Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:36 AM UTC

PDB ID	:	4U1U / pdb_00004u1u
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	:	2014-07-16
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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

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

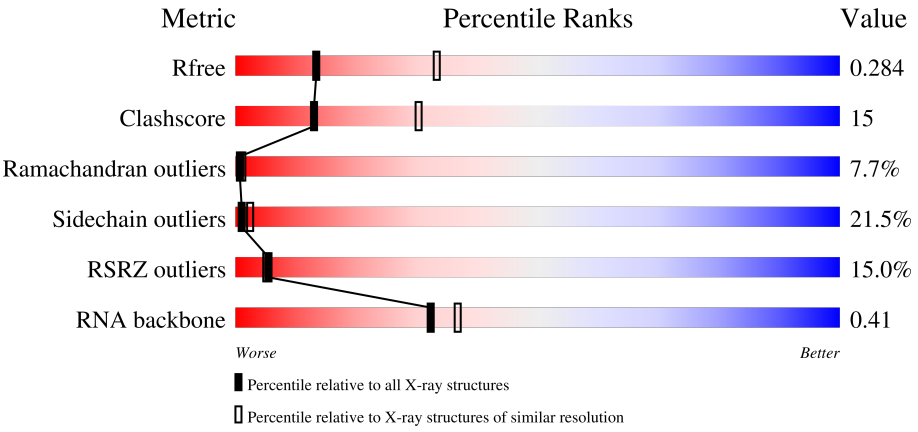
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.95 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}	180053	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)
RNA backbone	3983	1046 (3.16-2.76)

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

Mol	Chain	Length	Quality of chain
1	AA	1539	4% 43% 45% 12%
1	CA	1539	10% 43% 45% 12%
2	AB	218	10% 18% 47% 29% 6%
2	CB	218	26% 28% 44% 25%

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Mol	Chain	Length	Quality of chain
3	AC	206	5% 42% 42% 14%
3	CC	206	9% 48% 37% 15%
4	AD	205	17% 37% 45% 16%
4	CD	205	8% 43% 42% 13%
5	AE	150	8% 36% 43% 17%
5	CE	150	13% 47% 27% 19% 7%
6	AF	100	10% 36% 41% 21%
6	CF	100	9% 43% 37% 15% 5%
7	AG	151	20% 45% 42% 13%
7	CG	151	46% 38% 51% 9%
8	AH	129	2% 46% 37% 17%
8	CH	129	9% 44% 41% 14%
9	AI	127	20% 40% 43% 17%
9	CI	127	50% 31% 54% 14%
10	AJ	98	19% 27% 41% 31%
10	CJ	98	45% 37% 44% 17%
11	AK	117	12% 46% 38% 13%
11	CK	117	3% 42% 45% 10%
12	AL	123	8% 54% 35% 10%
12	CL	123	11% 41% 43% 15%
13	AM	114	16% 41% 39% 18%
13	CM	114	59% 44% 35% 21%
14	AN	100	26% 43% 31% 19%
14	CN	100	39% 32% 47% 16%
15	AO	88	6% 51% 40% 9%

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Mol	Chain	Length	Quality of chain
15	CO	88	6% 40% 42% 18%
16	AP	82	5% 41% 34% 22%
16	CP	82	24% 40% 45% 12%
17	AQ	80	14% 38% 42% 18%
17	CQ	80	30% 39% 42% 15%
18	AR	55	9% 56% 33% 11%
18	CR	55	7% 42% 44% 15%
19	AS	79	16% 44% 39% 10% 6%
19	CS	79	70% 38% 47% 13%
20	AT	85	7% 54% 29% 11% 6%
20	CT	85	26% 38% 46% 14%
21	AU	51	31% 22% 47% 22% 10%
21	CU	51	33% 29% 45% 16% 10%
22	BA	2903	5% 50% 40% 9%
22	DA	2903	10% 42% 46% 11%
23	BB	119	64% 30% 6%
23	DB	119	8% 49% 43% 8%
24	BC	271	2% 55% 38% 6%
24	DC	271	27% 47% 42% 11%
25	BD	209	% 65% 29% 5%
25	DD	209	23% 61% 32% 7%
26	BE	201	% 57% 36% 6%
26	DE	201	36% 49% 40% 10%
27	BF	177	10% 51% 38% 8%
27	DF	177	37% 44% 47% 9%

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Mol	Chain	Length	Quality of chain
28	BG	176	6% 53% 36% 9%
28	DG	176	28% 60% 32% 7%
29	BH	149	77% 26% 47% 22% 5%
29	DH	149	49% 36% 49% 11% 5%
30	BI	141	55% 38% 38% 21%
30	DI	141	70% 35% 51% 13%
31	BJ	142	3% 57% 35% 6%
31	DJ	142	21% 54% 40% 6%
32	BK	122	2% 63% 27% 8%
32	DK	122	11% 59% 31% 9%
33	BL	143	2% 58% 27% 13%
33	DL	143	47% 54% 35% 9%
34	BM	136	% 65% 29% 6%
34	DM	136	17% 63% 30% 7%
35	BN	120	% 60% 33% 6%
35	DN	120	46% 43% 43% 12%
36	BO	116	2% 54% 34% 9%
36	DO	116	29% 46% 45% 9%
37	BP	114	3% 58% 35% 6%
37	DP	114	24% 54% 35% 10%
38	BQ	117	% 58% 31% 11%
38	DQ	117	40% 59% 35% 6%
39	BR	103	3% 56% 33% 9%
39	DR	103	39% 52% 36% 11%
40	BS	110	2% 53% 36% 10%

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Mol	Chain	Length	Quality of chain
40	DS	110	35% 49% 43% 6%
41	BT	93	8% 45% 44% 11%
41	DT	93	57% 46% 37% 14%
42	BU	102	% 57% 37% 5%
42	DU	102	65% 41% 45% 12%
43	BV	94	% 66% 30%
43	DV	94	12% 57% 34% 9%
44	BW	76	4% 70% 30%
44	DW	76	20% 68% 21% 9%
45	BX	77	4% 44% 47% 9%
45	DX	77	26% 35% 52% 13%
46	BY	63	11% 41% 41% 16%
46	DY	63	43% 43% 43% 13%
47	BZ	58	71% 24% 5%
47	DZ	58	21% 52% 40% 7%
48	B0	56	48% 45% 7%
48	D0	56	41% 61% 30% 9%
49	B1	50	4% 52% 32% 16%
49	D1	50	34% 54% 34% 8%
50	B2	46	2% 57% 39%
50	D2	46	39% 52% 43%
51	B3	64	62% 31% 6%
51	D3	64	69% 69% 27% 5%
52	B4	38	5% 50% 45% 5%
52	D4	38	37% 47% 39% 13%

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Mol	Chain	Length	Quality of chain
53	B5	228	53% 49% 27% 7% 16%
54	B6	8	75% 25%
54	D6	8	12% 12% 62% 25%

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	DA	3060	-	-	-	X

2 Entry composition (i)

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	0	0	0
			947	604	192	151			
38	DQ	117	Total	C	N	O	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	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	0	0	0
			780	492	146	142			

- 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	0	0	0
			753	479	137	134	3			
43	DV	94	Total	C	N	O	S	0	0	0
			753	479	137	134	3			

- 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	0	0	0
			580	359	117	103	1			
44	DW	75	Total	C	N	O	S	0	0	0
			569	353	113	102	1			

- 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	0	0	0
			625	388	129	106	2			
45	DX	77	Total	C	N	O	S	0	0	0
			625	388	129	106	2			

- 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	0	0	0
			509	313	99	95	2			
46	DY	63	Total	C	N	O	S	0	0	0
			509	313	99	95	2			

- 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	0	0	0
			449	281	87	79	2			
47	DZ	58	Total	C	N	O	S	0	0	0
			449	281	87	79	2			

- 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 (CCD ID: MG) (formula: Mg).

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

- Molecule 56 is ZINC ION (CCD ID: 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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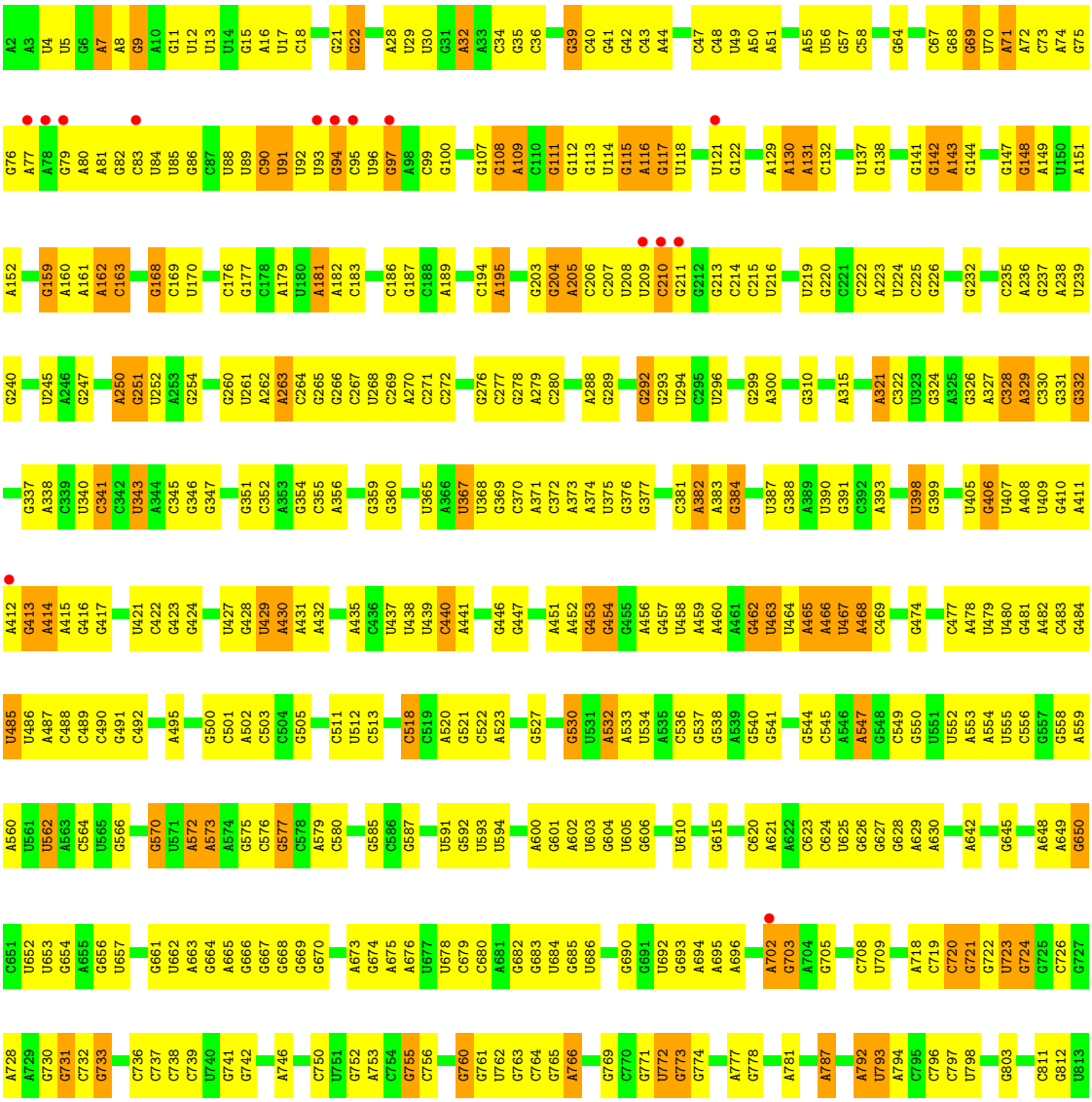
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	CT	4	Total O 4 4	0	0
57	CU	1	Total O 1 1	0	0
57	DA	612	Total O 612 612	0	0
57	DB	13	Total O 13 13	0	0
57	DC	7	Total O 7 7	0	0
57	DD	4	Total O 4 4	0	0
57	DE	4	Total O 4 4	0	0
57	DL	4	Total O 4 4	0	0
57	DN	1	Total O 1 1	0	0
57	DQ	2	Total O 2 2	0	0
57	DT	3	Total O 3 3	0	0
57	DV	1	Total O 1 1	0	0
57	D0	1	Total O 1 1	0	0
57	D2	2	Total O 2 2	0	0
57	D3	1	Total O 1 1	0	0
57	D4	1	Total O 1 1	0	0

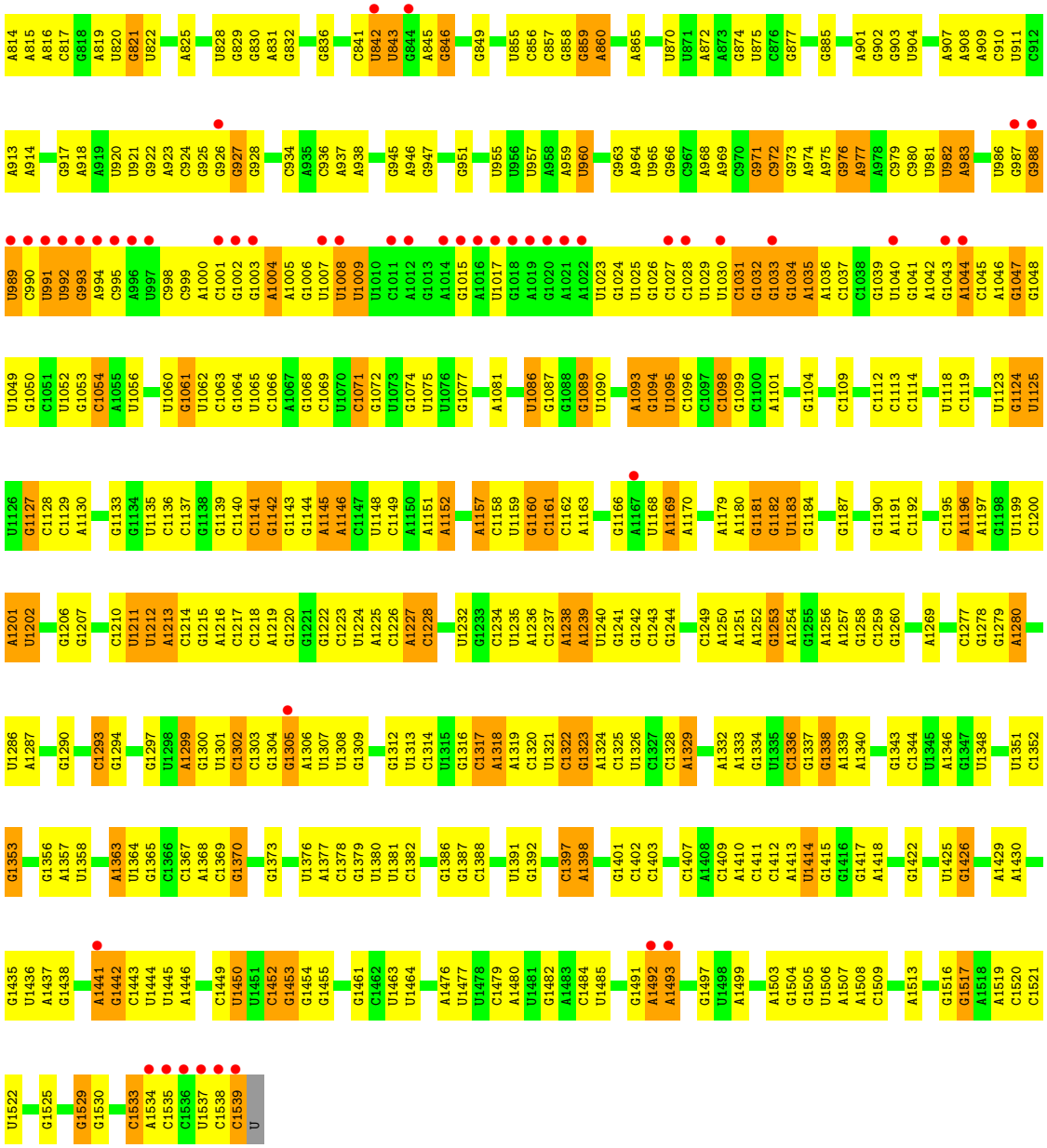
3 Residue-property plots (i)

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

- Molecule 1: 16S rRNA

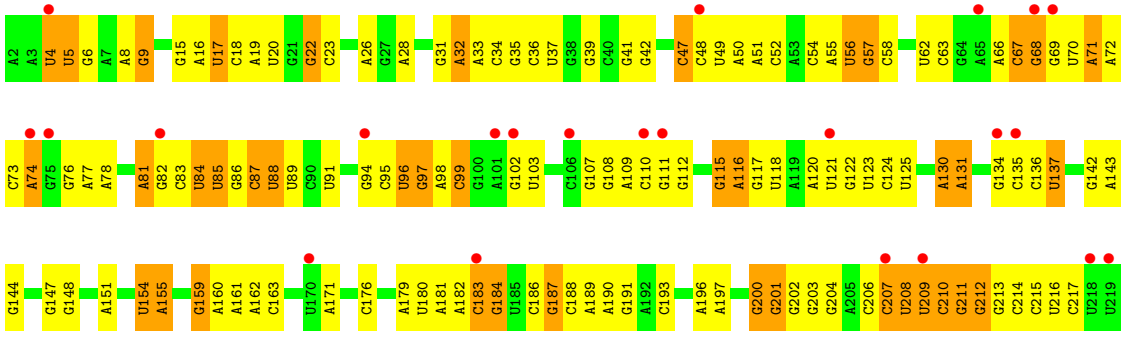
Chain AA:

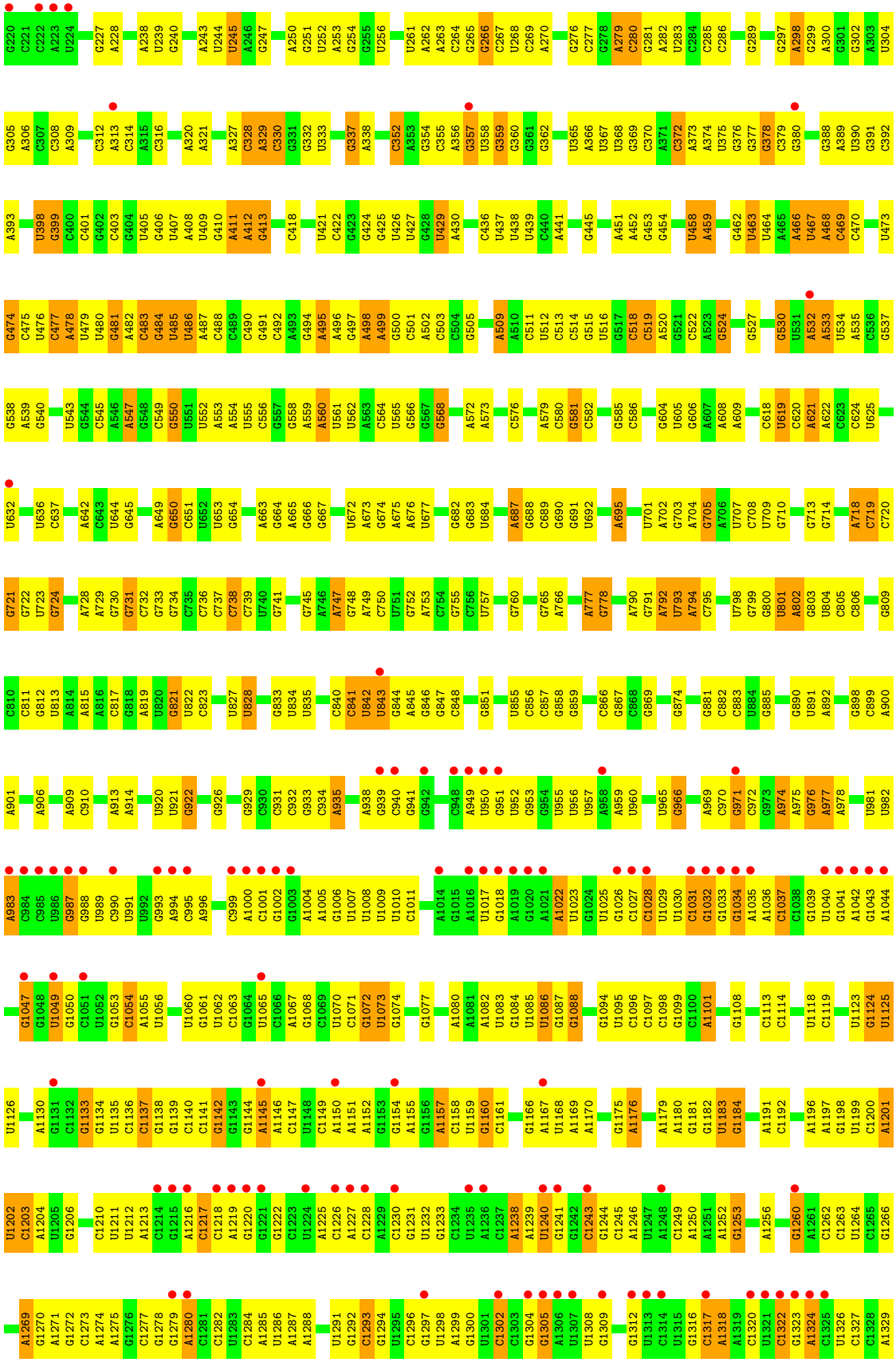


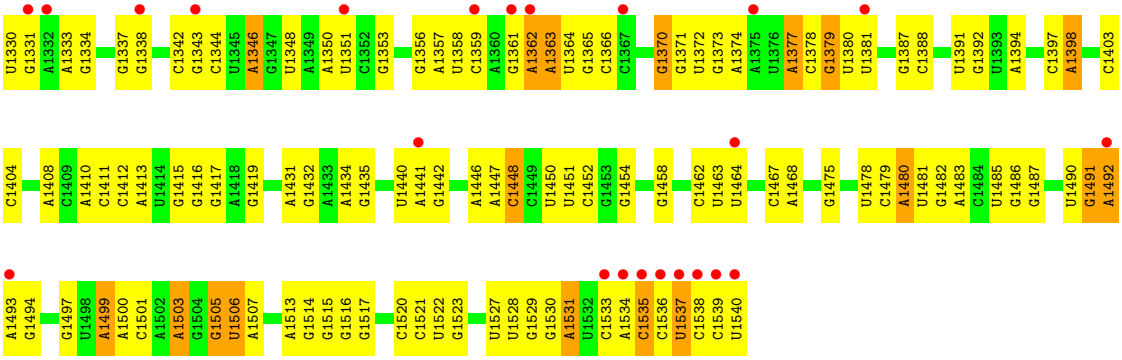


• Molecule 1: 16S rRNA

Chain CA:

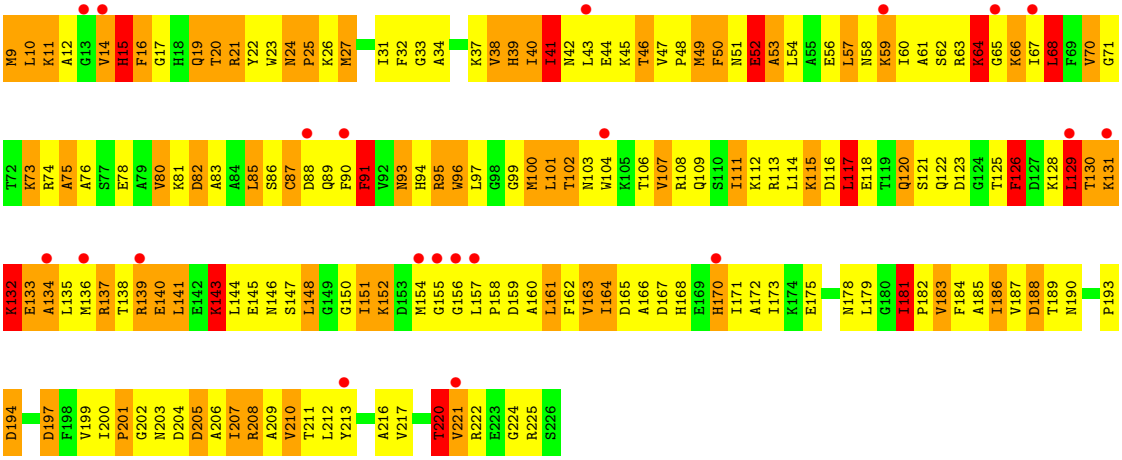



G220 C221 C222 A223 U224 G227 A228 A238 U239 G240 A243 U244 U245 A246 G247 A250 G251 U252 A253 G254 G255 U256 U261 A262 A263 C264 G265 G266 C267 U268 C269 A270 G276 C277 G278 A279 C280 G281 A282 U283 C284 C285 C286 G289 G297 A298 G299 A300 G301 G302 A303 U304
G305 A306 C307 C308 A309 C312 A313 C314 A315 C316 A320 A321 A327 C328 A329 C330 G331 G332 U333 G337 A338 C352 A353 G354 C355 A356 G357 U358 G359 G360 G361 G362 U365 A366 U367 U368 G369 C370 A371 C372 A373 A374 U375 G376 G377 G378 C379 G380 G388 A389 U390 G391 C392
A393 U398 G399 C400 C401 G402 C403 G404 U405 G406 U407 A408 U409 G410 A411 A412 G413 C418 U421 C422 G423 G424 G425 U426 U427 G428 U429 A430 C436 U437 U438 U439 C440 A441 G445 A451 A452 G453 G454 U458 A459 G462 U463 U464 A465 A466 U467 A468 C469 C470 U473
G474 C475 U476 C477 A478 U479 U480 G481 A482 C483 G484 U485 U486 A487 C488 C489 C490 G491 C492 A493 G494 A495 A496 G497 A498 A499 G500 C501 A502 C503 C504 G505 A509 A510 C511 U512 C513 C514 G515 U516 G517 C518 C519 A520 G521 C522 A523 G524 G527 G530 U531 A532 A533 U534 A535 C536 G537
G538 A539 G540 U543 G544 C545 A546 A547 G548 C549 G550 U551 U552 A553 A554 U555 C556 G557 G558 A559 A560 U561 U562 A563 C564 U565 G566 G567 G568 A572 A573 C576 A579 C580 G581 C582 G585 C586 G604 U605 G606 A607 A608 A609 C618 U619 C620 A621 A622 G623 C624 U625
U632 U636 C637 A642 C643 U644 G645 A649 G650 C651 U652 U653 G654 A663 G664 A665 G666 G667 U672 A673 G674 A675 A676 U677 G682 G683 U684 A687 G688 C689 G690 G691 U692 A695 U701 A702 G703 A704 G705 A706 U707 C708 U709 G710 G713 G714 A718 C719 C720
G721 G722 U723 G724 A728 A729 G730 G731 C732 G733 G734 G735 C736 C737 G738 C739 U740 G741 G745 A746 A747 G748 A749 C750 U751 G752 A753 C754 G755 G756 U757 G760 G765 A766 A777 G778 A790 G791 A792 U793 A794 C795 U798 G799 G800 U801 A802 G803 U804 C805 C806 G809
C810 C811 G812 U813 A814 A815 A816 C817 G818 A819 U820 G821 U822 C823 U827 U828 G833 U834 U835 C840 C841 U842 U843 G844 A845 G846 G847 C848 G851 U855 C856 C857 G858 G859 C866 G867 C868 G869 G874 G881 C882 C883 U884 G885 G890 U891 A892 G898 C899 A900
A901 A906 A909 C910 A913 A914 U920 U921 G922 G926 G929 C930 C931 C932 G933 C934 A935 A938 G939 C940 G941 G942 C948 A949 U950 G951 U952 G953 G954 U955 U956 U957 A958 A959 U960 U965 G966 A969 C970 G971 C972 G973 A974 A975 G976 A977 A978 U981 U982
A983 C984 C985 U986 G987 G988 U989 C990 U991 U992 G993 A994 C995 A996 C999 A1000 C1001 G1002 G1003 A1004 A1005 G1006 U1007 U1008 U1009 U1010 C1011 A1014 G1015 A1016 U1017 G1018 A1019 G1020 A1021 A1022 U1023 G1024 U1025 G1026 C1027 C1028 U1029 U1030 C1031 G1032 G1033 G1034 A1035 A1036 C1037 C1038 G1039 U1040 G1041 A1042 G1043 A1044
G1047 G1048 U1049 G1050 C1051 U1052 G1053 C1054 A1055 U1056 U1060 G1061 U1062 C1063 G1064 U1065 C1066 A1067 G1068 C1069 U1070 C1071 G1072 U1073 G1074 G1077 A1080 A1081 A1082 U1083 G1084 U1085 U1086 G1087 G1088 G1094 U1095 C1096 C1097 C1098 G1099 C1100 A1101 G1108 C1113 C1114 U1118 C1119 U1123 G1124 U1125
U1126 A1130 G1131 C1132 G1133 G1134 U1135 C1136 C1137 G1138 G1139 C1140 C1141 G1142 G1143 G1144 A1145 A1146 C1147 U1148 C1149 A1150 A1151 A1152 G1153 G1154 A1155 G1156 A1157 C1158 U1159 G1160 C1161 G1166 A1167 U1168 A1169 A1170 G1175 A1176 A1179 A1180 G1181 G1182 U1183 G1184 A1191 C1192 A1196 A1197 G1198 U1199 C1200 A1201
U1202 C1203 A1204 U1205 G1206 C1210 U1211 U1212 A1213 C1214 G1215 A1216 C1217 C1218 A1219 G1220 G1221 G1222 C1223 U1224 A1225 C1226 A1227 C1228 A1229 C1230 G1231 U1232 G1233 C1234 U1235 A1236 C1237 A1238 A1239 U1240 G1241 G1242 C1243 G1244 C1245 A1246 U1247 A1248 C1249 A1250 A1251 A1252 G1253 A1256 G1260 A1261 C1262 C1263 U1264 C1265 G1266
A1269 G1270 A1271 G1272 C1273 A1274 A1275 G1276 C1277 G1278 G1279 A1280 C1281 C1282 U1283 C1284 A1285 U1286 A1287 A1288 U1291 G1292 C1293 G1294 U1295 C1296 G1297 U1298 A1299 G1300 U1301 C1302 C1303 G1304 G1305 A1306 U1307 U1308 G1309 G1312 U1313 C1314 U1315 G1316 C1317 A1318 A1319 C1320 U1321 C1322 G1323 A1324 C1325 U1326 C1327 C1328 A1329



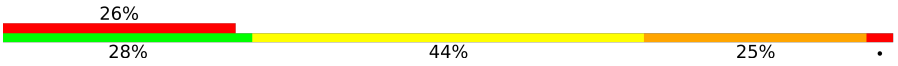
• Molecule 2: 30S ribosomal protein S2

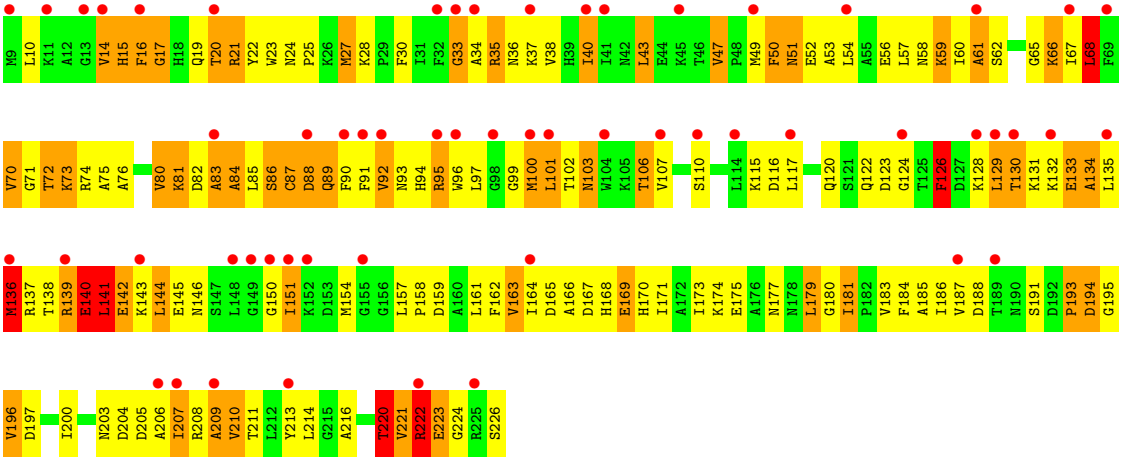
Chain AB:



• Molecule 2: 30S ribosomal protein S2

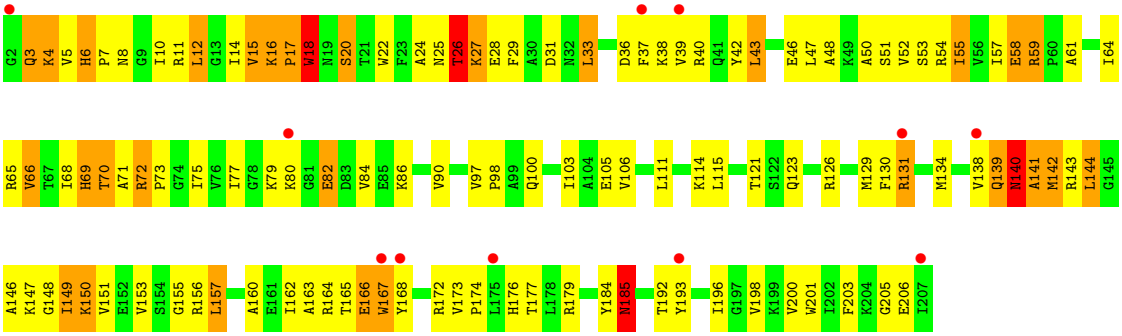
Chain CB:



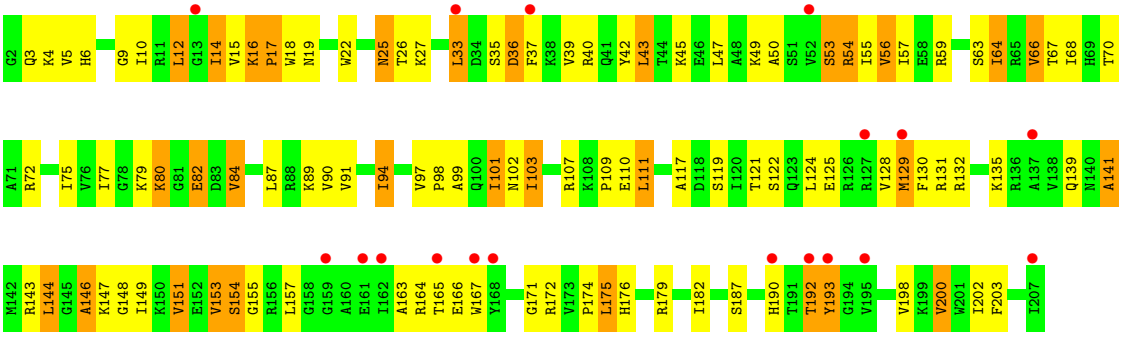


• Molecule 3: 30S ribosomal protein S3

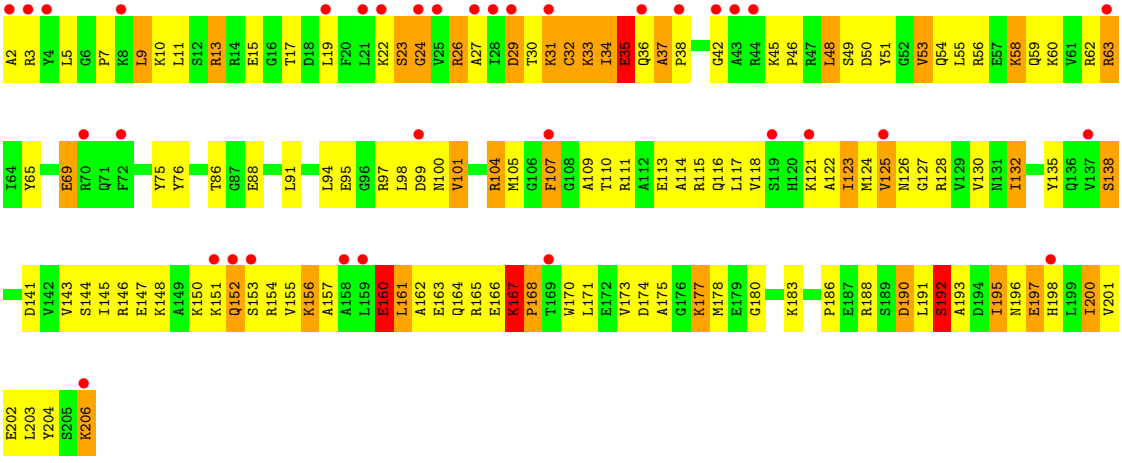
Chain AC:



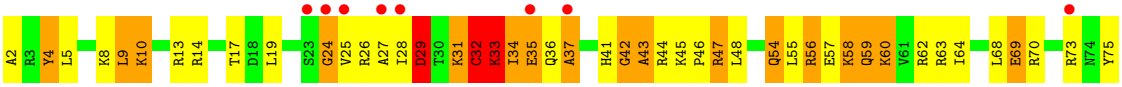
• Molecule 3: 30S ribosomal protein S3

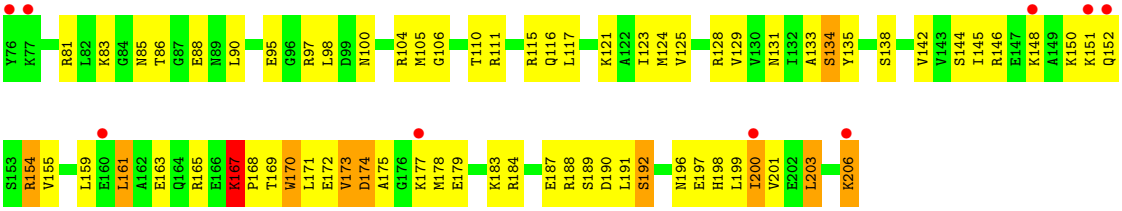


• Molecule 4: 30S ribosomal protein S4



• Molecule 4: 30S ribosomal protein S4





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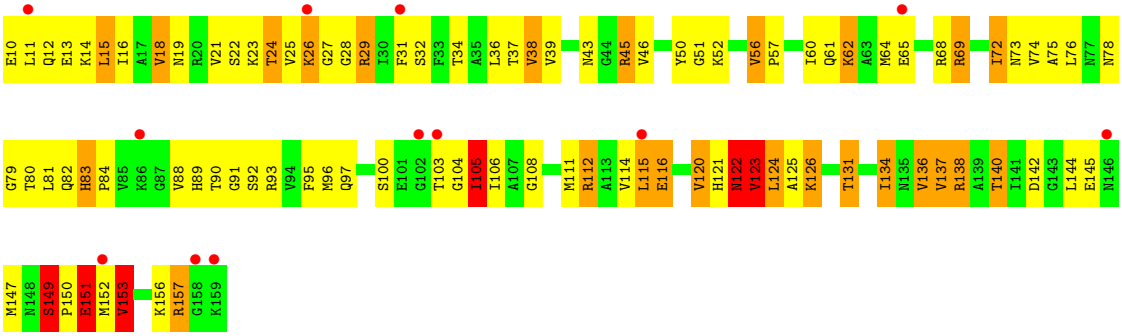
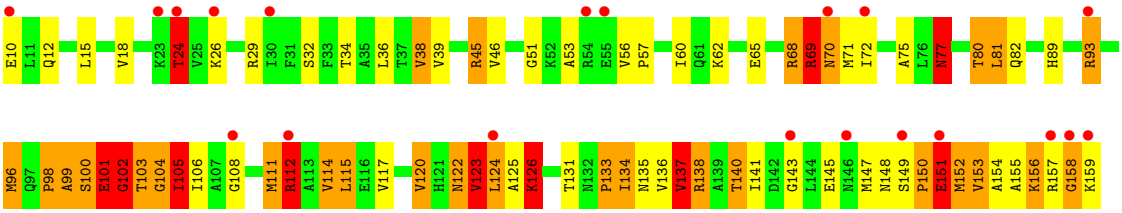
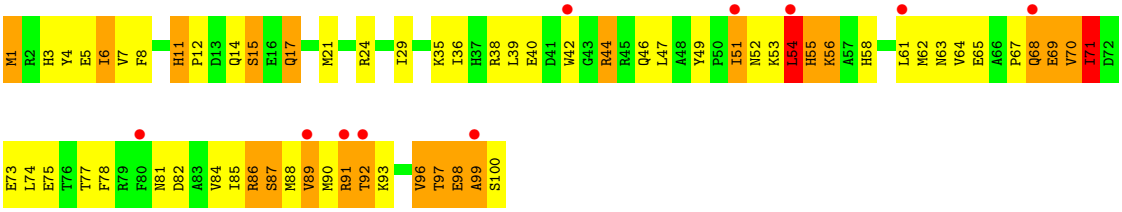


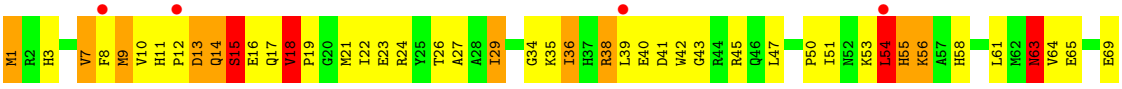
• Molecule 5: 30S ribosomal protein S5

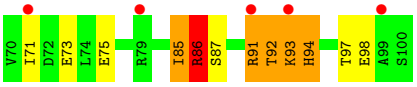


• Molecule 6: 30S ribosomal protein S6

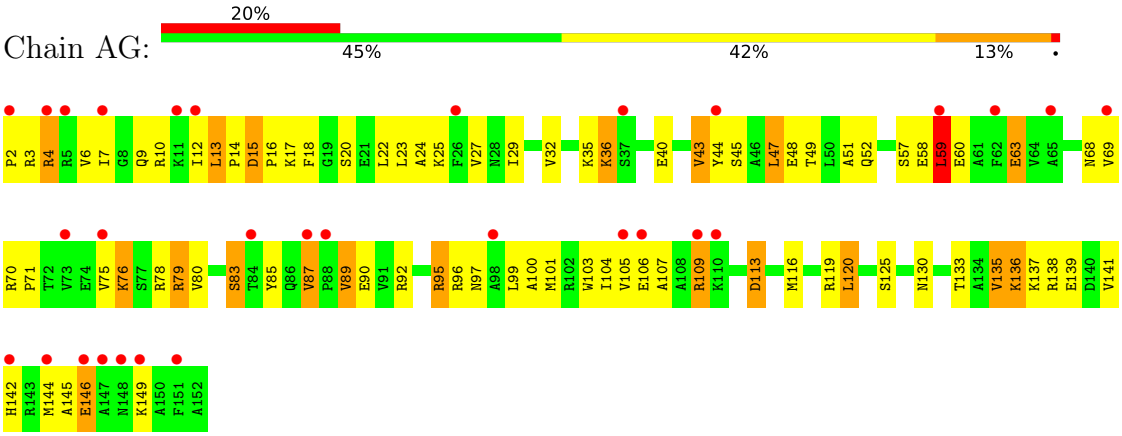


• Molecule 6: 30S ribosomal protein S6

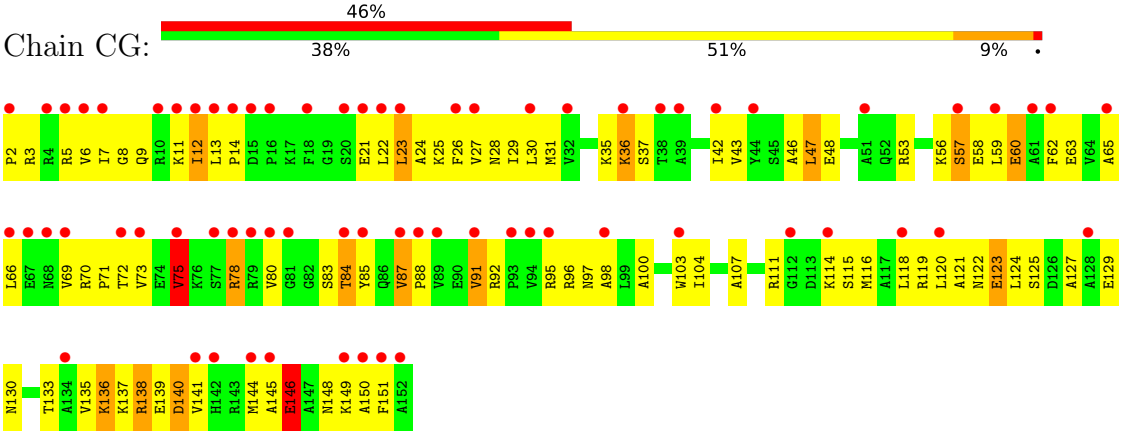




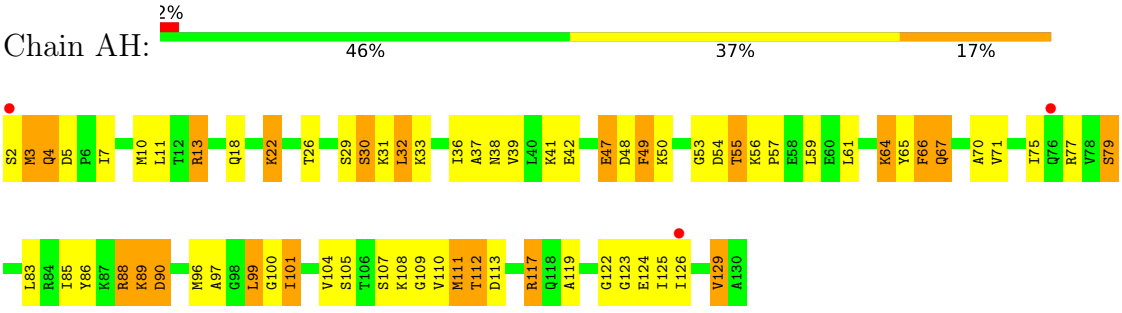
• Molecule 7: 30S ribosomal protein S7



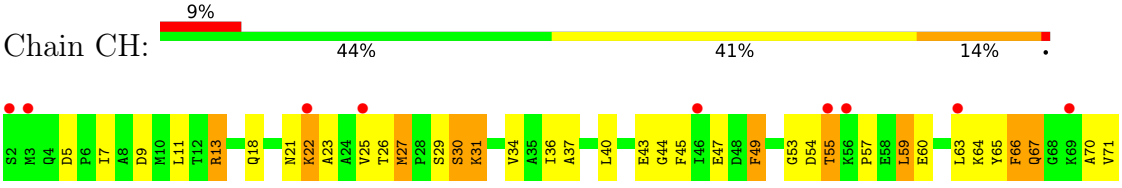
• Molecule 7: 30S ribosomal protein S7



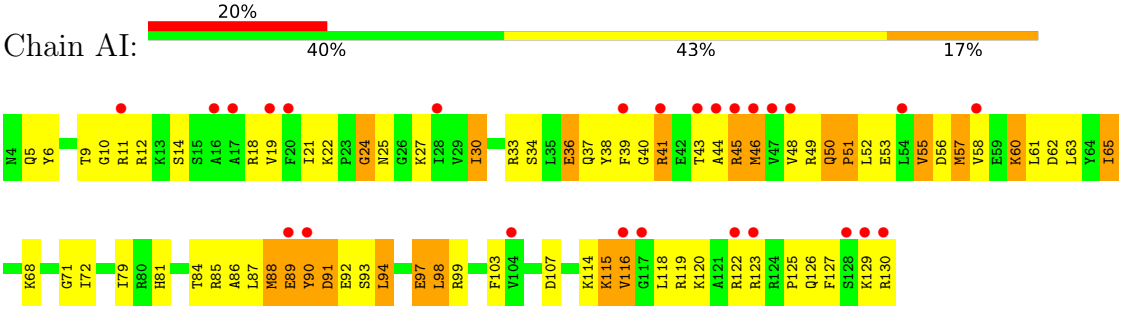
• Molecule 8: 30S ribosomal protein S8



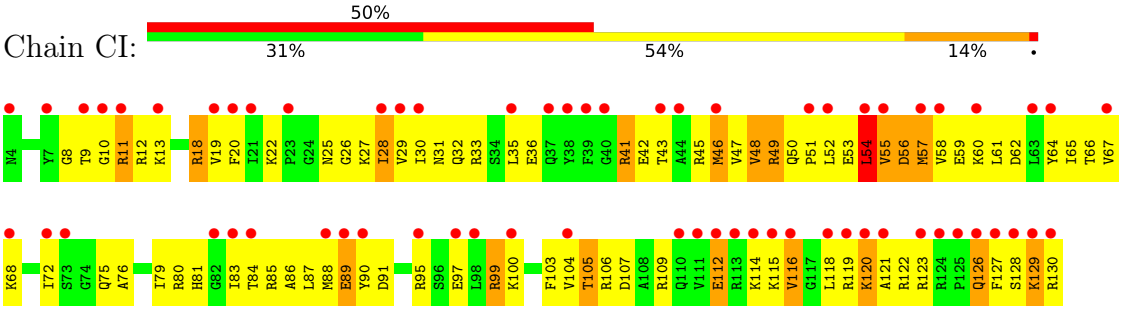
• Molecule 8: 30S ribosomal protein S8



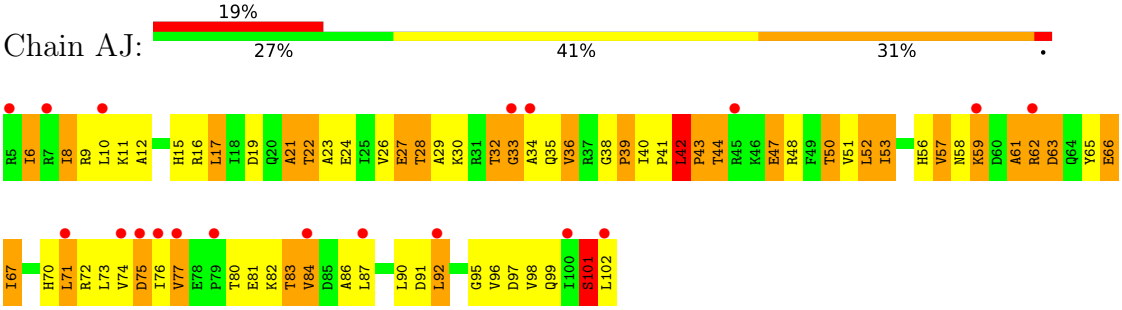
• Molecule 9: 30S ribosomal protein S9



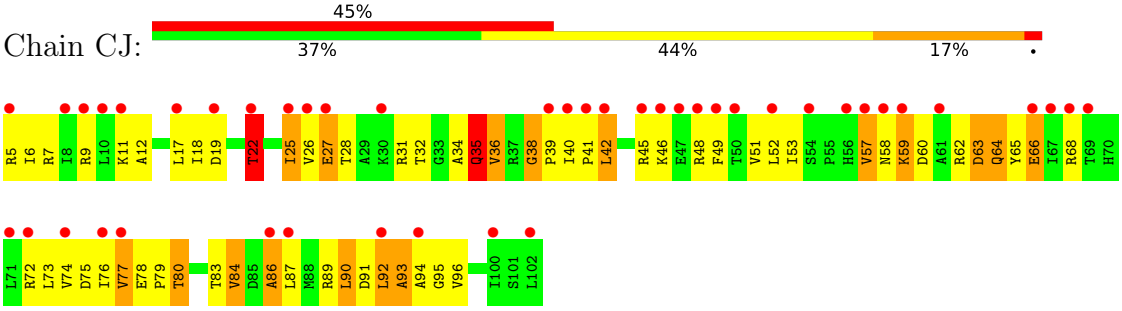
• Molecule 9: 30S ribosomal protein S9



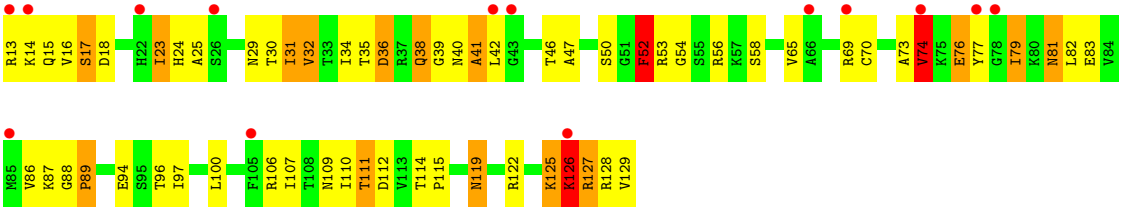
• Molecule 10: 30S ribosomal protein S10



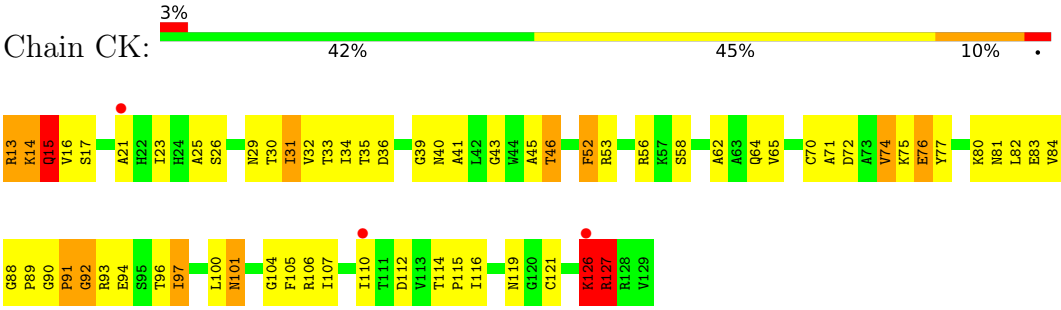
• Molecule 10: 30S ribosomal protein S10



• Molecule 11: 30S ribosomal protein S11



• Molecule 11: 30S ribosomal protein S11



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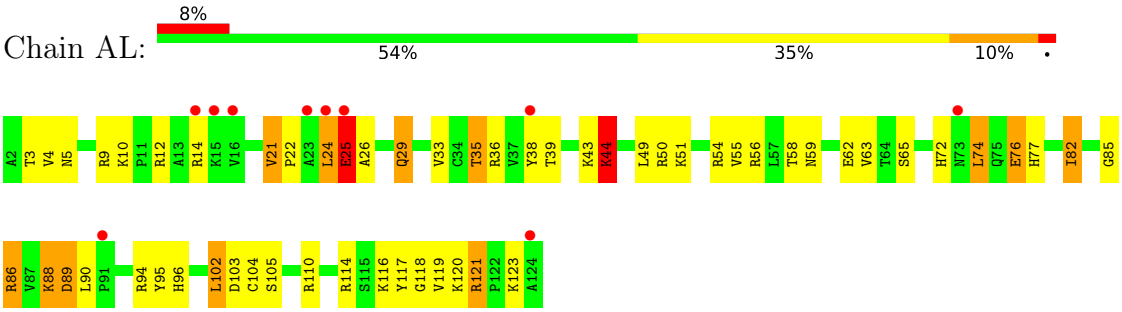

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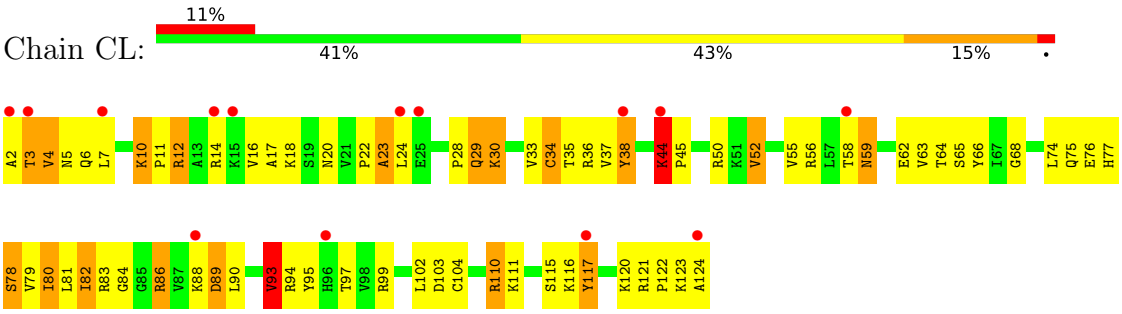

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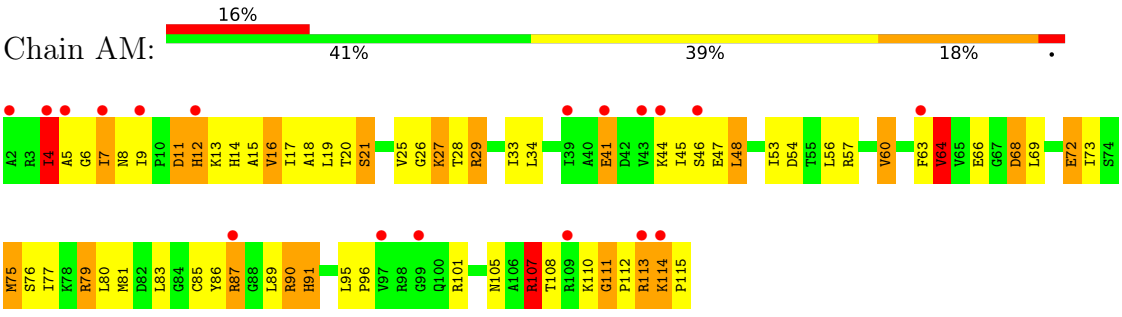

• Molecule 13: 30S ribosomal protein S13

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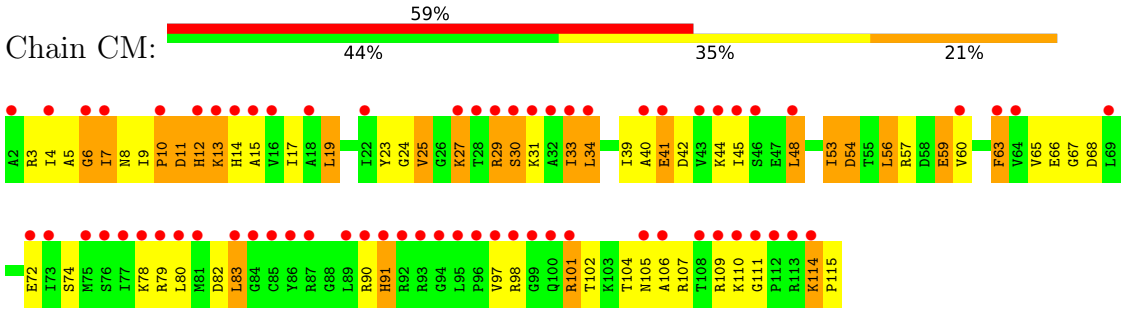

• Molecule 14: 30S ribosomal protein S14

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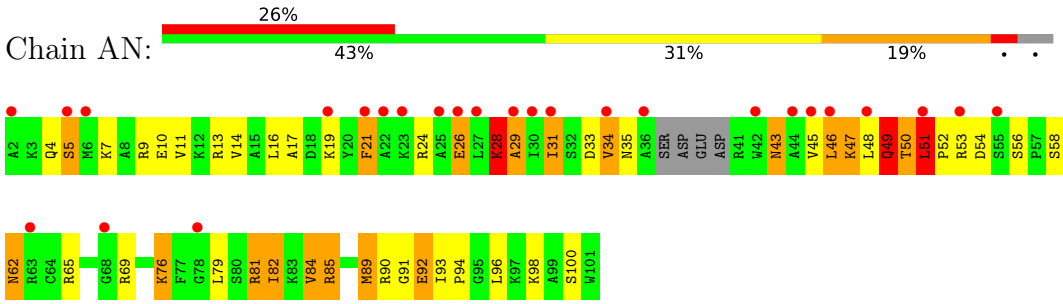

• Molecule 14: 30S ribosomal protein S14

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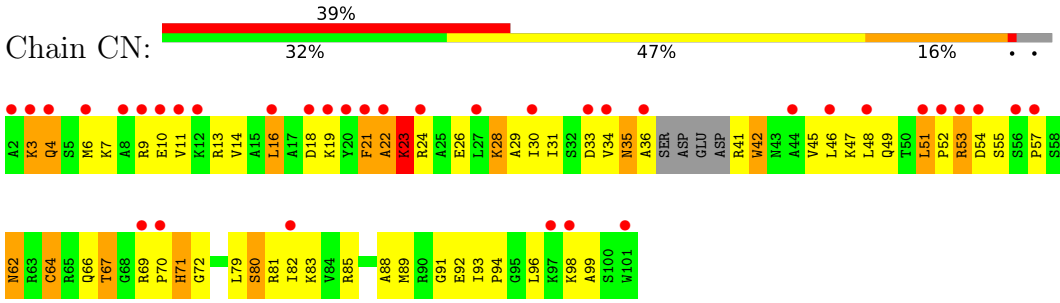

• Molecule 15: 30S ribosomal protein S15

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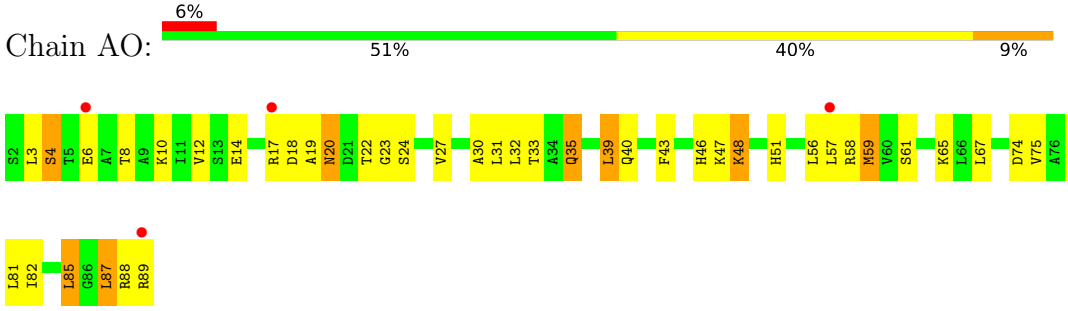

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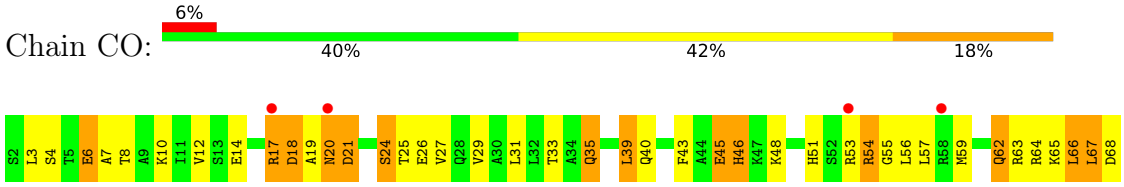

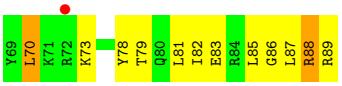

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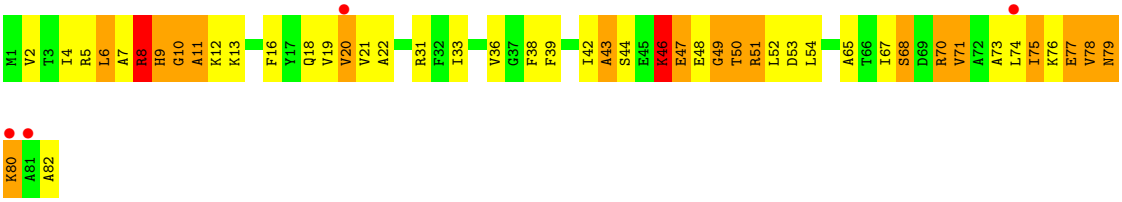

• Molecule 16: 30S ribosomal protein S16

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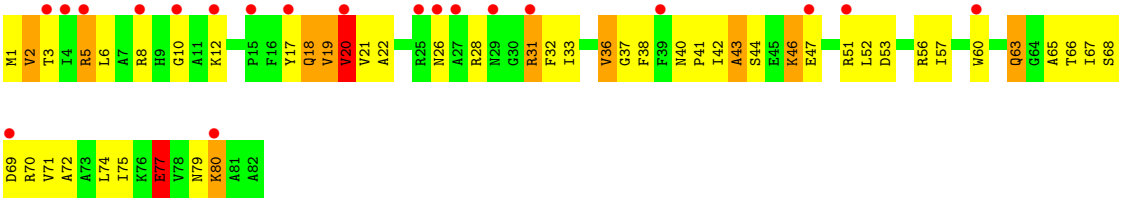

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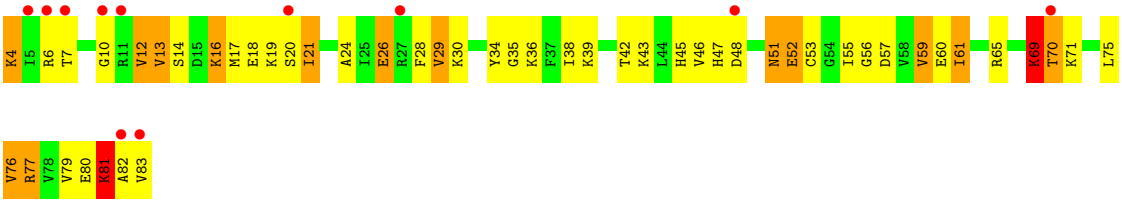

• Molecule 17: 30S ribosomal protein S17

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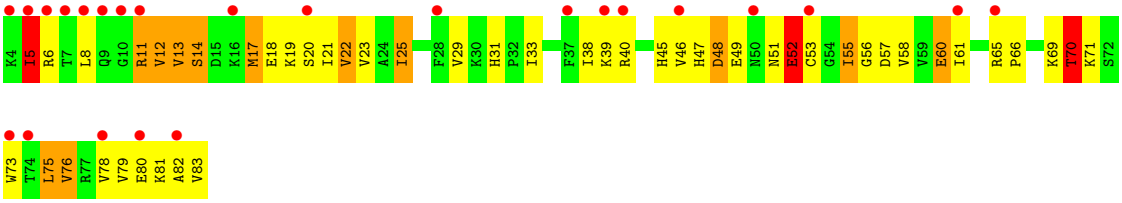
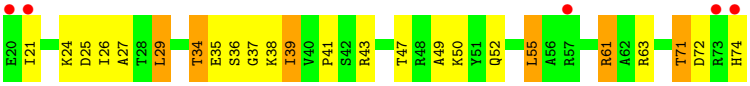


• Molecule 18: 30S ribosomal protein S18

Chain AR:



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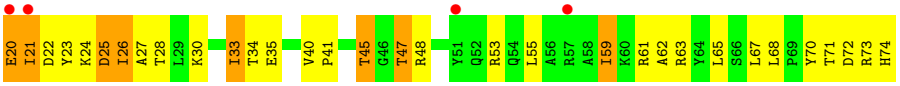

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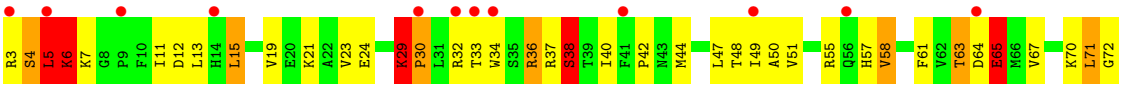

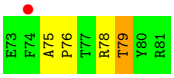

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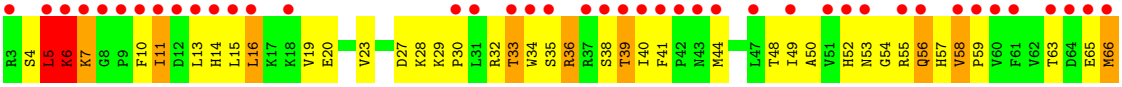

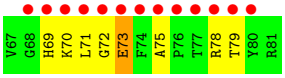

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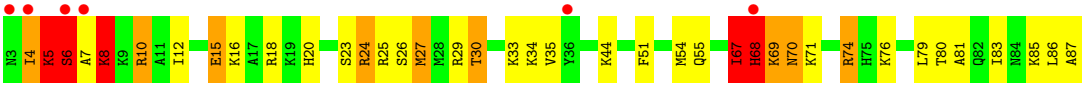

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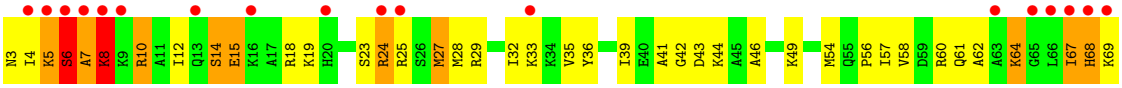

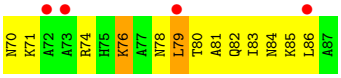

• Molecule 21: 30S ribosomal protein S21

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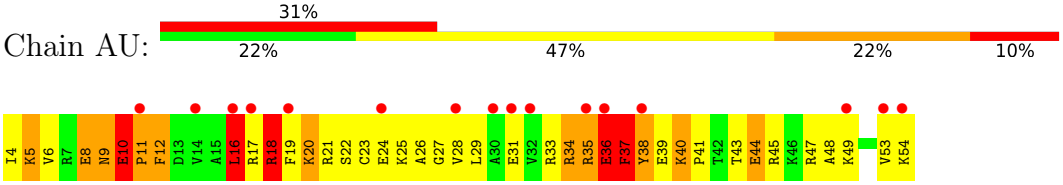

• Molecule 21: 30S ribosomal protein S21

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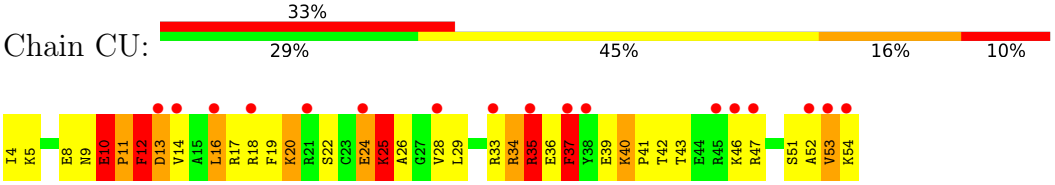
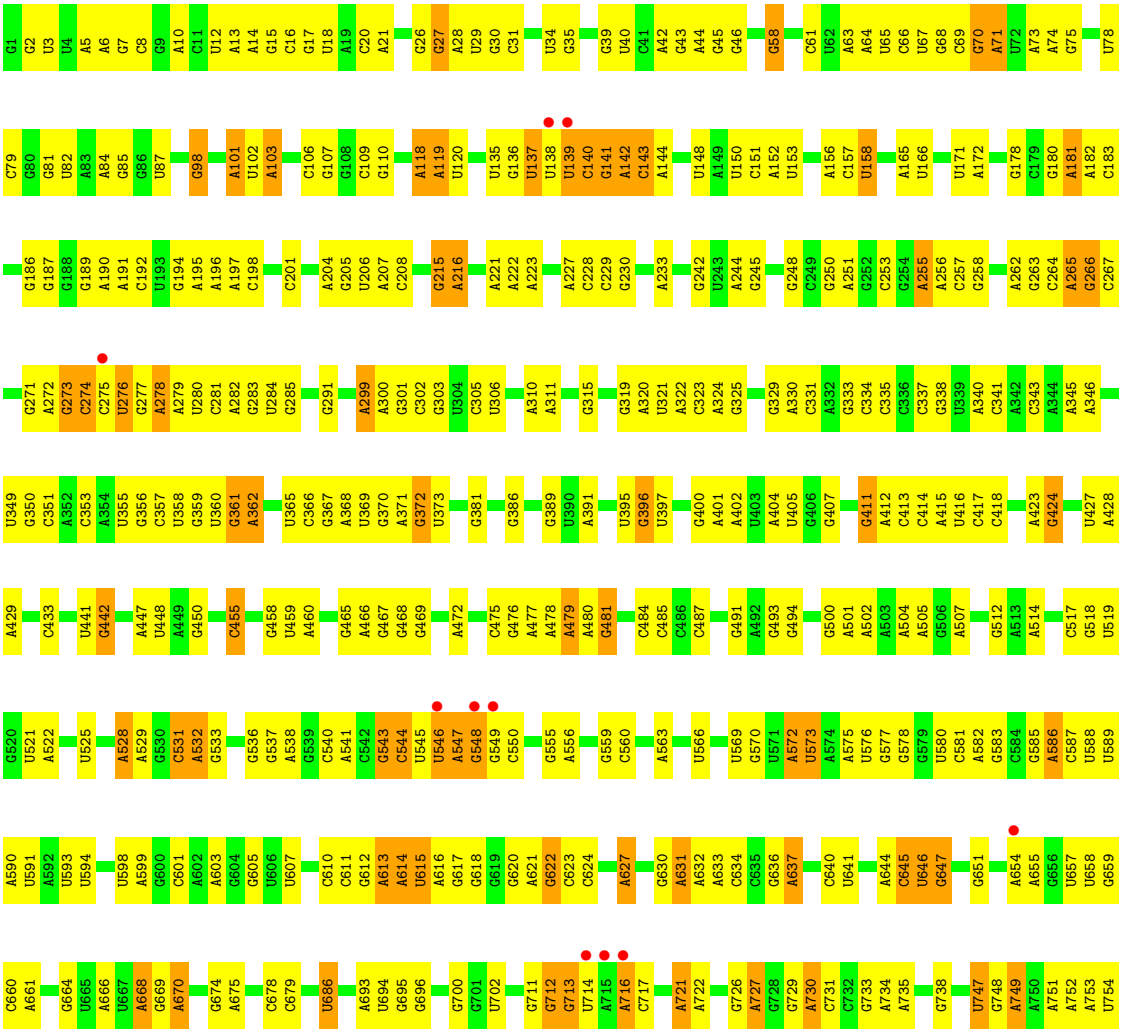
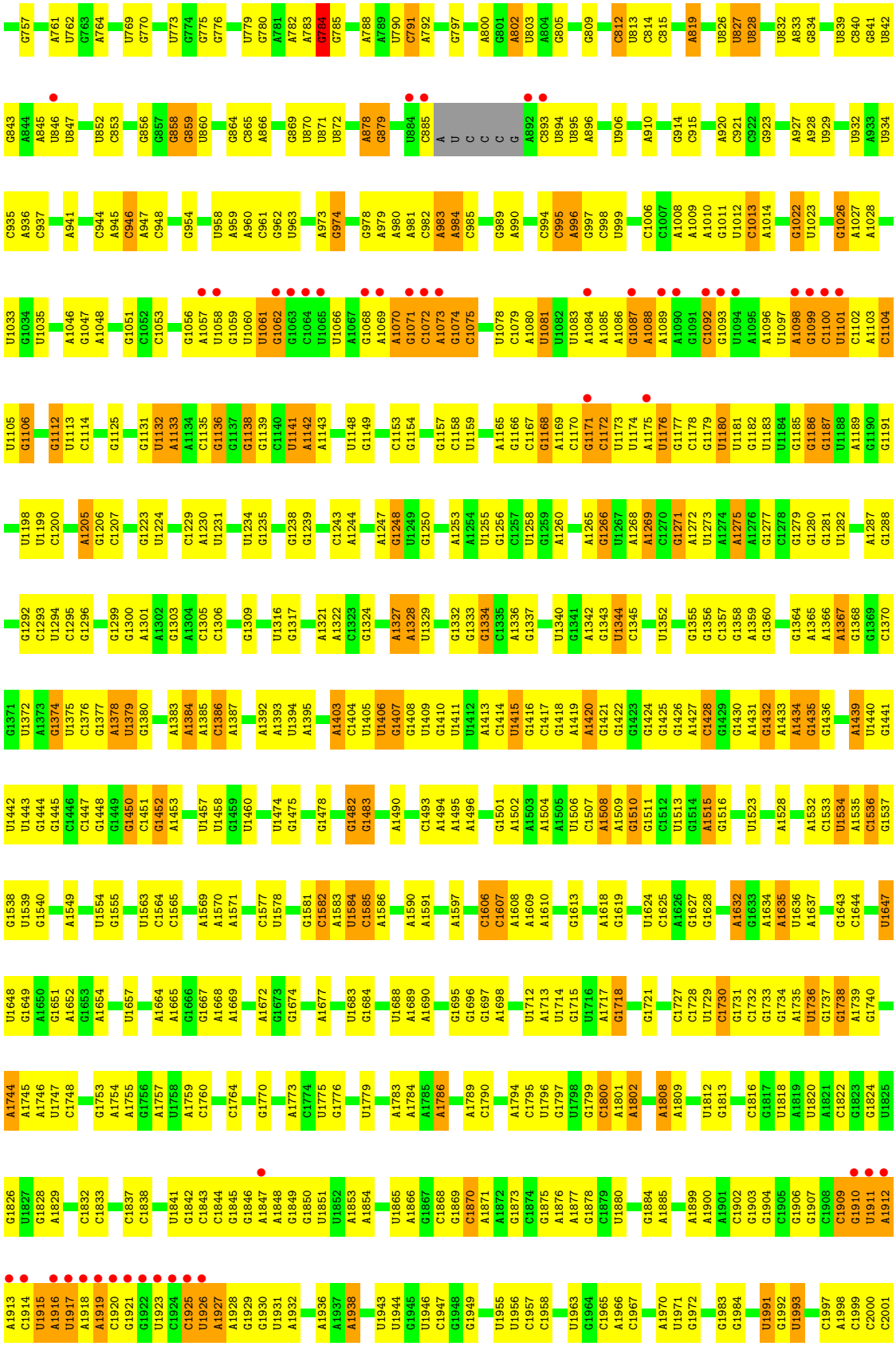


• Molecule 22: 23S rRNA

Chain BA:

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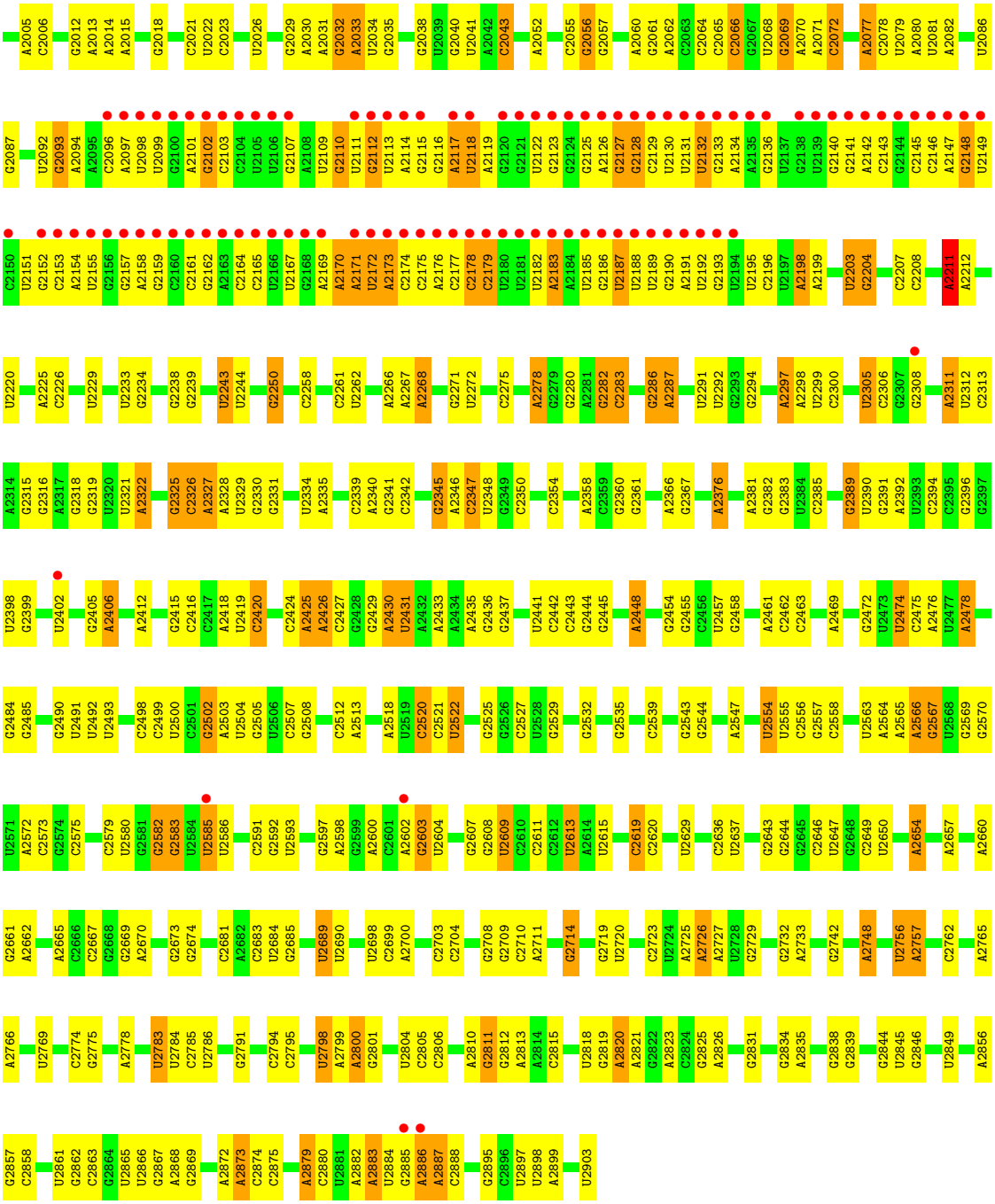

• Molecule 22: 23S rRNA

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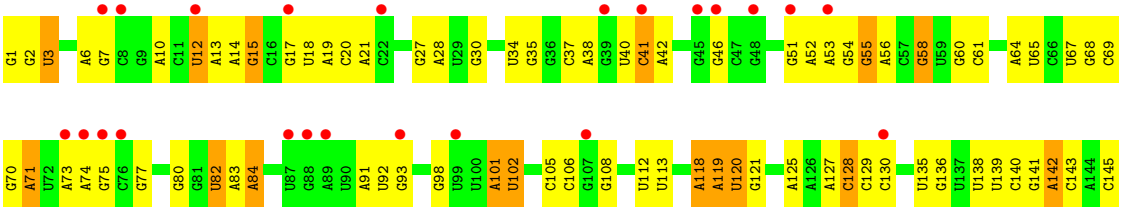

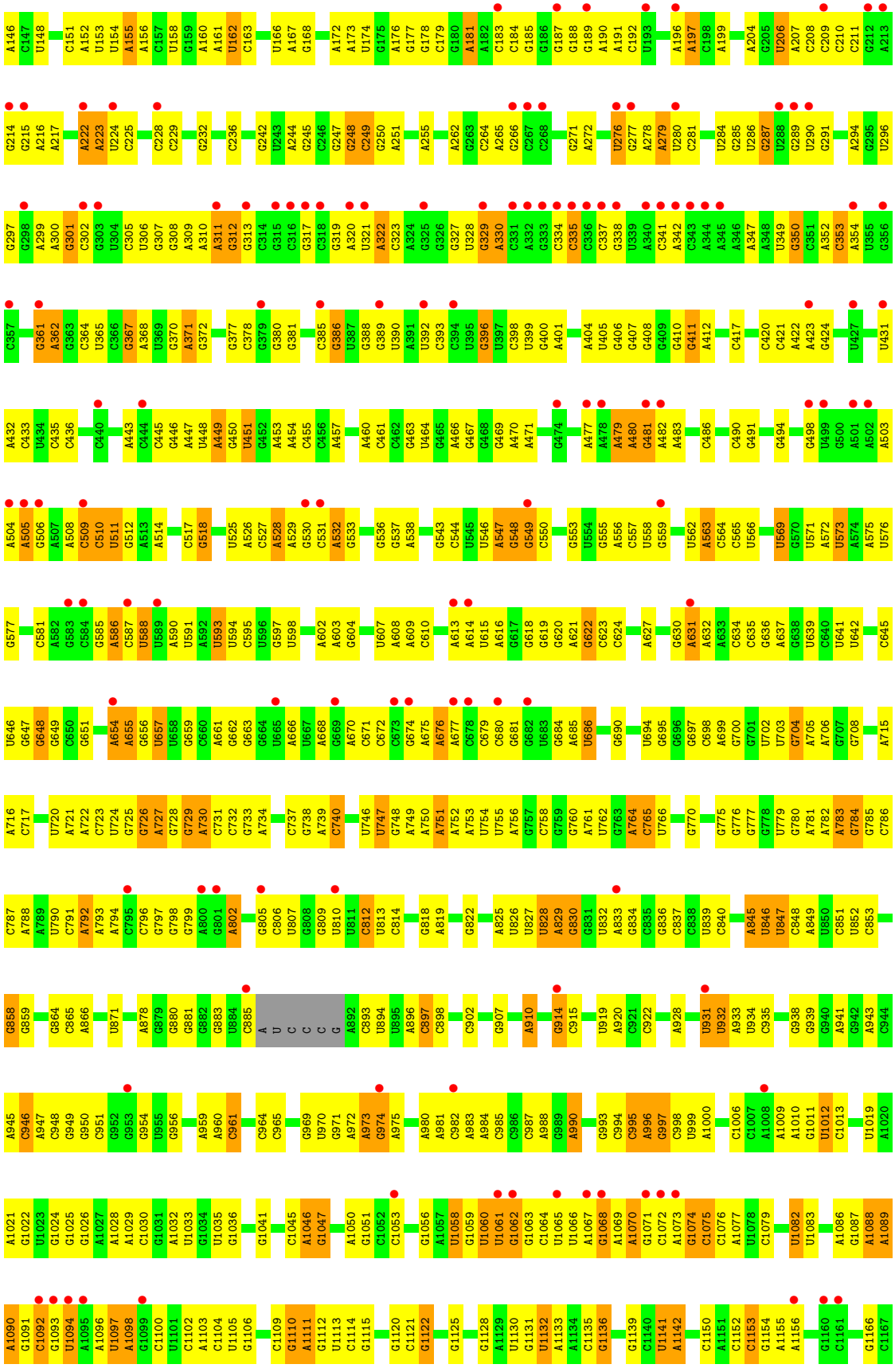

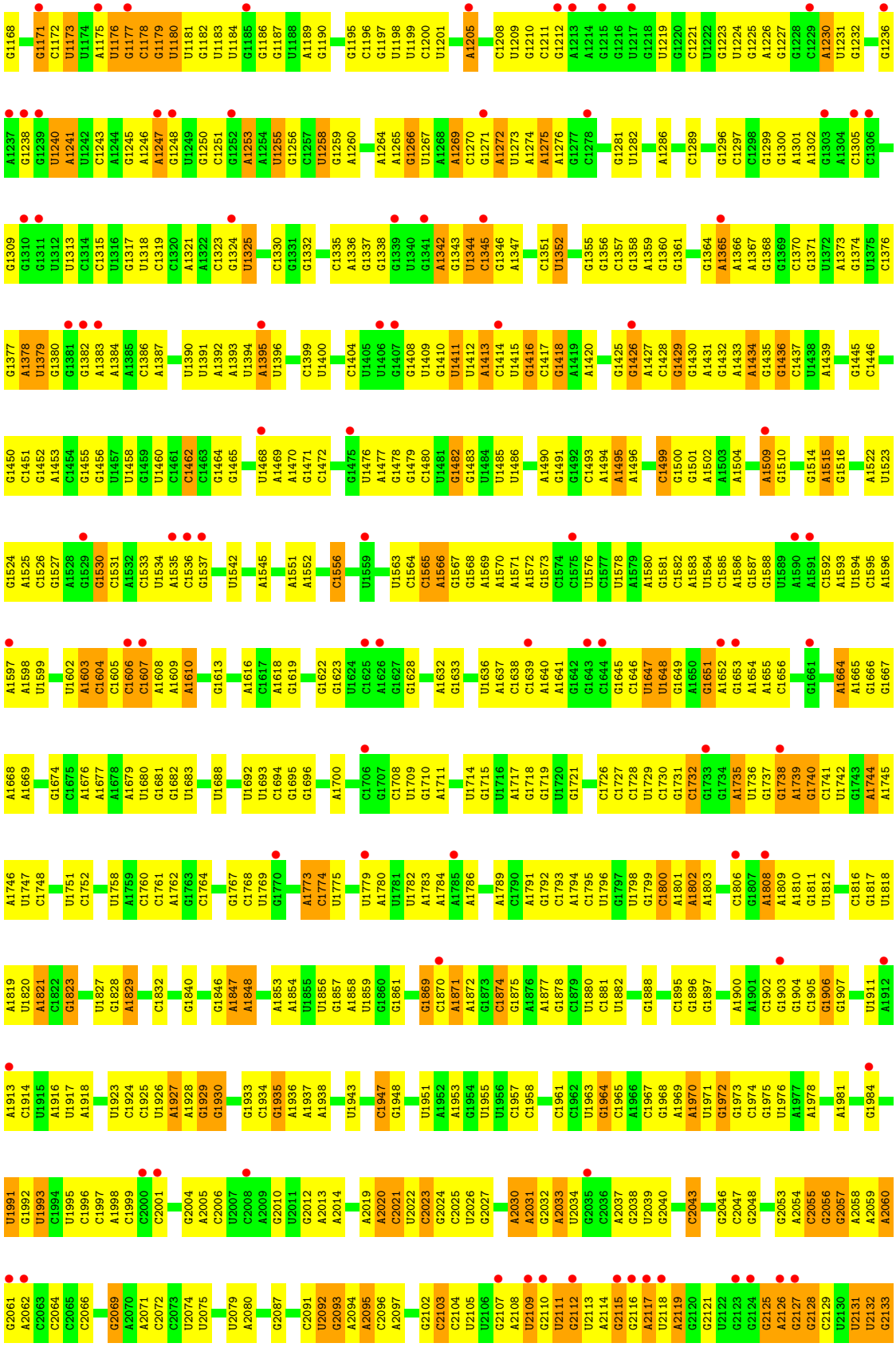
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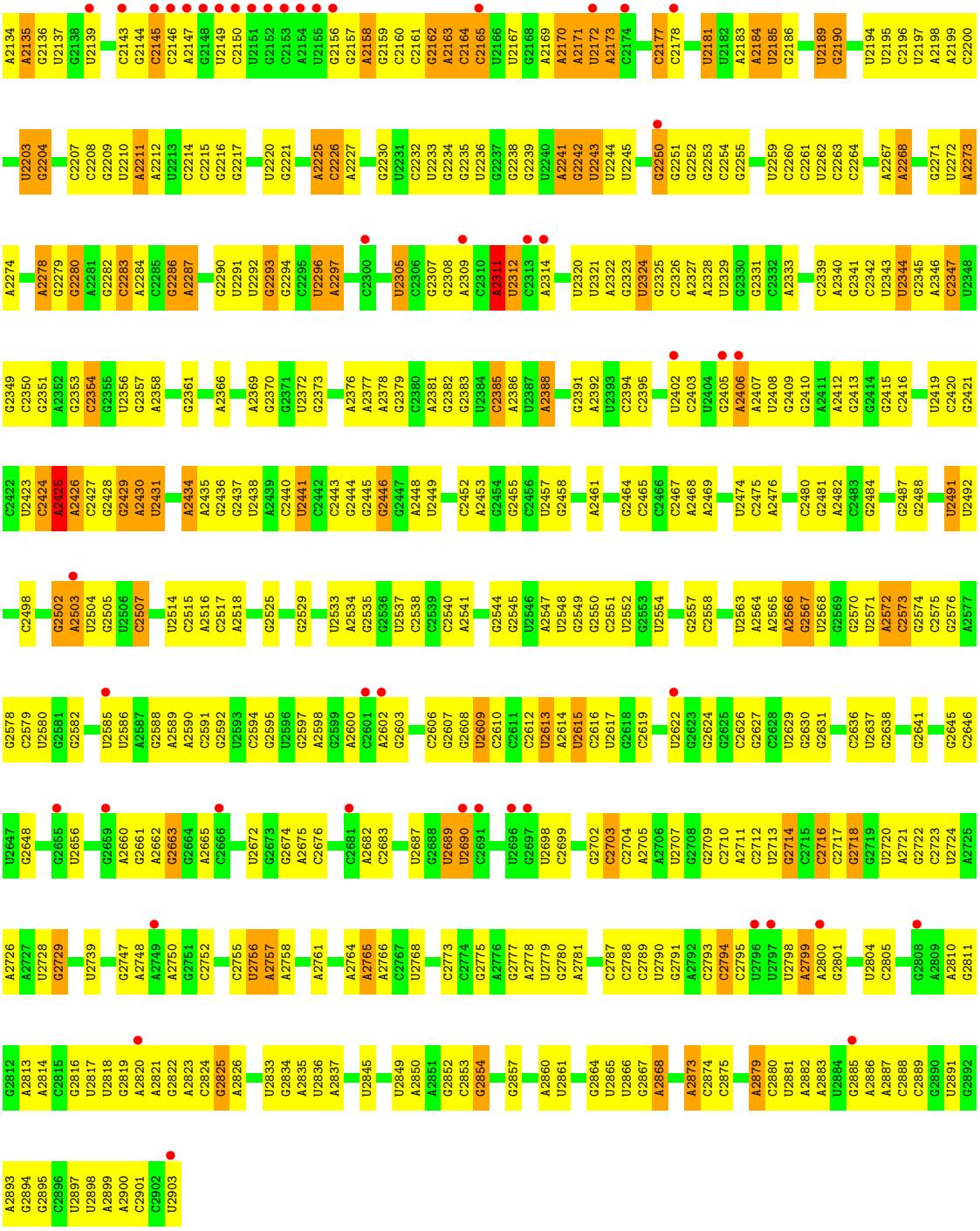
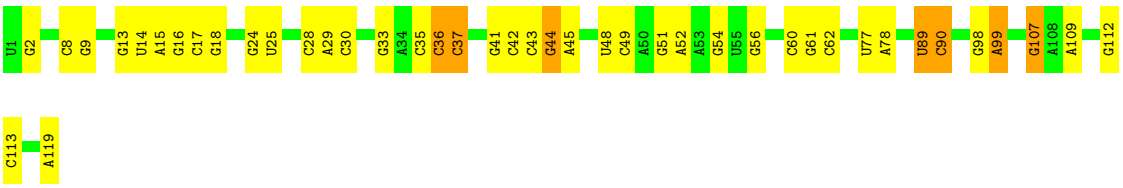


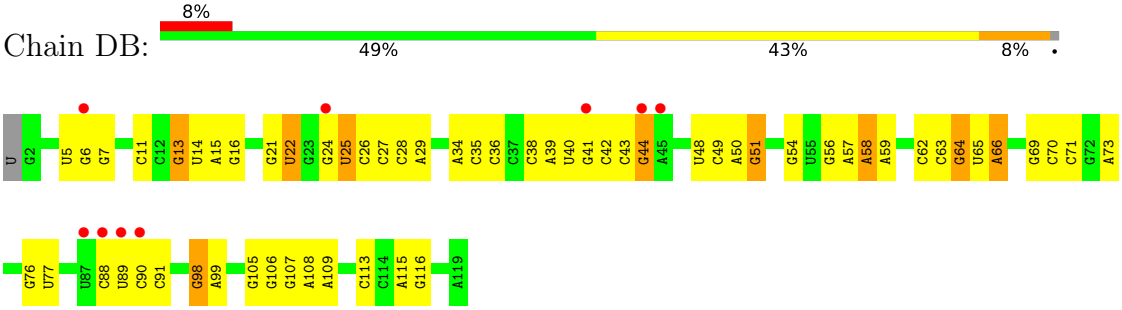
• Molecule 23: 5S rRNA

Chain BB:



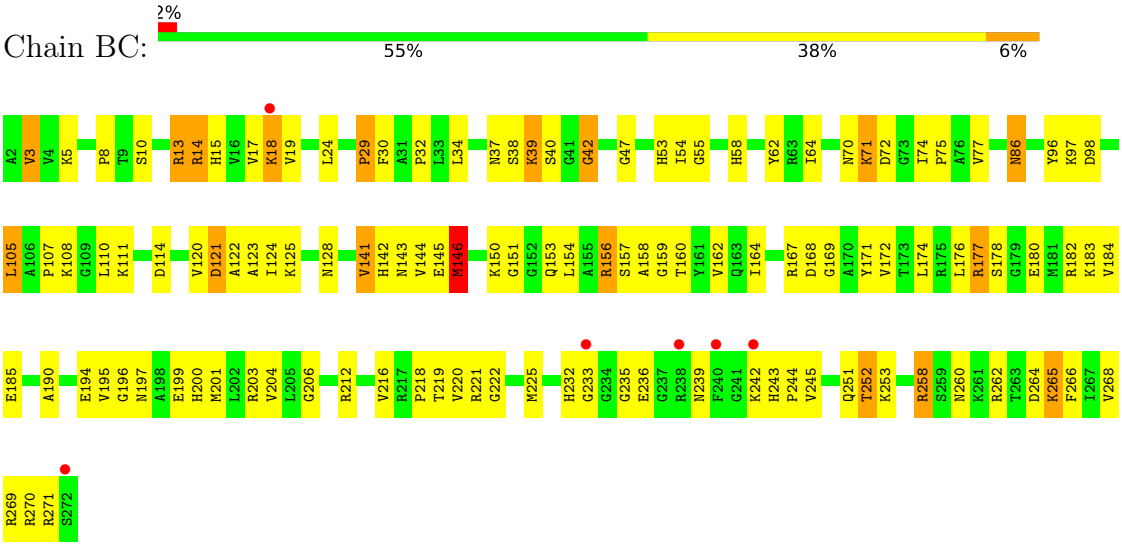
• Molecule 23: 5S rRNA

Chain DB:



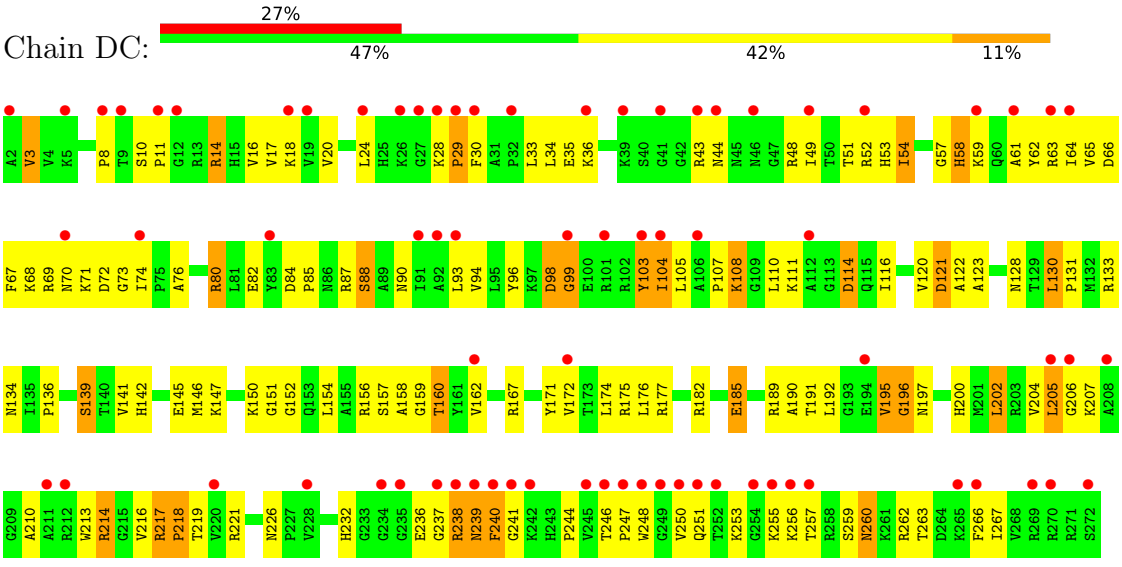
• Molecule 24: 50S ribosomal protein L2

Chain BC:



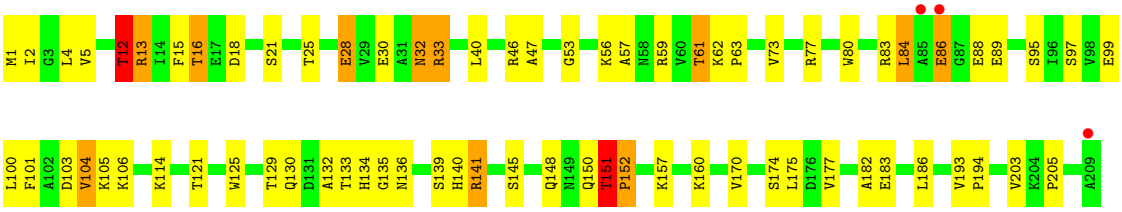
• Molecule 24: 50S ribosomal protein L2

Chain DC:



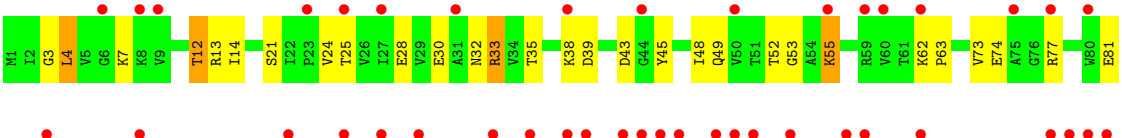
• Molecule 25: 50S ribosomal protein L3

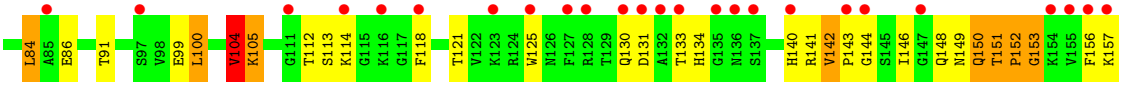
Chain BD:

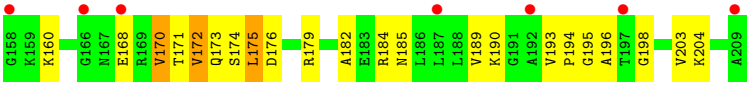


• Molecule 25: 50S ribosomal protein L3

Chain DD:

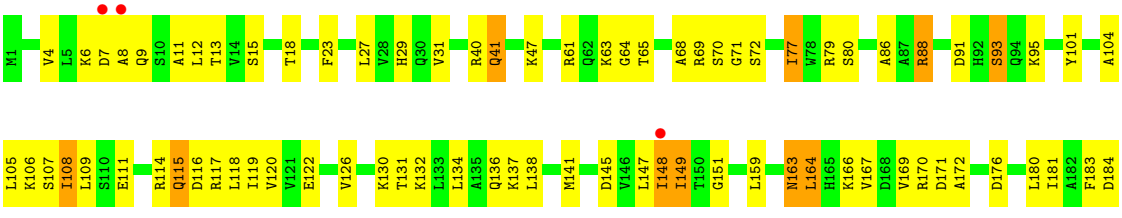


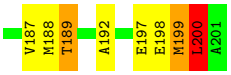




• Molecule 26: 50S ribosomal protein L4

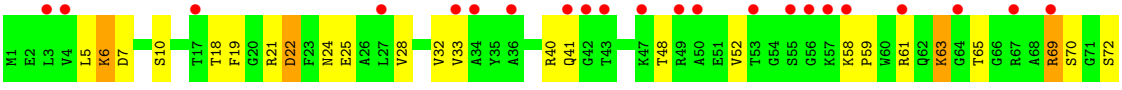
Chain BE:

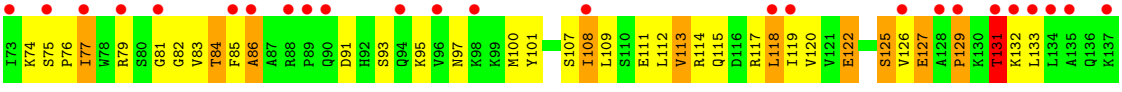


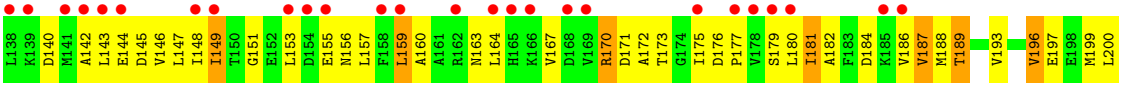


• Molecule 26: 50S ribosomal protein L4

Chain DE:

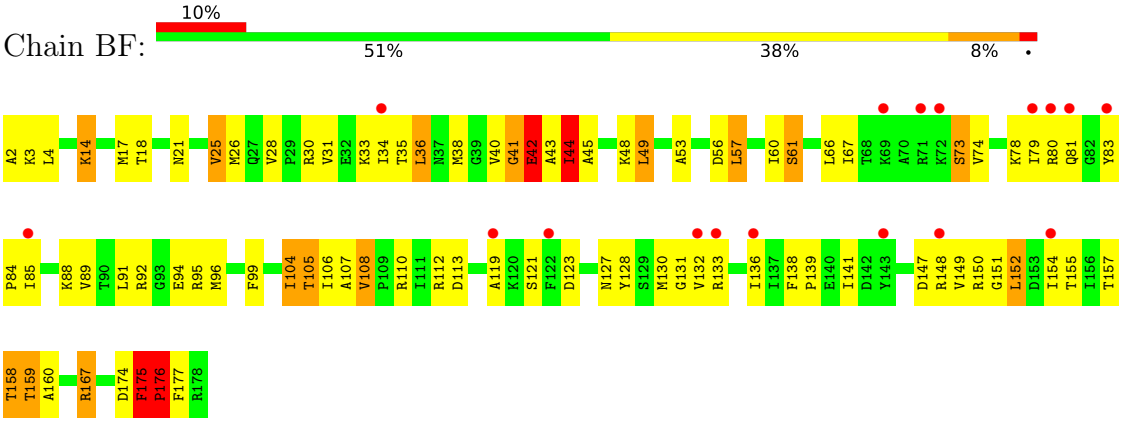






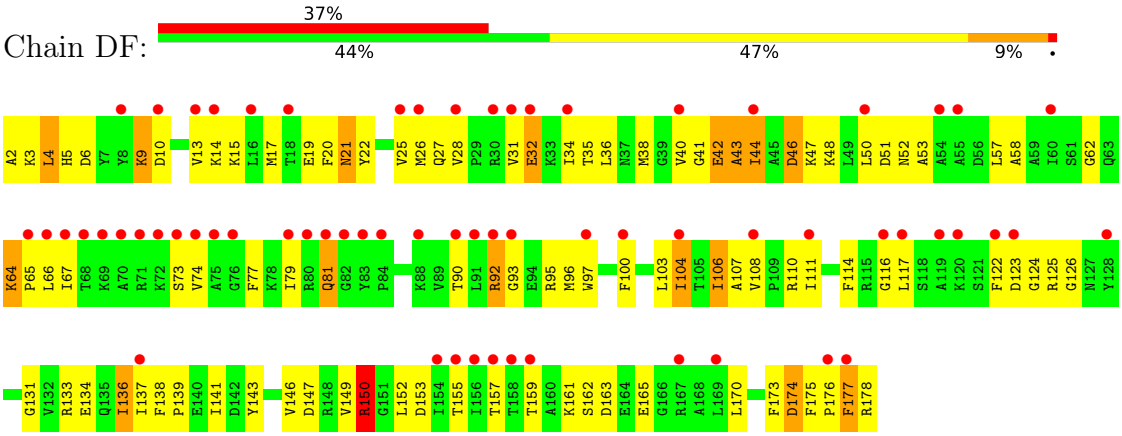
• Molecule 27: 50S ribosomal protein L5

Chain BF:



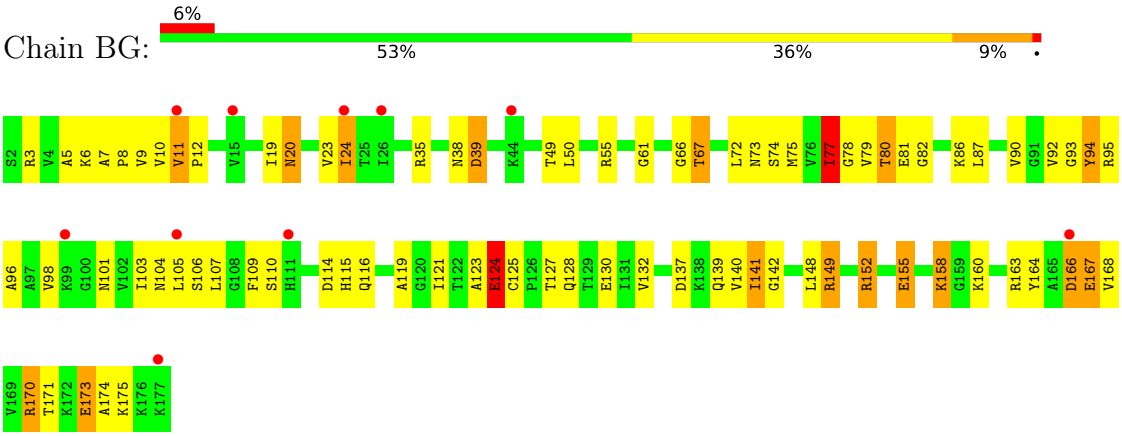
• Molecule 27: 50S ribosomal protein L5

Chain DF:



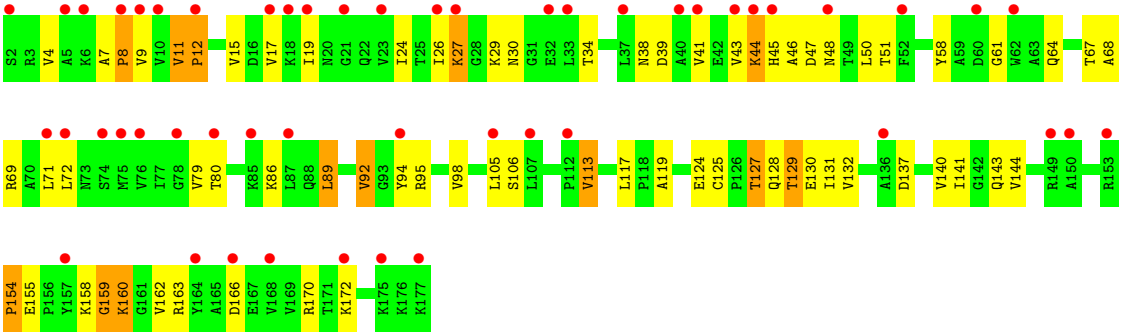
• Molecule 28: 50S ribosomal protein L6

Chain BG:



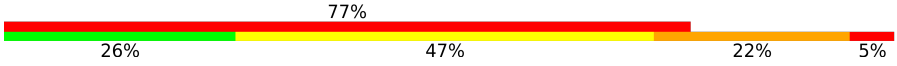
• Molecule 28: 50S ribosomal protein L6

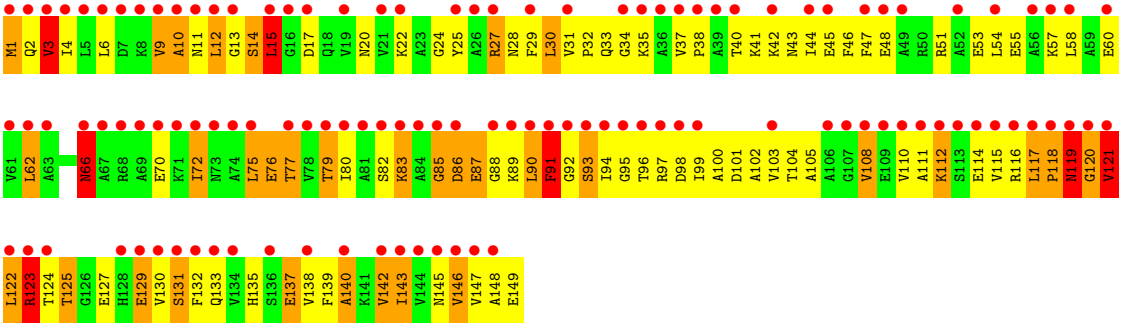
Chain DG:



• Molecule 29: 50S ribosomal protein L9

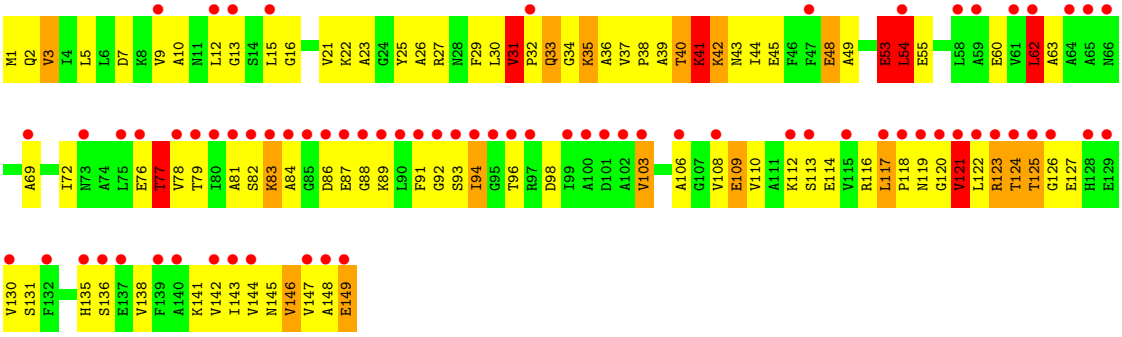
Chain BH:





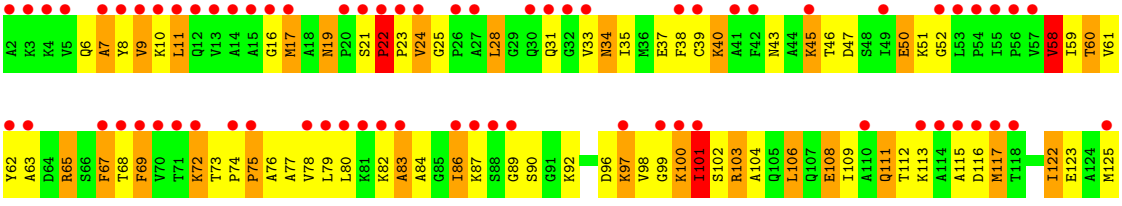
• Molecule 29: 50S ribosomal protein L9

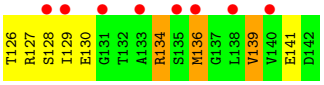
Chain DH:



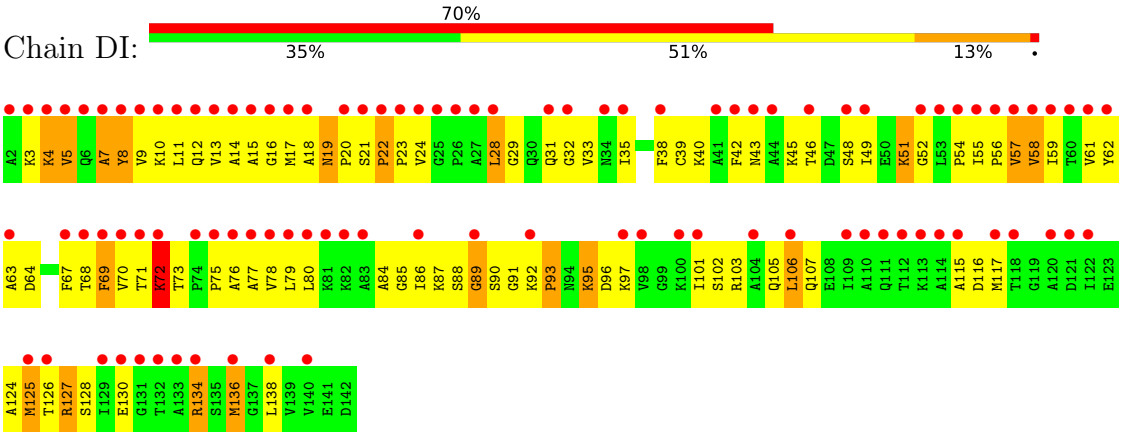
• Molecule 30: 50S ribosomal protein L11

Chain BI:

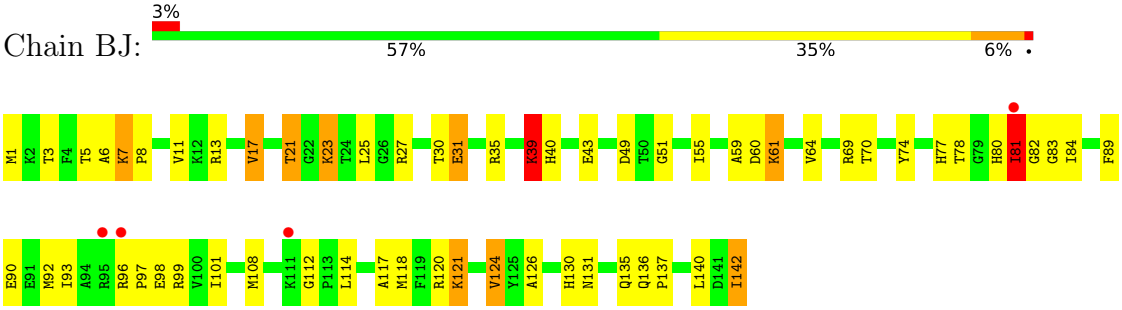




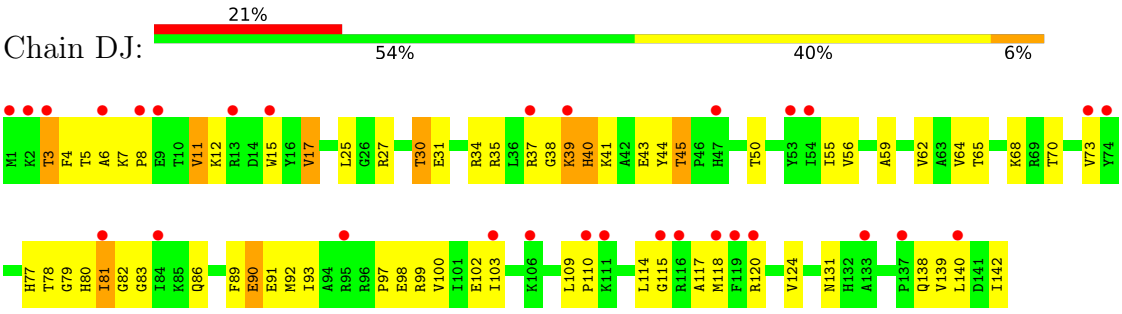
• Molecule 30: 50S ribosomal protein L11



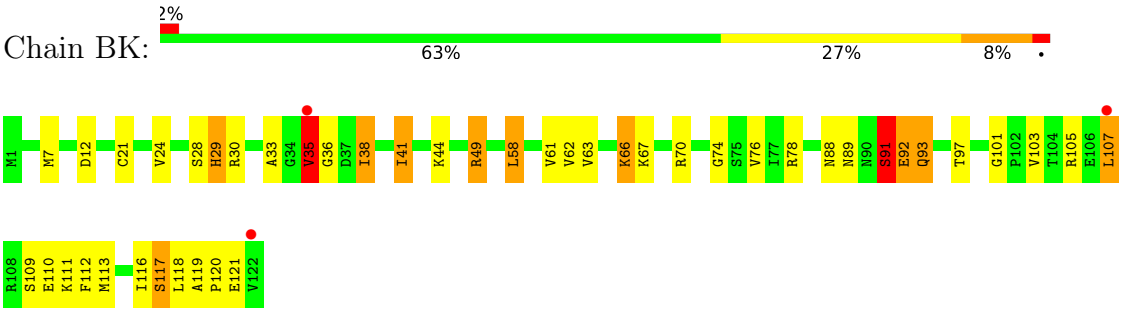
• Molecule 31: 50S ribosomal protein L13



• Molecule 31: 50S ribosomal protein L13

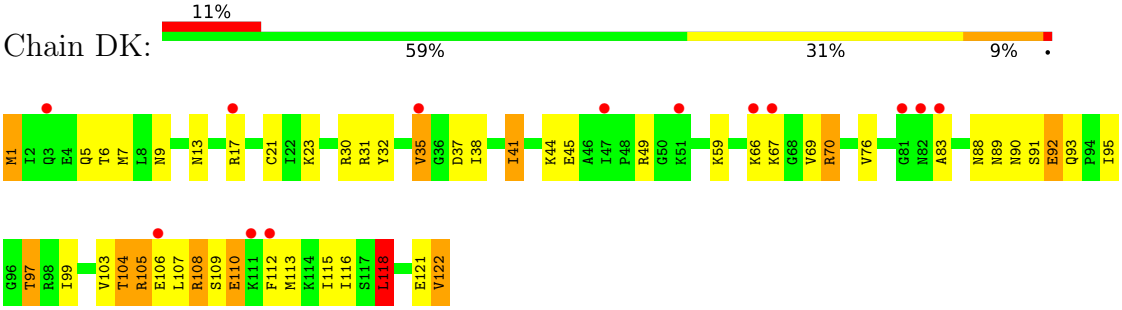


• Molecule 32: 50S ribosomal protein L14



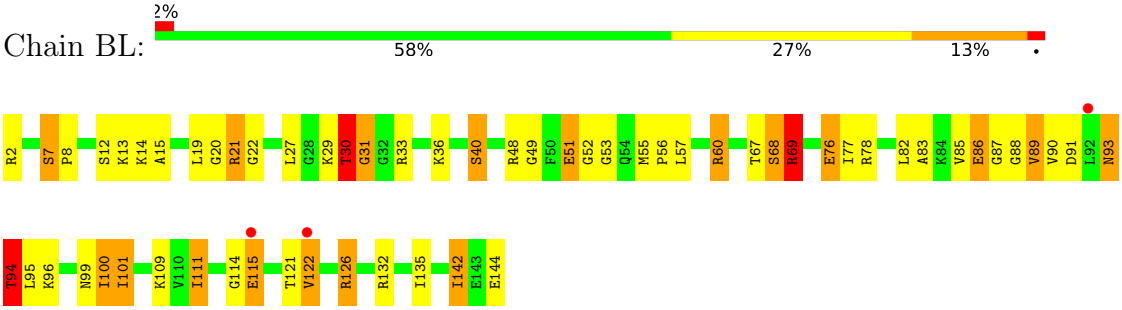
• Molecule 32: 50S ribosomal protein L14

Chain DK:



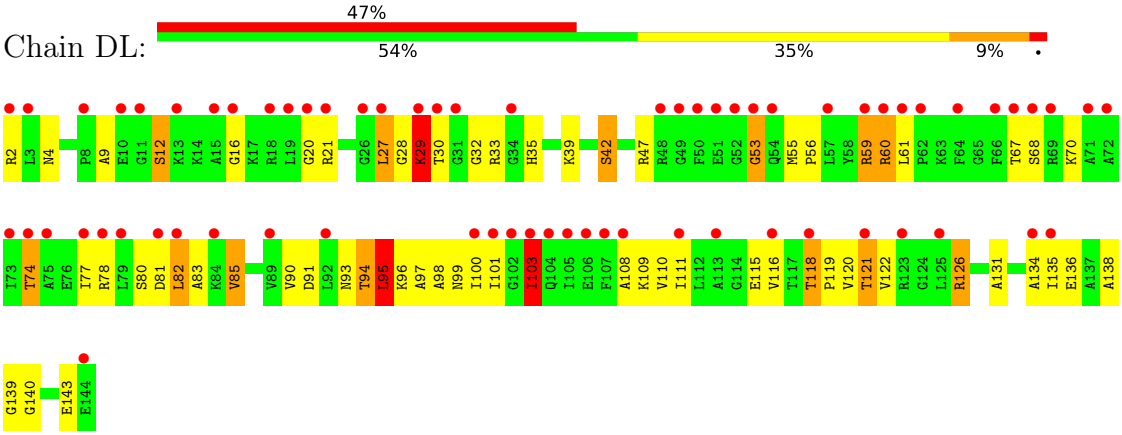
• Molecule 33: 50S ribosomal protein L15

Chain BL:



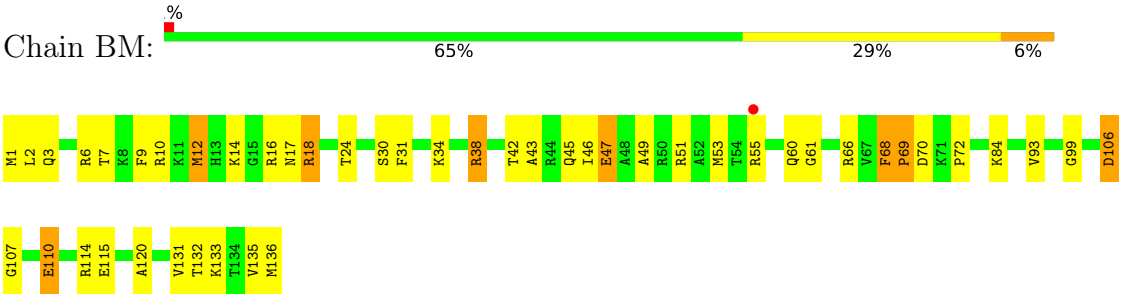
• Molecule 33: 50S ribosomal protein L15

Chain DL:



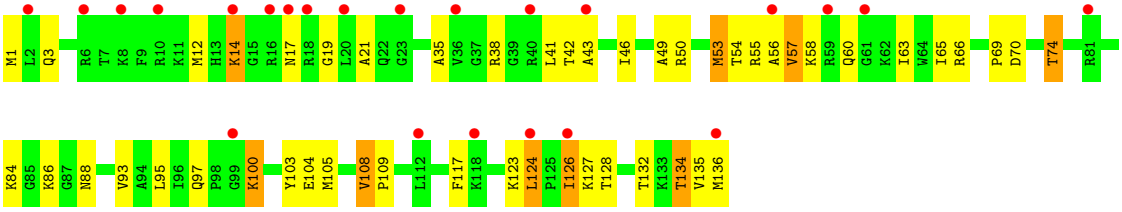
• Molecule 34: 50S ribosomal protein L16

Chain BM:



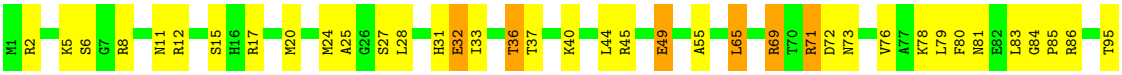
• Molecule 34: 50S ribosomal protein L16

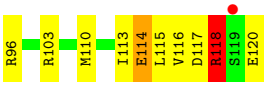
Chain DM:



• Molecule 35: 50S ribosomal protein L17

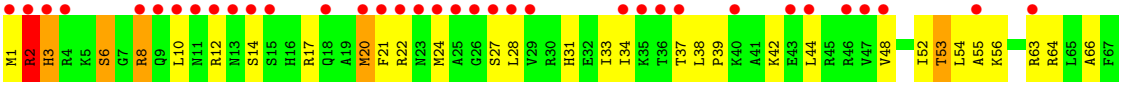
Chain BN:





• Molecule 35: 50S ribosomal protein L17

Chain DN:

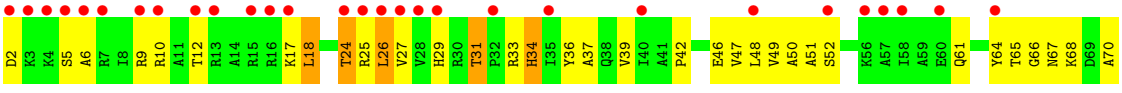


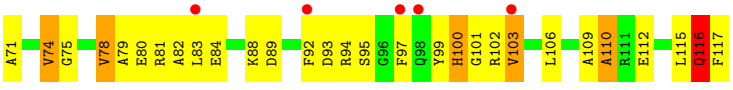
• Molecule 36: 50S ribosomal protein L18

Chain BO:

• Molecule 36: 50S ribosomal protein L18

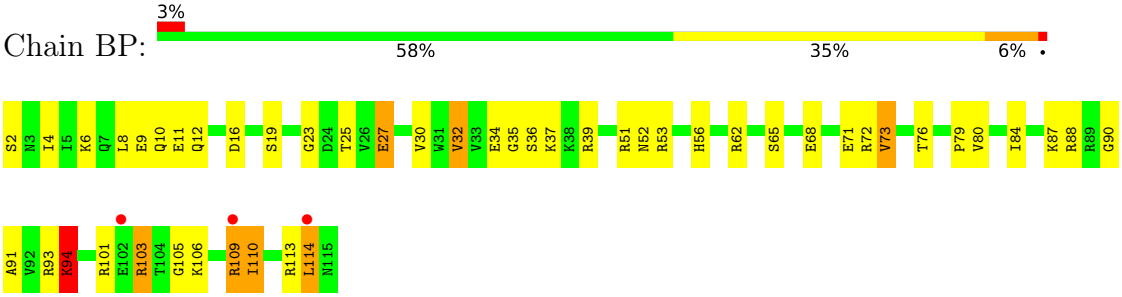
Chain DO:





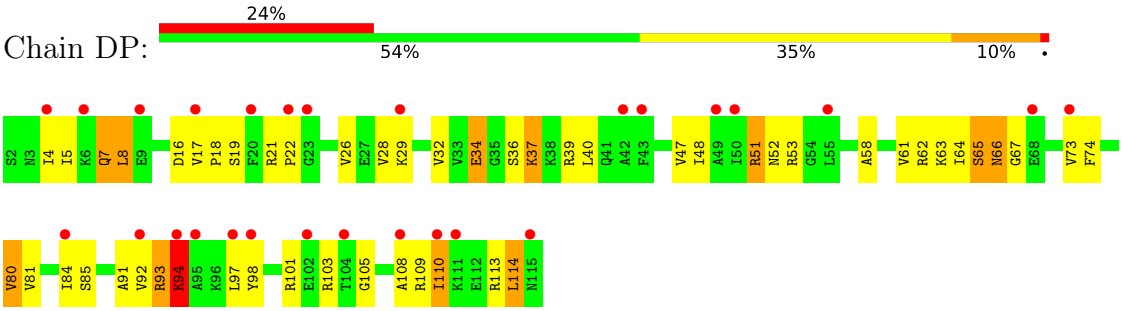
• Molecule 37: 50S ribosomal protein L19

Chain BP:



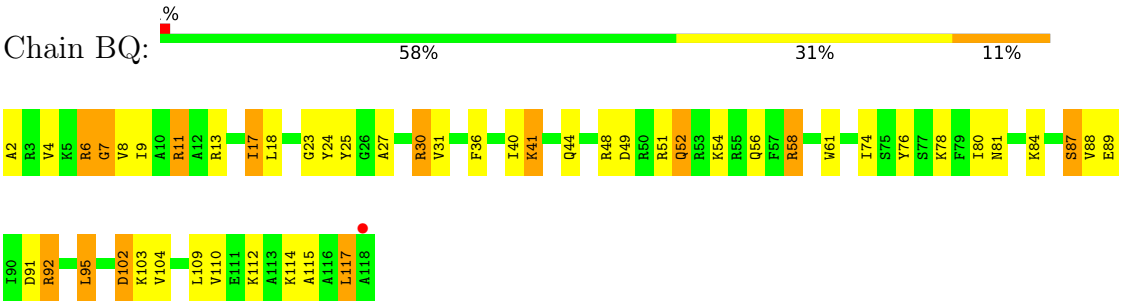
• Molecule 37: 50S ribosomal protein L19

Chain DP:



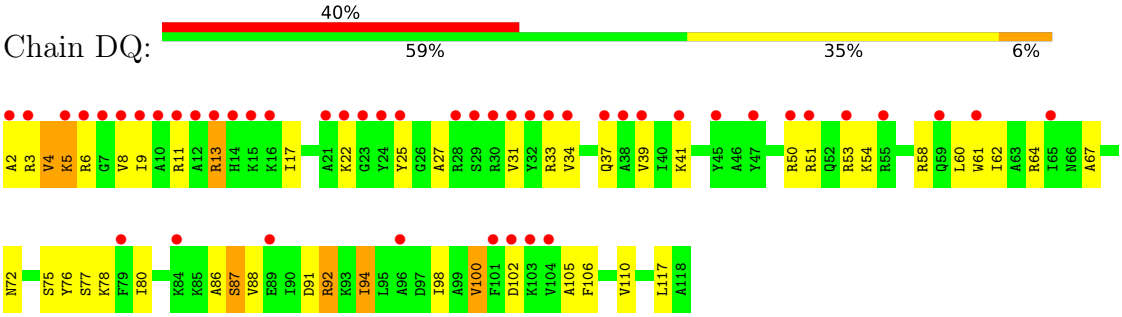
• Molecule 38: 50S ribosomal protein L20

Chain BQ:



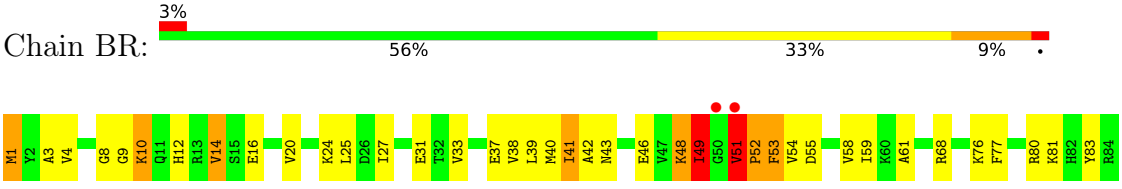
• Molecule 38: 50S ribosomal protein L20

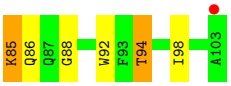
Chain DQ:



• Molecule 39: 50S ribosomal protein L21

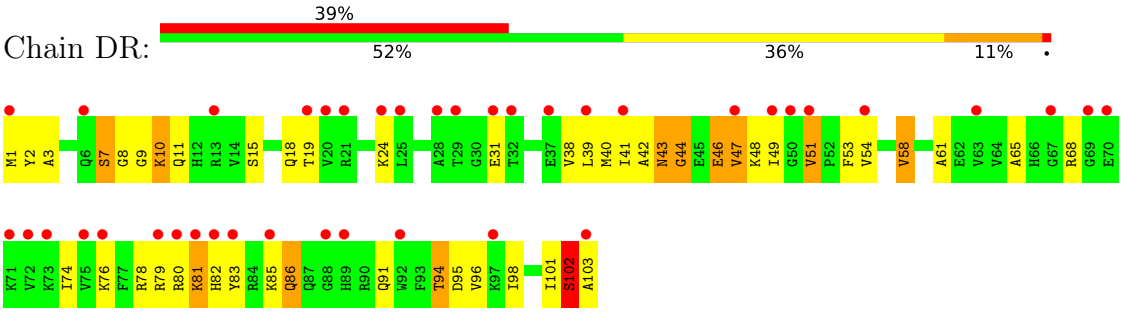
Chain BR:





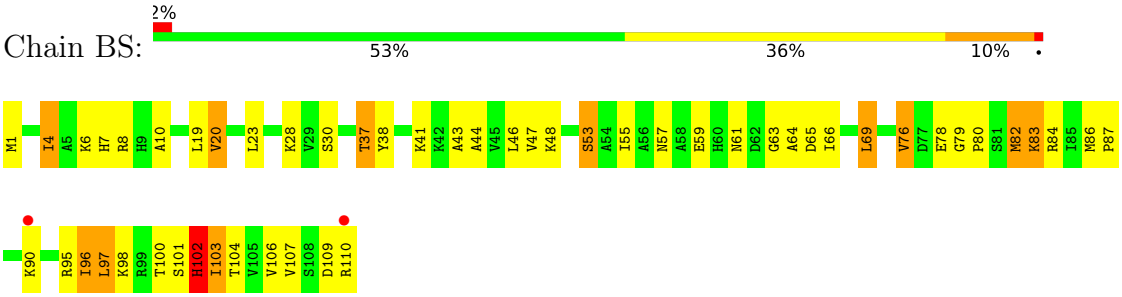
• Molecule 39: 50S ribosomal protein L21

Chain DR:



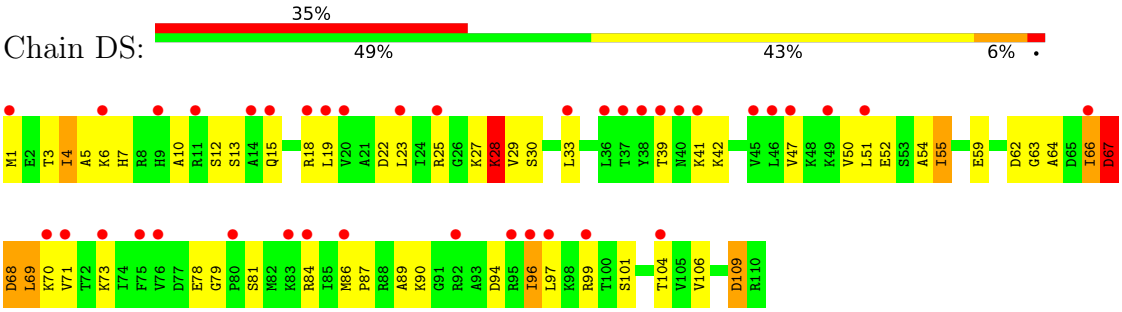
• Molecule 40: 50S ribosomal protein L22

Chain BS:



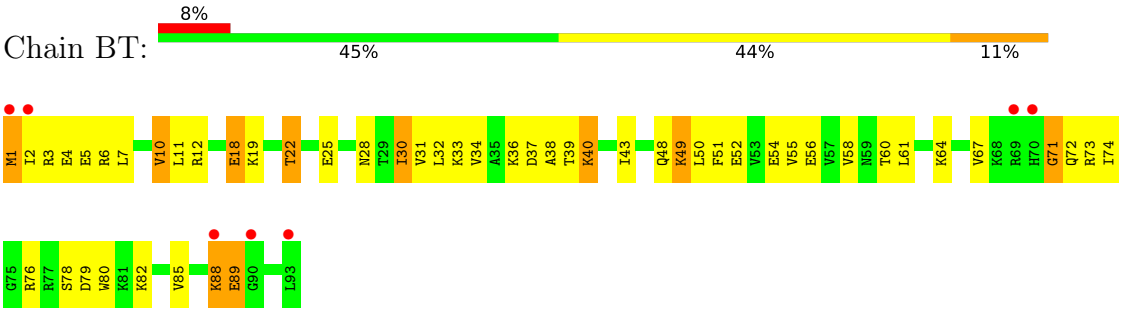
• Molecule 40: 50S ribosomal protein L22

Chain DS:



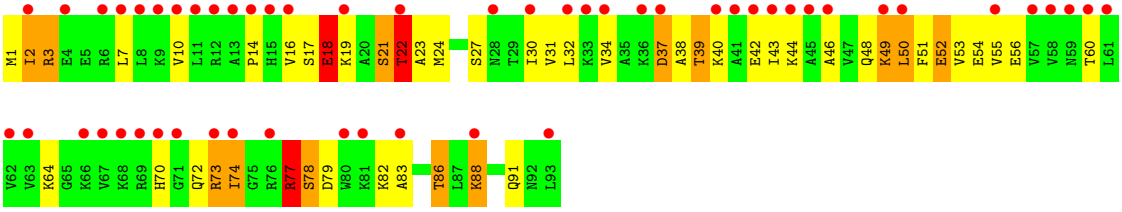
• Molecule 41: 50S ribosomal protein L23

Chain BT:

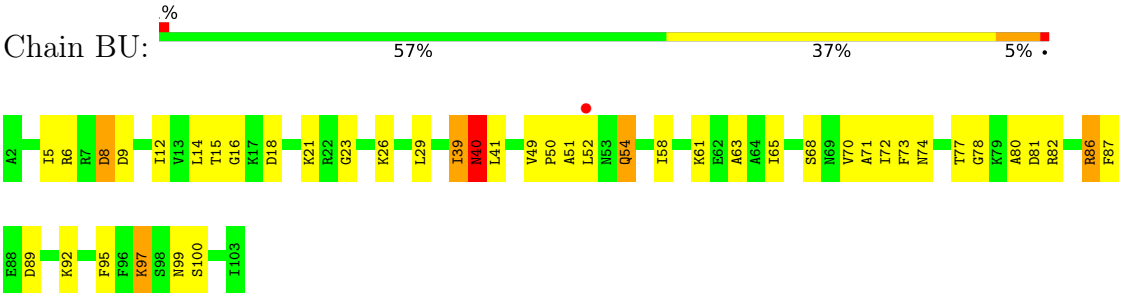


• Molecule 41: 50S ribosomal protein L23

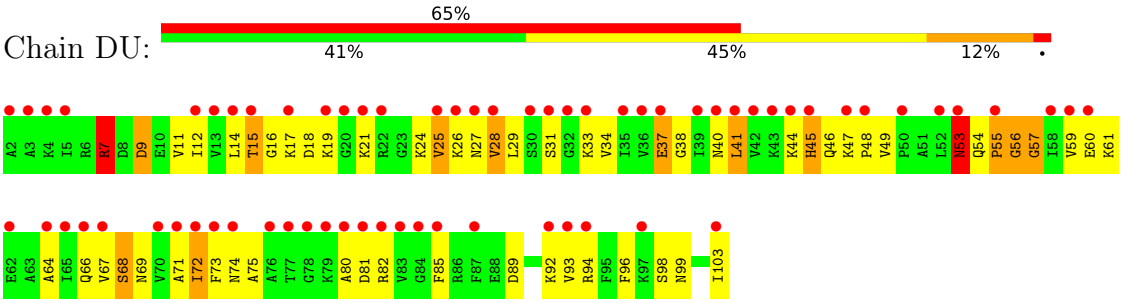
Chain DT:



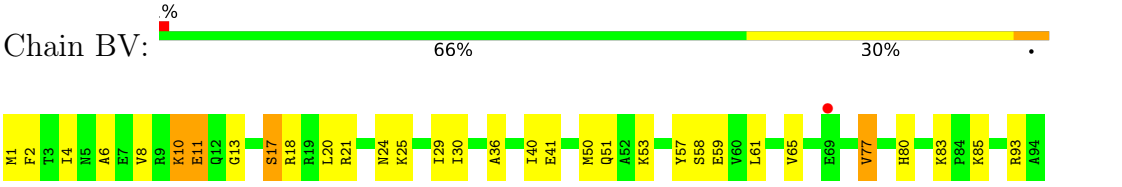
• Molecule 42: 50S ribosomal protein L24



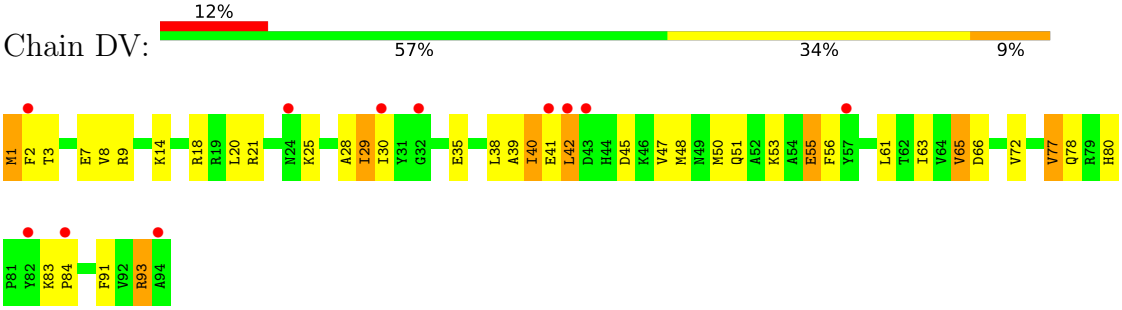
• Molecule 42: 50S ribosomal protein L24



• Molecule 43: 50S ribosomal protein L25



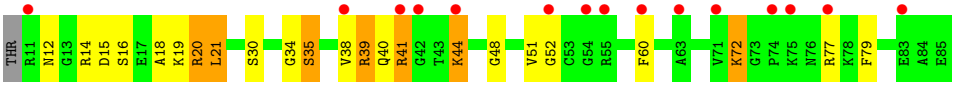
• Molecule 43: 50S ribosomal protein L25



• Molecule 44: 50S ribosomal protein L27

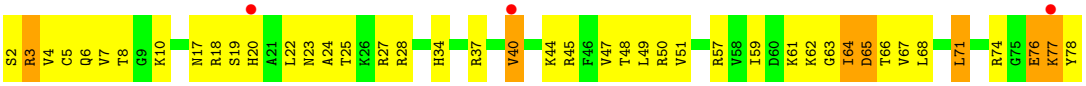
• Molecule 44: 50S ribosomal protein L27

Chain DW:



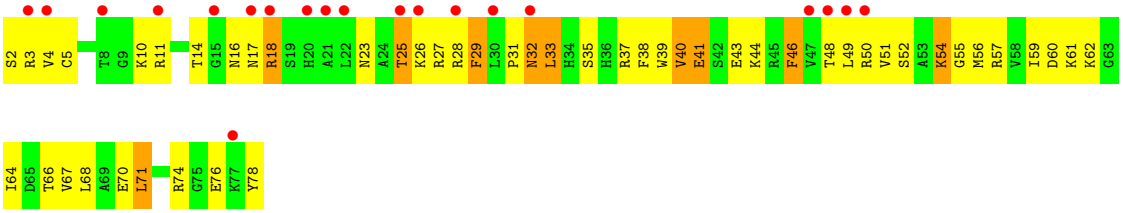
• Molecule 45: 50S ribosomal protein L28

Chain BX:



• Molecule 45: 50S ribosomal protein L28

Chain DX:

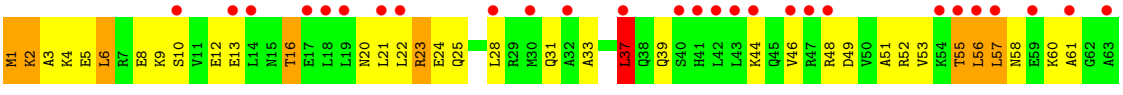


• Molecule 46: 50S ribosomal protein L29

Chain BY:

• Molecule 46: 50S ribosomal protein L29

Chain DY:

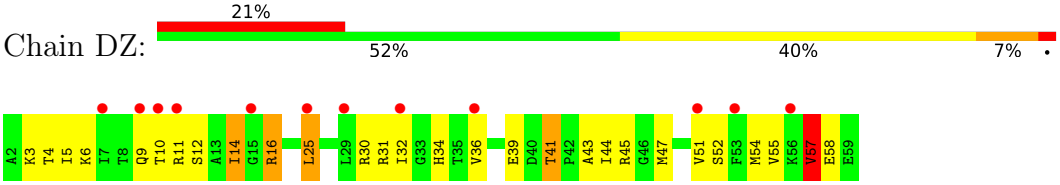


• Molecule 47: 50S ribosomal protein L30

Chain BZ:

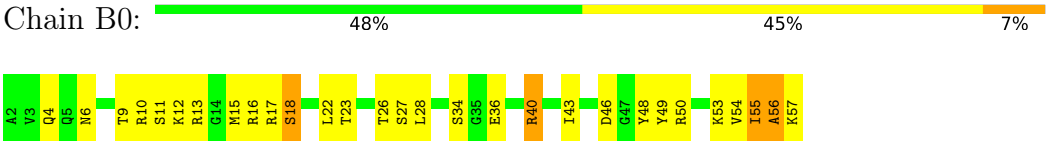
• Molecule 47: 50S ribosomal protein L30

Chain DZ:



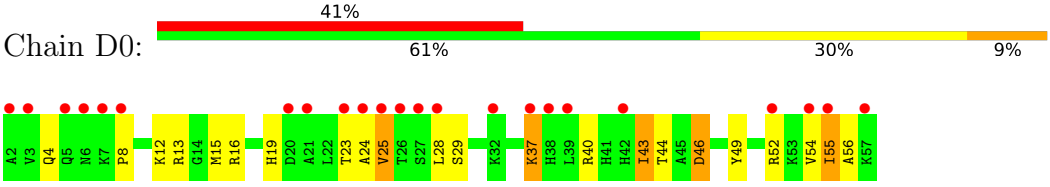
• Molecule 48: 50S ribosomal protein L32

Chain B0:



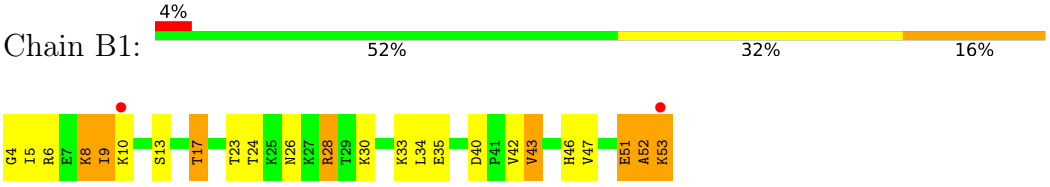
• Molecule 48: 50S ribosomal protein L32

Chain D0:



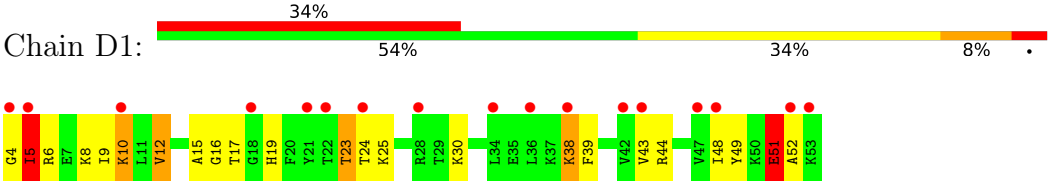
• Molecule 49: 50S ribosomal protein L33

Chain B1:



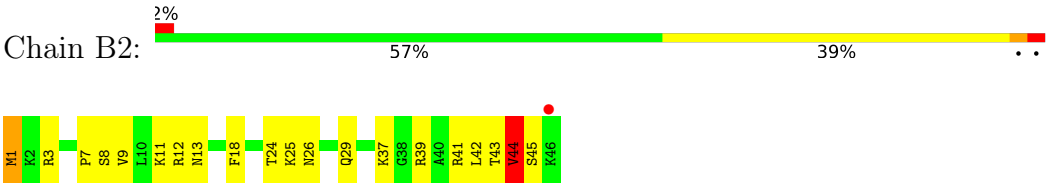
• Molecule 49: 50S ribosomal protein L33

Chain D1:



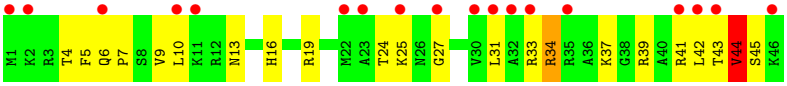
• Molecule 50: 50S ribosomal protein L34

Chain B2:



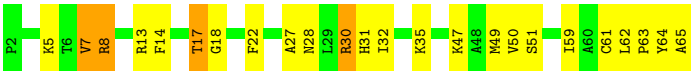
• Molecule 50: 50S ribosomal protein L34

Chain D2:



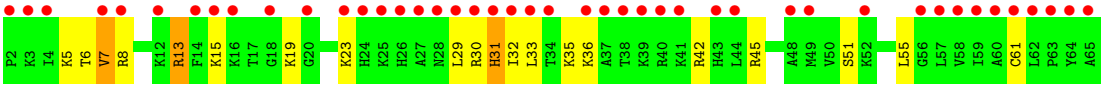
• Molecule 51: 50S ribosomal protein L35

Chain B3:



• Molecule 51: 50S ribosomal protein L35

Chain D3:

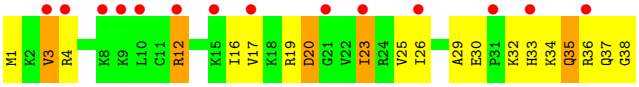


• Molecule 52: 50S ribosomal protein L36

Chain B4:

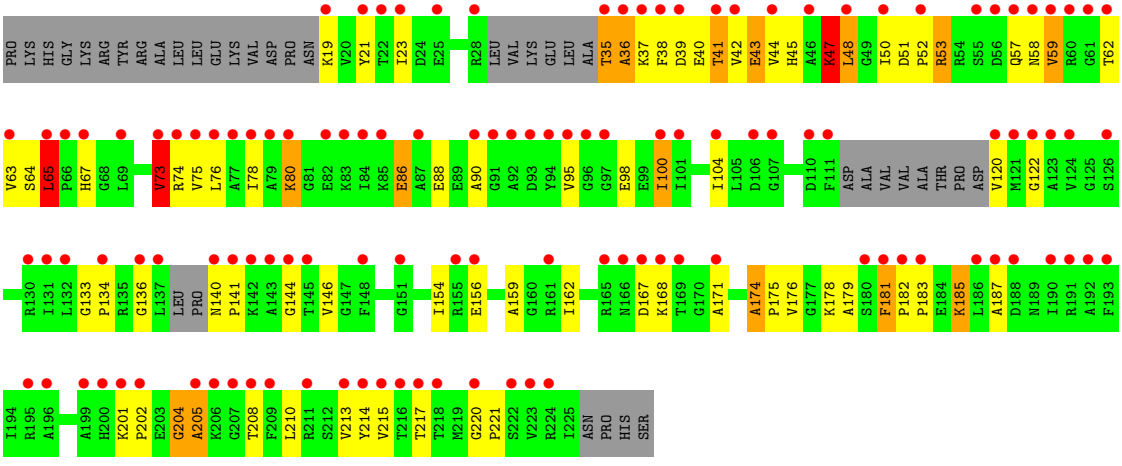
• Molecule 52: 50S ribosomal protein L36

Chain D4:



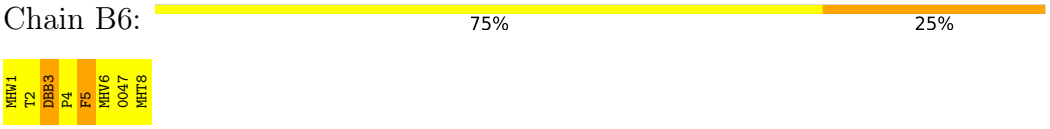
• Molecule 53: 50S ribosomal protein L1

Chain B5:



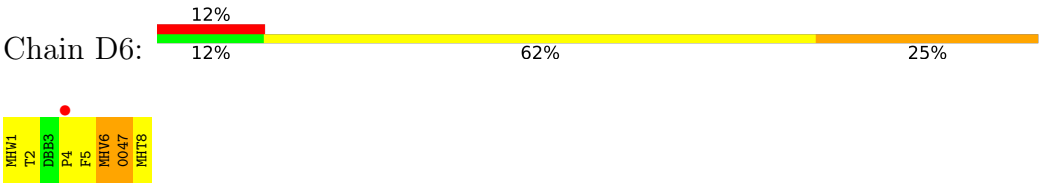
• Molecule 54: Quinupristin

Chain B6:



• Molecule 54: Quinupristin

Chain D6:



4 Data and refinement statistics (i)

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
$< I/\sigma(I) >$ [1]	1.44 (at 2.96Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, R_{free}	0.248 , 0.282 0.249 , 0.284	Depositor DCC
R_{free} test set	4515 reflections (0.40%)	wwPDB-VP
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 , 45.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	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.*

[1] Intensities estimated from amplitudes.

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

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.24	0/36944	0.47	0/57632
1	CA	0.21	0/36966	0.44	1/57666 (0.0%)
2	AB	0.48	0/1736	1.12	10/2338 (0.4%)
2	CB	0.46	0/1736	1.04	8/2338 (0.3%)
3	AC	0.46	0/1652	1.01	8/2225 (0.4%)
3	CC	0.44	0/1652	0.93	0/2225
4	AD	0.44	0/1665	1.02	3/2227 (0.1%)
4	CD	0.51	0/1665	1.04	4/2227 (0.2%)
5	AE	0.55	0/1119	1.15	7/1504 (0.5%)
5	CE	0.52	0/1119	1.09	7/1504 (0.5%)
6	AF	0.53	0/836	1.05	6/1128 (0.5%)
6	CF	0.49	0/836	1.03	5/1128 (0.4%)
7	AG	0.43	0/1196	1.01	4/1602 (0.2%)
7	CG	0.42	0/1196	0.95	3/1602 (0.2%)
8	AH	0.47	0/989	1.04	4/1326 (0.3%)
8	CH	0.40	0/989	0.90	4/1326 (0.3%)
9	AI	0.41	0/1034	0.97	2/1375 (0.1%)
9	CI	0.43	0/1034	1.01	3/1375 (0.2%)
10	AJ	0.52	0/797	0.98	3/1077 (0.3%)
10	CJ	0.44	0/797	0.98	3/1077 (0.3%)
11	AK	0.51	0/893	0.99	2/1205 (0.2%)
11	CK	0.44	0/893	0.99	5/1205 (0.4%)
12	AL	0.50	0/969	0.98	0/1300
12	CL	0.45	0/969	1.07	4/1300 (0.3%)
13	AM	0.49	0/893	1.07	4/1193 (0.3%)
13	CM	0.48	0/893	1.03	3/1193 (0.3%)
14	AN	0.40	0/785	1.04	6/1043 (0.6%)
14	CN	0.38	0/785	0.95	2/1043 (0.2%)
15	AO	0.41	0/718	0.89	1/959 (0.1%)
15	CO	0.38	0/718	0.97	2/959 (0.2%)
16	AP	0.53	0/659	1.01	0/884
16	CP	0.41	0/659	0.89	1/884 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	AQ	0.50	0/658	0.99	1/881 (0.1%)
17	CQ	0.50	0/658	0.92	0/881
18	AR	0.37	0/463	0.93	0/621
18	CR	0.41	0/463	0.87	0/621
19	AS	0.41	0/653	1.13	7/877 (0.8%)
19	CS	0.46	0/653	0.98	2/877 (0.2%)
20	AT	0.49	0/671	0.99	2/888 (0.2%)
20	CT	0.44	0/671	1.02	1/888 (0.1%)
21	AU	0.57	0/431	1.14	3/570 (0.5%)
21	CU	0.54	0/431	1.07	1/570 (0.2%)
22	BA	0.37	0/69659	0.60	2/108672 (0.0%)
22	DA	0.21	0/69659	0.44	2/108672 (0.0%)
23	BB	0.33	0/2850	0.56	0/4444
23	DB	0.17	0/2828	0.37	0/4410
24	BC	0.57	0/2122	1.06	5/2852 (0.2%)
24	DC	0.44	0/2122	0.98	4/2852 (0.1%)
25	BD	0.66	0/1586	1.12	6/2134 (0.3%)
25	DD	0.44	0/1586	0.90	1/2134 (0.0%)
26	BE	0.57	0/1571	1.00	3/2113 (0.1%)
26	DE	0.44	0/1571	0.94	1/2113 (0.0%)
27	BF	0.51	0/1435	0.94	3/1926 (0.2%)
27	DF	0.40	0/1435	0.95	4/1926 (0.2%)
28	BG	0.51	0/1343	1.11	8/1816 (0.4%)
28	DG	0.42	0/1343	0.93	4/1816 (0.2%)
29	BH	0.48	0/1121	0.98	5/1515 (0.3%)
29	DH	0.47	0/1121	0.92	5/1515 (0.3%)
30	BI	0.59	0/1046	1.12	6/1410 (0.4%)
30	DI	0.54	0/1046	1.16	8/1410 (0.6%)
31	BJ	0.64	0/1152	1.07	8/1551 (0.5%)
31	DJ	0.40	0/1152	0.98	2/1551 (0.1%)
32	BK	0.62	0/948	1.06	2/1268 (0.2%)
32	DK	0.42	0/948	0.91	0/1268
33	BL	0.64	0/1054	1.18	9/1403 (0.6%)
33	DL	0.45	0/1054	1.05	5/1403 (0.4%)
34	BM	0.61	0/1093	1.00	3/1460 (0.2%)
34	DM	0.39	0/1093	0.87	0/1460
35	BN	0.64	0/974	1.06	5/1301 (0.4%)
35	DN	0.45	0/974	0.92	0/1301
36	BO	0.57	0/902	0.98	2/1209 (0.2%)
36	DO	0.38	0/902	0.93	3/1209 (0.2%)
37	BP	0.59	0/929	0.98	0/1242
37	DP	0.40	0/929	0.93	4/1242 (0.3%)
38	BQ	0.67	0/960	1.06	1/1278 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	DQ	0.40	0/960	0.91	2/1278 (0.2%)
39	BR	0.62	0/829	1.23	4/1107 (0.4%)
39	DR	0.45	0/829	1.03	3/1107 (0.3%)
40	BS	1.02	6/864 (0.7%)	1.22	7/1156 (0.6%)
40	DS	0.48	0/864	0.98	1/1156 (0.1%)
41	BT	0.58	0/745	1.06	3/994 (0.3%)
41	DT	0.44	0/745	0.92	0/994
42	BU	0.56	0/788	1.09	4/1051 (0.4%)
42	DU	0.50	0/788	0.97	0/1051
43	BV	0.54	0/766	0.95	0/1025
43	DV	0.37	0/766	0.92	3/1025 (0.3%)
44	BW	0.65	0/587	1.01	2/776 (0.3%)
44	DW	0.35	0/576	0.85	1/762 (0.1%)
45	BX	0.51	0/635	0.98	0/848
45	DX	0.42	0/635	0.96	2/848 (0.2%)
46	BY	0.53	0/510	1.12	4/677 (0.6%)
46	DY	0.41	0/510	0.95	1/677 (0.1%)
47	BZ	0.69	0/453	1.07	1/605 (0.2%)
47	DZ	0.43	0/453	0.96	1/605 (0.2%)
48	B0	0.68	0/450	1.05	0/599
48	D0	0.41	0/450	0.87	1/599 (0.2%)
49	B1	0.58	0/417	0.98	0/554
49	D1	0.44	0/417	0.81	1/554 (0.2%)
50	B2	0.65	0/380	1.06	0/498
50	D2	0.39	0/380	1.01	3/498 (0.6%)
51	B3	0.56	0/513	1.01	0/676
51	D3	0.38	0/513	0.83	0/676
52	B4	0.60	0/303	0.99	0/397
52	D4	0.65	1/303 (0.3%)	0.96	0/397
53	B5	0.50	0/1145	1.43	15/1556 (1.0%)
54	B6	1.90	0/13	2.90	1/15 (6.7%)
54	D6	1.61	0/13	3.28	2/15 (13.3%)
All	All	0.36	7/310652 (0.0%)	0.68	305/464396 (0.1%)

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 (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	BS	103	ILE	CA-CB	-10.16	1.42	1.54
40	BS	102	HIS	ND1-CE1	-8.61	1.24	1.32
40	BS	102	HIS	CB-CG	-8.36	1.38	1.50
52	D4	33	HIS	ND1-CE1	6.63	1.39	1.32
40	BS	102	HIS	CD2-NE2	-6.39	1.30	1.37
40	BS	102	HIS	CE1-NE2	5.97	1.38	1.32
40	BS	102	HIS	CG-CD2	5.29	1.41	1.35

All (305) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
53	B5	220	GLY	CA-C-N	15.08	138.69	119.84
53	B5	220	GLY	C-N-CA	15.08	138.69	119.84
53	B5	174	ALA	CA-C-N	14.24	137.64	119.84
53	B5	174	ALA	C-N-CA	14.24	137.64	119.84
39	BR	51	VAL	CA-C-N	-14.12	102.19	119.84
39	BR	51	VAL	C-N-CA	-14.12	102.19	119.84
25	BD	151	THR	CA-C-N	13.36	136.53	119.84
25	BD	151	THR	C-N-CA	13.36	136.53	119.84
53	B5	182	PRO	CA-C-N	11.96	134.79	119.84
53	B5	182	PRO	C-N-CA	11.96	134.79	119.84
20	AT	8	LYS	N-CA-C	-10.04	99.58	112.23
19	AS	29	LYS	CA-C-N	-9.37	108.12	119.84
19	AS	29	LYS	C-N-CA	-9.37	108.12	119.84
40	BS	102	HIS	ND1-CG-CD2	-9.04	97.06	106.10
53	B5	140	ASN	CA-C-N	8.91	130.98	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
53	B5	140	ASN	C-N-CA	8.91	130.98	119.84
20	CT	8	LYS	N-CA-C	-8.85	101.08	112.23
28	BG	7	ALA	CA-C-N	8.80	128.87	119.89
28	BG	7	ALA	C-N-CA	8.80	128.87	119.89
5	AE	149	SER	CA-C-N	8.71	128.36	119.82
5	AE	149	SER	C-N-CA	8.71	128.36	119.82
27	DF	175	PHE	CA-C-N	8.70	130.71	119.84
27	DF	175	PHE	C-N-CA	8.70	130.71	119.84
42	BU	54	GLN	CA-C-N	-8.61	109.08	119.84
42	BU	54	GLN	C-N-CA	-8.61	109.08	119.84
7	AG	145	ALA	N-CA-C	-8.43	99.74	110.19
2	AB	181	ILE	CA-C-N	8.35	128.08	119.56
2	AB	181	ILE	C-N-CA	8.35	128.08	119.56
54	B6	2	THR	N-CA-CB	-8.34	97.31	111.50
46	BY	56	LEU	N-CA-C	-8.27	99.60	110.43
5	CE	153	VAL	N-CA-C	-8.21	101.09	112.50
46	BY	45	GLN	N-CA-C	-8.18	99.73	110.53
39	DR	9	GLY	N-CA-C	-8.15	102.53	115.08
11	CK	90	GLY	CA-C-N	8.02	129.86	119.84
11	CK	90	GLY	C-N-CA	8.02	129.86	119.84
10	CJ	91	ASP	N-CA-C	7.98	119.67	110.97
54	D6	2	THR	N-CA-CB	-7.83	98.19	111.50
27	BF	175	PHE	CA-C-N	7.74	129.52	119.84
27	BF	175	PHE	C-N-CA	7.74	129.52	119.84
24	DC	217	ARG	CA-C-N	7.74	129.51	119.84
24	DC	217	ARG	C-N-CA	7.74	129.51	119.84
15	AO	19	ALA	N-CA-C	-7.73	100.33	110.53
33	BL	101	ILE	N-CA-C	7.72	118.61	112.12
2	AB	15	HIS	N-CA-C	-7.71	104.76	114.56
4	CD	24	GLY	N-CA-C	7.69	122.70	111.24
30	DI	55	ILE	CA-C-N	7.66	127.82	120.31
30	DI	55	ILE	C-N-CA	7.66	127.82	120.31
21	AU	9	ASN	N-CA-C	7.65	121.11	108.48
36	BO	10	ARG	N-CA-C	-7.64	103.41	112.89
5	AE	112	ARG	N-CA-C	-7.63	102.97	111.82
7	AG	13	LEU	CA-C-N	7.61	129.35	119.84
7	AG	13	LEU	C-N-CA	7.61	129.35	119.84
2	AB	80	VAL	N-CA-C	-7.53	106.56	113.71
33	DL	95	LEU	N-CA-C	-7.53	103.09	111.82
24	DC	196	GLY	N-CA-C	7.49	123.94	114.66
36	DO	12	THR	N-CA-C	7.43	119.02	111.07
39	BR	9	GLY	N-CA-C	-7.38	105.05	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
31	BJ	7	LYS	CA-C-N	7.28	127.92	119.47
31	BJ	7	LYS	C-N-CA	7.28	127.92	119.47
53	B5	43	GLU	N-CA-C	7.26	120.35	108.52
29	BH	121	VAL	CA-C-N	7.18	134.62	121.70
29	BH	121	VAL	C-N-CA	7.18	134.62	121.70
4	CD	167	LYS	CA-C-N	7.07	127.32	119.90
4	CD	167	LYS	C-N-CA	7.07	127.32	119.90
2	CB	181	ILE	N-CA-C	7.06	114.70	108.63
28	BG	81	GLU	N-CA-C	-7.04	105.31	114.04
50	D2	6	GLN	CA-C-N	7.03	127.02	119.78
50	D2	6	GLN	C-N-CA	7.03	127.02	119.78
28	DG	7	ALA	CA-C-N	7.00	128.59	119.84
28	DG	7	ALA	C-N-CA	7.00	128.59	119.84
30	DI	73	THR	N-CA-C	6.96	114.49	108.22
14	CN	51	LEU	CA-C-N	6.90	128.46	119.84
14	CN	51	LEU	C-N-CA	6.90	128.46	119.84
47	DZ	57	VAL	N-CA-C	6.84	117.69	108.11
33	BL	52	GLY	N-CA-C	-6.81	99.83	112.37
6	CF	18	VAL	CA-C-N	-6.81	113.19	120.47
6	CF	18	VAL	C-N-CA	-6.81	113.19	120.47
25	BD	151	THR	C-N-CD	-6.78	97.20	125.00
15	CO	48	LYS	N-CA-C	-6.76	103.41	112.94
2	AB	221	VAL	N-CA-C	-6.72	105.20	111.45
43	DV	80	HIS	CA-C-N	6.72	128.24	119.84
43	DV	80	HIS	C-N-CA	6.72	128.24	119.84
3	AC	18	TRP	N-CA-C	-6.71	96.52	110.80
14	AN	56	SER	CA-C-N	6.70	126.15	118.85
14	AN	56	SER	C-N-CA	6.70	126.15	118.85
26	BE	41	GLN	N-CA-C	-6.68	101.13	110.35
39	DR	44	GLY	N-CA-C	-6.67	103.86	113.86
30	DI	70	VAL	N-CA-C	6.67	113.34	106.21
7	CG	75	VAL	N-CA-C	6.61	116.23	106.85
29	BH	123	ARG	N-CA-C	6.60	119.50	110.06
5	CE	18	VAL	N-CA-C	-6.58	102.88	110.05
42	BU	97	LYS	N-CA-C	-6.55	101.44	110.35
31	BJ	6	ALA	N-CA-C	-6.54	101.89	110.53
29	DH	121	VAL	N-CA-C	-6.54	106.30	113.43
3	AC	72	ARG	CA-C-N	6.50	125.93	118.85
3	AC	72	ARG	C-N-CA	6.50	125.93	118.85
30	BI	92	LYS	CA-C-N	6.50	126.26	119.05
30	BI	92	LYS	C-N-CA	6.50	126.26	119.05
25	BD	12	THR	CB-CA-C	-6.47	105.10	114.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
19	CS	36	ARG	N-CA-C	-6.47	105.31	113.72
6	AF	11	HIS	CA-C-N	6.45	127.90	119.84
6	AF	11	HIS	C-N-CA	6.45	127.90	119.84
46	BY	6	LEU	N-CA-C	-6.44	104.52	112.38
42	BU	23	GLY	N-CA-C	6.44	120.50	110.91
5	CE	112	ARG	N-CA-C	-6.43	103.96	110.97
12	CL	93	VAL	CB-CA-C	-6.42	104.99	111.80
26	BE	88	ARG	N-CA-C	-6.40	101.25	110.40
30	BI	123	GLU	N-CA-C	-6.39	105.12	114.39
35	BN	84	GLY	CA-C-N	6.37	125.87	119.24
35	BN	84	GLY	C-N-CA	6.37	125.87	119.24
33	DL	83	ALA	N-CA-C	-6.34	105.58	113.38
5	AE	123	VAL	CB-CA-C	-6.30	103.13	111.13
3	AC	6	HIS	CA-C-N	6.29	125.71	118.85
3	AC	6	HIS	C-N-CA	6.29	125.71	118.85
6	CF	11	HIS	CA-C-N	6.24	127.64	119.84
6	CF	11	HIS	C-N-CA	6.24	127.64	119.84
19	CS	58	VAL	N-CA-C	6.22	113.98	108.63
40	BS	103	ILE	N-CA-CB	-6.22	102.79	111.25
33	BL	60	ARG	N-CA-C	-6.21	104.62	111.82
53	B5	201	LYS	CA-C-N	6.20	127.59	119.84
53	B5	201	LYS	C-N-CA	6.20	127.59	119.84
9	AI	97	GLU	N-CA-C	-6.20	105.00	113.30
35	BN	49	GLU	CA-C-N	-6.16	112.14	119.84
35	BN	49	GLU	C-N-CA	-6.16	112.14	119.84
5	AE	11	LEU	N-CA-C	-6.16	103.51	111.02
10	AJ	42	LEU	CA-C-N	6.15	127.53	119.84
10	AJ	42	LEU	C-N-CA	6.15	127.53	119.84
22	DA	2311	A	C2'-C3'-O3'	6.15	118.72	109.50
8	CH	90	ASP	N-CA-C	-6.12	105.08	112.54
48	D0	25	VAL	N-CA-C	6.11	116.28	110.53
24	BC	146	MET	N-CA-C	-6.11	107.05	114.75
40	BS	102	HIS	N-CA-C	6.10	118.56	109.59
24	BC	42	GLY	N-CA-C	-6.10	106.67	115.27
10	AJ	21	ALA	N-CA-C	-6.10	104.46	113.61
3	AC	82	GLU	N-CA-C	6.07	118.42	111.02
13	AM	111	GLY	CA-C-N	6.06	127.42	119.84
13	AM	111	GLY	C-N-CA	6.06	127.42	119.84
31	BJ	112	GLY	CA-C-N	6.05	125.53	119.24
31	BJ	112	GLY	C-N-CA	6.05	125.53	119.24
9	CI	56	ASP	N-CA-C	6.04	119.40	110.46
28	BG	77	ILE	N-CA-C	-6.02	103.53	111.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	AB	24	ASN	CA-C-N	6.02	127.36	119.84
2	AB	24	ASN	C-N-CA	6.02	127.36	119.84
46	DY	56	LEU	N-CA-C	-5.95	101.47	110.28
2	AB	11	LYS	N-CA-C	-5.95	107.01	114.56
32	BK	12	ASP	N-CA-C	5.95	115.94	108.45
26	BE	148	ILE	CB-CA-C	-5.93	104.82	111.23
8	AH	55	THR	N-CA-C	-5.90	105.75	113.12
2	CB	83	ALA	N-CA-C	-5.88	105.94	114.12
8	CH	27	MET	N-CA-C	5.88	113.42	108.13
37	DP	17	VAL	CA-C-N	5.87	125.83	119.78
37	DP	17	VAL	C-N-CA	5.87	125.83	119.78
5	AE	151	GLU	N-CA-C	-5.87	105.20	112.72
45	DX	41	GLU	N-CA-C	-5.87	104.58	110.97
6	AF	71	ILE	N-CA-C	-5.85	103.61	111.44
26	DE	175	ILE	N-CA-C	5.84	117.12	109.58
29	DH	31	VAL	CA-C-N	-5.84	113.67	119.93
29	DH	31	VAL	C-N-CA	-5.84	113.67	119.93
40	BS	20	VAL	N-CA-C	-5.83	106.79	111.81
54	D6	4	PRO	N-CA-CB	5.83	109.42	103.00
41	BT	40	LYS	N-CA-C	-5.83	104.92	111.28
9	AI	98	LEU	N-CA-C	-5.80	104.92	112.23
28	DG	27	LYS	N-CA-C	5.77	117.30	109.11
40	DS	55	ILE	N-CA-C	-5.76	104.90	110.72
37	DP	61	VAL	N-CA-C	5.76	116.43	107.28
36	BO	13	ARG	N-CA-C	5.73	117.21	110.97
31	BJ	96	ARG	CA-C-N	5.72	125.40	119.05
31	BJ	96	ARG	C-N-CA	5.72	125.40	119.05
25	BD	151	THR	N-CA-C	-5.69	102.23	110.08
45	DX	29	PHE	N-CA-C	-5.68	101.11	109.81
24	BC	58	HIS	N-CA-C	5.68	118.07	110.35
2	CB	70	VAL	N-CA-C	5.67	116.02	107.75
8	CH	101	ILE	N-CA-C	5.67	118.31	108.90
17	AQ	29	VAL	N-CA-C	5.66	116.82	108.45
25	BD	104	VAL	N-CA-C	5.65	121.10	109.34
34	BM	68	PHE	CA-C-N	5.64	126.89	119.84
34	BM	68	PHE	C-N-CA	5.64	126.89	119.84
36	DO	110	ALA	N-CA-C	-5.64	107.05	114.04
27	DF	62	GLY	N-CA-C	-5.63	107.67	114.66
30	BI	22	PRO	N-CA-C	5.62	117.56	110.70
34	BM	38	ARG	N-CA-C	-5.62	101.02	109.95
33	BL	7	SER	CA-C-N	5.57	126.05	120.14
33	BL	7	SER	C-N-CA	5.57	126.05	120.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	CK	76	GLU	N-CA-C	-5.57	106.48	113.28
11	AK	74	VAL	CB-CA-C	-5.55	104.32	111.20
8	AH	5	ASP	CA-C-N	5.54	126.77	119.84
8	AH	5	ASP	C-N-CA	5.54	126.77	119.84
4	CD	25	VAL	N-CA-C	-5.54	106.80	111.56
31	DJ	45	THR	CA-C-N	5.54	125.63	119.32
31	DJ	45	THR	C-N-CA	5.54	125.63	119.32
21	AU	18	ARG	N-CA-C	-5.53	106.20	113.17
10	CJ	22	THR	N-CA-C	-5.52	105.90	113.30
30	DI	63	ALA	N-CA-C	-5.52	106.75	112.93
38	DQ	60	LEU	N-CA-C	-5.52	105.34	112.68
7	AG	87	VAL	N-CA-C	5.51	120.79	108.88
3	AC	185	ASN	N-CA-C	5.51	116.34	108.74
19	AS	34	TRP	N-CA-C	-5.51	105.77	112.88
16	CP	20	VAL	N-CA-C	5.51	115.62	108.35
33	DL	35	HIS	N-CA-C	5.50	117.17	107.61
3	AC	100	GLN	N-CA-C	-5.49	102.63	110.59
5	CE	137	VAL	N-CA-C	-5.49	101.72	109.63
29	BH	70	GLU	N-CA-C	-5.47	106.56	113.18
11	CK	126	LYS	N-CA-C	5.47	118.21	110.50
5	CE	123	VAL	N-CA-C	5.46	120.69	109.34
28	BG	164	TYR	N-CA-C	-5.45	102.93	110.35
5	CE	80	THR	N-CA-C	5.45	115.48	108.34
32	BK	58	LEU	N-CA-C	5.45	115.75	108.23
40	BS	104	THR	N-CA-C	5.45	117.29	108.41
4	AD	27	ALA	N-CA-C	5.44	115.72	108.38
33	BL	83	ALA	N-CA-C	-5.44	106.69	113.38
12	CL	44	LYS	CA-C-N	-5.43	114.23	119.87
12	CL	44	LYS	C-N-CA	-5.43	114.23	119.87
28	DG	92	VAL	N-CA-C	5.40	120.56	109.34
53	B5	168	LYS	N-CA-C	5.40	116.97	109.31
53	B5	122	GLY	N-CA-C	5.39	125.96	113.18
28	BG	167	GLU	N-CA-C	5.38	117.19	108.41
8	CH	109	GLY	N-CA-C	5.38	118.25	111.09
40	BS	102	HIS	ND1-CE1-NE2	-5.37	103.03	108.40
10	CJ	86	ALA	N-CA-C	-5.36	99.38	110.80
30	DI	5	VAL	N-CA-C	5.36	116.32	109.30
30	BI	50	GLU	N-CA-C	5.36	116.66	108.52
15	CO	45	GLU	N-CA-C	-5.35	103.63	110.53
19	AS	6	LYS	N-CA-C	5.35	122.19	110.80
47	BZ	16	ARG	N-CA-C	5.34	117.77	110.55
33	BL	20	GLY	N-CA-C	-5.34	107.95	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	DI	22	PRO	N-CA-C	5.33	117.21	110.70
7	CG	92	ARG	CA-C-N	5.33	126.50	119.84
7	CG	92	ARG	C-N-CA	5.33	126.50	119.84
30	DI	57	VAL	N-CA-C	5.32	120.40	109.34
11	AK	126	LYS	N-CA-C	5.32	117.15	110.24
24	DC	214	ARG	N-CA-C	-5.31	105.45	112.94
14	AN	50	THR	N-CA-C	-5.31	105.46	112.94
19	AS	75	ALA	CA-C-N	5.30	126.47	119.84
19	AS	75	ALA	C-N-CA	5.30	126.47	119.84
5	AE	153	VAL	N-CA-C	-5.28	105.63	113.39
13	AM	107	ARG	N-CA-C	5.28	122.05	110.80
35	BN	25	ALA	N-CA-C	-5.28	105.53	111.28
39	BR	86	GLN	N-CA-C	5.28	117.70	109.52
2	CB	84	ALA	N-CA-C	-5.28	106.34	112.89
2	CB	47	VAL	CA-C-N	-5.27	115.46	120.83
2	CB	47	VAL	C-N-CA	-5.27	115.46	120.83
29	BH	91	PHE	N-CA-C	-5.26	106.86	113.28
5	CE	69	ARG	N-CA-C	-5.26	103.20	110.35
22	BA	2211	A	P-O3'-C3'	5.25	128.08	120.20
6	CF	86	ARG	N-CA-C	5.25	121.99	110.80
38	DQ	4	VAL	N-CA-C	5.25	113.94	106.53
2	AB	91	PHE	N-CA-C	5.24	117.03	109.07
53	B5	208	THR	N-CA-C	5.24	118.11	108.58
14	AN	26	GLU	N-CA-C	-5.23	106.29	113.30
21	AU	53	VAL	N-CA-C	-5.23	106.70	111.67
24	BC	54	ILE	N-CA-C	5.23	115.38	107.75
21	CU	25	LYS	CB-CA-C	-5.22	110.53	116.54
9	CI	54	LEU	CA-C-N	5.21	131.36	121.97
9	CI	54	LEU	C-N-CA	5.21	131.36	121.97
25	DD	153	GLY	N-CA-C	-5.21	107.33	114.67
2	CB	110	SER	N-CA-C	-5.19	106.10	112.90
53	B5	47	LYS	N-CA-C	5.19	116.79	110.41
27	BF	44	ILE	N-CA-C	-5.18	105.33	110.62
33	DL	118	THR	CA-C-N	5.18	125.10	119.76
33	DL	118	THR	C-N-CA	5.18	125.10	119.76
41	BT	55	VAL	N-CA-C	5.17	115.50	107.28
27	DF	104	ILE	N-CA-C	5.17	117.51	111.05
6	AF	70	VAL	N-CA-C	-5.16	106.87	113.22
19	AS	38	SER	N-CA-C	5.16	117.51	110.24
2	AB	139	ARG	N-CA-C	-5.16	105.84	111.82
20	AT	68	HIS	N-CA-C	5.14	121.76	110.80
37	DP	110	ILE	N-CA-C	5.14	115.44	107.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	AH	101	ILE	N-CA-C	5.14	115.09	108.82
40	BS	8	ARG	N-CA-C	5.13	118.18	109.76
12	CL	80	ILE	N-CA-C	5.13	115.08	108.82
4	AD	34	ILE	N-CA-C	5.13	120.01	109.34
33	BL	22	GLY	N-CA-C	5.12	118.02	112.29
29	DH	123	ARG	N-CA-C	-5.11	105.36	112.30
6	AF	97	THR	N-CA-C	5.10	117.14	109.23
43	DV	77	VAL	N-CA-C	5.10	115.46	108.12
31	BJ	124	VAL	N-CA-C	5.08	114.89	107.37
2	CB	61	ALA	N-CA-C	-5.08	106.24	112.90
14	AN	51	LEU	CA-C-N	5.08	126.19	119.84
14	AN	51	LEU	C-N-CA	5.08	126.19	119.84
13	CM	111	GLY	CA-C-N	5.08	124.84	119.76
13	CM	111	GLY	C-N-CA	5.08	124.84	119.76
13	CM	7	ILE	N-CA-C	5.07	119.89	109.34
13	AM	113	ARG	N-CA-C	5.07	117.22	110.53
46	BY	59	GLU	N-CA-C	-5.07	106.61	112.89
28	BG	123	ALA	N-CA-C	5.06	117.08	109.23
36	DO	25	ARG	N-CA-C	5.06	116.89	109.24
1	CA	96	U	P-O3'-C3'	5.06	127.79	120.20
29	DH	62	LEU	N-CA-C	-5.06	107.06	113.18
50	D2	27	GLY	N-CA-C	-5.06	108.04	114.16
22	BA	784	G	C4'-C3'-O3'	-5.06	105.42	113.00
33	BL	30	THR	N-CA-C	5.05	121.56	110.80
44	DW	44	LYS	N-CA-C	-5.04	106.82	112.87
49	D1	5	ILE	N-CA-C	5.04	119.83	109.34
44	BW	73	GLY	CA-C-N	5.04	125.11	119.87
44	BW	73	GLY	C-N-CA	5.04	125.11	119.87
11	CK	52	PHE	N-CA-C	5.04	121.53	110.80
24	BC	216	VAL	N-CA-C	5.04	114.54	106.88
39	DR	65	ALA	N-CA-C	5.03	115.79	108.14
4	AD	48	LEU	N-CA-C	5.02	117.59	109.06
6	AF	96	VAL	N-CA-C	5.02	114.48	108.06
41	BT	82	LYS	N-CA-C	-5.02	101.97	109.95
28	BG	124	GLU	N-CA-C	5.02	115.66	108.74
22	DA	2425	A	P-O3'-C3'	5.02	127.72	120.20
38	BQ	84	LYS	N-CA-C	-5.00	105.73	111.14
30	BI	73	THR	N-CA-C	5.00	117.89	110.39

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
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	609	14
1	CA	33015	0	16616	649	0
2	AB	1705	0	1732	138	0
2	CB	1705	0	1732	117	0
3	AC	1625	0	1696	77	0
3	CC	1625	0	1696	69	0
4	AD	1643	0	1707	98	0
4	CD	1643	0	1707	78	0
5	AE	1106	0	1148	64	0
5	CE	1106	0	1148	78	0
6	AF	818	0	808	38	0
6	CF	818	0	808	36	0
7	AG	1182	0	1238	50	0
7	CG	1182	0	1238	53	0
8	AH	979	0	1031	42	0
8	CH	979	0	1031	46	0
9	AI	1022	0	1070	56	0
9	CI	1022	0	1070	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	AJ	787	0	828	60	0
10	CJ	787	0	828	44	0
11	AK	877	0	887	56	0
11	CK	877	0	887	41	0
12	AL	955	0	1016	39	0
12	CL	955	0	1016	50	0
13	AM	884	0	941	48	0
13	CM	884	0	941	41	0
14	AN	774	0	824	43	0
14	CN	774	0	824	47	0
15	AO	710	0	728	23	0
15	CO	710	0	728	38	0
16	AP	649	0	666	36	0
16	CP	649	0	666	32	0
17	AQ	649	0	691	35	0
17	CQ	649	0	691	34	0
18	AR	456	0	478	13	0
18	CR	456	0	478	24	0
19	AS	638	0	665	32	0
19	CS	638	0	665	31	0
20	AT	665	0	714	30	0
20	CT	665	0	714	35	0
21	AU	426	0	449	41	0
21	CU	426	0	449	28	0
22	BA	62195	0	31280	1058	0
22	DA	62195	0	31280	1204	1
23	BB	2549	0	1291	21	0
23	DB	2529	0	1281	44	0
24	BC	2083	0	2154	78	0
24	DC	2083	0	2154	97	0
25	BD	1565	0	1616	49	0
25	DD	1565	0	1616	58	0
26	BE	1552	0	1619	48	0
26	DE	1552	0	1619	65	0
27	BF	1411	0	1444	54	0
27	DF	1411	0	1444	52	0
28	BG	1323	0	1371	45	0
28	DG	1323	0	1371	39	0
29	BH	1110	0	1145	200	0
29	DH	1110	0	1148	96	13
30	BI	1032	0	1085	52	0
30	DI	1032	0	1085	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	BJ	1129	0	1162	31	0
31	DJ	1129	0	1162	50	0
32	BK	939	0	1012	36	0
32	DK	939	0	1012	29	0
33	BL	1045	0	1117	40	0
33	DL	1045	0	1117	46	0
34	BM	1074	0	1157	32	0
34	DM	1074	0	1157	28	0
35	BN	961	0	1000	39	0
35	DN	961	0	1000	49	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	35	0
38	BQ	947	0	1019	38	0
38	DQ	947	0	1019	46	0
39	BR	816	0	839	38	0
39	DR	816	0	839	37	0
40	BS	857	0	922	37	0
40	DS	857	0	922	27	0
41	BT	739	0	807	27	0
41	DT	739	0	807	28	0
42	BU	780	0	831	17	0
42	DU	780	0	831	45	0
43	BV	753	0	780	16	0
43	DV	753	0	780	29	0
44	BW	580	0	594	14	0
44	DW	569	0	581	19	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	17	0
49	B1	410	0	440	15	0
49	D1	410	0	440	15	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	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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	6953	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 (6953) 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:97:ARG:HD2	1:CA:369:G:O2'	1.51	1.09
29:BH:123:ARG:O	29:BH:124:THR:CG2	2.01	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:89:LYS:HB3	1:CA:359:G:H5"	1.43	1.00
29:BH:117:LEU:HD21	29:BH:121:VAL:H	1.23	1.00
22:BA:730:A:OP2	57:BA:3697:HOH:O	1.76	1.00
29:BH:120:GLY:C	29:BH:122:LEU:HA	1.85	0.99
29:BH:123:ARG:O	29:BH:124:THR:HG23	1.61	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:117:LEU:C	29:BH:121:VAL:HG23	1.93	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
22:BA:2819:G:OP1	57:BA:3807:HOH:O	1.88	0.90
17:CQ:46:VAL:HG21	17:CQ:61:ILE:HD11	1.50	0.90
22:DA:1936:A:H2	22:DA:1943:U:H3	1.13	0.90
22:BA:2720:U:OP1	37:BP:53:ARG:NH2	2.04	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
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: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
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
1:AA:702:A:N6	22:BA:1846:G:O2'	2.10	0.84
2:AB:21:ARG:O	2:AB:23:TRP:N	2.08	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:397:U:OP2	45:BX:10:LYS:NZ	2.09	0.84
22:BA:2478:A:H5'	52:B4:32:LYS:HD3	1.59	0.84
22:DA:1847:A:HO2'	22:DA:1848:A:H8	1.21	0.84
25:DD:140:HIS:NE2	57:DD:302:HOH:O	2.10	0.84
32:DK:7:MET:HE1	32:DK:44:LYS:HG3	1.59	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
29:DH:82:SER:O	29:DH:84:ALA:N	2.10	0.83
29:BH:86:ASP:H	1:CA:359:G:C4'	1.91	0.83
5:CE:99:ALA:O	5:CE:122:ASN:ND2	2.11	0.83
25:DD:3:GLY:HA3	25:DD:204:LYS:HG2	1.58	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
22:BA:1936:A:H2	22:BA:1943:U:H3	1.23	0.83
26:DE:108:ILE:HD11	26:DE:180:LEU:HB2	1.60	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
36:BO:31:THR:O	36:BO:102:ARG:NH1	2.11	0.82
22:DA:1371:G:N7	57:DA:3396:HOH:O	2.11	0.82
6:AF:3:HIS:H	6:AF:92:THR:HG23	1.42	0.82
10:AJ:11:LYS:HG3	10:AJ:97:ASP:HB3	1.62	0.82
22:BA:1482:G:H1'	22:BA:1509:A:H61	1.45	0.82
29:DH:94:ILE:HB	29:DH:122:LEU:HD12	1.60	0.82
22:BA:84:A:H62	22:BA:101:A:H2	1.25	0.82
1:AA:1228:C:OP2	13:AM:107:ARG:NH2	2.13	0.82
22:DA:370:G:N7	57:DA:3557:HOH:O	2.13	0.82
1:CA:1266:G:N2	1:CA:1269:A:OP2	2.13	0.81
4:CD:100:ASN:OD1	4:CD:111:ARG:NH1	2.12	0.81
22:DA:1427:A:N6	22:DA:1571:A:OP2	2.13	0.81
49:B1:34:LEU:H	49:B1:52:ALA:HB3	1.43	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
11:AK:17:SER:HA	11:AK:79:ILE:HA	1.61	0.81
45:DX:71:LEU:HA	45:DX:74:ARG:HG2	1.62	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:AB:15:HIS:HB2	2:AB:209:ALA:HB2	1.64	0.80
22:BA:1746:A:H2'	22:BA:1747:U:C6	2.17	0.80
12:CL:59:ASN:H	12:CL:59:ASN:HD22	1.29	0.80
22:DA:2279:G:N7	44:DW:14:ARG:NH2	2.30	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
22:DA:2343:U:HO2'	22:DA:2373:G:HO2'	1.24	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
22:BA:1277:G:H5'	35:BN:20:MET:HE2	1.63	0.79
50:D2:9:VAL:O	50:D2:13:ASN:ND2	2.15	0.79
31:BJ:114:LEU:HG	31:BJ:118:MET:HE3	1.63	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
22:BA:2029:G:N1	22:BA:2033:A:OP2	2.13	0.79
24:DC:226:ASN:ND2	57:DC:303:HOH:O	2.15	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
2:CB:97:LEU:H	2:CB:100:MET:HE3	1.48	0.79
10:AJ:28:THR:HG22	10:AJ:86:ALA:HB1	1.64	0.79
29:BH:123:ARG:C	29:BH:124:THR:HG23	2.06	0.79
21:CU:34:ARG:HE	21:CU:35:ARG:HB2	1.48	0.79
24:DC:157:SER:O	24:DC:160:THR:OG1	2.00	0.79
22:DA:602:A:HO2'	22:DA:604:G:HO2'	1.29	0.79
22:DA:1840:G:O6	22:DA:1902:C:N4	2.16	0.79
2:AB:95:ARG:HH12	2:AB:97:LEU:HA	1.47	0.78
22:DA:1258:U:H2'	22:DA:1259:G:C8	2.18	0.78
22:BA:1179:G:C5	22:BA:1180:U:H1'	2.18	0.78
22:BA:1907:G:N1	22:BA:1923:U:O2	2.12	0.78
26:DE:52:VAL:HG21	26:DE:81:GLY:HA2	1.64	0.78
22:BA:1434:A:HO2'	22:BA:1435:G:H8	1.30	0.78
29:BH:120:GLY:C	29:BH:122:LEU:CA	2.47	0.78
22:DA:2627:G:O2'	22:DA:2781:A:N1	2.17	0.78
1:AA:142:G:H3'	1:AA:143:A:H8	1.48	0.78
1:CA:1379:G:N2	1:CA:1381:U:O4	2.17	0.78
22:DA:783:A:O2'	22:DA:1779:U:O2	2.01	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:95:GLY:N	1:CA:368:U:OP1	2.16	0.78
22:BA:1287:A:H5'	35:BN:103:ARG:HD2	1.65	0.78
29:BH:83:LYS:HD2	1:CA:55:A:C2'	2.14	0.78
2:CB:221:VAL:O	2:CB:223:GLU:N	2.17	0.78
2:AB:41:ILE:HG21	2:AB:202:GLY:HA2	1.66	0.77
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
9:AI:24:GLY:H	9:AI:61:LEU:HA	1.49	0.77
31:BJ:81:ILE:HG23	31:BJ:82:GLY:H	1.49	0.77
2:CB:99:GLY:O	2:CB:103:ASN:N	2.16	0.77
29:DH:27:ARG:HE	45:DX:60:ASP:CG	1.93	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
1:AA:278:G:OP2	17:AQ:43:LYS:NZ	2.14	0.77
1:AA:405:U:O4	4:AD:2:ALA:N	2.18	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
39:DR:8:GLY:O	39:DR:10:LYS:NZ	2.16	0.77
22:BA:2131:U:H5'	22:BA:2132:U:H5"	1.67	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
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:2268:A:OP1	57:BA:3513:HOH:O	2.01	0.76
22:BA:2714:G:OP2	57:BA:3552:HOH:O	2.03	0.76
22:BA:674:G:H1'	26:BE:69:ARG:HD3	1.66	0.76
22:BA:228:C:H4'	22:BA:229:C:H5"	1.65	0.76
6:CF:9:MET:HG3	6:CF:86:ARG:HB2	1.66	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
20:AT:68:HIS:HB3	20:AT:69:LYS:HE3	1.67	0.76
36:BO:31:THR:HG22	36:BO:34:HIS:H	1.50	0.76
53:B5:42:VAL:HG12	53:B5:214:TYR:HA	1.66	0.76
22:DA:756:A:N7	57:DA:3298:HOH:O	2.18	0.76
29:DH:53:GLU:O	29:DH:55:GLU:N	2.19	0.76
10:AJ:10:LEU:HB2	10:AJ:72:ARG:HB2	1.65	0.76
29:BH:86:ASP:N	1:CA:359:G:H4'	2.00	0.76
22:BA:2005:A:OP1	57:BA:3386:HOH:O	2.02	0.76
22:DA:15:G:OP2	57:DA:3546:HOH:O	2.03	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2271:G:O6	57:DA:3506:HOH:O	2.02	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
23:BB:54:G:H21	27:BF:26:MET:HE3	1.50	0.76
5:CE:111:MET:HE2	5:CE:125:ALA:HB1	1.66	0.76
4:AD:58:LYS:HG2	4:AD:203:LEU:HD22	1.69	0.75
10:CJ:65:TYR:HB3	14:CN:96:LEU:HD11	1.69	0.75
22:BA:2507:C:OP1	57:BA:3716:HOH:O	2.03	0.75
29:DH:32:PRO:HB3	45:DX:39:TRP:HB3	1.69	0.75
35:DN:87:PHE:O	35:DN:89:SER:N	2.18	0.75
22:BA:946:C:OP2	57:BA:3350:HOH:O	2.04	0.75
28:DG:170:ARG:NH1	52:D4:29:ALA:O	2.19	0.75
29:DH:124:THR:OG1	29:DH:125:THR:N	2.17	0.75
22:BA:194:G:N7	57:BA:3764:HOH:O	2.19	0.75
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:DA:1064:C:H4'	30:DI:91:GLY:H	1.52	0.75
3:AC:77:ILE:HA	3:AC:84:VAL:HG23	1.69	0.75
11:AK:34:ILE:HG13	11:AK:74:VAL:HG21	1.68	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
5:CE:106:ILE:HD11	5:CE:124:LEU:HD23	1.67	0.75
22:DA:2438:U:O2'	22:DA:2440:C:OP1	2.05	0.75
42:DU:38:GLY:HA2	42:DU:41:LEU:HD21	1.68	0.75
1:AA:536:C:OP1	57:AA:1884:HOH:O	2.05	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
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
26:BE:106:LYS:HG3	26:BE:200:LEU:HG	1.68	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
22:BA:1439:A:OP2	57:BA:3636:HOH:O	2.05	0.74
26:DE:21:ARG:O	26:DE:114:ARG:NH2	2.19	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:297:G:H5"	42:DU:85:PHE:HB2	1.70	0.74
22:DA:2164:C:H2'	22:DA:2165:C:H6	1.51	0.74
2:AB:99:GLY:O	2:AB:103:ASN:N	2.13	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
22:BA:1565:C:H3'	24:BC:18:LYS:HZ2	1.52	0.74
22:DA:483:A:H1'	42:DU:45:HIS:HB2	1.69	0.74
44:DW:18:ALA:HB3	44:DW:20:ARG:HH21	1.50	0.74
1:AA:675:A:OP1	18:AR:74:HIS:NE2	2.20	0.74
27:BF:4:LEU:HD11	27:BF:104:ILE:HD11	1.70	0.74
1:CA:1001:C:H2'	1:CA:1002:G:C8	2.22	0.74
37:DP:39:ARG:HG3	37:DP:40:LEU:H	1.52	0.74
22:BA:455:C:N3	22:BA:472:A:H2'	2.02	0.74
33:BL:111:ILE:H	33:BL:111:ILE:HD12	1.51	0.74
22:DA:450:G:O6	57:DA:3239:HOH:O	2.05	0.73
22:BA:301:G:OP2	42:BU:82:ARG:NH1	2.22	0.73
35:DN:55:ALA:HB1	35:DN:80:PHE:H	1.53	0.73
36:DO:49:VAL:HG21	36:DO:82:ALA:HA	1.70	0.73
1:AA:1166:G:N1	1:AA:1169:A:OP2	2.19	0.73
22:BA:622:G:OP2	57:BA:3294:HOH:O	2.07	0.73
10:CJ:19:ASP:HA	10:CJ:22:THR:HB	1.70	0.73
18:CR:25:ASP:O	18:CR:27:ALA:N	2.21	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
1:CA:1499:A:OP2	57:CA:1880:HOH:O	2.06	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
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
22:BA:135:U:H3	22:BA:144:A:H61	1.37	0.73
22:BA:1565:C:H3'	24:BC:18:LYS:NZ	2.03	0.73
5:CE:101:GLU:O	5:CE:103:THR:N	2.22	0.73
22:BA:587:C:N3	33:BL:33:ARG:NH2	2.37	0.73
1:CA:1198:G:OP1	57:CA:1835:HOH:O	2.07	0.73
22:DA:618:G:O6	57:DA:3289:HOH:O	2.06	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
1:AA:1491:G:H5"	12:AL:43:LYS:HG3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:780:G:H21	22:BA:783:A:H62	1.37	0.72
3:AC:36:ASP:OD1	3:AC:59:ARG:NH1	2.22	0.72
22:BA:948:C:O2	22:BA:984:A:O2'	2.08	0.72
24:BC:107:PRO:HD2	24:BC:110:LEU:HD22	1.69	0.72
22:BA:370:G:O2'	22:BA:424:G:OP1	2.06	0.72
33:BL:29:LYS:HG2	33:BL:30:THR:HG23	1.70	0.72
33:BL:132:ARG:HG3	33:BL:142:ILE:HD13	1.71	0.72
1:CA:1198:G:N7	57:CA:1849:HOH:O	2.22	0.72
22:DA:668:A:N6	22:DA:670:A:O2'	2.22	0.72
22:DA:1265:A:OP1	57:DA:3745:HOH:O	2.07	0.72
28:BG:124:GLU:CD	28:BG:125:CYS:H	1.97	0.72
5:CE:82:GLN:H	5:CE:147:MET:HE3	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
27:DF:64:LYS:H	27:DF:64:LYS:HE2	1.54	0.72
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
25:BD:1:MET:HG3	25:BD:205:PRO:HG2	1.72	0.72
22:DA:151:C:H2'	22:DA:152:A:C8	2.25	0.72
22:DA:206:U:H2'	22:DA:207:A:H8	1.54	0.72
22:DA:471:A:OP1	26:DE:79:ARG:NH1	2.22	0.72
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.22	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
16:CP:42:ILE:O	16:CP:44:SER:N	2.21	0.72
17:CQ:12:VAL:HG12	17:CQ:13:VAL:H	1.51	0.72
17:CQ:52:GLU:HG2	17:CQ:53:CYS:H	1.53	0.72
4:AD:125:VAL:O	4:AD:127:GLY:N	2.21	0.72
32:BK:121:GLU:OE2	37:BP:65:SER:OG	2.07	0.72
1:CA:1124:G:O2'	1:CA:1145:A:N6	2.23	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
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
6:CF:1:MET:HG2	6:CF:65:GLU:HG2	1.71	0.72
3:AC:54:ARG:HB3	3:AC:69:HIS:HB2	1.72	0.71
22:BA:1266:G:OP1	48:B0:16:ARG:NE	2.19	0.71
1:CA:683:G:N2	11:CK:39:GLY:O	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
8:CH:75:ILE:HD13	8:CH:129:VAL:HG22	1.71	0.71
22:BA:1993:U:H4'	25:BD:133:THR:HG21	1.71	0.71
1:AA:1441:A:H62	1:AA:1461:G:H21	1.38	0.71
22:BA:447:A:OP2	57:BA:3210:HOH:O	2.08	0.71
22:BA:1869:G:H3'	22:BA:1870:C:H5'	1.70	0.71
22:DA:1153:C:H5'	38:DQ:62:ILE:HD13	1.72	0.71
27:DF:131:GLY:HA2	27:DF:153:ASP:HA	1.71	0.71
1:AA:376:G:H1	1:AA:387:U:H3	1.38	0.71
12:AL:24:LEU:HB2	12:AL:59:ASN:HD22	1.55	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
22:DA:1251:C:OP2	38:DQ:6:ARG:NH2	2.22	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
22:BA:2897:U:H2'	22:BA:2898:U:C6	2.25	0.71
1:CA:728:A:H2'	1:CA:729:A:C8	2.24	0.71
26:DE:58:LYS:NZ	26:DE:70:SER:O	2.22	0.71
37:DP:29:LYS:HB3	37:DP:40:LEU:HD21	1.72	0.71
1:AA:537:G:OP1	12:AL:110:ARG:NH2	2.23	0.71
1:CA:8:A:C6	4:CD:206:LYS:HB3	2.26	0.71
22:DA:249:C:O5'	22:DA:2394:C:O2'	2.09	0.71
22:DA:732:C:OP2	57:DA:3295:HOH:O	2.07	0.71
22:BA:136:G:H1	22:BA:143:C:H42	1.36	0.71
25:DD:121:THR:HG21	25:DD:143:PRO:HB3	1.72	0.71
22:BA:2278:A:OP1	34:BM:10:ARG:NH2	2.24	0.71
25:BD:140:HIS:NE2	57:BD:302:HOH:O	1.98	0.71
1:CA:1458:G:H5'	20:CT:27:MET:HB3	1.73	0.71
22:DA:161:A:H3'	22:DA:162:U:H5"	1.73	0.71
22:DA:733:G:OP2	57:DA:3293:HOH:O	2.09	0.71
22:DA:1378:A:O2'	22:DA:1380:G:N7	2.20	0.71
7:AG:146:GLU:HA	7:AG:149:LYS:HB2	1.72	0.71
48:B0:15:MET:O	48:B0:18:SER:HB3	1.91	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
22:DA:449:A:OP2	57:DA:3240:HOH:O	2.08	0.71
42:DU:33:LYS:HB3	42:DU:64:ALA:HB1	1.71	0.71
22:BA:2742:G:OP2	52:B4:24:ARG:NH1	2.24	0.71
29:BH:97:ARG:HH12	1:CA:369:G:H21	1.39	0.71
1:CA:619:U:H3	4:CD:131:ASN:HB3	1.56	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1255:U:O2'	57:DA:3269:HOH:O	2.07	0.71
1:AA:877:G:H21	8:AH:2:SER:N	1.89	0.70
22:BA:1265:A:OP1	57:BA:3753:HOH:O	2.07	0.70
22:BA:2151:U:H2'	22:BA:2152:G:C8	2.25	0.70
37:BP:103:ARG:HH11	37:BP:103:ARG:HG3	1.56	0.70
38:BQ:89:GLU:H	39:BR:49:ILE:HD12	1.56	0.70
19:CS:53:ASN:HB3	19:CS:75:ALA:HB1	1.73	0.70
22:DA:729:G:OP2	24:DC:207:LYS:NZ	2.24	0.70
23:DB:34:A:N6	23:DB:44:G:O2'	2.24	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
23:DB:57:A:H1'	27:DF:27:GLN:HA	1.71	0.70
28:DG:89:LEU:HB2	28:DG:129:THR:HG22	1.71	0.70
1:AA:562:U:OP2	12:AL:14:ARG:NH1	2.24	0.70
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
22:DA:2046:G:OP1	48:D0:12:LYS:NZ	2.23	0.70
1:AA:131:A:H2'	1:AA:132:C:C6	2.27	0.70
6:AF:46:GLN:HB2	6:AF:56:LYS:HE2	1.73	0.70
1:CA:1500:A:OP2	57:CA:1880:HOH:O	2.09	0.70
16:AP:77:GLU:C	16:AP:79:ASN:H	1.99	0.70
22:BA:1808:A:O2'	45:BX:3:ARG:NH1	2.25	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
51:B3:17:THR:OG1	51:B3:18:GLY:N	2.19	0.70
22:DA:740:C:H5'	22:DA:1784:A:H3'	1.72	0.70
22:BA:273:G:N2	22:BA:365:U:O2	2.23	0.70
1:CA:736:C:OP1	18:CR:61:ARG:NH1	2.24	0.70
22:DA:833:A:H2'	22:DA:834:G:C8	2.26	0.70
22:DA:1010:A:OP2	57:DA:3778:HOH:O	2.10	0.70
35:DN:83:LEU:HD21	35:DN:115:LEU:HD13	1.74	0.70
1:AA:1161:C:H2'	1:AA:1162:C:H6	1.55	0.70
20:AT:67:ILE:HD11	20:AT:71:LYS:HE3	1.72	0.70
22:BA:265:A:N1	22:BA:427:U:O2'	2.21	0.70
1:CA:811:C:O2'	1:CA:901:A:N1	2.24	0.70
1:CA:858:G:N7	57:CA:1817:HOH:O	2.25	0.70
2:CB:103:ASN:ND2	2:CB:106:THR:OG1	2.25	0.70
22:DA:1709:U:H2'	22:DA:1710:G:H8	1.54	0.70
2:CB:33:GLY:HA2	2:CB:40:ILE:H	1.55	0.70
22:DA:381:G:OP1	45:DX:18:ARG:NH2	2.25	0.70
22:DA:1010:A:N7	57:DA:3776:HOH:O	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
34:DM:66:ARG:NH1	34:DM:104:GLU:OE1	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:1248:G:C4	38:DQ:3:ARG:HG3	2.26	0.70
22:DA:1709:U:H2'	22:DA:1710:G:C8	2.26	0.70
22:DA:2899:A:H2'	22:DA:2900:A:C8	2.27	0.70
38:BQ:109:LEU:HD11	39:BR:40:MET:HE1	1.73	0.70
1:CA:1047:G:H1	1:CA:1210:C:H42	1.37	0.70
1:AA:989:U:H2'	1:AA:990:C:H6	1.57	0.69
22:BA:2199:A:H4'	29:BH:28:ASN:OD1	1.91	0.69
22:DA:1325:U:OP1	22:DA:1647:U:O2'	2.08	0.69
22:DA:1380:G:OP2	57:DA:3751:HOH:O	2.08	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
22:BA:1799:G:OP2	24:BC:270:ARG:NH2	2.21	0.69
29:BH:122:LEU:C	29:BH:123:ARG:HG2	2.17	0.69
10:CJ:46:LYS:HG2	10:CJ:68:ARG:HG2	1.74	0.69
15:CO:19:ALA:O	15:CO:20:ASN:HB2	1.92	0.69
22:DA:228:C:H4'	22:DA:229:C:H5"	1.74	0.69
22:BA:2199:A:C1'	29:BH:28:ASN:HD21	2.05	0.69
2:AB:96:TRP:HZ2	2:AB:101:LEU:HD23	1.57	0.69
30:BI:83:ALA:HB1	30:BI:109:ILE:HD13	1.73	0.69
1:CA:933:G:N7	7:CG:3:ARG:NH2	2.39	0.69
23:DB:28:C:OP1	36:DO:36:TYR:OH	2.07	0.69
22:DA:587:C:OP2	33:DL:21:ARG:NH1	2.24	0.69
22:DA:833:A:H2'	22:DA:834:G:H8	1.57	0.69
16:AP:4:ILE:HG12	16:AP:21:VAL:HG22	1.75	0.69
46:BY:9:LYS:HB3	46:BY:12:GLU:HG3	1.73	0.69
1:CA:1513:A:H2'	1:CA:1514:G:C8	2.27	0.69
33:DL:56:PRO:HD2	33:DL:59:ARG:HB2	1.73	0.69
10:AJ:57:VAL:HG22	10:AJ:58:ASN:H	1.57	0.69
2:CB:203:ASN:OD1	2:CB:204:ASP:N	2.26	0.69
8:CH:53:GLY:HA3	8:CH:57:PRO:HA	1.75	0.69
22:DA:2262:U:OP1	44:DW:41:ARG:NH2	2.26	0.69
43:DV:48:MET:O	43:DV:51:GLN:NE2	2.25	0.69
22:BA:1171:G:N2	22:BA:1178:C:O2	2.25	0.69
22:BA:2455:G:O6	57:BA:3532:HOH:O	2.09	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1049:U:OP1	57:CA:1843:HOH:O	2.11	0.69
13:CM:33:ILE:HD13	13:CM:59:GLU:HB3	1.75	0.69
22:DA:2243:U:OP1	57:DA:3736:HOH:O	2.11	0.69
23:DB:48:U:H4'	36:DO:100:HIS:CD2	2.28	0.69
1:AA:532:A:N6	3:AC:192:THR:OG1	2.25	0.69
1:CA:890:G:O2'	1:CA:906:A:N6	2.25	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
4:AD:32:CYS:SG	4:AD:33:LYS:N	2.66	0.69
22:BA:2093:G:H4'	29:BH:25:TYR:N	2.08	0.69
29:BH:91:PHE:CD1	1:CA:358:U:H1'	2.28	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
22:BA:192:C:OP1	57:BA:3745:HOH:O	2.11	0.68
22:BA:1563:U:H2'	22:BA:1564:C:C6	2.28	0.68
26:BE:31:VAL:HG21	26:BE:104:ALA:HB2	1.75	0.68
10:CJ:6:ILE:HD12	10:CJ:76:ILE:HB	1.75	0.68
22:DA:1395:A:OP2	57:DA:3400:HOH:O	2.10	0.68
17:AQ:12:VAL:HB	17:AQ:56:GLY:H	1.57	0.68
22:BA:1070:A:O2'	22:BA:1097:U:OP1	2.11	0.68
5:CE:150:PRO:HD2	5:CE:151:GLU:HG2	1.74	0.68
22:DA:2720:U:OP1	37:DP:53:ARG:NH2	2.27	0.68
35:DN:90:ARG:CZ	35:DN:116:VAL:HG11	2.23	0.68
1:AA:620:C:H1'	4:AD:132:ILE:HD11	1.74	0.68
10:AJ:10:LEU:HG	10:AJ:98:VAL:HG12	1.75	0.68
22:BA:349:U:H2'	22:BA:350:G:H8	1.58	0.68
22:BA:997:G:OP1	38:BQ:92:ARG:HG3	1.94	0.68
53:B5:64:SER:O	53:B5:65:LEU:HB2	1.92	0.68
22:DA:602:A:O2'	22:DA:604:G:O2'	2.07	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
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
2:AB:136:MET:N	2:AB:136:MET:SD	2.67	0.68
6:AF:98:GLU:HG3	6:AF:99:ALA:H	1.57	0.68
23:BB:8:C:O3'	36:BO:25:ARG:NH1	2.23	0.68
27:BF:108:VAL:HG11	27:BF:176:PRO:HG2	1.75	0.68
1:CA:1305:G:N7	57:CA:1866:HOH:O	2.25	0.68
22:BA:2286:G:OP2	49:B1:6:ARG:NH2	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:AB:138:THR:HA	2:AB:141:LEU:HB2	1.74	0.68
4:AD:59:GLN:O	4:AD:63:ARG:HG2	1.94	0.68
11:AK:74:VAL:C	11:AK:76:GLU:H	1.99	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
22:DA:2162:G:H4'	22:DA:2163:A:OP1	1.94	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
23:BB:30:C:OP1	36:BO:3:LYS:NZ	2.26	0.68
30:BI:77:ALA:HA	30:BI:80:LEU:HD12	1.76	0.68
10:CJ:36:VAL:HG12	10:CJ:38:GLY:H	1.59	0.68
22:DA:1469:A:H2'	22:DA:1470:A:C8	2.29	0.68
22:BA:14:A:OP2	57:BA:3555:HOH:O	2.11	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
1:AA:1015:G:H21	1:AA:1218:C:H1'	1.59	0.67
15:AO:30:ALA:HA	15:AO:85:LEU:HD21	1.75	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: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
1:AA:973:G:H1'	10:AJ:56:HIS:CD2	2.27	0.67
4:AD:150:LYS:NZ	4:AD:177:LYS:O	2.25	0.67
7:AG:135:VAL:HB	7:AG:138:ARG:HH21	1.59	0.67
22:BA:487:C:O2	40:BS:53:SER:OG	2.13	0.67
30:BI:108:GLU:HA	30:BI:111:GLN:HB3	1.76	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
3:AC:25:ASN:O	3:AC:27:LYS:N	2.27	0.67
26:BE:108:ILE:HD13	26:BE:181:ILE:HG12	1.76	0.67
29:BH:122:LEU:HD23	29:BH:123:ARG:N	2.10	0.67
1:CA:439:U:H4'	4:CD:121:LYS:HG3	1.74	0.67
22:DA:1638:C:H4'	22:DA:2710:C:O2	1.94	0.67
1:AA:1161:C:H2'	1:AA:1162:C:C6	2.29	0.67
3:AC:53:SER:HB3	3:AC:115:LEU:HG	1.76	0.67
5:AE:142:ASP:HA	5:AE:145:GLU:HB3	1.75	0.67
22:BA:617:G:N7	57:BA:3289:HOH:O	2.27	0.67
22:BA:1260:A:N6	57:BA:3278:HOH:O	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2800:A:H3'	22:BA:2801:G:H5'	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
30:DI:90:SER:HB3	30:DI:93:PRO:HG3	1.77	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:2291:U:H2'	22:DA:2292:U:C6	2.30	0.67
22:BA:1794:A:H2'	22:BA:1795:C:H6	1.60	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: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
6:AF:1:MET:HG2	6:AF:65:GLU:HG2	1.75	0.67
32:BK:7:MET:HE1	32:BK:44:LYS:HG3	1.76	0.67
5:CE:156:LYS:HD2	8:CH:71:VAL:HG13	1.76	0.67
22:DA:2058:A:N7	57:DA:3484:HOH:O	2.27	0.67
24:DC:147:LYS:HB2	24:DC:150:LYS:HB2	1.77	0.67
39:DR:58:VAL:HG13	39:DR:102:SER:HB2	1.75	0.67
25:BD:103:ASP:O	25:BD:105:LYS:N	2.27	0.67
5:CE:157:ARG:O	5:CE:159:LYS:N	2.28	0.67
13:CM:54:ASP:HA	13:CM:57:ARG:HB3	1.77	0.67
35:DN:76:VAL:HA	35:DN:79:LEU:HD12	1.77	0.67
1:AA:965:U:OP2	57:AA:1832:HOH:O	2.12	0.67
16:AP:75:ILE:HG22	16:AP:80:LYS:HE2	1.77	0.67
22:BA:1131:G:OP1	31:BJ:82:GLY:HA2	1.94	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
22:DA:761:A:OP2	57:DA:3292:HOH:O	2.12	0.67
22:BA:1667:G:O2'	22:BA:1991:U:O4	2.12	0.67
29:BH:27:ARG:O	29:BH:28:ASN:HB2	1.95	0.67
35:BN:32:GLU:CD	35:BN:86:ARG:HH22	2.02	0.67
22:DA:310:A:H5"	42:DU:15:THR:HG22	1.76	0.67
22:DA:1269:A:OP2	57:DA:3381:HOH:O	2.12	0.67
2:AB:82:ASP:O	2:AB:85:LEU:N	2.29	0.66
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
1:AA:601:G:H2'	1:AA:602:A:C8	2.30	0.66
12:AL:24:LEU:O	12:AL:26:ALA:N	2.28	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
22:DA:84:A:H62	22:DA:101:A:H2	1.40	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:AA:1040:U:H2'	1:AA:1041:G:C8	2.31	0.66
1:AA:1348:U:H4'	9:AI:122:ARG:HG3	1.77	0.66
22:DA:2171:A:O2'	22:DA:2173:A:OP1	2.13	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
9:CI:52:LEU:HD13	9:CI:57:MET:HG2	1.77	0.66
13:CM:107:ARG:HH22	13:CM:110:LYS:HE2	1.60	0.66
34:DM:53:MET:HE1	34:DM:103:TYR:CG	2.30	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
29:BH:94:ILE:CG2	29:BH:99:ILE:HG13	2.26	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
9:AI:57:MET:SD	9:AI:58:VAL:N	2.67	0.66
9:AI:90:TYR:HB3	9:AI:94:LEU:HD21	1.76	0.66
24:BC:39:LYS:HE3	24:BC:55:GLY:HA2	1.78	0.66
46:DY:9:LYS:H	46:DY:12:GLU:HG3	1.61	0.66
2:AB:73:LYS:O	2:AB:75:ALA:N	2.27	0.66
22:BA:587:C:OP2	33:BL:21:ARG:NH1	2.28	0.66
22:BA:2485:G:OP1	34:BM:45:GLN:NE2	2.28	0.66
4:CD:59:GLN:O	4:CD:63:ARG:HG3	1.95	0.66
22:DA:1847:A:O2'	22:DA:1848:A:H8	1.78	0.66
41:DT:14:PRO:HD2	46:DY:33:ALA:HB1	1.78	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
21:AU:4:ILE:HA	21:AU:20:LYS:HE3	1.76	0.66
22:BA:197:A:H62	22:BA:2430:A:H2'	1.60	0.66
1:AA:1182:G:H4'	1:AA:1183:U:H5'	1.78	0.66
22:BA:517:C:OP2	48:B0:10:ARG:NH2	2.29	0.66
22:BA:612:G:H4'	22:BA:613:A:C2	2.31	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
33:BL:87:GLY:O	33:BL:89:VAL:N	2.29	0.66
2:CB:73:LYS:O	2:CB:75:ALA:N	2.29	0.66
22:DA:2788:C:H2'	22:DA:2789:C:C6	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
22:BA:2128:G:H2'	22:BA:2129:C:O4'	1.96	0.66
43:BV:13:GLY:O	43:BV:17:SER:OG	2.14	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:10:LEU:HD12	2:CB:43:LEU:HD22	1.76	0.66
5:AE:15:LEU:HB3	5:AE:37:THR:HG22	1.78	0.65
20:CT:25:ARG:O	20:CT:29:ARG:HG2	1.96	0.65
40:DS:73:LYS:HB2	40:DS:106:VAL:HB	1.78	0.65
50:D2:43:THR:O	50:D2:44:VAL:HB	1.96	0.65
1:AA:376:G:H5"	16:AP:5:ARG:HB3	1.79	0.65
1:AA:1238:A:H5'	1:AA:1336:C:H41	1.60	0.65
19:AS:51:VAL:HG22	19:AS:71:LEU:HD13	1.76	0.65
22:BA:281:C:H2'	22:BA:282:A:C8	2.30	0.65
22:BA:627:A:OP1	33:BL:78:ARG:NH1	2.28	0.65
1:CA:1323:G:O2'	1:CA:1362:A:N3	2.27	0.65
3:CC:143:ARG:HG2	3:CC:144:LEU:HD13	1.78	0.65
22:DA:1789:A:H5"	24:DC:219:THR:O	1.96	0.65
22:DA:2498:C:OP2	57:DA:3681:HOH:O	2.13	0.65
22:DA:2609:U:H6	54:D6:7:004:HA	1.61	0.65
33:DL:136:GLU:HA	33:DL:140:GLY:HA3	1.77	0.65
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
3:AC:58:GLU:HG3	3:AC:65:ARG:HB3	1.78	0.65
12:AL:24:LEU:HB2	12:AL:59:ASN:ND2	2.11	0.65
22:BA:1073:A:H3'	22:BA:1074:G:C5'	2.25	0.65
15:CO:89:ARG:NH1	22:DA:716:A:OP1	2.29	0.65
11:AK:69:ARG:HH11	22:BA:2146:C:H42	1.45	0.65
22:BA:1056:G:H5"	22:BA:1057:A:H5'	1.77	0.65
1:CA:1273:C:H2'	1:CA:1274:A:O4'	1.97	0.65
15:CO:64:ARG:NH1	15:CO:68:ASP:OD2	2.26	0.65
34:DM:49:ALA:HB2	34:DM:123:LYS:HB2	1.79	0.65
1:AA:1077:G:N7	57:AA:1789:HOH:O	2.28	0.65
24:BC:107:PRO:HB3	24:BC:142:HIS:HE1	1.62	0.65
29:BH:114:GLU:HB3	29:BH:133:GLN:O	1.97	0.65
1:CA:403:C:OP1	4:CD:134:SER:HB3	1.97	0.65
22:DA:2134:A:H62	22:DA:2157:G:H1'	1.60	0.65
1:AA:79:G:H2'	1:AA:80:A:H8	1.61	0.65
12:AL:21:VAL:HG23	12:AL:95:TYR:CE1	2.31	0.65
22:BA:2820:A:OP1	57:BA:3811:HOH:O	2.15	0.65
29:BH:89:LYS:CB	1:CA:359:G:H5"	2.21	0.65
35:BN:79:LEU:O	35:BN:81:ASN:N	2.30	0.65
2:CB:21:ARG:O	2:CB:23:TRP:N	2.27	0.65
4:CD:35:GLU:O	4:CD:37:ALA:N	2.24	0.65
22:DA:1992:G:N2	22:DA:1996:C:O2'	2.30	0.65
26:DE:131:THR:HA	26:DE:160:ALA:HB1	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:DR:61:ALA:HB2	39:DR:98:ILE:HD13	1.78	0.65
40:DS:4:ILE:HG12	40:DS:106:VAL:HG22	1.77	0.65
1:AA:1422:G:O3'	32:BK:49:ARG:NH2	2.29	0.65
22:BA:2243:U:OP1	57:BA:3748:HOH:O	2.14	0.65
29:BH:139:PHE:O	29:BH:140:ALA:CB	2.44	0.65
37:BP:93:ARG:O	37:BP:94:LYS:HB2	1.95	0.65
51:B3:31:HIS:CD2	51:B3:32:ILE:HG13	2.31	0.65
1:CA:801:U:H2'	1:CA:802:A:H8	1.59	0.65
3:AC:140:ASN:HA	3:AC:143:ARG:HB3	1.78	0.65
6:AF:46:GLN:HA	6:AF:56:LYS:HG2	1.79	0.65
22:BA:1796:U:H2'	22:BA:1797:G:H8	1.62	0.65
38:BQ:88:VAL:HG13	39:BR:49:ILE:HD11	1.79	0.65
1:CA:1296:C:H4'	1:CA:1302:C:N4	2.12	0.65
22:DA:1035:U:H2'	22:DA:1036:G:H8	1.62	0.65
3:AC:16:LYS:HG3	3:AC:17:PRO:HD2	1.77	0.65
14:AN:91:GLY:O	14:AN:93:ILE:N	2.30	0.65
22:BA:1364:G:OP2	45:BX:2:SER:N	2.29	0.65
28:BG:90:VAL:HG21	28:BG:163:ARG:HE	1.61	0.65
43:BV:36:ALA:O	43:BV:93:ARG:NH2	2.28	0.65
1:CA:1540:U:O3'	21:CU:18:ARG:NE	2.30	0.65
22:DA:398:C:OP1	45:DX:32:ASN:ND2	2.30	0.65
9:AI:38:TYR:HD2	9:AI:39:PHE:HD2	1.45	0.64
13:AM:11:ASP:OD1	13:AM:12:HIS:N	2.30	0.64
22:BA:1916:A:H2'	22:BA:1917:U:O4'	1.96	0.64
22:BA:1936:A:H2	22:BA:1943:U:N3	1.94	0.64
27:BF:158:THR:HG22	27:BF:160:ALA:H	1.62	0.64
33:BL:68:SER:OG	33:BL:69:ARG:N	2.29	0.64
35:BN:24:MET:HE3	35:BN:44:LEU:HD13	1.79	0.64
4:CD:201:VAL:HG11	5:CE:103:THR:HB	1.78	0.64
22:DA:1094:U:H2'	22:DA:1096:A:OP2	1.96	0.64
21:AU:37:PHE:HA	21:AU:40:LYS:HE3	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
34:BM:42:THR:HG22	34:BM:93:VAL:HG12	1.79	0.64
1:CA:651:C:N4	1:CA:753:A:OP2	2.29	0.64
4:CD:88:GLU:HG2	4:CD:188:ARG:HD3	1.79	0.64
22:DA:777:G:N7	22:DA:793:A:H2	1.96	0.64
22:DA:1476:U:H1'	22:DA:1732:C:C2	2.31	0.64
22:DA:2054:A:OP1	22:DA:2055:C:O2'	2.14	0.64
24:DC:123:ALA:O	24:DC:128:ASN:ND2	2.29	0.64
4:AD:32:CYS:O	4:AD:33:LYS:HB2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.79	0.64
25:BD:13:ARG:HD3	25:BD:21:SER:OG	1.96	0.64
7:CG:27:VAL:HG12	7:CG:43:VAL:HG21	1.79	0.64
21:CU:25:LYS:HD3	21:CU:26:ALA:H	1.62	0.64
22:DA:2328:A:H2'	22:DA:2329:U:C6	2.33	0.64
24:DC:145:GLU:HG2	24:DC:152:GLY:N	2.12	0.64
1:CA:464:U:N3	1:CA:467:U:OP2	2.27	0.64
22:DA:17:G:H4'	38:DQ:25:TYR:CE1	2.33	0.64
22:DA:1097:U:C5	22:DA:1098:A:H1'	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:BA:580:U:H2'	22:BA:581:C:H6	1.61	0.64
1:CA:757:U:OP1	1:CA:822:U:O2'	2.15	0.64
20:CT:43:ASP:HB3	20:CT:46:ALA:HB3	1.78	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
51:D3:15:LYS:HD3	51:D3:23:LYS:HE2	1.79	0.64
4:AD:11:LEU:HD22	4:AD:63:ARG:HD3	1.80	0.64
8:AH:10:MET:HE1	8:AH:33:LYS:HA	1.79	0.64
22:BA:465:G:H2'	22:BA:466:A:C8	2.32	0.64
22:BA:2311:A:N3	27:BF:85:ILE:HD11	2.13	0.64
38:BQ:76:TYR:OH	38:BQ:92:ARG:NH1	2.30	0.64
11:CK:17:SER:O	11:CK:80:LYS:N	2.30	0.64
11:CK:25:ALA:HA	11:CK:30:THR:HG22	1.80	0.64
22:DA:2210:U:H4'	22:DA:2211:A:H5'	1.79	0.64
2:AB:163:VAL:HG13	2:AB:185:ALA:HB2	1.80	0.64
22:BA:2243:U:OP1	57:BA:3745:HOH:O	2.15	0.64
12:CL:74:LEU:HD11	12:CL:80:ILE:HG21	1.80	0.64
24:DC:72:ASP:O	24:DC:74:ILE:N	2.25	0.64
28:DG:38:ASN:HB3	28:DG:41:VAL:HG23	1.79	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
22:DA:1342:A:OP2	57:DA:3710:HOH:O	2.15	0.64
41:DT:73:ARG:NH1	41:DT:74:ILE:O	2.30	0.64
22:BA:361:G:H8	22:BA:361:G:OP2	1.81	0.64
1:CA:1291:U:OP1	7:CG:37:SER:HB3	1.97	0.64
14:CN:51:LEU:O	14:CN:53:ARG:N	2.31	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2817:U:O2	22:DA:2836:U:H1'	1.98	0.64
24:DC:70:ASN:O	24:DC:72:ASP:N	2.31	0.64
29:DH:117:LEU:CD1	29:DH:130:VAL:HG22	2.28	0.64
4:AD:58:LYS:HB3	4:AD:200:ILE:HB	1.80	0.64
1:CA:748:G:H2'	1:CA:749:A:C8	2.33	0.64
1:CA:798:U:O4	57:CA:1805:HOH:O	2.11	0.64
1:CA:1279:G:OP2	10:CJ:11:LYS:NZ	2.31	0.64
1:CA:1391:U:H2'	1:CA:1392:G:C8	2.33	0.64
4:CD:29:ASP:C	4:CD:31:LYS:H	2.05	0.64
22:DA:1809:A:H2'	22:DA:1810:A:C8	2.33	0.64
22:DA:2750:A:O2'	22:DA:2752:C:N4	2.32	0.64
28:DG:98:VAL:HG21	28:DG:124:GLU:HA	1.78	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
27:BF:73:SER:HB2	27:BF:81:GLN:H	1.63	0.63
28:BG:149:ARG:NH2	28:BG:167:GLU:OE2	2.31	0.63
1:CA:214:C:H2'	1:CA:215:C:C6	2.33	0.63
20:CT:70:ASN:O	20:CT:74:ARG:N	2.25	0.63
22:DA:197:A:N6	22:DA:2430:A:H2'	2.13	0.63
9:AI:118:LEU:HA	9:AI:125:PRO:HD3	1.78	0.63
16:AP:7:ALA:O	16:AP:9:HIS:N	2.30	0.63
22:BA:39:G:H2'	22:BA:40:U:C6	2.33	0.63
22:BA:197:A:N6	22:BA:2430:A:H2'	2.13	0.63
34:BM:18:ARG:HG2	34:BM:18:ARG:HH21	1.64	0.63
7:CG:145:ALA:O	7:CG:146:GLU:HB2	1.97	0.63
35:DN:96:ARG:HH11	35:DN:116:VAL:HG22	1.63	0.63
1:AA:1004:A:H2'	1:AA:1005:A:O4'	1.98	0.63
2:AB:148:LEU:HD22	2:AB:151:ILE:HG21	1.81	0.63
11:AK:83:GLU:HG3	11:AK:109:ASN:HD22	1.63	0.63
19:AS:32:ARG:HA	19:AS:50:ALA:HB3	1.81	0.63
20:AT:6:SER:OG	20:AT:7:ALA:N	2.31	0.63
29:BH:83:LYS:CG	1:CA:55:A:N3	2.55	0.63
3:CC:9:GLY:HA2	3:CC:12:LEU:HG	1.81	0.63
22:DA:411:G:OP2	22:DA:2406:A:O2'	2.13	0.63
30:DI:39:CYS:HA	30:DI:42:PHE:HB3	1.80	0.63
45:DX:41:GLU:OE1	45:DX:44:LYS:NZ	2.31	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
2:CB:21:ARG:C	2:CB:23:TRP:H	2.06	0.63
3:CC:72:ARG:HB3	3:CC:75:ILE:HG22	1.80	0.63
13:CM:11:ASP:OD1	13:CM:12:HIS:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:848:C:H2'	22:DA:849:A:H8	1.64	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
2:AB:154:MET:HE2	2:AB:158:PRO:HG3	1.79	0.63
14:AN:33:ASP:O	14:AN:35:ASN:N	2.30	0.63
36:BO:88:LYS:O	36:BO:89:ASP:HB2	1.99	0.63
20:CT:6:SER:OG	20:CT:7:ALA:N	2.32	0.63
22:DA:2638:G:O2'	22:DA:2775:G:N2	2.26	0.63
29:DH:117:LEU:HG	29:DH:120:GLY:O	1.98	0.63
45:DX:41:GLU:O	45:DX:44:LYS:HD2	1.98	0.63
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.16	0.63
2:AB:14:VAL:H	2:AB:208:ARG:HH12	1.46	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
22:BA:721:A:H2'	22:BA:722:A:C8	2.32	0.63
22:BA:945:A:N7	57:BA:3261:HOH:O	2.31	0.63
35:BN:49:GLU:OE2	35:BN:95:THR:HG22	1.98	0.63
8:CH:18:GLN:HG2	8:CH:63:LEU:HD13	1.81	0.63
22:DA:2125:G:N1	22:DA:2171:A:OP1	2.31	0.63
22:DA:2131:U:H1'	22:DA:2158:A:H61	1.64	0.63
22:DA:2189:U:H2'	22:DA:2190:G:H5"	1.80	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:BA:1428:C:N4	22:BA:1570:A:OP2	2.28	0.63
1:CA:211:G:H21	1:CA:212:G:H1'	1.63	0.63
13:CM:27:LYS:HA	13:CM:30:SER:HB2	1.81	0.63
16:CP:38:PHE:HE2	16:CP:51:ARG:HD3	1.64	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
1:AA:315:A:O2'	1:AA:330:C:H4'	1.99	0.63
8:AH:79:SER:HA	8:AH:85:ILE:HG12	1.80	0.63
9:AI:22:LYS:O	9:AI:62:ASP:N	2.27	0.63
9:AI:91:ASP:OD2	9:AI:93:SER:N	2.31	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
29:BH:83:LYS:CE	1:CA:55:A:C2'	2.77	0.63
22:DA:1315:C:O2'	22:DA:1392:A:N3	2.31	0.63
32:DK:38:ILE:HD11	32:DK:112:PHE:HZ	1.64	0.63
5:AE:25:VAL:O	5:AE:28:GLY:N	2.31	0.62
5:AE:97:GLN:HB2	5:AE:124:LEU:HD12	1.81	0.62
7:AG:70:ARG:HG3	7:AG:96:ARG:HG2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:AA:951:G:OP2	13:AM:101:ARG:NH2	2.31	0.62
3:AC:130:PHE:CZ	3:AC:131:ARG:HD2	2.33	0.62
53:B5:45:HIS:CD2	53:B5:176:VAL:HA	2.34	0.62
1:CA:49:U:O4	1:CA:362:G:N2	2.33	0.62
1:CA:374:A:H5"	1:CA:452:A:N1	2.13	0.62
6:CF:91:ARG:O	6:CF:92:THR:OG1	2.13	0.62
17:CQ:11:ARG:HA	17:CQ:58:VAL:HA	1.80	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
22:DA:2857:G:N2	22:DA:2860:A:OP2	2.20	0.62
30:DI:29:GLY:HA2	30:DI:33:VAL:HB	1.81	0.62
36:DO:79:ALA:HA	36:DO:115:LEU:HD22	1.81	0.62
43:DV:55:GLU:CD	43:DV:55:GLU:H	2.07	0.62
22:BA:2198:A:N3	29:BH:29:PHE:HB2	2.15	0.62
1:CA:1040:U:H2'	1:CA:1041:G:C8	2.33	0.62
7:CG:146:GLU:HA	7:CG:149:LYS:HB2	1.80	0.62
20:CT:80:THR:O	20:CT:83:ILE:HG13	1.99	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
52:D4:16:ILE:HD13	52:D4:25:VAL:HG22	1.80	0.62
6:AF:67:PRO:O	6:AF:69:GLU:N	2.32	0.62
16:AP:51:ARG:HG2	16:AP:51:ARG:HH11	1.64	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
46:BY:32:ALA:HB2	46:BY:37:LEU:HD23	1.80	0.62
1:CA:1225:A:H2'	1:CA:1226:C:C5	2.34	0.62
1:CA:1233:G:OP1	9:CI:119:ARG:NH2	2.32	0.62
35:DN:20:MET:HG3	35:DN:21:PHE:N	2.15	0.62
1:AA:1377:A:N3	7:AG:2:PRO:HG3	2.15	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: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: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
5:CE:105:ILE:N	5:CE:122:ASN:O	2.27	0.62
9:CI:84:THR:HG21	9:CI:103:PHE:HB3	1.81	0.62
22:DA:2121:G:N2	22:DA:2177:C:O2	2.25	0.62
1:AA:1232:U:OP1	9:AI:126:GLN:NE2	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1965:C:OP1	22:BA:1966:A:O2'	2.13	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
50:B2:12:ARG:HD2	50:B2:44:VAL:HG11	1.81	0.62
8:CH:111:MET:HE2	8:CH:115:ALA:HB1	1.82	0.62
22:DA:1096:A:H2'	22:DA:1097:U:O4'	1.99	0.62
22:DA:1570:A:H2'	22:DA:1571:A:C8	2.34	0.62
1:AA:269:C:H2'	1:AA:270:A:C8	2.34	0.62
1:AA:913:A:OP1	12:AL:88:LYS:NZ	2.27	0.62
22:BA:576:U:H2'	22:BA:577:G:C8	2.34	0.62
35:BN:73:ASN:HA	35:BN:76:VAL:HG12	1.80	0.62
4:CD:188:ARG:HH12	4:CD:192:SER:HB3	1.65	0.62
22:DA:527:C:OP2	22:DA:2779:U:N3	2.29	0.62
24:DC:69:ARG:HD3	24:DC:104:ILE:HG21	1.82	0.62
1:AA:1226:C:O2'	13:AM:110:LYS:NZ	2.33	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
24:DC:260:ASN:OD1	24:DC:263:THR:N	2.23	0.62
1:AA:276:G:P	17:AQ:17:MET:HE2	2.40	0.62
12:AL:86:ARG:NE	12:AL:88:LYS:HB3	2.15	0.62
17:AQ:46:VAL:HG11	17:AQ:61:ILE:HG13	1.82	0.62
22:BA:2585:U:H2'	54:B6:3:DBB:HG1	1.82	0.62
1:CA:374:A:H5"	1:CA:452:A:C2	2.35	0.62
5:CE:105:ILE:H	5:CE:122:ASN:C	2.08	0.62
22:DA:798:G:H2'	22:DA:799:G:H8	1.65	0.62
22:DA:973:A:OP2	39:DR:81:LYS:NZ	2.29	0.62
27:DF:93:GLY:H	27:DF:96:MET:HE2	1.65	0.62
8:AH:111:MET:HE1	8:AH:119:ALA:HB2	1.80	0.62
22:BA:1062:G:OP1	22:BA:1070:A:H4'	2.00	0.62
22:BA:2182:U:H2'	22:BA:2183:A:C8	2.35	0.62
28:BG:149:ARG:HH21	28:BG:167:GLU:CD	2.07	0.62
1:CA:398:U:H2'	1:CA:399:G:H8	1.64	0.62
1:AA:512:U:H2'	1:AA:513:C:C6	2.34	0.61
4:AD:118:VAL:HA	4:AD:123:ILE:HD12	1.81	0.61
14:AN:61:ARG:O	14:AN:62:ASN:HB2	1.99	0.61
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.35	0.61
1:CA:1326:U:H2'	1:CA:1327:C:C6	2.35	0.61
22:DA:118:A:N3	22:DA:178:G:H1'	2.14	0.61
22:DA:608:A:H2'	22:DA:609:A:C8	2.35	0.61
28:DG:159:GLY:O	28:DG:163:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DI:69:PHE:N	30:DI:69:PHE:HD1	1.98	0.61
35:DN:69:ARG:O	35:DN:71:ARG:N	2.25	0.61
1:AA:988:G:N2	1:AA:1217:C:O2	2.33	0.61
7:AG:15:ASP:HB3	7:AG:20:SER:H	1.64	0.61
10:AJ:42:LEU:HD23	10:AJ:43:PRO:HD2	1.81	0.61
16:AP:42:ILE:O	16:AP:44:SER:N	2.32	0.61
22:BA:1170:C:H2'	22:BA:1171:G:C8	2.34	0.61
34:BM:110:GLU:OE2	34:BM:114:ARG:NH2	2.34	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
17:CQ:31:HIS:HD2	17:CQ:33:ILE:H	1.48	0.61
22:DA:247:G:H4'	22:DA:386:G:C4	2.35	0.61
22:DA:2184:A:H2'	22:DA:2185:U:C6	2.35	0.61
2:AB:91:PHE:H	2:AB:150:GLY:HA3	1.65	0.61
22:BA:1417:C:H2'	22:BA:1418:G:O4'	1.99	0.61
22:BA:1794:A:H2'	22:BA:1795:C:C6	2.34	0.61
22:BA:1925:C:H4'	22:BA:1926:U:C5	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
1:CA:983:A:OP1	14:CN:9:ARG:NH2	2.32	0.61
1:CA:1147:C:O2'	9:CI:18:ARG:NH1	2.32	0.61
5:CE:134:ILE:H	5:CE:134:ILE:HD12	1.65	0.61
10:CJ:36:VAL:HA	10:CJ:76:ILE:HA	1.82	0.61
22:DA:250:G:OP2	51:D3:13:ARG:NH1	2.33	0.61
22:DA:594:U:H2'	22:DA:595:C:C6	2.35	0.61
22:DA:1679:A:N6	57:DA:3436:HOH:O	2.33	0.61
22:DA:1738:G:O2'	22:DA:1739:A:O5'	2.18	0.61
25:DD:12:THR:OG1	25:DD:13:ARG:N	2.25	0.61
29:DH:32:PRO:O	29:DH:33:GLN:CB	2.48	0.61
42:DU:24:LYS:H	42:DU:37:GLU:CD	2.08	0.61
1:AA:1031:C:O2'	1:AA:1032:G:OP2	2.17	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:1336:A:H2'	22:DA:1337:G:C8	2.35	0.61
29:DH:62:LEU:HD13	29:DH:62:LEU:C	2.25	0.61
1:AA:1441:A:H2	37:BP:114:LEU:HD22	1.65	0.61
2:AB:64:LYS:HB3	2:AB:66:LYS:HE2	1.83	0.61
35:BN:12:ARG:CZ	35:BN:20:MET:HE1	2.31	0.61
22:DA:192:C:O2'	22:DA:802:A:N3	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:DZ:6:LYS:HB2	47:DZ:58:GLU:HG3	1.83	0.61
50:D2:43:THR:OG1	50:D2:44:VAL:N	2.32	0.61
1:AA:109:A:H2'	1:AA:326:G:N2	2.15	0.61
1:AA:1425:U:O2'	1:AA:1426:G:H5'	2.01	0.61
2:AB:88:ASP:HB2	2:AB:221:VAL:HG12	1.83	0.61
22:BA:1730:C:H4'	22:BA:1730:C:OP1	1.99	0.61
25:BD:16:THR:OG1	25:BD:18:ASP:OD1	2.18	0.61
9:CI:31:ASN:HA	9:CI:66:THR:HG22	1.83	0.61
1:AA:721:G:H4'	1:AA:722:G:O4'	2.00	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
29:BH:123:ARG:C	29:BH:124:THR:CG2	2.65	0.61
5:CE:77:ASN:HB2	5:CE:82:GLN:HG2	1.81	0.61
22:DA:58:G:OP1	41:DT:78:SER:OG	2.17	0.61
22:DA:250:G:H2'	22:DA:251:A:C8	2.36	0.61
25:DD:7:LYS:HD3	25:DD:198:GLY:HA2	1.82	0.61
1:AA:1313:U:OP2	19:AS:6:LYS:HB3	2.01	0.61
22:BA:560:C:O2	38:BQ:48:ARG:NH1	2.34	0.61
22:BA:1086:A:O2'	22:BA:1087:G:N7	2.34	0.61
25:BD:125:TRP:CD2	25:BD:160:LYS:HD3	2.36	0.61
31:BJ:140:LEU:HD11	31:BJ:142:ILE:HD13	1.82	0.61
1:CA:477:C:H2'	1:CA:478:A:C8	2.34	0.61
1:CA:1182:G:H5'	1:CA:1184:G:H5"	1.83	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
29:DH:83:LYS:H	29:DH:149:GLU:HG2	1.64	0.61
45:DX:52:SER:OG	45:DX:55:GLY:N	2.32	0.61
1:AA:1129:C:O2	1:AA:1130:A:N6	2.34	0.61
2:AB:46:THR:HG23	2:AB:201:PRO:HB2	1.82	0.61
2:AB:115:LYS:O	2:AB:117:LEU:N	2.33	0.61
22:BA:1563:U:H2'	22:BA:1564:C:H6	1.65	0.61
1:CA:1006:G:H2'	1:CA:1007:U:C6	2.35	0.61
22:DA:7:G:H4'	31:DJ:15:TRP:CZ2	2.35	0.61
22:DA:1592:C:H2'	22:DA:1593:A:C8	2.36	0.61
28:DG:12:PRO:HD2	28:DG:15:VAL:HG21	1.83	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:BA:265:A:H4'	22:BA:266:G:OP1	2.01	0.61
29:BH:117:LEU:O	29:BH:121:VAL:HG22	1.93	0.61
22:DA:306:U:O2	22:DA:312:G:N2	2.34	0.61
22:DA:2134:A:OP2	22:DA:2157:G:N2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1179:A:H2'	1:AA:1180:A:O4'	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
7:AG:135:VAL:O	7:AG:139:GLU:HG2	2.01	0.60
19:AS:11:ILE:HG13	19:AS:38:SER:HB3	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
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
53:B5:42:VAL:O	53:B5:179:ALA:N	2.34	0.60
7:CG:42:ILE:HD13	7:CG:116:MET:HB3	1.83	0.60
22:DA:2134:A:N6	22:DA:2157:G:O2'	2.33	0.60
27:DF:134:GLU:HG3	27:DF:136:ILE:HD12	1.83	0.60
9:AI:46:MET:SD	9:AI:46:MET:N	2.74	0.60
22:BA:1342:A:OP2	57:BA:3719:HOH:O	2.17	0.60
29:BH:100:ALA:HB1	29:BH:112:LYS:HA	1.83	0.60
35:BN:12:ARG:O	35:BN:17:ARG:NH2	2.34	0.60
1:CA:909:A:H2'	1:CA:910:C:O4'	2.01	0.60
24:DC:237:GLY:O	24:DC:239:ASN:N	2.34	0.60
1:AA:219:U:H2'	1:AA:220:G:H8	1.65	0.60
21:AU:8:GLU:HB3	21:AU:12:PHE:HZ	1.65	0.60
29:BH:121:VAL:N	29:BH:122:LEU:HB2	2.16	0.60
1:CA:728:A:H2'	1:CA:729:A:H8	1.66	0.60
5:CE:104:GLY:O	5:CE:105:ILE:HG22	2.01	0.60
22:DA:661:A:H1'	33:DL:12:SER:O	2.00	0.60
22:DA:848:C:H2'	22:DA:849:A:C8	2.36	0.60
22:DA:1177:G:H2'	22:DA:1178:C:O4'	2.00	0.60
22:DA:2346:A:H3'	22:DA:2347:C:H5"	1.84	0.60
22:DA:2421:G:O6	51:D3:31:HIS:HD2	1.83	0.60
24:DC:121:ASP:OD1	24:DC:121:ASP:N	2.33	0.60
52:D4:23:ILE:HB	52:D4:38:GLY:HA3	1.84	0.60
3:AC:20:SER:HB3	14:AN:94:PRO:HG3	1.82	0.60
22:BA:528:A:C8	22:BA:528:A:H3'	2.36	0.60
22:BA:580:U:H2'	22:BA:581:C:C6	2.36	0.60
22:BA:1026:G:H2'	22:BA:1027:A:C8	2.36	0.60
22:BA:1070:A:C2	22:BA:1097:U:H4'	2.36	0.60
22:BA:1508:A:O2'	22:BA:1509:A:O4'	2.17	0.60
22:BA:2539:C:H5'	52:B4:3:VAL:HG21	1.83	0.60
22:BA:2667:C:N3	28:BG:110:SER:OG	2.32	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DV:30:ILE:HG12	43:DV:91:PHE:HB2	1.83	0.60
1:AA:407:U:H2'	1:AA:408:A:H8	1.66	0.60
1:AA:532:A:O3'	57:AA:1847:HOH:O	2.16	0.60
16:AP:46:LYS:HD3	16:AP:47:GLU:N	2.17	0.60
22:BA:726:G:O2'	22:BA:727:A:OP2	2.17	0.60
29:BH:117:LEU:CD2	29:BH:121:VAL:HA	2.31	0.60
33:BL:100:ILE:HG13	33:BL:101:ILE:HG23	1.84	0.60
1:CA:159:G:N2	1:CA:162:A:OP2	2.34	0.60
1:CA:475:C:H2'	1:CA:476:U:C6	2.36	0.60
2:CB:15:HIS:O	2:CB:17:GLY:N	2.35	0.60
22:DA:1178:C:H2'	22:DA:1179:G:C8	2.36	0.60
22:DA:1394:U:H4'	22:DA:1603:A:H4'	1.83	0.60
22:DA:2043:C:OP1	22:DA:2777:G:O2'	2.18	0.60
22:DA:2215:C:H2'	22:DA:2216:G:C8	2.37	0.60
22:DA:2286:G:H4'	22:DA:2287:A:O5'	2.01	0.60
22:DA:2428:G:H5"	22:DA:2429:G:OP1	2.02	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
46:DY:31:GLN:HG2	46:DY:37:LEU:HB2	1.84	0.60
22:BA:1342:A:OP2	57:BA:3721:HOH:O	2.16	0.60
30:BI:99:GLY:O	30:BI:139:VAL:HG23	2.02	0.60
1:CA:1346:A:H5"	9:CI:122:ARG:HH12	1.67	0.60
6:CF:64:VAL:HG12	6:CF:65:GLU:H	1.65	0.60
22:DA:2226:C:H2'	22:DA:2227:A:O4'	2.01	0.60
26:DE:113:VAL:HG23	26:DE:118:LEU:HD23	1.83	0.60
1:AA:32:A:OP1	1:AA:398:U:H1'	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
10:CJ:53:ILE:HG13	14:CN:85:ARG:HD2	1.84	0.60
22:DA:208:C:H2'	22:DA:209:C:C6	2.35	0.60
22:DA:2874:C:H2'	22:DA:2875:C:C6	2.37	0.60
22:DA:2885:G:N7	48:D0:40:ARG:NH2	2.50	0.60
22:BA:2703:C:H2'	22:BA:2704:C:H6	1.66	0.60
1:CA:102:G:O2'	1:CA:151:A:N3	2.31	0.60
1:CA:1181:G:O2'	1:CA:1182:G:N7	2.35	0.60
3:CC:49:LYS:O	3:CC:72:ARG:NH1	2.34	0.60
8:CH:96:MET:HB2	8:CH:99:LEU:O	2.01	0.60
19:CS:15:LEU:HD13	19:CS:33:THR:HG21	1.82	0.60
19:CS:36:ARG:NH2	19:CS:75:ALA:O	2.34	0.60
22:DA:18:U:O4	57:DA:3205:HOH:O	2.11	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:724:U:H2'	22:DA:725:G:O4'	2.02	0.60
22:DA:1377:G:OP2	57:DA:3391:HOH:O	2.15	0.60
22:DA:2143:C:H2'	22:DA:2144:G:O4'	2.01	0.60
36:DO:92:PHE:HB2	36:DO:117:PHE:CD1	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
10:AJ:19:ASP:HA	10:AJ:22:THR:HB	1.84	0.60
25:BD:99:GLU:HG2	25:BD:182:ALA:HB2	1.84	0.60
39:BR:37:GLU:HB3	39:BR:53:PHE:CE1	2.36	0.60
53:B5:35:THR:O	53:B5:35:THR:OG1	2.15	0.60
1:CA:1203:C:H4'	14:CN:67:THR:HB	1.83	0.60
2:CB:210:VAL:O	2:CB:214:LEU:HB2	2.02	0.60
20:CT:57:ILE:O	20:CT:61:GLN:HG2	2.01	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
29:DH:126:GLY:O	29:DH:146:VAL:HG23	2.00	0.60
40:DS:66:ILE:O	40:DS:68:ASP:N	2.35	0.60
1:AA:427:U:OP2	1:AA:428:G:O2'	2.15	0.60
2:AB:33:GLY:HA3	2:AB:40:ILE:H	1.66	0.60
13:AM:68:ASP:N	13:AM:68:ASP:OD2	2.34	0.60
22:BA:1403:A:H2'	22:BA:1404:C:C6	2.37	0.60
1:CA:268:U:H2'	1:CA:269:C:C6	2.36	0.60
1:CA:518:C:H2'	1:CA:530:G:C8	2.36	0.60
3:CC:149:ILE:HG13	3:CC:202:ILE:HG12	1.83	0.60
4:CD:104:ARG:HH11	4:CD:111:ARG:HH12	1.50	0.60
9:CI:29:VAL:HB	9:CI:64:TYR:HD2	1.66	0.60
12:CL:90:LEU:HB2	12:CL:93:VAL:HG21	1.84	0.60
22:DA:13:A:N1	22:DA:525:U:H2'	2.17	0.60
22:DA:2111:U:H5	22:DA:2145:C:H2'	1.67	0.60
22:DA:2290:G:H4'	22:DA:2381:A:O2'	2.02	0.60
29:DH:126:GLY:O	29:DH:146:VAL:N	2.35	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
1:AA:79:G:H2'	1:AA:80:A:C8	2.37	0.59
1:AA:972:C:H4'	10:AJ:59:LYS:HE3	1.83	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
22:BA:588:U:H2'	22:BA:589:U:C6	2.36	0.59
22:BA:636:G:OP2	33:BL:109:LYS:NZ	2.28	0.59
22:BA:2502:G:H5'	22:BA:2503:A:H5"	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BC:8:PRO:HB3	24:BC:14:ARG:HB2	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
1:CA:308:C:H2'	1:CA:309:A:C8	2.37	0.59
1:CA:1087:G:N2	1:CA:1099:G:H1'	2.17	0.59
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.37	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
22:DA:910:A:N3	22:DA:2264:C:O2'	2.33	0.59
22:DA:990:A:N1	39:DR:78:ARG:NH1	2.50	0.59
30:DI:106:LEU:HD13	30:DI:130:GLU:HG3	1.84	0.59
35:DN:79:LEU:O	35:DN:81:ASN:N	2.30	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
2:CB:54:LEU:HA	2:CB:57:LEU:HB3	1.84	0.59
30:DI:18:ALA:HB1	30:DI:43:ASN:HD21	1.67	0.59
35:DN:54:LEU:HD23	35:DN:66:ALA:HB2	1.83	0.59
36:DO:80:GLU:HA	36:DO:83:LEU:HD12	1.83	0.59
40:DS:22:ASP:CG	40:DS:25:ARG:HH22	2.10	0.59
1:AA:9:G:OP2	5:AE:126:LYS:NZ	2.26	0.59
1:AA:673:A:H5"	6:AF:86:ARG:NH1	2.16	0.59
25:BD:4:LEU:HD12	25:BD:32:ASN:CG	2.27	0.59
30:BI:74:PRO:HB2	30:BI:78:VAL:HG21	1.83	0.59
33:BL:77:ILE:HD12	33:BL:100:ILE:HD11	1.85	0.59
13:CM:39:ILE:HG13	13:CM:56:LEU:HD11	1.83	0.59
14:CN:47:LYS:HE3	19:CS:16:LEU:HD23	1.83	0.59
22:DA:309:A:H5'	42:DU:17:LYS:HG2	1.83	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:DL:82:LEU:HA	33:DL:85:VAL:HG13	1.84	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
28:BG:125:CYS:HA	28:BG:130:GLU:O	2.02	0.59
29:BH:99:ILE:HB	29:BH:115:VAL:HG11	1.84	0.59
1:CA:252:U:O4	1:CA:253:A:N6	2.36	0.59
1:CA:1175:G:H2'	1:CA:1176:A:H8	1.65	0.59
10:CJ:57:VAL:HG22	10:CJ:58:ASN:H	1.67	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
49:D1:4:GLY:O	49:D1:6:ARG:N	2.31	0.59
1:AA:796:C:OP1	11:AK:126:LYS:HB2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1225:A:H2'	1:AA:1226:C:C5	2.38	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
22:BA:2615:U:C2	48:B0:4:GLN:HA	2.38	0.59
22:BA:2846:G:OP2	37:BP:52:ASN:HB2	2.02	0.59
29:BH:94:ILE:HG22	29:BH:99:ILE:CG1	2.32	0.59
33:BL:122:VAL:HG21	33:BL:135:ILE:HD13	1.84	0.59
2:CB:59:LYS:HA	2:CB:62:SER:HB2	1.84	0.59
10:CJ:12:ALA:HB3	10:CJ:18:ILE:HB	1.83	0.59
22:DA:420:C:H2'	22:DA:421:C:H6	1.67	0.59
22:DA:2591:C:H2'	22:DA:2592:G:C8	2.38	0.59
24:DC:136:PRO:O	24:DC:139:SER:OG	2.21	0.59
1:AA:1151:A:O2'	1:AA:1152:A:O5'	2.19	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
22:BA:2287:A:OP1	49:B1:30:LYS:NZ	2.31	0.59
22:BA:2794:C:H2'	22:BA:2795:C:H6	1.67	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
22:DA:400:G:N7	45:DX:57:ARG:NH1	2.50	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
31:DJ:80:HIS:O	31:DJ:82:GLY:N	2.36	0.59
1:AA:129:A:H2	1:AA:232:G:H22	1.51	0.59
1:AA:1003:G:H21	1:AA:1005:A:H5'	1.67	0.59
17:AQ:19:LYS:O	17:AQ:71:LYS:NZ	2.35	0.59
21:AU:34:ARG:CZ	21:AU:35:ARG:HB2	2.32	0.59
22:BA:2092:U:H4'	29:BH:24:GLY:HA3	1.85	0.59
29:BH:1:MET:O	29:BH:20:ASN:ND2	2.35	0.59
39:BR:25:LEU:H	39:BR:94:THR:CG2	2.15	0.59
1:CA:688:G:O2'	1:CA:704:A:N1	2.33	0.59
1:CA:1372:U:OP2	9:CI:13:LYS:NZ	2.35	0.59
4:CD:169:THR:O	4:CD:171:LEU:N	2.35	0.59
10:CJ:27:GLU:O	10:CJ:31:ARG:HB3	2.02	0.59
22:DA:143:C:O2	41:DT:1:MET:N	2.35	0.59
22:DA:1019:U:OP1	22:DA:1035:U:O2'	2.17	0.59
22:DA:1869:G:N2	22:DA:1871:A:O2'	2.36	0.59
41:DT:18:GLU:O	41:DT:22:THR:OG1	2.18	0.59
41:DT:54:GLU:HB3	41:DT:88:LYS:HG3	1.84	0.59
1:AA:34:C:H2'	1:AA:35:G:H8	1.68	0.59
1:AA:398:U:H2'	1:AA:399:G:C8	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1033:G:H2'	1:AA:1034:G:H5'	1.84	0.59
3:AC:57:ILE:HG12	3:AC:66:VAL:HG22	1.85	0.59
29:BH:14:SER:OG	29:BH:17:ASP:CG	2.46	0.59
2:CB:82:ASP:OD1	2:CB:82:ASP:N	2.36	0.59
5:CE:65:GLU:OE2	5:CE:69:ARG:NH1	2.35	0.59
20:CT:62:ALA:HA	20:CT:68:HIS:H	1.68	0.59
22:DA:1309:G:H4'	50:D2:7:PRO:HB2	1.84	0.59
22:DA:1425:G:H2'	22:DA:1426:G:C8	2.38	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
31:DJ:99:ARG:HB3	31:DJ:103:ILE:HD12	1.85	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:414:C:H2'	22:BA:415:A:C8	2.37	0.59
22:BA:1910:G:H2'	22:BA:1911:U:O4'	2.03	0.59
22:BA:2882:A:OP1	35:BN:96:ARG:HD3	2.03	0.59
1:CA:509:A:N3	1:CA:543:U:O2'	2.36	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
10:CJ:80:THR:O	10:CJ:84:VAL:HB	2.02	0.59
38:DQ:72:ASN:HB3	38:DQ:110:VAL:HG11	1.85	0.59
47:DZ:31:ARG:HG2	47:DZ:34:HIS:HB2	1.84	0.59
1:AA:8:A:C6	4:AD:206:LYS:HB3	2.37	0.59
1:AA:999:C:H2'	1:AA:1000:A:C8	2.38	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
30:BI:75:PRO:HB2	30:BI:78:VAL:HG13	1.85	0.59
6:CF:19:PRO:HA	6:CF:22:ILE:HB	1.85	0.59
22:DA:2573:C:OP1	22:DA:2574:G:H5"	2.03	0.59
22:BA:528:A:H3'	22:BA:528:A:H8	1.67	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
1:CA:41:G:H2'	1:CA:42:G:C8	2.38	0.58
1:CA:131:A:O2'	1:CA:262:A:N3	2.36	0.58
1:CA:147:G:H2'	1:CA:148:G:C8	2.37	0.58
1:CA:1522:U:H2'	1:CA:1523:G:H8	1.67	0.58
10:CJ:52:LEU:HB2	14:CN:81:ARG:HD2	1.84	0.58
22:DA:1064:C:N3	22:DA:1074:G:N2	2.51	0.58
22:DA:1774:C:O2	24:DC:11:PRO:HB2	2.02	0.58
22:DA:2074:U:H2'	22:DA:2075:U:C6	2.38	0.58
29:DH:34:GLY:O	29:DH:35:LYS:CB	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DX:71:LEU:HB2	45:DX:76:GLU:HB2	1.83	0.58
3:AC:155:GLY:HA2	3:AC:163:ALA:HB1	1.84	0.58
5:AE:153:VAL:HG11	8:AH:99:LEU:HD13	1.84	0.58
22:BA:84:A:N1	22:BA:98:G:O2'	2.28	0.58
22:BA:139:U:C4	41:BT:2:ILE:HD13	2.38	0.58
22:BA:668:A:H2'	22:BA:670:A:H62	1.67	0.58
22:BA:1059:G:H5"	22:BA:1060:U:H3'	1.85	0.58
1:CA:407:U:H2'	1:CA:408:A:C8	2.38	0.58
1:CA:1071:C:H2'	1:CA:1072:G:H8	1.67	0.58
22:DA:2096:C:H2'	22:DA:2097:A:C8	2.38	0.58
22:DA:2572:A:OP1	22:DA:2574:G:O2'	2.18	0.58
40:DS:84:ARG:HB2	40:DS:96:ILE:HG12	1.84	0.58
6:AF:88:MET:HG2	6:AF:90:MET:HE2	1.85	0.58
9:AI:10:GLY:HA2	9:AI:81:HIS:ND1	2.19	0.58
11:AK:125:LYS:O	21:AU:34:ARG:NE	2.32	0.58
22:BA:395:U:O2'	22:BA:396:G:N7	2.34	0.58
42:BU:16:GLY:O	42:BU:18:ASP:N	2.30	0.58
1:CA:1220:G:H21	19:CS:54:GLY:HA2	1.68	0.58
15:CO:59:MET:O	15:CO:63:ARG:N	2.33	0.58
25:DD:179:ARG:NH1	37:DP:8:LEU:HD21	2.18	0.58
1:AA:429:U:H3'	4:AD:9:LEU:HD23	1.84	0.58
1:AA:645:G:N7	57:AA:1749:HOH:O	2.32	0.58
5:AE:82:GLN:H	5:AE:147:MET:CE	2.16	0.58
15:AO:46:HIS:O	15:AO:48:LYS:N	2.29	0.58
22:BA:660:C:H2'	22:BA:661:A:H8	1.68	0.58
22:BA:1403:A:H2'	22:BA:1404:C:H6	1.68	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:CE:69:ARG:O	5:CE:70:ASN:HB2	2.02	0.58
4:AD:151:LYS:HA	4:AD:178:MET:HE1	1.84	0.58
22:BA:1736:U:H2'	22:BA:1737:G:O4'	2.04	0.58
29:BH:31:VAL:N	29:BH:32:PRO:HD2	2.18	0.58
1:CA:355:C:H2'	1:CA:356:A:O4'	2.03	0.58
22:DA:679:C:H2'	22:DA:680:C:H6	1.69	0.58
22:DA:2111:U:C5	22:DA:2145:C:H2'	2.38	0.58
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
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:BA:1818:U:OP2	24:BC:156:ARG:NH1	2.36	0.58
1:CA:841:C:H3'	1:CA:843:U:H5"	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
21:CU:34:ARG:NE	21:CU:35:ARG:HB2	2.16	0.58
22:DA:1272:A:C5	22:DA:1618:A:H1'	2.38	0.58
1:AA:1307:U:H2'	1:AA:1308:U:C6	2.38	0.58
22:BA:572:A:OP2	39:BR:80:ARG:NH2	2.29	0.58
22:BA:1056:G:O2'	22:BA:1086:A:H8	1.87	0.58
22:BA:2390:U:OP2	51:B3:35:LYS:NZ	2.33	0.58
24:BC:182:ARG:NH2	24:BC:183:LYS:O	2.36	0.58
28:BG:24:ILE:HD12	28:BG:72:LEU:HD21	1.85	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
22:DA:616:A:H4'	26:DE:101:TYR:CZ	2.38	0.58
24:DC:232:HIS:NE2	24:DC:244:PRO:HA	2.18	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
5:AE:149:SER:HB2	5:AE:152:MET:HB2	1.86	0.58
22:BA:637:A:N1	22:BA:651:G:O2'	2.34	0.58
22:BA:819:A:OP2	22:BA:1187:G:N2	2.27	0.58
22:BA:1651:G:OP1	35:BN:40:LYS:HE3	2.04	0.58
24:BC:70:ASN:O	24:BC:72:ASP:N	2.37	0.58
1:CA:161:A:H2'	1:CA:162:A:C8	2.39	0.58
9:CI:116:VAL:HG21	10:CJ:62:ARG:HB2	1.85	0.58
17:CQ:31:HIS:CD2	17:CQ:33:ILE:H	2.21	0.58
22:DA:276:U:O2'	22:DA:278:A:N7	2.37	0.58
22:DA:1993:U:H4'	25:DD:133:THR:CG2	2.34	0.58
24:DC:8:PRO:HB3	24:DC:14:ARG:HB2	1.86	0.58
24:DC:61:ALA:O	24:DC:63:ARG:NH2	2.36	0.58
27:DF:73:SER:HB2	27:DF:81:GLN:HB3	1.85	0.58
15:AO:35:GLN:HB3	15:AO:59:MET:HE2	1.86	0.58
22:BA:1073:A:C3'	22:BA:1074:G:H5"	2.29	0.58
29:BH:97:ARG:HD2	1:CA:369:G:C2'	2.33	0.58
42:BU:14:LEU:HD11	42:BU:71:ALA:HB2	1.85	0.58
3:CC:64:ILE:HG12	3:CC:66:VAL:HG23	1.85	0.58
26:DE:196:VAL:HA	26:DE:199:MET:HE2	1.86	0.58
33:DL:96:LYS:HD3	33:DL:103:ILE:HA	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
22:BA:64:A:H2'	22:BA:65:U:C6	2.39	0.58
22:BA:906:U:O2'	34:BM:66:ARG:NH2	2.28	0.58
22:BA:2117:A:N6	22:BA:2170:A:N1	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
24:DC:67:PHE:HB3	24:DC:151:GLY:O	2.04	0.58
32:DK:70:ARG:HD3	32:DK:76:VAL:HB	1.86	0.58
33:DL:109:LYS:HG2	33:DL:126:ARG:HB3	1.86	0.58
1:AA:686:U:O4	1:AA:703:G:O2'	2.18	0.57
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.85	0.57
10:AJ:32:THR:HG21	10:AJ:86:ALA:HB2	1.86	0.57
10:AJ:44:THR:HG22	10:AJ:70:HIS:HA	1.86	0.57
22:BA:627:A:C6	22:BA:637:A:C8	2.92	0.57
22:BA:1141:U:H4'	22:BA:1142:A:O4'	2.04	0.57
22:DA:155:A:H2'	22:DA:156:A:C8	2.39	0.57
22:DA:2311:A:O2'	22:DA:2312:U:O4'	2.20	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
1:AA:181:A:N6	1:AA:195:A:OP2	2.37	0.57
3:AC:73:PRO:HG2	3:AC:105:GLU:OE1	2.04	0.57
3:AC:143:ARG:HG3	3:AC:144:LEU:HD13	1.86	0.57
22:BA:585:G:N7	38:BQ:6:ARG:NH1	2.51	0.57
3:CC:10:ILE:HD12	14:CN:98:LYS:HG3	1.85	0.57
9:CI:67:VAL:HG11	9:CI:79:ILE:HD11	1.85	0.57
22:DA:328:U:H4'	42:DU:66:GLN:HE21	1.69	0.57
40:DS:52:GLU:HA	40:DS:55:ILE:HD12	1.86	0.57
44:DW:21:LEU:HA	44:DW:39:ARG:HB2	1.86	0.57
51:D3:31:HIS:ND1	51:D3:32:ILE:HG13	2.20	0.57
1:AA:345:C:N3	32:BK:117:SER:OG	2.37	0.57
1:AA:669:G:H2'	1:AA:670:G:H8	1.69	0.57
1:AA:960:U:H2'	1:AA:1225:A:H62	1.69	0.57
5:AE:104:GLY:O	5:AE:105:ILE:HG22	2.04	0.57
22:BA:481:G:C4	22:BA:507:A:C2	2.93	0.57
22:BA:1182:G:H2'	22:BA:1183:U:O4'	2.04	0.57
22:BA:1536:C:H4'	22:BA:1537:G:H5"	1.86	0.57
22:BA:2186:G:H2'	22:BA:2187:U:C6	2.39	0.57
22:BA:2204:G:H4'	24:BC:150:LYS:HG3	1.87	0.57
27:BF:40:VAL:O	27:BF:42:GLU:N	2.37	0.57
27:BF:80:ARG:NE	27:BF:81:GLN:O	2.35	0.57
32:BK:93:GLN:NE2	32:BK:111:LYS:HB2	2.19	0.57
40:BS:43:ALA:HA	40:BS:46:LEU:HD12	1.86	0.57
1:CA:1041:G:H2'	1:CA:1042:A:C8	2.39	0.57
22:DA:788:A:OP1	22:DA:791:C:N4	2.33	0.57
29:DH:40:THR:O	29:DH:41:LYS:C	2.48	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
1:AA:989:U:H2'	1:AA:990:C:C6	2.38	0.57
2:AB:73:LYS:HE3	2:AB:205:ASP:HB2	1.87	0.57
8:AH:30:SER:HB3	8:AH:33:LYS:HG3	1.85	0.57
17:AQ:69:LYS:O	17:AQ:70:THR:HB	2.04	0.57
22:BA:974:G:H8	22:BA:990:A:H62	1.53	0.57
50:B2:18:PHE:HA	50:B2:43:THR:HG21	1.85	0.57
1:CA:67:C:O2'	1:CA:171:A:N3	2.37	0.57
1:CA:519:C:H2'	1:CA:520:A:O4'	2.04	0.57
14:CN:45:VAL:HG23	14:CN:46:LEU:H	1.67	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
22:DA:1799:G:C8	24:DC:176:LEU:HD13	2.39	0.57
22:DA:1827:U:H2'	22:DA:1828:G:O4'	2.05	0.57
22:DA:2641:G:H5"	31:DJ:78:THR:HB	1.87	0.57
28:DG:17:VAL:HG12	28:DG:19:ILE:HD11	1.86	0.57
29:DH:108:VAL:O	29:DH:110:VAL:N	2.36	0.57
1:AA:322:C:O2'	20:AT:18:ARG:HG3	2.03	0.57
2:AB:160:ALA:O	2:AB:161:LEU:HB2	2.03	0.57
5:AE:82:GLN:NE2	5:AE:150:PRO:HD3	2.19	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
29:BH:117:LEU:CD2	29:BH:121:VAL:H	2.08	0.57
41:BT:71:GLY:O	41:BT:73:ARG:N	2.37	0.57
45:BX:17:ASN:OD1	45:BX:27:ARG:HD2	2.05	0.57
46:BY:6:LEU:HD13	46:BY:56:LEU:HD22	1.86	0.57
53:B5:50:ILE:C	53:B5:52:PRO:HD3	2.29	0.57
1:CA:899:C:O2'	22:DA:1832:C:OP1	2.22	0.57
7:CG:13:LEU:HD13	7:CG:14:PRO:HD2	1.85	0.57
19:CS:69:HIS:ND1	19:CS:73:GLU:OE2	2.37	0.57
22:DA:450:G:N1	22:DA:454:A:OP2	2.30	0.57
22:DA:2096:C:H2'	22:DA:2097:A:H8	1.69	0.57
22:DA:2591:C:H2'	22:DA:2592:G:H8	1.69	0.57
22:DA:2793:C:H2'	22:DA:2794:C:C6	2.38	0.57
24:DC:210:ALA:HA	24:DC:213:TRP:CE2	2.39	0.57
30:DI:7:ALA:O	30:DI:59:ILE:HB	2.03	0.57
1:AA:8:A:N6	4:AD:202:GLU:O	2.38	0.57
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.39	0.57
22:BA:323:C:O2	26:BE:163:ASN:ND2	2.38	0.57
24:BC:260:ASN:O	24:BC:262:ARG:N	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:95:GLY:HA2	29:BH:117:LEU:HD22	1.87	0.57
30:BI:34:ASN:OD1	30:BI:65:ARG:NH2	2.36	0.57
1:CA:1348:U:OP1	9:CI:112:GLU:N	2.30	0.57
20:CT:35:VAL:HG21	20:CT:54:MET:HG2	1.86	0.57
22:DA:674:G:N2	22:DA:2445:G:OP1	2.38	0.57
1:AA:570:G:O6	1:AA:865:A:N6	2.38	0.57
9:AI:19:VAL:HA	9:AI:65:ILE:HG22	1.86	0.57
22:BA:381:G:OP1	45:BX:18:ARG:NH2	2.32	0.57
22:BA:582:A:H2'	22:BA:583:G:C8	2.39	0.57
33:BL:109:LYS:HG2	33:BL:126:ARG:HB2	1.85	0.57
46:BY:61:ALA:O	46:BY:63:ALA:N	2.38	0.57
1:CA:1239:A:H2'	1:CA:1298:U:O4	2.05	0.57
2:CB:33:GLY:HA2	2:CB:40:ILE:N	2.19	0.57
3:CC:47:LEU:HB3	3:CC:50:ALA:HB3	1.86	0.57
22:DA:1009:A:N3	22:DA:1153:C:O2'	2.36	0.57
23:DB:29:A:O2'	23:DB:58:A:N1	2.28	0.57
1:AA:337:G:H2'	1:AA:338:A:C8	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
10:AJ:53:ILE:HG22	10:AJ:61:ALA:HB1	1.87	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
22:BA:2532:G:O2'	22:BA:2657:A:N6	2.36	0.57
25:BD:5:VAL:HG21	25:BD:80:TRP:CD2	2.40	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
40:BS:78:GLU:C	40:BS:102:HIS:HE1	2.13	0.57
1:CA:32:A:OP1	1:CA:398:U:H1'	2.03	0.57
1:CA:304:U:H2'	1:CA:305:G:C8	2.39	0.57
1:CA:1070:U:H2'	1:CA:1071:C:C6	2.40	0.57
2:CB:50:PHE:HD1	2:CB:54:LEU:HD23	1.69	0.57
13:CM:40:ALA:O	13:CM:42:ASP:N	2.38	0.57
22:DA:92:U:H2'	22:DA:93:G:O4'	2.04	0.57
22:DA:2636:C:H2'	22:DA:2637:U:C6	2.39	0.57
29:DH:117:LEU:HB3	29:DH:120:GLY:O	2.05	0.57
30:DI:15:ALA:HB3	30:DI:52:GLY:H	1.68	0.57
33:DL:29:LYS:HG3	33:DL:30:THR:HG23	1.86	0.57
37:DP:65:SER:O	37:DP:67:GLY:N	2.37	0.57
1:AA:1278:G:H4'	1:AA:1279:G:C8	2.40	0.57
24:BC:10:SER:O	24:BC:13:ARG:HB3	2.05	0.57
30:BI:101:ILE:O	30:BI:141:GLU:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:689:C:OP1	11:CK:46:THR:OG1	2.15	0.57
22:DA:631:A:N3	22:DA:2415:G:O2'	2.34	0.57
22:DA:2346:A:H3'	22:DA:2347:C:C5'	2.35	0.57
23:DB:41:G:H8	27:DF:66:LEU:HD11	1.69	0.57
31:DJ:114:LEU:HG	31:DJ:118:MET:HE3	1.86	0.57
37:DP:22:PRO:HA	37:DP:47:VAL:HG12	1.87	0.57
2:AB:103:ASN:O	2:AB:106:THR:N	2.25	0.57
22:BA:1028:A:N6	22:BA:1125:G:H2'	2.20	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
19:CS:4:SER:O	19:CS:5:LEU:HB2	2.05	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
22:DA:2674:G:H4'	32:DK:30:ARG:HD2	1.85	0.57
31:DJ:17:VAL:HG22	31:DJ:55:ILE:HB	1.87	0.57
51:D3:33:LEU:HA	51:D3:36:LYS:HD2	1.87	0.57
52:D4:36:ARG:HG2	52:D4:37:GLN:H	1.69	0.57
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:AA:1144:G:N2	1:AA:1146:A:H62	2.02	0.56
3:AC:40:ARG:NH1	3:AC:55:ILE:O	2.37	0.56
12:AL:5:ASN:HB3	12:AL:9:ARG:HH12	1.70	0.56
22:BA:1584:U:O2	22:BA:1585:C:H5'	2.04	0.56
31:BJ:130:HIS:CE1	31:BJ:137:PRO:HG3	2.40	0.56
43:BV:4:ILE:HG13	43:BV:50:MET:HE1	1.85	0.56
1:CA:54:C:H2'	1:CA:352:C:H41	1.70	0.56
1:CA:687:A:N3	1:CA:688:G:H1'	2.19	0.56
1:CA:1108:G:H5"	3:CC:176:HIS:CD2	2.40	0.56
6:CF:45:ARG:O	6:CF:56:LYS:HA	2.05	0.56
38:DQ:87:SER:HB3	39:DR:51:VAL:HA	1.85	0.56
2:AB:23:TRP:CH2	2:AB:25:PRO:HA	2.39	0.56
11:AK:88:GLY:H	11:AK:114:THR:HG22	1.69	0.56
33:BL:85:VAL:HG11	33:BL:95:LEU:HD23	1.85	0.56
38:BQ:88:VAL:HG22	39:BR:49:ILE:HG13	1.87	0.56
1:CA:1166:G:C6	1:CA:1168:U:H5"	2.41	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
22:DA:328:U:O3'	42:DU:66:GLN:HG3	2.05	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1181:U:H2'	22:DA:1182:G:C8	2.40	0.56
22:DA:1187:G:N7	57:DA:3575:HOH:O	2.32	0.56
24:DC:17:VAL:H	24:DC:204:VAL:HG22	1.69	0.56
28:DG:44:LYS:H	28:DG:44:LYS:HE3	1.70	0.56
49:D1:23:THR:OG1	49:D1:24:THR:N	2.34	0.56
1:AA:215:C:H2'	1:AA:216:U:O4'	2.04	0.56
1:AA:587:G:H4'	8:AH:4:GLN:HA	1.88	0.56
1:AA:1129:C:H5'	9:AI:18:ARG:HH22	1.70	0.56
2:AB:85:LEU:HG	2:AB:86:SER:N	2.20	0.56
4:AD:107:PHE:CG	4:AD:145:ILE:HD11	2.41	0.56
4:AD:168:PRO:HG2	4:AD:171:LEU:HD11	1.88	0.56
11:AK:23:ILE:HD11	11:AK:86:VAL:HG13	1.86	0.56
20:AT:25:ARG:HG2	20:AT:29:ARG:HH11	1.71	0.56
22:BA:450:G:O6	57:BA:3243:HOH:O	2.16	0.56
22:BA:979:A:H2'	22:BA:982:C:H42	1.68	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
22:BA:2198:A:C2	29:BH:29:PHE:HB2	2.40	0.56
22:BA:2591:C:H2'	22:BA:2592:G:C8	2.39	0.56
22:BA:2674:G:H4'	32:BK:30:ARG:HD2	1.85	0.56
22:BA:2683:C:O2	32:BK:70:ARG:NH2	2.35	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
29:BH:83:LYS:CD	1:CA:55:A:HO2'	2.03	0.56
43:BV:6:ALA:HB1	43:BV:40:ILE:HG23	1.87	0.56
44:BW:66:LYS:HD2	44:BW:85:GLU:HB3	1.86	0.56
1:CA:56:U:H2'	1:CA:57:G:C8	2.40	0.56
1:CA:718:A:H5'	11:CK:119:ASN:ND2	2.21	0.56
1:CA:1036:A:H3'	1:CA:1037:C:C6	2.40	0.56
1:CA:1226:C:H2'	13:CM:102:THR:HB	1.87	0.56
1:CA:1342:C:H2'	1:CA:1343:G:C8	2.39	0.56
13:CM:8:ASN:ND2	13:CM:10:PRO:HG3	2.20	0.56
15:CO:39:LEU:HG	15:CO:43:PHE:CE1	2.40	0.56
20:CT:10:ARG:O	20:CT:14:SER:OG	2.21	0.56
22:DA:279:A:H61	22:DA:361:G:H1'	1.70	0.56
22:DA:750:A:H5"	22:DA:751:A:OP2	2.05	0.56
22:DA:1076:C:H1'	30:DI:93:PRO:HG2	1.86	0.56
22:DA:1823:G:N7	57:DA:3651:HOH:O	2.32	0.56
22:DA:2461:A:H1'	22:DA:2492:U:C2	2.41	0.56
22:DA:2849:U:OP2	37:DP:93:ARG:NH2	2.35	0.56
37:DP:92:VAL:HG21	37:DP:97:LEU:HD11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DV:21:ARG:HA	43:DV:25:LYS:O	2.06	0.56
1:AA:276:G:OP1	17:AQ:17:MET:HE2	2.05	0.56
18:AR:36:SER:HA	18:AR:72:ASP:HB3	1.87	0.56
22:BA:30:G:H2'	22:BA:31:C:C6	2.40	0.56
22:BA:2339:C:H2'	22:BA:2340:A:C8	2.41	0.56
39:BR:76:LYS:HD3	39:BR:85:LYS:HD2	1.87	0.56
1:CA:955:U:H2'	1:CA:956:U:O4'	2.06	0.56
22:DA:538:A:H5"	31:DJ:7:LYS:HE3	1.88	0.56
22:DA:1197:G:H2'	22:DA:1198:U:C6	2.40	0.56
22:DA:1259:G:H2'	22:DA:1260:A:H8	1.69	0.56
22:DA:1267:U:OP2	22:DA:2012:G:N1	2.24	0.56
22:DA:2341:G:H2'	22:DA:2342:C:C6	2.40	0.56
23:DB:27:C:OP1	36:DO:34:HIS:NE2	2.38	0.56
24:DC:88:SER:HB2	24:DC:158:ALA:H	1.70	0.56
29:DH:21:VAL:HG22	29:DH:22:LYS:N	2.19	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:1441:G:H2'	22:BA:1442:U:C6	2.41	0.56
1:CA:1219:A:H2'	1:CA:1220:G:C8	2.39	0.56
22:DA:27:G:N2	22:DA:512:G:H1'	2.20	0.56
22:DA:222:A:H3'	22:DA:421:C:H5'	1.87	0.56
22:DA:223:A:N1	22:DA:407:G:O2'	2.29	0.56
22:DA:536:G:N2	22:DA:557:C:O2	2.39	0.56
22:DA:1060:U:O4'	22:DA:1062:G:H5'	2.06	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
29:DH:83:LYS:N	29:DH:149:GLU:HG2	2.20	0.56
1:AA:702:A:H61	22:BA:1846:G:H4'	1.71	0.56
1:AA:983:A:H2	1:AA:1222:G:H22	1.53	0.56
3:AC:114:LYS:HD3	3:AC:185:ASN:OD1	2.06	0.56
12:AL:21:VAL:HG23	12:AL:95:TYR:HE1	1.70	0.56
13:AM:80:LEU:HD21	13:AM:87:ARG:HE	1.69	0.56
22:BA:70:G:H4'	22:BA:71:A:OP1	2.05	0.56
22:BA:1073:A:N7	22:BA:1074:G:H8	2.04	0.56
22:BA:2032:G:H1'	25:BD:150:GLN:OE1	2.06	0.56
22:BA:2275:C:O2	34:BM:84:LYS:HD3	2.06	0.56
6:CF:13:ASP:O	6:CF:15:SER:N	2.36	0.56
6:CF:14:GLN:C	6:CF:16:GLU:H	2.14	0.56
22:DA:120:U:H3'	22:DA:120:U:OP2	2.06	0.56
22:DA:1501:G:H2'	22:DA:1502:A:H8	1.69	0.56
24:DC:159:GLY:N	24:DC:195:VAL:HG22	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DF:43:ALA:O	27:DF:47:LYS:HD2	2.05	0.56
36:DO:109:ALA:HA	36:DO:112:GLU:HB2	1.88	0.56
38:DQ:72:ASN:CB	38:DQ:110:VAL:HG11	2.36	0.56
4:AD:10:LYS:HA	4:AD:13:ARG:HG3	1.88	0.56
6:AF:70:VAL:HA	6:AF:73:GLU:HG2	1.86	0.56
22:BA:441:U:H2'	22:BA:442:G:C8	2.41	0.56
22:BA:1179:G:N7	22:BA:1180:U:H1'	2.20	0.56
22:BA:1783:A:H5'	22:BA:2608:G:H4'	1.87	0.56
27:BF:36:LEU:HD21	27:BF:99:PHE:CE1	2.40	0.56
30:BI:78:VAL:HG23	30:BI:79:LEU:HG	1.87	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
1:CA:1320:C:N3	19:CS:36:ARG:NH1	2.54	0.56
5:CE:155:ALA:HB3	5:CE:156:LYS:HE3	1.87	0.56
14:CN:21:PHE:O	14:CN:23:LYS:N	2.39	0.56
1:AA:41:G:H2'	1:AA:42:G:C8	2.41	0.56
2:AB:160:ALA:HA	2:AB:182:PRO:HD2	1.87	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
39:BR:49:ILE:HB	39:BR:51:VAL:O	2.06	0.56
1:CA:663:A:O3'	18:CR:53:ARG:NH2	2.38	0.56
1:CA:703:G:H4'	1:CA:704:A:H5'	1.87	0.56
8:CH:77:ARG:NE	8:CH:79:SER:O	2.38	0.56
12:CL:50:ARG:HB2	12:CL:90:LEU:HD11	1.88	0.56
22:DA:214:G:H1'	22:DA:217:A:H5'	1.88	0.56
22:DA:1231:U:H2'	22:DA:1232:G:C8	2.41	0.56
22:DA:1258:U:H2'	22:DA:1259:G:H8	1.66	0.56
35:DN:98:LEU:HD13	48:D0:54:VAL:HG21	1.87	0.56
1:AA:91:U:C2	1:AA:92:U:H1'	2.41	0.56
22:BA:65:U:H2'	22:BA:66:C:H6	1.69	0.56
22:BA:118:A:N3	22:BA:178:G:H1'	2.21	0.56
22:BA:151:C:H2'	22:BA:152:A:C8	2.41	0.56
42:BU:49:VAL:O	42:BU:51:ALA:N	2.39	0.56
49:B1:26:ASN:OD1	49:B1:28:ARG:HB2	2.06	0.56
1:CA:620:C:H2'	1:CA:621:A:O4'	2.06	0.56
1:CA:1540:U:H4'	21:CU:18:ARG:HG2	1.88	0.56
5:CE:115:LEU:O	5:CE:120:VAL:HG23	2.06	0.56
22:DA:286:U:H2'	22:DA:287:G:C8	2.40	0.56
22:DA:352:A:H2'	22:DA:353:C:O4'	2.06	0.56
22:DA:1187:G:H5"	39:DR:83:TYR:CE2	2.41	0.56
22:DA:2114:A:C5	22:DA:2167:U:H4'	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1094:G:O2'	1:AA:1095:U:OP2	2.23	0.56
1:AA:1351:U:H2'	1:AA:1352:C:C6	2.41	0.56
2:AB:58:ASN:HA	2:AB:61:ALA:HB3	1.88	0.56
22:BA:360:U:H3'	22:BA:361:G:C8	2.40	0.56
22:BA:2128:G:H5'	53:B5:36:ALA:HA	1.88	0.56
22:BA:2198:A:N1	29:BH:25:TYR:HD1	2.04	0.56
29:BH:40:THR:OG1	29:BH:43:ASN:OD1	2.24	0.56
33:BL:93:ASN:HA	33:BL:96:LYS:HB2	1.87	0.56
46:BY:46:VAL:HA	46:BY:49:ASP:HB2	1.86	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
1:CA:1330:U:H4'	13:CM:23:TYR:CE1	2.41	0.56
4:CD:167:LYS:HE2	4:CD:173:VAL:HG11	1.88	0.56
7:CG:65:ALA:O	7:CG:127:ALA:HB1	2.06	0.56
11:CK:15:GLN:HA	11:CK:77:TYR:HA	1.88	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
22:DA:1652:A:OP1	35:DN:8:ARG:NH2	2.35	0.56
22:DA:1947:C:H2'	22:DA:1948:G:H8	1.70	0.56
22:DA:2773:C:OP1	25:DD:171:THR:OG1	2.22	0.56
25:DD:25:THR:HG21	25:DD:193:VAL:HG22	1.87	0.56
29:DH:53:GLU:O	29:DH:54:LEU:C	2.49	0.56
39:DR:78:ARG:HB3	39:DR:83:TYR:HB3	1.88	0.56
1:AA:723:U:H5'	1:AA:724:G:OP1	2.05	0.55
7:AG:146:GLU:HG3	7:AG:149:LYS:HE2	1.87	0.55
8:AH:22:LYS:N	8:AH:65:TYR:OH	2.39	0.55
11:AK:76:GLU:O	22:BA:2141:G:H5"	2.06	0.55
16:AP:71:VAL:O	16:AP:75:ILE:HG13	2.06	0.55
22:BA:26:G:H1'	22:BA:514:A:H61	1.71	0.55
22:BA:282:A:H2'	22:BA:283:G:C8	2.41	0.55
22:BA:1168:G:H2'	22:BA:1169:A:O4'	2.06	0.55
22:BA:2199:A:C4'	29:BH:28:ASN:CG	2.79	0.55
22:BA:2313:C:H5"	27:BF:88:LYS:HD3	1.88	0.55
35:BN:11:ASN:ND2	57:BN:203:HOH:O	2.39	0.55
37:BP:91:ALA:HB2	37:BP:113:ARG:HA	1.86	0.55
1:CA:978:A:O2'	1:CA:1322:C:H5	1.89	0.55
1:CA:1277:C:O2'	1:CA:1279:G:H1'	2.06	0.55
1:CA:1356:G:H2'	1:CA:1357:A:C8	2.41	0.55
2:CB:15:HIS:C	2:CB:15:HIS:ND1	2.63	0.55
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.87	0.55
22:DA:648:G:H2'	22:DA:649:G:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:753:A:H2'	22:DA:754:U:C6	2.41	0.55
22:DA:1794:A:H2'	22:DA:1795:C:H6	1.70	0.55
35:DN:38:LEU:HD11	35:DN:42:LYS:HE3	1.88	0.55
54:D6:6:MHV:CE	54:D6:7:004:HNA	2.19	0.55
1:AA:376:G:H2'	1:AA:377:G:H8	1.71	0.55
2:AB:57:LEU:O	2:AB:60:ILE:HG13	2.06	0.55
2:AB:83:ALA:HA	2:AB:86:SER:OG	2.06	0.55
2:AB:117:LEU:HB3	2:AB:141:LEU:HD11	1.87	0.55
5:AE:24:THR:HA	5:AE:29:ARG:HA	1.87	0.55
6:AF:42:TRP:HZ2	6:AF:61:LEU:HD22	1.70	0.55
10:AJ:81:GLU:HA	10:AJ:84:VAL:HG12	1.87	0.55
15:AO:33:THR:HG21	15:AO:85:LEU:HG	1.88	0.55
22:BA:5:A:H2'	22:BA:6:A:C8	2.41	0.55
22:BA:151:C:H2'	22:BA:152:A:H8	1.71	0.55
40:BS:66:ILE:HA	40:BS:69:LEU:HD22	1.88	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
1:CA:376:G:H5"	16:CP:5:ARG:HB2	1.88	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
2:CB:187:VAL:HB	2:CB:191:SER:HB2	1.89	0.55
3:CC:67:THR:HA	3:CC:102:ASN:HB2	1.88	0.55
22:DA:764:A:N1	22:DA:1789:A:O2'	2.38	0.55
22:DA:2391:G:OP2	51:D3:35:LYS:NZ	2.23	0.55
1:AA:159:G:H8	1:AA:159:G:H5"	1.71	0.55
2:AB:186:ILE:HA	2:AB:200:ILE:HB	1.89	0.55
3:AC:140:ASN:HA	3:AC:143:ARG:CB	2.36	0.55
22:BA:58:G:OP1	41:BT:78:SER:HB2	2.06	0.55
22:BA:1178:C:H2'	22:BA:1179:G:N7	2.21	0.55
22:BA:2321:U:H5'	22:BA:2322:A:OP2	2.06	0.55
24:BC:232:HIS:NE2	24:BC:244:PRO:HA	2.22	0.55
27:BF:119:ALA:HB1	27:BF:167:ARG:HD2	1.88	0.55
28:BG:121:ILE:HD12	28:BG:141:ILE:HG23	1.88	0.55
1:CA:1343:G:O2'	9:CI:123:ARG:HD2	2.05	0.55
2:CB:80:VAL:HG13	2:CB:214:LEU:HD11	1.86	0.55
2:CB:157:LEU:HD12	2:CB:181:ILE:HD11	1.89	0.55
22:DA:1266:G:O2'	22:DA:2012:G:O6	2.23	0.55
24:DC:247:PRO:HG2	24:DC:248:TRP:CZ3	2.42	0.55
1:AA:694:A:N1	1:AA:787:A:O2'	2.39	0.55
1:AA:998:C:H2'	1:AA:999:C:C6	2.41	0.55
1:AA:1277:C:H2'	1:AA:1279:G:H8	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:646:U:H5'	22:BA:647:G:H5"	1.88	0.55
22:BA:2094:A:H5'	29:BH:25:TYR:CG	2.41	0.55
22:BA:2315:G:H2'	22:BA:2316:G:H8	1.72	0.55
22:BA:2683:C:H4'	25:BD:13:ARG:NH1	2.22	0.55
23:BB:48:U:H2'	23:BB:49:C:C6	2.42	0.55
29:BH:83:LYS:CD	1:CA:55:A:H2'	2.36	0.55
29:BH:86:ASP:O	29:BH:87:GLU:CB	2.53	0.55
5:CE:102:GLY:O	5:CE:104:GLY:N	2.39	0.55
20:CT:67:ILE:HD11	20:CT:71:LYS:HD3	1.88	0.55
22:DA:674:G:H1'	26:DE:69:ARG:NE	2.21	0.55
22:DA:704:G:H1'	22:DA:726:G:H22	1.72	0.55
22:DA:2564:A:H5'	22:DA:2648:G:H4'	1.88	0.55
22:DA:2780:G:N1	31:DJ:102:GLU:OE2	2.32	0.55
31:DJ:4:PHE:HB3	38:DQ:64:ARG:HH12	1.71	0.55
31:DJ:65:THR:O	31:DJ:68:LYS:HB2	2.06	0.55
1:AA:593:U:H2'	1:AA:594:U:C6	2.42	0.55
8:AH:36:ILE:HD11	8:AH:126:ILE:HG21	1.87	0.55
22:BA:605:G:N3	22:BA:657:U:O2'	2.37	0.55
22:BA:994:C:H1'	39:BR:10:LYS:HE3	1.89	0.55
22:BA:1006:C:P	57:BA:3787:HOH:O	2.64	0.55
22:BA:2498:C:OP2	57:BA:3689:HOH:O	2.18	0.55
24:BC:235:GLY:HA2	24:BC:239:ASN:HB2	1.89	0.55
25:BD:47:ALA:HA	25:BD:84:LEU:H	1.71	0.55
29:BH:98:ASP:O	29:BH:102:ALA:HB3	2.07	0.55
30:BI:39:CYS:O	30:BI:43:ASN:HB2	2.07	0.55
34:BM:17:ASN:O	34:BM:38:ARG:HD3	2.07	0.55
41:BT:3:ARG:HB3	41:BT:6:ARG:HB3	1.89	0.55
1:CA:33:A:H2'	1:CA:34:C:C6	2.42	0.55
1:CA:866:C:C4	1:CA:867:G:H1'	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
22:DA:2372:U:H2'	22:DA:2373:G:C8	2.42	0.55
31:DJ:77:HIS:HA	31:DJ:83:GLY:O	2.07	0.55
33:DL:77:ILE:HG23	33:DL:81:ASP:OD2	2.07	0.55
36:DO:97:PHE:HB2	36:DO:103:VAL:HG11	1.88	0.55
41:DT:34:VAL:HG21	41:DT:43:ILE:HD11	1.87	0.55
2:AB:206:ALA:O	2:AB:208:ARG:N	2.40	0.55
3:AC:153:VAL:HG12	3:AC:198:VAL:HG22	1.88	0.55
5:AE:45:ARG:HG2	5:AE:73:ASN:HB3	1.87	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BC:40:SER:C	24:BC:42:GLY:H	2.14	0.55
29:BH:90:LEU:O	1:CA:358:U:C4'	2.43	0.55
29:BH:121:VAL:N	29:BH:122:LEU:CA	2.69	0.55
42:BU:81:ASP:OD1	42:BU:82:ARG:N	2.40	0.55
1:CA:1113:C:H4'	3:CC:14:ILE:HD12	1.88	0.55
1:CA:1492:A:H3'	1:CA:1493:A:C8	2.41	0.55
11:CK:23:ILE:HD11	11:CK:86:VAL:HG13	1.87	0.55
11:CK:97:ILE:HD13	11:CK:110:ILE:HD11	1.89	0.55
16:CP:19:VAL:HG22	16:CP:36:VAL:HG12	1.87	0.55
22:DA:153:U:H2'	22:DA:154:U:C6	2.42	0.55
22:DA:1153:C:OP1	38:DQ:92:ARG:NH1	2.40	0.55
22:DA:2115:G:O2'	22:DA:2117:A:N6	2.40	0.55
1:AA:1053:G:O5'	1:AA:1054:C:H5'	2.06	0.55
4:AD:198:HIS:HA	4:AD:201:VAL:HB	1.88	0.55
22:BA:660:C:H2'	22:BA:661:A:C8	2.42	0.55
22:BA:1056:G:HO2'	22:BA:1086:A:H8	1.54	0.55
22:BA:1582:C:O2'	22:BA:1585:C:N3	2.38	0.55
29:BH:94:ILE:C	1:CA:368:U:OP1	2.50	0.55
29:BH:120:GLY:CA	29:BH:122:LEU:HA	2.37	0.55
29:BH:121:VAL:N	29:BH:122:LEU:CB	2.70	0.55
22:DA:1230:A:H2'	22:DA:1231:U:C6	2.42	0.55
22:DA:1779:U:H5	22:DA:1784:A:N7	2.05	0.55
30:DI:28:LEU:HD13	30:DI:38:PHE:CD2	2.42	0.55
38:DQ:78:LYS:HE2	38:DQ:117:LEU:HD21	1.88	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:250:G:OP2	51:B3:13:ARG:NH1	2.39	0.55
22:BA:610:C:O2	22:BA:618:G:N2	2.28	0.55
22:BA:927:A:H2'	22:BA:928:A:C8	2.42	0.55
22:BA:1358:G:H1'	22:BA:1374:G:N2	2.22	0.55
22:BA:2757:A:N1	28:BG:67:THR:HG21	2.22	0.55
32:BK:93:GLN:HE22	32:BK:111:LYS:HB2	1.72	0.55
39:BR:49:ILE:HB	39:BR:52:PRO:HA	1.88	0.55
1:CA:466:A:H2'	1:CA:468:A:H2	1.71	0.55
7:CG:136:LYS:O	7:CG:140:ASP:HB2	2.07	0.55
19:CS:41:PHE:HB2	19:CS:44:MET:HG3	1.89	0.55
22:DA:494:G:H4'	40:DS:6:LYS:HG3	1.89	0.55
22:DA:981:A:N1	22:DA:2027:G:O2'	2.29	0.55
22:DA:2185:U:H2'	22:DA:2186:G:C8	2.42	0.55
26:DE:108:ILE:HB	33:DL:2:ARG:HH22	1.72	0.55
31:DJ:11:VAL:HG11	31:DJ:50:THR:HA	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:34:C:H2'	1:AA:35:G:C8	2.42	0.55
1:AA:41:G:H2'	1:AA:42:G:H8	1.72	0.55
3:AC:6:HIS:HB3	14:AN:89:MET:HG3	1.89	0.55
4:AD:50:ASP:O	4:AD:54:GLN:HB2	2.07	0.55
7:AG:18:PHE:HZ	7:AG:58:GLU:HG2	1.72	0.55
17:AQ:52:GLU:H	17:AQ:52:GLU:CD	2.13	0.55
22:BA:528:A:C2	22:BA:2043:C:H4'	2.42	0.55
29:BH:10:ALA:O	29:BH:12:LEU:N	2.40	0.55
41:BT:51:PHE:HE1	46:BY:26:PHE:HZ	1.55	0.55
1:CA:805:C:H2'	1:CA:806:C:H6	1.72	0.55
2:CB:135:LEU:HA	2:CB:138:THR:HG1	1.71	0.55
2:CB:142:GLU:HA	2:CB:145:GLU:HB2	1.88	0.55
8:CH:93:PRO:HG3	8:CH:125:ILE:HD12	1.88	0.55
22:DA:335:C:H6	22:DA:335:C:O5'	1.90	0.55
22:DA:448:U:H5"	57:DA:3241:HOH:O	2.07	0.55
22:DA:679:C:H2'	22:DA:680:C:C6	2.42	0.55
22:DA:1951:U:H2'	22:DA:1953:A:OP2	2.07	0.55
35:DN:1:MET:O	35:DN:3:HIS:N	2.40	0.55
1:AA:1234:C:H2'	1:AA:1235:U:H6	1.70	0.55
13:AM:75:MET:SD	27:BF:112:ARG:HB2	2.46	0.55
22:BA:1386:C:H2'	22:BA:1387:A:C8	2.42	0.55
22:BA:1926:U:H2'	22:BA:1926:U:O2	2.06	0.55
22:BA:2127:G:H4'	22:BA:2128:G:OP1	2.06	0.55
48:B0:34:SER:OG	48:B0:36:GLU:HG2	2.06	0.55
20:CT:81:ALA:O	20:CT:85:LYS:HG2	2.07	0.55
22:DA:883:G:N2	22:DA:894:U:O2	2.40	0.55
28:DG:140:VAL:O	28:DG:144:VAL:HG23	2.06	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
1:AA:903:G:H2'	1:AA:904:U:H6	1.72	0.54
22:BA:20:C:H2'	22:BA:21:A:C8	2.41	0.54
22:BA:417:C:H2'	22:BA:418:C:H6	1.72	0.54
22:BA:878:A:H5'	22:BA:879:G:OP2	2.07	0.54
22:BA:1322:A:O3'	40:BS:84:ARG:NH1	2.36	0.54
24:BC:71:LYS:HD2	24:BC:74:ILE:HD12	1.89	0.54
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.42	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:DA:532:A:N1	22:DA:2020:A:H1'	2.21	0.54
22:DA:893:C:H2'	22:DA:894:U:O4'	2.08	0.54
22:DA:1358:G:H1'	22:DA:1374:G:N2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1935:G:H1'	22:DA:1964:G:N2	2.22	0.54
22:DA:2267:A:H5"	22:DA:2268:A:H5'	1.88	0.54
22:DA:2790:U:H5'	22:DA:2893:A:N7	2.22	0.54
32:DK:99:ILE:HD13	32:DK:118:LEU:HD12	1.89	0.54
35:DN:72:ASP:HB3	35:DN:75:ILE:HB	1.90	0.54
1:AA:772:U:O2'	1:AA:773:G:OP1	2.23	0.54
1:AA:1160:G:OP1	2:AB:132:LYS:NZ	2.26	0.54
1:AA:1442:G:H2'	1:AA:1443:C:H6	1.71	0.54
2:AB:173:ILE:HG23	2:AB:183:VAL:HG11	1.89	0.54
6:AF:8:PHE:HA	6:AF:87:SER:HA	1.88	0.54
22:BA:1430:G:H2'	22:BA:1431:A:C8	2.42	0.54
22:BA:1442:U:H2'	22:BA:1443:U:C6	2.43	0.54
22:BA:1799:G:O6	24:BC:178:SER:HB3	2.06	0.54
22:BA:1927:A:H2'	22:BA:1928:A:C8	2.42	0.54
39:BR:8:GLY:O	39:BR:10:LYS:NZ	2.41	0.54
1:CA:736:C:H2'	1:CA:737:C:C6	2.41	0.54
1:CA:1252:A:H2'	1:CA:1253:G:O4'	2.08	0.54
3:CC:111:LEU:HD13	3:CC:146:ALA:HB2	1.88	0.54
12:CL:22:PRO:C	12:CL:24:LEU:H	2.14	0.54
22:DA:2057:G:H2'	22:DA:2058:A:O4'	2.07	0.54
26:DE:24:ASN:O	26:DE:28:VAL:HG23	2.07	0.54
33:DL:116:VAL:HG11	33:DL:134:ALA:HB1	1.89	0.54
34:DM:41:LEU:HD21	34:DM:124:LEU:HD13	1.89	0.54
42:DU:74:ASN:HA	42:DU:96:PHE:CZ	2.41	0.54
42:DU:96:PHE:CE1	42:DU:103:ILE:HG12	2.42	0.54
6:AF:90:MET:HG2	18:AR:61:ARG:HH21	1.72	0.54
7:AG:57:SER:OG	7:AG:58:GLU:N	2.40	0.54
22:BA:1796:U:H2'	22:BA:1797:G:C8	2.40	0.54
22:BA:2153:C:H2'	22:BA:2154:A:O4'	2.07	0.54
22:BA:2547:A:H5"	32:BK:29:HIS:NE2	2.23	0.54
22:BA:2845:U:H5"	37:BP:52:ASN:O	2.08	0.54
1:CA:1492:A:H3'	1:CA:1493:A:H8	1.72	0.54
3:CC:130:PHE:CE2	3:CC:131:ARG:HD3	2.43	0.54
11:CK:35:THR:OG1	11:CK:40:ASN:N	2.38	0.54
22:DA:1045:C:H41	22:DA:1111:A:H2'	1.72	0.54
22:DA:1299:G:O6	22:DA:1639:C:H5"	2.07	0.54
26:DE:97:ASN:HB2	26:DE:100:MET:HB2	1.89	0.54
46:DY:3:ALA:HA	46:DY:6:LEU:HB2	1.88	0.54
1:AA:545:C:H5'	4:AD:69:GLU:HB2	1.89	0.54
1:AA:1152:A:H5'	10:AJ:15:HIS:CD2	2.43	0.54
4:AD:62:ARG:NH1	4:AD:69:GLU:HG2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:88:ARG:O	8:AH:122:GLY:HA3	2.08	0.54
11:AK:13:ARG:HG3	11:AK:77:TYR:HE1	1.73	0.54
11:AK:24:HIS:HB3	11:AK:31:ILE:HG23	1.89	0.54
11:AK:88:GLY:N	11:AK:114:THR:HG22	2.23	0.54
22:BA:616:A:O2'	26:BE:199:MET:HE1	2.08	0.54
22:BA:2199:A:O4'	29:BH:28:ASN:CG	2.49	0.54
29:BH:90:LEU:HA	29:BH:125:THR:HG23	1.90	0.54
4:CD:26:ARG:HG3	4:CD:27:ALA:N	2.23	0.54
7:CG:91:VAL:HG23	7:CG:95:ARG:HB3	1.89	0.54
22:DA:999:U:OP2	57:DA:3357:HOH:O	2.18	0.54
22:DA:1747:U:H2'	22:DA:1748:C:C6	2.43	0.54
22:DA:2540:C:H2'	22:DA:2541:A:H8	1.71	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
1:AA:928:G:O2'	1:AA:1533:C:OP1	2.24	0.54
1:AA:1142:G:C2	1:AA:1143:G:H1'	2.42	0.54
2:AB:21:ARG:C	2:AB:23:TRP:H	2.09	0.54
2:AB:167:ASP:OD1	2:AB:168:HIS:N	2.40	0.54
14:AN:81:ARG:HA	14:AN:84:VAL:HB	1.90	0.54
22:BA:423:A:H5"	22:BA:424:G:H5'	1.90	0.54
22:BA:588:U:H2'	22:BA:589:U:H6	1.70	0.54
22:BA:1672:A:C2	22:BA:2582:G:H5'	2.43	0.54
22:BA:2140:G:N3	22:BA:2140:G:H2'	2.23	0.54
22:BA:2572:A:N7	25:BD:150:GLN:HB2	2.23	0.54
29:BH:77:THR:O	29:BH:77:THR:CG2	2.56	0.54
29:BH:90:LEU:CD2	29:BH:93:SER:HA	2.37	0.54
36:BO:94:ARG:O	36:BO:96:GLY:N	2.40	0.54
1:CA:689:C:OP2	11:CK:53:ARG:NH2	2.40	0.54
14:CN:91:GLY:O	14:CN:93:ILE:N	2.40	0.54
20:CT:5:LYS:O	20:CT:7:ALA:N	2.40	0.54
22:DA:17:G:H4'	38:DQ:25:TYR:HE1	1.72	0.54
22:DA:119:A:H4'	22:DA:120:U:O5'	2.07	0.54
22:DA:858:G:N2	22:DA:919:U:O4	2.38	0.54
27:DF:44:ILE:HG21	27:DF:79:ILE:HG22	1.89	0.54
29:DH:81:ALA:C	29:DH:149:GLU:HB3	2.33	0.54
33:DL:77:ILE:HD11	33:DL:101:ILE:HG21	1.89	0.54
36:DO:26:LEU:HB3	36:DO:92:PHE:HD1	1.72	0.54
37:DP:18:PRO:HG3	37:DP:84:ILE:O	2.07	0.54
1:AA:93:U:H2'	1:AA:94:G:H5"	1.88	0.54
1:AA:522:C:H2'	1:AA:523:A:O4'	2.06	0.54
1:AA:859:G:H2'	1:AA:860:A:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1239:A:H62	1:AA:1299:A:N6	2.05	0.54
2:AB:71:GLY:HA2	2:AB:164:ILE:HG22	1.90	0.54
14:AN:43:ASN:HA	14:AN:45:VAL:HG22	1.90	0.54
24:BC:62:TYR:HD2	24:BC:86:ASN:HD22	1.54	0.54
29:BH:103:VAL:HG21	29:BH:132:PHE:CE1	2.42	0.54
38:BQ:44:GLN:NE2	39:BR:77:PHE:HB3	2.22	0.54
40:BS:83:LYS:O	40:BS:84:ARG:HD3	2.07	0.54
15:CO:45:GLU:HG2	15:CO:46:HIS:H	1.73	0.54
22:DA:447:A:H5'	22:DA:449:A:C5	2.42	0.54
22:DA:1439:A:N7	22:DA:1552:A:H2	2.04	0.54
22:DA:2544:G:H2'	22:DA:2545:G:H8	1.73	0.54
22:DA:2615:U:C2	48:D0:4:GLN:HA	2.41	0.54
23:DB:62:C:H2'	23:DB:63:C:H6	1.71	0.54
33:DL:93:ASN:OD1	33:DL:94:THR:N	2.40	0.54
34:DM:54:THR:HA	34:DM:57:VAL:HG22	1.89	0.54
34:DM:63:ILE:HG12	34:DM:105:MET:HE2	1.89	0.54
37:DP:51:ARG:O	37:DP:58:ALA:N	2.34	0.54
38:DQ:94:ILE:HD13	39:DR:11:GLN:HB2	1.89	0.54
45:DX:54:LYS:HA	45:DX:57:ARG:HB2	1.88	0.54
1:AA:116:A:H2'	1:AA:117:G:H8	1.73	0.54
1:AA:381:C:H2'	1:AA:382:A:O4'	2.08	0.54
2:AB:54:LEU:HD22	2:AB:54:LEU:H	1.72	0.54
6:AF:47:LEU:HB3	6:AF:49:TYR:O	2.08	0.54
7:AG:40:GLU:HB2	7:AG:44:TYR:CE2	2.43	0.54
16:AP:38:PHE:CZ	16:AP:51:ARG:HB2	2.43	0.54
22:BA:65:U:H2'	22:BA:66:C:C6	2.42	0.54
22:BA:1006:C:OP2	57:BA:3787:HOH:O	2.18	0.54
22:BA:1266:G:O2'	22:BA:2012:G:O6	2.18	0.54
22:BA:2683:C:OP1	37:BP:51:ARG:NH2	2.41	0.54
20:CT:29:ARG:O	20:CT:33:LYS:HG2	2.08	0.54
22:DA:82:U:H5'	22:DA:296:U:H5"	1.89	0.54
22:DA:740:C:H5'	22:DA:1784:A:C3'	2.37	0.54
22:DA:2899:A:H2'	22:DA:2900:A:H8	1.71	0.54
25:DD:104:VAL:O	25:DD:105:LYS:HB3	2.07	0.54
44:DW:21:LEU:HD22	44:DW:39:ARG:HB3	1.90	0.54
2:AB:122:GLN:H	2:AB:122:GLN:CD	2.16	0.54
9:AI:114:LYS:HG2	9:AI:120:LYS:HA	1.90	0.54
22:BA:1590:A:H2'	22:BA:1591:A:C8	2.43	0.54
37:BP:103:ARG:HH11	37:BP:103:ARG:CG	2.21	0.54
1:CA:644:U:H2'	1:CA:645:G:O4'	2.08	0.54
1:CA:1308:U:H2'	1:CA:1309:G:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CG:69:VAL:HG21	7:CG:104:ILE:HD11	1.88	0.54
11:CK:16:VAL:HG12	11:CK:77:TYR:HB3	1.90	0.54
22:DA:135:U:H2'	22:DA:136:G:C8	2.43	0.54
22:DA:1270:C:O2'	22:DA:1648:U:OP2	2.25	0.54
22:DA:1726:C:H2'	22:DA:1727:C:H6	1.73	0.54
30:DI:5:VAL:HA	30:DI:8:TYR:CE1	2.43	0.54
42:DU:53:ASN:C	42:DU:55:PRO:HD3	2.33	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
10:AJ:36:VAL:HA	10:AJ:75:ASP:O	2.08	0.54
22:BA:18:U:OP1	38:BQ:30:ARG:NH2	2.41	0.54
25:BD:13:ARG:HD2	25:BD:15:PHE:CZ	2.43	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
22:DA:1411:U:H2'	22:DA:1412:U:O4'	2.07	0.54
22:DA:2291:U:H2'	22:DA:2292:U:H6	1.72	0.54
27:DF:32:GLU:OE1	27:DF:92:ARG:NH1	2.40	0.54
31:DJ:109:LEU:HD22	31:DJ:118:MET:HG3	1.88	0.54
37:DP:62:ARG:CZ	37:DP:101:ARG:HA	2.38	0.54
1:AA:398:U:H2'	1:AA:399:G:H8	1.72	0.54
13:AM:16:VAL:HG22	13:AM:41:GLU:O	2.08	0.54
13:AM:77:ILE:HG22	13:AM:81:MET:HE2	1.89	0.54
22:BA:250:G:OP1	57:BA:3818:HOH:O	2.19	0.54
22:BA:1509:A:O2'	22:BA:1510:G:OP2	2.21	0.54
28:BG:155:GLU:OE2	28:BG:158:LYS:N	2.41	0.54
29:BH:97:ARG:CD	1:CA:369:G:O2'	2.42	0.54
40:BS:84:ARG:HB2	40:BS:96:ILE:HG13	1.90	0.54
1:CA:673:A:O3'	6:CF:86:ARG:NH2	2.41	0.54
1:CA:778:G:O2'	11:CK:121:CYS:HB3	2.08	0.54
1:CA:1067:A:H4'	1:CA:1068:G:O5'	2.07	0.54
1:CA:1362:A:OP1	1:CA:1362:A:H4'	2.06	0.54
1:CA:1491:G:H2'	1:CA:1492:A:C8	2.43	0.54
2:CB:173:ILE:O	2:CB:177:ASN:ND2	2.40	0.54
22:DA:1141:U:H4'	22:DA:1142:A:O4'	2.08	0.54
22:DA:1432:G:H2'	22:DA:1433:A:C8	2.42	0.54
29:DH:79:THR:HA	29:DH:145:ASN:HB2	1.89	0.54
30:DI:5:VAL:HG22	30:DI:8:TYR:HE1	1.72	0.54
33:DL:59:ARG:CZ	33:DL:59:ARG:HB3	2.38	0.54
1:AA:487:A:H3'	1:AA:488:C:C6	2.43	0.53
1:AA:1157:A:H5'	1:AA:1158:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.43	0.53
22:BA:858:G:H3'	22:BA:859:G:C8	2.43	0.53
22:BA:2376:A:N3	36:BO:111:ARG:NH1	2.56	0.53
1:CA:1206:G:H4'	3:CC:192:THR:O	2.07	0.53
1:CA:1317:C:OP1	14:CN:57:PRO:HD2	2.08	0.53
4:CD:42:GLY:C	4:CD:44:ARG:H	2.16	0.53
17:CQ:52:GLU:CG	17:CQ:53:CYS:H	2.20	0.53
22:DA:37:C:H2'	22:DA:38:A:C8	2.42	0.53
22:DA:2215:C:H2'	22:DA:2216:G:H8	1.73	0.53
29:DH:32:PRO:O	29:DH:33:GLN:HB2	2.08	0.53
46:DY:51:ALA:O	46:DY:55:THR:OG1	2.24	0.53
5:AE:79:GLY:O	5:AE:121:HIS:N	2.34	0.53
11:AK:25:ALA:HA	11:AK:30:THR:HG22	1.89	0.53
22:BA:68:G:H2'	22:BA:69:C:O4'	2.08	0.53
22:BA:559:G:H1'	38:BQ:56:GLN:NE2	2.23	0.53
22:BA:1515:A:H3'	22:BA:1516:G:H8	1.73	0.53
22:BA:1668:A:H4'	22:BA:1669:A:O5'	2.08	0.53
22:BA:2394:C:OP1	51:B3:30:ARG:NH2	2.41	0.53
27:BF:107:ALA:O	27:BF:110:ARG:N	2.41	0.53
1:CA:1053:G:N7	1:CA:1200:C:H5"	2.23	0.53
9:CI:114:LYS:HG3	9:CI:120:LYS:HA	1.88	0.53
22:DA:1317:G:H2'	22:DA:1318:U:O4'	2.07	0.53
22:DA:1551:A:N6	57:DA:3629:HOH:O	2.40	0.53
23:DB:48:U:H2'	23:DB:49:C:C6	2.43	0.53
42:DU:7:ARG:O	42:DU:25:VAL:HB	2.08	0.53
1:AA:206:C:H2'	1:AA:207:C:O4'	2.07	0.53
1:AA:254:G:OP1	17:AQ:70:THR:HB	2.09	0.53
1:AA:667:G:H4'	15:AO:51:HIS:ND1	2.23	0.53
1:AA:1369:C:H2'	1:AA:1370:G:C8	2.43	0.53
4:AD:3:ARG:CZ	4:AD:115:ARG:HD3	2.38	0.53
7:AG:68:ASN:C	7:AG:70:ARG:H	2.16	0.53
13:AM:11:ASP:CG	13:AM:12:HIS:N	2.66	0.53
15:AO:24:SER:HB3	15:AO:27:VAL:HG23	1.89	0.53
22:BA:372:G:OP2	45:BX:61:LYS:HD3	2.07	0.53
22:BA:630:G:H5"	22:BA:631:A:OP2	2.08	0.53
22:BA:1169:A:H2'	22:BA:1170:C:O4'	2.08	0.53
22:BA:1936:A:N6	22:BA:1963:U:H3	2.05	0.53
22:BA:2118:U:O4	22:BA:2148:G:O2'	2.24	0.53
1:CA:33:A:H2'	1:CA:34:C:H6	1.73	0.53
1:CA:102:G:H2'	1:CA:103:U:H6	1.73	0.53
1:CA:1096:C:H2'	1:CA:1097:C:H6	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:86:ARG:CG	6:CF:86:ARG:HH11	2.21	0.53
7:CG:12:ILE:HD12	7:CG:24:ALA:HB1	1.90	0.53
15:CO:35:GLN:NE2	15:CO:39:LEU:HD22	2.22	0.53
19:CS:6:LYS:HB2	19:CS:7:LYS:HG2	1.90	0.53
20:CT:15:GLU:OE2	20:CT:18:ARG:NH2	2.24	0.53
22:DA:2811:G:OP1	25:DD:62:LYS:N	2.40	0.53
1:AA:558:G:H8	1:AA:558:G:O5'	1.90	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
4:AD:91:LEU:HD11	4:AD:195:ILE:HD11	1.90	0.53
8:AH:41:LYS:HD2	8:AH:48:ASP:HA	1.89	0.53
16:AP:6:LEU:HD13	16:AP:71:VAL:HG23	1.91	0.53
20:AT:80:THR:O	20:AT:83:ILE:HG13	2.09	0.53
22:BA:832:U:H2'	22:BA:833:A:C8	2.44	0.53
22:BA:947:A:HO2'	22:BA:984:A:H2	1.55	0.53
22:BA:994:C:OP2	38:BQ:54:LYS:NZ	2.41	0.53
53:B5:73:VAL:HG12	53:B5:74:ARG:H	1.72	0.53
1:CA:9:G:H5'	5:CE:108:GLY:HA3	1.89	0.53
1:CA:483:C:H2'	1:CA:484:G:C8	2.44	0.53
1:CA:1088:G:H21	1:CA:1167:A:N6	2.07	0.53
1:CA:1182:G:H4'	1:CA:1183:U:H5"	1.89	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
2:CB:62:SER:HA	2:CB:224:GLY:HA2	1.90	0.53
3:CC:5:VAL:HG21	3:CC:10:ILE:HD13	1.90	0.53
5:CE:156:LYS:HG2	8:CH:71:VAL:HG22	1.91	0.53
22:DA:1231:U:H2'	22:DA:1232:G:H8	1.71	0.53
22:DA:1266:G:OP1	48:D0:16:ARG:NE	2.40	0.53
22:DA:1799:G:N2	22:DA:1818:U:O2'	2.38	0.53
22:DA:2609:U:C6	54:D6:7:004:HA	2.41	0.53
22:DA:2886:A:C2	48:D0:29:SER:HB3	2.43	0.53
22:DA:2898:U:H2'	22:DA:2899:A:C8	2.43	0.53
24:DC:68:LYS:HG2	24:DC:151:GLY:HA2	1.88	0.53
2:AB:16:PHE:HD1	2:AB:17:GLY:H	1.56	0.53
5:AE:89:HIS:CE1	5:AE:138:ARG:HD3	2.43	0.53
9:AI:57:MET:HA	9:AI:60:LYS:HB2	1.90	0.53
22:BA:141:G:H5"	22:BA:142:A:C5	2.44	0.53
22:BA:1097:U:H1'	30:BI:9:VAL:HG12	1.90	0.53
28:BG:98:VAL:HG22	28:BG:103:ILE:HG12	1.90	0.53
30:BI:69:PHE:H	30:BI:69:PHE:HD1	1.55	0.53
33:BL:90:VAL:HG13	33:BL:95:LEU:HD21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:B1:13:SER:OG	49:B1:40:ASP:OD2	2.24	0.53
8:CH:29:SER:HB2	8:CH:59:LEU:HB2	1.90	0.53
12:CL:66:TYR:O	12:CL:97:THR:OG1	2.24	0.53
14:CN:66:GLN:HG3	14:CN:79:LEU:HD21	1.89	0.53
22:DA:125:A:H3'	50:D2:19:ARG:HG3	1.90	0.53
22:DA:954:G:O2'	22:DA:2274:A:N1	2.36	0.53
22:DA:2250:G:O5'	22:DA:2250:G:H8	1.90	0.53
22:DA:2716:C:H2'	22:DA:2717:C:H6	1.74	0.53
23:DB:41:G:C8	27:DF:66:LEU:HD11	2.44	0.53
29:DH:37:VAL:CG2	29:DH:38:PRO:HD2	2.39	0.53
29:DH:103:VAL:HA	29:DH:106:ALA:HB3	1.89	0.53
41:DT:40:LYS:HG3	41:DT:60:THR:HG23	1.91	0.53
1:AA:337:G:H2'	1:AA:338:A:H8	1.74	0.53
1:AA:591:U:H2'	1:AA:592:G:C8	2.44	0.53
2:AB:94:HIS:ND1	2:AB:146:ASN:HB2	2.24	0.53
8:AH:96:MET:HB2	8:AH:99:LEU:O	2.08	0.53
12:AL:86:ARG:CZ	12:AL:88:LYS:HB3	2.38	0.53
21:AU:8:GLU:HB3	21:AU:12:PHE:CZ	2.44	0.53
22:BA:1078:U:H1'	22:BA:1088:A:C2	2.43	0.53
22:BA:2142:A:H2'	22:BA:2143:C:C6	2.44	0.53
26:BE:15:SER:N	26:BE:197:GLU:OE2	2.30	0.53
28:BG:86:LYS:HG2	28:BG:132:VAL:HG13	1.91	0.53
29:BH:93:SER:OG	1:CA:357:G:C4'	2.51	0.53
32:BK:101:GLY:O	32:BK:120:PRO:HD2	2.08	0.53
34:BM:30:SER:N	34:BM:106:ASP:HB2	2.24	0.53
46:BY:13:GLU:HG2	46:BY:57:LEU:HD13	1.90	0.53
1:CA:123:U:H2'	1:CA:124:C:C6	2.44	0.53
1:CA:501:C:H1'	1:CA:549:C:H1'	1.91	0.53
1:CA:1308:U:H2'	1:CA:1309:G:H8	1.74	0.53
7:CG:88:PRO:HD2	7:CG:151:PHE:O	2.08	0.53
22:DA:548:G:H4'	22:DA:549:G:C2	2.43	0.53
22:DA:1289:C:O2'	22:DA:1330:C:H4'	2.09	0.53
22:DA:1938:A:C6	22:DA:2590:A:H1'	2.43	0.53
22:DA:2578:G:H21	25:DD:130:GLN:NE2	2.07	0.53
24:DC:24:LEU:HD11	24:DC:90:ASN:HD21	1.73	0.53
32:DK:76:VAL:HG12	37:DP:73:VAL:HG22	1.90	0.53
49:D1:9:ILE:HG21	49:D1:25:LYS:HD2	1.89	0.53
1:AA:825:A:O2'	8:AH:13:ARG:NH1	2.42	0.53
2:AB:63:ARG:O	2:AB:64:LYS:HB2	2.07	0.53
7:AG:135:VAL:HB	7:AG:138:ARG:NH2	2.22	0.53
13:AM:34:LEU:HD22	13:AM:41:GLU:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:893:C:H2'	22:BA:894:U:O4'	2.09	0.53
22:BA:2305:U:H2'	22:BA:2306:C:C6	2.44	0.53
22:BA:2366:A:H2'	22:BA:2367:G:O4'	2.08	0.53
22:BA:2698:U:H2'	22:BA:2699:C:C6	2.44	0.53
22:BA:2756:U:H1'	22:BA:2757:A:H5"	1.91	0.53
24:BC:144:VAL:HG12	24:BC:145:GLU:O	2.09	0.53
26:BE:164:LEU:HB3	26:BE:167:VAL:HB	1.91	0.53
36:BO:31:THR:HG22	36:BO:34:HIS:N	2.20	0.53
1:CA:505:G:H5'	1:CA:534:U:C2	2.44	0.53
1:CA:581:G:H8	1:CA:581:G:OP2	1.91	0.53
5:CE:150:PRO:C	5:CE:152:MET:H	2.16	0.53
13:CM:33:ILE:HG23	13:CM:59:GLU:HB3	1.90	0.53
17:CQ:12:VAL:HG23	17:CQ:57:ASP:O	2.09	0.53
21:CU:40:LYS:H	21:CU:41:PRO:HD2	1.73	0.53
22:DA:1338:G:H4'	41:DT:18:GLU:OE2	2.09	0.53
22:DA:1745:A:H2'	22:DA:1746:A:H8	1.73	0.53
22:DA:1969:A:O2'	22:DA:1972:G:N3	2.29	0.53
22:DA:2540:C:H2'	22:DA:2541:A:C8	2.44	0.53
23:DB:43:C:H1'	27:DF:90:THR:HB	1.91	0.53
24:DC:160:THR:H	24:DC:195:VAL:HG13	1.73	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
29:DH:2:GLN:O	29:DH:3:VAL:HG22	2.09	0.53
39:DR:41:ILE:HD13	39:DR:103:ALA:HA	1.91	0.53
1:AA:219:U:H2'	1:AA:220:G:C8	2.43	0.53
1:AA:1539:C:H5"	21:AU:18:ARG:HG3	1.91	0.53
9:AI:56:ASP:O	9:AI:60:LYS:NZ	2.31	0.53
22:BA:458:G:N2	22:BA:459:U:O4	2.36	0.53
22:BA:1072:C:OP2	22:BA:1075:C:N4	2.41	0.53
28:BG:20:ASN:O	28:BG:20:ASN:ND2	2.40	0.53
28:BG:93:GLY:O	28:BG:95:ARG:HG2	2.09	0.53
29:BH:147:VAL:CG1	29:BH:149:GLU:HG3	2.36	0.53
51:B3:17:THR:HG21	51:B3:49:MET:HE1	1.90	0.53
53:B5:53:ARG:HD3	53:B5:204:GLY:HA3	1.90	0.53
53:B5:59:VAL:HG21	53:B5:167:ASP:C	2.33	0.53
1:CA:499:A:C6	1:CA:547:A:C8	2.96	0.53
13:CM:106:ALA:O	13:CM:110:LYS:HB3	2.09	0.53
22:DA:329:G:O4'	22:DA:477:A:H1'	2.09	0.53
22:DA:1063:G:O2'	30:DI:89:GLY:HA3	2.09	0.53
22:DA:1199:U:H2'	22:DA:1200:C:C6	2.44	0.53
22:DA:1568:G:O4'	24:DC:58:HIS:HE1	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DH:31:VAL:HB	29:DH:32:PRO:HD3	1.89	0.53
10:AJ:48:ARG:NH1	10:AJ:66:GLU:OE1	2.42	0.53
22:BA:752:A:H3'	50:B2:1:MET:SD	2.48	0.53
22:BA:1385:A:H1'	22:BA:1386:C:C6	2.44	0.53
22:BA:1410:G:H2'	22:BA:1411:U:C6	2.44	0.53
22:BA:2794:C:H2'	22:BA:2795:C:C6	2.43	0.53
31:BJ:80:HIS:HB3	31:BJ:81:ILE:HG22	1.91	0.53
1:CA:1191:A:H5"	3:CC:4:LYS:HE3	1.91	0.53
5:CE:155:ALA:HB1	8:CH:66:PHE:CD2	2.44	0.53
11:CK:26:SER:HG	11:CK:29:ASN:H	1.55	0.53
21:CU:51:SER:O	21:CU:53:VAL:N	2.42	0.53
22:DA:27:G:O2'	22:DA:28:A:OP2	2.20	0.53
22:DA:463:G:N2	22:DA:466:A:OP2	2.36	0.53
22:DA:622:G:H2'	22:DA:623:C:C6	2.44	0.53
22:DA:2612:C:H5"	22:DA:2613:U:OP1	2.08	0.53
26:DE:127:GLU:O	26:DE:156:ASN:ND2	2.42	0.53
29:DH:31:VAL:CB	29:DH:32:PRO:CD	2.86	0.53
30:DI:45:LYS:HA	30:DI:48:SER:HB3	1.90	0.53
1:AA:205:A:OP1	1:AA:205:A:H4'	2.07	0.53
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.44	0.53
4:AD:190:ASP:OD2	4:AD:190:ASP:N	2.32	0.53
8:AH:64:LYS:HB2	8:AH:71:VAL:HG21	1.90	0.53
9:AI:50:GLN:C	9:AI:52:LEU:H	2.17	0.53
21:AU:6:VAL:HB	21:AU:8:GLU:HG2	1.90	0.53
22:BA:572:A:H5"	22:BA:573:U:OP2	2.09	0.53
22:BA:1061:U:O4	30:BI:11:LEU:HA	2.09	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
34:BM:136:MET:HE3	43:BV:77:VAL:HG12	1.91	0.53
52:B4:36:ARG:HG2	52:B4:37:GLN:H	1.74	0.53
2:CB:175:GLU:O	2:CB:179:LEU:N	2.39	0.53
3:CC:68:ILE:HD12	3:CC:101:ILE:HD11	1.91	0.53
9:CI:57:MET:O	9:CI:59:GLU:N	2.41	0.53
12:CL:38:TYR:HB2	12:CL:52:VAL:HG13	1.89	0.53
14:CN:54:ASP:OD1	14:CN:59:ARG:NH1	2.42	0.53
16:CP:40:ASN:HB3	16:CP:43:ALA:HB2	1.91	0.53
22:DA:142:A:H2'	22:DA:143:C:C6	2.44	0.53
22:DA:1656:C:H5"	25:DD:141:ARG:HB2	1.90	0.53
22:DA:2537:U:H2'	22:DA:2538:C:C6	2.43	0.53
24:DC:159:GLY:H	24:DC:195:VAL:HG22	1.74	0.53
28:DG:45:HIS:HA	28:DG:50:LEU:HD23	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DH:34:GLY:O	29:DH:35:LYS:HB2	2.08	0.53
33:DL:81:ASP:O	33:DL:82:LEU:HB3	2.08	0.53
1:AA:762:U:H2'	1:AA:763:G:H8	1.73	0.52
1:AA:1441:A:C2	37:BP:114:LEU:HD22	2.44	0.52
4:AD:151:LYS:HB2	4:AD:156:LYS:HE3	1.90	0.52
5:AE:96:MET:HB3	5:AE:125:ALA:HB2	1.91	0.52
22:BA:1695:G:H1'	24:BC:8:PRO:O	2.08	0.52
27:BF:14:LYS:O	27:BF:18:THR:HG23	2.08	0.52
28:BG:19:ILE:HG12	28:BG:24:ILE:HD13	1.90	0.52
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:CA:1202:U:H2'	1:CA:1203:C:O4'	2.09	0.52
11:CK:25:ALA:N	11:CK:87:LYS:O	2.41	0.52
22:DA:183:C:H1'	22:DA:433:C:H1'	1.90	0.52
22:DA:482:A:N6	22:DA:506:G:O2'	2.41	0.52
22:DA:1651:G:H4'	35:DN:39:PRO:HG2	1.91	0.52
22:DA:2345:G:H5'	22:DA:2347:C:O4'	2.09	0.52
28:DG:89:LEU:HD12	28:DG:162:VAL:HG22	1.91	0.52
33:DL:90:VAL:HB	33:DL:122:VAL:HA	1.91	0.52
2:AB:168:HIS:ND1	2:AB:168:HIS:O	2.42	0.52
3:AC:46:GLU:C	3:AC:48:ALA:H	2.17	0.52
27:BF:60:ILE:HG22	27:BF:99:PHE:HE1	1.74	0.52
40:BS:80:PRO:O	40:BS:100:THR:OG1	2.25	0.52
40:BS:90:LYS:NZ	54:B6:8:MHT:H7	2.24	0.52
53:B5:43:GLU:O	53:B5:213:VAL:HA	2.09	0.52
1:CA:1074:G:H4'	2:CB:103:ASN:CB	2.36	0.52
2:CB:169:GLU:O	2:CB:171:ILE:N	2.43	0.52
17:CQ:70:THR:HG22	17:CQ:71:LYS:H	1.73	0.52
18:CR:25:ASP:C	18:CR:27:ALA:H	2.17	0.52
22:DA:27:G:H22	22:DA:512:G:H1'	1.73	0.52
22:DA:482:A:H1'	22:DA:498:G:N2	2.23	0.52
22:DA:1152:C:H4'	38:DQ:77:SER:HA	1.91	0.52
22:DA:1881:C:H2'	22:DA:1882:U:O4'	2.09	0.52
22:DA:1999:C:O2	22:DA:2687:U:O2'	2.27	0.52
22:DA:2765:A:H5'	22:DA:2766:A:OP2	2.09	0.52
27:DF:126:GLY:HA2	27:DF:163:ASP:HA	1.92	0.52
39:DR:41:ILE:O	39:DR:47:VAL:N	2.42	0.52
1:AA:1269:A:N1	1:AA:1312:G:O2'	2.32	0.52
2:AB:95:ARG:NH1	2:AB:97:LEU:HA	2.23	0.52
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.08	0.52
12:AL:76:GLU:O	12:AL:77:HIS:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:7:G:H2'	22:BA:8:C:C6	2.45	0.52
22:BA:2298:A:H61	22:BA:2318:G:H1'	1.74	0.52
1:CA:1203:C:H2'	1:CA:1204:A:H8	1.73	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
22:DA:2344:U:H4'	22:DA:2345:G:OP1	2.09	0.52
39:DR:76:LYS:HB2	39:DR:85:LYS:HB2	1.91	0.52
41:DT:21:SER:O	41:DT:24:MET:N	2.42	0.52
1:AA:593:U:H2'	1:AA:594:U:H6	1.75	0.52
1:AA:642:A:N3	8:AH:105:SER:OG	2.38	0.52
1:AA:723:U:H5"	21:AU:49:LYS:HG2	1.92	0.52
1:AA:731:G:OP1	1:AA:766:A:H1'	2.09	0.52
1:AA:1112:C:O2	3:AC:179:ARG:HG3	2.10	0.52
2:AB:20:THR:OG1	2:AB:21:ARG:N	2.30	0.52
12:AL:72:HIS:ND1	12:AL:74:LEU:HB2	2.25	0.52
22:BA:479:A:N3	22:BA:481:G:H5"	2.24	0.52
22:BA:1877:A:H2'	22:BA:1878:G:O4'	2.10	0.52
22:BA:2315:G:H2'	22:BA:2316:G:C8	2.44	0.52
29:BH:77:THR:HA	29:BH:143:ILE:O	2.10	0.52
33:BL:89:VAL:O	33:BL:94:THR:HG21	2.09	0.52
2:CB:131:LYS:O	2:CB:135:LEU:N	2.42	0.52
3:CC:59:ARG:HB2	3:CC:63:SER:O	2.10	0.52
5:CE:148:ASN:OD1	8:CH:96:MET:HE1	2.09	0.52
6:CF:40:GLU:HB2	6:CF:42:TRP:HE1	1.75	0.52
22:DA:102:U:C2	46:DY:2:LYS:HE2	2.43	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
22:DA:846:U:H1'	22:DA:847:U:H5	1.74	0.52
22:DA:987:C:H2'	22:DA:988:A:O4'	2.09	0.52
22:DA:1597:A:O3'	22:DA:1598:A:H8	1.91	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
29:DH:34:GLY:O	29:DH:35:LYS:HD2	2.10	0.52
35:DN:28:LEU:HD23	35:DN:48:VAL:HG21	1.90	0.52
1:AA:92:U:H2'	1:AA:93:U:C6	2.45	0.52
1:AA:390:U:H2'	1:AA:391:G:H8	1.74	0.52
1:AA:600:A:H2'	1:AA:601:G:H8	1.70	0.52
1:AA:1227:A:O2'	13:AM:115:PRO:HD2	2.10	0.52
5:AE:111:MET:O	5:AE:115:LEU:HB2	2.08	0.52
9:AI:52:LEU:HD13	9:AI:57:MET:HG2	1.90	0.52
18:AR:26:ILE:HA	18:AR:29:LEU:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:BB:77:U:P	43:BV:21:ARG:HH22	2.33	0.52
29:BH:51:ARG:NH1	29:BH:55:GLU:OE1	2.43	0.52
1:CA:412:A:O2'	1:CA:413:G:H4'	2.09	0.52
1:CA:518:C:H4'	1:CA:519:C:O5'	2.10	0.52
1:CA:1361:G:C2	1:CA:1362:A:N7	2.77	0.52
2:CB:206:ALA:O	2:CB:208:ARG:N	2.43	0.52
5:CE:105:ILE:HG13	5:CE:112:ARG:HG3	1.90	0.52
13:CM:14:HIS:HB2	13:CM:17:ILE:HD12	1.90	0.52
22:DA:1783:A:H5'	22:DA:2608:G:H4'	1.90	0.52
22:DA:1911:U:H2'	22:DA:1918:A:C2	2.44	0.52
22:DA:2053:G:H2'	22:DA:2054:A:O4'	2.10	0.52
22:DA:2557:G:H2'	22:DA:2558:C:C6	2.45	0.52
26:DE:22:ASP:OD2	26:DE:22:ASP:N	2.37	0.52
26:DE:146:VAL:HG22	26:DE:167:VAL:HG22	1.91	0.52
1:AA:1277:C:HO2'	1:AA:1279:G:H8	1.57	0.52
3:AC:55:ILE:O	3:AC:55:ILE:HG13	2.09	0.52
5:AE:83:HIS:CE1	5:AE:147:MET:HG3	2.43	0.52
15:AO:4:SER:O	15:AO:8:THR:HG23	2.09	0.52
15:AO:81:LEU:HD11	15:AO:85:LEU:HD22	1.92	0.52
22:BA:2689:U:OP2	22:BA:2719:G:N2	2.29	0.52
24:BC:3:VAL:HG12	24:BC:19:VAL:HG22	1.92	0.52
26:BE:12:LEU:HD23	26:BE:13:THR:N	2.25	0.52
35:BN:31:HIS:C	35:BN:33:ILE:H	2.18	0.52
1:CA:463:U:H5'	1:CA:464:U:OP2	2.09	0.52
1:CA:545:C:H5'	4:CD:69:GLU:CG	2.40	0.52
1:CA:690:G:H2'	1:CA:691:G:O4'	2.09	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
5:CE:80:THR:HA	5:CE:120:VAL:HG12	1.92	0.52
7:CG:71:PRO:HD2	7:CG:96:ARG:O	2.10	0.52
8:CH:9:ASP:OD2	8:CH:13:ARG:NH1	2.41	0.52
14:CN:16:LEU:HB3	14:CN:55:SER:HA	1.92	0.52
22:DA:2850:A:OP2	22:DA:2866:U:N3	2.31	0.52
23:DB:64:G:H2'	23:DB:65:U:C6	2.45	0.52
29:DH:72:ILE:HG22	29:DH:72:ILE:O	2.09	0.52
31:DJ:56:VAL:HB	31:DJ:124:VAL:HG12	1.91	0.52
1:AA:1313:U:P	19:AS:6:LYS:HB3	2.50	0.52
1:AA:1338:G:H2'	1:AA:1339:A:C8	2.45	0.52
2:AB:197:ASP:N	2:AB:197:ASP:OD1	2.41	0.52
9:AI:120:LYS:HG3	9:AI:123:ARG:HB3	1.92	0.52
13:AM:18:ALA:O	13:AM:21:SER:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AS:15:LEU:HD13	19:AS:33:THR:HG21	1.92	0.52
20:AT:24:ARG:O	20:AT:27:MET:HG3	2.10	0.52
22:BA:583:G:OP1	38:BQ:7:GLY:HA2	2.09	0.52
22:BA:1287:A:C5'	35:BN:103:ARG:HD2	2.38	0.52
29:BH:94:ILE:CG2	29:BH:99:ILE:CG1	2.88	0.52
1:CA:425:G:H2'	1:CA:426:U:O4'	2.10	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
5:CE:149:SER:HB2	5:CE:152:MET:HG2	1.92	0.52
7:CG:137:LYS:O	7:CG:141:VAL:HG23	2.10	0.52
15:CO:3:LEU:HD22	15:CO:35:GLN:HG2	1.91	0.52
17:CQ:12:VAL:HG12	17:CQ:13:VAL:N	2.22	0.52
22:DA:934:U:H2'	22:DA:935:C:C6	2.45	0.52
22:DA:1450:G:C6	22:DA:1451:C:N4	2.77	0.52
22:DA:1773:A:N7	22:DA:1829:A:H1'	2.24	0.52
22:DA:1973:G:OP1	57:DA:3460:HOH:O	2.19	0.52
22:DA:2094:A:H2'	22:DA:2095:A:H8	1.75	0.52
24:DC:114:ASP:OD2	24:DC:114:ASP:N	2.40	0.52
28:DG:127:THR:HG22	28:DG:128:GLN:H	1.74	0.52
35:DN:85:PRO:HA	35:DN:88:ALA:HB2	1.91	0.52
2:AB:166:ALA:HB2	2:AB:187:VAL:HG12	1.92	0.52
3:AC:205:GLY:O	3:AC:206:GLU:HG2	2.10	0.52
6:AF:51:ILE:HD12	6:AF:86:ARG:CZ	2.39	0.52
9:AI:22:LYS:HZ2	9:AI:24:GLY:HA3	1.75	0.52
13:AM:95:LEU:HB3	13:AM:96:PRO:HD2	1.92	0.52
22:BA:372:G:OP1	45:BX:62:LYS:NZ	2.43	0.52
22:BA:1779:U:H5	22:BA:1784:A:N7	2.07	0.52
22:BA:2649:C:H2'	22:BA:2650:U:H6	1.75	0.52
28:BG:74:SER:HA	28:BG:77:ILE:HG13	1.92	0.52
29:BH:94:ILE:HD12	29:BH:98:ASP:HB3	1.92	0.52
34:BM:18:ARG:HH21	34:BM:18:ARG:CG	2.22	0.52
1:CA:200:G:H2'	1:CA:201:G:H5"	1.92	0.52
1:CA:791:G:C6	1:CA:792:A:N7	2.78	0.52
1:CA:940:C:H2'	1:CA:941:G:C8	2.45	0.52
8:CH:7:ILE:HB	8:CH:77:ARG:NH1	2.25	0.52
22:DA:224:U:OP2	22:DA:408:G:N2	2.41	0.52
22:DA:320:A:H4'	22:DA:322:A:N7	2.25	0.52
22:DA:1681:G:O2'	22:DA:1762:A:N3	2.39	0.52
22:DA:2567:G:H2'	22:DA:2568:U:C6	2.44	0.52
29:DH:23:ALA:O	29:DH:27:ARG:N	2.38	0.52
29:DH:25:TYR:CZ	29:DH:30:LEU:HD21	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DJ:78:THR:OG1	31:DJ:80:HIS:HB2	2.10	0.52
33:DL:56:PRO:O	33:DL:60:ARG:HB3	2.09	0.52
42:DU:14:LEU:HD11	42:DU:71:ALA:HB2	1.91	0.52
1:AA:452:A:C8	1:AA:452:A:H3'	2.45	0.52
4:AD:147:GLU:O	4:AD:150:LYS:HB2	2.10	0.52
10:AJ:6:ILE:HD12	10:AJ:76:ILE:HB	1.92	0.52
11:AK:110:ILE:HB	21:AU:6:VAL:HG22	1.91	0.52
13:AM:29:ARG:NH2	13:AM:63:PHE:HB2	2.25	0.52
22:BA:780:G:N2	22:BA:783:A:H62	2.04	0.52
22:BA:1070:A:C2	30:BI:10:LYS:HG3	2.45	0.52
22:BA:2636:C:H2'	22:BA:2637:U:C6	2.45	0.52
27:BF:38:MET:HE3	27:BF:57:LEU:HG	1.92	0.52
27:BF:136:ILE:HD11	27:BF:149:VAL:HG12	1.92	0.52
29:BH:2:GLN:O	29:BH:3:VAL:HG22	2.10	0.52
29:BH:117:LEU:CD2	29:BH:121:VAL:N	2.70	0.52
1:CA:821:G:H2'	1:CA:822:U:C6	2.45	0.52
1:CA:858:G:O6	1:CA:869:G:H3'	2.10	0.52
1:CA:950:U:H2'	1:CA:951:G:C8	2.45	0.52
1:CA:1053:G:O5'	1:CA:1054:C:H5'	2.10	0.52
22:DA:1259:G:H2'	22:DA:1260:A:C8	2.45	0.52
22:DA:1567:G:H2'	24:DC:85:PRO:HG3	1.90	0.52
25:DD:172:VAL:HG23	25:DD:194:PRO:HD3	1.91	0.52
36:DO:2:ASP:O	36:DO:6:ALA:HB2	2.10	0.52
46:DY:9:LYS:N	46:DY:12:GLU:HG3	2.24	0.52
1:AA:946:A:H2'	1:AA:947:G:C8	2.45	0.52
1:AA:1217:C:P	14:AN:9:ARG:HH21	2.33	0.52
2:AB:67:ILE:HB	2:AB:89:GLN:HB3	1.92	0.52
8:AH:18:GLN:NE2	8:AH:70:ALA:HB1	2.25	0.52
12:AL:29:GLN:HB2	12:AL:82:ILE:O	2.10	0.52
22:BA:2199:A:H4'	29:BH:28:ASN:CG	2.34	0.52
30:BI:117:MET:SD	30:BI:129:ILE:HD11	2.50	0.52
40:BS:57:ASN:O	40:BS:61:ASN:HB2	2.10	0.52
53:B5:75:VAL:HA	53:B5:120:VAL:O	2.10	0.52
1:CA:266:G:H3'	17:CQ:69:LYS:HB2	1.92	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
9:CI:8:GLY:N	9:CI:86:ALA:HB2	2.25	0.52
22:DA:845:A:H5'	22:DA:846:U:OP2	2.10	0.52
23:DB:29:A:OP2	36:DO:31:THR:HG23	2.10	0.52
25:DD:48:ILE:HG23	25:DD:84:LEU:HD21	1.90	0.52
32:DK:107:LEU:O	32:DK:109:SER:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:AA:466:A:H5'	1:AA:467:U:OP2	2.10	0.51
1:AA:1001:C:H2'	1:AA:1002:G:C8	2.45	0.51
1:AA:1321:U:O3'	19:AS:78:ARG:NH2	2.43	0.51
6:AF:38:ARG:HB3	6:AF:63:ASN:HB2	1.92	0.51
11:AK:74:VAL:C	11:AK:76:GLU:N	2.65	0.51
19:AS:5:LEU:O	19:AS:7:LYS:N	2.42	0.51
22:BA:84:A:H4'	22:BA:85:G:O5'	2.09	0.51
22:BA:543:G:C2	22:BA:544:C:H1'	2.45	0.51
22:BA:593:U:H2'	22:BA:594:U:C6	2.45	0.51
22:BA:1340:U:OP1	41:BT:19:LYS:NZ	2.39	0.51
22:BA:1435:G:O2'	22:BA:1436:G:H5'	2.09	0.51
22:BA:2563:U:H2'	22:BA:2565:A:OP2	2.10	0.51
32:BK:92:GLU:HG3	32:BK:111:LYS:NZ	2.25	0.51
50:B2:8:SER:OG	50:B2:11:LYS:HG3	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
5:CE:56:VAL:N	5:CE:57:PRO:HD2	2.24	0.51
6:CF:39:LEU:HD12	6:CF:40:GLU:N	2.25	0.51
8:CH:55:THR:C	8:CH:57:PRO:HD3	2.35	0.51
22:DA:328:U:H4'	42:DU:66:GLN:NE2	2.25	0.51
22:DA:671:C:H2'	22:DA:672:C:C6	2.45	0.51
22:DA:1323:C:N4	22:DA:1324:G:O6	2.43	0.51
22:DA:1719:G:N2	22:DA:1742:U:H1'	2.25	0.51
22:DA:2127:G:H4'	22:DA:2128:G:OP1	2.10	0.51
22:DA:2761:A:H1'	28:DG:143:GLN:NE2	2.25	0.51
24:DC:141:VAL:O	24:DC:162:VAL:N	2.41	0.51
30:DI:8:TYR:HB2	30:DI:59:ILE:H	1.75	0.51
46:DY:1:MET:O	46:DY:5:GLU:HG3	2.10	0.51
1:AA:152:A:N6	1:AA:170:U:C2	2.78	0.51
1:AA:340:U:H2'	1:AA:341:C:H6	1.75	0.51
1:AA:1317:C:H4'	14:AN:49:GLN:HE21	1.75	0.51
5:AE:95:PHE:CZ	5:AE:97:GLN:HG3	2.45	0.51
13:AM:114:LYS:HB2	13:AM:115:PRO:HD3	1.91	0.51
15:AO:8:THR:O	15:AO:12:VAL:HG23	2.10	0.51
19:AS:79:THR:O	19:AS:79:THR:OG1	2.26	0.51
20:AT:69:LYS:HB2	20:AT:70:ASN:OD1	2.10	0.51
22:BA:282:A:H2'	22:BA:283:G:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:856:G:H1'	44:BW:27:GLY:H	1.75	0.51
32:BK:76:VAL:HB	37:BP:73:VAL:HG13	1.92	0.51
38:BQ:27:ALA:HB1	38:BQ:31:VAL:HB	1.91	0.51
1:CA:952:U:H2'	1:CA:953:G:C8	2.45	0.51
2:CB:222:ARG:HE	2:CB:223:GLU:H	1.57	0.51
5:CE:122:ASN:CG	5:CE:123:VAL:H	2.18	0.51
8:CH:78:VAL:N	8:CH:126:ILE:O	2.42	0.51
14:CN:61:ARG:O	14:CN:62:ASN:HB2	2.10	0.51
22:DA:511:U:O4	22:DA:512:G:N1	2.43	0.51
22:DA:765:C:H2'	22:DA:766:U:C6	2.46	0.51
22:DA:847:U:O2	22:DA:934:U:H1'	2.10	0.51
22:DA:851:C:O2'	47:DZ:43:ALA:O	2.28	0.51
27:DF:15:LYS:O	27:DF:19:GLU:HG3	2.09	0.51
32:DK:38:ILE:HD11	32:DK:112:PHE:CZ	2.46	0.51
1:AA:118:U:O4	1:AA:288:A:H2'	2.09	0.51
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.43	0.51
1:AA:601:G:H2'	1:AA:602:A:H8	1.74	0.51
2:AB:104:TRP:CZ2	2:AB:154:MET:HG2	2.45	0.51
20:AT:4:ILE:HG12	20:AT:8:LYS:HZ1	1.74	0.51
22:BA:276:U:H2'	22:BA:276:U:O2	2.11	0.51
22:BA:1538:G:OP2	22:BA:1538:G:H8	1.93	0.51
22:BA:1869:G:C3'	22:BA:1870:C:H5'	2.40	0.51
22:BA:2305:U:N3	27:BF:151:GLY:HA3	2.25	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
39:BR:49:ILE:HG22	39:BR:52:PRO:C	2.34	0.51
1:CA:261:U:OP2	20:CT:71:LYS:HD2	2.11	0.51
2:CB:87:CYS:C	2:CB:89:GLN:H	2.19	0.51
22:DA:172:A:H2'	22:DA:173:A:C8	2.46	0.51
22:DA:420:C:H2'	22:DA:421:C:C6	2.46	0.51
22:DA:858:G:O2'	22:DA:2268:A:N3	2.40	0.51
22:DA:1063:G:H2'	22:DA:1064:C:O4'	2.09	0.51
22:DA:1572:A:H2'	22:DA:1573:G:H8	1.74	0.51
22:DA:1682:G:H2'	22:DA:1683:U:C6	2.45	0.51
24:DC:145:GLU:HA	24:DC:152:GLY:HA2	1.92	0.51
24:DC:171:TYR:HD2	24:DC:185:GLU:HA	1.75	0.51
33:DL:94:THR:HA	33:DL:97:ALA:HB3	1.92	0.51
5:AE:50:TYR:CE2	5:AE:134:ILE:HD11	2.45	0.51
6:AF:47:LEU:HD12	6:AF:55:HIS:HA	1.93	0.51
16:AP:77:GLU:C	16:AP:79:ASN:N	2.66	0.51
22:BA:1100:C:H2'	22:BA:1101:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1442:U:H2'	22:BA:1443:U:H6	1.75	0.51
29:BH:99:ILE:O	29:BH:103:VAL:CG2	2.58	0.51
29:BH:110:VAL:HG22	29:BH:114:GLU:HB2	1.90	0.51
1:CA:328:C:H4'	1:CA:329:A:H5"	1.92	0.51
1:CA:1071:C:H2'	1:CA:1072:G:C8	2.45	0.51
1:CA:1329:A:H5"	13:CM:25:VAL:HA	1.91	0.51
18:CR:62:ALA:HB3	18:CR:68:LEU:HD12	1.92	0.51
22:DA:118:A:H1'	22:DA:178:G:O4'	2.09	0.51
22:DA:469:G:O6	50:D2:37:LYS:HE2	2.11	0.51
22:DA:727:A:H2'	22:DA:728:G:C8	2.45	0.51
22:DA:1594:U:H2'	22:DA:1595:C:C6	2.45	0.51
27:DF:40:VAL:O	27:DF:42:GLU:N	2.42	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
38:DQ:17:ILE:HG23	38:DQ:39:VAL:HG21	1.92	0.51
45:DX:31:PRO:HB2	45:DX:33:LEU:HD13	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
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
22:BA:645:C:O2'	22:BA:646:U:H5"	2.11	0.51
22:BA:1917:U:C4	22:BA:1918:A:C5	2.99	0.51
22:BA:2086:U:H2'	22:BA:2087:G:C8	2.45	0.51
29:BH:100:ALA:CB	29:BH:112:LYS:HA	2.41	0.51
29:BH:132:PHE:O	29:BH:139:PHE:HB3	2.11	0.51
38:BQ:40:ILE:O	38:BQ:44:GLN:HG3	2.11	0.51
40:BS:4:ILE:HG23	40:BS:106:VAL:HG22	1.92	0.51
1:CA:408:A:OP1	4:CD:110:THR:OG1	2.27	0.51
1:CA:562:U:OP2	12:CL:14:ARG:NH2	2.44	0.51
1:CA:847:G:H2'	1:CA:848:C:O4'	2.10	0.51
3:CC:130:PHE:CE1	3:CC:157:LEU:HB3	2.46	0.51
7:CG:114:LYS:HB2	7:CG:118:LEU:HD12	1.93	0.51
11:CK:35:THR:OG1	11:CK:36:ASP:N	2.44	0.51
15:CO:26:GLU:HG2	15:CO:81:LEU:HD13	1.92	0.51
22:DA:451:U:H2'	22:DA:453:A:N7	2.25	0.51
23:DB:58:A:H2'	23:DB:59:A:O4'	2.11	0.51
24:DC:167:ARG:HG3	24:DC:172:VAL:HG12	1.91	0.51
34:DM:136:MET:HE3	43:DV:77:VAL:HG12	1.93	0.51
1:AA:264:C:H2'	1:AA:265:G:O4'	2.11	0.51
1:AA:974:A:P	14:AN:69:ARG:HH22	2.34	0.51
5:AE:153:VAL:O	5:AE:156:LYS:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:15:ASP:H	7:AG:24:ALA:HB2	1.75	0.51
22:BA:171:U:H2'	22:BA:172:A:C8	2.45	0.51
22:BA:934:U:H2'	22:BA:935:C:C6	2.45	0.51
22:BA:1131:G:O2'	22:BA:2026:U:H5'	2.10	0.51
22:BA:1364:G:P	45:BX:50:ARG:HH22	2.33	0.51
22:BA:1837:C:H2'	22:BA:1899:A:H61	1.76	0.51
22:BA:1853:A:N1	22:BA:2087:G:H1'	2.25	0.51
22:BA:2093:G:O2'	29:BH:25:TYR:HB2	2.11	0.51
22:BA:2804:U:H2'	22:BA:2805:C:H6	1.75	0.51
27:BF:80:ARG:HG2	27:BF:81:GLN:N	2.26	0.51
34:BM:2:LEU:O	34:BM:3:GLN:HB3	2.10	0.51
39:BR:25:LEU:H	39:BR:94:THR:HG21	1.75	0.51
39:BR:40:MET:C	39:BR:41:ILE:HG12	2.34	0.51
45:BX:49:LEU:HB3	45:BX:51:VAL:HG13	1.91	0.51
46:BY:34:SER:O	46:BY:36:GLN:N	2.42	0.51
1:CA:790:A:C6	1:CA:791:G:C6	2.98	0.51
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.11	0.51
1:CA:1377:A:N3	7:CG:2:PRO:HG3	2.26	0.51
12:CL:59:ASN:H	12:CL:59:ASN:ND2	2.05	0.51
13:CM:48:LEU:HD22	13:CM:53:ILE:HG13	1.92	0.51
15:CO:62:GLN:HA	15:CO:65:LYS:HE3	1.92	0.51
22:DA:674:G:H1'	26:DE:69:ARG:HE	1.76	0.51
22:DA:919:U:H2'	22:DA:920:A:O4'	2.11	0.51
22:DA:987:C:O2'	22:DA:1000:A:N3	2.39	0.51
22:DA:1009:A:O2'	22:DA:1153:C:H4'	2.10	0.51
22:DA:1090:A:N6	22:DA:1091:G:O6	2.43	0.51
22:DA:1515:A:H5'	22:DA:1516:G:OP2	2.11	0.51
22:DA:2112:G:H2'	22:DA:2112:G:N3	2.26	0.51
26:DE:117:ARG:HH21	26:DE:184:ASP:HA	1.74	0.51
27:DF:5:HIS:HB2	27:DF:97:TRP:CG	2.45	0.51
30:DI:28:LEU:HD11	30:DI:35:ILE:HG23	1.91	0.51
41:DT:56:GLU:HB3	41:DT:86:THR:HB	1.92	0.51
42:DU:57:GLY:O	42:DU:59:VAL:HG23	2.10	0.51
46:DY:9:LYS:HG2	46:DY:10:SER:N	2.26	0.51
46:DY:16:THR:O	46:DY:20:ASN:ND2	2.32	0.51
46:DY:28:LEU:HD11	46:DY:46:VAL:HG21	1.92	0.51
1:AA:374:A:H5"	1:AA:452:A:H2	1.75	0.51
1:AA:797:C:H2'	1:AA:798:U:C6	2.45	0.51
2:AB:9:MET:N	2:AB:9:MET:SD	2.84	0.51
2:AB:51:ASN:O	2:AB:52:GLU:HB2	2.11	0.51
5:AE:13:GLU:HB3	5:AE:39:VAL:HG12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:AU:35:ARG:O	21:AU:37:PHE:N	2.44	0.51
22:BA:973:A:H5"	39:BR:81:LYS:HG3	1.93	0.51
22:BA:1753:G:H5"	37:BP:93:ARG:HH11	1.75	0.51
44:BW:19:LYS:HG3	44:BW:41:ARG:HH21	1.75	0.51
1:CA:50:A:H1'	1:CA:52:C:O4'	2.10	0.51
1:CA:313:A:H2'	1:CA:314:C:C6	2.46	0.51
5:CE:111:MET:HG3	5:CE:140:THR:HG21	1.92	0.51
6:CF:64:VAL:HG12	6:CF:65:GLU:N	2.24	0.51
17:CQ:46:VAL:HG22	17:CQ:73:TRP:HB2	1.93	0.51
22:DA:388:G:N7	22:DA:390:U:H2'	2.25	0.51
22:DA:1802:A:H2'	22:DA:1803:A:C8	2.46	0.51
22:DA:1820:U:OP1	24:DC:177:ARG:HG2	2.10	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:2382:G:OP1	22:DA:2382:G:H3'	2.10	0.51
22:DA:2576:G:O2'	22:DA:2579:C:OP2	2.26	0.51
22:DA:2822:G:H2'	22:DA:2823:A:H5"	1.92	0.51
35:DN:117:ASP:O	35:DN:118:ARG:HB2	2.10	0.51
44:DW:52:GLY:HA3	44:DW:60:PHE:CZ	2.45	0.51
1:AA:501:C:H1'	1:AA:549:C:H1'	1.91	0.51
22:BA:1414:C:N3	22:BA:1415:U:H5	2.08	0.51
22:BA:1539:U:H2'	22:BA:1540:G:C8	2.45	0.51
22:BA:1754:A:C6	22:BA:1755:A:C6	2.99	0.51
22:BA:2345:G:N3	22:BA:2381:A:H2'	2.26	0.51
22:BA:2346:A:H4'	22:BA:2347:C:OP2	2.09	0.51
29:BH:85:GLY:HA2	29:BH:91:PHE:CE2	2.46	0.51
1:CA:1031:C:H4'	1:CA:1032:G:C2	2.45	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
2:CB:81:LYS:HG3	2:CB:91:PHE:CZ	2.46	0.51
17:CQ:60:GLU:HB3	17:CQ:76:VAL:HG23	1.93	0.51
22:DA:796:C:H2'	22:DA:797:G:C8	2.45	0.51
22:DA:1131:G:OP1	31:DJ:82:GLY:HA2	2.11	0.51
22:DA:1477:A:N6	22:DA:1514:G:O2'	2.44	0.51
27:DF:110:ARG:HH11	27:DF:137:ILE:C	2.19	0.51
32:DK:99:ILE:HG12	32:DK:115:ILE:HG23	1.92	0.51
38:DQ:76:TYR:CZ	38:DQ:80:ILE:HG13	2.46	0.51
41:DT:44:LYS:HE3	41:DT:55:VAL:HB	1.92	0.51
1:AA:9:G:H5'	5:AE:108:GLY:HA3	1.92	0.51
1:AA:1450:U:H2'	1:AA:1452:C:C5	2.46	0.51
10:AJ:10:LEU:HD23	10:AJ:96:VAL:HG11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:87:LYS:HA	11:AK:114:THR:HG22	1.92	0.51
17:AQ:47:HIS:HB2	17:AQ:71:LYS:HE3	1.93	0.51
22:BA:137:U:H2'	22:BA:140:C:C2	2.46	0.51
22:BA:357:C:H2'	22:BA:358:U:C6	2.45	0.51
22:BA:894:U:H2'	22:BA:895:U:C6	2.46	0.51
22:BA:1186:G:H5'	57:BA:3603:HOH:O	2.10	0.51
22:BA:1288:G:C4	22:BA:1327:A:C2	2.98	0.51
22:BA:1376:C:H3'	57:BA:3399:HOH:O	2.10	0.51
22:BA:1753:G:OP1	37:BP:93:ARG:HD3	2.11	0.51
22:BA:1999:C:OP1	22:BA:2723:C:O2'	2.26	0.51
22:BA:2856:A:N6	22:BA:2857:G:C6	2.79	0.51
28:BG:9:VAL:HG13	28:BG:50:LEU:HB2	1.93	0.51
29:BH:117:LEU:CD2	29:BH:121:VAL:CA	2.89	0.51
30:BI:59:ILE:HG22	30:BI:61:VAL:HG23	1.93	0.51
34:BM:47:GLU:OE2	34:BM:51:ARG:NE	2.44	0.51
1:CA:214:C:H2'	1:CA:215:C:H6	1.76	0.51
1:CA:636:U:H2'	1:CA:637:C:C6	2.46	0.51
3:CC:172:ARG:O	3:CC:174:PRO:HD3	2.09	0.51
4:CD:44:ARG:NE	4:CD:44:ARG:HA	2.25	0.51
20:CT:3:ASN:O	20:CT:5:LYS:N	2.43	0.51
22:DA:720:U:H2'	22:DA:721:A:C8	2.46	0.51
22:DA:832:U:OP1	33:DL:39:LYS:N	2.36	0.51
22:DA:1364:G:H5"	45:DX:3:ARG:NH1	2.26	0.51
22:DA:1468:U:H2'	22:DA:1522:A:N6	2.25	0.51
22:DA:2852:G:H2'	22:DA:2853:C:O4'	2.11	0.51
23:DB:25:U:H2'	23:DB:26:C:O4'	2.10	0.51
30:DI:46:THR:HG22	30:DI:51:LYS:HG3	1.93	0.51
1:AA:452:A:H3'	1:AA:452:A:H8	1.76	0.51
1:AA:981:U:O2'	14:AN:61:ARG:NE	2.44	0.51
1:AA:994:A:N1	1:AA:1047:G:H4'	2.26	0.51
1:AA:1202:U:H1'	14:AN:69:ARG:HD2	1.93	0.51
2:AB:126:PHE:CD2	2:AB:126:PHE:N	2.79	0.51
7:AG:116:MET:O	7:AG:120:LEU:HB2	2.11	0.51
13:AM:46:SER:O	13:AM:47:GLU:HB3	2.10	0.51
22:BA:1759:A:H2'	22:BA:1760:C:C6	2.46	0.51
29:BH:83:LYS:HA	29:BH:148:ALA:HA	1.93	0.51
31:BJ:49:ASP:OD1	31:BJ:121:LYS:NZ	2.43	0.51
1:CA:280:C:H4'	1:CA:281:G:OP2	2.11	0.51
1:CA:568:G:O6	12:CL:2:ALA:HB2	2.11	0.51
1:CA:684:U:O2'	11:CK:40:ASN:O	2.24	0.51
1:CA:805:C:H2'	1:CA:806:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1493:A:H8	1:CA:1493:A:OP2	1.94	0.51
5:CE:57:PRO:O	5:CE:60:ILE:HG13	2.11	0.51
16:CP:67:ILE:HG22	16:CP:68:SER:O	2.11	0.51
22:DA:1296:G:OP1	22:DA:2709:G:O2'	2.27	0.51
22:DA:1846:G:H5"	22:DA:1847:A:OP2	2.11	0.51
25:DD:38:LYS:HD2	25:DD:45:TYR:OH	2.11	0.51
29:DH:26:ALA:HA	29:DH:30:LEU:HB2	1.92	0.51
1:AA:591:U:H2'	1:AA:592:G:H8	1.76	0.50
1:AA:995:C:N3	1:AA:1046:A:O2'	2.37	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
2:AB:65:GLY:C	2:AB:66:LYS:HD3	2.36	0.50
9:AI:84:THR:HG21	9:AI:103:PHE:CB	2.41	0.50
22:BA:1812:U:H2'	22:BA:1813:G:H8	1.76	0.50
22:BA:2064:C:H2'	22:BA:2065:C:C6	2.46	0.50
22:BA:2261:C:OP1	44:BW:19:LYS:NZ	2.44	0.50
22:BA:2557:G:H2'	22:BA:2558:C:C6	2.46	0.50
24:BC:160:THR:O	24:BC:195:VAL:HG12	2.10	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
28:BG:149:ARG:CG	28:BG:149:ARG:HH11	2.24	0.50
29:BH:14:SER:OG	29:BH:17:ASP:OD1	2.29	0.50
29:BH:66:ASN:OD1	29:BH:138:VAL:HG21	2.11	0.50
33:BL:30:THR:O	33:BL:33:ARG:HG2	2.11	0.50
34:BM:49:ALA:HB1	34:BM:120:ALA:HB1	1.92	0.50
1:CA:503:C:OP1	12:CL:116:LYS:NZ	2.43	0.50
1:CA:677:U:H3	1:CA:713:G:H22	1.57	0.50
1:CA:931:C:H2'	1:CA:932:C:H6	1.76	0.50
4:CD:29:ASP:C	4:CD:31:LYS:N	2.69	0.50
5:CE:72:ILE:HD13	5:CE:145:GLU:CD	2.36	0.50
6:CF:16:GLU:C	6:CF:18:VAL:H	2.18	0.50
19:CS:55:ARG:HG3	19:CS:56:GLN:H	1.77	0.50
22:DA:121:G:H4'	22:DA:148:U:H2'	1.92	0.50
22:DA:1345:C:H5'	22:DA:1396:U:H5	1.75	0.50
22:DA:1676:A:H2'	22:DA:1677:A:O4'	2.12	0.50
22:DA:1895:C:H2'	22:DA:1896:G:H8	1.75	0.50
22:DA:2216:G:H2'	22:DA:2217:G:C8	2.46	0.50
23:DB:106:G:H2'	23:DB:107:G:O4'	2.11	0.50
25:DD:14:ILE:HG12	25:DD:24:VAL:HG21	1.93	0.50
39:DR:81:LYS:HD3	39:DR:81:LYS:N	2.27	0.50
1:AA:468:A:C2	1:AA:469:C:C4	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1032:G:H5'	1:AA:1033:G:OP2	2.11	0.50
14:AN:45:VAL:HG23	14:AN:46:LEU:H	1.76	0.50
22:BA:136:G:H1	22:BA:143:C:N4	2.08	0.50
22:BA:1721:G:O2'	22:BA:1739:A:N6	2.44	0.50
22:BA:1846:G:H2'	22:BA:1847:A:C8	2.45	0.50
22:BA:1946:U:H2'	22:BA:1947:C:C6	2.46	0.50
36:BO:51:ALA:HB3	36:BO:78:VAL:HG13	1.93	0.50
1:CA:227:G:H2'	1:CA:228:A:O4'	2.10	0.50
1:CA:1086:U:H4'	1:CA:1086:U:OP1	2.10	0.50
4:CD:98:LEU:HB2	4:CD:135:TYR:HB3	1.93	0.50
9:CI:76:ALA:HA	9:CI:79:ILE:HD12	1.92	0.50
10:CJ:49:PHE:O	10:CJ:65:TYR:N	2.35	0.50
16:CP:17:TYR:HE1	16:CP:41:PRO:HG3	1.76	0.50
19:CS:16:LEU:O	19:CS:20:GLU:HG2	2.10	0.50
20:CT:79:LEU:O	20:CT:83:ILE:HG23	2.12	0.50
22:DA:236:C:O2'	22:DA:431:U:H4'	2.11	0.50
25:DD:125:TRP:CG	25:DD:160:LYS:HB3	2.46	0.50
31:DJ:4:PHE:O	38:DQ:64:ARG:NH2	2.33	0.50
47:DZ:10:THR:HG22	47:DZ:54:MET:C	2.37	0.50
1:AA:340:U:H2'	1:AA:341:C:C6	2.46	0.50
1:AA:1060:U:H2'	1:AA:1061:G:H8	1.76	0.50
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.46	0.50
1:AA:1397:C:O2'	1:AA:1398:A:OP1	2.24	0.50
12:AL:24:LEU:CG	12:AL:25:GLU:H	2.13	0.50
14:AN:28:LYS:HG3	14:AN:29:ALA:N	2.26	0.50
14:AN:47:LYS:HD3	19:AS:13:LEU:HD21	1.93	0.50
22:BA:305:C:H2'	22:BA:306:U:C6	2.45	0.50
22:BA:337:C:H2'	22:BA:338:G:O4'	2.11	0.50
22:BA:869:G:H2'	22:BA:870:U:O4'	2.10	0.50
22:BA:1585:C:H2'	22:BA:1586:A:O4'	2.11	0.50
22:BA:1734:G:H2'	22:BA:1735:A:H8	1.76	0.50
22:BA:2040:G:H2'	22:BA:2041:U:O4'	2.11	0.50
22:BA:2128:G:OP2	53:B5:37:LYS:HE3	2.11	0.50
1:CA:32:A:H3'	1:CA:33:A:H8	1.74	0.50
1:CA:605:U:H2'	1:CA:606:G:C8	2.46	0.50
7:CG:136:LYS:HE2	7:CG:140:ASP:OD1	2.11	0.50
22:DA:236:C:H4'	22:DA:431:U:O2'	2.10	0.50
22:DA:933:A:H5'	22:DA:934:U:OP2	2.12	0.50
22:DA:1075:C:H2'	22:DA:1076:C:C6	2.45	0.50
22:DA:1779:U:C5	22:DA:1784:A:N7	2.80	0.50
22:DA:1973:G:C6	22:DA:1974:C:C4	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DH:5:LEU:HA	29:DH:36:ALA:HA	1.93	0.50
33:DL:135:ILE:HG22	33:DL:140:GLY:HA2	1.94	0.50
38:DQ:102:ASP:OD1	39:DR:2:TYR:OH	2.17	0.50
1:AA:71:A:H3'	1:AA:71:A:OP2	2.11	0.50
1:AA:237:G:H2'	1:AA:238:A:O4'	2.12	0.50
1:AA:579:A:H2'	1:AA:580:C:H6	1.76	0.50
1:AA:792:A:H4'	1:AA:793:U:O5'	2.11	0.50
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.46	0.50
1:AA:1504:G:OP2	1:AA:1507:A:O2'	2.24	0.50
2:AB:164:ILE:HG23	2:AB:165:ASP:H	1.75	0.50
7:AG:100:ALA:O	7:AG:104:ILE:HG13	2.11	0.50
11:AK:52:PHE:HB3	11:AK:56:ARG:HB3	1.93	0.50
22:BA:493:G:H2'	22:BA:494:G:O4'	2.11	0.50
22:BA:1425:G:O2'	22:BA:1426:G:H5'	2.11	0.50
22:BA:2683:C:H5"	37:BP:56:HIS:HB3	1.92	0.50
27:BF:158:THR:CG2	27:BF:160:ALA:H	2.25	0.50
35:BN:28:LEU:O	35:BN:32:GLU:N	2.44	0.50
42:BU:5:ILE:C	42:BU:6:ARG:HG2	2.37	0.50
1:CA:299:G:N2	1:CA:565:U:O2	2.44	0.50
1:CA:667:G:OP1	1:CA:732:C:O2'	2.27	0.50
1:CA:1232:U:H5"	9:CI:126:GLN:O	2.11	0.50
2:CB:213:TYR:HA	2:CB:216:ALA:HB3	1.93	0.50
8:CH:75:ILE:HA	8:CH:128:TYR:O	2.12	0.50
19:CS:56:GLN:CD	19:CS:57:HIS:H	2.19	0.50
21:CU:25:LYS:O	21:CU:29:LEU:HB2	2.11	0.50
22:DA:1297:C:O2'	22:DA:1302:A:N1	2.31	0.50
22:DA:1871:A:O2'	22:DA:1872:A:N7	2.44	0.50
29:DH:127:GLU:HG3	29:DH:145:ASN:HA	1.93	0.50
36:DO:71:ALA:O	36:DO:75:GLY:N	2.39	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
52:D4:30:GLU:HG3	52:D4:32:LYS:H	1.74	0.50
1:AA:39:G:N7	1:AA:547:A:H8	2.10	0.50
1:AA:108:G:C6	20:AT:10:ARG:HG2	2.46	0.50
1:AA:1048:G:O6	1:AA:1210:C:N4	2.44	0.50
1:AA:1243:C:H2'	1:AA:1244:G:C8	2.46	0.50
1:AA:1508:A:H2'	1:AA:1509:C:O4'	2.11	0.50
5:AE:136:VAL:O	5:AE:140:THR:OG1	2.29	0.50
9:AI:52:LEU:HA	9:AI:55:VAL:HG23	1.93	0.50
13:AM:85:CYS:SG	13:AM:87:ARG:HG3	2.52	0.50
22:BA:812:C:H4'	38:BQ:13:ARG:NH2	2.22	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1059:G:H3'	22:BA:1060:U:H2'	1.93	0.50
22:BA:1296:G:OP1	22:BA:2709:G:O2'	2.26	0.50
22:BA:1327:A:H2'	22:BA:1328:A:O4'	2.12	0.50
22:BA:2297:A:N1	22:BA:2321:U:H5	2.09	0.50
27:BF:60:ILE:HD13	27:BF:152:LEU:HD21	1.93	0.50
27:BF:158:THR:O	57:BF:201:HOH:O	2.18	0.50
41:BT:12:ARG:HH11	41:BT:12:ARG:HG3	1.77	0.50
1:CA:4:U:H5"	1:CA:5:U:OP1	2.11	0.50
1:CA:558:G:O5'	1:CA:558:G:H8	1.94	0.50
1:CA:581:G:OP1	15:CO:65:LYS:NZ	2.45	0.50
3:CC:77:ILE:HA	3:CC:84:VAL:HG23	1.92	0.50
4:CD:145:ILE:HD13	4:CD:178:MET:HB3	1.94	0.50
22:DA:323:C:H6	22:DA:1205:A:N1	2.09	0.50
22:DA:2544:G:H2'	22:DA:2545:G:C8	2.45	0.50
22:DA:2597:G:H2'	22:DA:2598:A:C8	2.47	0.50
38:DQ:76:TYR:OH	38:DQ:92:ARG:NH1	2.43	0.50
39:DR:42:ALA:HA	39:DR:46:GLU:HA	1.93	0.50
40:DS:79:GLY:H	40:DS:101:SER:HA	1.75	0.50
1:AA:374:A:H5"	1:AA:452:A:C2	2.47	0.50
1:AA:855:U:H2'	1:AA:856:C:C6	2.45	0.50
1:AA:1299:A:H2'	1:AA:1299:A:N3	2.27	0.50
2:AB:19:GLN:HG2	2:AB:190:ASN:OD1	2.11	0.50
2:AB:217:VAL:O	2:AB:221:VAL:HG23	2.11	0.50
17:AQ:21:ILE:HD13	17:AQ:48:ASP:OD1	2.11	0.50
22:BA:366:C:H2'	22:BA:367:G:O4'	2.12	0.50
22:BA:381:G:OP1	45:BX:18:ARG:HD3	2.12	0.50
22:BA:1613:G:H4'	50:B2:3:ARG:HD3	1.93	0.50
27:BF:33:LYS:HG2	27:BF:157:THR:HB	1.93	0.50
29:BH:80:ILE:O	29:BH:147:VAL:N	2.44	0.50
37:BP:62:ARG:HH21	37:BP:71:GLU:HG3	1.77	0.50
43:BV:51:GLN:OE1	43:BV:57:TYR:OH	2.29	0.50
49:B1:17:THR:HG21	49:B1:43:VAL:HG12	1.93	0.50
1:CA:186:C:O4'	20:CT:76:LYS:HD2	2.11	0.50
1:CA:302:G:O2'	1:CA:556:C:H5"	2.11	0.50
1:CA:1084:G:C5	1:CA:1085:U:C4	3.00	0.50
1:CA:1097:C:H2'	1:CA:1098:C:C6	2.46	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
3:CC:87:LEU:O	3:CC:91:VAL:HG23	2.11	0.50
22:DA:607:U:O4	22:DA:619:G:H2'	2.11	0.50
22:DA:655:A:O3'	22:DA:656:G:H8	1.95	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1434:A:H2'	22:DA:1435:G:C8	2.47	0.50
22:DA:1721:G:H2'	22:DA:1738:G:H22	1.76	0.50
24:DC:141:VAL:HG11	24:DC:190:ALA:HB1	1.92	0.50
26:DE:48:THR:O	26:DE:52:VAL:HG23	2.12	0.50
34:DM:56:ALA:C	34:DM:58:LYS:H	2.19	0.50
1:AA:693:G:P	11:AK:127:ARG:HH22	2.33	0.50
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.46	0.50
4:AD:151:LYS:CA	4:AD:178:MET:HE1	2.42	0.50
7:AG:137:LYS:O	7:AG:141:VAL:HG23	2.11	0.50
22:BA:2405:G:O2'	22:BA:2406:A:OP1	2.28	0.50
22:BA:2461:A:H2'	22:BA:2462:C:H6	1.77	0.50
23:BB:60:C:N4	57:BB:303:HOH:O	2.44	0.50
25:BD:61:THR:OG1	25:BD:63:PRO:HD2	2.12	0.50
28:BG:9:VAL:HG21	28:BG:73:ASN:HA	1.94	0.50
51:B3:63:PRO:HG2	51:B3:64:TYR:CD2	2.47	0.50
1:CA:495:A:C2	1:CA:496:A:C6	2.99	0.50
1:CA:750:C:H4'	15:CO:21:ASP:HA	1.94	0.50
5:CE:138:ARG:H	5:CE:141:ILE:HD13	1.77	0.50
22:DA:242:G:N7	51:D3:5:LYS:HG2	2.27	0.50
22:DA:289:G:H2'	22:DA:290:U:O4'	2.12	0.50
22:DA:422:A:OP2	57:DA:3558:HOH:O	2.20	0.50
22:DA:457:A:N1	22:DA:470:A:H5"	2.27	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
34:DM:17:ASN:OD1	34:DM:95:LEU:HB3	2.11	0.50
1:AA:668:G:H2'	1:AA:669:G:C8	2.47	0.50
1:AA:702:A:N6	22:BA:1846:G:H4'	2.26	0.50
1:AA:1202:U:C2	14:AN:82:ILE:HG21	2.47	0.50
1:AA:1236:A:H2'	1:AA:1237:C:C6	2.46	0.50
1:AA:1442:G:H2'	1:AA:1443:C:C6	2.47	0.50
2:AB:20:THR:HB	2:AB:37:LYS:O	2.12	0.50
22:BA:157:C:H2'	22:BA:158:U:O4'	2.12	0.50
22:BA:165:A:H2'	22:BA:166:U:O4'	2.12	0.50
22:BA:636:G:C6	33:BL:111:ILE:HD11	2.47	0.50
22:BA:1440:U:H2'	22:BA:1441:G:H8	1.77	0.50
22:BA:2056:G:H2'	22:BA:2056:G:N3	2.26	0.50
22:BA:2070:A:H2'	22:BA:2071:A:O4'	2.12	0.50
24:BC:251:GLN:HG3	24:BC:252:THR:O	2.10	0.50
31:BJ:98:GLU:CD	31:BJ:126:ALA:HB2	2.36	0.50
40:BS:69:LEU:HG	40:BS:107:VAL:HG22	1.93	0.50
51:B3:62:LEU:HB3	51:B3:65:ALA:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:28:A:OP1	4:CD:73:ARG:NH2	2.44	0.50
1:CA:73:C:H1'	1:CA:74:A:H5'	1.94	0.50
1:CA:821:G:H2'	1:CA:822:U:H6	1.76	0.50
1:CA:1478:U:H2'	1:CA:1479:C:H6	1.77	0.50
5:CE:68:ARG:O	5:CE:71:MET:HE3	2.12	0.50
6:CF:91:ARG:HG2	6:CF:93:LYS:NZ	2.27	0.50
7:CG:125:SER:C	7:CG:127:ALA:H	2.18	0.50
8:CH:87:LYS:HG3	8:CH:91:GLU:HB3	1.93	0.50
13:CM:11:ASP:HA	13:CM:45:ILE:HD13	1.94	0.50
16:CP:38:PHE:CZ	16:CP:51:ARG:HB3	2.46	0.50
22:DA:631:A:H8	22:DA:631:A:OP1	1.94	0.50
22:DA:1877:A:H2'	22:DA:1878:G:C8	2.47	0.50
24:DC:29:PRO:HG3	24:DC:63:ARG:CZ	2.42	0.50
26:DE:149:ILE:HG23	26:DE:188:MET:HG2	1.93	0.50
33:DL:90:VAL:N	33:DL:121:THR:O	2.45	0.50
34:DM:21:ALA:HB1	34:DM:100:LYS:HG2	1.93	0.50
42:DU:28:VAL:HA	42:DU:34:VAL:HG12	1.93	0.50
1:AA:130:A:N7	17:AQ:65:ARG:HB2	2.26	0.50
1:AA:1314:C:H41	19:AS:4:SER:HA	1.77	0.50
5:AE:34:THR:HG22	5:AE:52:LYS:HB3	1.94	0.50
9:AI:40:GLY:HA2	9:AI:45:ARG:HB2	1.94	0.50
12:AL:74:LEU:HD21	12:AL:104:CYS:HA	1.93	0.50
19:AS:37:ARG:O	19:AS:70:LYS:HD2	2.11	0.50
22:BA:18:U:O4	57:BA:3205:HOH:O	2.19	0.50
22:BA:30:G:H2'	22:BA:31:C:H6	1.76	0.50
22:BA:198:C:H4'	22:BA:2243:U:O2'	2.12	0.50
22:BA:545:U:H2'	22:BA:546:U:O3'	2.11	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
22:BA:2014:A:H2'	22:BA:2015:A:C8	2.47	0.50
27:BF:25:VAL:O	27:BF:28:VAL:HG12	2.12	0.50
38:BQ:102:ASP:C	38:BQ:104:VAL:H	2.20	0.50
40:BS:79:GLY:CA	40:BS:102:HIS:CE1	2.94	0.50
48:B0:11:SER:O	48:B0:15:MET:HG3	2.11	0.50
49:B1:4:GLY:C	49:B1:6:ARG:H	2.20	0.50
2:CB:72:THR:HA	2:CB:93:ASN:O	2.12	0.50
4:CD:14:ARG:HG2	4:CD:56:ARG:HH21	1.75	0.50
10:CJ:28:THR:HG21	10:CJ:90:LEU:HD12	1.93	0.50
10:CJ:52:LEU:HD22	10:CJ:59:LYS:HA	1.94	0.50
14:CN:23:LYS:HG3	14:CN:24:ARG:HG3	1.94	0.50
16:CP:72:ALA:HA	16:CP:75:ILE:HD12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:189:G:P	45:DX:26:LYS:HE2	2.51	0.50
22:DA:311:A:C2	22:DA:330:A:H3'	2.46	0.50
22:DA:624:C:O2'	22:DA:657:U:H5"	2.12	0.50
22:DA:632:A:H5"	33:DL:68:SER:HB2	1.92	0.50
22:DA:846:U:O2'	22:DA:847:U:O5'	2.29	0.50
22:DA:2780:G:P	31:DJ:120:ARG:HE	2.35	0.50
24:DC:154:LEU:HD13	24:DC:176:LEU:HD21	1.93	0.50
29:DH:44:ILE:O	29:DH:48:GLU:HB2	2.12	0.50
31:DJ:89:PHE:CE2	31:DJ:100:VAL:HG11	2.47	0.50
32:DK:113:MET:SD	32:DK:116:ILE:HD11	2.52	0.50
38:DQ:98:ILE:HG22	38:DQ:106:PHE:HB2	1.94	0.50
1:AA:147:G:H2'	1:AA:148:G:C8	2.47	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
10:AJ:21:ALA:HA	10:AJ:24:GLU:HB3	1.94	0.49
10:AJ:67:ILE:HG13	14:AN:96:LEU:HD13	1.94	0.49
22:BA:2092:U:OP2	29:BH:27:ARG:CD	2.60	0.49
24:BC:53:HIS:NE2	24:BC:219:THR:HG23	2.27	0.49
29:BH:91:PHE:HB3	1:CA:55:A:C4	2.47	0.49
30:BI:34:ASN:HB3	30:BI:37:GLU:H	1.77	0.49
33:BL:111:ILE:H	33:BL:111:ILE:CD1	2.24	0.49
42:BU:86:ARG:HG2	42:BU:95:PHE:CD2	2.47	0.49
52:B4:11:CYS:HB3	52:B4:33:HIS:HE1	1.76	0.49
1:CA:502:A:H2'	1:CA:503:C:O4'	2.12	0.49
2:CB:223:GLU:OE2	2:CB:226:SER:HA	2.12	0.49
5:CE:82:GLN:OE1	5:CE:149:SER:HA	2.12	0.49
8:CH:86:TYR:C	8:CH:87:LYS:HD2	2.37	0.49
8:CH:89:LYS:HG3	8:CH:90:ASP:N	2.27	0.49
15:CO:6:GLU:O	15:CO:10:LYS:N	2.43	0.49
22:DA:118:A:C8	22:DA:119:A:C8	3.00	0.49
22:DA:1240:U:O2'	22:DA:1241:A:O5'	2.28	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
41:DT:37:ASP:OD2	41:DT:38:ALA:N	2.42	0.49
42:DU:28:VAL:HB	42:DU:34:VAL:HG12	1.94	0.49
1:AA:1071:C:H2'	1:AA:1072:G:H8	1.76	0.49
2:AB:17:GLY:HA2	2:AB:41:ILE:HG23	1.93	0.49
3:AC:138:VAL:HA	3:AC:149:ILE:HD13	1.93	0.49
5:AE:80:THR:HA	5:AE:122:ASN:HD21	1.77	0.49
11:AK:52:PHE:CB	11:AK:56:ARG:HB3	2.43	0.49
22:BA:78:U:H2'	22:BA:79:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1098:A:H5'	22:BA:1099:G:OP2	2.12	0.49
22:BA:1820:U:OP1	24:BC:177:ARG:NH2	2.46	0.49
27:BF:34:ILE:HG13	27:BF:96:MET:HG3	1.94	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
46:BY:15:ASN:O	46:BY:19:LEU:HG	2.12	0.49
52:B4:36:ARG:HG2	52:B4:37:GLN:N	2.27	0.49
1:CA:624:C:H2'	1:CA:625:U:O4'	2.13	0.49
3:CC:90:VAL:O	3:CC:94:ILE:HG13	2.11	0.49
15:CO:10:LYS:O	15:CO:14:GLU:HG3	2.12	0.49
22:DA:747:U:O2	22:DA:2014:A:H1'	2.12	0.49
22:DA:1097:U:H3'	22:DA:1098:A:O4'	2.12	0.49
22:DA:1130:U:C2	22:DA:2025:C:H5"	2.47	0.49
22:DA:1665:A:H5"	32:DK:66:LYS:HG3	1.93	0.49
27:DF:136:ILE:HG23	27:DF:141:ILE:HG22	1.94	0.49
29:DH:86:ASP:C	29:DH:88:GLY:H	2.19	0.49
43:DV:30:ILE:HG13	43:DV:40:ILE:HG13	1.94	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:BA:521:U:H2'	22:BA:522:A:C8	2.47	0.49
22:BA:1731:G:C6	22:BA:1733:G:C5	3.00	0.49
22:BA:1789:A:P	24:BC:221:ARG:HH11	2.35	0.49
22:BA:2079:U:H4'	22:BA:2433:A:H2	1.78	0.49
51:B3:27:ALA:O	51:B3:28:ASN:HB2	2.11	0.49
11:CK:43:GLY:HA3	11:CK:74:VAL:HG12	1.93	0.49
16:CP:8:ARG:HB3	16:CP:28:ARG:NH1	2.27	0.49
22:DA:931:U:O4	22:DA:1166:G:N2	2.45	0.49
22:DA:1058:U:H2'	22:DA:1059:G:C8	2.47	0.49
22:DA:1184:U:OP1	47:DZ:30:ARG:HD3	2.12	0.49
22:DA:2718:G:H5'	37:DP:98:TYR:CD1	2.47	0.49
29:DH:5:LEU:HD11	29:DH:13:GLY:HA2	1.93	0.49
37:DP:16:ASP:OD2	37:DP:16:ASP:N	2.44	0.49
1:AA:22:G:H4'	1:AA:885:G:C8	2.47	0.49
1:AA:532:A:N7	3:AC:193:TYR:HB3	2.26	0.49
1:AA:763:G:H2'	1:AA:764:C:H6	1.77	0.49
1:AA:1258:G:H2'	1:AA:1259:C:C6	2.48	0.49
1:AA:1277:C:C2'	1:AA:1279:G:H8	2.25	0.49
1:AA:1435:G:H2'	1:AA:1436:U:H6	1.75	0.49
2:AB:50:PHE:HA	2:AB:213:TYR:OH	2.12	0.49
3:AC:142:MET:HE1	3:AC:148:GLY:HA2	1.94	0.49
4:AD:109:ALA:N	4:AD:113:GLU:OE2	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:91:ARG:HG2	6:AF:93:LYS:HD3	1.94	0.49
10:AJ:80:THR:HB	10:AJ:83:THR:H	1.77	0.49
11:AK:111:THR:HG23	21:AU:5:LYS:HB3	1.95	0.49
22:BA:400:G:N7	45:BX:57:ARG:NH1	2.59	0.49
22:BA:622:G:H2'	22:BA:623:C:C6	2.47	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:BA:2643:G:H2'	22:BA:2644:G:O4'	2.13	0.49
23:BB:112:G:H2'	23:BB:113:C:C6	2.47	0.49
29:BH:86:ASP:O	29:BH:87:GLU:HB2	2.11	0.49
29:BH:99:ILE:O	29:BH:99:ILE:HG22	2.12	0.49
41:BT:18:GLU:CD	41:BT:18:GLU:H	2.18	0.49
1:CA:392:C:H2'	1:CA:393:A:C8	2.46	0.49
5:CE:36:LEU:HD21	5:CE:137:VAL:HG11	1.93	0.49
5:CE:150:PRO:O	5:CE:153:VAL:HG22	2.12	0.49
9:CI:99:ARG:HG2	9:CI:104:VAL:HG21	1.95	0.49
14:CN:36:ALA:HB2	14:CN:41:ARG:HG3	1.95	0.49
17:CQ:8:LEU:HD22	17:CQ:73:TRP:CH2	2.47	0.49
18:CR:71:THR:OG1	18:CR:72:ASP:N	2.45	0.49
22:DA:20:C:H2'	22:DA:21:A:C8	2.47	0.49
22:DA:320:A:H2'	26:DE:131:THR:HG21	1.94	0.49
22:DA:370:G:O2'	22:DA:423:A:H3'	2.12	0.49
22:DA:562:U:H2'	22:DA:572:A:O4'	2.12	0.49
22:DA:586:A:N1	22:DA:809:G:O2'	2.38	0.49
22:DA:813:U:H2'	22:DA:814:C:C6	2.48	0.49
22:DA:1011:G:OP1	38:DQ:75:SER:HB2	2.12	0.49
22:DA:1810:A:H2'	22:DA:1811:G:O4'	2.13	0.49
22:DA:2267:A:H5"	22:DA:2268:A:C5'	2.43	0.49
22:DA:2376:A:H2'	22:DA:2377:A:O4'	2.11	0.49
26:DE:147:LEU:HB3	26:DE:186:VAL:HG13	1.94	0.49
27:DF:38:MET:HB2	27:DF:57:LEU:HD11	1.95	0.49
28:DG:8:PRO:HG3	28:DG:51:THR:HG22	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
37:DP:48:ILE:HD13	37:DP:62:ARG:HB2	1.94	0.49
1:AA:1096:C:HO2'	1:AA:1170:A:HO2'	1.55	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
4:AD:13:ARG:HH12	4:AD:37:ALA:C	2.20	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:20:HIS:O	20:AT:24:ARG:HG2	2.12	0.49
22:BA:300:A:OP2	42:BU:97:LYS:NZ	2.45	0.49
22:BA:659:G:H4'	26:BE:95:LYS:HD3	1.93	0.49
22:BA:714:U:H2'	22:BA:716:A:N7	2.27	0.49
22:BA:749:A:H4'	22:BA:1271:G:N3	2.28	0.49
22:BA:1234:U:H2'	22:BA:1235:G:O4'	2.13	0.49
22:BA:1357:C:H2'	22:BA:1358:G:O4'	2.12	0.49
22:BA:2649:C:H2'	22:BA:2650:U:C6	2.48	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
1:CA:312:C:H2'	1:CA:313:A:C8	2.47	0.49
1:CA:401:C:OP2	4:CD:70:ARG:HD3	2.13	0.49
1:CA:532:A:N6	3:CC:193:TYR:HD2	2.10	0.49
1:CA:949:A:N7	13:CM:105:ASN:ND2	2.60	0.49
2:CB:72:THR:HG22	2:CB:95:ARG:NH1	2.28	0.49
7:CG:57:SER:HB3	7:CG:60:GLU:HG3	1.93	0.49
9:CI:10:GLY:HA2	9:CI:81:HIS:ND1	2.28	0.49
20:CT:44:LYS:NZ	20:CT:86:LEU:O	2.36	0.49
22:DA:1563:U:H2'	22:DA:1564:C:H6	1.77	0.49
22:DA:1751:U:H2'	22:DA:1752:C:C6	2.47	0.49
22:DA:2293:G:H2'	22:DA:2294:G:O4'	2.12	0.49
22:DA:2718:G:H5'	37:DP:98:TYR:HD1	1.78	0.49
22:DA:2834:G:H2'	22:DA:2879:A:N6	2.28	0.49
39:DR:49:ILE:HG22	39:DR:54:VAL:N	2.28	0.49
46:DY:9:LYS:HB3	46:DY:12:GLU:HG2	1.95	0.49
1:AA:1118:U:O3'	9:AI:85:ARG:NH2	2.45	0.49
1:AA:1141:C:O2'	1:AA:1142:G:H8	1.96	0.49
1:AA:1219:A:H2'	1:AA:1220:G:C8	2.47	0.49
4:AD:105:MET:HE2	4:AD:171:LEU:HB2	1.95	0.49
19:AS:4:SER:O	19:AS:6:LYS:N	2.46	0.49
22:BA:1717:A:H2'	22:BA:1718:G:O4'	2.12	0.49
31:BJ:7:LYS:O	31:BJ:11:VAL:HG23	2.13	0.49
32:BK:63:VAL:HG12	32:BK:107:LEU:HD21	1.94	0.49
39:BR:3:ALA:HB3	39:BR:59:ILE:HD11	1.93	0.49
41:BT:56:GLU:HB2	41:BT:88:LYS:HA	1.95	0.49
1:CA:206:C:H2'	1:CA:207:C:H4'	1.94	0.49
1:CA:642:A:N3	8:CH:105:SER:OG	2.32	0.49
1:CA:1060:U:H2'	1:CA:1061:G:C8	2.48	0.49
1:CA:1096:C:H2'	1:CA:1097:C:C6	2.47	0.49
1:CA:1263:C:H2'	1:CA:1264:U:C6	2.47	0.49
8:CH:113:ASP:OD1	8:CH:114:ARG:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:14:HIS:HB2	13:CM:17:ILE:CD1	2.43	0.49
13:CM:114:LYS:HB2	13:CM:115:PRO:HD3	1.93	0.49
22:DA:1269:A:C6	22:DA:1270:C:N4	2.81	0.49
22:DA:1599:U:P	41:DT:40:LYS:HD2	2.53	0.49
22:DA:1916:A:H2'	22:DA:1917:U:O4'	2.13	0.49
22:DA:2369:A:H2'	22:DA:2370:G:O4'	2.13	0.49
30:DI:4:LYS:HD2	30:DI:5:VAL:H	1.77	0.49
1:AA:921:U:H2'	1:AA:922:G:O4'	2.13	0.49
1:AA:1053:G:N7	1:AA:1199:U:H3'	2.27	0.49
1:AA:1253:G:H2'	1:AA:1254:A:H8	1.77	0.49
22:BA:2462:C:H2'	22:BA:2463:C:H6	1.78	0.49
22:BA:2748:A:N1	57:BA:3815:HOH:O	2.35	0.49
24:BC:145:GLU:HG2	24:BC:151:GLY:H	1.77	0.49
27:BF:36:LEU:HD22	27:BF:91:LEU:HD11	1.95	0.49
31:BJ:78:THR:OG1	31:BJ:80:HIS:HB2	2.13	0.49
1:CA:34:C:H2'	1:CA:35:G:C8	2.48	0.49
1:CA:81:A:H2'	1:CA:82:G:C8	2.47	0.49
1:CA:714:G:H21	1:CA:777:A:H1'	1.77	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
11:CK:14:LYS:HD2	11:CK:14:LYS:C	2.38	0.49
19:CS:36:ARG:HA	19:CS:71:LEU:HB2	1.93	0.49
22:DA:69:C:HO2'	22:DA:73:A:HO2'	1.59	0.49
22:DA:973:A:H5"	39:DR:81:LYS:HG3	1.95	0.49
22:DA:1019:U:O2'	22:DA:1021:A:N7	2.37	0.49
22:DA:1628:G:H21	22:DA:2699:C:P	2.35	0.49
22:DA:2747:G:O6	22:DA:2755:C:H5"	2.11	0.49
37:DP:37:LYS:NZ	37:DP:39:ARG:HD2	2.28	0.49
47:DZ:9:GLN:HB3	47:DZ:32:ILE:HA	1.95	0.49
51:D3:7:VAL:HB	51:D3:61:CYS:HB3	1.93	0.49
1:AA:203:G:H5'	1:AA:468:A:H8	1.77	0.49
1:AA:624:C:H4'	16:AP:11:ALA:HB2	1.94	0.49
1:AA:718:A:H5'	11:AK:119:ASN:HB2	1.94	0.49
1:AA:1380:U:C4	7:AG:3:ARG:HD3	2.47	0.49
1:AA:1538:C:C2'	1:AA:1539:C:H5'	2.43	0.49
4:AD:170:TRP:CG	4:AD:186:PRO:HG3	2.47	0.49
22:BA:66:C:H2'	22:BA:67:U:C6	2.47	0.49
22:BA:305:C:H2'	22:BA:306:U:H6	1.78	0.49
22:BA:417:C:H2'	22:BA:418:C:C6	2.47	0.49
22:BA:538:A:O2'	31:BJ:8:PRO:HD2	2.13	0.49
22:BA:1199:U:H2'	22:BA:1200:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1747:U:H2'	22:BA:1748:C:C6	2.47	0.49
22:BA:1779:U:C5	22:BA:1784:A:N7	2.80	0.49
22:BA:2033:A:H4'	22:BA:2034:U:OP1	2.13	0.49
23:BB:14:U:O2	23:BB:107:G:H4'	2.13	0.49
27:BF:44:ILE:HG22	27:BF:83:TYR:CZ	2.48	0.49
31:BJ:59:ALA:C	31:BJ:61:LYS:H	2.21	0.49
33:BL:95:LEU:O	33:BL:100:ILE:HG23	2.13	0.49
36:BO:24:THR:HG22	36:BO:42:PRO:HD3	1.95	0.49
1:CA:929:G:H5"	1:CA:1535:C:C5'	2.43	0.49
2:CB:57:LEU:O	2:CB:60:ILE:HG13	2.13	0.49
2:CB:151:ILE:HG13	2:CB:154:MET:HE3	1.94	0.49
6:CF:13:ASP:C	6:CF:15:SER:H	2.19	0.49
16:CP:6:LEU:HD12	16:CP:71:VAL:HG23	1.95	0.49
22:DA:790:U:N3	22:DA:794:A:O2'	2.45	0.49
22:DA:1264:A:H5'	48:D0:8:PRO:HG2	1.93	0.49
22:DA:1688:U:O2	22:DA:1700:A:H8	1.95	0.49
22:DA:1861:G:N2	22:DA:1882:U:H1'	2.27	0.49
24:DC:131:PRO:HB2	24:DC:133:ARG:HG2	1.95	0.49
24:DC:141:VAL:CG1	24:DC:190:ALA:HB1	2.43	0.49
35:DN:2:ARG:HG3	35:DN:3:HIS:N	2.28	0.49
35:DN:90:ARG:HG2	35:DN:92:GLY:O	2.12	0.49
37:DP:93:ARG:O	37:DP:94:LYS:HB2	2.12	0.49
1:AA:483:C:O2	16:AP:13:LYS:NZ	2.45	0.49
2:AB:87:CYS:HB2	2:AB:89:GLN:NE2	2.27	0.49
2:AB:126:PHE:N	2:AB:126:PHE:HD2	2.10	0.49
22:BA:484:C:H2'	22:BA:485:C:H6	1.78	0.49
22:BA:623:C:H2'	22:BA:624:C:C6	2.48	0.49
22:BA:946:C:H2'	22:BA:947:A:H8	1.78	0.49
22:BA:998:C:P	38:BQ:92:ARG:HH21	2.35	0.49
22:BA:2079:U:H4'	22:BA:2433:A:C2	2.48	0.49
22:BA:2508:G:HO2'	22:BA:2554:U:HO2'	1.61	0.49
22:BA:2619:C:H2'	22:BA:2620:C:H6	1.78	0.49
1:CA:972:C:H4'	10:CJ:59:LYS:CG	2.43	0.49
3:CC:151:VAL:HG12	3:CC:200:VAL:HB	1.94	0.49
10:CJ:19:ASP:OD2	10:CJ:72:ARG:NH2	2.46	0.49
10:CJ:63:ASP:OD1	14:CN:85:ARG:NH1	2.41	0.49
12:CL:22:PRO:O	12:CL:24:LEU:N	2.44	0.49
20:CT:78:ASN:O	20:CT:82:GLN:HG2	2.13	0.49
22:DA:680:C:H2'	22:DA:681:G:C8	2.48	0.49
22:DA:697:G:H2'	22:DA:698:C:C6	2.48	0.49
22:DA:971:G:H2'	22:DA:972:A:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:DB:38:C:H2'	23:DB:39:A:O4'	2.12	0.49
29:DH:21:VAL:CG2	29:DH:22:LYS:N	2.76	0.49
30:DI:103:ARG:O	30:DI:107:GLN:HB2	2.12	0.49
1:AA:73:C:O2'	1:AA:74:A:H8	1.96	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
2:AB:33:GLY:HA3	2:AB:40:ILE:N	2.27	0.49
2:AB:151:ILE:HG23	2:AB:152:LYS:H	1.78	0.49
2:AB:164:ILE:O	2:AB:186:ILE:HG12	2.12	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
20:AT:71:LYS:HA	20:AT:74:ARG:NH2	2.27	0.49
21:AU:19:PHE:O	21:AU:22:SER:HB3	2.13	0.49
22:BA:751:A:H5'	40:BS:90:LYS:HA	1.95	0.49
22:BA:1802:A:N1	22:BA:1822:C:H1'	2.28	0.49
22:BA:2330:G:O3'	44:BW:44:LYS:HE3	2.12	0.49
22:BA:2654:A:N1	22:BA:2665:A:H5"	2.28	0.49
24:BC:17:VAL:N	24:BC:204:VAL:HG22	2.28	0.49
25:BD:133:THR:HG23	25:BD:134:HIS:CD2	2.47	0.49
28:BG:6:LYS:O	28:BG:8:PRO:HD3	2.13	0.49
29:BH:121:VAL:H	29:BH:122:LEU:HB2	1.77	0.49
33:BL:29:LYS:C	33:BL:31:GLY:H	2.19	0.49
1:CA:19:A:H2'	1:CA:20:U:H6	1.78	0.49
1:CA:136:C:H2'	1:CA:137:U:C6	2.48	0.49
1:CA:552:U:O2'	12:CL:83:ARG:O	2.29	0.49
2:CB:23:TRP:O	2:CB:23:TRP:CG	2.66	0.49
9:CI:19:VAL:HG11	9:CI:83:ILE:HA	1.94	0.49
17:CQ:8:LEU:HD23	17:CQ:25:ILE:HD12	1.95	0.49
22:DA:232:G:N1	22:DA:420:C:OP1	2.35	0.49
22:DA:309:A:H4'	42:DU:16:GLY:HA2	1.95	0.49
22:DA:1926:U:H2'	22:DA:1928:A:N7	2.28	0.49
25:DD:133:THR:HG23	25:DD:134:HIS:N	2.27	0.49
28:DG:4:VAL:HG12	28:DG:69:ARG:HG2	1.95	0.49
28:DG:158:LYS:O	28:DG:160:LYS:N	2.46	0.49
30:DI:97:LYS:N	30:DI:97:LYS:HD2	2.27	0.49
32:DK:103:VAL:O	32:DK:122:VAL:HB	2.13	0.49
39:DR:19:THR:HA	39:DR:96:VAL:O	2.13	0.49
1:AA:71:A:N6	1:AA:100:G:N7	2.61	0.48
1:AA:1086:U:O2'	1:AA:1087:G:H5'	2.13	0.48
10:AJ:32:THR:OG1	10:AJ:33:GLY:N	2.46	0.48
12:AL:63:VAL:HG21	12:AL:95:TYR:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:52:LEU:O	16:AP:54:LEU:N	2.46	0.48
22:BA:528:A:C8	22:BA:528:A:C3'	2.96	0.48
26:BE:18:THR:HA	26:BE:106:LYS:HG2	1.95	0.48
38:BQ:76:TYR:CZ	38:BQ:80:ILE:HG13	2.48	0.48
46:BY:20:ASN:O	46:BY:24:GLU:HB2	2.12	0.48
48:B0:46:ASP:O	48:B0:53:LYS:HE3	2.13	0.48
1:CA:890:G:O2'	1:CA:891:U:OP2	2.30	0.48
2:CB:99:GLY:O	2:CB:101:LEU:N	2.46	0.48
3:CC:57:ILE:HG13	3:CC:66:VAL:HG22	1.94	0.48
3:CC:155:GLY:HA2	3:CC:163:ALA:HB1	1.94	0.48
5:CE:99:ALA:O	5:CE:101:GLU:N	2.46	0.48
22:DA:1668:A:H4'	22:DA:1669:A:O5'	2.13	0.48
22:DA:2038:G:H2'	22:DA:2039:U:O4'	2.13	0.48
22:DA:2131:U:H5'	22:DA:2132:U:H5"	1.94	0.48
22:DA:2241:A:H2'	22:DA:2242:G:C8	2.48	0.48
29:DH:72:ILE:O	29:DH:141:LYS:O	2.30	0.48
31:DJ:34:ARG:O	31:DJ:39:LYS:HB2	2.11	0.48
34:DM:42:THR:HA	34:DM:93:VAL:HG12	1.95	0.48
45:DX:49:LEU:HD11	45:DX:68:LEU:HD21	1.95	0.48
1:AA:537:G:H2'	1:AA:538:G:C8	2.48	0.48
1:AA:682:G:H2'	1:AA:683:G:H8	1.78	0.48
1:AA:1063:C:H2'	1:AA:1064:G:C8	2.48	0.48
2:AB:23:TRP:CZ3	2:AB:25:PRO:HA	2.48	0.48
2:AB:154:MET:O	2:AB:156:GLY:N	2.37	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
6:AF:53:LYS:O	6:AF:54:LEU:HB3	2.12	0.48
14:AN:13:ARG:O	14:AN:17:ALA:HB2	2.13	0.48
22:BA:616:A:H4'	26:BE:101:TYR:CE2	2.48	0.48
22:BA:1074:G:H2'	22:BA:1075:C:H5'	1.95	0.48
22:BA:1410:G:N7	57:BA:3628:HOH:O	2.35	0.48
22:BA:1508:A:H4'	22:BA:1508:A:OP1	2.13	0.48
22:BA:2462:C:H2'	22:BA:2463:C:C6	2.48	0.48
57:BA:3785:HOH:O	31:BJ:39:LYS:HE3	2.12	0.48
25:BD:125:TRP:CE3	25:BD:160:LYS:HD3	2.48	0.48
29:BH:139:PHE:O	29:BH:140:ALA:HB2	2.14	0.48
30:BI:122:ILE:HG23	30:BI:125:MET:SD	2.53	0.48
1:CA:243:A:H4'	1:CA:244:U:H5"	1.95	0.48
1:CA:605:U:H2'	1:CA:606:G:H8	1.78	0.48
1:CA:1101:A:N6	2:CB:102:THR:HG21	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1490:U:H2'	1:CA:1491:G:C8	2.49	0.48
2:CB:87:CYS:O	2:CB:89:GLN:N	2.41	0.48
5:CE:96:MET:HE3	5:CE:96:MET:HB3	1.69	0.48
7:CG:121:ALA:HA	7:CG:124:LEU:HB2	1.95	0.48
8:CH:40:LEU:O	8:CH:45:PHE:HB2	2.12	0.48
8:CH:113:ASP:OD2	8:CH:117:ARG:NH2	2.46	0.48
18:CR:35:GLU:HB2	21:CU:19:PHE:HZ	1.76	0.48
22:DA:184:C:H2'	22:DA:185:G:C8	2.47	0.48
22:DA:760:G:H2'	22:DA:761:A:O4'	2.12	0.48
22:DA:1246:A:O2'	26:DE:40:ARG:NH2	2.46	0.48
22:DA:1874:C:H3'	22:DA:1875:G:C8	2.47	0.48
24:DC:76:ALA:HB2	24:DC:96:TYR:CD2	2.49	0.48
26:DE:19:PHE:HB3	26:DE:113:VAL:HG21	1.94	0.48
1:AA:552:U:H2'	1:AA:553:A:H8	1.79	0.48
1:AA:992:U:H4'	1:AA:993:G:O5'	2.12	0.48
5:AE:137:VAL:O	5:AE:138:ARG:HB2	2.13	0.48
10:AJ:52:LEU:HD22	10:AJ:62:ARG:HG2	1.94	0.48
10:AJ:80:THR:HB	10:AJ:83:THR:HB	1.95	0.48
12:AL:22:PRO:C	12:AL:24:LEU:N	2.72	0.48
12:AL:51:LYS:HD3	12:AL:51:LYS:N	2.28	0.48
22:BA:712:G:C2'	22:BA:713:G:H5'	2.44	0.48
22:BA:790:U:O2'	22:BA:791:C:O5'	2.28	0.48
22:BA:1444:G:H2'	22:BA:1445:G:H8	1.75	0.48
22:BA:2267:A:H5"	22:BA:2268:A:C5'	2.43	0.48
22:BA:2474:U:H5"	22:BA:2475:C:OP2	2.14	0.48
31:BJ:74:TYR:CD1	31:BJ:92:MET:HG3	2.49	0.48
1:CA:211:G:N3	1:CA:211:G:H2'	2.29	0.48
1:CA:476:U:O2'	1:CA:477:C:H5'	2.13	0.48
1:CA:515:G:H2'	1:CA:516:U:O4'	2.13	0.48
5:CE:45:ARG:HA	5:CE:72:ILE:O	2.13	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
16:CP:6:LEU:HD23	16:CP:17:TYR:CG	2.48	0.48
16:CP:21:VAL:HG21	16:CP:60:TRP:CD1	2.49	0.48
18:CR:20:GLU:O	18:CR:22:ASP:N	2.46	0.48
22:DA:108:G:O2'	22:DA:347:A:N3	2.41	0.48
22:DA:232:G:H22	22:DA:420:C:H5'	1.78	0.48
22:DA:244:A:H2'	22:DA:245:G:O4'	2.13	0.48
22:DA:279:A:C2	22:DA:362:A:H4'	2.48	0.48
22:DA:622:G:H2'	22:DA:623:C:H6	1.77	0.48
22:DA:1638:C:O2	22:DA:2698:U:O2'	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:DB:70:C:H2'	23:DB:71:C:C6	2.48	0.48
30:DI:62:TYR:HB3	30:DI:64:ASP:H	1.78	0.48
40:DS:5:ALA:HB3	40:DS:54:ALA:HB2	1.96	0.48
45:DX:33:LEU:HD23	45:DX:50:ARG:CZ	2.43	0.48
49:D1:9:ILE:HB	49:D1:52:ALA:HA	1.95	0.48
49:D1:15:ALA:C	49:D1:17:THR:H	2.20	0.48
52:D4:12:ARG:NH1	52:D4:12:ARG:HB2	2.28	0.48
7:AG:12:ILE:HD11	7:AG:25:LYS:HG3	1.95	0.48
9:AI:40:GLY:O	9:AI:41:ARG:HB2	2.14	0.48
11:AK:31:ILE:HB	11:AK:46:THR:HG22	1.94	0.48
11:AK:126:LYS:H	11:AK:126:LYS:HD3	1.79	0.48
19:AS:44:MET:HA	19:AS:47:LEU:HD12	1.95	0.48
22:BA:257:C:H2'	22:BA:258:G:O4'	2.12	0.48
22:BA:839:U:H2'	22:BA:840:C:C6	2.49	0.48
22:BA:858:G:H5"	22:BA:858:G:H8	1.78	0.48
22:BA:1058:U:H1'	22:BA:1081:U:O2	2.13	0.48
22:BA:1087:G:N2	22:BA:1102:C:O2	2.45	0.48
22:BA:1474:U:O4	22:BA:1475:G:N2	2.46	0.48
33:BL:21:ARG:HD3	33:BL:21:ARG:HA	1.56	0.48
35:BN:103:ARG:HD3	35:BN:110:MET:HE2	1.95	0.48
48:B0:48:TYR:CE2	48:B0:53:LYS:HB2	2.49	0.48
1:CA:582:C:N3	1:CA:760:G:C6	2.81	0.48
1:CA:1118:U:H2'	1:CA:1119:C:C6	2.47	0.48
1:CA:1366:C:O2'	10:CJ:62:ARG:NH2	2.45	0.48
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.49	0.48
2:CB:66:LYS:NZ	2:CB:154:MET:O	2.46	0.48
4:CD:129:VAL:HG23	4:CD:146:ARG:HD3	1.94	0.48
5:CE:101:GLU:HA	5:CE:122:ASN:HB2	1.94	0.48
8:CH:30:SER:O	8:CH:34:VAL:HG23	2.12	0.48
9:CI:26:GLY:H	9:CI:59:GLU:HA	1.76	0.48
19:CS:30:PRO:HA	19:CS:48:THR:O	2.12	0.48
22:DA:70:G:H5"	22:DA:112:U:O2	2.13	0.48
22:DA:659:G:H4'	26:DE:95:LYS:HD3	1.94	0.48
22:DA:748:G:C8	40:DS:89:ALA:HB1	2.48	0.48
22:DA:1273:U:H4'	22:DA:1275:A:P	2.53	0.48
22:DA:1435:G:C2'	22:DA:1436:G:H5'	2.42	0.48
22:DA:1746:A:H2'	22:DA:1747:U:C6	2.49	0.48
22:DA:2207:C:H2'	22:DA:2208:C:H6	1.77	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
26:DE:148:ILE:HG21	26:DE:157:LEU:HD21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DG:129:THR:C	28:DG:130:GLU:HG2	2.37	0.48
30:DI:71:THR:OG1	30:DI:72:LYS:N	2.46	0.48
1:AA:652:U:O4	1:AA:752:G:O2'	2.24	0.48
1:AA:763:G:H2'	1:AA:764:C:C6	2.48	0.48
4:AD:152:GLN:O	4:AD:155:VAL:HG12	2.13	0.48
7:AG:71:PRO:O	7:AG:96:ARG:HG3	2.14	0.48
10:AJ:27:GLU:C	10:AJ:29:ALA:H	2.21	0.48
22:BA:1435:G:H2'	22:BA:1436:G:C8	2.49	0.48
37:BP:25:THR:HB	37:BP:88:ARG:HB3	1.94	0.48
37:BP:27:GLU:HG2	37:BP:87:LYS:HE2	1.95	0.48
39:BR:14:VAL:HG13	39:BR:98:ILE:HG13	1.94	0.48
41:BT:30:ILE:HD11	41:BT:32:LEU:HD21	1.95	0.48
1:CA:663:A:H2'	1:CA:664:G:O4'	2.13	0.48
3:CC:129:MET:CG	3:CC:131:ARG:HH11	2.27	0.48
9:CI:25:ASN:O	9:CI:62:ASP:HA	2.14	0.48
9:CI:87:LEU:C	9:CI:89:GLU:H	2.22	0.48
14:CN:64:CYS:HB3	14:CN:69:ARG:H	1.79	0.48
22:DA:301:G:H1'	22:DA:302:C:C6	2.48	0.48
22:DA:783:A:C8	22:DA:784:G:H4'	2.48	0.48
22:DA:1343:G:H1'	22:DA:1597:A:C4	2.48	0.48
22:DA:1874:C:H3'	22:DA:1875:G:H8	1.78	0.48
22:DA:2480:C:H2'	22:DA:2481:G:O4'	2.13	0.48
23:DB:115:A:H2'	23:DB:116:G:C8	2.48	0.48
25:DD:172:VAL:CG2	25:DD:194:PRO:HD3	2.43	0.48
26:DE:179:SER:HA	26:DE:182:ALA:HB3	1.94	0.48
31:DJ:4:PHE:CG	38:DQ:100:VAL:HG11	2.48	0.48
36:DO:37:ALA:HB2	36:DO:106:LEU:HD11	1.95	0.48
46:DY:9:LYS:HG2	46:DY:10:SER:H	1.78	0.48
1:AA:355:C:H2'	1:AA:356:A:O4'	2.13	0.48
1:AA:771:G:H2'	1:AA:772:U:C6	2.49	0.48
1:AA:1181:G:C2	1:AA:1182:G:N2	2.82	0.48
4:AD:124:MET:HE2	4:AD:146:ARG:HD2	1.95	0.48
10:AJ:51:VAL:HB	14:AN:81:ARG:HB2	1.96	0.48
13:AM:45:ILE:HG13	13:AM:48:LEU:HD13	1.94	0.48
20:AT:26:SER:O	20:AT:30:THR:OG1	2.31	0.48
22:BA:441:U:O2'	26:BE:41:GLN:NE2	2.46	0.48
22:BA:477:A:H2'	22:BA:478:A:C8	2.48	0.48
22:BA:674:G:H5"	26:BE:71:GLY:HA3	1.94	0.48
22:BA:833:A:H2'	22:BA:834:G:C8	2.49	0.48
22:BA:1092:C:H2'	22:BA:1093:G:O4'	2.13	0.48
22:BA:1275:A:N1	22:BA:1295:C:O2'	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1490:A:O2'	24:BC:98:ASP:OD2	2.31	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
22:BA:2502:G:C5'	22:BA:2503:A:H5"	2.44	0.48
23:BB:28:C:H2'	23:BB:29:A:O4'	2.14	0.48
39:BR:68:ARG:HD3	39:BR:92:TRP:CZ2	2.48	0.48
1:CA:898:G:N2	1:CA:901:A:OP2	2.41	0.48
1:CA:957:U:O2	1:CA:959:A:C8	2.67	0.48
1:CA:1175:G:H2'	1:CA:1176:A:C8	2.47	0.48
1:CA:1277:C:H2'	1:CA:1278:G:H5"	1.96	0.48
2:CB:208:ARG:O	2:CB:211:THR:N	2.47	0.48
3:CC:36:ASP:O	3:CC:40:ARG:HG3	2.14	0.48
6:CF:86:ARG:HH11	6:CF:86:ARG:HG2	1.77	0.48
9:CI:115:LYS:HD2	9:CI:118:LEU:HD22	1.96	0.48
15:CO:33:THR:HA	15:CO:63:ARG:NH1	2.29	0.48
17:CQ:47:HIS:N	17:CQ:73:TRP:O	2.30	0.48
22:DA:635:C:H2'	22:DA:636:G:H8	1.78	0.48
22:DA:734:A:OP2	22:DA:761:A:N6	2.42	0.48
22:DA:897:C:H2'	22:DA:898:C:C6	2.48	0.48
22:DA:1379:U:OP1	22:DA:1379:U:C6	2.66	0.48
22:DA:1769:U:O2'	22:DA:1958:C:OP1	2.31	0.48
22:DA:1933:G:H2'	22:DA:1934:C:O4'	2.14	0.48
22:DA:2440:C:N3	22:DA:2441:U:H1'	2.28	0.48
22:DA:2834:G:H2'	22:DA:2879:A:H61	1.77	0.48
25:DD:35:THR:OG1	25:DD:49:GLN:OE1	2.24	0.48
27:DF:134:GLU:HB3	27:DF:137:ILE:HG23	1.94	0.48
29:DH:117:LEU:HD11	29:DH:130:VAL:HG22	1.95	0.48
31:DJ:4:PHE:C	38:DQ:64:ARG:HH22	2.21	0.48
36:DO:2:ASP:OD1	36:DO:5:SER:OG	2.28	0.48
45:DX:38:PHE:HZ	45:DX:56:MET:HG2	1.77	0.48
1:AA:375:U:OP1	16:AP:70:ARG:NH1	2.47	0.48
1:AA:1144:G:N1	1:AA:1145:A:H2	2.11	0.48
2:AB:132:LYS:O	2:AB:134:ALA:N	2.47	0.48
2:AB:172:ALA:O	2:AB:175:GLU:HB2	2.13	0.48
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.44	0.48
3:AC:72:ARG:O	3:AC:75:ILE:HG22	2.14	0.48
4:AD:138:SER:N	4:AD:141:ASP:OD2	2.43	0.48
10:AJ:26:VAL:HG12	10:AJ:30:LYS:HD3	1.95	0.48
12:AL:35:THR:O	12:AL:36:ARG:HG3	2.13	0.48
12:AL:39:THR:O	12:AL:39:THR:OG1	2.32	0.48
13:AM:56:LEU:O	13:AM:60:VAL:HG12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2207:C:H2'	22:BA:2208:C:C6	2.49	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
29:BH:103:VAL:HG21	29:BH:132:PHE:CZ	2.49	0.48
53:B5:185:LYS:C	53:B5:187:ALA:H	2.22	0.48
1:CA:130:A:OP1	17:CQ:65:ARG:HD2	2.14	0.48
1:CA:1467:C:H2'	1:CA:1468:A:H8	1.78	0.48
2:CB:65:GLY:HA3	2:CB:159:ASP:HB2	1.95	0.48
2:CB:66:LYS:HB2	2:CB:158:PRO:HA	1.96	0.48
5:CE:65:GLU:HG2	5:CE:69:ARG:NH2	2.29	0.48
18:CR:33:ILE:HA	18:CR:40:VAL:HG23	1.95	0.48
22:DA:1062:G:C5	22:DA:1088:A:H2'	2.49	0.48
22:DA:2039:U:H2'	22:DA:2040:G:H8	1.78	0.48
22:DA:2391:G:H1'	22:DA:2424:C:H41	1.79	0.48
25:DD:52:THR:O	25:DD:77:ARG:HG2	2.14	0.48
26:DE:189:THR:O	26:DE:193:VAL:HG23	2.12	0.48
1:AA:413:G:N1	4:AD:32:CYS:O	2.43	0.48
1:AA:575:G:O2'	1:AA:821:G:H5'	2.14	0.48
1:AA:1145:A:O2'	1:AA:1146:A:O5'	2.31	0.48
8:AH:66:PHE:CD2	8:AH:67:GLN:HG2	2.49	0.48
10:AJ:59:LYS:HD2	10:AJ:59:LYS:C	2.38	0.48
11:AK:70:CYS:O	11:AK:74:VAL:HG22	2.13	0.48
14:AN:79:LEU:HB2	14:AN:84:VAL:HG23	1.96	0.48
22:BA:43:G:H2'	22:BA:44:A:O4'	2.12	0.48
22:BA:1447:C:H2'	22:BA:1448:G:C8	2.49	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
30:BI:43:ASN:OD1	30:BI:46:THR:HB	2.13	0.48
36:BO:53:THR:HB	36:BO:65:THR:HG22	1.96	0.48
40:BS:109:ASP:OD1	40:BS:110:ARG:N	2.44	0.48
1:CA:66:A:C6	1:CA:67:C:C5	3.02	0.48
1:CA:72:A:N6	1:CA:99:C:H1'	2.29	0.48
1:CA:834:U:H2'	1:CA:835:U:C6	2.49	0.48
2:CB:222:ARG:HE	2:CB:223:GLU:N	2.12	0.48
5:CE:75:ALA:O	5:CE:147:MET:HE2	2.14	0.48
7:CG:57:SER:CB	7:CG:60:GLU:HG3	2.43	0.48
12:CL:37:VAL:HG21	12:CL:75:GLN:HA	1.95	0.48
22:DA:690:G:H1'	22:DA:779:U:O3'	2.14	0.48
22:DA:1415:U:H2'	22:DA:1416:G:H4'	1.95	0.48
22:DA:1565:C:H5'	24:DC:18:LYS:NZ	2.29	0.48
22:DA:1747:U:H2'	22:DA:1748:C:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2109:U:H1'	22:DA:2181:U:O2	2.14	0.48
24:DC:80:ARG:NE	24:DC:82:GLU:OE2	2.47	0.48
29:DH:32:PRO:HB3	45:DX:39:TRP:CB	2.42	0.48
29:DH:127:GLU:HG3	29:DH:144:VAL:O	2.14	0.48
35:DN:27:SER:HB3	35:DN:34:ILE:HG21	1.95	0.48
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.13	0.48
4:AD:46:PRO:O	4:AD:48:LEU:HD22	2.13	0.48
10:AJ:23:ALA:O	10:AJ:27:GLU:HB2	2.14	0.48
13:AM:79:ARG:O	13:AM:83:LEU:HG	2.13	0.48
22:BA:614:A:H5'	22:BA:614:A:H8	1.78	0.48
22:BA:753:A:H2'	22:BA:754:U:H6	1.79	0.48
22:BA:1430:G:H2'	22:BA:1431:A:H8	1.79	0.48
22:BA:2261:C:C6	44:BW:16:SER:HB3	2.49	0.48
22:BA:2391:G:H3'	51:B3:32:ILE:HD12	1.96	0.48
25:BD:132:ALA:HA	25:BD:140:HIS:ND1	2.29	0.48
37:BP:27:GLU:O	37:BP:27:GLU:HG3	2.14	0.48
46:BY:61:ALA:C	46:BY:63:ALA:H	2.22	0.48
48:B0:13:ARG:O	48:B0:17:ARG:HG3	2.14	0.48
1:CA:22:G:O2'	1:CA:913:A:N1	2.42	0.48
1:CA:285:C:H2'	1:CA:286:C:C6	2.49	0.48
1:CA:309:A:H1'	1:CA:608:A:C2	2.48	0.48
1:CA:632:U:O2	1:CA:632:U:H2'	2.14	0.48
4:CD:33:LYS:HG3	4:CD:33:LYS:O	2.14	0.48
9:CI:99:ARG:HA	9:CI:104:VAL:CG2	2.44	0.48
15:CO:40:GLN:HE22	22:DA:716:A:H1'	1.79	0.48
22:DA:392:U:H2'	22:DA:393:C:H6	1.79	0.48
22:DA:704:G:H1'	22:DA:726:G:N2	2.29	0.48
22:DA:1410:G:H2'	22:DA:1411:U:C6	2.49	0.48
22:DA:1693:U:O4	22:DA:1976:U:O2'	2.26	0.48
22:DA:1789:A:OP2	24:DC:221:ARG:NH1	2.46	0.48
25:DD:125:TRP:HB3	25:DD:160:LYS:HD3	1.95	0.48
25:DD:157:LYS:HD2	31:DJ:79:GLY:O	2.13	0.48
27:DF:106:ILE:HD11	27:DF:139:PRO:HG2	1.96	0.48
28:DG:26:ILE:HD11	28:DG:72:LEU:HD23	1.95	0.48
49:D1:10:LYS:O	49:D1:51:GLU:HG2	2.14	0.48
1:AA:39:G:H2'	1:AA:40:C:H6	1.78	0.48
5:AE:131:THR:OG1	5:AE:131:THR:O	2.29	0.48
10:AJ:52:LEU:HD11	10:AJ:59:LYS:HA	1.96	0.48
22:BA:186:G:O2'	22:BA:187:G:H5'	2.14	0.48
22:BA:590:A:H2'	22:BA:591:U:C6	2.49	0.48
22:BA:944:C:H2'	57:BA:3354:HOH:O	2.13	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
22:BA:1010:A:OP2	57:BA:3786:HOH:O	2.20	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
30:BI:17:MET:HE2	30:BI:17:MET:HA	1.96	0.48
1:CA:31:G:N7	1:CA:306:A:H1'	2.29	0.48
4:CD:75:TYR:OH	4:CD:97:ARG:NH1	2.46	0.48
7:CG:138:ARG:HE	7:CG:138:ARG:HB3	1.43	0.48
9:CI:20:PHE:HB2	9:CI:64:TYR:HB3	1.96	0.48
12:CL:3:THR:HB	12:CL:6:GLN:HG3	1.96	0.48
15:CO:33:THR:HA	15:CO:63:ARG:HH11	1.79	0.48
22:DA:609:A:H2'	22:DA:610:C:O4'	2.14	0.48
22:DA:996:A:O3'	38:DQ:91:ASP:HB2	2.14	0.48
22:DA:1800:C:O2'	22:DA:1818:U:N3	2.38	0.48
22:DA:2023:C:H2'	22:DA:2024:G:H8	1.79	0.48
22:DA:2244:U:H2'	22:DA:2245:U:O4'	2.14	0.48
28:DG:11:VAL:HG13	28:DG:48:ASN:C	2.39	0.48
28:DG:67:THR:O	28:DG:71:LEU:N	2.47	0.48
36:DO:34:HIS:N	36:DO:65:THR:O	2.45	0.48
1:AA:17:U:H2'	1:AA:18:C:C6	2.49	0.47
1:AA:57:G:H2'	1:AA:58:C:C6	2.49	0.47
1:AA:204:G:H2'	1:AA:205:A:O4'	2.13	0.47
1:AA:250:A:H4'	1:AA:251:G:O5'	2.13	0.47
1:AA:374:A:C6	1:AA:375:U:C4	3.02	0.47
1:AA:477:C:H2'	1:AA:478:A:C8	2.49	0.47
1:AA:1386:G:H2'	1:AA:1387:G:H8	1.79	0.47
1:AA:1516:G:N2	1:AA:1519:A:OP2	2.45	0.47
7:AG:133:THR:O	7:AG:136:LYS:HB3	2.14	0.47
8:AH:53:GLY:HA3	8:AH:57:PRO:HA	1.94	0.47
15:AO:61:SER:O	15:AO:65:LYS:HG3	2.14	0.47
17:AQ:17:MET:HB2	17:AQ:20:SER:HB3	1.96	0.47
22:BA:244:A:C2	22:BA:255:A:C4	3.02	0.47
22:BA:1074:G:C2'	22:BA:1075:C:H5'	2.44	0.47
22:BA:1255:U:C5	26:BE:68:ALA:HA	2.49	0.47
22:BA:2798:U:H6	22:BA:2798:U:H5'	1.79	0.47
22:BA:2800:A:C2	22:BA:2895:G:H1'	2.49	0.47
26:BE:117:ARG:HH12	33:BL:2:ARG:HD3	1.79	0.47
32:BK:92:GLU:HG3	32:BK:111:LYS:HZ3	1.79	0.47
32:BK:113:MET:O	32:BK:116:ILE:HG13	2.13	0.47
44:BW:41:ARG:HH11	44:BW:41:ARG:HG3	1.78	0.47
1:CA:619:U:H3	4:CD:131:ASN:CB	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1534:A:H4'	1:CA:1535:C:H2'	1.96	0.47
4:CD:31:LYS:N	4:CD:31:LYS:HD3	2.28	0.47
15:CO:67:LEU:HD23	15:CO:78:TYR:CE1	2.49	0.47
17:CQ:61:ILE:HA	17:CQ:75:LEU:HA	1.95	0.47
22:DA:1243:C:H1'	33:DL:4:ASN:O	2.14	0.47
22:DA:1274:A:N3	22:DA:1297:C:H1'	2.29	0.47
22:DA:1853:A:N3	22:DA:2233:U:O2'	2.38	0.47
22:DA:2103:C:H2'	22:DA:2104:C:C6	2.49	0.47
24:DC:147:LYS:HG3	24:DC:150:LYS:HD2	1.96	0.47
25:DD:55:LYS:HG3	25:DD:77:ARG:HA	1.96	0.47
29:DH:82:SER:O	29:DH:83:LYS:C	2.57	0.47
37:DP:39:ARG:CG	37:DP:40:LEU:H	2.22	0.47
42:DU:72:ILE:H	42:DU:72:ILE:HG13	1.37	0.47
43:DV:14:LYS:HD3	43:DV:18:ARG:NH2	2.29	0.47
1:AA:623:C:H2'	1:AA:624:C:H6	1.79	0.47
2:AB:10:LEU:HG	2:AB:11:LYS:N	2.29	0.47
2:AB:139:ARG:HG3	2:AB:140:GLU:N	2.29	0.47
4:AD:188:ARG:NH2	4:AD:197:GLU:OE1	2.47	0.47
22:BA:27:G:O2'	22:BA:512:G:N2	2.47	0.47
22:BA:242:G:C8	51:B3:5:LYS:HG2	2.49	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
22:BA:1230:A:H2'	22:BA:1231:U:O4'	2.13	0.47
29:BH:116:ARG:O	29:BH:118:PRO:HD3	2.14	0.47
30:BI:58:VAL:HG12	30:BI:59:ILE:H	1.80	0.47
32:BK:21:CYS:HA	32:BK:41:ILE:HG22	1.96	0.47
43:BV:2:PHE:CD1	43:BV:50:MET:HE3	2.49	0.47
3:CC:141:ALA:O	3:CC:146:ALA:HB3	2.14	0.47
5:CE:81:LEU:O	5:CE:98:PRO:HB3	2.14	0.47
22:DA:2:G:C6	22:DA:3:U:C4	3.03	0.47
22:DA:301:G:C6	22:DA:317:G:C6	3.03	0.47
22:DA:1199:U:H1'	38:DQ:4:VAL:HG22	1.97	0.47
22:DA:1351:C:O2'	22:DA:1571:A:N3	2.44	0.47
22:DA:1708:C:H2'	22:DA:1709:U:C6	2.49	0.47
22:DA:1794:A:H2'	22:DA:1795:C:C6	2.49	0.47
22:DA:2550:G:OP1	57:DA:3719:HOH:O	2.20	0.47
22:DA:2689:U:H4'	22:DA:2690:U:OP2	2.13	0.47
26:DE:48:THR:HG22	26:DE:86:ALA:HB3	1.97	0.47
43:DV:30:ILE:HD13	43:DV:72:VAL:HG11	1.95	0.47
1:AA:194:C:O2'	1:AA:195:A:H5'	2.15	0.47
1:AA:235:C:H2'	1:AA:236:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:406:G:H8	1:AA:406:G:OP2	1.97	0.47
1:AA:678:U:O2	1:AA:777:A:H4'	2.13	0.47
2:AB:20:THR:HA	2:AB:38:VAL:HA	1.96	0.47
4:AD:65:TYR:CG	4:AD:94:LEU:HD22	2.49	0.47
7:AG:116:MET:HE3	7:AG:120:LEU:HG	1.95	0.47
22:BA:773:U:H4'	24:BC:47:GLY:HA3	1.96	0.47
22:BA:1818:U:O2'	24:BC:153:GLN:O	2.22	0.47
22:BA:2485:G:H5"	34:BM:45:GLN:HE21	1.79	0.47
29:BH:89:LYS:HD3	1:CA:359:G:OP1	2.15	0.47
29:BH:111:ALA:O	29:BH:114:GLU:HB2	2.14	0.47
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.49	0.47
7:CG:75:VAL:HG11	7:CG:144:MET:HG3	1.96	0.47
9:CI:18:ARG:O	9:CI:65:ILE:HA	2.14	0.47
12:CL:59:ASN:HD22	12:CL:59:ASN:N	1.99	0.47
16:CP:44:SER:O	16:CP:46:LYS:HG3	2.15	0.47
22:DA:634:C:OP2	33:DL:70:LYS:HD3	2.14	0.47
22:DA:948:C:H2'	22:DA:949:G:C8	2.48	0.47
22:DA:1179:G:C5	22:DA:1180:U:H1'	2.49	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:1936:A:H2	22:DA:1943:U:N3	1.95	0.47
22:DA:2268:A:OP1	57:DA:3505:HOH:O	2.20	0.47
23:DB:14:U:OP2	23:DB:70:C:O2'	2.31	0.47
25:DD:99:GLU:HG2	25:DD:182:ALA:HB2	1.96	0.47
29:DH:83:LYS:CG	29:DH:149:GLU:CG	2.86	0.47
33:DL:110:VAL:HG12	33:DL:131:ALA:HB1	1.95	0.47
40:DS:28:LYS:O	40:DS:30:SER:N	2.48	0.47
1:AA:8:A:H1'	5:AE:108:GLY:HA2	1.96	0.47
1:AA:773:G:H2'	1:AA:774:G:O4'	2.14	0.47
1:AA:1071:C:H2'	1:AA:1072:G:C8	2.49	0.47
1:AA:1224:U:O2'	1:AA:1322:C:OP1	2.26	0.47
4:AD:125:VAL:HG11	4:AD:135:TYR:CE2	2.50	0.47
17:AQ:16:LYS:O	17:AQ:17:MET:HE3	2.13	0.47
19:AS:51:VAL:O	19:AS:58:VAL:HG13	2.14	0.47
21:AU:44:GLU:OE2	21:AU:45:ARG:NH1	2.47	0.47
22:BA:150:U:H2'	22:BA:151:C:C6	2.50	0.47
22:BA:201:C:OP1	45:BX:18:ARG:NH1	2.47	0.47
22:BA:1868:C:H2'	22:BA:1869:G:O4'	2.15	0.47
22:BA:2154:A:H2'	22:BA:2155:U:C6	2.49	0.47
22:BA:2233:U:H2'	22:BA:2234:G:C8	2.50	0.47
22:BA:2520:C:O2'	22:BA:2521:C:H5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:618:C:H5”	1:CA:619:U:H5”	1.96	0.47
1:CA:1230:C:O5’	1:CA:1230:C:H6	1.98	0.47
2:CB:126:PHE:CD2	2:CB:126:PHE:N	2.82	0.47
9:CI:30:ILE:HA	9:CI:65:ILE:O	2.14	0.47
22:DA:300:A:O5’	42:DU:82:ARG:NH1	2.47	0.47
22:DA:563:A:OP2	39:DR:79:ARG:NH2	2.39	0.47
22:DA:607:U:H5	22:DA:619:G:C4	2.32	0.47
22:DA:686:U:H6	22:DA:788:A:N1	2.13	0.47
22:DA:1495:A:H2’	22:DA:1496:A:C8	2.50	0.47
22:DA:1760:C:H2’	22:DA:1761:C:O4’	2.15	0.47
36:DO:70:ALA:O	36:DO:74:VAL:HB	2.15	0.47
1:AA:383:A:C5	1:AA:384:G:H1’	2.49	0.47
1:AA:591:U:OP1	8:AH:31:LYS:HD2	2.13	0.47
1:AA:692:U:O4	11:AK:54:GLY:HA2	2.15	0.47
3:AC:7:PRO:HG2	3:AC:184:TYR:CD1	2.49	0.47
3:AC:36:ASP:C	3:AC:38:LYS:H	2.22	0.47
5:AE:15:LEU:HA	5:AE:37:THR:HA	1.96	0.47
5:AE:34:THR:HB	5:AE:50:TYR:CE2	2.50	0.47
6:AF:6:ILE:HG23	6:AF:89:VAL:HG12	1.96	0.47
7:AG:60:GLU:HA	7:AG:63:GLU:HB2	1.96	0.47
8:AH:29:SER:HB2	8:AH:59:LEU:HB2	1.96	0.47
13:AM:107:ARG:HA	13:AM:107:ARG:HH11	1.78	0.47
22:BA:81:G:H2’	22:BA:82:U:O4’	2.15	0.47
22:BA:1299:G:H8	22:BA:1299:G:O5’	1.97	0.47
22:BA:1820:U:OP1	24:BC:177:ARG:HG2	2.14	0.47
22:BA:2171:A:O2’	22:BA:2172:U:H5’	2.14	0.47
22:BA:2189:U:H2’	22:BA:2190:G:O4’	2.15	0.47
22:BA:2334:U:C4	36:BO:16:ARG:HD3	2.48	0.47
29:BH:117:LEU:HD23	29:BH:121:VAL:HA	1.95	0.47
46:BY:9:LYS:H	46:BY:12:GLU:HG3	1.80	0.47
1:CA:107:G:O2’	1:CA:378:G:H4’	2.14	0.47
1:CA:372:C:H4’	1:CA:373:A:OP1	2.15	0.47
1:CA:608:A:H2’	1:CA:609:A:O4’	2.14	0.47
1:CA:1181:G:O2’	1:CA:1182:G:C8	2.65	0.47
4:CD:95:GLU:OE2	4:CD:100:ASN:ND2	2.33	0.47
4:CD:124:MET:HE3	4:CD:146:ARG:HD2	1.96	0.47
7:CG:25:LYS:O	7:CG:29:ILE:HG12	2.15	0.47
19:CS:63:THR:HB	19:CS:66:MET:HG3	1.95	0.47
22:DA:380:G:O3’	45:DX:16:ASN:HB2	2.15	0.47
22:DA:586:A:H2	22:DA:809:G:N3	2.12	0.47
22:DA:731:C:OP2	57:DA:3689:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:974:G:H1'	22:DA:975:A:C8	2.50	0.47
22:DA:1370:C:O4'	22:DA:1810:A:H2	1.97	0.47
22:DA:1567:G:H4'	24:DC:58:HIS:CE1	2.50	0.47
22:DA:2024:G:OP2	22:DA:2034:U:H4'	2.14	0.47
22:DA:2660:A:H2'	22:DA:2661:G:C8	2.49	0.47
23:DB:49:C:OP1	36:DO:101:GLY:HA3	2.14	0.47
24:DC:53:HIS:O	24:DC:217:ARG:N	2.45	0.47
27:DF:100:PHE:O	27:DF:104:ILE:HG12	2.15	0.47
29:DH:5:LEU:HD13	29:DH:13:GLY:HA3	1.96	0.47
29:DH:62:LEU:O	29:DH:62:LEU:HD22	2.14	0.47
35:DN:93:GLY:C	35:DN:95:THR:H	2.23	0.47
42:DU:9:ASP:OD1	42:DU:94:ARG:NH1	2.34	0.47
45:DX:40:VAL:CG2	45:DX:43:GLU:HB2	2.45	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
1:AA:292:G:N7	1:AA:293:G:H1'	2.30	0.47
1:AA:327:A:O3'	1:AA:328:C:H4'	2.14	0.47
1:AA:489:C:H2'	1:AA:490:C:H6	1.80	0.47
1:AA:781:A:H4'	1:AA:1522:U:O2'	2.15	0.47
1:AA:1280:A:H5"	10:AJ:42:LEU:HD21	1.96	0.47
6:AF:71:ILE:HD11	6:AF:89:VAL:HG21	1.96	0.47
7:AG:29:ILE:HG22	7:AG:105:VAL:HG21	1.96	0.47
13:AM:66:GLU:O	13:AM:69:LEU:N	2.48	0.47
13:AM:86:TYR:HA	13:AM:89:LEU:HD12	1.97	0.47
22:BA:171:U:H2'	22:BA:172:A:H8	1.80	0.47
22:BA:2569:G:C2	22:BA:2570:G:C8	3.03	0.47
25:BD:12:THR:HB	25:BD:13:ARG:H	1.41	0.47
25:BD:84:LEU:HD22	25:BD:88:GLU:HB3	1.97	0.47
29:BH:14:SER:O	29:BH:15:LEU:CB	2.61	0.47
34:BM:31:PHE:CZ	34:BM:110:GLU:HA	2.49	0.47
41:BT:2:ILE:HA	41:BT:3:ARG:C	2.39	0.47
41:BT:18:GLU:O	41:BT:22:THR:HG23	2.14	0.47
46:BY:9:LYS:HG2	46:BY:10:SER:N	2.28	0.47
1:CA:279:A:H5"	1:CA:281:G:H5'	1.97	0.47
1:CA:970:C:H5"	1:CA:971:G:OP1	2.14	0.47
1:CA:1243:C:H2'	1:CA:1244:G:C8	2.50	0.47
4:CD:33:LYS:O	4:CD:34:ILE:C	2.58	0.47
8:CH:27:MET:HG2	8:CH:59:LEU:HB3	1.96	0.47
11:CK:127:ARG:O	21:CU:34:ARG:NH1	2.44	0.47
22:DA:349:U:H2'	22:DA:350:G:H8	1.79	0.47
22:DA:699:A:H2'	22:DA:700:G:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1352:U:H5	57:DA:3392:HOH:O	1.97	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
22:DA:2610:C:O4'	54:D6:7:004:HD2	2.13	0.47
22:DA:2707:U:O2	35:DN:71:ARG:NH1	2.47	0.47
22:DA:2804:U:H2'	22:DA:2805:C:C6	2.50	0.47
23:DB:11:C:O5'	23:DB:11:C:H6	1.98	0.47
27:DF:34:ILE:HA	27:DF:155:THR:O	2.14	0.47
45:DX:68:LEU:HD23	45:DX:68:LEU:HA	1.81	0.47
1:AA:251:G:H4'	1:AA:252:U:O5'	2.14	0.47
1:AA:1192:C:OP2	3:AC:4:LYS:HE2	2.15	0.47
1:AA:1493:A:OP2	1:AA:1493:A:H8	1.96	0.47
2:AB:16:PHE:HB2	2:AB:40:ILE:HG23	1.97	0.47
2:AB:162:PHE:HA	2:AB:184:PHE:O	2.14	0.47
4:AD:30:THR:HG22	4:AD:31:LYS:H	1.80	0.47
4:AD:76:TYR:CG	4:AD:204:TYR:HD1	2.33	0.47
7:AG:146:GLU:HA	7:AG:149:LYS:CB	2.41	0.47
8:AH:2:SER:C	8:AH:4:GLN:N	2.71	0.47
10:AJ:11:LYS:HA	10:AJ:70:HIS:O	2.15	0.47
12:AL:85:GLY:O	12:AL:96:HIS:ND1	2.47	0.47
15:AO:39:LEU:HD12	15:AO:39:LEU:HA	1.73	0.47
16:AP:39:PHE:CD2	16:AP:74:LEU:HD11	2.49	0.47
17:AQ:60:GLU:HB3	17:AQ:76:VAL:HG23	1.96	0.47
22:BA:770:G:H1'	22:BA:1379:U:C4	2.49	0.47
22:BA:783:A:C8	22:BA:784:G:H4'	2.50	0.47
22:BA:783:A:H8	22:BA:784:G:H4'	1.78	0.47
22:BA:980:A:C6	22:BA:981:A:N1	2.83	0.47
22:BA:1167:C:H2'	22:BA:1168:G:H5"	1.97	0.47
22:BA:1414:C:C4	22:BA:1415:U:H5	2.33	0.47
22:BA:1570:A:C6	22:BA:1571:A:C6	3.03	0.47
22:BA:1683:U:H2'	22:BA:1684:G:C8	2.50	0.47
22:BA:1789:A:O3'	24:BC:218:PRO:HB3	2.14	0.47
22:BA:2192:U:C2	22:BA:2193:G:C8	3.03	0.47
22:BA:2591:C:H2'	22:BA:2592:G:H8	1.78	0.47
25:BD:13:ARG:HD2	25:BD:15:PHE:CE1	2.49	0.47
25:BD:101:PHE:HZ	25:BD:203:VAL:O	1.98	0.47
27:BF:73:SER:HB2	27:BF:81:GLN:N	2.29	0.47
28:BG:74:SER:HA	28:BG:77:ILE:CG1	2.44	0.47
28:BG:90:VAL:HG21	28:BG:163:ARG:NE	2.29	0.47
30:BI:28:LEU:HD12	30:BI:28:LEU:O	2.14	0.47
38:BQ:11:ARG:HD2	38:BQ:11:ARG:HA	1.53	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BR:4:VAL:HA	39:BR:12:HIS:O	2.13	0.47
42:BU:40:ASN:O	42:BU:63:ALA:N	2.47	0.47
45:BX:6:GLN:O	45:BX:74:ARG:NH1	2.48	0.47
46:BY:9:LYS:HB3	46:BY:12:GLU:CG	2.41	0.47
48:B0:10:ARG:HB2	48:B0:13:ARG:NH2	2.29	0.47
1:CA:466:A:H2'	1:CA:468:A:C2	2.47	0.47
1:CA:792:A:O2'	1:CA:794:A:N7	2.41	0.47
1:CA:999:C:H2'	1:CA:1000:A:C8	2.50	0.47
2:CB:165:ASP:O	2:CB:168:HIS:HB3	2.15	0.47
3:CC:97:VAL:HB	3:CC:98:PRO:HD2	1.97	0.47
4:CD:24:GLY:O	4:CD:161:LEU:HD11	2.14	0.47
5:CE:150:PRO:C	5:CE:152:MET:N	2.72	0.47
6:CF:36:ILE:HB	6:CF:64:VAL:HG13	1.97	0.47
7:CG:60:GLU:HA	7:CG:63:GLU:HB3	1.97	0.47
10:CJ:28:THR:HG23	10:CJ:31:ARG:NH2	2.29	0.47
11:CK:88:GLY:H	11:CK:114:THR:HG22	1.79	0.47
11:CK:91:PRO:HB2	11:CK:92:GLY:H	1.48	0.47
14:CN:4:GLN:OE1	14:CN:7:LYS:NZ	2.42	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:DA:1076:C:H2'	22:DA:1077:A:O4'	2.14	0.47
22:DA:1338:G:O2'	22:DA:1393:A:N1	2.40	0.47
22:DA:1906:G:OP1	22:DA:1930:G:C8	2.68	0.47
22:DA:2385:C:H2'	22:DA:2386:A:C8	2.49	0.47
22:DA:2405:G:H1'	22:DA:2412:A:N6	2.29	0.47
22:DA:2813:A:H2'	22:DA:2814:A:H8	1.78	0.47
23:DB:66:A:H61	23:DB:107:G:H2'	1.79	0.47
24:DC:57:GLY:HA3	24:DC:213:TRP:HA	1.96	0.47
26:DE:5:LEU:HD23	26:DE:122:GLU:HG2	1.97	0.47
26:DE:125:SER:OG	26:DE:126:VAL:N	2.44	0.47
26:DE:140:ASP:C	26:DE:142:ALA:H	2.22	0.47
36:DO:50:ALA:O	36:DO:81:ARG:NH2	2.47	0.47
37:DP:4:ILE:HD12	37:DP:4:ILE:H	1.80	0.47
40:DS:51:LEU:O	40:DS:55:ILE:HG13	2.14	0.47
1:AA:35:G:H2'	1:AA:36:C:C6	2.50	0.47
2:AB:61:ALA:HA	2:AB:65:GLY:CA	2.45	0.47
2:AB:71:GLY:O	2:AB:93:ASN:HA	2.14	0.47
2:AB:188:ASP:HB2	2:AB:204:ASP:OD1	2.15	0.47
5:AE:18:VAL:HA	5:AE:34:THR:O	2.14	0.47
6:AF:12:PRO:O	6:AF:15:SER:HB2	2.15	0.47
9:AI:57:MET:SD	9:AI:57:MET:N	2.86	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:74:ASP:OD1	15:AO:77:ARG:HD3	2.14	0.47
20:AT:71:LYS:HD2	20:AT:74:ARG:HH21	1.80	0.47
22:BA:460:A:P	50:B2:41:ARG:HH12	2.38	0.47
22:BA:686:U:O4	50:B2:12:ARG:HB2	2.15	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
22:BA:1268:A:C2	22:BA:2013:A:C4	3.03	0.47
22:BA:1549:A:O3'	22:BA:1740:G:N2	2.47	0.47
22:BA:2112:G:H2'	22:BA:2112:G:N3	2.30	0.47
32:BK:116:ILE:HD12	32:BK:117:SER:N	2.30	0.47
40:BS:37:THR:HG22	40:BS:38:TYR:CD1	2.50	0.47
1:CA:282:A:H3'	1:CA:283:U:C6	2.50	0.47
1:CA:649:A:H2'	1:CA:650:G:O4'	2.14	0.47
1:CA:974:A:OP1	14:CN:69:ARG:NH1	2.46	0.47
1:CA:1034:G:H2'	1:CA:1035:A:C8	2.50	0.47
1:CA:1260:G:OP1	1:CA:1284:C:O2'	2.29	0.47
6:CF:50:PRO:HD3	18:CR:74:HIS:HB3	1.96	0.47
14:CN:33:ASP:O	14:CN:35:ASN:N	2.48	0.47
17:CQ:13:VAL:HG12	17:CQ:22:VAL:O	2.15	0.47
22:DA:737:C:H2'	22:DA:738:G:O4'	2.15	0.47
22:DA:1231:U:O5'	22:DA:1231:U:H6	1.98	0.47
22:DA:1479:G:H2'	22:DA:1480:C:O4'	2.15	0.47
22:DA:1645:G:H5"	22:DA:1646:C:O4'	2.14	0.47
22:DA:2060:A:N6	26:DE:69:ARG:HH12	2.13	0.47
33:DL:119:PRO:HB3	33:DL:139:GLY:HA3	1.97	0.47
1:AA:552:U:H2'	1:AA:553:A:C8	2.50	0.47
1:AA:982:U:H4'	1:AA:983:A:H5'	1.97	0.47
4:AD:123:ILE:HD13	4:AD:123:ILE:N	2.30	0.47
5:AE:60:ILE:HG13	5:AE:61:GLN:N	2.30	0.47
8:AH:29:SER:HB2	8:AH:59:LEU:H	1.79	0.47
12:AL:102:LEU:HB3	12:AL:103:ASP:H	1.56	0.47
17:AQ:12:VAL:HG23	17:AQ:57:ASP:O	2.14	0.47
22:BA:1171:G:C2	22:BA:1172:C:C2	3.03	0.47
22:BA:1185:G:H5"	22:BA:1186:G:OP1	2.14	0.47
22:BA:2081:U:H2'	22:BA:2082:A:C8	2.50	0.47
22:BA:2812:G:H2'	22:BA:2813:A:O4'	2.15	0.47
38:BQ:91:ASP:O	38:BQ:95:LEU:HD12	2.15	0.47
47:BZ:47:MET:O	47:BZ:51:VAL:HG22	2.15	0.47
53:B5:65:LEU:C	53:B5:67:HIS:H	2.22	0.47
1:CA:487:A:H3'	1:CA:488:C:C6	2.50	0.47
1:CA:1029:U:O2	1:CA:1029:U:H2'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:79:VAL:O	12:CL:103:ASP:HB2	2.15	0.47
22:DA:371:A:H61	22:DA:401:A:H3'	1.80	0.47
22:DA:392:U:H2'	22:DA:393:C:C6	2.50	0.47
22:DA:607:U:O4	22:DA:620:G:H5'	2.15	0.47
22:DA:826:U:H5"	22:DA:2429:G:OP2	2.15	0.47
22:DA:830:G:P	22:DA:830:G:H8	2.38	0.47
22:DA:959:A:H2'	22:DA:960:A:C8	2.50	0.47
22:DA:1367:A:C5	22:DA:1368:G:H1'	2.49	0.47
22:DA:1605:C:O2	22:DA:1610:A:O2'	2.29	0.47
22:DA:1645:G:OP1	22:DA:1646:C:H5'	2.15	0.47
22:DA:1803:A:O3'	24:DC:257:THR:HB	2.15	0.47
22:DA:2235:G:H2'	22:DA:2236:U:O4'	2.15	0.47
22:DA:2810:A:C8	22:DA:2811:G:C8	3.03	0.47
22:DA:2819:G:O5'	22:DA:2819:G:H8	1.98	0.47
24:DC:17:VAL:N	24:DC:204:VAL:HG22	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
44:DW:40:GLN:OE1	44:DW:44:LYS:N	2.48	0.47
46:DY:22:LEU:HG	46:DY:23:ARG:HE	1.80	0.47
1:AA:463:U:H3'	1:AA:464:U:C6	2.50	0.47
1:AA:1449:C:H2'	1:AA:1450:U:O4'	2.15	0.47
6:AF:38:ARG:HH12	6:AF:99:ALA:HB3	1.79	0.47
7:AG:47:LEU:HD12	7:AG:47:LEU:HA	1.78	0.47
21:AU:47:ARG:HA	21:AU:47:ARG:HE	1.80	0.47
22:BA:468:G:N7	50:B2:39:ARG:NH2	2.60	0.47
22:BA:582:A:H2'	22:BA:583:G:H8	1.78	0.47
22:BA:674:G:H5"	26:BE:71:GLY:CA	2.45	0.47
22:BA:674:G:H5"	26:BE:71:GLY:N	2.30	0.47
22:BA:700:G:O2'	22:BA:1632:A:N3	2.41	0.47
22:BA:1056:G:H4'	22:BA:1086:A:C8	2.50	0.47
27:BF:121:SER:HB2	27:BF:128:TYR:CE1	2.49	0.47
29:BH:91:PHE:HB3	1:CA:55:A:N3	2.30	0.47
30:BI:127:ARG:HA	30:BI:130:GLU:HG3	1.97	0.47
47:BZ:30:ARG:HG3	47:BZ:34:HIS:CE1	2.50	0.47
53:B5:48:LEU:HD12	53:B5:57:GLN:HG2	1.95	0.47
1:CA:8:A:C5	4:CD:206:LYS:HB3	2.50	0.47
1:CA:206:C:H2'	1:CA:207:C:C4'	2.45	0.47
1:CA:935:A:N1	7:CG:3:ARG:NH1	2.63	0.47
1:CA:1296:C:N4	1:CA:1297:G:O6	2.48	0.47
1:CA:1520:C:H2'	1:CA:1521:C:H6	1.80	0.47
2:CB:165:ASP:O	2:CB:169:GLU:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:167:ASP:OD2	2:CB:191:SER:HA	2.15	0.47
3:CC:153:VAL:HB	3:CC:198:VAL:HG22	1.97	0.47
20:CT:35:VAL:O	20:CT:39:ILE:HG13	2.15	0.47
22:DA:703:U:C2'	22:DA:704:G:H5'	2.46	0.47
22:DA:1434:A:H2'	22:DA:1435:G:H8	1.80	0.47
22:DA:2043:C:H1'	22:DA:2779:U:O4	2.14	0.47
22:DA:2836:U:H2'	22:DA:2837:A:C8	2.50	0.47
26:DE:155:GLU:O	26:DE:159:LEU:HD12	2.15	0.47
32:DK:66:LYS:HA	32:DK:66:LYS:HD2	1.79	0.47
3:AC:27:LYS:H	3:AC:27:LYS:HD2	1.79	0.46
4:AD:118:VAL:HA	4:AD:123:ILE:CD1	2.43	0.46
8:AH:75:ILE:HD13	8:AH:129:VAL:HG13	1.97	0.46
22:BA:962:G:O2'	22:BA:963:U:H5'	2.15	0.46
22:BA:1380:G:OP2	57:BA:3757:HOH:O	2.19	0.46
22:BA:1590:A:H2'	22:BA:1591:A:H8	1.80	0.46
22:BA:1916:A:N3	22:BA:1917:U:H1'	2.31	0.46
26:BE:199:MET:HE2	26:BE:199:MET:HB3	1.73	0.46
27:BF:2:ALA:HB2	27:BF:94:GLU:OE1	2.15	0.46
30:BI:58:VAL:HG12	30:BI:59:ILE:N	2.30	0.46
30:BI:80:LEU:HD13	30:BI:136:MET:SD	2.55	0.46
31:BJ:70:THR:HG22	31:BJ:90:GLU:OE2	2.16	0.46
33:BL:95:LEU:HB3	33:BL:101:ILE:HG23	1.97	0.46
37:BP:34:GLU:N	37:BP:37:LYS:O	2.44	0.46
40:BS:84:ARG:HB2	40:BS:96:ILE:CG1	2.44	0.46
1:CA:109:A:C6	1:CA:327:A:C6	3.03	0.46
1:CA:978:A:P	1:CA:1362:A:N6	2.89	0.46
4:CD:144:SER:HB3	4:CD:179:GLU:HB2	1.97	0.46
5:CE:122:ASN:CG	5:CE:123:VAL:N	2.72	0.46
22:DA:211:C:OP1	50:D2:25:LYS:NZ	2.44	0.46
22:DA:307:G:N1	22:DA:310:A:OP2	2.48	0.46
22:DA:406:G:H2'	22:DA:407:G:O4'	2.16	0.46
22:DA:518:G:OP2	48:D0:13:ARG:NH2	2.48	0.46
22:DA:864:G:O2'	22:DA:914:G:O6	2.33	0.46
22:DA:2487:G:H2'	22:DA:2488:G:C8	2.49	0.46
22:DA:2487:G:H2'	22:DA:2488:G:H8	1.79	0.46
25:DD:13:ARG:HD3	25:DD:21:SER:OG	2.15	0.46
29:DH:112:LYS:CG	29:DH:113:SER:N	2.76	0.46
35:DN:55:ALA:CB	35:DN:79:LEU:HB3	2.45	0.46
45:DX:10:LYS:HE3	45:DX:54:LYS:HD2	1.96	0.46
1:AA:328:C:O2	1:AA:328:C:H2'	2.15	0.46
1:AA:560:A:H5'	1:AA:566:G:N2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:738:C:H2'	1:AA:739:C:H6	1.80	0.46
1:AA:1142:G:H2'	1:AA:1143:G:O4'	2.14	0.46
1:AA:1290:G:OP1	7:AG:35:LYS:NZ	2.48	0.46
1:AA:1417:G:N2	1:AA:1482:G:H2'	2.29	0.46
2:AB:97:LEU:O	2:AB:100:MET:HB3	2.15	0.46
5:AE:69:ARG:H	5:AE:69:ARG:HG2	1.42	0.46
17:AQ:4:LYS:HE3	17:AQ:4:LYS:HB3	1.49	0.46
20:AT:5:LYS:O	20:AT:7:ALA:N	2.49	0.46
21:AU:37:PHE:HB3	21:AU:41:PRO:CG	2.41	0.46
22:BA:958:U:H2'	23:BB:89:U:C2	2.50	0.46
22:BA:1786:A:H1'	22:BA:1938:A:N6	2.31	0.46
22:BA:2579:C:O5'	22:BA:2579:C:H6	1.97	0.46
27:BF:30:ARG:O	27:BF:159:THR:HG23	2.16	0.46
35:BN:44:LEU:HD23	35:BN:113:ILE:HG21	1.98	0.46
1:CA:940:C:H2'	1:CA:941:G:H8	1.81	0.46
11:CK:23:ILE:HG22	11:CK:32:VAL:HG13	1.97	0.46
11:CK:88:GLY:H	11:CK:114:THR:CG2	2.28	0.46
14:CN:10:GLU:O	14:CN:14:VAL:HG23	2.15	0.46
15:CO:29:VAL:HG13	15:CO:63:ARG:HD2	1.97	0.46
22:DA:1645:G:H4'	22:DA:1646:C:C6	2.51	0.46
22:DA:1930:G:N2	22:DA:1968:G:H2'	2.30	0.46
22:DA:2544:G:H5'	22:DA:2645:G:C2	2.50	0.46
22:DA:2816:G:O3'	35:DN:99:LYS:HE2	2.15	0.46
29:DH:41:LYS:O	29:DH:44:ILE:HG12	2.15	0.46
31:DJ:35:ARG:HG2	31:DJ:40:HIS:HD2	1.80	0.46
43:DV:41:GLU:C	43:DV:42:LEU:HD23	2.40	0.46
45:DX:17:ASN:HB2	45:DX:25:THR:HB	1.97	0.46
1:AA:207:C:H2'	1:AA:208:U:C2	2.49	0.46
1:AA:294:U:OP1	1:AA:610:U:O2'	2.22	0.46
1:AA:453:G:H2'	1:AA:454:G:C8	2.50	0.46
1:AA:537:G:H2'	1:AA:538:G:H8	1.80	0.46
1:AA:1089:G:H2'	1:AA:1090:U:O4'	2.15	0.46
1:AA:1258:G:H2'	1:AA:1259:C:H6	1.79	0.46
3:AC:7:PRO:HG2	3:AC:184:TYR:CG	2.51	0.46
4:AD:99:ASP:OD2	4:AD:115:ARG:NH2	2.47	0.46
4:AD:148:LYS:CD	4:AD:148:LYS:H	2.28	0.46
5:AE:75:ALA:O	5:AE:82:GLN:NE2	2.49	0.46
8:AH:113:ASP:O	8:AH:117:ARG:HB2	2.16	0.46
10:AJ:80:THR:HG22	10:AJ:82:LYS:H	1.80	0.46
16:AP:51:ARG:HH11	16:AP:51:ARG:CG	2.27	0.46
21:AU:38:TYR:C	21:AU:41:PRO:HD2	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:26:G:H1'	22:BA:514:A:N6	2.29	0.46
22:BA:264:C:O2'	22:BA:265:A:H2'	2.15	0.46
22:BA:632:A:H2'	22:BA:633:A:C8	2.50	0.46
22:BA:734:A:C5	22:BA:735:A:C8	3.04	0.46
22:BA:1510:G:H2'	22:BA:1511:G:O4'	2.16	0.46
22:BA:2580:U:H5"	25:BD:135:GLY:O	2.15	0.46
26:BE:7:ASP:O	26:BE:9:GLN:N	2.48	0.46
29:BH:132:PHE:CD2	29:BH:142:VAL:CG2	2.99	0.46
32:BK:103:VAL:HB	32:BK:107:LEU:HD13	1.98	0.46
34:BM:12:MET:HE3	34:BM:72:PRO:HD2	1.96	0.46
37:BP:10:GLN:C	37:BP:12:GLN:H	2.22	0.46
38:BQ:17:ILE:HG12	38:BQ:36:PHE:HD2	1.80	0.46
53:B5:59:VAL:HG21	53:B5:167:ASP:H	1.80	0.46
1:CA:15:G:C2	1:CA:16:A:C4	3.03	0.46
1:CA:107:G:H22	20:CT:5:LYS:NZ	2.13	0.46
1:CA:1447:A:P	1:CA:1448:C:H41	2.39	0.46
8:CH:5:ASP:OD1	8:CH:81:PRO:HD3	2.15	0.46
17:CQ:14:SER:C	17:CQ:17:MET:HE1	2.41	0.46
22:DA:19:A:O2'	22:DA:553:G:H4'	2.16	0.46
22:DA:1265:A:N1	22:DA:2013:A:H5"	2.30	0.46
22:DA:1269:A:H8	22:DA:1269:A:O5'	1.99	0.46
22:DA:1527:G:H21	22:DA:1545:A:H62	1.63	0.46
22:DA:1666:G:O3'	32:DK:6:THR:HG23	2.15	0.46
22:DA:1895:C:H2'	22:DA:1896:G:C8	2.50	0.46
22:DA:2461:A:H1'	22:DA:2492:U:N3	2.31	0.46
22:DA:2545:G:N3	22:DA:2565:A:H2	2.13	0.46
25:DD:30:GLU:HG2	25:DD:185:ASN:ND2	2.30	0.46
29:DH:53:GLU:C	29:DH:55:GLU:N	2.72	0.46
30:DI:92:LYS:HB3	30:DI:95:LYS:HE3	1.97	0.46
41:DT:46:ALA:O	41:DT:50:LEU:HB2	2.15	0.46
6:AF:17:GLN:NE2	6:AF:17:GLN:O	2.49	0.46
8:AH:7:ILE:HD11	8:AH:32:LEU:HG	1.97	0.46
22:BA:26:G:C6	22:BA:27:G:N1	2.83	0.46
22:BA:555:G:O2'	22:BA:556:A:OP2	2.34	0.46
22:BA:686:U:H2'	22:BA:788:A:C2	2.50	0.46
22:BA:1085:A:C6	22:BA:1086:A:N6	2.83	0.46
22:BA:1176:U:H2'	22:BA:1177:G:N9	2.31	0.46
22:BA:1657:U:P	25:BD:141:ARG:HG3	2.56	0.46
22:BA:1820:U:O2'	24:BC:158:ALA:O	2.29	0.46
22:BA:2012:G:OP1	40:BS:98:LYS:NZ	2.39	0.46
22:BA:2436:G:C2	22:BA:2437:G:C8	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2839:G:O2'	35:BN:49:GLU:OE1	2.26	0.46
23:BB:90:C:H5"	34:BM:18:ARG:HG3	1.97	0.46
24:BC:204:VAL:O	24:BC:206:GLY:N	2.48	0.46
25:BD:16:THR:O	37:BP:79:PRO:HG2	2.15	0.46
29:BH:37:VAL:CG2	29:BH:38:PRO:HD2	2.45	0.46
29:BH:80:ILE:HG21	29:BH:94:ILE:CG1	2.45	0.46
30:BI:21:SER:HA	30:BI:25:GLY:HA2	1.98	0.46
30:BI:102:SER:OG	30:BI:103:ARG:N	2.48	0.46
35:BN:73:ASN:HA	35:BN:76:VAL:CG1	2.46	0.46
1:CA:313:A:H2'	1:CA:314:C:H6	1.80	0.46
1:CA:458:U:H2'	1:CA:459:A:C8	2.50	0.46
1:CA:473:U:H2'	1:CA:474:G:H8	1.80	0.46
1:CA:1342:C:H1'	9:CI:126:GLN:HG3	1.97	0.46
1:CA:1417:G:C6	1:CA:1482:G:C6	3.04	0.46
4:CD:117:LEU:HB3	4:CD:123:ILE:HD11	1.98	0.46
9:CI:12:ARG:HD2	9:CI:107:ASP:HB3	1.98	0.46
13:CM:4:ILE:HA	13:CM:57:ARG:CZ	2.45	0.46
22:DA:1:G:C2	22:DA:2:G:C4	3.03	0.46
22:DA:784:G:OP1	22:DA:2588:G:H5"	2.15	0.46
22:DA:812:C:H4'	38:DQ:13:ARG:HH12	1.81	0.46
22:DA:1012:U:O4	31:DJ:30:THR:HG21	2.16	0.46
22:DA:1073:A:H2'	22:DA:1074:G:H5'	1.97	0.46
22:DA:1344:U:O5'	22:DA:1344:U:H6	1.98	0.46
22:DA:1593:A:H2'	22:DA:1594:U:O4'	2.16	0.46
24:DC:130:LEU:HD12	24:DC:134:ASN:HB2	1.97	0.46
25:DD:179:ARG:HH12	37:DP:8:LEU:HD21	1.79	0.46
27:DF:170:LEU:HA	27:DF:170:LEU:HD23	1.78	0.46
32:DK:21:CYS:HA	32:DK:41:ILE:HG22	1.97	0.46
1:AA:111:G:H5"	1:AA:112:G:OP2	2.15	0.46
1:AA:310:G:H5"	16:AP:31:ARG:HB2	1.97	0.46
1:AA:667:G:OP1	1:AA:732:C:O2'	2.18	0.46
1:AA:872:A:C8	1:AA:874:G:C8	3.03	0.46
9:AI:84:THR:HG21	9:AI:103:PHE:HB3	1.97	0.46
11:AK:16:VAL:HG22	11:AK:18:ASP:H	1.79	0.46
11:AK:83:GLU:HG3	11:AK:109:ASN:ND2	2.30	0.46
22:BA:250:G:C6	22:BA:251:A:C6	3.04	0.46
22:BA:852:U:H2'	22:BA:853:C:C6	2.50	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:BA:2469:A:H4'	34:BM:55:ARG:HH12	1.81	0.46
29:BH:93:SER:O	1:CA:368:U:O4'	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
47:BZ:31:ARG:HG2	47:BZ:34:HIS:HB2	1.97	0.46
1:CA:478:A:H8	1:CA:478:A:OP2	1.99	0.46
1:CA:988:G:N2	1:CA:1217:C:O2	2.49	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
4:CD:168:PRO:HB2	4:CD:171:LEU:CD1	2.45	0.46
6:CF:47:LEU:HG	6:CF:56:LYS:N	2.30	0.46
9:CI:22:LYS:O	9:CI:62:ASP:N	2.40	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
14:CN:13:ARG:HG2	14:CN:54:ASP:CG	2.40	0.46
22:DA:480:A:H5"	42:DU:44:LYS:HD2	1.97	0.46
22:DA:1196:C:H1'	22:DA:1226:A:C4	2.51	0.46
22:DA:1904:G:O2'	22:DA:1927:A:N6	2.40	0.46
22:DA:2351:G:O2'	22:DA:2366:A:N6	2.43	0.46
24:DC:51:THR:HG22	24:DC:54:ILE:HD11	1.97	0.46
29:DH:34:GLY:O	29:DH:35:LYS:CG	2.64	0.46
36:DO:27:VAL:HA	36:DO:93:ASP:HB3	1.97	0.46
45:DX:39:TRP:HB2	45:DX:46:PHE:CE2	2.51	0.46
45:DX:40:VAL:HG21	45:DX:43:GLU:HB2	1.98	0.46
1:AA:676:A:H5"	11:AK:115:PRO:HB3	1.96	0.46
1:AA:903:G:H2'	1:AA:904:U:C6	2.51	0.46
1:AA:991:U:C4	1:AA:1212:U:H1'	2.50	0.46
1:AA:1157:A:C4	1:AA:1181:G:C6	3.04	0.46
1:AA:1216:A:OP1	14:AN:5:SER:OG	2.29	0.46
2:AB:64:LYS:HD3	2:AB:65:GLY:N	2.30	0.46
5:AE:81:LEU:HD21	5:AE:123:VAL:HG13	1.97	0.46
7:AG:109:ARG:HH21	7:AG:119:ARG:NH1	2.14	0.46
16:AP:50:THR:O	16:AP:50:THR:HG22	2.15	0.46
22:BA:58:G:O2'	22:BA:73:A:N1	2.45	0.46
22:BA:195:A:N7	57:BA:3764:HOH:O	2.36	0.46
22:BA:349:U:H2'	22:BA:350:G:C8	2.44	0.46
22:BA:601:C:O2	22:BA:605:G:H4'	2.16	0.46
22:BA:640:C:H2'	22:BA:641:U:C6	2.51	0.46
22:BA:2271:G:H2'	22:BA:2272:U:H6	1.80	0.46
22:BA:2425:A:H4'	22:BA:2426:A:O5'	2.15	0.46
25:BD:2:ILE:HG13	25:BD:100:LEU:HD21	1.97	0.46
29:BH:94:ILE:HG23	29:BH:98:ASP:HB2	1.98	0.46
47:BZ:37:GLU:O	47:BZ:38:ARG:HD3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:63:C:O2'	1:CA:380:G:H4'	2.15	0.46
1:CA:77:A:H2'	1:CA:78:A:O4'	2.14	0.46
1:CA:441:A:N6	1:CA:494:G:H22	2.14	0.46
1:CA:497:G:O2'	1:CA:498:A:H5'	2.15	0.46
1:CA:1126:U:H3	10:CJ:42:LEU:HD21	1.80	0.46
1:CA:1150:A:N6	1:CA:1151:A:H62	2.14	0.46
1:CA:1527:U:H2'	1:CA:1528:U:C6	2.50	0.46
7:CG:11:LYS:HB3	7:CG:21:GLU:OE1	2.15	0.46
13:CM:6:GLY:C	13:CM:8:ASN:H	2.23	0.46
13:CM:66:GLU:HB3	13:CM:67:GLY:H	1.54	0.46
14:CN:88:ALA:HB2	14:CN:96:LEU:HD23	1.97	0.46
15:CO:70:LEU:HD22	15:CO:78:TYR:HB2	1.97	0.46
22:DA:53:A:C2	22:DA:179:C:H4'	2.50	0.46
22:DA:129:C:H2'	22:DA:130:C:H6	1.80	0.46
22:DA:327:G:N2	42:DU:68:SER:HB2	2.30	0.46
22:DA:814:C:OP1	39:DR:86:GLN:HG3	2.16	0.46
22:DA:1113:U:H2'	22:DA:1114:C:C6	2.51	0.46
22:DA:1430:G:H2'	22:DA:1431:A:O4'	2.16	0.46
22:DA:2290:G:N2	22:DA:2343:U:H1'	2.30	0.46
22:DA:2572:A:N7	25:DD:150:GLN:HB3	2.30	0.46
24:DC:66:ASP:N	24:DC:103:TYR:O	2.40	0.46
29:DH:27:ARG:HE	45:DX:60:ASP:CB	2.27	0.46
34:DM:108:VAL:HG12	34:DM:109:PRO:HD2	1.98	0.46
44:DW:34:GLY:O	44:DW:60:PHE:HB2	2.15	0.46
47:DZ:16:ARG:H	47:DZ:16:ARG:HG2	1.52	0.46
49:D1:15:ALA:O	49:D1:17:THR:N	2.48	0.46
49:D1:38:LYS:HB2	49:D1:49:TYR:CD2	2.51	0.46
1:AA:572:A:H5'	1:AA:573:A:OP2	2.15	0.46
1:AA:1166:G:O2'	1:AA:1169:A:N6	2.48	0.46
1:AA:1312:G:N7	19:AS:3:ARG:N	2.63	0.46
1:AA:1351:U:H2'	1:AA:1352:C:H6	1.81	0.46
1:AA:1417:G:C6	1:AA:1482:G:C6	3.04	0.46
2:AB:47:VAL:HB	2:AB:48:PRO:HD3	1.98	0.46
2:AB:216:ALA:O	2:AB:220:THR:HG22	2.16	0.46
4:AD:148:LYS:H	4:AD:148:LYS:HD3	1.79	0.46
12:AL:3:THR:HG22	12:AL:5:ASN:N	2.30	0.46
17:AQ:79:VAL:HG12	17:AQ:80:GLU:HG3	1.98	0.46
18:AR:72:ASP:OD2	21:AU:4:ILE:HG13	2.15	0.46
21:AU:12:PHE:N	21:AU:12:PHE:CD2	2.83	0.46
22:BA:923:G:H4'	44:BW:29:GLU:HG3	1.97	0.46
22:BA:1048:A:N1	22:BA:1112:G:O2'	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1069:A:N1	22:BA:1073:A:N6	2.63	0.46
22:BA:1474:U:H2'	22:BA:1475:G:H5'	1.97	0.46
22:BA:1845:G:H2'	22:BA:1846:G:O4'	2.15	0.46
26:BE:23:PHE:HB2	26:BE:114:ARG:HH12	1.81	0.46
29:BH:89:LYS:O	29:BH:90:LEU:C	2.58	0.46
31:BJ:31:GLU:OE2	31:BJ:35:ARG:NH1	2.46	0.46
36:BO:64:TYR:HB3	36:BO:67:ASN:ND2	2.30	0.46
44:BW:41:ARG:O	44:BW:57:HIS:ND1	2.33	0.46
44:BW:46:HIS:CE1	44:BW:77:ARG:HD3	2.51	0.46
48:B0:43:ILE:HG22	48:B0:49:TYR:HB2	1.96	0.46
1:CA:81:A:H2'	1:CA:82:G:H8	1.80	0.46
1:CA:159:G:H21	1:CA:161:A:H3'	1.81	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
1:CA:1219:A:N6	1:CA:1220:G:O6	2.49	0.46
8:CH:59:LEU:HD12	8:CH:60:GLU:N	2.31	0.46
12:CL:86:ARG:CZ	12:CL:88:LYS:HB3	2.45	0.46
14:CN:64:CYS:SG	14:CN:80:SER:HB2	2.56	0.46
15:CO:67:LEU:HD23	15:CO:78:TYR:HE1	1.81	0.46
22:DA:190:A:H2'	22:DA:191:A:O4'	2.15	0.46
22:DA:1571:A:H8	22:DA:1571:A:O5'	1.98	0.46
22:DA:2799:A:O2'	22:DA:2800:A:H5"	2.16	0.46
24:DC:197:ASN:OD1	24:DC:200:HIS:HB2	2.16	0.46
26:DE:149:ILE:CG2	26:DE:188:MET:HG2	2.46	0.46
41:DT:64:LYS:HA	41:DT:79:ASP:OD1	2.16	0.46
1:AA:168:G:C6	1:AA:169:C:C4	3.04	0.46
1:AA:390:U:H2'	1:AA:391:G:C8	2.50	0.46
1:AA:1410:A:H2'	1:AA:1411:C:C6	2.50	0.46
3:AC:22:TRP:CB	3:AC:59:ARG:HG2	2.45	0.46
3:AC:134:MET:HE2	3:AC:168:TYR:HD1	1.81	0.46
4:AD:122:ALA:HA	4:AD:146:ARG:HG3	1.97	0.46
4:AD:151:LYS:HB2	4:AD:156:LYS:CE	2.46	0.46
9:AI:81:HIS:O	9:AI:84:THR:OG1	2.29	0.46
12:AL:36:ARG:HB3	12:AL:38:TYR:HE2	1.80	0.46
22:BA:936:A:H2'	22:BA:937:C:C6	2.51	0.46
22:BA:1744:A:H3'	22:BA:1745:A:H8	1.81	0.46
22:BA:1789:A:OP1	24:BC:221:ARG:HD3	2.14	0.46
22:BA:2334:U:O4	36:BO:16:ARG:NH2	2.49	0.46
22:BA:2566:A:N1	32:BK:28:SER:OG	2.41	0.46
22:BA:2815:C:O2'	48:B0:40:ARG:HB3	2.16	0.46
27:BF:136:ILE:H	27:BF:136:ILE:HD12	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BQ:41:LYS:HB2	38:BQ:41:LYS:HE3	1.53	0.46
43:BV:30:ILE:HG22	43:BV:93:ARG:HG3	1.98	0.46
45:BX:5:CYS:SG	45:BX:8:THR:HG23	2.55	0.46
1:CA:524:G:O5'	1:CA:524:G:H8	1.98	0.46
1:CA:676:A:H5"	11:CK:115:PRO:HB3	1.97	0.46
1:CA:1160:G:O6	1:CA:1181:G:C6	2.69	0.46
1:CA:1222:G:H5"	19:CS:78:ARG:NH1	2.30	0.46
3:CC:42:TYR:CE1	3:CC:90:VAL:HG21	2.50	0.46
4:CD:169:THR:C	4:CD:171:LEU:H	2.24	0.46
8:CH:26:THR:HA	8:CH:59:LEU:O	2.16	0.46
9:CI:47:VAL:O	9:CI:50:GLN:HB2	2.16	0.46
13:CM:3:ARG:HA	13:CM:9:ILE:HG12	1.96	0.46
15:CO:89:ARG:HH12	22:DA:716:A:P	2.38	0.46
19:CS:10:PHE:O	19:CS:39:THR:OG1	2.33	0.46
19:CS:70:LYS:O	19:CS:73:GLU:HB2	2.16	0.46
22:DA:635:C:H2'	22:DA:636:G:C8	2.50	0.46
22:DA:866:A:O4'	22:DA:914:G:N2	2.48	0.46
22:DA:2408:U:H2'	22:DA:2409:G:C8	2.51	0.46
22:DA:2721:A:H2'	22:DA:2722:G:C8	2.50	0.46
28:DG:9:VAL:HG23	28:DG:69:ARG:HD2	1.97	0.46
30:DI:127:ARG:H	30:DI:127:ARG:HD3	1.81	0.46
32:DK:104:THR:O	32:DK:106:GLU:N	2.48	0.46
35:DN:53:THR:HA	35:DN:56:LYS:HG2	1.96	0.46
45:DX:49:LEU:O	45:DX:51:VAL:HG13	2.15	0.46
52:D4:25:VAL:HB	52:D4:35:GLN:HG3	1.98	0.46
1:AA:222:C:H2'	1:AA:223:A:H8	1.81	0.46
1:AA:375:U:C4	1:AA:376:G:N7	2.84	0.46
1:AA:720:C:H5'	18:AR:41:PRO:HA	1.98	0.46
3:AC:147:LYS:HB2	3:AC:203:PHE:CD2	2.51	0.46
4:AD:31:LYS:HE2	4:AD:31:LYS:HB2	1.56	0.46
5:AE:104:GLY:HA3	5:AE:122:ASN:HA	1.97	0.46
6:AF:11:HIS:HA	6:AF:12:PRO:HD2	1.67	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:BA:714:U:HO2'	22:BA:716:A:H62	1.56	0.46
22:BA:1165:A:H2'	22:BA:1166:G:H8	1.81	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
22:BA:2813:A:H2	22:BA:2887:A:H61	1.63	0.46
24:BC:71:LYS:HE3	24:BC:96:TYR:CD2	2.51	0.46
24:BC:212:ARG:HA	24:BC:212:ARG:HD2	1.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BF:41:GLY:O	27:BF:43:ALA:N	2.49	0.46
29:BH:45:GLU:C	29:BH:47:PHE:N	2.72	0.46
39:BR:61:ALA:HB2	39:BR:98:ILE:HD13	1.98	0.46
53:B5:65:LEU:HD12	53:B5:67:HIS:HB2	1.97	0.46
1:CA:801:U:H2'	1:CA:802:A:C8	2.46	0.46
1:CA:990:C:C4	1:CA:991:U:O4	2.69	0.46
2:CB:27:MET:SD	2:CB:193:PRO:HD3	2.56	0.46
2:CB:83:ALA:HA	2:CB:86:SER:HB3	1.98	0.46
4:CD:41:HIS:O	4:CD:44:ARG:HG2	2.16	0.46
18:CR:40:VAL:HA	18:CR:41:PRO:HD2	1.77	0.46
22:DA:528:A:C2	22:DA:2043:C:H4'	2.50	0.46
22:DA:564:C:O4'	38:DQ:37:GLN:NE2	2.49	0.46
22:DA:593:U:H2'	22:DA:594:U:C6	2.51	0.46
22:DA:1091:G:O2'	22:DA:1092:C:OP2	2.25	0.46
22:DA:1800:C:OP2	24:DC:182:ARG:NH1	2.49	0.46
22:DA:2704:C:H3'	22:DA:2705:A:H8	1.81	0.46
23:DB:13:G:H1	23:DB:69:G:HO2'	1.64	0.46
27:DF:53:ALA:HB2	27:DF:150:ARG:HD2	1.96	0.46
29:DH:60:GLU:HA	29:DH:60:GLU:OE2	2.15	0.46
30:DI:15:ALA:HB3	30:DI:52:GLY:N	2.31	0.46
31:DJ:40:HIS:O	38:DQ:67:ALA:HB1	2.16	0.46
3:AC:47:LEU:HB3	3:AC:50:ALA:HB3	1.97	0.46
3:AC:139:GLN:O	3:AC:141:ALA:N	2.49	0.46
4:AD:165:ARG:O	4:AD:167:LYS:N	2.49	0.46
22:BA:570:G:H2'	22:BA:2030:A:N7	2.31	0.46
22:BA:589:U:H2'	22:BA:590:A:C8	2.51	0.46
22:BA:714:U:O2'	22:BA:716:A:N6	2.32	0.46
22:BA:864:G:C6	22:BA:865:C:N4	2.84	0.46
22:BA:954:G:OP2	34:BM:16:ARG:NH2	2.44	0.46
22:BA:2052:A:H4'	25:BD:148:GLN:O	2.16	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
32:BK:36:GLY:HA2	32:BK:62:VAL:O	2.16	0.46
1:CA:110:C:H2'	1:CA:111:G:O4'	2.16	0.46
1:CA:1238:A:N3	1:CA:1241:G:O2'	2.45	0.46
1:CA:1240:U:O4	7:CG:116:MET:HE2	2.16	0.46
2:CB:35:ARG:O	2:CB:38:VAL:HG12	2.16	0.46
2:CB:90:PHE:HB3	2:CB:150:GLY:O	2.16	0.46
3:CC:39:VAL:O	3:CC:43:LEU:HB2	2.16	0.46
4:CD:187:GLU:N	4:CD:190:ASP:OD1	2.45	0.46
12:CL:90:LEU:HB2	12:CL:93:VAL:CG2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:188:G:C6	22:DA:189:G:C4	3.04	0.46
22:DA:635:C:O2'	22:DA:639:U:H5"	2.16	0.46
22:DA:1073:A:H4'	22:DA:2474:U:H4'	1.97	0.46
22:DA:1190:G:H5"	33:DL:32:GLY:O	2.15	0.46
22:DA:1525:A:H2'	22:DA:1526:C:O4'	2.16	0.46
22:DA:1592:C:H2'	22:DA:1593:A:H8	1.78	0.46
22:DA:1957:C:H5'	22:DA:1984:G:O2'	2.15	0.46
22:DA:1998:A:H4'	22:DA:2724:U:O2'	2.16	0.46
22:DA:2053:G:H5'	25:DD:149:ASN:O	2.16	0.46
22:DA:2093:G:O6	22:DA:2225:A:H5"	2.15	0.46
22:DA:2627:G:N2	22:DA:2777:G:OP2	2.48	0.46
28:DG:105:LEU:HB2	28:DG:113:VAL:HB	1.97	0.46
1:AA:971:G:O6	1:AA:1364:U:O2'	2.34	0.45
4:AD:29:ASP:C	4:AD:30:THR:O	2.58	0.45
5:AE:14:LYS:NZ	5:AE:116:GLU:OE1	2.36	0.45
9:AI:30:ILE:HD12	9:AI:79:ILE:HD11	1.97	0.45
10:AJ:80:THR:O	10:AJ:84:VAL:N	2.41	0.45
13:AM:26:GLY:O	13:AM:28:THR:N	2.49	0.45
18:AR:47:THR:HG21	18:AR:52:GLN:HB2	1.99	0.45
22:BA:711:G:H2'	22:BA:712:G:O4'	2.16	0.45
22:BA:721:A:H2'	22:BA:722:A:H8	1.79	0.45
22:BA:2849:U:H4'	22:BA:2868:A:C2	2.51	0.45
29:BH:129:GLU:C	29:BH:130:VAL:CG2	2.90	0.45
29:BH:129:GLU:C	29:BH:130:VAL:HG23	2.41	0.45
32:BK:70:ARG:NH1	32:BK:74:GLY:O	2.44	0.45
37:BP:109:ARG:HB2	37:BP:109:ARG:HH21	1.81	0.45
1:CA:81:A:H61	1:CA:87:C:N4	2.13	0.45
1:CA:687:A:O2'	1:CA:701:U:O4	2.12	0.45
1:CA:1010:U:H2'	1:CA:1011:C:C6	2.51	0.45
1:CA:1060:U:H2'	1:CA:1061:G:H8	1.80	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
7:CG:23:LEU:HD23	7:CG:26:PHE:HB3	1.98	0.45
11:CK:30:THR:HG21	11:CK:92:GLY:HA3	1.99	0.45
12:CL:99:ARG:HB2	12:CL:117:TYR:HA	1.98	0.45
13:CM:19:LEU:HG	13:CM:34:LEU:HD21	1.99	0.45
15:CO:39:LEU:HD12	15:CO:39:LEU:HA	1.85	0.45
22:DA:67:U:H2'	22:DA:68:G:O4'	2.16	0.45
22:DA:310:A:O2'	22:DA:311:A:OP2	2.26	0.45
22:DA:1494:A:H2'	22:DA:1495:A:C8	2.51	0.45
22:DA:1736:U:H2'	22:DA:1737:G:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1738:G:O2'	22:DA:1739:A:H8	1.99	0.45
22:DA:1995:U:OP1	57:DA:3809:HOH:O	2.21	0.45
22:DA:2419:U:H2'	22:DA:2420:C:C6	2.50	0.45
39:DR:43:ASN:HB3	39:DR:44:GLY:H	1.52	0.45
47:DZ:41:THR:HG23	47:DZ:44:ILE:CG1	2.42	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
1:AA:1520:C:H2'	1:AA:1521:C:C6	2.52	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
7:AG:29:ILE:HD12	7:AG:101:MET:HE3	1.97	0.45
22:BA:156:A:H2'	22:BA:157:C:O4'	2.16	0.45
22:BA:1008:A:N6	22:BA:1136:G:C6	2.84	0.45
22:BA:1712:U:OP2	22:BA:1713:A:O2'	2.29	0.45
29:BH:30:LEU:C	29:BH:32:PRO:HD2	2.41	0.45
29:BH:79:THR:HG23	29:BH:147:VAL:HB	1.98	0.45
29:BH:88:GLY:C	29:BH:125:THR:OG1	2.59	0.45
29:BH:94:ILE:HG23	29:BH:98:ASP:CB	2.47	0.45
30:BI:67:PHE:CD2	30:BI:67:PHE:N	2.84	0.45
45:BX:68:LEU:HD13	45:BX:78:TYR:CE1	2.51	0.45
1:CA:484:G:C5	1:CA:486:U:H1'	2.51	0.45
1:CA:1478:U:H2'	1:CA:1479:C:C6	2.50	0.45
1:CA:1537:U:H5"	1:CA:1538:C:OP2	2.16	0.45
2:CB:14:VAL:H	2:CB:208:ARG:NH1	2.15	0.45
9:CI:99:ARG:HA	9:CI:104:VAL:HG21	1.97	0.45
22:DA:783:A:H8	22:DA:784:G:H4'	1.81	0.45
22:DA:825:A:H4'	22:DA:2428:G:C5	2.51	0.45
22:DA:961:C:C2	22:DA:2031:A:C6	3.05	0.45
22:DA:1998:A:OP2	25:DD:141:ARG:NH2	2.48	0.45
22:DA:2033:A:H4'	22:DA:2034:U:OP1	2.15	0.45
22:DA:2091:C:H3'	22:DA:2092:U:H5"	1.98	0.45
22:DA:2353:G:H2'	22:DA:2354:C:O4'	2.16	0.45
27:DF:106:ILE:O	27:DF:110:ARG:HD3	2.16	0.45
27:DF:106:ILE:HG12	27:DF:107:ALA:N	2.31	0.45
29:DH:83:LYS:HG3	29:DH:149:GLU:HG3	1.93	0.45
32:DK:59:LYS:HG3	32:DK:89:ASN:OD1	2.16	0.45
35:DN:87:PHE:HE1	35:DN:116:VAL:HG12	1.81	0.45
40:DS:86:MET:HE3	40:DS:87:PRO:HD2	1.98	0.45
1:AA:451:A:H5"	16:AP:70:ARG:NH2	2.32	0.45
1:AA:675:A:H5'	18:AR:71:THR:HG21	1.99	0.45
1:AA:719:C:O2'	18:AR:38:LYS:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:843:U:OP1	1:AA:846:G:N2	2.42	0.45
1:AA:1008:U:H2'	1:AA:1009:U:C6	2.51	0.45
1:AA:1060:U:OP1	14:AN:85:ARG:NH2	2.42	0.45
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.51	0.45
13:AM:15:ALA:O	13:AM:19:LEU:HD23	2.16	0.45
21:AU:12:PHE:N	21:AU:12:PHE:HD2	2.14	0.45
21:AU:16:LEU:C	21:AU:18:ARG:HD2	2.42	0.45
22:BA:1113:U:OP1	28:BG:3:ARG:NH1	2.49	0.45
22:BA:1324:G:C4	22:BA:1328:A:N6	2.84	0.45
22:BA:2844:G:H2'	22:BA:2845:U:O4'	2.16	0.45
33:BL:91:ASP:O	33:BL:94:THR:HB	2.17	0.45
40:BS:55:ILE:HG23	40:BS:66:ILE:HG12	1.97	0.45
41:BT:33:LYS:HG3	41:BT:80:TRP:CE3	2.50	0.45
42:BU:39:ILE:HG22	42:BU:40:ASN:N	2.31	0.45
1:CA:673:A:H2'	1:CA:674:G:C8	2.51	0.45
1:CA:705:G:N2	11:CK:31:ILE:HD12	2.32	0.45
1:CA:745:G:H5"	1:CA:851:G:O2'	2.16	0.45
1:CA:976:G:OP2	1:CA:1358:U:O2'	2.34	0.45
2:CB:72:THR:HG22	2:CB:95:ARG:HH11	1.80	0.45
2:CB:183:VAL:HG12	2:CB:196:VAL:HG13	1.98	0.45
4:CD:4:TYR:O	4:CD:5:LEU:HB2	2.15	0.45
5:CE:101:GLU:HA	5:CE:122:ASN:CB	2.46	0.45
17:CQ:19:LYS:O	17:CQ:71:LYS:NZ	2.39	0.45
22:DA:12:U:O2	22:DA:12:U:H2'	2.15	0.45
22:DA:40:U:H2'	22:DA:41:C:C6	2.50	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:DA:2293:G:H5"	36:DO:94:ARG:HH22	1.80	0.45
22:DA:2575:C:O2'	22:DA:2578:G:N7	2.45	0.45
25:DD:170:VAL:HG23	25:DD:194:PRO:HB3	1.97	0.45
29:DH:112:LYS:HG2	29:DH:113:SER:N	2.32	0.45
30:DI:21:SER:HB3	30:DI:22:PRO:HD3	1.98	0.45
35:DN:22:ARG:HG3	35:DN:70:THR:HA	1.97	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
4:AD:123:ILE:N	4:AD:146:ARG:HG3	2.31	0.45
4:AD:195:ILE:HG13	4:AD:197:GLU:OE2	2.16	0.45
11:AK:29:ASN:OD1	11:AK:47:ALA:HB3	2.16	0.45
13:AM:54:ASP:HB3	13:AM:57:ARG:HH21	1.81	0.45
16:AP:4:ILE:HA	16:AP:20:VAL:O	2.17	0.45
22:BA:284:U:H2'	22:BA:285:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:BB:42:C:C5	27:BF:66:LEU:HD22	2.51	0.45
24:BC:252:THR:HG22	24:BC:253:LYS:H	1.82	0.45
36:BO:26:LEU:HD22	36:BO:115:LEU:HD23	1.99	0.45
46:BY:45:GLN:O	46:BY:46:VAL:HB	2.16	0.45
1:CA:898:G:O2'	1:CA:900:A:N7	2.48	0.45
1:CA:922:G:N3	1:CA:1398:A:H2	2.15	0.45
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.52	0.45
2:CB:35:ARG:O	2:CB:37:LYS:N	2.50	0.45
4:CD:9:LEU:HD12	4:CD:9:LEU:HA	1.63	0.45
4:CD:29:ASP:O	4:CD:31:LYS:NZ	2.33	0.45
5:CE:138:ARG:H	5:CE:141:ILE:CD1	2.29	0.45
10:CJ:36:VAL:HG22	10:CJ:76:ILE:HG12	1.99	0.45
12:CL:34:CYS:HB3	12:CL:55:VAL:HG22	1.98	0.45
18:CR:25:ASP:O	18:CR:28:THR:N	2.49	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
22:DA:675:A:C6	22:DA:676:A:C6	3.04	0.45
22:DA:1223:G:N2	22:DA:1226:A:OP2	2.46	0.45
22:DA:1669:A:O4'	32:DK:5:GLN:HG3	2.16	0.45
22:DA:1906:G:OP2	22:DA:1929:G:O2'	2.35	0.45
22:DA:2093:G:O2'	22:DA:2094:A:H5'	2.16	0.45
22:DA:2243:U:H2'	22:DA:2244:U:C6	2.52	0.45
22:DA:2864:G:H2'	22:DA:2865:U:O4'	2.16	0.45
26:DE:177:PRO:O	26:DE:181:ILE:HG13	2.16	0.45
29:DH:34:GLY:O	29:DH:35:LYS:CD	2.65	0.45
30:DI:62:TYR:CB	30:DI:64:ASP:H	2.28	0.45
36:DO:24:THR:HG23	36:DO:42:PRO:HD3	1.97	0.45
44:DW:48:GLY:H	44:DW:51:VAL:HB	1.82	0.45
48:D0:55:ILE:HG22	48:D0:56:ALA:N	2.30	0.45
1:AA:205:A:H2'	1:AA:205:A:N3	2.30	0.45
1:AA:271:C:H2'	1:AA:272:C:C6	2.52	0.45
1:AA:1095:U:H2'	1:AA:1096:C:O4'	2.17	0.45
1:AA:1444:U:H2'	1:AA:1445:U:C6	2.52	0.45
1:AA:1538:C:H2'	1:AA:1539:C:H5'	1.99	0.45
2:AB:42:ASN:HB3	2:AB:45:LYS:HB3	1.98	0.45
3:AC:5:VAL:HG21	3:AC:10:ILE:HD13	1.98	0.45
4:AD:160:GLU:O	4:AD:162:ALA:N	2.50	0.45
5:AE:157:ARG:NH2	8:AH:100:GLY:H	2.14	0.45
15:AO:43:PHE:CE1	15:AO:56:LEU:HD22	2.51	0.45
19:AS:36:ARG:HB3	19:AS:72:GLY:HA3	1.98	0.45
22:BA:1084:A:C2	22:BA:1106:G:H1'	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1424:G:H2'	22:BA:1425:G:O4'	2.16	0.45
22:BA:1435:G:H2'	22:BA:1436:G:H8	1.82	0.45
22:BA:1915:U:C2'	22:BA:1916:A:H5'	2.46	0.45
28:BG:170:ARG:HH12	52:B4:29:ALA:HA	1.82	0.45
29:BH:90:LEU:HG	29:BH:92:GLY:C	2.42	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
1:CA:857:C:H2'	1:CA:858:G:O4'	2.16	0.45
2:CB:72:THR:HG23	2:CB:94:HIS:O	2.17	0.45
2:CB:173:ILE:HG22	2:CB:177:ASN:ND2	2.31	0.45
3:CC:63:SER:OG	3:CC:64:ILE:N	2.48	0.45
22:DA:479:A:N3	22:DA:481:G:H5"	2.31	0.45
22:DA:651:G:H5'	51:D3:19:LYS:HG3	1.98	0.45
22:DA:708:G:N2	22:DA:724:U:H1'	2.31	0.45
22:DA:1087:G:H2'	22:DA:1088:A:H5'	1.99	0.45
22:DA:1089:A:O2'	22:DA:1090:A:N7	2.42	0.45
22:DA:1120:G:C6	22:DA:1121:C:C4	3.05	0.45
22:DA:1926:U:H1'	22:DA:1929:G:C6	2.52	0.45
22:DA:2280:G:O2'	22:DA:2388:A:N1	2.48	0.45
22:DA:2533:U:OP1	22:DA:2665:A:O2'	2.33	0.45
22:DA:2888:C:H2'	22:DA:2889:C:C6	2.52	0.45
24:DC:43:ARG:NH2	24:DC:49:ILE:HD11	2.31	0.45
29:DH:93:SER:HB3	29:DH:123:ARG:HG3	1.99	0.45
30:DI:62:TYR:C	30:DI:64:ASP:H	2.23	0.45
35:DN:69:ARG:C	35:DN:71:ARG:H	2.19	0.45
36:DO:39:VAL:N	36:DO:49:VAL:O	2.43	0.45
45:DX:17:ASN:OD1	45:DX:27:ARG:HB3	2.17	0.45
1:AA:67:C:H2'	1:AA:68:G:C8	2.52	0.45
1:AA:484:G:H4'	1:AA:485:U:OP1	2.16	0.45
1:AA:540:G:H2'	1:AA:541:G:H8	1.81	0.45
1:AA:695:A:H2'	1:AA:696:A:O4'	2.17	0.45
1:AA:762:U:H2'	1:AA:763:G:C8	2.51	0.45
1:AA:1001:C:H3'	1:AA:1001:C:H6	1.82	0.45
1:AA:1052:U:O2	1:AA:1207:G:N2	2.50	0.45
1:AA:1094:G:HO2'	1:AA:1095:U:P	2.40	0.45
1:AA:1387:G:H2'	1:AA:1388:C:C6	2.51	0.45
9:AI:33:ARG:HG2	9:AI:37:GLN:HB3	1.98	0.45
22:BA:118:A:C8	22:BA:119:A:C8	3.04	0.45
22:BA:500:G:N2	22:BA:502:A:H3'	2.32	0.45
22:BA:1224:U:H4'	39:BR:88:GLY:O	2.16	0.45
22:BA:1333:G:C2	22:BA:1334:G:C8	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1689:A:H2'	22:BA:1690:A:H8	1.81	0.45
22:BA:2065:C:H2'	22:BA:2066:C:H6	1.81	0.45
22:BA:2834:G:H2'	22:BA:2879:A:H61	1.81	0.45
25:BD:12:THR:HG21	37:BP:9:GLU:HG3	1.98	0.45
27:BF:130:MET:HE2	27:BF:132:VAL:HG13	1.99	0.45
35:BN:32:GLU:HA	35:BN:115:LEU:HD12	1.98	0.45
40:BS:86:MET:HE3	40:BS:87:PRO:HD2	1.98	0.45
41:BT:49:LYS:HD3	41:BT:49:LYS:HA	1.71	0.45
45:BX:63:GLY:O	45:BX:65:ASP:N	2.50	0.45
1:CA:206:C:N4	1:CA:213:G:H1	2.15	0.45
1:CA:487:A:H3'	1:CA:488:C:H6	1.81	0.45
1:CA:931:C:H2'	1:CA:932:C:C6	2.51	0.45
1:CA:972:C:H4'	10:CJ:59:LYS:HG2	1.98	0.45
1:CA:1462:C:H2'	1:CA:1463:U:C6	2.51	0.45
4:CD:174:ASP:OD1	4:CD:177:LYS:N	2.46	0.45
5:CE:156:LYS:HA	5:CE:159:LYS:NZ	2.32	0.45
6:CF:43:GLY:HA2	6:CF:58:HIS:NE2	2.32	0.45
8:CH:43:GLU:OE1	8:CH:112:THR:HG21	2.16	0.45
12:CL:79:VAL:HG12	12:CL:102:LEU:HD23	1.99	0.45
16:CP:38:PHE:CE2	16:CP:51:ARG:HD3	2.47	0.45
22:DA:82:U:H2'	22:DA:83:A:C8	2.52	0.45
22:DA:300:A:P	42:DU:82:ARG:HH12	2.39	0.45
22:DA:305:C:H1'	22:DA:313:G:N2	2.32	0.45
22:DA:327:G:H2'	22:DA:328:U:O4'	2.17	0.45
22:DA:334:C:OP1	22:DA:335:C:N4	2.48	0.45
22:DA:367:G:C2	22:DA:368:A:H1'	2.52	0.45
22:DA:1045:C:H1'	22:DA:1047:G:C6	2.52	0.45
22:DA:1063:G:N3	30:DI:90:SER:OG	2.48	0.45
22:DA:1360:G:H5"	57:DA:3614:HOH:O	2.16	0.45
22:DA:1640:A:H2'	22:DA:1641:A:C8	2.51	0.45
22:DA:2311:A:H5"	27:DF:77:PHE:CE1	2.52	0.45
22:DA:2370:G:H4'	49:D1:44:ARG:NH1	2.31	0.45
22:DA:2622:U:O2'	22:DA:2825:G:N7	2.50	0.45
22:DA:2712:C:OP1	22:DA:2714:G:H4'	2.17	0.45
25:DD:113:SER:HB3	25:DD:170:VAL:HG21	1.97	0.45
29:DH:147:VAL:HG12	29:DH:148:ALA:N	2.32	0.45
47:DZ:12:SER:OG	47:DZ:14:ILE:HG13	2.17	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
1:AA:1157:A:C5	1:AA:1180:A:C6	3.05	0.45
2:AB:68:LEU:HD22	2:AB:70:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:78:GLU:C	2:AB:80:VAL:H	2.23	0.45
4:AD:97:ARG:O	4:AD:101:VAL:HG23	2.16	0.45
8:AH:64:LYS:HB2	8:AH:71:VAL:CG2	2.47	0.45
13:AM:15:ALA:HB3	13:AM:34:LEU:HD21	1.99	0.45
22:BA:324:A:N6	22:BA:338:G:O2'	2.48	0.45
22:BA:729:G:H2'	22:BA:1775:U:H1'	1.99	0.45
22:BA:1013:C:O2'	22:BA:1014:A:H5'	2.17	0.45
22:BA:1198:U:H2'	22:BA:1199:U:C6	2.52	0.45
22:BA:1206:G:C6	22:BA:1207:C:C4	3.05	0.45
22:BA:1287:A:C5	22:BA:1288:G:C6	3.05	0.45
22:BA:2094:A:OP2	29:BH:22:LYS:CE	2.65	0.45
22:BA:2579:C:OP1	57:BA:3546:HOH:O	2.21	0.45
22:BA:2820:A:OP2	35:BN:2:ARG:NH1	2.46	0.45
22:BA:2872:A:O2'	22:BA:2873:A:H5'	2.17	0.45
23:BB:17:C:H2'	23:BB:18:G:O4'	2.15	0.45
23:BB:61:G:H2'	23:BB:62:C:H6	1.80	0.45
29:BH:72:ILE:HG23	29:BH:142:VAL:HG22	1.99	0.45
36:BO:28:VAL:HG11	36:BO:92:PHE:CZ	2.51	0.45
49:B1:9:ILE:HD12	49:B1:52:ALA:HB1	1.97	0.45
1:CA:87:C:H2'	1:CA:88:U:C6	2.52	0.45
1:CA:183:C:O2'	1:CA:184:G:O5'	2.34	0.45
1:CA:490:C:H2'	1:CA:491:G:C8	2.52	0.45
1:CA:568:G:N2	1:CA:883:C:C2	2.85	0.45
1:CA:794:A:H2'	1:CA:795:C:C6	2.50	0.45
1:CA:1113:C:H2'	1:CA:1114:C:H6	1.82	0.45
2:CB:82:ASP:H	2:CB:85:LEU:HB3	1.81	0.45
4:CD:105:MET:HE3	4:CD:171:LEU:HD23	1.97	0.45
7:CG:111:ARG:CZ	7:CG:122:ASN:HB3	2.47	0.45
10:CJ:93:ALA:C	10:CJ:95:GLY:H	2.24	0.45
11:CK:71:ALA:O	11:CK:74:VAL:HG22	2.16	0.45
13:CM:27:LYS:O	13:CM:27:LYS:HD3	2.16	0.45
16:CP:46:LYS:HD3	16:CP:47:GLU:H	1.82	0.45
16:CP:52:LEU:HD21	16:CP:57:ILE:HD12	1.99	0.45
22:DA:467:G:P	50:D2:33:ARG:HH11	2.40	0.45
22:DA:588:U:H1'	26:DE:85:PHE:CD1	2.51	0.45
22:DA:1482:G:H1'	22:DA:1509:A:H61	1.81	0.45
22:DA:1499:C:H2'	22:DA:1500:G:H8	1.82	0.45
22:DA:1566:A:H5'	24:DC:214:ARG:CZ	2.46	0.45
22:DA:1717:A:H2'	22:DA:1718:G:O4'	2.16	0.45
22:DA:2093:G:N7	22:DA:2225:A:H2'	2.31	0.45
22:DA:2172:U:H4'	22:DA:2173:A:H5'	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2282:G:N3	22:DA:2425:A:N6	2.65	0.45
22:DA:2286:G:H5"	22:DA:2287:A:OP1	2.17	0.45
26:DE:193:VAL:O	26:DE:197:GLU:HB2	2.16	0.45
29:DH:39:ALA:O	29:DH:41:LYS:N	2.47	0.45
37:DP:28:VAL:HG21	37:DP:74:PHE:CE2	2.52	0.45
47:DZ:51:VAL:O	47:DZ:55:VAL:HG22	2.16	0.45
48:D0:37:LYS:H	48:D0:37:LYS:HG3	1.59	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
1:AA:1479:C:H2'	1:AA:1480:A:O4'	2.17	0.45
3:AC:39:VAL:O	3:AC:43:LEU:HB2	2.17	0.45
3:AC:71:ALA:HB2	3:AC:106:VAL:HB	1.98	0.45
8:AH:109:GLY:O	8:AH:111:MET:HG3	2.17	0.45
22:BA:152:A:H2'	22:BA:153:U:C6	2.52	0.45
22:BA:323:C:H6	22:BA:1205:A:N1	2.14	0.45
22:BA:636:G:N7	33:BL:109:LYS:NZ	2.48	0.45
22:BA:1903:G:H2'	22:BA:1904:G:H8	1.81	0.45
24:BC:121:ASP:OD1	24:BC:121:ASP:N	2.48	0.45
24:BC:157:SER:O	24:BC:195:VAL:HG11	2.17	0.45
25:BD:151:THR:HG22	25:BD:152:PRO:CD	2.47	0.45
28:BG:124:GLU:CD	28:BG:125:CYS:N	2.69	0.45
30:BI:7:ALA:HB2	30:BI:61:VAL:HB	1.99	0.45
38:BQ:110:VAL:HG12	38:BQ:114:LYS:HE2	1.99	0.45
40:BS:10:ALA:N	40:BS:101:SER:O	2.47	0.45
40:BS:82:MET:HG3	40:BS:98:LYS:HB2	1.97	0.45
49:B1:34:LEU:H	49:B1:52:ALA:CB	2.19	0.45
1:CA:238:A:O2'	1:CA:239:U:H5'	2.17	0.45
1:CA:337:G:H2'	1:CA:338:A:H8	1.80	0.45
1:CA:664:G:P	18:CR:53:ARG:HH21	2.40	0.45
1:CA:892:A:O2'	1:CA:1415:G:H4'	2.16	0.45
1:CA:1119:C:OP1	9:CI:11:ARG:NH2	2.50	0.45
1:CA:1144:G:H5"	1:CA:1145:A:OP2	2.17	0.45
3:CC:66:VAL:O	3:CC:101:ILE:HG13	2.16	0.45
9:CI:120:LYS:HG2	9:CI:123:ARG:HB3	1.99	0.45
18:CR:73:ARG:HB2	18:CR:74:HIS:HD2	1.81	0.45
22:DA:722:A:H2'	22:DA:723:C:O4'	2.16	0.45
22:DA:780:G:H21	22:DA:783:A:H62	1.63	0.45
22:DA:846:U:H1'	22:DA:847:U:C5	2.52	0.45
22:DA:1198:U:O2	38:DQ:4:VAL:HG11	2.17	0.45
22:DA:2267:A:H2	57:DA:3506:HOH:O	1.99	0.45
22:DA:2845:U:H5"	37:DP:52:ASN:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DE:119:ILE:HB	26:DE:187:VAL:HG23	1.99	0.45
29:DH:31:VAL:CG1	29:DH:32:PRO:HD3	2.47	0.45
34:DM:134:THR:HB	34:DM:135:VAL:H	1.68	0.45
35:DN:55:ALA:HA	35:DN:80:PHE:CE1	2.52	0.45
36:DO:26:LEU:HB3	36:DO:92:PHE:CD1	2.50	0.45
1:AA:429:U:H4'	1:AA:430:A:OP1	2.17	0.45
1:AA:518:C:H5	1:AA:530:G:OP2	2.00	0.45
1:AA:1093:A:N3	1:AA:1109:C:O2'	2.47	0.45
1:AA:1123:U:O3'	10:AJ:38:GLY:HA3	2.17	0.45
3:AC:42:TYR:OH	3:AC:90:VAL:HG21	2.17	0.45
5:AE:151:GLU:C	5:AE:153:VAL:H	2.25	0.45
9:AI:25:ASN:H	9:AI:62:ASP:CG	2.25	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
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
22:BA:2178:C:H2'	22:BA:2179:C:C6	2.52	0.45
22:BA:2203:U:H5"	22:BA:2204:G:OP1	2.17	0.45
26:BE:149:ILE:HG23	26:BE:188:MET:HG2	1.99	0.45
28:BG:115:HIS:CD2	28:BG:148:LEU:HD21	2.52	0.45
29:BH:12:LEU:HG	29:BH:13:GLY:N	2.31	0.45
29:BH:40:THR:O	29:BH:42:LYS:N	2.48	0.45
29:BH:76:GLU:HA	29:BH:142:VAL:CG1	2.46	0.45
32:BK:91:SER:OG	32:BK:93:GLN:HB2	2.16	0.45
36:BO:37:ALA:HB2	36:BO:106:LEU:HD11	1.99	0.45
49:B1:10:LYS:O	49:B1:51:GLU:HG2	2.17	0.45
1:CA:32:A:C2	1:CA:33:A:C5	3.05	0.45
1:CA:790:A:H2'	1:CA:791:G:C8	2.52	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
6:CF:3:HIS:CD2	6:CF:94:HIS:HA	2.52	0.45
18:CR:34:THR:OG1	18:CR:35:GLU:N	2.49	0.45
22:DA:173:A:H2'	22:DA:174:U:C6	2.52	0.45
22:DA:1462:C:C1'	22:DA:2702:G:H21	2.29	0.45
22:DA:1800:C:H5'	24:DC:146:MET:HE1	1.98	0.45
22:DA:1924:C:H2'	22:DA:1925:C:O4'	2.17	0.45
22:DA:2551:C:H2'	22:DA:2552:U:C6	2.51	0.45
22:DA:2672:U:O5'	22:DA:2672:U:H6	1.99	0.45
28:DG:125:CYS:SG	28:DG:131:ILE:HG12	2.57	0.45
29:DH:5:LEU:CD1	29:DH:13:GLY:CA	2.95	0.45
29:DH:15:LEU:HD22	29:DH:15:LEU:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DI:72:LYS:HG3	30:DI:116:ASP:OD2	2.17	0.45
31:DJ:38:GLY:O	31:DJ:44:TYR:HB2	2.17	0.45
32:DK:17:ARG:N	32:DK:45:GLU:O	2.43	0.45
40:DS:33:LEU:HD21	40:DS:52:GLU:CG	2.47	0.45
40:DS:59:GLU:HA	40:DS:64:ALA:HA	1.99	0.45
1:AA:224:U:H2'	1:AA:225:C:C6	2.52	0.45
1:AA:629:A:H2'	1:AA:630:A:H8	1.82	0.45
1:AA:708:C:H2'	1:AA:709:U:H6	1.82	0.45
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.52	0.45
3:AC:26:THR:HG23	14:AN:76:LYS:HD3	1.99	0.45
4:AD:156:LYS:HD3	4:AD:156:LYS:HA	1.77	0.45
5:AE:83:HIS:HE1	5:AE:147:MET:HG3	1.82	0.45
11:AK:69:ARG:NH1	22:BA:2146:C:H42	2.13	0.45
20:AT:18:ARG:HE	20:AT:18:ARG:HB3	1.67	0.45
22:BA:142:A:C5	22:BA:143:C:C4	3.05	0.45
22:BA:281:C:H2'	22:BA:282:A:H8	1.78	0.45
22:BA:1060:U:OP2	30:BI:76:ALA:N	2.51	0.45
22:BA:1392:A:C6	22:BA:1393:A:C6	3.05	0.45
22:BA:1440:U:H2'	22:BA:1441:G:C8	2.50	0.45
22:BA:1509:A:O2'	22:BA:1510:G:P	2.74	0.45
22:BA:1998:A:OP2	25:BD:141:ARG:NH2	2.50	0.45
22:BA:2685:G:OP1	32:BK:78:ARG:NH2	2.49	0.45
25:BD:136:ASN:HD21	25:BD:139:SER:H	1.65	0.45
27:BF:4:LEU:HD23	27:BF:4:LEU:HA	1.87	0.45
33:BL:36:LYS:O	33:BL:40:SER:HB3	2.17	0.45
34:BM:136:MET:HE2	34:BM:136:MET:HB3	1.71	0.45
38:BQ:115:ALA:C	38:BQ:117:LEU:H	2.25	0.45
40:BS:20:VAL:HA	40:BS:23:LEU:HD12	1.99	0.45
1:CA:1486:G:H2'	1:CA:1487:G:O4'	2.16	0.45
3:CC:111:LEU:HD21	3:CC:144:LEU:O	2.16	0.45
3:CC:124:LEU:HD23	3:CC:124:LEU:HA	1.84	0.45
5:CE:111:MET:O	5:CE:115:LEU:HB2	2.17	0.45
22:DA:53:A:C8	22:DA:54:G:C8	3.04	0.45
22:DA:947:A:O2'	22:DA:984:A:H2	2.00	0.45
22:DA:950:G:H2'	22:DA:951:C:O4'	2.17	0.45
22:DA:1654:A:P	35:DN:1:MET:HA	2.56	0.45
22:DA:1806:C:H1'	24:DC:44:ASN:HD21	1.82	0.45
22:DA:2125:G:H5'	22:DA:2126:A:OP2	2.16	0.45
22:DA:2262:U:H4'	22:DA:2328:A:C2	2.52	0.45
22:DA:2514:U:H2'	22:DA:2515:C:C6	2.52	0.45
22:DA:2662:A:H2'	22:DA:2663:G:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DQ:86:ALA:HB3	38:DQ:88:VAL:HG23	1.99	0.45
39:DR:1:MET:HE1	39:DR:101:ILE:HB	1.99	0.45
42:DU:33:LYS:HE2	42:DU:66:GLN:CD	2.42	0.45
1:AA:11:G:C6	1:AA:12:U:C4	3.05	0.44
1:AA:356:A:H2	1:AA:368:U:O2	2.00	0.44
1:AA:741:G:H2'	1:AA:742:G:O4'	2.16	0.44
1:AA:761:G:H2'	1:AA:762:U:C6	2.51	0.44
1:AA:1124:G:H3'	1:AA:1145:A:N6	2.32	0.44
6:AF:44:ARG:HA	6:AF:58:HIS:HA	1.99	0.44
7:AG:92:ARG:O	7:AG:96:ARG:HB2	2.17	0.44
9:AI:114:LYS:NZ	9:AI:118:LEU:O	2.48	0.44
10:AJ:52:LEU:HD21	10:AJ:59:LYS:HA	2.00	0.44
17:AQ:4:LYS:HG3	17:AQ:7:THR:HG22	1.98	0.44
22:BA:18:U:O3'	38:BQ:23:GLY:HA2	2.17	0.44
22:BA:610:C:H2'	22:BA:611:C:H6	1.82	0.44
22:BA:815:C:OP1	39:BR:85:LYS:NZ	2.50	0.44
22:BA:1176:U:H2'	22:BA:1177:G:C8	2.52	0.44
22:BA:1586:A:H8	22:BA:1586:A:O5'	2.00	0.44
22:BA:1637:A:H4'	22:BA:2711:A:O2'	2.17	0.44
22:BA:1754:A:H2'	22:BA:1755:A:C8	2.51	0.44
22:BA:2199:A:C4'	29:BH:28:ASN:ND2	2.80	0.44
22:BA:2418:A:C6	22:BA:2419:U:C4	3.06	0.44
24:BC:40:SER:C	24:BC:42:GLY:N	2.73	0.44
27:BF:105:THR:HG23	27:BF:106:ILE:HG23	1.98	0.44
29:BH:75:LEU:C	29:BH:75:LEU:HD22	2.41	0.44
37:BP:71:GLU:OE1	37:BP:101:ARG:NE	2.36	0.44
42:BU:74:ASN:O	42:BU:78:GLY:N	2.47	0.44
1:CA:393:A:OP2	16:CP:12:LYS:HD2	2.17	0.44
1:CA:1000:A:H2'	1:CA:1001:C:O4'	2.17	0.44
1:CA:1130:A:H5"	9:CI:64:TYR:HE1	1.82	0.44
1:CA:1222:G:O6	57:CA:1861:HOH:O	2.21	0.44
1:CA:1350:A:H2'	1:CA:1351:U:O4'	2.17	0.44
1:CA:1515:G:H2'	1:CA:1516:G:C8	2.52	0.44
4:CD:150:LYS:O	4:CD:151:LYS:HG2	2.17	0.44
5:CE:81:LEU:CD2	5:CE:96:MET:HG3	2.48	0.44
5:CE:157:ARG:HD3	5:CE:158:GLY:H	1.82	0.44
12:CL:14:ARG:HD2	12:CL:14:ARG:HA	1.71	0.44
12:CL:64:THR:HG23	12:CL:93:VAL:HG13	1.99	0.44
21:CU:12:PHE:HD1	21:CU:13:ASP:N	2.15	0.44
22:DA:1:G:H2'	22:DA:2:G:H8	1.81	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)
22:DA:828:U:O2'	22:DA:829:A:H5'	2.17	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:DA:1182:G:H2'	22:DA:1183:U:O4'	2.16	0.44
22:DA:1224:U:C4	22:DA:1225:G:C6	3.05	0.44
22:DA:2014:A:H5'	40:DS:94:ASP:OD1	2.17	0.44
22:DA:2131:U:H1'	22:DA:2158:A:N6	2.31	0.44
22:DA:2170:A:H1'	22:DA:2171:A:C8	2.52	0.44
22:DA:2339:C:H2'	22:DA:2340:A:C8	2.52	0.44
22:DA:2594:C:N4	22:DA:2595:G:O6	2.50	0.44
26:DE:108:ILE:HD11	26:DE:180:LEU:CB	2.40	0.44
29:DH:32:PRO:CB	45:DX:39:TRP:HB3	2.44	0.44
34:DM:53:MET:HE2	34:DM:117:PHE:CD1	2.52	0.44
42:DU:71:ALA:HB3	42:DU:80:ALA:HB1	1.99	0.44
1:AA:555:U:H2'	1:AA:556:C:C6	2.52	0.44
1:AA:771:G:H2'	1:AA:772:U:H6	1.81	0.44
1:AA:1484:C:H2'	1:AA:1485:U:O4'	2.17	0.44
2:AB:66:LYS:HE3	2:AB:159:ASP:OD2	2.16	0.44
7:AG:18:PHE:CZ	7:AG:58:GLU:HG2	2.50	0.44
7:AG:83:SER:HB2	7:AG:85:TYR:CD2	2.52	0.44
11:AK:35:THR:HA	11:AK:41:ALA:HA	1.99	0.44
14:AN:90:ARG:NH1	14:AN:92:GLU:HG3	2.32	0.44
22:BA:361:G:HO2'	22:BA:362:A:P	2.39	0.44
22:BA:580:U:O3'	38:BQ:31:VAL:HG13	2.16	0.44
22:BA:605:G:H1'	22:BA:657:U:H1'	1.99	0.44
22:BA:1374:G:H2'	22:BA:1375:U:O4'	2.17	0.44
22:BA:1450:G:C6	22:BA:1451:C:N4	2.85	0.44
22:BA:2065:C:H2'	22:BA:2066:C:C6	2.52	0.44
22:BA:2298:A:N6	22:BA:2318:G:H1'	2.32	0.44
29:BH:57:LYS:CG	29:BH:58:LEU:N	2.81	0.44
34:BM:43:ALA:O	34:BM:47:GLU:HB2	2.18	0.44
39:BR:25:LEU:H	39:BR:94:THR:HG23	1.81	0.44
1:CA:160:A:H2'	1:CA:161:A:O4'	2.17	0.44
1:CA:206:C:H42	1:CA:213:G:H1	1.63	0.44
1:CA:269:C:H2'	1:CA:270:A:C8	2.52	0.44
3:CC:19:ASN:HA	3:CC:56:VAL:HG13	1.99	0.44
5:CE:137:VAL:O	5:CE:138:ARG:CB	2.64	0.44
5:CE:153:VAL:O	5:CE:157:ARG:N	2.39	0.44
6:CF:42:TRP:CZ2	6:CF:61:LEU:HB2	2.52	0.44
7:CG:13:LEU:CD1	7:CG:14:PRO:HD2	2.47	0.44
21:CU:29:LEU:O	21:CU:33:ARG:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:161:A:C3'	22:DA:162:U:H5"	2.43	0.44
22:DA:327:G:H21	42:DU:68:SER:HB2	1.82	0.44
22:DA:566:U:O2'	22:DA:809:G:OP2	2.26	0.44
22:DA:732:C:H2'	22:DA:733:G:O4'	2.17	0.44
22:DA:928:A:H5'	47:DZ:39:GLU:OE1	2.17	0.44
22:DA:969:G:H2'	22:DA:970:U:C6	2.52	0.44
22:DA:1200:C:H2'	22:DA:1201:U:H6	1.81	0.44
22:DA:1651:G:C6	22:DA:1652:A:C5	3.05	0.44
22:DA:2392:A:OP2	51:D3:31:HIS:CE1	2.69	0.44
22:DA:2690:U:C4	22:DA:2873:A:N1	2.85	0.44
22:DA:2897:U:H2'	22:DA:2898:U:C6	2.52	0.44
23:DB:5:U:H2'	23:DB:6:G:C8	2.53	0.44
29:DH:1:MET:CE	29:DH:27:ARG:NH1	2.80	0.44
35:DN:8:ARG:HB3	35:DN:10:LEU:HG	1.98	0.44
1:AA:39:G:H2'	1:AA:40:C:C6	2.52	0.44
1:AA:276:G:O3'	17:AQ:45:HIS:CE1	2.70	0.44
1:AA:393:A:H5'	1:AA:483:C:O2'	2.18	0.44
2:AB:113:ARG:O	2:AB:117:LEU:HB2	2.17	0.44
2:AB:118:GLU:HA	2:AB:121:SER:HB2	1.99	0.44
4:AD:51:TYR:CE2	4:AD:55:LEU:HD12	2.51	0.44
4:AD:170:TRP:CD2	4:AD:186:PRO:HG3	2.52	0.44
5:AE:74:VAL:HG11	5:AE:144:LEU:HB3	2.00	0.44
10:AJ:47:GLU:OE2	14:AN:76:LYS:NZ	2.50	0.44
22:BA:7:G:H2'	22:BA:8:C:H6	1.82	0.44
22:BA:15:G:C6	22:BA:16:C:C4	3.04	0.44
22:BA:423:A:H5"	22:BA:424:G:C5'	2.48	0.44
22:BA:585:G:H5"	22:BA:586:A:OP1	2.17	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
22:BA:2056:G:C2	22:BA:2057:G:C8	3.05	0.44
22:BA:2415:G:H2'	22:BA:2416:C:C6	2.53	0.44
22:BA:2774:C:H2'	22:BA:2775:G:O4'	2.16	0.44
24:BC:146:MET:HE2	24:BC:146:MET:HB3	1.80	0.44
30:BI:76:ALA:HB1	30:BI:129:ILE:HG23	2.00	0.44
30:BI:106:LEU:HA	30:BI:109:ILE:HB	1.99	0.44
35:BN:12:ARG:NH1	35:BN:20:MET:HE1	2.33	0.44
35:BN:65:LEU:HD11	35:BN:69:ARG:NH2	2.33	0.44
53:B5:52:PRO:HB2	53:B5:205:ALA:HB3	1.99	0.44
1:CA:19:A:H2'	1:CA:20:U:C6	2.52	0.44
1:CA:513:C:H2'	1:CA:514:C:C6	2.52	0.44
1:CA:543:U:P	4:CD:14:ARG:HH21	2.39	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:580:C:H2'	1:CA:581:G:O4'	2.17	0.44
1:CA:1481:U:H2'	1:CA:1482:G:C8	2.52	0.44
1:CA:1492:A:H8	1:CA:1492:A:OP2	2.00	0.44
5:CE:101:GLU:C	5:CE:103:THR:N	2.75	0.44
5:CE:133:PRO:O	5:CE:135:ASN:N	2.49	0.44
6:CF:3:HIS:H	6:CF:92:THR:HG23	1.82	0.44
7:CG:125:SER:C	7:CG:127:ALA:N	2.75	0.44
14:CN:16:LEU:HA	14:CN:19:LYS:HE2	1.99	0.44
18:CR:24:LYS:O	18:CR:26:ILE:N	2.42	0.44
22:DA:7:G:H4'	31:DJ:15:TRP:CH2	2.53	0.44
22:DA:187:G:C2	22:DA:210:C:C2	3.06	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
22:DA:445:C:O2'	22:DA:449:A:N3	2.47	0.44
22:DA:677:A:O2'	22:DA:2071:A:H5'	2.18	0.44
22:DA:787:C:OP1	57:DA:3753:HOH:O	2.21	0.44
22:DA:1408:G:H2'	22:DA:1409:U:C6	2.53	0.44
22:DA:2297:A:N1	22:DA:2321:U:C5	2.85	0.44
22:DA:2323:G:O2'	22:DA:2324:U:H5'	2.17	0.44
22:DA:2819:G:H2'	22:DA:2821:A:N7	2.32	0.44
26:DE:170:ARG:HH12	26:DE:176:ASP:CG	2.25	0.44
29:DH:37:VAL:HG22	29:DH:38:PRO:HD2	1.98	0.44
30:DI:72:LYS:HG3	30:DI:116:ASP:CG	2.43	0.44
39:DR:39:LEU:HG	39:DR:49:ILE:HD13	1.99	0.44
47:DZ:47:MET:O	47:DZ:51:VAL:HG22	2.17	0.44
48:D0:44:THR:C	48:D0:46:ASP:H	2.26	0.44
50:D2:39:ARG:HB2	50:D2:42:LEU:HD22	1.99	0.44
1:AA:36:C:OP1	12:AL:120:LYS:HE3	2.17	0.44
1:AA:43:C:H2'	1:AA:44:A:O4'	2.18	0.44
1:AA:49:U:O4	1:AA:365:U:H5	1.99	0.44
1:AA:374:A:C5'	1:AA:452:A:H2	2.31	0.44
1:AA:414:A:H2'	1:AA:415:A:H8	1.81	0.44
2:AB:134:ALA:O	2:AB:138:THR:HG23	2.18	0.44
4:AD:15:GLU:HG3	4:AD:19:LEU:HD11	1.98	0.44
4:AD:157:ALA:O	4:AD:160:GLU:HB3	2.17	0.44
5:AE:25:VAL:O	5:AE:26:LYS:C	2.60	0.44
5:AE:57:PRO:O	5:AE:61:GLN:HB2	2.17	0.44
7:AG:68:ASN:O	7:AG:70:ARG:N	2.47	0.44
9:AI:51:PRO:HB3	9:AI:84:THR:HG23	1.98	0.44
13:AM:29:ARG:O	13:AM:33:ILE:HG12	2.17	0.44
22:BA:355:U:H2'	22:BA:356:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1360:G:C6	22:BA:1372:U:C2	3.06	0.44
22:BA:1696:G:C6	22:BA:1697:G:C4	3.06	0.44
22:BA:1812:U:H2'	22:BA:1813:G:C8	2.52	0.44
22:BA:2207:C:H2'	22:BA:2208:C:H6	1.81	0.44
22:BA:2229:U:O2	45:BX:34:HIS:HE1	1.99	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
25:BD:28:GLU:OE2	25:BD:30:GLU:HG3	2.18	0.44
28:BG:11:VAL:HA	28:BG:12:PRO:HD3	1.73	0.44
30:BI:19:ASN:ND2	30:BI:35:ILE:O	2.47	0.44
1:CA:62:U:O2'	1:CA:379:C:O2	2.34	0.44
1:CA:203:G:N2	1:CA:215:C:C2	2.86	0.44
1:CA:800:G:O5'	1:CA:800:G:H8	2.00	0.44
1:CA:1133:G:C2	1:CA:1142:G:C2	3.05	0.44
1:CA:1271:A:H2'	1:CA:1272:G:C8	2.52	0.44
2:CB:130:THR:HB	2:CB:132:LYS:HB3	1.99	0.44
3:CC:43:LEU:HD21	3:CC:68:ILE:HD11	1.99	0.44
3:CC:135:LYS:HG2	3:CC:139:GLN:OE1	2.17	0.44
4:CD:46:PRO:O	4:CD:47:ARG:C	2.61	0.44
6:CF:14:GLN:C	6:CF:16:GLU:N	2.76	0.44
10:CJ:59:LYS:O	10:CJ:62:ARG:HD2	2.18	0.44
11:CK:92:GLY:O	11:CK:94:GLU:N	2.51	0.44
13:CM:4:ILE:O	13:CM:6:GLY:N	2.50	0.44
14:CN:41:ARG:HG2	14:CN:42:TRP:N	2.31	0.44
16:CP:2:VAL:HG23	16:CP:65:ALA:HA	2.00	0.44
22:DA:432:A:H2'	22:DA:433:C:O4'	2.18	0.44
22:DA:547:A:H3'	22:DA:548:G:C5'	2.46	0.44
22:DA:686:U:H2'	22:DA:788:A:N1	2.33	0.44
22:DA:758:C:O2'	22:DA:1981:A:N3	2.44	0.44
22:DA:931:U:H4'	22:DA:932:U:OP2	2.17	0.44
22:DA:1073:A:O2'	22:DA:2474:U:H5'	2.17	0.44
22:DA:1313:U:H4'	22:DA:1332:G:H4'	1.99	0.44
22:DA:2395:C:H42	22:DA:2421:G:H1	1.63	0.44
22:DA:2683:C:H4'	25:DD:13:ARG:NH1	2.33	0.44
25:DD:33:ARG:NH1	25:DD:53:GLY:O	2.50	0.44
25:DD:112:THR:O	25:DD:195:GLY:HA2	2.17	0.44
29:DH:25:TYR:O	29:DH:29:PHE:HB3	2.18	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
1:AA:1029:U:O2	1:AA:1032:G:N2	2.44	0.44
1:AA:1251:A:H2'	1:AA:1252:A:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:24:ALA:HB1	3:AC:28:GLU:HG2	1.99	0.44
4:AD:58:LYS:HG3	4:AD:59:GLN:N	2.32	0.44
4:AD:114:ALA:O	4:AD:117:LEU:HB2	2.17	0.44
5:AE:115:LEU:HG	5:AE:120:VAL:HG21	1.99	0.44
7:AG:16:PRO:HB2	9:AI:46:MET:HE3	2.00	0.44
7:AG:146:GLU:CG	7:AG:149:LYS:HE2	2.46	0.44
10:AJ:51:VAL:O	10:AJ:62:ARG:HA	2.18	0.44
17:AQ:4:LYS:HG3	17:AQ:7:THR:CG2	2.48	0.44
21:AU:25:LYS:HD2	21:AU:26:ALA:N	2.32	0.44
22:BA:340:A:H2'	22:BA:341:C:O4'	2.17	0.44
22:BA:570:G:H2'	22:BA:2030:A:C8	2.53	0.44
22:BA:578:G:C5	22:BA:2018:G:H5'	2.53	0.44
22:BA:747:U:C5	22:BA:2613:U:C5	3.06	0.44
22:BA:1414:C:C4	22:BA:1415:U:C5	3.06	0.44
22:BA:2282:G:H4'	22:BA:2389:G:O2'	2.17	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
25:BD:106:LYS:HA	25:BD:175:LEU:O	2.18	0.44
29:BH:14:SER:HG	29:BH:17:ASP:CG	2.21	0.44
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
40:BS:41:LYS:HD2	48:B0:22:LEU:HD11	1.98	0.44
47:BZ:45:ARG:HD3	47:BZ:45:ARG:HA	1.65	0.44
1:CA:36:C:OP1	12:CL:120:LYS:HE3	2.17	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
1:CA:1450:U:O2'	1:CA:1451:U:H2'	2.18	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
9:CI:107:ASP:OD2	9:CI:109:ARG:HG3	2.18	0.44
15:CO:17:ARG:CZ	15:CO:24:SER:HB2	2.48	0.44
22:DA:396:G:H1'	45:DX:29:PHE:HB3	1.99	0.44
22:DA:1380:G:H21	22:DA:1570:A:H2	1.65	0.44
22:DA:1609:A:H5"	57:DA:3642:HOH:O	2.18	0.44
22:DA:2292:U:H2'	22:DA:2293:G:C8	2.53	0.44
23:DB:48:U:H4'	36:DO:100:HIS:NE2	2.32	0.44
32:DK:88:ASN:HB3	32:DK:92:GLU:O	2.17	0.44
38:DQ:105:ALA:HB1	39:DR:40:MET:HE1	1.99	0.44
40:DS:10:ALA:O	40:DS:12:SER:N	2.49	0.44
1:AA:971:G:C8	1:AA:1365:G:H4'	2.53	0.44
1:AA:1157:A:C6	1:AA:1180:A:C5	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1182:G:C4'	1:AA:1183:U:H5'	2.45	0.44
1:AA:1329:A:OP1	13:AM:29:ARG:HB2	2.18	0.44
1:AA:1333:A:C2	1:AA:1334:G:H1'	2.53	0.44
1:AA:1367:C:P	9:AI:114:LYS:HZ1	2.39	0.44
1:AA:1517:G:N3	22:BA:1919:A:O2'	2.26	0.44
2:AB:23:TRP:HB3	2:AB:39:HIS:CE1	2.52	0.44
2:AB:181:ILE:O	2:AB:183:VAL:HG23	2.17	0.44
3:AC:157:LEU:H	3:AC:157:LEU:HG	1.60	0.44
15:AO:10:LYS:O	15:AO:14:GLU:HG3	2.18	0.44
15:AO:32:LEU:HA	15:AO:32:LEU:HD23	1.72	0.44
17:AQ:52:GLU:OE1	17:AQ:52:GLU:N	2.34	0.44
20:AT:4:ILE:HA	20:AT:8:LYS:HZ2	1.82	0.44
22:BA:299:A:H8	22:BA:299:A:OP2	2.00	0.44
22:BA:747:U:O2	22:BA:2014:A:H1'	2.17	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
22:BA:2077:A:H2'	22:BA:2078:C:H6	1.83	0.44
22:BA:2527:C:H5"	52:B4:31:PRO:HB3	2.00	0.44
22:BA:2710:C:OP1	57:BA:3553:HOH:O	2.21	0.44
24:BC:171:TYR:HA	24:BC:185:GLU:HA	1.99	0.44
27:BF:38:MET:SD	27:BF:53:ALA:HB1	2.57	0.44
29:BH:31:VAL:N	29:BH:32:PRO:CD	2.80	0.44
29:BH:89:LYS:CE	29:BH:124:THR:HG22	2.48	0.44
29:BH:100:ALA:HB2	29:BH:115:VAL:HG21	1.98	0.44
31:BJ:99:ARG:HA	31:BJ:99:ARG:HD2	1.77	0.44
32:BK:113:MET:HE2	32:BK:113:MET:HB2	1.80	0.44
53:B5:59:VAL:HG12	53:B5:63:VAL:HG21	2.00	0.44
1:CA:822:U:H2'	1:CA:823:C:C6	2.53	0.44
4:CD:168:PRO:HB3	4:CD:170:TRP:CH2	2.52	0.44
8:CH:21:ASN:O	8:CH:23:ALA:N	2.51	0.44
11:CK:116:ILE:HD12	21:CU:28:VAL:HG23	2.00	0.44
22:DA:443:A:C8	26:DE:40:ARG:HD3	2.53	0.44
22:DA:446:G:H5"	38:DQ:5:LYS:HZ3	1.81	0.44
22:DA:576:U:H2'	22:DA:577:G:C8	2.52	0.44
22:DA:1344:U:HO2'	22:DA:1345:C:P	2.36	0.44
22:DA:1647:U:H3'	22:DA:1647:U:OP2	2.18	0.44
22:DA:2283:C:H2'	22:DA:2284:A:O4'	2.18	0.44
22:DA:2722:G:H2'	22:DA:2723:C:C6	2.52	0.44
25:DD:151:THR:HG22	25:DD:152:PRO:CD	2.48	0.44
26:DE:69:ARG:H	26:DE:69:ARG:HG3	1.47	0.44
27:DF:48:LYS:O	27:DF:51:ASP:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DK:1:MET:HE2	32:DK:32:TYR:CE1	2.52	0.44
38:DQ:50:ARG:HH22	39:DR:74:ILE:HA	1.83	0.44
1:AA:666:G:C5	1:AA:741:G:C6	3.05	0.44
1:AA:831:A:OP1	2:AB:21:ARG:HG3	2.17	0.44
1:AA:937:A:N1	7:AG:2:PRO:HG2	2.32	0.44
1:AA:1211:U:HO2'	1:AA:1212:U:P	2.41	0.44
1:AA:1250:A:H2'	1:AA:1251:A:C8	2.53	0.44
2:AB:19:GLN:O	2:AB:38:VAL:HG23	2.17	0.44
3:AC:165:THR:O	3:AC:166:GLU:HB2	2.18	0.44
4:AD:51:TYR:CZ	4:AD:55:LEU:HD12	2.52	0.44
8:AH:18:GLN:CD	8:AH:70:ALA:HB1	2.43	0.44
8:AH:75:ILE:HD13	8:AH:129:VAL:HG22	1.99	0.44
10:AJ:42:LEU:HB3	10:AJ:71:LEU:HB3	1.99	0.44
22:BA:17:G:H2'	22:BA:18:U:C6	2.53	0.44
22:BA:1496:A:N3	22:BA:1577:C:O2'	2.36	0.44
22:BA:1570:A:H2'	22:BA:1571:A:C8	2.52	0.44
22:BA:2102:G:H5'	22:BA:2103:C:OP2	2.18	0.44
22:BA:2243:U:H2'	22:BA:2244:U:C6	2.53	0.44
22:BA:2726:A:N3	32:BK:67:LYS:NZ	2.61	0.44
22:BA:2868:A:H2'	22:BA:2869:G:C8	2.53	0.44
22:BA:2883:A:OP2	48:B0:50:ARG:NH1	2.51	0.44
28:BG:5:ALA:HB2	28:BG:66:GLY:HA2	2.00	0.44
29:BH:57:LYS:HG3	29:BH:58:LEU:N	2.33	0.44
29:BH:62:LEU:HD12	29:BH:62:LEU:O	2.17	0.44
29:BH:99:ILE:CD1	29:BH:117:LEU:HD13	2.48	0.44
30:BI:84:ALA:HB1	30:BI:101:ILE:HD12	1.99	0.44
40:BS:97:LEU:HD12	40:BS:97:LEU:HA	1.82	0.44
1:CA:952:U:H2'	1:CA:953:G:H8	1.82	0.44
1:CA:1137:C:H1'	1:CA:1138:G:N2	2.33	0.44
2:CB:166:ALA:HB2	2:CB:187:VAL:HG12	1.99	0.44
3:CC:129:MET:HB2	3:CC:132:ARG:HG3	2.00	0.44
5:CE:126:LYS:HE2	5:CE:126:LYS:HA	1.98	0.44
9:CI:13:LYS:N	9:CI:106:ARG:HH12	1.99	0.44
12:CL:28:PRO:HB2	12:CL:29:GLN:OE1	2.18	0.44
21:CU:8:GLU:HB3	21:CU:12:PHE:CE2	2.53	0.44
22:DA:129:C:H2'	22:DA:130:C:C6	2.53	0.44
22:DA:830:G:H22	22:DA:2446:G:C5'	2.31	0.44
22:DA:2060:A:H62	26:DE:69:ARG:HH12	1.64	0.44
28:DG:137:ASP:HB3	28:DG:140:VAL:HG23	2.00	0.44
34:DM:35:ALA:HB1	34:DM:126:ILE:HD11	1.99	0.44
43:DV:7:GLU:HB2	43:DV:41:GLU:OE2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DV:30:ILE:HD11	43:DV:63:ILE:HD12	1.99	0.44
45:DX:51:VAL:HG21	45:DX:56:MET:HG3	2.00	0.44
1:AA:626:G:C6	1:AA:627:G:C5	3.06	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
2:AB:47:VAL:C	2:AB:49:MET:H	2.25	0.44
2:AB:108:ARG:O	2:AB:111:ILE:HB	2.18	0.44
3:AC:155:GLY:O	3:AC:196:ILE:HG12	2.17	0.44
5:AE:72:ILE:HD13	5:AE:145:GLU:CD	2.43	0.44
7:AG:76:LYS:HB3	7:AG:89:VAL:HG11	1.98	0.44
9:AI:34:SER:HB3	9:AI:37:GLN:HB2	2.00	0.44
10:AJ:35:GLN:HG2	10:AJ:77:VAL:HB	2.00	0.44
10:AJ:42:LEU:HA	10:AJ:43:PRO:HD2	1.73	0.44
12:AL:50:ARG:HG3	12:AL:90:LEU:HD11	1.98	0.44
17:AQ:59:VAL:HG23	17:AQ:77:ARG:O	2.17	0.44
22:BA:255:A:C6	22:BA:256:A:C5	3.06	0.44
22:BA:2190:G:H3'	22:BA:2191:A:H8	1.82	0.44
22:BA:2898:U:H2'	22:BA:2899:A:C8	2.53	0.44
28:BG:94:TYR:HA	28:BG:106:SER:O	2.18	0.44
29:BH:4:ILE:HG23	29:BH:17:ASP:O	2.17	0.44
1:CA:115:G:H4'	1:CA:116:A:O5'	2.18	0.44
1:CA:298:A:H2'	1:CA:299:G:O4'	2.18	0.44
1:CA:765:G:C6	1:CA:812:G:C4	3.06	0.44
1:CA:1028:C:O2	1:CA:1028:C:H2'	2.17	0.44
1:CA:1359:C:O2'	1:CA:1361:G:N7	2.48	0.44
2:CB:82:ASP:N	2:CB:85:LEU:HB3	2.32	0.44
4:CD:19:LEU:HD22	4:CD:64:ILE:HG13	2.00	0.44
5:CE:104:GLY:HA3	5:CE:122:ASN:HA	1.99	0.44
9:CI:49:ARG:HH21	9:CI:53:GLU:HA	1.83	0.44
9:CI:57:MET:O	9:CI:60:LYS:N	2.51	0.44
10:CJ:38:GLY:HA2	10:CJ:39:PRO:HD2	1.82	0.44
16:CP:38:PHE:CE2	16:CP:51:ARG:HB3	2.53	0.44
22:DA:27:G:C2	22:DA:512:G:N3	2.86	0.44
22:DA:68:G:H2'	22:DA:69:C:O4'	2.18	0.44
22:DA:77:G:OP1	46:DY:52:ARG:HD3	2.18	0.44
22:DA:190:A:OP2	45:DX:26:LYS:NZ	2.50	0.44
22:DA:291:G:H1	22:DA:349:U:H3	1.66	0.44
22:DA:675:A:N3	22:DA:2443:C:O2'	2.48	0.44
22:DA:777:G:N7	22:DA:793:A:C2	2.83	0.44
22:DA:839:U:H2'	22:DA:840:C:C6	2.53	0.44
22:DA:1526:C:H2'	22:DA:1527:G:O4'	2.17	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
22:DA:2104:C:H2'	22:DA:2105:U:O4'	2.18	0.44
22:DA:2135:A:C2	22:DA:2136:G:H1'	2.53	0.44
22:DA:2354:C:O2'	44:DW:35:SER:HA	2.18	0.44
22:DA:2507:C:H5'	22:DA:2573:C:N4	2.33	0.44
24:DC:240:PHE:HB3	24:DC:241:GLY:H	1.64	0.44
26:DE:59:PRO:HG2	26:DE:70:SER:HB2	1.99	0.44
27:DF:4:LEU:H	27:DF:4:LEU:HG	1.40	0.44
28:DG:64:GLN:O	28:DG:67:THR:OG1	2.36	0.44
29:DH:127:GLU:CG	29:DH:144:VAL:O	2.65	0.44
31:DJ:40:HIS:CE1	31:DJ:41:LYS:HG3	2.53	0.44
40:DS:28:LYS:HA	40:DS:70:LYS:HG3	1.99	0.44
46:DY:31:GLN:OE1	46:DY:37:LEU:HD12	2.17	0.44
1:AA:79:G:N2	1:AA:91:U:O4	2.51	0.44
1:AA:131:A:O2'	1:AA:262:A:N3	2.38	0.44
1:AA:437:U:C2'	1:AA:438:U:H5'	2.48	0.44
1:AA:452:A:H1'	16:AP:70:ARG:NH1	2.33	0.44
1:AA:955:U:O4'	1:AA:1227:A:N6	2.51	0.44
1:AA:1293:C:H5'	1:AA:1294:G:OP2	2.18	0.44
2:AB:26:LYS:NZ	2:AB:194:ASP:OD2	2.36	0.44
2:AB:53:ALA:HB3	2:AB:54:LEU:HD22	2.00	0.44
2:AB:66:LYS:HG2	2:AB:156:GLY:HA3	2.00	0.44
6:AF:92:THR:O	6:AF:93:LYS:HG2	2.17	0.44
9:AI:36:GLU:HA	9:AI:40:GLY:HA3	2.00	0.44
12:AL:33:VAL:HG23	12:AL:56:ARG:HB3	2.00	0.44
21:AU:4:ILE:CA	21:AU:20:LYS:HE3	2.44	0.44
22:BA:69:C:H2'	22:BA:70:G:C8	2.53	0.44
22:BA:1011:G:H1'	22:BA:1013:C:O4'	2.17	0.44
22:BA:1073:A:OP1	22:BA:1073:A:C8	2.71	0.44
22:BA:1105:U:H2'	22:BA:1106:G:H8	1.83	0.44
22:BA:1366:A:C5	22:BA:1367:A:C8	3.06	0.44
22:BA:1854:A:H2	22:BA:2087:G:N3	2.16	0.44
22:BA:2070:A:C2	22:BA:2442:C:C2	3.06	0.44
22:BA:2348:U:O4	22:BA:2382:G:N1	2.51	0.44
23:BB:52:A:N7	36:BO:64:TYR:OH	2.41	0.44
24:BC:98:ASP:OD1	24:BC:98:ASP:N	2.47	0.44
24:BC:108:LYS:HD2	24:BC:194:GLU:OE1	2.17	0.44
27:BF:56:ASP:O	27:BF:60:ILE:HG13	2.18	0.44
33:BL:49:GLY:O	33:BL:51:GLU:HG2	2.18	0.44
35:BN:32:GLU:OE1	35:BN:118:ARG:HA	2.18	0.44
47:BZ:31:ARG:HG3	47:BZ:32:ILE:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:68:G:C5	1:CA:69:G:H1'	2.53	0.44
1:CA:117:G:H2'	1:CA:118:U:O4'	2.18	0.44
1:CA:154:U:O4	1:CA:155:A:N6	2.51	0.44
1:CA:179:A:H2'	1:CA:180:U:C6	2.53	0.44
1:CA:604:G:H2'	1:CA:605:U:O4'	2.18	0.44
1:CA:689:C:O2'	1:CA:705:G:O2'	2.33	0.44
1:CA:747:A:H2'	1:CA:748:G:O4'	2.18	0.44
1:CA:1371:G:OP2	9:CI:13:LYS:HD3	2.18	0.44
3:CC:165:THR:O	3:CC:166:GLU:HB3	2.18	0.44
6:CF:41:ASP:OD2	6:CF:43:GLY:N	2.43	0.44
6:CF:50:PRO:HD2	18:CR:74:HIS:ND1	2.33	0.44
9:CI:13:LYS:H	9:CI:106:ARG:NH1	2.00	0.44
9:CI:57:MET:N	9:CI:57:MET:SD	2.91	0.44
10:CJ:48:ARG:HG3	10:CJ:48:ARG:HH11	1.82	0.44
13:CM:91:HIS:HA	13:CM:109:ARG:NH2	2.33	0.44
15:CO:27:VAL:O	15:CO:31:LEU:HD12	2.18	0.44
22:DA:1142:A:H4'	31:DJ:27:ARG:HH22	1.82	0.44
22:DA:1171:G:N3	22:DA:1179:G:N1	2.65	0.44
22:DA:1336:A:H2'	22:DA:1337:G:H8	1.80	0.44
23:DB:49:C:H2'	23:DB:50:A:H8	1.83	0.44
25:DD:173:GLN:O	25:DD:175:LEU:N	2.51	0.44
27:DF:20:PHE:HB2	27:DF:22:TYR:CE2	2.53	0.44
29:DH:29:PHE:O	29:DH:30:LEU:C	2.61	0.44
30:DI:125:MET:HE2	30:DI:125:MET:HB2	1.59	0.44
35:DN:115:LEU:H	35:DN:115:LEU:HG	1.67	0.44
36:DO:80:GLU:O	36:DO:84:GLU:HG3	2.18	0.44
37:DP:51:ARG:HD3	37:DP:58:ALA:HB3	2.00	0.44
43:DV:72:VAL:HG12	43:DV:93:ARG:HA	2.00	0.44
52:D4:1:MET:HB2	52:D4:34:LYS:HB3	2.00	0.44
1:AA:440:C:H2'	1:AA:441:A:H8	1.83	0.43
1:AA:452:A:C8	1:AA:452:A:C3'	3.01	0.43
1:AA:540:G:H2'	1:AA:541:G:C8	2.53	0.43
1:AA:1044:A:C5	1:AA:1045:C:H1'	2.53	0.43
1:AA:1301:U:HO2'	1:AA:1302:C:P	2.41	0.43
2:AB:102:THR:HB	2:AB:175:GLU:OE1	2.18	0.43
2:AB:120:GLN:N	2:AB:123:ASP:HB2	2.33	0.43
3:AC:130:PHE:O	3:AC:134:MET:HG3	2.18	0.43
4:AD:75:TYR:OH	4:AD:97:ARG:NH1	2.48	0.43
8:AH:29:SER:OG	8:AH:30:SER:N	2.51	0.43
19:AS:48:THR:HG22	19:AS:61:PHE:HD1	1.82	0.43
20:AT:71:LYS:HD2	20:AT:74:ARG:NH2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1406:U:O2'	22:BA:1407:G:O5'	2.31	0.43
22:BA:1635:A:C6	22:BA:1636:U:C2	3.05	0.43
22:BA:1738:G:O2'	22:BA:1739:A:H8	2.01	0.43
22:BA:1800:C:OP1	24:BC:258:ARG:NH2	2.51	0.43
22:BA:2125:G:N2	22:BA:2173:A:H62	2.16	0.43
22:BA:2258:C:O2'	22:BA:2427:C:OP2	2.30	0.43
22:BA:2660:A:H2'	22:BA:2661:G:O4'	2.18	0.43
24:BC:62:TYR:HA	24:BC:86:ASN:HD21	1.83	0.43
24:BC:269:ARG:HH11	24:BC:269:ARG:HG2	1.83	0.43
27:BF:61:SER:HB2	27:BF:91:LEU:HD21	2.00	0.43
29:BH:89:LYS:HE3	29:BH:124:THR:HG22	1.98	0.43
33:BL:76:GLU:C	33:BL:77:ILE:HD13	2.43	0.43
34:BM:34:LYS:HE2	34:BM:99:GLY:O	2.18	0.43
38:BQ:58:ARG:HA	38:BQ:61:TRP:CE3	2.52	0.43
39:BR:27:ILE:HG21	39:BR:33:VAL:HG12	2.00	0.43
40:BS:78:GLU:O	40:BS:102:HIS:HE1	2.01	0.43
1:CA:533:A:O2'	1:CA:535:A:OP2	2.27	0.43
2:CB:134:ALA:O	2:CB:138:THR:HG23	2.17	0.43
4:CD:100:ASN:O	4:CD:104:ARG:HG2	2.17	0.43
5:CE:155:ALA:HB1	8:CH:66:PHE:CE2	2.53	0.43
10:CJ:46:LYS:HB3	10:CJ:66:GLU:OE1	2.18	0.43
12:CL:12:ARG:HH11	12:CL:12:ARG:HG3	1.83	0.43
12:CL:102:LEU:HB3	12:CL:103:ASP:H	1.67	0.43
21:CU:34:ARG:HH21	21:CU:35:ARG:HD2	1.83	0.43
22:DA:410:G:H8	22:DA:410:G:O5'	2.01	0.43
22:DA:1652:A:H3'	22:DA:1653:G:C8	2.53	0.43
22:DA:1911:U:H2'	22:DA:1918:A:N1	2.33	0.43
22:DA:2597:G:H5"	24:DC:240:PHE:O	2.18	0.43
24:DC:84:ASP:HB3	24:DC:87:ARG:HG2	2.00	0.43
31:DJ:93:ILE:HA	31:DJ:97:PRO:HB3	1.99	0.43
40:DS:73:LYS:CB	40:DS:106:VAL:HB	2.46	0.43
1:AA:213:G:O5'	1:AA:213:G:H8	2.00	0.43
1:AA:520:A:N1	1:AA:536:C:H1'	2.33	0.43
1:AA:1005:A:H2'	1:AA:1006:G:O4'	2.19	0.43
2:AB:81:LYS:HG2	2:AB:85:LEU:HD22	2.00	0.43
2:AB:139:ARG:O	2:AB:143:LYS:HB2	2.18	0.43
7:AG:15:ASP:OD1	7:AG:18:PHE:HB2	2.18	0.43
7:AG:107:ALA:HB1	7:AG:133:THR:HB	2.00	0.43
13:AM:11:ASP:OD1	13:AM:45:ILE:HB	2.18	0.43
13:AM:54:ASP:HA	13:AM:57:ARG:HB2	2.00	0.43
14:AN:21:PHE:CE1	14:AN:51:LEU:HD12	2.53	0.43

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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	0.43
22:BA:528:A:H2'	22:BA:529:A:H5"	2.00	0.43
22:BA:871:U:H2'	22:BA:872:U:C6	2.53	0.43
22:BA:1113:U:H2'	22:BA:1114:C:C6	2.53	0.43
22:BA:2097:A:C2	22:BA:2193:G:C6	3.06	0.43
22:BA:2318:G:C6	22:BA:2319:G:N1	2.86	0.43
22:BA:2420:C:H5"	49:B1:8:LYS:HE3	2.00	0.43
22:BA:2472:G:H2'	22:BA:2475:C:H42	1.84	0.43
22:BA:2725:A:C4	22:BA:2727:A:C8	3.06	0.43
25:BD:32:ASN:HD22	25:BD:32:ASN:N	2.17	0.43
28:BG:137:ASP:HB3	28:BG:140:VAL:HB	2.00	0.43
31:BJ:17:VAL:HG23	31:BJ:55:ILE:HD12	2.00	0.43
41:BT:34:VAL:HG21	41:BT:43:ILE:HD11	2.00	0.43
41:BT:64:LYS:HA	41:BT:79:ASP:OD1	2.19	0.43
45:BX:71:LEU:O	45:BX:76:GLU:HB2	2.19	0.43
48:B0:54:VAL:HG23	48:B0:55:ILE:HG12	1.99	0.43
49:B1:17:THR:HG21	49:B1:42:VAL:HB	1.99	0.43
1:CA:55:A:N7	1:CA:56:U:C4	2.85	0.43
1:CA:667:G:H4'	15:CO:51:HIS:ND1	2.33	0.43
1:CA:731:G:H5'	1:CA:766:A:H4'	1.99	0.43
1:CA:855:U:H2'	1:CA:856:C:C6	2.53	0.43
1:CA:1072:G:C6	1:CA:1073:U:C4	3.06	0.43
2:CB:91:PHE:O	2:CB:150:GLY:HA3	2.17	0.43
6:CF:16:GLU:O	6:CF:18:VAL:N	2.51	0.43
11:CK:112:ASP:HB3	21:CU:4:ILE:CG2	2.48	0.43
20:CT:28:MET:O	20:CT:32:ILE:HG13	2.18	0.43
22:DA:997:G:OP1	38:DQ:92:ARG:HG2	2.17	0.43
22:DA:1092:C:H3'	22:DA:1093:G:H8	1.83	0.43
22:DA:1491:G:C6	22:DA:1500:G:C2	3.06	0.43
22:DA:1821:A:H5'	24:DC:157:SER:OG	2.16	0.43
22:DA:2196:C:O2'	22:DA:2197:U:H5'	2.18	0.43
22:DA:2369:A:N6	22:DA:2382:G:O6	2.51	0.43
22:DA:2794:C:H2'	22:DA:2795:C:O4'	2.17	0.43
23:DB:42:C:H4'	27:DF:64:LYS:HE3	1.99	0.43
30:DI:10:LYS:HB3	30:DI:56:PRO:HB2	1.99	0.43
30:DI:54:PRO:O	30:DI:75:PRO:HD2	2.18	0.43
30:DI:76:ALA:HA	30:DI:79:LEU:HB2	2.00	0.43
31:DJ:30:THR:HG22	31:DJ:31:GLU:N	2.32	0.43
31:DJ:110:PRO:O	31:DJ:115:GLY:HA3	2.18	0.43
32:DK:9:ASN:HB2	32:DK:83:ALA:HB2	2.00	0.43
35:DN:37:THR:HG22	35:DN:110:MET:HE1	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DV:29:ILE:HG12	43:DV:38:LEU:O	2.18	0.43
49:D1:8:LYS:HG3	49:D1:24:THR:HG22	1.99	0.43
1:AA:238:A:H2'	1:AA:239:U:O4'	2.18	0.43
1:AA:585:G:OP1	17:AQ:39:LYS:HE3	2.18	0.43
1:AA:649:A:H2'	1:AA:650:G:O4'	2.18	0.43
1:AA:746:A:H8	1:AA:746:A:O5'	2.00	0.43
1:AA:920:U:H2'	1:AA:921:U:C6	2.53	0.43
1:AA:1307:U:H2'	1:AA:1308:U:H6	1.82	0.43
1:AA:1437:A:H2'	1:AA:1438:G:H8	1.83	0.43
1:AA:1463:U:H2'	1:AA:1464:U:C6	2.53	0.43
2:AB:41:ILE:HG21	2:AB:202:GLY:CA	2.45	0.43
5:AE:90:THR:HG22	5:AE:91:GLY:N	2.34	0.43
8:AH:47:GLU:HG2	8:AH:64:LYS:HG2	2.00	0.43
10:AJ:101:SER:HB2	10:AJ:102:LEU:H	1.61	0.43
22:BA:566:U:O2'	22:BA:809:G:OP2	2.25	0.43
22:BA:959:A:N3	22:BA:2457:U:O2'	2.42	0.43
22:BA:1306:C:H41	22:BA:1606:C:H2'	1.83	0.43
22:BA:1665:A:H5"	32:BK:66:LYS:HB3	2.00	0.43
22:BA:1850:G:C5	22:BA:1851:U:C4	3.07	0.43
22:BA:1956:U:H2'	22:BA:1957:C:H5'	2.00	0.43
22:BA:2360:G:OP1	51:B3:51:SER:OG	2.36	0.43
22:BA:2555:U:C5	22:BA:2556:C:C2	3.06	0.43
24:BC:141:VAL:CG1	24:BC:190:ALA:HB1	2.48	0.43
28:BG:72:LEU:HA	28:BG:75:MET:HB2	1.99	0.43
29:BH:27:ARG:O	29:BH:28:ASN:CB	2.66	0.43
29:BH:80:ILE:HG21	29:BH:94:ILE:HG13	2.00	0.43
37:BP:6:LYS:HA	37:BP:6:LYS:HD2	1.80	0.43
37:BP:30:VAL:HG13	37:BP:80:VAL:HG12	1.99	0.43
42:BU:87:PHE:CZ	42:BU:92:LYS:HG3	2.53	0.43
46:BY:30:MET:O	46:BY:34:SER:OG	2.30	0.43
1:CA:97:G:H2'	1:CA:98:A:O4'	2.18	0.43
1:CA:134:G:H2'	1:CA:135:C:O4'	2.18	0.43
1:CA:409:U:H2'	1:CA:410:G:O4'	2.18	0.43
2:CB:102:THR:HA	2:CB:179:LEU:HD21	1.99	0.43
3:CC:122:SER:HA	3:CC:125:GLU:OE2	2.17	0.43
3:CC:164:ARG:NH1	3:CC:166:GLU:OE1	2.51	0.43
5:CE:154:ALA:HA	5:CE:157:ARG:C	2.43	0.43
8:CH:11:LEU:HD22	8:CH:75:ILE:HD11	1.99	0.43
9:CI:25:ASN:H	9:CI:62:ASP:CG	2.27	0.43
10:CJ:77:VAL:O	10:CJ:79:PRO:HD3	2.18	0.43
11:CK:58:SER:O	11:CK:91:PRO:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CK:101:ASN:C	11:CK:101:ASN:OD1	2.61	0.43
14:CN:79:LEU:HB3	14:CN:80:SER:H	1.62	0.43
19:CS:15:LEU:HD22	19:CS:35:SER:HB3	2.01	0.43
20:CT:60:ARG:O	20:CT:64:LYS:HB2	2.18	0.43
21:CU:4:ILE:HA	21:CU:20:LYS:HZ1	1.83	0.43
22:DA:532:A:H1'	22:DA:2021:C:N4	2.33	0.43
22:DA:964:C:O2'	22:DA:2273:A:N3	2.47	0.43
22:DA:1370:C:H2'	22:DA:1371:G:C8	2.53	0.43
22:DA:1552:A:N6	57:DA:3627:HOH:O	2.39	0.43
22:DA:1786:A:H1'	22:DA:1938:A:N6	2.33	0.43
22:DA:1795:C:C4	22:DA:1796:U:C4	3.07	0.43
22:DA:2261:C:H1'	22:DA:2388:A:N3	2.33	0.43
24:DC:82:GLU:OE1	24:DC:103:TYR:OH	2.31	0.43
24:DC:246:THR:C	24:DC:248:TRP:H	2.26	0.43
29:DH:31:VAL:CB	29:DH:32:PRO:HD3	2.47	0.43
31:DJ:35:ARG:HG2	31:DJ:40:HIS:CD2	2.54	0.43
39:DR:82:HIS:CG	39:DR:82:HIS:O	2.70	0.43
1:AA:268:U:H2'	1:AA:269:C:C6	2.54	0.43
1:AA:343:U:H2'	1:AA:345:C:C5	2.54	0.43
1:AA:562:U:H1'	12:AL:12:ARG:HD3	2.01	0.43
1:AA:830:G:H2'	1:AA:831:A:H8	1.84	0.43
1:AA:1373:G:H5"	7:AG:36:LYS:HB2	2.00	0.43
3:AC:156:ARG:HD3	3:AC:193:TYR:O	2.17	0.43
9:AI:22:LYS:HE3	9:AI:22:LYS:HB3	1.71	0.43
22:BA:274:C:H2'	22:BA:275:C:O4'	2.17	0.43
22:BA:1688:U:N3	22:BA:1698:A:C2	2.87	0.43
22:BA:1786:A:C4	22:BA:1938:A:C6	3.06	0.43
22:BA:2328:A:H2'	22:BA:2329:U:C6	2.53	0.43
22:BA:2708:G:O2'	35:BN:71:ARG:HD3	2.18	0.43
29:BH:96:THR:O	29:BH:100:ALA:N	2.50	0.43
37:BP:2:SER:O	37:BP:6:LYS:HG2	2.18	0.43
37:BP:6:LYS:O	37:BP:10:GLN:HG2	2.18	0.43
42:BU:12:ILE:HG21	42:BU:80:ALA:HB2	1.99	0.43
1:CA:23:C:H5	1:CA:561:U:O4	2.01	0.43
1:CA:702:A:C8	22:DA:1848:A:H1'	2.53	0.43
1:CA:1431:A:C6	1:CA:1432:G:C6	3.06	0.43
7:CG:111:ARG:HH11	7:CG:123:GLU:HG2	1.83	0.43
17:CQ:65:ARG:HA	17:CQ:66:PRO:HD3	1.87	0.43
22:DA:167:A:C2	22:DA:168:G:H1'	2.54	0.43
22:DA:528:A:OP1	57:DA:3243:HOH:O	2.21	0.43
22:DA:980:A:C4	22:DA:1136:G:O4'	2.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1366:A:C4	22:DA:1367:A:C8	3.06	0.43
22:DA:1802:A:C6	22:DA:1803:A:C6	3.07	0.43
22:DA:2160:C:H2'	22:DA:2161:C:O4'	2.18	0.43
22:DA:2263:C:H41	44:DW:15:ASP:CG	2.27	0.43
27:DF:104:ILE:HA	27:DF:108:VAL:HB	1.99	0.43
28:DG:39:ASP:HB3	28:DG:58:TYR:OH	2.17	0.43
30:DI:8:TYR:HB3	30:DI:59:ILE:O	2.18	0.43
34:DM:1:MET:HE3	34:DM:43:ALA:HB3	2.00	0.43
40:DS:7:HIS:HB2	40:DS:50:VAL:HG21	2.00	0.43
47:DZ:5:ILE:HD11	47:DZ:57:VAL:HG21	2.00	0.43
1:AA:162:A:H5"	1:AA:163:C:OP2	2.18	0.43
1:AA:299:G:C6	1:AA:300:A:C6	3.06	0.43
1:AA:462:G:H3'	1:AA:463:U:H6	1.83	0.43
1:AA:731:G:H2'	1:AA:732:C:H6	1.83	0.43
1:AA:936:C:O2'	1:AA:1382:C:N3	2.52	0.43
1:AA:1308:U:O3'	13:AM:91:HIS:HE1	2.02	0.43
7:AG:40:GLU:HA	7:AG:43:VAL:HG23	2.00	0.43
11:AK:23:ILE:HD13	11:AK:96:THR:HG21	2.01	0.43
13:AM:64:VAL:O	13:AM:69:LEU:HB2	2.18	0.43
17:AQ:52:GLU:CD	17:AQ:52:GLU:N	2.76	0.43
21:AU:21:ARG:NH1	21:AU:25:LYS:HG3	2.33	0.43
22:BA:78:U:H2'	22:BA:79:C:H6	1.83	0.43
22:BA:1061:U:C2	30:BI:10:LYS:HB2	2.53	0.43
22:BA:1269:A:N7	57:BA:3387:HOH:O	2.37	0.43
22:BA:1627:G:C2	22:BA:1628:G:C8	3.07	0.43
22:BA:2176:A:C6	22:BA:2177:C:N4	2.86	0.43
22:BA:2458:G:C2	22:BA:2490:G:N2	2.87	0.43
24:BC:258:ARG:NH1	24:BC:264:ASP:OD2	2.51	0.43
29:BH:76:GLU:HA	29:BH:142:VAL:HG12	2.00	0.43
36:BO:35:ILE:HG12	36:BO:106:LEU:HD12	2.00	0.43
40:BS:1:MET:HE3	40:BS:1:MET:HB3	1.82	0.43
51:B3:22:PHE:O	51:B3:50:VAL:HG23	2.18	0.43
3:CC:110:GLU:H	3:CC:110:GLU:CD	2.26	0.43
9:CI:46:MET:O	9:CI:49:ARG:HB3	2.19	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
12:CL:122:PRO:O	12:CL:124:ALA:N	2.52	0.43
13:CM:13:LYS:HB3	13:CM:14:HIS:H	1.58	0.43
22:DA:648:G:H1'	22:DA:2351:G:OP1	2.18	0.43
22:DA:661:A:H2'	22:DA:662:G:O4'	2.18	0.43
22:DA:810:U:C4	33:DL:30:THR:HA	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:1050:A:H2'	22:DA:1051:G:C8	2.53	0.43
22:DA:1247:A:O3'	38:DQ:2:ALA:HB3	2.19	0.43
22:DA:1640:A:H2'	22:DA:1641:A:H8	1.84	0.43
22:DA:2057:G:OP1	57:DA:3668:HOH:O	2.21	0.43
22:DA:2607:G:H2'	22:DA:2608:G:O4'	2.18	0.43
22:DA:2849:U:P	37:DP:93:ARG:HH21	2.40	0.43
24:DC:93:LEU:HD13	24:DC:103:TYR:CE1	2.54	0.43
31:DJ:5:THR:HG23	31:DJ:45:THR:HG21	2.01	0.43
44:DW:21:LEU:HB3	44:DW:39:ARG:O	2.18	0.43
1:AA:71:A:C6	1:AA:100:G:C8	3.07	0.43
1:AA:109:A:C6	1:AA:326:G:C6	3.07	0.43
1:AA:570:G:H1'	1:AA:820:U:C4	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:AF:40:GLU:HB2	6:AF:61:LEU:HB3	2.00	0.43
22:BA:335:C:H5"	42:BU:82:ARG:HD3	2.00	0.43
22:BA:695:G:C2	22:BA:696:G:C8	3.07	0.43
22:BA:973:A:H5"	39:BR:81:LYS:CG	2.49	0.43
22:BA:1506:U:H2'	22:BA:1507:C:C6	2.54	0.43
22:BA:1664:A:H1'	22:BA:2726:A:N1	2.33	0.43
22:BA:1949:G:N2	22:BA:1958:C:C2	2.87	0.43
26:BE:145:ASP:HB3	26:BE:184:ASP:HB2	2.00	0.43
26:BE:180:LEU:HA	26:BE:180:LEU:HD23	1.69	0.43
28:BG:96:ALA:HB2	28:BG:105:LEU:HD23	2.00	0.43
29:BH:41:LYS:HA	29:BH:44:ILE:HG12	2.01	0.43
29:BH:103:VAL:O	29:BH:108:VAL:O	2.37	0.43
35:BN:36:THR:HG23	35:BN:37:THR:O	2.17	0.43
36:BO:111:ARG:HD3	36:BO:117:PHE:OXT	2.19	0.43
41:BT:40:LYS:HD3	41:BT:58:VAL:O	2.19	0.43
45:BX:64:ILE:HG13	45:BX:68:LEU:HG	2.01	0.43
46:BY:57:LEU:HA	46:BY:60:LYS:HB3	2.01	0.43
1:CA:17:U:H2'	1:CA:18:C:C6	2.53	0.43
1:CA:411:A:C6	1:CA:429:U:C5	3.06	0.43
1:CA:664:G:H22	1:CA:741:G:H1	1.66	0.43
1:CA:939:G:C6	1:CA:940:C:C4	3.07	0.43
1:CA:977:A:OP1	14:CN:71:HIS:HE1	2.01	0.43
2:CB:50:PHE:CD1	2:CB:54:LEU:HD23	2.53	0.43
7:CG:57:SER:OG	7:CG:58:GLU:N	2.50	0.43
8:CH:65:TYR:HA	8:CH:70:ALA:HA	2.00	0.43
9:CI:120:LYS:CG	9:CI:123:ARG:HB3	2.48	0.43
14:CN:18:ASP:HA	14:CN:22:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CN:69:ARG:HA	14:CN:70:PRO:HD3	1.85	0.43
22:DA:105:C:H2'	22:DA:106:C:C6	2.54	0.43
22:DA:335:C:H5"	42:DU:82:ARG:HD3	2.00	0.43
22:DA:738:G:H2'	22:DA:739:A:C8	2.53	0.43
22:DA:2094:A:H2'	22:DA:2095:A:C8	2.53	0.43
22:DA:2271:G:OP1	44:DW:18:ALA:HB1	2.19	0.43
22:DA:2323:G:H2'	22:DA:2324:U:O4'	2.17	0.43
22:DA:2392:A:C8	22:DA:2429:G:C2	3.06	0.43
26:DE:129:PRO:HB3	26:DE:159:LEU:HB2	1.99	0.43
31:DJ:117:ALA:HA	31:DJ:120:ARG:HD2	1.99	0.43
43:DV:20:LEU:O	43:DV:25:LYS:HB2	2.18	0.43
43:DV:38:LEU:HB3	43:DV:40:ILE:HD11	1.99	0.43
44:DW:72:LYS:HB2	44:DW:79:PHE:CD2	2.53	0.43
46:DY:28:LEU:HD23	46:DY:37:LEU:HD11	2.01	0.43
1:AA:684:U:H2'	1:AA:685:G:O4'	2.19	0.43
1:AA:722:G:C8	1:AA:724:G:H1'	2.54	0.43
1:AA:760:G:C5	1:AA:761:G:C8	3.07	0.43
1:AA:957:U:O2	1:AA:959:A:H8	2.01	0.43
1:AA:1068:G:O2'	1:AA:1191:A:N1	2.47	0.43
4:AD:105:MET:HG2	4:AD:171:LEU:HD22	2.00	0.43
6:AF:46:GLN:HB2	6:AF:56:LYS:CE	2.45	0.43
9:AI:6:TYR:HB3	9:AI:89:GLU:HG2	2.01	0.43
19:AS:11:ILE:HA	19:AS:38:SER:HB3	2.00	0.43
22:BA:20:C:O2'	22:BA:21:A:H5'	2.18	0.43
22:BA:416:U:H2'	22:BA:417:C:C6	2.53	0.43
22:BA:1138:G:N3	31:BJ:108:MET:HE2	2.33	0.43
22:BA:1248:G:OP1	38:BQ:2:ALA:N	2.52	0.43
22:BA:2094:A:C2	22:BA:2196:C:C2	3.06	0.43
22:BA:2127:G:H2'	22:BA:2128:G:C8	2.54	0.43
22:BA:2191:A:C6	22:BA:2192:U:C4	3.06	0.43
22:BA:2522:U:O2'	22:BA:2647:U:OP1	2.35	0.43
22:BA:2661:G:H2'	22:BA:2662:A:C8	2.54	0.43
22:BA:2810:A:O3'	25:BD:62:LYS:HB2	2.17	0.43
24:BC:265:LYS:HB3	24:BC:266:PHE:CD1	2.53	0.43
28:BG:166:ASP:OD1	28:BG:166:ASP:N	2.45	0.43
29:BH:9:VAL:O	29:BH:10:ALA:O	2.36	0.43
29:BH:94:ILE:CD1	29:BH:98:ASP:HB3	2.48	0.43
30:BI:103:ARG:HE	30:BI:104:ALA:N	2.17	0.43
39:BR:1:MET:HG2	39:BR:42:ALA:O	2.19	0.43
40:BS:20:VAL:O	40:BS:23:LEU:HB2	2.18	0.43
40:BS:90:LYS:NZ	54:B6:8:MHT:H6A	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:552:U:C2	1:CA:553:A:C8	3.07	0.43
1:CA:822:U:H2'	1:CA:823:C:H6	1.82	0.43
1:CA:1245:C:H2'	1:CA:1246:A:H8	1.84	0.43
1:CA:1250:A:N3	1:CA:1370:G:O2'	2.45	0.43
4:CD:172:GLU:HG2	4:CD:183:LYS:HD3	2.00	0.43
5:CE:29:ARG:H	5:CE:29:ARG:HG2	1.63	0.43
7:CG:116:MET:HA	7:CG:119:ARG:HD3	2.00	0.43
10:CJ:38:GLY:O	10:CJ:40:ILE:HG13	2.18	0.43
15:CO:45:GLU:HG2	15:CO:46:HIS:N	2.33	0.43
22:DA:754:U:H2'	22:DA:755:U:C6	2.53	0.43
22:DA:1109:C:H5"	22:DA:1110:G:OP2	2.19	0.43
22:DA:1209:U:H2'	22:DA:1210:G:H21	1.83	0.43
22:DA:1360:G:N1	22:DA:1361:G:H1'	2.33	0.43
22:DA:1655:A:C6	22:DA:1656:C:C2	3.06	0.43
22:DA:2005:A:OP2	22:DA:2006:C:N4	2.40	0.43
22:DA:2636:C:H4'	25:DD:81:GLU:CD	2.43	0.43
27:DF:13:VAL:O	27:DF:17:MET:HG2	2.19	0.43
27:DF:38:MET:HG3	27:DF:152:LEU:HB3	2.00	0.43
27:DF:46:ASP:N	27:DF:46:ASP:OD1	2.50	0.43
30:DI:58:VAL:O	30:DI:69:PHE:HB3	2.19	0.43
34:DM:19:GLY:O	34:DM:38:ARG:NH1	2.37	0.43
44:DW:19:LYS:HA	44:DW:19:LYS:HD3	1.80	0.43
1:AA:96:U:HO2'	1:AA:97:G:P	2.41	0.43
1:AA:1032:G:C2	1:AA:1033:G:H1'	2.54	0.43
1:AA:1537:U:H2'	1:AA:1538:C:O4'	2.19	0.43
7:AG:103:TRP:CH2	7:AG:141:VAL:HG21	2.54	0.43
15:AO:46:HIS:C	15:AO:48:LYS:H	2.21	0.43
22:BA:39:G:H2'	22:BA:40:U:H6	1.79	0.43
22:BA:106:C:H2'	22:BA:107:G:C8	2.53	0.43
22:BA:401:A:H2'	22:BA:402:A:C8	2.53	0.43
22:BA:540:C:C2	22:BA:541:A:C8	3.07	0.43
22:BA:598:U:H2'	22:BA:599:A:H8	1.83	0.43
22:BA:644:A:H2'	22:BA:645:C:O4'	2.18	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:BA:1229:C:H2'	22:BA:1230:A:C8	2.54	0.43
22:BA:1378:A:O2'	22:BA:1380:G:OP2	2.37	0.43
22:BA:1457:U:H5"	22:BA:1458:U:OP1	2.18	0.43
22:BA:2071:A:H2'	22:BA:2072:C:C6	2.53	0.43
28:BG:101:ASN:ND2	28:BG:116:GLN:OE1	2.51	0.43
29:BH:97:ARG:HH12	1:CA:369:G:N2	2.12	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BO:36:TYR:N	36:BO:36:TYR:CD2	2.86	0.43
37:BP:37:LYS:HE3	37:BP:39:ARG:HE	1.84	0.43
42:BU:39:ILE:O	42:BU:41:LEU:N	2.51	0.43
43:BV:58:SER:OG	43:BV:59:GLU:N	2.50	0.43
49:B1:4:GLY:O	49:B1:6:ARG:N	2.48	0.43
53:B5:47:LYS:HE3	53:B5:48:LEU:H	1.83	0.43
1:CA:35:G:C2	1:CA:550:G:C2	3.07	0.43
1:CA:245:U:H3	1:CA:283:U:H3	1.65	0.43
1:CA:256:U:H3	1:CA:270:A:H61	1.66	0.43
1:CA:987:G:N2	1:CA:1218:C:O2	2.52	0.43
1:CA:1269:A:H2	1:CA:1312:G:N3	2.16	0.43
1:CA:1394:A:C5	1:CA:1501:C:H4'	2.53	0.43
2:CB:71:GLY:O	2:CB:93:ASN:HA	2.19	0.43
3:CC:175:LEU:HD12	3:CC:175:LEU:O	2.19	0.43
7:CG:28:ASN:O	7:CG:31:MET:HB3	2.19	0.43
12:CL:65:SER:OG	12:CL:97:THR:HG23	2.18	0.43
20:CT:6:SER:C	20:CT:8:LYS:H	2.26	0.43
22:DA:35:G:N2	22:DA:450:G:H1'	2.34	0.43
22:DA:297:G:H5"	42:DU:85:PHE:CB	2.46	0.43
22:DA:319:G:OP2	26:DE:132:LYS:HE2	2.18	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:DA:1299:G:O2'	22:DA:1640:A:N6	2.50	0.43
22:DA:1654:A:O2'	25:DD:118:PHE:O	2.31	0.43
22:DA:1668:A:O4'	22:DA:1669:A:C2	2.72	0.43
22:DA:1791:A:C8	22:DA:1792:G:C8	3.07	0.43
22:DA:1969:A:H2'	22:DA:1972:G:H21	1.84	0.43
22:DA:2616:C:H2'	22:DA:2617:U:H6	1.84	0.43
23:DB:49:C:O3'	36:DO:68:LYS:HE2	2.19	0.43
23:DB:76:G:N3	43:DV:78:GLN:NE2	2.60	0.43
26:DE:149:ILE:HD11	26:DE:172:ALA:HA	2.01	0.43
27:DF:40:VAL:HG11	27:DF:50:LEU:HD13	2.00	0.43
31:DJ:31:GLU:HG3	31:DJ:142:ILE:HD11	2.00	0.43
40:DS:1:MET:HB3	40:DS:109:ASP:OD2	2.18	0.43
40:DS:67:ASP:OD1	40:DS:67:ASP:N	2.48	0.43
1:AA:279:A:H5"	1:AA:279:A:H8	1.83	0.43
1:AA:579:A:H2'	1:AA:580:C:C6	2.53	0.43
1:AA:685:G:N1	1:AA:686:U:O4	2.52	0.43
1:AA:855:U:H2'	1:AA:856:C:H6	1.83	0.43
1:AA:1181:G:O2'	1:AA:1182:G:N7	2.51	0.43
1:AA:1409:C:H2'	1:AA:1410:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:16:PHE:O	2:AB:41:ILE:HD12	2.19	0.43
3:AC:167:TRP:HE3	3:AC:167:TRP:O	2.01	0.43
5:AE:56:VAL:N	5:AE:57:PRO:HD2	2.34	0.43
6:AF:47:LEU:HD13	6:AF:51:ILE:HG23	2.00	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:137:U:H2'	22:BA:140:C:N1	2.33	0.43
22:BA:319:G:H2'	22:BA:320:A:O4'	2.18	0.43
22:BA:657:U:H2'	22:BA:658:U:C6	2.54	0.43
22:BA:747:U:C4	22:BA:2613:U:C4	3.07	0.43
22:BA:826:U:H2'	22:BA:828:U:O4'	2.18	0.43
22:BA:839:U:H1'	22:BA:1191:G:H1'	2.00	0.43
22:BA:1097:U:O2'	30:BI:9:VAL:HA	2.19	0.43
22:BA:1171:G:C5	22:BA:1172:C:C4	3.07	0.43
22:BA:1432:G:O2'	22:BA:1433:A:H5'	2.19	0.43
22:BA:1624:U:H2'	22:BA:1625:C:C6	2.51	0.43
22:BA:1697:G:OP2	22:BA:1698:A:O2'	2.32	0.43
22:BA:1917:U:H2'	22:BA:1918:A:H5'	2.00	0.43
22:BA:2172:U:H4'	22:BA:2173:A:H5'	2.00	0.43
22:BA:2294:G:H5"	36:BO:10:ARG:HD3	2.00	0.43
22:BA:2669:G:O2'	22:BA:2670:A:H5'	2.19	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:BJ:114:LEU:O	31:BJ:118:MET:HG3	2.18	0.43
41:BT:58:VAL:HG22	41:BT:85:VAL:HG22	2.01	0.43
1:CA:71:A:N1	1:CA:99:C:O2'	2.52	0.43
1:CA:709:U:H2'	1:CA:710:G:C8	2.50	0.43
1:CA:1216:A:H2'	1:CA:1217:C:H6	1.84	0.43
3:CC:33:LEU:O	3:CC:36:ASP:HB2	2.19	0.43
3:CC:182:ILE:HD13	3:CC:182:ILE:HA	1.86	0.43
5:CE:157:ARG:C	5:CE:159:LYS:N	2.76	0.43
17:CQ:12:VAL:CG1	17:CQ:13:VAL:H	2.28	0.43
22:DA:830:G:H22	22:DA:2446:G:H5"	1.84	0.43
22:DA:1223:G:OP2	39:DR:68:ARG:NH1	2.52	0.43
22:DA:1318:U:H2'	22:DA:1319:C:C6	2.54	0.43
22:DA:1586:A:H8	22:DA:1586:A:O5'	2.02	0.43
22:DA:2037:A:C6	22:DA:2038:G:C6	3.07	0.43
22:DA:2047:C:H2'	22:DA:2048:G:H8	1.83	0.43
22:DA:2056:G:C2	22:DA:2057:G:C8	3.06	0.43
22:DA:2093:G:C6	22:DA:2225:A:C8	3.07	0.43
22:DA:2464:G:H2'	22:DA:2465:C:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2469:A:C4'	34:DM:55:ARG:HD3	2.46	0.43
23:DB:65:U:C4	23:DB:108:A:C4	3.06	0.43
29:DH:31:VAL:O	29:DH:32:PRO:C	2.61	0.43
30:DI:33:VAL:HG22	30:DI:67:PHE:CD2	2.54	0.43
30:DI:75:PRO:HG2	30:DI:78:VAL:HG22	2.01	0.43
31:DJ:70:THR:HG22	31:DJ:90:GLU:OE1	2.19	0.43
37:DP:48:ILE:HA	37:DP:97:LEU:HB2	2.01	0.43
43:DV:9:ARG:HG3	43:DV:41:GLU:HB3	2.01	0.43
1:AA:56:U:H2'	1:AA:57:G:C8	2.53	0.43
1:AA:91:U:C4	1:AA:92:U:C2	3.07	0.43
1:AA:683:G:H21	11:AK:40:ASN:HA	1.84	0.43
1:AA:761:G:H2'	1:AA:762:U:H6	1.83	0.43
1:AA:821:G:H2'	1:AA:822:U:C6	2.53	0.43
1:AA:901:A:N7	1:AA:902:G:H1'	2.34	0.43
2:AB:129:LEU:HB3	2:AB:130:THR:H	1.60	0.43
7:AG:4:ARG:HB2	7:AG:4:ARG:HH11	1.83	0.43
9:AI:56:ASP:OD2	9:AI:57:MET:N	2.45	0.43
12:AL:117:TYR:O	12:AL:119:VAL:HG23	2.19	0.43
22:BA:27:G:N2	22:BA:512:G:H1'	2.33	0.43
22:BA:102:U:H4'	22:BA:103:A:OP1	2.19	0.43
22:BA:223:A:N1	22:BA:407:G:O2'	2.49	0.43
22:BA:299:A:C5	22:BA:300:A:C6	3.07	0.43
22:BA:645:C:H2'	22:BA:647:G:C5	2.54	0.43
22:BA:1281:G:H2'	22:BA:1282:U:C6	2.54	0.43
22:BA:1965:C:H5"	22:BA:1966:A:H2'	2.00	0.43
22:BA:2602:A:H4'	22:BA:2603:G:OP2	2.18	0.43
22:BA:2800:A:H3'	22:BA:2801:G:C5'	2.47	0.43
22:BA:2862:G:H2'	22:BA:2863:C:C6	2.53	0.43
29:BH:79:THR:CG2	29:BH:147:VAL:CG2	2.97	0.43
49:B1:23:THR:OG1	49:B1:24:THR:N	2.51	0.43
1:CA:390:U:H2'	1:CA:391:G:C8	2.53	0.43
1:CA:537:G:H2'	1:CA:538:G:C8	2.54	0.43
2:CB:82:ASP:CG	2:CB:83:ALA:H	2.26	0.43
2:CB:183:VAL:N	2:CB:197:ASP:OD1	2.52	0.43
2:CB:222:ARG:NE	2:CB:223:GLU:HB2	2.33	0.43
9:CI:19:VAL:HG21	9:CI:83:ILE:N	2.33	0.43
13:CM:54:ASP:HA	13:CM:57:ARG:CB	2.44	0.43
14:CN:72:GLY:O	14:CN:80:SER:HA	2.19	0.43
16:CP:21:VAL:HG12	16:CP:33:ILE:HB	2.00	0.43
22:DA:371:A:N6	22:DA:401:A:H3'	2.34	0.43
22:DA:654:A:H3'	22:DA:654:A:N3	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:659:G:H4'	26:DE:95:LYS:HB3	2.00	0.43
22:DA:786:C:H5"	22:DA:1780:A:N7	2.34	0.43
22:DA:1105:U:H2'	22:DA:1106:G:H8	1.83	0.43
22:DA:1399:C:H2'	22:DA:1400:U:C6	2.53	0.43
22:DA:2282:G:C4	22:DA:2425:A:N6	2.87	0.43
25:DD:104:VAL:HG23	25:DD:105:LYS:H	1.83	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
32:DK:108:ARG:HE	32:DK:108:ARG:HB2	1.67	0.43
36:DO:97:PHE:CB	36:DO:103:VAL:HG11	2.49	0.43
41:DT:77:ARG:HB3	41:DT:78:SER:H	1.49	0.43
1:AA:237:G:OP1	17:AQ:42:THR:OG1	2.36	0.42
1:AA:369:G:OP2	1:AA:388:G:N1	2.45	0.42
1:AA:755:G:N2	1:AA:756:C:C2	2.87	0.42
1:AA:764:C:H2'	1:AA:765:G:O4'	2.18	0.42
1:AA:945:G:C2	1:AA:946:A:C8	3.07	0.42
1:AA:1409:C:H2'	1:AA:1410:A:H8	1.84	0.42
3:AC:123:GLN:HA	3:AC:126:ARG:HB2	2.00	0.42
4:AD:177:LYS:HD3	4:AD:177:LYS:N	2.34	0.42
8:AH:55:THR:HG22	8:AH:56:LYS:HG3	2.00	0.42
9:AI:55:VAL:HG21	9:AI:87:LEU:HD21	2.01	0.42
10:AJ:65:TYR:HB3	14:AN:96:LEU:HD11	2.01	0.42
10:AJ:71:LEU:HD13	10:AJ:71:LEU:HA	1.82	0.42
12:AL:114:ARG:HB3	12:AL:119:VAL:HB	2.01	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
14:AN:43:ASN:C	14:AN:45:VAL:N	2.74	0.42
20:AT:51:PHE:HE1	20:AT:55:GLN:NE2	2.17	0.42
22:BA:276:U:H2'	22:BA:278:A:H62	1.84	0.42
22:BA:1223:G:OP2	39:BR:68:ARG:NH1	2.52	0.42
22:BA:1452:G:H2'	22:BA:1457:U:O4	2.19	0.42
22:BA:1606:C:H4'	22:BA:1607:C:H5'	2.00	0.42
22:BA:2093:G:P	29:BH:24:GLY:H	2.41	0.42
22:BA:2109:U:H2'	22:BA:2110:G:C8	2.54	0.42
25:BD:183:GLU:H	25:BD:183:GLU:CD	2.23	0.42
26:BE:111:GLU:OE1	26:BE:115:GLN:HG2	2.19	0.42
50:B2:9:VAL:HG12	50:B2:13:ASN:ND2	2.33	0.42
1:CA:308:C:H2'	1:CA:309:A:H8	1.82	0.42
1:CA:554:A:H2'	1:CA:555:U:H6	1.84	0.42
1:CA:562:U:H1'	12:CL:12:ARG:CG	2.49	0.42
1:CA:1537:U:H3'	1:CA:1538:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:95:ARG:HA	2:CB:95:ARG:HD3	1.88	0.42
2:CB:165:ASP:HB3	2:CB:169:GLU:OE2	2.19	0.42
7:CG:95:ARG:HA	7:CG:98:ALA:HB3	2.01	0.42
22:DA:71:A:OP2	22:DA:113:U:H5'	2.19	0.42
22:DA:464:U:H5'	50:D2:5:PHE:CE2	2.54	0.42
22:DA:571:U:H1'	22:DA:573:U:C6	2.54	0.42
22:DA:621:A:H2'	22:DA:622:G:O4'	2.19	0.42
22:DA:764:A:H2	24:DC:218:PRO:HG3	1.84	0.42
22:DA:814:C:H1'	22:DA:1225:G:N2	2.34	0.42
22:DA:833:A:P	33:DL:39:LYS:HE2	2.59	0.42
22:DA:1173:U:O2'	22:DA:1176:U:O2	2.20	0.42
22:DA:1365:A:OP2	45:DX:3:ARG:N	2.43	0.42
22:DA:2203:U:H5"	22:DA:2204:G:OP1	2.19	0.42
23:DB:70:C:H2'	23:DB:71:C:H6	1.84	0.42
29:DH:62:LEU:HD13	29:DH:63:ALA:N	2.34	0.42
30:DI:80:LEU:HD13	30:DI:136:MET:SD	2.59	0.42
34:DM:50:ARG:HG3	34:DM:65:ILE:HD11	2.00	0.42
42:DU:66:GLN:O	42:DU:69:ASN:N	2.45	0.42
45:DX:68:LEU:HD22	45:DX:78:TYR:CZ	2.53	0.42
46:DY:60:LYS:HE3	46:DY:60:LYS:HB2	1.91	0.42
51:D3:29:LEU:HD12	51:D3:29:LEU:HA	1.87	0.42
1:AA:64:G:C8	1:AA:99:C:N4	2.87	0.42
1:AA:917:G:H2'	1:AA:918:A:C8	2.54	0.42
1:AA:1098:C:H2'	1:AA:1099:G:O4'	2.19	0.42
1:AA:1119:C:P	9:AI:85:ARG:HH22	2.42	0.42
2:AB:54:LEU:HB3	2:AB:220:THR:HG21	2.02	0.42
2:AB:68:LEU:HD13	2:AB:161:LEU:HD21	2.00	0.42
2:AB:164:ILE:HG23	2:AB:165:ASP:N	2.34	0.42
2:AB:181:ILE:HA	2:AB:182:PRO:HD3	1.75	0.42
12:AL:36:ARG:HB3	12:AL:38:TYR:CE2	2.54	0.42
15:AO:87:LEU:C	15:AO:89:ARG:H	2.27	0.42
17:AQ:81:LYS:HB2	17:AQ:81:LYS:HE2	1.58	0.42
20:AT:15:GLU:CD	20:AT:18:ARG:HH21	2.27	0.42
21:AU:10:GLU:CD	21:AU:11:PRO:HD3	2.43	0.42
22:BA:206:U:O2'	22:BA:207:A:H5'	2.18	0.42
22:BA:233:A:N6	22:BA:428:A:H61	2.18	0.42
22:BA:531:C:C5	22:BA:2035:G:C2	3.07	0.42
22:BA:974:G:C8	22:BA:989:G:C2	3.07	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
22:BA:2297:A:N1	22:BA:2321:U:C5	2.86	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:2415:G:H2'	22:BA:2416:C:H6	1.84	0.42
22:BA:2454:G:O6	57:BA:3529:HOH:O	2.21	0.42
28:BG:125:CYS:HB3	28:BG:127:THR:O	2.19	0.42
29:BH:114:GLU:CB	29:BH:133:GLN:O	2.66	0.42
34:BM:49:ALA:O	34:BM:53:MET:HG2	2.18	0.42
41:BT:4:GLU:HA	41:BT:7:LEU:HB2	2.00	0.42
44:BW:47:ALA:HB2	44:BW:59:LEU:HD22	2.01	0.42
46:BY:56:LEU:O	46:BY:57:LEU:CB	2.66	0.42
1:CA:193:C:O3'	20:CT:56:PRO:HB3	2.20	0.42
1:CA:209:U:O2	1:CA:209:U:H2'	2.19	0.42
1:CA:585:G:OP1	17:CQ:39:LYS:HE3	2.19	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
4:CD:173:VAL:HG13	4:CD:174:ASP:N	2.25	0.42
5:CE:53:ALA:HB2	5:CE:62:LYS:NZ	2.34	0.42
8:CH:11:LEU:HD11	8:CH:127:CYS:CB	2.49	0.42
12:CL:35:THR:HG22	12:CL:36:ARG:HE	1.83	0.42
16:CP:18:GLN:O	16:CP:20:VAL:HG12	2.20	0.42
16:CP:77:GLU:C	16:CP:79:ASN:H	2.26	0.42
21:CU:19:PHE:HA	21:CU:22:SER:HB3	2.01	0.42
22:DA:389:G:C8	22:DA:2413:G:H4'	2.53	0.42
22:DA:572:A:OP2	39:DR:79:ARG:NH1	2.52	0.42
22:DA:1060:U:OP2	30:DI:75:PRO:HA	2.19	0.42
22:DA:1189:A:H2'	22:DA:1190:G:O4'	2.19	0.42
22:DA:1356:G:C2	22:DA:1357:C:C2	3.08	0.42
22:DA:1856:U:O4	22:DA:1857:G:C6	2.72	0.42
22:DA:2824:C:C4	22:DA:2825:G:C5	3.07	0.42
22:DA:2852:G:H2'	22:DA:2853:C:C6	2.54	0.42
24:DC:107:PRO:HB3	24:DC:142:HIS:NE2	2.34	0.42
30:DI:124:ALA:C	30:DI:126:THR:H	2.27	0.42
34:DM:74:THR:HA	34:DM:88:ASN:O	2.18	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
1:AA:21:G:H2'	1:AA:22:G:C8	2.55	0.42
1:AA:502:A:C2	1:AA:503:C:C2	3.07	0.42
1:AA:629:A:H2'	1:AA:630:A:C8	2.55	0.42
1:AA:1200:C:H4'	1:AA:1201:A:H3'	2.01	0.42
1:AA:1206:G:H4'	3:AC:192:THR:O	2.19	0.42
1:AA:1308:U:O2'	1:AA:1309:G:H5'	2.20	0.42
1:AA:1322:C:OP1	19:AS:78:ARG:NH2	2.53	0.42
2:AB:56:GLU:HA	2:AB:59:LYS:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:95:ARG:HG2	2:AB:95:ARG:HH11	1.84	0.42
2:AB:151:ILE:HG23	2:AB:152:LYS:N	2.34	0.42
3:AC:7:PRO:HD2	3:AC:184:TYR:CD2	2.53	0.42
3:AC:12:LEU:HD23	3:AC:12:LEU:HA	1.79	0.42
10:AJ:63:ASP:OD1	14:AN:85:ARG:HD2	2.19	0.42
11:AK:35:THR:OG1	11:AK:40:ASN:N	2.52	0.42
11:AK:42:LEU:HB3	11:AK:77:TYR:CD2	2.55	0.42
13:AM:107:ARG:HH21	13:AM:113:ARG:HB3	1.85	0.42
14:AN:16:LEU:HD23	14:AN:19:LYS:HE2	2.01	0.42
21:AU:34:ARG:NH2	21:AU:35:ARG:HB2	2.34	0.42
22:BA:2:G:H2'	22:BA:3:U:H6	1.84	0.42
22:BA:1022:G:N2	22:BA:1142:A:C2	2.82	0.42
22:BA:1153:C:H2'	22:BA:1154:G:O4'	2.18	0.42
25:BD:84:LEU:HD23	25:BD:84:LEU:HA	1.47	0.42
28:BG:173:GLU:HB3	28:BG:174:ALA:H	1.76	0.42
40:BS:37:THR:HG22	40:BS:38:TYR:CE1	2.54	0.42
48:B0:12:LYS:HD2	48:B0:12:LYS:HA	1.75	0.42
1:CA:31:G:H22	1:CA:47:C:H4'	1.83	0.42
1:CA:263:A:OP1	20:CT:74:ARG:HD3	2.18	0.42
1:CA:483:C:H2'	1:CA:484:G:N7	2.34	0.42
1:CA:1483:A:O5'	1:CA:1483:A:H8	2.03	0.42
2:CB:161:LEU:HD12	2:CB:161:LEU:HA	1.83	0.42
3:CC:6:HIS:CD2	14:CN:89:MET:HB3	2.55	0.42
12:CL:10:LYS:HA	12:CL:11:PRO:HD3	1.88	0.42
17:CQ:20:SER:N	17:CQ:48:ASP:OD1	2.53	0.42
17:CQ:52:GLU:HG2	17:CQ:53:CYS:N	2.28	0.42
20:CT:6:SER:O	20:CT:8:LYS:N	2.53	0.42
22:DA:176:A:H3'	22:DA:177:G:N2	2.33	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
22:DA:938:G:C2	22:DA:939:G:N7	2.87	0.42
22:DA:998:C:OP2	38:DQ:58:ARG:NH2	2.53	0.42
22:DA:1490:A:H2'	22:DA:1490:A:N3	2.35	0.42
22:DA:1530:G:N2	22:DA:1542:U:O2	2.53	0.42
22:DA:2272:U:H5"	22:DA:2273:A:OP1	2.19	0.42
22:DA:2391:G:H1'	22:DA:2424:C:N4	2.33	0.42
22:DA:2571:U:C4	22:DA:2574:G:C8	3.06	0.42
22:DA:2800:A:C2	22:DA:2895:G:H1'	2.55	0.42
29:DH:72:ILE:O	29:DH:72:ILE:CG2	2.67	0.42
33:DL:70:LYS:O	33:DL:74:THR:HG23	2.19	0.42
40:DS:15:GLN:HA	40:DS:18:ARG:HD2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:324:G:N2	1:AA:326:G:H3'	2.34	0.42
1:AA:605:U:O2'	1:AA:606:G:H5'	2.19	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
8:AH:37:ALA:HB1	8:AH:61:LEU:HD21	2.02	0.42
10:AJ:42:LEU:HD23	10:AJ:43:PRO:CD	2.48	0.42
11:AK:114:THR:HA	11:AK:115:PRO:HD3	1.79	0.42
14:AN:58:SER:O	57:AN:201:HOH:O	2.21	0.42
15:AO:82:ILE:HD12	15:AO:88:ARG:HG2	2.02	0.42
17:AQ:10:GLY:HA3	17:AQ:24:ALA:O	2.20	0.42
22:BA:300:A:H2'	22:BA:334:C:H1'	2.01	0.42
22:BA:1083:U:O2	22:BA:1086:A:N1	2.52	0.42
22:BA:1536:C:H4'	22:BA:1537:G:C5'	2.48	0.42
22:BA:1870:C:H5"	22:BA:1871:A:C8	2.54	0.42
22:BA:2305:U:H5"	27:BF:131:GLY:HA3	2.00	0.42
22:BA:2492:U:H2'	22:BA:2493:U:H6	1.83	0.42
22:BA:2742:G:P	52:B4:24:ARG:HH12	2.42	0.42
25:BD:140:HIS:CD2	57:BD:302:HOH:O	2.59	0.42
28:BG:105:LEU:HD13	28:BG:107:LEU:HD11	2.01	0.42
33:BL:57:LEU:HG	51:B3:14:PHE:HZ	1.84	0.42
37:BP:23:GLY:O	37:BP:110:ILE:HD11	2.18	0.42
45:BX:77:LYS:HA	45:BX:77:LYS:HD2	1.60	0.42
52:B4:7:VAL:HG22	52:B4:38:GLY:HA3	2.02	0.42
1:CA:427:U:P	4:CD:13:ARG:HH22	2.42	0.42
1:CA:554:A:H2'	1:CA:555:U:C6	2.55	0.42
1:CA:1180:A:P	9:CI:99:ARG:HH22	2.42	0.42
22:DA:35:G:H1'	22:DA:454:A:C4	2.54	0.42
22:DA:188:G:HO2'	22:DA:1365:A:N6	2.18	0.42
22:DA:703:U:H2'	22:DA:704:G:H5'	2.00	0.42
22:DA:1154:G:P	38:DQ:58:ARG:HH11	2.41	0.42
22:DA:1273:U:H4'	22:DA:1275:A:OP1	2.20	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
22:DA:1696:G:H21	22:DA:1978:A:H5'	1.84	0.42
22:DA:1767:G:H2'	22:DA:1768:C:H6	1.82	0.42
22:DA:2025:C:H2'	22:DA:2026:U:C6	2.54	0.42
22:DA:2189:U:C2'	22:DA:2190:G:H5"	2.49	0.42
22:DA:2209:G:C2	22:DA:2216:G:C2	3.07	0.42
22:DA:2349:G:OP2	51:D3:42:ARG:NH2	2.52	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:DC:65:VAL:HG22	24:DC:103:TYR:HB3	2.02	0.42
24:DC:84:ASP:HA	24:DC:85:PRO:HD3	1.89	0.42
24:DC:107:PRO:HD2	24:DC:110:LEU:HD22	2.00	0.42
28:DG:127:THR:HB	28:DG:130:GLU:HG3	2.00	0.42
29:DH:31:VAL:HB	29:DH:32:PRO:HD2	2.00	0.42
35:DN:12:ARG:O	35:DN:17:ARG:NH2	2.51	0.42
42:DU:14:LEU:HD21	42:DU:71:ALA:HB3	2.00	0.42
43:DV:38:LEU:HD12	43:DV:38:LEU:HA	1.90	0.42
46:DY:21:LEU:HA	46:DY:25:GLN:HB3	2.00	0.42
1:AA:186:C:H2'	1:AA:187:G:O4'	2.19	0.42
1:AA:321:A:N7	1:AA:328:C:O2'	2.43	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
2:AB:163:VAL:HG21	2:AB:173:ILE:HD11	1.99	0.42
3:AC:6:HIS:CB	14:AN:89:MET:HG3	2.49	0.42
3:AC:130:PHE:CE1	3:AC:131:ARG:HD2	2.54	0.42
4:AD:15:GLU:OE2	4:AD:56:ARG:NH2	2.51	0.42
12:AL:43:LYS:HG2	12:AL:44:LYS:HD3	2.01	0.42
19:AS:7:LYS:HB3	19:AS:7:LYS:HE3	1.86	0.42
21:AU:35:ARG:O	21:AU:36:GLU:C	2.62	0.42
22:BA:973:A:OP2	39:BR:81:LYS:HE3	2.19	0.42
22:BA:1564:C:O2'	22:BA:1565:C:H5'	2.19	0.42
22:BA:2129:C:H2'	22:BA:2130:U:C6	2.55	0.42
22:BA:2394:C:P	51:B3:30:ARG:HH21	2.41	0.42
22:BA:2564:A:C2	22:BA:2647:U:H4'	2.54	0.42
22:BA:2865:U:C4	22:BA:2866:U:C4	3.07	0.42
24:BC:105:LEU:HD22	24:BC:143:ASN:HD22	1.84	0.42
30:BI:125:MET:HA	30:BI:128:SER:HB3	2.02	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
1:CA:57:G:H2'	1:CA:58:C:C6	2.54	0.42
1:CA:89:U:H6	1:CA:89:U:O5'	2.02	0.42
1:CA:137:U:H1'	1:CA:227:G:N2	2.34	0.42
1:CA:491:G:O2'	1:CA:492:C:H5'	2.20	0.42
1:CA:718:A:H3'	1:CA:719:C:H6	1.85	0.42
1:CA:1077:G:N2	1:CA:1080:A:OP2	2.49	0.42
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.61	0.42
1:CA:1216:A:H2'	1:CA:1217:C:C6	2.54	0.42
1:CA:1416:G:N2	1:CA:1485:U:H1'	2.35	0.42
13:CM:79:ARG:O	13:CM:83:LEU:HD23	2.20	0.42
20:CT:8:LYS:H	20:CT:8:LYS:HG2	1.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:160:A:C8	22:DA:167:A:C6	3.07	0.42
22:DA:176:A:C5	22:DA:177:G:C6	3.07	0.42
22:DA:537:G:C6	22:DA:555:G:C2	3.08	0.42
22:DA:597:G:H2'	22:DA:598:U:O4'	2.19	0.42
22:DA:1417:C:H2'	22:DA:1418:G:O4'	2.19	0.42
22:DA:1439:A:N7	22:DA:1552:A:C2	2.85	0.42
22:DA:1604:C:O2'	22:DA:1610:A:N1	2.41	0.42
22:DA:1881:C:O5'	22:DA:1881:C:H6	2.02	0.42
22:DA:2254:C:H2'	22:DA:2255:G:O4'	2.20	0.42
22:DA:2548:U:H2'	22:DA:2549:G:O4'	2.20	0.42
22:DA:2728:U:O2'	22:DA:2729:G:H5"	2.19	0.42
23:DB:76:G:OP1	43:DV:9:ARG:NH2	2.52	0.42
28:DG:125:CYS:HB3	28:DG:127:THR:O	2.19	0.42
29:DH:69:ALA:HB2	29:DH:138:VAL:HG12	2.02	0.42
29:DH:121:VAL:O	29:DH:122:LEU:CB	2.67	0.42
29:DH:127:GLU:HA	29:DH:144:VAL:O	2.19	0.42
37:DP:39:ARG:HG3	37:DP:40:LEU:N	2.27	0.42
41:DT:51:PHE:O	41:DT:53:VAL:N	2.53	0.42
45:DX:18:ARG:HA	45:DX:18:ARG:HD2	1.83	0.42
1:AA:277:C:H2'	1:AA:278:G:H5'	2.01	0.42
1:AA:428:G:O4'	1:AA:430:A:C8	2.72	0.42
1:AA:1516:G:N1	1:AA:1519:A:OP2	2.49	0.42
3:AC:68:ILE:O	3:AC:70:THR:HG22	2.20	0.42
19:AS:29:LYS:HB3	19:AS:30:PRO:CD	2.48	0.42
19:AS:42:PRO:HD3	19:AS:67:VAL:HG13	2.00	0.42
19:AS:49:ILE:HG21	19:AS:71:LEU:HD11	2.01	0.42
22:BA:42:A:H2'	22:BA:43:G:O4'	2.20	0.42
22:BA:303:G:C6	22:BA:315:G:C6	3.08	0.42
22:BA:319:G:C4	22:BA:333:G:N2	2.87	0.42
22:BA:532:A:N3	22:BA:532:A:H2'	2.35	0.42
22:BA:581:C:H2'	22:BA:582:A:C8	2.54	0.42
22:BA:693:A:H2'	22:BA:694:U:O4'	2.19	0.42
22:BA:958:U:C2	23:BB:89:U:H1'	2.54	0.42
22:BA:1317:G:C2	22:BA:1336:A:C2	3.08	0.42
22:BA:2504:U:H6	22:BA:2504:U:O5'	2.02	0.42
22:BA:2600:A:N6	57:BA:3794:HOH:O	2.52	0.42
22:BA:2766:A:N3	22:BA:2766:A:H2'	2.34	0.42
23:BB:43:C:H2'	23:BB:44:G:H5'	2.00	0.42
26:BE:61:ARG:NH2	26:BE:64:GLY:HA3	2.35	0.42
29:BH:89:LYS:HB3	1:CA:359:G:H5'	1.98	0.42
39:BR:48:LYS:HB3	39:BR:48:LYS:HE2	1.24	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:84:U:O2'	1:CA:85:U:H5'	2.20	0.42
1:CA:297:G:N2	1:CA:300:A:OP2	2.52	0.42
1:CA:1022:A:C6	1:CA:1023:U:C4	3.08	0.42
1:CA:1270:G:H8	1:CA:1270:G:OP2	2.03	0.42
5:CE:36:LEU:HD12	5:CE:36:LEU:HA	1.94	0.42
5:CE:153:VAL:HG23	5:CE:157:ARG:CB	2.49	0.42
6:CF:38:ARG:HG2	6:CF:63:ASN:HB3	2.02	0.42
7:CG:65:ALA:HB1	7:CG:127:ALA:HB3	2.01	0.42
9:CI:87:LEU:C	9:CI:89:GLU:N	2.78	0.42
9:CI:95:ARG:O	9:CI:99:ARG:N	2.41	0.42
10:CJ:7:ARG:HD3	10:CJ:75:ASP:OD1	2.20	0.42
10:CJ:48:ARG:NH1	10:CJ:66:GLU:OE1	2.52	0.42
14:CN:93:ILE:HA	14:CN:94:PRO:HD3	1.91	0.42
16:CP:31:ARG:HG3	16:CP:32:PHE:N	2.34	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
22:DA:445:C:H2'	22:DA:446:G:C8	2.54	0.42
22:DA:590:A:N6	22:DA:666:A:H61	2.18	0.42
22:DA:818:G:H5'	22:DA:839:U:OP1	2.20	0.42
22:DA:822:G:O6	22:DA:943:A:H2	2.02	0.42
22:DA:836:G:H2'	22:DA:837:C:C6	2.54	0.42
22:DA:970:U:O2'	22:DA:985:C:OP2	2.35	0.42
22:DA:1068:G:N3	22:DA:1068:G:H2'	2.34	0.42
22:DA:1654:A:OP2	35:DN:1:MET:HA	2.19	0.42
22:DA:1735:A:H2'	22:DA:1736:U:O4'	2.20	0.42
22:DA:1789:A:P	24:DC:221:ARG:HH11	2.41	0.42
22:DA:2233:U:H2'	22:DA:2234:G:C8	2.55	0.42
22:DA:2436:G:C2	22:DA:2437:G:C8	3.08	0.42
22:DA:2886:A:H2	48:D0:29:SER:HB3	1.84	0.42
24:DC:266:PHE:N	24:DC:266:PHE:CD1	2.88	0.42
27:DF:138:PHE:HA	27:DF:139:PRO:HD3	1.83	0.42
29:DH:31:VAL:HG12	29:DH:32:PRO:HD3	2.02	0.42
30:DI:14:ALA:C	30:DI:16:GLY:H	2.28	0.42
33:DL:93:ASN:O	33:DL:95:LEU:N	2.42	0.42
35:DN:79:LEU:C	35:DN:81:ASN:H	2.23	0.42
41:DT:82:LYS:HG2	41:DT:83:ALA:N	2.34	0.42
45:DX:59:ILE:HG12	45:DX:67:VAL:HG21	2.02	0.42
46:DY:1:MET:HG2	46:DY:5:GLU:OE2	2.19	0.42
1:AA:79:G:H22	1:AA:90:C:N4	2.17	0.42
1:AA:885:G:C2	1:AA:913:A:N1	2.87	0.42
1:AA:1249:C:O2'	9:AI:71:GLY:HA2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1520:C:H2'	1:AA:1521:C:H6	1.83	0.42
8:AH:41:LYS:NZ	8:AH:48:ASP:OD2	2.38	0.42
10:AJ:53:ILE:CG2	10:AJ:61:ALA:HB1	2.50	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
22:BA:622:G:H2'	22:BA:623:C:H6	1.84	0.42
22:BA:790:U:O2'	22:BA:791:C:P	2.77	0.42
22:BA:920:A:H2'	22:BA:921:C:C6	2.55	0.42
22:BA:962:G:H21	22:BA:2250:G:H1	1.66	0.42
22:BA:1309:G:H4'	50:B2:7:PRO:HG2	2.01	0.42
22:BA:2271:G:H2'	22:BA:2272:U:C6	2.54	0.42
22:BA:2582:G:C2	22:BA:2583:G:C8	3.08	0.42
22:BA:2783:U:H2'	22:BA:2784:U:C6	2.54	0.42
22:BA:2786:U:O2'	25:BD:63:PRO:O	2.38	0.42
22:BA:2804:U:H2'	22:BA:2805:C:C6	2.54	0.42
23:BB:54:G:N2	27:BF:26:MET:HE3	2.27	0.42
29:BH:116:ARG:HB3	29:BH:131:SER:O	2.20	0.42
30:BI:33:VAL:HG21	30:BI:59:ILE:HG23	2.01	0.42
30:BI:43:ASN:HA	30:BI:46:THR:HB	2.01	0.42
34:BM:42:THR:O	34:BM:46:ILE:HG13	2.19	0.42
35:BN:8:ARG:HH21	35:BN:8:ARG:HD3	1.71	0.42
52:B4:33:HIS:O	52:B4:35:GLN:HG3	2.19	0.42
1:CA:49:U:O4	1:CA:365:U:H5	2.02	0.42
1:CA:209:U:H4'	1:CA:210:C:OP2	2.18	0.42
1:CA:389:A:C6	1:CA:390:U:H1'	2.54	0.42
1:CA:549:C:H2'	1:CA:550:G:O4'	2.19	0.42
1:CA:1125:U:H4'	10:CJ:7:ARG:NH1	2.35	0.42
1:CA:1505:G:H4'	1:CA:1506:U:H5"	2.00	0.42
3:CC:12:LEU:HD23	3:CC:12:LEU:HA	1.74	0.42
3:CC:53:SER:O	3:CC:54:ARG:HB2	2.19	0.42
3:CC:154:SER:HA	3:CC:165:THR:HA	2.01	0.42
6:CF:7:VAL:HG23	6:CF:9:MET:HE3	2.02	0.42
11:CK:13:ARG:HE	11:CK:13:ARG:HB3	1.57	0.42
19:CS:36:ARG:HH21	19:CS:75:ALA:HB3	1.85	0.42
20:CT:24:ARG:O	20:CT:27:MET:HG3	2.19	0.42
22:DA:55:G:C2	22:DA:56:A:C8	3.08	0.42
22:DA:69:C:O2'	22:DA:73:A:O2'	2.31	0.42
22:DA:676:A:H2	22:DA:2069:G:N3	2.18	0.42
22:DA:1028:A:N6	22:DA:1125:G:H2'	2.35	0.42
22:DA:1029:A:N1	22:DA:2465:C:O2'	2.43	0.42
22:DA:1384:A:O2'	22:DA:1404:C:O2	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2074:U:C2	22:DA:2436:G:C2	3.08	0.42
22:DA:2445:G:O2'	22:DA:2446:G:H5'	2.19	0.42
24:DC:98:ASP:CG	24:DC:99:GLY:H	2.28	0.42
24:DC:207:LYS:HG3	24:DC:210:ALA:H	1.83	0.42
26:DE:111:GLU:O	26:DE:115:GLN:HG2	2.20	0.42
28:DG:154:PRO:HA	28:DG:160:LYS:O	2.20	0.42
29:DH:43:ASN:C	29:DH:45:GLU:H	2.27	0.42
30:DI:89:GLY:HA2	30:DI:136:MET:HE3	2.01	0.42
36:DO:6:ALA:O	36:DO:10:ARG:HB2	2.20	0.42
36:DO:33:ARG:HG2	36:DO:34:HIS:CD2	2.55	0.42
38:DQ:61:TRP:HB3	38:DQ:92:ARG:O	2.19	0.42
39:DR:8:GLY:C	39:DR:10:LYS:HG2	2.45	0.42
42:DU:53:ASN:OD1	42:DU:53:ASN:N	2.52	0.42
43:DV:9:ARG:HB2	43:DV:39:ALA:HB1	2.01	0.42
48:D0:12:LYS:HA	48:D0:15:MET:HB2	2.01	0.42
54:D6:7:004:O	54:D6:7:004:HG1	2.19	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
1:AA:857:C:H2'	1:AA:858:G:C8	2.55	0.42
1:AA:909:A:H2'	1:AA:910:C:O4'	2.19	0.42
1:AA:1130:A:O2'	9:AI:5:GLN:HG3	2.20	0.42
1:AA:1187:G:H5'	9:AI:115:LYS:HE3	2.01	0.42
1:AA:1201:A:H1'	1:AA:1202:U:OP2	2.20	0.42
1:AA:1325:C:H2'	1:AA:1326:U:H6	1.84	0.42
3:AC:150:LYS:HG3	3:AC:201:TRP:CE3	2.55	0.42
4:AD:13:ARG:HB3	4:AD:13:ARG:HH11	1.84	0.42
4:AD:130:VAL:HG11	4:AD:135:TYR:CD1	2.55	0.42
5:AE:36:LEU:HD21	5:AE:137:VAL:HG11	2.02	0.42
7:AG:95:ARG:CZ	7:AG:99:LEU:HD21	2.50	0.42
8:AH:39:VAL:HG13	8:AH:112:THR:HG22	2.02	0.42
14:AN:11:VAL:O	14:AN:14:VAL:HG12	2.20	0.42
14:AN:21:PHE:HE1	14:AN:51:LEU:HD12	1.84	0.42
15:AO:85:LEU:HD12	15:AO:85:LEU:HA	1.93	0.42
17:AQ:16:LYS:C	17:AQ:17:MET:HE3	2.44	0.42
18:AR:55:LEU:HD22	18:AR:55:LEU:HA	1.83	0.42
22:BA:391:A:C6	22:BA:411:G:C2	3.08	0.42
22:BA:413:C:H4'	22:BA:1880:U:H4'	2.02	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
22:BA:1132:U:H3'	22:BA:1133:A:H5"	2.01	0.42
22:BA:1808:A:H3'	22:BA:1809:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:1909:C:H5'	22:BA:1910:G:OP2	2.19	0.42
22:BA:2299:U:H2'	22:BA:2300:C:C6	2.55	0.42
22:BA:2874:C:H2'	22:BA:2875:C:H6	1.85	0.42
23:BB:78:A:C2	23:BB:99:A:C4	3.08	0.42
26:BE:108:ILE:HD13	26:BE:181:ILE:CG1	2.48	0.42
26:BE:137:LYS:O	26:BE:141:MET:HG2	2.20	0.42
29:BH:118:PRO:O	29:BH:119:ASN:CB	2.68	0.42
31:BJ:23:LYS:HE3	31:BJ:142:ILE:OXT	2.20	0.42
52:B4:2:LYS:HE2	52:B4:4:ARG:NE	2.34	0.42
1:CA:6:G:H22	5:CE:102:GLY:HA2	1.85	0.42
1:CA:728:A:C8	15:CO:54:ARG:CZ	3.03	0.42
1:CA:965:U:OP1	1:CA:1198:G:H5"	2.20	0.42
1:CA:1244:G:C6	1:CA:1245:C:N4	2.87	0.42
2:CB:15:HIS:HD2	2:CB:209:ALA:HB2	1.85	0.42
4:CD:56:ARG:NH1	4:CD:56:ARG:HA	2.34	0.42
5:CE:98:PRO:O	5:CE:122:ASN:ND2	2.52	0.42
7:CG:78:ARG:HG3	7:CG:87:VAL:HG21	2.00	0.42
10:CJ:34:ALA:N	10:CJ:78:GLU:HG2	2.35	0.42
12:CL:30:LYS:O	12:CL:81:LEU:HD12	2.19	0.42
12:CL:84:GLY:HA2	12:CL:95:TYR:HD1	1.85	0.42
14:CN:53:ARG:C	14:CN:55:SER:N	2.78	0.42
15:CO:8:THR:O	15:CO:12:VAL:HG23	2.20	0.42
21:CU:24:GLU:HA	21:CU:28:VAL:HG22	2.01	0.42
22:DA:127:A:H5"	22:DA:128:C:C6	2.55	0.42
22:DA:1029:A:N7	22:DA:1030:C:C2	2.88	0.42
22:DA:2019:A:H4'	38:DQ:34:VAL:CG2	2.49	0.42
22:DA:2452:C:C4	22:DA:2453:A:C6	3.07	0.42
22:DA:2873:A:O4'	35:DN:6:SER:HB2	2.19	0.42
23:DB:28:C:H6	23:DB:28:C:O5'	2.03	0.42
24:DC:29:PRO:HB2	24:DC:30:PHE:H	1.62	0.42
26:DE:143:LEU:HB3	26:DE:146:VAL:CG1	2.50	0.42
27:DF:100:PHE:HE2	27:DF:173:PHE:CD2	2.37	0.42
33:DL:61:LEU:O	51:D3:13:ARG:HD3	2.20	0.42
33:DL:82:LEU:HG	33:DL:120:VAL:HG21	2.00	0.42
34:DM:12:MET:O	34:DM:86:LYS:HE2	2.19	0.42
40:DS:23:LEU:HD22	48:D0:24:ALA:HB2	2.02	0.42
42:DU:9:ASP:O	42:DU:25:VAL:HG23	2.20	0.42
44:DW:21:LEU:HD13	44:DW:40:GLN:HA	2.01	0.42
52:D4:19:ARG:O	52:D4:20:ASP:HB2	2.20	0.42
1:AA:208:U:C5	1:AA:210:C:C4	3.07	0.42
1:AA:407:U:H2'	1:AA:408:A:C8	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:484:G:H8	1:AA:484:G:OP1	2.01	0.42
1:AA:663:A:H5'	1:AA:836:G:OP1	2.20	0.42
1:AA:705:G:N2	11:AK:31:ILE:HD13	2.35	0.42
1:AA:719:C:O2'	18:AR:39:ILE:O	2.37	0.42
1:AA:721:G:C6	1:AA:733:G:C2	3.07	0.42
1:AA:1160:G:O2'	1:AA:1161:C:P	2.78	0.42
1:AA:1170:A:H8	1:AA:1170:A:O5'	2.02	0.42
2:AB:106:THR:HA	2:AB:109:GLN:HE22	1.85	0.42
3:AC:53:SER:CB	3:AC:115:LEU:HG	2.47	0.42
6:AF:81:ASN:O	6:AF:84:VAL:HG12	2.19	0.42
7:AG:97:ASN:HA	7:AG:100:ALA:HB3	2.01	0.42
11:AK:126:LYS:HD3	11:AK:126:LYS:N	2.35	0.42
20:AT:25:ARG:HG2	20:AT:29:ARG:NH1	2.33	0.42
21:AU:25:LYS:HD2	21:AU:26:ALA:H	1.84	0.42
22:BA:13:A:N1	22:BA:525:U:H2'	2.35	0.42
22:BA:253:C:OP2	51:B3:5:LYS:NZ	2.28	0.42
22:BA:441:U:H2'	22:BA:442:G:H8	1.85	0.42
22:BA:458:G:C8	50:B2:37:LYS:HG2	2.55	0.42
22:BA:1098:A:C5	22:BA:1099:G:C6	3.08	0.42
22:BA:1316:U:C2	22:BA:1337:G:N2	2.88	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
22:BA:1946:U:H2'	22:BA:1947:C:H6	1.84	0.42
22:BA:2093:G:O3'	29:BH:25:TYR:HB2	2.20	0.42
22:BA:2444:G:OP2	26:BE:63:LYS:HD2	2.20	0.42
23:BB:36:C:H5"	23:BB:37:C:OP2	2.20	0.42
24:BC:74:ILE:HA	24:BC:75:PRO:HD3	1.91	0.42
25:BD:86:GLU:O	25:BD:86:GLU:HG3	2.20	0.42
26:BE:79:ARG:HG2	26:BE:79:ARG:HH11	1.84	0.42
26:BE:171:ASP:OD1	26:BE:171:ASP:C	2.62	0.42
30:BI:11:LEU:O	30:BI:24:VAL:HG11	2.20	0.42
30:BI:58:VAL:HB	30:BI:69:PHE:HB2	2.02	0.42
31:BJ:77:HIS:HA	31:BJ:83:GLY:O	2.20	0.42
32:BK:38:ILE:HD11	32:BK:112:PHE:HZ	1.85	0.42
40:BS:41:LYS:O	40:BS:44:ALA:HB3	2.20	0.42
42:BU:40:ASN:HB3	42:BU:63:ALA:O	2.19	0.42
43:BV:80:HIS:CE1	43:BV:83:LYS:HE3	2.54	0.42
1:CA:200:G:C3'	1:CA:201:G:H5"	2.50	0.42
1:CA:445:G:C2	1:CA:490:C:C2	3.08	0.42
1:CA:976:G:OP1	14:CN:71:HIS:ND1	2.47	0.42
1:CA:1098:C:H2'	1:CA:1099:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1123:U:O3'	10:CJ:38:GLY:HA3	2.20	0.42
1:CA:1361:G:H2'	1:CA:1362:A:H5"	2.01	0.42
2:CB:186:ILE:HA	2:CB:200:ILE:HB	2.00	0.42
12:CL:44:LYS:H	12:CL:44:LYS:HD3	1.84	0.42
15:CO:39:LEU:HG	15:CO:43:PHE:HE1	1.80	0.42
16:CP:5:ARG:O	16:CP:19:VAL:HA	2.20	0.42
17:CQ:5:ILE:HB	17:CQ:6:ARG:H	1.47	0.42
17:CQ:69:LYS:O	17:CQ:70:THR:OG1	2.33	0.42
19:CS:40:ILE:HA	19:CS:44:MET:SD	2.60	0.42
21:CU:35:ARG:NH2	57:CU:101:HOH:O	2.52	0.42
22:DA:13:A:H4'	22:DA:14:A:OP1	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
22:DA:965:C:O5'	22:DA:2273:A:H1'	2.20	0.42
22:DA:2278:A:H5"	44:DW:12:ASN:HD21	1.85	0.42
22:DA:2415:G:C6	22:DA:2416:C:C4	3.08	0.42
25:DD:12:THR:HG21	37:DP:5:ILE:HG23	2.02	0.42
25:DD:32:ASN:HA	25:DD:52:THR:HB	2.00	0.42
25:DD:151:THR:C	25:DD:153:GLY:N	2.78	0.42
27:DF:117:LEU:O	27:DF:177:PHE:HA	2.19	0.42
30:DI:80:LEU:HD22	30:DI:138:LEU:HD11	2.00	0.42
35:DN:74:GLU:O	35:DN:77:ALA:HB3	2.19	0.42
44:DW:52:GLY:HA3	44:DW:60:PHE:CE1	2.55	0.42
49:D1:12:VAL:HG23	49:D1:51:GLU:HB3	2.02	0.42
1:AA:151:A:H2'	1:AA:152:A:O4'	2.20	0.42
1:AA:223:A:H2'	1:AA:224:U:C6	2.55	0.42
1:AA:625:U:H4'	16:AP:16:PHE:CE2	2.54	0.42
1:AA:1034:G:H2'	1:AA:1035:A:O4'	2.19	0.42
1:AA:1226:C:P	13:AM:90:ARG:HH22	2.42	0.42
4:AD:30:THR:O	4:AD:31:LYS:C	2.63	0.42
4:AD:95:GLU:OE2	4:AD:104:ARG:NH1	2.52	0.42
5:AE:106:ILE:HG13	5:AE:124:LEU:HB3	2.02	0.42
6:AF:42:TRP:CZ2	6:AF:61:LEU:HD22	2.53	0.42
17:AQ:17:MET:HG2	17:AQ:20:SER:HB3	2.01	0.42
19:AS:63:THR:O	19:AS:65:GLU:N	2.43	0.42
22:BA:2:G:H2'	22:BA:3:U:C6	2.55	0.42
22:BA:476:G:N2	22:BA:479:A:O4'	2.52	0.42
22:BA:2392:A:O2'	33:BL:60:ARG:O	2.35	0.42
22:BA:2886:A:C5	22:BA:2887:A:C8	3.08	0.42
28:BG:49:THR:O	28:BG:50:LEU:HD23	2.20	0.42
34:BM:16:ARG:HA	34:BM:16:ARG:HD3	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BN:72:ASP:O	35:BN:76:VAL:HG12	2.20	0.42
35:BN:81:ASN:O	35:BN:85:PRO:HG2	2.20	0.42
43:BV:10:LYS:HG2	43:BV:11:GLU:HG2	2.01	0.42
46:BY:56:LEU:O	46:BY:57:LEU:HB3	2.19	0.42
52:B4:3:VAL:HG12	52:B4:36:ARG:HB3	2.02	0.42
1:CA:276:G:C6	1:CA:277:C:C4	3.08	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
1:CA:518:C:H2'	1:CA:530:G:H8	1.81	0.42
1:CA:560:A:H5'	1:CA:566:G:N2	2.34	0.42
1:CA:747:A:N6	1:CA:748:G:C6	2.88	0.42
1:CA:828:U:O2	2:CB:25:PRO:HG2	2.20	0.42
1:CA:938:A:O3'	7:CG:95:ARG:NH2	2.53	0.42
1:CA:1293:C:H3'	1:CA:1294:G:H8	1.84	0.42
1:CA:1408:A:C2	1:CA:1494:G:C4	3.08	0.42
1:CA:1538:C:H2'	1:CA:1539:C:C6	2.55	0.42
2:CB:47:VAL:O	2:CB:51:ASN:ND2	2.53	0.42
2:CB:128:LYS:HA	2:CB:128:LYS:HD2	1.86	0.42
2:CB:128:LYS:O	2:CB:129:LEU:HB2	2.19	0.42
5:CE:153:VAL:HG23	5:CE:157:ARG:HB2	2.02	0.42
7:CG:148:ASN:C	7:CG:150:ALA:H	2.28	0.42
10:CJ:35:GLN:HB3	10:CJ:36:VAL:H	1.53	0.42
12:CL:116:LYS:H	12:CL:116:LYS:HG3	1.68	0.42
13:CM:29:ARG:NH1	13:CM:33:ILE:HD11	2.35	0.42
13:CM:74:SER:O	13:CM:78:LYS:HG3	2.20	0.42
21:CU:10:GLU:CG	21:CU:11:PRO:HD3	2.40	0.42
22:DA:262:A:H5'	22:DA:610:C:O2'	2.20	0.42
22:DA:565:C:H4'	22:DA:1253:A:N6	2.35	0.42
22:DA:662:G:O3'	33:DL:16:GLY:HA2	2.20	0.42
22:DA:1132:U:O2'	22:DA:1133:A:H5'	2.20	0.42
22:DA:1373:A:C4	22:DA:1374:G:H1'	2.54	0.42
22:DA:1567:G:O2'	24:DC:63:ARG:NH1	2.53	0.42
22:DA:1896:G:H2'	22:DA:1897:G:O4'	2.20	0.42
22:DA:2259:U:H2'	22:DA:2260:C:C6	2.55	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
22:DA:2698:U:H2'	22:DA:2699:C:C6	2.55	0.42
23:DB:41:G:P	23:DB:43:C:H41	2.43	0.42
24:DC:3:VAL:HG11	24:DC:202:LEU:HD23	2.00	0.42
26:DE:129:PRO:HG3	26:DE:156:ASN:OD1	2.20	0.42
31:DJ:59:ALA:O	31:DJ:62:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DN:24:MET:HE3	35:DN:44:LEU:HD22	2.01	0.42
36:DO:100:HIS:CD2	36:DO:101:GLY:N	2.88	0.42
38:DQ:58:ARG:HA	38:DQ:61:TRP:CE3	2.54	0.42
39:DR:24:LYS:HA	39:DR:94:THR:OG1	2.20	0.42
41:DT:23:ALA:O	41:DT:27:SER:N	2.43	0.42
41:DT:49:LYS:O	41:DT:51:PHE:N	2.53	0.42
52:D4:3:VAL:HG12	52:D4:36:ARG:HB3	2.01	0.42
1:AA:620:C:H2'	1:AA:621:A:O4'	2.19	0.41
1:AA:679:C:H2'	1:AA:680:C:C6	2.55	0.41
1:AA:907:A:C4	1:AA:908:A:C8	3.07	0.41
1:AA:1211:U:H1'	1:AA:1213:A:C2	2.55	0.41
1:AA:1222:G:C6	1:AA:1223:C:C4	3.08	0.41
9:AI:51:PRO:HB3	9:AI:84:THR:CG2	2.50	0.41
19:AS:19:VAL:O	19:AS:23:VAL:HG23	2.20	0.41
20:AT:4:ILE:HG12	20:AT:8:LYS:NZ	2.35	0.41
22:BA:58:G:OP1	41:BT:78:SER:CB	2.68	0.41
22:BA:66:C:H2'	22:BA:67:U:H6	1.84	0.41
22:BA:109:C:H2'	22:BA:110:G:O4'	2.19	0.41
22:BA:361:G:O2'	22:BA:362:A:O5'	2.36	0.41
22:BA:607:U:O4	22:BA:620:G:H5'	2.19	0.41
22:BA:1534:U:H3'	22:BA:1536:C:H41	1.84	0.41
22:BA:2093:G:O5'	29:BH:24:GLY:HA3	2.20	0.41
22:BA:2127:G:H21	22:BA:2173:A:H1'	1.85	0.41
24:BC:40:SER:O	24:BC:42:GLY:N	2.53	0.41
24:BC:243:HIS:O	24:BC:245:VAL:HG13	2.20	0.41
24:BC:266:PHE:CD1	24:BC:266:PHE:N	2.86	0.41
29:BH:41:LYS:O	29:BH:42:LYS:C	2.62	0.41
29:BH:104:THR:CG2	29:BH:110:VAL:O	2.68	0.41
31:BJ:13:ARG:HB3	31:BJ:51:GLY:O	2.20	0.41
34:BM:61:GLY:HA2	34:BM:107:GLY:HA3	2.02	0.41
41:BT:37:ASP:OD1	41:BT:37:ASP:N	2.43	0.41
1:CA:501:C:H2'	1:CA:502:A:C8	2.55	0.41
1:CA:512:U:H2'	1:CA:513:C:C6	2.55	0.41
1:CA:608:A:H3'	1:CA:609:A:H8	1.85	0.41
1:CA:841:C:H2'	1:CA:843:U:O4'	2.20	0.41
1:CA:1249:C:O3'	9:CI:75:GLN:NE2	2.50	0.41
1:CA:1262:C:H2'	1:CA:1263:C:O4'	2.20	0.41
2:CB:27:MET:HE3	2:CB:30:PHE:CD2	2.55	0.41
3:CC:22:TRP:CZ3	14:CN:94:PRO:HG2	2.54	0.41
3:CC:129:MET:HG2	3:CC:131:ARG:HH11	1.84	0.41
5:CE:93:ARG:NH1	5:CE:93:ARG:HB3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:9:MET:CG	6:CF:86:ARG:HB2	2.44	0.41
6:CF:29:ILE:HG22	6:CF:34:GLY:O	2.20	0.41
9:CI:49:ARG:NH2	9:CI:53:GLU:HA	2.34	0.41
10:CJ:35:GLN:NE2	10:CJ:77:VAL:HB	2.35	0.41
16:CP:19:VAL:HG13	16:CP:37:GLY:C	2.45	0.41
19:CS:11:ILE:HB	19:CS:38:SER:CB	2.50	0.41
22:DA:308:G:C6	22:DA:309:A:C6	3.08	0.41
22:DA:377:G:C6	22:DA:378:C:C4	3.08	0.41
22:DA:806:C:H2'	22:DA:807:U:C6	2.55	0.41
22:DA:971:G:C2	22:DA:972:A:H1'	2.55	0.41
22:DA:1211:C:H5"	22:DA:1212:G:C8	2.55	0.41
22:DA:1364:G:N2	22:DA:1367:A:OP2	2.26	0.41
22:DA:1572:A:H2'	22:DA:1573:G:C8	2.55	0.41
22:DA:1669:A:OP2	57:DA:3719:HOH:O	2.22	0.41
22:DA:1726:C:H2'	22:DA:1727:C:C6	2.54	0.41
22:DA:2163:A:C6	22:DA:2164:C:H1'	2.54	0.41
22:DA:2296:U:H4'	22:DA:2297:A:OP1	2.19	0.41
22:DA:2340:A:H2'	22:DA:2341:G:C8	2.55	0.41
26:DE:181:ILE:HG23	33:DL:2:ARG:NH1	2.35	0.41
30:DI:127:ARG:HA	30:DI:130:GLU:HB2	2.00	0.41
36:DO:88:LYS:HD3	36:DO:116:GLN:NE2	2.35	0.41
52:D4:12:ARG:HB2	52:D4:12:ARG:CZ	2.50	0.41
1:AA:16:A:H4'	5:AE:22:SER:H	1.85	0.41
1:AA:93:U:C2'	1:AA:94:G:H5"	2.49	0.41
1:AA:628:G:H2'	1:AA:629:A:O4'	2.21	0.41
1:AA:803:G:H8	1:AA:803:G:O5'	2.03	0.41
1:AA:874:G:C6	1:AA:875:U:C4	3.08	0.41
2:AB:120:GLN:HG2	2:AB:125:THR:O	2.20	0.41
12:AL:114:ARG:NH2	12:AL:121:ARG:HA	2.34	0.41
16:AP:75:ILE:HG13	16:AP:75:ILE:H	1.50	0.41
17:AQ:26:GLU:OE2	17:AQ:39:LYS:HB3	2.20	0.41
22:BA:675:A:N3	22:BA:2443:C:O2'	2.50	0.41
22:BA:747:U:C4	22:BA:2613:U:C5	3.08	0.41
22:BA:1250:G:H5'	38:BQ:6:ARG:HD3	2.02	0.41
22:BA:1820:U:O2	24:BC:200:HIS:HB3	2.20	0.41
22:BA:2006:C:H6	22:BA:2006:C:O5'	2.03	0.41
22:BA:2684:U:C4	22:BA:2685:G:N7	2.89	0.41
24:BC:141:VAL:HG11	24:BC:190:ALA:HB1	2.01	0.41
26:BE:29:HIS:CE1	33:BL:8:PRO:HB3	2.55	0.41
28:BG:141:ILE:HD12	28:BG:142:GLY:N	2.35	0.41
29:BH:90:LEU:HD13	29:BH:125:THR:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BH:139:PHE:O	29:BH:140:ALA:HB3	2.20	0.41
45:BX:22:LEU:HD23	45:BX:22:LEU:HA	1.77	0.41
49:B1:53:LYS:H	49:B1:53:LYS:HG2	1.45	0.41
50:B2:9:VAL:HG12	50:B2:13:ASN:HD21	1.86	0.41
1:CA:26:A:H61	1:CA:558:G:H1'	1.85	0.41
1:CA:115:G:H1'	1:CA:116:A:N7	2.35	0.41
1:CA:765:G:N2	1:CA:813:U:H5	2.18	0.41
1:CA:1053:G:N7	1:CA:1199:U:H3'	2.35	0.41
1:CA:1316:G:N2	1:CA:1318:A:H3'	2.35	0.41
2:CB:206:ALA:O	2:CB:210:VAL:HG13	2.19	0.41
5:CE:100:SER:O	5:CE:101:GLU:C	2.63	0.41
13:CM:63:PHE:O	13:CM:65:VAL:HG13	2.20	0.41
22:DA:181:A:H1'	22:DA:435:C:O4'	2.20	0.41
22:DA:223:A:H2'	22:DA:408:G:N3	2.35	0.41
22:DA:319:G:H2'	22:DA:320:A:O4'	2.20	0.41
22:DA:852:U:H2'	22:DA:853:C:C6	2.55	0.41
22:DA:1045:C:C3'	22:DA:1046:A:H5'	2.50	0.41
22:DA:1069:A:N1	22:DA:1073:A:N7	2.69	0.41
22:DA:1596:A:C6	22:DA:1597:A:C6	3.08	0.41
22:DA:2305:U:O4'	27:DF:131:GLY:HA3	2.20	0.41
27:DF:114:PHE:HE1	27:DF:117:LEU:HD22	1.85	0.41
29:DH:41:LYS:HE2	29:DH:44:ILE:CD1	2.50	0.41
29:DH:135:HIS:CG	29:DH:136:SER:N	2.89	0.41
35:DN:55:ALA:HB2	35:DN:79:LEU:HB3	2.00	0.41
36:DO:71:ALA:HB1	36:DO:106:LEU:HB2	2.02	0.41
36:DO:74:VAL:O	36:DO:78:VAL:HG23	2.20	0.41
39:DR:19:THR:CG2	39:DR:95:ASP:HB3	2.50	0.41
47:DZ:25:LEU:HD23	47:DZ:25:LEU:HA	1.89	0.41
1:AA:579:A:H4'	1:AA:728:A:H1'	2.02	0.41
1:AA:730:G:N3	1:AA:730:G:H2'	2.35	0.41
1:AA:977:A:O2'	1:AA:979:C:OP2	2.35	0.41
1:AA:983:A:N3	1:AA:983:A:H2'	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
3:AC:97:VAL:HB	3:AC:98:PRO:HD2	2.01	0.41
6:AF:64:VAL:HG12	6:AF:65:GLU:N	2.34	0.41
6:AF:75:GLU:HA	6:AF:78:PHE:HB2	2.00	0.41
7:AG:58:GLU:HB3	7:AG:59:LEU:H	1.59	0.41
8:AH:89:LYS:HG3	8:AH:90:ASP:H	1.85	0.41
11:AK:16:VAL:HG12	11:AK:77:TYR:HB3	2.02	0.41
11:AK:76:GLU:C	22:BA:2141:G:OP1	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:215:G:H4'	22:BA:216:A:OP1	2.21	0.41
22:BA:320:A:H4'	22:BA:322:A:N7	2.35	0.41
22:BA:2398:U:H2'	22:BA:2399:G:H8	1.85	0.41
26:BE:27:LEU:O	26:BE:31:VAL:HG23	2.20	0.41
27:BF:148:ARG:HG2	27:BF:149:VAL:H	1.84	0.41
28:BG:77:ILE:H	28:BG:77:ILE:HG12	1.45	0.41
28:BG:127:THR:HG22	28:BG:128:GLN:N	2.34	0.41
38:BQ:102:ASP:C	38:BQ:104:VAL:N	2.78	0.41
45:BX:18:ARG:NE	45:BX:24:ALA:HB2	2.35	0.41
45:BX:59:ILE:HA	45:BX:67:VAL:HG21	2.02	0.41
1:CA:1118:U:H1'	1:CA:1179:A:C5	2.55	0.41
1:CA:1479:C:H2'	1:CA:1480:A:H8	1.85	0.41
2:CB:58:ASN:OD1	2:CB:61:ALA:HB3	2.19	0.41
2:CB:68:LEU:HD21	2:CB:92:VAL:HG23	2.01	0.41
2:CB:193:PRO:HB2	2:CB:194:ASP:H	1.68	0.41
6:CF:18:VAL:O	6:CF:21:MET:HB2	2.21	0.41
7:CG:103:TRP:O	7:CG:107:ALA:N	2.48	0.41
8:CH:40:LEU:HD21	8:CH:129:VAL:HG21	2.03	0.41
9:CI:54:LEU:O	9:CI:55:VAL:HG13	2.20	0.41
12:CL:38:TYR:N	12:CL:52:VAL:O	2.46	0.41
15:CO:24:SER:O	15:CO:27:VAL:HB	2.19	0.41
19:CS:34:TRP:HA	19:CS:52:HIS:HB2	2.02	0.41
22:DA:483:A:O3'	42:DU:48:PRO:HD3	2.20	0.41
22:DA:705:A:H2'	22:DA:706:A:C8	2.54	0.41
22:DA:1056:G:H4'	22:DA:1086:A:C8	2.55	0.41
22:DA:1819:A:H4'	22:DA:1820:U:H5"	2.02	0.41
22:DA:2347:C:O2'	49:D1:39:PHE:HB3	2.19	0.41
22:DA:2824:C:N4	22:DA:2825:G:N7	2.69	0.41
32:DK:105:ARG:NH1	37:DP:34:GLU:HG3	2.35	0.41
35:DN:31:HIS:C	35:DN:33:ILE:H	2.28	0.41
42:DU:18:ASP:OD2	42:DU:18:ASP:N	2.52	0.41
42:DU:26:LYS:HD2	42:DU:26:LYS:HA	1.73	0.41
45:DX:5:CYS:SG	45:DX:52:SER:HB3	2.60	0.41
1:AA:544:G:C6	1:AA:545:C:C4	3.08	0.41
1:AA:603:U:H2'	1:AA:604:G:C8	2.55	0.41
1:AA:1162:C:C2	1:AA:1163:A:C8	3.08	0.41
1:AA:1217:C:OP1	14:AN:9:ARG:NE	2.38	0.41
1:AA:1318:A:H1'	19:AS:37:ARG:NH1	2.35	0.41
2:AB:23:TRP:HB3	2:AB:39:HIS:HE1	1.85	0.41
4:AD:157:ALA:O	4:AD:161:LEU:HD13	2.21	0.41
4:AD:197:GLU:O	4:AD:200:ILE:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:55:THR:C	8:AH:57:PRO:HD3	2.44	0.41
11:AK:36:ASP:CG	11:AK:38:GLN:HG2	2.46	0.41
13:AM:7:ILE:HD12	13:AM:8:ASN:H	1.85	0.41
22:BA:14:A:H8	22:BA:14:A:O5'	2.03	0.41
22:BA:182:A:H2	22:BA:433:C:O2	2.03	0.41
22:BA:620:G:H4'	22:BA:621:A:O5'	2.20	0.41
22:BA:753:A:H2'	22:BA:754:U:C6	2.56	0.41
22:BA:1074:G:C6	22:BA:1075:C:C4	3.09	0.41
22:BA:1355:G:C2	22:BA:1356:G:C8	3.09	0.41
22:BA:1384:A:H1'	22:BA:1405:U:H1'	2.03	0.41
22:BA:1759:A:H2'	22:BA:1760:C:H6	1.84	0.41
22:BA:1770:G:C5	22:BA:1983:G:C6	3.09	0.41
22:BA:1837:C:C2	22:BA:1899:A:N6	2.89	0.41
22:BA:2646:C:OP2	22:BA:2732:G:O2'	2.28	0.41
27:BF:175:PHE:HD1	27:BF:177:PHE:CE1	2.39	0.41
32:BK:28:SER:C	32:BK:30:ARG:H	2.28	0.41
32:BK:105:ARG:HH21	37:BP:32:VAL:HG21	1.85	0.41
40:BS:96:ILE:HD12	40:BS:98:LYS:HG3	2.02	0.41
43:BV:80:HIS:CE1	43:BV:83:LYS:HG3	2.56	0.41
51:B3:7:VAL:HB	51:B3:61:CYS:HB3	2.02	0.41
54:B6:4:PRO:HA	54:B6:5:MHU:HM1	1.83	0.41
1:CA:200:G:C2'	1:CA:201:G:H5"	2.51	0.41
2:CB:33:GLY:CA	2:CB:40:ILE:H	2.28	0.41
4:CD:57:GLU:O	4:CD:60:LYS:N	2.54	0.41
7:CG:47:LEU:HD12	7:CG:47:LEU:HA	1.88	0.41
8:CH:64:LYS:HE2	8:CH:64:LYS:HB3	1.76	0.41
11:CK:112:ASP:OD1	11:CK:114:THR:HG23	2.20	0.41
12:CL:56:ARG:NH1	12:CL:62:GLU:HB2	2.35	0.41
15:CO:55:GLY:O	15:CO:59:MET:HG3	2.19	0.41
18:CR:20:GLU:HG3	18:CR:55:LEU:HD13	2.01	0.41
18:CR:59:ILE:HG22	18:CR:63:ARG:HD2	2.02	0.41
21:CU:12:PHE:CD1	21:CU:13:ASP:N	2.87	0.41
21:CU:39:GLU:HA	21:CU:42:THR:OG1	2.21	0.41
22:DA:188:G:C2	22:DA:209:C:N3	2.88	0.41
22:DA:505:A:HO2'	22:DA:509:C:HO2'	1.64	0.41
22:DA:517:C:O2'	40:DS:18:ARG:NH2	2.48	0.41
22:DA:1346:G:H2'	22:DA:1347:A:H8	1.86	0.41
22:DA:1464:G:H2'	22:DA:1465:G:C8	2.55	0.41
22:DA:1692:U:O2'	22:DA:1693:U:H2'	2.20	0.41
22:DA:2033:A:OP1	22:DA:2033:A:H2'	2.20	0.41
22:DA:2467:C:N4	22:DA:2468:A:C6	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2886:A:C2	22:DA:2887:A:H1'	2.56	0.41
26:DE:58:LYS:HA	26:DE:59:PRO:HD3	1.95	0.41
26:DE:75:SER:C	26:DE:77:ILE:H	2.28	0.41
28:DG:27:LYS:HB2	28:DG:27:LYS:HE2	1.75	0.41
28:DG:86:LYS:HG3	28:DG:132:VAL:HG22	2.02	0.41
31:DJ:7:LYS:HA	31:DJ:8:PRO:HD3	1.92	0.41
39:DR:3:ALA:HB2	39:DR:101:ILE:HG23	2.03	0.41
50:D2:31:LEU:HD21	50:D2:43:THR:HG22	2.02	0.41
1:AA:430:A:OP1	4:AD:9:LEU:HB2	2.21	0.41
1:AA:662:U:H2'	1:AA:663:A:C8	2.55	0.41
1:AA:982:U:H4'	1:AA:983:A:C5'	2.51	0.41
1:AA:1074:G:C2	1:AA:1075:U:C2	3.09	0.41
2:AB:24:ASN:HA	2:AB:25:PRO:HD2	1.93	0.41
2:AB:57:LEU:HB2	2:AB:184:PHE:CE1	2.56	0.41
2:AB:66:LYS:O	2:AB:159:ASP:HB2	2.20	0.41
2:AB:104:TRP:CH2	2:AB:154:MET:HG2	2.56	0.41
2:AB:117:LEU:HD13	2:AB:117:LEU:HA	1.92	0.41
3:AC:155:GLY:N	3:AC:164:ARG:O	2.37	0.41
5:AE:122:ASN:C	5:AE:122:ASN:HD22	2.28	0.41
7:AG:45:SER:HA	7:AG:48:GLU:HB2	2.01	0.41
10:AJ:27:GLU:HA	10:AJ:30:LYS:HE2	2.02	0.41
13:AM:20:THR:HA	13:AM:25:VAL:HG23	2.01	0.41
16:AP:47:GLU:HB2	16:AP:48:GLU:H	1.70	0.41
16:AP:75:ILE:O	16:AP:78:VAL:HG12	2.21	0.41
22:BA:321:U:OP2	26:BE:130:LYS:HD3	2.21	0.41
22:BA:1394:U:H2'	22:BA:1395:A:O4'	2.19	0.41
22:BA:1501:G:O2'	22:BA:1502:A:H5'	2.20	0.41
22:BA:2125:G:H21	22:BA:2173:A:H62	1.68	0.41
24:BC:180:GLU:HG3	24:BC:269:ARG:O	2.20	0.41
25:BD:57:ALA:C	25:BD:59:ARG:H	2.29	0.41
27:BF:74:VAL:O	27:BF:79:ILE:HG13	2.20	0.41
29:BH:33:GLN:O	29:BH:35:LYS:N	2.53	0.41
30:BI:130:GLU:HB3	30:BI:134:ARG:NH2	2.36	0.41
33:BL:96:LYS:HG3	33:BL:101:ILE:HD11	2.00	0.41
35:BN:114:GLU:HG3	35:BN:115:LEU:O	2.20	0.41
36:BO:79:ALA:HB2	36:BO:110:ALA:HA	2.03	0.41
40:BS:90:LYS:HZ3	54:B6:8:MHT:H5	1.85	0.41
41:BT:10:VAL:HG12	41:BT:11:LEU:HD23	2.03	0.41
1:CA:190:A:H2'	1:CA:191:G:O4'	2.20	0.41
1:CA:418:C:O2'	1:CA:540:G:H1'	2.20	0.41
1:CA:462:G:H5"	1:CA:463:U:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:729:A:H2'	1:CA:730:G:O4'	2.20	0.41
1:CA:938:A:N6	1:CA:939:G:C6	2.89	0.41
1:CA:1053:G:O5'	1:CA:1054:C:H3'	2.20	0.41
1:CA:1403:C:H2'	1:CA:1404:C:C6	2.54	0.41
1:CA:1480:A:H2'	1:CA:1481:U:O4'	2.20	0.41
2:CB:83:ALA:O	2:CB:86:SER:OG	2.36	0.41
2:CB:206:ALA:C	2:CB:208:ARG:N	2.78	0.41
4:CD:146:ARG:O	4:CD:150:LYS:HB2	2.21	0.41
5:CE:149:SER:O	5:CE:153:VAL:HG13	2.21	0.41
21:CU:53:VAL:HG13	21:CU:54:LYS:H	1.85	0.41
22:DA:222:A:H3'	22:DA:421:C:C5'	2.49	0.41
22:DA:248:G:H5'	22:DA:250:G:N7	2.36	0.41
22:DA:371:A:N3	45:DX:61:LYS:NZ	2.65	0.41
22:DA:749:A:C5	22:DA:750:A:C8	3.08	0.41
22:DA:1021:A:H8	22:DA:1122:G:O2'	2.03	0.41
22:DA:1431:A:H2'	22:DA:1432:G:O4'	2.21	0.41
22:DA:1485:U:H2'	22:DA:1486:U:C6	2.56	0.41
22:DA:1744:A:H3'	22:DA:1745:A:H8	1.86	0.41
22:DA:2136:G:H1	22:DA:2156:G:H1'	1.83	0.41
22:DA:2631:G:N3	22:DA:2810:A:H2	2.18	0.41
22:DA:2853:C:H2'	22:DA:2854:G:H8	1.83	0.41
25:DD:148:GLN:HB2	25:DD:152:PRO:HG2	2.02	0.41
29:DH:2:GLN:O	29:DH:3:VAL:O	2.38	0.41
32:DK:13:ASN:OD1	32:DK:97:THR:N	2.38	0.41
43:DV:83:LYS:HA	43:DV:84:PRO:HD3	1.93	0.41
45:DX:17:ASN:ND2	45:DX:27:ARG:HD2	2.36	0.41
49:D1:48:ILE:H	49:D1:48:ILE:HD12	1.84	0.41
1:AA:176:C:H2'	1:AA:177:G:N3	2.36	0.41
1:AA:1190:G:P	3:AC:5:VAL:H	2.44	0.41
2:AB:94:HIS:CE1	2:AB:146:ASN:HB2	2.55	0.41
2:AB:175:GLU:O	2:AB:178:ASN:HB3	2.21	0.41
4:AD:105:MET:HE1	4:AD:180:GLY:C	2.46	0.41
4:AD:173:VAL:HG22	4:AD:174:ASP:N	2.36	0.41
6:AF:4:TYR:CE2	6:AF:71:ILE:HG21	2.55	0.41
9:AI:50:GLN:HG2	9:AI:53:GLU:OE2	2.20	0.41
9:AI:86:ALA:C	9:AI:88:MET:N	2.78	0.41
20:AT:35:VAL:HG11	20:AT:79:LEU:HD13	2.01	0.41
20:AT:44:LYS:HD3	20:AT:87:ALA:HA	2.03	0.41
22:BA:204:A:H8	22:BA:204:A:OP1	2.04	0.41
22:BA:262:A:H2'	22:BA:263:G:O4'	2.20	0.41
22:BA:518:G:H2'	22:BA:519:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:547:A:C8	22:BA:548:G:N3	2.88	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
22:BA:1148:U:C2'	22:BA:1149:G:H5'	2.51	0.41
22:BA:1279:G:H4'	35:BN:31:HIS:CD2	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:1515:A:H3'	22:BA:1516:G:C8	2.53	0.41
22:BA:1917:U:C2'	22:BA:1918:A:H5'	2.51	0.41
22:BA:2069:G:C2	22:BA:2443:C:C2	3.08	0.41
22:BA:2543:G:H2'	22:BA:2544:G:C8	2.56	0.41
31:BJ:117:ALA:HA	31:BJ:120:ARG:HD2	2.02	0.41
34:BM:2:LEU:HD12	34:BM:68:PHE:CE1	2.56	0.41
37:BP:34:GLU:O	37:BP:36:SER:N	2.53	0.41
44:BW:69:PHE:CE1	44:BW:80:ILE:HD11	2.56	0.41
45:BX:19:SER:OG	45:BX:20:HIS:N	2.52	0.41
46:BY:57:LEU:CA	46:BY:60:LYS:HB3	2.51	0.41
48:B0:55:ILE:HG22	48:B0:56:ALA:N	2.35	0.41
50:B2:26:ASN:HA	50:B2:29:GLN:HB2	2.03	0.41
1:CA:1149:C:O5'	1:CA:1149:C:H6	2.04	0.41
1:CA:1434:A:H2'	1:CA:1435:G:O4'	2.20	0.41
1:CA:1520:C:H2'	1:CA:1521:C:C6	2.55	0.41
7:CG:22:LEU:HA	7:CG:25:LYS:HE2	2.02	0.41
7:CG:97:ASN:O	7:CG:100:ALA:HB3	2.21	0.41
8:CH:7:ILE:HB	8:CH:77:ARG:HH12	1.86	0.41
9:CI:28:ILE:HB	9:CI:35:LEU:HB2	2.01	0.41
11:CK:71:ALA:O	11:CK:75:LYS:HG3	2.19	0.41
15:CO:53:ARG:O	15:CO:56:LEU:HB3	2.21	0.41
16:CP:22:ALA:HA	16:CP:33:ILE:HD12	2.01	0.41
19:CS:58:VAL:HA	19:CS:59:PRO:HD3	1.85	0.41
22:DA:247:G:OP2	22:DA:249:C:N4	2.54	0.41
22:DA:532:A:H2'	22:DA:532:A:N3	2.36	0.41
22:DA:694:U:O2'	22:DA:1378:A:H2	2.03	0.41
22:DA:770:G:H1'	22:DA:1379:U:C4	2.56	0.41
22:DA:1856:U:C4	22:DA:1857:G:C6	3.08	0.41
22:DA:1923:U:H2'	22:DA:1924:C:C6	2.56	0.41
22:DA:2286:G:OP1	49:D1:30:LYS:HE3	2.21	0.41
22:DA:2563:U:H1'	22:DA:2566:A:N6	2.35	0.41
22:DA:2591:C:P	24:DC:238:ARG:HG3	2.60	0.41
24:DC:158:ALA:HB1	24:DC:197:ASN:O	2.20	0.41
25:DD:114:LYS:HE2	25:DD:196:ALA:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DH:40:THR:OG1	29:DH:43:ASN:ND2	2.53	0.41
30:DI:71:THR:C	30:DI:72:LYS:HD3	2.44	0.41
30:DI:130:GLU:HG2	30:DI:134:ARG:HH22	1.86	0.41
31:DJ:4:PHE:CD1	38:DQ:100:VAL:HG11	2.55	0.41
33:DL:77:ILE:HB	33:DL:109:LYS:O	2.21	0.41
43:DV:9:ARG:CG	43:DV:41:GLU:HB3	2.50	0.41
45:DX:2:SER:O	45:DX:4:VAL:N	2.53	0.41
49:D1:17:THR:C	49:D1:19:HIS:H	2.28	0.41
1:AA:262:A:C6	1:AA:263:A:C6	3.09	0.41
1:AA:811:C:C5	1:AA:812:G:C6	3.08	0.41
1:AA:901:A:C5	1:AA:902:G:H1'	2.56	0.41
1:AA:1003:G:N2	1:AA:1004:A:O2'	2.54	0.41
1:AA:1226:C:H4'	1:AA:1227:A:OP1	2.21	0.41
13:AM:95:LEU:HB3	13:AM:96:PRO:CD	2.51	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
21:AU:19:PHE:O	21:AU:19:PHE:HD2	2.04	0.41
22:BA:191:A:H2'	22:BA:192:C:C6	2.56	0.41
22:BA:1385:A:C6	22:BA:1403:A:C5	3.09	0.41
22:BA:2810:A:H2'	22:BA:2811:G:O4'	2.21	0.41
29:BH:10:ALA:C	29:BH:12:LEU:H	2.27	0.41
29:BH:95:GLY:HA2	29:BH:117:LEU:CD2	2.51	0.41
29:BH:100:ALA:HB2	29:BH:115:VAL:CG2	2.50	0.41
32:BK:91:SER:HG	32:BK:93:GLN:HB2	1.85	0.41
34:BM:18:ARG:HG2	34:BM:18:ARG:NH2	2.34	0.41
36:BO:115:LEU:HD12	36:BO:115:LEU:HA	1.64	0.41
38:BQ:102:ASP:O	38:BQ:104:VAL:N	2.53	0.41
1:CA:264:C:H2'	1:CA:265:G:O4'	2.20	0.41
1:CA:539:A:H2'	1:CA:540:G:C8	2.56	0.41
1:CA:881:G:C6	1:CA:882:C:C4	3.09	0.41
1:CA:966:G:O2'	9:CI:130:ARG:OXT	2.37	0.41
1:CA:1503:A:C8	1:CA:1531:A:H1'	2.56	0.41
2:CB:52:GLU:HG3	2:CB:56:GLU:HG2	2.01	0.41
3:CC:107:ARG:H	3:CC:107:ARG:HD3	1.85	0.41
3:CC:109:PRO:C	3:CC:111:LEU:H	2.29	0.41
4:CD:68:LEU:HA	4:CD:68:LEU:HD23	1.84	0.41
5:CE:155:ALA:C	5:CE:156:LYS:HG3	2.46	0.41
9:CI:33:ARG:HD3	9:CI:33:ARG:HA	1.88	0.41
12:CL:74:LEU:HD21	12:CL:104:CYS:SG	2.61	0.41
15:CO:78:TYR:OH	15:CO:88:ARG:NE	2.53	0.41
15:CO:82:ILE:HG13	15:CO:83:GLU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:64:A:H2'	22:DA:65:U:C6	2.56	0.41
22:DA:555:G:O2'	22:DA:556:A:OP2	2.33	0.41
22:DA:994:C:H1'	39:DR:10:LYS:HE3	2.01	0.41
22:DA:1070:A:H2'	22:DA:1097:U:OP1	2.20	0.41
22:DA:1281:G:H2'	22:DA:1282:U:C6	2.55	0.41
22:DA:1346:G:H2'	22:DA:1347:A:C8	2.56	0.41
22:DA:2058:A:N6	22:DA:2059:A:N6	2.68	0.41
22:DA:2064:C:O3'	22:DA:2251:G:N2	2.54	0.41
22:DA:2066:C:H5"	57:DA:3502:HOH:O	2.19	0.41
22:DA:2134:A:N3	22:DA:2159:G:H1'	2.36	0.41
22:DA:2220:U:H2'	22:DA:2221:G:C8	2.55	0.41
22:DA:2444:G:OP2	26:DE:63:LYS:HD2	2.21	0.41
22:DA:2516:A:O2'	22:DA:2517:C:H5'	2.19	0.41
22:DA:2636:C:OP1	25:DD:81:GLU:HB2	2.20	0.41
24:DC:177:ARG:HA	24:DC:177:ARG:HD2	1.79	0.41
27:DF:161:LYS:HB2	27:DF:165:GLU:CD	2.46	0.41
29:DH:76:GLU:O	29:DH:76:GLU:CD	2.63	0.41
29:DH:130:VAL:CG1	29:DH:131:SER:N	2.82	0.41
31:DJ:90:GLU:HG3	31:DJ:91:GLU:H	1.85	0.41
31:DJ:98:GLU:O	31:DJ:102:GLU:HG3	2.21	0.41
34:DM:58:LYS:C	34:DM:60:GLN:H	2.29	0.41
40:DS:69:LEU:C	40:DS:70:LYS:HD2	2.45	0.41
45:DX:68:LEU:HB3	45:DX:78:TYR:OH	2.20	0.41
1:AA:664:G:H22	1:AA:741:G:H1	1.69	0.41
1:AA:683:G:N2	11:AK:39:GLY:O	2.54	0.41
2:AB:65:GLY:O	2:AB:66:LYS:HD3	2.21	0.41
2:AB:222:ARG:CZ	2:AB:222:ARG:HB3	2.51	0.41
4:AD:48:LEU:HD21	4:AD:53:VAL:HG12	2.02	0.41
19:AS:11:ILE:HG12	19:AS:12:ASP:O	2.21	0.41
21:AU:37:PHE:HA	21:AU:37:PHE:HD1	1.73	0.41
22:BA:373:U:OP2	22:BA:400:G:N1	2.30	0.41
22:BA:769:U:C2	22:BA:770:G:C8	3.09	0.41
22:BA:827:U:H2'	22:BA:2068:U:C2	2.56	0.41
22:BA:1243:C:H2'	22:BA:1244:A:O4'	2.20	0.41
22:BA:1727:C:H2'	22:BA:1728:C:C6	2.56	0.41
22:BA:2021:C:P	48:B0:9:THR:HG21	2.61	0.41
23:BB:61:G:H2'	23:BB:62:C:C6	2.55	0.41
24:BC:30:PHE:CD2	24:BC:32:PRO:HD2	2.56	0.41
27:BF:104:ILE:H	27:BF:104:ILE:HG12	1.71	0.41
27:BF:138:PHE:HE2	27:BF:152:LEU:HD23	1.86	0.41
37:BP:8:LEU:O	37:BP:11:GLU:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BT:88:LYS:O	41:BT:89:GLU:HG2	2.21	0.41
1:CA:111:G:C6	1:CA:330:C:N4	2.87	0.41
1:CA:672:U:H2'	1:CA:673:A:C8	2.56	0.41
1:CA:1082:A:C6	1:CA:1083:U:N3	2.89	0.41
2:CB:100:MET:CA	2:CB:107:VAL:HG21	2.49	0.41
2:CB:131:LYS:HA	2:CB:134:ALA:HB3	2.03	0.41
3:CC:64:ILE:HG23	3:CC:99:ALA:HB2	2.03	0.41
3:CC:131:ARG:HE	3:CC:131:ARG:HB2	1.76	0.41
8:CH:34:VAL:O	8:CH:37:ALA:N	2.52	0.41
11:CK:21:ALA:HA	11:CK:34:ILE:HD13	2.02	0.41
13:CM:10:PRO:HB2	13:CM:11:ASP:H	1.66	0.41
13:CM:15:ALA:O	13:CM:19:LEU:HD23	2.21	0.41
22:DA:1082:U:H5"	22:DA:1083:U:OP2	2.21	0.41
22:DA:1436:G:C2	22:DA:1437:C:H1'	2.56	0.41
22:DA:1638:C:O2'	22:DA:2698:U:O2	2.38	0.41
22:DA:1856:U:O4	22:DA:1857:G:N1	2.54	0.41
22:DA:2259:U:H1'	22:DA:2427:C:C2	2.56	0.41
23:DB:21:G:H2'	23:DB:22:U:O4'	2.21	0.41
24:DC:33:LEU:HD23	24:DC:33:LEU:HA	1.88	0.41
26:DE:108:ILE:O	26:DE:112:LEU:HG	2.21	0.41
34:DM:97:GLN:O	34:DM:100:LYS:HB2	2.20	0.41
43:DV:51:GLN:HA	43:DV:56:PHE:CB	2.50	0.41
51:D3:51:SER:O	51:D3:55:LEU:HG	2.21	0.41
1:AA:15:G:C4	1:AA:16:A:C8	3.08	0.41
1:AA:44:A:OP2	16:AP:12:LYS:HE2	2.21	0.41
1:AA:922:G:C6	1:AA:923:A:C6	3.08	0.41
1:AA:1305:G:O2'	1:AA:1306:A:H8	2.04	0.41
1:AA:1386:G:H2'	1:AA:1387:G:C8	2.56	0.41
2:AB:131:LYS:HA	2:AB:131:LYS:HD3	1.50	0.41
2:AB:147:SER:O	2:AB:147:SER:OG	2.35	0.41
3:AC:22:TRP:CG	3:AC:59:ARG:HG2	2.56	0.41
4:AD:9:LEU:HD13	4:AD:9:LEU:HA	1.74	0.41
4:AD:58:LYS:CB	4:AD:200:ILE:HB	2.50	0.41
4:AD:122:ALA:O	4:AD:123:ILE:HG23	2.20	0.41
5:AE:60:ILE:O	5:AE:64:MET:HG2	2.21	0.41
8:AH:86:TYR:HD2	8:AH:124:GLU:HA	1.86	0.41
8:AH:105:SER:O	8:AH:123:GLY:HA3	2.21	0.41
10:AJ:8:ILE:HA	10:AJ:99:GLN:O	2.21	0.41
10:AJ:9:ARG:O	10:AJ:98:VAL:HA	2.20	0.41
11:AK:38:GLN:HB2	11:AK:40:ASN:HD22	1.85	0.41
11:AK:128:ARG:HG2	11:AK:128:ARG:HH11	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:79:ASN:ND2	16:AP:82:ALA:O	2.52	0.41
17:AQ:69:LYS:O	17:AQ:70:THR:CB	2.69	0.41
20:AT:23:SER:OG	20:AT:24:ARG:N	2.53	0.41
22:BA:29:U:H2'	22:BA:30:G:C8	2.56	0.41
22:BA:190:A:C4	22:BA:207:A:C2	3.08	0.41
22:BA:322:A:C5	22:BA:340:A:C2	3.09	0.41
22:BA:572:A:C6	22:BA:573:U:N3	2.89	0.41
22:BA:657:U:O5'	22:BA:657:U:H6	2.04	0.41
22:BA:666:A:H4'	33:BL:48:ARG:HD3	2.03	0.41
22:BA:802:A:H2'	22:BA:803:U:C6	2.56	0.41
22:BA:842:U:H2'	22:BA:843:G:O4'	2.21	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:997:G:C2	22:BA:1159:U:C2	3.09	0.41
22:BA:1408:G:C6	22:BA:1409:U:C4	3.09	0.41
22:BA:1474:U:C2'	22:BA:1475:G:H5'	2.51	0.41
22:BA:1643:G:H2'	22:BA:1644:C:O4'	2.21	0.41
22:BA:1776:G:N3	22:BA:1776:G:H2'	2.36	0.41
22:BA:1838:C:N4	22:BA:1899:A:C4	2.89	0.41
22:BA:1911:U:H2'	22:BA:1918:A:C2	2.56	0.41
22:BA:1916:A:C2	22:BA:1917:U:H1'	2.55	0.41
22:BA:2080:A:O5'	45:BX:19:SER:OG	2.33	0.41
22:BA:2098:U:H2'	22:BA:2099:U:C6	2.55	0.41
22:BA:2128:G:N2	22:BA:2173:A:O2'	2.52	0.41
22:BA:2174:C:O2'	22:BA:2175:C:H5'	2.21	0.41
22:BA:2636:C:H2'	22:BA:2637:U:H6	1.84	0.41
26:BE:101:TYR:O	26:BE:104:ALA:HB3	2.21	0.41
26:BE:147:LEU:HB2	26:BE:183:PHE:CD1	2.55	0.41
28:BG:35:ARG:N	28:BG:75:MET:HE1	2.36	0.41
29:BH:82:SER:HB3	29:BH:146:VAL:HG12	2.03	0.41
29:BH:82:SER:HG	29:BH:90:LEU:HG	1.85	0.41
30:BI:22:PRO:HB2	30:BI:23:PRO:HD3	2.01	0.41
31:BJ:7:LYS:HA	31:BJ:8:PRO:HD3	1.81	0.41
31:BJ:69:ARG:HA	31:BJ:89:PHE:CD1	2.55	0.41
38:BQ:81:ASN:HD22	38:BQ:81:ASN:HA	1.76	0.41
42:BU:73:PHE:CZ	42:BU:78:GLY:HA2	2.56	0.41
43:BV:85:LYS:HE3	43:BV:85:LYS:HB3	1.82	0.41
45:BX:40:VAL:HG23	45:BX:45:ARG:O	2.21	0.41
53:B5:19:LYS:HD3	53:B5:19:LYS:HA	1.88	0.41
53:B5:80:LYS:HA	53:B5:98:GLU:HG3	2.03	0.41
1:CA:50:A:N1	1:CA:360:G:O2'	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:187:G:H5”	1:CA:188:C:OP2	2.20	0.41
1:CA:437:U:O4’	4:CD:154:ARG:NH1	2.54	0.41
1:CA:1346:A:N6	1:CA:1374:A:C8	2.89	0.41
2:CB:20:THR:OG1	2:CB:21:ARG:N	2.52	0.41
2:CB:140:GLU:HB3	2:CB:144:LEU:HD21	2.03	0.41
3:CC:148:GLY:O	3:CC:203:PHE:N	2.40	0.41
4:CD:148:LYS:HB2	4:CD:148:LYS:HE2	1.77	0.41
7:CG:31:MET:HG3	7:CG:35:LYS:O	2.21	0.41
7:CG:83:SER:O	7:CG:85:TYR:N	2.53	0.41
9:CI:83:ILE:O	9:CI:87:LEU:HG	2.21	0.41
12:CL:22:PRO:C	12:CL:24:LEU:N	2.78	0.41
17:CQ:45:HIS:O	17:CQ:71:LYS:HA	2.21	0.41
18:CR:23:TYR:HE1	18:CR:65:LEU:HD12	1.86	0.41
18:CR:27:ALA:O	18:CR:30:LYS:HG2	2.21	0.41
22:DA:648:G:H2’	22:DA:649:G:C8	2.53	0.41
22:DA:740:C:H5’	22:DA:1784:A:C2’	2.51	0.41
22:DA:784:G:H5”	24:DC:226:ASN:OD1	2.21	0.41
22:DA:814:C:H1’	22:DA:1225:G:H21	1.86	0.41
22:DA:871:U:C2	22:DA:907:G:C6	3.09	0.41
22:DA:995:C:N3	31:DJ:3:THR:N	2.56	0.41
22:DA:1102:C:H2’	22:DA:1103:A:C8	2.56	0.41
22:DA:1179:G:C6	22:DA:1180:U:H1’	2.56	0.41
22:DA:1515:A:O2’	22:DA:1556:C:O2’	2.27	0.41
22:DA:1565:C:H5’	24:DC:18:LYS:HZ2	1.86	0.41
22:DA:1740:G:H2’	22:DA:1741:C:C6	2.56	0.41
22:DA:1769:U:H1’	22:DA:1984:G:N2	2.35	0.41
22:DA:2195:U:H2’	22:DA:2196:C:H6	1.86	0.41
22:DA:2214:C:H2’	22:DA:2215:C:O4’	2.21	0.41
22:DA:2252:G:H2’	22:DA:2253:G:O4’	2.20	0.41
22:DA:2431:U:N3	22:DA:2434:A:OP2	2.43	0.41
22:DA:2443:C:H2’	22:DA:2444:G:O4’	2.21	0.41
22:DA:2491:U:H5’	22:DA:2570:G:H5’	2.02	0.41
22:DA:2881:U:H2’	22:DA:2882:A:C8	2.56	0.41
24:DC:159:GLY:HA2	24:DC:195:VAL:O	2.21	0.41
25:DD:142:VAL:HG23	25:DD:144:GLY:H	1.85	0.41
25:DD:176:ASP:HB2	25:DD:190:LYS:HB3	2.02	0.41
26:DE:155:GLU:HG3	26:DE:159:LEU:CD1	2.51	0.41
28:DG:24:ILE:HD13	28:DG:72:LEU:HD21	2.02	0.41
28:DG:94:TYR:HA	28:DG:106:SER:O	2.21	0.41
31:DJ:6:ALA:O	31:DJ:7:LYS:HG3	2.20	0.41
33:DL:77:ILE:HD13	33:DL:108:ALA:HB1	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DO:17:LYS:HA	36:DO:17:LYS:HD3	1.89	0.41
38:DQ:78:LYS:HE2	38:DQ:78:LYS:HB3	1.76	0.41
42:DU:73:PHE:CE2	42:DU:75:ALA:HA	2.55	0.41
43:DV:1:MET:HE3	43:DV:1:MET:HB2	1.93	0.41
43:DV:30:ILE:HG12	43:DV:91:PHE:CB	2.50	0.41
1:AA:670:G:N2	1:AA:736:C:O2	2.47	0.41
1:AA:737:C:H2'	1:AA:738:C:H6	1.86	0.41
1:AA:750:C:O2	15:AO:23:GLY:HA3	2.21	0.41
1:AA:979:C:OP2	1:AA:980:C:H5	2.04	0.41
1:AA:1023:U:H2'	1:AA:1024:G:O4'	2.20	0.41
3:AC:29:PHE:HE2	3:AC:33:LEU:HD23	1.85	0.41
3:AC:144:LEU:HD22	3:AC:144:LEU:H	1.85	0.41
5:AE:16:ILE:HD11	5:AE:38:VAL:HB	2.03	0.41
5:AE:156:LYS:HA	8:AH:66:PHE:CD2	2.56	0.41
16:AP:73:ALA:O	16:AP:77:GLU:HB2	2.21	0.41
21:AU:35:ARG:NH2	57:AU:101:HOH:O	2.39	0.41
22:BA:198:C:O5'	22:BA:198:C:H6	2.04	0.41
22:BA:345:A:H1'	22:BA:346:A:N7	2.36	0.41
22:BA:358:U:H2'	22:BA:359:G:C8	2.56	0.41
22:BA:1096:A:H2'	22:BA:1097:U:O4'	2.21	0.41
22:BA:1413:A:C6	22:BA:1414:C:N3	2.89	0.41
22:BA:1789:A:H2'	22:BA:1790:C:O4'	2.21	0.41
22:BA:1847:A:P	22:BA:1847:A:H8	2.44	0.41
22:BA:1912:A:C2	22:BA:1919:A:C4	3.09	0.41
22:BA:2001:C:H4'	22:BA:2689:U:H2'	2.03	0.41
22:BA:2190:G:C6	22:BA:2191:A:C5	3.09	0.41
22:BA:2785:C:H2'	22:BA:2786:U:O4'	2.20	0.41
24:BC:239:ASN:ND2	57:BC:307:HOH:O	2.54	0.41
26:BE:170:ARG:NH2	26:BE:176:ASP:OD2	2.45	0.41
27:BF:49:LEU:HD12	27:BF:49:LEU:HA	1.85	0.41
29:BH:75:LEU:C	29:BH:75:LEU:CD2	2.93	0.41
39:BR:24:LYS:HE2	39:BR:24:LYS:HB3	1.91	0.41
53:B5:88:GLU:HG3	53:B5:95:VAL:HG23	2.03	0.41
1:CA:37:U:O2'	1:CA:500:G:H4'	2.21	0.41
1:CA:102:G:H2'	1:CA:103:U:C6	2.55	0.41
1:CA:369:G:OP2	1:CA:388:G:C2	2.73	0.41
1:CA:452:A:H62	1:CA:480:U:H3	1.69	0.41
1:CA:803:G:C5	1:CA:804:U:C4	3.09	0.41
1:CA:1145:A:O2'	1:CA:1146:A:H8	2.04	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:18:VAL:O	6:CF:22:ILE:HG13	2.20	0.41
8:CH:11:LEU:HD11	8:CH:127:CYS:HB3	2.02	0.41
19:CS:15:LEU:HD23	19:CS:38:SER:HB2	2.03	0.41
22:DA:160:A:H2'	22:DA:161:A:C8	2.56	0.41
22:DA:380:G:H4'	45:DX:16:ASN:O	2.20	0.41
22:DA:460:A:H2'	22:DA:461:C:O4'	2.21	0.41
22:DA:1418:G:H21	22:DA:1580:A:H62	1.68	0.41
22:DA:1680:U:H2'	22:DA:1681:G:O4'	2.21	0.41
22:DA:2446:G:H8	22:DA:2446:G:OP2	2.03	0.41
23:DB:51:G:C8	36:DO:64:TYR:HE2	2.38	0.41
33:DL:55:MET:SD	33:DL:59:ARG:NH2	2.94	0.41
43:DV:28:ALA:HB3	43:DV:42:LEU:HD21	2.03	0.41
1:AA:219:U:C2	1:AA:220:G:C8	3.08	0.40
1:AA:359:G:H2'	1:AA:360:G:O4'	2.21	0.40
1:AA:431:A:C4	1:AA:432:A:C8	3.09	0.40
1:AA:1072:G:OP1	5:AE:62:LYS:NZ	2.50	0.40
1:AA:1401:G:N2	1:AA:1402:C:H1'	2.36	0.40
3:AC:174:PRO:C	3:AC:176:HIS:H	2.28	0.40
4:AD:35:GLU:O	4:AD:38:PRO:HD3	2.21	0.40
9:AI:50:GLN:O	9:AI:52:LEU:N	2.50	0.40
11:AK:125:LYS:O	21:AU:34:ARG:NH2	2.54	0.40
13:AM:7:ILE:H	13:AM:7:ILE:HG13	1.41	0.40
21:AU:25:LYS:O	21:AU:29:LEU:HB2	2.20	0.40
21:AU:40:LYS:O	21:AU:44:GLU:HB2	2.21	0.40
22:BA:947:A:O2'	22:BA:984:A:H2	2.03	0.40
22:BA:1027:A:H8	22:BA:1027:A:O5'	2.05	0.40
22:BA:1343:G:C4	22:BA:1344:U:C5	3.08	0.40
22:BA:1753:G:H5"	37:BP:93:ARG:NH1	2.36	0.40
22:BA:1799:G:H4'	22:BA:1800:C:O5'	2.21	0.40
22:BA:1902:C:H4'	24:BC:242:LYS:O	2.21	0.40
22:BA:2282:G:H5"	22:BA:2283:C:O4'	2.21	0.40
22:BA:2305:U:O2'	27:BF:133:ARG:NE	2.54	0.40
29:BH:132:PHE:CE2	29:BH:142:VAL:CG2	3.04	0.40
30:BI:40:LYS:HD3	30:BI:40:LYS:HA	1.81	0.40
31:BJ:93:ILE:O	31:BJ:97:PRO:HG3	2.21	0.40
32:BK:35:VAL:HB	32:BK:36:GLY:H	1.67	0.40
35:BN:55:ALA:HA	35:BN:80:PHE:CE1	2.55	0.40
35:BN:78:LYS:C	35:BN:79:LEU:O	2.60	0.40
45:BX:18:ARG:CZ	45:BX:24:ALA:HB2	2.50	0.40
1:CA:72:A:C6	1:CA:73:C:N4	2.89	0.40
1:CA:375:U:OP1	16:CP:70:ARG:HD3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:721:G:H4'	1:CA:722:G:O5'	2.20	0.40
1:CA:981:U:H2'	1:CA:982:U:C5	2.57	0.40
1:CA:1317:C:O2'	14:CN:49:GLN:HG2	2.22	0.40
4:CD:197:GLU:H	4:CD:197:GLU:CD	2.29	0.40
7:CG:46:ALA:HA	7:CG:121:ALA:HB2	2.01	0.40
9:CI:46:MET:HA	9:CI:48:VAL:HG23	2.02	0.40
9:CI:120:LYS:O	9:CI:121:ALA:HB3	2.20	0.40
22:DA:242:G:C6	51:D3:5:LYS:HE2	2.55	0.40
22:DA:309:A:O3'	42:DU:16:GLY:HA2	2.21	0.40
22:DA:569:U:H5'	22:DA:946:C:H1'	2.04	0.40
22:DA:571:U:C4	22:DA:2030:A:C6	3.09	0.40
22:DA:1357:C:H2'	22:DA:1358:G:O4'	2.21	0.40
22:DA:1695:G:C8	24:DC:8:PRO:HG2	2.56	0.40
22:DA:1930:G:H1'	22:DA:1968:G:N1	2.36	0.40
22:DA:2119:A:N6	22:DA:2167:U:H1'	2.36	0.40
22:DA:2131:U:C4'	22:DA:2133:G:H1'	2.50	0.40
22:DA:2278:A:N6	44:DW:14:ARG:O	2.55	0.40
22:DA:2457:U:C4	22:DA:2458:G:C6	3.09	0.40
22:DA:2474:U:H5"	22:DA:2475:C:OP2	2.21	0.40
22:DA:2674:G:H2'	22:DA:2675:A:C8	2.56	0.40
22:DA:2702:G:C6	22:DA:2703:C:C4	3.10	0.40
24:DC:24:LEU:HD11	24:DC:90:ASN:ND2	2.35	0.40
24:DC:34:LEU:HA	24:DC:62:TYR:O	2.21	0.40
24:DC:260:ASN:HD21	24:DC:263:THR:HG23	1.86	0.40
25:DD:184:ARG:CZ	37:DP:7:GLN:HE22	2.34	0.40
27:DF:64:LYS:HA	27:DF:65:PRO:HD3	1.87	0.40
29:DH:1:MET:HB3	29:DH:21:VAL:O	2.20	0.40
30:DI:136:MET:H	30:DI:136:MET:HG2	1.67	0.40
35:DN:38:LEU:HB3	35:DN:39:PRO:HD3	2.03	0.40
35:DN:55:ALA:HB1	35:DN:80:PHE:N	2.28	0.40
36:DO:36:TYR:HD2	36:DO:52:SER:HB2	1.87	0.40
43:DV:2:PHE:HD1	43:DV:2:PHE:HA	1.75	0.40
45:DX:67:VAL:O	45:DX:70:GLU:N	2.54	0.40
46:DY:48:ARG:O	46:DY:51:ALA:HB3	2.21	0.40
1:AA:109:A:H2'	1:AA:326:G:H21	1.86	0.40
1:AA:179:A:OP2	57:AA:1880:HOH:O	2.22	0.40
1:AA:414:A:H2'	1:AA:415:A:C8	2.56	0.40
1:AA:437:U:H4'	4:AD:154:ARG:HH22	1.86	0.40
1:AA:453:G:H2'	1:AA:454:G:O4'	2.22	0.40
1:AA:663:A:H2'	1:AA:664:G:O4'	2.21	0.40
1:AA:1491:G:H2'	1:AA:1492:A:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:147:SER:O	2:AB:148:LEU:HG	2.21	0.40
2:AB:184:PHE:N	2:AB:184:PHE:CD2	2.88	0.40
3:AC:31:ASP:HA	14:AN:65:ARG:HH22	1.86	0.40
5:AE:22:SER:HB2	5:AE:31:PHE:CD2	2.56	0.40
5:AE:80:THR:CA	5:AE:122:ASN:HD21	2.34	0.40
7:AG:43:VAL:O	7:AG:47:LEU:HB2	2.21	0.40
9:AI:91:ASP:CG	9:AI:93:SER:H	2.29	0.40
11:AK:89:PRO:HD3	21:AU:29:LEU:HD11	2.02	0.40
21:AU:41:PRO:HA	21:AU:45:ARG:NH1	2.36	0.40
22:BA:598:U:H2'	22:BA:599:A:C8	2.56	0.40
22:BA:749:A:N3	22:BA:1618:A:H2'	2.35	0.40
22:BA:1084:A:C5	22:BA:1085:A:C6	3.09	0.40
22:BA:1292:G:H2'	22:BA:1293:C:C6	2.57	0.40
22:BA:2000:C:O2'	22:BA:2001:C:H5'	2.21	0.40
22:BA:2092:U:OP1	22:BA:2199:A:O2'	2.33	0.40
22:BA:2192:U:H2'	22:BA:2193:G:O4'	2.22	0.40
22:BA:2458:G:N3	22:BA:2490:G:N2	2.69	0.40
22:BA:2500:U:O2'	22:BA:2504:U:OP1	2.39	0.40
22:BA:2838:G:C6	22:BA:2839:G:C5	3.09	0.40
24:BC:29:PRO:CG	24:BC:34:LEU:HD21	2.51	0.40
26:BE:145:ASP:HA	26:BE:166:LYS:O	2.21	0.40
29:BH:90:LEU:HB2	29:BH:124:THR:C	2.46	0.40
40:BS:41:LYS:HE3	48:B0:22:LEU:HD21	2.03	0.40
40:BS:76:VAL:HG13	40:BS:103:ILE:HG12	2.03	0.40
41:BT:61:LEU:C	41:BT:61:LEU:HD12	2.47	0.40
46:BY:36:GLN:O	46:BY:37:LEU:HB3	2.21	0.40
1:CA:124:C:H2'	1:CA:125:U:C6	2.55	0.40
1:CA:438:U:C2	1:CA:494:G:C6	3.09	0.40
1:CA:453:G:H2'	1:CA:454:G:C8	2.56	0.40
1:CA:469:C:H2'	1:CA:470:C:O4'	2.21	0.40
1:CA:490:C:H2'	1:CA:491:G:H8	1.85	0.40
1:CA:982:U:H5"	14:CN:6:MET:HE2	2.03	0.40
1:CA:1086:U:O2'	1:CA:1087:G:H5'	2.22	0.40
1:CA:1220:G:H1'	19:CS:52:HIS:CD2	2.56	0.40
1:CA:1499:A:H3'	57:CA:1880:HOH:O	2.20	0.40
2:CB:53:ALA:C	2:CB:54:LEU:HD22	2.46	0.40
4:CD:148:LYS:CD	4:CD:148:LYS:H	2.34	0.40
5:CE:133:PRO:O	5:CE:136:VAL:N	2.54	0.40
8:CH:102:ALA:O	8:CH:112:THR:HA	2.21	0.40
10:CJ:25:ILE:CG2	10:CJ:74:VAL:HG21	2.51	0.40
11:CK:84:VAL:HG11	11:CK:97:ILE:HG22	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CS:36:ARG:HB3	19:CS:72:GLY:CA	2.51	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:364:C:H2'	22:DA:365:U:O4'	2.21	0.40
22:DA:585:G:H5"	22:DA:586:A:OP1	2.20	0.40
22:DA:607:U:H5	22:DA:619:G:C5	2.40	0.40
22:DA:1445:G:C6	22:DA:1446:C:C4	3.09	0.40
22:DA:1798:U:O2'	22:DA:1802:A:N3	2.51	0.40
22:DA:2311:A:C2	27:DF:79:ILE:HG21	2.56	0.40
22:DA:2756:U:H1'	22:DA:2757:A:H5"	2.02	0.40
23:DB:71:C:C2	23:DB:106:G:C2	3.09	0.40
28:DG:11:VAL:HA	28:DG:12:PRO:HD3	1.88	0.40
29:DH:96:THR:O	29:DH:98:ASP:N	2.54	0.40
30:DI:57:VAL:CG2	30:DI:71:THR:HB	2.51	0.40
32:DK:23:LYS:HD3	32:DK:23:LYS:HA	1.89	0.40
35:DN:94:TYR:O	35:DN:116:VAL:N	2.49	0.40
42:DU:61:LYS:HA	42:DU:61:LYS:HD2	1.87	0.40
46:DY:49:ASP:O	46:DY:53:VAL:HG23	2.21	0.40
1:AA:29:U:C2'	1:AA:30:U:H5'	2.50	0.40
1:AA:29:U:H5'	1:AA:296:U:OP1	2.21	0.40
1:AA:57:G:H2'	1:AA:58:C:O4'	2.21	0.40
1:AA:113:G:H2'	1:AA:114:U:C6	2.57	0.40
1:AA:468:A:H5'	1:AA:469:C:OP2	2.21	0.40
1:AA:577:G:C8	1:AA:816:A:C6	3.10	0.40
1:AA:731:G:H2'	1:AA:732:C:C6	2.57	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
1:AA:1113:C:H2'	1:AA:1114:C:H6	1.86	0.40
1:AA:1195:C:H5"	1:AA:1196:A:OP2	2.20	0.40
1:AA:1223:C:OP2	19:AS:78:ARG:NH1	2.54	0.40
1:AA:1491:G:H2'	1:AA:1492:A:C8	2.56	0.40
2:AB:62:SER:C	2:AB:64:LYS:N	2.77	0.40
3:AC:68:ILE:O	3:AC:70:THR:N	2.55	0.40
5:AE:25:VAL:O	5:AE:27:GLY:N	2.55	0.40
5:AE:105:ILE:HD12	5:AE:105:ILE:HA	1.83	0.40
7:AG:15:ASP:OD2	7:AG:17:LYS:N	2.49	0.40
16:AP:38:PHE:CD1	16:AP:38:PHE:C	2.99	0.40
16:AP:43:ALA:O	16:AP:46:LYS:HD2	2.21	0.40
22:BA:135:U:H3	22:BA:144:A:N6	2.12	0.40
22:BA:181:A:C2	22:BA:182:A:C4	3.09	0.40
22:BA:678:C:H2'	22:BA:679:C:H6	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:974:G:O2'	22:BA:989:G:N2	2.54	0.40
22:BA:974:G:C4	22:BA:1186:G:C2	3.09	0.40
22:BA:983:A:C6	22:BA:984:A:C2	3.09	0.40
22:BA:995:C:O2	31:BJ:3:THR:OG1	2.28	0.40
22:BA:1688:U:H2'	22:BA:1698:A:N6	2.36	0.40
22:BA:1744:A:H2'	22:BA:1745:A:O4'	2.21	0.40
22:BA:1832:C:N4	22:BA:1833:C:C4	2.90	0.40
22:BA:1927:A:C6	22:BA:1928:A:C6	3.09	0.40
22:BA:1983:G:C6	22:BA:1984:G:N7	2.89	0.40
22:BA:2186:G:C5	22:BA:2187:U:C4	3.09	0.40
22:BA:2592:G:C6	22:BA:2593:U:C4	3.09	0.40
22:BA:2597:G:O2'	22:BA:2598:A:H5'	2.21	0.40
22:BA:2756:U:OP2	52:B4:19:ARG:NE	2.54	0.40
24:BC:159:GLY:H	24:BC:195:VAL:HG13	1.86	0.40
26:BE:134:LEU:O	26:BE:138:LEU:HG	2.22	0.40
32:BK:105:ARG:C	32:BK:107:LEU:N	2.80	0.40
33:BL:55:MET:HA	33:BL:56:PRO:HD3	1.92	0.40
35:BN:79:LEU:HA	35:BN:83:LEU:HB2	2.02	0.40
38:BQ:112:LYS:HD3	39:BR:48:LYS:HD2	2.02	0.40
1:CA:202:G:H2'	1:CA:203:G:O4'	2.20	0.40
1:CA:522:C:H41	12:CL:50:ARG:NH2	2.20	0.40
1:CA:793:U:O2	1:CA:1516:G:H4'	2.20	0.40
1:CA:950:U:H2'	1:CA:951:G:H8	1.85	0.40
1:CA:1037:C:H6	1:CA:1037:C:OP2	2.05	0.40
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.56	0.40
1:CA:1271:A:H2'	1:CA:1272:G:H8	1.86	0.40
1:CA:1380:U:C4	7:CG:3:ARG:HD3	2.56	0.40
2:CB:162:PHE:HA	2:CB:184:PHE:O	2.21	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
8:CH:96:MET:HE2	8:CH:96:MET:HB3	1.81	0.40
9:CI:25:ASN:C	9:CI:27:LYS:H	2.29	0.40
11:CK:36:ASP:OD2	11:CK:40:ASN:HB2	2.21	0.40
12:CL:64:THR:HG23	12:CL:93:VAL:CG1	2.51	0.40
13:CM:101:ARG:HD2	13:CM:104:THR:OG1	2.21	0.40
14:CN:30:ILE:O	14:CN:33:ASP:HB3	2.21	0.40
15:CO:4:SER:HB2	15:CO:7:ALA:HB3	2.03	0.40
16:CP:43:ALA:O	16:CP:44:SER:OG	2.29	0.40
22:DA:320:A:O3'	22:DA:321:U:H3'	2.21	0.40
22:DA:956:G:O6	34:DM:14:LYS:NZ	2.52	0.40
22:DA:1335:C:H2'	22:DA:1336:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:DA:2024:G:C4	22:DA:2040:G:N2	2.90	0.40
22:DA:2114:A:C4	22:DA:2167:U:H4'	2.56	0.40
22:DA:2183:A:H2'	22:DA:2184:A:C8	2.57	0.40
22:DA:2378:A:N7	22:DA:2379:G:H1'	2.37	0.40
22:DA:2590:A:H5"	24:DC:238:ARG:HE	1.87	0.40
22:DA:2626:C:H2'	22:DA:2627:G:O4'	2.21	0.40
23:DB:76:G:H2'	23:DB:77:U:O4'	2.22	0.40
25:DD:4:LEU:HD22	25:DD:100:LEU:HD23	2.03	0.40
26:DE:114:ARG:HE	26:DE:114:ARG:HB2	1.55	0.40
26:DE:149:ILE:CD1	26:DE:172:ALA:HA	2.52	0.40
27:DF:143:TYR:O	27:DF:146:VAL:HG22	2.21	0.40
35:DN:48:VAL:O	35:DN:52:ILE:HG13	2.22	0.40
35:DN:66:ALA:O	35:DN:70:THR:HG23	2.22	0.40
36:DO:18:LEU:HD13	36:DO:18:LEU:HA	1.84	0.40
41:DT:2:ILE:HG23	41:DT:3:ARG:C	2.46	0.40
54:D6:6:MHV:OD1	54:D6:8:MHT:H4	2.21	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
1:AA:1125:U:C5	1:AA:1127:G:C6	3.09	0.40
2:AB:90:PHE:HB3	2:AB:150:GLY:O	2.21	0.40
2:AB:130:THR:HB	2:AB:132:LYS:HB3	2.02	0.40
10:AJ:53:ILE:HB	10:AJ:62:ARG:N	2.36	0.40
13:AM:72:GLU:O	13:AM:75:MET:HB3	2.21	0.40
14:AN:43:ASN:C	14:AN:45:VAL:H	2.30	0.40
16:AP:8:ARG:C	16:AP:10:GLY:H	2.29	0.40
22:BA:368:A:N6	22:BA:369:U:O4	2.54	0.40
22:BA:458:G:H22	22:BA:469:G:H2'	1.85	0.40
22:BA:475:C:C4	22:BA:481:G:O6	2.73	0.40
22:BA:1009:A:H8	22:BA:1009:A:O5'	2.05	0.40
22:BA:1918:A:O3'	22:BA:1919:A:C8	2.75	0.40
22:BA:1936:A:H61	22:BA:1963:U:H3	1.69	0.40
22:BA:2093:G:O2'	29:BH:25:TYR:HA	2.22	0.40
24:BC:77:VAL:HA	24:BC:114:ASP:O	2.21	0.40
27:BF:138:PHE:HA	27:BF:139:PRO:HD3	1.95	0.40
30:BI:100:LYS:HB3	30:BI:139:VAL:HB	2.04	0.40
34:BM:7:THR:OG1	34:BM:9:PHE:O	2.34	0.40
34:BM:132:THR:HG22	34:BM:133:LYS:N	2.36	0.40
35:BN:37:THR:HA	35:BN:110:MET:SD	2.61	0.40
46:BY:23:ARG:O	46:BY:27:ASN:HB2	2.22	0.40
46:BY:43:LEU:HD23	46:BY:43:LEU:HA	1.86	0.40
1:CA:254:G:O2'	17:CQ:20:SER:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:957:U:O3'	19:CS:79:THR:OG1	2.39	0.40
1:CA:1088:G:H21	1:CA:1167:A:H61	1.68	0.40
1:CA:1180:A:OP1	9:CI:105:THR:OG1	2.39	0.40
2:CB:133:GLU:O	2:CB:137:ARG:HB3	2.21	0.40
3:CC:40:ARG:CG	3:CC:55:ILE:HD11	2.45	0.40
7:CG:148:ASN:C	7:CG:150:ALA:N	2.80	0.40
9:CI:115:LYS:HB2	9:CI:118:LEU:HD22	2.03	0.40
11:CK:56:ARG:O	11:CK:62:ALA:HB2	2.21	0.40
16:CP:56:ARG:HD2	16:CP:56:ARG:HA	1.85	0.40
17:CQ:55:ILE:HG12	17:CQ:56:GLY:N	2.37	0.40
18:CR:45:THR:O	18:CR:45:THR:OG1	2.32	0.40
22:DA:558:U:H2'	22:DA:559:G:C8	2.57	0.40
22:DA:585:G:H8	22:DA:585:G:O5'	2.04	0.40
22:DA:1587:G:H2'	22:DA:1588:G:H8	1.87	0.40
22:DA:1632:A:C6	22:DA:1633:G:C6	3.09	0.40
22:DA:1664:A:OP2	22:DA:1664:A:C8	2.74	0.40
22:DA:1854:A:O4'	22:DA:2233:U:H4'	2.22	0.40
22:DA:2200:C:O2	22:DA:2226:C:N4	2.55	0.40
22:DA:2704:C:H3'	22:DA:2705:A:C8	2.57	0.40
24:DC:210:ALA:HA	24:DC:213:TRP:NE1	2.37	0.40
26:DE:109:LEU:HD12	26:DE:109:LEU:HA	1.79	0.40
28:DG:68:ALA:HA	28:DG:71:LEU:HB2	2.03	0.40
34:DM:56:ALA:C	34:DM:58:LYS:N	2.79	0.40
34:DM:136:MET:HE2	34:DM:136:MET:HB3	1.78	0.40
46:DY:24:GLU:HB3	46:DY:46:VAL:HG21	2.03	0.40
1:AA:39:G:N7	1:AA:547:A:C8	2.89	0.40
1:AA:417:G:N2	1:AA:540:G:O2'	2.55	0.40
1:AA:505:G:H4'	1:AA:534:U:C4	2.56	0.40
1:AA:1241:G:H2'	1:AA:1242:G:H8	1.85	0.40
1:AA:1476:A:H2'	1:AA:1477:U:O4'	2.21	0.40
2:AB:120:GLN:HE22	2:AB:137:ARG:HH22	1.68	0.40
4:AD:95:GLU:O	4:AD:100:ASN:ND2	2.54	0.40
4:AD:174:ASP:OD2	4:AD:177:LYS:N	2.30	0.40
5:AE:81:LEU:HD12	5:AE:147:MET:SD	2.62	0.40
6:AF:1:MET:HE3	6:AF:1:MET:HB2	1.71	0.40
10:AJ:15:HIS:CG	10:AJ:16:ARG:N	2.89	0.40
11:AK:13:ARG:HG2	22:BA:2142:A:OP1	2.22	0.40
12:AL:25:GLU:O	12:AL:26:ALA:C	2.63	0.40
21:AU:16:LEU:O	21:AU:18:ARG:HD2	2.22	0.40
21:AU:45:ARG:HA	21:AU:48:ALA:HB3	2.03	0.40
22:BA:28:A:C5	22:BA:29:U:C5	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BA:182:A:C6	22:BA:183:C:C4	3.08	0.40
22:BA:189:G:O6	22:BA:205:G:O2'	2.29	0.40
22:BA:826:U:O2'	33:BL:53:GLY:HA3	2.21	0.40
22:BA:2512:C:H2'	22:BA:2513:A:O4'	2.21	0.40
22:BA:2805:C:C4	22:BA:2806:C:C4	3.10	0.40
24:BC:222:GLY:HA2	24:BC:225:MET:HE3	2.02	0.40
25:BD:46:ARG:HH22	25:BD:86:GLU:HA	1.87	0.40
29:BH:120:GLY:HA2	29:BH:122:LEU:HA	2.04	0.40
30:BI:11:LEU:HD12	30:BI:24:VAL:HG12	2.04	0.40
30:BI:97:LYS:N	30:BI:97:LYS:HD2	2.37	0.40
30:BI:115:ALA:O	30:BI:116:ASP:HB2	2.21	0.40
37:BP:90:GLY:O	37:BP:113:ARG:NH1	2.52	0.40
43:BV:40:ILE:HA	43:BV:40:ILE:HD13	1.73	0.40
44:BW:28:GLY:O	44:BW:66:LYS:HG2	2.22	0.40
1:CA:112:G:H5'	1:CA:389:A:O2'	2.21	0.40
1:CA:196:A:OP1	20:CT:64:LYS:NZ	2.54	0.40
1:CA:208:U:C5	1:CA:210:C:H6	2.40	0.40
1:CA:279:A:OP1	1:CA:280:C:O2'	2.38	0.40
1:CA:585:G:C6	1:CA:586:C:C4	3.10	0.40
1:CA:1280:A:C8	10:CJ:42:LEU:HD23	2.57	0.40
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.22	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
3:CC:67:THR:HG23	3:CC:102:ASN:HB2	2.03	0.40
4:CD:45:LYS:HB2	4:CD:45:LYS:HE3	1.89	0.40
5:CE:150:PRO:O	5:CE:152:MET:N	2.54	0.40
8:CH:49:PHE:C	8:CH:49:PHE:CD1	2.98	0.40
14:CN:53:ARG:C	14:CN:55:SER:H	2.28	0.40
16:CP:53:ASP:O	16:CP:57:ILE:HG13	2.21	0.40
20:CT:62:ALA:HA	20:CT:68:HIS:N	2.36	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:993:G:H1'	39:DR:91:GLN:OE1	2.22	0.40
22:DA:1412:U:H2'	22:DA:1413:A:C8	2.57	0.40
22:DA:1974:C:H2'	22:DA:1975:G:H8	1.86	0.40
22:DA:2079:U:H2'	22:DA:2080:A:O4'	2.21	0.40
22:DA:2199:A:C6	22:DA:2200:C:C2	3.10	0.40
26:DE:155:GLU:HG3	26:DE:159:LEU:HD12	2.04	0.40
29:DH:77:THR:HA	29:DH:143:ILE:O	2.22	0.40
29:DH:96:THR:C	29:DH:98:ASP:N	2.79	0.40
31:DJ:31:GLU:O	31:DJ:35:ARG:HG3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DL:136:GLU:C	33:DL:138:ALA:H	2.29	0.40
37:DP:37:LYS:HZ1	37:DP:39:ARG:HD2	1.86	0.40
41:DT:38:ALA:O	41:DT:39:THR:HB	2.21	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
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 0
3	AC	204/206 (99%)	158 (78%)	30 (15%)	16 (8%)	1 1
3	CC	204/206 (99%)	156 (76%)	33 (16%)	15 (7%)	1 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AD	203/205 (99%)	150 (74%)	29 (14%)	24 (12%)	0	0
4	CD	203/205 (99%)	152 (75%)	29 (14%)	22 (11%)	0	0
5	AE	148/150 (99%)	112 (76%)	20 (14%)	16 (11%)	0	0
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	0
6	CF	98/100 (98%)	69 (70%)	14 (14%)	15 (15%)	0	0
7	AG	149/151 (99%)	110 (74%)	30 (20%)	9 (6%)	1	2
7	CG	149/151 (99%)	118 (79%)	22 (15%)	9 (6%)	1	2
8	AH	127/129 (98%)	94 (74%)	26 (20%)	7 (6%)	1	3
8	CH	127/129 (98%)	103 (81%)	17 (13%)	7 (6%)	1	3
9	AI	125/127 (98%)	96 (77%)	20 (16%)	9 (7%)	1	1
9	CI	125/127 (98%)	97 (78%)	20 (16%)	8 (6%)	1	2
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	0
11	AK	115/117 (98%)	90 (78%)	16 (14%)	9 (8%)	1	1
11	CK	115/117 (98%)	85 (74%)	21 (18%)	9 (8%)	1	1
12	AL	121/123 (98%)	96 (79%)	19 (16%)	6 (5%)	1	3
12	CL	121/123 (98%)	97 (80%)	13 (11%)	11 (9%)	0	1
13	AM	112/114 (98%)	85 (76%)	16 (14%)	11 (10%)	0	1
13	CM	112/114 (98%)	82 (73%)	19 (17%)	11 (10%)	0	1
14	AN	92/100 (92%)	61 (66%)	20 (22%)	11 (12%)	0	0
14	CN	92/100 (92%)	61 (66%)	15 (16%)	16 (17%)	0	0
15	AO	86/88 (98%)	65 (76%)	18 (21%)	3 (4%)	3	7
15	CO	86/88 (98%)	68 (79%)	14 (16%)	4 (5%)	2	4
16	AP	80/82 (98%)	49 (61%)	15 (19%)	16 (20%)	0	0
16	CP	80/82 (98%)	59 (74%)	17 (21%)	4 (5%)	1	3
17	AQ	78/80 (98%)	57 (73%)	11 (14%)	10 (13%)	0	0
17	CQ	78/80 (98%)	53 (68%)	17 (22%)	8 (10%)	0	0
18	AR	53/55 (96%)	45 (85%)	4 (8%)	4 (8%)	1	1
18	CR	53/55 (96%)	40 (76%)	8 (15%)	5 (9%)	0	1
19	AS	77/79 (98%)	55 (71%)	14 (18%)	8 (10%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
19	CS	77/79 (98%)	61 (79%)	13 (17%)	3 (4%)	2 5
20	AT	83/85 (98%)	66 (80%)	12 (14%)	5 (6%)	1 2
20	CT	83/85 (98%)	68 (82%)	9 (11%)	6 (7%)	1 1
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%)	2 5
24	DC	269/271 (99%)	209 (78%)	42 (16%)	18 (7%)	1 1
25	BD	207/209 (99%)	183 (88%)	19 (9%)	5 (2%)	4 13
25	DD	207/209 (99%)	173 (84%)	29 (14%)	5 (2%)	4 13
26	BE	199/201 (99%)	171 (86%)	22 (11%)	6 (3%)	3 9
26	DE	199/201 (99%)	157 (79%)	29 (15%)	13 (6%)	1 1
27	BF	175/177 (99%)	144 (82%)	23 (13%)	8 (5%)	2 4
27	DF	175/177 (99%)	146 (83%)	17 (10%)	12 (7%)	1 1
28	BG	174/176 (99%)	147 (84%)	15 (9%)	12 (7%)	1 1
28	DG	174/176 (99%)	138 (79%)	25 (14%)	11 (6%)	1 2
29	BH	147/149 (99%)	89 (60%)	37 (25%)	21 (14%)	0 0
29	DH	147/149 (99%)	100 (68%)	32 (22%)	15 (10%)	0 0
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 0
31	BJ	140/142 (99%)	124 (89%)	11 (8%)	5 (4%)	2 6
31	DJ	140/142 (99%)	123 (88%)	15 (11%)	2 (1%)	9 24
32	BK	120/122 (98%)	98 (82%)	13 (11%)	9 (8%)	1 1
32	DK	120/122 (98%)	100 (83%)	14 (12%)	6 (5%)	1 3
33	BL	141/143 (99%)	109 (77%)	20 (14%)	12 (8%)	0 1
33	DL	141/143 (99%)	105 (74%)	29 (21%)	7 (5%)	1 3
34	BM	134/136 (98%)	117 (87%)	15 (11%)	2 (2%)	8 23
34	DM	134/136 (98%)	112 (84%)	19 (14%)	3 (2%)	5 15
35	BN	118/120 (98%)	96 (81%)	21 (18%)	1 (1%)	16 37
35	DN	118/120 (98%)	97 (82%)	11 (9%)	10 (8%)	0 1
36	BO	114/116 (98%)	95 (83%)	15 (13%)	4 (4%)	3 7
36	DO	114/116 (98%)	96 (84%)	14 (12%)	4 (4%)	3 7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
37	BP	112/114 (98%)	98 (88%)	9 (8%)	5 (4%)	2 4
37	DP	112/114 (98%)	91 (81%)	16 (14%)	5 (4%)	2 4
38	BQ	115/117 (98%)	107 (93%)	3 (3%)	5 (4%)	2 4
38	DQ	115/117 (98%)	108 (94%)	6 (5%)	1 (1%)	14 34
39	BR	101/103 (98%)	86 (85%)	8 (8%)	7 (7%)	1 1
39	DR	101/103 (98%)	77 (76%)	20 (20%)	4 (4%)	2 5
40	BS	108/110 (98%)	100 (93%)	5 (5%)	3 (3%)	4 11
40	DS	108/110 (98%)	89 (82%)	14 (13%)	5 (5%)	2 4
41	BT	91/93 (98%)	70 (77%)	13 (14%)	8 (9%)	0 1
41	DT	91/93 (98%)	70 (77%)	9 (10%)	12 (13%)	0 0
42	BU	100/102 (98%)	80 (80%)	12 (12%)	8 (8%)	1 1
42	DU	100/102 (98%)	73 (73%)	17 (17%)	10 (10%)	0 0
43	BV	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	11 29
43	DV	92/94 (98%)	82 (89%)	8 (9%)	2 (2%)	5 15
44	BW	74/76 (97%)	67 (90%)	7 (10%)	0	100 100
44	DW	73/76 (96%)	65 (89%)	6 (8%)	2 (3%)	4 11
45	BX	75/77 (97%)	72 (96%)	1 (1%)	2 (3%)	4 11
45	DX	75/77 (97%)	64 (85%)	9 (12%)	2 (3%)	4 11
46	BY	61/63 (97%)	40 (66%)	12 (20%)	9 (15%)	0 0
46	DY	61/63 (97%)	49 (80%)	8 (13%)	4 (7%)	1 1
47	BZ	56/58 (97%)	52 (93%)	4 (7%)	0	100 100
47	DZ	56/58 (97%)	53 (95%)	1 (2%)	2 (4%)	2 6
48	B0	54/56 (96%)	46 (85%)	5 (9%)	3 (6%)	1 2
48	D0	54/56 (96%)	41 (76%)	11 (20%)	2 (4%)	2 6
49	B1	48/50 (96%)	38 (79%)	6 (12%)	4 (8%)	0 1
49	D1	48/50 (96%)	37 (77%)	8 (17%)	3 (6%)	1 2
50	B2	44/46 (96%)	39 (89%)	3 (7%)	2 (4%)	2 4
50	D2	44/46 (96%)	38 (86%)	4 (9%)	2 (4%)	2 4
51	B3	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	7 21
51	D3	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7 21
52	B4	36/38 (95%)	33 (92%)	3 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
52	D4	36/38 (95%)	33 (92%)	1 (3%)	2 (6%)	1 2
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 1

All (881) Ramachandran outliers are listed below:

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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 (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	180/180 (100%)	113 (63%)	67 (37%)	0	0
2	CB	180/180 (100%)	127 (71%)	53 (29%)	0	0
3	AC	170/170 (100%)	131 (77%)	39 (23%)	1	2
3	CC	170/170 (100%)	134 (79%)	36 (21%)	1	2
4	AD	172/172 (100%)	129 (75%)	43 (25%)	0	1
4	CD	172/172 (100%)	136 (79%)	36 (21%)	1	2
5	AE	113/113 (100%)	79 (70%)	34 (30%)	0	0
5	CE	113/113 (100%)	84 (74%)	29 (26%)	0	1
6	AF	87/87 (100%)	60 (69%)	27 (31%)	0	0
6	CF	87/87 (100%)	60 (69%)	27 (31%)	0	0
7	AG	124/124 (100%)	89 (72%)	35 (28%)	0	0
7	CG	124/124 (100%)	92 (74%)	32 (26%)	0	1
8	AH	104/104 (100%)	75 (72%)	29 (28%)	0	0
8	CH	104/104 (100%)	80 (77%)	24 (23%)	1	2
9	AI	105/105 (100%)	77 (73%)	28 (27%)	0	0
9	CI	105/105 (100%)	75 (71%)	30 (29%)	0	0
10	AJ	86/86 (100%)	60 (70%)	26 (30%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	CJ	86/86 (100%)	63 (73%)	23 (27%)	0	0
11	AK	90/90 (100%)	68 (76%)	22 (24%)	1	1
11	CK	90/90 (100%)	66 (73%)	24 (27%)	0	0
12	AL	103/103 (100%)	80 (78%)	23 (22%)	1	2
12	CL	103/103 (100%)	78 (76%)	25 (24%)	1	1
13	AM	92/92 (100%)	71 (77%)	21 (23%)	1	2
13	CM	92/92 (100%)	69 (75%)	23 (25%)	0	1
14	AN	79/83 (95%)	59 (75%)	20 (25%)	0	1
14	CN	79/83 (95%)	67 (85%)	12 (15%)	3	8
15	AO	75/76 (99%)	59 (79%)	16 (21%)	1	2
15	CO	75/76 (99%)	58 (77%)	17 (23%)	1	2
16	AP	65/65 (100%)	51 (78%)	14 (22%)	1	2
16	CP	65/65 (100%)	48 (74%)	17 (26%)	0	1
17	AQ	74/74 (100%)	52 (70%)	22 (30%)	0	0
17	CQ	74/74 (100%)	52 (70%)	22 (30%)	0	0
18	AR	48/48 (100%)	39 (81%)	9 (19%)	1	4
18	CR	48/48 (100%)	40 (83%)	8 (17%)	2	6
19	AS	70/70 (100%)	57 (81%)	13 (19%)	1	4
19	CS	70/70 (100%)	51 (73%)	19 (27%)	0	0
20	AT	65/65 (100%)	46 (71%)	19 (29%)	0	0
20	CT	65/65 (100%)	45 (69%)	20 (31%)	0	0
21	AU	44/44 (100%)	28 (64%)	16 (36%)	0	0
21	CU	44/44 (100%)	32 (73%)	12 (27%)	0	0
24	BC	216/216 (100%)	183 (85%)	33 (15%)	3	8
24	DC	216/216 (100%)	175 (81%)	41 (19%)	1	3
25	BD	164/164 (100%)	142 (87%)	22 (13%)	4	11
25	DD	164/164 (100%)	142 (87%)	22 (13%)	4	11
26	BE	165/165 (100%)	137 (83%)	28 (17%)	2	5
26	DE	165/165 (100%)	128 (78%)	37 (22%)	1	2
27	BF	148/148 (100%)	116 (78%)	32 (22%)	1	2
27	DF	148/148 (100%)	114 (77%)	34 (23%)	1	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
28	BG	137/137 (100%)	114 (83%)	23 (17%)	2 6
28	DG	137/137 (100%)	121 (88%)	16 (12%)	5 16
29	BH	114/114 (100%)	81 (71%)	33 (29%)	0 0
29	DH	114/114 (100%)	89 (78%)	25 (22%)	1 2
30	BI	109/109 (100%)	78 (72%)	31 (28%)	0 0
30	DI	109/109 (100%)	83 (76%)	26 (24%)	1 1
31	BJ	116/116 (100%)	96 (83%)	20 (17%)	2 5
31	DJ	116/116 (100%)	99 (85%)	17 (15%)	3 9
32	BK	103/103 (100%)	90 (87%)	13 (13%)	4 13
32	DK	103/103 (100%)	88 (85%)	15 (15%)	3 9
33	BL	102/102 (100%)	79 (78%)	23 (22%)	1 2
33	DL	102/102 (100%)	80 (78%)	22 (22%)	1 2
34	BM	109/109 (100%)	95 (87%)	14 (13%)	4 13
34	DM	109/109 (100%)	96 (88%)	13 (12%)	5 15
35	BN	100/100 (100%)	87 (87%)	13 (13%)	4 12
35	DN	100/100 (100%)	83 (83%)	17 (17%)	2 5
36	BO	86/86 (100%)	57 (66%)	29 (34%)	0 0
36	DO	86/86 (100%)	69 (80%)	17 (20%)	1 3
37	BP	99/99 (100%)	86 (87%)	13 (13%)	4 12
37	DP	99/99 (100%)	77 (78%)	22 (22%)	1 2
38	BQ	89/89 (100%)	71 (80%)	18 (20%)	1 3
38	DQ	89/89 (100%)	75 (84%)	14 (16%)	2 8
39	BR	84/84 (100%)	70 (83%)	14 (17%)	2 6
39	DR	84/84 (100%)	69 (82%)	15 (18%)	2 4
40	BS	93/93 (100%)	75 (81%)	18 (19%)	1 3
40	DS	93/93 (100%)	72 (77%)	21 (23%)	1 2
41	BT	80/80 (100%)	67 (84%)	13 (16%)	2 7
41	DT	80/80 (100%)	64 (80%)	16 (20%)	1 3
42	BU	83/83 (100%)	67 (81%)	16 (19%)	1 3
42	DU	83/83 (100%)	61 (74%)	22 (26%)	0 1
43	BV	78/78 (100%)	65 (83%)	13 (17%)	2 6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
43	DV	78/78 (100%)	64 (82%)	14 (18%)	2 4
44	BW	57/58 (98%)	51 (90%)	6 (10%)	6 19
44	DW	56/58 (97%)	48 (86%)	8 (14%)	3 9
45	BX	67/67 (100%)	54 (81%)	13 (19%)	1 3
45	DX	67/67 (100%)	52 (78%)	15 (22%)	1 2
46	BY	55/55 (100%)	46 (84%)	9 (16%)	2 7
46	DY	55/55 (100%)	42 (76%)	13 (24%)	1 1
47	BZ	48/48 (100%)	39 (81%)	9 (19%)	1 4
47	DZ	48/48 (100%)	39 (81%)	9 (19%)	1 4
48	B0	47/47 (100%)	40 (85%)	7 (15%)	3 8
48	D0	47/47 (100%)	41 (87%)	6 (13%)	4 13
49	B1	45/45 (100%)	36 (80%)	9 (20%)	1 3
49	D1	45/45 (100%)	38 (84%)	7 (16%)	2 8
50	B2	38/38 (100%)	33 (87%)	5 (13%)	4 12
50	D2	38/38 (100%)	32 (84%)	6 (16%)	2 8
51	B3	51/51 (100%)	46 (90%)	5 (10%)	7 21
51	D3	51/51 (100%)	46 (90%)	5 (10%)	7 21
52	B4	34/34 (100%)	29 (85%)	5 (15%)	3 9
52	D4	34/34 (100%)	28 (82%)	6 (18%)	2 5
53	B5	61/180 (34%)	44 (72%)	17 (28%)	0 0
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%)	7373 (78%)	2017 (22%)	1 2

All (2017) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	9	MET
2	AB	10	LEU
2	AB	14	VAL
2	AB	15	HIS
2	AB	19	GLN
2	AB	20	THR
2	AB	21	ARG

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Mol	Chain	Res	Type
2	AB	27	MET
2	AB	31	ILE
2	AB	32	PHE
2	AB	38	VAL
2	AB	39	HIS
2	AB	40	ILE
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	57	LEU
2	AB	59	LYS
2	AB	64	LYS
2	AB	66	LYS
2	AB	68	LEU
2	AB	70	VAL
2	AB	82	ASP
2	AB	85	LEU
2	AB	91	PHE
2	AB	93	ASN
2	AB	100	MET
2	AB	101	LEU
2	AB	102	THR
2	AB	107	VAL
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	137	ARG
2	AB	140	GLU
2	AB	141	LEU
2	AB	143	LYS
2	AB	144	LEU

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Mol	Chain	Res	Type
2	AB	151	ILE
2	AB	163	VAL
2	AB	164	ILE
2	AB	170	HIS
2	AB	171	ILE
2	AB	179	LEU
2	AB	181	ILE
2	AB	186	ILE
2	AB	188	ASP
2	AB	194	ASP
2	AB	197	ASP
2	AB	199	VAL
2	AB	205	ASP
2	AB	207	ILE
2	AB	208	ARG
2	AB	210	VAL
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	33	LEU
3	AC	37	PHE
3	AC	43	LEU
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	111	LEU
3	AC	121	THR

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Mol	Chain	Res	Type
3	AC	129	MET
3	AC	131	ARG
3	AC	140	ASN
3	AC	142	MET
3	AC	144	LEU
3	AC	149	ILE
3	AC	150	LYS
3	AC	151	VAL
3	AC	157	LEU
3	AC	162	ILE
3	AC	166	GLU
3	AC	167	TRP
3	AC	173	VAL
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	23	SER
4	AD	26	ARG
4	AD	31	LYS
4	AD	32	CYS
4	AD	35	GLU
4	AD	45	LYS
4	AD	53	VAL
4	AD	58	LYS
4	AD	60	LYS
4	AD	63	ARG
4	AD	69	GLU
4	AD	86	THR
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	132	ILE
4	AD	138	SER
4	AD	143	VAL

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Mol	Chain	Res	Type
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	167	LYS
4	AD	177	LYS
4	AD	183	LYS
4	AD	190	ASP
4	AD	192	SER
4	AD	195	ILE
4	AD	196	ASN
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	19	ASN
5	AE	21	VAL
5	AE	29	ARG
5	AE	32	SER
5	AE	38	VAL
5	AE	46	VAL
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	103	THR
5	AE	105	ILE
5	AE	114	VAL
5	AE	115	LEU
5	AE	116	GLU
5	AE	120	VAL
5	AE	122	ASN
5	AE	123	VAL
5	AE	124	LEU
5	AE	126	LYS

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Mol	Chain	Res	Type
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	151	GLU
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	21	MET
6	AF	24	ARG
6	AF	35	LYS
6	AF	39	LEU
6	AF	44	ARG
6	AF	51	ILE
6	AF	52	ASN
6	AF	54	LEU
6	AF	55	HIS
6	AF	62	MET
6	AF	68	GLN
6	AF	71	ILE
6	AF	74	LEU
6	AF	77	THR
6	AF	82	ASP
6	AF	85	ILE
6	AF	86	ARG
6	AF	87	SER
6	AF	89	VAL
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	22	LEU

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Mol	Chain	Res	Type
7	AG	23	LEU
7	AG	32	VAL
7	AG	36	LYS
7	AG	43	VAL
7	AG	47	LEU
7	AG	49	THR
7	AG	52	GLN
7	AG	59	LEU
7	AG	63	GLU
7	AG	75	VAL
7	AG	76	LYS
7	AG	78	ARG
7	AG	79	ARG
7	AG	80	VAL
7	AG	83	SER
7	AG	89	VAL
7	AG	90	GLU
7	AG	95	ARG
7	AG	106	GLU
7	AG	109	ARG
7	AG	113	ASP
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
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	47	GLU
8	AH	49	PHE
8	AH	50	LYS
8	AH	64	LYS
8	AH	77	ARG

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Mol	Chain	Res	Type
8	AH	79	SER
8	AH	83	LEU
8	AH	89	LYS
8	AH	90	ASP
8	AH	99	LEU
8	AH	101	ILE
8	AH	104	VAL
8	AH	107	SER
8	AH	108	LYS
8	AH	110	VAL
8	AH	111	MET
8	AH	112	THR
8	AH	117	ARG
8	AH	125	ILE
8	AH	129	VAL
9	AI	11	ARG
9	AI	14	SER
9	AI	30	ILE
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
9	AI	65	ILE
9	AI	68	LYS
9	AI	88	MET
9	AI	89	GLU
9	AI	90	TYR
9	AI	92	GLU
9	AI	94	LEU
9	AI	97	GLU
9	AI	98	LEU
9	AI	99	ARG
9	AI	115	LYS
9	AI	116	VAL
9	AI	127	PHE
9	AI	129	LYS

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Mol	Chain	Res	Type
9	AI	130	ARG
10	AJ	6	ILE
10	AJ	8	ILE
10	AJ	17	LEU
10	AJ	22	THR
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	67	ILE
10	AJ	71	LEU
10	AJ	73	LEU
10	AJ	77	VAL
10	AJ	83	THR
10	AJ	84	VAL
10	AJ	87	LEU
10	AJ	91	ASP
10	AJ	92	LEU
10	AJ	101	SER
11	AK	17	SER
11	AK	23	ILE
11	AK	31	ILE
11	AK	32	VAL
11	AK	38	GLN
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	94	GLU

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Mol	Chain	Res	Type
11	AK	97	ILE
11	AK	100	LEU
11	AK	107	ILE
11	AK	111	THR
11	AK	119	ASN
11	AK	126	LYS
11	AK	129	VAL
12	AL	4	VAL
12	AL	10	LYS
12	AL	21	VAL
12	AL	25	GLU
12	AL	29	GLN
12	AL	35	THR
12	AL	44	LYS
12	AL	49	LEU
12	AL	54	ARG
12	AL	55	VAL
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	9	ILE
13	AM	13	LYS
13	AM	16	VAL
13	AM	21	SER
13	AM	27	LYS
13	AM	29	ARG
13	AM	44	LYS
13	AM	48	LEU
13	AM	60	VAL
13	AM	64	VAL

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Mol	Chain	Res	Type
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	91	HIS
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	31	ILE
14	AN	34	VAL
14	AN	43	ASN
14	AN	46	LEU
14	AN	49	GLN
14	AN	51	LEU
14	AN	59	ARG
14	AN	76	LYS
14	AN	82	ILE
14	AN	84	VAL
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
15	AO	59	MET
15	AO	67	LEU

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Mol	Chain	Res	Type
15	AO	75	VAL
15	AO	85	LEU
15	AO	87	LEU
16	AP	2	VAL
16	AP	6	LEU
16	AP	8	ARG
16	AP	18	GLN
16	AP	19	VAL
16	AP	20	VAL
16	AP	46	LYS
16	AP	47	GLU
16	AP	51	ARG
16	AP	67	ILE
16	AP	70	ARG
16	AP	71	VAL
16	AP	75	ILE
16	AP	76	LYS
17	AQ	4	LYS
17	AQ	13	VAL
17	AQ	14	SER
17	AQ	16	LYS
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	61	ILE
17	AQ	69	LYS
17	AQ	75	LEU
17	AQ	76	VAL
17	AQ	77	ARG
17	AQ	81	LYS
17	AQ	83	VAL
18	AR	21	ILE
18	AR	24	LYS
18	AR	29	LEU

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Mol	Chain	Res	Type
18	AR	34	THR
18	AR	39	ILE
18	AR	43	ARG
18	AR	55	LEU
18	AR	61	ARG
18	AR	71	THR
19	AS	5	LEU
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	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	54	MET
20	AT	67	ILE
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

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Mol	Chain	Res	Type
21	AU	16	LEU
21	AU	18	ARG
21	AU	20	LYS
21	AU	23	CYS
21	AU	28	VAL
21	AU	33	ARG
21	AU	34	ARG
21	AU	36	GLU
21	AU	37	PHE
21	AU	43	THR
21	AU	44	GLU
21	AU	54	LYS
24	BC	3	VAL
24	BC	5	LYS
24	BC	14	ARG
24	BC	18	LYS
24	BC	24	LEU
24	BC	38	SER
24	BC	39	LYS
24	BC	64	ILE
24	BC	86	ASN
24	BC	97	LYS
24	BC	105	LEU
24	BC	111	LYS
24	BC	120	VAL
24	BC	121	ASP
24	BC	125	LYS
24	BC	141	VAL
24	BC	146	MET
24	BC	156	ARG
24	BC	162	VAL
24	BC	164	ILE
24	BC	172	VAL
24	BC	174	LEU
24	BC	177	ARG
24	BC	184	VAL
24	BC	197	ASN
24	BC	199	GLU
24	BC	203	ARG
24	BC	220	VAL
24	BC	252	THR
24	BC	258	ARG

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Mol	Chain	Res	Type
24	BC	265	LYS
24	BC	268	VAL
24	BC	271	ARG
25	BD	12	THR
25	BD	13	ARG
25	BD	16	THR
25	BD	25	THR
25	BD	28	GLU
25	BD	32	ASN
25	BD	33	ARG
25	BD	61	THR
25	BD	73	VAL
25	BD	77	ARG
25	BD	83	ARG
25	BD	84	LEU
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
25	BD	193	VAL
26	BE	4	VAL
26	BE	47	LYS
26	BE	65	THR
26	BE	70	SER
26	BE	72	SER
26	BE	77	ILE
26	BE	80	SER
26	BE	88	ARG
26	BE	93	SER
26	BE	105	LEU
26	BE	107	SER
26	BE	108	ILE
26	BE	109	LEU
26	BE	115	GLN
26	BE	116	ASP
26	BE	120	VAL
26	BE	122	GLU

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Mol	Chain	Res	Type
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	189	THR
26	BE	198	GLU
26	BE	199	MET
26	BE	200	LEU
27	BF	3	LYS
27	BF	14	LYS
27	BF	17	MET
27	BF	25	VAL
27	BF	31	VAL
27	BF	35	THR
27	BF	36	LEU
27	BF	42	GLU
27	BF	44	ILE
27	BF	48	LYS
27	BF	49	LEU
27	BF	57	LEU
27	BF	61	SER
27	BF	67	ILE
27	BF	78	LYS
27	BF	89	VAL
27	BF	92	ARG
27	BF	95	ARG
27	BF	104	ILE
27	BF	105	THR
27	BF	108	VAL
27	BF	113	ASP
27	BF	141	ILE
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	167	ARG
27	BF	174	ASP

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Mol	Chain	Res	Type
27	BF	176	PRO
28	BG	10	VAL
28	BG	11	VAL
28	BG	20	ASN
28	BG	23	VAL
28	BG	24	ILE
28	BG	39	ASP
28	BG	55	ARG
28	BG	67	THR
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	141	ILE
28	BG	149	ARG
28	BG	152	ARG
28	BG	155	GLU
28	BG	160	LYS
28	BG	166	ASP
28	BG	168	VAL
28	BG	170	ARG
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	54	LEU
29	BH	60	GLU
29	BH	62	LEU
29	BH	66	ASN
29	BH	72	ILE
29	BH	75	LEU
29	BH	76	GLU
29	BH	77	THR
29	BH	79	THR
29	BH	86	ASP
29	BH	91	PHE
29	BH	108	VAL

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Mol	Chain	Res	Type
29	BH	112	LYS
29	BH	117	LEU
29	BH	119	ASN
29	BH	121	VAL
29	BH	122	LEU
29	BH	123	ARG
29	BH	125	THR
29	BH	127	GLU
29	BH	129	GLU
29	BH	131	SER
29	BH	137	GLU
29	BH	142	VAL
29	BH	143	ILE
29	BH	145	ASN
29	BH	146	VAL
30	BI	8	TYR
30	BI	9	VAL
30	BI	11	LEU
30	BI	17	MET
30	BI	28	LEU
30	BI	34	ASN
30	BI	38	PHE
30	BI	40	LYS
30	BI	45	LYS
30	BI	47	ASP
30	BI	50	GLU
30	BI	58	VAL
30	BI	60	THR
30	BI	62	TYR
30	BI	67	PHE
30	BI	68	THR
30	BI	69	PHE
30	BI	72	LYS
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	101	ILE
30	BI	103	ARG
30	BI	108	GLU

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Mol	Chain	Res	Type
30	BI	111	GLN
30	BI	112	THR
30	BI	136	MET
30	BI	139	VAL
31	BJ	1	MET
31	BJ	5	THR
31	BJ	17	VAL
31	BJ	23	LYS
31	BJ	30	THR
31	BJ	31	GLU
31	BJ	39	LYS
31	BJ	40	HIS
31	BJ	43	GLU
31	BJ	61	LYS
31	BJ	64	VAL
31	BJ	81	ILE
31	BJ	84	ILE
31	BJ	101	ILE
31	BJ	121	LYS
31	BJ	124	VAL
31	BJ	131	ASN
31	BJ	135	GLN
31	BJ	136	GLN
31	BJ	142	ILE
32	BK	35	VAL
32	BK	38	ILE
32	BK	41	ILE
32	BK	49	ARG
32	BK	58	LEU
32	BK	61	VAL
32	BK	66	LYS
32	BK	88	ASN
32	BK	91	SER
32	BK	92	GLU
32	BK	97	THR
32	BK	107	LEU
32	BK	117	SER
33	BL	7	SER
33	BL	13	LYS
33	BL	14	LYS
33	BL	19	LEU
33	BL	21	ARG

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Mol	Chain	Res	Type
33	BL	27	LEU
33	BL	40	SER
33	BL	51	GLU
33	BL	67	THR
33	BL	69	ARG
33	BL	76	GLU
33	BL	82	LEU
33	BL	86	GLU
33	BL	89	VAL
33	BL	93	ASN
33	BL	94	THR
33	BL	100	ILE
33	BL	115	GLU
33	BL	121	THR
33	BL	122	VAL
33	BL	126	ARG
33	BL	142	ILE
33	BL	144	GLU
34	BM	1	MET
34	BM	12	MET
34	BM	14	LYS
34	BM	18	ARG
34	BM	24	THR
34	BM	47	GLU
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	6	SER
35	BN	15	SER
35	BN	27	SER
35	BN	32	GLU
35	BN	36	THR
35	BN	65	LEU
35	BN	69	ARG
35	BN	71	ARG
35	BN	114	GLU
35	BN	116	VAL

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Mol	Chain	Res	Type
35	BN	117	ASP
35	BN	118	ARG
35	BN	120	GLU
36	BO	2	ASP
36	BO	3	LYS
36	BO	4	LYS
36	BO	5	SER
36	BO	9	ARG
36	BO	17	LYS
36	BO	18	LEU
36	BO	24	THR
36	BO	25	ARG
36	BO	27	VAL
36	BO	28	VAL
36	BO	31	THR
36	BO	35	ILE
36	BO	36	TYR
36	BO	45	SER
36	BO	47	VAL
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	85	LYS
36	BO	88	LYS
36	BO	89	ASP
36	BO	102	ARG
36	BO	116	GLN
37	BP	19	SER
37	BP	27	GLU
37	BP	32	VAL
37	BP	68	GLU
37	BP	72	ARG
37	BP	73	VAL
37	BP	84	ILE
37	BP	94	LYS
37	BP	103	ARG
37	BP	106	LYS

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Mol	Chain	Res	Type
37	BP	109	ARG
37	BP	110	ILE
37	BP	114	LEU
38	BQ	4	VAL
38	BQ	6	ARG
38	BQ	8	VAL
38	BQ	9	ILE
38	BQ	11	ARG
38	BQ	17	ILE
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	74	ILE
38	BQ	78	LYS
38	BQ	87	SER
38	BQ	92	ARG
38	BQ	95	LEU
38	BQ	117	LEU
39	BR	1	MET
39	BR	10	LYS
39	BR	14	VAL
39	BR	16	GLU
39	BR	20	VAL
39	BR	38	VAL
39	BR	41	ILE
39	BR	46	GLU
39	BR	48	LYS
39	BR	49	ILE
39	BR	54	VAL
39	BR	58	VAL
39	BR	85	LYS
39	BR	94	THR
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	37	THR

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Mol	Chain	Res	Type
40	BS	47	VAL
40	BS	53	SER
40	BS	59	GLU
40	BS	69	LEU
40	BS	76	VAL
40	BS	82	MET
40	BS	83	LYS
40	BS	95	ARG
40	BS	96	ILE
40	BS	97	LEU
40	BS	102	HIS
41	BT	1	MET
41	BT	5	GLU
41	BT	10	VAL
41	BT	18	GLU
41	BT	22	THR
41	BT	30	ILE
41	BT	31	VAL
41	BT	36	LYS
41	BT	39	THR
41	BT	49	LYS
41	BT	50	LEU
41	BT	60	THR
41	BT	74	ILE
42	BU	8	ASP
42	BU	9	ASP
42	BU	15	THR
42	BU	21	LYS
42	BU	26	LYS
42	BU	29	LEU
42	BU	40	ASN
42	BU	52	LEU
42	BU	58	ILE
42	BU	61	LYS
42	BU	65	ILE
42	BU	68	SER
42	BU	70	VAL
42	BU	72	ILE
42	BU	77	THR
42	BU	86	ARG
43	BV	1	MET
43	BV	8	VAL

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Mol	Chain	Res	Type
43	BV	10	LYS
43	BV	11	GLU
43	BV	17	SER
43	BV	18	ARG
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
44	BW	20	ARG
44	BW	31	VAL
44	BW	38	VAL
44	BW	64	ASP
44	BW	81	SER
44	BW	82	ILE
45	BX	23	ASN
45	BX	25	THR
45	BX	28	ARG
45	BX	37	ARG
45	BX	40	VAL
45	BX	44	LYS
45	BX	47	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	17	GLU
46	BY	22	LEU
46	BY	29	ARG
46	BY	54	LYS
46	BY	59	GLU
47	BZ	3	LYS
47	BZ	10	THR
47	BZ	30	ARG

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Mol	Chain	Res	Type
47	BZ	32	ILE
47	BZ	36	VAL
47	BZ	45	ARG
47	BZ	52	SER
47	BZ	57	VAL
47	BZ	59	GLU
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	33	LYS
49	B1	35	GLU
49	B1	43	VAL
49	B1	46	HIS
49	B1	47	VAL
49	B1	51	GLU
49	B1	53	LYS
50	B2	1	MET
50	B2	24	THR
50	B2	42	LEU
50	B2	44	VAL
50	B2	45	SER
51	B3	8	ARG
51	B3	17	THR
51	B3	30	ARG
51	B3	47	LYS
51	B3	59	ILE
52	B4	2	LYS
52	B4	3	VAL
52	B4	6	SER
52	B4	9	LYS
52	B4	12	ARG
53	B5	21	TYR
53	B5	23	ILE
53	B5	35	THR
53	B5	38	PHE
53	B5	39	ASP

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Mol	Chain	Res	Type
53	B5	41	THR
53	B5	47	LYS
53	B5	48	LEU
53	B5	58	ASN
53	B5	59	VAL
53	B5	65	LEU
53	B5	73	VAL
53	B5	76	LEU
53	B5	78	ILE
53	B5	80	LYS
53	B5	86	GLU
53	B5	100	ILE
2	CB	14	VAL
2	CB	15	HIS
2	CB	16	PHE
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	66	LYS
2	CB	67	ILE
2	CB	68	LEU
2	CB	72	THR
2	CB	80	VAL
2	CB	81	LYS
2	CB	88	ASP
2	CB	89	GLN
2	CB	92	VAL
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

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Mol	Chain	Res	Type
2	CB	123	ASP
2	CB	126	PHE
2	CB	130	THR
2	CB	133	GLU
2	CB	136	MET
2	CB	139	ARG
2	CB	140	GLU
2	CB	141	LEU
2	CB	142	GLU
2	CB	143	LYS
2	CB	144	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	196	VAL
2	CB	207	ILE
2	CB	210	VAL
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	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	94	ILE
3	CC	103	ILE

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Mol	Chain	Res	Type
3	CC	111	LEU
3	CC	119	SER
3	CC	121	THR
3	CC	128	VAL
3	CC	129	MET
3	CC	144	LEU
3	CC	147	LYS
3	CC	151	VAL
3	CC	153	VAL
3	CC	154	SER
3	CC	167	TRP
3	CC	175	LEU
3	CC	179	ARG
3	CC	190	HIS
3	CC	192	THR
3	CC	193	TYR
3	CC	200	VAL
4	CD	8	LYS
4	CD	9	LEU
4	CD	10	LYS
4	CD	28	ILE
4	CD	29	ASP
4	CD	31	LYS
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	86	THR
4	CD	116	GLN
4	CD	125	VAL
4	CD	128	ARG
4	CD	134	SER
4	CD	138	SER
4	CD	142	VAL

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Mol	Chain	Res	Type
4	CD	152	GLN
4	CD	155	VAL
4	CD	161	LEU
4	CD	163	GLU
4	CD	184	ARG
4	CD	189	SER
4	CD	191	LEU
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	24	THR
5	CE	26	LYS
5	CE	32	SER
5	CE	34	THR
5	CE	38	VAL
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	105	ILE
5	CE	112	ARG
5	CE	114	VAL
5	CE	115	LEU
5	CE	117	VAL
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
6	CF	1	MET
6	CF	7	VAL

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Mol	Chain	Res	Type
6	CF	8	PHE
6	CF	9	MET
6	CF	10	VAL
6	CF	15	SER
6	CF	18	VAL
6	CF	23	GLU
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
6	CF	54	LEU
6	CF	55	HIS
6	CF	63	ASN
6	CF	69	GLU
6	CF	71	ILE
6	CF	73	GLU
6	CF	75	GLU
6	CF	85	ILE
6	CF	86	ARG
6	CF	87	SER
6	CF	94	HIS
6	CF	97	THR
7	CG	5	ARG
7	CG	6	VAL
7	CG	7	ILE
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

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Mol	Chain	Res	Type
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
7	CG	129	GLU
7	CG	133	THR
7	CG	135	VAL
7	CG	136	LYS
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	36	ILE
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	75	ILE
8	CH	77	ARG
8	CH	80	ARG
8	CH	83	LEU
8	CH	87	LYS
8	CH	94	LYS
8	CH	101	ILE
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

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Mol	Chain	Res	Type
9	CI	28	ILE
9	CI	32	GLN
9	CI	36	GLU
9	CI	41	ARG
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
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	105	THR
9	CI	112	GLU
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	51	VAL
10	CJ	59	LYS
10	CJ	60	ASP
10	CJ	63	ASP
10	CJ	64	GLN
10	CJ	66	GLU
10	CJ	73	LEU

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Mol	Chain	Res	Type
10	CJ	77	VAL
10	CJ	80	THR
10	CJ	83	THR
10	CJ	84	VAL
10	CJ	87	LEU
10	CJ	89	ARG
10	CJ	92	LEU
10	CJ	96	VAL
11	CK	13	ARG
11	CK	14	LYS
11	CK	15	GLN
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	74	VAL
11	CK	76	GLU
11	CK	81	ASN
11	CK	82	LEU
11	CK	83	GLU
11	CK	86	VAL
11	CK	96	THR
11	CK	97	ILE
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	127	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

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Mol	Chain	Res	Type
12	CL	33	VAL
12	CL	44	LYS
12	CL	52	VAL
12	CL	58	THR
12	CL	59	ASN
12	CL	63	VAL
12	CL	78	SER
12	CL	82	ILE
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
13	CM	34	LEU
13	CM	41	GLU
13	CM	48	LEU
13	CM	53	ILE
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

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Mol	Chain	Res	Type
14	CN	35	ASN
14	CN	48	LEU
14	CN	53	ARG
14	CN	60	GLN
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	35	GLN
15	CO	39	LEU
15	CO	54	ARG
15	CO	62	GLN
15	CO	66	LEU
15	CO	67	LEU
15	CO	70	LEU
15	CO	73	LYS
15	CO	79	THR
15	CO	85	LEU
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	36	VAL
16	CP	46	LYS
16	CP	63	GLN
16	CP	66	THR
16	CP	69	ASP
16	CP	74	LEU
16	CP	77	GLU
16	CP	80	LYS

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Mol	Chain	Res	Type
17	CQ	5	ILE
17	CQ	11	ARG
17	CQ	14	SER
17	CQ	17	MET
17	CQ	18	GLU
17	CQ	22	VAL
17	CQ	23	VAL
17	CQ	25	ILE
17	CQ	29	VAL
17	CQ	38	ILE
17	CQ	40	ARG
17	CQ	48	ASP
17	CQ	52	GLU
17	CQ	55	ILE
17	CQ	60	GLU
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
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	7	LYS
19	CS	11	ILE
19	CS	13	LEU
19	CS	14	HIS
19	CS	16	LEU
19	CS	19	VAL
19	CS	23	VAL
19	CS	27	ASP
19	CS	28	LYS
19	CS	29	LYS

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Mol	Chain	Res	Type
19	CS	33	THR
19	CS	39	THR
19	CS	49	ILE
19	CS	56	GLN
19	CS	65	GLU
19	CS	66	MET
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	23	SER
20	CT	24	ARG
20	CT	27	MET
20	CT	36	TYR
20	CT	49	LYS
20	CT	58	VAL
20	CT	64	LYS
20	CT	67	ILE
20	CT	69	LYS
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	14	VAL
21	CU	16	LEU
21	CU	17	ARG
21	CU	20	LYS
21	CU	25	LYS
21	CU	34	ARG
21	CU	37	PHE
21	CU	43	THR
21	CU	47	ARG
24	DC	3	VAL
24	DC	10	SER
24	DC	14	ARG

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Mol	Chain	Res	Type
24	DC	20	VAL
24	DC	48	ARG
24	DC	52	ARG
24	DC	54	ILE
24	DC	59	LYS
24	DC	64	ILE
24	DC	80	ARG
24	DC	88	SER
24	DC	94	VAL
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	116	ILE
24	DC	120	VAL
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	192	LEU
24	DC	195	VAL
24	DC	202	LEU
24	DC	205	LEU
24	DC	216	VAL
24	DC	236	GLU
24	DC	250	VAL
24	DC	256	LYS
24	DC	259	SER
24	DC	262	ARG
24	DC	267	ILE
25	DD	4	LEU
25	DD	12	THR
25	DD	28	GLU
25	DD	33	ARG

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Mol	Chain	Res	Type
25	DD	39	ASP
25	DD	55	LYS
25	DD	73	VAL
25	DD	84	LEU
25	DD	86	GLU
25	DD	91	THR
25	DD	100	LEU
25	DD	104	VAL
25	DD	131	ASP
25	DD	142	VAL
25	DD	146	ILE
25	DD	150	GLN
25	DD	168	GLU
25	DD	170	VAL
25	DD	172	VAL
25	DD	175	LEU
25	DD	189	VAL
25	DD	203	VAL
26	DE	6	LYS
26	DE	10	SER
26	DE	22	ASP
26	DE	25	GLU
26	DE	32	VAL
26	DE	33	VAL
26	DE	41	GLN
26	DE	63	LYS
26	DE	65	THR
26	DE	69	ARG
26	DE	74	LYS
26	DE	77	ILE
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	113	VAL
26	DE	118	LEU
26	DE	120	VAL
26	DE	125	SER
26	DE	127	GLU
26	DE	131	THR

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Mol	Chain	Res	Type
26	DE	133	LEU
26	DE	149	ILE
26	DE	159	LEU
26	DE	163	ASN
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	189	THR
26	DE	196	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	25	VAL
27	DF	26	MET
27	DF	28	VAL
27	DF	31	VAL
27	DF	32	GLU
27	DF	35	THR
27	DF	36	LEU
27	DF	42	GLU
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	92	ARG
27	DF	95	ARG
27	DF	106	ILE
27	DF	125	ARG
27	DF	133	ARG
27	DF	136	ILE
27	DF	147	ASP
27	DF	149	VAL
27	DF	150	ARG

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Mol	Chain	Res	Type
27	DF	157	THR
27	DF	159	THR
27	DF	162	SER
27	DF	174	ASP
27	DF	178	ARG
28	DG	11	VAL
28	DG	29	LYS
28	DG	30	ASN
28	DG	34	THR
28	DG	44	LYS
28	DG	89	LEU
28	DG	95	ARG
28	DG	113	VAL
28	DG	117	LEU
28	DG	127	THR
28	DG	129	THR
28	DG	141	ILE
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	53	GLU
29	DH	54	LEU
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	103	VAL
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

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Mol	Chain	Res	Type
29	DH	125	THR
29	DH	142	VAL
29	DH	146	VAL
29	DH	149	GLU
30	DI	3	LYS
30	DI	4	LYS
30	DI	8	TYR
30	DI	11	LEU
30	DI	12	GLN
30	DI	17	MET
30	DI	24	VAL
30	DI	28	LEU
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	86	ILE
30	DI	87	LYS
30	DI	95	LYS
30	DI	96	ASP
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	11	VAL
31	DJ	17	VAL
31	DJ	30	THR
31	DJ	39	LYS
31	DJ	40	HIS
31	DJ	43	GLU
31	DJ	64	VAL
31	DJ	73	VAL
31	DJ	81	ILE
31	DJ	86	GLN
31	DJ	90	GLU

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Mol	Chain	Res	Type
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
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	110	GLU
32	DK	118	LEU
32	DK	121	GLU
32	DK	122	VAL
33	DL	12	SER
33	DL	27	LEU
33	DL	29	LYS
33	DL	42	SER
33	DL	47	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	95	LEU
33	DL	99	ASN
33	DL	100	ILE
33	DL	103	ILE
33	DL	118	THR
33	DL	121	THR
33	DL	126	ARG
33	DL	143	GLU

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Mol	Chain	Res	Type
34	DM	14	LYS
34	DM	46	ILE
34	DM	57	VAL
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
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	47	VAL
36	DO	48	LEU
36	DO	61	GLN
36	DO	67	ASN
36	DO	74	VAL
36	DO	78	VAL
36	DO	89	ASP

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Mol	Chain	Res	Type
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	37	LYS
37	DP	51	ARG
37	DP	63	LYS
37	DP	64	ILE
37	DP	65	SER
37	DP	66	ASN
37	DP	80	VAL
37	DP	81	VAL
37	DP	85	SER
37	DP	93	ARG
37	DP	94	LYS
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
38	DQ	100	VAL
39	DR	7	SER

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Mol	Chain	Res	Type
39	DR	10	LYS
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	81	LYS
39	DR	86	GLN
39	DR	94	THR
39	DR	102	SER
40	DS	3	THR
40	DS	4	ILE
40	DS	13	SER
40	DS	19	LEU
40	DS	28	LYS
40	DS	39	THR
40	DS	41	LYS
40	DS	42	LYS
40	DS	47	VAL
40	DS	66	ILE
40	DS	67	ASP
40	DS	68	ASP
40	DS	69	LEU
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	2	ILE
41	DT	3	ARG
41	DT	7	LEU
41	DT	16	VAL
41	DT	18	GLU
41	DT	22	THR
41	DT	30	ILE

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Mol	Chain	Res	Type
41	DT	31	VAL
41	DT	49	LYS
41	DT	52	GLU
41	DT	70	HIS
41	DT	74	ILE
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	25	VAL
42	DU	27	ASN
42	DU	28	VAL
42	DU	29	LEU
42	DU	31	SER
42	DU	40	ASN
42	DU	41	LEU
42	DU	45	HIS
42	DU	46	GLN
42	DU	47	LYS
42	DU	49	VAL
42	DU	53	ASN
42	DU	54	GLN
42	DU	60	GLU
42	DU	67	VAL
42	DU	68	SER
42	DU	72	ILE
42	DU	81	ASP
42	DU	93	VAL
42	DU	99	ASN
43	DV	1	MET
43	DV	3	THR
43	DV	8	VAL
43	DV	29	ILE
43	DV	35	GLU
43	DV	40	ILE
43	DV	42	LEU
43	DV	45	ASP
43	DV	50	MET
43	DV	53	LYS
43	DV	55	GLU

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Mol	Chain	Res	Type
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	72	LYS
44	DW	77	ARG
45	DX	11	ARG
45	DX	14	THR
45	DX	18	ARG
45	DX	23	ASN
45	DX	25	THR
45	DX	33	LEU
45	DX	35	SER
45	DX	37	ARG
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	1	MET
46	DY	2	LYS
46	DY	6	LEU
46	DY	8	GLU
46	DY	13	GLU
46	DY	16	THR
46	DY	37	LEU
46	DY	39	GLN
46	DY	44	LYS
46	DY	55	THR
46	DY	56	LEU
46	DY	57	LEU
46	DY	58	ASN
47	DZ	3	LYS
47	DZ	11	ARG
47	DZ	16	ARG

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Mol	Chain	Res	Type
47	DZ	25	LEU
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	25	VAL
48	D0	28	LEU
48	D0	37	LYS
48	D0	46	ASP
48	D0	52	ARG
49	D1	5	ILE
49	D1	10	LYS
49	D1	12	VAL
49	D1	23	THR
49	D1	38	LYS
49	D1	43	VAL
49	D1	51	GLU
50	D2	4	THR
50	D2	10	LEU
50	D2	24	THR
50	D2	34	ARG
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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (101) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	89	GLN
4	AD	36	GLN

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Mol	Chain	Res	Type
4	AD	74	ASN
5	AE	43	ASN
5	AE	70	ASN
5	AE	77	ASN
5	AE	122	ASN
10	AJ	99	GLN
11	AK	40	ASN
13	AM	14	HIS
13	AM	91	HIS
14	AN	4	GLN
14	AN	35	ASN
14	AN	49	GLN
14	AN	66	GLN
20	AT	52	ASN
20	AT	55	GLN
20	AT	68	HIS
20	AT	78	ASN
20	AT	84	ASN
24	BC	163	GLN
24	BC	239	ASN
24	BC	251	GLN
25	BD	136	ASN
27	BF	37	ASN
29	BH	20	ASN
29	BH	28	ASN
29	BH	119	ASN
29	BH	135	HIS
32	BK	93	GLN
33	BL	93	ASN
33	BL	99	ASN
35	BN	31	HIS
35	BN	81	ASN
36	BO	19	GLN
36	BO	29	HIS
37	BP	66	ASN
38	BQ	52	GLN
39	BR	86	GLN
40	BS	15	GLN
40	BS	102	HIS
41	BT	70	HIS
43	BV	5	ASN
50	B2	26	ASN

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Mol	Chain	Res	Type
2	CB	42	ASN
2	CB	51	ASN
2	CB	89	GLN
2	CB	103	ASN
3	CC	176	HIS
4	CD	196	ASN
5	CE	89	HIS
6	CF	14	GLN
6	CF	37	HIS
7	CG	68	ASN
7	CG	130	ASN
7	CG	148	ASN
8	CH	18	GLN
10	CJ	58	ASN
10	CJ	70	HIS
11	CK	15	GLN
12	CL	59	ASN
14	CN	43	ASN
15	CO	46	HIS
16	CP	18	GLN
17	CQ	31	HIS
18	CR	52	GLN
19	CS	43	ASN
19	CS	52	HIS
20	CT	52	ASN
20	CT	84	ASN
24	DC	90	ASN
24	DC	251	GLN
26	DE	94	GLN
26	DE	163	ASN
27	DF	21	ASN
27	DF	23	ASN
27	DF	52	ASN
28	DG	143	GLN
29	DH	20	ASN
29	DH	128	HIS
30	DI	43	ASN
31	DJ	80	HIS
32	DK	93	GLN
33	DL	38	GLN
34	DM	13	HIS
36	DO	116	GLN

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Mol	Chain	Res	Type
37	DP	12	GLN
37	DP	56	HIS
37	DP	66	ASN
37	DP	115	ASN
39	DR	89	HIS
40	DS	15	GLN
41	DT	28	ASN
41	DT	59	ASN
42	DU	69	ASN
43	DV	24	ASN
44	DW	50	ASN
44	DW	57	HIS
44	DW	76	ASN
46	DY	45	GLN
51	D3	31	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1537/1539 (99%)	358 (23%)	16 (1%)
1	CA	1538/1539 (99%)	338 (21%)	9 (0%)
22	BA	2895/2903 (99%)	563 (19%)	28 (0%)
22	DA	2895/2903 (99%)	645 (22%)	34 (1%)
23	BB	118/119 (99%)	23 (19%)	0
23	DB	117/119 (98%)	25 (21%)	0
All	All	9100/9122 (99%)	1952 (21%)	87 (0%)

All (1952) 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

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Mol	Chain	Res	Type
1	AA	50	A
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	115	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

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Mol	Chain	Res	Type
1	AA	168	G
1	AA	181	A
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

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Mol	Chain	Res	Type
1	AA	398	U
1	AA	406	G
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

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Mol	Chain	Res	Type
1	AA	527	G
1	AA	530	G
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

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Mol	Chain	Res	Type
1	AA	817	C
1	AA	821	G
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

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Mol	Chain	Res	Type
1	AA	1009	U
1	AA	1017	U
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

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Mol	Chain	Res	Type
1	AA	1137	C
1	AA	1139	G
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

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Mol	Chain	Res	Type
1	AA	1302	C
1	AA	1303	C
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

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Mol	Chain	Res	Type
1	AA	1499	A
1	AA	1503	A
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

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Mol	Chain	Res	Type
22	BA	196	A
22	BA	208	C
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

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Mol	Chain	Res	Type
22	BA	411	G
22	BA	412	A
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

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Mol	Chain	Res	Type
22	BA	654	A
22	BA	655	A
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

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Mol	Chain	Res	Type
22	BA	878	A
22	BA	879	G
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

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Mol	Chain	Res	Type
22	BA	1092	C
22	BA	1098	A
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

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Mol	Chain	Res	Type
22	BA	1280	G
22	BA	1294	U
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

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Mol	Chain	Res	Type
22	BA	1482	G
22	BA	1483	G
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

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Mol	Chain	Res	Type
22	BA	1718	G
22	BA	1729	U
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

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Mol	Chain	Res	Type
22	BA	1929	G
22	BA	1930	G
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

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Mol	Chain	Res	Type
22	BA	2118	U
22	BA	2119	A
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

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Mol	Chain	Res	Type
22	BA	2239	G
22	BA	2243	U
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

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Mol	Chain	Res	Type
22	BA	2435	A
22	BA	2441	U
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

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Mol	Chain	Res	Type
22	BA	2762	C
22	BA	2765	A
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

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Mol	Chain	Res	Type
23	BB	51	G
23	BB	56	G
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

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Mol	Chain	Res	Type
1	CA	121	U
1	CA	122	G
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

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Mol	Chain	Res	Type
1	CA	328	C
1	CA	329	A
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

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Mol	Chain	Res	Type
1	CA	485	U
1	CA	486	U
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	560	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

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Mol	Chain	Res	Type
1	CA	723	U
1	CA	724	G
1	CA	731	G
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

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Mol	Chain	Res	Type
1	CA	975	A
1	CA	976	G
1	CA	977	A
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

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Mol	Chain	Res	Type
1	CA	1124	G
1	CA	1125	U
1	CA	1133	G
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

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Mol	Chain	Res	Type
1	CA	1286	U
1	CA	1287	A
1	CA	1292	G
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

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Mol	Chain	Res	Type
1	CA	1505	G
1	CA	1506	U
1	CA	1507	A
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

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Mol	Chain	Res	Type
22	DA	155	A
22	DA	158	U
22	DA	162	U
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

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Mol	Chain	Res	Type
22	DA	354	A
22	DA	361	G
22	DA	362	A
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

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Mol	Chain	Res	Type
22	DA	548	G
22	DA	549	G
22	DA	550	C
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	614	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

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Mol	Chain	Res	Type
22	DA	746	U
22	DA	747	U
22	DA	751	A
22	DA	752	A
22	DA	762	U
22	DA	764	A
22	DA	765	C
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

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Mol	Chain	Res	Type
22	DA	945	A
22	DA	946	C
22	DA	961	C
22	DA	974	G
22	DA	982	C
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

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Mol	Chain	Res	Type
22	DA	1098	A
22	DA	1100	C
22	DA	1104	C
22	DA	1110	G
22	DA	1111	A
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

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Mol	Chain	Res	Type
22	DA	1255	U
22	DA	1256	G
22	DA	1258	U
22	DA	1266	G
22	DA	1269	A
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

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Mol	Chain	Res	Type
22	DA	1453	A
22	DA	1455	G
22	DA	1456	G
22	DA	1458	U
22	DA	1460	U
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

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Mol	Chain	Res	Type
22	DA	1610	A
22	DA	1613	G
22	DA	1616	A
22	DA	1623	G
22	DA	1647	U
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

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Mol	Chain	Res	Type
22	DA	1869	G
22	DA	1870	C
22	DA	1871	A
22	DA	1874	C
22	DA	1880	U
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

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Mol	Chain	Res	Type
22	DA	2061	G
22	DA	2062	A
22	DA	2069	G
22	DA	2072	C
22	DA	2087	G
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

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Mol	Chain	Res	Type
22	DA	2171	A
22	DA	2172	U
22	DA	2173	A
22	DA	2177	C
22	DA	2178	C
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

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Mol	Chain	Res	Type
22	DA	2327	A
22	DA	2331	G
22	DA	2333	A
22	DA	2344	U
22	DA	2347	C
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

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Mol	Chain	Res	Type
22	DA	2525	G
22	DA	2529	G
22	DA	2534	A
22	DA	2535	G
22	DA	2547	A
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

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Mol	Chain	Res	Type
22	DA	2764	A
22	DA	2765	A
22	DA	2768	U
22	DA	2778	A
22	DA	2791	G
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

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Mol	Chain	Res	Type
23	DB	73	A
23	DB	88	C
23	DB	89	U
23	DB	90	C
23	DB	91	C
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

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Mol	Chain	Res	Type
22	BA	1378	A
22	BA	1434	A
22	BA	1494	A
22	BA	1606	C
22	BA	1610	A
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

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Mol	Chain	Res	Type
22	DA	1738	G
22	DA	2109	U
22	DA	2111	U
22	DA	2127	G
22	DA	2146	C
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	DBB	B6	3	54	4,5,6	1.54	1 (25%)	1,5,7	0.12	0
54	004	D6	7	54	9,10,11	0.56	0	9,12,14	1.08	1 (11%)
54	MHW	D6	1	54	9,9,10	1.75	2 (22%)	10,11,13	3.23	3 (30%)
54	MHU	B6	5	54	14,15,16	1.76	3 (21%)	18,19,21	1.58	4 (22%)
54	MHW	B6	1	54	9,9,10	1.63	1 (11%)	10,11,13	2.57	4 (40%)
54	MHV	B6	6	54	7,9,10	1.45	1 (14%)	8,11,13	3.40	3 (37%)
54	DBB	D6	3	54	4,5,6	1.19	0	1,5,7	0.73	0
54	MHU	D6	5	54	14,15,16	1.98	3 (21%)	18,19,21	2.14	2 (11%)
54	MHV	D6	6	54	7,9,10	0.93	0	8,11,13	3.59	3 (37%)
54	004	B6	7	54	9,10,11	1.59	1 (11%)	9,12,14	2.23	3 (33%)

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	DBB	B6	3	54	-	0/3/4/6	-
54	004	D6	7	54	-	0/4/6/8	0/1/1/1
54	MHW	D6	1	54	-	0/2/2/4	0/1/1/1
54	MHU	B6	5	54	-	0/9/12/14	0/1/1/1
54	MHW	B6	1	54	-	0/2/2/4	0/1/1/1
54	MHV	B6	6	54	-	0/1/12/14	0/1/1/1
54	DBB	D6	3	54	-	0/3/4/6	-
54	MHU	D6	5	54	-	0/9/12/14	0/1/1/1
54	MHV	D6	6	54	-	0/1/12/14	0/1/1/1
54	004	B6	7	54	-	0/4/6/8	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	D6	5	MHU	CZ-NZ	5.63	1.50	1.37
54	B6	5	MHU	CZ-NZ	5.10	1.49	1.37
54	B6	7	004	CB-CA	-4.48	1.48	1.52
54	D6	1	MHW	CA-C	4.12	1.53	1.48
54	B6	1	MHW	CA-C	3.61	1.52	1.48
54	B6	6	MHV	CB-CG	-3.08	1.45	1.50
54	D6	5	MHU	CB-CG	3.03	1.58	1.51
54	D6	5	MHU	CD2-CE2	2.65	1.43	1.38
54	B6	3	DBB	CB-CA	-2.48	1.46	1.53
54	B6	5	MHU	CD2-CE2	2.29	1.42	1.38
54	B6	5	MHU	CB-CG	2.05	1.56	1.51
54	D6	1	MHW	CG2-CB	2.01	1.43	1.39

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	D6	6	MHV	CD2-CE-N	-8.99	90.50	109.98
54	B6	6	MHV	CD2-CE-N	-8.20	92.22	109.98
54	D6	5	MHU	CG-CB-CA	8.03	124.94	113.51
54	D6	1	MHW	CD-CE-N	7.27	134.92	123.42
54	B6	1	MHW	CD-CE-N	5.16	131.58	123.42
54	D6	1	MHW	CG2-CD-CE	-5.10	111.55	118.92
54	B6	1	MHW	CG2-CD-CE	-4.46	112.47	118.92
54	D6	1	MHW	O-C-CA	-4.41	118.84	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	B6	7	004	CD1-CG1-CB	-3.92	115.96	120.65
54	B6	7	004	CE-CD2-CG2	-3.32	116.14	120.24
54	B6	1	MHW	CB-CA-C	-3.10	117.78	120.09
54	D6	7	004	CB-CA-C	-3.07	103.48	112.09
54	B6	5	MHU	CB-CA-N	3.03	114.94	110.48
54	B6	6	MHV	OD1-CG-CB	-3.03	117.81	121.95
54	B6	5	MHU	O-C-CA	-2.93	117.22	124.77
54	D6	6	MHV	CB-CA-N	-2.92	106.46	112.50
54	B6	5	MHU	CB-CA-C	-2.82	106.20	111.81
54	B6	6	MHV	CD2-CG-CB	2.81	120.15	115.89
54	B6	7	004	CG2-CB-CG1	2.50	121.40	118.30
54	D6	5	MHU	O-C-CA	-2.41	118.57	124.77
54	B6	5	MHU	CM-N-CA	2.30	120.58	113.70
54	D6	6	MHV	CD2-CG-CB	2.19	119.21	115.89
54	B6	1	MHW	O-C-CA	-2.17	121.65	124.37

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	D6	7	004	6	0
54	B6	5	MHU	1	0
54	D6	6	MHV	3	0

5.5 Carbohydrates (i)

There are no oligosaccharides 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, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AA	1538/1539 (99%)	0.13	62 (4%) 42 35	15, 50, 134, 177	0
1	CA	1539/1539 (100%)	0.66	147 (9%) 13 12	29, 70, 143, 176	0
2	AB	218/218 (100%)	0.87	21 (9%) 13 12	39, 71, 98, 131	0
2	CB	218/218 (100%)	1.53	57 (26%) 1 1	55, 80, 108, 126	0
3	AC	206/206 (100%)	0.48	11 (5%) 32 27	36, 56, 81, 95	0
3	CC	206/206 (100%)	0.98	18 (8%) 16 14	52, 73, 93, 114	0
4	AD	205/205 (100%)	1.03	35 (17%) 4 3	33, 55, 80, 109	0
4	CD	205/205 (100%)	0.53	17 (8%) 17 15	23, 40, 75, 93	0
5	AE	150/150 (100%)	0.70	12 (8%) 18 16	32, 49, 82, 111	0
5	CE	150/150 (100%)	0.89	20 (13%) 7 7	35, 56, 83, 105	0
6	AF	100/100 (100%)	0.83	10 (10%) 12 11	34, 55, 75, 85	0
6	CF	100/100 (100%)	0.85	9 (9%) 15 13	44, 72, 97, 105	0
7	AG	151/151 (100%)	1.40	30 (19%) 3 3	48, 73, 96, 107	0
7	CG	151/151 (100%)	1.98	69 (45%) 0 0	75, 92, 105, 113	0
8	AH	129/129 (100%)	0.31	3 (2%) 61 53	28, 47, 71, 80	0
8	CH	129/129 (100%)	0.95	12 (9%) 14 12	46, 63, 83, 90	0
9	AI	127/127 (100%)	1.24	26 (20%) 2 2	42, 68, 96, 115	0
9	CI	127/127 (100%)	2.15	64 (50%) 0 0	64, 87, 106, 131	0
10	AJ	98/98 (100%)	1.26	19 (19%) 3 3	42, 62, 93, 120	0
10	CJ	98/98 (100%)	2.14	44 (44%) 0 0	66, 89, 108, 122	0
11	AK	117/117 (100%)	1.08	14 (11%) 9 8	29, 61, 88, 106	0
11	CK	117/117 (100%)	0.48	3 (2%) 57 49	35, 63, 82, 90	0
12	AL	123/123 (100%)	0.58	10 (8%) 18 16	23, 36, 72, 102	0
12	CL	123/123 (100%)	0.93	14 (11%) 10 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%)	0.97	18 (15%) 5 4	43, 66, 91, 105	0
13	CM	114/114 (100%)	2.49	67 (58%) 0 0	80, 98, 113, 118	0
14	AN	96/100 (96%)	1.39	26 (27%) 1 1	39, 56, 93, 108	0
14	CN	96/100 (96%)	1.83	39 (40%) 0 0	60, 88, 106, 119	0
15	AO	88/88 (100%)	0.66	5 (5%) 29 24	31, 49, 66, 99	0
15	CO	88/88 (100%)	0.75	5 (5%) 29 24	42, 62, 84, 108	0
16	AP	82/82 (100%)	0.76	4 (4%) 35 29	35, 46, 80, 103	0
16	CP	82/82 (100%)	1.28	20 (24%) 2 2	43, 61, 87, 105	0
17	AQ	80/80 (100%)	0.92	11 (13%) 6 6	30, 55, 85, 123	0
17	CQ	80/80 (100%)	1.54	24 (30%) 1 1	42, 69, 97, 108	0
18	AR	55/55 (100%)	0.81	5 (9%) 15 13	38, 51, 76, 113	0
18	CR	55/55 (100%)	0.68	4 (7%) 21 18	40, 54, 83, 113	0
19	AS	79/79 (100%)	0.98	13 (16%) 4 4	45, 66, 92, 97	0
19	CS	79/79 (100%)	2.69	55 (69%) 0 0	79, 98, 113, 126	0
20	AT	85/85 (100%)	0.73	6 (7%) 22 19	35, 48, 74, 115	0
20	CT	85/85 (100%)	1.59	22 (25%) 1 1	52, 69, 91, 98	0
21	AU	51/51 (100%)	1.84	16 (31%) 1 1	49, 70, 92, 105	0
21	CU	51/51 (100%)	1.72	17 (33%) 1 1	43, 67, 92, 107	0
22	BA	2897/2903 (99%)	-0.33	153 (5%) 32 27	3, 18, 128, 196	0
22	DA	2897/2903 (99%)	1.03	286 (9%) 13 11	42, 82, 142, 182	0
23	BB	119/119 (100%)	-0.59	0 100 100	6, 26, 52, 94	0
23	DB	118/119 (99%)	0.94	9 (7%) 20 18	68, 109, 131, 143	0
24	BC	271/271 (100%)	0.01	6 (2%) 62 54	8, 24, 44, 65	0
24	DC	271/271 (100%)	1.43	74 (27%) 1 1	40, 60, 76, 84	0
25	BD	209/209 (100%)	-0.19	3 (1%) 73 67	4, 15, 42, 69	0
25	DD	209/209 (100%)	1.41	49 (23%) 2 2	47, 64, 83, 99	0
26	BE	201/201 (100%)	-0.01	3 (1%) 72 65	4, 27, 54, 95	0
26	DE	201/201 (100%)	1.81	73 (36%) 1 1	38, 76, 96, 108	0
27	BF	177/177 (100%)	0.53	17 (9%) 13 12	23, 44, 86, 104	0
27	DF	177/177 (100%)	1.83	65 (36%) 1 1	79, 97, 113, 125	0
28	BG	176/176 (100%)	0.44	10 (5%) 29 24	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%)	1.65	50 (28%) 1 1	66, 85, 103, 117	0
29	BH	149/149 (100%)	3.08	115 (77%) 0 0	25, 102, 121, 129	0
29	DH	149/149 (100%)	2.31	73 (48%) 0 0	25, 92, 107, 115	0
30	BI	141/141 (100%)	2.36	78 (55%) 0 0	80, 104, 120, 136	0
30	DI	141/141 (100%)	2.91	98 (69%) 0 0	91, 110, 121, 124	0
31	BJ	142/142 (100%)	-0.19	4 (2%) 55 47	5, 12, 32, 54	0
31	DJ	142/142 (100%)	1.32	30 (21%) 2 2	49, 64, 80, 96	0
32	BK	122/122 (100%)	-0.23	3 (2%) 58 50	7, 16, 40, 68	0
32	DK	122/122 (100%)	1.01	13 (10%) 11 10	47, 60, 81, 95	0
33	BL	143/143 (100%)	0.21	3 (2%) 63 55	4, 26, 49, 80	0
33	DL	143/143 (100%)	2.01	67 (46%) 0 0	45, 72, 90, 111	0
34	BM	136/136 (100%)	-0.28	1 (0%) 84 80	6, 16, 34, 93	0
34	DM	136/136 (100%)	1.11	23 (16%) 4 4	40, 64, 82, 110	0
35	BN	120/120 (100%)	-0.27	1 (0%) 82 78	7, 13, 25, 70	0
35	DN	120/120 (100%)	2.04	55 (45%) 0 0	50, 71, 88, 109	0
36	BO	116/116 (100%)	0.09	2 (1%) 69 62	18, 29, 52, 59	0
36	DO	116/116 (100%)	1.69	34 (29%) 1 1	64, 86, 100, 113	0
37	BP	114/114 (100%)	-0.04	3 (2%) 57 49	10, 22, 49, 73	0
37	DP	114/114 (100%)	1.37	27 (23%) 2 2	51, 66, 84, 91	0
38	BQ	117/117 (100%)	-0.37	1 (0%) 81 76	3, 8, 21, 57	0
38	DQ	117/117 (100%)	1.75	47 (40%) 0 0	46, 65, 79, 83	0
39	BR	103/103 (100%)	-0.13	3 (2%) 53 46	4, 15, 37, 64	0
39	DR	103/103 (100%)	1.89	40 (38%) 1 0	49, 72, 86, 96	0
40	BS	110/110 (100%)	-0.40	2 (1%) 67 59	4, 9, 27, 89	0
40	DS	110/110 (100%)	1.82	39 (35%) 1 1	53, 69, 89, 97	0
41	BT	93/93 (100%)	0.37	7 (7%) 20 18	15, 28, 83, 100	0
41	DT	93/93 (100%)	2.31	53 (56%) 0 0	60, 79, 102, 110	0
42	BU	102/102 (100%)	0.23	1 (0%) 79 74	15, 32, 62, 95	0
42	DU	102/102 (100%)	2.63	66 (64%) 0 0	61, 82, 103, 109	0
43	BV	94/94 (100%)	-0.15	1 (1%) 78 73	11, 24, 48, 59	0
43	DV	94/94 (100%)	1.08	11 (11%) 9 8	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%)	-0.02	3 (3%) 43 35	10, 17, 37, 56	0
44	DW	75/76 (98%)	1.53	15 (20%) 3 3	49, 75, 86, 107	0
45	BX	77/77 (100%)	0.28	3 (3%) 43 35	11, 28, 53, 81	0
45	DX	77/77 (100%)	1.51	20 (25%) 1 1	49, 66, 84, 89	0
46	BY	63/63 (100%)	0.65	7 (11%) 10 9	21, 42, 71, 93	0
46	DY	63/63 (100%)	2.07	27 (42%) 0 0	63, 86, 95, 104	0
47	BZ	58/58 (100%)	-0.17	0 100 100	7, 11, 34, 40	0
47	DZ	58/58 (100%)	1.44	12 (20%) 2 2	50, 69, 82, 89	0
48	B0	56/56 (100%)	-0.33	0 100 100	4, 14, 38, 77	0
48	D0	56/56 (100%)	1.94	23 (41%) 0 0	49, 69, 90, 106	0
49	B1	50/50 (100%)	0.28	2 (4%) 42 35	19, 33, 61, 95	0
49	D1	50/50 (100%)	1.58	17 (34%) 1 1	63, 79, 91, 103	0
50	B2	46/46 (100%)	-0.05	1 (2%) 62 54	8, 14, 22, 97	0
50	D2	46/46 (100%)	1.91	18 (39%) 1 0	47, 64, 78, 100	0
51	B3	64/64 (100%)	-0.07	0 100 100	10, 16, 26, 37	0
51	D3	64/64 (100%)	2.49	44 (68%) 0 0	53, 67, 79, 83	0
52	B4	38/38 (100%)	0.30	2 (5%) 32 27	13, 23, 38, 60	0
52	D4	38/38 (100%)	1.70	14 (36%) 1 1	56, 71, 84, 96	0
53	B5	191/228 (83%)	2.44	121 (63%) 0 0	71, 107, 119, 133	0
54	B6	2/8 (25%)	-0.27	0 100 100	6, 6, 6, 8	0
54	D6	2/8 (25%)	1.55	1 (50%) 0 0	41, 41, 41, 44	0
All	All	20738/20810 (99%)	0.76	3113 (15%) 5 5	3, 61, 117, 196	0

All (3113) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
29	BH	144	VAL	9.6
48	D0	27	SER	9.2
20	CT	4	ILE	8.4
10	AJ	102	LEU	8.2
4	CD	25	VAL	8.2
30	DI	53	LEU	8.2
7	CG	62	PHE	8.0
29	DH	144	VAL	8.0
22	BA	2190	G	7.9

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Mol	Chain	Res	Type	RSRZ
33	DL	92	LEU	7.9
22	BA	2135	A	7.8
22	BA	2100	G	7.8
29	DH	92	GLY	7.7
1	AA	1017	U	7.6
7	AG	147	ALA	7.6
22	BA	2184	A	7.6
50	B2	46	LYS	7.2
22	BA	1926	U	7.2
22	BA	2103	C	7.1
50	D2	46	LYS	7.1
22	BA	715	A	7.1
30	BI	53	LEU	7.1
19	CS	49	ILE	7.0
22	BA	2113	U	7.0
12	AL	25	GLU	6.9
1	AA	994	A	6.8
44	DW	44	LYS	6.8
29	BH	81	ALA	6.7
19	CS	74	PHE	6.7
22	BA	2112	G	6.7
21	AU	32	VAL	6.7
30	DI	11	LEU	6.6
11	CK	126	LYS	6.6
21	AU	38	TYR	6.6
29	BH	96	THR	6.5
30	DI	78	VAL	6.5
22	BA	2185	U	6.5
22	BA	2159	G	6.5
22	BA	2193	G	6.5
34	DM	56	ALA	6.5
30	DI	58	VAL	6.5
22	BA	2101	A	6.5
10	CJ	74	VAL	6.3
19	CS	34	TRP	6.3
22	BA	2104	C	6.3
22	BA	2098	U	6.3
22	BA	2189	U	6.3
30	DI	38	PHE	6.3
24	DC	27	GLY	6.2
22	BA	2099	U	6.2
22	BA	2102	G	6.2

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Mol	Chain	Res	Type	RSRZ
42	DU	13	VAL	6.1
1	AA	990	C	6.1
2	CB	151	ILE	6.1
14	AN	21	PHE	6.1
22	BA	2191	A	6.1
29	DH	90	LEU	6.1
29	DH	124	THR	6.1
25	DD	128	ARG	6.1
30	DI	70	VAL	6.1
30	DI	129	ILE	6.0
9	CI	54	LEU	5.9
33	DL	19	LEU	5.9
24	DC	251	GLN	5.9
22	BA	2144	G	5.9
7	AG	109	ARG	5.9
13	CM	86	TYR	5.9
29	DH	79	THR	5.9
7	AG	5	ARG	5.9
13	CM	101	ARG	5.9
41	BT	69	ARG	5.9
1	AA	1018	G	5.9
29	DH	125	THR	5.9
41	DT	34	VAL	5.9
41	DT	36	LYS	5.9
1	AA	1016	A	5.8
30	DI	3	LYS	5.8
8	AH	2	SER	5.8
46	DY	10	SER	5.8
21	CU	38	TYR	5.8
10	CJ	76	ILE	5.8
35	DN	2	ARG	5.8
22	BA	2136	G	5.8
22	BA	2158	A	5.8
9	AI	43	THR	5.7
53	B5	35	THR	5.7
22	BA	1921	G	5.7
30	DI	4	LYS	5.7
45	DX	11	ARG	5.7
30	DI	74	PRO	5.7
29	BH	120	GLY	5.7
12	CL	14	ARG	5.7
20	AT	68	HIS	5.7

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Mol	Chain	Res	Type	RSRZ
17	AQ	20	SER	5.7
4	AD	22	LYS	5.6
29	BH	119	ASN	5.6
33	DL	107	PHE	5.6
22	BA	2114	A	5.6
42	DU	58	ILE	5.6
49	D1	36	LEU	5.6
30	DI	2	ALA	5.6
22	BA	2160	C	5.6
29	DH	120	GLY	5.6
1	CA	994	A	5.5
29	BH	94	ILE	5.5
2	CB	132	LYS	5.5
35	DN	47	VAL	5.5
20	AT	4	ILE	5.5
19	CS	71	LEU	5.5
30	DI	54	PRO	5.5
2	AB	157	LEU	5.5
17	AQ	83	VAL	5.5
42	DU	39	ILE	5.5
50	D2	33	ARG	5.4
30	BI	79	LEU	5.4
29	BH	37	VAL	5.4
24	DC	254	GLY	5.4
19	CS	37	ARG	5.4
19	CS	76	PRO	5.4
22	BA	2156	G	5.4
42	DU	71	ALA	5.3
7	CG	12	ILE	5.3
30	DI	55	ILE	5.3
2	AB	155	GLY	5.3
30	DI	79	LEU	5.3
1	CA	1535	C	5.3
9	CI	129	LYS	5.3
29	BH	121	VAL	5.3
29	DH	142	VAL	5.3
22	BA	2140	G	5.3
1	AA	78	A	5.3
53	B5	94	TYR	5.3
35	DN	25	ALA	5.2
13	CM	89	LEU	5.2
30	DI	28	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
13	CM	96	PRO	5.2
22	BA	2192	U	5.2
29	DH	93	SER	5.2
29	BH	95	GLY	5.2
4	CD	152	GLN	5.2
13	CM	98	ARG	5.2
42	DU	26	LYS	5.2
1	AA	995	C	5.2
22	BA	1919	A	5.1
13	CM	109	ARG	5.1
42	DU	12	ILE	5.1
29	DH	82	SER	5.1
22	BA	716	A	5.1
2	CB	136	MET	5.1
1	AA	1534	A	5.1
29	BH	69	ALA	5.1
30	DI	14	ALA	5.1
9	CI	119	ARG	5.1
11	AK	126	LYS	5.1
22	BA	2175	C	5.1
29	BH	117	LEU	5.1
35	DN	102	PHE	5.1
26	DE	168	ASP	5.1
26	DE	42	GLY	5.0
33	DL	15	ALA	5.0
30	DI	75	PRO	5.0
30	BI	55	ILE	5.0
22	BA	2153	C	5.0
24	DC	242	LYS	5.0
1	AA	1019	A	5.0
29	DH	128	HIS	5.0
13	CM	80	LEU	5.0
26	DE	73	ILE	5.0
30	BI	11	LEU	5.0
22	DA	12	U	5.0
30	DI	68	THR	5.0
29	BH	38	PRO	5.0
29	BH	110	VAL	5.0
30	DI	13	VAL	5.0
13	CM	99	GLY	4.9
29	BH	123	ARG	4.9
12	CL	44	LYS	4.9

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Mol	Chain	Res	Type	RSRZ
29	BH	118	PRO	4.9
21	AU	28	VAL	4.9
30	DI	9	VAL	4.9
19	CS	69	HIS	4.9
29	BH	134	VAL	4.9
24	DC	49	ILE	4.9
52	D4	9	LYS	4.9
29	DH	99	ILE	4.8
30	DI	10	LYS	4.8
13	CM	87	ARG	4.8
30	BI	14	ALA	4.8
53	B5	216	THR	4.8
42	DU	31	SER	4.8
3	AC	37	PHE	4.8
9	CI	20	PHE	4.8
30	BI	67	PHE	4.8
51	D3	57	LEU	4.8
10	CJ	59	LYS	4.8
41	DT	43	ILE	4.8
22	BA	2186	G	4.8
30	BI	78	VAL	4.8
19	CS	3	ARG	4.8
26	DE	88	ARG	4.8
7	CG	151	PHE	4.8
29	DH	12	LEU	4.7
8	CH	3	MET	4.7
28	DG	6	LYS	4.7
29	BH	99	ILE	4.7
2	CB	213	TYR	4.7
31	DJ	1	MET	4.7
35	DN	97	ILE	4.7
10	AJ	75	ASP	4.7
41	DT	76	ARG	4.7
20	CT	68	HIS	4.7
1	CA	1536	C	4.7
22	BA	1918	A	4.7
26	DE	158	PHE	4.7
22	BA	2145	C	4.7
42	DU	20	GLY	4.7
22	DA	2172	U	4.7
42	DU	67	VAL	4.7
53	B5	28	ARG	4.7

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Mol	Chain	Res	Type	RSRZ
12	CL	124	ALA	4.7
29	DH	88	GLY	4.7
53	B5	76	LEU	4.7
36	DO	2	ASP	4.7
6	CF	54	LEU	4.7
9	CI	44	ALA	4.7
25	DD	31	ALA	4.7
29	BH	11	ASN	4.7
30	BI	115	ALA	4.7
35	DN	43	GLU	4.7
53	B5	166	ASN	4.7
53	B5	202	PRO	4.7
29	BH	78	VAL	4.7
29	BH	124	THR	4.6
53	B5	218	THR	4.6
14	CN	2	ALA	4.6
53	B5	50	ILE	4.6
22	BA	2157	G	4.6
1	AA	121	U	4.6
29	DH	100	ALA	4.6
30	DI	15	ALA	4.6
33	DL	34	GLY	4.6
42	DU	80	ALA	4.6
3	CC	162	ILE	4.6
29	BH	113	SER	4.6
30	DI	109	ILE	4.6
12	CL	15	LYS	4.6
22	BA	549	G	4.6
22	BA	2885	G	4.6
40	DS	46	LEU	4.6
4	AD	28	ILE	4.6
29	BH	56	ALA	4.6
44	DW	41	ARG	4.6
12	AL	15	LYS	4.6
38	DQ	16	LYS	4.6
30	DI	69	PHE	4.5
9	CI	43	THR	4.5
13	CM	93	ARG	4.5
29	BH	52	ALA	4.5
30	BI	52	GLY	4.5
9	CI	100	LYS	4.5
22	BA	1925	C	4.5

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Mol	Chain	Res	Type	RSRZ
29	DH	78	VAL	4.5
22	DA	75	G	4.5
31	DJ	119	PHE	4.5
13	CM	69	LEU	4.5
13	CM	106	ALA	4.5
30	BI	27	ALA	4.5
4	AD	152	GLN	4.5
22	BA	2174	C	4.5
6	AF	92	THR	4.5
17	AQ	5	ILE	4.5
30	BI	15	ALA	4.5
37	DP	95	ALA	4.5
36	DO	16	ARG	4.5
30	DI	35	ILE	4.5
30	DI	82	LYS	4.5
38	DQ	22	LYS	4.5
22	BA	2152	G	4.5
2	CB	129	LEU	4.5
40	DS	73	LYS	4.4
42	DU	70	VAL	4.4
1	CA	4	U	4.4
14	AN	27	LEU	4.4
22	BA	2155	U	4.4
29	BH	5	LEU	4.4
33	DL	61	LEU	4.4
17	AQ	6	ARG	4.4
36	DO	58	ILE	4.4
19	CS	33	THR	4.4
30	DI	7	ALA	4.4
38	DQ	11	ARG	4.4
41	DT	73	ARG	4.4
50	D2	42	LEU	4.4
1	AA	993	G	4.4
22	BA	2125	G	4.4
22	BA	2168	G	4.4
38	DQ	8	VAL	4.4
33	DL	27	LEU	4.4
41	DT	11	LEU	4.4
1	CA	1320	C	4.4
29	DH	83	LYS	4.4
51	D3	61	CYS	4.4
9	AI	17	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
19	CS	35	SER	4.4
29	DH	95	GLY	4.4
30	DI	17	MET	4.4
13	CM	83	LEU	4.4
52	D4	10	LEU	4.4
51	D3	14	PHE	4.4
1	AA	1535	C	4.4
22	BA	885	C	4.4
30	BI	75	PRO	4.4
45	DX	49	LEU	4.3
30	BI	86	ILE	4.3
29	DH	84	ALA	4.3
40	DS	37	THR	4.3
4	AD	36	GLN	4.3
22	BA	2141	G	4.3
22	DA	1537	G	4.3
13	CM	27	LYS	4.3
41	DT	60	THR	4.3
13	CM	45	ILE	4.3
2	AB	156	GLY	4.3
4	CD	24	GLY	4.3
7	CG	5	ARG	4.3
9	AI	129	LYS	4.3
22	BA	1922	G	4.3
26	DE	153	LEU	4.3
30	DI	118	THR	4.3
9	CI	21	ILE	4.3
7	AG	88	PRO	4.3
26	DE	67	ARG	4.3
29	BH	49	ALA	4.3
53	B5	124	VAL	4.3
2	CB	150	GLY	4.3
29	BH	122	LEU	4.3
12	CL	25	GLU	4.3
22	DA	1808	A	4.2
35	DN	1	MET	4.2
6	CF	91	ARG	4.2
29	BH	147	VAL	4.2
38	DQ	15	LYS	4.2
41	DT	10	VAL	4.2
9	CI	39	PHE	4.2
13	CM	85	CYS	4.2

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Mol	Chain	Res	Type	RSRZ
1	AA	991	U	4.2
22	BA	2585	U	4.2
9	CI	90	TYR	4.2
5	CE	157	ARG	4.2
21	CU	47	ARG	4.2
40	DS	95	ARG	4.2
21	AU	14	VAL	4.2
7	CG	150	ALA	4.2
30	BI	16	GLY	4.2
30	DI	59	ILE	4.2
1	CA	121	U	4.2
21	CU	35	ARG	4.2
29	BH	115	VAL	4.2
45	DX	50	ARG	4.2
10	CJ	52	LEU	4.2
13	CM	97	VAL	4.2
22	BA	2142	A	4.2
27	DF	66	LEU	4.2
41	DT	57	VAL	4.2
42	DU	65	ILE	4.2
40	DS	41	LYS	4.1
20	AT	36	TYR	4.1
22	BA	2188	U	4.1
27	DF	156	ILE	4.1
2	CB	32	PHE	4.1
27	DF	100	PHE	4.1
5	CE	93	ARG	4.1
1	AA	1538	C	4.1
7	AG	69	VAL	4.1
42	DU	30	SER	4.1
22	BA	1847	A	4.1
30	BI	38	PHE	4.1
28	DG	153	ARG	4.1
42	DU	77	THR	4.1
42	DU	14	LEU	4.1
1	CA	1033	G	4.1
53	B5	38	PHE	4.1
29	BH	68	ARG	4.1
33	DL	81	ASP	4.1
48	D0	39	LEU	4.1
30	DI	5	VAL	4.1
40	DS	80	PRO	4.1

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Mol	Chain	Res	Type	RSRZ
13	CM	77	ILE	4.1
28	DG	26	ILE	4.1
22	BA	2182	U	4.1
42	DU	82	ARG	4.1
42	DU	85	PHE	4.1
41	DT	32	LEU	4.0
41	DT	93	LEU	4.0
46	DY	19	LEU	4.0
22	BA	2147	A	4.0
53	B5	120	VAL	4.0
24	DC	106	ALA	4.0
40	DS	40	ASN	4.0
53	B5	97	GLY	4.0
18	CR	20	GLU	4.0
28	BG	166	ASP	4.0
21	AU	35	ARG	4.0
7	CG	23	LEU	4.0
30	DI	80	LEU	4.0
38	DQ	59	GLN	4.0
1	CA	1539	C	4.0
29	BH	3	VAL	4.0
29	BH	79	THR	4.0
42	DU	47	LYS	4.0
53	B5	77	ALA	4.0
13	AM	4	ILE	4.0
21	CU	45	ARG	4.0
12	AL	38	TYR	4.0
36	DO	48	LEU	4.0
9	CI	114	LYS	4.0
13	CM	31	LYS	4.0
27	BF	69	LYS	4.0
29	BH	71	LYS	4.0
29	DH	121	VAL	4.0
33	DL	89	VAL	4.0
41	BT	70	HIS	4.0
45	DX	20	HIS	4.0
7	CG	61	ALA	4.0
4	CD	28	ILE	4.0
22	BA	2143	C	4.0
3	CC	193	TYR	4.0
7	CG	66	LEU	4.0
35	DN	44	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
1	CA	1032	G	4.0
8	CH	2	SER	4.0
7	AG	73	VAL	4.0
25	DD	75	ALA	3.9
36	DO	40	ILE	3.9
43	DV	43	ASP	3.9
51	D3	28	ASN	3.9
29	DH	62	LEU	3.9
38	DQ	14	HIS	3.9
29	BH	80	ILE	3.9
29	BH	143	ILE	3.9
33	DL	71	ALA	3.9
41	DT	2	ILE	3.9
42	DU	103	ILE	3.9
53	B5	100	ILE	3.9
1	AA	1020	G	3.9
22	BA	1923	U	3.9
22	DA	2690	U	3.9
28	DG	52	PHE	3.9
29	BH	90	LEU	3.9
30	BI	80	LEU	3.9
53	B5	132	LEU	3.9
27	DF	8	TYR	3.9
40	DS	38	TYR	3.9
30	DI	98	VAL	3.9
48	D0	3	VAL	3.9
29	BH	93	SER	3.9
1	AA	412	A	3.9
26	DE	162	ARG	3.9
53	B5	211	ARG	3.9
1	CA	1307	U	3.9
1	CA	94	G	3.9
14	CN	3	LYS	3.9
19	CS	15	LEU	3.9
26	DE	164	LEU	3.9
35	DN	28	LEU	3.9
28	DG	157	TYR	3.9
31	DJ	74	TYR	3.9
9	CI	128	SER	3.9
19	CS	55	ARG	3.9
19	CS	70	LYS	3.9
36	DO	4	LYS	3.9

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Mol	Chain	Res	Type	RSRZ
28	DG	9	VAL	3.9
29	BH	108	VAL	3.9
33	DL	116	VAL	3.9
22	BA	2115	G	3.9
9	AI	123	ARG	3.9
29	DH	102	ALA	3.9
51	D3	37	ALA	3.9
38	DQ	29	SER	3.9
24	DC	18	LYS	3.8
24	DC	26	LYS	3.8
35	DN	26	GLY	3.8
9	CI	112	GLU	3.8
14	AN	45	VAL	3.8
51	D3	58	VAL	3.8
24	DC	112	ALA	3.8
53	B5	36	ALA	3.8
53	B5	87	ALA	3.8
22	BA	2124	G	3.8
22	BA	2127	G	3.8
49	B1	53	LYS	3.8
1	AA	989	U	3.8
1	CA	1219	A	3.8
22	BA	2097	A	3.8
22	DA	2149	U	3.8
38	DQ	13	ARG	3.8
2	CB	34	ALA	3.8
29	BH	67	ALA	3.8
25	DD	157	LYS	3.8
29	BH	54	LEU	3.8
33	DL	106	GLU	3.8
1	CA	1002	G	3.8
22	BA	2178	C	3.8
29	BH	146	VAL	3.8
22	BA	2154	A	3.8
8	CH	22	LYS	3.8
51	D3	52	LYS	3.8
30	DI	133	ALA	3.8
46	DY	22	LEU	3.8
16	CP	3	THR	3.8
30	BI	118	THR	3.8
30	DI	60	THR	3.8
39	DR	50	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
53	B5	208	THR	3.8
18	AR	20	GLU	3.8
4	CD	73	ARG	3.8
1	CA	987	G	3.8
9	CI	68	LYS	3.8
25	DD	154	LYS	3.8
40	DS	83	LYS	3.8
41	DT	68	LYS	3.8
14	CN	20	TYR	3.8
19	CS	5	LEU	3.8
22	BA	2176	A	3.8
3	CC	192	THR	3.8
29	BH	91	PHE	3.8
9	CI	124	ARG	3.7
29	BH	130	VAL	3.7
39	DR	85	LYS	3.7
45	BX	20	HIS	3.7
9	CI	38	TYR	3.7
15	AO	57	LEU	3.7
22	BA	1072	C	3.7
22	BA	2130	U	3.7
24	DC	239	ASN	3.7
25	DD	135	GLY	3.7
29	BH	107	GLY	3.7
22	BA	2169	A	3.7
29	BH	97	ARG	3.7
7	CG	141	VAL	3.7
13	CM	16	VAL	3.7
40	DS	20	VAL	3.7
27	DF	67	ILE	3.7
35	DN	113	ILE	3.7
20	CT	63	ALA	3.7
26	DE	128	ALA	3.7
27	DF	83	TYR	3.7
30	BI	8	TYR	3.7
38	DQ	25	TYR	3.7
2	CB	155	GLY	3.7
22	BA	2096	C	3.7
17	AQ	70	THR	3.7
29	BH	77	THR	3.7
22	BA	2123	G	3.7
31	DJ	37	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
26	DE	132	LYS	3.7
45	BX	77	LYS	3.7
2	CB	67	ILE	3.7
29	BH	4	ILE	3.7
29	BH	44	ILE	3.7
42	DU	5	ILE	3.7
53	B5	44	VAL	3.7
46	DY	40	SER	3.7
21	AU	16	LEU	3.7
21	CU	16	LEU	3.7
27	DF	117	LEU	3.7
36	BO	50	ALA	3.7
46	DY	56	LEU	3.7
29	BH	7	ASP	3.7
53	B5	21	TYR	3.7
1	CA	1321	U	3.7
9	CI	130	ARG	3.7
18	AR	73	ARG	3.7
31	BJ	96	ARG	3.7
31	BJ	111	LYS	3.7
49	D1	53	LYS	3.7
22	BA	1920	C	3.7
29	BH	19	VAL	3.7
40	DS	45	VAL	3.7
41	BT	2	ILE	3.7
1	AA	987	G	3.7
1	AA	988	G	3.7
7	CG	2	PRO	3.7
30	BI	54	PRO	3.7
9	CI	98	LEU	3.7
29	BH	36	ALA	3.7
24	DC	12	GLY	3.7
40	DS	99	ARG	3.7
22	DA	2155	U	3.7
26	DE	131	THR	3.7
27	DF	79	ILE	3.7
29	DH	94	ILE	3.7
36	DO	28	VAL	3.7
22	DA	1278	C	3.6
29	DH	118	PRO	3.6
1	AA	1021	A	3.6
22	BA	2183	A	3.6

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Mol	Chain	Res	Type	RSRZ
1	CA	1305	G	3.6
4	AD	29	ASP	3.6
6	AF	91	ARG	3.6
9	CI	60	LYS	3.6
30	DI	62	TYR	3.6
21	CU	53	VAL	3.6
7	CG	72	THR	3.6
3	AC	175	LEU	3.6
9	AI	44	ALA	3.6
49	D1	52	ALA	3.6
22	DA	336	C	3.6
22	BA	654	A	3.6
30	DI	81	LYS	3.6
40	DS	84	ARG	3.6
41	DT	33	LYS	3.6
46	DY	47	ARG	3.6
29	DH	132	PHE	3.6
7	CG	6	VAL	3.6
22	DA	805	G	3.6
29	BH	138	VAL	3.6
30	BI	5	VAL	3.6
32	DK	35	VAL	3.6
41	DT	55	VAL	3.6
8	CH	55	THR	3.6
53	B5	62	THR	3.6
10	CJ	102	LEU	3.6
22	BA	2111	U	3.6
22	BA	2402	U	3.6
48	D0	2	ALA	3.6
38	DQ	41	LYS	3.6
39	DR	71	LYS	3.6
13	CM	84	GLY	3.6
33	DL	49	GLY	3.6
22	DA	1205	A	3.6
51	D3	32	ILE	3.6
10	AJ	74	VAL	3.6
19	CS	58	VAL	3.6
39	DR	72	VAL	3.6
3	AC	168	TYR	3.6
26	DE	53	THR	3.6
35	DN	10	LEU	3.6
1	CA	1537	U	3.6

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Mol	Chain	Res	Type	RSRZ
22	BA	1093	G	3.6
19	CS	75	ALA	3.6
26	DE	36	ALA	3.6
29	BH	39	ALA	3.6
30	BI	63	ALA	3.6
48	D0	57	LYS	3.6
51	D3	15	LYS	3.6
19	CS	38	SER	3.6
30	DI	67	PHE	3.6
19	CS	51	VAL	3.6
33	BL	115	GLU	3.6
7	CG	13	LEU	3.6
30	BI	23	PRO	3.6
7	CG	152	ALA	3.5
10	CJ	9	ARG	3.5
27	DF	30	ARG	3.5
36	DO	9	ARG	3.5
22	BA	2148	G	3.5
29	BH	88	GLY	3.5
42	DU	78	GLY	3.5
28	DG	76	VAL	3.5
29	BH	12	LEU	3.5
42	DU	48	PRO	3.5
49	D1	10	LYS	3.5
1	AA	1014	A	3.5
1	AA	1536	C	3.5
1	CA	999	C	3.5
14	CN	59	ARG	3.5
28	DG	136	ALA	3.5
39	DR	103	ALA	3.5
22	BA	2139	U	3.5
13	CM	7	ILE	3.5
33	DL	20	GLY	3.5
48	D0	55	ILE	3.5
52	D4	23	ILE	3.5
13	AM	97	VAL	3.5
30	DI	140	VAL	3.5
53	B5	95	VAL	3.5
53	B5	126	SER	3.5
37	DP	9	GLU	3.5
20	CT	79	LEU	3.5
36	DO	17	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
29	DH	66	ASN	3.5
30	BI	68	THR	3.5
46	BY	23	ARG	3.5
29	DH	148	ALA	3.5
30	BI	2	ALA	3.5
30	DI	120	ALA	3.5
48	D0	5	GLN	3.5
1	CA	1236	A	3.5
22	DA	1092	C	3.5
30	DI	122	ILE	3.5
42	DU	87	PHE	3.5
14	CN	11	VAL	3.5
28	BG	15	VAL	3.5
30	BI	24	VAL	3.5
19	CS	44	MET	3.5
21	AU	24	GLU	3.5
29	DH	149	GLU	3.5
37	DP	102	GLU	3.5
2	CB	148	LEU	3.5
10	CJ	42	LEU	3.5
29	BH	89	LYS	3.5
37	DP	111	LYS	3.5
51	D3	39	LYS	3.5
51	D3	41	LYS	3.5
19	CS	12	ASP	3.5
26	BE	7	ASP	3.5
42	DU	55	PRO	3.5
3	CC	168	TYR	3.5
41	DT	6	ARG	3.5
22	DA	2152	G	3.5
36	DO	6	ALA	3.5
24	DC	240	PHE	3.5
26	DE	85	PHE	3.5
53	B5	111	PHE	3.5
1	CA	1538	C	3.5
33	DL	53	GLY	3.5
26	DE	186	VAL	3.5
32	BK	35	VAL	3.5
41	DT	63	VAL	3.5
42	DU	36	VAL	3.5
22	BA	2149	U	3.5
22	DA	2585	U	3.5

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Mol	Chain	Res	Type	RSRZ
9	CI	13	LYS	3.5
24	DC	28	LYS	3.5
26	DE	143	LEU	3.5
41	DT	81	LYS	3.5
50	D2	2	LYS	3.5
13	CM	113	ARG	3.5
26	DE	61	ARG	3.5
39	DR	80	ARG	3.5
39	DR	32	THR	3.5
29	BH	111	ALA	3.5
5	CE	30	ILE	3.4
29	DH	80	ILE	3.4
29	DH	139	PHE	3.4
29	DH	143	ILE	3.4
42	DU	73	PHE	3.4
24	DC	241	GLY	3.4
27	DF	82	GLY	3.4
4	AD	151	LYS	3.4
39	DR	51	VAL	3.4
29	BH	60	GLU	3.4
22	BA	1912	A	3.4
22	BA	2122	U	3.4
31	DJ	116	ARG	3.4
53	B5	130	ARG	3.4
53	B5	52	PRO	3.4
3	AC	193	TYR	3.4
14	CN	8	ALA	3.4
29	BH	74	ALA	3.4
17	CQ	9	GLN	3.4
35	DN	9	GLN	3.4
33	DL	101	ILE	3.4
5	CE	158	GLY	3.4
19	CS	18	LYS	3.4
51	D3	49	MET	3.4
7	CG	30	LEU	3.4
9	CI	55	VAL	3.4
14	AN	51	LEU	3.4
26	DE	169	VAL	3.4
28	DG	10	VAL	3.4
29	BH	61	VAL	3.4
30	DI	24	VAL	3.4
19	AS	32	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
22	DA	329	G	3.4
32	DK	17	ARG	3.4
22	DA	2151	U	3.4
22	DA	2796	U	3.4
22	BA	2886	A	3.4
53	B5	141	PRO	3.4
33	DL	68	SER	3.4
29	BH	128	HIS	3.4
30	DI	27	ALA	3.4
19	CS	39	THR	3.4
26	DE	17	THR	3.4
29	DH	86	ASP	3.4
26	DE	77	ILE	3.4
35	DN	40	LYS	3.4
14	CN	16	LEU	3.4
19	CS	8	GLY	3.4
35	DN	105	GLY	3.4
35	DN	4	ARG	3.4
9	CI	125	PRO	3.4
30	BI	74	PRO	3.4
30	DI	23	PRO	3.4
22	BA	2172	U	3.4
22	DA	1382	G	3.4
31	DJ	47	HIS	3.4
9	CI	84	THR	3.4
13	CM	13	LYS	3.4
32	DK	66	LYS	3.4
10	AJ	84	VAL	3.4
14	CN	51	LEU	3.4
26	DE	96	VAL	3.4
32	DK	81	GLY	3.4
41	DT	62	VAL	3.4
29	BH	70	GLU	3.4
46	DY	17	GLU	3.4
10	CJ	41	PRO	3.4
19	AS	9	PRO	3.4
35	DN	111	ALA	3.4
16	AP	80	LYS	3.4
27	DF	88	LYS	3.4
31	DJ	111	LYS	3.4
39	DR	73	LYS	3.4
52	D4	26	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
24	DC	9	THR	3.4
27	DF	97	TRP	3.4
5	AE	31	PHE	3.4
19	CS	41	PHE	3.4
22	BA	1073	A	3.4
13	CM	43	VAL	3.3
36	DO	103	VAL	3.3
2	CB	13	GLY	3.3
22	DA	2300	C	3.3
9	CI	113	ARG	3.3
13	AM	113	ARG	3.3
37	BP	109	ARG	3.3
37	BP	102	GLU	3.3
30	BI	22	PRO	3.3
10	CJ	46	LYS	3.3
14	AN	36	ALA	3.3
14	AN	44	ALA	3.3
29	BH	84	ALA	3.3
41	DT	9	LYS	3.3
44	DW	75	LYS	3.3
30	DI	125	MET	3.3
31	DJ	81	ILE	3.3
46	BY	63	ALA	3.3
30	DI	42	PHE	3.3
53	B5	22	THR	3.3
29	BH	58	LEU	3.3
9	CI	104	VAL	3.3
29	BH	98	ASP	3.3
45	DX	47	VAL	3.3
29	BH	16	GLY	3.3
35	DN	22	ARG	3.3
22	BA	2146	C	3.3
22	DA	1606	C	3.3
22	DA	474	G	3.3
29	BH	42	LYS	3.3
42	DU	92	LYS	3.3
19	CS	66	MET	3.3
26	DE	135	ALA	3.3
30	DI	110	ALA	3.3
9	CI	127	PHE	3.3
10	CJ	71	LEU	3.3
25	DD	156	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
30	DI	106	LEU	3.3
47	DZ	9	GLN	3.3
53	B5	217	THR	3.3
30	BI	13	VAL	3.3
38	DQ	28	ARG	3.3
42	DU	83	VAL	3.3
25	DD	158	GLY	3.3
22	BA	2134	A	3.3
20	CT	16	LYS	3.3
42	DU	79	LYS	3.3
24	DC	104	ILE	3.3
25	DD	132	ALA	3.3
30	DI	44	ALA	3.3
34	DM	126	ILE	3.3
38	DQ	9	ILE	3.3
1	AA	1015	G	3.3
1	AA	1043	G	3.3
22	BA	1087	G	3.3
22	DA	2250	G	3.3
11	AK	105	PHE	3.3
34	DM	2	LEU	3.3
35	DN	29	VAL	3.3
35	DN	46	ARG	3.3
36	DO	24	THR	3.3
7	CG	85	TYR	3.3
9	CI	64	TYR	3.3
5	AE	65	GLU	3.3
13	CM	110	LYS	3.3
53	B5	201	LYS	3.3
35	DN	24	MET	3.3
7	CG	42	ILE	3.3
25	DD	27	ILE	3.3
26	DE	149	ILE	3.3
42	DU	35	ILE	3.3
9	CI	121	ALA	3.3
13	CM	18	ALA	3.3
29	BH	140	ALA	3.3
29	DH	135	HIS	3.3
2	CB	114	LEU	3.3
10	CJ	72	ARG	3.3
30	DI	134	ARG	3.3
45	DX	28	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
24	DC	245	VAL	3.3
44	DW	71	VAL	3.3
46	DY	46	VAL	3.3
29	DH	96	THR	3.3
22	BA	2138	G	3.3
26	DE	64	GLY	3.3
53	B5	96	GLY	3.3
24	BC	272	SER	3.3
5	AE	159	LYS	3.2
53	B5	83	LYS	3.2
30	DI	20	PRO	3.2
9	AI	46	MET	3.2
28	BG	26	ILE	3.2
28	DG	45	HIS	3.2
29	DH	140	ALA	3.2
30	BI	133	ALA	3.2
46	DY	41	HIS	3.2
51	D3	27	ALA	3.2
7	CG	118	LEU	3.2
46	DY	18	LEU	3.2
16	CP	39	PHE	3.2
10	CJ	26	VAL	3.2
27	DF	31	VAL	3.2
2	CB	33	GLY	3.2
22	DA	268	C	3.2
22	DA	2000	C	3.2
7	CG	36	LYS	3.2
14	AN	42	TRP	3.2
26	DE	57	LYS	3.2
39	DR	92	TRP	3.2
53	B5	156	GLU	3.2
7	CG	68	ASN	3.2
22	BA	1094	U	3.2
22	DA	333	G	3.2
22	DA	810	U	3.2
22	DA	2903	U	3.2
53	B5	183	PRO	3.2
33	DL	77	ILE	3.2
19	CS	10	PHE	3.2
7	CG	27	VAL	3.2
7	CG	73	VAL	3.2
7	CG	80	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	AA	1044	A	3.2
1	CA	1362	A	3.2
53	B5	142	LYS	3.2
30	DI	46	THR	3.2
1	CA	135	C	3.2
22	DA	302	C	3.2
28	DG	2	SER	3.2
29	BH	131	SER	3.2
14	CN	30	ILE	3.2
20	CT	67	ILE	3.2
22	BA	1058	U	3.2
22	BA	1917	U	3.2
22	DA	2109	U	3.2
28	DG	33	LEU	3.2
28	DG	105	LEU	3.2
29	BH	148	ALA	3.2
31	DJ	6	ALA	3.2
33	DL	72	ALA	3.2
37	DP	108	ALA	3.2
42	DU	2	ALA	3.2
46	DY	43	LEU	3.2
53	B5	137	LEU	3.2
7	CG	4	ARG	3.2
53	B5	143	ALA	3.2
1	CA	1220	G	3.2
22	BA	1171	G	3.2
25	DD	62	LYS	3.2
39	DR	76	LYS	3.2
46	DY	44	LYS	3.2
51	D3	12	LYS	3.2
3	AC	2	GLY	3.2
13	CM	94	GLY	3.2
31	DJ	115	GLY	3.2
10	CJ	66	GLU	3.2
38	DQ	89	GLU	3.2
28	DG	62	TRP	3.2
1	AA	1539	C	3.2
2	CB	95	ARG	3.2
4	AD	27	ALA	3.2
16	AP	81	ALA	3.2
18	CR	57	ARG	3.2
29	DH	58	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
26	DE	86	ALA	3.2
29	DH	106	ALA	3.2
41	DT	12	ARG	3.2
53	B5	195	ARG	3.2
22	BA	884	U	3.2
40	DS	9	HIS	3.2
20	CT	8	LYS	3.2
25	DD	8	LYS	3.2
28	DG	177	LYS	3.2
19	CS	68	GLY	3.2
22	DA	1093	G	3.2
22	DA	1099	G	3.2
22	DA	2112	G	3.2
13	CM	108	THR	3.2
27	DF	18	THR	3.2
14	AN	26	GLU	3.2
46	DY	13	GLU	3.2
19	CS	11	ILE	3.2
31	DJ	84	ILE	3.2
39	DR	49	ILE	3.2
53	B5	23	ILE	3.2
9	AI	54	LEU	3.1
10	CJ	87	LEU	3.1
30	DI	8	TYR	3.1
19	CS	78	ARG	3.1
38	DQ	33	ARG	3.1
45	DX	22	LEU	3.1
51	D3	30	ARG	3.1
17	AQ	82	ALA	3.1
48	D0	21	ALA	3.1
51	D3	48	ALA	3.1
22	DA	76	C	3.1
22	DA	795	C	3.1
29	DH	108	VAL	3.1
38	DQ	34	VAL	3.1
36	DO	32	PRO	3.1
1	CA	993	G	3.1
22	DA	88	G	3.1
22	DA	801	G	3.1
31	DJ	120	ARG	3.1
33	DL	3	LEU	3.1
39	DR	39	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
41	BT	93	LEU	3.1
12	AL	124	ALA	3.1
13	CM	46	SER	3.1
16	CP	27	ALA	3.1
20	AT	6	SER	3.1
20	CT	33	LYS	3.1
30	BI	4	LYS	3.1
30	BI	128	SER	3.1
38	DQ	38	ALA	3.1
51	D3	24	HIS	3.1
51	D3	26	HIS	3.1
53	B5	85	LYS	3.1
22	DA	2126	A	3.1
22	DA	2154	A	3.1
25	DD	131	ASP	3.1
35	DN	23	ASN	3.1
41	DT	59	ASN	3.1
7	CG	87	VAL	3.1
11	AK	74	VAL	3.1
21	CU	14	VAL	3.1
22	BA	2106	U	3.1
22	BA	2181	U	3.1
22	BA	2194	U	3.1
29	BH	2	GLN	3.1
22	DA	267	C	3.1
53	B5	91	GLY	3.1
53	B5	122	GLY	3.1
10	CJ	40	ILE	3.1
26	DE	43	THR	3.1
26	DE	175	ILE	3.1
27	DF	84	PRO	3.1
30	DI	26	PRO	3.1
19	CS	16	LEU	3.1
26	DE	134	LEU	3.1
45	DX	3	ARG	3.1
24	DC	265	LYS	3.1
9	CI	7	TYR	3.1
25	DD	192	ALA	3.1
29	DH	81	ALA	3.1
18	AR	74	HIS	3.1
30	BI	88	SER	3.1
22	BA	2121	G	3.1

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Mol	Chain	Res	Type	RSRZ
22	DA	1248	G	3.1
35	DN	73	ASN	3.1
41	DT	58	VAL	3.1
42	DU	40	ASN	3.1
51	D3	7	VAL	3.1
52	B4	20	ASP	3.1
1	AA	1493	A	3.1
1	CA	1441	A	3.1
22	BA	2117	A	3.1
22	DA	504	A	3.1
22	DA	654	A	3.1
22	DA	1073	A	3.1
1	CA	1017	U	3.1
22	BA	2131	U	3.1
35	DN	18	GLN	3.1
24	DC	41	GLY	3.1
30	BI	99	GLY	3.1
33	DL	11	GLY	3.1
41	BT	90	GLY	3.1
10	CJ	25	ILE	3.1
2	CB	135	LEU	3.1
2	CB	139	ARG	3.1
30	DI	22	PRO	3.1
36	DO	12	THR	3.1
53	B5	165	ARG	3.1
7	AG	110	LYS	3.1
27	DF	72	LYS	3.1
42	DU	33	LYS	3.1
39	BR	103	ALA	3.1
51	D3	60	ALA	3.1
2	AB	14	VAL	3.1
26	DE	4	VAL	3.1
33	DL	64	PHE	3.1
29	BH	136	SER	3.1
53	B5	180	SER	3.1
35	DN	11	ASN	3.1
30	DI	12	GLN	3.1
41	DT	71	GLY	3.1
45	DX	15	GLY	3.1
1	CA	983	A	3.1
1	CA	1014	A	3.1
1	CA	1312	G	3.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1361	G	3.1
22	DA	332	A	3.1
22	DA	1407	G	3.1
47	DZ	7	ILE	3.1
7	AG	106	GLU	3.1
33	DL	21	ARG	3.1
40	DS	92	ARG	3.1
12	AL	24	LEU	3.1
25	DD	55	LYS	3.1
26	DE	177	PRO	3.1
34	DM	118	LYS	3.1
37	DP	94	LYS	3.1
52	D4	8	LYS	3.1
53	B5	69	LEU	3.1
22	BA	1092	C	3.1
22	DA	331	C	3.1
2	CB	14	VAL	3.0
7	AG	151	PHE	3.0
7	CG	91	VAL	3.0
38	DQ	31	VAL	3.0
49	D1	21	TYR	3.0
51	D3	64	TYR	3.0
5	AE	158	GLY	3.0
10	AJ	5	ARG	3.0
19	CS	40	ILE	3.0
25	DD	59	ARG	3.0
5	CE	55	GLU	3.0
7	AG	146	GLU	3.0
30	BI	3	LYS	3.0
39	DR	37	GLU	3.0
47	DZ	29	LEU	3.0
51	D3	33	LEU	3.0
1	CA	1224	U	3.0
9	CI	9	THR	3.0
7	CG	145	ALA	3.0
10	CJ	77	VAL	3.0
29	DH	61	VAL	3.0
49	D1	47	VAL	3.0
52	D4	33	HIS	3.0
53	B5	209	PHE	3.0
1	CA	995	C	3.0
1	CA	1031	C	3.0

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Mol	Chain	Res	Type	RSRZ
1	CA	1322	C	3.0
22	BA	2164	C	3.0
25	DD	97	SER	3.0
27	DF	73	SER	3.0
2	CB	164	ILE	3.0
14	CN	61	ARG	3.0
27	BF	71	ARG	3.0
29	DH	126	GLY	3.0
49	D1	4	GLY	3.0
53	B5	107	GLY	3.0
24	BC	18	LYS	3.0
42	DU	43	LYS	3.0
42	DU	52	LEU	3.0
24	DC	8	PRO	3.0
26	DE	144	GLU	3.0
22	BA	138	U	3.0
22	DA	1217	U	3.0
22	DA	340	A	3.0
30	DI	76	ALA	3.0
53	B5	187	ALA	3.0
53	B5	196	ALA	3.0
2	CB	92	VAL	3.0
7	AG	105	VAL	3.0
7	AG	142	HIS	3.0
21	CU	37	PHE	3.0
29	DH	91	PHE	3.0
30	BI	42	PHE	3.0
30	BI	57	VAL	3.0
1	CA	220	G	3.0
3	AC	167	TRP	3.0
22	BA	2128	G	3.0
22	DA	1215	G	3.0
14	AN	23	LYS	3.0
21	CU	54	LYS	3.0
22	BA	2177	C	3.0
22	DA	228	C	3.0
22	DA	1536	C	3.0
7	CG	59	LEU	3.0
7	CG	88	PRO	3.0
30	BI	39	CYS	3.0
30	BI	56	PRO	3.0
39	DR	19	THR	3.0

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Mol	Chain	Res	Type	RSRZ
2	CB	100	MET	3.0
13	CM	81	MET	3.0
22	BA	714	U	3.0
25	DD	209	ALA	3.0
26	DE	34	ALA	3.0
24	DC	172	VAL	3.0
24	DC	228	VAL	3.0
28	DG	17	VAL	3.0
30	BI	70	VAL	3.0
22	BA	1913	A	3.0
22	BA	2602	A	3.0
22	DA	1095	A	3.0
2	AB	131	LYS	3.0
9	CI	120	LYS	3.0
12	CL	38	TYR	3.0
34	DM	14	LYS	3.0
13	CM	73	ILE	3.0
16	CP	51	ARG	3.0
36	DO	35	ILE	3.0
39	DR	21	ARG	3.0
40	DS	11	ARG	3.0
53	B5	78	ILE	3.0
53	B5	101	ILE	3.0
5	CE	124	LEU	3.0
24	DC	237	GLY	3.0
30	BI	12	GLN	3.0
44	DW	52	GLY	3.0
22	DA	7	G	3.0
14	CN	54	ASP	3.0
48	D0	20	ASP	3.0
53	B5	110	ASP	3.0
17	CQ	80	GLU	3.0
22	DA	1306	C	3.0
29	DH	87	GLU	3.0
7	CG	38	THR	3.0
30	BI	71	THR	3.0
30	DI	71	THR	3.0
13	CM	64	VAL	3.0
14	CN	34	VAL	3.0
19	CS	60	VAL	3.0
21	AU	53	VAL	3.0
25	DD	60	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
27	DF	28	VAL	3.0
27	DF	74	VAL	3.0
27	DF	122	PHE	3.0
29	BH	21	VAL	3.0
29	DH	130	VAL	3.0
1	CA	1540	U	3.0
19	AS	14	HIS	3.0
47	DZ	53	PHE	3.0
22	DA	665	U	3.0
4	CD	151	LYS	2.9
10	CJ	30	LYS	2.9
24	DC	256	LYS	2.9
25	DD	114	LYS	2.9
4	AD	63	ARG	2.9
24	DC	52	ARG	2.9
34	DM	40	ARG	2.9
53	B5	60	ARG	2.9
1	CA	1493	A	2.9
22	DA	1365	A	2.9
22	DA	2062	A	2.9
29	BH	72	ILE	2.9
6	CF	39	LEU	2.9
10	CJ	19	ASP	2.9
10	CJ	39	PRO	2.9
26	DE	129	PRO	2.9
37	DP	22	PRO	2.9
51	D3	2	PRO	2.9
1	CA	1018	G	2.9
2	AB	136	MET	2.9
22	BA	1063	G	2.9
22	BA	1068	G	2.9
22	BA	2107	G	2.9
22	DA	481	G	2.9
22	DA	1311	G	2.9
1	CA	1243	C	2.9
24	DC	92	ALA	2.9
35	DN	104	ALA	2.9
17	CQ	37	PHE	2.9
19	CS	77	THR	2.9
33	DL	30	THR	2.9
34	DM	36	VAL	2.9
35	DN	48	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
46	DY	55	THR	2.9
52	D4	3	VAL	2.9
28	BG	111	HIS	2.9
2	CB	45	LYS	2.9
8	CH	56	LYS	2.9
11	AK	14	LYS	2.9
28	DG	172	LYS	2.9
30	BI	87	LYS	2.9
1	CA	209	U	2.9
12	AL	14	ARG	2.9
20	CT	25	ARG	2.9
9	CI	28	ILE	2.9
30	DI	49	ILE	2.9
37	DP	110	ILE	2.9
40	DS	66	ILE	2.9
29	DH	75	LEU	2.9
40	DS	97	LEU	2.9
20	CT	13	GLN	2.9
30	DI	111	GLN	2.9
19	CS	9	PRO	2.9
22	BA	2163	A	2.9
22	DA	1175	A	2.9
21	AU	31	GLU	2.9
29	BH	109	GLU	2.9
2	CB	88	ASP	2.9
50	D2	22	MET	2.9
2	CB	206	ALA	2.9
14	AN	22	ALA	2.9
20	CT	72	ALA	2.9
27	DF	54	ALA	2.9
30	BI	114	ALA	2.9
25	DD	25	THR	2.9
28	BG	177	LYS	2.9
28	DG	85	LYS	2.9
29	BH	132	PHE	2.9
39	DR	75	VAL	2.9
2	CB	37	LYS	2.9
13	AM	44	LYS	2.9
14	AN	19	LYS	2.9
47	DZ	10	THR	2.9
14	AN	63	ARG	2.9
22	DA	673	C	2.9

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Mol	Chain	Res	Type	RSRZ
22	DA	2153	C	2.9
36	DO	15	ARG	2.9
22	DA	669	G	2.9
19	AS	49	ILE	2.9
53	B5	131	ILE	2.9
35	DN	83	LEU	2.9
4	AD	24	GLY	2.9
9	CI	82	GLY	2.9
24	BC	233	GLY	2.9
24	DC	249	GLY	2.9
28	DG	164	TYR	2.9
1	AA	1167	A	2.9
9	AI	58	VAL	2.9
10	CJ	57	VAL	2.9
13	CM	32	ALA	2.9
24	DC	255	LYS	2.9
29	DH	69	ALA	2.9
42	DU	19	LYS	2.9
53	B5	193	PHE	2.9
6	CF	79	ARG	2.9
9	CI	83	ILE	2.9
42	DU	72	ILE	2.9
26	DE	159	LEU	2.9
1	CA	1218	C	2.9
22	DA	318	C	2.9
22	DA	509	C	2.9
22	BA	546	U	2.9
14	CN	4	GLN	2.9
7	AG	2	PRO	2.9
22	DA	266	G	2.9
26	DE	94	GLN	2.9
42	DU	66	GLN	2.9
9	CI	46	MET	2.9
27	DF	32	GLU	2.9
2	CB	143	LYS	2.9
45	DX	26	LYS	2.9
53	B5	37	LYS	2.9
41	DT	28	ASN	2.9
2	CB	209	ALA	2.9
4	AD	25	VAL	2.9
7	CG	75	VAL	2.9
10	CJ	61	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
28	DG	23	VAL	2.9
29	DH	147	VAL	2.9
30	BI	83	ALA	2.9
30	DI	77	ALA	2.9
53	B5	75	VAL	2.9
11	AK	69	ARG	2.9
21	AU	17	ARG	2.9
22	DA	345	A	2.9
22	DA	833	A	2.9
22	DA	1912	A	2.9
29	DH	123	ARG	2.9
36	DO	13	ARG	2.9
6	AF	54	LEU	2.9
7	CG	120	LEU	2.9
10	CJ	92	LEU	2.9
10	CJ	100	ILE	2.9
13	CM	22	ILE	2.9
17	CQ	5	ILE	2.9
26	DE	119	ILE	2.9
27	DF	50	LEU	2.9
35	DN	98	LEU	2.9
30	DI	117	MET	2.8
31	DJ	110	PRO	2.8
50	D2	1	MET	2.8
53	B5	121	MET	2.8
22	DA	87	U	2.8
7	CG	44	TYR	2.8
22	DA	343	C	2.8
41	BT	88	LYS	2.8
14	AN	34	VAL	2.8
22	DA	506	G	2.8
22	DA	1068	G	2.8
22	DA	2156	G	2.8
29	BH	103	VAL	2.8
10	CJ	48	ARG	2.8
16	CP	25	ARG	2.8
26	DE	49	ARG	2.8
30	DI	43	ASN	2.8
36	DO	57	ALA	2.8
42	DU	22	ARG	2.8
36	DO	5	SER	2.8
2	AB	129	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
14	CN	27	LEU	2.8
19	CS	47	LEU	2.8
24	DC	93	LEU	2.8
40	DS	19	LEU	2.8
44	BW	10	THR	2.8
49	D1	24	THR	2.8
22	BA	1090	A	2.8
25	DD	23	PRO	2.8
14	CN	97	LYS	2.8
39	DR	24	LYS	2.8
41	DT	40	LYS	2.8
10	CJ	27	GLU	2.8
41	DT	80	TRP	2.8
1	AA	992	U	2.8
1	CA	219	U	2.8
16	CP	17	TYR	2.8
24	DC	103	TYR	2.8
29	BH	25	TYR	2.8
1	CA	1325	C	2.8
3	CC	195	VAL	2.8
7	AG	4	ARG	2.8
11	AK	13	ARG	2.8
14	CN	24	ARG	2.8
20	CT	24	ARG	2.8
22	BA	1100	C	2.8
22	BA	1924	C	2.8
22	BA	2161	C	2.8
22	DA	1072	C	2.8
29	BH	26	ALA	2.8
31	DJ	13	ARG	2.8
46	DY	48	ARG	2.8
53	B5	161	ARG	2.8
35	DN	21	PHE	2.8
5	CE	72	ILE	2.8
29	BH	62	LEU	2.8
29	DH	54	LEU	2.8
33	DL	100	ILE	2.8
51	D3	43	HIS	2.8
40	DS	36	LEU	2.8
4	CD	23	SER	2.8
27	DF	158	THR	2.8
35	DN	27	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	CA	1047	G	2.8
1	CA	1331	G	2.8
22	DA	356	G	2.8
22	DA	2127	G	2.8
45	DX	48	THR	2.8
2	AB	13	GLY	2.8
10	AJ	33	GLY	2.8
22	DA	2749	A	2.8
34	DM	61	GLY	2.8
2	CB	128	LYS	2.8
4	AD	8	LYS	2.8
8	CH	69	LYS	2.8
36	DO	56	LYS	2.8
48	D0	7	LYS	2.8
51	D3	25	LYS	2.8
26	DE	89	PRO	2.8
19	AS	34	TRP	2.8
46	BY	13	GLU	2.8
24	DC	220	VAL	2.8
35	DN	96	ARG	2.8
40	DS	47	VAL	2.8
53	B5	74	ARG	2.8
53	B5	191	ARG	2.8
13	CM	40	ALA	2.8
14	AN	2	ALA	2.8
22	BA	2105	U	2.8
22	DA	2402	U	2.8
27	DF	177	PHE	2.8
46	DY	61	ALA	2.8
3	CC	190	HIS	2.8
28	DG	107	LEU	2.8
29	BH	66	ASN	2.8
29	BH	75	LEU	2.8
46	DY	28	LEU	2.8
53	B5	186	LEU	2.8
1	CA	948	C	2.8
22	DA	2150	C	2.8
28	DG	18	LYS	2.8
31	DJ	39	LYS	2.8
40	BS	90	LYS	2.8
5	AE	102	GLY	2.8
27	DF	76	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
30	DI	25	GLY	2.8
1	CA	988	G	2.8
9	CI	23	PRO	2.8
14	CN	70	PRO	2.8
15	AO	80	GLN	2.8
22	DA	93	G	2.8
22	DA	1339	G	2.8
53	B5	134	PRO	2.8
1	CA	65	A	2.8
42	DU	37	GLU	2.8
4	AD	3	ARG	2.8
13	AM	87	ARG	2.8
13	CM	90	ARG	2.8
39	DR	13	ARG	2.8
42	DU	42	VAL	2.8
48	D0	25	VAL	2.8
53	B5	63	VAL	2.8
53	B5	73	VAL	2.8
7	AG	62	PHE	2.8
7	AG	98	ALA	2.8
7	CG	39	ALA	2.8
9	AI	20	PHE	2.8
17	CQ	28	PHE	2.8
24	DC	208	ALA	2.8
28	DG	5	ALA	2.8
37	DP	98	TYR	2.8
38	DQ	2	ALA	2.8
38	DQ	96	ALA	2.8
53	B5	79	ALA	2.8
1	AA	1537	U	2.8
1	CA	632	U	2.8
13	CM	34	LEU	2.8
14	AN	31	ILE	2.8
17	CQ	61	ILE	2.8
18	AR	21	ILE	2.8
22	BA	1065	U	2.8
26	DE	148	ILE	2.8
29	DH	117	LEU	2.8
53	B5	104	ILE	2.8
13	CM	75	MET	2.8
17	CQ	39	LYS	2.8
26	DE	141	MET	2.8

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Mol	Chain	Res	Type	RSRZ
30	BI	10	LYS	2.8
30	BI	136	MET	2.8
30	DI	113	LYS	2.8
38	DQ	84	LYS	2.8
40	DS	104	THR	2.8
42	DU	44	LYS	2.8
53	B5	41	THR	2.8
22	BA	2129	C	2.8
22	DA	209	C	2.8
53	B5	55	SER	2.8
24	DC	206	GLY	2.8
29	DH	32	PRO	2.8
30	BI	20	PRO	2.8
30	DI	56	PRO	2.8
6	AF	68	GLN	2.7
3	CC	127	ARG	2.7
7	CG	10	ARG	2.7
13	CM	79	ARG	2.7
14	CN	9	ARG	2.7
27	BF	133	ARG	2.7
27	DF	167	ARG	2.7
3	CC	52	VAL	2.7
7	CG	128	ALA	2.7
2	CB	207	ILE	2.7
11	AK	77	TYR	2.7
22	DA	1381	G	2.7
22	DA	2309	A	2.7
27	DF	55	ALA	2.7
30	BI	110	ALA	2.7
13	AM	12	HIS	2.7
34	DM	136	MET	2.7
37	DP	6	LYS	2.7
45	DX	77	LYS	2.7
51	D3	16	LYS	2.7
29	DH	73	ASN	2.7
19	CS	79	THR	2.7
35	DN	37	THR	2.7
14	AN	55	SER	2.7
14	CN	57	PRO	2.7
1	CA	1028	C	2.7
1	CA	1533	C	2.7
9	CI	110	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
33	DL	69	ARG	2.7
46	BY	7	ARG	2.7
22	BA	1914	C	2.7
22	BA	2165	C	2.7
53	B5	25	GLU	2.7
17	CQ	78	VAL	2.7
28	BG	11	VAL	2.7
2	CB	16	PHE	2.7
9	CI	52	LEU	2.7
14	CN	44	ALA	2.7
17	CQ	82	ALA	2.7
24	DC	2	ALA	2.7
37	BP	114	LEU	2.7
45	DX	21	ALA	2.7
50	D2	23	ALA	2.7
10	CJ	67	ILE	2.7
30	BI	49	ILE	2.7
19	CS	14	HIS	2.7
27	BF	83	TYR	2.7
30	BI	62	TYR	2.7
38	DQ	32	TYR	2.7
7	AG	144	MET	2.7
22	DA	73	A	2.7
22	DA	213	A	2.7
32	DK	67	LYS	2.7
46	BY	9	LYS	2.7
46	DY	30	MET	2.7
1	AA	844	G	2.7
1	CA	1034	G	2.7
22	BA	139	U	2.7
22	BA	2133	G	2.7
22	DA	1653	G	2.7
17	CQ	50	ASN	2.7
48	D0	6	ASN	2.7
25	DD	197	THR	2.7
4	AD	42	GLY	2.7
5	CE	108	GLY	2.7
13	CM	6	GLY	2.7
39	BR	50	GLY	2.7
51	D3	20	GLY	2.7
9	AI	130	ARG	2.7
33	DL	8	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
28	DG	168	VAL	2.7
39	DR	47	VAL	2.7
1	CA	940	C	2.7
1	CA	1302	C	2.7
2	CB	101	LEU	2.7
6	AF	61	LEU	2.7
12	CL	7	LEU	2.7
14	AN	30	ILE	2.7
22	BA	2179	C	2.7
22	DA	41	C	2.7
22	DA	337	C	2.7
22	DA	2601	C	2.7
24	DC	91	ILE	2.7
49	D1	48	ILE	2.7
53	B5	205	ALA	2.7
29	BH	22	LYS	2.7
36	DO	3	LYS	2.7
46	BY	2	LYS	2.7
48	D0	37	LYS	2.7
14	CN	6	MET	2.7
27	BF	143	TYR	2.7
22	BA	1057	A	2.7
1	CA	1235	U	2.7
14	AN	78	GLY	2.7
14	CN	69	ARG	2.7
24	DC	235	GLY	2.7
24	DC	257	THR	2.7
33	DL	16	GLY	2.7
36	DO	7	ARG	2.7
38	DQ	23	GLY	2.7
44	DW	55	ARG	2.7
48	D0	52	ARG	2.7
53	B5	145	THR	2.7
1	CA	942	G	2.7
22	DA	498	G	2.7
22	DA	583	G	2.7
22	DA	2808	G	2.7
2	CB	107	VAL	2.7
21	AU	36	GLU	2.7
27	DF	81	GLN	2.7
31	DJ	9	GLU	2.7
7	CG	7	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
10	AJ	71	LEU	2.7
10	AJ	92	LEU	2.7
3	CC	37	PHE	2.7
24	DC	30	PHE	2.7
24	DC	64	ILE	2.7
27	BF	122	PHE	2.7
29	BH	106	ALA	2.7
30	BI	101	ILE	2.7
30	DI	18	ALA	2.7
30	DI	86	ILE	2.7
31	DJ	54	ILE	2.7
32	DK	112	PHE	2.7
36	DO	92	PHE	2.7
13	CM	78	LYS	2.7
32	DK	51	LYS	2.7
28	DG	75	MET	2.7
3	CC	167	TRP	2.7
13	CM	12	HIS	2.7
25	DD	80	TRP	2.7
39	DR	89	HIS	2.7
41	DT	70	HIS	2.7
48	D0	42	HIS	2.7
1	CA	48	C	2.7
1	CA	106	C	2.7
1	CA	222	C	2.7
22	DA	335	C	2.7
22	DA	2666	C	2.7
27	DF	128	TYR	2.7
26	DE	56	GLY	2.7
28	DG	8	PRO	2.7
42	DU	27	ASN	2.7
42	DU	53	ASN	2.7
1	AA	842	U	2.7
1	AA	997	U	2.7
1	CA	1035	A	2.7
22	BA	1069	A	2.7
22	BA	2173	A	2.7
22	DA	342	A	2.7
22	DA	482	A	2.7
7	CG	32	VAL	2.7
9	CI	19	VAL	2.7
33	DL	51	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
43	BV	69	GLU	2.7
14	AN	48	LEU	2.7
24	DC	205	LEU	2.7
25	DD	137	SER	2.7
33	BL	92	LEU	2.7
50	D2	10	LEU	2.7
26	DE	98	LYS	2.6
49	D1	38	LYS	2.6
50	D2	25	LYS	2.6
30	BI	41	ALA	2.6
30	DI	41	ALA	2.6
33	DL	75	ALA	2.6
1	AA	926	G	2.6
1	AA	1003	G	2.6
1	AA	1305	G	2.6
22	DA	325	G	2.6
41	DT	15	HIS	2.6
2	CB	104	TRP	2.6
18	CR	51	TYR	2.6
2	CB	222	ARG	2.6
10	CJ	45	ARG	2.6
10	CJ	68	ARG	2.6
14	AN	53	ARG	2.6
19	AS	3	ARG	2.6
24	DC	238	ARG	2.6
1	CA	984	C	2.6
22	DA	2008	C	2.6
22	DA	2313	C	2.6
13	CM	112	PRO	2.6
34	DM	99	GLY	2.6
39	DR	69	GLY	2.6
41	DT	14	PRO	2.6
27	DF	157	THR	2.6
1	CA	986	U	2.6
13	CM	60	VAL	2.6
13	CM	114	LYS	2.6
21	CU	24	GLU	2.6
22	BA	2166	U	2.6
26	DE	185	LYS	2.6
30	BI	30	GLN	2.6
30	DI	61	VAL	2.6
37	DP	55	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
38	DQ	39	VAL	2.6
53	B5	80	LYS	2.6
1	AA	1492	A	2.6
22	BA	2171	A	2.6
4	AD	153	SER	2.6
9	AI	39	PHE	2.6
28	DG	74	SER	2.6
30	BI	21	SER	2.6
38	DQ	12	ALA	2.6
41	BT	1	MET	2.6
44	DW	63	ALA	2.6
53	B5	90	ALA	2.6
53	B5	92	ALA	2.6
25	DD	125	TRP	2.6
9	CI	123	ARG	2.6
15	CO	17	ARG	2.6
22	DA	549	G	2.6
22	DA	682	G	2.6
22	DA	1239	G	2.6
22	DA	2110	G	2.6
23	DB	41	G	2.6
29	DH	97	ARG	2.6
35	DN	12	ARG	2.6
51	D3	40	ARG	2.6
2	CB	124	GLY	2.6
13	CM	111	GLY	2.6
16	CP	15	PRO	2.6
27	DF	65	PRO	2.6
50	D2	27	GLY	2.6
53	B5	61	GLY	2.6
1	AA	1001	C	2.6
9	CI	111	VAL	2.6
10	CJ	10	LEU	2.6
22	DA	587	C	2.6
22	DA	1625	C	2.6
22	DA	2174	C	2.6
24	DC	39	LYS	2.6
25	DD	133	THR	2.6
25	DD	130	GLN	2.6
29	BH	31	VAL	2.6
29	DH	115	VAL	2.6
46	DY	21	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
53	B5	65	LEU	2.6
9	CI	126	GLN	2.6
27	DF	154	ILE	2.6
29	DH	129	GLU	2.6
29	DH	137	GLU	2.6
30	DI	101	ILE	2.6
33	DL	73	ILE	2.6
44	BW	17	GLU	2.6
2	AB	154	MET	2.6
35	DN	72	ASP	2.6
40	DS	1	MET	2.6
25	BD	209	ALA	2.6
30	DI	114	ALA	2.6
41	DT	46	ALA	2.6
1	CA	1167	A	2.6
2	CB	110	SER	2.6
4	AD	119	SER	2.6
17	CQ	20	SER	2.6
22	DA	1156	A	2.6
22	DA	2117	A	2.6
26	DE	75	SER	2.6
9	CI	11	ARG	2.6
10	CJ	5	ARG	2.6
17	CQ	65	ARG	2.6
24	BC	238	ARG	2.6
27	BF	80	ARG	2.6
47	DZ	11	ARG	2.6
24	DC	248	TRP	2.6
31	DJ	15	TRP	2.6
10	AJ	79	PRO	2.6
19	CS	42	PRO	2.6
19	CS	72	GLY	2.6
7	CG	114	LYS	2.6
19	CS	7	LYS	2.6
26	DE	139	LYS	2.6
1	CA	1215	G	2.6
4	AD	159	LEU	2.6
22	BA	2162	G	2.6
22	DA	1310	G	2.6
27	DF	25	VAL	2.6
29	DH	122	LEU	2.6
34	DM	112	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
35	DN	76	VAL	2.6
37	DP	92	VAL	2.6
39	DR	20	VAL	2.6
48	D0	26	THR	2.6
4	CD	160	GLU	2.6
8	AH	76	GLN	2.6
19	CS	53	ASN	2.6
2	CB	91	PHE	2.6
9	AI	16	ALA	2.6
19	CS	61	PHE	2.6
25	DD	85	ALA	2.6
46	DY	63	ALA	2.6
1	CA	1228	C	2.6
22	DA	1639	C	2.6
22	DA	2001	C	2.6
22	DA	2165	C	2.6
53	B5	188	ASP	2.6
22	DA	931	U	2.6
22	DA	1094	U	2.6
22	DA	2118	U	2.6
13	CM	14	HIS	2.6
24	DC	63	ARG	2.6
34	DM	6	ARG	2.6
10	CJ	11	LYS	2.6
14	CN	52	PRO	2.6
19	CS	30	PRO	2.6
25	DD	144	GLY	2.6
29	BH	92	GLY	2.6
30	BI	32	GLY	2.6
31	DJ	8	PRO	2.6
53	B5	182	PRO	2.6
54	D6	4	PRO	2.6
4	AD	21	LEU	2.6
30	BI	138	LEU	2.6
37	DP	97	LEU	2.6
9	CI	72	ILE	2.6
9	CI	116	VAL	2.6
30	DI	136	MET	2.6
33	DL	121	THR	2.6
35	DN	34	ILE	2.6
37	DP	104	THR	2.6
51	D3	34	THR	2.6

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Mol	Chain	Res	Type	RSRZ
29	BH	45	GLU	2.6
33	DL	104	GLN	2.6
13	AM	63	PHE	2.6
13	CM	63	PHE	2.6
27	DF	70	ALA	2.6
29	BH	10	ALA	2.6
29	BH	145	ASN	2.6
30	DI	115	ALA	2.6
39	DR	28	ALA	2.6
1	AA	211	G	2.5
22	DA	289	G	2.5
22	DA	315	G	2.5
22	DA	389	G	2.5
1	AA	1008	U	2.5
1	AA	1030	U	2.5
22	BA	2167	U	2.5
22	DA	290	U	2.5
36	DO	29	HIS	2.5
38	DQ	3	ARG	2.5
39	DR	82	HIS	2.5
51	D3	31	HIS	2.5
11	AK	26	SER	2.5
22	DA	22	C	2.5
22	DA	341	C	2.5
53	B5	222	SER	2.5
12	CL	88	LYS	2.5
27	DF	69	LYS	2.5
30	BI	81	LYS	2.5
51	D3	36	LYS	2.5
7	CG	103	TRP	2.5
22	DA	1237	A	2.5
3	CC	13	GLY	2.5
33	DL	26	GLY	2.5
33	DL	62	PRO	2.5
25	DD	187	LEU	2.5
26	DE	138	LEU	2.5
38	DQ	7	GLY	2.5
41	DT	61	LEU	2.5
43	DV	42	LEU	2.5
51	D3	44	LEU	2.5
7	CG	144	MET	2.5
9	CI	67	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
27	DF	13	VAL	2.5
28	DG	41	VAL	2.5
31	DJ	103	ILE	2.5
33	DL	103	ILE	2.5
52	D4	17	VAL	2.5
5	AE	103	THR	2.5
9	CI	97	GLU	2.5
29	BH	40	THR	2.5
7	CG	98	ALA	2.5
27	DF	75	ALA	2.5
30	BI	7	ALA	2.5
40	DS	75	PHE	2.5
34	DM	17	ASN	2.5
7	CG	95	ARG	2.5
10	AJ	62	ARG	2.5
15	CO	53	ARG	2.5
15	CO	58	ARG	2.5
34	DM	10	ARG	2.5
34	DM	16	ARG	2.5
53	B5	56	ASP	2.5
53	B5	224	ARG	2.5
1	CA	1065	U	2.5
35	DN	15	SER	2.5
35	DN	35	LYS	2.5
42	DU	97	LYS	2.5
22	DA	39	G	2.5
22	DA	303	G	2.5
22	DA	1252	G	2.5
22	DA	394	C	2.5
22	DA	2145	C	2.5
2	CB	96	TRP	2.5
8	CH	82	GLY	2.5
9	CI	63	LEU	2.5
29	DH	85	GLY	2.5
44	DW	42	GLY	2.5
13	AM	7	ILE	2.5
4	CD	76	TYR	2.5
24	DC	250	VAL	2.5
42	DU	93	VAL	2.5
1	CA	1216	A	2.5
22	DA	2800	A	2.5
10	CJ	50	THR	2.5

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Mol	Chain	Res	Type	RSRZ
12	AL	23	ALA	2.5
12	CL	2	ALA	2.5
33	DL	108	ALA	2.5
37	DP	42	ALA	2.5
12	AL	73	ASN	2.5
13	CM	92	ARG	2.5
25	DD	136	ASN	2.5
27	DF	92	ARG	2.5
28	DG	48	ASN	2.5
7	CG	142	HIS	2.5
4	CD	177	LYS	2.5
13	AM	114	LYS	2.5
29	BH	35	LYS	2.5
29	DH	112	LYS	2.5
30	DI	92	LYS	2.5
30	DI	100	LYS	2.5
33	DL	84	LYS	2.5
40	DS	6	LYS	2.5
47	DZ	56	LYS	2.5
1	CA	1240	U	2.5
26	DE	3	LEU	2.5
35	DN	115	LEU	2.5
48	D0	8	PRO	2.5
27	BF	34	ILE	2.5
28	DG	78	GLY	2.5
29	BH	34	GLY	2.5
47	DZ	15	GLY	2.5
6	AF	42	TRP	2.5
39	DR	63	VAL	2.5
53	B5	42	VAL	2.5
1	CA	1226	C	2.5
1	AA	97	G	2.5
22	DA	1661	G	2.5
9	CI	89	GLU	2.5
29	BH	114	GLU	2.5
25	BD	85	ALA	2.5
26	DE	41	GLN	2.5
27	DF	68	THR	2.5
30	BI	69	PHE	2.5
37	DP	20	PHE	2.5
46	DY	59	GLU	2.5
7	CG	84	THR	2.5

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Mol	Chain	Res	Type	RSRZ
11	AK	66	ALA	2.5
32	DK	83	ALA	2.5
33	DL	134	ALA	2.5
45	DX	25	THR	2.5
49	D1	22	THR	2.5
1	CA	223	A	2.5
1	CA	1534	A	2.5
22	DA	320	A	2.5
22	DA	502	A	2.5
22	DA	1213	A	2.5
38	DQ	6	ARG	2.5
52	D4	36	ARG	2.5
7	CG	11	LYS	2.5
13	CM	44	LYS	2.5
33	DL	13	LYS	2.5
46	DY	54	LYS	2.5
42	DU	45	HIS	2.5
41	DT	37	ASP	2.5
7	AG	59	LEU	2.5
9	CI	35	LEU	2.5
11	AK	42	LEU	2.5
28	DG	87	LEU	2.5
29	BH	15	LEU	2.5
41	DT	8	LEU	2.5
19	CS	59	PRO	2.5
26	DE	179	SER	2.5
52	D4	31	PRO	2.5
7	CG	81	GLY	2.5
22	BA	2132	U	2.5
22	DA	1406	U	2.5
29	BH	13	GLY	2.5
41	DT	74	ILE	2.5
51	D3	18	GLY	2.5
53	B5	84	ILE	2.5
53	B5	220	GLY	2.5
17	CQ	46	VAL	2.5
48	D0	54	VAL	2.5
49	D1	43	VAL	2.5
24	BC	240	PHE	2.5
33	DL	10	GLU	2.5
44	DW	60	PHE	2.5
3	AC	131	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
4	AD	2	ALA	2.5
10	AJ	7	ARG	2.5
15	AO	89	ARG	2.5
20	CT	7	ALA	2.5
21	AU	30	ALA	2.5
21	CU	33	ARG	2.5
24	DC	101	ARG	2.5
24	DC	270	ARG	2.5
26	DE	69	ARG	2.5
33	DL	54	GLN	2.5
38	DQ	55	ARG	2.5
24	DC	246	THR	2.5
30	DI	126	THR	2.5
35	DN	70	THR	2.5
53	B5	199	ALA	2.5
1	CA	1314	C	2.5
4	AD	121	LYS	2.5
9	CI	115	LYS	2.5
17	CQ	4	LYS	2.5
20	CT	69	LYS	2.5
22	BA	2150	C	2.5
22	DA	357	C	2.5
24	DC	5	LYS	2.5
49	B1	10	LYS	2.5
1	AA	1033	G	2.5
1	CA	111	G	2.5
1	CA	1279	G	2.5
22	DA	1271	G	2.5
1	CA	1042	A	2.5
22	BA	892	A	2.5
22	BA	1084	A	2.5
22	DA	613	A	2.5
48	D0	38	HIS	2.5
19	CS	64	ASP	2.4
27	DF	26	MET	2.4
29	DH	15	LEU	2.4
39	DR	25	LEU	2.4
51	D3	29	LEU	2.4
53	B5	93	ASP	2.4
24	DC	32	PRO	2.4
26	DE	108	ILE	2.4
27	DF	60	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
24	DC	19	VAL	2.4
24	DC	272	SER	2.4
26	DE	55	SER	2.4
29	BH	9	VAL	2.4
30	DI	32	GLY	2.4
29	BH	82	SER	2.4
31	DJ	73	VAL	2.4
32	BK	122	VAL	2.4
35	DN	116	VAL	2.4
41	DT	67	VAL	2.4
44	DW	38	VAL	2.4
22	DA	193	U	2.4
29	BH	47	PHE	2.4
29	DH	47	PHE	2.4
30	DI	130	GLU	2.4
35	DN	103	ARG	2.4
37	DP	43	PHE	2.4
41	DT	42	GLU	2.4
42	DU	60	GLU	2.4
4	AD	43	ALA	2.4
14	CN	98	LYS	2.4
17	CQ	16	LYS	2.4
19	CS	80	TYR	2.4
24	DC	83	TYR	2.4
28	DG	40	ALA	2.4
28	DG	44	LYS	2.4
29	DH	59	ALA	2.4
30	BI	100	LYS	2.4
30	DI	63	ALA	2.4
46	BY	4	LYS	2.4
51	D3	3	LYS	2.4
30	DI	132	THR	2.4
1	AA	210	C	2.4
22	DA	8	C	2.4
22	DA	531	C	2.4
22	DA	680	C	2.4
22	DA	1305	C	2.4
22	DA	2143	C	2.4
2	CB	9	MET	2.4
19	CS	43	ASN	2.4
20	AT	3	ASN	2.4
24	DC	70	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
53	B5	58	ASN	2.4
8	CH	63	LEU	2.4
1	AA	702	A	2.4
1	CA	1016	A	2.4
1	CA	1021	A	2.4
22	DA	311	A	2.4
22	DA	1008	A	2.4
1	AA	79	G	2.4
16	CP	4	ILE	2.4
22	DA	214	G	2.4
22	DA	953	G	2.4
28	DG	12	PRO	2.4
30	BI	26	PRO	2.4
29	DH	13	GLY	2.4
30	DI	52	GLY	2.4
36	DO	27	VAL	2.4
53	B5	207	GLY	2.4
20	CT	6	SER	2.4
29	BH	27	ARG	2.4
29	BH	116	ARG	2.4
33	DL	123	ARG	2.4
35	DN	90	ARG	2.4
1	CA	1351	U	2.4
2	AB	104	TRP	2.4
7	CG	21	GLU	2.4
10	CJ	49	PHE	2.4
13	AM	41	GLU	2.4
14	CN	21	PHE	2.4
22	DA	1468	U	2.4
25	DD	123	LYS	2.4
29	BH	29	PHE	2.4
32	DK	106	GLU	2.4
39	DR	97	LYS	2.4
42	DU	62	GLU	2.4
27	BF	119	ALA	2.4
42	DU	64	ALA	2.4
5	CE	24	THR	2.4
28	DG	80	THR	2.4
35	DN	36	THR	2.4
53	B5	169	THR	2.4
11	AK	22	HIS	2.4
3	CC	33	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
10	AJ	10	LEU	2.4
33	DL	57	LEU	2.4
45	DX	30	LEU	2.4
46	DY	42	LEU	2.4
5	CE	70	ASN	2.4
30	DI	34	ASN	2.4
7	AG	7	ILE	2.4
38	DQ	65	ILE	2.4
1	AA	95	C	2.4
1	CA	985	C	2.4
5	CE	143	GLY	2.4
25	DD	166	GLY	2.4
28	DG	21	GLY	2.4
28	DG	60	ASP	2.4
29	DH	9	VAL	2.4
38	DQ	102	ASP	2.4
53	B5	167	ASP	2.4
1	CA	101	A	2.4
22	DA	2602	A	2.4
2	CB	225	ARG	2.4
6	CF	93	LYS	2.4
16	CP	31	ARG	2.4
26	DE	47	LYS	2.4
27	DF	80	ARG	2.4
28	DG	149	ARG	2.4
51	D3	23	LYS	2.4
1	CA	951	G	2.4
2	CB	90	PHE	2.4
3	CC	161	GLU	2.4
13	CM	76	SER	2.4
14	AN	5	SER	2.4
22	DA	338	G	2.4
22	DA	1212	G	2.4
22	DA	2148	G	2.4
23	DB	6	G	2.4
24	DC	194	GLU	2.4
25	DD	127	PHE	2.4
2	AB	134	ALA	2.4
17	CQ	73	TRP	2.4
22	DA	276	U	2.4
22	DA	1061	U	2.4
22	DA	2797	U	2.4

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Mol	Chain	Res	Type	RSRZ
2	AB	213	TYR	2.4
38	DQ	45	TYR	2.4
3	CC	165	THR	2.4
10	CJ	56	HIS	2.4
14	AN	6	MET	2.4
39	DR	1	MET	2.4
4	AD	19	LEU	2.4
17	CQ	8	LEU	2.4
2	AB	67	ILE	2.4
27	BF	79	ILE	2.4
24	DC	11	PRO	2.4
53	B5	140	ASN	2.4
9	AI	116	VAL	2.4
9	CI	29	VAL	2.4
2	AB	59	LYS	2.4
11	AK	43	GLY	2.4
26	DE	33	VAL	2.4
29	DH	89	LYS	2.4
30	BI	131	GLY	2.4
37	DP	73	VAL	2.4
39	BR	51	VAL	2.4
2	AB	88	ASP	2.4
9	AI	11	ARG	2.4
27	DF	71	ARG	2.4
31	BJ	95	ARG	2.4
31	DJ	106	LYS	2.4
40	DS	49	LYS	2.4
41	DT	19	LYS	2.4
52	D4	15	LYS	2.4
53	B5	19	LYS	2.4
1	CA	1001	C	2.4
22	DA	385	C	2.4
22	DA	1053	C	2.4
22	DA	1345	C	2.4
22	DA	1607	C	2.4
1	CA	313	A	2.4
1	CA	532	A	2.4
1	CA	949	A	2.4
1	CA	1248	A	2.4
22	BA	1098	A	2.4
22	DA	1590	A	2.4
23	DB	45	A	2.4

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Mol	Chain	Res	Type	RSRZ
33	DL	50	PHE	2.4
10	CJ	86	ALA	2.4
11	CK	21	ALA	2.4
28	DG	150	ALA	2.4
51	D3	65	ALA	2.4
53	B5	171	ALA	2.4
5	CE	149	SER	2.4
1	CA	134	G	2.4
1	CA	1041	G	2.4
1	CA	1043	G	2.4
17	CQ	7	THR	2.4
22	BA	548	G	2.4
22	DA	189	G	2.4
22	DA	317	G	2.4
22	DA	392	U	2.4
22	DA	1529	G	2.4
30	BI	117	MET	2.4
12	CL	24	LEU	2.4
19	AS	5	LEU	2.4
33	DL	82	LEU	2.4
48	D0	28	LEU	2.4
8	CH	46	ILE	2.4
26	BE	148	ILE	2.4
24	DC	247	PRO	2.4
5	CE	159	LYS	2.3
7	AG	75	VAL	2.3
7	AG	149	LYS	2.3
2	CB	149	GLY	2.3
15	CO	72	ARG	2.3
16	AP	20	VAL	2.3
21	CU	28	VAL	2.3
24	DC	212	ARG	2.3
26	DE	126	VAL	2.3
26	DE	178	VAL	2.3
28	BG	99	LYS	2.3
30	BI	97	LYS	2.3
34	DM	81	ARG	2.3
37	DP	115	ASN	2.3
41	DT	44	LYS	2.3
45	BX	40	VAL	2.3
30	BI	89	GLY	2.3
30	DI	131	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
42	DU	32	GLY	2.3
42	DU	84	GLY	2.3
7	AG	26	PHE	2.3
53	B5	181	PHE	2.3
14	AN	25	ALA	2.3
14	CN	22	ALA	2.3
15	AO	6	GLU	2.3
29	DH	64	ALA	2.3
29	DH	76	GLU	2.3
30	DI	104	ALA	2.3
14	CN	60	GLN	2.3
22	DA	316	C	2.3
7	CG	20	SER	2.3
14	CN	101	TRP	2.3
22	BA	2126	A	2.3
2	AB	170	HIS	2.3
10	AJ	87	LEU	2.3
28	DG	37	LEU	2.3
33	DL	67	THR	2.3
36	DO	64	TYR	2.3
39	DR	29	THR	2.3
40	DS	23	LEU	2.3
53	B5	67	HIS	2.3
1	AA	209	U	2.3
1	CA	170	U	2.3
1	CA	1049	U	2.3
13	CM	4	ILE	2.3
27	DF	34	ILE	2.3
28	BG	24	ILE	2.3
33	DL	111	ILE	2.3
41	DT	30	ILE	2.3
16	CP	80	LYS	2.3
20	CT	5	LYS	2.3
27	DF	120	LYS	2.3
33	DL	29	LYS	2.3
42	DU	50	PRO	2.3
51	D3	63	PRO	2.3
53	B5	206	LYS	2.3
1	AA	1002	G	2.3
1	CA	1297	G	2.3
8	CH	110	VAL	2.3
10	AJ	45	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
18	AR	57	ARG	2.3
21	CU	21	ARG	2.3
22	DA	313	G	2.3
22	DA	2116	G	2.3
22	DA	2659	G	2.3
24	DC	43	ARG	2.3
24	DC	269	ARG	2.3
27	DF	40	VAL	2.3
33	DL	48	ARG	2.3
33	DL	59	ARG	2.3
2	CB	98	GLY	2.3
7	AG	148	ASN	2.3
16	CP	10	GLY	2.3
29	BH	85	GLY	2.3
32	DK	82	ASN	2.3
35	DN	13	ASN	2.3
39	DR	88	GLY	2.3
45	DX	17	ASN	2.3
45	DX	32	ASN	2.3
33	DL	66	PHE	2.3
9	AI	89	GLU	2.3
13	CM	15	ALA	2.3
19	CS	65	GLU	2.3
29	BH	17	ASP	2.3
30	BI	116	ASP	2.3
20	AT	7	ALA	2.3
20	CT	73	ALA	2.3
36	DO	60	GLU	2.3
38	BQ	118	ALA	2.3
50	D2	32	ALA	2.3
19	CS	13	LEU	2.3
27	DF	169	LEU	2.3
29	BH	6	LEU	2.3
1	CA	1317	C	2.3
19	CS	52	HIS	2.3
22	DA	130	C	2.3
22	DA	334	C	2.3
22	DA	1870	C	2.3
35	DN	3	HIS	2.3
31	BJ	81	ILE	2.3
33	DL	74	THR	2.3
1	AA	996	A	2.3

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Mol	Chain	Res	Type	RSRZ
1	CA	1227	A	2.3
22	DA	1509	A	2.3
22	DA	2820	A	2.3
49	D1	5	ILE	2.3
51	D3	4	ILE	2.3
28	DG	175	LYS	2.3
29	BH	8	LYS	2.3
30	BI	45	LYS	2.3
30	BI	72	LYS	2.3
38	DQ	5	LYS	2.3
41	DT	49	LYS	2.3
1	CA	1040	U	2.3
21	AU	11	PRO	2.3
25	DD	143	PRO	2.3
35	DN	63	ARG	2.3
16	CP	20	VAL	2.3
40	DS	71	VAL	2.3
42	DU	28	VAL	2.3
42	DU	59	VAL	2.3
45	DX	4	VAL	2.3
47	DZ	36	VAL	2.3
20	CT	65	GLY	2.3
24	DC	99	GLY	2.3
7	CG	18	PHE	2.3
22	BA	1071	G	2.3
22	BA	2120	G	2.3
22	DA	2124	G	2.3
22	DA	2655	G	2.3
26	DE	155	GLU	2.3
35	DN	55	ALA	2.3
35	DN	68	ALA	2.3
37	DP	68	GLU	2.3
39	DR	31	GLU	2.3
7	CG	15	ASP	2.3
9	CI	88	MET	2.3
2	CB	117	LEU	2.3
9	CI	118	LEU	2.3
13	CM	100	GLN	2.3
4	AD	198	HIS	2.3
4	CD	206	LYS	2.3
7	AG	11	LYS	2.3
9	CI	30	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
10	AJ	76	ILE	2.3
10	CJ	8	ILE	2.3
10	CJ	54	SER	2.3
14	CN	56	SER	2.3
18	CR	21	ILE	2.3
20	CT	20	HIS	2.3
25	DD	140	HIS	2.3
30	BI	113	LYS	2.3
36	BO	95	SER	2.3
40	DS	96	ILE	2.3
41	DT	66	LYS	2.3
53	B5	190	ILE	2.3
2	CB	20	THR	2.3
50	D2	43	THR	2.3
51	D3	38	THR	2.3
5	CE	54	ARG	2.3
9	AI	41	ARG	2.3
16	CP	8	ARG	2.3
33	DL	2	ARG	2.3
34	DM	59	ARG	2.3
44	DW	77	ARG	2.3
1	AA	1027	C	2.3
1	CA	1332	A	2.3
3	AC	138	VAL	2.3
9	CI	58	VAL	2.3
22	BA	1089	A	2.3
22	BA	2187	U	2.3
22	DA	344	A	2.3
22	DA	614	A	2.3
22	DA	982	C	2.3
22	DA	1067	A	2.3
22	DA	1535	A	2.3
22	DA	2146	C	2.3
22	BA	2118	U	2.3
24	DC	234	GLY	2.3
25	DD	111	GLY	2.3
27	DF	116	GLY	2.3
10	CJ	58	ASN	2.3
4	AD	158	ALA	2.3
7	AG	65	ALA	2.3
7	CG	65	ALA	2.3
9	CI	57	MET	2.3

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Mol	Chain	Res	Type	RSRZ
26	BE	8	ALA	2.3
28	DG	32	GLU	2.3
2	CB	54	LEU	2.3
5	AE	115	LEU	2.3
17	AQ	48	ASP	2.3
19	CS	31	LEU	2.3
29	BH	133	GLN	2.3
31	DJ	140	LEU	2.3
32	BK	107	LEU	2.3
38	DQ	37	GLN	2.3
39	DR	6	GLN	2.3
53	B5	57	GLN	2.3
20	CT	9	LYS	2.3
26	DE	166	LYS	2.3
30	DI	72	LYS	2.3
48	D0	32	LYS	2.3
1	CA	68	G	2.3
22	DA	48	G	2.3
22	DA	277	G	2.3
22	DA	530	G	2.3
22	DA	1236	G	2.3
7	CG	77	SER	2.3
27	DF	159	THR	2.3
33	DL	18	ARG	2.3
41	DT	69	ARG	2.3
44	DW	11	ARG	2.3
45	DX	18	ARG	2.3
48	D0	23	THR	2.3
2	AB	221	VAL	2.3
3	AC	39	VAL	2.3
6	CF	12	PRO	2.3
7	CG	16	PRO	2.3
25	DD	9	VAL	2.3
27	DF	108	VAL	2.3
27	DF	176	PRO	2.3
43	DV	57	TYR	2.3
28	DG	43	VAL	2.3
42	DU	25	VAL	2.3
43	DV	84	PRO	2.3
39	DR	67	GLY	2.3
22	DA	280	U	2.3
22	DA	2622	U	2.3

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Mol	Chain	Res	Type	RSRZ
1	CA	1145	A	2.2
4	AD	107	PHE	2.2
22	BA	1175	A	2.2
22	DA	74	A	2.2
22	DA	1383	A	2.2
22	DA	1644	C	2.2
22	DA	2406	A	2.2
22	DA	2503	A	2.2
24	DC	211	ALA	2.2
41	DT	83	ALA	2.2
53	B5	82	GLU	2.2
53	B5	123	ALA	2.2
42	DU	41	LEU	2.2
5	CE	26	LYS	2.2
19	CS	6	LYS	2.2
28	BG	44	LYS	2.2
34	DM	8	LYS	2.2
26	DE	154	ASP	2.2
30	DI	121	ASP	2.2
27	BF	148	ARG	2.2
31	DJ	95	ARG	2.2
36	DO	25	ARG	2.2
39	DR	79	ARG	2.2
50	D2	35	ARG	2.2
17	CQ	53	CYS	2.2
45	DX	8	THR	2.2
4	AD	125	VAL	2.2
9	AI	48	VAL	2.2
30	BI	33	VAL	2.2
47	DZ	51	VAL	2.2
35	DN	112	TYR	2.2
1	AA	94	G	2.2
1	CA	1026	G	2.2
22	DA	379	G	2.2
22	DA	1185	G	2.2
22	DA	1341	G	2.2
22	DA	2115	G	2.2
17	AQ	10	GLY	2.2
49	D1	18	GLY	2.2
6	AF	80	PHE	2.2
31	DJ	118	MET	2.2
1	CA	218	U	2.2

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Mol	Chain	Res	Type	RSRZ
22	BA	1101	U	2.2
22	DA	99	U	2.2
23	DB	89	U	2.2
5	CE	10	GLU	2.2
6	AF	99	ALA	2.2
14	CN	36	ALA	2.2
7	CG	22	LEU	2.2
13	CM	41	GLU	2.2
30	DI	83	ALA	2.2
41	DT	45	ALA	2.2
1	AA	1022	A	2.2
1	CA	1492	A	2.2
2	CB	11	LYS	2.2
4	CD	77	LYS	2.2
14	CN	48	LEU	2.2
16	AP	74	LEU	2.2
22	BA	893	C	2.2
22	DA	89	A	2.2
22	DA	196	A	2.2
22	DA	354	A	2.2
22	DA	631	A	2.2
22	DA	800	A	2.2
22	DA	1575	C	2.2
22	DA	1591	A	2.2
22	DA	1597	A	2.2
24	DC	46	ASN	2.2
26	DE	133	LEU	2.2
30	BI	82	LYS	2.2
34	DM	124	LEU	2.2
35	DN	99	LYS	2.2
36	DO	26	LEU	2.2
42	BU	52	LEU	2.2
46	DY	57	LEU	2.2
19	AS	56	GLN	2.2
27	BF	136	ILE	2.2
16	CP	69	ASP	2.2
21	CU	13	ASP	2.2
53	B5	39	ASP	2.2
2	CB	187	VAL	2.2
4	AD	38	PRO	2.2
19	AS	33	THR	2.2
25	DD	50	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
49	D1	42	VAL	2.2
35	DN	14	SER	2.2
2	AB	65	GLY	2.2
7	CG	112	GLY	2.2
11	AK	78	GLY	2.2
44	DW	54	GLY	2.2
25	DD	118	PHE	2.2
38	DQ	101	PHE	2.2
16	CP	12	LYS	2.2
24	DC	36	LYS	2.2
1	CA	75	G	2.2
2	AB	43	LEU	2.2
13	CM	48	LEU	2.2
25	DD	116	LYS	2.2
29	BH	112	LYS	2.2
22	DA	51	G	2.2
22	DA	215	G	2.2
22	DA	298	G	2.2
22	DA	674	G	2.2
22	DA	1171	G	2.2
22	DA	2405	G	2.2
42	DU	3	ALA	2.2
44	BW	85	GLU	2.2
46	DY	14	LEU	2.2
50	D2	31	LEU	2.2
1	AA	1007	U	2.2
1	CA	1381	U	2.2
22	BA	846	U	2.2
22	DA	2139	U	2.2
15	CO	20	ASN	2.2
43	DV	24	ASN	2.2
4	AD	70	ARG	2.2
7	AG	12	ILE	2.2
9	CI	37	GLN	2.2
14	CN	82	ILE	2.2
30	BI	129	ILE	2.2
32	DK	47	ILE	2.2
33	DL	105	ILE	2.2
38	DQ	53	ARG	2.2
1	CA	1324	A	2.2
1	CA	1375	A	2.2
22	DA	1395	A	2.2

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Mol	Chain	Res	Type	RSRZ
22	DA	1913	A	2.2
1	AA	1011	C	2.2
1	CA	110	C	2.2
1	CA	1359	C	2.2
22	DA	2681	C	2.2
53	B5	200	HIS	2.2
27	DF	10	ASP	2.2
9	AI	19	VAL	2.2
27	BF	132	VAL	2.2
40	DS	76	VAL	2.2
50	D2	30	VAL	2.2
38	DQ	61	TRP	2.2
40	DS	39	THR	2.2
41	DT	22	THR	2.2
7	CG	57	SER	2.2
9	CI	10	GLY	2.2
30	BI	17	MET	2.2
40	DS	86	MET	2.2
13	CM	30	SER	2.2
43	DV	82	TYR	2.2
53	B5	136	GLY	2.2
53	B5	214	TYR	2.2
2	CB	152	LYS	2.2
4	AD	31	LYS	2.2
21	AU	54	LYS	2.2
24	BC	242	LYS	2.2
42	DU	17	LYS	2.2
10	CJ	17	LEU	2.2
40	DS	33	LEU	2.2
41	DT	7	LEU	2.2
41	DT	50	LEU	2.2
6	CF	99	ALA	2.2
16	CP	47	GLU	2.2
19	CS	73	GLU	2.2
41	DT	13	ALA	2.2
2	CB	40	ILE	2.2
6	CF	71	ILE	2.2
9	AI	45	ARG	2.2
9	AI	122	ARG	2.2
17	AQ	27	ARG	2.2
17	CQ	11	ARG	2.2
17	CQ	40	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
26	DE	79	ARG	2.2
27	DF	111	ILE	2.2
13	CM	105	ASN	2.2
22	DA	427	U	2.2
35	DN	8	ARG	2.2
51	D3	8	ARG	2.2
52	B4	12	ARG	2.2
30	BI	31	GLN	2.2
30	DI	6	GLN	2.2
1	CA	69	G	2.2
1	CA	357	G	2.2
22	DA	1160	G	2.2
22	DA	1475	G	2.2
22	DA	1984	G	2.2
26	DE	165	HIS	2.2
7	AG	87	VAL	2.2
12	AL	16	VAL	2.2
22	DA	677	A	2.2
22	DA	2147	A	2.2
25	DD	155	VAL	2.2
29	DH	103	VAL	2.2
30	DI	57	VAL	2.2
37	DP	17	VAL	2.2
53	B5	106	ASP	2.2
1	CA	1230	C	2.2
2	CB	49	MET	2.2
22	DA	444	C	2.2
22	DA	1229	C	2.2
2	CB	130	THR	2.2
5	AE	152	MET	2.2
3	CC	159	GLY	2.2
9	AI	117	GLY	2.2
14	AN	68	GLY	2.2
24	DC	59	LYS	2.2
25	DD	38	LYS	2.2
28	DG	27	LYS	2.2
40	DS	70	LYS	2.2
53	B5	151	GLY	2.2
7	AG	37	SER	2.2
7	CG	26	PHE	2.2
9	AI	128	SER	2.2
21	AU	19	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
27	DF	16	LEU	2.2
30	DI	21	SER	2.2
36	DO	52	SER	2.2
53	B5	148	PHE	2.2
13	CM	95	LEU	2.2
47	DZ	25	LEU	2.2
4	CD	35	GLU	2.2
8	CH	130	ALA	2.2
13	AM	2	ALA	2.2
29	DH	65	ALA	2.2
5	CE	112	ARG	2.1
10	AJ	100	ILE	2.1
11	CK	110	ILE	2.1
16	CP	5	ARG	2.1
27	BF	154	ILE	2.1
34	BM	55	ARG	2.1
37	DP	4	ILE	2.1
52	D4	4	ARG	2.1
26	DE	90	GLN	2.1
29	BH	73	ASN	2.1
29	DH	119	ASN	2.1
53	B5	66	PRO	2.1
14	CN	33	ASP	2.1
30	BI	125	MET	2.1
5	CE	23	LYS	2.1
14	CN	12	LYS	2.1
14	CN	19	LYS	2.1
1	AA	1441	A	2.1
1	CA	958	A	2.1
1	CA	971	G	2.1
1	CA	1131	G	2.1
1	CA	1221	G	2.1
1	CA	1306	A	2.1
1	CA	1323	G	2.1
7	CG	149	LYS	2.1
10	AJ	59	LYS	2.1
10	CJ	22	THR	2.1
13	AM	99	GLY	2.1
19	CS	63	THR	2.1
22	BA	1099	G	2.1
22	DA	361	G	2.1
22	DA	477	A	2.1

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Mol	Chain	Res	Type	RSRZ
22	DA	974	G	2.1
22	DA	1303	G	2.1
22	DA	2314	A	2.1
23	DB	44	G	2.1
29	BH	83	LYS	2.1
30	DI	112	THR	2.1
31	DJ	3	THR	2.1
33	DL	52	GLY	2.1
37	DP	23	GLY	2.1
43	DV	32	GLY	2.1
51	D3	56	GLY	2.1
52	D4	21	GLY	2.1
1	AA	83	C	2.1
1	AA	1028	C	2.1
5	AE	11	LEU	2.1
6	CF	8	PHE	2.1
22	DA	440	C	2.1
22	DA	678	C	2.1
22	DA	1161	C	2.1
22	DA	1706	C	2.1
22	DA	1806	C	2.1
39	DR	83	TYR	2.1
4	CD	37	ALA	2.1
13	AM	46	SER	2.1
29	BH	63	ALA	2.1
29	DH	136	SER	2.1
30	DI	48	SER	2.1
33	DL	113	ALA	2.1
37	DP	49	ALA	2.1
42	DU	76	ALA	2.1
43	DV	94	ALA	2.1
2	AB	139	ARG	2.1
4	AD	44	ARG	2.1
25	DD	168	GLU	2.1
40	DS	25	ARG	2.1
41	DT	4	GLU	2.1
49	D1	28	ARG	2.1
8	AH	126	ILE	2.1
13	AM	9	ILE	2.1
28	DG	19	ILE	2.1
39	DR	41	ILE	2.1
47	DZ	32	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
51	D3	59	ILE	2.1
19	CS	56	GLN	2.1
32	DK	3	GLN	2.1
42	DU	74	ASN	2.1
7	CG	69	VAL	2.1
7	CG	89	VAL	2.1
12	AL	91	PRO	2.1
13	AM	43	VAL	2.1
3	CC	129	MET	2.1
19	AS	30	PRO	2.1
22	DA	1559	U	2.1
24	DC	29	PRO	2.1
30	BI	9	VAL	2.1
39	DR	54	VAL	2.1
53	B5	59	VAL	2.1
27	DF	14	LYS	2.1
29	BH	57	LYS	2.1
30	DI	97	LYS	2.1
19	AS	64	ASP	2.1
28	DG	166	ASP	2.1
42	DU	81	ASP	2.1
12	CL	58	THR	2.1
25	DD	44	GLY	2.1
2	CB	69	PHE	2.1
26	DE	180	LEU	2.1
27	DF	91	LEU	2.1
28	DG	71	LEU	2.1
36	DO	97	PHE	2.1
40	DS	51	LEU	2.1
4	AD	4	TYR	2.1
7	CG	51	ALA	2.1
7	CG	78	ARG	2.1
10	CJ	94	ALA	2.1
13	CM	29	ARG	2.1
22	DA	478	A	2.1
22	DA	505	A	2.1
22	DA	1247	A	2.1
26	DE	50	ALA	2.1
27	DF	119	ALA	2.1
33	DL	78	ARG	2.1
38	DQ	47	TYR	2.1
40	DS	18	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1020	G	2.1
7	CG	67	GLU	2.1
13	AM	39	ILE	2.1
13	CM	72	GLU	2.1
22	BA	1062	G	2.1
22	DA	17	G	2.1
22	DA	212	G	2.1
22	DA	914	G	2.1
22	DA	1062	G	2.1
22	DA	1071	G	2.1
22	DA	1238	G	2.1
22	DA	1643	G	2.1
22	DA	1738	G	2.1
22	DA	2123	G	2.1
23	DB	24	G	2.1
30	BI	135	SER	2.1
33	DL	135	ILE	2.1
35	BN	119	SER	2.1
39	DR	70	GLU	2.1
44	DW	83	GLU	2.1
1	CA	183	C	2.1
1	CA	990	C	2.1
1	CA	1367	C	2.1
23	DB	90	C	2.1
30	DI	31	GLN	2.1
36	DO	98	GLN	2.1
40	DS	15	GLN	2.1
50	D2	6	GLN	2.1
4	AD	206	LYS	2.1
4	CD	148	LYS	2.1
5	AE	146	ASN	2.1
24	DC	44	ASN	2.1
24	DC	162	VAL	2.1
26	DE	58	LYS	2.1
53	B5	168	LYS	2.1
53	B5	223	VAL	2.1
1	CA	950	U	2.1
22	BA	2180	U	2.1
22	DA	224	U	2.1
22	DA	288	U	2.1
22	DA	431	U	2.1
22	DA	1065	U	2.1

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Mol	Chain	Res	Type	RSRZ
22	DA	2696	U	2.1
14	AN	46	LEU	2.1
25	DD	6	GLY	2.1
26	DE	81	GLY	2.1
26	DE	118	LEU	2.1
27	DF	123	ASP	2.1
30	DI	16	GLY	2.1
30	DI	89	GLY	2.1
33	DL	79	LEU	2.1
33	DL	102	GLY	2.1
33	DL	125	LEU	2.1
46	DY	37	LEU	2.1
53	B5	48	LEU	2.1
4	AD	169	THR	2.1
17	AQ	7	THR	2.1
33	DL	118	THR	2.1
42	DU	15	THR	2.1
40	BS	110	ARG	2.1
42	DU	94	ARG	2.1
50	D2	41	ARG	2.1
3	AC	207	ILE	2.1
3	CC	137	ALA	2.1
10	AJ	34	ALA	2.1
14	AN	29	ALA	2.1
24	DC	61	ALA	2.1
25	BD	86	GLU	2.1
27	DF	104	ILE	2.1
27	DF	137	ILE	2.1
34	DM	43	ALA	2.1
37	DP	84	ILE	2.1
40	DS	14	ALA	2.1
43	DV	30	ILE	2.1
53	B5	46	ALA	2.1
7	AG	44	TYR	2.1
10	CJ	47	GLU	2.1
28	DG	94	TYR	2.1
29	BH	48	GLU	2.1
31	DJ	53	TYR	2.1
22	BA	1916	A	2.1
22	DA	53	A	2.1
22	DA	1626	A	2.1
27	BF	81	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	CA	82	G	2.1
1	CA	207	C	2.1
1	CA	939	G	2.1
1	CA	1003	G	2.1
1	CA	1214	C	2.1
1	CA	1304	G	2.1
3	AC	80	LYS	2.1
4	AD	137	VAL	2.1
5	AE	26	LYS	2.1
11	AK	85	MET	2.1
12	CL	96	HIS	2.1
8	CH	25	VAL	2.1
21	CU	46	LYS	2.1
22	BA	2308	G	2.1
22	DA	45	G	2.1
22	DA	187	G	2.1
22	DA	559	G	2.1
22	DA	1324	G	2.1
22	DA	1903	G	2.1
22	DA	2035	G	2.1
30	BI	140	VAL	2.1
31	DJ	2	LYS	2.1
42	DU	21	LYS	2.1
28	DG	112	PRO	2.1
5	CE	146	ASN	2.1
9	CI	4	ASN	2.1
16	CP	26	ASN	2.1
24	DC	24	LEU	2.1
30	DI	138	LEU	2.1
49	D1	34	LEU	2.1
2	AB	90	PHE	2.1
4	AD	72	PHE	2.1
17	CQ	10	GLY	2.1
19	AS	41	PHE	2.1
22	DA	499	U	2.1
27	DF	93	GLY	2.1
53	B5	144	GLY	2.1
7	AG	84	THR	2.1
10	CJ	69	THR	2.1
14	CN	53	ARG	2.1
17	AQ	11	ARG	2.1
17	CQ	6	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
27	DF	90	THR	2.1
27	DF	155	THR	2.1
38	DQ	50	ARG	2.1
2	CB	41	ILE	2.1
2	CB	61	ALA	2.1
4	CD	27	ALA	2.1
6	AF	51	ILE	2.1
13	AM	5	ALA	2.1
26	DE	142	ALA	2.1
27	DF	44	ILE	2.1
38	DQ	21	ALA	2.1
33	DL	144	GLU	2.1
43	DV	41	GLU	2.1
38	DQ	24	TYR	2.1
9	CI	73	SER	2.0
27	BF	72	LYS	2.0
29	DH	113	SER	2.0
38	DQ	103	LYS	2.0
39	DR	81	LYS	2.0
42	DU	4	LYS	2.0
13	CM	91	HIS	2.0
1	AA	77	A	2.0
1	CA	74	A	2.0
1	CA	1044	A	2.0
1	CA	1280	A	2.0
6	AF	89	VAL	2.0
9	AI	47	VAL	2.0
22	DA	423	A	2.0
22	DA	1652	A	2.0
22	DA	1785	A	2.0
38	DQ	104	VAL	2.0
53	B5	215	VAL	2.0
31	DJ	137	PRO	2.0
44	DW	74	PRO	2.0
16	CP	29	ASN	2.0
22	BA	1064	C	2.0
36	DO	83	LEU	2.0
1	CA	1154	G	2.0
1	CA	1343	G	2.0
9	CI	95	ARG	2.0
15	AO	17	ARG	2.0
22	BA	1910	G	2.0

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Mol	Chain	Res	Type	RSRZ
22	DA	107	G	2.0
22	DA	1177	G	2.0
22	DA	1426	G	2.0
22	DA	1770	G	2.0
22	DA	2061	G	2.0
22	DA	2697	G	2.0
22	DA	2885	G	2.0
33	DL	31	GLY	2.0
33	DL	60	ARG	2.0
34	DM	18	ARG	2.0
34	DM	23	GLY	2.0
36	DO	10	ARG	2.0
52	D4	12	ARG	2.0
1	AA	1040	U	2.0
1	CA	224	U	2.0
1	CA	843	U	2.0
1	CA	1464	U	2.0
2	CB	189	THR	2.0
4	CD	200	ILE	2.0
9	AI	28	ILE	2.0
13	CM	33	ILE	2.0
22	DA	321	U	2.0
22	DA	589	U	2.0
13	CM	2	ALA	2.0
14	CN	18	ASP	2.0
24	DC	74	ILE	2.0
29	BH	86	ASP	2.0
37	DP	50	ILE	2.0
38	DQ	10	ALA	2.0
48	D0	24	ALA	2.0
53	B5	192	ALA	2.0
5	CE	151	GLU	2.0
14	CN	10	GLU	2.0
16	CP	60	TRP	2.0
5	AE	86	LYS	2.0
9	AI	90	TYR	2.0
12	CL	117	TYR	2.0
21	AU	49	LYS	2.0
26	DE	137	LYS	2.0
37	DP	29	LYS	2.0
50	D2	11	LYS	2.0
29	BH	1	MET	2.0

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Mol	Chain	Res	Type	RSRZ
10	AJ	77	VAL	2.0
29	BH	142	VAL	2.0
33	BL	122	VAL	2.0
41	DT	16	VAL	2.0
53	B5	213	VAL	2.0
7	CG	14	PRO	2.0
7	CG	93	PRO	2.0
9	CI	51	PRO	2.0
13	CM	10	PRO	2.0
1	AA	1012	A	2.0
1	CA	1000	A	2.0
1	CA	1019	A	2.0
1	CA	1150	A	2.0
14	CN	46	LEU	2.0
20	CT	66	LEU	2.0
20	CT	86	LEU	2.0
22	DA	222	A	2.0
22	DA	501	A	2.0
26	DE	27	LEU	2.0
28	BG	105	LEU	2.0
28	DG	72	LEU	2.0
34	DM	20	LEU	2.0
51	D3	62	LEU	2.0
7	CG	79	ARG	2.0
13	AM	109	ARG	2.0
21	CU	18	ARG	2.0
25	DD	77	ARG	2.0
38	DQ	30	ARG	2.0
38	DQ	51	ARG	2.0
53	B5	155	ARG	2.0
9	CI	40	GLY	2.0
19	AS	74	PHE	2.0
24	DC	266	PHE	2.0
25	DD	147	GLY	2.0
38	DQ	79	PHE	2.0
43	DV	2	PHE	2.0
1	CA	1027	C	2.0
1	CA	1051	C	2.0
3	CC	207	ILE	2.0
22	BA	275	C	2.0
22	DA	183	C	2.0
22	DA	584	C	2.0

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Mol	Chain	Res	Type	RSRZ
22	DA	885	C	2.0
22	DA	1414	C	2.0
22	DA	2178	C	2.0
22	DA	2691	C	2.0
23	DB	88	C	2.0
27	BF	85	ILE	2.0
2	CB	83	ALA	2.0
7	CG	134	ALA	2.0
12	CL	3	THR	2.0
13	CM	28	THR	2.0
17	CQ	74	THR	2.0
21	CU	52	ALA	2.0
24	DC	252	THR	2.0
31	DJ	133	ALA	2.0
41	DT	41	ALA	2.0
46	DY	32	ALA	2.0
1	AA	93	U	2.0
1	CA	1313	U	2.0
4	AD	99	ASP	2.0
22	BA	1911	U	2.0
22	DA	1779	U	2.0
23	DB	87	U	2.0
29	BH	129	GLU	2.0
29	DH	101	ASP	2.0
1	CA	102	G	2.0
1	CA	380	G	2.0
1	CA	1241	G	2.0
1	CA	1260	G	2.0
1	CA	1309	G	2.0
1	CA	1338	G	2.0
22	DA	46	G	2.0
22	DA	1733	G	2.0
22	DA	2107	G	2.0
32	DK	111	LYS	2.0
41	DT	88	LYS	2.0
35	DN	20	MET	2.0
7	CG	94	VAL	2.0
9	AI	104	VAL	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	004	D6	7	10/11	0.82	0.17	38,42,48,48	0
54	DBB	D6	3	6/7	0.83	0.16	37,40,41,43	0
54	MHW	D6	1	9/10	0.83	0.19	49,54,56,59	0
54	MHU	D6	5	15/16	0.85	0.19	37,42,54,56	0
54	MHV	D6	6	9/10	0.89	0.10	39,40,42,43	0
54	MHU	B6	5	15/16	0.95	0.10	0,5,18,21	0
54	004	B6	7	10/11	0.95	0.11	3,6,7,10	0
54	MHW	B6	1	9/10	0.95	0.10	12,14,18,21	0
54	MHV	B6	6	9/10	0.96	0.07	2,6,13,14	0
54	DBB	B6	3	6/7	0.97	0.09	6,8,10,15	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	AA	1648	1/1	0.45	0.10	38,38,38,38	0
55	MG	DA	3060	1/1	0.46	0.56	61,61,61,61	0
55	MG	CA	1636	1/1	0.53	0.21	79,79,79,79	0
55	MG	DA	3070	1/1	0.54	0.25	58,58,58,58	0
55	MG	DA	3119	1/1	0.61	0.36	68,68,68,68	0
55	MG	AA	1614	1/1	0.65	0.34	53,53,53,53	0
55	MG	DA	3158	1/1	0.65	0.14	55,55,55,55	0
55	MG	BA	3040	1/1	0.66	0.28	7,7,7,7	0
55	MG	DA	3155	1/1	0.66	0.31	44,44,44,44	0
55	MG	DA	3015	1/1	0.66	0.34	56,56,56,56	0
55	MG	AA	1657	1/1	0.67	0.24	40,40,40,40	0
55	MG	BA	3188	1/1	0.68	0.15	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	DA	3137	1/1	0.69	0.27	42,42,42,42	0
55	MG	DA	3041	1/1	0.70	0.25	53,53,53,53	0
55	MG	CA	1633	1/1	0.71	0.27	54,54,54,54	0
55	MG	BA	3098	1/1	0.71	0.37	58,58,58,58	0
55	MG	DA	3057	1/1	0.71	0.36	54,54,54,54	0
55	MG	AA	1615	1/1	0.72	0.13	46,46,46,46	0
55	MG	DA	3091	1/1	0.72	0.30	71,71,71,71	0
55	MG	DA	3076	1/1	0.73	0.24	48,48,48,48	0
55	MG	DA	3151	1/1	0.73	0.22	45,45,45,45	0
55	MG	DA	3161	1/1	0.73	0.11	42,42,42,42	0
55	MG	DA	3143	1/1	0.74	0.09	46,46,46,46	0
55	MG	CA	1652	1/1	0.75	0.12	39,39,39,39	0
55	MG	DA	3124	1/1	0.75	0.21	59,59,59,59	0
55	MG	DA	3131	1/1	0.75	0.36	71,71,71,71	0
55	MG	DA	3033	1/1	0.76	0.16	45,45,45,45	0
55	MG	BA	3060	1/1	0.76	0.37	33,33,33,33	0
55	MG	DA	3163	1/1	0.76	0.16	51,51,51,51	0
55	MG	BA	3061	1/1	0.77	0.32	55,55,55,55	0
55	MG	DA	3126	1/1	0.77	0.10	57,57,57,57	0
55	MG	DA	3090	1/1	0.77	0.16	58,58,58,58	0
55	MG	CA	1643	1/1	0.77	0.23	44,44,44,44	0
55	MG	BA	3179	1/1	0.77	0.21	39,39,39,39	0
55	MG	CM	201	1/1	0.78	0.13	46,46,46,46	0
55	MG	DA	3040	1/1	0.78	0.18	57,57,57,57	0
55	MG	DA	3115	1/1	0.79	0.13	58,58,58,58	0
55	MG	DA	3148	1/1	0.79	0.19	45,45,45,45	0
55	MG	CA	1609	1/1	0.79	0.17	58,58,58,58	0
55	MG	DA	3153	1/1	0.79	0.13	52,52,52,52	0
55	MG	CA	1628	1/1	0.79	0.26	64,64,64,64	0
55	MG	AA	1652	1/1	0.79	0.23	43,43,43,43	0
55	MG	DA	3046	1/1	0.79	0.18	53,53,53,53	0
55	MG	BA	3105	1/1	0.79	0.19	4,4,4,4	0
55	MG	CA	1635	1/1	0.80	0.14	76,76,76,76	0
55	MG	CA	1605	1/1	0.80	0.22	57,57,57,57	0
55	MG	BA	3157	1/1	0.80	0.23	26,26,26,26	0
55	MG	DA	3045	1/1	0.80	0.13	53,53,53,53	0
55	MG	DA	3016	1/1	0.80	0.26	53,53,53,53	0
55	MG	DA	3102	1/1	0.81	0.16	45,45,45,45	0
55	MG	BA	3015	1/1	0.81	0.24	52,52,52,52	0
55	MG	DA	3099	1/1	0.81	0.19	53,53,53,53	0
55	MG	DA	3034	1/1	0.82	0.26	56,56,56,56	0
55	MG	CA	1642	1/1	0.82	0.21	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	CA	1655	1/1	0.82	0.10	44,44,44,44	0
55	MG	DA	3092	1/1	0.82	0.24	62,62,62,62	0
55	MG	BA	3102	1/1	0.82	0.29	23,23,23,23	0
55	MG	DA	3047	1/1	0.83	0.20	66,66,66,66	0
55	MG	DA	3054	1/1	0.83	0.19	44,44,44,44	0
55	MG	DA	3055	1/1	0.83	0.34	53,53,53,53	0
55	MG	DA	3056	1/1	0.83	0.21	51,51,51,51	0
55	MG	DA	3039	1/1	0.83	0.08	53,53,53,53	0
55	MG	BA	3150	1/1	0.83	0.27	42,42,42,42	0
55	MG	BA	3116	1/1	0.83	0.15	11,11,11,11	0
55	MG	BA	3126	1/1	0.83	0.23	7,7,7,7	0
55	MG	DA	3006	1/1	0.83	0.19	64,64,64,64	0
55	MG	DA	3135	1/1	0.84	0.21	47,47,47,47	0
55	MG	DA	3093	1/1	0.84	0.10	65,65,65,65	0
55	MG	DA	3140	1/1	0.84	0.24	37,37,37,37	0
55	MG	BA	3191	1/1	0.84	0.14	35,35,35,35	0
55	MG	AA	1638	1/1	0.84	0.14	51,51,51,51	0
55	MG	DA	3106	1/1	0.84	0.08	56,56,56,56	0
55	MG	BA	3109	1/1	0.84	0.13	9,9,9,9	0
55	MG	BA	3173	1/1	0.84	0.10	20,20,20,20	0
55	MG	AA	1608	1/1	0.84	0.11	24,24,24,24	0
55	MG	AA	1671	1/1	0.84	0.13	35,35,35,35	0
55	MG	DA	3004	1/1	0.84	0.19	64,64,64,64	0
55	MG	DA	3098	1/1	0.85	0.28	63,63,63,63	0
55	MG	CA	1604	1/1	0.85	0.11	70,70,70,70	0
55	MG	DA	3013	1/1	0.85	0.24	45,45,45,45	0
55	MG	CA	1650	1/1	0.85	0.37	40,40,40,40	0
55	MG	DA	3111	1/1	0.85	0.09	42,42,42,42	0
55	MG	BA	3055	1/1	0.85	0.17	23,23,23,23	0
55	MG	DA	3026	1/1	0.85	0.10	53,53,53,53	0
55	MG	BA	3161	1/1	0.85	0.09	24,24,24,24	0
55	MG	DA	3125	1/1	0.85	0.09	51,51,51,51	0
55	MG	CA	1638	1/1	0.85	0.15	55,55,55,55	0
55	MG	AA	1620	1/1	0.85	0.09	44,44,44,44	0
55	MG	DA	3164	1/1	0.85	0.14	47,47,47,47	0
55	MG	DA	3031	1/1	0.86	0.19	50,50,50,50	0
55	MG	DA	3113	1/1	0.86	0.09	42,42,42,42	0
55	MG	DA	3147	1/1	0.86	0.10	49,49,49,49	0
55	MG	DA	3010	1/1	0.86	0.09	48,48,48,48	0
55	MG	AA	1664	1/1	0.86	0.10	36,36,36,36	0
55	MG	BA	3154	1/1	0.86	0.09	29,29,29,29	0
55	MG	BA	3143	1/1	0.86	0.17	7,7,7,7	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	DA	3025	1/1	0.86	0.34	49,49,49,49	0
55	MG	DA	3009	1/1	0.86	0.09	57,57,57,57	0
55	MG	DA	3104	1/1	0.86	0.12	54,54,54,54	0
55	MG	DA	3029	1/1	0.86	0.26	41,41,41,41	0
55	MG	AA	1605	1/1	0.87	0.10	32,32,32,32	0
55	MG	BA	3079	1/1	0.87	0.09	28,28,28,28	0
55	MG	BA	3146	1/1	0.87	0.19	23,23,23,23	0
55	MG	DA	3138	1/1	0.87	0.26	41,41,41,41	0
55	MG	BA	3087	1/1	0.87	0.12	18,18,18,18	0
55	MG	AA	1660	1/1	0.87	0.20	40,40,40,40	0
55	MG	CA	1611	1/1	0.87	0.17	55,55,55,55	0
55	MG	DA	3059	1/1	0.87	0.20	53,53,53,53	0
55	MG	BA	3034	1/1	0.87	0.29	18,18,18,18	0
55	MG	DA	3005	1/1	0.87	0.14	66,66,66,66	0
55	MG	DA	3116	1/1	0.87	0.11	51,51,51,51	0
55	MG	AA	1662	1/1	0.87	0.07	41,41,41,41	0
55	MG	DA	3160	1/1	0.87	0.10	35,35,35,35	0
55	MG	BA	3171	1/1	0.87	0.08	29,29,29,29	0
55	MG	AA	1646	1/1	0.87	0.09	44,44,44,44	0
55	MG	AA	1668	1/1	0.87	0.06	18,18,18,18	0
55	MG	BA	3117	1/1	0.88	0.04	4,4,4,4	0
55	MG	CA	1637	1/1	0.88	0.20	51,51,51,51	0
55	MG	BA	3119	1/1	0.88	0.28	21,21,21,21	0
55	MG	DA	3008	1/1	0.88	0.31	51,51,51,51	0
55	MG	BA	3036	1/1	0.88	0.18	19,19,19,19	0
55	MG	DA	3062	1/1	0.88	0.09	44,44,44,44	0
55	MG	DA	3112	1/1	0.88	0.11	52,52,52,52	0
55	MG	BA	3133	1/1	0.88	0.26	40,40,40,40	0
55	MG	CA	1647	1/1	0.88	0.16	24,24,24,24	0
55	MG	DA	3086	1/1	0.88	0.08	53,53,53,53	0
55	MG	DA	3087	1/1	0.88	0.11	51,51,51,51	0
55	MG	BA	3029	1/1	0.88	0.13	15,15,15,15	0
55	MG	BA	3111	1/1	0.88	0.10	23,23,23,23	0
55	MG	BA	3025	1/1	0.88	0.23	40,40,40,40	0
55	MG	BA	3190	1/1	0.88	0.13	33,33,33,33	0
55	MG	AM	201	1/1	0.89	0.07	29,29,29,29	0
55	MG	BA	3175	1/1	0.89	0.11	27,27,27,27	0
55	MG	BA	3077	1/1	0.89	0.07	26,26,26,26	0
55	MG	AA	1617	1/1	0.89	0.18	44,44,44,44	0
55	MG	BA	3023	1/1	0.89	0.11	15,15,15,15	0
55	MG	DA	3152	1/1	0.89	0.09	41,41,41,41	0
55	MG	AA	1669	1/1	0.89	0.17	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	DA	3036	1/1	0.89	0.13	61,61,61,61	0
55	MG	DA	3014	1/1	0.89	0.08	43,43,43,43	0
55	MG	DA	3061	1/1	0.89	0.40	53,53,53,53	0
55	MG	BA	3057	1/1	0.89	0.16	20,20,20,20	0
55	MG	AA	1654	1/1	0.89	0.31	40,40,40,40	0
55	MG	DA	3023	1/1	0.89	0.09	35,35,35,35	0
55	MG	DA	3165	1/1	0.89	0.29	34,34,34,34	0
55	MG	DA	3166	1/1	0.89	0.07	34,34,34,34	0
55	MG	DQ	201	1/1	0.89	0.19	32,32,32,32	0
55	MG	AA	1653	1/1	0.90	0.16	24,24,24,24	0
55	MG	BA	3004	1/1	0.90	0.14	33,33,33,33	0
55	MG	AA	1632	1/1	0.90	0.11	40,40,40,40	0
55	MG	DA	3139	1/1	0.90	0.24	31,31,31,31	0
55	MG	BA	3159	1/1	0.90	0.13	19,19,19,19	0
55	MG	DA	3142	1/1	0.90	0.26	38,38,38,38	0
55	MG	CA	1644	1/1	0.90	0.11	32,32,32,32	0
55	MG	BA	3160	1/1	0.90	0.20	7,7,7,7	0
55	MG	CA	1649	1/1	0.90	0.14	35,35,35,35	0
55	MG	BA	3045	1/1	0.90	0.10	13,13,13,13	0
55	MG	CA	1651	1/1	0.90	0.13	48,48,48,48	0
55	MG	BA	3170	1/1	0.90	0.09	35,35,35,35	0
55	MG	DA	3154	1/1	0.90	0.11	45,45,45,45	0
55	MG	DA	3114	1/1	0.90	0.18	64,64,64,64	0
55	MG	CA	1653	1/1	0.90	0.13	47,47,47,47	0
55	MG	CA	1614	1/1	0.90	0.07	44,44,44,44	0
55	MG	BA	3046	1/1	0.90	0.14	8,8,8,8	0
55	MG	DA	3123	1/1	0.90	0.09	47,47,47,47	0
55	MG	CA	1631	1/1	0.90	0.19	62,62,62,62	0
55	MG	AA	1637	1/1	0.90	0.10	18,18,18,18	0
55	MG	AA	1659	1/1	0.90	0.24	34,34,34,34	0
55	MG	AA	1630	1/1	0.90	0.11	49,49,49,49	0
55	MG	AA	1651	1/1	0.91	0.22	32,32,32,32	0
55	MG	CA	1621	1/1	0.91	0.08	53,53,53,53	0
55	MG	DA	3144	1/1	0.91	0.12	52,52,52,52	0
55	MG	DA	3145	1/1	0.91	0.10	37,37,37,37	0
55	MG	AA	1667	1/1	0.91	0.05	37,37,37,37	0
55	MG	DA	3084	1/1	0.91	0.20	56,56,56,56	0
55	MG	DA	3149	1/1	0.91	0.35	36,36,36,36	0
55	MG	DA	3011	1/1	0.91	0.25	46,46,46,46	0
55	MG	DA	3118	1/1	0.91	0.16	45,45,45,45	0
55	MG	BA	3125	1/1	0.91	0.10	8,8,8,8	0
55	MG	CA	1601	1/1	0.91	0.09	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	BA	3076	1/1	0.91	0.15	17,17,17,17	0
55	MG	BA	3174	1/1	0.91	0.08	20,20,20,20	0
55	MG	CA	1606	1/1	0.91	0.21	52,52,52,52	0
55	MG	CA	1608	1/1	0.91	0.18	50,50,50,50	0
55	MG	DA	3001	1/1	0.91	0.14	43,43,43,43	0
55	MG	DA	3028	1/1	0.91	0.10	50,50,50,50	0
55	MG	CA	1641	1/1	0.91	0.35	46,46,46,46	0
55	MG	BA	3113	1/1	0.91	0.15	10,10,10,10	0
55	MG	AA	1624	1/1	0.91	0.17	39,39,39,39	0
55	MG	DA	3127	1/1	0.92	0.10	47,47,47,47	0
55	MG	DA	3078	1/1	0.92	0.07	64,64,64,64	0
55	MG	CA	1602	1/1	0.92	0.07	61,61,61,61	0
55	MG	BA	3019	1/1	0.92	0.19	3,3,3,3	0
55	MG	AA	1665	1/1	0.92	0.11	34,34,34,34	0
55	MG	AA	1649	1/1	0.92	0.08	27,27,27,27	0
55	MG	AA	1643	1/1	0.92	0.10	19,19,19,19	0
55	MG	DA	3141	1/1	0.92	0.17	28,28,28,28	0
55	MG	DA	3044	1/1	0.92	0.08	61,61,61,61	0
55	MG	BA	3112	1/1	0.92	0.06	11,11,11,11	0
55	MG	CA	1646	1/1	0.92	0.07	40,40,40,40	0
55	MG	BA	3176	1/1	0.92	0.11	24,24,24,24	0
55	MG	DA	3146	1/1	0.92	0.04	35,35,35,35	0
55	MG	DA	3048	1/1	0.92	0.15	51,51,51,51	0
55	MG	DA	3051	1/1	0.92	0.06	35,35,35,35	0
55	MG	DA	3053	1/1	0.92	0.10	43,43,43,43	0
55	MG	DA	3109	1/1	0.92	0.15	37,37,37,37	0
55	MG	AA	1644	1/1	0.92	0.06	32,32,32,32	0
55	MG	BA	3182	1/1	0.92	0.14	22,22,22,22	0
55	MG	CA	1627	1/1	0.92	0.18	59,59,59,59	0
55	MG	DA	3024	1/1	0.92	0.12	45,45,45,45	0
55	MG	AA	1661	1/1	0.92	0.06	22,22,22,22	0
55	MG	CA	1630	1/1	0.92	0.19	66,66,66,66	0
55	MG	AA	1627	1/1	0.92	0.22	43,43,43,43	0
55	MG	AA	1663	1/1	0.92	0.08	35,35,35,35	0
55	MG	BB	201	1/1	0.92	0.07	28,28,28,28	0
55	MG	DA	3071	1/1	0.92	0.22	59,59,59,59	0
55	MG	DA	3074	1/1	0.92	0.10	41,41,41,41	0
55	MG	AA	1635	1/1	0.92	0.12	37,37,37,37	0
55	MG	DA	3133	1/1	0.93	0.38	57,57,57,57	0
55	MG	BA	3093	1/1	0.93	0.10	16,16,16,16	0
55	MG	BA	3194	1/1	0.93	0.07	28,28,28,28	0
55	MG	CA	1629	1/1	0.93	0.08	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	DA	3018	1/1	0.93	0.14	57,57,57,57	0
55	MG	AA	1634	1/1	0.93	0.07	36,36,36,36	0
55	MG	BA	3123	1/1	0.93	0.09	18,18,18,18	0
55	MG	DA	3101	1/1	0.93	0.07	40,40,40,40	0
55	MG	BA	3009	1/1	0.93	0.08	6,6,6,6	0
55	MG	BA	3090	1/1	0.93	0.06	17,17,17,17	0
55	MG	DA	3105	1/1	0.93	0.07	37,37,37,37	0
55	MG	BA	3128	1/1	0.93	0.15	9,9,9,9	0
55	MG	BA	3177	1/1	0.93	0.16	24,24,24,24	0
55	MG	DA	3002	1/1	0.93	0.25	52,52,52,52	0
55	MG	BA	3178	1/1	0.93	0.19	20,20,20,20	0
55	MG	DA	3066	1/1	0.93	0.06	39,39,39,39	0
55	MG	DA	3068	1/1	0.93	0.20	52,52,52,52	0
55	MG	CA	1639	1/1	0.93	0.07	34,34,34,34	0
55	MG	BA	3108	1/1	0.93	0.18	1,1,1,1	0
55	MG	DA	3073	1/1	0.93	0.10	37,37,37,37	0
55	MG	DA	3007	1/1	0.93	0.16	54,54,54,54	0
55	MG	BA	3136	1/1	0.93	0.21	24,24,24,24	0
55	MG	BA	3163	1/1	0.93	0.17	27,27,27,27	0
55	MG	DA	3080	1/1	0.93	0.10	39,39,39,39	0
55	MG	BA	3168	1/1	0.93	0.08	18,18,18,18	0
55	MG	CA	1645	1/1	0.93	0.13	41,41,41,41	0
55	MG	DA	3128	1/1	0.93	0.08	57,57,57,57	0
55	MG	CA	1624	1/1	0.93	0.09	33,33,33,33	0
55	MG	DA	3077	1/1	0.94	0.08	59,59,59,59	0
55	MG	AA	1650	1/1	0.94	0.08	35,35,35,35	0
55	MG	CA	1615	1/1	0.94	0.18	35,35,35,35	0
55	MG	CA	1618	1/1	0.94	0.08	28,28,28,28	0
55	MG	BA	3038	1/1	0.94	0.05	8,8,8,8	0
55	MG	AA	1655	1/1	0.94	0.07	34,34,34,34	0
55	MG	BA	3044	1/1	0.94	0.07	20,20,20,20	0
55	MG	AA	1622	1/1	0.94	0.18	21,21,21,21	0
55	MG	DA	3121	1/1	0.94	0.11	41,41,41,41	0
55	MG	DA	3150	1/1	0.94	0.07	42,42,42,42	0
55	MG	BA	3137	1/1	0.94	0.32	4,4,4,4	0
55	MG	BA	3082	1/1	0.94	0.20	15,15,15,15	0
55	MG	BA	3085	1/1	0.94	0.08	7,7,7,7	0
55	MG	BA	3115	1/1	0.94	0.15	35,35,35,35	0
55	MG	DA	3043	1/1	0.94	0.18	54,54,54,54	0
55	MG	CA	1634	1/1	0.94	0.08	49,49,49,49	0
55	MG	DA	3103	1/1	0.94	0.13	48,48,48,48	0
55	MG	BA	3030	1/1	0.94	0.15	10,10,10,10	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	BA	3047	1/1	0.94	0.10	34,34,34,34	0
55	MG	BA	3033	1/1	0.94	0.15	4,4,4,4	0
55	MG	DA	3107	1/1	0.94	0.08	49,49,49,49	0
55	MG	BA	3003	1/1	0.94	0.06	20,20,20,20	0
55	MG	DA	3110	1/1	0.94	0.24	57,57,57,57	0
55	MG	DA	3067	1/1	0.95	0.06	49,49,49,49	0
55	MG	BA	3181	1/1	0.95	0.09	14,14,14,14	0
55	MG	BA	3144	1/1	0.95	0.09	25,25,25,25	0
55	MG	BA	3114	1/1	0.95	0.07	19,19,19,19	0
55	MG	AA	1623	1/1	0.95	0.11	42,42,42,42	0
55	MG	BA	3152	1/1	0.95	0.07	11,11,11,11	0
55	MG	BA	3153	1/1	0.95	0.13	2,2,2,2	0
55	MG	BA	3195	1/1	0.95	0.07	20,20,20,20	0
55	MG	AA	1631	1/1	0.95	0.10	42,42,42,42	0
55	MG	BB	204	1/1	0.95	0.21	4,4,4,4	0
55	MG	DA	3081	1/1	0.95	0.12	43,43,43,43	0
55	MG	BA	3156	1/1	0.95	0.17	12,12,12,12	0
55	MG	AA	1656	1/1	0.95	0.10	37,37,37,37	0
55	MG	BA	3066	1/1	0.95	0.07	6,6,6,6	0
55	MG	BA	3120	1/1	0.95	0.07	7,7,7,7	0
55	MG	CA	1648	1/1	0.95	0.20	42,42,42,42	0
55	MG	DA	3038	1/1	0.95	0.05	42,42,42,42	0
55	MG	BA	3073	1/1	0.95	0.06	13,13,13,13	0
55	MG	BA	3162	1/1	0.95	0.17	21,21,21,21	0
55	MG	BA	3075	1/1	0.95	0.07	15,15,15,15	0
55	MG	BA	3166	1/1	0.95	0.15	25,25,25,25	0
55	MG	CA	1613	1/1	0.95	0.08	19,19,19,19	0
55	MG	CA	1654	1/1	0.95	0.04	26,26,26,26	0
55	MG	BA	3167	1/1	0.95	0.05	28,28,28,28	0
55	MG	AA	1603	1/1	0.95	0.09	34,34,34,34	0
55	MG	CA	1617	1/1	0.95	0.12	35,35,35,35	0
55	MG	AA	1658	1/1	0.95	0.04	33,33,33,33	0
55	MG	BA	3052	1/1	0.95	0.06	8,8,8,8	0
55	MG	BA	3135	1/1	0.95	0.15	17,17,17,17	0
55	MG	CA	1625	1/1	0.95	0.12	25,25,25,25	0
55	MG	DA	3159	1/1	0.95	0.12	39,39,39,39	0
55	MG	BA	3080	1/1	0.95	0.08	18,18,18,18	0
55	MG	AA	1602	1/1	0.95	0.11	33,33,33,33	0
55	MG	DA	3162	1/1	0.95	0.12	46,46,46,46	0
55	MG	BA	3138	1/1	0.95	0.17	4,4,4,4	0
55	MG	BA	3139	1/1	0.95	0.23	1,1,1,1	0
55	MG	BA	3140	1/1	0.95	0.13	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	DA	3012	1/1	0.95	0.06	40,40,40,40	0
55	MG	DA	3167	1/1	0.95	0.11	59,59,59,59	0
55	MG	BA	3084	1/1	0.95	0.17	12,12,12,12	0
55	MG	CA	1607	1/1	0.96	0.10	42,42,42,42	0
55	MG	DA	3069	1/1	0.96	0.05	63,63,63,63	0
55	MG	DA	3120	1/1	0.96	0.08	49,49,49,49	0
55	MG	AA	1639	1/1	0.96	0.06	51,51,51,51	0
55	MG	DA	3122	1/1	0.96	0.10	42,42,42,42	0
55	MG	BA	3172	1/1	0.96	0.11	23,23,23,23	0
55	MG	DA	3027	1/1	0.96	0.26	51,51,51,51	0
55	MG	AA	1666	1/1	0.96	0.07	30,30,30,30	0
55	MG	DA	3075	1/1	0.96	0.10	48,48,48,48	0
55	MG	BA	3145	1/1	0.96	0.09	15,15,15,15	0
55	MG	AA	1612	1/1	0.96	0.08	24,24,24,24	0
55	MG	BA	3149	1/1	0.96	0.05	1,1,1,1	0
55	MG	DA	3132	1/1	0.96	0.13	45,45,45,45	0
55	MG	DA	3079	1/1	0.96	0.05	62,62,62,62	0
55	MG	BA	3016	1/1	0.96	0.12	17,17,17,17	0
55	MG	DA	3136	1/1	0.96	0.16	57,57,57,57	0
55	MG	AA	1619	1/1	0.96	0.22	43,43,43,43	0
55	MG	BA	3121	1/1	0.96	0.08	22,22,22,22	0
55	MG	DA	3085	1/1	0.96	0.05	42,42,42,42	0
55	MG	BA	3101	1/1	0.96	0.07	2,2,2,2	0
55	MG	BA	3155	1/1	0.96	0.11	15,15,15,15	0
55	MG	DA	3088	1/1	0.96	0.18	51,51,51,51	0
55	MG	BA	3183	1/1	0.96	0.06	24,24,24,24	0
55	MG	BA	3187	1/1	0.96	0.13	28,28,28,28	0
55	MG	AA	1626	1/1	0.96	0.10	26,26,26,26	0
55	MG	BA	3103	1/1	0.96	0.06	9,9,9,9	0
55	MG	DA	3095	1/1	0.96	0.06	49,49,49,49	0
55	MG	DA	3097	1/1	0.96	0.04	44,44,44,44	0
55	MG	BA	3158	1/1	0.96	0.08	20,20,20,20	0
55	MG	CA	1632	1/1	0.96	0.09	54,54,54,54	0
55	MG	DA	3100	1/1	0.96	0.08	43,43,43,43	0
55	MG	BA	3193	1/1	0.96	0.04	12,12,12,12	0
55	MG	DA	3049	1/1	0.96	0.08	49,49,49,49	0
55	MG	AA	1606	1/1	0.96	0.06	31,31,31,31	0
55	MG	BA	3107	1/1	0.96	0.10	6,6,6,6	0
55	MG	DA	3157	1/1	0.96	0.07	47,47,47,47	0
55	MG	BA	3134	1/1	0.96	0.06	8,8,8,8	0
55	MG	BA	3028	1/1	0.96	0.06	4,4,4,4	0
55	MG	AA	1629	1/1	0.96	0.06	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	BA	3048	1/1	0.96	0.08	16,16,16,16	0
55	MG	CA	1603	1/1	0.96	0.09	44,44,44,44	0
55	MG	AA	1601	1/1	0.96	0.06	49,49,49,49	0
55	MG	BA	3083	1/1	0.96	0.15	32,32,32,32	0
55	MG	DA	3021	1/1	0.96	0.06	38,38,38,38	0
55	MG	DA	3063	1/1	0.96	0.11	41,41,41,41	0
55	MG	DA	3022	1/1	0.96	0.08	54,54,54,54	0
55	MG	DB	201	1/1	0.96	0.05	69,69,69,69	0
55	MG	BA	3031	1/1	0.96	0.07	8,8,8,8	0
55	MG	DA	3037	1/1	0.97	0.04	45,45,45,45	0
55	MG	DA	3083	1/1	0.97	0.12	61,61,61,61	0
55	MG	BA	3078	1/1	0.97	0.05	33,33,33,33	0
55	MG	CA	1619	1/1	0.97	0.07	26,26,26,26	0
55	MG	DA	3130	1/1	0.97	0.04	51,51,51,51	0
55	MG	AA	1613	1/1	0.97	0.04	20,20,20,20	0
55	MG	CA	1622	1/1	0.97	0.08	40,40,40,40	0
55	MG	CA	1623	1/1	0.97	0.19	40,40,40,40	0
55	MG	DA	3134	1/1	0.97	0.06	34,34,34,34	0
55	MG	DA	3089	1/1	0.97	0.19	58,58,58,58	0
55	MG	BA	3010	1/1	0.97	0.07	3,3,3,3	0
55	MG	DA	3003	1/1	0.97	0.05	52,52,52,52	0
55	MG	BA	3148	1/1	0.97	0.15	16,16,16,16	0
55	MG	CA	1626	1/1	0.97	0.05	42,42,42,42	0
55	MG	BA	3051	1/1	0.97	0.07	6,6,6,6	0
55	MG	DA	3096	1/1	0.97	0.15	52,52,52,52	0
55	MG	BA	3012	1/1	0.97	0.10	4,4,4,4	0
55	MG	BA	3151	1/1	0.97	0.12	31,31,31,31	0
55	MG	BA	3054	1/1	0.97	0.07	5,5,5,5	0
55	MG	AA	1616	1/1	0.97	0.06	42,42,42,42	0
55	MG	BA	3086	1/1	0.97	0.08	9,9,9,9	0
55	MG	AA	1645	1/1	0.97	0.08	39,39,39,39	0
55	MG	BA	3088	1/1	0.97	0.13	32,32,32,32	0
55	MG	BA	3059	1/1	0.97	0.16	16,16,16,16	0
55	MG	BA	3091	1/1	0.97	0.06	28,28,28,28	0
55	MG	BA	3092	1/1	0.97	0.11	20,20,20,20	0
55	MG	BA	3002	1/1	0.97	0.10	15,15,15,15	0
55	MG	DA	3020	1/1	0.97	0.20	42,42,42,42	0
55	MG	BA	3129	1/1	0.97	0.08	5,5,5,5	0
55	MG	BA	3132	1/1	0.97	0.12	27,27,27,27	0
55	MG	DA	3156	1/1	0.97	0.09	30,30,30,30	0
55	MG	BA	3020	1/1	0.97	0.06	7,7,7,7	0
55	MG	AA	1610	1/1	0.97	0.12	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	BA	3067	1/1	0.97	0.08	5,5,5,5	0
55	MG	BA	3071	1/1	0.97	0.10	11,11,11,11	0
55	MG	BA	3041	1/1	0.97	0.05	11,11,11,11	0
55	MG	DA	3117	1/1	0.97	0.05	49,49,49,49	0
55	MG	BA	3106	1/1	0.97	0.19	0,0,0,0	0
55	MG	AA	1618	1/1	0.97	0.05	35,35,35,35	0
55	MG	BA	3027	1/1	0.97	0.09	22,22,22,22	0
55	MG	DA	3032	1/1	0.97	0.10	49,49,49,49	0
55	MG	BA	3141	1/1	0.97	0.28	4,4,4,4	0
55	MG	BA	3142	1/1	0.97	0.28	15,15,15,15	0
55	MG	DB	203	1/1	0.97	0.04	56,56,56,56	0
55	MG	BA	3007	1/1	0.97	0.05	25,25,25,25	0
55	MG	BA	3169	1/1	0.98	0.14	24,24,24,24	0
55	MG	DA	3030	1/1	0.98	0.06	44,44,44,44	0
55	MG	AA	1636	1/1	0.98	0.13	26,26,26,26	0
55	MG	BA	3089	1/1	0.98	0.03	12,12,12,12	0
55	MG	BA	3021	1/1	0.98	0.06	1,1,1,1	0
55	MG	AA	1604	1/1	0.98	0.06	45,45,45,45	0
55	MG	DA	3035	1/1	0.98	0.06	38,38,38,38	0
55	MG	BA	3024	1/1	0.98	0.09	7,7,7,7	0
55	MG	BA	3074	1/1	0.98	0.08	20,20,20,20	0
55	MG	BA	3147	1/1	0.98	0.18	13,13,13,13	0
55	MG	CA	1616	1/1	0.98	0.04	29,29,29,29	0
55	MG	AA	1609	1/1	0.98	0.08	20,20,20,20	0
55	MG	BA	3100	1/1	0.98	0.06	6,6,6,6	0
55	MG	DA	3042	1/1	0.98	0.05	49,49,49,49	0
55	MG	BA	3124	1/1	0.98	0.18	21,21,21,21	0
55	MG	CA	1620	1/1	0.98	0.10	46,46,46,46	0
55	MG	DA	3094	1/1	0.98	0.14	59,59,59,59	0
55	MG	BA	3026	1/1	0.98	0.05	7,7,7,7	0
55	MG	BA	3008	1/1	0.98	0.04	9,9,9,9	0
55	MG	BA	3127	1/1	0.98	0.04	1,1,1,1	0
55	MG	BA	3184	1/1	0.98	0.12	23,23,23,23	0
55	MG	BA	3185	1/1	0.98	0.07	11,11,11,11	0
55	MG	BA	3186	1/1	0.98	0.24	18,18,18,18	0
55	MG	DA	3052	1/1	0.98	0.04	35,35,35,35	0
55	MG	AA	1621	1/1	0.98	0.07	33,33,33,33	0
55	MG	BA	3104	1/1	0.98	0.11	1,1,1,1	0
55	MG	BA	3189	1/1	0.98	0.09	3,3,3,3	0
55	MG	BA	3130	1/1	0.98	0.10	4,4,4,4	0
55	MG	BA	3131	1/1	0.98	0.16	35,35,35,35	0
55	MG	BA	3192	1/1	0.98	0.08	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	DA	3108	1/1	0.98	0.12	35,35,35,35	0
55	MG	AA	1670	1/1	0.98	0.20	26,26,26,26	0
55	MG	BA	3011	1/1	0.98	0.14	13,13,13,13	0
55	MG	DA	3017	1/1	0.98	0.03	40,40,40,40	0
55	MG	AA	1640	1/1	0.98	0.07	39,39,39,39	0
55	MG	DA	3019	1/1	0.98	0.09	47,47,47,47	0
55	MG	BA	3014	1/1	0.98	0.04	6,6,6,6	0
55	MG	BB	202	1/1	0.98	0.04	11,11,11,11	0
55	MG	BB	203	1/1	0.98	0.04	10,10,10,10	0
55	MG	BA	3058	1/1	0.98	0.04	13,13,13,13	0
55	MG	BA	3110	1/1	0.98	0.10	23,23,23,23	0
55	MG	DA	3072	1/1	0.98	0.17	42,42,42,42	0
55	MG	BA	3164	1/1	0.98	0.29	21,21,21,21	0
55	MG	AA	1641	1/1	0.98	0.05	20,20,20,20	0
55	MG	DB	202	1/1	0.98	0.03	42,42,42,42	0
55	MG	BA	3001	1/1	0.98	0.06	10,10,10,10	0
55	MG	AA	1625	1/1	0.98	0.06	31,31,31,31	0
56	ZN	B4	101	1/1	0.98	0.08	131,131,131,131	0
55	MG	BA	3070	1/1	0.99	0.13	9,9,9,9	0
55	MG	DA	3129	1/1	0.99	0.03	38,38,38,38	0
55	MG	AA	1647	1/1	0.99	0.04	39,39,39,39	0
55	MG	BA	3072	1/1	0.99	0.10	4,4,4,4	0
55	MG	BA	3017	1/1	0.99	0.04	6,6,6,6	0
55	MG	BA	3018	1/1	0.99	0.04	27,27,27,27	0
55	MG	BA	3180	1/1	0.99	0.12	25,25,25,25	0
55	MG	AA	1642	1/1	0.99	0.03	24,24,24,24	0
55	MG	AA	1611	1/1	0.99	0.04	18,18,18,18	0
55	MG	BA	3049	1/1	0.99	0.04	9,9,9,9	0
55	MG	BA	3050	1/1	0.99	0.03	11,11,11,11	0
55	MG	BA	3032	1/1	0.99	0.05	8,8,8,8	0
55	MG	DA	3050	1/1	0.99	0.05	29,29,29,29	0
55	MG	AA	1628	1/1	0.99	0.04	37,37,37,37	0
55	MG	BA	3081	1/1	0.99	0.07	1,1,1,1	0
55	MG	BA	3053	1/1	0.99	0.07	4,4,4,4	0
55	MG	BA	3022	1/1	0.99	0.07	3,3,3,3	0
55	MG	BA	3118	1/1	0.99	0.05	11,11,11,11	0
55	MG	BA	3035	1/1	0.99	0.04	2,2,2,2	0
55	MG	BA	3056	1/1	0.99	0.08	10,10,10,10	0
55	MG	DA	3058	1/1	0.99	0.04	37,37,37,37	0
55	MG	AA	1607	1/1	0.99	0.03	33,33,33,33	0
55	MG	BA	3122	1/1	0.99	0.14	2,2,2,2	0
55	MG	AA	1633	1/1	0.99	0.03	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	BA	3039	1/1	0.99	0.03	1,1,1,1	0
55	MG	BA	3005	1/1	0.99	0.04	31,31,31,31	0
55	MG	DA	3065	1/1	0.99	0.03	33,33,33,33	0
55	MG	BA	3006	1/1	0.99	0.04	20,20,20,20	0
55	MG	BA	3062	1/1	0.99	0.08	3,3,3,3	0
55	MG	CA	1640	1/1	0.99	0.14	23,23,23,23	0
55	MG	BA	3063	1/1	0.99	0.06	0,0,0,0	0
55	MG	BA	3064	1/1	0.99	0.05	2,2,2,2	0
55	MG	BA	3165	1/1	0.99	0.07	2,2,2,2	0
55	MG	BA	3094	1/1	0.99	0.04	17,17,17,17	0
55	MG	BA	3096	1/1	0.99	0.03	5,5,5,5	0
55	MG	BA	3097	1/1	0.99	0.03	6,6,6,6	0
55	MG	BA	3065	1/1	0.99	0.04	7,7,7,7	0
55	MG	BA	3099	1/1	0.99	0.04	3,3,3,3	0
55	MG	BA	3042	1/1	0.99	0.06	6,6,6,6	0
55	MG	CA	1610	1/1	0.99	0.03	47,47,47,47	0
55	MG	BA	3043	1/1	0.99	0.02	15,15,15,15	0
55	MG	CA	1612	1/1	0.99	0.04	30,30,30,30	0
55	MG	BA	3068	1/1	0.99	0.04	6,6,6,6	0
55	MG	DA	3082	1/1	0.99	0.10	50,50,50,50	0
55	MG	BA	3069	1/1	0.99	0.06	39,39,39,39	0
56	ZN	D4	101	1/1	0.99	0.07	79,79,79,79	0
55	MG	BA	3095	1/1	1.00	0.03	8,8,8,8	0
55	MG	BA	3037	1/1	1.00	0.08	2,2,2,2	0
55	MG	DA	3064	1/1	1.00	0.02	38,38,38,38	0
55	MG	BA	3013	1/1	1.00	0.07	0,0,0,0	0

6.5 Other polymers (i)

There are no such residues in this entry.