD13	36:DO:18:LEU:HA	1.84	0.40
22:BA:1338:G:O6	41:BT:66:LYS:NZ	2.48	0.40
13:CM:101:ARG:HD2	13:CM:104:THR:OG1	2.21	0.40
22:DA:956:G:O6	34:DM:14:LYS:NZ	2.52	0.40
3:CC:79:LYS:H	3:CC:82:GLU:HB3	1.87	0.40
4:CD:115:ARG:HG3	4:CD:133:ALA:HB2	2.03	0.40
1:AA:29:U:H5'	1:AA:296:U:OP1	2.21	0.40
1:AA:29:U:C2'	1:AA:30:U:H5'	2.50	0.40
22:BA:2093:G:O2'	29:BH:25:TYR:HA	2.22	0.40
1:CA:1088:G:H21	1:CA:1167:A:H61	1.68	0.40
22:BA:1936:A:H61	22:BA:1963:U:H3	1.69	0.40
3:CC:40:ARG:CG	3:CC:55:ILE:HD11	2.45	0.40
1:CA:254:G:O2'	17:CQ:20:SER:HB2	2.21	0.40
2:AB:130:THR:HB	2:AB:132:LYS:HB3	2.02	0.40
22:BA:1918:A:O3'	22:BA:1919:A:C8	2.75	0.40
24:DC:210:ALA:HA	24:DC:213:TRP:NE1	2.37	0.40
28:DG:68:ALA:HA	28:DG:71:LEU:HB2	2.03	0.40
2:AB:90:PHE:HB3	2:AB:150:GLY:O	2.21	0.40
46:DY:24:GLU:HB3	46:DY:46:VAL:HG21	2.03	0.40
22:DA:2200:C:O2	22:DA:2226:C:N4	2.55	0.40
30:BI:100:LYS:HB3	30:BI:139:VAL:HB	2.04	0.40
10:AJ:53:ILE:HB	10:AJ:62:ARG:N	2.36	0.40
22:BA:475:C:C4	22:BA:481:G:O6	2.73	0.40
22:DA:27:G:HO2'	22:DA:28:A:P	2.43	0.40
27:BF:138:PHE:HA	27:BF:139:PRO:HD3	1.95	0.40
13:AM:72:GLU:O	13:AM:75:MET:HB3	2.21	0.40
22:BA:1490:A:HO2'	22:BA:1491:G:H5'	1.87	0.40
1:CA:1252:A:H2	1:CA:1355:G:HO2'	1.67	0.40
22:BA:458:G:H22	22:BA:469:G:H2'	1.85	0.40
1:CA:957:U:O3'	19:CS:79:THR:OG1	2.39	0.40
1:AA:1125:U:C5	1:AA:1127:G:C6	3.09	0.40
1:CA:1180:A:OP1	9:CI:105:THR:OG1	2.39	0.40
9:CI:115:LYS:HB2	9:CI:118:LEU:HD22	2.03	0.40
22:DA:1854:A:O4'	22:DA:2233:U:H4'	2.22	0.40
22:DA:585:G:O5'	22:DA:585:G:H8	2.04	0.40
22:DA:2704:C:H3'	22:DA:2705:A:C8	2.57	0.40
35:BN:37:THR:HA	35:BN:110:MET:SD	2.61	0.40
34:BM:132:THR:HG22	34:BM:133:LYS:N	2.36	0.40
22:BA:368:A:N6	22:BA:369:U:O4	2.54	0.40
11:CK:56:ARG:O	11:CK:62:ALA:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CQ:55:ILE:HG12	17:CQ:56:GLY:N	2.37	0.40
22:DA:1632:A:C6	22:DA:1633:G:C6	3.09	0.40
46:BY:23:ARG:O	46:BY:27:ASN:HB2	2.22	0.40
22:DA:558:U:H2'	22:DA:559:G:C8	2.57	0.40
22:DA:1664:A:OP2	22:DA:1664:A:C8	2.74	0.40
24:BC:77:VAL:HA	24:BC:114:ASP:O	2.21	0.40
46:BY:43:LEU:HA	46:BY:43:LEU:HD23	1.86	0.40
26:DE:109:LEU:HA	26:DE:109:LEU:HD12	1.79	0.40
16:CP:56:ARG:HD2	16:CP:56:ARG:HA	1.85	0.40
22:BA:1009:A:O5'	22:BA:1009:A:H8	2.05	0.40
18:CR:45:THR:OG1	18:CR:45:THR:O	2.32	0.40
1:AA:819:A:N7	1:AA:1529:G:C2	2.88	0.40
1:AA:911:U:OP2	12:AL:94:ARG:NH1	2.55	0.40
22:DA:1587:G:H2'	22:DA:1588:G:H8	1.87	0.40
2:CB:133:GLU:O	2:CB:137:ARG:HB3	2.21	0.40
29:BH:120:GLY:HA2	29:BH:122:LEU:HA	2.04	0.40
29:BH:82:SER:HG	29:BH:90:LEU:HG	1.86	0.40
30:BI:11:LEU:HD12	30:BI:24:VAL:HG12	2.04	0.40
4:AD:174:ASP:OD2	4:AD:177:LYS:N	2.30	0.40
5:CE:150:PRO:O	5:CE:152:MET:N	2.54	0.40
11:AK:13:ARG:HG2	22:BA:2142:A:OP1	2.22	0.40
21:AU:45:ARG:HA	21:AU:48:ALA:HB3	2.03	0.40
22:DA:203:A:OP2	22:DA:204:A:O2'	2.36	0.40
1:AA:1440:U:HO2'	1:AA:1441:A:H8	1.70	0.40
31:DJ:31:GLU:O	31:DJ:35:ARG:HG3	2.22	0.40
22:BA:182:A:C6	22:BA:183:C:C4	3.08	0.40
22:DA:1412:U:H2'	22:DA:1413:A:C8	2.57	0.40
22:DA:792:A:H3'	22:DA:793:A:H5'	2.04	0.40
22:DA:972:A:C6	22:DA:973:A:C6	3.09	0.40
22:DA:2199:A:C6	22:DA:2200:C:C2	3.10	0.40
41:DT:38:ALA:O	41:DT:39:THR:HB	2.21	0.40
20:CT:62:ALA:HA	20:CT:68:HIS:N	2.36	0.40
5:AE:81:LEU:HD12	5:AE:147:MET:SD	2.62	0.40
44:BW:28:GLY:O	44:BW:66:LYS:HG2	2.22	0.40
43:BV:40:ILE:HA	43:BV:40:ILE:HD13	1.73	0.40
22:BA:28:A:C5	22:BA:29:U:C5	3.09	0.40
37:BP:90:GLY:O	37:BP:113:ARG:NH1	2.52	0.40
3:CC:67:THR:HG23	3:CC:102:ASN:HB2	2.03	0.40
10:AJ:15:HIS:CG	10:AJ:16:ARG:N	2.89	0.40
21:AU:16:LEU:O	21:AU:18:ARG:HD2	2.22	0.40
26:DE:155:GLU:HG3	26:DE:159:LEU:HD12	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1974:C:H2'	22:DA:1975:G:H8	1.86	0.40
22:BA:1277:G:H5'	35:BN:20:MET:CE	2.52	0.40
22:BA:2805:C:C4	22:BA:2806:C:C4	3.10	0.40
1:AA:39:G:N7	1:AA:547:A:C8	2.89	0.40
22:DA:2079:U:H2'	22:DA:2080:A:O4'	2.21	0.40
1:CA:1280:A:C8	10:CJ:42:LEU:HD23	2.57	0.40
1:AA:417:G:N2	1:AA:540:G:O2'	2.55	0.40
16:CP:53:ASP:O	16:CP:57:ILE:HG13	2.21	0.40
1:CA:1515:G:H2'	1:CA:1516:G:H8	1.86	0.40
2:CB:132:LYS:HA	2:CB:136:MET:HB2	2.03	0.40
2:AB:120:GLN:HE22	2:AB:137:ARG:HH22	1.68	0.40
1:CA:196:A:OP1	20:CT:64:LYS:NZ	2.54	0.40
22:BA:2726:A:N3	32:BK:67:LYS:NZ	2.61	0.40
22:BA:826:U:O2'	33:BL:53:GLY:HA3	2.21	0.40
1:CA:112:G:H5'	1:CA:389:A:O2'	2.21	0.40
1:CA:585:G:C6	1:CA:586:C:C4	3.10	0.40
1:CA:208:U:C5	1:CA:210:C:H6	2.40	0.40
25:BD:46:ARG:HH22	25:BD:86:GLU:HA	1.87	0.40
4:AD:95:GLU:O	4:AD:100:ASN:ND2	2.54	0.40
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.22	0.40
22:BA:189:G:O6	22:BA:205:G:O2'	2.29	0.40
1:AA:1476:A:H2'	1:AA:1477:U:O4'	2.21	0.40
22:DA:993:G:H1'	39:DR:91:GLN:OE1	2.22	0.40
30:BI:115:ALA:O	30:BI:116:ASP:HB2	2.21	0.40
22:BA:2512:C:H2'	22:BA:2513:A:O4'	2.21	0.40
1:AA:505:G:H4'	1:AA:534:U:C4	2.56	0.40
4:CD:45:LYS:HE3	4:CD:45:LYS:HB2	1.89	0.40
30:BI:97:LYS:HD2	30:BI:97:LYS:N	2.37	0.40
29:DH:77:THR:HA	29:DH:143:ILE:O	2.22	0.40
1:AA:1241:G:H2'	1:AA:1242:G:H8	1.85	0.40

All (14) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:368:U:OP2	29:DH:123:ARG:NE[4_455]	1.50	0.70
1:AA:55:A:N1	29:DH:91:PHE:CE1[4_455]	1.60	0.60
1:AA:55:A:N3	29:DH:91:PHE:CZ[4_455]	1.66	0.54
1:AA:55:A:C2	29:DH:91:PHE:CE1[4_455]	1.70	0.50
1:AA:55:A:C2	29:DH:91:PHE:CZ[4_455]	1.71	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:368:U:OP2	29:DH:123:ARG:CZ[4_455]	1.75	0.45
1:AA:55:A:N1	29:DH:91:PHE:CD1[4_455]	1.78	0.42
1:AA:367:U:O3'	29:DH:123:ARG:NH2[4_455]	1.83	0.37
1:AA:368:U:C6	29:DH:92:GLY:N[4_455]	2.02	0.18
1:AA:416:G:OP1	22:DA:2139:U:O2'[4_455]	2.06	0.14
1:AA:55:A:C6	29:DH:91:PHE:CE1[4_455]	2.08	0.12
1:AA:368:U:O4'	29:DH:91:PHE:O[4_455]	2.11	0.09
1:AA:368:U:N3	29:DH:91:PHE:CB[4_455]	2.18	0.02
1:AA:368:U:C5	29:DH:92:GLY:N[4_455]	2.18	0.02

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	216/218 (99%)	130 (60%)	40 (18%)	46 (21%)	0	0
2	CB	216/218 (99%)	134 (62%)	47 (22%)	35 (16%)	0	1
3	AC	204/206 (99%)	158 (78%)	30 (15%)	16 (8%)	1	5
3	CC	204/206 (99%)	156 (76%)	33 (16%)	15 (7%)	1	5
4	AD	203/205 (99%)	150 (74%)	29 (14%)	24 (12%)	0	1
4	CD	203/205 (99%)	152 (75%)	29 (14%)	22 (11%)	0	2
5	AE	148/150 (99%)	112 (76%)	20 (14%)	16 (11%)	0	2
5	CE	148/150 (99%)	103 (70%)	20 (14%)	25 (17%)	0	0
6	AF	98/100 (98%)	72 (74%)	15 (15%)	11 (11%)	0	2
6	CF	98/100 (98%)	69 (70%)	14 (14%)	15 (15%)	0	1
7	AG	149/151 (99%)	110 (74%)	30 (20%)	9 (6%)	2	9
7	CG	149/151 (99%)	118 (79%)	22 (15%)	9 (6%)	2	9
8	AH	127/129 (98%)	94 (74%)	26 (20%)	7 (6%)	2	11
8	CH	127/129 (98%)	103 (81%)	17 (13%)	7 (6%)	2	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	AI	125/127 (98%)	96 (77%)	20 (16%)	9 (7%)	1	6
9	CI	125/127 (98%)	97 (78%)	20 (16%)	8 (6%)	2	7
10	AJ	96/98 (98%)	67 (70%)	12 (12%)	17 (18%)	0	0
10	CJ	96/98 (98%)	70 (73%)	14 (15%)	12 (12%)	0	1
11	AK	115/117 (98%)	90 (78%)	16 (14%)	9 (8%)	1	5
11	CK	115/117 (98%)	85 (74%)	21 (18%)	9 (8%)	1	5
12	AL	121/123 (98%)	96 (79%)	19 (16%)	6 (5%)	3	13
12	CL	121/123 (98%)	97 (80%)	13 (11%)	11 (9%)	1	3
13	AM	112/114 (98%)	85 (76%)	16 (14%)	11 (10%)	1	3
13	CM	112/114 (98%)	82 (73%)	19 (17%)	11 (10%)	1	3
14	AN	92/100 (92%)	61 (66%)	20 (22%)	11 (12%)	0	1
14	CN	92/100 (92%)	61 (66%)	15 (16%)	16 (17%)	0	0
15	AO	86/88 (98%)	65 (76%)	18 (21%)	3 (4%)	4	22
15	CO	86/88 (98%)	68 (79%)	14 (16%)	4 (5%)	3	15
16	AP	80/82 (98%)	49 (61%)	15 (19%)	16 (20%)	0	0
16	CP	80/82 (98%)	59 (74%)	17 (21%)	4 (5%)	3	13
17	AQ	78/80 (98%)	57 (73%)	11 (14%)	10 (13%)	0	1
17	CQ	78/80 (98%)	53 (68%)	17 (22%)	8 (10%)	1	2
18	AR	53/55 (96%)	45 (85%)	4 (8%)	4 (8%)	1	5
18	CR	53/55 (96%)	40 (76%)	8 (15%)	5 (9%)	1	3
19	AS	77/79 (98%)	55 (71%)	14 (18%)	8 (10%)	1	2
19	CS	77/79 (98%)	61 (79%)	13 (17%)	3 (4%)	4	19
20	AT	83/85 (98%)	66 (80%)	12 (14%)	5 (6%)	2	9
20	CT	83/85 (98%)	68 (82%)	9 (11%)	6 (7%)	1	6
21	AU	49/51 (96%)	29 (59%)	9 (18%)	11 (22%)	0	0
21	CU	49/51 (96%)	29 (59%)	6 (12%)	14 (29%)	0	0
24	BC	269/271 (99%)	217 (81%)	41 (15%)	11 (4%)	3	17
24	DC	269/271 (99%)	209 (78%)	42 (16%)	18 (7%)	1	6
25	BD	207/209 (99%)	183 (88%)	19 (9%)	5 (2%)	7	33
25	DD	207/209 (99%)	173 (84%)	29 (14%)	5 (2%)	7	33
26	BE	199/201 (99%)	171 (86%)	22 (11%)	6 (3%)	5	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	DE	199/201 (99%)	157 (79%)	29 (15%)	13 (6%)	1	7
27	BF	175/177 (99%)	144 (82%)	23 (13%)	8 (5%)	3	15
27	DF	175/177 (99%)	146 (83%)	17 (10%)	12 (7%)	1	6
28	BG	174/176 (99%)	147 (84%)	15 (9%)	12 (7%)	1	6
28	DG	174/176 (99%)	138 (79%)	25 (14%)	11 (6%)	2	8
29	BH	147/149 (99%)	89 (60%)	37 (25%)	21 (14%)	0	1
29	DH	147/149 (99%)	100 (68%)	32 (22%)	15 (10%)	1	2
30	BI	139/141 (99%)	78 (56%)	37 (27%)	24 (17%)	0	0
30	DI	139/141 (99%)	80 (58%)	44 (32%)	15 (11%)	0	2
31	BJ	140/142 (99%)	124 (89%)	11 (8%)	5 (4%)	4	21
31	DJ	140/142 (99%)	123 (88%)	15 (11%)	2 (1%)	14	49
32	BK	120/122 (98%)	98 (82%)	13 (11%)	9 (8%)	1	5
32	DK	120/122 (98%)	100 (83%)	14 (12%)	6 (5%)	3	13
33	BL	141/143 (99%)	109 (77%)	20 (14%)	12 (8%)	1	4
33	DL	141/143 (99%)	105 (74%)	29 (21%)	7 (5%)	3	13
34	BM	134/136 (98%)	117 (87%)	15 (11%)	2 (2%)	13	47
34	DM	134/136 (98%)	112 (84%)	19 (14%)	3 (2%)	8	35
35	BN	118/120 (98%)	96 (81%)	21 (18%)	1 (1%)	24	64
35	DN	118/120 (98%)	97 (82%)	11 (9%)	10 (8%)	1	4
36	BO	114/116 (98%)	95 (83%)	15 (13%)	4 (4%)	4	22
36	DO	114/116 (98%)	96 (84%)	14 (12%)	4 (4%)	4	22
37	BP	112/114 (98%)	98 (88%)	9 (8%)	5 (4%)	3	15
37	DP	112/114 (98%)	91 (81%)	16 (14%)	5 (4%)	3	15
38	BQ	115/117 (98%)	107 (93%)	3 (3%)	5 (4%)	3	16
38	DQ	115/117 (98%)	108 (94%)	6 (5%)	1 (1%)	21	61
39	BR	101/103 (98%)	86 (85%)	8 (8%)	7 (7%)	1	6
39	DR	101/103 (98%)	77 (76%)	20 (20%)	4 (4%)	4	18
40	BS	108/110 (98%)	100 (93%)	5 (5%)	3 (3%)	6	28
40	DS	108/110 (98%)	89 (82%)	14 (13%)	5 (5%)	3	15
41	BT	91/93 (98%)	70 (77%)	13 (14%)	8 (9%)	1	4
41	DT	91/93 (98%)	70 (77%)	9 (10%)	12 (13%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	BU	100/102 (98%)	80 (80%)	12 (12%)	8 (8%)	1	4
42	DU	100/102 (98%)	73 (73%)	17 (17%)	10 (10%)	1	2
43	BV	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	17	56
43	DV	92/94 (98%)	82 (89%)	8 (9%)	2 (2%)	8	35
44	BW	74/76 (97%)	67 (90%)	7 (10%)	0	100	100
44	DW	73/76 (96%)	65 (89%)	6 (8%)	2 (3%)	6	29
45	BX	75/77 (97%)	72 (96%)	1 (1%)	2 (3%)	6	29
45	DX	75/77 (97%)	64 (85%)	9 (12%)	2 (3%)	6	29
46	BY	61/63 (97%)	40 (66%)	12 (20%)	9 (15%)	0	1
46	DY	61/63 (97%)	49 (80%)	8 (13%)	4 (7%)	1	7
47	BZ	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
47	DZ	56/58 (97%)	53 (95%)	1 (2%)	2 (4%)	4	21
48	B0	54/56 (96%)	46 (85%)	5 (9%)	3 (6%)	2	11
48	D0	54/56 (96%)	41 (76%)	11 (20%)	2 (4%)	4	20
49	B1	48/50 (96%)	38 (79%)	6 (12%)	4 (8%)	1	4
49	D1	48/50 (96%)	37 (77%)	8 (17%)	3 (6%)	2	8
50	B2	44/46 (96%)	39 (89%)	3 (7%)	2 (4%)	3	15
50	D2	44/46 (96%)	38 (86%)	4 (9%)	2 (4%)	3	15
51	B3	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	12	45
51	D3	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	12	45
52	B4	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
52	D4	36/38 (95%)	33 (92%)	1 (3%)	2 (6%)	2	11
53	B5	183/228 (80%)	94 (51%)	54 (30%)	35 (19%)	0	0
54	B6	2/8 (25%)	2 (100%)	0	0	100	100
54	D6	2/8 (25%)	2 (100%)	0	0	100	100
All	All	11422/11688 (98%)	8887 (78%)	1654 (14%)	881 (8%)	1	5

All (881) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	16	PHE
2	AB	22	TYR
2	AB	34	ALA

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Mol	Chain	Res	Type
2	AB	64	LYS
2	AB	73	LYS
2	AB	74	ARG
2	AB	75	ALA
2	AB	76	ALA
2	AB	107	VAL
2	AB	116	ASP
2	AB	120	GLN
2	AB	129	LEU
2	AB	134	ALA
2	AB	148	LEU
2	AB	152	LYS
2	AB	170	HIS
2	AB	207	ILE
2	AB	210	VAL
2	AB	212	LEU
3	AC	15	VAL
3	AC	26	THR
4	AD	23	SER
4	AD	29	ASP
4	AD	33	LYS
4	AD	35	GLU
4	AD	49	SER
4	AD	126	ASN
4	AD	192	SER
5	AE	26	LYS
5	AE	43	ASN
5	AE	105	ILE
5	AE	122	ASN
5	AE	138	ARG
6	AF	6	ILE
6	AF	7	VAL
6	AF	68	GLN
6	AF	91	ARG
6	AF	92	THR
7	AG	59	LEU
7	AG	130	ASN
8	AH	3	MET
9	AI	41	ARG
9	AI	44	ALA
9	AI	91	ASP
10	AJ	34	ALA

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Mol	Chain	Res	Type
10	AJ	57	VAL
10	AJ	101	SER
11	AK	52	PHE
12	AL	24	LEU
12	AL	25	GLU
12	AL	44	LYS
12	AL	89	ASP
13	AM	4	ILE
13	AM	5	ALA
13	AM	11	ASP
13	AM	12	HIS
13	AM	41	GLU
13	AM	64	VAL
13	AM	114	LYS
14	AN	28	LYS
14	AN	47	LYS
14	AN	49	GLN
14	AN	52	PRO
14	AN	62	ASN
16	AP	8	ARG
16	AP	43	ALA
16	AP	46	LYS
16	AP	53	ASP
17	AQ	13	VAL
17	AQ	18	GLU
19	AS	6	LYS
19	AS	29	LYS
20	AT	5	LYS
20	AT	6	SER
21	AU	11	PRO
21	AU	24	GLU
21	AU	36	GLU
21	AU	37	PHE
21	AU	38	TYR
21	AU	40	LYS
24	BC	236	GLU
25	BD	86	GLU
25	BD	104	VAL
25	BD	152	PRO
26	BE	86	ALA
27	BF	41	GLY
27	BF	42	GLU

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Mol	Chain	Res	Type
27	BF	176	PRO
28	BG	39	ASP
28	BG	119	ALA
29	BH	10	ALA
29	BH	34	GLY
29	BH	53	GLU
29	BH	87	GLU
29	BH	90	LEU
29	BH	118	PRO
29	BH	121	VAL
29	BH	140	ALA
30	BI	19	ASN
30	BI	58	VAL
30	BI	65	ARG
31	BJ	81	ILE
32	BK	29	HIS
32	BK	35	VAL
32	BK	91	SER
32	BK	110	GLU
33	BL	30	THR
33	BL	68	SER
33	BL	88	GLY
33	BL	94	THR
33	BL	115	GLU
34	BM	69	PRO
36	BO	87	ILE
36	BO	95	SER
37	BP	16	ASP
37	BP	94	LYS
37	BP	105	GLY
38	BQ	25	TYR
39	BR	31	GLU
39	BR	49	ILE
39	BR	51	VAL
39	BR	53	PHE
39	BR	55	ASP
40	BS	64	ALA
41	BT	72	GLN
41	BT	88	LYS
41	BT	89	GLU
42	BU	99	ASN
45	BX	3	ARG

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Mol	Chain	Res	Type
46	BY	22	LEU
46	BY	24	GLU
46	BY	36	GLN
48	B0	56	ALA
49	B1	17	THR
53	B5	51	ASP
53	B5	53	ARG
53	B5	134	PRO
53	B5	141	PRO
53	B5	146	VAL
53	B5	154	ILE
53	B5	174	ALA
53	B5	175	PRO
53	B5	205	ALA
53	B5	210	LEU
53	B5	221	PRO
2	CB	16	PHE
2	CB	73	LYS
2	CB	74	ARG
2	CB	86	SER
2	CB	88	ASP
2	CB	126	PHE
2	CB	170	HIS
2	CB	193	PRO
2	CB	194	ASP
2	CB	207	ILE
2	CB	220	THR
2	CB	222	ARG
3	CC	17	PRO
3	CC	82	GLU
3	CC	146	ALA
4	CD	33	LYS
4	CD	34	ILE
4	CD	35	GLU
4	CD	36	GLN
4	CD	42	GLY
4	CD	47	ARG
4	CD	170	TRP
4	CD	174	ASP
5	CE	45	ARG
5	CE	101	GLU
5	CE	103	THR

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Mol	Chain	Res	Type
5	CE	111	MET
5	CE	123	VAL
5	CE	138	ARG
6	CF	14	GLN
6	CF	55	HIS
6	CF	86	ARG
6	CF	91	ARG
6	CF	92	THR
6	CF	98	GLU
7	CG	9	GLN
7	CG	130	ASN
7	CG	146	GLU
8	CH	22	LYS
8	CH	66	PHE
9	CI	55	VAL
9	CI	91	ASP
9	CI	129	LYS
10	CJ	93	ALA
11	CK	52	PHE
11	CK	91	PRO
11	CK	127	ARG
12	CL	34	CYS
12	CL	44	LYS
12	CL	76	GLU
12	CL	123	LYS
13	CM	7	ILE
13	CM	11	ASP
13	CM	41	GLU
13	CM	114	LYS
14	CN	22	ALA
14	CN	52	PRO
14	CN	62	ASN
14	CN	92	GLU
17	CQ	5	ILE
17	CQ	51	ASN
17	CQ	52	GLU
17	CQ	70	THR
18	CR	47	THR
19	CS	5	LEU
20	CT	4	ILE
20	CT	6	SER
21	CU	9	ASN

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Mol	Chain	Res	Type
21	CU	12	PHE
21	CU	24	GLU
21	CU	36	GLU
21	CU	37	PHE
21	CU	40	LYS
24	DC	29	PRO
24	DC	35	GLU
24	DC	36	LYS
24	DC	58	HIS
24	DC	71	LYS
24	DC	218	PRO
24	DC	239	ASN
24	DC	255	LYS
25	DD	104	VAL
25	DD	105	LYS
25	DD	152	PRO
25	DD	174	SER
27	DF	123	ASP
27	DF	150	ARG
27	DF	176	PRO
28	DG	92	VAL
28	DG	119	ALA
29	DH	3	VAL
29	DH	10	ALA
29	DH	33	GLN
29	DH	35	LYS
29	DH	41	LYS
29	DH	53	GLU
29	DH	54	LEU
29	DH	83	LYS
29	DH	109	GLU
30	DI	7	ALA
30	DI	19	ASN
30	DI	93	PRO
31	DJ	81	ILE
32	DK	105	ARG
32	DK	108	ARG
34	DM	69	PRO
35	DN	2	ARG
35	DN	70	THR
35	DN	88	ALA
35	DN	104	ALA

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Mol	Chain	Res	Type
35	DN	119	SER
36	DO	116	GLN
37	DP	66	ASN
37	DP	94	LYS
38	DQ	87	SER
39	DR	31	GLU
40	DS	29	VAL
40	DS	63	GLY
40	DS	67	ASP
41	DT	18	GLU
41	DT	52	GLU
41	DT	77	ARG
41	DT	88	LYS
42	DU	7	ARG
42	DU	53	ASN
42	DU	55	PRO
42	DU	89	ASP
45	DX	62	LYS
46	DY	57	LEU
46	DY	61	ALA
47	DZ	4	THR
49	D1	5	ILE
50	D2	44	VAL
50	D2	45	SER
2	AB	41	ILE
2	AB	53	ALA
2	AB	87	CYS
2	AB	95	ARG
2	AB	117	LEU
2	AB	128	LYS
2	AB	133	GLU
2	AB	143	LYS
2	AB	183	VAL
2	AB	201	PRO
2	AB	220	THR
3	AC	17	PRO
3	AC	69	HIS
3	AC	79	LYS
3	AC	140	ASN
3	AC	141	ALA
3	AC	146	ALA
4	AD	7	PRO

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Mol	Chain	Res	Type
4	AD	24	GLY
4	AD	153	SER
4	AD	156	LYS
4	AD	160	GLU
4	AD	166	GLU
4	AD	175	ALA
4	AD	191	LEU
5	AE	78	ASN
5	AE	100	SER
6	AF	36	ILE
6	AF	69	GLU
7	AG	15	ASP
7	AG	51	ALA
7	AG	69	VAL
7	AG	79	ARG
8	AH	54	ASP
8	AH	67	GLN
8	AH	88	ARG
9	AI	9	THR
10	AJ	32	THR
10	AJ	33	GLY
10	AJ	61	ALA
11	AK	14	LYS
11	AK	41	ALA
11	AK	73	ALA
11	AK	125	LYS
12	AL	118	GLY
12	AL	123	LYS
14	AN	34	VAL
14	AN	53	ARG
14	AN	81	ARG
14	AN	92	GLU
16	AP	65	ALA
16	AP	68	SER
16	AP	77	GLU
16	AP	80	LYS
17	AQ	12	VAL
17	AQ	51	ASN
17	AQ	70	THR
18	AR	27	ALA
19	AS	64	ASP
21	AU	31	GLU

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Mol	Chain	Res	Type
21	AU	35	ARG
24	BC	13	ARG
24	BC	71	LYS
24	BC	122	ALA
24	BC	196	GLY
26	BE	8	ALA
27	BF	21	ASN
28	BG	61	GLY
28	BG	79	VAL
29	BH	3	VAL
29	BH	11	ASN
29	BH	14	SER
29	BH	15	LEU
29	BH	66	ASN
29	BH	119	ASN
30	BI	6	GLN
30	BI	24	VAL
30	BI	45	LYS
30	BI	60	THR
30	BI	98	VAL
30	BI	106	LEU
30	BI	117	MET
30	BI	126	THR
30	BI	134	ARG
31	BJ	25	LEU
32	BK	109	SER
33	BL	15	ALA
33	BL	69	ARG
33	BL	86	GLU
33	BL	114	GLY
36	BO	88	LYS
37	BP	35	GLY
38	BQ	7	GLY
38	BQ	102	ASP
40	BS	63	GLY
41	BT	71	GLY
42	BU	8	ASP
46	BY	35	GLY
46	BY	62	GLY
49	B1	28	ARG
49	B1	52	ALA
50	B2	25	LYS

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Mol	Chain	Res	Type
50	B2	44	VAL
53	B5	36	ALA
53	B5	41	THR
53	B5	62	THR
53	B5	136	GLY
53	B5	185	LYS
2	CB	22	TYR
2	CB	33	GLY
2	CB	36	ASN
2	CB	51	ASN
2	CB	59	LYS
2	CB	87	CYS
2	CB	100	MET
2	CB	120	GLN
2	CB	124	GLY
2	CB	141	LEU
3	CC	101	ILE
4	CD	32	CYS
4	CD	85	ASN
4	CD	165	ARG
5	CE	51	GLY
5	CE	70	ASN
5	CE	77	ASN
5	CE	98	PRO
5	CE	100	SER
5	CE	102	GLY
5	CE	134	ILE
5	CE	150	PRO
5	CE	151	GLU
5	CE	158	GLY
6	CF	27	ALA
6	CF	54	LEU
6	CF	56	LYS
6	CF	63	ASN
6	CF	93	LYS
7	CG	56	LYS
7	CG	80	VAL
7	CG	84	THR
8	CH	67	GLN
8	CH	89	LYS
9	CI	120	LYS
10	CJ	35	GLN

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Mol	Chain	Res	Type
10	CJ	57	VAL
10	CJ	86	ALA
10	CJ	92	LEU
11	CK	92	GLY
11	CK	93	ARG
12	CL	23	ALA
12	CL	89	ASP
13	CM	12	HIS
14	CN	29	ALA
14	CN	42	TRP
14	CN	59	ARG
15	CO	20	ASN
16	CP	10	GLY
16	CP	80	LYS
17	CQ	13	VAL
18	CR	21	ILE
18	CR	25	ASP
18	CR	26	ILE
20	CT	7	ALA
20	CT	41	ALA
20	CT	68	HIS
21	CU	11	PRO
21	CU	13	ASP
21	CU	46	LYS
21	CU	52	ALA
24	DC	73	GLY
24	DC	238	ARG
24	DC	240	PHE
24	DC	251	GLN
26	DE	7	ASP
26	DE	61	ARG
26	DE	84	THR
26	DE	122	GLU
26	DE	131	THR
27	DF	41	GLY
27	DF	103	LEU
28	DG	46	ALA
28	DG	61	GLY
28	DG	159	GLY
29	DH	31	VAL
29	DH	77	THR
29	DH	118	PRO

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Mol	Chain	Res	Type
30	DI	88	SER
30	DI	102	SER
30	DI	106	LEU
31	DJ	25	LEU
32	DK	35	VAL
33	DL	9	ALA
33	DL	42	SER
33	DL	103	ILE
33	DL	111	ILE
35	DN	3	HIS
36	DO	34	HIS
37	DP	105	GLY
37	DP	114	LEU
39	DR	102	SER
40	DS	62	ASP
41	DT	37	ASP
41	DT	72	GLN
41	DT	73	ARG
42	DU	9	ASP
42	DU	19	LYS
42	DU	57	GLY
44	DW	35	SER
46	DY	37	LEU
47	DZ	14	ILE
48	D0	55	ILE
2	AB	12	ALA
2	AB	68	LEU
2	AB	96	TRP
2	AB	126	PHE
2	AB	155	GLY
2	AB	203	ASN
2	AB	211	THR
3	AC	18	TRP
3	AC	61	ALA
3	AC	80	LYS
3	AC	139	GLN
4	AD	36	GLN
4	AD	107	PHE
4	AD	167	LYS
5	AE	24	THR
5	AE	45	ARG
5	AE	62	LYS

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Mol	Chain	Res	Type
5	AE	76	LEU
5	AE	157	ARG
6	AF	56	LYS
6	AF	99	ALA
7	AG	14	PRO
7	AG	87	VAL
7	AG	113	ASP
8	AH	4	GLN
8	AH	66	PHE
8	AH	97	ALA
10	AJ	17	LEU
10	AJ	43	PRO
10	AJ	75	ASP
11	AK	15	GLN
11	AK	89	PRO
13	AM	27	LYS
15	AO	20	ASN
16	AP	49	GLY
16	AP	79	ASN
18	AR	25	ASP
18	AR	49	ALA
18	AR	50	LYS
19	AS	5	LEU
19	AS	30	PRO
19	AS	65	GLU
20	AT	68	HIS
24	BC	37	ASN
24	BC	167	ARG
25	BD	40	LEU
25	BD	114	LYS
26	BE	6	LYS
27	BF	73	SER
28	BG	158	LYS
28	BG	175	LYS
29	BH	9	VAL
29	BH	30	LEU
29	BH	85	GLY
29	BH	93	SER
29	BH	105	ALA
30	BI	31	GLN
30	BI	63	ALA
30	BI	75	PRO

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Mol	Chain	Res	Type
30	BI	83	ALA
30	BI	90	SER
30	BI	113	LYS
31	BJ	21	THR
31	BJ	39	LYS
32	BK	93	GLN
32	BK	118	LEU
32	BK	119	ALA
33	BL	111	ILE
38	BQ	24	TYR
38	BQ	103	LYS
41	BT	25	GLU
42	BU	50	PRO
46	BY	10	SER
46	BY	14	LEU
48	B0	55	ILE
53	B5	73	VAL
53	B5	90	ALA
53	B5	156	GLU
53	B5	217	THR
2	CB	17	GLY
2	CB	21	ARG
2	CB	129	LEU
2	CB	134	ALA
2	CB	136	MET
2	CB	209	ALA
3	CC	54	ARG
3	CC	64	ILE
3	CC	89	LYS
4	CD	4	TYR
4	CD	10	LYS
4	CD	154	ARG
4	CD	173	VAL
4	CD	175	ALA
4	CD	192	SER
5	CE	12	GLN
5	CE	68	ARG
5	CE	99	ALA
5	CE	122	ASN
5	CE	143	GLY
6	CF	17	GLN
7	CG	140	ASP

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Mol	Chain	Res	Type
9	CI	41	ARG
10	CJ	17	LEU
10	CJ	36	VAL
10	CJ	41	PRO
10	CJ	94	ALA
11	CK	15	GLN
11	CK	41	ALA
12	CL	77	HIS
13	CM	5	ALA
13	CM	10	PRO
13	CM	82	ASP
14	CN	23	LYS
14	CN	28	LYS
14	CN	34	VAL
15	CO	18	ASP
16	CP	43	ALA
18	CR	70	TYR
19	CS	6	LYS
21	CU	16	LEU
24	DC	108	LYS
24	DC	205	LEU
24	DC	260	ASN
26	DE	6	LYS
26	DE	86	ALA
26	DE	144	GLU
27	DF	21	ASN
28	DG	47	ASP
29	DH	16	GLY
29	DH	40	THR
30	DI	84	ALA
30	DI	115	ALA
32	DK	93	GLN
33	DL	29	LYS
35	DN	105	GLY
40	DS	28	LYS
41	DT	10	VAL
42	DU	98	SER
43	DV	93	ARG
52	D4	20	ASP
52	D4	23	ILE
2	AB	52	GLU
2	AB	132	LYS

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Mol	Chain	Res	Type
2	AB	145	GLU
3	AC	3	GLN
3	AC	12	LEU
5	AE	12	GLN
5	AE	68	ARG
6	AF	54	LEU
6	AF	98	GLU
10	AJ	36	VAL
10	AJ	42	LEU
10	AJ	62	ARG
10	AJ	95	GLY
11	AK	127	ARG
13	AM	105	ASN
14	AN	21	PHE
14	AN	29	ALA
15	AO	3	LEU
16	AP	11	ALA
16	AP	50	THR
17	AQ	6	ARG
17	AQ	82	ALA
19	AS	4	SER
26	BE	200	LEU
27	BF	45	ALA
27	BF	175	PHE
28	BG	173	GLU
29	BH	83	LYS
30	BI	72	LYS
32	BK	89	ASN
33	BL	31	GLY
34	BM	6	ARG
35	BN	118	ARG
36	BO	89	ASP
39	BR	43	ASN
39	BR	52	PRO
40	BS	65	ASP
41	BT	28	ASN
41	BT	38	ALA
42	BU	39	ILE
42	BU	89	ASP
45	BX	64	ILE
53	B5	65	LEU
53	B5	86	GLU

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Mol	Chain	Res	Type
53	B5	162	ILE
53	B5	171	ALA
2	CB	34	ALA
2	CB	205	ASP
3	CC	25	ASN
3	CC	80	LYS
3	CC	141	ALA
4	CD	17	THR
4	CD	37	ALA
7	CG	57	SER
8	CH	31	LYS
8	CH	44	GLY
9	CI	42	GLU
9	CI	72	ILE
10	CJ	90	LEU
11	CK	89	PRO
12	CL	4	VAL
12	CL	17	ALA
12	CL	78	SER
12	CL	117	TYR
13	CM	24	GLY
14	CN	16	LEU
15	CO	46	HIS
16	CP	77	GLU
17	CQ	80	GLU
17	CQ	82	ALA
19	CS	32	ARG
24	DC	122	ALA
26	DE	18	THR
26	DE	151	GLY
27	DF	3	LYS
27	DF	9	LYS
27	DF	43	ALA
27	DF	174	ASP
29	DH	9	VAL
30	DI	9	VAL
30	DI	72	LYS
30	DI	101	ILE
32	DK	110	GLU
33	DL	53	GLY
34	DM	3	GLN
35	DN	106	ASP

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Mol	Chain	Res	Type
36	DO	99	TYR
41	DT	22	THR
41	DT	39	THR
41	DT	50	LEU
44	DW	21	LEU
46	DY	23	ARG
2	AB	25	PRO
2	AB	115	LYS
2	AB	161	LEU
2	AB	224	GLY
3	AC	66	VAL
4	AD	101	VAL
4	AD	193	ALA
9	AI	72	ILE
10	AJ	41	PRO
10	AJ	74	VAL
11	AK	36	ASP
13	AM	112	PRO
16	AP	9	HIS
16	AP	36	VAL
17	AQ	69	LYS
17	AQ	81	LYS
20	AT	4	ILE
20	AT	67	ILE
21	AU	10	GLU
21	AU	16	LEU
21	AU	27	GLY
24	BC	201	MET
26	BE	11	ALA
28	BG	38	ASN
28	BG	80	THR
28	BG	94	TYR
31	BJ	60	ASP
33	BL	12	SER
41	BT	52	GLU
42	BU	100	SER
46	BY	33	ALA
48	B0	26	THR
53	B5	104	ILE
53	B5	133	GLY
53	B5	144	GLY
53	B5	159	ALA

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Mol	Chain	Res	Type
53	B5	183	PRO
2	CB	140	GLU
3	CC	12	LEU
3	CC	14	ILE
4	CD	29	ASP
4	CD	43	ALA
4	CD	167	LYS
5	CE	126	LYS
6	CF	13	ASP
6	CF	53	LYS
9	CI	58	VAL
13	CM	6	GLY
14	CN	21	PHE
21	CU	53	VAL
24	DC	253	LYS
25	DD	43	ASP
26	DE	153	LEU
27	DF	116	GLY
27	DF	177	PHE
28	DG	80	THR
30	DI	13	VAL
32	DK	118	LEU
33	DL	115	GLU
35	DN	82	GLU
35	DN	118	ARG
39	DR	7	SER
39	DR	53	PHE
42	DU	37	GLU
45	DX	32	ASN
49	D1	51	GLU
2	AB	193	PRO
3	AC	160	ALA
4	AD	34	ILE
4	AD	37	ALA
5	AE	51	GLY
9	AI	50	GLN
9	AI	116	VAL
10	AJ	39	PRO
10	AJ	92	LEU
15	AO	47	LYS
29	BH	120	GLY
30	BI	7	ALA

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Mol	Chain	Res	Type
37	BP	76	THR
42	BU	40	ASN
43	BV	24	ASN
46	BY	57	LEU
49	B1	5	ILE
2	CB	68	LEU
3	CC	84	VAL
5	CE	24	THR
6	CF	15	SER
13	CM	13	LYS
14	CN	3	LYS
14	CN	64	CYS
17	CQ	12	VAL
21	CU	35	ARG
26	DE	72	SER
28	DG	8	PRO
28	DG	12	PRO
28	DG	154	PRO
34	DM	53	MET
36	DO	66	GLY
37	DP	80	VAL
41	DT	21	SER
4	AD	125	VAL
4	AD	168	PRO
5	AE	88	VAL
9	AI	24	GLY
13	AM	111	GLY
24	BC	29	PRO
28	BG	82	GLY
30	BI	52	GLY
30	BI	101	ILE
2	CB	180	GLY
3	CC	66	VAL
3	CC	103	ILE
5	CE	105	ILE
5	CE	133	PRO
8	CH	75	ILE
10	CJ	38	GLY
11	CK	104	GLY
14	CN	31	ILE
42	DU	56	GLY
49	D1	16	GLY

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Mol	Chain	Res	Type
17	AQ	35	GLY
28	BG	78	GLY
7	CG	8	GLY
24	DC	99	GLY
28	DG	79	VAL
30	DI	58	VAL
30	DI	85	GLY
2	AB	157	LEU
9	AI	51	PRO
16	AP	10	GLY
24	BC	124	ILE
24	BC	233	GLY
26	BE	151	GLY
51	B3	7	VAL
53	B5	44	VAL
53	B5	100	ILE
53	B5	181	PHE
2	CB	221	VAL
10	CJ	42	LEU
14	CN	11	VAL
20	CT	42	GLY
26	DE	129	PRO
16	AP	78	VAL
19	AS	76	PRO
27	BF	84	PRO
42	BU	54	GLN
53	B5	202	PRO
2	CB	151	ILE
15	CO	86	GLY
21	CU	10	GLU
30	DI	89	GLY
43	DV	65	VAL
48	D0	43	ILE
51	D3	7	VAL
30	BI	22	PRO
30	BI	122	ILE
53	B5	204	GLY
53	B5	215	VAL

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	180/180 (100%)	113 (63%)	67 (37%)	0	1
2	CB	180/180 (100%)	129 (72%)	51 (28%)	0	2
3	AC	170/170 (100%)	132 (78%)	38 (22%)	1	4
3	CC	170/170 (100%)	131 (77%)	39 (23%)	1	4
4	AD	172/172 (100%)	129 (75%)	43 (25%)	1	3
4	CD	172/172 (100%)	138 (80%)	34 (20%)	1	7
5	AE	113/113 (100%)	85 (75%)	28 (25%)	1	3
5	CE	113/113 (100%)	85 (75%)	28 (25%)	1	3
6	AF	87/87 (100%)	64 (74%)	23 (26%)	0	2
6	CF	87/87 (100%)	63 (72%)	24 (28%)	0	2
7	AG	124/124 (100%)	94 (76%)	30 (24%)	1	3
7	CG	124/124 (100%)	91 (73%)	33 (27%)	0	2
8	AH	104/104 (100%)	79 (76%)	25 (24%)	1	3
8	CH	104/104 (100%)	83 (80%)	21 (20%)	1	6
9	AI	105/105 (100%)	74 (70%)	31 (30%)	0	1
9	CI	105/105 (100%)	77 (73%)	28 (27%)	0	2
10	AJ	86/86 (100%)	64 (74%)	22 (26%)	0	2
10	CJ	86/86 (100%)	67 (78%)	19 (22%)	1	4
11	AK	90/90 (100%)	66 (73%)	24 (27%)	0	2
11	CK	90/90 (100%)	69 (77%)	21 (23%)	1	4
12	AL	103/103 (100%)	84 (82%)	19 (18%)	2	9
12	CL	103/103 (100%)	78 (76%)	25 (24%)	1	3
13	AM	92/92 (100%)	74 (80%)	18 (20%)	1	7
13	CM	92/92 (100%)	70 (76%)	22 (24%)	1	3
14	AN	79/83 (95%)	61 (77%)	18 (23%)	1	4
14	CN	79/83 (95%)	68 (86%)	11 (14%)	4	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	AO	75/76 (99%)	59 (79%)	16 (21%)	1	5
15	CO	75/76 (99%)	57 (76%)	18 (24%)	1	3
16	AP	65/65 (100%)	52 (80%)	13 (20%)	1	7
16	CP	65/65 (100%)	49 (75%)	16 (25%)	1	3
17	AQ	74/74 (100%)	52 (70%)	22 (30%)	0	1
17	CQ	74/74 (100%)	53 (72%)	21 (28%)	0	2
18	AR	48/48 (100%)	41 (85%)	7 (15%)	4	16
18	CR	48/48 (100%)	39 (81%)	9 (19%)	2	8
19	AS	70/70 (100%)	57 (81%)	13 (19%)	2	9
19	CS	70/70 (100%)	55 (79%)	15 (21%)	1	5
20	AT	65/65 (100%)	46 (71%)	19 (29%)	0	2
20	CT	65/65 (100%)	48 (74%)	17 (26%)	0	2
21	AU	44/44 (100%)	27 (61%)	17 (39%)	0	0
21	CU	44/44 (100%)	32 (73%)	12 (27%)	0	2
24	BC	216/216 (100%)	190 (88%)	26 (12%)	6	24
24	DC	216/216 (100%)	180 (83%)	36 (17%)	3	11
25	BD	164/164 (100%)	147 (90%)	17 (10%)	9	30
25	DD	164/164 (100%)	144 (88%)	20 (12%)	6	23
26	BE	165/165 (100%)	138 (84%)	27 (16%)	3	12
26	DE	165/165 (100%)	133 (81%)	32 (19%)	2	7
27	BF	148/148 (100%)	121 (82%)	27 (18%)	2	9
27	DF	148/148 (100%)	118 (80%)	30 (20%)	1	6
28	BG	137/137 (100%)	117 (85%)	20 (15%)	4	16
28	DG	137/137 (100%)	123 (90%)	14 (10%)	9	31
29	BH	114/114 (100%)	88 (77%)	26 (23%)	1	4
29	DH	114/114 (100%)	88 (77%)	26 (23%)	1	4
30	BI	109/109 (100%)	86 (79%)	23 (21%)	1	5
30	DI	109/109 (100%)	84 (77%)	25 (23%)	1	4
31	BJ	116/116 (100%)	103 (89%)	13 (11%)	7	27
31	DJ	116/116 (100%)	102 (88%)	14 (12%)	6	23
32	BK	103/103 (100%)	93 (90%)	10 (10%)	10	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	DK	103/103 (100%)	90 (87%)	13 (13%)	5	22
33	BL	102/102 (100%)	85 (83%)	17 (17%)	3	11
33	DL	102/102 (100%)	81 (79%)	21 (21%)	1	6
34	BM	109/109 (100%)	97 (89%)	12 (11%)	8	27
34	DM	109/109 (100%)	97 (89%)	12 (11%)	8	27
35	BN	100/100 (100%)	87 (87%)	13 (13%)	5	20
35	DN	100/100 (100%)	83 (83%)	17 (17%)	2	11
36	BO	86/86 (100%)	64 (74%)	22 (26%)	0	2
36	DO	86/86 (100%)	72 (84%)	14 (16%)	3	12
37	BP	99/99 (100%)	88 (89%)	11 (11%)	8	27
37	DP	99/99 (100%)	80 (81%)	19 (19%)	2	8
38	BQ	89/89 (100%)	74 (83%)	15 (17%)	2	11
38	DQ	89/89 (100%)	76 (85%)	13 (15%)	4	16
39	BR	84/84 (100%)	73 (87%)	11 (13%)	5	20
39	DR	84/84 (100%)	70 (83%)	14 (17%)	3	11
40	BS	93/93 (100%)	78 (84%)	15 (16%)	3	12
40	DS	93/93 (100%)	77 (83%)	16 (17%)	2	10
41	BT	80/80 (100%)	68 (85%)	12 (15%)	3	15
41	DT	80/80 (100%)	66 (82%)	14 (18%)	2	10
42	BU	83/83 (100%)	68 (82%)	15 (18%)	2	9
42	DU	83/83 (100%)	64 (77%)	19 (23%)	1	4
43	BV	78/78 (100%)	66 (85%)	12 (15%)	3	14
43	DV	78/78 (100%)	67 (86%)	11 (14%)	4	17
44	BW	57/58 (98%)	53 (93%)	4 (7%)	19	53
44	DW	56/58 (97%)	49 (88%)	7 (12%)	6	22
45	BX	67/67 (100%)	55 (82%)	12 (18%)	2	9
45	DX	67/67 (100%)	55 (82%)	12 (18%)	2	9
46	BY	55/55 (100%)	48 (87%)	7 (13%)	5	21
46	DY	55/55 (100%)	43 (78%)	12 (22%)	1	5
47	BZ	48/48 (100%)	43 (90%)	5 (10%)	9	30
47	DZ	48/48 (100%)	38 (79%)	10 (21%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	B0	47/47 (100%)	40 (85%)	7 (15%)	4	15
48	D0	47/47 (100%)	42 (89%)	5 (11%)	8	29
49	B1	45/45 (100%)	38 (84%)	7 (16%)	3	13
49	D1	45/45 (100%)	39 (87%)	6 (13%)	5	19
50	B2	38/38 (100%)	32 (84%)	6 (16%)	3	13
50	D2	38/38 (100%)	32 (84%)	6 (16%)	3	13
51	B3	51/51 (100%)	46 (90%)	5 (10%)	10	34
51	D3	51/51 (100%)	46 (90%)	5 (10%)	10	34
52	B4	34/34 (100%)	30 (88%)	4 (12%)	6	24
52	D4	34/34 (100%)	28 (82%)	6 (18%)	2	10
53	B5	61/180 (34%)	48 (79%)	13 (21%)	1	5
54	B6	2/2 (100%)	2 (100%)	0	100	100
54	D6	2/2 (100%)	2 (100%)	0	100	100
All	All	9390/9522 (99%)	7570 (81%)	1820 (19%)	2	7

All (1820) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	10	LEU
2	AB	14	VAL
2	AB	15	HIS
2	AB	20	THR
2	AB	21	ARG
2	AB	22	TYR
2	AB	27	MET
2	AB	31	ILE
2	AB	32	PHE
2	AB	38	VAL
2	AB	39	HIS
2	AB	41	ILE
2	AB	43	LEU
2	AB	44	GLU
2	AB	46	THR
2	AB	49	MET
2	AB	50	PHE
2	AB	52	GLU
2	AB	56	GLU

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Mol	Chain	Res	Type
2	AB	57	LEU
2	AB	59	LYS
2	AB	64	LYS
2	AB	66	LYS
2	AB	68	LEU
2	AB	82	ASP
2	AB	85	LEU
2	AB	91	PHE
2	AB	93	ASN
2	AB	100	MET
2	AB	102	THR
2	AB	107	VAL
2	AB	108	ARG
2	AB	111	ILE
2	AB	112	LYS
2	AB	117	LEU
2	AB	126	PHE
2	AB	129	LEU
2	AB	130	THR
2	AB	131	LYS
2	AB	132	LYS
2	AB	133	GLU
2	AB	135	LEU
2	AB	136	MET
2	AB	137	ARG
2	AB	139	ARG
2	AB	140	GLU
2	AB	141	LEU
2	AB	143	LYS
2	AB	144	LEU
2	AB	151	ILE
2	AB	152	LYS
2	AB	163	VAL
2	AB	164	ILE
2	AB	170	HIS
2	AB	174	LYS
2	AB	181	ILE
2	AB	186	ILE
2	AB	188	ASP
2	AB	194	ASP
2	AB	197	ASP
2	AB	205	ASP

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Mol	Chain	Res	Type
2	AB	207	ILE
2	AB	208	ARG
2	AB	210	VAL
2	AB	213	TYR
2	AB	220	THR
2	AB	225	ARG
3	AC	3	GLN
3	AC	4	LYS
3	AC	14	ILE
3	AC	15	VAL
3	AC	16	LYS
3	AC	18	TRP
3	AC	20	SER
3	AC	26	THR
3	AC	27	LYS
3	AC	29	PHE
3	AC	33	LEU
3	AC	37	PHE
3	AC	51	SER
3	AC	52	VAL
3	AC	55	ILE
3	AC	58	GLU
3	AC	59	ARG
3	AC	64	ILE
3	AC	70	THR
3	AC	82	GLU
3	AC	86	LYS
3	AC	103	ILE
3	AC	107	ARG
3	AC	111	LEU
3	AC	121	THR
3	AC	131	ARG
3	AC	140	ASN
3	AC	142	MET
3	AC	144	LEU
3	AC	150	LYS
3	AC	157	LEU
3	AC	161	GLU
3	AC	162	ILE
3	AC	166	GLU
3	AC	167	TRP
3	AC	173	VAL

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Mol	Chain	Res	Type
3	AC	185	ASN
3	AC	200	VAL
4	AD	5	LEU
4	AD	9	LEU
4	AD	13	ARG
4	AD	17	THR
4	AD	20	PHE
4	AD	23	SER
4	AD	26	ARG
4	AD	31	LYS
4	AD	32	CYS
4	AD	35	GLU
4	AD	44	ARG
4	AD	53	VAL
4	AD	58	LYS
4	AD	60	LYS
4	AD	63	ARG
4	AD	69	GLU
4	AD	70	ARG
4	AD	83	LYS
4	AD	98	LEU
4	AD	104	ARG
4	AD	110	THR
4	AD	111	ARG
4	AD	116	GLN
4	AD	121	LYS
4	AD	123	ILE
4	AD	128	ARG
4	AD	138	SER
4	AD	143	VAL
4	AD	144	SER
4	AD	152	GLN
4	AD	160	GLU
4	AD	161	LEU
4	AD	163	GLU
4	AD	164	GLN
4	AD	171	LEU
4	AD	177	LYS
4	AD	190	ASP
4	AD	192	SER
4	AD	195	ILE
4	AD	196	ASN

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Mol	Chain	Res	Type
4	AD	197	GLU
4	AD	200	ILE
4	AD	206	LYS
5	AE	10	GLU
5	AE	15	LEU
5	AE	18	VAL
5	AE	29	ARG
5	AE	32	SER
5	AE	38	VAL
5	AE	46	VAL
5	AE	54	ARG
5	AE	56	VAL
5	AE	65	GLU
5	AE	69	ARG
5	AE	72	ILE
5	AE	83	HIS
5	AE	92	SER
5	AE	93	ARG
5	AE	114	VAL
5	AE	115	LEU
5	AE	122	ASN
5	AE	123	VAL
5	AE	124	LEU
5	AE	126	LYS
5	AE	131	THR
5	AE	134	ILE
5	AE	136	VAL
5	AE	137	VAL
5	AE	140	THR
5	AE	149	SER
5	AE	153	VAL
6	AF	1	MET
6	AF	5	GLU
6	AF	14	GLN
6	AF	15	SER
6	AF	17	GLN
6	AF	24	ARG
6	AF	35	LYS
6	AF	39	LEU
6	AF	44	ARG
6	AF	46	GLN
6	AF	51	ILE

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Mol	Chain	Res	Type
6	AF	52	ASN
6	AF	54	LEU
6	AF	55	HIS
6	AF	62	MET
6	AF	69	GLU
6	AF	77	THR
6	AF	82	ASP
6	AF	85	ILE
6	AF	87	SER
6	AF	96	VAL
6	AF	97	THR
6	AF	100	SER
7	AG	4	ARG
7	AG	6	VAL
7	AG	7	ILE
7	AG	9	GLN
7	AG	10	ARG
7	AG	13	LEU
7	AG	23	LEU
7	AG	26	PHE
7	AG	36	LYS
7	AG	43	VAL
7	AG	49	THR
7	AG	52	GLN
7	AG	59	LEU
7	AG	63	GLU
7	AG	70	ARG
7	AG	75	VAL
7	AG	76	LYS
7	AG	78	ARG
7	AG	79	ARG
7	AG	80	VAL
7	AG	89	VAL
7	AG	95	ARG
7	AG	111	ARG
7	AG	120	LEU
7	AG	125	SER
7	AG	135	VAL
7	AG	136	LYS
7	AG	142	HIS
7	AG	144	MET
7	AG	146	GLU

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Mol	Chain	Res	Type
8	AH	3	MET
8	AH	11	LEU
8	AH	13	ARG
8	AH	22	LYS
8	AH	26	THR
8	AH	30	SER
8	AH	32	LEU
8	AH	38	ASN
8	AH	42	GLU
8	AH	49	PHE
8	AH	64	LYS
8	AH	77	ARG
8	AH	79	SER
8	AH	83	LEU
8	AH	87	LYS
8	AH	89	LYS
8	AH	90	ASP
8	AH	99	LEU
8	AH	104	VAL
8	AH	107	SER
8	AH	108	LYS
8	AH	111	MET
8	AH	112	THR
8	AH	125	ILE
8	AH	129	VAL
9	AI	7	TYR
9	AI	11	ARG
9	AI	12	ARG
9	AI	14	SER
9	AI	22	LYS
9	AI	30	ILE
9	AI	33	ARG
9	AI	36	GLU
9	AI	43	THR
9	AI	45	ARG
9	AI	46	MET
9	AI	48	VAL
9	AI	49	ARG
9	AI	55	VAL
9	AI	57	MET
9	AI	60	LYS
9	AI	63	LEU

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Mol	Chain	Res	Type
9	AI	65	ILE
9	AI	68	LYS
9	AI	85	ARG
9	AI	88	MET
9	AI	89	GLU
9	AI	90	TYR
9	AI	92	GLU
9	AI	94	LEU
9	AI	99	ARG
9	AI	115	LYS
9	AI	116	VAL
9	AI	127	PHE
9	AI	129	LYS
9	AI	130	ARG
10	AJ	6	ILE
10	AJ	8	ILE
10	AJ	15	HIS
10	AJ	27	GLU
10	AJ	28	THR
10	AJ	40	ILE
10	AJ	42	LEU
10	AJ	44	THR
10	AJ	47	GLU
10	AJ	50	THR
10	AJ	52	LEU
10	AJ	53	ILE
10	AJ	59	LYS
10	AJ	63	ASP
10	AJ	66	GLU
10	AJ	73	LEU
10	AJ	83	THR
10	AJ	84	VAL
10	AJ	89	ARG
10	AJ	91	ASP
10	AJ	92	LEU
10	AJ	101	SER
11	AK	17	SER
11	AK	18	ASP
11	AK	23	ILE
11	AK	31	ILE
11	AK	32	VAL
11	AK	38	GLN

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Mol	Chain	Res	Type
11	AK	50	SER
11	AK	52	PHE
11	AK	58	SER
11	AK	65	VAL
11	AK	74	VAL
11	AK	76	GLU
11	AK	79	ILE
11	AK	81	ASN
11	AK	82	LEU
11	AK	95	SER
11	AK	97	ILE
11	AK	100	LEU
11	AK	101	ASN
11	AK	107	ILE
11	AK	111	THR
11	AK	119	ASN
11	AK	126	LYS
11	AK	128	ARG
12	AL	4	VAL
12	AL	21	VAL
12	AL	25	GLU
12	AL	29	GLN
12	AL	44	LYS
12	AL	54	ARG
12	AL	58	THR
12	AL	62	GLU
12	AL	65	SER
12	AL	74	LEU
12	AL	76	GLU
12	AL	82	ILE
12	AL	86	ARG
12	AL	88	LYS
12	AL	89	ASP
12	AL	102	LEU
12	AL	105	SER
12	AL	116	LYS
12	AL	121	ARG
13	AM	4	ILE
13	AM	7	ILE
13	AM	13	LYS
13	AM	14	HIS
13	AM	16	VAL

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Mol	Chain	Res	Type
13	AM	21	SER
13	AM	27	LYS
13	AM	29	ARG
13	AM	48	LEU
13	AM	64	VAL
13	AM	68	ASP
13	AM	72	GLU
13	AM	75	MET
13	AM	79	ARG
13	AM	87	ARG
13	AM	90	ARG
13	AM	107	ARG
13	AM	108	THR
14	AN	4	GLN
14	AN	5	SER
14	AN	7	LYS
14	AN	24	ARG
14	AN	26	GLU
14	AN	28	LYS
14	AN	43	ASN
14	AN	46	LEU
14	AN	49	GLN
14	AN	51	LEU
14	AN	59	ARG
14	AN	62	ASN
14	AN	63	ARG
14	AN	76	LYS
14	AN	85	ARG
14	AN	89	MET
14	AN	98	LYS
14	AN	100	SER
15	AO	4	SER
15	AO	6	GLU
15	AO	17	ARG
15	AO	18	ASP
15	AO	31	LEU
15	AO	35	GLN
15	AO	39	LEU
15	AO	40	GLN
15	AO	48	LYS
15	AO	57	LEU
15	AO	58	ARG

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Mol	Chain	Res	Type
15	AO	59	MET
15	AO	67	LEU
15	AO	75	VAL
15	AO	85	LEU
15	AO	87	LEU
16	AP	1	MET
16	AP	2	VAL
16	AP	6	LEU
16	AP	8	ARG
16	AP	20	VAL
16	AP	39	PHE
16	AP	46	LYS
16	AP	51	ARG
16	AP	67	ILE
16	AP	70	ARG
16	AP	71	VAL
16	AP	75	ILE
16	AP	80	LYS
17	AQ	4	LYS
17	AQ	11	ARG
17	AQ	13	VAL
17	AQ	14	SER
17	AQ	16	LYS
17	AQ	17	MET
17	AQ	21	ILE
17	AQ	26	GLU
17	AQ	28	PHE
17	AQ	29	VAL
17	AQ	30	LYS
17	AQ	38	ILE
17	AQ	51	ASN
17	AQ	52	GLU
17	AQ	53	CYS
17	AQ	55	ILE
17	AQ	59	VAL
17	AQ	75	LEU
17	AQ	76	VAL
17	AQ	77	ARG
17	AQ	81	LYS
17	AQ	83	VAL
18	AR	29	LEU
18	AR	30	LYS

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Mol	Chain	Res	Type
18	AR	34	THR
18	AR	43	ARG
18	AR	48	ARG
18	AR	55	LEU
18	AR	71	THR
19	AS	6	LYS
19	AS	15	LEU
19	AS	21	LYS
19	AS	24	GLU
19	AS	36	ARG
19	AS	38	SER
19	AS	41	PHE
19	AS	55	ARG
19	AS	58	VAL
19	AS	63	THR
19	AS	65	GLU
19	AS	71	LEU
19	AS	79	THR
20	AT	5	LYS
20	AT	6	SER
20	AT	8	LYS
20	AT	10	ARG
20	AT	12	ILE
20	AT	15	GLU
20	AT	16	LYS
20	AT	24	ARG
20	AT	27	MET
20	AT	30	THR
20	AT	34	LYS
20	AT	36	TYR
20	AT	54	MET
20	AT	68	HIS
20	AT	69	LYS
20	AT	70	ASN
20	AT	74	ARG
20	AT	76	LYS
20	AT	86	LEU
21	AU	5	LYS
21	AU	9	ASN
21	AU	10	GLU
21	AU	12	PHE
21	AU	16	LEU

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Mol	Chain	Res	Type
21	AU	18	ARG
21	AU	19	PHE
21	AU	20	LYS
21	AU	28	VAL
21	AU	33	ARG
21	AU	34	ARG
21	AU	37	PHE
21	AU	38	TYR
21	AU	43	THR
21	AU	44	GLU
21	AU	47	ARG
21	AU	54	LYS
24	BC	3	VAL
24	BC	5	LYS
24	BC	18	LYS
24	BC	24	LEU
24	BC	38	SER
24	BC	39	LYS
24	BC	86	ASN
24	BC	97	LYS
24	BC	111	LYS
24	BC	121	ASP
24	BC	125	LYS
24	BC	156	ARG
24	BC	164	ILE
24	BC	172	VAL
24	BC	174	LEU
24	BC	177	ARG
24	BC	181	MET
24	BC	187	ASP
24	BC	197	ASN
24	BC	199	GLU
24	BC	203	ARG
24	BC	213	TRP
24	BC	252	THR
24	BC	258	ARG
24	BC	265	LYS
24	BC	271	ARG
25	BD	12	THR
25	BD	16	THR
25	BD	28	GLU
25	BD	32	ASN

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Mol	Chain	Res	Type
25	BD	61	THR
25	BD	73	VAL
25	BD	77	ARG
25	BD	83	ARG
25	BD	89	GLU
25	BD	95	SER
25	BD	97	SER
25	BD	121	THR
25	BD	141	ARG
25	BD	145	SER
25	BD	157	LYS
25	BD	174	SER
25	BD	177	VAL
26	BE	44	ARG
26	BE	65	THR
26	BE	70	SER
26	BE	72	SER
26	BE	77	ILE
26	BE	80	SER
26	BE	93	SER
26	BE	107	SER
26	BE	108	ILE
26	BE	109	LEU
26	BE	111	GLU
26	BE	115	GLN
26	BE	116	ASP
26	BE	120	VAL
26	BE	122	GLU
26	BE	126	VAL
26	BE	132	LYS
26	BE	136	GLN
26	BE	149	ILE
26	BE	159	LEU
26	BE	163	ASN
26	BE	164	LEU
26	BE	170	ARG
26	BE	189	THR
26	BE	198	GLU
26	BE	199	MET
26	BE	200	LEU
27	BF	3	LYS
27	BF	14	LYS

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Mol	Chain	Res	Type
27	BF	17	MET
27	BF	25	VAL
27	BF	35	THR
27	BF	36	LEU
27	BF	42	GLU
27	BF	44	ILE
27	BF	48	LYS
27	BF	51	ASP
27	BF	57	LEU
27	BF	61	SER
27	BF	78	LYS
27	BF	83	TYR
27	BF	92	ARG
27	BF	95	ARG
27	BF	104	ILE
27	BF	105	THR
27	BF	113	ASP
27	BF	147	ASP
27	BF	152	LEU
27	BF	154	ILE
27	BF	155	THR
27	BF	158	THR
27	BF	159	THR
27	BF	174	ASP
27	BF	176	PRO
28	BG	10	VAL
28	BG	20	ASN
28	BG	23	VAL
28	BG	39	ASP
28	BG	45	HIS
28	BG	67	THR
28	BG	69	ARG
28	BG	77	ILE
28	BG	80	THR
28	BG	87	LEU
28	BG	92	VAL
28	BG	124	GLU
28	BG	139	GLN
28	BG	149	ARG
28	BG	152	ARG
28	BG	155	GLU
28	BG	160	LYS

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Mol	Chain	Res	Type
28	BG	166	ASP
28	BG	168	VAL
28	BG	171	THR
29	BH	1	MET
29	BH	3	VAL
29	BH	6	LEU
29	BH	12	LEU
29	BH	15	LEU
29	BH	27	ARG
29	BH	50	ARG
29	BH	60	GLU
29	BH	62	LEU
29	BH	66	ASN
29	BH	75	LEU
29	BH	77	THR
29	BH	79	THR
29	BH	86	ASP
29	BH	91	PHE
29	BH	112	LYS
29	BH	119	ASN
29	BH	122	LEU
29	BH	123	ARG
29	BH	125	THR
29	BH	129	GLU
29	BH	131	SER
29	BH	137	GLU
29	BH	142	VAL
29	BH	145	ASN
29	BH	146	VAL
30	BI	8	TYR
30	BI	9	VAL
30	BI	11	LEU
30	BI	28	LEU
30	BI	34	ASN
30	BI	38	PHE
30	BI	47	ASP
30	BI	50	GLU
30	BI	60	THR
30	BI	62	TYR
30	BI	67	PHE
30	BI	69	PHE
30	BI	72	LYS

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Mol	Chain	Res	Type
30	BI	82	LYS
30	BI	86	ILE
30	BI	87	LYS
30	BI	96	ASP
30	BI	97	LYS
30	BI	100	LYS
30	BI	103	ARG
30	BI	108	GLU
30	BI	136	MET
30	BI	141	GLU
31	BJ	1	MET
31	BJ	5	THR
31	BJ	17	VAL
31	BJ	23	LYS
31	BJ	30	THR
31	BJ	40	HIS
31	BJ	43	GLU
31	BJ	61	LYS
31	BJ	64	VAL
31	BJ	124	VAL
31	BJ	131	ASN
31	BJ	135	GLN
31	BJ	136	GLN
32	BK	35	VAL
32	BK	38	ILE
32	BK	49	ARG
32	BK	58	LEU
32	BK	61	VAL
32	BK	88	ASN
32	BK	91	SER
32	BK	92	GLU
32	BK	107	LEU
32	BK	117	SER
33	BL	7	SER
33	BL	13	LYS
33	BL	19	LEU
33	BL	21	ARG
33	BL	40	SER
33	BL	51	GLU
33	BL	69	ARG
33	BL	76	GLU
33	BL	82	LEU

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Mol	Chain	Res	Type
33	BL	86	GLU
33	BL	89	VAL
33	BL	93	ASN
33	BL	100	ILE
33	BL	115	GLU
33	BL	126	ARG
33	BL	142	ILE
33	BL	144	GLU
34	BM	12	MET
34	BM	14	LYS
34	BM	18	ARG
34	BM	24	THR
34	BM	60	GLN
34	BM	69	PRO
34	BM	70	ASP
34	BM	106	ASP
34	BM	110	GLU
34	BM	115	GLU
34	BM	131	VAL
34	BM	135	VAL
35	BN	2	ARG
35	BN	4	ARG
35	BN	6	SER
35	BN	15	SER
35	BN	27	SER
35	BN	36	THR
35	BN	65	LEU
35	BN	69	ARG
35	BN	71	ARG
35	BN	114	GLU
35	BN	117	ASP
35	BN	118	ARG
35	BN	120	GLU
36	BO	2	ASP
36	BO	4	LYS
36	BO	5	SER
36	BO	9	ARG
36	BO	18	LEU
36	BO	24	THR
36	BO	25	ARG
36	BO	28	VAL
36	BO	31	THR

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Mol	Chain	Res	Type
36	BO	36	TYR
36	BO	45	SER
36	BO	49	VAL
36	BO	55	GLU
36	BO	58	ILE
36	BO	63	LYS
36	BO	65	THR
36	BO	74	VAL
36	BO	78	VAL
36	BO	83	LEU
36	BO	89	ASP
36	BO	102	ARG
36	BO	116	GLN
37	BP	19	SER
37	BP	27	GLU
37	BP	63	LYS
37	BP	68	GLU
37	BP	72	ARG
37	BP	73	VAL
37	BP	93	ARG
37	BP	103	ARG
37	BP	106	LYS
37	BP	109	ARG
37	BP	110	ILE
38	BQ	4	VAL
38	BQ	6	ARG
38	BQ	8	VAL
38	BQ	9	ILE
38	BQ	11	ARG
38	BQ	18	LEU
38	BQ	30	ARG
38	BQ	41	LYS
38	BQ	51	ARG
38	BQ	52	GLN
38	BQ	58	ARG
38	BQ	78	LYS
38	BQ	87	SER
38	BQ	92	ARG
38	BQ	95	LEU
39	BR	10	LYS
39	BR	14	VAL
39	BR	16	GLU

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Mol	Chain	Res	Type
39	BR	20	VAL
39	BR	38	VAL
39	BR	41	ILE
39	BR	46	GLU
39	BR	48	LYS
39	BR	58	VAL
39	BR	85	LYS
39	BR	94	THR
40	BS	1	MET
40	BS	4	ILE
40	BS	6	LYS
40	BS	7	HIS
40	BS	19	LEU
40	BS	28	LYS
40	BS	30	SER
40	BS	47	VAL
40	BS	53	SER
40	BS	59	GLU
40	BS	69	LEU
40	BS	82	MET
40	BS	95	ARG
40	BS	97	LEU
40	BS	102	HIS
41	BT	1	MET
41	BT	5	GLU
41	BT	18	GLU
41	BT	22	THR
41	BT	30	ILE
41	BT	36	LYS
41	BT	39	THR
41	BT	49	LYS
41	BT	50	LEU
41	BT	59	ASN
41	BT	60	THR
41	BT	74	ILE
42	BU	6	ARG
42	BU	8	ASP
42	BU	9	ASP
42	BU	26	LYS
42	BU	29	LEU
42	BU	30	SER
42	BU	40	ASN

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Mol	Chain	Res	Type
42	BU	52	LEU
42	BU	61	LYS
42	BU	65	ILE
42	BU	68	SER
42	BU	72	ILE
42	BU	77	THR
42	BU	81	ASP
42	BU	86	ARG
43	BV	1	MET
43	BV	8	VAL
43	BV	10	LYS
43	BV	17	SER
43	BV	20	LEU
43	BV	29	ILE
43	BV	41	GLU
43	BV	53	LYS
43	BV	61	LEU
43	BV	65	VAL
43	BV	77	VAL
43	BV	90	ASP
44	BW	20	ARG
44	BW	38	VAL
44	BW	64	ASP
44	BW	82	ILE
45	BX	5	CYS
45	BX	23	ASN
45	BX	25	THR
45	BX	28	ARG
45	BX	37	ARG
45	BX	40	VAL
45	BX	48	THR
45	BX	65	ASP
45	BX	66	THR
45	BX	71	LEU
45	BX	76	GLU
45	BX	77	LYS
46	BY	6	LEU
46	BY	12	GLU
46	BY	13	GLU
46	BY	16	THR
46	BY	22	LEU
46	BY	29	ARG

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Mol	Chain	Res	Type
46	BY	59	GLU
47	BZ	3	LYS
47	BZ	10	THR
47	BZ	36	VAL
47	BZ	45	ARG
47	BZ	52	SER
48	B0	6	ASN
48	B0	18	SER
48	B0	23	THR
48	B0	27	SER
48	B0	28	LEU
48	B0	40	ARG
48	B0	57	LYS
49	B1	8	LYS
49	B1	9	ILE
49	B1	35	GLU
49	B1	46	HIS
49	B1	47	VAL
49	B1	51	GLU
49	B1	53	LYS
50	B2	3	ARG
50	B2	24	THR
50	B2	29	GLN
50	B2	42	LEU
50	B2	44	VAL
50	B2	45	SER
51	B3	15	LYS
51	B3	17	THR
51	B3	30	ARG
51	B3	31	HIS
51	B3	47	LYS
52	B4	2	LYS
52	B4	3	VAL
52	B4	6	SER
52	B4	12	ARG
53	B5	21	TYR
53	B5	28	ARG
53	B5	35	THR
53	B5	38	PHE
53	B5	39	ASP
53	B5	41	THR
53	B5	47	LYS

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Mol	Chain	Res	Type
53	B5	48	LEU
53	B5	58	ASN
53	B5	59	VAL
53	B5	65	LEU
53	B5	73	VAL
53	B5	78	ILE
2	CB	14	VAL
2	CB	15	HIS
2	CB	16	PHE
2	CB	18	HIS
2	CB	19	GLN
2	CB	20	THR
2	CB	24	ASN
2	CB	27	MET
2	CB	28	LYS
2	CB	35	ARG
2	CB	40	ILE
2	CB	43	LEU
2	CB	49	MET
2	CB	50	PHE
2	CB	51	ASN
2	CB	66	LYS
2	CB	67	ILE
2	CB	68	LEU
2	CB	88	ASP
2	CB	89	GLN
2	CB	91	PHE
2	CB	92	VAL
2	CB	94	HIS
2	CB	95	ARG
2	CB	96	TRP
2	CB	101	LEU
2	CB	103	ASN
2	CB	106	THR
2	CB	116	ASP
2	CB	117	LEU
2	CB	122	GLN
2	CB	123	ASP
2	CB	126	PHE
2	CB	130	THR
2	CB	133	GLU
2	CB	136	MET

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Mol	Chain	Res	Type
2	CB	139	ARG
2	CB	140	GLU
2	CB	143	LYS
2	CB	144	LEU
2	CB	157	LEU
2	CB	163	VAL
2	CB	164	ILE
2	CB	169	GLU
2	CB	174	LYS
2	CB	179	LEU
2	CB	188	ASP
2	CB	207	ILE
2	CB	220	THR
2	CB	222	ARG
2	CB	223	GLU
3	CC	3	GLN
3	CC	15	VAL
3	CC	16	LYS
3	CC	18	TRP
3	CC	25	ASN
3	CC	26	THR
3	CC	27	LYS
3	CC	28	GLU
3	CC	29	PHE
3	CC	33	LEU
3	CC	35	SER
3	CC	36	ASP
3	CC	37	PHE
3	CC	43	LEU
3	CC	45	LYS
3	CC	53	SER
3	CC	56	VAL
3	CC	70	THR
3	CC	80	LYS
3	CC	103	ILE
3	CC	107	ARG
3	CC	111	LEU
3	CC	119	SER
3	CC	121	THR
3	CC	128	VAL
3	CC	129	MET
3	CC	131	ARG

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Mol	Chain	Res	Type
3	CC	144	LEU
3	CC	147	LYS
3	CC	151	VAL
3	CC	153	VAL
3	CC	167	TRP
3	CC	168	TYR
3	CC	175	LEU
3	CC	179	ARG
3	CC	185	ASN
3	CC	190	HIS
3	CC	192	THR
3	CC	193	TYR
4	CD	8	LYS
4	CD	9	LEU
4	CD	10	LYS
4	CD	28	ILE
4	CD	29	ASP
4	CD	32	CYS
4	CD	33	LYS
4	CD	48	LEU
4	CD	54	GLN
4	CD	55	LEU
4	CD	56	ARG
4	CD	58	LYS
4	CD	59	GLN
4	CD	60	LYS
4	CD	69	GLU
4	CD	81	ARG
4	CD	83	LYS
4	CD	116	GLN
4	CD	125	VAL
4	CD	128	ARG
4	CD	134	SER
4	CD	138	SER
4	CD	142	VAL
4	CD	148	LYS
4	CD	152	GLN
4	CD	155	VAL
4	CD	161	LEU
4	CD	163	GLU
4	CD	184	ARG
4	CD	191	LEU

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Mol	Chain	Res	Type
4	CD	199	LEU
4	CD	200	ILE
4	CD	203	LEU
4	CD	206	LYS
5	CE	10	GLU
5	CE	15	LEU
5	CE	19	ASN
5	CE	24	THR
5	CE	26	LYS
5	CE	32	SER
5	CE	34	THR
5	CE	39	VAL
5	CE	46	VAL
5	CE	69	ARG
5	CE	77	ASN
5	CE	81	LEU
5	CE	93	ARG
5	CE	96	MET
5	CE	101	GLU
5	CE	112	ARG
5	CE	114	VAL
5	CE	115	LEU
5	CE	120	VAL
5	CE	124	LEU
5	CE	126	LYS
5	CE	131	THR
5	CE	137	VAL
5	CE	140	THR
5	CE	151	GLU
5	CE	152	MET
5	CE	156	LYS
5	CE	157	ARG
6	CF	1	MET
6	CF	8	PHE
6	CF	15	SER
6	CF	24	ARG
6	CF	26	THR
6	CF	29	ILE
6	CF	35	LYS
6	CF	36	ILE
6	CF	38	ARG
6	CF	51	ILE

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Mol	Chain	Res	Type
6	CF	53	LYS
6	CF	54	LEU
6	CF	55	HIS
6	CF	63	ASN
6	CF	68	GLN
6	CF	69	GLU
6	CF	71	ILE
6	CF	73	GLU
6	CF	75	GLU
6	CF	80	PHE
6	CF	85	ILE
6	CF	87	SER
6	CF	93	LYS
6	CF	97	THR
7	CG	3	ARG
7	CG	4	ARG
7	CG	5	ARG
7	CG	6	VAL
7	CG	7	ILE
7	CG	11	LYS
7	CG	12	ILE
7	CG	23	LEU
7	CG	30	LEU
7	CG	36	LYS
7	CG	47	LEU
7	CG	48	GLU
7	CG	53	ARG
7	CG	59	LEU
7	CG	60	GLU
7	CG	62	PHE
7	CG	66	LEU
7	CG	70	ARG
7	CG	72	THR
7	CG	73	VAL
7	CG	75	VAL
7	CG	78	ARG
7	CG	84	THR
7	CG	87	VAL
7	CG	91	VAL
7	CG	115	SER
7	CG	120	LEU
7	CG	123	GLU

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Mol	Chain	Res	Type
7	CG	129	GLU
7	CG	133	THR
7	CG	138	ARG
7	CG	139	GLU
7	CG	146	GLU
8	CH	13	ARG
8	CH	22	LYS
8	CH	25	VAL
8	CH	30	SER
8	CH	31	LYS
8	CH	33	LYS
8	CH	45	PHE
8	CH	47	GLU
8	CH	49	PHE
8	CH	54	ASP
8	CH	55	THR
8	CH	59	LEU
8	CH	67	GLN
8	CH	77	ARG
8	CH	80	ARG
8	CH	87	LYS
8	CH	104	VAL
8	CH	111	MET
8	CH	112	THR
8	CH	121	LEU
8	CH	125	ILE
9	CI	9	THR
9	CI	11	ARG
9	CI	18	ARG
9	CI	32	GLN
9	CI	33	ARG
9	CI	36	GLU
9	CI	43	THR
9	CI	45	ARG
9	CI	46	MET
9	CI	48	VAL
9	CI	49	ARG
9	CI	54	LEU
9	CI	56	ASP
9	CI	57	MET
9	CI	61	LEU
9	CI	68	LYS

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Mol	Chain	Res	Type
9	CI	85	ARG
9	CI	88	MET
9	CI	89	GLU
9	CI	90	TYR
9	CI	97	GLU
9	CI	99	ARG
9	CI	100	LYS
9	CI	106	ARG
9	CI	116	VAL
9	CI	126	GLN
9	CI	127	PHE
9	CI	129	LYS
10	CJ	9	ARG
10	CJ	22	THR
10	CJ	25	ILE
10	CJ	26	VAL
10	CJ	27	GLU
10	CJ	32	THR
10	CJ	35	GLN
10	CJ	45	ARG
10	CJ	59	LYS
10	CJ	60	ASP
10	CJ	63	ASP
10	CJ	66	GLU
10	CJ	73	LEU
10	CJ	80	THR
10	CJ	83	THR
10	CJ	84	VAL
10	CJ	87	LEU
10	CJ	89	ARG
10	CJ	92	LEU
11	CK	13	ARG
11	CK	14	LYS
11	CK	15	GLN
11	CK	27	PHE
11	CK	31	ILE
11	CK	33	THR
11	CK	46	THR
11	CK	64	GLN
11	CK	65	VAL
11	CK	72	ASP
11	CK	77	TYR

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Mol	Chain	Res	Type
11	CK	81	ASN
11	CK	82	LEU
11	CK	96	THR
11	CK	100	LEU
11	CK	101	ASN
11	CK	105	PHE
11	CK	106	ARG
11	CK	107	ILE
11	CK	126	LYS
11	CK	128	ARG
12	CL	3	THR
12	CL	4	VAL
12	CL	5	ASN
12	CL	10	LYS
12	CL	12	ARG
12	CL	16	VAL
12	CL	18	LYS
12	CL	20	ASN
12	CL	29	GLN
12	CL	30	LYS
12	CL	33	VAL
12	CL	44	LYS
12	CL	58	THR
12	CL	59	ASN
12	CL	63	VAL
12	CL	78	SER
12	CL	82	ILE
12	CL	83	ARG
12	CL	86	ARG
12	CL	89	ASP
12	CL	93	VAL
12	CL	94	ARG
12	CL	110	ARG
12	CL	111	LYS
12	CL	121	ARG
13	CM	19	LEU
13	CM	25	VAL
13	CM	27	LYS
13	CM	29	ARG
13	CM	30	SER
13	CM	31	LYS
13	CM	33	ILE

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Mol	Chain	Res	Type
13	CM	34	LEU
13	CM	41	GLU
13	CM	48	LEU
13	CM	54	ASP
13	CM	56	LEU
13	CM	59	GLU
13	CM	60	VAL
13	CM	63	PHE
13	CM	68	ASP
13	CM	72	GLU
13	CM	80	LEU
13	CM	83	LEU
13	CM	90	ARG
13	CM	91	HIS
13	CM	101	ARG
14	CN	4	GLN
14	CN	23	LYS
14	CN	26	GLU
14	CN	28	LYS
14	CN	48	LEU
14	CN	53	ARG
14	CN	54	ASP
14	CN	67	THR
14	CN	71	HIS
14	CN	80	SER
14	CN	82	ILE
15	CO	6	GLU
15	CO	17	ARG
15	CO	18	ASP
15	CO	21	ASP
15	CO	24	SER
15	CO	26	GLU
15	CO	35	GLN
15	CO	39	LEU
15	CO	48	LYS
15	CO	54	ARG
15	CO	62	GLN
15	CO	64	ARG
15	CO	70	LEU
15	CO	73	LYS
15	CO	79	THR
15	CO	85	LEU

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Mol	Chain	Res	Type
15	CO	87	LEU
15	CO	88	ARG
16	CP	1	MET
16	CP	2	VAL
16	CP	3	THR
16	CP	5	ARG
16	CP	18	GLN
16	CP	19	VAL
16	CP	20	VAL
16	CP	26	ASN
16	CP	31	ARG
16	CP	46	LYS
16	CP	51	ARG
16	CP	63	GLN
16	CP	69	ASP
16	CP	74	LEU
16	CP	77	GLU
16	CP	80	LYS
17	CQ	5	ILE
17	CQ	11	ARG
17	CQ	14	SER
17	CQ	17	MET
17	CQ	18	GLU
17	CQ	23	VAL
17	CQ	25	ILE
17	CQ	28	PHE
17	CQ	29	VAL
17	CQ	40	ARG
17	CQ	48	ASP
17	CQ	52	GLU
17	CQ	55	ILE
17	CQ	65	ARG
17	CQ	70	THR
17	CQ	75	LEU
17	CQ	76	VAL
17	CQ	78	VAL
17	CQ	79	VAL
17	CQ	81	LYS
17	CQ	83	VAL
18	CR	20	GLU
18	CR	21	ILE
18	CR	33	ILE

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Mol	Chain	Res	Type
18	CR	42	SER
18	CR	45	THR
18	CR	47	THR
18	CR	48	ARG
18	CR	59	ILE
18	CR	67	LEU
19	CS	5	LEU
19	CS	6	LYS
19	CS	11	ILE
19	CS	13	LEU
19	CS	14	HIS
19	CS	16	LEU
19	CS	23	VAL
19	CS	27	ASP
19	CS	28	LYS
19	CS	33	THR
19	CS	39	THR
19	CS	49	ILE
19	CS	56	GLN
19	CS	65	GLU
19	CS	73	GLU
20	CT	5	LYS
20	CT	6	SER
20	CT	8	LYS
20	CT	10	ARG
20	CT	12	ILE
20	CT	14	SER
20	CT	15	GLU
20	CT	19	LYS
20	CT	24	ARG
20	CT	27	MET
20	CT	36	TYR
20	CT	49	LYS
20	CT	64	LYS
20	CT	67	ILE
20	CT	76	LYS
20	CT	79	LEU
20	CT	84	ASN
21	CU	5	LYS
21	CU	10	GLU
21	CU	12	PHE
21	CU	16	LEU

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Mol	Chain	Res	Type
21	CU	19	PHE
21	CU	22	SER
21	CU	25	LYS
21	CU	34	ARG
21	CU	37	PHE
21	CU	38	TYR
21	CU	43	THR
21	CU	47	ARG
24	DC	3	VAL
24	DC	10	SER
24	DC	14	ARG
24	DC	20	VAL
24	DC	48	ARG
24	DC	52	ARG
24	DC	54	ILE
24	DC	64	ILE
24	DC	80	ARG
24	DC	88	SER
24	DC	98	ASP
24	DC	103	TYR
24	DC	104	ILE
24	DC	105	LEU
24	DC	111	LYS
24	DC	114	ASP
24	DC	121	ASP
24	DC	130	LEU
24	DC	139	SER
24	DC	156	ARG
24	DC	160	THR
24	DC	174	LEU
24	DC	175	ARG
24	DC	185	GLU
24	DC	189	ARG
24	DC	191	THR
24	DC	195	VAL
24	DC	202	LEU
24	DC	205	LEU
24	DC	213	TRP
24	DC	236	GLU
24	DC	250	VAL
24	DC	256	LYS
24	DC	259	SER

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Mol	Chain	Res	Type
24	DC	262	ARG
24	DC	266	PHE
25	DD	1	MET
25	DD	4	LEU
25	DD	12	THR
25	DD	13	ARG
25	DD	28	GLU
25	DD	33	ARG
25	DD	39	ASP
25	DD	73	VAL
25	DD	84	LEU
25	DD	86	GLU
25	DD	91	THR
25	DD	104	VAL
25	DD	131	ASP
25	DD	141	ARG
25	DD	146	ILE
25	DD	150	GLN
25	DD	170	VAL
25	DD	172	VAL
25	DD	175	LEU
25	DD	189	VAL
26	DE	6	LYS
26	DE	10	SER
26	DE	22	ASP
26	DE	32	VAL
26	DE	41	GLN
26	DE	63	LYS
26	DE	65	THR
26	DE	69	ARG
26	DE	77	ILE
26	DE	78	TRP
26	DE	83	VAL
26	DE	84	THR
26	DE	91	ASP
26	DE	93	SER
26	DE	107	SER
26	DE	108	ILE
26	DE	114	ARG
26	DE	118	LEU
26	DE	120	VAL
26	DE	125	SER

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Mol	Chain	Res	Type
26	DE	127	GLU
26	DE	131	THR
26	DE	133	LEU
26	DE	149	ILE
26	DE	159	LEU
26	DE	164	LEU
26	DE	170	ARG
26	DE	171	ASP
26	DE	173	THR
26	DE	181	ILE
26	DE	187	VAL
26	DE	200	LEU
27	DF	4	LEU
27	DF	6	ASP
27	DF	10	ASP
27	DF	14	LYS
27	DF	21	ASN
27	DF	26	MET
27	DF	28	VAL
27	DF	31	VAL
27	DF	35	THR
27	DF	36	LEU
27	DF	44	ILE
27	DF	46	ASP
27	DF	52	ASN
27	DF	64	LYS
27	DF	67	ILE
27	DF	74	VAL
27	DF	81	GLN
27	DF	83	TYR
27	DF	92	ARG
27	DF	95	ARG
27	DF	106	ILE
27	DF	125	ARG
27	DF	133	ARG
27	DF	147	ASP
27	DF	149	VAL
27	DF	150	ARG
27	DF	157	THR
27	DF	162	SER
27	DF	174	ASP
27	DF	178	ARG

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Mol	Chain	Res	Type
28	DG	11	VAL
28	DG	30	ASN
28	DG	44	LYS
28	DG	89	LEU
28	DG	95	ARG
28	DG	117	LEU
28	DG	127	THR
28	DG	129	THR
28	DG	137	ASP
28	DG	152	ARG
28	DG	155	GLU
28	DG	160	LYS
28	DG	166	ASP
28	DG	172	LYS
29	DH	7	ASP
29	DH	12	LEU
29	DH	41	LYS
29	DH	42	LYS
29	DH	48	GLU
29	DH	50	ARG
29	DH	53	GLU
29	DH	54	LEU
29	DH	57	LYS
29	DH	62	LEU
29	DH	77	THR
29	DH	78	VAL
29	DH	87	GLU
29	DH	89	LYS
29	DH	94	ILE
29	DH	109	GLU
29	DH	114	GLU
29	DH	116	ARG
29	DH	117	LEU
29	DH	119	ASN
29	DH	121	VAL
29	DH	124	THR
29	DH	125	THR
29	DH	129	GLU
29	DH	142	VAL
29	DH	149	GLU
30	DI	3	LYS
30	DI	4	LYS

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Mol	Chain	Res	Type
30	DI	8	TYR
30	DI	11	LEU
30	DI	12	GLN
30	DI	17	MET
30	DI	24	VAL
30	DI	31	GLN
30	DI	40	LYS
30	DI	49	ILE
30	DI	51	LYS
30	DI	68	THR
30	DI	69	PHE
30	DI	72	LYS
30	DI	87	LYS
30	DI	95	LYS
30	DI	96	ASP
30	DI	97	LYS
30	DI	105	GLN
30	DI	117	MET
30	DI	125	MET
30	DI	127	ARG
30	DI	128	SER
30	DI	134	ARG
30	DI	136	MET
31	DJ	3	THR
31	DJ	30	THR
31	DJ	37	ARG
31	DJ	39	LYS
31	DJ	40	HIS
31	DJ	43	GLU
31	DJ	81	ILE
31	DJ	86	GLN
31	DJ	90	GLU
31	DJ	92	MET
31	DJ	131	ASN
31	DJ	138	GLN
31	DJ	139	VAL
31	DJ	140	LEU
32	DK	1	MET
32	DK	41	ILE
32	DK	49	ARG
32	DK	67	LYS
32	DK	70	ARG

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Mol	Chain	Res	Type
32	DK	90	ASN
32	DK	91	SER
32	DK	92	GLU
32	DK	95	ILE
32	DK	97	THR
32	DK	104	THR
32	DK	114	LYS
32	DK	121	GLU
33	DL	12	SER
33	DL	27	LEU
33	DL	29	LYS
33	DL	42	SER
33	DL	47	ARG
33	DL	48	ARG
33	DL	59	ARG
33	DL	60	ARG
33	DL	74	THR
33	DL	78	ARG
33	DL	80	SER
33	DL	82	LEU
33	DL	85	VAL
33	DL	91	ASP
33	DL	94	THR
33	DL	96	LYS
33	DL	100	ILE
33	DL	103	ILE
33	DL	118	THR
33	DL	126	ARG
33	DL	143	GLU
34	DM	6	ARG
34	DM	14	LYS
34	DM	70	ASP
34	DM	74	THR
34	DM	100	LYS
34	DM	108	VAL
34	DM	124	LEU
34	DM	126	ILE
34	DM	127	LYS
34	DM	128	THR
34	DM	132	THR
34	DM	134	THR
35	DN	2	ARG

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Mol	Chain	Res	Type
35	DN	6	SER
35	DN	8	ARG
35	DN	14	SER
35	DN	20	MET
35	DN	53	THR
35	DN	63	ARG
35	DN	69	ARG
35	DN	70	THR
35	DN	71	ARG
35	DN	76	VAL
35	DN	79	LEU
35	DN	82	GLU
35	DN	100	CYS
35	DN	114	GLU
35	DN	115	LEU
35	DN	116	VAL
36	DO	9	ARG
36	DO	18	LEU
36	DO	24	THR
36	DO	26	LEU
36	DO	31	THR
36	DO	48	LEU
36	DO	67	ASN
36	DO	78	VAL
36	DO	89	ASP
36	DO	95	SER
36	DO	100	HIS
36	DO	102	ARG
36	DO	103	VAL
36	DO	116	GLN
37	DP	7	GLN
37	DP	8	LEU
37	DP	19	SER
37	DP	21	ARG
37	DP	26	VAL
37	DP	32	VAL
37	DP	34	GLU
37	DP	36	SER
37	DP	51	ARG
37	DP	63	LYS
37	DP	64	ILE
37	DP	65	SER

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Mol	Chain	Res	Type
37	DP	66	ASN
37	DP	81	VAL
37	DP	85	SER
37	DP	93	ARG
37	DP	109	ARG
37	DP	110	ILE
37	DP	114	LEU
38	DQ	5	LYS
38	DQ	8	VAL
38	DQ	9	ILE
38	DQ	11	ARG
38	DQ	13	ARG
38	DQ	22	LYS
38	DQ	33	ARG
38	DQ	41	LYS
38	DQ	51	ARG
38	DQ	53	ARG
38	DQ	54	LYS
38	DQ	92	ARG
38	DQ	94	ILE
39	DR	7	SER
39	DR	12	HIS
39	DR	15	SER
39	DR	18	GLN
39	DR	38	VAL
39	DR	43	ASN
39	DR	46	GLU
39	DR	47	VAL
39	DR	48	LYS
39	DR	51	VAL
39	DR	58	VAL
39	DR	86	GLN
39	DR	94	THR
39	DR	102	SER
40	DS	3	THR
40	DS	13	SER
40	DS	19	LEU
40	DS	22	ASP
40	DS	28	LYS
40	DS	66	ILE
40	DS	67	ASP
40	DS	68	ASP

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Mol	Chain	Res	Type
40	DS	78	GLU
40	DS	81	SER
40	DS	90	LYS
40	DS	96	ILE
40	DS	97	LEU
40	DS	99	ARG
40	DS	104	THR
40	DS	109	ASP
41	DT	3	ARG
41	DT	7	LEU
41	DT	16	VAL
41	DT	22	THR
41	DT	30	ILE
41	DT	31	VAL
41	DT	32	LEU
41	DT	49	LYS
41	DT	52	GLU
41	DT	70	HIS
41	DT	77	ARG
41	DT	78	SER
41	DT	86	THR
41	DT	91	GLN
42	DU	7	ARG
42	DU	15	THR
42	DU	18	ASP
42	DU	25	VAL
42	DU	27	ASN
42	DU	28	VAL
42	DU	29	LEU
42	DU	31	SER
42	DU	40	ASN
42	DU	45	HIS
42	DU	46	GLN
42	DU	49	VAL
42	DU	53	ASN
42	DU	54	GLN
42	DU	68	SER
42	DU	72	ILE
42	DU	81	ASP
42	DU	93	VAL
42	DU	99	ASN
43	DV	1	MET

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Mol	Chain	Res	Type
43	DV	8	VAL
43	DV	29	ILE
43	DV	40	ILE
43	DV	42	LEU
43	DV	45	ASP
43	DV	50	MET
43	DV	53	LYS
43	DV	61	LEU
43	DV	65	VAL
43	DV	66	ASP
44	DW	16	SER
44	DW	20	ARG
44	DW	30	SER
44	DW	38	VAL
44	DW	39	ARG
44	DW	41	ARG
44	DW	77	ARG
45	DX	11	ARG
45	DX	18	ARG
45	DX	23	ASN
45	DX	33	LEU
45	DX	35	SER
45	DX	40	VAL
45	DX	46	PHE
45	DX	48	THR
45	DX	54	LYS
45	DX	64	ILE
45	DX	66	THR
45	DX	71	LEU
46	DY	2	LYS
46	DY	6	LEU
46	DY	13	GLU
46	DY	16	THR
46	DY	29	ARG
46	DY	37	LEU
46	DY	39	GLN
46	DY	44	LYS
46	DY	48	ARG
46	DY	56	LEU
46	DY	57	LEU
46	DY	58	ASN
47	DZ	3	LYS

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Mol	Chain	Res	Type
47	DZ	11	ARG
47	DZ	16	ARG
47	DZ	25	LEU
47	DZ	31	ARG
47	DZ	36	VAL
47	DZ	41	THR
47	DZ	45	ARG
47	DZ	52	SER
47	DZ	57	VAL
48	D0	23	THR
48	D0	28	LEU
48	D0	37	LYS
48	D0	46	ASP
48	D0	52	ARG
49	D1	10	LYS
49	D1	12	VAL
49	D1	23	THR
49	D1	25	LYS
49	D1	26	ASN
49	D1	51	GLU
50	D2	4	THR
50	D2	10	LEU
50	D2	24	THR
50	D2	25	LYS
50	D2	41	ARG
50	D2	44	VAL
51	D3	6	THR
51	D3	8	ARG
51	D3	13	ARG
51	D3	30	ARG
51	D3	31	HIS
52	D4	3	VAL
52	D4	4	ARG
52	D4	12	ARG
52	D4	17	VAL
52	D4	26	ILE
52	D4	35	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (57) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	89	GLN

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Mol	Chain	Res	Type
4	AD	36	GLN
5	AE	82	GLN
5	AE	122	ASN
10	AJ	56	HIS
11	AK	40	ASN
11	AK	109	ASN
13	AM	91	HIS
14	AN	4	GLN
14	AN	66	GLN
15	AO	46	HIS
19	AS	52	HIS
20	AT	55	GLN
24	BC	163	GLN
24	BC	239	ASN
25	BD	136	ASN
28	BG	104	ASN
29	BH	28	ASN
29	BH	119	ASN
29	BH	135	HIS
32	BK	93	GLN
33	BL	99	ASN
38	BQ	81	ASN
40	BS	15	GLN
40	BS	102	HIS
45	BX	34	HIS
2	CB	18	HIS
2	CB	36	ASN
2	CB	51	ASN
2	CB	89	GLN
2	CB	103	ASN
3	CC	176	HIS
7	CG	68	ASN
7	CG	130	ASN
8	CH	18	GLN
10	CJ	70	HIS
12	CL	59	ASN
17	CQ	31	HIS
18	CR	52	GLN
19	CS	52	HIS
24	DC	90	ASN
24	DC	251	GLN
25	DD	130	GLN

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Mol	Chain	Res	Type
26	DE	163	ASN
27	DF	63	GLN
28	DG	143	GLN
29	DH	128	HIS
30	DI	43	ASN
36	DO	116	GLN
37	DP	7	GLN
39	DR	89	HIS
40	DS	15	GLN
41	DT	59	ASN
44	DW	50	ASN
46	DY	45	GLN
49	D1	26	ASN
51	D3	31	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1537/1539 (99%)	357 (23%)	16 (1%)
1	CA	1538/1539 (99%)	337 (21%)	9 (0%)
22	BA	2895/2903 (99%)	563 (19%)	28 (0%)
22	DA	2895/2903 (99%)	643 (22%)	34 (1%)
23	BB	118/119 (99%)	23 (19%)	0
23	DB	117/119 (98%)	25 (21%)	0
All	All	9100/9122 (99%)	1948 (21%)	87 (0%)

All (1948) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	4	U
1	AA	5	U
1	AA	7	A
1	AA	9	G
1	AA	13	U
1	AA	22	G
1	AA	28	A
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	50	A

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Mol	Chain	Res	Type
1	AA	51	A
1	AA	69	G
1	AA	70	U
1	AA	71	A
1	AA	72	A
1	AA	75	G
1	AA	76	G
1	AA	77	A
1	AA	81	A
1	AA	82	G
1	AA	83	C
1	AA	84	U
1	AA	85	U
1	AA	86	G
1	AA	88	U
1	AA	89	U
1	AA	90	C
1	AA	91	U
1	AA	94	G
1	AA	95	C
1	AA	97	G
1	AA	108	G
1	AA	109	A
1	AA	111	G
1	AA	116	A
1	AA	117	G
1	AA	121	U
1	AA	122	G
1	AA	130	A
1	AA	131	A
1	AA	137	U
1	AA	138	G
1	AA	141	G
1	AA	142	G
1	AA	143	A
1	AA	144	G
1	AA	149	A
1	AA	159	G
1	AA	162	A
1	AA	163	C
1	AA	168	G
1	AA	181	A

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Mol	Chain	Res	Type
1	AA	182	A
1	AA	183	C
1	AA	189	A
1	AA	195	A
1	AA	204	G
1	AA	205	A
1	AA	209	U
1	AA	210	C
1	AA	211	G
1	AA	214	C
1	AA	226	G
1	AA	240	G
1	AA	245	U
1	AA	247	G
1	AA	250	A
1	AA	251	G
1	AA	263	A
1	AA	266	G
1	AA	267	C
1	AA	280	C
1	AA	289	G
1	AA	292	G
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	331	G
1	AA	332	G
1	AA	341	C
1	AA	343	U
1	AA	346	G
1	AA	347	G
1	AA	352	C
1	AA	354	G
1	AA	367	U
1	AA	370	C
1	AA	371	A
1	AA	372	C
1	AA	373	A
1	AA	382	A
1	AA	384	G
1	AA	398	U
1	AA	406	G

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Mol	Chain	Res	Type
1	AA	409	U
1	AA	410	G
1	AA	411	A
1	AA	412	A
1	AA	413	G
1	AA	414	A
1	AA	421	U
1	AA	422	C
1	AA	423	G
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	435	A
1	AA	439	U
1	AA	440	C
1	AA	453	G
1	AA	454	G
1	AA	456	A
1	AA	457	G
1	AA	458	U
1	AA	459	A
1	AA	460	A
1	AA	462	G
1	AA	463	U
1	AA	465	A
1	AA	466	A
1	AA	467	U
1	AA	468	A
1	AA	474	G
1	AA	479	U
1	AA	481	G
1	AA	482	A
1	AA	485	U
1	AA	486	U
1	AA	491	G
1	AA	492	C
1	AA	495	A
1	AA	511	C
1	AA	518	C
1	AA	521	G
1	AA	527	G
1	AA	530	G

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Mol	Chain	Res	Type
1	AA	532	A
1	AA	533	A
1	AA	547	A
1	AA	550	G
1	AA	559	A
1	AA	562	U
1	AA	564	C
1	AA	570	G
1	AA	572	A
1	AA	573	A
1	AA	576	C
1	AA	577	G
1	AA	615	G
1	AA	650	G
1	AA	653	U
1	AA	654	G
1	AA	656	G
1	AA	661	G
1	AA	665	A
1	AA	702	A
1	AA	703	G
1	AA	720	C
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	733	G
1	AA	753	A
1	AA	755	G
1	AA	760	G
1	AA	766	A
1	AA	772	U
1	AA	773	G
1	AA	778	G
1	AA	787	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	814	A
1	AA	815	A
1	AA	817	C
1	AA	821	G

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Mol	Chain	Res	Type
1	AA	828	U
1	AA	829	G
1	AA	832	G
1	AA	841	C
1	AA	842	U
1	AA	843	U
1	AA	845	A
1	AA	846	G
1	AA	849	G
1	AA	859	G
1	AA	860	A
1	AA	870	U
1	AA	914	A
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	938	A
1	AA	960	U
1	AA	963	G
1	AA	964	A
1	AA	966	G
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	972	C
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	982	U
1	AA	983	A
1	AA	986	U
1	AA	987	G
1	AA	988	G
1	AA	989	U
1	AA	991	U
1	AA	992	U
1	AA	993	G
1	AA	1004	A
1	AA	1007	U
1	AA	1008	U
1	AA	1009	U
1	AA	1017	U

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Mol	Chain	Res	Type
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1030	U
1	AA	1031	C
1	AA	1032	G
1	AA	1033	G
1	AA	1034	G
1	AA	1035	A
1	AA	1036	A
1	AA	1037	C
1	AA	1039	G
1	AA	1042	A
1	AA	1043	G
1	AA	1044	A
1	AA	1047	G
1	AA	1049	U
1	AA	1050	G
1	AA	1054	C
1	AA	1056	U
1	AA	1061	G
1	AA	1065	U
1	AA	1066	C
1	AA	1069	C
1	AA	1071	C
1	AA	1086	U
1	AA	1089	G
1	AA	1093	A
1	AA	1094	G
1	AA	1095	U
1	AA	1098	C
1	AA	1101	A
1	AA	1104	G
1	AA	1124	G
1	AA	1125	U
1	AA	1127	G
1	AA	1133	G
1	AA	1135	U
1	AA	1136	C
1	AA	1137	C
1	AA	1139	G

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Mol	Chain	Res	Type
1	AA	1140	C
1	AA	1141	C
1	AA	1142	G
1	AA	1145	A
1	AA	1146	A
1	AA	1149	C
1	AA	1152	A
1	AA	1157	A
1	AA	1159	U
1	AA	1160	G
1	AA	1161	C
1	AA	1168	U
1	AA	1169	A
1	AA	1181	G
1	AA	1182	G
1	AA	1183	U
1	AA	1184	G
1	AA	1196	A
1	AA	1197	A
1	AA	1202	U
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1215	G
1	AA	1227	A
1	AA	1228	C
1	AA	1238	A
1	AA	1239	A
1	AA	1240	U
1	AA	1253	G
1	AA	1256	A
1	AA	1257	A
1	AA	1260	G
1	AA	1280	A
1	AA	1286	U
1	AA	1287	A
1	AA	1293	C
1	AA	1297	G
1	AA	1299	A
1	AA	1300	G
1	AA	1302	C
1	AA	1303	C

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Mol	Chain	Res	Type
1	AA	1304	G
1	AA	1305	G
1	AA	1317	C
1	AA	1318	A
1	AA	1320	C
1	AA	1322	C
1	AA	1323	G
1	AA	1328	C
1	AA	1329	A
1	AA	1332	A
1	AA	1336	C
1	AA	1337	G
1	AA	1338	G
1	AA	1340	A
1	AA	1346	A
1	AA	1353	G
1	AA	1363	A
1	AA	1368	A
1	AA	1370	G
1	AA	1378	C
1	AA	1379	G
1	AA	1381	U
1	AA	1397	C
1	AA	1398	A
1	AA	1414	U
1	AA	1418	A
1	AA	1426	G
1	AA	1429	A
1	AA	1430	A
1	AA	1441	A
1	AA	1442	G
1	AA	1446	A
1	AA	1450	U
1	AA	1452	C
1	AA	1453	G
1	AA	1454	G
1	AA	1455	G
1	AA	1492	A
1	AA	1493	A
1	AA	1497	G
1	AA	1499	A
1	AA	1503	A

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Mol	Chain	Res	Type
1	AA	1505	G
1	AA	1506	U
1	AA	1517	G
1	AA	1529	G
1	AA	1530	G
1	AA	1533	C
1	AA	1534	A
1	AA	1535	C
1	AA	1539	C
22	BA	10	A
22	BA	12	U
22	BA	27	G
22	BA	34	U
22	BA	35	G
22	BA	45	G
22	BA	46	G
22	BA	58	G
22	BA	61	C
22	BA	63	A
22	BA	71	A
22	BA	74	A
22	BA	75	G
22	BA	87	U
22	BA	98	G
22	BA	101	A
22	BA	103	A
22	BA	118	A
22	BA	119	A
22	BA	120	U
22	BA	137	U
22	BA	138	U
22	BA	139	U
22	BA	140	C
22	BA	141	G
22	BA	142	A
22	BA	143	C
22	BA	148	U
22	BA	158	U
22	BA	180	G
22	BA	181	A
22	BA	196	A
22	BA	208	C

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Mol	Chain	Res	Type
22	BA	215	G
22	BA	216	A
22	BA	221	A
22	BA	222	A
22	BA	227	A
22	BA	230	G
22	BA	248	G
22	BA	255	A
22	BA	265	A
22	BA	266	G
22	BA	267	C
22	BA	271	G
22	BA	272	A
22	BA	273	G
22	BA	274	C
22	BA	276	U
22	BA	277	G
22	BA	278	A
22	BA	279	A
22	BA	291	G
22	BA	299	A
22	BA	302	C
22	BA	310	A
22	BA	311	A
22	BA	325	G
22	BA	329	G
22	BA	330	A
22	BA	331	C
22	BA	343	C
22	BA	351	C
22	BA	353	C
22	BA	361	G
22	BA	362	A
22	BA	371	A
22	BA	372	G
22	BA	386	G
22	BA	389	G
22	BA	396	G
22	BA	404	A
22	BA	405	U
22	BA	411	G
22	BA	412	A

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Mol	Chain	Res	Type
22	BA	424	G
22	BA	429	A
22	BA	442	G
22	BA	448	U
22	BA	455	C
22	BA	467	G
22	BA	480	A
22	BA	481	G
22	BA	491	G
22	BA	501	A
22	BA	504	A
22	BA	505	A
22	BA	528	A
22	BA	531	C
22	BA	532	A
22	BA	533	G
22	BA	543	G
22	BA	544	C
22	BA	546	U
22	BA	547	A
22	BA	548	G
22	BA	549	G
22	BA	550	C
22	BA	563	A
22	BA	572	A
22	BA	573	U
22	BA	575	A
22	BA	586	A
22	BA	603	A
22	BA	613	A
22	BA	614	A
22	BA	615	U
22	BA	622	G
22	BA	627	A
22	BA	631	A
22	BA	634	C
22	BA	637	A
22	BA	645	C
22	BA	646	U
22	BA	647	G
22	BA	654	A
22	BA	655	A

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Mol	Chain	Res	Type
22	BA	664	G
22	BA	669	G
22	BA	670	A
22	BA	686	U
22	BA	702	U
22	BA	712	G
22	BA	713	G
22	BA	716	A
22	BA	721	A
22	BA	727	A
22	BA	730	A
22	BA	738	G
22	BA	747	U
22	BA	748	G
22	BA	749	A
22	BA	757	G
22	BA	762	U
22	BA	764	A
22	BA	775	G
22	BA	776	G
22	BA	779	U
22	BA	782	A
22	BA	784	G
22	BA	785	G
22	BA	791	C
22	BA	792	A
22	BA	800	A
22	BA	802	A
22	BA	805	G
22	BA	812	C
22	BA	819	A
22	BA	827	U
22	BA	828	U
22	BA	845	A
22	BA	846	U
22	BA	847	U
22	BA	858	G
22	BA	859	G
22	BA	860	U
22	BA	866	A
22	BA	878	A
22	BA	879	G

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Mol	Chain	Res	Type
22	BA	885	C
22	BA	896	A
22	BA	910	A
22	BA	914	G
22	BA	915	C
22	BA	932	U
22	BA	941	A
22	BA	946	C
22	BA	961	C
22	BA	974	G
22	BA	983	A
22	BA	984	A
22	BA	985	C
22	BA	995	C
22	BA	996	A
22	BA	1012	U
22	BA	1013	C
22	BA	1022	G
22	BA	1023	U
22	BA	1026	G
22	BA	1033	U
22	BA	1035	U
22	BA	1046	A
22	BA	1047	G
22	BA	1051	G
22	BA	1053	C
22	BA	1061	U
22	BA	1062	G
22	BA	1066	U
22	BA	1068	G
22	BA	1070	A
22	BA	1071	G
22	BA	1072	C
22	BA	1073	A
22	BA	1074	G
22	BA	1075	C
22	BA	1081	U
22	BA	1087	G
22	BA	1088	A
22	BA	1089	A
22	BA	1092	C
22	BA	1098	A

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Mol	Chain	Res	Type
22	BA	1099	G
22	BA	1100	C
22	BA	1101	U
22	BA	1104	C
22	BA	1106	G
22	BA	1112	G
22	BA	1132	U
22	BA	1133	A
22	BA	1135	C
22	BA	1136	G
22	BA	1138	G
22	BA	1139	G
22	BA	1141	U
22	BA	1142	A
22	BA	1168	G
22	BA	1171	G
22	BA	1172	C
22	BA	1173	U
22	BA	1174	U
22	BA	1175	A
22	BA	1176	U
22	BA	1180	U
22	BA	1181	U
22	BA	1186	G
22	BA	1187	G
22	BA	1189	A
22	BA	1205	A
22	BA	1238	G
22	BA	1239	G
22	BA	1247	A
22	BA	1248	G
22	BA	1253	A
22	BA	1256	G
22	BA	1258	U
22	BA	1266	G
22	BA	1269	A
22	BA	1271	G
22	BA	1272	A
22	BA	1273	U
22	BA	1275	A
22	BA	1280	G
22	BA	1294	U

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Mol	Chain	Res	Type
22	BA	1300	G
22	BA	1301	A
22	BA	1303	G
22	BA	1305	C
22	BA	1321	A
22	BA	1327	A
22	BA	1328	A
22	BA	1329	U
22	BA	1332	G
22	BA	1334	G
22	BA	1345	C
22	BA	1352	U
22	BA	1359	A
22	BA	1365	A
22	BA	1367	A
22	BA	1368	G
22	BA	1370	C
22	BA	1374	G
22	BA	1377	G
22	BA	1378	A
22	BA	1379	U
22	BA	1383	A
22	BA	1384	A
22	BA	1386	C
22	BA	1403	A
22	BA	1406	U
22	BA	1407	G
22	BA	1415	U
22	BA	1416	G
22	BA	1419	A
22	BA	1420	A
22	BA	1427	A
22	BA	1428	C
22	BA	1432	G
22	BA	1435	G
22	BA	1439	A
22	BA	1450	G
22	BA	1452	G
22	BA	1453	A
22	BA	1460	U
22	BA	1482	G
22	BA	1483	G

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Mol	Chain	Res	Type
22	BA	1493	C
22	BA	1494	A
22	BA	1495	A
22	BA	1504	A
22	BA	1508	A
22	BA	1510	G
22	BA	1515	A
22	BA	1523	U
22	BA	1528	A
22	BA	1532	A
22	BA	1533	C
22	BA	1534	U
22	BA	1535	A
22	BA	1536	C
22	BA	1554	U
22	BA	1555	G
22	BA	1569	A
22	BA	1578	U
22	BA	1581	G
22	BA	1582	C
22	BA	1583	A
22	BA	1584	U
22	BA	1585	C
22	BA	1597	A
22	BA	1607	C
22	BA	1608	A
22	BA	1609	A
22	BA	1610	A
22	BA	1619	G
22	BA	1632	A
22	BA	1634	A
22	BA	1635	A
22	BA	1647	U
22	BA	1648	U
22	BA	1649	G
22	BA	1652	A
22	BA	1674	G
22	BA	1677	A
22	BA	1714	U
22	BA	1715	G
22	BA	1718	G
22	BA	1729	U

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Mol	Chain	Res	Type
22	BA	1730	C
22	BA	1732	C
22	BA	1736	U
22	BA	1738	G
22	BA	1744	A
22	BA	1757	A
22	BA	1764	C
22	BA	1773	A
22	BA	1786	A
22	BA	1800	C
22	BA	1801	A
22	BA	1802	A
22	BA	1808	A
22	BA	1816	C
22	BA	1828	G
22	BA	1829	A
22	BA	1841	U
22	BA	1842	G
22	BA	1865	U
22	BA	1866	A
22	BA	1870	C
22	BA	1873	G
22	BA	1876	A
22	BA	1884	G
22	BA	1885	A
22	BA	1906	G
22	BA	1909	C
22	BA	1910	G
22	BA	1911	U
22	BA	1912	A
22	BA	1913	A
22	BA	1914	C
22	BA	1915	U
22	BA	1916	A
22	BA	1917	U
22	BA	1919	A
22	BA	1920	C
22	BA	1925	C
22	BA	1926	U
22	BA	1927	A
22	BA	1929	G
22	BA	1930	G

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Mol	Chain	Res	Type
22	BA	1931	U
22	BA	1932	A
22	BA	1938	A
22	BA	1944	U
22	BA	1955	U
22	BA	1967	C
22	BA	1970	A
22	BA	1972	G
22	BA	1991	U
22	BA	1992	G
22	BA	1993	U
22	BA	1997	C
22	BA	2022	U
22	BA	2023	C
22	BA	2031	A
22	BA	2032	G
22	BA	2033	A
22	BA	2038	G
22	BA	2043	C
22	BA	2055	C
22	BA	2056	G
22	BA	2060	A
22	BA	2061	G
22	BA	2062	A
22	BA	2066	C
22	BA	2069	G
22	BA	2072	C
22	BA	2077	A
22	BA	2093	G
22	BA	2096	C
22	BA	2101	A
22	BA	2102	G
22	BA	2107	G
22	BA	2110	G
22	BA	2111	U
22	BA	2112	G
22	BA	2113	U
22	BA	2115	G
22	BA	2116	G
22	BA	2117	A
22	BA	2118	U
22	BA	2119	A

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Mol	Chain	Res	Type
22	BA	2122	U
22	BA	2123	G
22	BA	2126	A
22	BA	2128	G
22	BA	2132	U
22	BA	2133	G
22	BA	2134	A
22	BA	2136	G
22	BA	2145	C
22	BA	2147	A
22	BA	2148	G
22	BA	2149	U
22	BA	2157	G
22	BA	2158	A
22	BA	2159	G
22	BA	2162	G
22	BA	2164	C
22	BA	2165	C
22	BA	2167	U
22	BA	2169	A
22	BA	2170	A
22	BA	2171	A
22	BA	2172	U
22	BA	2173	A
22	BA	2178	C
22	BA	2179	C
22	BA	2183	A
22	BA	2185	U
22	BA	2187	U
22	BA	2188	U
22	BA	2195	U
22	BA	2198	A
22	BA	2203	U
22	BA	2204	G
22	BA	2211	A
22	BA	2212	A
22	BA	2220	U
22	BA	2225	A
22	BA	2226	C
22	BA	2238	G
22	BA	2239	G
22	BA	2243	U

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Mol	Chain	Res	Type
22	BA	2250	G
22	BA	2266	A
22	BA	2268	A
22	BA	2278	A
22	BA	2280	G
22	BA	2283	C
22	BA	2286	G
22	BA	2287	A
22	BA	2297	A
22	BA	2305	U
22	BA	2308	G
22	BA	2311	A
22	BA	2312	U
22	BA	2322	A
22	BA	2325	G
22	BA	2326	C
22	BA	2327	A
22	BA	2331	G
22	BA	2335	A
22	BA	2345	G
22	BA	2347	C
22	BA	2350	C
22	BA	2354	C
22	BA	2358	A
22	BA	2361	G
22	BA	2376	A
22	BA	2383	G
22	BA	2385	C
22	BA	2389	G
22	BA	2396	G
22	BA	2402	U
22	BA	2406	A
22	BA	2412	A
22	BA	2420	C
22	BA	2424	C
22	BA	2425	A
22	BA	2426	A
22	BA	2429	G
22	BA	2430	A
22	BA	2431	U
22	BA	2435	A
22	BA	2441	U

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Mol	Chain	Res	Type
22	BA	2445	G
22	BA	2448	A
22	BA	2474	U
22	BA	2476	A
22	BA	2478	A
22	BA	2484	G
22	BA	2491	U
22	BA	2502	G
22	BA	2505	G
22	BA	2518	A
22	BA	2520	C
22	BA	2522	U
22	BA	2525	G
22	BA	2529	G
22	BA	2535	G
22	BA	2554	U
22	BA	2566	A
22	BA	2567	G
22	BA	2573	C
22	BA	2582	G
22	BA	2583	G
22	BA	2585	U
22	BA	2586	U
22	BA	2603	G
22	BA	2604	U
22	BA	2609	U
22	BA	2613	U
22	BA	2619	C
22	BA	2629	U
22	BA	2654	A
22	BA	2681	C
22	BA	2689	U
22	BA	2690	U
22	BA	2700	A
22	BA	2714	G
22	BA	2726	A
22	BA	2729	G
22	BA	2733	A
22	BA	2748	A
22	BA	2757	A
22	BA	2762	C
22	BA	2765	A

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Mol	Chain	Res	Type
22	BA	2769	U
22	BA	2778	A
22	BA	2783	U
22	BA	2791	G
22	BA	2798	U
22	BA	2799	A
22	BA	2800	A
22	BA	2811	G
22	BA	2818	U
22	BA	2820	A
22	BA	2821	A
22	BA	2825	G
22	BA	2826	A
22	BA	2835	A
22	BA	2858	C
22	BA	2861	U
22	BA	2867	G
22	BA	2873	A
22	BA	2879	A
22	BA	2880	C
22	BA	2883	A
22	BA	2884	U
22	BA	2885	G
22	BA	2886	A
22	BA	2887	A
22	BA	2903	U
23	BB	2	G
23	BB	9	G
23	BB	13	G
23	BB	15	A
23	BB	16	G
23	BB	24	G
23	BB	25	U
23	BB	33	G
23	BB	35	C
23	BB	36	C
23	BB	37	C
23	BB	41	G
23	BB	44	G
23	BB	45	A
23	BB	51	G
23	BB	56	G

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Mol	Chain	Res	Type
23	BB	89	U
23	BB	90	C
23	BB	98	G
23	BB	99	A
23	BB	107	G
23	BB	109	A
23	BB	119	A
1	CA	4	U
1	CA	5	U
1	CA	9	G
1	CA	17	U
1	CA	22	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	56	U
1	CA	57	G
1	CA	67	C
1	CA	68	G
1	CA	70	U
1	CA	71	A
1	CA	74	A
1	CA	76	G
1	CA	81	A
1	CA	83	C
1	CA	84	U
1	CA	85	U
1	CA	87	C
1	CA	88	U
1	CA	91	U
1	CA	94	G
1	CA	95	C
1	CA	97	G
1	CA	99	C
1	CA	108	G
1	CA	115	G
1	CA	116	A
1	CA	120	A
1	CA	121	U
1	CA	122	G

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Mol	Chain	Res	Type
1	CA	130	A
1	CA	131	A
1	CA	137	U
1	CA	142	G
1	CA	143	A
1	CA	144	G
1	CA	154	U
1	CA	155	A
1	CA	159	G
1	CA	163	C
1	CA	176	C
1	CA	181	A
1	CA	182	A
1	CA	183	C
1	CA	184	G
1	CA	187	G
1	CA	189	A
1	CA	197	A
1	CA	200	G
1	CA	201	G
1	CA	204	G
1	CA	207	C
1	CA	208	U
1	CA	210	C
1	CA	211	G
1	CA	212	G
1	CA	240	G
1	CA	245	U
1	CA	247	G
1	CA	250	A
1	CA	251	G
1	CA	266	G
1	CA	267	C
1	CA	279	A
1	CA	280	C
1	CA	289	G
1	CA	298	A
1	CA	316	C
1	CA	320	A
1	CA	321	A
1	CA	328	C
1	CA	329	A

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Mol	Chain	Res	Type
1	CA	330	C
1	CA	332	G
1	CA	333	U
1	CA	337	G
1	CA	352	C
1	CA	354	G
1	CA	357	G
1	CA	359	G
1	CA	367	U
1	CA	370	C
1	CA	372	C
1	CA	377	G
1	CA	378	G
1	CA	398	U
1	CA	399	G
1	CA	406	G
1	CA	411	A
1	CA	412	A
1	CA	413	G
1	CA	421	U
1	CA	422	C
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	436	C
1	CA	458	U
1	CA	459	A
1	CA	463	U
1	CA	466	A
1	CA	467	U
1	CA	468	A
1	CA	469	C
1	CA	474	G
1	CA	477	C
1	CA	478	A
1	CA	479	U
1	CA	481	G
1	CA	482	A
1	CA	483	C
1	CA	484	G
1	CA	485	U
1	CA	486	U

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Mol	Chain	Res	Type
1	CA	495	A
1	CA	498	A
1	CA	499	A
1	CA	509	A
1	CA	511	C
1	CA	518	C
1	CA	519	C
1	CA	524	G
1	CA	527	G
1	CA	530	G
1	CA	532	A
1	CA	533	A
1	CA	547	A
1	CA	550	G
1	CA	559	A
1	CA	564	C
1	CA	568	G
1	CA	572	A
1	CA	573	A
1	CA	576	C
1	CA	579	A
1	CA	581	G
1	CA	619	U
1	CA	621	A
1	CA	622	A
1	CA	650	G
1	CA	653	U
1	CA	654	G
1	CA	665	A
1	CA	666	G
1	CA	675	A
1	CA	682	G
1	CA	687	A
1	CA	695	A
1	CA	705	G
1	CA	718	A
1	CA	719	C
1	CA	720	C
1	CA	721	G
1	CA	723	U
1	CA	724	G
1	CA	731	G

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Mol	Chain	Res	Type
1	CA	734	G
1	CA	738	C
1	CA	747	A
1	CA	752	G
1	CA	755	G
1	CA	777	A
1	CA	778	G
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	799	G
1	CA	801	U
1	CA	802	A
1	CA	809	G
1	CA	815	A
1	CA	817	C
1	CA	819	A
1	CA	821	G
1	CA	827	U
1	CA	828	U
1	CA	841	C
1	CA	842	U
1	CA	843	U
1	CA	844	G
1	CA	845	A
1	CA	846	G
1	CA	859	G
1	CA	874	G
1	CA	885	G
1	CA	914	A
1	CA	922	G
1	CA	926	G
1	CA	934	C
1	CA	935	A
1	CA	960	U
1	CA	966	G
1	CA	969	A
1	CA	971	G
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A

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Mol	Chain	Res	Type
1	CA	983	A
1	CA	987	G
1	CA	989	U
1	CA	993	G
1	CA	994	A
1	CA	995	C
1	CA	996	A
1	CA	1004	A
1	CA	1005	A
1	CA	1008	U
1	CA	1009	U
1	CA	1017	U
1	CA	1018	G
1	CA	1022	A
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030	U
1	CA	1031	C
1	CA	1032	G
1	CA	1033	G
1	CA	1034	G
1	CA	1037	C
1	CA	1039	G
1	CA	1043	G
1	CA	1044	A
1	CA	1047	G
1	CA	1050	G
1	CA	1054	C
1	CA	1056	U
1	CA	1065	U
1	CA	1072	G
1	CA	1073	U
1	CA	1086	U
1	CA	1088	G
1	CA	1094	G
1	CA	1095	U
1	CA	1101	A
1	CA	1124	G
1	CA	1125	U
1	CA	1133	G

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Mol	Chain	Res	Type
1	CA	1134	G
1	CA	1135	U
1	CA	1136	C
1	CA	1137	C
1	CA	1139	G
1	CA	1140	C
1	CA	1141	C
1	CA	1142	G
1	CA	1145	A
1	CA	1154	G
1	CA	1155	A
1	CA	1157	A
1	CA	1159	U
1	CA	1160	G
1	CA	1161	C
1	CA	1176	A
1	CA	1183	U
1	CA	1184	G
1	CA	1192	C
1	CA	1196	A
1	CA	1197	A
1	CA	1202	U
1	CA	1203	C
1	CA	1212	U
1	CA	1213	A
1	CA	1217	C
1	CA	1227	A
1	CA	1228	C
1	CA	1238	A
1	CA	1240	U
1	CA	1243	C
1	CA	1253	G
1	CA	1256	A
1	CA	1260	G
1	CA	1269	A
1	CA	1275	A
1	CA	1280	A
1	CA	1282	C
1	CA	1285	A
1	CA	1286	U
1	CA	1287	A
1	CA	1292	G

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Mol	Chain	Res	Type
1	CA	1293	C
1	CA	1299	A
1	CA	1300	G
1	CA	1302	C
1	CA	1304	G
1	CA	1305	G
1	CA	1317	C
1	CA	1318	A
1	CA	1322	C
1	CA	1324	A
1	CA	1331	G
1	CA	1337	G
1	CA	1338	G
1	CA	1346	A
1	CA	1353	G
1	CA	1362	A
1	CA	1363	A
1	CA	1364	U
1	CA	1370	G
1	CA	1377	A
1	CA	1378	C
1	CA	1379	G
1	CA	1397	C
1	CA	1398	A
1	CA	1419	G
1	CA	1440	U
1	CA	1441	A
1	CA	1442	G
1	CA	1446	A
1	CA	1448	C
1	CA	1452	C
1	CA	1454	G
1	CA	1475	G
1	CA	1480	A
1	CA	1491	G
1	CA	1492	A
1	CA	1497	G
1	CA	1499	A
1	CA	1503	A
1	CA	1505	G
1	CA	1506	U
1	CA	1507	A

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Mol	Chain	Res	Type
1	CA	1517	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1533	C
1	CA	1535	C
1	CA	1536	C
1	CA	1537	U
22	DA	3	U
22	DA	10	A
22	DA	12	U
22	DA	15	G
22	DA	30	G
22	DA	34	U
22	DA	41	C
22	DA	42	A
22	DA	46	G
22	DA	55	G
22	DA	58	G
22	DA	61	C
22	DA	71	A
22	DA	74	A
22	DA	75	G
22	DA	80	G
22	DA	82	U
22	DA	84	A
22	DA	91	A
22	DA	98	G
22	DA	101	A
22	DA	102	U
22	DA	118	A
22	DA	119	A
22	DA	120	U
22	DA	128	C
22	DA	138	U
22	DA	139	U
22	DA	140	C
22	DA	141	G
22	DA	142	A
22	DA	155	A
22	DA	158	U
22	DA	162	U

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Mol	Chain	Res	Type
22	DA	163	C
22	DA	166	U
22	DA	181	A
22	DA	196	A
22	DA	197	A
22	DA	199	A
22	DA	206	U
22	DA	215	G
22	DA	216	A
22	DA	222	A
22	DA	223	A
22	DA	225	C
22	DA	248	G
22	DA	249	C
22	DA	255	A
22	DA	264	C
22	DA	265	A
22	DA	266	G
22	DA	271	G
22	DA	272	A
22	DA	276	U
22	DA	277	G
22	DA	279	A
22	DA	280	U
22	DA	281	C
22	DA	284	U
22	DA	285	G
22	DA	287	G
22	DA	294	A
22	DA	299	A
22	DA	301	G
22	DA	311	A
22	DA	312	G
22	DA	322	A
22	DA	329	G
22	DA	330	A
22	DA	335	C
22	DA	350	G
22	DA	353	C
22	DA	354	A
22	DA	361	G
22	DA	362	A

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Mol	Chain	Res	Type
22	DA	367	G
22	DA	371	A
22	DA	372	G
22	DA	385	C
22	DA	386	G
22	DA	396	G
22	DA	399	U
22	DA	405	U
22	DA	411	G
22	DA	412	A
22	DA	417	C
22	DA	424	G
22	DA	436	C
22	DA	449	A
22	DA	451	U
22	DA	455	C
22	DA	480	A
22	DA	481	G
22	DA	486	C
22	DA	490	C
22	DA	491	G
22	DA	504	A
22	DA	505	A
22	DA	508	A
22	DA	509	C
22	DA	510	C
22	DA	511	U
22	DA	518	G
22	DA	526	A
22	DA	528	A
22	DA	529	A
22	DA	530	G
22	DA	531	C
22	DA	532	A
22	DA	533	G
22	DA	543	G
22	DA	544	C
22	DA	546	U
22	DA	547	A
22	DA	548	G
22	DA	549	G
22	DA	550	C

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Mol	Chain	Res	Type
22	DA	563	A
22	DA	569	U
22	DA	573	U
22	DA	575	A
22	DA	586	A
22	DA	588	U
22	DA	593	U
22	DA	603	A
22	DA	613	A
22	DA	615	U
22	DA	622	G
22	DA	627	A
22	DA	630	G
22	DA	631	A
22	DA	637	A
22	DA	641	U
22	DA	642	U
22	DA	645	C
22	DA	646	U
22	DA	647	G
22	DA	648	G
22	DA	654	A
22	DA	655	A
22	DA	657	U
22	DA	663	G
22	DA	676	A
22	DA	685	A
22	DA	686	U
22	DA	695	G
22	DA	702	U
22	DA	704	G
22	DA	715	A
22	DA	717	C
22	DA	726	G
22	DA	727	A
22	DA	729	G
22	DA	730	A
22	DA	740	C
22	DA	746	U
22	DA	747	U
22	DA	751	A
22	DA	752	A

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Mol	Chain	Res	Type
22	DA	762	U
22	DA	764	A
22	DA	775	G
22	DA	776	G
22	DA	782	A
22	DA	783	A
22	DA	784	G
22	DA	785	G
22	DA	792	A
22	DA	802	A
22	DA	805	G
22	DA	812	C
22	DA	819	A
22	DA	827	U
22	DA	828	U
22	DA	829	A
22	DA	830	G
22	DA	845	A
22	DA	846	U
22	DA	847	U
22	DA	858	G
22	DA	859	G
22	DA	865	C
22	DA	878	A
22	DA	880	G
22	DA	881	G
22	DA	885	C
22	DA	896	A
22	DA	897	C
22	DA	902	C
22	DA	910	A
22	DA	914	G
22	DA	915	C
22	DA	922	C
22	DA	931	U
22	DA	932	U
22	DA	941	A
22	DA	945	A
22	DA	946	C
22	DA	961	C
22	DA	974	G
22	DA	982	C

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Mol	Chain	Res	Type
22	DA	983	A
22	DA	990	A
22	DA	995	C
22	DA	996	A
22	DA	997	G
22	DA	1012	U
22	DA	1013	C
22	DA	1022	G
22	DA	1024	G
22	DA	1025	G
22	DA	1026	G
22	DA	1033	U
22	DA	1041	G
22	DA	1046	A
22	DA	1047	G
22	DA	1053	C
22	DA	1058	U
22	DA	1060	U
22	DA	1061	U
22	DA	1062	G
22	DA	1065	U
22	DA	1066	U
22	DA	1067	A
22	DA	1068	G
22	DA	1070	A
22	DA	1071	G
22	DA	1072	C
22	DA	1074	G
22	DA	1075	C
22	DA	1079	C
22	DA	1082	U
22	DA	1088	A
22	DA	1089	A
22	DA	1090	A
22	DA	1092	C
22	DA	1094	U
22	DA	1097	U
22	DA	1098	A
22	DA	1100	C
22	DA	1104	C
22	DA	1110	G
22	DA	1111	A

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Mol	Chain	Res	Type
22	DA	1112	G
22	DA	1115	G
22	DA	1122	G
22	DA	1128	G
22	DA	1132	U
22	DA	1135	C
22	DA	1136	G
22	DA	1139	G
22	DA	1141	U
22	DA	1142	A
22	DA	1150	C
22	DA	1153	C
22	DA	1155	A
22	DA	1156	A
22	DA	1168	G
22	DA	1171	G
22	DA	1172	C
22	DA	1173	U
22	DA	1175	A
22	DA	1176	U
22	DA	1177	G
22	DA	1178	C
22	DA	1179	G
22	DA	1180	U
22	DA	1186	G
22	DA	1205	A
22	DA	1208	C
22	DA	1219	U
22	DA	1221	C
22	DA	1227	G
22	DA	1230	A
22	DA	1236	G
22	DA	1238	G
22	DA	1241	A
22	DA	1247	A
22	DA	1250	G
22	DA	1253	A
22	DA	1255	U
22	DA	1256	G
22	DA	1258	U
22	DA	1266	G
22	DA	1269	A

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Mol	Chain	Res	Type
22	DA	1271	G
22	DA	1272	A
22	DA	1276	A
22	DA	1286	A
22	DA	1300	G
22	DA	1301	A
22	DA	1305	C
22	DA	1321	A
22	DA	1325	U
22	DA	1342	A
22	DA	1345	C
22	DA	1352	U
22	DA	1355	G
22	DA	1359	A
22	DA	1365	A
22	DA	1376	C
22	DA	1378	A
22	DA	1379	U
22	DA	1382	G
22	DA	1383	A
22	DA	1386	C
22	DA	1387	A
22	DA	1390	U
22	DA	1391	U
22	DA	1395	A
22	DA	1411	U
22	DA	1413	A
22	DA	1414	C
22	DA	1416	G
22	DA	1418	G
22	DA	1420	A
22	DA	1426	G
22	DA	1428	C
22	DA	1429	G
22	DA	1434	A
22	DA	1436	G
22	DA	1452	G
22	DA	1453	A
22	DA	1455	G
22	DA	1456	G
22	DA	1458	U
22	DA	1460	U

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Mol	Chain	Res	Type
22	DA	1462	C
22	DA	1471	G
22	DA	1472	C
22	DA	1478	G
22	DA	1482	G
22	DA	1483	G
22	DA	1493	C
22	DA	1495	A
22	DA	1499	C
22	DA	1504	A
22	DA	1509	A
22	DA	1510	G
22	DA	1515	A
22	DA	1523	U
22	DA	1524	G
22	DA	1530	G
22	DA	1531	C
22	DA	1533	C
22	DA	1534	U
22	DA	1535	A
22	DA	1536	C
22	DA	1537	G
22	DA	1556	C
22	DA	1565	C
22	DA	1566	A
22	DA	1569	A
22	DA	1576	U
22	DA	1578	U
22	DA	1581	G
22	DA	1582	C
22	DA	1583	A
22	DA	1584	U
22	DA	1585	C
22	DA	1603	A
22	DA	1604	C
22	DA	1607	C
22	DA	1608	A
22	DA	1610	A
22	DA	1613	G
22	DA	1616	A
22	DA	1623	G
22	DA	1647	U

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Mol	Chain	Res	Type
22	DA	1648	U
22	DA	1649	G
22	DA	1651	G
22	DA	1664	A
22	DA	1674	G
22	DA	1694	C
22	DA	1711	A
22	DA	1714	U
22	DA	1715	G
22	DA	1728	C
22	DA	1729	U
22	DA	1730	C
22	DA	1731	G
22	DA	1732	C
22	DA	1735	A
22	DA	1738	G
22	DA	1739	A
22	DA	1740	G
22	DA	1744	A
22	DA	1758	U
22	DA	1764	C
22	DA	1773	A
22	DA	1774	C
22	DA	1782	U
22	DA	1800	C
22	DA	1801	A
22	DA	1802	A
22	DA	1808	A
22	DA	1812	U
22	DA	1816	C
22	DA	1821	A
22	DA	1823	G
22	DA	1829	A
22	DA	1847	A
22	DA	1848	A
22	DA	1858	A
22	DA	1859	U
22	DA	1869	G
22	DA	1870	C
22	DA	1871	A
22	DA	1874	C
22	DA	1880	U

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Mol	Chain	Res	Type
22	DA	1888	G
22	DA	1900	A
22	DA	1903	G
22	DA	1905	C
22	DA	1906	G
22	DA	1907	G
22	DA	1913	A
22	DA	1914	C
22	DA	1927	A
22	DA	1929	G
22	DA	1930	G
22	DA	1935	G
22	DA	1947	C
22	DA	1955	U
22	DA	1961	C
22	DA	1963	U
22	DA	1964	G
22	DA	1965	C
22	DA	1967	C
22	DA	1970	A
22	DA	1971	U
22	DA	1972	G
22	DA	1991	U
22	DA	1993	U
22	DA	1997	C
22	DA	2020	A
22	DA	2021	C
22	DA	2022	U
22	DA	2023	C
22	DA	2030	A
22	DA	2031	A
22	DA	2033	A
22	DA	2043	C
22	DA	2055	C
22	DA	2056	G
22	DA	2057	G
22	DA	2060	A
22	DA	2061	G
22	DA	2062	A
22	DA	2069	G
22	DA	2072	C
22	DA	2087	G

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Mol	Chain	Res	Type
22	DA	2092	U
22	DA	2093	G
22	DA	2095	A
22	DA	2102	G
22	DA	2103	C
22	DA	2107	G
22	DA	2108	A
22	DA	2110	G
22	DA	2111	U
22	DA	2112	G
22	DA	2113	U
22	DA	2115	G
22	DA	2116	G
22	DA	2117	A
22	DA	2118	U
22	DA	2119	A
22	DA	2125	G
22	DA	2126	A
22	DA	2127	G
22	DA	2128	G
22	DA	2131	U
22	DA	2132	U
22	DA	2133	G
22	DA	2135	A
22	DA	2137	U
22	DA	2145	C
22	DA	2146	C
22	DA	2147	A
22	DA	2149	U
22	DA	2150	C
22	DA	2158	A
22	DA	2162	G
22	DA	2163	A
22	DA	2164	C
22	DA	2165	C
22	DA	2169	A
22	DA	2170	A
22	DA	2171	A
22	DA	2172	U
22	DA	2173	A
22	DA	2177	C
22	DA	2178	C

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Mol	Chain	Res	Type
22	DA	2181	U
22	DA	2184	A
22	DA	2185	U
22	DA	2189	U
22	DA	2190	G
22	DA	2194	U
22	DA	2198	A
22	DA	2203	U
22	DA	2204	G
22	DA	2211	A
22	DA	2212	A
22	DA	2225	A
22	DA	2226	C
22	DA	2230	G
22	DA	2238	G
22	DA	2239	G
22	DA	2241	A
22	DA	2242	G
22	DA	2243	U
22	DA	2250	G
22	DA	2268	A
22	DA	2273	A
22	DA	2278	A
22	DA	2280	G
22	DA	2283	C
22	DA	2287	A
22	DA	2293	G
22	DA	2297	A
22	DA	2305	U
22	DA	2307	G
22	DA	2309	A
22	DA	2311	A
22	DA	2312	U
22	DA	2320	U
22	DA	2322	A
22	DA	2324	U
22	DA	2325	G
22	DA	2327	A
22	DA	2331	G
22	DA	2333	A
22	DA	2344	U
22	DA	2347	C

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Mol	Chain	Res	Type
22	DA	2350	C
22	DA	2354	C
22	DA	2356	U
22	DA	2357	G
22	DA	2361	G
22	DA	2383	G
22	DA	2385	C
22	DA	2388	A
22	DA	2402	U
22	DA	2403	C
22	DA	2406	A
22	DA	2407	A
22	DA	2410	G
22	DA	2423	U
22	DA	2424	C
22	DA	2425	A
22	DA	2426	A
22	DA	2429	G
22	DA	2430	A
22	DA	2431	U
22	DA	2434	A
22	DA	2435	A
22	DA	2441	U
22	DA	2446	G
22	DA	2448	A
22	DA	2449	U
22	DA	2455	G
22	DA	2476	A
22	DA	2482	A
22	DA	2484	G
22	DA	2491	U
22	DA	2502	G
22	DA	2503	A
22	DA	2504	U
22	DA	2505	G
22	DA	2507	C
22	DA	2518	A
22	DA	2525	G
22	DA	2529	G
22	DA	2534	A
22	DA	2535	G
22	DA	2547	A

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Mol	Chain	Res	Type
22	DA	2554	U
22	DA	2566	A
22	DA	2567	G
22	DA	2572	A
22	DA	2573	C
22	DA	2580	U
22	DA	2582	G
22	DA	2585	U
22	DA	2586	U
22	DA	2589	A
22	DA	2600	A
22	DA	2602	A
22	DA	2603	G
22	DA	2606	C
22	DA	2609	U
22	DA	2613	U
22	DA	2614	A
22	DA	2615	U
22	DA	2629	U
22	DA	2630	G
22	DA	2646	C
22	DA	2656	U
22	DA	2663	G
22	DA	2682	A
22	DA	2689	U
22	DA	2690	U
22	DA	2703	C
22	DA	2713	U
22	DA	2714	G
22	DA	2716	C
22	DA	2718	G
22	DA	2726	A
22	DA	2729	G
22	DA	2739	U
22	DA	2748	A
22	DA	2757	A
22	DA	2758	A
22	DA	2764	A
22	DA	2765	A
22	DA	2768	U
22	DA	2778	A
22	DA	2791	G

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Mol	Chain	Res	Type
22	DA	2794	C
22	DA	2798	U
22	DA	2799	A
22	DA	2801	G
22	DA	2820	A
22	DA	2825	G
22	DA	2826	A
22	DA	2833	U
22	DA	2835	A
22	DA	2854	G
22	DA	2861	U
22	DA	2867	G
22	DA	2868	A
22	DA	2873	A
22	DA	2879	A
22	DA	2880	C
22	DA	2883	A
22	DA	2891	U
22	DA	2894	G
22	DA	2901	C
22	DA	2903	U
23	DB	13	G
23	DB	15	A
23	DB	16	G
23	DB	22	U
23	DB	24	G
23	DB	25	U
23	DB	35	C
23	DB	36	C
23	DB	40	U
23	DB	44	G
23	DB	51	G
23	DB	54	G
23	DB	56	G
23	DB	58	A
23	DB	64	G
23	DB	66	A
23	DB	73	A
23	DB	88	C
23	DB	89	U
23	DB	90	C
23	DB	91	C

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Mol	Chain	Res	Type
23	DB	98	G
23	DB	99	A
23	DB	105	G
23	DB	109	A

All (87) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	148	G
1	AA	209	U
1	AA	351	G
1	AA	429	U
1	AA	481	G
1	AA	653	U
1	AA	702	A
1	AA	772	U
1	AA	1031	C
1	AA	1049	U
1	AA	1145	A
1	AA	1181	G
1	AA	1201	A
1	AA	1211	U
1	AA	1533	C
22	BA	70	G
22	BA	271	G
22	BA	310	A
22	BA	404	A
22	BA	479	A
22	BA	614	A
22	BA	668	A
22	BA	764	A
22	BA	858	G
22	BA	960	A
22	BA	984	A
22	BA	995	C
22	BA	1344	U
22	BA	1378	A
22	BA	1434	A
22	BA	1494	A
22	BA	1606	C
22	BA	1610	A

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Mol	Chain	Res	Type
22	BA	1875	G
22	BA	1919	A
22	BA	2127	G
22	BA	2211	A
22	BA	2282	G
22	BA	2286	G
22	BA	2326	C
22	BA	2406	A
22	BA	2425	A
22	BA	2756	U
1	CA	96	U
1	CA	115	G
1	CA	209	U
1	CA	429	U
1	CA	559	A
1	CA	733	G
1	CA	1049	U
1	CA	1201	A
1	CA	1211	U
22	DA	60	G
22	DA	196	A
22	DA	271	G
22	DA	404	A
22	DA	479	A
22	DA	503	A
22	DA	529	A
22	DA	614	A
22	DA	764	A
22	DA	781	A
22	DA	846	U
22	DA	973	A
22	DA	1089	A
22	DA	1240	U
22	DA	1275	A
22	DA	1344	U
22	DA	1378	A
22	DA	1606	C
22	DA	1738	G
22	DA	2109	U
22	DA	2111	U
22	DA	2127	G
22	DA	2146	C

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Mol	Chain	Res	Type
22	DA	2162	G
22	DA	2211	A
22	DA	2225	A
22	DA	2286	G
22	DA	2296	U
22	DA	2308	G
22	DA	2311	A
22	DA	2326	C
22	DA	2425	A
22	DA	2602	A
22	DA	2756	U

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

10 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	$\# Z > 2$
54	MHW	B6	1	54	9,9,10	1.44	1 (11%)	8,11,13	2.39	2 (25%)
54	DBB	B6	3	54	4,5,6	1.42	1 (25%)	3,5,7	2.22	2 (66%)
54	MHU	B6	5	54	13,15,16	1.71	2 (15%)	15,19,21	1.25	1 (6%)
54	MHV	B6	6	54	7,9,10	1.34	1 (14%)	8,11,13	4.22	4 (50%)
54	004	B6	7	54	9,10,11	1.57	1 (11%)	10,12,14	2.63	5 (50%)
54	MHW	D6	1	54	9,9,10	1.52	1 (11%)	8,11,13	3.10	3 (37%)
54	DBB	D6	3	54	4,5,6	1.09	0	3,5,7	1.83	1 (33%)
54	MHU	D6	5	54	13,15,16	1.95	3 (23%)	15,19,21	1.83	2 (13%)
54	MHV	D6	6	54	7,9,10	0.89	0	8,11,13	3.73	3 (37%)
54	004	D6	7	54	9,10,11	0.52	0	10,12,14	1.61	1 (10%)

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
54	MHW	B6	1	54	-	0/2/2/4	0/1/1/1
54	DBB	B6	3	54	-	0/2/4/6	0/0/0/0
54	MHU	B6	5	54	-	0/8/12/14	0/1/1/1
54	MHV	B6	6	54	-	0/1/12/14	0/1/1/1
54	004	B6	7	54	-	0/4/6/8	0/1/1/1
54	MHW	D6	1	54	-	0/2/2/4	0/1/1/1
54	DBB	D6	3	54	-	0/2/4/6	0/0/0/0
54	MHU	D6	5	54	-	0/8/12/14	0/1/1/1
54	MHV	D6	6	54	-	0/1/12/14	0/1/1/1
54	004	D6	7	54	-	0/4/6/8	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	B6	7	004	CB-CA	-4.46	1.48	1.52
54	B6	6	MHV	CB-CG	-2.75	1.45	1.50
54	B6	3	DBB	CB-CA	-2.40	1.46	1.53
54	B6	5	MHU	CD2-CE2	2.08	1.42	1.38
54	D6	5	MHU	CD2-CE2	2.41	1.43	1.38
54	D6	5	MHU	CB-CG	2.93	1.58	1.51
54	B6	1	MHW	CA-C	3.06	1.52	1.48
54	D6	1	MHW	CA-C	3.46	1.53	1.48
54	B6	5	MHU	CZ-NZ	4.85	1.49	1.37
54	D6	5	MHU	CZ-NZ	5.35	1.50	1.37

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	D6	6	MHV	CD2-CE-N	-9.82	90.50	109.82
54	B6	6	MHV	CD2-CE-N	-8.95	92.22	109.82
54	B6	6	MHV	CA-CB-CG	-6.31	104.80	111.87
54	B6	7	004	CB-CA-N	-4.83	101.15	112.54
54	D6	1	MHW	CG2-CD-CE	-4.75	111.55	118.90
54	B6	1	MHW	CG2-CD-CE	-4.15	112.47	118.90
54	B6	7	004	CD1-CG1-CB	-3.54	115.96	120.64
54	B6	6	MHV	OD1-CG-CB	-3.29	117.81	121.98
54	B6	5	MHU	O-C-CA	-3.11	117.22	125.44
54	B6	3	DBB	O-C-CA	-2.80	118.18	125.49
54	B6	7	004	CE-CD2-CG2	-2.77	116.14	120.19
54	B6	3	DBB	CG-CB-CA	-2.63	106.66	113.44
54	D6	5	MHU	O-C-CA	-2.60	118.57	125.44
54	D6	6	MHV	CE-CD2-CG	-2.58	107.51	112.01
54	D6	3	DBB	CG-CB-CA	-2.34	107.41	113.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	D6	1	MHW	CE-N-CA	-2.10	113.67	116.90
54	D6	6	MHV	CD2-CG-CB	2.41	119.21	115.89
54	B6	7	004	CG2-CB-CG1	2.42	121.40	118.31
54	B6	6	MHV	CD2-CG-CB	3.09	120.15	115.89
54	B6	7	004	C-CA-N	3.56	116.85	109.12
54	D6	7	004	C-CA-N	4.77	119.48	109.12
54	B6	1	MHW	CD-CE-N	4.88	131.58	123.44
54	D6	5	MHU	CG-CB-CA	6.20	124.94	114.26
54	D6	1	MHW	CD-CE-N	6.88	134.92	123.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	B6	3	DBB	1	0
54	B6	5	MHU	1	0
54	D6	6	MHV	3	0
54	D6	7	004	6	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 500 ligands modelled in this entry, 500 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1538/1539 (99%)	0.08	42 (2%) 58 37	15, 50, 134, 177	0
1	CA	1539/1539 (100%)	0.41	109 (7%) 19 10	29, 71, 143, 177	0
2	AB	218/218 (100%)	1.01	42 (19%) 2 1	39, 71, 98, 131	0
2	CB	218/218 (100%)	1.56	79 (36%) 0 0	55, 80, 108, 126	0
3	AC	206/206 (100%)	0.37	13 (6%) 23 12	36, 56, 81, 95	0
3	CC	206/206 (100%)	1.58	66 (32%) 1 0	52, 73, 93, 114	0
4	AD	205/205 (100%)	0.81	25 (12%) 5 3	33, 55, 80, 109	0
4	CD	205/205 (100%)	0.40	14 (6%) 20 11	23, 40, 75, 93	0
5	AE	150/150 (100%)	0.44	5 (3%) 50 31	32, 49, 82, 111	0
5	CE	150/150 (100%)	0.66	11 (7%) 18 9	35, 56, 83, 105	0
6	AF	100/100 (100%)	0.36	7 (7%) 19 10	34, 55, 75, 85	0
6	CF	100/100 (100%)	0.89	16 (16%) 3 1	44, 72, 97, 105	0
7	AG	151/151 (100%)	1.15	34 (22%) 1 1	48, 73, 96, 107	0
7	CG	151/151 (100%)	3.18	100 (66%) 0 0	75, 92, 105, 113	0
8	AH	129/129 (100%)	0.33	2 (1%) 74 55	28, 47, 71, 80	0
8	CH	129/129 (100%)	0.93	20 (15%) 3 1	46, 63, 83, 90	0
9	AI	127/127 (100%)	1.09	26 (20%) 1 1	42, 68, 96, 115	0
9	CI	127/127 (100%)	2.17	63 (49%) 0 0	64, 87, 106, 131	0
10	AJ	98/98 (100%)	1.09	17 (17%) 2 1	42, 62, 93, 120	0
10	CJ	98/98 (100%)	3.41	68 (69%) 0 0	66, 89, 108, 122	0
11	AK	117/117 (100%)	0.92	23 (19%) 1 1	29, 61, 88, 106	0
11	CK	117/117 (100%)	0.63	11 (9%) 11 5	35, 63, 82, 91	0
12	AL	123/123 (100%)	0.42	5 (4%) 41 24	23, 36, 72, 102	0
12	CL	123/123 (100%)	0.81	9 (7%) 18 9	38, 50, 80, 102	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	114/114 (100%)	0.67	15 (13%) 4 2	43, 66, 91, 105	0
13	CM	114/114 (100%)	3.49	85 (74%) 0 0	80, 98, 113, 118	0
14	AN	96/100 (96%)	0.83	17 (17%) 2 1	39, 56, 93, 108	0
14	CN	96/100 (96%)	2.81	57 (59%) 0 0	60, 88, 106, 119	0
15	AO	88/88 (100%)	0.48	6 (6%) 20 11	31, 49, 66, 99	0
15	CO	88/88 (100%)	0.76	8 (9%) 11 6	42, 62, 84, 108	0
16	AP	82/82 (100%)	0.97	14 (17%) 2 1	35, 46, 80, 103	0
16	CP	82/82 (100%)	1.59	20 (24%) 1 1	43, 61, 87, 105	0
17	AQ	80/80 (100%)	0.69	8 (10%) 9 5	30, 55, 85, 123	0
17	CQ	80/80 (100%)	1.63	25 (31%) 1 0	42, 69, 97, 108	0
18	AR	55/55 (100%)	0.70	6 (10%) 7 4	38, 51, 76, 113	0
18	CR	55/55 (100%)	0.94	9 (16%) 2 1	40, 54, 83, 113	0
19	AS	79/79 (100%)	0.90	12 (15%) 3 1	45, 66, 92, 97	0
19	CS	79/79 (100%)	4.05	58 (73%) 0 0	79, 98, 113, 126	0
20	AT	85/85 (100%)	0.73	7 (8%) 14 7	35, 48, 74, 115	0
20	CT	85/85 (100%)	2.33	41 (48%) 0 0	52, 69, 91, 98	0
21	AU	51/51 (100%)	1.52	13 (25%) 1 1	49, 70, 92, 105	0
21	CU	51/51 (100%)	1.07	9 (17%) 2 1	43, 67, 92, 107	0
22	BA	2897/2903 (99%)	0.31	121 (4%) 40 23	3, 18, 128, 196	0
22	DA	2897/2903 (99%)	0.58	194 (6%) 21 11	42, 82, 142, 182	0
23	BB	119/119 (100%)	-0.19	0 100 100	6, 26, 52, 94	0
23	DB	118/119 (99%)	0.40	5 (4%) 40 23	68, 109, 131, 143	0
24	BC	271/271 (100%)	0.07	3 (1%) 82 65	8, 24, 44, 65	0
24	DC	271/271 (100%)	1.29	62 (22%) 1 1	40, 60, 76, 84	0
25	BD	209/209 (100%)	0.09	0 100 100	4, 15, 42, 69	0
25	DD	209/209 (100%)	1.43	59 (28%) 1 0	47, 64, 83, 99	0
26	BE	201/201 (100%)	0.06	1 (0%) 91 81	4, 27, 54, 95	0
26	DE	201/201 (100%)	2.19	98 (48%) 0 0	38, 76, 96, 108	0
27	BF	177/177 (100%)	0.41	10 (5%) 28 15	23, 44, 86, 104	0
27	DF	177/177 (100%)	3.96	145 (81%) 0 0	79, 97, 113, 125	0
28	BG	176/176 (100%)	0.49	12 (6%) 20 11	21, 39, 66, 95	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DG	176/176 (100%)	2.49	101 (57%) 0 0	66, 85, 103, 117	0
29	BH	149/149 (100%)	4.67	113 (75%) 0 0	25, 102, 121, 129	0
29	DH	149/149 (100%)	2.46	74 (49%) 0 0	25, 92, 107, 115	0
30	BI	141/141 (100%)	3.88	95 (67%) 0 0	80, 104, 120, 136	0
30	DI	141/141 (100%)	5.77	129 (91%) 0 0	91, 110, 121, 124	0
31	BJ	142/142 (100%)	-0.05	1 (0%) 89 76	5, 12, 32, 54	0
31	DJ	142/142 (100%)	1.32	32 (22%) 1 1	49, 64, 80, 96	0
32	BK	122/122 (100%)	-0.06	1 (0%) 87 73	7, 16, 40, 68	0
32	DK	122/122 (100%)	1.42	36 (29%) 1 0	47, 60, 81, 95	0
33	BL	143/143 (100%)	0.14	3 (2%) 67 46	4, 26, 49, 80	0
33	DL	143/143 (100%)	2.50	77 (53%) 0 0	45, 72, 90, 111	0
34	BM	136/136 (100%)	-0.06	0 100 100	6, 16, 34, 93	0
34	DM	136/136 (100%)	1.31	38 (27%) 1 0	40, 64, 82, 110	0
35	BN	120/120 (100%)	-0.04	0 100 100	7, 13, 25, 70	0
35	DN	120/120 (100%)	1.89	41 (34%) 0 0	50, 71, 88, 109	0
36	BO	116/116 (100%)	0.13	1 (0%) 85 70	18, 29, 52, 59	0
36	DO	116/116 (100%)	3.15	78 (67%) 0 0	64, 86, 100, 113	0
37	BP	114/114 (100%)	0.09	2 (1%) 71 51	10, 22, 49, 73	0
37	DP	114/114 (100%)	1.44	37 (32%) 1 0	51, 66, 84, 91	0
38	BQ	117/117 (100%)	-0.03	0 100 100	3, 8, 21, 57	0
38	DQ	117/117 (100%)	1.51	40 (34%) 0 0	46, 65, 79, 83	0
39	BR	103/103 (100%)	-0.08	0 100 100	4, 15, 37, 64	0
39	DR	103/103 (100%)	2.04	45 (43%) 0 0	49, 72, 86, 96	0
40	BS	110/110 (100%)	0.03	1 (0%) 85 70	4, 9, 27, 89	0
40	DS	110/110 (100%)	2.52	63 (57%) 0 0	53, 69, 89, 97	0
41	BT	93/93 (100%)	0.59	8 (8%) 13 6	15, 28, 83, 100	0
41	DT	93/93 (100%)	3.21	66 (70%) 0 0	60, 79, 102, 111	0
42	BU	102/102 (100%)	0.17	4 (3%) 43 25	15, 32, 62, 95	0
42	DU	102/102 (100%)	4.19	75 (73%) 0 0	61, 82, 103, 109	0
43	BV	94/94 (100%)	0.03	2 (2%) 67 46	11, 24, 48, 59	0
43	DV	94/94 (100%)	1.14	19 (20%) 1 1	60, 78, 93, 98	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BW	76/76 (100%)	0.14	2 (2%) 59 38	10, 17, 37, 56	0
44	DW	75/76 (98%)	2.27	38 (50%) 0 0	49, 75, 86, 107	0
45	BX	77/77 (100%)	0.17	4 (5%) 31 17	11, 28, 53, 81	0
45	DX	77/77 (100%)	1.56	25 (32%) 1 0	49, 66, 84, 89	0
46	BY	63/63 (100%)	0.60	5 (7%) 15 8	21, 42, 71, 93	0
46	DY	63/63 (100%)	2.35	31 (49%) 0 0	63, 86, 95, 104	0
47	BZ	58/58 (100%)	-0.01	0 100 100	7, 11, 34, 40	0
47	DZ	58/58 (100%)	1.34	18 (31%) 1 0	50, 69, 82, 89	0
48	B0	56/56 (100%)	-0.09	0 100 100	4, 14, 38, 77	0
48	D0	56/56 (100%)	2.05	19 (33%) 0 0	49, 69, 90, 106	0
49	B1	50/50 (100%)	0.25	2 (4%) 42 25	19, 33, 61, 95	0
49	D1	50/50 (100%)	2.17	24 (48%) 0 0	63, 79, 91, 103	0
50	B2	46/46 (100%)	0.11	1 (2%) 65 44	8, 14, 22, 97	0
50	D2	46/46 (100%)	1.96	17 (36%) 0 0	47, 64, 78, 100	0
51	B3	64/64 (100%)	0.18	1 (1%) 74 55	10, 16, 26, 37	0
51	D3	64/64 (100%)	1.80	25 (39%) 0 0	53, 67, 79, 83	0
52	B4	38/38 (100%)	0.42	1 (2%) 59 38	13, 23, 38, 60	0
52	D4	38/38 (100%)	2.98	24 (63%) 0 0	56, 71, 84, 96	0
53	B5	191/228 (83%)	7.17	185 (96%) 0 0	71, 107, 119, 133	0
54	B6	2/8 (25%)	0.34	0 100 100	6, 6, 6, 8	0
54	D6	2/8 (25%)	1.07	1 (50%) 0 0	41, 41, 41, 44	0
All	All	20738/20810 (99%)	0.95	3532 (17%) 2 1	3, 61, 117, 196	0

All (3532) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
29	BH	96	THR	24.6
53	B5	111	PHE	23.5
30	DI	2	ALA	21.9
29	BH	113	SER	20.6
30	DI	3	LYS	20.6
22	BA	2104	C	20.2
22	BA	2184	A	19.0
53	B5	218	THR	18.9
42	DU	26	LYS	18.1

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Mol	Chain	Res	Type	RSRZ
22	BA	2135	A	17.6
48	D0	27	SER	17.2
53	B5	141	PRO	17.1
22	BA	2100	G	17.0
29	BH	97	ARG	16.6
53	B5	212	SER	16.6
30	BI	3	LYS	16.4
30	DI	6	GLN	16.3
30	BI	53	LEU	16.0
22	BA	2103	C	15.7
30	DI	68	THR	15.2
53	B5	55	SER	15.0
22	BA	2101	A	15.0
53	B5	204	GLY	14.8
1	CA	1536	C	14.8
7	CG	62	PHE	14.6
29	BH	115	VAL	14.6
53	B5	110	ASP	14.6
30	DI	67	PHE	14.4
22	BA	2159	G	14.0
22	BA	2158	A	13.9
30	DI	69	PHE	13.7
29	BH	54	LEU	13.7
53	B5	70	GLY	13.6
1	CA	1535	C	13.5
53	B5	200	HIS	13.4
33	DL	92	LEU	13.4
30	DI	4	LYS	13.3
53	B5	207	GLY	13.3
22	BA	2102	G	13.3
29	BH	95	GLY	13.2
53	B5	48	LEU	13.2
53	B5	157	ILE	13.2
29	BH	144	VAL	13.2
30	DI	60	THR	13.1
30	DI	34	ASN	12.9
10	AJ	102	LEU	12.8
30	BI	2	ALA	12.5
36	DO	40	ILE	12.1
53	B5	122	GLY	12.1
53	B5	67	HIS	12.0
53	B5	66	PRO	11.9

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Mol	Chain	Res	Type	RSRZ
53	B5	109	MET	11.8
53	B5	140	ASN	11.8
30	DI	58	VAL	11.7
22	BA	2117	A	11.7
36	DO	24	THR	11.6
53	B5	183	PRO	11.6
29	DH	79	THR	11.5
1	AA	1534	A	11.5
1	AA	1536	C	11.5
53	B5	77	ALA	11.5
19	CS	74	PHE	11.4
22	BA	2165	C	11.3
10	CJ	74	VAL	11.3
53	B5	107	GLY	11.2
42	DU	13	VAL	11.2
53	B5	95	VAL	11.2
29	DH	82	SER	11.2
29	DH	142	VAL	11.2
53	B5	217	THR	11.1
22	DA	1175	A	11.1
53	B5	131	ILE	11.1
53	B5	173	HIS	11.1
1	AA	1535	C	11.0
29	BH	112	LYS	11.0
30	BI	4	LYS	11.0
53	B5	145	THR	11.0
30	BI	87	LYS	10.9
42	DU	20	GLY	10.9
13	CM	85	CYS	10.9
53	B5	143	ALA	10.8
53	B5	97	GLY	10.8
53	B5	203	GLU	10.8
30	DI	31	GLN	10.8
42	DU	48	PRO	10.8
30	BI	39	CYS	10.7
30	DI	32	GLY	10.7
22	BA	2185	U	10.7
53	B5	52	PRO	10.6
22	BA	2144	G	10.6
29	BH	98	ASP	10.6
53	B5	84	ILE	10.6
22	BA	2127	G	10.6

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Mol	Chain	Res	Type	RSRZ
53	B5	202	PRO	10.6
27	DF	130	MET	10.6
22	BA	2145	C	10.6
17	AQ	83	VAL	10.5
13	CM	46	SER	10.5
30	BI	67	PHE	10.5
10	CJ	76	ILE	10.4
7	CG	18	PHE	10.4
42	DU	39	ILE	10.3
52	D4	9	LYS	10.3
22	BA	2140	G	10.3
2	AB	155	GLY	10.3
30	DI	7	ALA	10.3
27	DF	128	TYR	10.2
12	CL	124	ALA	10.2
24	DC	27	GLY	10.2
27	DF	117	LEU	10.2
29	BH	58	LEU	10.2
30	DI	5	VAL	10.2
22	BA	2178	C	10.2
46	DY	10	SER	10.1
14	CN	44	ALA	10.1
30	DI	53	LEU	10.1
30	BI	79	LEU	10.1
42	DU	12	ILE	10.1
53	B5	182	PRO	10.1
30	DI	35	ILE	10.0
30	DI	59	ILE	9.9
42	DU	78	GLY	9.9
19	CS	66	MET	9.9
53	B5	20	VAL	9.9
30	DI	48	SER	9.9
29	BH	124	THR	9.9
19	CS	24	GLU	9.8
42	DU	58	ILE	9.8
53	B5	76	LEU	9.8
53	B5	146	VAL	9.8
30	DI	54	PRO	9.8
22	BA	2136	G	9.8
9	CI	128	SER	9.7
29	BH	69	ALA	9.7
1	CA	1534	A	9.7

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Mol	Chain	Res	Type	RSRZ
41	DT	55	VAL	9.7
22	BA	2189	U	9.7
53	B5	133	GLY	9.6
29	BH	146	VAL	9.6
20	CT	4	ILE	9.6
22	BA	2148	G	9.6
53	B5	62	THR	9.6
2	AB	157	LEU	9.5
30	DI	13	VAL	9.5
17	CQ	4	LYS	9.5
53	B5	219	MET	9.5
29	BH	44	ILE	9.5
22	BA	2114	A	9.5
42	DU	40	ASN	9.4
22	BA	2174	C	9.4
30	DI	66	SER	9.4
27	DF	156	ILE	9.4
30	DI	62	TYR	9.3
30	DI	47	ASP	9.3
53	B5	63	VAL	9.3
30	DI	46	THR	9.3
52	D4	10	LEU	9.3
22	BA	2156	G	9.3
33	DL	144	GLU	9.3
22	BA	2115	G	9.2
41	DT	2	ILE	9.2
29	BH	55	GLU	9.2
30	BI	17	MET	9.1
1	CA	1539	C	9.1
53	B5	156	GLU	9.1
53	B5	142	LYS	9.1
29	DH	12	LEU	9.1
53	B5	108	TRP	9.0
1	CA	1032	G	9.0
53	B5	199	ALA	9.0
22	BA	2160	C	9.0
13	CM	77	ILE	9.0
22	BA	2106	U	9.0
22	BA	2112	G	9.0
53	B5	54	ARG	9.0
42	DU	36	VAL	9.0
30	BI	5	VAL	8.9

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Mol	Chain	Res	Type	RSRZ
30	BI	14	ALA	8.9
22	BA	2175	C	8.9
42	DU	60	GLU	8.9
30	DI	61	VAL	8.9
29	BH	80	ILE	8.9
30	BI	99	GLY	8.9
53	B5	79	ALA	8.9
30	BI	22	PRO	8.9
29	BH	136	SER	8.9
10	CJ	87	LEU	8.9
1	AA	1539	C	8.8
30	BI	41	ALA	8.8
49	D1	36	LEU	8.8
53	B5	223	VAL	8.8
53	B5	184	GLU	8.7
14	CN	27	LEU	8.7
22	DA	1537	G	8.7
24	DC	112	ALA	8.7
29	BH	87	GLU	8.7
1	AA	1538	C	8.7
22	BA	2147	A	8.7
53	B5	123	ALA	8.7
30	DI	20	PRO	8.7
41	DT	34	VAL	8.6
22	BA	2143	C	8.6
53	B5	94	TYR	8.6
53	B5	225	ILE	8.6
53	B5	45	HIS	8.6
53	B5	50	ILE	8.6
22	BA	2190	G	8.6
19	CS	71	LEU	8.5
30	DI	63	ALA	8.5
30	DI	70	VAL	8.5
29	BH	68	ARG	8.5
9	AI	43	THR	8.5
29	DH	144	VAL	8.5
9	CI	43	THR	8.5
42	DU	52	LEU	8.4
53	B5	104	ILE	8.4
28	DG	52	PHE	8.4
53	B5	159	ALA	8.4
41	DT	10	VAL	8.4

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Mol	Chain	Res	Type	RSRZ
28	DG	105	LEU	8.4
53	B5	132	LEU	8.4
53	B5	152	GLU	8.3
53	B5	134	PRO	8.3
33	DL	101	ILE	8.3
53	B5	69	LEU	8.3
10	CJ	71	LEU	8.3
10	CJ	72	ARG	8.3
53	B5	68	GLY	8.3
2	CB	136	MET	8.2
19	CS	38	SER	8.2
27	DF	120	LYS	8.2
53	B5	208	THR	8.2
4	CD	25	VAL	8.1
7	CG	66	LEU	8.1
22	BA	2139	U	8.1
30	BI	8	TYR	8.1
19	CS	42	PRO	8.1
22	BA	2183	A	8.1
29	BH	78	VAL	8.1
22	BA	2179	C	8.1
22	BA	2157	G	8.0
27	DF	100	PHE	8.0
53	B5	149	ASN	8.0
27	DF	21	ASN	8.0
53	B5	147	GLY	8.0
22	BA	2142	A	8.0
53	B5	194	ILE	8.0
30	BI	78	VAL	8.0
2	CB	9	MET	8.0
41	DT	15	HIS	8.0
53	B5	49	GLY	8.0
53	B5	158	LYS	8.0
27	DF	93	GLY	8.0
29	BH	119	ASN	8.0
22	BA	2186	G	8.0
53	B5	224	ARG	7.9
9	CI	129	LYS	7.9
22	BA	2125	G	7.9
27	DF	54	ALA	7.9
53	B5	89	GLU	7.9
19	CS	39	THR	7.9

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Mol	Chain	Res	Type	RSRZ
40	DS	84	ARG	7.9
34	DM	136	MET	7.9
30	BI	13	VAL	7.9
53	B5	160	GLY	7.9
30	BI	23	PRO	7.8
27	DF	67	ILE	7.8
53	B5	121	MET	7.8
2	CB	32	PHE	7.8
19	CS	41	PHE	7.8
7	CG	13	LEU	7.8
29	DH	90	LEU	7.8
7	CG	39	ALA	7.8
27	DF	65	PRO	7.8
4	AD	28	ILE	7.8
41	DT	43	ILE	7.8
53	B5	125	GLY	7.8
53	B5	165	ARG	7.8
22	BA	2154	A	7.8
30	DI	8	TYR	7.8
26	DE	186	VAL	7.8
10	CJ	16	ARG	7.7
29	BH	120	GLY	7.7
29	DH	124	THR	7.7
22	BA	2153	C	7.7
29	BH	67	ALA	7.7
53	B5	164	PHE	7.7
53	B5	209	PHE	7.7
42	DU	62	GLU	7.7
42	DU	79	LYS	7.7
40	DS	40	ASN	7.7
52	D4	8	LYS	7.7
29	BH	123	ARG	7.7
30	DI	49	ILE	7.7
53	B5	60	ARG	7.7
26	DE	17	THR	7.7
42	DU	50	PRO	7.7
22	BA	2124	G	7.6
22	BA	2152	G	7.6
10	CJ	77	VAL	7.6
36	DO	25	ARG	7.6
22	BA	2162	G	7.6
27	DF	85	ILE	7.6

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Mol	Chain	Res	Type	RSRZ
22	BA	2161	C	7.6
13	CM	12	HIS	7.6
7	AG	147	ALA	7.6
19	CS	13	LEU	7.6
44	DW	83	GLU	7.6
53	B5	78	ILE	7.6
29	DH	92	GLY	7.5
33	DL	3	LEU	7.5
30	DI	42	PHE	7.5
53	B5	191	ARG	7.5
53	B5	174	ALA	7.5
13	CM	45	ILE	7.5
53	B5	85	LYS	7.5
53	B5	98	GLU	7.5
50	D2	46	LYS	7.5
28	DG	9	VAL	7.5
29	BH	91	PHE	7.5
27	DF	154	ILE	7.5
53	B5	93	ASP	7.5
1	CA	94	G	7.5
50	D2	42	LEU	7.4
7	CG	88	PRO	7.4
2	CB	151	ILE	7.4
29	BH	116	ARG	7.4
30	DI	38	PHE	7.4
42	DU	25	VAL	7.4
28	DG	45	HIS	7.4
53	B5	96	GLY	7.4
22	BA	2099	U	7.4
30	DI	45	LYS	7.4
7	CG	16	PRO	7.4
49	D1	52	ALA	7.4
22	BA	2116	G	7.3
53	B5	28	ARG	7.3
25	DD	31	ALA	7.3
7	CG	151	PHE	7.3
53	B5	38	PHE	7.3
30	BI	11	LEU	7.3
22	BA	2177	C	7.3
29	BH	19	VAL	7.3
31	DJ	54	ILE	7.2
22	BA	2121	G	7.2

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Mol	Chain	Res	Type	RSRZ
22	BA	2123	G	7.2
53	B5	47	LYS	7.2
29	BH	101	ASP	7.2
14	CN	36	ALA	7.2
2	AB	156	GLY	7.2
22	DA	1536	C	7.1
42	DU	31	SER	7.1
9	CI	38	TYR	7.1
53	B5	216	THR	7.1
19	CS	69	HIS	7.1
31	DJ	119	PHE	7.1
20	CT	39	ILE	7.1
26	DE	119	ILE	7.1
42	DU	87	PHE	7.1
30	DI	14	ALA	7.1
18	AR	20	GLU	7.1
16	CP	39	PHE	7.1
10	CJ	11	LYS	7.1
30	BI	55	ILE	7.1
19	CS	44	MET	7.1
27	DF	32	GLU	7.1
13	CM	40	ALA	7.0
53	B5	53	ARG	7.0
22	BA	2163	A	7.0
36	DO	64	TYR	7.0
29	BH	121	VAL	7.0
30	BI	68	THR	7.0
22	BA	2169	A	7.0
22	BA	2182	U	7.0
27	DF	129	SER	7.0
13	CM	47	GLU	7.0
42	DU	27	ASN	7.0
10	CJ	41	PRO	7.0
53	B5	65	LEU	7.0
53	B5	148	PHE	7.0
30	DI	15	ALA	6.9
30	DI	30	GLN	6.9
27	DF	20	PHE	6.9
30	BI	135	SER	6.9
53	B5	75	VAL	6.9
46	DY	40	SER	6.9
29	DH	128	HIS	6.9

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Mol	Chain	Res	Type	RSRZ
42	DU	80	ALA	6.9
27	DF	8	TYR	6.9
42	DU	35	ILE	6.9
40	DS	92	ARG	6.9
9	CI	130	ARG	6.9
19	CS	49	ILE	6.9
49	D1	53	LYS	6.9
10	CJ	10	LEU	6.9
53	B5	150	ILE	6.9
36	DO	26	LEU	6.8
5	AE	159	LYS	6.8
7	CG	17	LYS	6.8
22	BA	2107	G	6.8
30	DI	11	LEU	6.8
27	DF	155	THR	6.8
30	DI	121	ASP	6.8
8	CH	2	SER	6.8
13	CM	48	LEU	6.8
25	DD	6	GLY	6.8
29	BH	142	VAL	6.8
19	CS	43	ASN	6.8
22	BA	2113	U	6.8
53	B5	106	ASP	6.8
13	CM	32	ALA	6.8
53	B5	211	ARG	6.8
13	CM	98	ARG	6.8
25	DD	55	LYS	6.8
39	DR	19	THR	6.8
53	B5	83	LYS	6.8
10	CJ	26	VAL	6.7
27	DF	138	PHE	6.7
29	BH	148	ALA	6.7
53	B5	59	VAL	6.7
13	CM	83	LEU	6.7
39	DR	39	LEU	6.7
22	BA	2176	A	6.7
53	B5	81	GLY	6.7
22	DA	1093	G	6.7
7	CG	12	ILE	6.7
27	DF	60	ILE	6.7
53	B5	198	GLU	6.7
27	DF	159	THR	6.7

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Mol	Chain	Res	Type	RSRZ
46	DY	33	ALA	6.7
30	DI	25	GLY	6.6
35	DN	29	VAL	6.6
29	BH	11	ASN	6.6
42	DU	43	LYS	6.6
22	BA	2120	G	6.6
27	DF	114	PHE	6.6
14	CN	11	VAL	6.6
19	CS	60	VAL	6.6
53	B5	39	ASP	6.6
29	DH	81	ALA	6.6
34	DM	56	ALA	6.6
36	DO	106	LEU	6.6
13	CM	63	PHE	6.6
7	CG	148	ASN	6.6
41	DT	36	LYS	6.6
35	DN	28	LEU	6.6
9	CI	90	TYR	6.6
42	DU	77	THR	6.6
7	CG	87	VAL	6.6
22	BA	2168	G	6.6
33	DL	19	LEU	6.6
30	DI	44	ALA	6.6
33	DL	89	VAL	6.5
22	BA	2134	A	6.5
6	CF	39	LEU	6.5
26	DE	164	LEU	6.5
30	BI	100	LYS	6.5
22	BA	2138	G	6.5
19	CS	37	ARG	6.5
22	BA	2141	G	6.5
30	BI	38	PHE	6.5
53	B5	41	THR	6.5
29	BH	109	GLU	6.5
50	D2	33	ARG	6.5
53	B5	161	ARG	6.5
53	B5	46	ALA	6.5
53	B5	126	SER	6.5
30	BI	52	GLY	6.5
30	DI	80	LEU	6.5
42	DU	30	SER	6.5
17	CQ	78	VAL	6.5

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Mol	Chain	Res	Type	RSRZ
27	DF	23	ASN	6.5
45	DX	11	ARG	6.4
29	BH	118	PRO	6.4
30	BI	69	PHE	6.4
16	CP	47	GLU	6.4
1	AA	1018	G	6.4
53	B5	19	LYS	6.4
42	DU	71	ALA	6.4
53	B5	192	ALA	6.4
53	B5	130	ARG	6.4
53	B5	169	THR	6.4
30	BI	12	GLN	6.4
41	DT	83	ALA	6.4
16	AP	80	LYS	6.4
7	CG	20	SER	6.4
28	DG	32	GLU	6.4
13	CM	86	TYR	6.4
42	DU	33	LYS	6.4
19	CS	11	ILE	6.4
53	B5	72	GLN	6.4
53	B5	82	GLU	6.4
20	CT	24	ARG	6.4
28	DG	62	TRP	6.3
30	DI	78	VAL	6.3
53	B5	210	LEU	6.3
1	CA	1538	C	6.3
3	CC	193	TYR	6.3
53	B5	124	VAL	6.3
22	DA	1870	C	6.3
53	B5	87	ALA	6.3
50	B2	46	LYS	6.3
13	CM	84	GLY	6.3
14	CN	48	LEU	6.3
29	BH	85	GLY	6.3
45	DX	49	LEU	6.3
29	DH	120	GLY	6.3
53	B5	215	VAL	6.3
26	DE	118	LEU	6.3
33	DL	106	GLU	6.3
27	DF	132	VAL	6.2
29	BH	72	ILE	6.2
27	DF	176	PRO	6.2

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Mol	Chain	Res	Type	RSRZ
2	CB	34	ALA	6.2
27	DF	66	LEU	6.2
1	CA	1031	C	6.2
7	CG	15	ASP	6.2
30	DI	24	VAL	6.2
11	AK	126	LYS	6.2
22	DA	2124	G	6.2
27	DF	77	PHE	6.2
51	D3	14	PHE	6.2
2	CB	67	ILE	6.2
27	DF	152	LEU	6.2
41	DT	71	GLY	6.2
36	DO	103	VAL	6.2
36	DO	2	ASP	6.2
19	CS	58	VAL	6.2
29	DH	130	VAL	6.2
7	CG	23	LEU	6.2
9	CI	39	PHE	6.2
20	CT	38	ALA	6.2
29	BH	86	ASP	6.2
30	DI	64	ASP	6.2
35	DN	25	ALA	6.2
30	BI	95	LYS	6.2
40	DS	36	LEU	6.1
33	DL	121	THR	6.1
19	CS	30	PRO	6.1
9	CI	58	VAL	6.1
43	DV	43	ASP	6.1
2	AB	9	MET	6.1
30	DI	17	MET	6.1
12	AL	25	GLU	6.1
29	BH	102	ALA	6.1
43	DV	94	ALA	6.1
53	B5	27	ALA	6.1
30	DI	139	VAL	6.1
27	DF	13	VAL	6.1
28	DG	87	LEU	6.1
22	BA	2150	C	6.1
28	DG	33	LEU	6.1
39	DR	96	VAL	6.1
30	DI	96	ASP	6.1
17	AQ	20	SER	6.1

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Mol	Chain	Res	Type	RSRZ
22	BA	2164	C	6.0
30	BI	96	ASP	6.0
53	B5	56	ASP	6.0
27	DF	14	LYS	6.0
7	AG	88	PRO	6.0
36	DO	85	LYS	6.0
29	DH	100	ALA	6.0
27	DF	68	THR	6.0
19	CS	29	LYS	6.0
33	DL	77	ILE	6.0
10	CJ	45	ARG	6.0
22	BA	2166	U	6.0
27	DF	175	PHE	6.0
36	DO	117	PHE	6.0
27	DF	57	LEU	6.0
10	CJ	99	GLN	6.0
30	BI	71	THR	6.0
41	DT	73	ARG	6.0
30	DI	85	GLY	6.0
3	CC	37	PHE	6.0
13	CM	30	SER	5.9
7	CG	49	THR	5.9
27	DF	157	THR	5.9
7	CG	53	ARG	5.9
19	CS	51	VAL	5.9
35	DN	24	MET	5.9
22	DA	1535	A	5.9
53	B5	214	TYR	5.9
30	DI	126	THR	5.9
7	CG	152	ALA	5.9
18	CR	20	GLU	5.9
36	DO	92	PHE	5.9
53	B5	181	PHE	5.9
30	DI	120	ALA	5.9
42	DU	51	ALA	5.9
26	DE	144	GLU	5.9
1	CA	1537	U	5.9
30	BI	133	ALA	5.9
53	B5	151	GLY	5.9
35	DN	111	ALA	5.9
36	DO	107	ALA	5.9
53	B5	74	ARG	5.9

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Mol	Chain	Res	Type	RSRZ
40	DS	20	VAL	5.9
53	B5	166	ASN	5.9
48	D0	57	LYS	5.9
22	BA	2172	U	5.9
9	CI	68	LYS	5.9
30	BI	138	LEU	5.9
46	DY	36	GLN	5.9
53	B5	61	GLY	5.9
46	BY	63	ALA	5.9
29	DH	83	LYS	5.8
27	DF	86	GLY	5.8
32	DK	81	GLY	5.8
36	DO	60	GLU	5.8
30	DI	112	THR	5.8
39	DR	29	THR	5.8
14	CN	35	ASN	5.8
30	DI	140	VAL	5.8
30	DI	21	SER	5.8
29	BH	47	PHE	5.8
29	DH	93	SER	5.8
2	AB	131	LYS	5.8
27	DF	113	ASP	5.8
28	DG	6	LYS	5.8
30	DI	43	ASN	5.8
13	CM	95	LEU	5.8
28	BG	166	ASP	5.8
13	CM	80	LEU	5.8
53	B5	105	LEU	5.8
27	DF	25	VAL	5.8
30	BI	98	VAL	5.8
19	CS	23	VAL	5.7
27	DF	177	PHE	5.7
35	DN	63	ARG	5.7
1	CA	999	C	5.7
30	BI	92	LYS	5.7
42	DU	61	LYS	5.7
29	BH	130	VAL	5.7
26	DE	173	THR	5.7
1	CA	82	G	5.7
29	BH	105	ALA	5.7
26	DE	138	LEU	5.7
49	D1	47	VAL	5.7

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Mol	Chain	Res	Type	RSRZ
29	BH	139	PHE	5.7
29	BH	89	LYS	5.7
53	B5	24	ASP	5.7
19	CS	16	LEU	5.7
30	DI	12	GLN	5.7
22	BA	2126	A	5.7
40	DS	37	THR	5.7
22	BA	2173	A	5.7
14	CN	51	LEU	5.7
30	DI	79	LEU	5.7
44	DW	72	LYS	5.7
25	DD	60	VAL	5.7
36	DO	16	ARG	5.7
41	BT	2	ILE	5.7
7	CG	61	ALA	5.7
2	CB	213	TYR	5.7
7	CG	118	LEU	5.7
53	B5	23	ILE	5.7
30	BI	114	ALA	5.7
53	B5	73	VAL	5.6
41	DT	6	ARG	5.6
22	DA	2112	G	5.6
53	B5	179	ALA	5.6
19	CS	76	PRO	5.6
40	DS	71	VAL	5.6
41	DT	16	VAL	5.6
27	DF	76	GLY	5.6
24	DC	239	ASN	5.6
26	DE	175	ILE	5.6
19	CS	12	ASP	5.6
28	DG	103	ILE	5.6
41	DT	50	LEU	5.6
29	DH	112	LYS	5.6
42	DU	21	LYS	5.6
19	CS	61	PHE	5.6
19	CS	64	ASP	5.6
22	BA	1847	A	5.6
42	DU	89	ASP	5.6
30	DI	9	VAL	5.6
30	DI	76	ALA	5.6
53	B5	90	ALA	5.6
10	CJ	89	ARG	5.6

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Mol	Chain	Res	Type	RSRZ
14	CN	34	VAL	5.5
30	DI	39	CYS	5.5
36	DO	61	GLN	5.5
53	B5	137	LEU	5.5
27	DF	122	PHE	5.5
33	DL	71	ALA	5.5
29	BH	129	GLU	5.5
50	D2	1	MET	5.5
2	CB	33	GLY	5.5
27	DF	131	GLY	5.5
33	DL	107	PHE	5.5
24	DC	49	ILE	5.5
33	DL	142	ILE	5.5
42	DU	72	ILE	5.5
1	CA	209	U	5.5
13	CM	89	LEU	5.5
26	DE	143	LEU	5.5
29	BH	122	LEU	5.5
35	DN	26	GLY	5.5
40	DS	110	ARG	5.5
27	DF	172	ALA	5.5
4	AD	36	GLN	5.5
20	CT	65	GLY	5.5
10	CJ	100	ILE	5.5
17	CQ	50	ASN	5.5
28	DG	20	ASN	5.5
53	B5	58	ASN	5.5
21	AU	35	ARG	5.5
1	AA	78	A	5.5
30	DI	89	GLY	5.5
20	CT	3	ASN	5.5
33	DL	15	ALA	5.4
44	DW	53	CYS	5.4
22	BA	2098	U	5.4
32	DK	111	LYS	5.4
26	DE	153	LEU	5.4
30	BI	61	VAL	5.4
30	DI	114	ALA	5.4
24	DC	249	GLY	5.4
27	DF	133	ARG	5.4
29	BH	17	ASP	5.4
19	CS	65	GLU	5.4

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Mol	Chain	Res	Type	RSRZ
13	CM	33	ILE	5.4
29	DH	78	VAL	5.4
7	AG	5	ARG	5.4
27	DF	142	ASP	5.4
13	CM	94	GLY	5.4
29	DH	143	ILE	5.4
52	D4	1	MET	5.4
1	CA	1020	G	5.4
19	CS	25	SER	5.4
30	DI	33	VAL	5.4
41	DT	1	MET	5.4
2	CB	206	ALA	5.4
28	DG	40	ALA	5.4
30	DI	133	ALA	5.4
22	BA	2105	U	5.4
22	BA	2155	U	5.4
22	BA	2193	G	5.4
53	B5	153	ILE	5.4
9	CI	67	VAL	5.3
29	BH	81	ALA	5.3
9	AI	130	ARG	5.3
53	B5	64	SER	5.3
33	DL	82	LEU	5.3
13	CM	68	ASP	5.3
13	CM	39	ILE	5.3
29	BH	143	ILE	5.3
30	DI	22	PRO	5.3
34	DM	99	GLY	5.3
16	CP	80	LYS	5.3
26	DE	55	SER	5.3
27	DF	165	GLU	5.3
29	BH	117	LEU	5.3
48	D0	39	LEU	5.3
13	CM	109	ARG	5.3
29	BH	93	SER	5.3
7	CG	68	ASN	5.3
13	CM	43	VAL	5.3
39	DR	88	GLY	5.3
53	B5	170	GLY	5.3
27	DF	9	LYS	5.3
22	DA	2313	C	5.3
40	DS	45	VAL	5.3

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Mol	Chain	Res	Type	RSRZ
29	DH	149	GLU	5.3
40	DS	2	GLU	5.3
30	BI	6	GLN	5.3
22	DA	613	A	5.3
33	DL	108	ALA	5.3
48	D0	55	ILE	5.3
10	CJ	27	GLU	5.3
7	CG	72	THR	5.3
10	CJ	8	ILE	5.3
2	CB	129	LEU	5.3
26	DE	165	HIS	5.3
7	CG	41	SER	5.3
19	CS	63	THR	5.2
49	D1	21	TYR	5.2
42	DU	86	ARG	5.2
2	AB	135	LEU	5.2
53	B5	187	ALA	5.2
21	CU	38	TYR	5.2
27	DF	153	ASP	5.2
33	DL	81	ASP	5.2
29	BH	90	LEU	5.2
40	DS	46	LEU	5.2
29	BH	135	HIS	5.2
7	CG	4	ARG	5.2
25	DD	209	ALA	5.2
35	DN	76	VAL	5.2
7	CG	85	TYR	5.2
21	AU	38	TYR	5.2
30	DI	129	ILE	5.2
53	B5	193	PHE	5.2
7	CG	139	GLU	5.2
10	CJ	73	LEU	5.2
13	CM	38	GLY	5.2
7	CG	14	PRO	5.2
13	CM	64	VAL	5.2
26	DE	172	ALA	5.2
22	BA	2181	U	5.2
53	B5	57	GLN	5.2
27	DF	108	VAL	5.2
41	DT	33	LYS	5.2
2	CB	148	LEU	5.2
30	BI	62	TYR	5.2

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Mol	Chain	Res	Type	RSRZ
33	DL	57	LEU	5.2
24	DC	242	LYS	5.2
53	B5	155	ARG	5.2
22	BA	2171	A	5.2
38	DQ	23	GLY	5.2
24	DC	106	ALA	5.2
3	CC	196	ILE	5.2
30	DI	86	ILE	5.2
27	DF	69	LYS	5.2
7	AG	75	VAL	5.2
36	DO	90	VAL	5.2
36	DO	87	ILE	5.1
29	BH	110	VAL	5.1
29	BH	79	THR	5.1
29	DH	104	THR	5.1
19	CS	72	GLY	5.1
41	DT	75	GLY	5.1
47	DZ	9	GLN	5.1
26	DE	148	ILE	5.1
27	DF	112	ARG	5.1
41	DT	32	LEU	5.1
27	DF	118	SER	5.1
7	CG	52	GLN	5.1
27	DF	51	ASP	5.1
13	CM	29	ARG	5.1
53	B5	144	GLY	5.1
53	B5	162	ILE	5.1
53	B5	172	ILE	5.1
3	CC	144	LEU	5.1
29	DH	117	LEU	5.1
29	DH	18	GLN	5.1
10	CJ	67	ILE	5.1
12	AL	124	ALA	5.1
30	DI	41	ALA	5.1
28	DG	168	VAL	5.1
30	BI	30	GLN	5.1
44	DW	52	GLY	5.1
31	DJ	140	LEU	5.1
29	BH	59	ALA	5.1
10	CJ	66	GLU	5.1
53	B5	201	LYS	5.1
28	DG	157	TYR	5.1

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Mol	Chain	Res	Type	RSRZ
29	BH	128	HIS	5.1
1	CA	1312	G	5.1
27	DF	28	VAL	5.1
38	DQ	29	SER	5.0
27	DF	169	LEU	5.0
13	CM	96	PRO	5.0
22	BA	2149	U	5.0
28	DG	10	VAL	5.0
45	DX	47	VAL	5.0
1	CA	1021	A	5.0
14	CN	24	ARG	5.0
29	BH	5	LEU	5.0
51	D3	57	LEU	5.0
27	DF	40	VAL	5.0
7	CG	111	ARG	5.0
14	CN	32	SER	5.0
20	CT	85	LYS	5.0
53	B5	221	PRO	5.0
29	BH	145	ASN	5.0
40	DS	19	LEU	5.0
22	DA	549	G	5.0
10	CJ	39	PRO	5.0
30	DI	98	VAL	5.0
30	DI	130	GLU	5.0
13	AM	114	LYS	5.0
30	BI	40	LYS	5.0
24	DC	47	GLY	5.0
9	AI	17	ALA	5.0
28	DG	2	SER	5.0
36	DO	37	ALA	5.0
45	DX	78	TYR	5.0
26	DE	168	ASP	5.0
35	DN	120	GLU	5.0
24	DC	26	LYS	5.0
2	CB	114	LEU	5.0
13	CM	55	THR	5.0
27	DF	22	TYR	5.0
30	BI	54	PRO	5.0
53	B5	80	LYS	5.0
53	B5	99	GLU	5.0
20	CT	25	ARG	5.0
46	DY	37	LEU	5.0

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Mol	Chain	Res	Type	RSRZ
13	CM	10	PRO	5.0
52	D4	15	LYS	5.0
31	DJ	118	MET	4.9
14	CN	45	VAL	4.9
53	B5	42	VAL	4.9
8	CH	122	GLY	4.9
10	CJ	90	LEU	4.9
44	DW	25	ARG	4.9
53	B5	43	GLU	4.9
53	B5	195	ARG	4.9
7	CG	133	THR	4.9
22	BA	2122	U	4.9
27	DF	170	LEU	4.9
14	CN	4	GLN	4.9
28	DG	43	VAL	4.9
14	CN	20	TYR	4.9
33	DL	30	THR	4.9
40	DS	3	THR	4.9
6	CF	91	ARG	4.9
7	CG	144	MET	4.9
22	BA	2130	U	4.9
42	DU	42	VAL	4.9
30	BI	103	ARG	4.9
40	DS	38	TYR	4.9
30	BI	66	SER	4.9
53	B5	154	ILE	4.9
9	CI	44	ALA	4.9
29	BH	84	ALA	4.9
2	CB	132	LYS	4.9
3	CC	127	ARG	4.9
4	CD	24	GLY	4.9
19	CS	15	LEU	4.9
22	BA	2110	G	4.9
28	DG	148	LEU	4.9
41	DT	58	VAL	4.9
41	DT	62	VAL	4.9
10	CJ	80	THR	4.9
16	CP	17	TYR	4.9
30	DI	56	PRO	4.9
51	D3	61	CYS	4.9
25	DD	97	SER	4.9
31	DJ	47	HIS	4.9

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Mol	Chain	Res	Type	RSRZ
31	DJ	142	ILE	4.9
27	DF	164	GLU	4.9
41	DT	76	ARG	4.8
28	DG	50	LEU	4.8
29	DH	15	LEU	4.8
30	DI	19	ASN	4.8
27	DF	107	ALA	4.8
48	D0	28	LEU	4.8
32	DK	89	ASN	4.8
40	DS	87	PRO	4.8
7	CG	134	ALA	4.8
13	CM	74	SER	4.8
29	BH	82	SER	4.8
27	DF	87	CYS	4.8
35	DN	83	LEU	4.8
42	DU	47	LYS	4.8
52	D4	33	HIS	4.8
27	DF	18	THR	4.8
1	CA	1314	C	4.8
22	BA	138	U	4.8
44	DW	63	ALA	4.8
53	B5	136	GLY	4.8
27	DF	121	SER	4.8
1	CA	207	C	4.8
14	CN	42	TRP	4.8
28	DG	59	ALA	4.8
13	CM	8	ASN	4.8
51	D3	58	VAL	4.8
1	CA	1540	U	4.8
46	DY	13	GLU	4.8
27	DF	61	SER	4.8
33	DL	68	SER	4.8
29	BH	137	GLU	4.8
10	CJ	17	LEU	4.8
14	CN	21	PHE	4.8
29	DH	80	ILE	4.8
21	CU	45	ARG	4.8
36	DO	39	VAL	4.8
30	DI	142	ASP	4.8
53	B5	88	GLU	4.8
1	AA	86	G	4.8
1	AA	1020	G	4.8

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Mol	Chain	Res	Type	RSRZ
25	DD	75	ALA	4.8
44	DW	73	GLY	4.8
3	CC	167	TRP	4.8
26	DE	155	GLU	4.8
30	BI	81	LYS	4.7
14	CN	63	ARG	4.7
10	CJ	94	ALA	4.7
22	BA	2128	G	4.7
53	B5	120	VAL	4.7
20	AT	36	TYR	4.7
33	DL	70	LYS	4.7
2	AB	139	ARG	4.7
29	BH	149	GLU	4.7
42	DU	49	VAL	4.7
10	CJ	15	HIS	4.7
13	CM	113	ARG	4.7
32	DK	82	ASN	4.7
30	BI	83	ALA	4.7
36	DO	66	GLY	4.7
30	DI	36	MET	4.7
24	DC	28	LYS	4.7
19	AS	9	PRO	4.7
3	CC	62	LYS	4.7
29	BH	20	ASN	4.7
13	CM	36	ALA	4.7
30	DI	110	ALA	4.7
52	D4	6	SER	4.7
29	BH	61	VAL	4.7
53	B5	22	THR	4.7
53	B5	213	VAL	4.7
9	CI	98	LEU	4.7
10	CJ	19	ASP	4.7
15	CO	17	ARG	4.7
30	DI	65	ARG	4.7
31	DJ	74	TYR	4.7
9	CI	83	ILE	4.7
1	AA	1030	U	4.7
30	DI	74	PRO	4.7
11	AK	14	LYS	4.7
30	BI	21	SER	4.7
26	DE	102	ARG	4.7
29	DH	125	THR	4.7

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Mol	Chain	Res	Type	RSRZ
14	CN	33	ASP	4.7
14	CN	57	PRO	4.7
19	CS	40	ILE	4.7
3	CC	173	VAL	4.7
42	DU	70	VAL	4.7
44	DW	38	VAL	4.7
30	DI	99	GLY	4.7
9	CI	20	PHE	4.6
26	DE	91	ASP	4.6
30	DI	28	LEU	4.6
49	D1	24	THR	4.6
47	DZ	7	ILE	4.6
12	CL	25	GLU	4.6
24	DC	245	VAL	4.6
17	CQ	8	LEU	4.6
29	BH	38	PRO	4.6
33	DL	132	ARG	4.6
30	BI	101	ILE	4.6
27	DF	82	GLY	4.6
41	DT	49	LYS	4.6
41	DT	74	ILE	4.6
35	DN	47	VAL	4.6
22	DA	2174	C	4.6
29	BH	132	PHE	4.6
22	BA	2188	U	4.6
3	CC	159	GLY	4.6
30	DI	131	GLY	4.6
14	CN	52	PRO	4.6
34	DM	126	ILE	4.6
22	BA	2191	A	4.6
30	DI	106	LEU	4.6
53	B5	197	LEU	4.6
13	CM	2	ALA	4.6
1	CA	1044	A	4.6
7	CG	59	LEU	4.6
14	AN	51	LEU	4.6
21	AU	24	GLU	4.6
22	BA	2118	U	4.6
27	DF	119	ALA	4.6
29	BH	14	SER	4.6
20	AT	68	HIS	4.6
7	CG	91	VAL	4.6

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Mol	Chain	Res	Type	RSRZ
3	CC	79	LYS	4.6
22	DA	2903	U	4.6
22	DA	1073	A	4.6
36	DO	62	LEU	4.6
14	CN	2	ALA	4.6
32	DK	60	ALA	4.6
28	DG	131	ILE	4.6
24	DC	103	TYR	4.6
51	D3	64	TYR	4.6
48	D0	34	SER	4.5
52	D4	16	ILE	4.5
28	DG	102	VAL	4.5
16	CP	60	TRP	4.5
28	DG	84	THR	4.5
26	DE	24	ASN	4.5
7	CG	131	LYS	4.5
1	AA	990	C	4.5
35	DN	119	SER	4.5
7	CG	27	VAL	4.5
35	DN	102	PHE	4.5
27	DF	161	LYS	4.5
1	AA	1017	U	4.5
27	DF	62	GLY	4.5
22	DA	2300	C	4.5
36	DO	52	SER	4.5
5	CE	124	LEU	4.5
7	AG	151	PHE	4.5
14	AN	21	PHE	4.5
42	DU	76	ALA	4.5
30	DI	52	GLY	4.5
13	CM	31	LYS	4.5
19	CS	28	LYS	4.5
13	CM	101	ARG	4.5
22	BA	885	C	4.5
53	B5	180	SER	4.5
2	CB	212	LEU	4.5
39	DR	35	PHE	4.5
46	DY	41	HIS	4.5
29	BH	74	ALA	4.5
41	DT	35	ALA	4.5
29	BH	92	GLY	4.5
48	D0	38	HIS	4.5

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Mol	Chain	Res	Type	RSRZ
53	B5	92	ALA	4.5
3	CC	195	VAL	4.5
48	D0	3	VAL	4.5
30	BI	91	GLY	4.5
39	DR	50	GLY	4.5
53	B5	86	GLU	4.5
14	CN	31	ILE	4.5
14	CN	14	VAL	4.5
11	CK	126	LYS	4.5
14	AN	52	PRO	4.5
27	DF	78	LYS	4.5
40	DS	49	LYS	4.5
14	AN	30	ILE	4.5
7	CG	75	VAL	4.5
16	CP	45	GLU	4.5
30	DI	75	PRO	4.5
10	CJ	97	ASP	4.4
17	CQ	23	VAL	4.4
28	DG	86	LYS	4.4
14	CN	50	THR	4.4
29	BH	75	LEU	4.4
29	BH	106	ALA	4.4
37	DP	108	ALA	4.4
41	DT	8	LEU	4.4
7	CG	37	SER	4.4
30	DI	82	LYS	4.4
27	DF	149	VAL	4.4
8	CH	59	LEU	4.4
13	AM	19	LEU	4.4
14	CN	46	LEU	4.4
44	DW	62	LYS	4.4
28	BG	26	ILE	4.4
29	BH	3	VAL	4.4
52	D4	25	VAL	4.4
22	DA	2158	A	4.4
30	DI	77	ALA	4.4
10	CJ	9	ARG	4.4
24	DC	18	LYS	4.4
30	DI	88	SER	4.4
16	CP	52	LEU	4.4
30	BI	15	ALA	4.4
30	DI	37	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
33	DL	85	VAL	4.4
36	DO	63	LYS	4.4
22	BA	2133	G	4.4
19	CS	31	LEU	4.4
36	DO	115	LEU	4.4
42	DU	38	GLY	4.4
22	DA	2126	A	4.4
3	CC	109	PRO	4.4
25	DD	25	THR	4.4
14	CN	30	ILE	4.4
39	DR	101	ILE	4.4
30	DI	97	LYS	4.4
37	DP	111	LYS	4.4
53	B5	103	LYS	4.4
19	CS	67	VAL	4.4
33	DL	122	VAL	4.4
7	CG	51	ALA	4.4
53	B5	26	ALA	4.4
22	BA	715	A	4.4
32	DK	106	GLU	4.4
53	B5	40	GLU	4.4
16	CP	51	ARG	4.4
22	BA	1175	A	4.4
2	CB	217	VAL	4.4
7	AG	69	VAL	4.4
7	CG	19	GLY	4.4
29	BH	29	PHE	4.4
37	DP	43	PHE	4.4
19	AS	3	ARG	4.3
39	DR	59	ILE	4.3
10	AJ	74	VAL	4.3
21	AU	32	VAL	4.3
36	DO	65	THR	4.3
41	DT	67	VAL	4.3
46	DY	16	THR	4.3
10	AJ	89	ARG	4.3
25	DD	186	LEU	4.3
27	DF	36	LEU	4.3
35	DN	46	ARG	4.3
13	CM	56	LEU	4.3
8	AH	2	SER	4.3
19	CS	75	ALA	4.3

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Mol	Chain	Res	Type	RSRZ
20	CT	77	ALA	4.3
29	BH	10	ALA	4.3
13	CM	87	ARG	4.3
27	DF	111	ILE	4.3
39	DR	24	LYS	4.3
30	BI	47	ASP	4.3
39	DR	63	VAL	4.3
37	DP	25	THR	4.3
25	DD	105	LYS	4.3
51	D3	49	MET	4.3
53	B5	101	ILE	4.3
30	BI	42	PHE	4.3
28	DG	92	VAL	4.3
29	BH	147	VAL	4.3
18	CR	74	HIS	4.3
30	DI	18	ALA	4.3
27	DF	35	THR	4.3
3	CC	172	ARG	4.3
22	DA	1170	C	4.3
27	DF	10	ASP	4.3
39	DR	32	THR	4.3
41	DT	30	ILE	4.3
42	DU	5	ILE	4.3
10	CJ	75	ASP	4.3
22	DA	1067	A	4.3
22	DA	2150	C	4.3
27	DF	102	ARG	4.3
30	DI	95	LYS	4.3
29	DH	140	ALA	4.3
33	DL	124	GLY	4.3
28	DG	166	ASP	4.3
33	DL	126	ARG	4.3
40	DS	16	LYS	4.3
36	DO	38	GLN	4.3
36	DO	93	ASP	4.3
1	CA	1302	C	4.3
26	DE	134	LEU	4.3
28	DG	167	GLU	4.3
14	CN	19	LYS	4.3
21	CU	47	ARG	4.3
29	BH	40	THR	4.3
37	DP	65	SER	4.3

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Mol	Chain	Res	Type	RSRZ
2	AB	90	PHE	4.3
30	BI	116	ASP	4.3
36	DO	19	GLN	4.3
53	B5	128	LEU	4.3
39	DR	37	GLU	4.3
2	CB	40	ILE	4.2
40	DS	103	ILE	4.2
50	D2	43	THR	4.2
28	DG	151	TYR	4.2
29	BH	133	GLN	4.2
36	DO	74	VAL	4.2
26	DE	128	ALA	4.2
7	CG	130	ASN	4.2
21	AU	4	ILE	4.2
27	DF	79	ILE	4.2
48	D0	23	THR	4.2
42	BU	53	ASN	4.2
1	CA	1325	C	4.2
39	DR	92	TRP	4.2
40	DS	66	ILE	4.2
25	DD	38	LYS	4.2
42	DU	59	VAL	4.2
28	DG	57	GLY	4.2
32	DK	112	PHE	4.2
36	DO	13	ARG	4.2
47	DZ	56	LYS	4.2
9	CI	112	GLU	4.2
30	DI	57	VAL	4.2
32	DK	69	VAL	4.2
28	DG	25	THR	4.2
13	AM	115	PRO	4.2
22	BA	2111	U	4.2
7	CG	129	GLU	4.2
6	CF	66	ALA	4.2
20	CT	72	ALA	4.2
25	DD	26	VAL	4.2
27	DF	90	THR	4.2
14	CN	47	LYS	4.2
15	AO	89	ARG	4.2
35	DN	118	ARG	4.2
38	DQ	84	LYS	4.2
19	CS	52	HIS	4.2

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Mol	Chain	Res	Type	RSRZ
19	AS	49	ILE	4.2
39	DR	75	VAL	4.2
41	BT	69	ARG	4.2
53	B5	135	ARG	4.2
32	DK	65	THR	4.2
22	BA	2131	U	4.2
22	DA	896	A	4.2
41	DT	87	LEU	4.2
27	DF	116	GLY	4.2
30	DI	71	THR	4.2
46	DY	59	GLU	4.2
29	DH	47	PHE	4.2
29	DH	132	PHE	4.2
37	DP	115	ASN	4.2
22	DA	344	A	4.2
7	AG	109	ARG	4.2
25	DD	96	ILE	4.2
28	DG	177	LYS	4.2
22	DA	228	C	4.2
39	DR	67	GLY	4.2
16	CP	50	THR	4.1
44	DW	50	ASN	4.1
46	DY	29	ARG	4.1
14	CN	60	GLN	4.1
26	DE	149	ILE	4.1
2	AB	221	VAL	4.1
22	DA	1171	G	4.1
30	BI	142	ASP	4.1
42	DU	32	GLY	4.1
22	DA	1172	C	4.1
45	DX	50	ARG	4.1
34	DM	7	THR	4.1
22	BA	2108	A	4.1
10	CJ	42	LEU	4.1
27	DF	12	VAL	4.1
29	BH	39	ALA	4.1
36	DO	77	ALA	4.1
40	DS	33	LEU	4.1
1	CA	1033	G	4.1
1	AA	1019	A	4.1
30	BI	115	ALA	4.1
13	CM	58	ASP	4.1

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Mol	Chain	Res	Type	RSRZ
13	CM	81	MET	4.1
9	AI	20	PHE	4.1
35	DN	97	ILE	4.1
37	DP	110	ILE	4.1
35	DN	43	GLU	4.1
40	DS	95	ARG	4.1
26	DE	158	PHE	4.1
2	CB	182	PRO	4.1
28	DG	82	GLY	4.1
28	DG	130	GLU	4.1
30	DI	118	THR	4.1
10	CJ	46	LYS	4.1
24	DC	240	PHE	4.1
36	DO	58	ILE	4.1
7	CG	103	TRP	4.1
20	CT	64	LYS	4.1
39	DR	27	ILE	4.1
35	DN	30	ARG	4.1
45	BX	77	LYS	4.1
33	DL	50	PHE	4.1
22	BA	1925	C	4.1
4	CD	177	LYS	4.1
7	CG	135	VAL	4.1
51	D3	48	ALA	4.1
53	B5	189	ASN	4.1
22	DA	2173	A	4.0
29	BH	1	MET	4.0
29	DH	13	GLY	4.0
7	CG	5	ARG	4.0
36	DO	113	ALA	4.0
27	BF	113	ASP	4.0
36	DO	46	GLU	4.0
42	DU	37	GLU	4.0
45	DX	20	HIS	4.0
20	CT	87	ALA	4.0
30	BI	49	ILE	4.0
26	BE	7	ASP	4.0
42	DU	95	PHE	4.0
2	CB	74	ARG	4.0
28	DG	170	ARG	4.0
35	DN	73	ASN	4.0
49	B1	4	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
37	DP	104	THR	4.0
1	CA	1018	G	4.0
1	CA	1305	G	4.0
29	BH	94	ILE	4.0
30	BI	20	PRO	4.0
9	CI	103	PHE	4.0
41	DT	3	ARG	4.0
53	B5	37	LYS	4.0
22	DA	138	U	4.0
30	DI	55	ILE	4.0
22	DA	2128	G	4.0
30	DI	81	LYS	4.0
30	DI	127	ARG	4.0
22	DA	1094	U	4.0
22	DA	2129	C	4.0
53	B5	167	ASP	4.0
41	DT	72	GLN	4.0
7	AG	144	MET	4.0
20	CT	67	ILE	4.0
29	DH	94	ILE	4.0
32	DK	104	THR	4.0
37	DP	95	ALA	4.0
39	DR	103	ALA	4.0
17	CQ	44	LEU	4.0
44	DW	32	LEU	4.0
47	DZ	29	LEU	4.0
26	DE	129	PRO	4.0
9	CI	11	ARG	4.0
2	CB	92	VAL	4.0
14	CN	16	LEU	4.0
22	DA	2125	G	4.0
28	DG	172	LYS	4.0
26	DE	127	GLU	4.0
30	BI	43	ASN	4.0
42	DU	63	ALA	4.0
27	DF	103	LEU	4.0
7	AG	62	PHE	4.0
20	CT	42	GLY	4.0
24	DC	241	GLY	4.0
26	DE	1	MET	4.0
1	AA	1537	U	4.0
9	CI	4	ASN	4.0

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Mol	Chain	Res	Type	RSRZ
11	AK	16	VAL	4.0
40	DS	97	LEU	4.0
2	CB	37	LYS	4.0
28	DG	44	LYS	4.0
53	B5	51	ASP	4.0
36	DO	51	ALA	3.9
41	DT	45	ALA	3.9
52	D4	26	ILE	3.9
19	CS	17	LYS	3.9
22	DA	1715	G	3.9
45	DX	74	ARG	3.9
22	DA	2169	A	3.9
52	D4	2	LYS	3.9
38	DQ	101	PHE	3.9
33	DL	104	GLN	3.9
30	DI	83	ALA	3.9
13	CM	19	LEU	3.9
25	DD	27	ILE	3.9
41	DT	12	ARG	3.9
51	D3	52	LYS	3.9
39	DR	100	GLY	3.9
53	B5	220	GLY	3.9
7	CG	76	LYS	3.9
13	CM	79	ARG	3.9
22	DA	1174	U	3.9
26	DE	104	ALA	3.9
17	CQ	13	VAL	3.9
34	DM	33	LEU	3.9
25	DD	74	GLU	3.9
1	CA	1043	G	3.9
9	AI	129	LYS	3.9
22	BA	139	U	3.9
29	DH	74	ALA	3.9
44	DW	61	ALA	3.9
13	AM	4	ILE	3.9
44	DW	51	VAL	3.9
2	CB	69	PHE	3.9
22	DA	2178	C	3.9
1	CA	1030	U	3.9
12	CL	44	LYS	3.9
22	DA	345	A	3.9
50	D2	32	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
28	DG	164	TYR	3.9
34	DM	41	LEU	3.9
40	DS	9	HIS	3.9
27	DF	80	ARG	3.9
41	DT	69	ARG	3.9
42	DU	73	PHE	3.9
53	B5	127	LYS	3.9
1	AA	1027	C	3.9
26	DE	131	THR	3.9
29	BH	104	THR	3.9
7	CG	141	VAL	3.9
26	DE	33	VAL	3.9
29	BH	51	ARG	3.9
29	DH	121	VAL	3.9
33	DL	100	ILE	3.9
34	DM	124	LEU	3.9
52	D4	38	GLY	3.9
27	DF	38	MET	3.9
30	BI	36	MET	3.9
31	DJ	15	TRP	3.9
4	AD	27	ALA	3.9
21	CU	44	GLU	3.9
26	DE	34	ALA	3.9
7	AG	73	VAL	3.9
26	DE	180	LEU	3.9
27	DF	137	ILE	3.9
40	DS	69	LEU	3.9
33	DL	67	THR	3.9
48	D0	25	VAL	3.9
3	AC	168	TYR	3.9
1	CA	1002	G	3.9
22	DA	2123	G	3.9
2	AB	88	ASP	3.9
14	CN	53	ARG	3.9
3	CC	192	THR	3.9
40	DS	73	LYS	3.9
22	DA	1095	A	3.8
30	BI	84	ALA	3.8
28	DG	162	VAL	3.8
42	DU	28	VAL	3.8
44	DW	71	VAL	3.8
13	CM	72	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
3	AC	81	GLY	3.8
22	DA	101	A	3.8
27	DF	34	ILE	3.8
20	CT	71	LYS	3.8
7	CG	57	SER	3.8
10	CJ	101	SER	3.8
11	CK	21	ALA	3.8
24	DC	99	GLY	3.8
25	DD	85	ALA	3.8
34	DM	61	GLY	3.8
18	AR	73	ARG	3.8
19	CS	47	LEU	3.8
22	BA	2146	C	3.8
41	DT	88	LYS	3.8
45	DX	22	LEU	3.8
34	DM	80	VAL	3.8
26	DE	89	PRO	3.8
9	CI	84	THR	3.8
8	AH	119	ALA	3.8
26	DE	98	LYS	3.8
16	CP	57	ILE	3.8
38	DQ	18	LEU	3.8
36	DO	78	VAL	3.8
19	AS	74	PHE	3.8
37	DP	9	GLU	3.8
43	DV	56	PHE	3.8
47	DZ	37	GLU	3.8
22	DA	1068	G	3.8
46	DY	30	MET	3.8
7	CG	38	THR	3.8
10	CJ	28	THR	3.8
14	CN	98	LYS	3.8
36	DO	102	ARG	3.8
46	DY	54	LYS	3.8
7	CG	107	ALA	3.8
26	DE	191	ASP	3.8
33	DL	20	GLY	3.8
20	CT	84	ASN	3.8
24	DC	93	LEU	3.8
38	DQ	117	LEU	3.8
9	AI	39	PHE	3.8
26	DE	183	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
31	DJ	13	ARG	3.8
36	DO	116	GLN	3.8
52	D4	35	GLN	3.8
22	DA	88	G	3.8
53	B5	188	ASP	3.8
28	DG	107	LEU	3.8
46	DY	42	LEU	3.8
9	CI	21	ILE	3.8
53	B5	100	ILE	3.8
4	AD	22	LYS	3.8
36	DO	88	LYS	3.8
50	D2	37	LYS	3.8
22	DA	343	C	3.8
13	CM	75	MET	3.8
22	DA	2109	U	3.8
25	DD	125	TRP	3.8
20	CT	63	ALA	3.8
30	BI	7	ALA	3.8
35	DN	68	ALA	3.8
43	DV	57	TYR	3.8
2	CB	135	LEU	3.8
4	AD	21	LEU	3.8
25	DD	133	THR	3.8
53	B5	25	GLU	3.8
2	CB	143	LYS	3.8
14	CN	28	LYS	3.8
22	DA	2103	C	3.8
3	CC	206	GLU	3.8
40	DS	32	ALA	3.8
47	DZ	2	ALA	3.8
3	CC	103	ILE	3.8
7	CG	43	VAL	3.8
13	CM	4	ILE	3.8
33	DL	135	ILE	3.8
40	DS	105	VAL	3.8
30	BI	34	ASN	3.8
27	DF	96	MET	3.8
1	CA	1270	G	3.7
2	CB	122	GLN	3.7
42	DU	23	GLY	3.7
10	AJ	10	LEU	3.7
10	CJ	91	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
40	DS	68	ASP	3.7
3	CC	14	ILE	3.7
19	AS	40	ILE	3.7
27	DF	83	TYR	3.7
36	DO	99	TYR	3.7
2	CB	65	GLY	3.7
30	DI	90	SER	3.7
22	DA	1092	C	3.7
32	DK	107	LEU	3.7
33	DL	91	ASP	3.7
2	CB	139	ARG	3.7
12	CL	123	LYS	3.7
34	DM	40	ARG	3.7
40	DS	41	LYS	3.7
7	CG	86	GLN	3.7
3	CC	155	GLY	3.7
9	CI	53	GLU	3.7
30	DI	94	ASN	3.7
27	DF	17	MET	3.7
1	AA	87	C	3.7
7	CG	137	LYS	3.7
7	CG	143	ARG	3.7
30	BI	80	LEU	3.7
40	DS	6	LYS	3.7
40	DS	85	ILE	3.7
2	CB	96	TRP	3.7
29	DH	88	GLY	3.7
28	DG	104	ASN	3.7
30	DI	23	PRO	3.7
53	B5	175	PRO	3.7
29	BH	35	LYS	3.7
33	DL	96	LYS	3.7
48	D0	37	LYS	3.7
22	DA	2168	G	3.7
29	DH	101	ASP	3.7
25	DD	180	VAL	3.7
40	DS	24	ILE	3.7
10	CJ	95	GLY	3.7
49	D1	45	GLN	3.7
27	DF	115	ARG	3.7
30	BI	94	ASN	3.7
42	DU	100	SER	3.7

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Mol	Chain	Res	Type	RSRZ
2	CB	10	LEU	3.7
13	CM	41	GLU	3.7
28	DG	4	VAL	3.7
2	AB	65	GLY	3.7
13	CM	52	GLN	3.7
33	DL	114	GLY	3.7
9	AI	123	ARG	3.7
10	CJ	82	LYS	3.7
27	DF	95	ARG	3.7
2	AB	51	ASN	3.7
28	DG	12	PRO	3.7
30	BI	88	SER	3.7
36	DO	12	THR	3.7
9	CI	63	LEU	3.7
13	CM	69	LEU	3.7
26	DE	23	PHE	3.7
27	DF	173	PHE	3.7
36	DO	80	GLU	3.7
39	DR	46	GLU	3.7
30	BI	140	VAL	3.7
25	DD	166	GLY	3.7
36	DO	23	ALA	3.7
11	CK	42	LEU	3.7
29	DH	139	PHE	3.7
29	BH	7	ASP	3.7
2	CB	31	ILE	3.7
27	DF	88	LYS	3.7
40	DS	17	VAL	3.7
46	BY	23	ARG	3.7
52	D4	12	ARG	3.7
1	CA	1028	C	3.7
22	DA	2172	U	3.7
20	CT	73	ALA	3.7
29	BH	63	ALA	3.7
30	BI	77	ALA	3.7
8	CH	49	PHE	3.6
13	CM	71	ARG	3.6
14	CN	43	ASN	3.6
25	DD	154	LYS	3.6
30	DI	10	LYS	3.6
38	DQ	39	VAL	3.6
27	DF	27	GLN	3.6

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Mol	Chain	Res	Type	RSRZ
51	D3	24	HIS	3.6
22	DA	281	C	3.6
26	DE	50	ALA	3.6
29	DH	111	ALA	3.6
40	DS	5	ALA	3.6
20	CT	9	LYS	3.6
52	D4	32	LYS	3.6
2	CB	161	LEU	3.6
20	CT	79	LEU	3.6
26	DE	178	VAL	3.6
31	DJ	97	PRO	3.6
37	DP	84	ILE	3.6
39	DR	87	GLN	3.6
53	B5	222	SER	3.6
7	CG	90	GLU	3.6
26	DE	162	ARG	3.6
36	DO	9	ARG	3.6
30	DI	101	ILE	3.6
22	BA	2170	A	3.6
23	DB	119	A	3.6
25	DD	8	LYS	3.6
36	DO	76	LYS	3.6
37	DP	102	GLU	3.6
2	CB	76	ALA	3.6
53	B5	205	ALA	3.6
1	CA	90	C	3.6
22	DA	357	C	3.6
26	DE	147	LEU	3.6
3	CC	106	VAL	3.6
7	CG	78	ARG	3.6
22	DA	2796	U	3.6
30	BI	122	ILE	3.6
3	CC	29	PHE	3.6
1	CA	1317	C	3.6
12	AL	24	LEU	3.6
33	DL	79	LEU	3.6
40	DS	91	GLY	3.6
27	DF	136	ILE	3.6
53	B5	102	GLN	3.6
53	B5	176	VAL	3.6
1	AA	412	A	3.6
29	DH	77	THR	3.6

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Mol	Chain	Res	Type	RSRZ
7	CG	8	GLY	3.6
25	DD	56	LYS	3.6
27	DF	39	GLY	3.6
29	BH	88	GLY	3.6
30	DI	119	GLY	3.6
26	DE	120	VAL	3.6
42	DU	83	VAL	3.6
42	DU	98	SER	3.6
24	DC	172	VAL	3.6
26	DE	122	GLU	3.6
27	DF	101	GLU	3.6
13	CM	9	ILE	3.6
28	DG	169	VAL	3.6
32	DK	99	ILE	3.6
17	CQ	65	ARG	3.6
17	CQ	82	ALA	3.6
28	DG	174	ALA	3.6
21	CU	37	PHE	3.6
26	DE	64	GLY	3.6
34	DM	36	VAL	3.6
36	DO	27	VAL	3.6
40	DS	107	VAL	3.6
2	AB	74	ARG	3.6
9	AI	41	ARG	3.6
22	DA	1076	C	3.6
16	AP	81	ALA	3.6
22	DA	12	U	3.6
28	DG	106	SER	3.6
2	CB	101	LEU	3.5
19	CS	48	THR	3.5
24	DC	110	LEU	3.5
33	DL	18	ARG	3.5
22	DA	1044	C	3.5
40	DS	54	ALA	3.5
32	DK	91	SER	3.5
41	DT	70	HIS	3.5
46	DY	14	LEU	3.5
44	BW	10	THR	3.5
29	DH	147	VAL	3.5
36	DO	28	VAL	3.5
29	DH	86	ASP	3.5
17	CQ	53	CYS	3.5

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Mol	Chain	Res	Type	RSRZ
51	D3	51	SER	3.5
10	CJ	51	VAL	3.5
19	AS	56	GLN	3.5
30	BI	121	ASP	3.5
30	DI	116	ASP	3.5
33	DL	23	ILE	3.5
47	DZ	4	THR	3.5
27	DF	94	GLU	3.5
31	DJ	137	PRO	3.5
45	DX	71	LEU	3.5
20	CT	13	GLN	3.5
25	DD	95	SER	3.5
30	DI	122	ILE	3.5
44	DW	64	ASP	3.5
48	D0	26	THR	3.5
7	CG	35	LYS	3.5
13	CM	23	TYR	3.5
16	CP	54	LEU	3.5
20	CT	86	LEU	3.5
43	DV	42	LEU	3.5
1	AA	844	G	3.5
29	BH	138	VAL	3.5
31	DJ	56	VAL	3.5
26	DE	13	THR	3.5
32	DK	101	GLY	3.5
22	BA	2167	U	3.5
2	CB	117	LEU	3.5
22	DA	2179	C	3.5
34	DM	6	ARG	3.5
1	AA	1492	A	3.5
29	DH	40	THR	3.5
34	DM	79	ALA	3.5
40	DS	98	LYS	3.5
10	AJ	84	VAL	3.5
38	DQ	89	GLU	3.5
22	DA	1103	A	3.5
14	CN	72	GLY	3.5
30	DI	16	GLY	3.5
51	D3	47	LYS	3.5
10	AJ	71	LEU	3.5
33	BL	92	LEU	3.5
17	CQ	83	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
50	D2	30	VAL	3.5
13	CM	114	LYS	3.5
26	DE	124	PHE	3.5
27	DF	7	TYR	3.5
27	DF	31	VAL	3.4
41	DT	53	VAL	3.4
7	CG	10	ARG	3.4
9	CI	30	ILE	3.4
13	CM	51	GLY	3.4
29	DH	97	ARG	3.4
35	DN	113	ILE	3.4
42	DU	53	ASN	3.4
1	CA	1035	A	3.4
9	AI	90	TYR	3.4
14	AN	48	LEU	3.4
7	CG	71	PRO	3.4
28	DG	8	PRO	3.4
38	DQ	44	GLN	3.4
2	CB	150	GLY	3.4
8	CH	123	GLY	3.4
30	BI	97	LYS	3.4
53	B5	91	GLY	3.4
1	AA	1001	C	3.4
8	CH	130	ALA	3.4
53	B5	196	ALA	3.4
27	DF	64	LYS	3.4
16	AP	71	VAL	3.4
39	DR	33	VAL	3.4
2	AB	67	ILE	3.4
34	DM	96	ILE	3.4
4	AD	29	ASP	3.4
38	DQ	10	ALA	3.4
27	DF	50	LEU	3.4
18	CR	51	TYR	3.4
38	DQ	25	TYR	3.4
24	DC	246	THR	3.4
30	BI	58	VAL	3.4
10	CJ	49	PHE	3.4
22	DA	143	C	3.4
22	DA	1100	C	3.4
33	DL	27	LEU	3.4
36	DO	21	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
3	CC	42	TYR	3.4
38	DQ	45	TYR	3.4
35	DN	37	THR	3.4
13	CM	14	HIS	3.4
20	CT	34	LYS	3.4
39	DR	31	GLU	3.4
42	DU	75	ALA	3.4
27	DF	105	THR	3.4
32	DK	110	GLU	3.4
16	CP	81	ALA	3.4
28	DG	111	HIS	3.4
3	CC	76	VAL	3.4
18	AR	32	TYR	3.4
29	DH	135	HIS	3.4
28	DG	73	ASN	3.4
33	DL	6	LEU	3.4
42	DU	22	ARG	3.4
9	CI	57	MET	3.4
30	DI	87	LYS	3.4
33	DL	31	GLY	3.4
13	CM	76	SER	3.4
14	CN	10	GLU	3.4
21	AU	31	GLU	3.4
25	DD	89	GLU	3.4
24	DC	104	ILE	3.4
27	DF	109	PRO	3.4
33	DL	73	ILE	3.4
9	CI	127	PHE	3.4
10	CJ	50	THR	3.4
24	DC	101	ARG	3.4
24	DC	232	HIS	3.4
28	DG	69	ARG	3.4
2	AB	85	LEU	3.4
9	CI	61	LEU	3.4
10	CJ	102	LEU	3.4
35	DN	9	GLN	3.4
7	CG	54	SER	3.3
25	DD	98	VAL	3.3
36	DO	95	SER	3.3
16	CP	4	ILE	3.3
2	CB	90	PHE	3.3
13	AM	92	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
27	DF	168	ALA	3.3
28	DG	163	ARG	3.3
30	BI	120	ALA	3.3
39	DR	28	ALA	3.3
44	DW	47	ALA	3.3
1	AA	1032	G	3.3
22	DA	2110	G	3.3
34	DM	62	LYS	3.3
41	DT	60	THR	3.3
7	CG	81	GLY	3.3
25	DD	84	LEU	3.3
26	DE	200	LEU	3.3
46	DY	31	GLN	3.3
9	CI	89	GLU	3.3
7	CG	73	VAL	3.3
32	DK	52	VAL	3.3
7	CG	79	ARG	3.3
2	AB	134	ALA	3.3
11	AK	77	TYR	3.3
27	BF	83	TYR	3.3
27	DF	139	PRO	3.3
36	DO	59	ALA	3.3
53	B5	168	LYS	3.3
1	CA	204	G	3.3
22	BA	2885	G	3.3
14	AN	24	ARG	3.3
46	DY	47	ARG	3.3
52	D4	7	VAL	3.3
13	CM	27	LYS	3.3
14	CN	23	LYS	3.3
37	DP	63	LYS	3.3
49	B1	53	LYS	3.3
34	DM	92	TRP	3.3
41	DT	80	TRP	3.3
9	CI	126	GLN	3.3
13	CM	99	GLY	3.3
46	DY	56	LEU	3.3
13	CM	70	ARG	3.3
26	DE	88	ARG	3.3
1	AA	1003	G	3.3
22	DA	1529	G	3.3
38	DQ	15	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
22	DA	2163	A	3.3
28	DG	24	ILE	3.3
2	CB	226	SER	3.3
27	DF	143	TYR	3.3
35	DN	82	GLU	3.3
29	DH	6	LEU	3.3
10	CJ	96	VAL	3.3
39	DR	51	VAL	3.3
10	CJ	88	MET	3.3
1	CA	1019	A	3.3
1	CA	1492	A	3.3
3	CC	71	ALA	3.3
33	DL	123	ARG	3.3
10	CJ	65	TYR	3.3
14	CN	49	GLN	3.3
36	DO	89	ASP	3.3
2	CB	107	VAL	3.3
29	BH	9	VAL	3.3
32	DK	35	VAL	3.3
7	CG	97	ASN	3.3
10	CJ	81	GLU	3.3
14	CN	8	ALA	3.3
16	AP	4	ILE	3.3
27	DF	99	PHE	3.3
29	BH	100	ALA	3.3
28	DG	29	LYS	3.3
28	DG	94	TYR	3.3
30	BI	75	PRO	3.3
3	CC	87	LEU	3.3
11	CK	129	VAL	3.3
41	DT	47	VAL	3.3
46	BY	7	ARG	3.3
7	AG	7	ILE	3.3
10	CJ	22	THR	3.3
26	DE	141	MET	3.3
26	DE	190	ALA	3.3
44	DW	26	PHE	3.3
47	DZ	8	THR	3.3
19	CS	68	GLY	3.3
27	DF	124	GLY	3.3
1	CA	86	G	3.3
1	CA	211	G	3.3

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Mol	Chain	Res	Type	RSRZ
25	DD	201	LEU	3.3
42	DU	9	ASP	3.3
22	DA	1075	C	3.3
22	DA	1278	C	3.3
1	CA	1017	U	3.3
17	CQ	73	TRP	3.3
10	CJ	34	ALA	3.3
11	AK	81	ASN	3.3
27	DF	147	ASP	3.3
22	DA	268	C	3.2
22	DA	1606	C	3.2
41	DT	68	LYS	3.2
25	DD	101	PHE	3.2
29	DH	67	ALA	3.2
3	CC	102	ASN	3.2
27	DF	41	GLY	3.2
43	DV	32	GLY	3.2
46	DY	21	LEU	3.2
31	DJ	53	TYR	3.2
41	DT	42	GLU	3.2
2	CB	210	VAL	3.2
27	DF	89	VAL	3.2
22	DA	356	G	3.2
7	CG	112	GLY	3.2
29	DH	68	ARG	3.2
30	BI	132	THR	3.2
44	DW	44	LYS	3.2
44	DW	75	LYS	3.2
41	DT	37	ASP	3.2
16	AP	47	GLU	3.2
4	AD	158	ALA	3.2
30	DI	115	ALA	3.2
22	DA	1168	G	3.2
29	BH	62	LEU	3.2
42	DU	14	LEU	3.2
6	CF	79	ARG	3.2
28	DG	58	TYR	3.2
30	BI	24	VAL	3.2
1	CA	1296	C	3.2
28	DG	5	ALA	3.2
46	DY	32	ALA	3.2
1	CA	1024	G	3.2

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Mol	Chain	Res	Type	RSRZ
36	DO	108	ASP	3.2
42	DU	81	ASP	3.2
19	CS	59	PRO	3.2
22	DA	1205	A	3.2
41	DT	40	LYS	3.2
26	DE	125	SER	3.2
39	DR	53	PHE	3.2
11	AK	79	ILE	3.2
22	BA	2192	U	3.2
22	DA	2402	U	3.2
34	DM	73	ILE	3.2
47	DZ	34	HIS	3.2
26	DE	30	GLN	3.2
9	CI	41	ARG	3.2
26	DE	12	LEU	3.2
27	DF	91	LEU	3.2
46	DY	58	ASN	3.2
1	AA	1016	A	3.2
22	BA	1171	G	3.2
22	DA	2602	A	3.2
39	DR	52	PRO	3.2
30	DI	91	GLY	3.2
53	B5	44	VAL	3.2
38	DQ	65	ILE	3.2
2	CB	89	GLN	3.2
3	CC	129	MET	3.2
34	DM	105	MET	3.2
10	AJ	75	ASP	3.2
28	DG	56	ASP	3.2
35	DN	62	ASN	3.2
7	CG	64	VAL	3.2
30	BI	139	VAL	3.2
32	DK	50	GLY	3.2
1	CA	1313	U	3.2
18	AR	74	HIS	3.2
20	CT	29	ARG	3.2
44	DW	23	VAL	3.2
33	DL	131	ALA	3.2
36	DO	109	ALA	3.2
49	D1	23	THR	3.2
18	CR	39	ILE	3.2
22	DA	75	G	3.2

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Mol	Chain	Res	Type	RSRZ
40	DS	31	GLN	3.2
41	BT	70	HIS	3.2
33	DL	69	ARG	3.1
2	CB	80	VAL	3.1
24	DC	70	ASN	3.1
30	BI	82	LYS	3.1
37	DP	74	PHE	3.1
42	DU	44	LYS	3.1
44	DW	60	PHE	3.1
7	CG	65	ALA	3.1
19	CS	50	ALA	3.1
31	DJ	6	ALA	3.1
19	AS	39	THR	3.1
27	DF	158	THR	3.1
29	DH	96	THR	3.1
47	DZ	5	ILE	3.1
2	CB	191	SER	3.1
7	CG	50	LEU	3.1
19	CS	5	LEU	3.1
22	BA	2180	U	3.1
5	CE	157	ARG	3.1
10	AJ	33	GLY	3.1
22	DA	183	C	3.1
38	DQ	102	ASP	3.1
41	DT	81	LYS	3.1
48	D0	46	ASP	3.1
8	CH	25	VAL	3.1
24	DC	91	ILE	3.1
3	CC	69	HIS	3.1
42	DU	41	LEU	3.1
53	B5	185	LYS	3.1
1	CA	1297	G	3.1
44	DW	42	GLY	3.1
2	AB	187	VAL	3.1
2	CB	91	PHE	3.1
5	AE	31	PHE	3.1
39	DR	38	VAL	3.1
2	CB	216	ALA	3.1
13	AM	5	ALA	3.1
38	DQ	99	ALA	3.1
3	CC	120	ILE	3.1
4	CD	28	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
46	BY	2	LYS	3.1
20	CT	66	LEU	3.1
30	DI	123	GLU	3.1
33	DL	80	SER	3.1
36	DO	48	LEU	3.1
2	AB	75	ALA	3.1
22	DA	267	C	3.1
51	D3	65	ALA	3.1
8	CH	46	ILE	3.1
30	DI	72	LYS	3.1
34	DM	63	ILE	3.1
45	DX	17	ASN	3.1
6	CF	54	LEU	3.1
41	DT	11	LEU	3.1
47	DZ	39	GLU	3.1
14	CN	6	MET	3.1
14	CN	95	GLY	3.1
21	AU	21	ARG	3.1
1	CA	4	U	3.1
4	AD	37	ALA	3.1
36	BO	50	ALA	3.1
22	DA	2156	G	3.1
9	CI	64	TYR	3.1
2	CB	147	SER	3.1
3	CC	126	ARG	3.1
27	DF	26	MET	3.1
30	DI	117	MET	3.1
10	CJ	30	LYS	3.1
51	D3	22	PHE	3.1
20	CT	45	ALA	3.1
36	DO	57	ALA	3.1
36	DO	73	ALA	3.1
27	DF	106	ILE	3.1
33	DL	62	PRO	3.1
22	BA	549	G	3.1
22	DA	279	A	3.1
28	BG	105	LEU	3.1
27	DF	24	SER	3.1
40	DS	108	SER	3.1
26	DE	169	VAL	3.1
28	DG	17	VAL	3.1
40	DS	93	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
29	DH	133	GLN	3.1
22	DA	1533	C	3.1
37	DP	109	ARG	3.1
38	DQ	13	ARG	3.1
1	AA	82	G	3.1
15	CO	13	SER	3.1
29	DH	91	PHE	3.1
42	DU	18	ASP	3.1
16	AP	22	ALA	3.1
30	DI	84	ALA	3.1
24	DC	64	ILE	3.1
30	DI	111	GLN	3.1
38	DQ	37	GLN	3.1
40	DS	11	ARG	3.1
36	DO	4	LYS	3.1
15	CO	56	LEU	3.1
49	D1	34	LEU	3.1
13	CM	54	ASP	3.0
14	CN	69	ARG	3.0
16	AP	20	VAL	3.0
9	CI	105	THR	3.0
25	DD	132	ALA	3.0
27	DF	171	ALA	3.0
29	BH	76	GLU	3.0
29	DH	64	ALA	3.0
31	DJ	94	ALA	3.0
31	DJ	98	GLU	3.0
39	DR	48	LYS	3.0
28	DG	72	LEU	3.0
36	DO	22	GLY	3.0
41	DT	61	LEU	3.0
1	CA	998	C	3.0
1	CA	1042	A	3.0
2	CB	187	VAL	3.0
13	CM	13	LYS	3.0
19	CS	19	VAL	3.0
35	DN	72	ASP	3.0
20	CT	8	LYS	3.0
29	BH	83	LYS	3.0
29	BH	77	THR	3.0
44	DW	35	SER	3.0
28	DG	53	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
13	CM	115	PRO	3.0
25	DD	59	ARG	3.0
50	D2	18	PHE	3.0
27	DF	43	ALA	3.0
29	DH	9	VAL	3.0
14	CN	100	SER	3.0
48	D0	5	GLN	3.0
33	DL	61	LEU	3.0
45	DX	18	ARG	3.0
38	DQ	103	LYS	3.0
1	CA	1271	A	3.0
36	DO	41	ALA	3.0
6	AF	68	GLN	3.0
27	DF	63	GLN	3.0
7	AG	79	ARG	3.0
17	CQ	5	ILE	3.0
21	CU	35	ARG	3.0
36	DO	114	GLY	3.0
14	AN	27	LEU	3.0
43	DV	34	LYS	3.0
7	CG	74	GLU	3.0
29	BH	114	GLU	3.0
29	BH	46	PHE	3.0
3	CC	32	ASN	3.0
6	CF	28	ALA	3.0
22	DA	546	U	3.0
36	DO	50	ALA	3.0
11	CK	110	ILE	3.0
17	CQ	21	ILE	3.0
20	CT	36	TYR	3.0
30	BI	119	GLY	3.0
36	DO	56	LYS	3.0
46	DY	9	LYS	3.0
26	DE	150	THR	3.0
29	DH	75	LEU	3.0
30	DI	73	THR	3.0
41	DT	4	GLU	3.0
9	AI	19	VAL	3.0
11	AK	13	ARG	3.0
22	DA	361	G	3.0
37	DP	73	VAL	3.0
38	DQ	96	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
51	D3	28	ASN	3.0
20	AT	61	GLN	3.0
51	D3	16	LYS	3.0
16	AP	33	ILE	3.0
20	CT	32	ILE	3.0
33	DL	58	TYR	3.0
6	CF	47	LEU	3.0
28	DG	133	LEU	3.0
46	DY	24	GLU	3.0
2	CB	63	ARG	3.0
41	DT	77	ARG	3.0
2	CB	73	LYS	3.0
19	CS	22	ALA	3.0
2	CB	104	TRP	3.0
24	DC	248	TRP	3.0
9	AI	21	ILE	3.0
29	BH	99	ILE	3.0
9	CI	87	LEU	3.0
30	DI	138	LEU	3.0
37	DP	97	LEU	3.0
14	CN	58	SER	3.0
28	DG	74	SER	3.0
45	DX	3	ARG	3.0
6	CF	32	ALA	3.0
22	BA	1926	U	3.0
30	BI	25	GLY	3.0
32	DK	68	GLY	3.0
42	DU	99	ASN	3.0
44	DW	54	GLY	3.0
52	D4	13	ASN	3.0
2	AB	18	HIS	3.0
22	DA	544	C	3.0
49	D1	48	ILE	3.0
7	AG	85	TYR	3.0
25	DD	77	ARG	3.0
22	DA	280	U	3.0
41	DT	82	LYS	3.0
13	CM	49	SER	3.0
45	DX	35	SER	3.0
6	CF	89	VAL	2.9
10	CJ	98	VAL	2.9
28	DG	165	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
36	DO	105	ALA	2.9
46	BY	62	GLY	2.9
46	DY	45	GLN	2.9
9	CI	31	ASN	2.9
17	CQ	11	ARG	2.9
29	BH	43	ASN	2.9
3	AC	47	LEU	2.9
20	CT	51	PHE	2.9
3	CC	52	VAL	2.9
9	CI	124	ARG	2.9
10	AJ	37	ARG	2.9
24	DC	250	VAL	2.9
26	DE	90	GLN	2.9
28	DG	51	THR	2.9
53	B5	129	GLY	2.9
53	B5	71	LYS	2.9
8	CH	36	ILE	2.9
38	DQ	17	ILE	2.9
1	CA	1228	C	2.9
14	AN	36	ALA	2.9
20	CT	11	ALA	2.9
29	BH	50	ARG	2.9
14	AN	23	LYS	2.9
22	DA	266	G	2.9
22	DA	329	G	2.9
26	DE	56	GLY	2.9
27	DF	33	LYS	2.9
50	D2	2	LYS	2.9
13	AM	7	ILE	2.9
32	DK	90	ASN	2.9
14	CN	41	ARG	2.9
24	DC	62	TYR	2.9
41	BT	51	PHE	2.9
50	D2	35	ARG	2.9
24	DC	92	ALA	2.9
44	DW	78	LYS	2.9
46	DY	62	GLY	2.9
30	BI	26	PRO	2.9
3	CC	77	ILE	2.9
27	DF	104	ILE	2.9
2	CB	144	LEU	2.9
7	CG	30	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
8	CH	63	LEU	2.9
18	AR	68	LEU	2.9
1	CA	1243	C	2.9
22	DA	1167	C	2.9
22	DA	2104	C	2.9
10	AJ	35	GLN	2.9
40	DS	47	VAL	2.9
2	AB	222	ARG	2.9
7	CG	2	PRO	2.9
33	DL	21	ARG	2.9
10	AJ	87	LEU	2.9
11	AK	96	THR	2.9
13	CM	103	LYS	2.9
22	BA	359	G	2.9
48	D0	6	ASN	2.9
22	DA	1085	A	2.9
1	CA	1226	C	2.9
2	CB	111	ILE	2.9
2	CB	164	ILE	2.9
32	DK	38	ILE	2.9
38	DQ	22	LYS	2.9
15	AO	57	LEU	2.9
19	CS	14	HIS	2.9
22	DA	214	G	2.9
22	DA	880	G	2.9
36	DO	67	ASN	2.9
30	DI	29	GLY	2.9
7	AG	27	VAL	2.9
13	AM	97	VAL	2.9
18	CR	23	TYR	2.9
40	DS	106	VAL	2.9
22	BA	2137	U	2.9
40	DS	48	LYS	2.9
24	DC	105	LEU	2.9
35	DN	10	LEU	2.9
28	DG	83	PHE	2.9
31	DJ	92	MET	2.9
35	DN	21	PHE	2.9
3	CC	156	ARG	2.9
7	CG	55	GLY	2.9
14	CN	17	ALA	2.9
20	CT	47	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
3	AC	138	VAL	2.9
1	CA	210	C	2.9
9	CI	72	ILE	2.9
43	DV	58	SER	2.9
49	D1	13	SER	2.9
7	CG	26	PHE	2.9
14	CN	73	PHE	2.9
21	AU	47	ARG	2.9
22	BA	1065	U	2.9
40	BS	110	ARG	2.9
9	CI	9	THR	2.9
31	DJ	78	THR	2.9
1	CA	1016	A	2.8
4	AD	67	VAL	2.8
9	AI	67	VAL	2.8
22	DA	2170	A	2.8
43	DV	82	TYR	2.8
49	D1	49	TYR	2.8
1	AA	79	G	2.8
22	DA	277	G	2.8
3	CC	124	LEU	2.8
9	AI	63	LEU	2.8
29	DH	113	SER	2.8
42	DU	29	LEU	2.8
30	BI	16	GLY	2.8
13	CM	37	ALA	2.8
33	DL	5	THR	2.8
42	DU	3	ALA	2.8
19	CS	80	TYR	2.8
22	BA	2119	A	2.8
40	DS	67	ASP	2.8
1	AA	1031	C	2.8
22	DA	1248	G	2.8
29	BH	12	LEU	2.8
30	BI	35	ILE	2.8
40	DS	4	ILE	2.8
45	DX	61	LYS	2.8
49	D1	18	GLY	2.8
3	CC	85	GLU	2.8
7	AG	105	VAL	2.8
32	DK	49	ARG	2.8
36	DO	47	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
37	DP	101	ARG	2.8
38	DQ	33	ARG	2.8
45	DX	45	ARG	2.8
1	CA	1000	A	2.8
4	AD	151	LYS	2.8
22	BA	716	A	2.8
31	DJ	49	ASP	2.8
37	DP	38	LYS	2.8
41	BT	88	LYS	2.8
2	CB	201	PRO	2.8
7	AG	2	PRO	2.8
22	DA	316	C	2.8
22	DA	2143	C	2.8
22	DA	2164	C	2.8
28	DG	28	GLY	2.8
33	DL	8	PRO	2.8
44	DW	81	SER	2.8
2	CB	225	ARG	2.8
14	CN	29	ALA	2.8
26	DE	201	ALA	2.8
27	DF	75	ALA	2.8
33	DL	10	GLU	2.8
33	DL	75	ALA	2.8
50	D2	36	ALA	2.8
29	BH	8	LYS	2.8
22	DA	213	A	2.8
22	DA	1046	A	2.8
22	DA	2309	A	2.8
28	DG	161	GLY	2.8
36	DO	97	PHE	2.8
7	AG	150	ALA	2.8
7	CG	123	GLU	2.8
28	DG	110	SER	2.8
49	D1	44	ARG	2.8
20	CT	49	LYS	2.8
22	DA	1176	U	2.8
51	D3	23	LYS	2.8
3	AC	39	VAL	2.8
9	CI	48	VAL	2.8
24	DC	94	VAL	2.8
28	DG	48	ASN	2.8
28	DG	49	THR	2.8

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Mol	Chain	Res	Type	RSRZ
31	DJ	5	THR	2.8
11	AK	19	GLY	2.8
38	DQ	7	GLY	2.8
5	CE	10	GLU	2.8
23	DB	118	C	2.8
24	DC	126	PRO	2.8
26	DE	199	MET	2.8
43	DV	84	PRO	2.8
4	CD	36	GLN	2.8
9	CI	111	VAL	2.8
1	CA	988	G	2.8
22	DA	2120	G	2.8
22	DA	2157	G	2.8
34	DM	64	TRP	2.8
7	CG	132	GLY	2.8
12	CL	80	ILE	2.8
13	CM	11	ASP	2.8
22	DA	2585	U	2.8
50	D2	12	ARG	2.8
1	CA	1257	A	2.8
22	DA	1808	A	2.8
2	CB	84	ALA	2.8
19	CS	35	SER	2.8
49	D1	43	VAL	2.8
2	CB	224	GLY	2.8
7	CG	60	GLU	2.8
10	CJ	63	ASP	2.8
13	CM	44	LYS	2.8
22	DA	1407	G	2.8
32	DK	47	ILE	2.8
33	DL	28	GLY	2.8
33	DL	49	GLY	2.8
15	CO	22	THR	2.8
21	AU	42	THR	2.8
44	DW	74	PRO	2.8
13	CM	97	VAL	2.8
19	AS	32	ARG	2.8
4	AD	182	PHE	2.8
20	CT	43	ASP	2.8
27	BF	170	LEU	2.8
28	BG	24	ILE	2.8
41	DT	79	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	CA	1331	G	2.8
9	AI	44	ALA	2.8
11	CK	15	GLN	2.8
15	CO	89	ARG	2.8
18	CR	57	ARG	2.8
26	DE	196	VAL	2.8
37	DP	33	VAL	2.8
41	DT	24	MET	2.8
22	DA	1049	C	2.7
4	AD	198	HIS	2.7
27	DF	4	LEU	2.7
6	AF	92	THR	2.7
10	CJ	20	GLN	2.7
19	CS	21	LYS	2.7
20	AT	87	ALA	2.7
28	DG	132	VAL	2.7
25	DD	64	GLU	2.7
22	DA	2177	C	2.7
19	AS	41	PHE	2.7
27	BF	169	LEU	2.7
30	BI	19	ASN	2.7
16	AP	60	TRP	2.7
22	DA	1077	A	2.7
28	DG	171	THR	2.7
22	DA	1087	G	2.7
22	DA	1452	G	2.7
22	DA	2307	G	2.7
36	DO	42	PRO	2.7
33	DL	78	ARG	2.7
3	CC	130	PHE	2.7
7	CG	47	LEU	2.7
7	CG	125	SER	2.7
24	BC	272	SER	2.7
19	CS	70	LYS	2.7
30	BI	59	ILE	2.7
24	DC	46	ASN	2.7
30	BI	76	ALA	2.7
7	CG	48	GLU	2.7
34	DM	103	TYR	2.7
10	CJ	32	THR	2.7
35	DN	96	ARG	2.7
40	DS	82	MET	2.7

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Mol	Chain	Res	Type	RSRZ
3	CC	43	LEU	2.7
4	CD	107	PHE	2.7
14	CN	7	LYS	2.7
22	DA	93	G	2.7
2	AB	34	ALA	2.7
14	AN	43	ASN	2.7
10	AJ	26	VAL	2.7
24	DC	220	VAL	2.7
35	DN	94	TYR	2.7
28	DG	129	THR	2.7
4	AD	19	LEU	2.7
28	DG	71	LEU	2.7
1	CA	1001	C	2.7
29	DH	137	GLU	2.7
42	DU	6	ARG	2.7
26	DE	81	GLY	2.7
1	CA	77	A	2.7
22	DA	1420	A	2.7
7	CG	116	MET	2.7
16	CP	3	THR	2.7
28	DG	112	PRO	2.7
2	CB	18	HIS	2.7
7	CG	109	ARG	2.7
26	DE	7	ASP	2.7
40	DS	34	ASP	2.7
26	DE	15	SER	2.7
33	DL	86	GLU	2.7
2	AB	128	LYS	2.7
22	DA	2165	C	2.7
22	DA	2175	C	2.7
26	DE	8	ALA	2.7
29	BH	36	ALA	2.7
29	DH	71	LYS	2.7
30	DI	40	LYS	2.7
44	DW	33	ALA	2.7
1	CA	1361	G	2.7
25	DD	185	ASN	2.7
28	DG	79	VAL	2.7
10	CJ	68	ARG	2.7
11	AK	82	LEU	2.7
35	DN	95	THR	2.7
46	DY	28	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
51	D3	2	PRO	2.7
6	CF	36	ILE	2.7
2	CB	88	ASP	2.7
12	CL	76	GLU	2.7
44	DW	85	GLU	2.7
53	B5	190	ILE	2.7
17	CQ	36	LYS	2.7
9	AI	128	SER	2.7
22	BA	2109	U	2.7
38	DQ	21	ALA	2.7
25	DD	158	GLY	2.7
26	DE	126	VAL	2.7
33	DL	93	ASN	2.7
42	DU	34	VAL	2.7
47	DZ	11	ARG	2.7
1	CA	1362	A	2.7
24	DC	205	LEU	2.7
25	DD	156	PHE	2.7
30	DI	141	GLU	2.7
41	DT	5	GLU	2.7
43	BV	69	GLU	2.7
47	DZ	3	LYS	2.7
49	D1	27	LYS	2.7
50	D2	31	LEU	2.7
47	DZ	44	ILE	2.7
19	CS	27	ASP	2.7
26	DE	60	TRP	2.7
27	DF	135	GLN	2.7
29	DH	136	SER	2.7
22	DA	1117	C	2.7
24	DC	238	ARG	2.7
26	DE	28	VAL	2.7
26	DE	67	ARG	2.7
28	DG	90	VAL	2.7
41	DT	85	VAL	2.7
1	CA	101	A	2.6
16	CP	48	GLU	2.6
21	CU	24	GLU	2.6
22	DA	2127	G	2.6
31	DJ	125	TYR	2.6
41	DT	52	GLU	2.6
19	AS	64	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
28	DG	80	THR	2.6
35	DN	36	THR	2.6
9	CI	108	ALA	2.6
2	AB	35	ARG	2.6
13	AM	113	ARG	2.6
24	DC	48	ARG	2.6
26	DE	9	GLN	2.6
51	D3	21	GLY	2.6
24	DC	272	SER	2.6
1	CA	1320	C	2.6
45	DX	38	PHE	2.6
46	DY	26	PHE	2.6
1	AA	1493	A	2.6
1	CA	1493	A	2.6
2	AB	40	ILE	2.6
22	DA	1413	A	2.6
34	DM	72	PRO	2.6
1	CA	79	G	2.6
22	DA	1311	G	2.6
3	CC	180	ALA	2.6
11	AK	66	ALA	2.6
14	CN	22	ALA	2.6
14	CN	99	ALA	2.6
32	DK	105	ARG	2.6
38	DQ	30	ARG	2.6
27	DF	151	GLY	2.6
29	DH	107	GLY	2.6
7	CG	77	SER	2.6
33	DL	120	VAL	2.6
41	DT	56	GLU	2.6
10	CJ	92	LEU	2.6
37	BP	114	LEU	2.6
3	AC	193	TYR	2.6
6	CF	6	ILE	2.6
16	CP	35	ARG	2.6
9	CI	125	PRO	2.6
24	DC	74	ILE	2.6
28	DG	176	LYS	2.6
30	DI	100	LYS	2.6
34	DM	8	LYS	2.6
42	DU	19	LYS	2.6
52	D4	29	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
22	DA	289	G	2.6
10	CJ	47	GLU	2.6
7	AG	148	ASN	2.6
35	DN	38	LEU	2.6
2	AB	136	MET	2.6
32	DK	2	ILE	2.6
26	DE	22	ASP	2.6
28	DG	7	ALA	2.6
22	DA	1177	G	2.6
22	DA	2121	G	2.6
4	AD	23	SER	2.6
32	DK	67	LYS	2.6
3	CC	64	ILE	2.6
16	CP	42	ILE	2.6
22	DA	1090	A	2.6
33	DL	133	ALA	2.6
43	DV	45	ASP	2.6
29	DH	109	GLU	2.6
52	B4	12	ARG	2.6
11	AK	74	VAL	2.6
18	CR	40	VAL	2.6
31	DJ	21	THR	2.6
37	DP	92	VAL	2.6
39	DR	58	VAL	2.6
22	BA	546	U	2.6
22	BA	2132	U	2.6
22	DA	139	U	2.6
1	CA	212	G	2.6
25	DD	199	SER	2.6
1	CA	1132	C	2.6
1	CA	1218	C	2.6
2	CB	155	GLY	2.6
28	DG	141	ILE	2.6
2	CB	133	GLU	2.6
1	CA	1324	A	2.6
3	CC	88	ARG	2.6
29	DH	65	ALA	2.6
37	BP	102	GLU	2.6
41	DT	91	GLN	2.6
27	DF	47	LYS	2.6
30	BI	60	THR	2.6
36	DO	5	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	AA	1026	G	2.6
1	CA	1454	G	2.6
2	CB	154	MET	2.6
22	DA	315	G	2.6
29	BH	73	ASN	2.6
30	DI	125	MET	2.6
51	D3	8	ARG	2.6
3	CC	133	ALA	2.6
13	CM	15	ALA	2.6
1	AA	841	C	2.6
32	DK	102	PRO	2.6
1	CA	205	A	2.6
22	DA	342	A	2.6
3	CC	15	VAL	2.6
11	AK	27	PHE	2.6
16	CP	56	ARG	2.6
20	CT	80	THR	2.6
22	DA	2797	U	2.6
9	CI	13	LYS	2.6
10	CJ	12	ALA	2.6
13	CM	100	GLN	2.6
20	CT	81	ALA	2.6
28	DG	88	GLN	2.6
41	BT	92	ASN	2.6
43	DV	1	MET	2.6
22	BA	1063	G	2.6
3	CC	23	PHE	2.5
6	CF	8	PHE	2.5
7	AG	48	GLU	2.5
12	CL	7	LEU	2.5
13	CM	62	LYS	2.5
29	DH	89	LYS	2.5
30	DI	50	GLU	2.5
33	DL	141	LYS	2.5
30	DI	27	ALA	2.5
37	DP	19	SER	2.5
24	DC	225	MET	2.5
42	BU	75	ALA	2.5
22	BA	846	U	2.5
9	CI	95	ARG	2.5
11	AK	84	VAL	2.5
14	CN	9	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
21	AU	28	VAL	2.5
22	BA	613	A	2.5
26	DE	14	VAL	2.5
27	DF	92	ARG	2.5
34	DM	10	ARG	2.5
38	DQ	100	VAL	2.5
39	DR	20	VAL	2.5
12	AL	123	LYS	2.5
13	AM	41	GLU	2.5
36	DO	20	GLU	2.5
49	D1	25	LYS	2.5
49	D1	30	LYS	2.5
3	CC	197	GLY	2.5
10	CJ	25	ILE	2.5
7	CG	150	ALA	2.5
9	CI	5	GLN	2.5
4	AD	119	SER	2.5
30	BI	48	SER	2.5
2	AB	123	ASP	2.5
8	CH	48	ASP	2.5
20	CT	60	ARG	2.5
14	CN	101	TRP	2.5
24	DC	3	VAL	2.5
26	DE	76	PRO	2.5
1	AA	998	C	2.5
22	BA	1913	A	2.5
22	DA	89	A	2.5
22	DA	2176	A	2.5
42	DU	10	GLU	2.5
11	CK	43	GLY	2.5
2	CB	83	ALA	2.5
3	CC	94	ILE	2.5
3	CC	207	ILE	2.5
2	CB	189	THR	2.5
13	CM	108	THR	2.5
28	DG	46	ALA	2.5
28	DG	127	THR	2.5
42	DU	64	ALA	2.5
26	DE	47	LYS	2.5
45	DX	10	LYS	2.5
9	AI	89	GLU	2.5
9	CI	92	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
28	DG	76	VAL	2.5
46	DY	17	GLU	2.5
19	CS	26	GLY	2.5
22	DA	654	A	2.5
22	DA	1111	A	2.5
22	DA	2008	C	2.5
6	AF	91	ARG	2.5
31	DJ	95	ARG	2.5
38	DQ	14	HIS	2.5
7	CG	98	ALA	2.5
22	DA	2116	G	2.5
26	DE	77	ILE	2.5
35	DN	77	ALA	2.5
33	DL	14	LYS	2.5
28	DG	60	ASP	2.5
35	DN	70	THR	2.5
4	CD	143	VAL	2.5
7	CG	105	VAL	2.5
25	DD	90	PHE	2.5
29	DH	61	VAL	2.5
36	DO	43	ASN	2.5
5	CE	128	TYR	2.5
5	CE	108	GLY	2.5
17	AQ	73	TRP	2.5
9	CI	100	LYS	2.5
1	CA	1034	G	2.5
22	DA	2308	G	2.5
7	CG	63	GLU	2.5
41	DT	54	GLU	2.5
42	DU	88	GLU	2.5
21	AU	51	SER	2.5
13	CM	105	ASN	2.5
34	DM	17	ASN	2.5
19	AS	71	LEU	2.5
53	B5	186	LEU	2.5
9	CI	37	GLN	2.5
24	DC	135	ILE	2.5
36	DO	110	ALA	2.5
7	CG	67	GLU	2.5
31	DJ	37	ARG	2.5
3	CC	39	VAL	2.5
13	CM	25	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
28	BG	101	ASN	2.5
42	DU	17	LYS	2.5
7	AG	59	LEU	2.5
12	CL	81	LEU	2.5
22	DA	1084	A	2.5
7	CG	142	HIS	2.5
22	DA	318	C	2.5
29	BH	65	ALA	2.5
32	DK	39	ILE	2.5
7	CG	70	ARG	2.5
27	DF	125	ARG	2.5
9	AI	104	VAL	2.5
15	AO	43	PHE	2.5
29	DH	46	PHE	2.5
33	BL	122	VAL	2.5
41	DT	31	VAL	2.5
53	B5	206	LYS	2.5
17	AQ	7	THR	2.5
9	AI	23	PRO	2.5
14	CN	79	LEU	2.5
22	DA	2152	G	2.5
30	BI	118	THR	2.5
12	AL	14	ARG	2.5
26	DE	181	ILE	2.5
30	DI	103	ARG	2.5
41	DT	41	ALA	2.5
45	BX	20	HIS	2.5
22	BA	2129	C	2.5
34	DM	100	LYS	2.5
17	CQ	17	MET	2.5
39	DR	69	GLY	2.5
24	DC	29	PRO	2.4
26	DE	43	THR	2.4
40	DS	88	ARG	2.4
46	DY	25	GLN	2.4
7	CG	56	LYS	2.4
22	DA	1868	C	2.4
15	CO	15	PHE	2.4
4	AD	178	MET	2.4
5	CE	46	VAL	2.4
9	CI	19	VAL	2.4
39	DR	1	MET	2.4

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Mol	Chain	Res	Type	RSRZ
5	CE	93	ARG	2.4
2	AB	226	SER	2.4
5	AE	65	GLU	2.4
26	DE	133	LEU	2.4
35	DN	115	LEU	2.4
9	CI	32	GLN	2.4
24	DC	244	PRO	2.4
28	DG	27	LYS	2.4
2	CB	209	ALA	2.4
27	DF	53	ALA	2.4
1	CA	81	A	2.4
1	CA	1279	G	2.4
22	DA	1538	G	2.4
7	AG	53	ARG	2.4
7	AG	81	GLY	2.4
45	DX	46	PHE	2.4
17	CQ	46	VAL	2.4
29	DH	134	VAL	2.4
19	CS	6	LYS	2.4
19	CS	73	GLU	2.4
33	DL	125	LEU	2.4
37	DP	112	GLU	2.4
44	BW	85	GLU	2.4
44	DW	29	GLU	2.4
9	CI	14	SER	2.4
14	CN	56	SER	2.4
30	DI	26	PRO	2.4
42	DU	46	GLN	2.4
25	DD	91	THR	2.4
1	CA	1248	A	2.4
19	CS	3	ARG	2.4
22	BA	1919	A	2.4
27	DF	71	ARG	2.4
32	DK	98	ARG	2.4
39	DR	66	HIS	2.4
23	DB	18	G	2.4
25	DD	200	ASP	2.4
2	AB	154	MET	2.4
4	AD	179	GLU	2.4
42	DU	91	LYS	2.4
6	AF	61	LEU	2.4
16	AP	18	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
34	DM	60	GLN	2.4
39	DR	6	GLN	2.4
1	CA	1025	U	2.4
4	AD	70	ARG	2.4
22	DA	2131	U	2.4
9	CI	7	TYR	2.4
1	CA	983	A	2.4
1	CA	1022	A	2.4
22	DA	1590	A	2.4
30	BI	137	GLY	2.4
44	DW	79	PHE	2.4
28	DG	41	VAL	2.4
7	AG	23	LEU	2.4
22	DA	885	C	2.4
45	BX	71	LEU	2.4
29	BH	111	ALA	2.4
36	DO	70	ALA	2.4
38	DQ	113	ALA	2.4
41	DT	13	ALA	2.4
11	AK	58	SER	2.4
34	DM	46	ILE	2.4
5	CE	103	THR	2.4
25	DD	126	ASN	2.4
41	DT	92	ASN	2.4
1	CA	72	A	2.4
1	CA	1287	A	2.4
9	CI	42	GLU	2.4
4	AD	143	VAL	2.4
8	CH	104	VAL	2.4
10	CJ	60	ASP	2.4
26	DE	29	HIS	2.4
27	DF	140	GLU	2.4
36	DO	112	GLU	2.4
13	AM	109	ARG	2.4
31	DJ	96	ARG	2.4
37	DP	72	ARG	2.4
1	CA	1013	G	2.4
2	CB	160	ALA	2.4
28	DG	121	ILE	2.4
41	DT	26	LYS	2.4
25	DD	80	TRP	2.4
1	CA	208	U	2.4

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Mol	Chain	Res	Type	RSRZ
7	CG	122	ASN	2.4
27	DF	162	SER	2.4
29	DH	16	GLY	2.4
19	CS	10	PHE	2.4
13	CM	60	VAL	2.4
22	DA	196	A	2.4
22	DA	1745	A	2.4
25	DD	188	LEU	2.4
29	BH	15	LEU	2.4
27	DF	81	GLN	2.4
29	BH	141	LYS	2.4
30	DI	92	LYS	2.4
39	DR	60	LYS	2.4
1	CA	1359	C	2.4
32	DK	83	ALA	2.4
22	DA	1091	G	2.4
23	DB	20	G	2.4
25	DD	88	GLU	2.4
27	DF	97	TRP	2.4
33	DL	130	GLY	2.4
2	AB	30	PHE	2.4
9	CI	12	ARG	2.4
38	DQ	32	TYR	2.4
13	CM	42	ASP	2.4
14	AN	33	ASP	2.4
24	DC	257	THR	2.4
40	DS	109	ASP	2.4
48	D0	42	HIS	2.4
2	CB	152	LYS	2.4
4	CD	185	LYS	2.4
28	BG	176	LYS	2.4
13	CM	5	ALA	2.4
33	DL	72	ALA	2.4
17	AQ	55	ILE	2.4
20	AT	67	ILE	2.4
41	DT	90	GLY	2.4
45	DX	76	GLU	2.4
51	D3	20	GLY	2.4
51	D3	59	ILE	2.4
31	DJ	46	PRO	2.4
35	DN	39	PRO	2.4
45	DX	72	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
29	BH	25	TYR	2.4
38	DQ	24	TYR	2.4
45	DX	7	VAL	2.4
7	AG	84	THR	2.4
25	DD	197	THR	2.4
1	AA	994	A	2.3
28	DG	22	GLN	2.3
35	DN	1	MET	2.3
27	DF	19	GLU	2.3
40	DS	43	ALA	2.3
33	DL	102	GLY	2.3
22	DA	275	C	2.3
38	DQ	74	ILE	2.3
40	DS	35	ILE	2.3
5	CE	114	VAL	2.3
16	AP	21	VAL	2.3
1	CA	1041	G	2.3
22	DA	317	G	2.3
2	CB	108	ARG	2.3
4	CD	35	GLU	2.3
22	DA	1744	A	2.3
40	DS	15	GLN	2.3
41	BT	91	GLN	2.3
6	AF	51	ILE	2.3
9	CI	8	GLY	2.3
24	BC	18	LYS	2.3
27	DF	44	ILE	2.3
28	DG	99	LYS	2.3
33	DL	84	LYS	2.3
1	CA	1209	C	2.3
4	AD	72	PHE	2.3
22	DA	2310	C	2.3
7	CG	45	SER	2.3
11	AK	53	ARG	2.3
29	DH	123	ARG	2.3
34	DM	106	ASP	2.3
39	DR	26	ASP	2.3
15	AO	3	LEU	2.3
1	AA	1000	A	2.3
3	AC	79	LYS	2.3
7	CG	108	ALA	2.3
21	AU	23	CYS	2.3

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Mol	Chain	Res	Type	RSRZ
22	DA	914	G	2.3
29	DH	105	ALA	2.3
38	DQ	41	LYS	2.3
51	D3	6	THR	2.3
33	DL	105	ILE	2.3
40	DS	96	ILE	2.3
49	D1	39	PHE	2.3
10	CJ	43	PRO	2.3
16	AP	51	ARG	2.3
50	D2	39	ARG	2.3
4	AD	93	LEU	2.3
4	AD	166	GLU	2.3
7	CG	124	LEU	2.3
26	DE	2	GLU	2.3
37	DP	6	LYS	2.3
40	DS	90	LYS	2.3
10	CJ	33	GLY	2.3
22	DA	2154	A	2.3
28	DG	36	THR	2.3
28	DG	78	GLY	2.3
30	BI	131	GLY	2.3
33	DL	83	ALA	2.3
33	DL	87	GLY	2.3
37	DP	23	GLY	2.3
40	DS	86	MET	2.3
1	CA	1455	G	2.3
3	CC	162	ILE	2.3
22	DA	1303	G	2.3
22	DA	1450	G	2.3
31	DJ	55	ILE	2.3
32	DK	115	ILE	2.3
21	CU	21	ARG	2.3
19	AS	21	LYS	2.3
24	DC	19	VAL	2.3
44	DW	70	GLU	2.3
2	AB	153	ASP	2.3
46	DY	4	LYS	2.3
9	AI	98	LEU	2.3
13	AM	95	LEU	2.3
29	DH	122	LEU	2.3
18	CR	32	TYR	2.3
24	DC	76	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
25	DD	115	GLY	2.3
29	BH	64	ALA	2.3
30	DI	124	ALA	2.3
37	DP	42	ALA	2.3
2	CB	130	THR	2.3
22	DA	603	A	2.3
29	DH	72	ILE	2.3
37	DP	31	TRP	2.3
25	DD	68	PHE	2.3
47	DZ	53	PHE	2.3
1	CA	954	G	2.3
1	CA	1242	G	2.3
22	BA	1921	G	2.3
33	DL	143	GLU	2.3
38	DQ	34	VAL	2.3
1	CA	206	C	2.3
3	AC	43	LEU	2.3
7	AG	86	GLN	2.3
27	BF	81	GLN	2.3
30	BI	107	GLN	2.3
38	DQ	71	GLN	2.3
39	DR	18	GLN	2.3
21	CU	9	ASN	2.3
26	DE	72	SER	2.3
49	D1	19	HIS	2.3
16	CP	1	MET	2.3
1	CA	74	A	2.3
22	DA	2749	A	2.3
37	DP	50	ILE	2.3
24	DC	36	LYS	2.3
14	CN	26	GLU	2.3
39	DR	62	GLU	2.3
27	DF	29	PRO	2.3
28	BG	113	VAL	2.3
1	CA	68	G	2.3
1	CA	1310	G	2.3
2	AB	57	LEU	2.3
2	AB	214	LEU	2.3
22	DA	2802	G	2.3
27	DF	16	LEU	2.3
31	DJ	14	ASP	2.3
2	CB	51	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
3	CC	27	LYS	2.3
3	CC	89	LYS	2.3
26	DE	179	SER	2.3
27	DF	37	ASN	2.3
30	DI	128	SER	2.3
3	AC	64	ILE	2.3
1	CA	250	A	2.3
2	AB	69	PHE	2.3
7	AG	26	PHE	2.3
14	AN	26	GLU	2.3
22	BA	1918	A	2.3
2	CB	125	THR	2.3
47	DZ	10	THR	2.3
6	AF	96	VAL	2.3
22	DA	1173	U	2.3
25	DD	104	VAL	2.3
26	DE	121	VAL	2.3
35	DN	116	VAL	2.3
4	CD	46	PRO	2.3
42	DU	66	GLN	2.3
43	DV	33	GLY	2.3
25	DD	54	ALA	2.3
43	DV	74	ALA	2.3
28	DG	125	CYS	2.3
38	DQ	90	ILE	2.3
38	DQ	106	PHE	2.3
3	CC	107	ARG	2.3
24	DC	223	THR	2.3
28	BG	11	VAL	2.3
4	AD	94	LEU	2.3
30	DI	105	GLN	2.3
51	D3	41	LYS	2.3
13	CM	61	ALA	2.2
1	AA	88	U	2.2
1	AA	1043	G	2.2
2	AB	213	TYR	2.2
25	DD	24	VAL	2.2
33	DL	90	VAL	2.2
28	DG	31	GLY	2.2
29	BH	16	GLY	2.2
40	DS	39	THR	2.2
41	DT	29	THR	2.2

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Mol	Chain	Res	Type	RSRZ
22	DA	1065	U	2.2
45	DX	21	ALA	2.2
27	DF	134	GLU	2.2
30	BI	50	GLU	2.2
36	DO	111	ARG	2.2
44	DW	77	ARG	2.2
46	DY	23	ARG	2.2
3	CC	149	ILE	2.2
30	DI	109	ILE	2.2
47	DZ	32	ILE	2.2
2	AB	27	MET	2.2
9	CI	73	SER	2.2
1	AA	1034	G	2.2
42	DU	24	LYS	2.2
1	AA	1004	A	2.2
1	CA	80	A	2.2
1	CA	1219	A	2.2
1	CA	1441	A	2.2
5	AE	117	VAL	2.2
7	CG	32	VAL	2.2
14	AN	84	VAL	2.2
2	CB	68	LEU	2.2
7	AG	66	LEU	2.2
20	AT	66	LEU	2.2
27	BF	117	LEU	2.2
49	D1	17	THR	2.2
3	CC	54	ARG	2.2
9	CI	119	ARG	2.2
10	CJ	86	ALA	2.2
14	AN	25	ALA	2.2
29	DH	148	ALA	2.2
42	DU	82	ARG	2.2
16	CP	38	PHE	2.2
27	BF	122	PHE	2.2
28	DG	19	ILE	2.2
43	DV	26	PHE	2.2
2	AB	100	MET	2.2
22	DA	2601	C	2.2
25	DD	1	MET	2.2
40	DS	1	MET	2.2
50	D2	16	HIS	2.2
41	DT	78	SER	2.2

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Mol	Chain	Res	Type	RSRZ
2	AB	114	LEU	2.2
20	CT	82	GLN	2.2
22	BA	654	A	2.2
37	DP	105	GLY	2.2
32	DK	3	GLN	2.2
42	BU	52	LEU	2.2
28	DG	124	GLU	2.2
33	BL	115	GLU	2.2
7	AG	71	PRO	2.2
17	CQ	39	LYS	2.2
45	DX	39	TRP	2.2
9	AI	28	ILE	2.2
17	CQ	61	ILE	2.2
1	CA	83	C	2.2
1	CA	1273	C	2.2
1	CA	1322	C	2.2
16	AP	40	ASN	2.2
33	DL	4	ASN	2.2
7	AG	143	ARG	2.2
13	CM	88	GLY	2.2
28	BG	15	VAL	2.2
52	D4	36	ARG	2.2
3	CC	33	LEU	2.2
9	CI	110	GLN	2.2
22	BA	2151	U	2.2
32	BK	107	LEU	2.2
37	DP	34	GLU	2.2
2	CB	159	ASP	2.2
26	DE	74	LYS	2.2
27	DF	45	ALA	2.2
43	DV	81	PRO	2.2
8	CH	7	ILE	2.2
14	AN	31	ILE	2.2
9	CI	33	ARG	2.2
36	DO	15	ARG	2.2
39	DR	68	ARG	2.2
44	DW	55	ARG	2.2
6	CF	21	MET	2.2
9	CI	82	GLY	2.2
22	DA	1030	C	2.2
22	DA	1104	C	2.2
22	DA	1732	C	2.2

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Mol	Chain	Res	Type	RSRZ
22	DA	2795	C	2.2
24	DC	12	GLY	2.2
11	CK	55	SER	2.2
17	CQ	43	LYS	2.2
26	DE	10	SER	2.2
29	BH	21	VAL	2.2
22	DA	1089	A	2.2
22	DA	1169	A	2.2
27	DF	2	ALA	2.2
1	CA	843	U	2.2
22	DA	288	U	2.2
22	DA	1116	G	2.2
22	DA	2107	G	2.2
23	DB	117	G	2.2
24	DC	231	PRO	2.2
29	DH	32	PRO	2.2
3	CC	143	ARG	2.2
9	CI	123	ARG	2.2
36	DO	81	ARG	2.2
2	CB	202	GLY	2.2
15	CO	6	GLU	2.2
28	DG	85	LYS	2.2
31	DJ	115	GLY	2.2
38	DQ	112	LYS	2.2
49	D1	7	GLU	2.2
29	DH	119	ASN	2.2
22	DA	1045	C	2.2
25	DD	73	VAL	2.2
14	AN	2	ALA	2.2
22	DA	1365	A	2.2
26	DE	154	ASP	2.2
31	DJ	60	ASP	2.2
37	DP	91	ALA	2.2
2	CB	48	PRO	2.2
21	AU	37	PHE	2.2
8	CH	75	ILE	2.2
10	AJ	100	ILE	2.2
11	CK	34	ILE	2.2
26	DE	65	THR	2.2
1	CA	76	G	2.2
7	AG	106	GLU	2.2
22	DA	548	G	2.2

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Mol	Chain	Res	Type	RSRZ
22	DA	1106	G	2.2
2	CB	199	VAL	2.2
8	CH	72	VAL	2.2
17	CQ	31	HIS	2.2
22	DA	2181	U	2.2
5	AE	115	LEU	2.2
5	CE	115	LEU	2.2
10	AJ	73	LEU	2.2
13	AM	80	LEU	2.2
24	DC	83	TYR	2.2
26	DE	135	ALA	2.2
26	DE	182	ALA	2.2
32	DK	33	ALA	2.2
44	DW	84	ALA	2.2
2	AB	127	ASP	2.2
22	DA	1551	A	2.2
22	DA	2142	A	2.2
30	BI	72	LYS	2.2
7	CG	21	GLU	2.2
24	DC	116	ILE	2.2
27	BF	44	ILE	2.2
28	DG	26	ILE	2.2
35	DN	85	PRO	2.2
52	D4	31	PRO	2.2
33	DL	76	GLU	2.2
11	AK	111	THR	2.2
36	DO	96	GLY	2.2
1	CA	1255	G	2.2
7	CG	120	LEU	2.2
13	CM	90	ARG	2.2
24	DC	65	VAL	2.2
26	DE	114	ARG	2.2
29	BH	18	GLN	2.2
31	DJ	124	VAL	2.2
39	DR	22	LEU	2.2
22	DA	22	C	2.1
22	DA	1053	C	2.1
22	DA	1614	A	2.1
26	DE	19	PHE	2.1
27	DF	174	ASP	2.1
3	CC	174	PRO	2.1
7	AG	8	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
13	CM	22	ILE	2.1
29	DH	4	ILE	2.1
9	AI	33	ARG	2.1
48	D0	30	VAL	2.1
6	AF	42	TRP	2.1
22	BA	1094	U	2.1
20	CT	46	ALA	2.1
25	DD	41	ALA	2.1
26	DE	45	ALA	2.1
44	DW	24	LYS	2.1
34	DM	88	ASN	2.1
37	DP	66	ASN	2.1
4	AD	189	SER	2.1
11	AK	18	ASP	2.1
16	AP	38	PHE	2.1
22	BA	140	C	2.1
22	DA	2145	C	2.1
22	DA	2666	C	2.1
41	DT	17	SER	2.1
2	AB	63	ARG	2.1
17	AQ	6	ARG	2.1
17	CQ	6	ARG	2.1
33	DL	103	ILE	2.1
42	BU	48	PRO	2.1
1	CA	121	U	2.1
3	AC	80	LYS	2.1
7	AG	110	LYS	2.1
8	CH	22	LYS	2.1
6	CF	62	MET	2.1
8	CH	55	THR	2.1
13	CM	65	VAL	2.1
26	DE	41	GLN	2.1
33	DL	128	THR	2.1
34	DM	132	THR	2.1
3	AC	37	PHE	2.1
15	AO	17	ARG	2.1
20	CT	14	SER	2.1
32	DK	37	ASP	2.1
22	DA	41	C	2.1
22	DA	1185	G	2.1
32	DK	108	ARG	2.1
10	AJ	38	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
18	AR	39	ILE	2.1
22	DA	1048	A	2.1
27	DF	141	ILE	2.1
39	DR	41	ILE	2.1
2	CB	105	LYS	2.1
24	DC	111	LYS	2.1
3	CC	128	VAL	2.1
9	AI	32	GLN	2.1
52	D4	37	GLN	2.1
30	BI	106	LEU	2.1
37	DP	8	LEU	2.1
37	DP	76	THR	2.1
3	CC	104	ALA	2.1
26	DE	152	GLU	2.1
44	DW	46	HIS	2.1
27	DF	178	ARG	2.1
24	DC	45	ASN	2.1
42	DU	96	PHE	2.1
3	CC	53	SER	2.1
14	CN	80	SER	2.1
34	DM	39	GLY	2.1
48	D0	29	SER	2.1
15	AO	11	ILE	2.1
38	DQ	40	ILE	2.1
1	AA	926	G	2.1
22	DA	1869	G	2.1
3	AC	100	GLN	2.1
10	CJ	36	VAL	2.1
34	DM	26	VAL	2.1
34	DM	89	VAL	2.1
3	CC	40	ARG	2.1
40	DS	23	LEU	2.1
49	D1	32	GLU	2.1
52	D4	19	ARG	2.1
6	CF	92	THR	2.1
7	AG	44	TYR	2.1
25	DD	114	LYS	2.1
3	CC	17	PRO	2.1
22	DA	354	A	2.1
10	AJ	31	ARG	2.1
11	AK	113	VAL	2.1
13	AM	107	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
2	CB	145	GLU	2.1
4	CD	159	LEU	2.1
13	AM	83	LEU	2.1
22	DA	953	G	2.1
27	DF	150	ARG	2.1
45	BX	72	ARG	2.1
47	DZ	24	LEU	2.1
48	D0	36	GLU	2.1
52	D4	22	VAL	2.1
2	AB	15	HIS	2.1
7	AG	17	LYS	2.1
14	AN	12	LYS	2.1
22	DA	2149	U	2.1
27	BF	116	GLY	2.1
53	B5	177	GLY	2.1
4	CD	144	SER	2.1
10	CJ	37	ARG	2.1
14	CN	61	ARG	2.1
28	BG	153	ARG	2.1
31	BJ	96	ARG	2.1
32	DK	109	SER	2.1
1	AA	995	C	2.1
9	CI	47	VAL	2.1
10	CJ	59	LYS	2.1
24	DC	154	LEU	2.1
29	DH	141	LYS	2.1
34	DM	11	LYS	2.1
45	DX	4	VAL	2.1
22	DA	1228	G	2.1
26	DE	26	ALA	2.1
36	DO	82	ALA	2.1
37	DP	13	MET	2.1
39	DR	61	ALA	2.1
2	AB	50	PHE	2.1
9	CI	81	HIS	2.1
33	DL	140	GLY	2.1
43	DV	55	GLU	2.1
24	DC	24	LEU	2.1
25	DD	5	VAL	2.1
28	BG	72	LEU	2.1
29	DH	110	VAL	2.1
44	DW	31	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
11	CK	71	ALA	2.1
24	DC	31	ALA	2.1
26	DE	161	ALA	2.1
43	DV	6	ALA	2.1
45	DX	73	ALA	2.1
3	CC	78	GLY	2.1
13	CM	111	GLY	2.1
24	BC	240	PHE	2.1
1	CA	1131	G	2.1
7	CG	119	ARG	2.1
9	AI	122	ARG	2.1
24	DC	237	GLY	2.1
46	DY	1	MET	2.1
25	DD	128	ARG	2.1
26	DE	21	ARG	2.1
28	BG	111	HIS	2.1
52	D4	24	ARG	2.1
2	CB	102	THR	2.1
3	CC	80	LYS	2.1
9	AI	27	LYS	2.1
10	AJ	30	LYS	2.1
31	DJ	75	TYR	2.1
2	CB	110	SER	2.1
12	CL	29	GLN	2.1
1	AA	1441	A	2.1
1	CA	1274	A	2.1
11	AK	129	VAL	2.1
29	BH	108	VAL	2.1
5	CE	110	ALA	2.1
22	BA	1100	C	2.1
1	CA	85	U	2.0
2	CB	126	PHE	2.0
38	DQ	11	ARG	2.1
50	D2	34	ARG	2.1
13	CM	67	GLY	2.0
26	DE	171	ASP	2.0
40	DS	94	ASP	2.0
1	CA	942	G	2.0
9	AI	83	ILE	2.0
17	CQ	7	THR	2.0
20	AT	39	ILE	2.0
22	DA	7	G	2.0

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Mol	Chain	Res	Type	RSRZ
22	DA	882	G	2.0
22	DA	1684	G	2.0
25	DD	22	ILE	2.0
35	DN	112	TYR	2.0
10	CJ	35	GLN	2.0
4	AD	115	ARG	2.0
4	CD	130	VAL	2.0
9	CI	113	ARG	2.0
15	CO	67	LEU	2.0
27	DF	110	ARG	2.0
29	DH	19	VAL	2.0
1	AA	1036	A	2.0
1	CA	1275	A	2.0
3	AC	104	ALA	2.0
11	AK	85	MET	2.0
7	CG	40	GLU	2.0
19	CS	20	GLU	2.0
39	DR	70	GLU	2.0
40	DS	74	ILE	2.0
43	BV	70	ILE	2.0
43	DV	89	ILE	2.0
3	CC	100	GLN	2.0
22	DA	2155	U	2.0
1	AA	993	G	2.0
17	AQ	23	VAL	2.0
22	DA	1530	G	2.0
25	DD	4	LEU	2.0
51	D3	55	LEU	2.0
1	CA	71	A	2.0
8	CH	50	LYS	2.0
11	CK	80	LYS	2.0
30	BI	89	GLY	2.0
41	DT	51	PHE	2.0
1	CA	87	C	2.0
22	DA	2151	U	2.0
28	DG	16	ASP	2.0
6	CF	44	ARG	2.0
24	DC	102	ARG	2.0
26	DE	79	ARG	2.0
49	D1	46	HIS	2.0
27	BF	156	ILE	2.0
28	DG	116	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
2	AB	129	LEU	2.0
4	CD	125	VAL	2.0
17	CQ	29	VAL	2.0
25	DD	116	LYS	2.0
30	BI	9	VAL	2.0
39	DR	47	VAL	2.0
41	BT	7	LEU	2.0
51	D3	36	LYS	2.0
1	AA	988	G	2.0
1	CA	102	G	2.0
11	AK	52	PHE	2.0
22	DA	180	G	2.0
22	DA	1066	U	2.0
29	BH	13	GLY	2.0
34	DM	29	GLY	2.0
10	CJ	24	GLU	2.0
8	CH	113	ASP	2.0
18	CR	22	ASP	2.0
22	DA	436	C	2.0
22	DA	531	C	2.0
10	CJ	40	ILE	2.0
10	CJ	70	HIS	2.0
51	B3	4	ILE	2.0
3	CC	135	LYS	2.0
11	AK	80	LYS	2.0
40	DS	27	LYS	2.0
9	AI	48	VAL	2.0
17	AQ	70	THR	2.0
20	CT	70	ASN	2.0
34	DM	107	GLY	2.0
3	CC	125	GLU	2.0
8	CH	81	PRO	2.0
9	CI	34	SER	2.0
13	CM	112	PRO	2.0
28	DG	54	PRO	2.0
37	DP	22	PRO	2.0
54	D6	4	PRO	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
54	004	D6	7	10/11	0.90	0.20	-	38,42,48,48	0
54	MHU	B6	5	15/16	0.97	0.23	-	0,5,18,21	0
54	MHV	B6	6	9/10	0.98	0.16	-	2,6,13,14	0
54	MHW	D6	1	9/10	0.77	0.33	-	49,54,56,59	0
54	MHW	B6	1	9/10	0.95	0.21	-	12,14,18,21	0
54	004	B6	7	10/11	0.97	0.29	-	3,6,7,10	0
54	DBB	D6	3	6/7	0.91	0.28	-	37,40,41,43	0
54	MHU	D6	5	15/16	0.89	0.36	-	37,42,54,56	0
54	MHV	D6	6	9/10	0.92	0.16	-	39,40,42,43	0
54	DBB	B6	3	6/7	0.97	0.22	-	6,8,10,15	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
55	MG	BA	3040	1/1	0.88	0.45	27.33	7,7,7,7	0
55	MG	BA	3178	1/1	0.91	0.46	27.24	20,20,20,20	0
55	MG	AA	1669	1/1	0.84	0.55	20.06	43,43,43,43	0
55	MG	DA	3057	1/1	0.78	0.62	17.12	54,54,54,54	0
55	MG	DA	3162	1/1	0.84	0.45	13.43	46,46,46,46	0
55	MG	BA	3186	1/1	0.98	0.35	12.55	18,18,18,18	0
55	MG	DA	3157	1/1	0.95	0.40	11.36	47,47,47,47	0
55	MG	DA	3153	1/1	0.93	0.48	10.59	52,52,52,52	0
55	MG	BA	3170	1/1	0.91	0.29	10.49	35,35,35,35	0
55	MG	DA	3002	1/1	0.89	0.41	10.01	52,52,52,52	0
55	MG	BA	3168	1/1	0.71	0.32	9.32	18,18,18,18	0
55	MG	BA	3116	1/1	0.86	0.31	8.59	11,11,11,11	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	BA	3113	1/1	0.92	0.32	8.46	10,10,10,10	0
55	MG	AA	1622	1/1	0.91	0.27	7.80	21,21,21,21	0
55	MG	BA	3070	1/1	0.94	0.25	7.67	9,9,9,9	0
55	MG	DA	3027	1/1	0.84	0.45	7.63	51,51,51,51	0
55	MG	BA	3108	1/1	0.78	0.28	6.43	1,1,1,1	0
55	MG	DA	3165	1/1	0.93	0.38	5.72	34,34,34,34	0
55	MG	BA	3130	1/1	0.95	0.24	4.49	4,4,4,4	0
55	MG	DA	3013	1/1	0.78	0.37	3.92	45,45,45,45	0
55	MG	DA	3124	1/1	0.76	0.38	3.78	59,59,59,59	0
55	MG	DA	3109	1/1	0.93	0.24	3.70	37,37,37,37	0
55	MG	DA	3070	1/1	0.38	0.35	3.33	58,58,58,58	0
55	MG	BA	3152	1/1	0.97	0.22	3.17	11,11,11,11	0
55	MG	BA	3163	1/1	0.93	0.23	3.16	27,27,27,27	0
55	MG	BA	3153	1/1	0.95	0.30	3.00	2,2,2,2	0
55	MG	DA	3005	1/1	0.35	0.23	2.92	66,66,66,66	0
55	MG	DA	3008	1/1	0.86	0.42	2.61	51,51,51,51	0
55	MG	DA	3071	1/1	0.90	0.28	2.56	59,59,59,59	0
55	MG	BA	3188	1/1	0.75	0.18	2.13	27,27,27,27	0
55	MG	BA	3161	1/1	0.84	0.22	2.02	24,24,24,24	0
55	MG	DA	3116	1/1	0.83	0.20	1.97	51,51,51,51	0
55	MG	BA	3155	1/1	0.92	0.27	1.92	15,15,15,15	0
55	MG	CA	1640	1/1	0.95	0.21	1.82	23,23,23,23	0
55	MG	DA	3047	1/1	0.70	0.31	1.65	66,66,66,66	0
55	MG	BA	3175	1/1	0.83	0.18	1.47	27,27,27,27	0
55	MG	BA	3053	1/1	0.96	0.20	1.41	4,4,4,4	0
55	MG	DA	3040	1/1	0.64	0.26	1.41	57,57,57,57	0
55	MG	DA	3031	1/1	0.80	0.23	1.41	50,50,50,50	0
55	MG	BA	3159	1/1	0.92	0.19	1.40	19,19,19,19	0
55	MG	BA	3107	1/1	0.97	0.20	1.30	6,6,6,6	0
55	MG	BA	3184	1/1	0.96	0.17	1.08	23,23,23,23	0
55	MG	DA	3046	1/1	0.47	0.25	1.05	53,53,53,53	0
55	MG	AA	1662	1/1	0.93	0.19	0.94	41,41,41,41	0
55	MG	AA	1630	1/1	0.65	0.20	0.73	49,49,49,49	0
55	MG	BA	3109	1/1	0.89	0.20	0.64	9,9,9,9	0
55	MG	BA	3034	1/1	0.89	0.20	0.64	18,18,18,18	0
55	MG	CA	1615	1/1	0.88	0.16	0.62	35,35,35,35	0
55	MG	BA	3062	1/1	0.96	0.21	0.57	3,3,3,3	0
55	MG	DA	3068	1/1	0.86	0.19	0.45	52,52,52,52	0
55	MG	DA	3114	1/1	0.94	0.33	0.40	64,64,64,64	0
55	MG	BA	3104	1/1	0.97	0.20	0.27	1,1,1,1	0
55	MG	AA	1641	1/1	0.95	0.18	0.26	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	BA	3012	1/1	0.91	0.21	0.23	4,4,4,4	0
55	MG	DA	3063	1/1	0.93	0.19	0.18	41,41,41,41	0
55	MG	BA	3063	1/1	0.98	0.20	0.15	0,0,0,0	0
55	MG	BA	3047	1/1	0.78	0.14	0.02	34,34,34,34	0
56	ZN	B4	101	1/1	0.96	0.21	-0.22	131,131,131,131	0
55	MG	BA	3105	1/1	0.88	0.19	-0.30	4,4,4,4	0
55	MG	AA	1634	1/1	0.72	0.17	-0.34	36,36,36,36	0
55	MG	BA	3132	1/1	0.91	0.19	-0.40	27,27,27,27	0
55	MG	CA	1603	1/1	0.83	0.14	-0.41	44,44,44,44	0
55	MG	DA	3105	1/1	0.92	0.17	-0.44	37,37,37,37	0
55	MG	AA	1636	1/1	0.97	0.20	-0.47	26,26,26,26	0
55	MG	DA	3018	1/1	0.71	0.18	-0.48	57,57,57,57	0
55	MG	BA	3097	1/1	0.97	0.19	-0.53	6,6,6,6	0
55	MG	AA	1617	1/1	0.77	0.18	-0.55	44,44,44,44	0
55	MG	BA	3165	1/1	0.97	0.16	-0.56	2,2,2,2	0
55	MG	DA	3108	1/1	0.95	0.18	-0.60	35,35,35,35	0
55	MG	BA	3036	1/1	0.90	0.19	-0.61	19,19,19,19	0
55	MG	CA	1630	1/1	0.88	0.26	-0.69	66,66,66,66	0
55	MG	BA	3013	1/1	0.93	0.19	-0.77	0,0,0,0	0
55	MG	DA	3023	1/1	0.64	0.18	-0.79	35,35,35,35	0
55	MG	AA	1607	1/1	0.91	0.15	-0.84	33,33,33,33	0
55	MG	DA	3022	1/1	0.93	0.15	-0.87	54,54,54,54	0
55	MG	DA	3081	1/1	0.93	0.15	-0.94	43,43,43,43	0
55	MG	DA	3107	1/1	0.90	0.14	-1.20	49,49,49,49	0
55	MG	DA	3012	1/1	0.80	0.16	-1.21	40,40,40,40	0
55	MG	DA	3132	1/1	0.88	0.11	-1.25	45,45,45,45	0
55	MG	CA	1614	1/1	0.87	0.09	-1.25	44,44,44,44	0
55	MG	DA	3062	1/1	0.77	0.14	-1.29	44,44,44,44	0
55	MG	DA	3096	1/1	0.93	0.17	-1.40	52,52,52,52	0
55	MG	BA	3112	1/1	0.94	0.16	-1.48	11,11,11,11	0
55	MG	DA	3104	1/1	0.77	0.14	-1.56	54,54,54,54	0
55	MG	BA	3134	1/1	0.87	0.17	-1.58	8,8,8,8	0
56	ZN	D4	101	1/1	0.97	0.05	-1.61	79,79,79,79	0
55	MG	BA	3049	1/1	0.91	0.14	-1.65	9,9,9,9	0
55	MG	DA	3077	1/1	0.61	0.08	-1.79	59,59,59,59	0
55	MG	BA	3071	1/1	0.89	0.16	-1.85	11,11,11,11	0
55	MG	AA	1604	1/1	0.87	0.10	-1.88	45,45,45,45	0
55	MG	CA	1635	1/1	0.60	0.18	-1.91	76,76,76,76	0
55	MG	AA	1629	1/1	0.95	0.12	-1.94	43,43,43,43	0
55	MG	BA	3120	1/1	0.83	0.16	-1.94	7,7,7,7	0
55	MG	DA	3079	1/1	0.82	0.11	-1.98	62,62,62,62	0
55	MG	AA	1642	1/1	0.96	0.13	-2.01	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	BB	201	1/1	0.76	0.10	-2.17	28,28,28,28	0
55	MG	DA	3136	1/1	0.59	0.10	-2.21	57,57,57,57	0
55	MG	BA	3021	1/1	0.92	0.16	-2.21	1,1,1,1	0
55	MG	BA	3022	1/1	0.96	0.16	-2.22	3,3,3,3	0
55	MG	CA	1617	1/1	0.72	0.15	-2.24	35,35,35,35	0
55	MG	DA	3049	1/1	0.63	0.10	-2.26	49,49,49,49	0
55	MG	CA	1632	1/1	0.92	0.13	-2.28	54,54,54,54	0
55	MG	DA	3128	1/1	0.91	0.10	-2.31	57,57,57,57	0
55	MG	BA	3064	1/1	0.90	0.17	-2.44	2,2,2,2	0
55	MG	CA	1624	1/1	0.85	0.13	-2.51	33,33,33,33	0
55	MG	BA	3023	1/1	0.76	0.15	-2.53	15,15,15,15	0
55	MG	BA	3077	1/1	0.83	0.08	-2.54	26,26,26,26	0
55	MG	DA	3095	1/1	0.80	0.10	-2.60	49,49,49,49	0
55	MG	DA	3134	1/1	0.86	0.10	-2.60	34,34,34,34	0
55	MG	AA	1618	1/1	0.81	0.11	-2.62	35,35,35,35	0
55	MG	DA	3053	1/1	0.92	0.12	-2.75	43,43,43,43	0
55	MG	AA	1616	1/1	0.87	0.10	-2.78	42,42,42,42	0
55	MG	BA	3136	1/1	0.96	0.14	-2.79	24,24,24,24	0
55	MG	DA	3078	1/1	0.71	0.10	-2.98	64,64,64,64	0
55	MG	DA	3021	1/1	0.79	0.12	-3.03	38,38,38,38	0
55	MG	DA	3145	1/1	0.95	0.10	-3.05	37,37,37,37	0
55	MG	DA	3026	1/1	0.69	0.10	-3.10	53,53,53,53	0
55	MG	CA	1621	1/1	0.70	0.11	-3.14	53,53,53,53	0
55	MG	BA	3008	1/1	0.82	0.12	-3.18	9,9,9,9	0
55	MG	DA	3097	1/1	0.88	0.08	-3.30	44,44,44,44	0
55	MG	BA	3129	1/1	0.95	0.16	-3.34	5,5,5,5	0
55	MG	BA	3024	1/1	0.94	0.14	-3.34	7,7,7,7	0
55	MG	BA	3177	1/1	0.94	0.09	-3.37	24,24,24,24	0
55	MG	BA	3066	1/1	0.89	0.13	-3.57	6,6,6,6	0
55	MG	BA	3050	1/1	0.92	0.11	-3.70	11,11,11,11	0
55	MG	CA	1616	1/1	0.93	0.11	-3.72	29,29,29,29	0
55	MG	BA	3068	1/1	0.90	0.17	-3.79	6,6,6,6	0
55	MG	CA	1601	1/1	0.72	0.11	-3.83	33,33,33,33	0
55	MG	CA	1610	1/1	0.96	0.09	-3.88	47,47,47,47	0
55	MG	DA	3120	1/1	0.90	0.09	-3.96	49,49,49,49	0
55	MG	BA	3059	1/1	0.94	0.14	-3.97	16,16,16,16	0
55	MG	BA	3079	1/1	0.77	0.11	-4.05	28,28,28,28	0
55	MG	DB	201	1/1	0.92	0.06	-4.12	69,69,69,69	0
55	MG	CA	1619	1/1	0.93	0.11	-4.23	26,26,26,26	0
55	MG	AA	1606	1/1	0.95	0.09	-4.24	31,31,31,31	0
55	MG	BA	3017	1/1	0.97	0.13	-4.25	6,6,6,6	0
55	MG	BA	3065	1/1	0.97	0.11	-4.30	7,7,7,7	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	AA	1613	1/1	0.90	0.11	-4.55	20,20,20,20	0
55	MG	BA	3027	1/1	0.89	0.09	-4.72	22,22,22,22	0
55	MG	DA	3038	1/1	0.81	0.09	-4.76	42,42,42,42	0
55	MG	DA	3050	1/1	0.94	0.07	-4.82	29,29,29,29	0
55	MG	AA	1640	1/1	0.91	0.06	-4.83	39,39,39,39	0
55	MG	DA	3017	1/1	0.80	0.13	-4.97	40,40,40,40	0
55	MG	CA	1626	1/1	0.81	0.08	-5.07	42,42,42,42	0
55	MG	BA	3009	1/1	0.78	0.13	-5.22	6,6,6,6	0
55	MG	BA	3101	1/1	0.92	0.14	-5.57	2,2,2,2	0
55	MG	BA	3110	1/1	0.89	0.08	-5.71	23,23,23,23	0
55	MG	DA	3073	1/1	0.84	0.10	-5.77	37,37,37,37	0
55	MG	BA	3058	1/1	0.94	0.08	-5.80	13,13,13,13	0
55	MG	CA	1607	1/1	0.89	0.10	-6.05	42,42,42,42	0
55	MG	AA	1633	1/1	0.94	0.09	-6.32	31,31,31,31	0
55	MG	BA	3118	1/1	0.96	0.07	-6.54	11,11,11,11	0
55	MG	AA	1625	1/1	0.97	0.07	-6.69	31,31,31,31	0
55	MG	CA	1622	1/1	0.95	0.05	-6.74	40,40,40,40	0
55	MG	AA	1609	1/1	0.96	0.08	-6.98	20,20,20,20	0
55	MG	DA	3129	1/1	0.94	0.11	-7.08	38,38,38,38	0
55	MG	BA	3073	1/1	0.86	0.12	-7.12	13,13,13,13	0
55	MG	BA	3096	1/1	0.97	0.11	-7.45	5,5,5,5	0
55	MG	DA	3065	1/1	0.94	0.06	-7.54	33,33,33,33	0
55	MG	DA	3058	1/1	0.96	0.05	-7.98	37,37,37,37	0
55	MG	BA	3002	1/1	0.89	0.08	-9.89	15,15,15,15	0
55	MG	BA	3131	1/1	0.93	0.11	-10.21	35,35,35,35	0
55	MG	BA	3005	1/1	0.97	0.05	-12.66	31,31,31,31	0
55	MG	BA	3028	1/1	0.92	0.11	-24.90	4,4,4,4	0
55	MG	AA	1665	1/1	0.90	0.16	-	34,34,34,34	0
55	MG	DA	3025	1/1	0.72	0.45	-	49,49,49,49	0
55	MG	DA	3092	1/1	0.77	0.45	-	62,62,62,62	0
55	MG	AA	1626	1/1	0.92	0.19	-	26,26,26,26	0
55	MG	BA	3067	1/1	0.93	0.20	-	5,5,5,5	0
55	MG	BA	3102	1/1	0.91	0.33	-	23,23,23,23	0
55	MG	BA	3115	1/1	0.89	0.19	-	35,35,35,35	0
55	MG	AA	1647	1/1	0.98	0.18	-	39,39,39,39	0
55	MG	BA	3151	1/1	0.89	0.20	-	31,31,31,31	0
55	MG	BA	3037	1/1	0.98	0.23	-	2,2,2,2	0
55	MG	DA	3043	1/1	0.66	0.21	-	54,54,54,54	0
55	MG	BA	3187	1/1	0.90	0.17	-	28,28,28,28	0
55	MG	BA	3045	1/1	0.68	0.20	-	13,13,13,13	0
55	MG	AA	1623	1/1	0.78	0.13	-	42,42,42,42	0
55	MG	DA	3084	1/1	0.78	0.30	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	BA	3146	1/1	0.95	0.25	-	23,23,23,23	0
55	MG	BA	3080	1/1	0.91	0.10	-	18,18,18,18	0
55	MG	CA	1631	1/1	0.82	0.25	-	62,62,62,62	0
55	MG	BA	3085	1/1	0.77	0.15	-	7,7,7,7	0
55	MG	DA	3086	1/1	0.65	0.13	-	53,53,53,53	0
55	MG	CA	1612	1/1	0.98	0.05	-	30,30,30,30	0
55	MG	BA	3141	1/1	0.98	0.42	-	4,4,4,4	0
55	MG	AA	1610	1/1	0.72	0.17	-	49,49,49,49	0
55	MG	BA	3169	1/1	0.95	0.12	-	24,24,24,24	0
55	MG	BB	202	1/1	0.94	0.08	-	11,11,11,11	0
55	MG	DA	3054	1/1	0.78	0.28	-	44,44,44,44	0
55	MG	BA	3086	1/1	0.91	0.21	-	9,9,9,9	0
55	MG	BA	3093	1/1	0.87	0.16	-	16,16,16,16	0
55	MG	CA	1649	1/1	0.92	0.16	-	35,35,35,35	0
55	MG	BA	3154	1/1	0.79	0.20	-	29,29,29,29	0
55	MG	DA	3066	1/1	0.86	0.11	-	39,39,39,39	0
55	MG	CA	1609	1/1	0.31	0.21	-	58,58,58,58	0
55	MG	AM	201	1/1	0.93	0.29	-	29,29,29,29	0
55	MG	BA	3142	1/1	0.94	0.41	-	15,15,15,15	0
55	MG	DA	3141	1/1	0.93	0.20	-	28,28,28,28	0
55	MG	CA	1636	1/1	0.30	0.26	-	79,79,79,79	0
55	MG	BA	3011	1/1	0.95	0.07	-	13,13,13,13	0
55	MG	DA	3080	1/1	0.81	0.11	-	39,39,39,39	0
55	MG	DA	3072	1/1	0.95	0.12	-	42,42,42,42	0
55	MG	BA	3126	1/1	0.88	0.28	-	7,7,7,7	0
55	MG	BA	3174	1/1	0.95	0.12	-	20,20,20,20	0
55	MG	BA	3038	1/1	0.88	0.14	-	8,8,8,8	0
55	MG	AA	1643	1/1	0.91	0.16	-	19,19,19,19	0
55	MG	AA	1650	1/1	0.94	0.17	-	35,35,35,35	0
55	MG	AA	1644	1/1	0.82	0.26	-	32,32,32,32	0
55	MG	BA	3143	1/1	0.96	0.28	-	7,7,7,7	0
55	MG	DA	3056	1/1	0.64	0.24	-	51,51,51,51	0
55	MG	DA	3032	1/1	0.85	0.06	-	49,49,49,49	0
55	MG	AA	1603	1/1	0.95	0.15	-	34,34,34,34	0
55	MG	DA	3123	1/1	0.86	0.17	-	47,47,47,47	0
55	MG	AA	1632	1/1	0.78	0.14	-	40,40,40,40	0
55	MG	DB	202	1/1	0.90	0.05	-	42,42,42,42	0
55	MG	CA	1653	1/1	0.96	0.31	-	47,47,47,47	0
55	MG	DA	3014	1/1	0.85	0.09	-	43,43,43,43	0
55	MG	DA	3009	1/1	0.65	0.12	-	57,57,57,57	0
55	MG	BA	3082	1/1	0.89	0.19	-	15,15,15,15	0
55	MG	BA	3158	1/1	0.94	0.18	-	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	BA	3171	1/1	0.96	0.14	-	29,29,29,29	0
55	MG	DA	3117	1/1	0.78	0.06	-	49,49,49,49	0
55	MG	BA	3167	1/1	0.94	0.15	-	28,28,28,28	0
55	MG	BA	3121	1/1	0.93	0.08	-	22,22,22,22	0
55	MG	DA	3060	1/1	0.47	1.18	-	61,61,61,61	0
55	MG	DA	3036	1/1	0.84	0.16	-	61,61,61,61	0
55	MG	DA	3024	1/1	0.80	0.17	-	45,45,45,45	0
55	MG	CA	1644	1/1	0.96	0.25	-	32,32,32,32	0
55	MG	DA	3074	1/1	0.84	0.10	-	41,41,41,41	0
55	MG	BA	3010	1/1	0.84	0.15	-	3,3,3,3	0
55	MG	BA	3076	1/1	0.84	0.19	-	17,17,17,17	0
55	MG	BA	3166	1/1	0.92	0.21	-	25,25,25,25	0
55	MG	DA	3034	1/1	0.76	0.29	-	56,56,56,56	0
55	MG	CA	1646	1/1	0.91	0.14	-	40,40,40,40	0
55	MG	DA	3152	1/1	0.92	0.16	-	41,41,41,41	0
55	MG	DA	3061	1/1	0.79	0.99	-	53,53,53,53	0
55	MG	BA	3015	1/1	0.58	0.41	-	52,52,52,52	0
55	MG	AA	1671	1/1	0.93	0.20	-	35,35,35,35	0
55	MG	BA	3083	1/1	0.92	0.21	-	32,32,32,32	0
55	MG	BA	3078	1/1	0.92	0.10	-	33,33,33,33	0
55	MG	BA	3125	1/1	0.88	0.20	-	8,8,8,8	0
55	MG	AA	1638	1/1	0.62	0.12	-	51,51,51,51	0
55	MG	DA	3133	1/1	0.81	0.58	-	57,57,57,57	0
55	MG	DA	3158	1/1	0.83	0.16	-	55,55,55,55	0
55	MG	DB	203	1/1	0.85	0.06	-	56,56,56,56	0
55	MG	CA	1606	1/1	0.78	0.29	-	52,52,52,52	0
55	MG	BA	3176	1/1	0.93	0.14	-	24,24,24,24	0
55	MG	BA	3018	1/1	0.96	0.09	-	27,27,27,27	0
55	MG	DA	3111	1/1	0.66	0.12	-	42,42,42,42	0
55	MG	DA	3125	1/1	0.85	0.17	-	51,51,51,51	0
55	MG	CA	1627	1/1	0.83	0.12	-	59,59,59,59	0
55	MG	BA	3191	1/1	0.93	0.24	-	35,35,35,35	0
55	MG	CA	1654	1/1	0.85	0.14	-	26,26,26,26	0
55	MG	AA	1645	1/1	0.98	0.13	-	39,39,39,39	0
55	MG	BA	3150	1/1	0.80	0.24	-	42,42,42,42	0
55	MG	AA	1605	1/1	0.80	0.16	-	32,32,32,32	0
55	MG	DA	3137	1/1	0.82	0.47	-	42,42,42,42	0
55	MG	DA	3166	1/1	0.87	0.15	-	34,34,34,34	0
55	MG	CA	1648	1/1	0.93	0.19	-	42,42,42,42	0
55	MG	BA	3052	1/1	0.70	0.15	-	8,8,8,8	0
55	MG	AA	1664	1/1	0.91	0.19	-	36,36,36,36	0
55	MG	AA	1663	1/1	0.93	0.17	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	BA	3084	1/1	0.94	0.12	-	12,12,12,12	0
55	MG	AA	1621	1/1	0.93	0.06	-	33,33,33,33	0
55	MG	AA	1648	1/1	0.78	0.29	-	38,38,38,38	0
55	MG	DA	3167	1/1	0.83	0.12	-	59,59,59,59	0
55	MG	BA	3031	1/1	0.84	0.14	-	8,8,8,8	0
55	MG	DA	3159	1/1	0.80	0.17	-	39,39,39,39	0
55	MG	DA	3041	1/1	0.66	0.36	-	53,53,53,53	0
55	MG	DA	3067	1/1	0.95	0.10	-	49,49,49,49	0
55	MG	DA	3144	1/1	0.97	0.04	-	52,52,52,52	0
55	MG	CA	1645	1/1	0.97	0.19	-	41,41,41,41	0
55	MG	BA	3147	1/1	0.98	0.46	-	13,13,13,13	0
55	MG	AA	1659	1/1	0.77	0.52	-	34,34,34,34	0
55	MG	BA	3069	1/1	0.97	0.07	-	39,39,39,39	0
55	MG	DA	3139	1/1	0.98	0.36	-	31,31,31,31	0
55	MG	AA	1608	1/1	0.67	0.21	-	24,24,24,24	0
55	MG	BA	3185	1/1	0.90	0.17	-	11,11,11,11	0
55	MG	AA	1653	1/1	0.95	0.30	-	24,24,24,24	0
55	MG	DA	3100	1/1	0.88	0.07	-	43,43,43,43	0
55	MG	DA	3138	1/1	0.86	0.72	-	41,41,41,41	0
55	MG	BA	3060	1/1	0.82	0.38	-	33,33,33,33	0
55	MG	BA	3123	1/1	0.86	0.13	-	18,18,18,18	0
55	MG	BA	3192	1/1	0.94	0.16	-	15,15,15,15	0
55	MG	BA	3048	1/1	0.72	0.09	-	16,16,16,16	0
55	MG	BA	3072	1/1	0.98	0.20	-	4,4,4,4	0
55	MG	BA	3189	1/1	0.97	0.20	-	3,3,3,3	0
55	MG	DA	3010	1/1	0.69	0.11	-	48,48,48,48	0
55	MG	DA	3083	1/1	0.88	0.27	-	61,61,61,61	0
55	MG	BA	3194	1/1	0.99	0.17	-	28,28,28,28	0
55	MG	BA	3103	1/1	0.84	0.12	-	9,9,9,9	0
55	MG	DA	3029	1/1	0.81	0.28	-	41,41,41,41	0
55	MG	AA	1646	1/1	0.89	0.20	-	44,44,44,44	0
55	MG	DA	3127	1/1	0.58	0.13	-	47,47,47,47	0
55	MG	BA	3014	1/1	0.91	0.11	-	6,6,6,6	0
55	MG	DA	3112	1/1	0.83	0.28	-	52,52,52,52	0
55	MG	DA	3131	1/1	0.54	0.89	-	71,71,71,71	0
55	MG	AA	1661	1/1	0.94	0.20	-	22,22,22,22	0
55	MG	DA	3090	1/1	0.71	0.21	-	58,58,58,58	0
55	MG	AA	1658	1/1	0.96	0.08	-	33,33,33,33	0
55	MG	BA	3128	1/1	0.88	0.22	-	9,9,9,9	0
55	MG	DA	3076	1/1	0.80	0.33	-	48,48,48,48	0
55	MG	DA	3135	1/1	0.67	0.24	-	47,47,47,47	0
55	MG	DA	3037	1/1	0.77	0.10	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	CA	1638	1/1	0.62	0.21	-	55,55,55,55	0
55	MG	BA	3160	1/1	0.90	0.26	-	7,7,7,7	0
55	MG	BA	3039	1/1	0.95	0.18	-	1,1,1,1	0
55	MG	CA	1643	1/1	0.95	0.28	-	44,44,44,44	0
55	MG	BA	3030	1/1	0.79	0.28	-	10,10,10,10	0
55	MG	BB	204	1/1	0.98	0.29	-	4,4,4,4	0
55	MG	AA	1652	1/1	0.88	0.20	-	43,43,43,43	0
55	MG	DA	3089	1/1	0.94	0.22	-	58,58,58,58	0
55	MG	DA	3082	1/1	0.97	0.06	-	50,50,50,50	0
55	MG	DA	3085	1/1	0.93	0.10	-	42,42,42,42	0
55	MG	DA	3048	1/1	0.35	0.20	-	51,51,51,51	0
55	MG	CA	1641	1/1	0.93	0.83	-	46,46,46,46	0
55	MG	DA	3006	1/1	0.81	0.37	-	64,64,64,64	0
55	MG	DA	3122	1/1	0.85	0.18	-	42,42,42,42	0
55	MG	BA	3094	1/1	0.91	0.05	-	17,17,17,17	0
55	MG	DA	3088	1/1	0.92	0.29	-	51,51,51,51	0
55	MG	BA	3190	1/1	0.90	0.25	-	33,33,33,33	0
55	MG	BA	3054	1/1	0.90	0.11	-	5,5,5,5	0
55	MG	AA	1668	1/1	0.88	0.18	-	18,18,18,18	0
55	MG	AA	1620	1/1	0.80	0.11	-	44,44,44,44	0
55	MG	AA	1667	1/1	0.86	0.20	-	37,37,37,37	0
55	MG	DA	3160	1/1	0.79	0.30	-	35,35,35,35	0
55	MG	DA	3044	1/1	0.83	0.10	-	61,61,61,61	0
55	MG	DA	3154	1/1	0.87	0.13	-	45,45,45,45	0
55	MG	CA	1651	1/1	0.90	0.15	-	48,48,48,48	0
55	MG	AA	1654	1/1	0.96	0.33	-	40,40,40,40	0
55	MG	DA	3118	1/1	0.81	0.12	-	45,45,45,45	0
55	MG	DA	3069	1/1	0.85	0.08	-	63,63,63,63	0
55	MG	CA	1613	1/1	0.90	0.15	-	19,19,19,19	0
55	MG	AA	1612	1/1	0.84	0.14	-	24,24,24,24	0
55	MG	BA	3057	1/1	0.75	0.20	-	20,20,20,20	0
55	MG	BA	3193	1/1	0.96	0.13	-	12,12,12,12	0
55	MG	DA	3020	1/1	0.95	0.36	-	42,42,42,42	0
55	MG	AA	1601	1/1	0.92	0.14	-	49,49,49,49	0
55	MG	BA	3032	1/1	0.95	0.17	-	8,8,8,8	0
55	MG	BA	3098	1/1	0.77	0.34	-	58,58,58,58	0
55	MG	DA	3143	1/1	0.71	0.29	-	46,46,46,46	0
55	MG	BA	3099	1/1	0.89	0.14	-	3,3,3,3	0
55	MG	AA	1656	1/1	0.94	0.12	-	37,37,37,37	0
55	MG	DA	3015	1/1	0.66	0.63	-	56,56,56,56	0
55	MG	BA	3003	1/1	0.83	0.11	-	20,20,20,20	0
55	MG	BA	3007	1/1	0.87	0.08	-	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	CA	1628	1/1	0.78	0.40	-	64,64,64,64	0
55	MG	BA	3162	1/1	0.93	0.19	-	21,21,21,21	0
55	MG	DA	3148	1/1	0.90	0.26	-	45,45,45,45	0
55	MG	BA	3091	1/1	0.88	0.07	-	28,28,28,28	0
55	MG	DA	3151	1/1	0.85	0.40	-	45,45,45,45	0
55	MG	DA	3087	1/1	0.69	0.14	-	51,51,51,51	0
55	MG	DA	3115	1/1	0.70	0.18	-	58,58,58,58	0
55	MG	DA	3051	1/1	0.90	0.07	-	35,35,35,35	0
55	MG	BA	3144	1/1	0.97	0.19	-	25,25,25,25	0
55	MG	DA	3156	1/1	0.96	0.13	-	30,30,30,30	0
55	MG	BA	3181	1/1	0.91	0.22	-	14,14,14,14	0
55	MG	BA	3055	1/1	0.89	0.22	-	23,23,23,23	0
55	MG	CA	1623	1/1	0.93	0.29	-	40,40,40,40	0
55	MG	BA	3149	1/1	0.97	0.15	-	1,1,1,1	0
55	MG	AA	1639	1/1	0.82	0.06	-	51,51,51,51	0
55	MG	CA	1634	1/1	0.89	0.07	-	49,49,49,49	0
55	MG	BA	3164	1/1	0.96	0.45	-	21,21,21,21	0
55	MG	AA	1627	1/1	0.83	0.34	-	43,43,43,43	0
55	MG	BB	203	1/1	0.82	0.09	-	10,10,10,10	0
55	MG	DA	3033	1/1	0.76	0.23	-	45,45,45,45	0
55	MG	DA	3093	1/1	0.68	0.14	-	65,65,65,65	0
55	MG	CA	1642	1/1	0.94	0.27	-	27,27,27,27	0
55	MG	DA	3101	1/1	0.95	0.10	-	40,40,40,40	0
55	MG	BA	3006	1/1	0.94	0.10	-	20,20,20,20	0
55	MG	AA	1602	1/1	0.90	0.07	-	33,33,33,33	0
55	MG	DA	3155	1/1	0.57	0.74	-	44,44,44,44	0
55	MG	AA	1619	1/1	0.88	0.26	-	43,43,43,43	0
55	MG	BA	3145	1/1	0.90	0.21	-	15,15,15,15	0
55	MG	DA	3019	1/1	0.95	0.16	-	47,47,47,47	0
55	MG	BA	3061	1/1	0.79	0.47	-	55,55,55,55	0
55	MG	BA	3122	1/1	0.94	0.24	-	2,2,2,2	0
55	MG	DA	3119	1/1	0.68	0.63	-	68,68,68,68	0
55	MG	DA	3146	1/1	0.89	0.21	-	35,35,35,35	0
55	MG	DA	3106	1/1	0.62	0.13	-	56,56,56,56	0
55	MG	BA	3172	1/1	0.96	0.19	-	23,23,23,23	0
55	MG	BA	3133	1/1	0.86	0.39	-	40,40,40,40	0
55	MG	AA	1637	1/1	0.78	0.18	-	18,18,18,18	0
55	MG	BA	3019	1/1	0.82	0.24	-	3,3,3,3	0
55	MG	DA	3113	1/1	0.66	0.16	-	42,42,42,42	0
55	MG	BA	3041	1/1	0.96	0.12	-	11,11,11,11	0
55	MG	DA	3130	1/1	0.87	0.09	-	51,51,51,51	0
55	MG	CA	1605	1/1	0.76	0.37	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	CA	1637	1/1	0.73	0.37	-	51,51,51,51	0
55	MG	BA	3148	1/1	0.95	0.24	-	16,16,16,16	0
55	MG	CA	1655	1/1	0.82	0.61	-	44,44,44,44	0
55	MG	DA	3028	1/1	0.80	0.08	-	50,50,50,50	0
55	MG	DA	3035	1/1	0.96	0.15	-	38,38,38,38	0
55	MG	AA	1615	1/1	0.70	0.12	-	46,46,46,46	0
55	MG	DA	3099	1/1	0.49	0.18	-	53,53,53,53	0
55	MG	BA	3033	1/1	0.91	0.24	-	4,4,4,4	0
55	MG	DA	3094	1/1	0.85	0.30	-	59,59,59,59	0
55	MG	BA	3182	1/1	0.93	0.21	-	22,22,22,22	0
55	MG	CA	1650	1/1	0.86	0.49	-	40,40,40,40	0
55	MG	CA	1652	1/1	0.71	0.16	-	39,39,39,39	0
55	MG	AA	1660	1/1	0.94	0.22	-	40,40,40,40	0
55	MG	AA	1666	1/1	0.91	0.22	-	30,30,30,30	0
55	MG	BA	3114	1/1	0.90	0.20	-	19,19,19,19	0
55	MG	CA	1625	1/1	0.91	0.21	-	25,25,25,25	0
55	MG	BA	3025	1/1	0.78	0.25	-	40,40,40,40	0
55	MG	CA	1633	1/1	0.67	0.45	-	54,54,54,54	0
55	MG	DA	3059	1/1	0.89	0.35	-	53,53,53,53	0
55	MG	BA	3042	1/1	0.91	0.17	-	6,6,6,6	0
55	MG	DA	3103	1/1	0.74	0.14	-	48,48,48,48	0
55	MG	BA	3117	1/1	0.98	0.15	-	4,4,4,4	0
55	MG	BA	3056	1/1	0.97	0.11	-	10,10,10,10	0
55	MG	BA	3020	1/1	0.93	0.11	-	7,7,7,7	0
55	MG	DA	3126	1/1	0.89	0.14	-	57,57,57,57	0
55	MG	BA	3075	1/1	0.86	0.15	-	15,15,15,15	0
55	MG	BA	3157	1/1	0.96	0.26	-	26,26,26,26	0
55	MG	BA	3092	1/1	0.93	0.09	-	20,20,20,20	0
55	MG	DA	3140	1/1	0.96	0.44	-	37,37,37,37	0
55	MG	AA	1651	1/1	0.96	0.27	-	32,32,32,32	0
55	MG	DA	3004	1/1	0.46	0.33	-	64,64,64,64	0
55	MG	CA	1618	1/1	0.92	0.16	-	28,28,28,28	0
55	MG	CA	1629	1/1	0.85	0.08	-	63,63,63,63	0
55	MG	CA	1639	1/1	0.94	0.12	-	34,34,34,34	0
55	MG	BA	3195	1/1	0.86	0.12	-	20,20,20,20	0
55	MG	BA	3026	1/1	0.97	0.07	-	7,7,7,7	0
55	MG	DA	3098	1/1	0.87	0.56	-	63,63,63,63	0
55	MG	BA	3087	1/1	0.81	0.10	-	18,18,18,18	0
55	MG	AA	1631	1/1	0.77	0.13	-	42,42,42,42	0
55	MG	CA	1608	1/1	0.89	0.30	-	50,50,50,50	0
55	MG	DA	3091	1/1	0.67	0.66	-	71,71,71,71	0
55	MG	BA	3001	1/1	0.95	0.08	-	10,10,10,10	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	DA	3163	1/1	0.56	0.31	-	51,51,51,51	0
55	MG	DA	3039	1/1	0.93	0.17	-	53,53,53,53	0
55	MG	BA	3043	1/1	0.99	0.08	-	15,15,15,15	0
55	MG	DA	3142	1/1	0.87	0.34	-	38,38,38,38	0
55	MG	DA	3007	1/1	0.80	0.27	-	54,54,54,54	0
55	MG	AA	1624	1/1	0.66	0.17	-	39,39,39,39	0
55	MG	DA	3149	1/1	0.90	0.32	-	36,36,36,36	0
55	MG	AA	1614	1/1	0.64	0.44	-	53,53,53,53	0
55	MG	DA	3055	1/1	0.76	0.50	-	53,53,53,53	0
55	MG	BA	3137	1/1	0.99	0.45	-	4,4,4,4	0
55	MG	BA	3119	1/1	0.86	0.34	-	21,21,21,21	0
55	MG	AA	1635	1/1	0.81	0.18	-	37,37,37,37	0
55	MG	DA	3011	1/1	0.78	0.17	-	46,46,46,46	0
55	MG	BA	3074	1/1	0.95	0.07	-	20,20,20,20	0
55	MG	CM	201	1/1	0.79	0.32	-	46,46,46,46	0
55	MG	AA	1611	1/1	0.98	0.07	-	18,18,18,18	0
55	MG	BA	3106	1/1	0.96	0.33	-	0,0,0,0	0
55	MG	AA	1655	1/1	0.92	0.12	-	34,34,34,34	0
55	MG	BA	3140	1/1	0.89	0.20	-	14,14,14,14	0
55	MG	AA	1649	1/1	0.96	0.22	-	27,27,27,27	0
55	MG	BA	3046	1/1	0.94	0.22	-	8,8,8,8	0
55	MG	BA	3089	1/1	0.94	0.10	-	12,12,12,12	0
55	MG	AA	1657	1/1	0.64	0.62	-	40,40,40,40	0
55	MG	DA	3110	1/1	0.82	0.37	-	57,57,57,57	0
55	MG	CA	1604	1/1	0.51	0.17	-	70,70,70,70	0
55	MG	BA	3127	1/1	0.96	0.09	-	1,1,1,1	0
55	MG	CA	1647	1/1	0.94	0.19	-	24,24,24,24	0
55	MG	CA	1602	1/1	0.53	0.10	-	61,61,61,61	0
55	MG	BA	3051	1/1	0.86	0.12	-	6,6,6,6	0
55	MG	BA	3035	1/1	0.93	0.15	-	2,2,2,2	0
55	MG	DA	3102	1/1	0.53	0.21	-	45,45,45,45	0
55	MG	AA	1670	1/1	0.97	0.37	-	26,26,26,26	0
55	MG	BA	3124	1/1	0.96	0.25	-	21,21,21,21	0
55	MG	BA	3088	1/1	0.94	0.16	-	32,32,32,32	0
55	MG	DA	3150	1/1	0.93	0.22	-	42,42,42,42	0
55	MG	BA	3081	1/1	0.98	0.17	-	1,1,1,1	0
55	MG	BA	3138	1/1	0.91	0.40	-	4,4,4,4	0
55	MG	DA	3161	1/1	0.92	0.10	-	42,42,42,42	0
55	MG	CA	1620	1/1	0.92	0.10	-	46,46,46,46	0
55	MG	BA	3016	1/1	0.92	0.07	-	17,17,17,17	0
55	MG	BA	3095	1/1	0.97	0.09	-	8,8,8,8	0
55	MG	BA	3173	1/1	0.94	0.19	-	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
55	MG	DA	3052	1/1	0.91	0.08	-	35,35,35,35	0
55	MG	BA	3100	1/1	0.93	0.14	-	6,6,6,6	0
55	MG	DA	3045	1/1	0.75	0.21	-	53,53,53,53	0
55	MG	AA	1628	1/1	0.93	0.05	-	37,37,37,37	0
55	MG	DA	3147	1/1	0.94	0.19	-	49,49,49,49	0
55	MG	BA	3111	1/1	0.90	0.12	-	23,23,23,23	0
55	MG	BA	3029	1/1	0.71	0.11	-	15,15,15,15	0
55	MG	BA	3004	1/1	0.61	0.15	-	33,33,33,33	0
55	MG	BA	3044	1/1	0.57	0.15	-	20,20,20,20	0
55	MG	DA	3064	1/1	0.96	0.08	-	38,38,38,38	0
55	MG	DA	3003	1/1	0.92	0.09	-	52,52,52,52	0
55	MG	BA	3180	1/1	0.92	0.26	-	25,25,25,25	0
55	MG	BA	3156	1/1	0.98	0.24	-	12,12,12,12	0
55	MG	BA	3135	1/1	0.96	0.09	-	17,17,17,17	0
55	MG	BA	3090	1/1	0.80	0.08	-	17,17,17,17	0
55	MG	DA	3016	1/1	0.68	0.41	-	53,53,53,53	0
55	MG	DA	3042	1/1	0.91	0.11	-	49,49,49,49	0
55	MG	BA	3179	1/1	0.77	0.47	-	39,39,39,39	0
55	MG	DA	3121	1/1	0.70	0.16	-	41,41,41,41	0
55	MG	CA	1611	1/1	0.59	0.19	-	55,55,55,55	0
55	MG	BA	3139	1/1	0.91	0.40	-	1,1,1,1	0
55	MG	DA	3001	1/1	0.53	0.19	-	43,43,43,43	0
55	MG	DA	3075	1/1	0.96	0.11	-	48,48,48,48	0
55	MG	DQ	201	1/1	0.86	0.25	-	32,32,32,32	0
55	MG	DA	3164	1/1	0.96	0.13	-	47,47,47,47	0
55	MG	BA	3183	1/1	0.96	0.17	-	24,24,24,24	0
55	MG	DA	3030	1/1	0.95	0.15	-	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.