Full wwPDB EM Validation Report

Nov 20, 2022 – 03:20 AM EST

PDB ID	:	4V7B
EMDB ID	:	EMD-5775
Title	:	Visualization of two tRNAs trapped in transit during EF-G-mediated translocation
Authors	:	Ramrath, D.J.F.; Lancaster, L.; Sprink, T.; Mielke, T.; Loerke, J.; Noller, H.F.; Spahn, C.M.T.
Deposited on	:	2013-10-27
Resolution	:	6.80 Å(reported)
Based on initial model	:	4KIY

This is a Full wwPDB EM 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/EMValidationReportHelp
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:

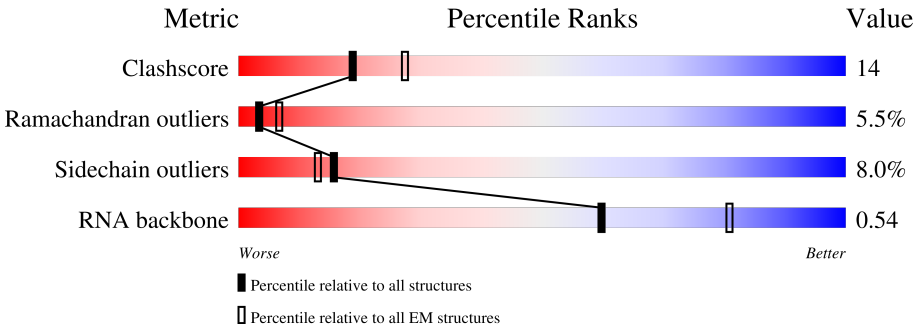
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 6.80 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)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1542	58% 31% 8%
2	AB	241	84% 54% 32% 5% 10%
3	AC	233	41% 63% 22% 12%
4	AD	206	50% 63% 31% 6%
5	AE	167	31% 50% 36% 10%
6	AF	135	28% 53% 16% 24%
7	AG	179	69% 61% 21% 16%

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Mol	Chain	Length	Quality of chain
8	AH	130	32% 71% 23% 5%
9	AI	130	38% 44% 45% 8%
10	AJ	103	48% 60% 30% 5% 5%
11	AK	129	37% 66% 21% 9%
12	AL	124	50% 66% 27% 6%
13	AM	118	45% 69% 21% 7%
14	AN	101	32% 54% 37% 5%
15	AO	89	16% 78% 20%
16	AP	82	29% 72% 26%
17	AQ	84	25% 65% 27% 5%
18	AR	75	25% 53% 20% 27%
19	AS	92	26% 58% 23% 5% 14%
20	AT	87	21% 75% 22%
21	AU	71	51% 28% 39% 28%
22	AV	77	13% 19% 64% 14%
23	AW	77	8% 16% 52% 31%
24	AX	19	37% 26% 74%
25	AY	704	47% 64% 26% 5% 5%
26	BB	120	66% 25% 8%
27	BC	273	41% 69% 26%
28	BA	2904	58% 31% 9%
29	BD	209	35% 65% 29% 5%
30	BE	201	46% 70% 24% 5%
31	BF	179	42% 65% 30%
32	BG	177	26% 62% 29% 8%

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Mol	Chain	Length	Quality of chain
33	BH	50	90% 60% 32% 8%
34	BI	142	92% 51% 44% 5%
35	BJ	142	29% 61% 28% 9%
36	BK	123	52% 54% 35% 8%
37	BL	144	31% 71% 24%
38	BM	136	34% 63% 28% 8%
39	BN	127	16% 62% 29% 6%
40	BO	117	15% 67% 28%
41	BP	115	43% 65% 25% 6%
42	BQ	118	25% 63% 31% 5%
43	BR	103	34% 63% 34%
44	BS	110	35% 69% 24% 6%
45	BT	100	28% 54% 32% 6% 7%
46	BU	104	43% 57% 36% 5%
47	BV	94	21% 76% 22%
48	BW	85	29% 32% 40% 20% 7%
49	BX	78	31% 69% 23% 5%
50	BY	63	29% 60% 38%
51	BZ	59	25% 54% 34% 8%
52	B0	57	35% 74% 21%
53	B1	55	73% 56% 27% 7% 9%
54	B2	46	39% 78% 20%
55	B3	65	32% 75% 18% 5%
56	B4	38	21% 58% 37%
57	B5	165	83% 24% 38% 19% 8% 10%

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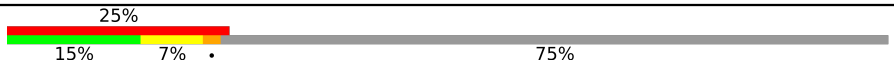
Mol	Chain	Length	Quality of chain
58	B6	121	

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
59	FUA	AY	801	-	-	X	-
60	GDP	AY	802	-	-	X	-

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 150958 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	1533	32895	14671	6036	10655	1533	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AB	218	1704	1081	305	311	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AC	206	1624	1028	305	288	3	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AE	150	1105	687	211	201	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AF	102	832	525	150	150	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	55	Total	C	N	O	0	0
			455	288	86	81		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 22 is a RNA chain called modified formyl-methionine specific initiator transfer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 23 is a RNA chain called formyl-methionine specific initiator transfer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	77	Total	C	N	O	P	0	0
			1635	732	291	536	76		

- Molecule 24 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	19	Total	C	N	O	P	0	0
			416	187	86	124	19		

- Molecule 25 is a protein called Elongation Factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	671	Total	C	N	O	S	0	0
			5194	3278	895	998	23		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BB	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BC	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 28 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	2854	Total	C	N	O	P	0	0
			61274	27334	11279	19807	2854		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BF	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BH	50	Total	C	N	O	S	0	0
			384	247	68	68	1		

- Molecule 34 is a protein called 50S ribosomal protein L11.

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

- Molecule 35 is a protein called 50S ribosomal protein L13.

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

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BK	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 37 is a protein called 50S ribosomal protein L15.

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

- Molecule 38 is a protein called 50S ribosomal protein L16.

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

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BN	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 40 is a protein called 50S ribosomal protein L18.

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

- Molecule 41 is a protein called 50S ribosomal protein L19.

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

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	BQ	117	Total 947	C 604	N 192	O 151	0	0

- Molecule 43 is a protein called 50S ribosomal protein L21.

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

- Molecule 44 is a protein called 50S ribosomal protein L22.

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

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BT	93	Total 738	C 466	N 139	O 131	S 2	0	0

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	BU	102	Total 779	C 492	N 146	O 141	0	0

- Molecule 47 is a protein called 50S ribosomal protein L25.

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

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BW	79	Total 596	C 367	N 120	O 108	S 1	0	0

- Molecule 49 is a protein called 50S ribosomal protein L28.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L30.

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
53	B1	50	Total	C	N	O	0	0
			409	263	75	71		

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

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

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

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

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

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

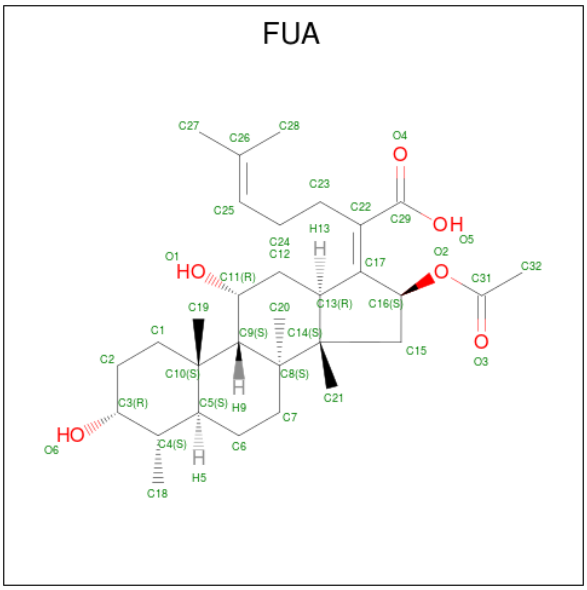
- Molecule 57 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	B5	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 58 is a protein called 50S ribosomal protein L7/L12.

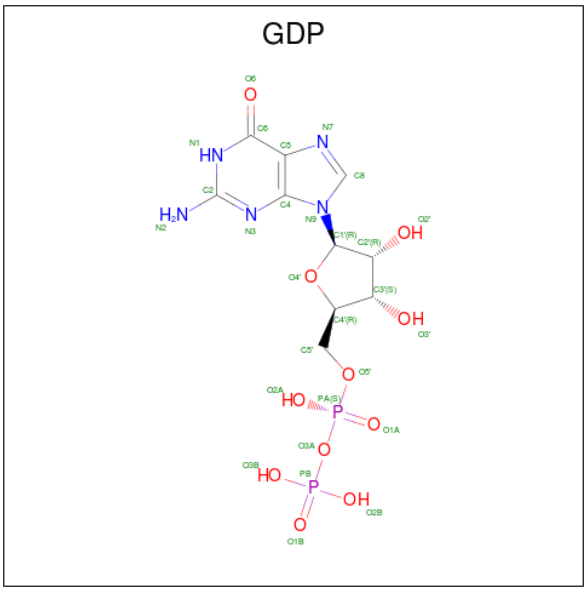
Mol	Chain	Residues	Atoms					AltConf	Trace
58	B6	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 59 is FUSIDIC ACID (three-letter code: FUA) (formula: $C_{31}H_{48}O_6$).



Mol	Chain	Residues	Atoms			AltConf
59	AY	1	Total	C	O	0
			37	31	6	

- Molecule 60 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



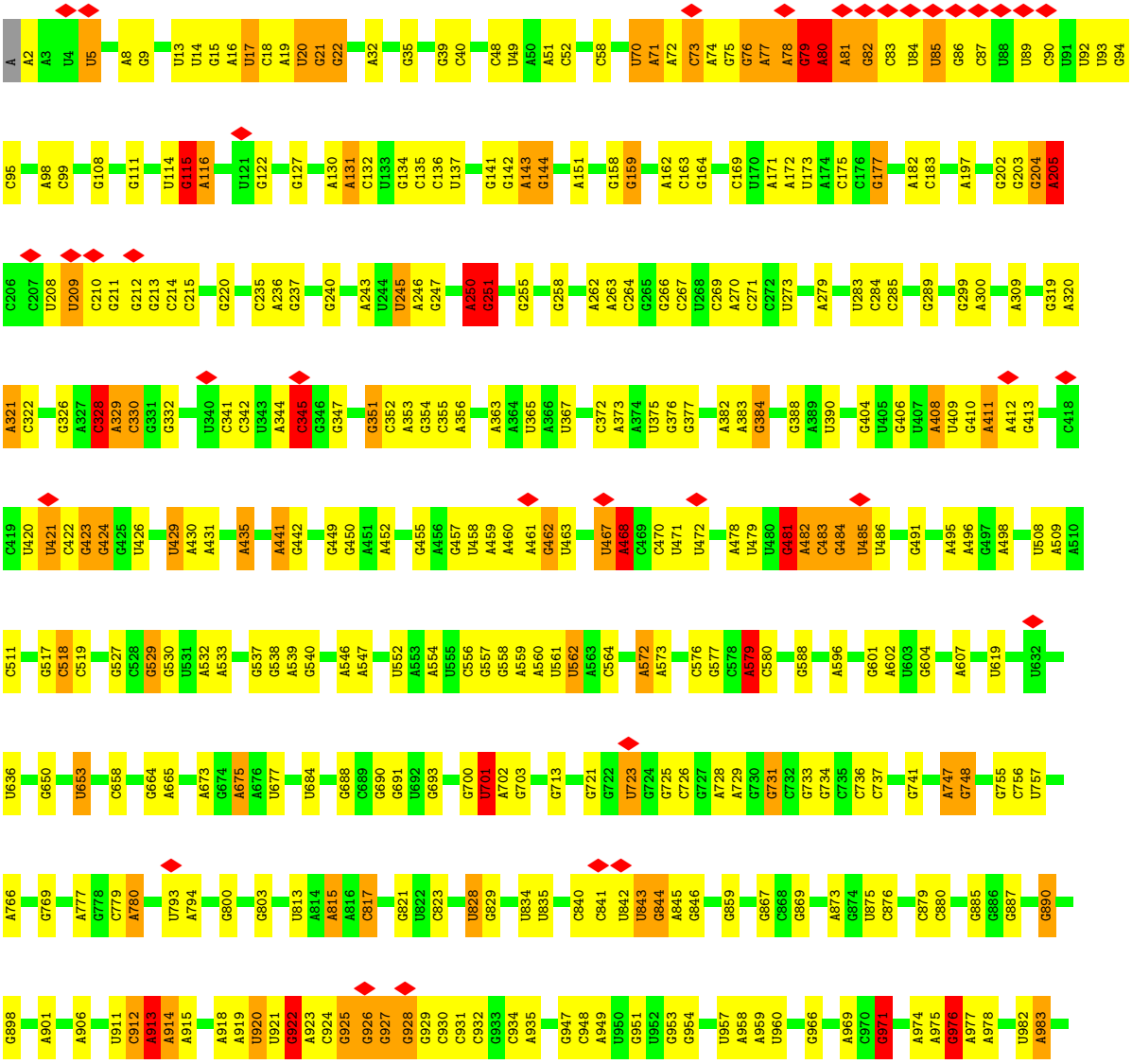
Mol	Chain	Residues	Atoms					AltConf
60	AY	1	Total	C	N	O	P	0
			28	10	5	11	2	

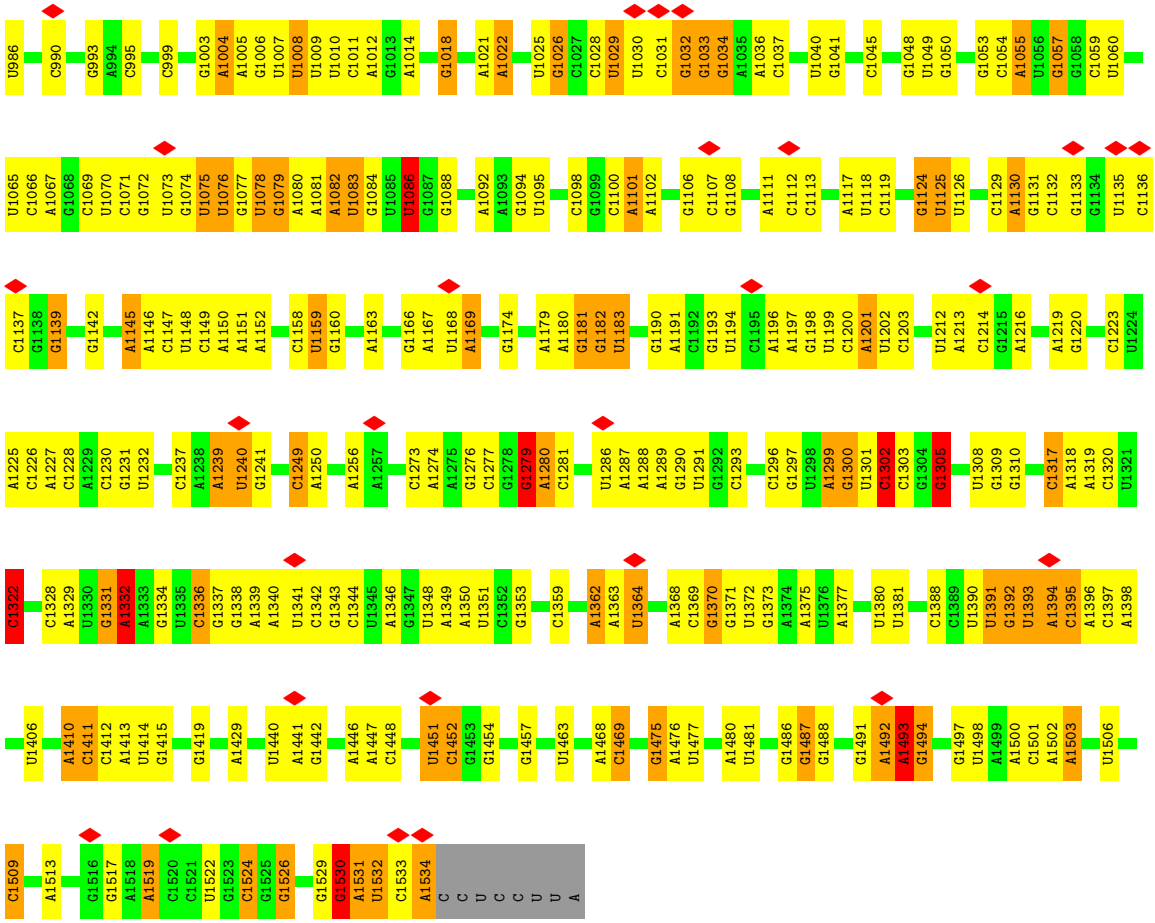
3 Residue-property plots (i)

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 16S ribosomal RNA

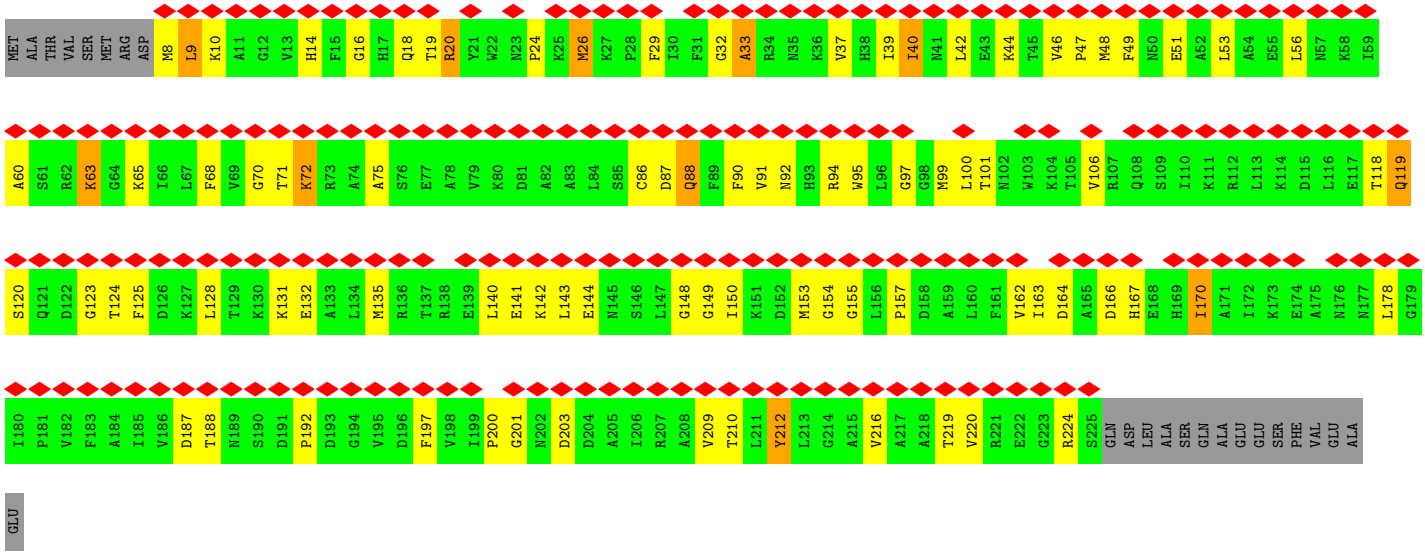
Chain AA:





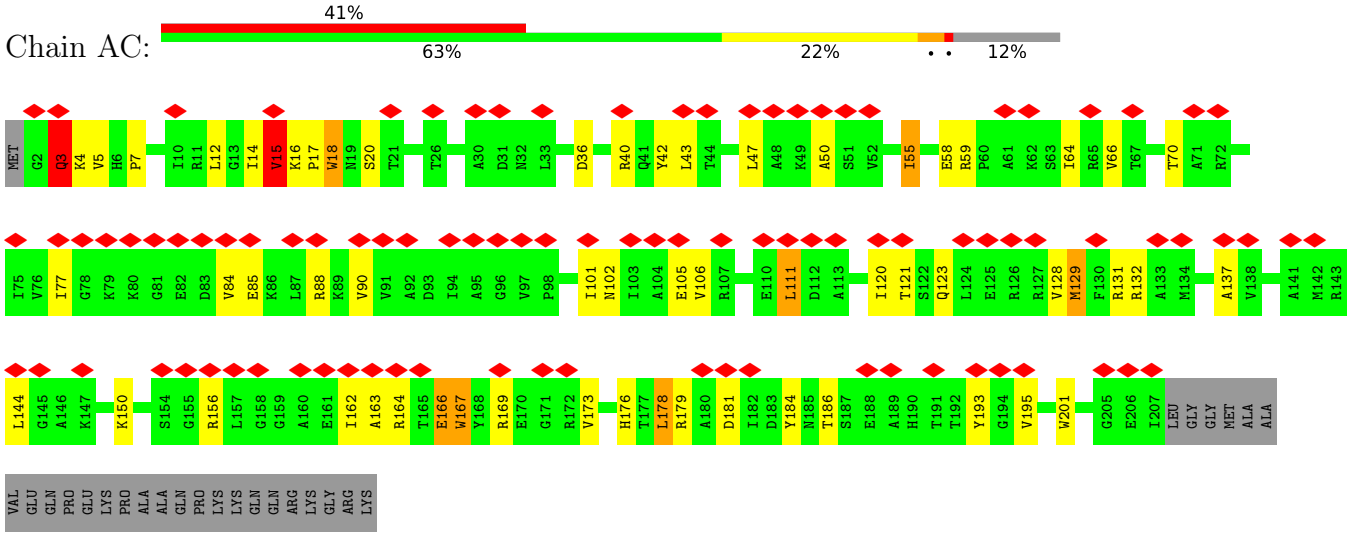
• Molecule 2: 30S ribosomal protein S2

Chain AB:



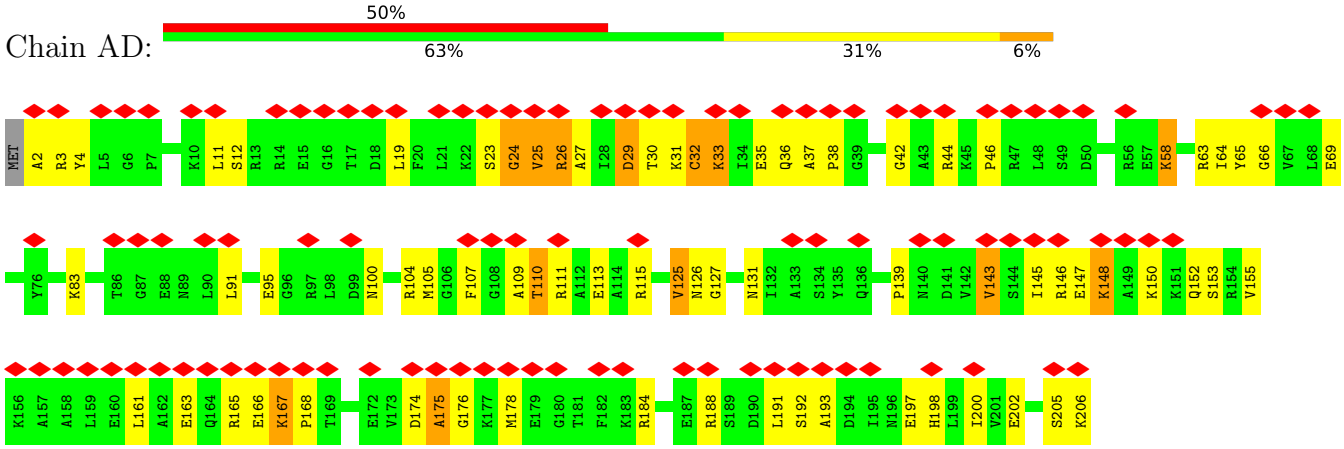
• Molecule 3: 30S ribosomal protein S3

Chain AC:



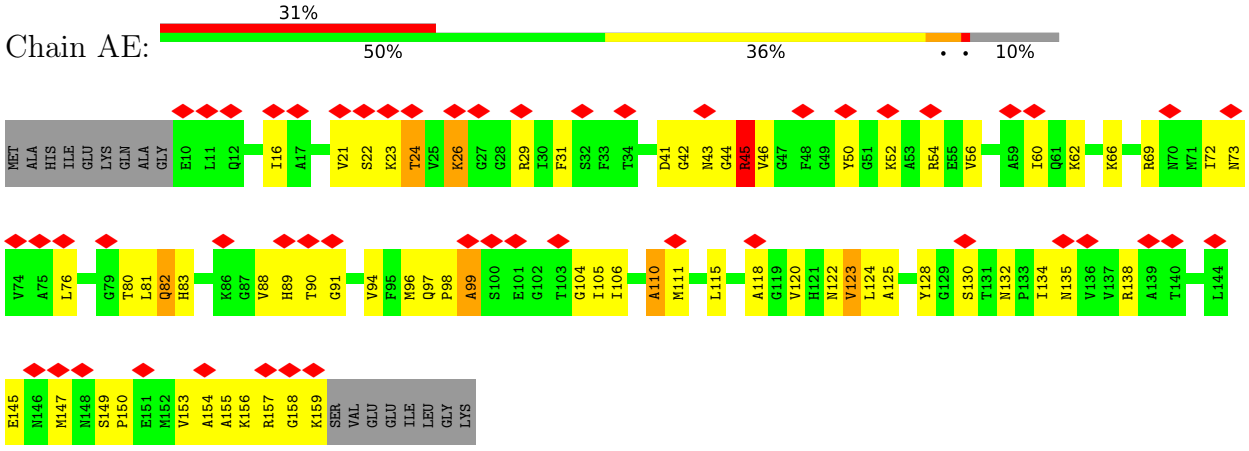
• Molecule 4: 30S ribosomal protein S4

Chain AD:



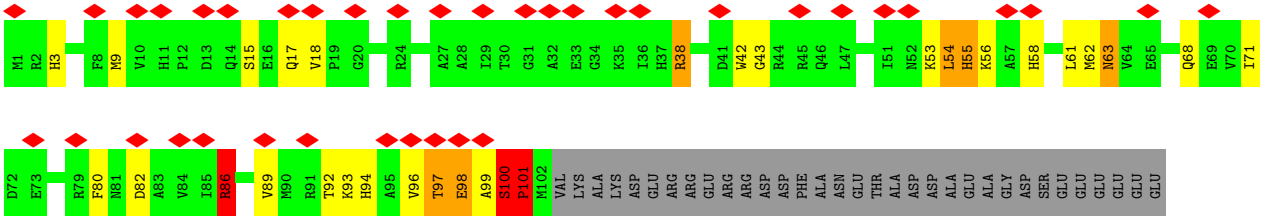
• Molecule 5: 30S ribosomal protein S5

Chain AE:

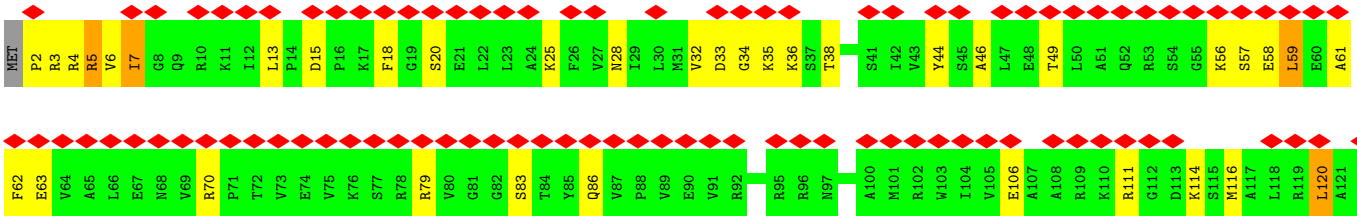


• Molecule 6: 30S ribosomal protein S6

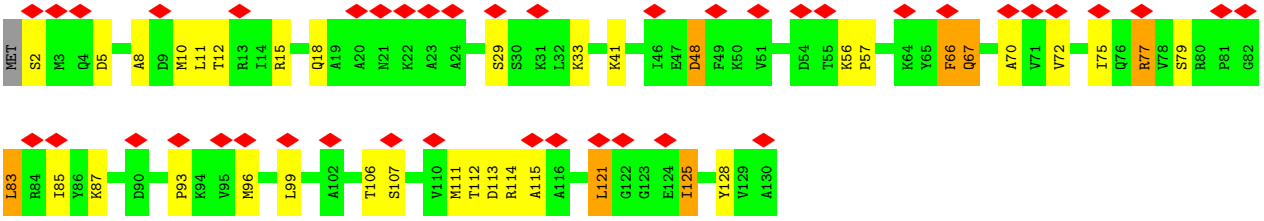
Chain AF:



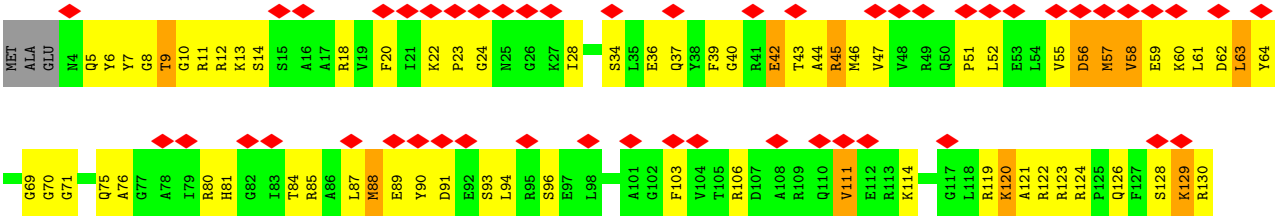
• Molecule 7: 30S ribosomal protein S7



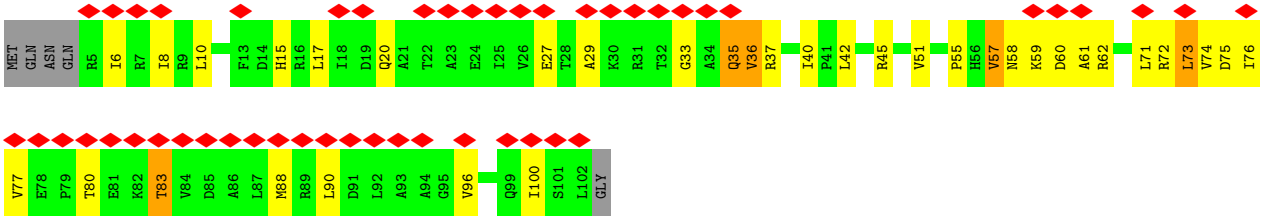
• Molecule 8: 30S ribosomal protein S8



• Molecule 9: 30S ribosomal protein S9

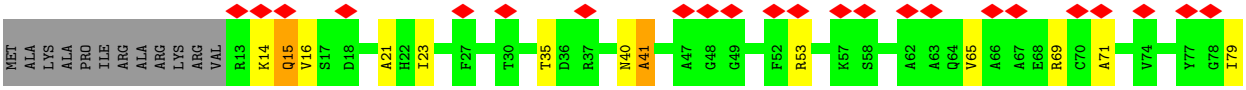


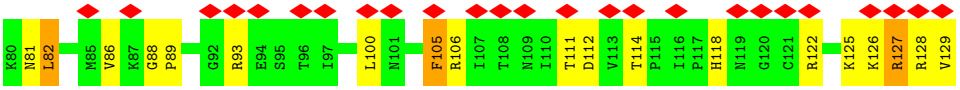
• Molecule 10: 30S ribosomal protein S10



• Molecule 11: 30S ribosomal protein S11

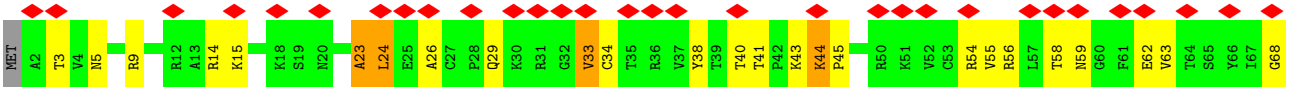
Chain AK:

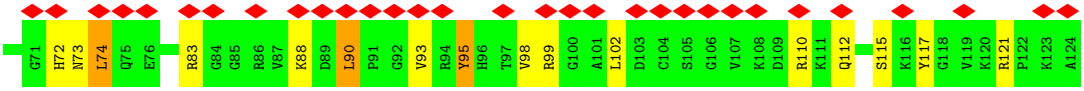




• Molecule 12: 30S ribosomal protein S12

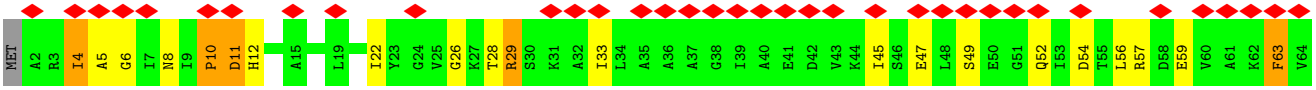
Chain AL:

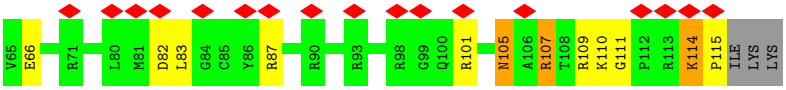




• Molecule 13: 30S ribosomal protein S13

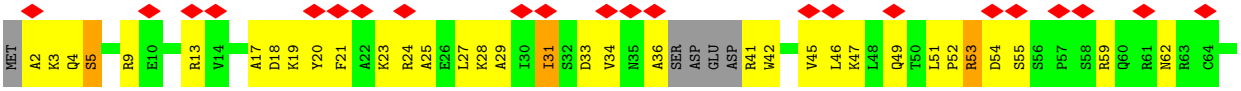
Chain AM:

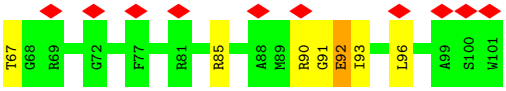




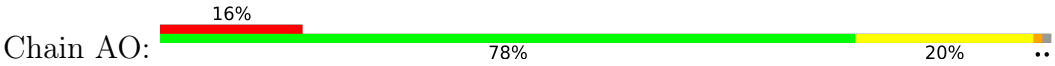
• Molecule 14: 30S ribosomal protein S14

Chain AN:

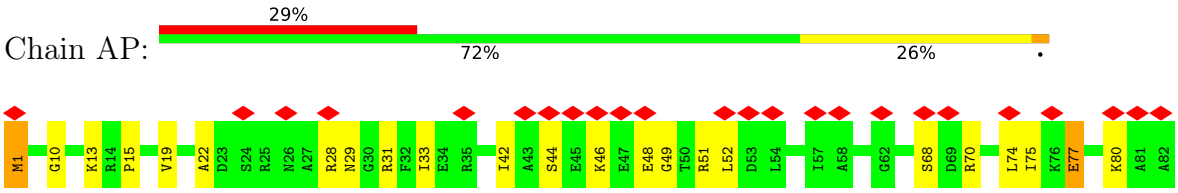




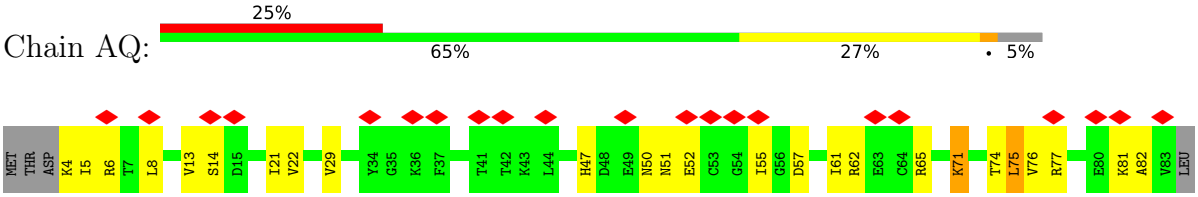
• Molecule 15: 30S ribosomal protein S15



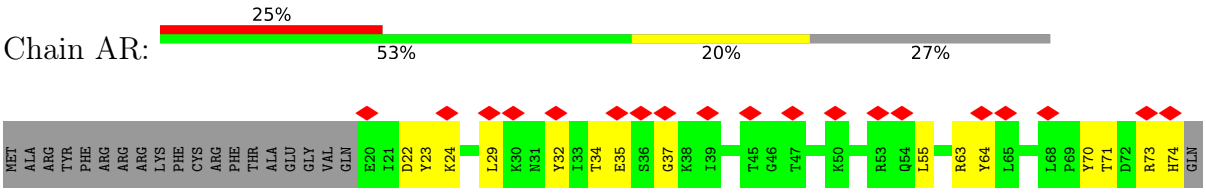
• Molecule 16: 30S ribosomal protein S16



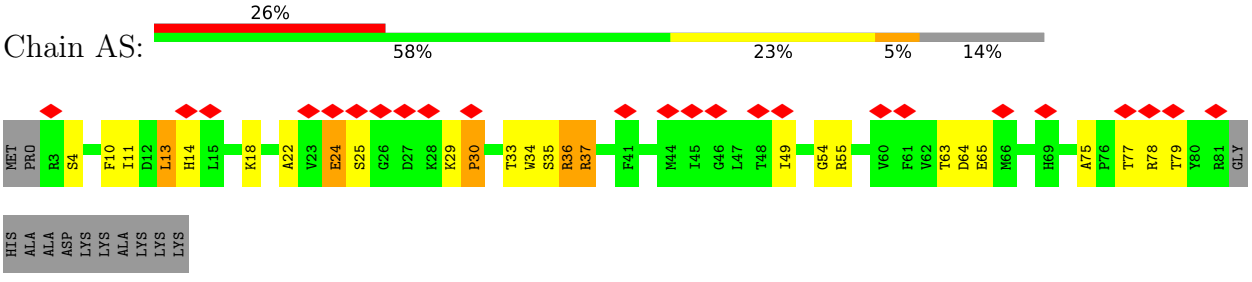
• Molecule 17: 30S ribosomal protein S17



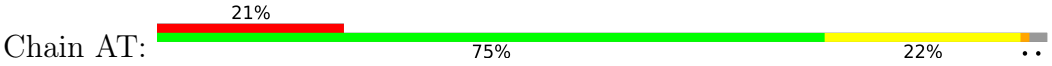
• Molecule 18: 30S ribosomal protein S18

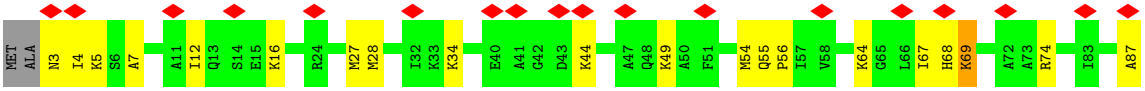


• Molecule 19: 30S ribosomal protein S19

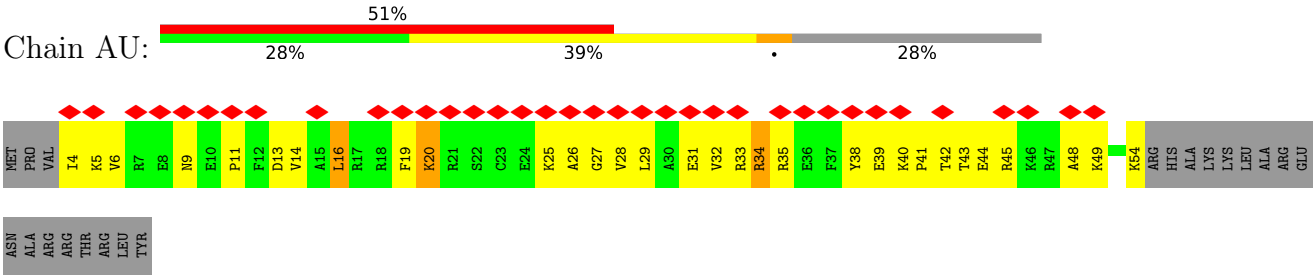


• Molecule 20: 30S ribosomal protein S20

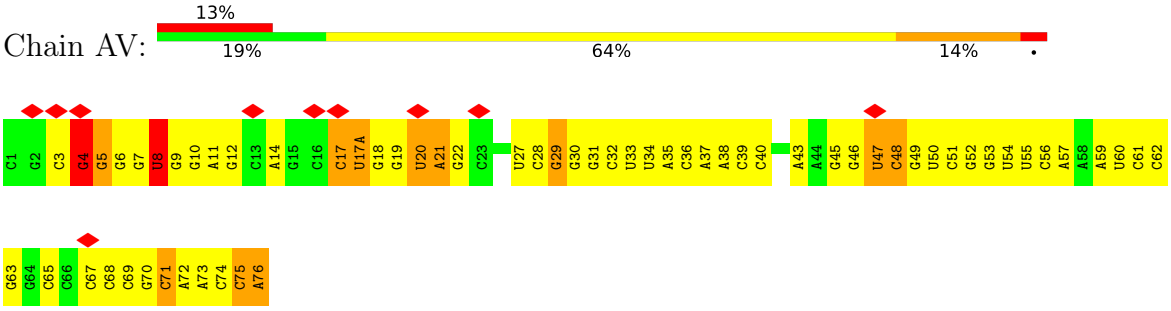




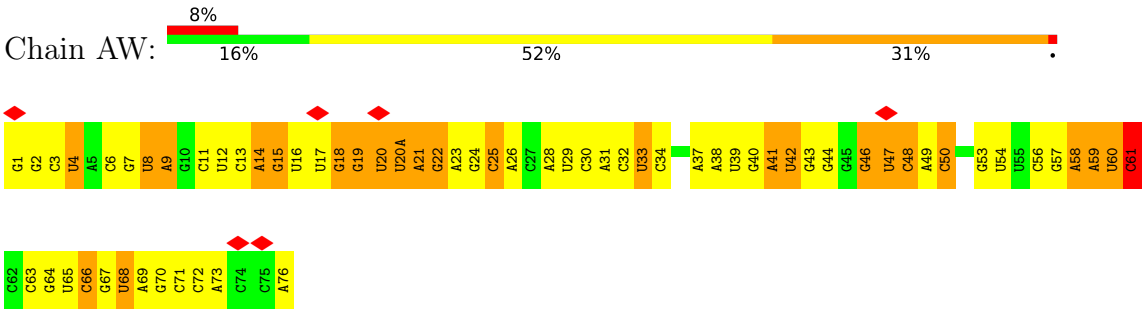
• Molecule 21: 30S ribosomal protein S21



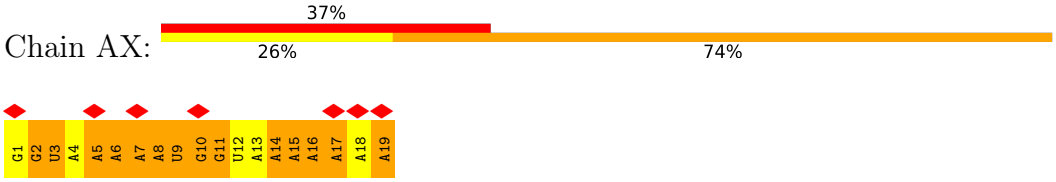
• Molecule 22: modified formyl-methionine specific initiator transfer RNA



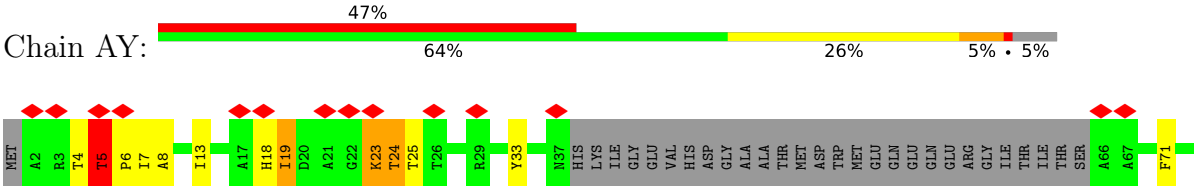
• Molecule 23: formyl-methionine specific initiator transfer RNA

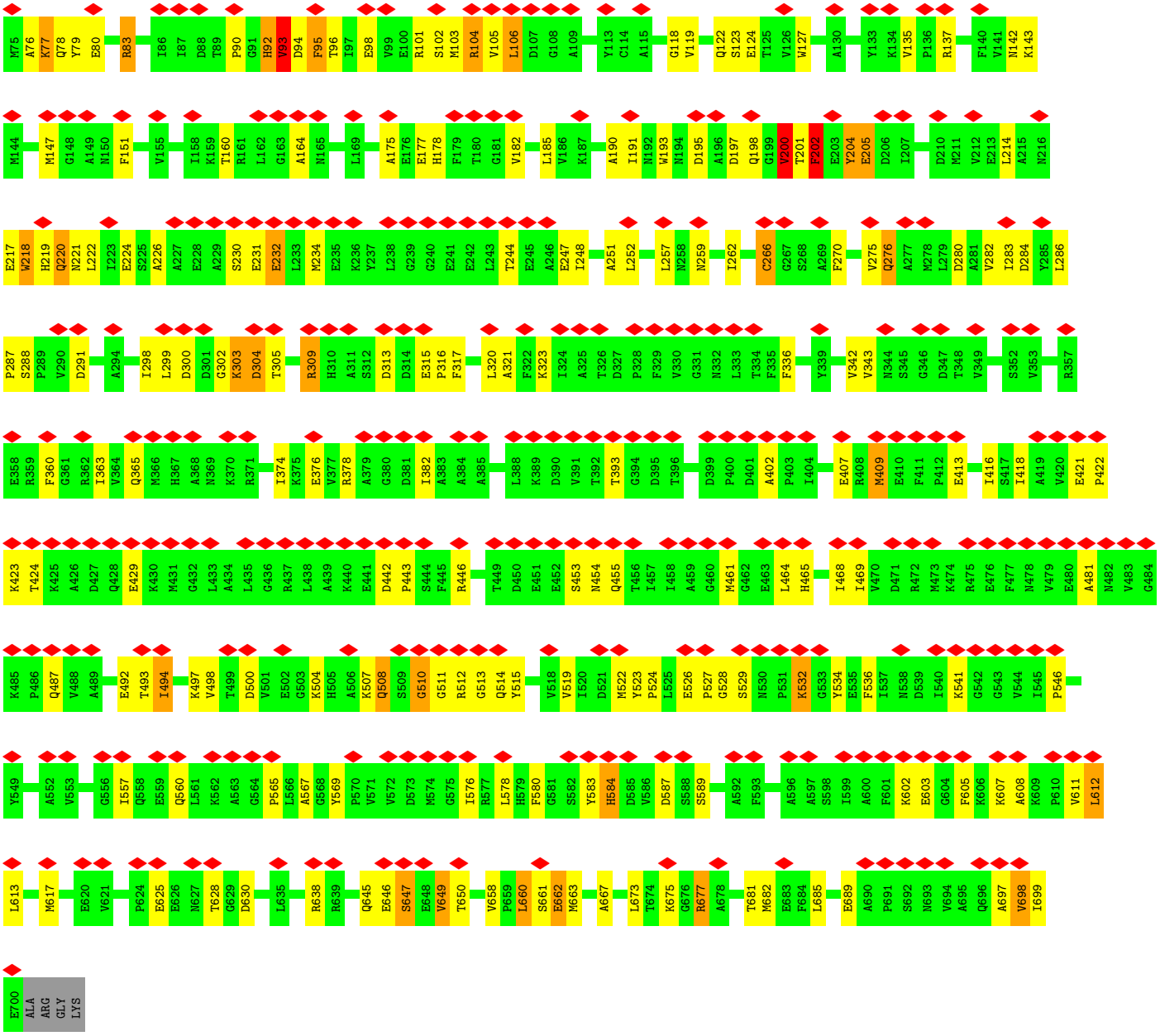


• Molecule 24: messenger RNA



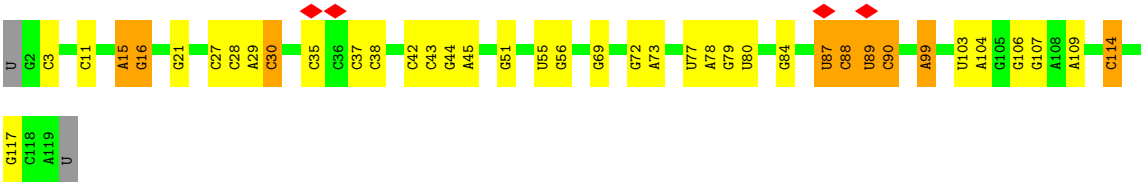
• Molecule 25: Elongation Factor G





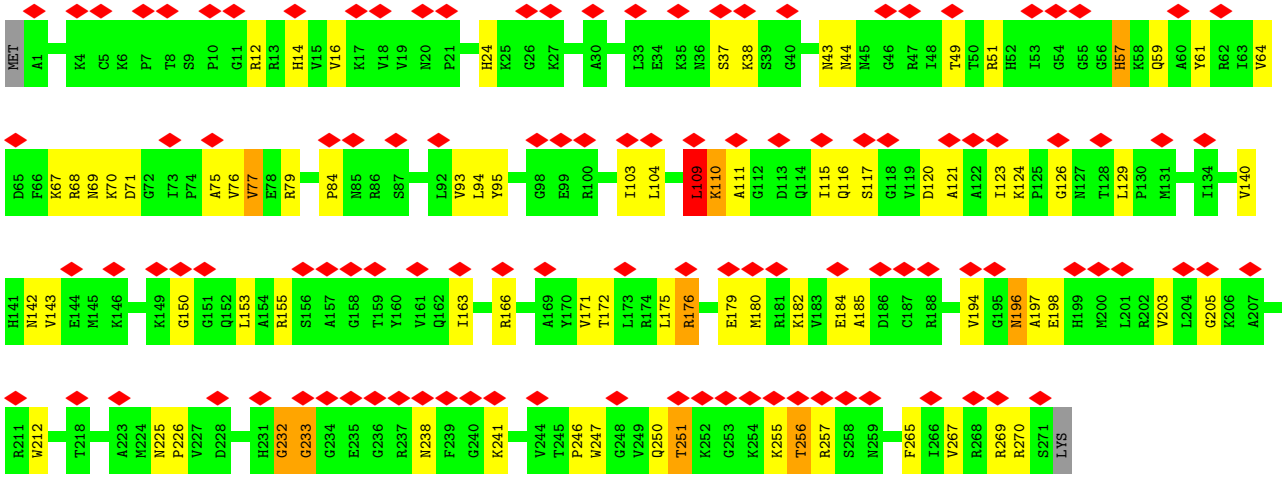
• Molecule 26: 5S ribosomal RNA

Chain BB:



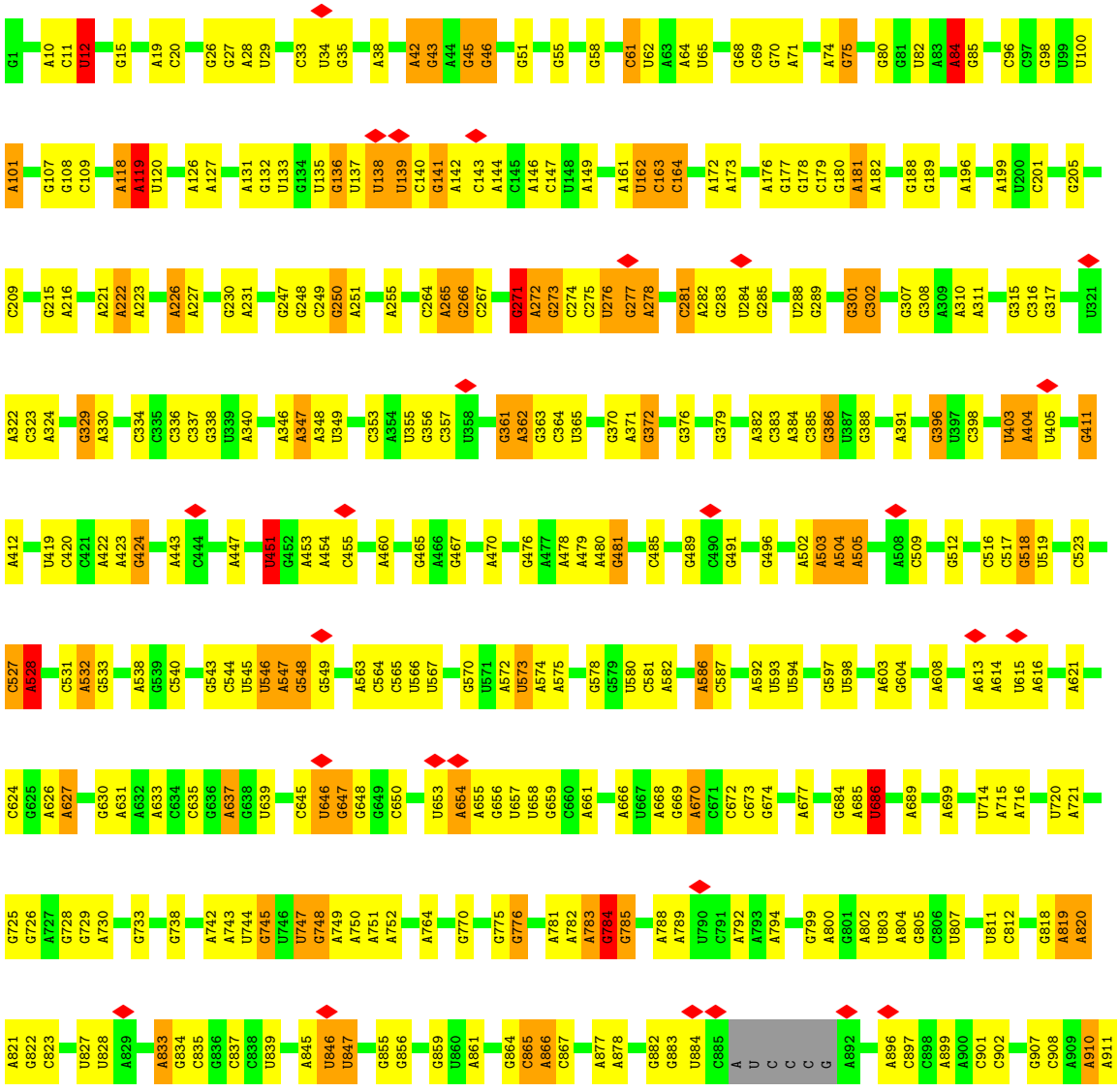
• Molecule 27: 50S ribosomal protein L2

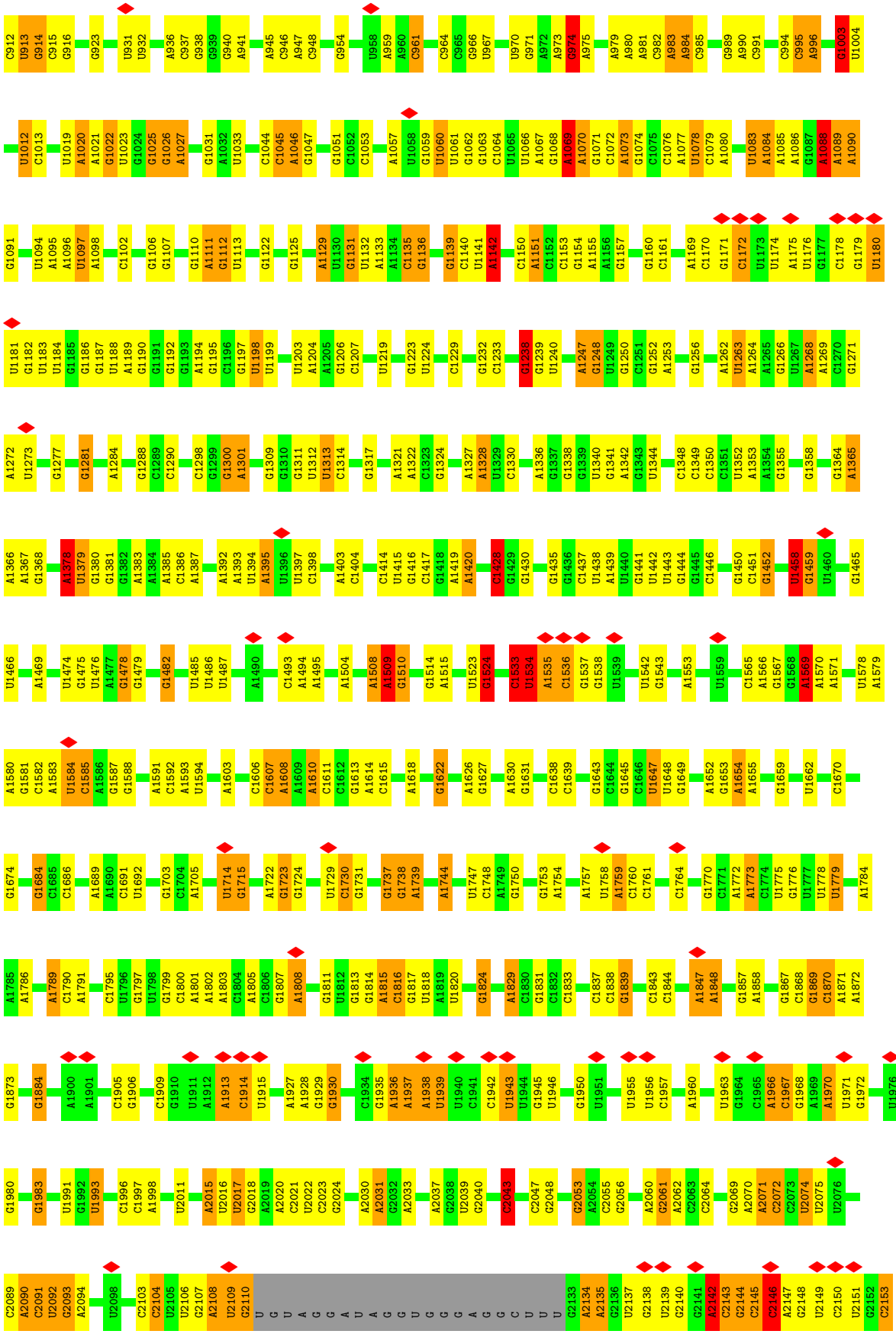
Chain BC:

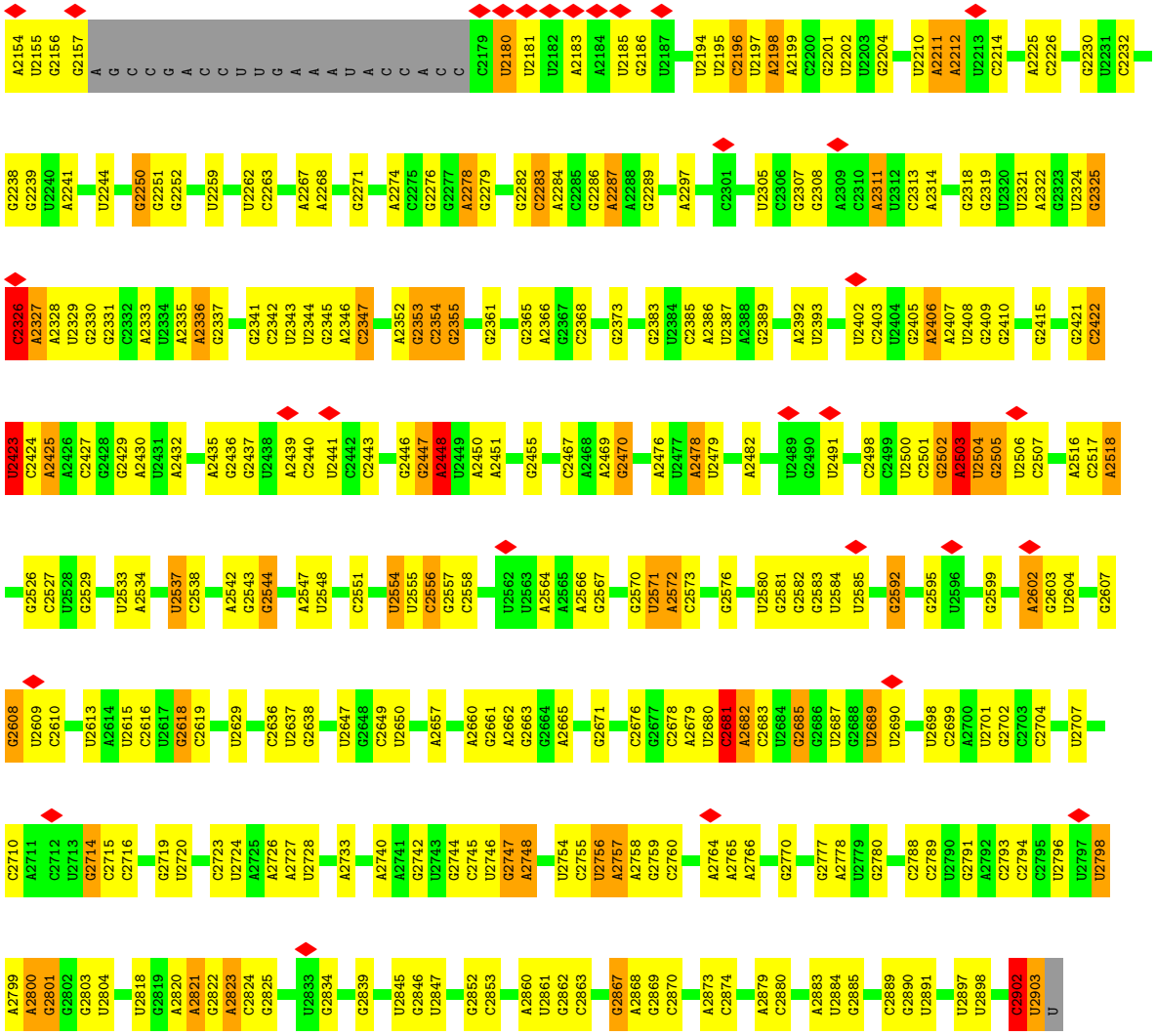


• Molecule 28: 23S ribosomal RNA

Chain BA:

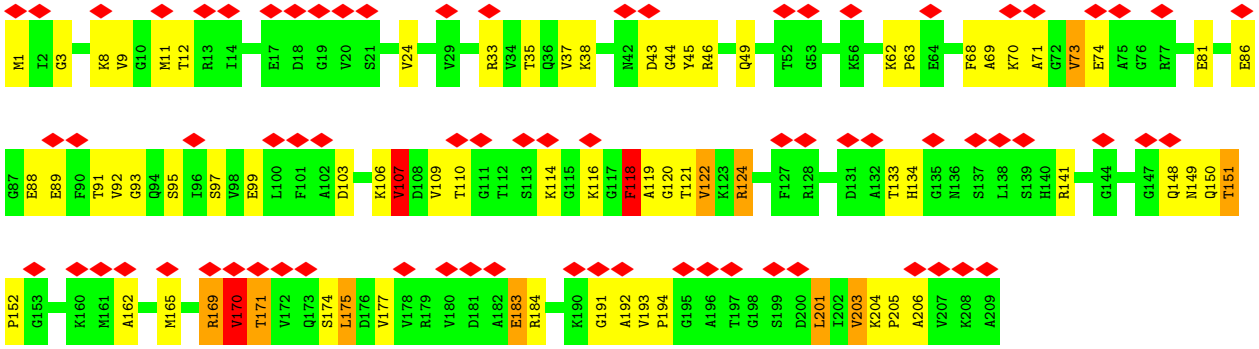






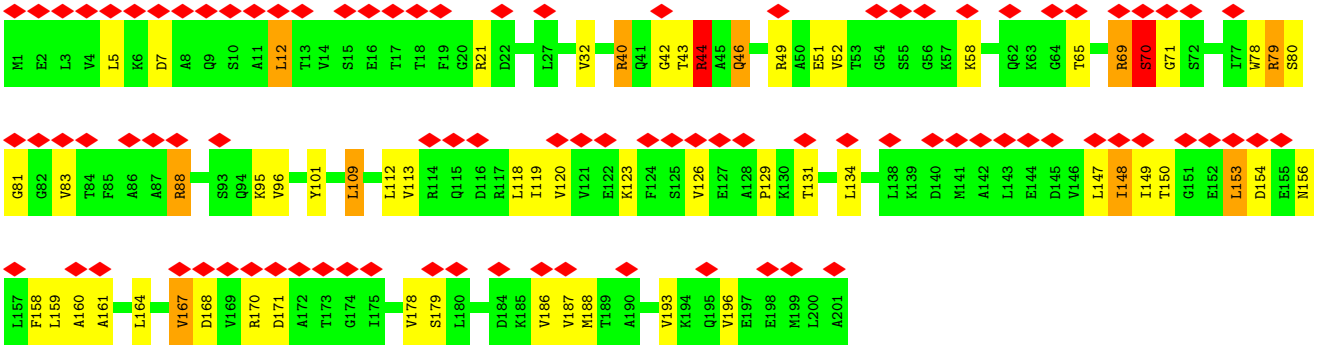
• Molecule 29: 50S ribosomal protein L3

Chain BD:



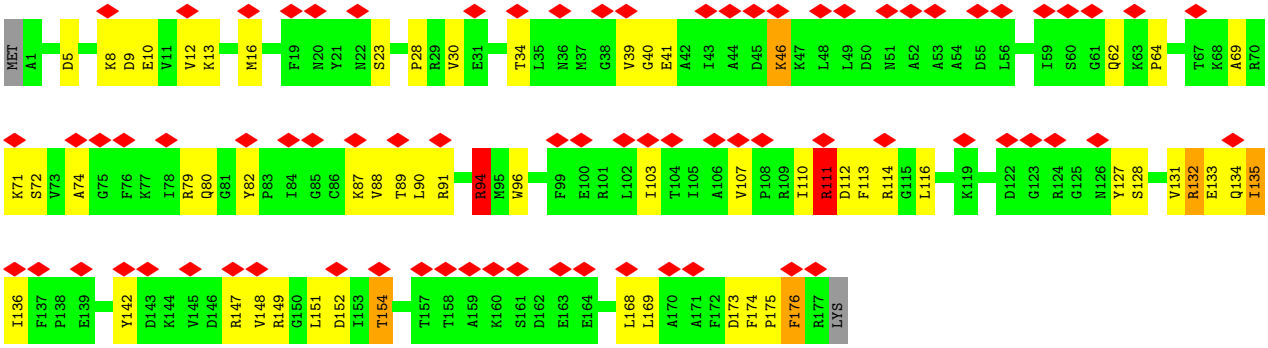
• Molecule 30: 50S ribosomal protein L4

Chain BE:



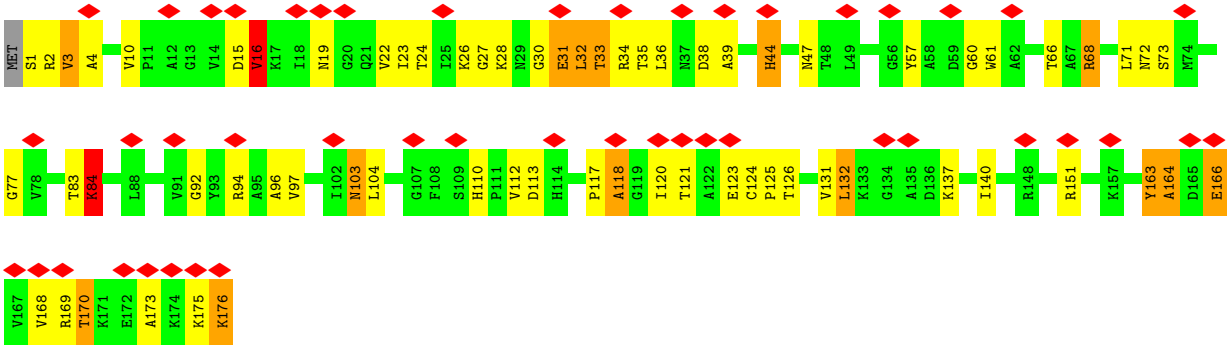
• Molecule 31: 50S ribosomal protein L5

Chain BF:



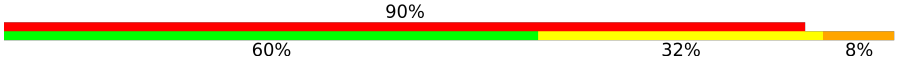
• Molecule 32: 50S ribosomal protein L6

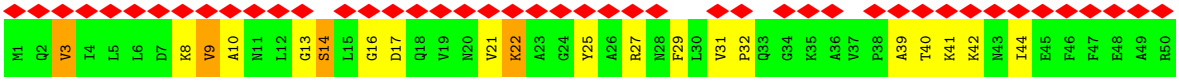
Chain BG:



• Molecule 33: 50S ribosomal protein L9

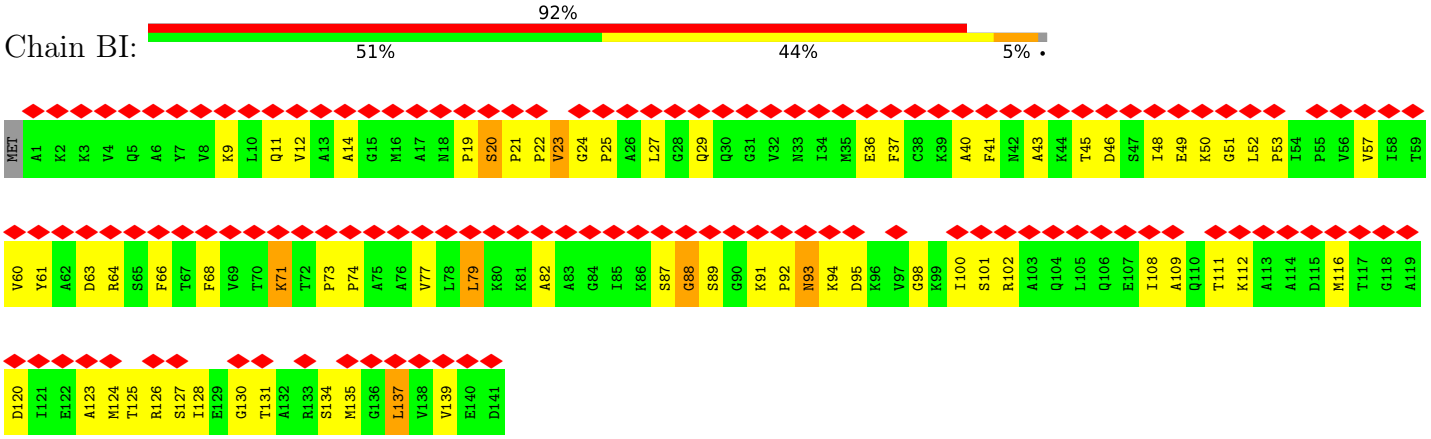
Chain BH:





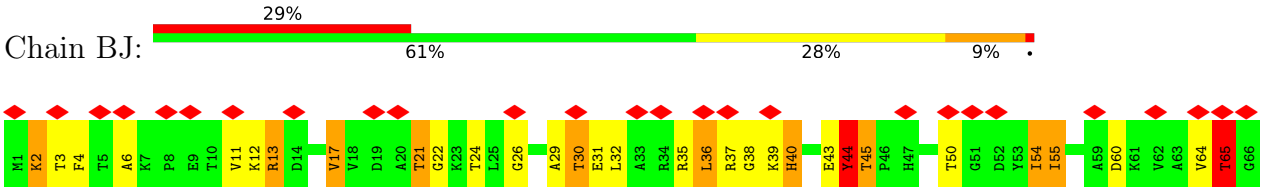
• Molecule 34: 50S ribosomal protein L11

Chain BI:



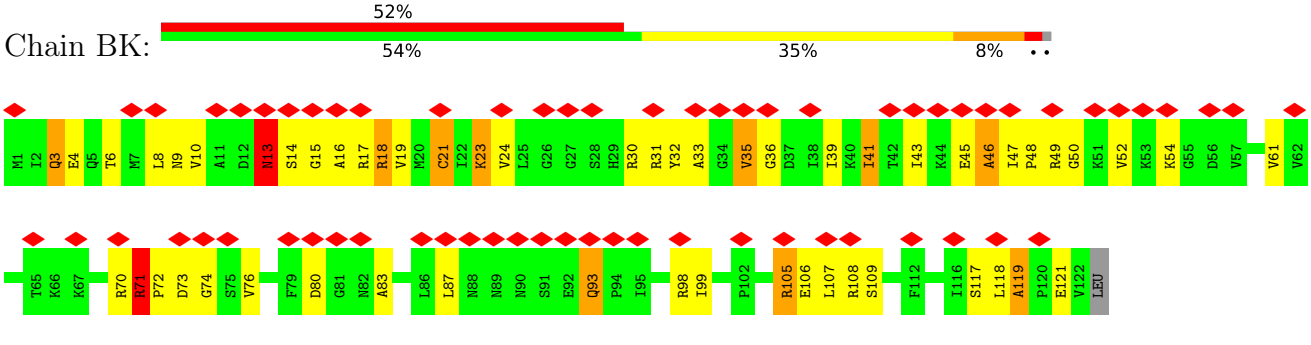
• Molecule 35: 50S ribosomal protein L13

Chain BJ:



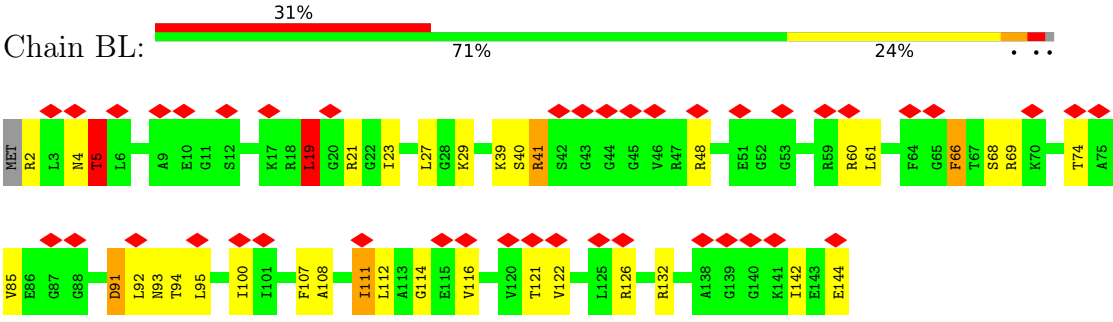
• Molecule 36: 50S ribosomal protein L14

Chain BK:



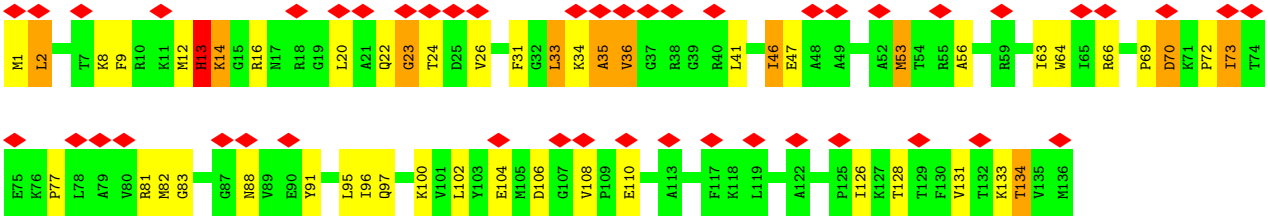
• Molecule 37: 50S ribosomal protein L15

Chain BL:

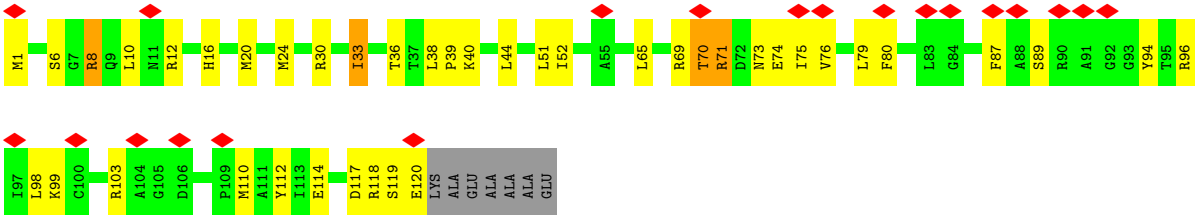


• Molecule 38: 50S ribosomal protein L16

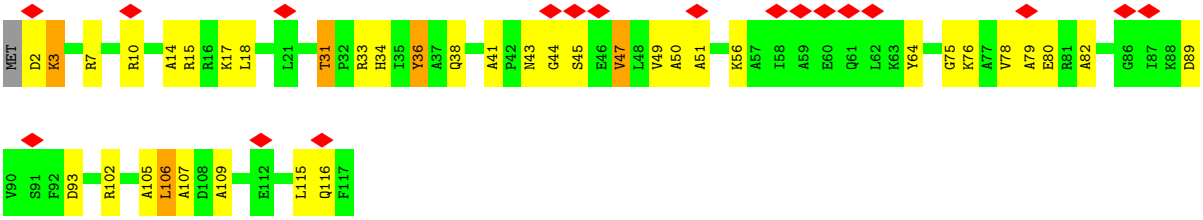
Chain BM:



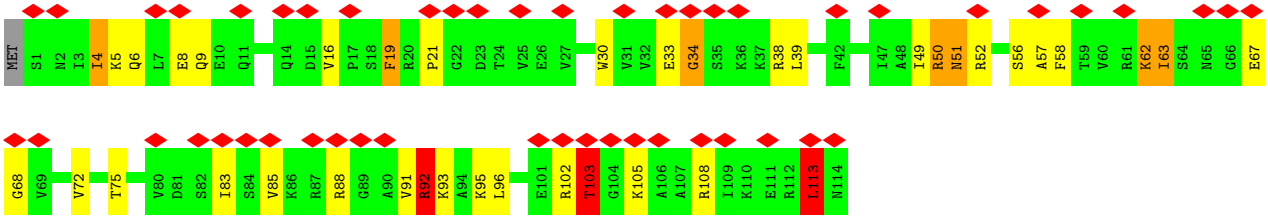
• Molecule 39: 50S ribosomal protein L17



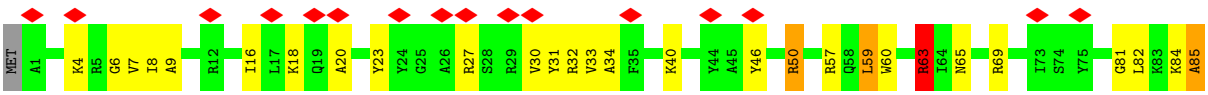
• Molecule 40: 50S ribosomal protein L18

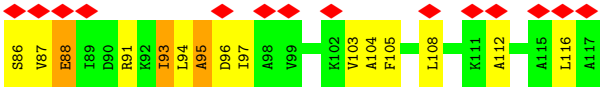


• Molecule 41: 50S ribosomal protein L19



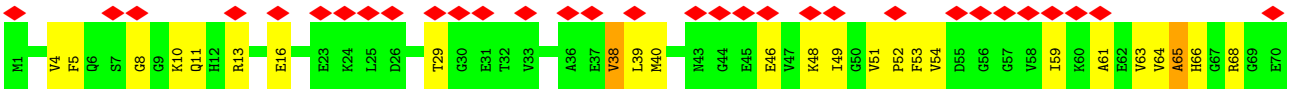
• Molecule 42: 50S ribosomal protein L20

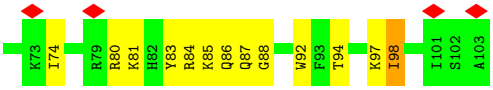




• Molecule 43: 50S ribosomal protein L21

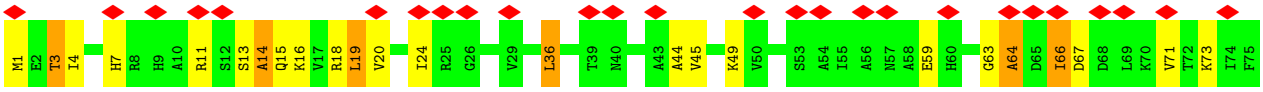
Chain BR:

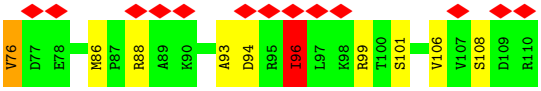




• Molecule 44: 50S ribosomal protein L22

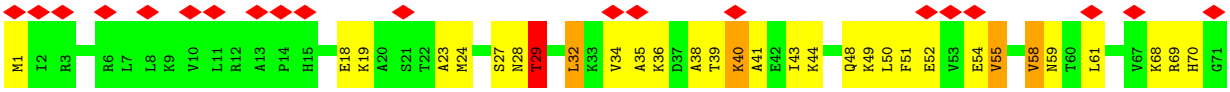
Chain BS:

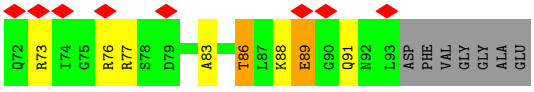




• Molecule 45: 50S ribosomal protein L23

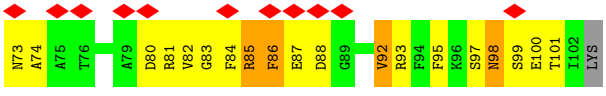
Chain BT:





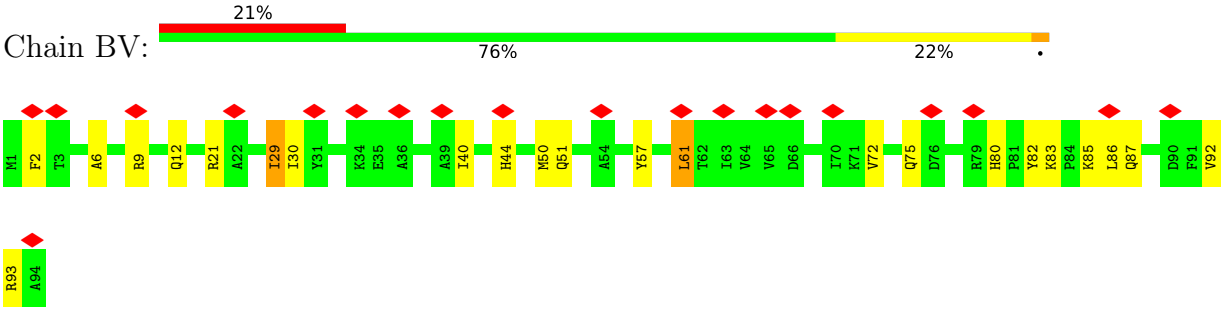
• Molecule 46: 50S ribosomal protein L24

Chain BU:



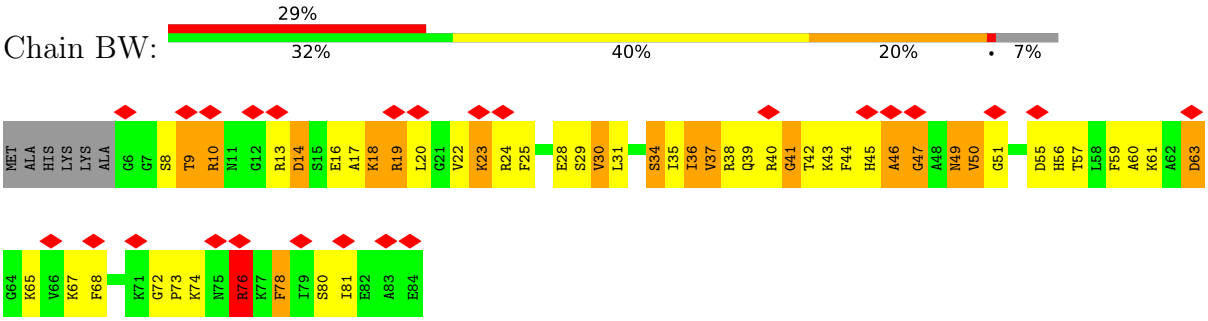
• Molecule 47: 50S ribosomal protein L25

Chain BV:



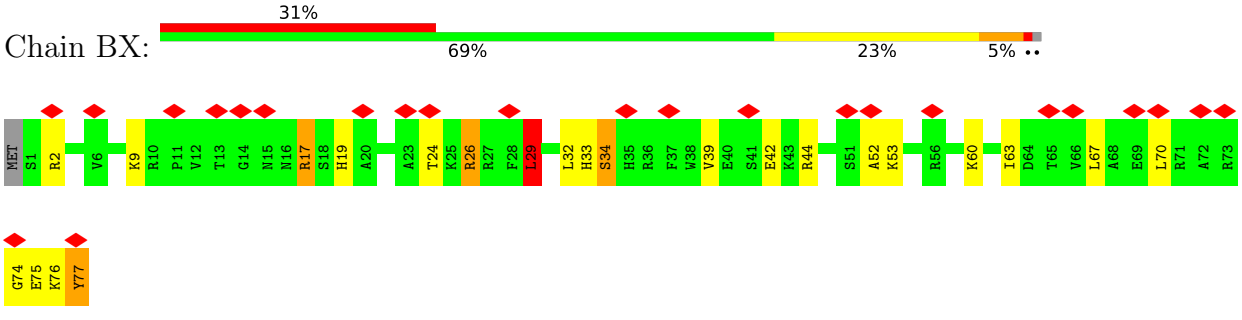
• Molecule 48: 50S ribosomal protein L27

Chain BW:



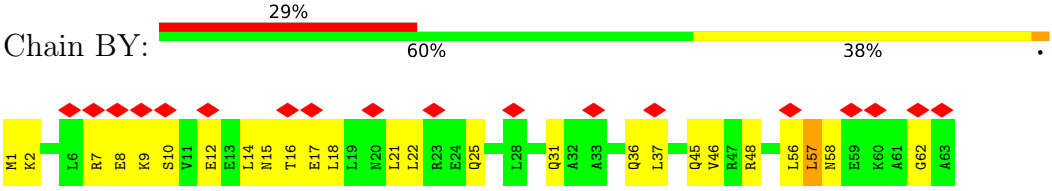
• Molecule 49: 50S ribosomal protein L28

Chain BX:



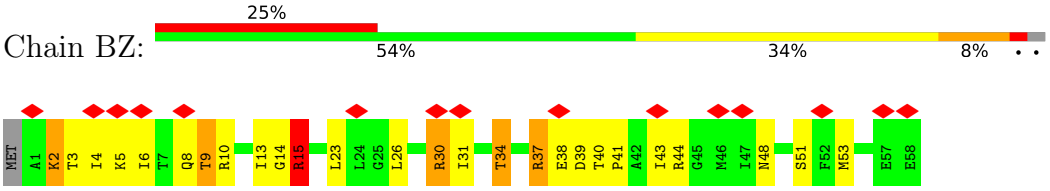
• Molecule 50: 50S ribosomal protein L29

Chain BY:



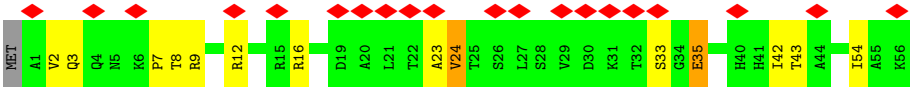
• Molecule 51: 50S ribosomal protein L30

Chain BZ:

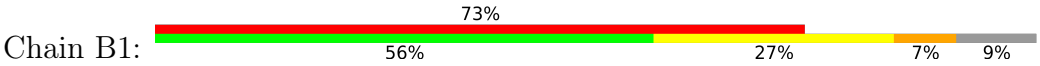


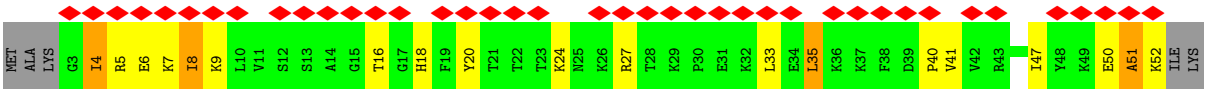
• Molecule 52: 50S ribosomal protein L32

Chain B0:

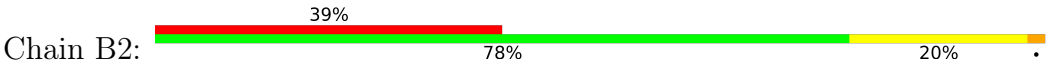


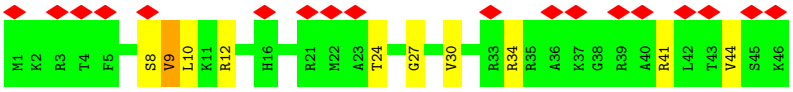
• Molecule 53: 50S ribosomal protein L33



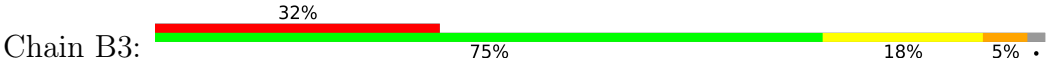


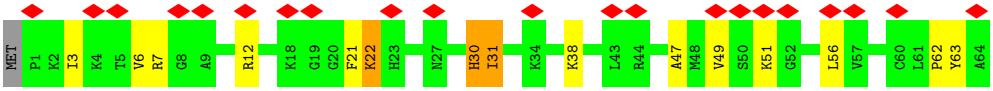
• Molecule 54: 50S ribosomal protein L34



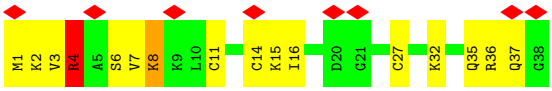


• Molecule 55: 50S ribosomal protein L35

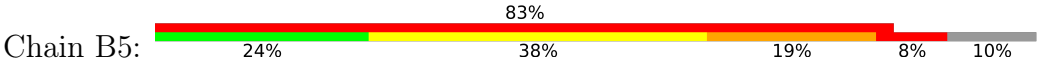


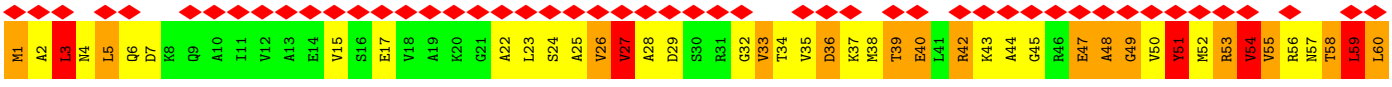


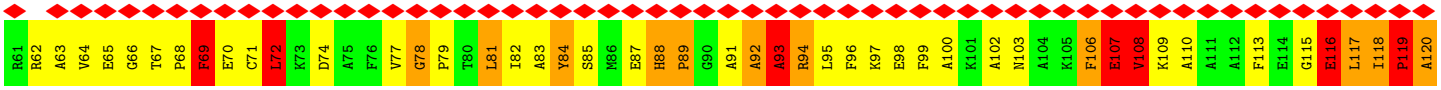
• Molecule 56: 50S ribosomal protein L36

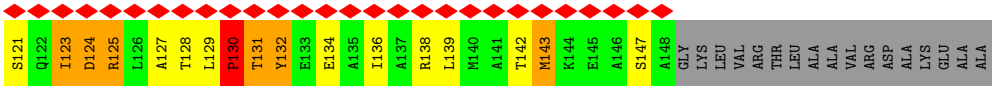


• Molecule 57: 50S ribosomal protein L10



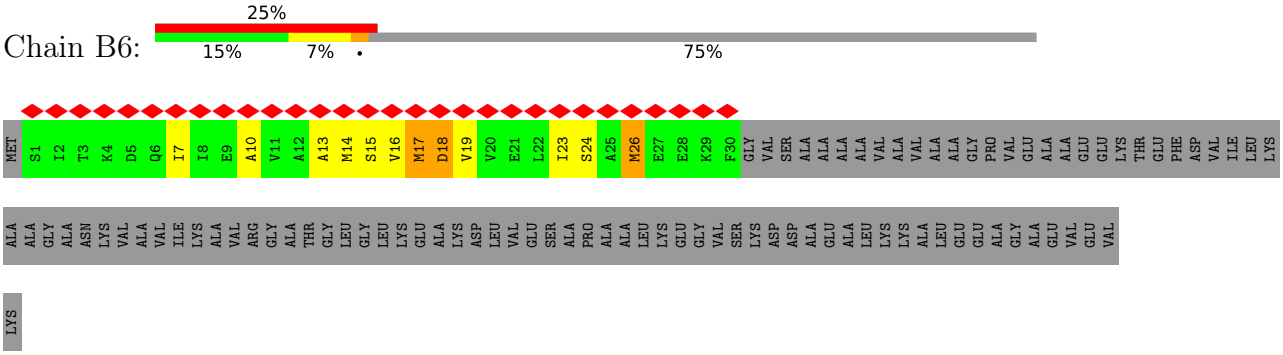






• Molecule 58: 50S ribosomal protein L7/L12

Chain B6:


25%
15%
7%
75%
MET S1 I2 T3 K4 D5 Q6 I7 I8 E9 A10 V11 A12 A13 M14 S15 V16 M17 D18 V19 V20 E21 L22 I23 S24 A25 M26 E27 E28 K29 F30 GLY VAL SER ALA ALA ALA VAL ALA VAL ALA ALA ALA GLY PRO VAL GLU ALA ALA GLU GLU LYS THR GLU PHE ASP VAL ILE LEU LYS
ALA ALA GLY ALA ASN LYS VAL ALA VAL ILE LYS ALA VAL ARG GLY ALA THR GLY LEU GLY LEU LYS GLU ALA LYS ASP LEU VAL GLU SER ALA PRO ALA ALA LEU LYS GLU GLY VAL SER LYS ASP ASP ALA GLU ALA LEU LYS LYS ALA LEU GLU GLU ALA GLY ALA GLU VAL GLU VAL
LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	279309	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	The volumes were CTF-corrected in defocus groups with an average of approximately 906 individual images per group.	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20.00	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	12.702	Depositor
Minimum map value	-5.078	Depositor
Average map value	0.197	Depositor
Map value standard deviation	0.875	Depositor
Recommended contour level	3.0	Depositor
Map size (Å)	378.0, 378.0, 378.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.26, 1.26, 1.26	Depositor

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: GDP, FUA, 5MU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	AA	0.65	4/36834 (0.0%)	1.13	100/57462 (0.2%)
2	AB	0.49	0/1735	0.72	0/2338
3	AC	0.45	0/1651	0.69	0/2225
4	AD	0.53	0/1665	0.79	0/2227
5	AE	0.49	0/1118	0.76	0/1504
6	AF	0.50	0/851	0.70	0/1150
7	AG	0.49	0/1195	0.67	0/1602
8	AH	0.48	0/989	0.65	0/1326
9	AI	0.54	0/1034	0.81	0/1375
10	AJ	0.54	0/796	0.80	0/1077
11	AK	0.50	0/893	0.74	0/1205
12	AL	0.54	0/969	0.82	0/1300
13	AM	0.48	0/892	0.70	0/1193
14	AN	0.48	0/785	0.78	0/1043
15	AO	0.44	0/722	0.66	0/964
16	AP	0.48	0/659	0.74	0/884
17	AQ	0.46	0/657	0.73	0/881
18	AR	0.45	0/462	0.62	0/621
19	AS	0.47	0/652	0.81	0/877
20	AT	0.47	0/671	0.61	0/888
21	AU	0.66	0/430	0.84	0/570
22	AV	0.57	0/1810	0.74	0/2821
23	AW	0.43	0/1827	1.14	6/2845 (0.2%)
24	AX	0.30	0/469	0.70	0/730
25	AY	0.46	0/5291	0.67	2/7160 (0.0%)
26	BB	0.66	0/2828	1.10	2/4410 (0.0%)
27	BC	0.54	0/2121	0.79	2/2852 (0.1%)
28	BA	0.81	17/68626 (0.0%)	1.22	303/107056 (0.3%)
29	BD	0.57	0/1586	0.77	1/2134 (0.0%)
30	BE	0.53	0/1571	0.76	2/2113 (0.1%)
31	BF	0.49	0/1434	0.71	1/1926 (0.1%)
32	BG	0.55	0/1343	0.73	0/1816

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	BH	0.53	0/389	0.73	0/523
34	BI	0.62	0/1046	0.84	1/1410 (0.1%)
35	BJ	0.63	1/1152 (0.1%)	0.78	0/1551
36	BK	0.65	1/947 (0.1%)	0.77	0/1268
37	BL	0.56	0/1054	0.79	2/1403 (0.1%)
38	BM	0.61	0/1093	0.77	0/1460
39	BN	0.51	0/973	0.68	0/1301
40	BO	0.46	0/902	0.70	0/1209
41	BP	0.52	0/929	0.78	1/1242 (0.1%)
42	BQ	0.62	0/960	0.71	1/1278 (0.1%)
43	BR	0.61	1/829 (0.1%)	0.76	0/1107
44	BS	0.54	0/864	0.73	0/1156
45	BT	0.55	0/744	0.85	1/994 (0.1%)
46	BU	0.56	0/787	0.78	0/1051
47	BV	0.48	0/766	0.67	1/1025 (0.1%)
48	BW	0.69	0/603	1.00	1/797 (0.1%)
49	BX	0.50	0/635	0.79	1/848 (0.1%)
50	BY	0.46	0/510	0.75	0/677
51	BZ	0.54	0/453	0.84	1/605 (0.2%)
52	B0	0.54	0/450	0.69	0/599
53	B1	0.53	0/416	0.74	0/554
54	B2	0.53	0/380	0.70	0/498
55	B3	0.53	0/513	0.75	0/676
56	B4	0.58	0/303	0.84	0/397
57	B5	0.74	0/1131	1.32	26/1524 (1.7%)
58	B6	0.59	0/227	0.65	0/304
All	All	0.69	24/163622 (0.0%)	1.08	455/244032 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	AF	0	1
12	AL	0	1
22	AV	0	3
25	AY	0	1
27	BC	0	1
29	BD	0	1
35	BJ	0	1
36	BK	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
57	B5	0	1
All	All	0	11

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	922	G	O3'-P	9.48	1.72	1.61
28	BA	984	A	N9-C4	-8.58	1.32	1.37
1	AA	1362	A	N7-C5	7.93	1.44	1.39
28	BA	528	A	N9-C4	-6.68	1.33	1.37
28	BA	1142	A	N9-C4	-6.58	1.33	1.37
28	BA	2504	U	C4-O4	6.28	1.28	1.23
28	BA	783	A	N9-C4	-6.22	1.34	1.37
28	BA	1569	A	N9-C4	-6.20	1.34	1.37
28	BA	783	A	N3-C4	-5.90	1.31	1.34
28	BA	1073	A	C5-C6	5.76	1.46	1.41
28	BA	2504	U	C2-N3	5.67	1.41	1.37
28	BA	2504	U	N3-C4	5.59	1.43	1.38
35	BJ	44	TYR	CD2-CE2	-5.57	1.30	1.39
1	AA	1362	A	N3-C4	5.41	1.38	1.34
43	BR	86	GLN	CB-CG	5.40	1.67	1.52
28	BA	1142	A	C5-C6	-5.36	1.36	1.41
28	BA	528	A	N3-C4	-5.33	1.31	1.34
28	BA	783	A	N7-C5	-5.29	1.36	1.39
36	BK	21	CYS	CB-SG	-5.25	1.73	1.81
28	BA	1321	A	N9-C4	5.21	1.41	1.37
28	BA	2053	G	C6-O6	5.20	1.28	1.24
28	BA	2478	A	N9-C4	-5.06	1.34	1.37
28	BA	783	A	C5-C6	-5.01	1.36	1.41
1	AA	1500	A	N9-C4	-5.00	1.34	1.37

All (455) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	BA	1073	A	N1-C6-N6	-20.01	106.59	118.60
28	BA	1073	A	C5-C6-N6	14.04	134.94	123.70
28	BA	2053	G	N1-C6-O6	13.92	128.25	119.90
1	AA	922	G	P-O3'-C3'	13.08	135.40	119.70
28	BA	2504	U	N3-C4-O4	13.06	128.54	119.40
28	BA	984	A	C2-N3-C4	-12.08	104.56	110.60
28	BA	961	C	O5'-P-OP2	-11.80	95.08	105.70
28	BA	2053	G	C6-C5-N7	-11.57	123.46	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	BA	1073	A	C6-C5-N7	11.42	140.29	132.30
1	AA	1362	A	C4-C5-C6	-11.40	111.30	117.00
28	BA	2053	G	C5-C6-N1	-11.33	105.83	111.50
1	AA	1362	A	N1-C6-N6	-11.20	111.88	118.60
28	BA	1073	A	C4-C5-N7	-11.18	105.11	110.70
28	BA	783	A	C5-N7-C8	-10.82	98.49	103.90
1	AA	1362	A	C6-C5-N7	10.77	139.84	132.30
28	BA	974	G	C6-C5-N7	-10.48	124.11	130.40
28	BA	2504	U	C5-C6-N1	10.47	127.94	122.70
28	BA	2053	G	C4-C5-C6	10.14	124.89	118.80
1	AA	1362	A	C8-N9-C4	9.99	109.80	105.80
1	AA	1362	A	C4-N9-C1’	-9.89	108.49	126.30
28	BA	2504	U	C6-N1-C2	-9.85	115.09	121.00
28	BA	974	G	C4-C5-N7	9.79	114.71	110.80
28	BA	783	A	N7-C8-N9	9.62	118.61	113.80
57	B5	92	ALA	C-N-CA	9.60	145.69	121.70
28	BA	1534	U	C2-N1-C1’	9.30	128.86	117.70
28	BA	1073	A	C5-N7-C8	9.22	108.51	103.90
28	BA	528	A	C2-N3-C4	-9.11	106.04	110.60
57	B5	93	ALA	C-N-CA	9.06	144.35	121.70
1	AA	1362	A	N7-C8-N9	-9.04	109.28	113.80
1	AA	1362	A	O4’-C1’-N9	8.98	115.38	108.20
28	BA	1950	G	N1-C6-O6	8.95	125.27	119.90
28	BA	465	G	C8-N9-C4	-8.83	102.87	106.40
28	BA	1533	C	N1-C2-O2	8.64	124.08	118.90
28	BA	1073	A	N9-C4-C5	8.61	109.24	105.80
28	BA	783	A	C8-N9-C4	-8.58	102.37	105.80
28	BA	2074	U	O5’-P-OP2	-8.55	98.01	105.70
1	AA	922	G	OP1-P-O3’	8.54	123.99	105.20
28	BA	1936	A	C2-N3-C4	-8.51	106.35	110.60
28	BA	2534	A	N1-C6-N6	8.45	123.67	118.60
28	BA	974	G	C4-N9-C1’	8.45	137.48	126.50
1	AA	922	G	O5’-P-OP2	-8.42	98.12	105.70
28	BA	1533	C	C2-N1-C1’	8.40	128.04	118.80
28	BA	1142	A	C2-N3-C4	-8.34	106.43	110.60
28	BA	2572	A	N1-C6-N6	8.34	123.60	118.60
1	AA	529	G	N1-C6-O6	8.29	124.87	119.90
57	B5	27	VAL	CG1-CB-CG2	8.19	124.01	110.90
28	BA	586	A	O5’-P-OP1	-8.12	98.39	105.70
29	BD	151	THR	C-N-CD	8.01	145.22	128.40
28	BA	783	A	C4-C5-N7	7.87	114.64	110.70
28	BA	1533	C	C6-N1-C2	-7.87	117.15	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	BA	984	A	N3-C4-C5	7.72	132.20	126.80
28	BA	1795	C	C6-N1-C2	-7.72	117.21	120.30
28	BA	2053	G	C4-N9-C1'	7.69	136.49	126.50
1	AA	1362	A	C8-N9-C1'	7.68	141.52	127.70
28	BA	1478	G	N1-C6-O6	7.68	124.51	119.90
57	B5	51	TYR	C-N-CA	7.67	140.87	121.70
23	AW	68	U	C2-N1-C1'	-7.66	108.50	117.70
28	BA	2504	U	N3-C4-C5	-7.66	110.01	114.60
57	B5	49	GLY	C-N-CA	7.65	140.83	121.70
48	BW	76	ARG	NE-CZ-NH2	7.63	124.11	120.30
28	BA	783	A	N1-C6-N6	7.63	123.18	118.60
57	B5	123	ILE	CG1-CB-CG2	7.63	128.18	111.40
28	BA	465	G	N3-C4-C5	-7.61	124.79	128.60
28	BA	974	G	C8-N9-C1'	-7.61	117.11	127.00
28	BA	2053	G	C2-N3-C4	-7.61	108.09	111.90
28	BA	2146	C	N3-C4-C5	-7.59	118.86	121.90
57	B5	119	PRO	C-N-CA	7.57	140.61	121.70
28	BA	776	G	C5-C6-O6	7.51	133.11	128.60
28	BA	783	A	C6-C5-N7	-7.48	127.06	132.30
28	BA	1839	G	N1-C6-O6	7.41	124.35	119.90
28	BA	2504	U	C5-C4-O4	-7.41	121.45	125.90
57	B5	72	LEU	C-N-CA	7.38	140.14	121.70
30	BE	44	ARG	NE-CZ-NH2	7.37	123.98	120.30
1	AA	1362	A	N1-C2-N3	-7.33	125.64	129.30
28	BA	1533	C	N3-C2-O2	-7.31	116.78	121.90
57	B5	81	LEU	CB-CG-CD2	7.28	123.37	111.00
28	BA	1950	G	C6-C5-N7	-7.26	126.04	130.40
28	BA	2053	G	N1-C2-N3	7.25	128.25	123.90
1	AA	922	G	O3'-P-O5'	-7.24	90.24	104.00
28	BA	1073	A	O5'-P-OP2	7.24	119.39	110.70
28	BA	2250	G	C6-C5-N7	-7.24	126.05	130.40
28	BA	1534	U	C6-N1-C1'	-7.22	111.08	121.20
28	BA	974	G	C5-N7-C8	-7.20	100.70	104.30
28	BA	2501	C	C2-N1-C1'	-7.20	110.88	118.80
28	BA	776	G	C5-C6-N1	-7.18	107.91	111.50
28	BA	2447	G	O5'-P-OP1	-7.16	99.25	105.70
1	AA	1086	U	N3-C2-O2	-7.16	117.19	122.20
57	B5	28	ALA	C-N-CA	7.15	139.57	121.70
28	BA	2053	G	C8-N9-C1'	-7.13	117.73	127.00
28	BA	1142	A	N1-C6-N6	7.10	122.86	118.60
57	B5	47	GLU	C-N-CA	7.04	139.30	121.70
28	BA	2423	U	P-O3'-C3'	7.00	128.09	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	B5	54	VAL	CG1-CB-CG2	6.98	122.07	110.90
28	BA	2250	G	N1-C6-O6	6.94	124.06	119.90
28	BA	2061	G	C6-C5-N7	-6.93	126.25	130.40
28	BA	2448	A	N1-C6-N6	6.92	122.75	118.60
28	BA	1284	A	O5'-P-OP2	-6.92	99.48	105.70
28	BA	783	A	C2-N3-C4	-6.91	107.14	110.60
28	BA	2503	A	C5-C6-N6	-6.91	118.17	123.70
28	BA	1935	G	O5'-P-OP2	-6.91	99.48	105.70
1	AA	1524	C	O5'-P-OP1	-6.91	99.48	105.70
28	BA	1839	G	C6-C5-N7	-6.90	126.26	130.40
28	BA	2504	U	C2-N1-C1'	6.90	125.98	117.70
28	BA	984	A	N3-C4-N9	-6.89	121.89	127.40
28	BA	802	A	N1-C6-N6	-6.89	114.47	118.60
28	BA	1378	A	P-O3'-C3'	6.85	127.92	119.70
28	BA	1192	G	C8-N9-C4	6.83	109.13	106.40
28	BA	1311	G	C8-N9-C4	-6.83	103.67	106.40
28	BA	1654	A	O5'-P-OP1	-6.83	99.56	105.70
1	AA	971	G	N1-C6-O6	6.82	123.99	119.90
28	BA	12	U	N3-C2-O2	-6.80	117.44	122.20
1	AA	328	C	N3-C2-O2	-6.80	117.14	121.90
28	BA	974	G	N1-C6-O6	6.79	123.97	119.90
28	BA	2823	A	C8-N9-C4	-6.75	103.10	105.80
28	BA	974	G	N3-C4-N9	6.75	130.05	126.00
28	BA	2681	C	C6-N1-C2	6.75	123.00	120.30
1	AA	328	C	N1-C2-O2	6.70	122.92	118.90
28	BA	503	A	C8-N9-C4	-6.69	103.12	105.80
28	BA	974	G	N9-C4-C5	-6.69	102.72	105.40
28	BA	974	G	C5-C6-O6	-6.68	124.59	128.60
28	BA	974	G	N7-C8-N9	6.67	116.44	113.10
37	BL	19	LEU	CA-CB-CG	6.67	130.64	115.30
31	BF	94	ARG	NE-CZ-NH1	6.63	123.61	120.30
28	BA	2610	C	N3-C2-O2	-6.61	117.27	121.90
27	BC	233	GLY	N-CA-C	-6.59	96.62	113.10
28	BA	528	A	N1-C6-N6	6.58	122.55	118.60
28	BA	1815	A	N9-C4-C5	6.53	108.41	105.80
1	AA	1086	U	N1-C2-O2	6.52	127.36	122.80
1	AA	1305	G	O5'-P-OP1	-6.50	99.85	105.70
1	AA	1530	G	O4'-C1'-N9	6.49	113.39	108.20
28	BA	2146	C	C2-N3-C4	6.49	123.14	119.90
57	B5	84	TYR	C-N-CA	6.47	137.87	121.70
28	BA	2447	G	N1-C6-O6	6.45	123.77	119.90
57	B5	40	GLU	C-N-CA	6.45	137.81	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	B5	147	SER	C-N-CA	6.44	137.81	121.70
23	AW	68	U	C6-N1-C1'	6.43	130.20	121.20
28	BA	2689	U	C5-C4-O4	6.42	129.75	125.90
28	BA	1263	U	N3-C4-C5	-6.41	110.75	114.60
28	BA	984	A	N1-C6-N6	6.41	122.45	118.60
28	BA	404	A	P-O3'-C3'	6.41	127.39	119.70
28	BA	670	A	O4'-C1'-N9	-6.40	103.08	108.20
28	BA	820	A	O5'-P-OP1	-6.38	99.95	105.70
28	BA	2754	U	N3-C4-O4	6.38	123.86	119.40
57	B5	50	VAL	C-N-CA	6.37	137.62	121.70
28	BA	2551	C	OP2-P-O3'	6.37	119.20	105.20
28	BA	2267	A	C8-N9-C4	-6.35	103.26	105.80
1	AA	1332	A	C2-N3-C4	-6.34	107.43	110.60
28	BA	2142	A	OP2-P-O3'	6.32	119.11	105.20
28	BA	1142	A	N3-C4-C5	6.31	131.22	126.80
28	BA	1125	G	N1-C6-O6	6.31	123.69	119.90
1	AA	5	U	N1-C2-O2	6.29	127.20	122.80
30	BE	44	ARG	NE-CZ-NH1	-6.26	117.17	120.30
57	B5	108	VAL	CG1-CB-CG2	6.26	120.91	110.90
28	BA	2770	G	N1-C6-O6	-6.25	116.15	119.90
28	BA	2250	G	C4-C5-N7	6.25	113.30	110.80
25	AY	302	GLY	N-CA-C	-6.23	97.52	113.10
57	B5	39	THR	C-N-CA	6.23	137.28	121.70
1	AA	1279	G	C4-N9-C1'	6.23	134.60	126.50
1	AA	701	U	P-O3'-C3'	6.22	127.17	119.70
1	AA	995	C	C6-N1-C2	6.21	122.78	120.30
57	B5	60	LEU	CB-CG-CD1	6.21	121.56	111.00
28	BA	1950	G	C5-C6-O6	-6.20	124.88	128.60
1	AA	468	A	C8-N9-C4	-6.20	103.32	105.80
1	AA	1370	G	N1-C6-O6	6.20	123.62	119.90
28	BA	748	G	O4'-C1'-N9	6.20	113.16	108.20
28	BA	2250	G	C5-N7-C8	-6.18	101.21	104.30
27	BC	109	LEU	CA-CB-CG	6.17	129.49	115.30
28	BA	1142	A	C4-C5-N7	6.17	113.78	110.70
28	BA	1839	G	C5-C6-O6	-6.15	124.91	128.60
28	BA	1142	A	C5-N7-C8	-6.15	100.82	103.90
28	BA	1003	G	O5'-P-OP2	-6.15	100.16	105.70
1	AA	5	U	N3-C2-O2	-6.13	117.91	122.20
28	BA	2505	G	O5'-P-OP2	-6.13	100.19	105.70
23	AW	61	C	C2-N1-C1'	6.12	125.53	118.80
28	BA	379	G	N1-C6-O6	6.12	123.57	119.90
28	BA	2592	G	O5'-P-OP2	-6.11	100.20	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	BA	567	U	N1-C2-O2	-6.10	118.53	122.80
28	BA	784	G	O4'-C1'-N9	-6.09	103.33	108.20
1	AA	452	A	N1-C6-N6	6.08	122.25	118.60
1	AA	1509	C	C6-N1-C2	-6.07	117.87	120.30
28	BA	2241	A	C8-N9-C4	-6.07	103.37	105.80
57	B5	59	LEU	C-N-CA	6.05	136.83	121.70
28	BA	2534	A	C4-C5-N7	6.05	113.72	110.70
28	BA	2043	C	C6-N1-C2	-6.05	117.88	120.30
28	BA	784	G	P-O3'-C3'	6.05	126.96	119.70
1	AA	1069	C	O5'-P-OP1	-6.04	100.27	105.70
37	BL	82	LEU	CA-CB-CG	6.03	129.18	115.30
28	BA	548	G	C8-N9-C4	-6.03	103.99	106.40
1	AA	1279	G	C8-N9-C1'	-6.02	119.18	127.00
1	AA	237	G	N3-C4-C5	6.01	131.60	128.60
1	AA	971	G	N3-C2-N2	-6.01	115.70	119.90
1	AA	1370	G	C5-C6-N1	-6.00	108.50	111.50
28	BA	1069	A	OP2-P-O3'	6.00	118.39	105.20
28	BA	1073	A	N7-C8-N9	-6.00	110.80	113.80
28	BA	1328	A	O5'-P-OP2	-5.99	100.31	105.70
28	BA	1025	G	P-O3'-C3'	5.99	126.89	119.70
28	BA	528	A	C5-C6-N1	-5.95	114.72	117.70
28	BA	964	C	O5'-P-OP2	-5.95	100.35	105.70
57	B5	53	ARG	C-N-CA	5.94	136.56	121.70
1	AA	330	C	N3-C4-C5	5.94	124.28	121.90
28	BA	2747	G	OP2-P-O3'	5.94	118.26	105.20
1	AA	80	A	O4'-C1'-N9	5.93	112.95	108.20
28	BA	1094	U	N3-C4-C5	-5.93	111.04	114.60
28	BA	1815	A	C8-N9-C4	-5.92	103.43	105.80
1	AA	330	C	C6-N1-C2	5.90	122.66	120.30
1	AA	529	G	C5-C6-O6	-5.90	125.06	128.60
28	BA	1069	A	C8-N9-C4	-5.90	103.44	105.80
28	BA	2554	U	O5'-P-OP1	-5.89	100.39	105.70
28	BA	527	C	P-O3'-C3'	5.89	126.77	119.70
1	AA	1302	C	P-O3'-C3'	5.89	126.77	119.70
28	BA	2447	G	C5-C6-O6	-5.89	125.07	128.60
28	BA	119	A	O5'-P-OP2	-5.89	100.40	105.70
28	BA	1670	C	N1-C2-O2	-5.88	115.37	118.90
28	BA	1428	C	O5'-P-OP1	-5.87	100.41	105.70
1	AA	1201	A	N1-C6-N6	-5.87	115.08	118.60
28	BA	2610	C	N1-C2-O2	5.86	122.42	118.90
28	BA	2448	A	C6-C5-N7	-5.86	128.20	132.30
28	BA	1779	U	N3-C4-O4	-5.84	115.31	119.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	BA	1509	A	O4'-C1'-N9	5.83	112.86	108.20
1	AA	79	G	P-O3'-C3'	5.82	126.69	119.70
28	BA	2241	A	N9-C4-C5	5.82	108.13	105.80
28	BA	1837	C	O5'-P-OP1	-5.81	100.47	105.70
1	AA	262	A	O5'-P-OP1	-5.81	100.47	105.70
1	AA	108	G	C4-N9-C1'	5.80	134.05	126.50
28	BA	516	C	O5'-P-OP1	-5.80	100.48	105.70
28	BA	2715	C	C6-N1-C2	5.79	122.62	120.30
28	BA	1606	C	C2-N3-C4	-5.76	117.02	119.90
1	AA	529	G	C6-C5-N7	-5.76	126.95	130.40
28	BA	1192	G	N9-C4-C5	-5.74	103.10	105.40
1	AA	251	G	N1-C6-O6	5.73	123.34	119.90
28	BA	1066	U	N3-C2-O2	-5.73	118.19	122.20
28	BA	2534	A	C5-N7-C8	-5.72	101.04	103.90
28	BA	1645	G	N3-C4-C5	-5.72	125.74	128.60
28	BA	2061	G	N3-C4-N9	5.71	129.42	126.00
57	B5	117	LEU	C-N-CA	5.71	135.96	121.70
1	AA	844	G	C4-N9-C1'	5.70	133.91	126.50
1	AA	990	C	C6-N1-C2	-5.70	118.02	120.30
28	BA	2604	U	N3-C4-O4	-5.70	115.41	119.40
28	BA	1789	A	O5'-P-OP1	-5.69	100.58	105.70
28	BA	1358	G	C8-N9-C4	-5.68	104.13	106.40
1	AA	1279	G	O4'-C1'-N9	-5.67	103.67	108.20
1	AA	1279	G	N7-C8-N9	5.65	115.93	113.10
28	BA	1534	U	C5-C6-N1	5.65	125.53	122.70
28	BA	1247	A	P-O3'-C3'	5.65	126.47	119.70
28	BA	1263	U	C6-N1-C2	-5.65	117.61	121.00
28	BA	1207	C	C6-N1-C2	-5.64	118.04	120.30
28	BA	2544	G	C6-C5-N7	-5.64	127.01	130.40
28	BA	1088	A	O4'-C1'-N9	-5.64	103.69	108.20
28	BA	1157	G	N1-C6-O6	5.64	123.28	119.90
28	BA	1979	U	C6-N1-C2	-5.64	117.62	121.00
28	BA	2271	G	C5-C6-O6	-5.63	125.22	128.60
28	BA	271	G	OP1-P-O3'	5.62	117.58	105.20
28	BA	2501	C	N3-C4-C5	5.62	124.15	121.90
28	BA	2719	G	C5-C6-N1	-5.62	108.69	111.50
1	AA	431	A	C8-N9-C4	5.61	108.05	105.80
28	BA	2146	C	C6-N1-C2	-5.60	118.06	120.30
28	BA	1198	U	O5'-P-OP2	-5.60	100.66	105.70
23	AW	61	C	N1-C2-O2	5.60	122.26	118.90
1	AA	1493	A	P-O3'-C3'	5.59	126.41	119.70
28	BA	2719	G	N1-C6-O6	5.59	123.25	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	BA	1509	A	P-O3'-C3'	5.58	126.40	119.70
1	AA	1359	C	N1-C2-O2	5.58	122.25	118.90
28	BA	1611	C	N1-C2-O2	-5.58	115.55	118.90
28	BA	1153	C	N1-C2-O2	-5.57	115.56	118.90
28	BA	1073	A	C4-N9-C1'	-5.57	116.27	126.30
28	BA	2053	G	N3-C2-N2	-5.57	116.00	119.90
1	AA	1362	A	C2-N3-C4	5.57	113.38	110.60
1	AA	1519	A	C4-C5-C6	5.56	119.78	117.00
1	AA	237	G	C8-N9-C4	5.54	108.62	106.40
23	AW	66	C	N1-C2-O2	5.53	122.22	118.90
1	AA	1362	A	C5-C6-N1	5.52	120.46	117.70
28	BA	1027	A	O4'-C1'-N9	-5.52	103.79	108.20
1	AA	1410	A	N1-C6-N6	-5.51	115.29	118.60
1	AA	844	G	C8-N9-C1'	-5.51	119.84	127.00
28	BA	1229	C	C6-N1-C2	5.51	122.50	120.30
28	BA	29	U	OP2-P-O3'	5.50	117.29	105.20
28	BA	672	C	N1-C2-O2	5.49	122.19	118.90
28	BA	1125	G	C6-C5-N7	-5.49	127.11	130.40
28	BA	626	A	N1-C6-N6	5.49	121.89	118.60
28	BA	1069	A	O4'-C1'-N9	5.49	112.59	108.20
28	BA	209	C	C6-N1-C2	5.48	122.49	120.30
28	BA	2326	C	C5-C4-N4	-5.48	116.36	120.20
1	AA	1078	U	O3'-P-O5'	-5.48	93.59	104.00
28	BA	451	U	O4'-C1'-N1	5.48	112.58	108.20
28	BA	1759	A	N1-C6-N6	5.47	121.88	118.60
28	BA	989	G	O4'-C1'-N9	5.47	112.58	108.20
1	AA	913	A	P-O3'-C3'	5.46	126.26	119.70
26	BB	80	U	N1-C2-N3	5.46	118.18	114.90
23	AW	68	U	N1-C2-O2	-5.46	118.98	122.80
28	BA	2446	G	OP2-P-O3'	5.46	117.20	105.20
28	BA	1311	G	N7-C8-N9	5.45	115.83	113.10
28	BA	55	G	C5-C6-O6	-5.45	125.33	128.60
28	BA	984	A	C5-C6-N1	-5.45	114.98	117.70
28	BA	1190	G	C5-N7-C8	-5.45	101.58	104.30
28	BA	532	A	C8-N9-C4	-5.45	103.62	105.80
28	BA	2604	U	C5-C4-O4	5.44	129.16	125.90
28	BA	2689	U	N3-C4-O4	-5.44	115.59	119.40
28	BA	2271	G	N1-C6-O6	5.43	123.16	119.90
28	BA	1430	G	N1-C6-O6	5.42	123.15	119.90
1	AA	976	G	C5-C6-O6	5.42	131.85	128.60
28	BA	2282	G	C8-N9-C4	-5.42	104.23	106.40
28	BA	598	U	OP2-P-O3'	5.41	117.11	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	BA	2353	G	N1-C6-O6	-5.41	116.65	119.90
28	BA	1950	G	C8-N9-C1'	-5.41	119.97	127.00
28	BA	2250	G	N7-C8-N9	5.41	115.80	113.10
28	BA	2544	G	N1-C6-O6	5.41	123.14	119.90
1	AA	351	G	C4-C5-N7	5.40	112.96	110.80
1	AA	481	G	C4-N9-C1'	-5.40	119.48	126.50
28	BA	2263	C	N3-C4-C5	-5.39	119.74	121.90
1	AA	115	G	N3-C4-C5	-5.39	125.90	128.60
1	AA	328	C	C2-N1-C1'	5.39	124.73	118.80
1	AA	1359	C	C6-N1-C2	5.39	122.46	120.30
28	BA	1025	G	C8-N9-C4	-5.39	104.24	106.40
28	BA	2439	A	N1-C6-N6	5.39	121.83	118.60
28	BA	1420	A	O4'-C1'-N9	5.38	112.51	108.20
1	AA	844	G	N3-C4-N9	5.38	129.23	126.00
28	BA	1129	A	O5'-P-OP1	-5.38	100.86	105.70
28	BA	2244	U	C5-C4-O4	-5.38	122.67	125.90
1	AA	1241	G	C5-C6-O6	5.38	131.83	128.60
28	BA	1073	A	C8-N9-C1'	5.38	137.38	127.70
28	BA	1824	G	N9-C4-C5	5.38	107.55	105.40
28	BA	837	C	N1-C2-O2	-5.37	115.68	118.90
28	BA	2153	C	O4'-C1'-N1	5.37	112.50	108.20
28	BA	677	A	OP1-P-O3'	5.37	117.00	105.20
1	AA	1526	G	O5'-P-OP1	-5.36	100.88	105.70
28	BA	1350	C	C6-N1-C2	5.36	122.44	120.30
28	BA	2250	G	C2-N3-C4	-5.35	109.22	111.90
1	AA	1301	U	O5'-P-OP2	-5.35	100.89	105.70
28	BA	2353	G	C2-N3-C4	5.35	114.57	111.90
28	BA	2355	G	C8-N9-C4	5.35	108.54	106.40
41	BP	113	LEU	CA-CB-CG	5.34	127.58	115.30
28	BA	2608	G	C2-N3-C4	-5.34	109.23	111.90
28	BA	1970	A	C8-N9-C4	-5.33	103.67	105.80
28	BA	250	G	O5'-P-OP2	-5.33	100.91	105.70
28	BA	2704	C	C6-N1-C2	5.32	122.43	120.30
28	BA	1206	G	N3-C4-C5	-5.32	125.94	128.60
1	AA	912	C	N3-C4-N4	5.31	121.72	118.00
28	BA	2571	U	C2-N1-C1'	-5.31	111.33	117.70
57	B5	50	VAL	CG1-CB-CG2	5.31	119.39	110.90
1	AA	976	G	C4-C5-N7	-5.31	108.68	110.80
1	AA	108	G	C4-C5-N7	5.30	112.92	110.80
57	B5	131	THR	N-CA-C	-5.30	96.68	111.00
28	BA	1355	G	C8-N9-C4	-5.30	104.28	106.40
28	BA	1831	G	C8-N9-C4	-5.30	104.28	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	BA	2071	A	OP2-P-O3'	5.29	116.83	105.20
1	AA	250	A	P-O3'-C3'	5.28	126.04	119.70
28	BA	1458	U	P-O3'-C3'	5.28	126.04	119.70
28	BA	2015	A	N1-C6-N6	-5.28	115.43	118.60
28	BA	748	G	C4-C5-N7	-5.27	108.69	110.80
28	BA	776	G	C4-N9-C1'	5.27	133.35	126.50
28	BA	2037	A	N9-C4-C5	5.27	107.91	105.80
28	BA	518	G	O5'-P-OP1	-5.27	100.96	105.70
28	BA	2470	G	OP2-P-O3'	5.27	116.79	105.20
28	BA	1565	C	C6-N1-C2	-5.26	118.19	120.30
28	BA	1131	G	OP1-P-O3'	5.26	116.78	105.20
1	AA	134	G	N1-C2-N2	-5.26	111.47	116.20
28	BA	548	G	N3-C4-C5	-5.26	125.97	128.60
28	BA	1533	C	C5-C6-N1	5.26	123.63	121.00
57	B5	50	VAL	CA-CB-CG1	5.25	118.78	110.90
28	BA	2501	C	C6-N1-C1'	5.25	127.10	120.80
28	BA	916	G	C6-C5-N7	-5.24	127.25	130.40
28	BA	2723	C	C6-N1-C2	-5.24	118.20	120.30
28	BA	84	A	N1-C6-N6	-5.24	115.46	118.60
28	BA	2584	U	N3-C4-O4	5.23	123.06	119.40
28	BA	2537	U	C5-C4-O4	5.23	129.04	125.90
28	BA	733	G	C8-N9-C4	-5.23	104.31	106.40
25	AY	93	VAL	N-CA-C	-5.23	96.88	111.00
28	BA	2685	G	C5-C6-N1	-5.23	108.89	111.50
51	BZ	15	ARG	NE-CZ-NH1	5.22	122.91	120.30
28	BA	1446	C	C6-N1-C2	-5.22	118.21	120.30
49	BX	29	LEU	CA-CB-CG	5.22	127.31	115.30
28	BA	940	G	N1-C6-O6	5.22	123.03	119.90
28	BA	404	A	C8-N9-C4	-5.22	103.71	105.80
1	AA	572	A	N1-C6-N6	-5.22	115.47	118.60
28	BA	2618	G	C5-C6-N1	-5.21	108.89	111.50
28	BA	776	G	C4-C5-C6	5.21	121.92	118.80
28	BA	1943	U	C5-C4-O4	5.21	129.02	125.90
1	AA	1057	G	N1-C6-O6	-5.20	116.78	119.90
28	BA	1264	A	O5'-P-OP1	-5.20	101.02	105.70
28	BA	1639	C	C6-N1-C2	5.20	122.38	120.30
28	BA	1936	A	N3-C4-C5	5.20	130.44	126.80
28	BA	991	C	C6-N1-C2	-5.20	118.22	120.30
28	BA	454	A	O5'-P-OP2	-5.19	101.03	105.70
28	BA	2825	G	N3-C4-N9	5.19	129.11	126.00
28	BA	2534	A	C5-C6-N6	-5.18	119.55	123.70
1	AA	52	C	O5'-P-OP2	-5.18	101.04	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AA	1201	A	P-O3'-C3'	5.18	125.92	119.70
1	AA	1241	G	N3-C4-N9	-5.18	122.89	126.00
28	BA	119	A	P-O3'-C3'	5.18	125.91	119.70
28	BA	1122	G	N3-C4-N9	-5.18	122.89	126.00
57	B5	130	PRO	CA-N-CD	-5.17	104.26	111.50
1	AA	869	G	C5-C6-O6	-5.17	125.50	128.60
1	AA	1370	G	N3-C2-N2	-5.17	116.28	119.90
1	AA	890	G	O5'-P-OP1	5.17	116.90	110.70
1	AA	931	C	C5-C4-N4	5.17	123.81	120.20
28	BA	1538	G	N3-C4-C5	5.17	131.18	128.60
42	BQ	63	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	AA	1322	C	N1-C2-O2	5.16	122.00	118.90
1	AA	467	U	P-O3'-C3'	5.16	125.89	119.70
28	BA	1355	G	N3-C2-N2	-5.16	116.29	119.90
28	BA	1452	G	C4-C5-N7	5.16	112.86	110.80
28	BA	2015	A	N9-C4-C5	5.16	107.86	105.80
28	BA	699	A	N1-C6-N6	5.16	121.69	118.60
28	BA	1238	G	O5'-P-OP2	-5.16	101.06	105.70
28	BA	807	U	N3-C4-O4	5.15	123.01	119.40
28	BA	1534	U	N1-C2-O2	5.15	126.41	122.80
1	AA	479	U	O4'-C1'-N1	5.15	112.32	108.20
1	AA	326	G	N3-C4-N9	-5.13	122.92	126.00
28	BA	465	G	C4-C5-C6	5.13	121.88	118.80
1	AA	319	G	C4-N9-C1'	-5.13	119.83	126.50
28	BA	1779	U	C5-C6-N1	-5.13	120.14	122.70
26	BB	114	C	C5-C4-N4	-5.13	116.61	120.20
28	BA	1025	G	N3-C4-C5	-5.13	126.04	128.60
28	BA	752	A	C2-N3-C4	-5.13	108.04	110.60
28	BA	2368	C	C6-N1-C2	5.12	122.35	120.30
1	AA	351	G	C5-N7-C8	-5.12	101.74	104.30
1	AA	345	C	O5'-P-OP1	-5.12	101.09	105.70
28	BA	833	A	C8-N9-C4	-5.12	103.75	105.80
28	BA	1395	A	O4'-C1'-N9	5.12	112.30	108.20
47	BV	61	LEU	CA-CB-CG	5.12	127.07	115.30
1	AA	205	A	O4'-C1'-N9	-5.11	104.11	108.20
28	BA	2422	C	N1-C2-O2	5.11	121.97	118.90
34	BI	79	LEU	CA-CB-CG	5.11	127.04	115.30
28	BA	1684	G	N3-C4-C5	-5.10	126.05	128.60
1	AA	1336	C	P-O3'-C3'	5.09	125.81	119.70
28	BA	2503	A	C5-C6-N1	5.09	120.25	117.70
28	BA	1928	A	N1-C6-N6	5.09	121.65	118.60
28	BA	2443	C	C6-N1-C2	-5.08	118.27	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	BA	1524	G	C8-N9-C4	-5.08	104.37	106.40
1	AA	579	A	OP2-P-O3'	5.08	116.38	105.20
1	AA	780	A	N1-C6-N6	-5.08	115.55	118.60
28	BA	650	C	C6-N1-C2	-5.08	118.27	120.30
28	BA	2448	A	C5-C6-N6	-5.08	119.64	123.70
28	BA	376	G	C6-C5-N7	-5.07	127.36	130.40
28	BA	403	U	P-O3'-C3'	5.07	125.78	119.70
28	BA	1533	C	C6-N1-C1'	-5.06	114.73	120.80
28	BA	1659	G	N3-C4-C5	5.06	131.13	128.60
28	BA	2518	A	N1-C6-N6	5.06	121.63	118.60
28	BA	2537	U	N1-C2-N3	5.05	117.93	114.90
28	BA	1983	G	C5-C6-N1	-5.04	108.98	111.50
28	BA	2455	G	O5'-P-OP2	-5.04	101.16	105.70
1	AA	1279	G	C6-C5-N7	-5.04	127.38	130.40
28	BA	1314	C	C2-N1-C1'	5.04	124.34	118.80
28	BA	1606	C	P-O3'-C3'	5.03	125.74	119.70
28	BA	2902	C	P-O3'-C3'	5.03	125.73	119.70
28	BA	984	A	N1-C2-N3	5.02	131.81	129.30
28	BA	970	U	N1-C2-O2	-5.02	119.29	122.80
45	BT	29	THR	N-CA-C	5.01	124.54	111.00
28	BA	2278	A	OP2-P-O3'	5.01	116.23	105.20
28	BA	686	U	C2-N1-C1'	-5.01	111.69	117.70
1	AA	328	C	C6-N1-C1'	-5.00	114.80	120.80
28	BA	745	G	N3-C4-N9	5.00	129.00	126.00
28	BA	1622	G	C8-N9-C4	-5.00	104.40	106.40
28	BA	467	G	N7-C8-N9	-5.00	110.60	113.10
28	BA	1122	G	N3-C4-C5	5.00	131.10	128.60

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	AF	101	PRO	Peptide
12	AL	23	ALA	Peptide
22	AV	29	G	Sidechain
22	AV	4	G	Sidechain
22	AV	8	U	Sidechain
25	AY	218	TRP	Peptide
57	B5	130	PRO	Peptide
27	BC	233	GLY	Peptide
29	BD	9	VAL	Peptide
35	BJ	110	PRO	Peptide

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Mol	Chain	Res	Type	Group
36	BK	71	ARG	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32895	0	16542	956	0
2	AB	1704	0	1732	90	0
3	AC	1624	0	1696	41	0
4	AD	1643	0	1707	68	0
5	AE	1105	0	1147	147	0
6	AF	832	0	824	26	0
7	AG	1181	0	1236	53	0
8	AH	979	0	1031	28	0
9	AI	1022	0	1067	121	0
10	AJ	786	0	828	23	0
11	AK	877	0	887	32	0
12	AL	955	0	1016	36	0
13	AM	883	0	941	31	0
14	AN	774	0	824	35	0
15	AO	714	0	733	11	0
16	AP	649	0	666	14	0
17	AQ	648	0	691	11	0
18	AR	455	0	478	10	0
19	AS	637	0	665	39	0
20	AT	665	0	714	11	0
21	AU	425	0	449	43	0
22	AV	1640	0	832	136	0
23	AW	1635	0	829	97	0
24	AX	416	0	207	169	0
25	AY	5194	0	5170	222	0
26	BB	2529	0	1281	21	0
27	BC	2082	0	2157	50	0
28	BA	61274	0	30812	852	0
29	BD	1565	0	1616	52	0
30	BE	1552	0	1619	37	0
31	BF	1410	0	1442	59	0
32	BG	1323	0	1374	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	BH	384	0	405	35	0
34	BI	1032	0	1088	57	0
35	BJ	1129	0	1162	52	0
36	BK	938	0	1012	40	0
37	BL	1045	0	1117	34	0
38	BM	1074	0	1156	48	0
39	BN	960	0	1000	30	0
40	BO	892	0	923	22	0
41	BP	917	0	965	51	0
42	BQ	947	0	1022	50	0
43	BR	816	0	839	35	0
44	BS	857	0	922	28	0
45	BT	738	0	807	35	0
46	BU	779	0	834	29	0
47	BV	753	0	780	14	0
48	BW	596	0	610	82	0
49	BX	625	0	655	16	0
50	BY	509	0	543	12	0
51	BZ	449	0	491	17	0
52	B0	444	0	461	17	0
53	B1	409	0	440	16	0
54	B2	377	0	418	5	0
55	B3	504	0	574	10	0
56	B4	302	0	340	15	0
57	B5	1117	0	1155	120	0
58	B6	227	0	237	7	0
59	AY	37	0	44	59	0
60	AY	28	0	12	26	0
All	All	150958	0	103225	3593	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All (3593) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:92:HIS:CE1	59:AY:801:FUA:H283	1.23	1.69
1:AA:1498:U:C5	24:AX:12:U:H5”	1.26	1.64
1:AA:1498:U:C4	24:AX:12:U:H5”	1.32	1.61
24:AX:14:A:H2’	24:AX:15:A:C5’	1.24	1.58
24:AX:14:A:C2’	24:AX:15:A:H5”	1.16	1.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:92:HIS:CE1	59:AY:801:FUA:C28	1.90	1.52
1:AA:1498:U:C5	24:AX:12:U:C5'	1.89	1.51
1:AA:1530:G:H2'	1:AA:1531:A:C8	1.47	1.47
1:AA:828:U:O2	2:AB:24:PRO:CG	1.63	1.44
1:AA:1075:U:H4'	1:AA:1101:A:C6	1.57	1.39
25:AY:92:HIS:NE2	59:AY:801:FUA:H283	1.35	1.39
1:AA:1082:A:C2'	1:AA:1083:U:H5'	1.53	1.36
15:AO:89:ARG:NH1	28:BA:716:A:OP1	1.59	1.35
1:AA:1074:G:C2'	1:AA:1075:U:H5'	1.58	1.34
1:AA:1081:A:C5'	5:AE:23:LYS:HG3	1.56	1.33
1:AA:15:G:N2	5:AE:22:SER:O	1.60	1.33
22:AV:57:A:C5'	31:BF:74:ALA:HB2	1.59	1.33
1:AA:922:G:N1	1:AA:1395:C:N3	1.77	1.32
9:AI:130:ARG:NH2	23:AW:34:C:H5"	1.43	1.32
2:AB:178:LEU:HD11	5:AE:69:ARG:NH1	1.39	1.32
1:AA:1530:G:H2'	1:AA:1531:A:N7	1.43	1.31
25:AY:270:PHE:CB	60:AY:802:GDP:N1	1.92	1.31
1:AA:1075:U:C4'	1:AA:1101:A:C6	2.13	1.31
1:AA:1498:U:C6	24:AX:12:U:OP1	1.84	1.30
24:AX:8:A:C2'	24:AX:9:U:H5'	1.58	1.30
1:AA:828:U:C2	2:AB:24:PRO:HG2	1.67	1.29
28:BA:2197:U:O2'	33:BH:29:PHE:CD1	1.85	1.29
1:AA:1075:U:H4'	1:AA:1101:A:N6	1.43	1.29
1:AA:1530:G:C6	1:AA:1531:A:N6	2.00	1.29
1:AA:1074:G:O2'	1:AA:1075:U:C5'	1.80	1.28
1:AA:1074:G:O2'	1:AA:1075:U:H5'	1.23	1.28
1:AA:1392:G:C2'	1:AA:1393:U:H5'	1.65	1.27
25:AY:95:PHE:CE1	59:AY:801:FUA:H122	1.69	1.26
28:BA:2197:U:H2'	28:BA:2198:A:C8	1.69	1.25
23:AW:76:A:N6	28:BA:2422:C:O4'	1.67	1.25
1:AA:928:G:O4'	1:AA:1533:C:OP1	1.55	1.24
1:AA:1075:U:C2'	1:AA:1076:U:H5'	1.67	1.24
25:AY:95:PHE:CE1	59:AY:801:FUA:C12	2.19	1.23
28:BA:2197:U:O2'	33:BH:29:PHE:CG	1.91	1.23
1:AA:19:A:C2'	1:AA:20:U:H5'	1.67	1.23
1:AA:1498:U:OP2	24:AX:11:G:H4'	1.16	1.23
5:AE:31:PHE:HE2	24:AX:19:A:N1	1.35	1.23
1:AA:920:U:O2'	1:AA:921:U:H5'	1.36	1.23
1:AA:1392:G:O2'	1:AA:1503:A:OP2	1.54	1.22
25:AY:270:PHE:HB2	60:AY:802:GDP:N1	1.51	1.22
25:AY:464:LEU:HD11	59:AY:801:FUA:C27	1.70	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1149:C:OP2	9:AI:11:ARG:NH1	1.68	1.22
22:AV:75:C:OP2	28:BA:2602:A:N6	1.72	1.22
22:AV:76:A:C8	28:BA:2451:A:O2'	1.82	1.21
1:AA:15:G:N2	1:AA:1080:A:O3'	1.70	1.21
1:AA:1530:G:C5	1:AA:1531:A:N6	2.08	1.21
25:AY:95:PHE:CD1	59:AY:801:FUA:C12	2.24	1.20
1:AA:1498:U:OP2	24:AX:11:G:C4'	1.90	1.19
1:AA:1463:U:P	41:BP:108:ARG:HH11	1.64	1.18
25:AY:95:PHE:CZ	59:AY:801:FUA:H122	1.78	1.18
22:AV:17:C:H5"	22:AV:17(A):U:H6	1.08	1.18
1:AA:1394:A:H1'	1:AA:1395:C:OP1	1.38	1.17
2:AB:178:LEU:CD1	5:AE:69:ARG:NH1	2.08	1.17
22:AV:36:C:H5'	25:AY:513:GLY:HA2	1.24	1.17
1:AA:1530:G:C2'	1:AA:1531:A:C8	2.28	1.16
1:AA:928:G:H4'	1:AA:1533:C:C5	1.80	1.16
24:AX:3:U:H2'	24:AX:4:A:C8	1.80	1.16
28:BA:2198:A:H2'	28:BA:2198:A:OP2	1.40	1.16
1:AA:1498:U:C4	24:AX:12:U:C5'	2.20	1.16
1:AA:1149:C:P	9:AI:11:ARG:NH1	2.19	1.15
1:AA:1391:U:C2'	1:AA:1392:G:H5'	1.76	1.15
25:AY:270:PHE:HB2	60:AY:802:GDP:C6	1.81	1.15
1:AA:1393:U:C4'	1:AA:1502:A:H4'	1.78	1.14
24:AX:9:U:C2'	24:AX:10:G:H5'	1.75	1.14
1:AA:16:A:H2'	1:AA:17:U:H5'	1.28	1.14
1:AA:1394:A:N7	1:AA:1501:C:H4'	1.61	1.14
1:AA:18:C:H5"	5:AE:132:ASN:HD21	0.98	1.14
1:AA:19:A:O2'	1:AA:20:U:H5'	1.46	1.13
25:AY:464:LEU:CD1	59:AY:801:FUA:H272	1.78	1.13
1:AA:1129:C:H4'	9:AI:18:ARG:HH22	1.13	1.12
1:AA:1394:A:C5	1:AA:1501:C:H4'	1.83	1.12
21:AU:48:ALA:O	24:AX:3:U:OP2	1.66	1.12
25:AY:95:PHE:CG	59:AY:801:FUA:H121	1.84	1.12
28:BA:2197:U:O3'	33:BH:29:PHE:CE1	2.02	1.12
1:AA:21:G:H1'	1:AA:914:A:N6	1.65	1.12
1:AA:1498:U:O4	24:AX:12:U:H5"	1.50	1.12
1:AA:1289:A:O3'	7:AG:35:LYS:NZ	1.81	1.11
1:AA:1498:U:N1	24:AX:12:U:OP1	1.82	1.11
28:BA:911:A:C5	38:BM:8:LYS:HE3	1.65	1.11
1:AA:926:G:H22	24:AX:8:A:P	1.73	1.11
1:AA:1079:G:OP1	5:AE:50:TYR:CE2	2.03	1.11
2:AB:178:LEU:HD12	5:AE:69:ARG:HD2	1.30	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:2090:A:H2'	28:BA:2091:C:H5'	1.18	1.11
1:AA:1130:A:OP2	9:AI:64:TYR:CE2	2.04	1.10
1:AA:20:U:H2'	1:AA:21:G:H5'	1.21	1.10
1:AA:1075:U:H2'	1:AA:1076:U:H5'	1.11	1.10
28:BA:2091:C:OP2	28:BA:2092:U:H3'	1.49	1.10
1:AA:1149:C:P	9:AI:11:ARG:HH11	1.75	1.10
28:BA:2195:U:C2'	28:BA:2196:C:H5'	1.82	1.10
1:AA:1392:G:O2'	1:AA:1393:U:H5'	1.49	1.10
22:AV:37:A:O4'	25:AY:508:GLN:OE1	1.70	1.09
1:AA:1395:C:N4	1:AA:1396:A:N6	2.00	1.09
1:AA:1082:A:H2'	1:AA:1083:U:H5'	1.12	1.09
25:AY:95:PHE:CD1	59:AY:801:FUA:H11	1.88	1.09
1:AA:1348:U:H4'	9:AI:122:ARG:HG3	1.34	1.09
25:AY:95:PHE:CD1	59:AY:801:FUA:H121	1.85	1.09
1:AA:1193:G:O2'	5:AE:26:LYS:NZ	1.86	1.08
1:AA:1377:A:C2	7:AG:2:PRO:HD3	1.88	1.08
5:AE:31:PHE:CE2	24:AX:19:A:N1	2.21	1.08
22:AV:17:C:H5"	22:AV:17(A):U:C6	1.88	1.08
59:AY:801:FUA:H202	59:AY:801:FUA:H5	1.29	1.08
57:B5:71:CYS:HB3	57:B5:117:LEU:HD12	1.33	1.08
25:AY:92:HIS:NE2	59:AY:801:FUA:C28	2.04	1.08
1:AA:16:A:H1'	1:AA:1080:A:H4'	1.36	1.07
1:AA:1240:U:OP2	7:AG:116:MET:N	1.87	1.07
1:AA:1498:U:H5	24:AX:12:U:H5'	1.20	1.07
24:AX:9:U:O2'	24:AX:10:G:H5'	1.51	1.07
1:AA:1072:G:OP1	5:AE:54:ARG:CD	2.01	1.07
22:AV:21:A:H61	22:AV:46:G:H2'	1.20	1.07
1:AA:928:G:O2'	1:AA:929:G:H5'	1.52	1.06
5:AE:31:PHE:HE2	24:AX:19:A:C2	1.72	1.06
1:AA:1533:C:H3'	1:AA:1534:A:C5'	1.85	1.06
1:AA:16:A:N3	1:AA:1080:A:O4'	1.89	1.06
1:AA:1076:U:O2	1:AA:1081:A:C2	2.07	1.06
1:AA:1372:U:OP2	9:AI:13:LYS:NZ	1.88	1.06
1:AA:1073:U:P	5:AE:62:LYS:NZ	2.30	1.05
1:AA:18:C:H5"	5:AE:132:ASN:ND2	1.71	1.05
1:AA:1081:A:C5'	5:AE:23:LYS:CG	2.34	1.05
1:AA:1498:U:H5	24:AX:12:U:C5'	1.47	1.05
22:AV:57:A:H5'	31:BF:74:ALA:CB	1.87	1.05
24:AX:14:A:O2'	24:AX:15:A:H5"	1.56	1.05
25:AY:270:PHE:HB3	60:AY:802:GDP:N1	1.64	1.05
1:AA:16:A:C2'	1:AA:17:U:H5'	1.85	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:178:LEU:HD11	5:AE:69:ARG:HH11	0.88	1.04
1:AA:1074:G:OP2	5:AE:62:LYS:HD3	1.58	1.04
1:AA:1391:U:O2'	1:AA:1392:G:H5'	1.58	1.04
1:AA:1498:U:C2	24:AX:12:U:OP1	2.10	1.04
1:AA:1429:A:H4'	28:BA:1703:G:O2'	1.58	1.03
25:AY:25:THR:N	60:AY:802:GDP:O2A	1.90	1.03
1:AA:1081:A:H5'	5:AE:23:LYS:CG	1.88	1.03
28:BA:2091:C:H2'	28:BA:2092:U:H5	1.21	1.03
1:AA:1498:U:C5	24:AX:12:U:OP1	2.12	1.03
1:AA:1390:U:H2'	1:AA:1391:U:C6	1.94	1.03
22:AV:34:U:N3	24:AX:13:A:N1	2.06	1.03
2:AB:178:LEU:CD1	5:AE:69:ARG:HD2	1.88	1.03
22:AV:75:C:OP2	28:BA:2602:A:C6	1.83	1.03
25:AY:95:PHE:CD1	59:AY:801:FUA:C11	2.42	1.02
1:AA:1130:A:O2'	9:AI:5:GLN:HG3	1.57	1.02
1:AA:1073:U:P	5:AE:62:LYS:HZ1	1.80	1.02
1:AA:20:U:C2'	1:AA:21:G:H5'	1.87	1.02
1:AA:1130:A:OP1	9:AI:18:ARG:NH2	1.91	1.02
23:AW:50:C:N4	23:AW:64:G:H1	1.58	1.01
28:BA:2195:U:H2'	28:BA:2196:C:H5'	1.38	1.01
24:AX:8:A:H2'	24:AX:9:U:C5'	1.89	1.01
57:B5:26:VAL:HG21	57:B5:115:GLY:H	1.23	1.01
28:BA:2197:U:C2'	28:BA:2198:A:C5	2.44	1.01
28:BA:2091:C:P	28:BA:2092:U:H5"	2.01	1.00
1:AA:1074:G:H2'	1:AA:1075:U:H5'	1.42	1.00
22:AV:46:G:H4'	22:AV:47:U:H5	1.25	1.00
1:AA:21:G:H1'	1:AA:914:A:H61	1.20	1.00
9:AI:130:ARG:NH2	23:AW:34:C:C5'	2.23	1.00
1:AA:1081:A:C6	1:AA:1082:A:N6	2.30	0.99
1:AA:1463:U:P	41:BP:108:ARG:NH1	2.35	0.99
1:AA:926:G:N2	24:AX:8:A:P	2.35	0.99
23:AW:12:U:H3	23:AW:23:A:N6	1.60	0.99
1:AA:1079:G:O2'	1:AA:1080:A:H5'	1.62	0.99
57:B5:3:LEU:O	57:B5:7:ASP:OD1	1.79	0.99
24:AX:14:A:N3	24:AX:15:A:H5'	1.78	0.99
25:AY:270:PHE:HB3	60:AY:802:GDP:HN1	1.24	0.99
1:AA:1392:G:H2'	1:AA:1393:U:H5'	1.44	0.99
28:BA:2090:A:C2'	28:BA:2091:C:H5'	1.93	0.99
1:AA:1076:U:O2	1:AA:1081:A:N1	1.94	0.99
1:AA:1130:A:OP2	9:AI:64:TYR:HE2	1.43	0.99
1:AA:1442:G:H4'	41:BP:113:LEU:HD12	1.43	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:910:A:C2	38:BM:9:PHE:CE1	2.45	0.99
1:AA:1075:U:C4'	1:AA:1101:A:N6	2.20	0.99
22:AV:36:C:H5'	25:AY:513:GLY:CA	1.93	0.99
1:AA:21:G:O2'	1:AA:22:G:O4'	1.79	0.99
28:BA:2197:U:C2	28:BA:2198:A:N7	2.30	0.98
22:AV:35:A:O2'	25:AY:513:GLY:HA3	1.63	0.98
1:AA:19:A:H2'	1:AA:20:U:H5'	1.45	0.98
24:AX:9:U:H2'	24:AX:10:G:H5'	1.41	0.98
1:AA:17:U:H1'	1:AA:1079:G:H1'	1.42	0.98
1:AA:1077:G:N2	1:AA:1080:A:N7	2.11	0.98
25:AY:270:PHE:CB	60:AY:802:GDP:C6	2.41	0.98
1:AA:1493:A:C4'	24:AX:14:A:H4'	1.94	0.98
23:AW:11:C:H42	23:AW:24:G:H1	1.09	0.97
24:AX:8:A:C2'	24:AX:9:U:C5'	2.40	0.97
1:AA:1377:A:N3	7:AG:2:PRO:HD3	1.80	0.97
25:AY:147:MET:CE	32:BG:92:GLY:HA2	1.94	0.97
1:AA:17:U:H2'	1:AA:18:C:C6	1.99	0.97
22:AV:34:U:C4	24:AX:13:A:N1	2.33	0.97
1:AA:1393:U:H4'	1:AA:1502:A:H4'	1.46	0.96
22:AV:35:A:N6	24:AX:13:A:N6	2.12	0.96
28:BA:2092:U:H4'	28:BA:2093:G:O5'	1.63	0.96
1:AA:1158:C:O2'	2:AB:131:LYS:HD2	1.66	0.96
28:BA:2197:U:H2'	28:BA:2198:A:N7	1.80	0.96
24:AX:13:A:O4'	25:AY:511:GLY:HA2	1.66	0.96
1:AA:1072:G:OP1	5:AE:54:ARG:HD3	1.65	0.96
13:AM:82:ASP:OD2	31:BF:142:TYR:HE1	1.47	0.95
1:AA:927:G:OP1	1:AA:1503:A:C6	2.20	0.95
1:AA:1077:G:N1	1:AA:1080:A:OP2	1.99	0.95
28:BA:912:C:H2'	28:BA:913:U:H5'	1.46	0.95
24:AX:3:U:C2'	24:AX:4:A:H8	1.79	0.95
24:AX:6:A:H3'	24:AX:6:A:N3	1.82	0.95
28:BA:2089:C:C2'	28:BA:2090:A:H5'	1.96	0.95
1:AA:18:C:C5'	5:AE:132:ASN:HD21	1.78	0.95
1:AA:1391:U:H2'	1:AA:1392:G:H5'	1.46	0.94
24:AX:3:U:H2'	24:AX:4:A:H8	1.22	0.94
1:AA:17:U:C1'	1:AA:1079:G:H1'	1.97	0.94
1:AA:1081:A:C6	1:AA:1082:A:C6	2.55	0.94
22:AV:74:C:C2	28:BA:2252:G:N1	2.28	0.94
1:AA:1147:C:H4'	9:AI:7:TYR:CE2	2.01	0.94
1:AA:15:G:O2'	5:AE:22:SER:CB	2.16	0.94
57:B5:117:LEU:CD2	57:B5:120:ALA:HA	1.97	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:927:G:H2'	1:AA:928:G:H5'	1.49	0.94
1:AA:1442:G:C4'	41:BP:113:LEU:HD12	1.95	0.94
23:AW:76:A:N6	28:BA:2422:C:C1'	2.31	0.94
25:AY:270:PHE:HB2	60:AY:802:GDP:C2	2.03	0.94
28:BA:2197:U:C2'	28:BA:2198:A:N7	2.30	0.94
1:AA:1498:U:C5	24:AX:12:U:P	2.61	0.94
1:AA:1530:G:C6	1:AA:1531:A:C6	2.56	0.94
22:AV:76:A:H8	28:BA:2451:A:O2'	1.43	0.94
1:AA:1317:C:OP2	14:AN:28:LYS:NZ	2.01	0.94
1:AA:1075:U:C4	1:AA:1076:U:C4	2.56	0.94
28:BA:2196:C:C2	28:BA:2197:U:N3	2.36	0.93
1:AA:1394:A:C8	1:AA:1501:C:H4'	2.04	0.93
28:BA:2197:U:C1'	28:BA:2198:A:N7	2.32	0.93
25:AY:92:HIS:HE1	59:AY:801:FUA:C28	1.75	0.93
25:AY:649:VAL:HA	34:BI:25:PRO:CB	1.99	0.93
1:AA:1074:G:C5	1:AA:1075:U:C4	2.57	0.93
1:AA:1493:A:H4'	24:AX:14:A:H4'	1.48	0.93
24:AX:12:U:O2'	24:AX:13:A:H5'	1.69	0.93
22:AV:35:A:C6	24:AX:13:A:C6	2.57	0.93
1:AA:927:G:H1'	1:AA:1532:U:H4'	1.50	0.92
57:B5:71:CYS:HB3	57:B5:117:LEU:CD1	1.98	0.92
1:AA:928:G:H4'	1:AA:1533:C:H5	1.19	0.92
25:AY:147:MET:HE2	32:BG:92:GLY:HA2	1.51	0.92
1:AA:16:A:C2	1:AA:1080:A:H1'	2.05	0.92
1:AA:921:U:OP1	1:AA:1082:A:H5"	1.68	0.92
1:AA:1475:G:H4'	28:BA:1689:A:H4'	1.48	0.92
1:AA:1079:G:OP1	5:AE:50:TYR:CZ	2.21	0.92
24:AX:14:A:C2'	24:AX:15:A:C5'	2.04	0.92
1:AA:21:G:N3	1:AA:914:A:N6	2.18	0.92
57:B5:71:CYS:CB	57:B5:117:LEU:HD12	2.00	0.92
22:AV:35:A:O2'	25:AY:513:GLY:CA	2.17	0.91
28:BA:2197:U:H2'	28:BA:2198:A:C5	2.05	0.91
1:AA:920:U:HO2'	1:AA:921:U:H5'	1.33	0.91
25:AY:92:HIS:CE1	59:AY:801:FUA:H282	2.03	0.91
1:AA:828:U:O2	2:AB:24:PRO:HG2	0.74	0.91
24:AX:8:A:H2'	24:AX:9:U:H5'	0.93	0.91
28:BA:1154:G:OP2	42:BQ:57:ARG:NH1	2.03	0.91
22:AV:57:A:C5'	31:BF:74:ALA:CB	2.45	0.91
1:AA:926:G:N2	24:AX:8:A:OP2	2.04	0.91
28:BA:2091:C:OP2	28:BA:2092:U:H5"	1.71	0.91
1:AA:1533:C:H3'	1:AA:1534:A:H5"	1.50	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:178:LEU:CD1	5:AE:69:ARG:CZ	2.49	0.91
13:AM:82:ASP:CG	31:BF:142:TYR:HE1	1.73	0.91
25:AY:469:ILE:HD13	59:AY:801:FUA:H3	1.52	0.91
1:AA:1082:A:O2'	1:AA:1083:U:H5'	1.71	0.91
1:AA:1394:A:O2'	1:AA:1501:C:O2	1.89	0.91
22:AV:36:C:C5'	25:AY:513:GLY:HA2	2.01	0.91
28:BA:2197:U:H4'	33:BH:29:PHE:CZ	2.06	0.91
1:AA:1081:A:H2'	1:AA:1082:A:C8	2.05	0.90
1:AA:1147:C:O2	9:AI:18:ARG:NH1	2.03	0.90
15:AO:89:ARG:NH1	28:BA:716:A:P	2.45	0.90
24:AX:12:U:C2'	24:AX:13:A:H5'	2.01	0.90
1:AA:1375:A:OP1	7:AG:25:LYS:HE3	1.71	0.90
1:AA:1412:C:OP1	12:AL:54:ARG:NH1	2.05	0.90
57:B5:24:SER:HB2	57:B5:116:GLU:HG2	1.54	0.90
1:AA:1079:G:H5"	5:AE:50:TYR:OH	1.70	0.90
1:AA:1074:G:O2'	1:AA:1075:U:H5"	1.71	0.90
1:AA:1129:C:H4'	9:AI:18:ARG:NH2	1.85	0.90
28:BA:1248:G:OP2	30:BE:44:ARG:NH1	2.04	0.90
28:BA:2091:C:C6	28:BA:2092:U:C5	2.60	0.90
1:AA:1083:U:C5	1:AA:1084:G:C5	2.58	0.90
28:BA:2197:U:O2'	33:BH:29:PHE:CE1	2.25	0.90
22:AV:34:U:N3	24:AX:13:A:C2	2.40	0.90
23:AW:20:U:OP1	28:BA:2145:C:H2'	1.71	0.90
28:BA:2279:G:N7	48:BW:10:ARG:NH2	2.20	0.90
1:AA:1530:G:H2'	1:AA:1531:A:H8	1.36	0.89
23:AW:50:C:H42	23:AW:64:G:H1	1.14	0.89
1:AA:1392:G:H4'	1:AA:1531:A:C5'	2.02	0.89
57:B5:71:CYS:CB	57:B5:117:LEU:CD1	2.50	0.89
22:AV:34:U:O4	24:AX:13:A:N6	2.05	0.89
1:AA:15:G:C5'	5:AE:29:ARG:NH1	2.36	0.89
26:BB:43:C:O2	31:BF:91:ARG:NH2	2.04	0.89
1:AA:1101:A:H61	2:AB:101:THR:HG21	1.36	0.89
5:AE:31:PHE:CE2	24:AX:19:A:C2	2.61	0.89
1:AA:1076:U:O2'	1:AA:1077:G:C5'	2.20	0.89
22:AV:20:U:H3'	22:AV:21:A:H5'	1.55	0.89
28:BA:2091:C:H2'	28:BA:2092:U:C5	2.08	0.89
1:AA:1346:A:H5"	9:AI:122:ARG:HH12	1.37	0.88
46:BU:98:ASN:O	46:BU:100:GLU:N	2.06	0.88
1:AA:1075:U:C5'	1:AA:1101:A:N6	2.36	0.88
23:AW:20:U:OP1	28:BA:2145:C:C2'	2.21	0.88
28:BA:864:G:O2'	28:BA:914:G:O6	1.90	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:996:A:OP2	42:BQ:91:ARG:NH2	2.07	0.88
22:AV:57:A:H5'	31:BF:74:ALA:HB2	0.91	0.88
1:AA:1075:U:C5'	1:AA:1101:A:C6	2.57	0.88
1:AA:1081:A:N1	1:AA:1082:A:C6	2.41	0.88
1:AA:1290:G:P	7:AG:35:LYS:NZ	2.45	0.88
1:AA:15:G:H4'	5:AE:29:ARG:NH1	1.89	0.88
1:AA:1082:A:H2'	1:AA:1083:U:C5'	2.02	0.88
1:AA:1074:G:C6	1:AA:1075:U:C4	2.62	0.87
28:BA:1336:A:OP2	45:BT:68:LYS:NZ	2.06	0.87
28:BA:2091:C:C6	28:BA:2092:U:C6	2.62	0.87
28:BA:2089:C:H2'	28:BA:2090:A:H5'	1.55	0.87
1:AA:927:G:C2'	1:AA:928:G:H5'	2.03	0.87
1:AA:1075:U:C5	1:AA:1076:U:C4	2.62	0.87
22:AV:75:C:N4	28:BA:2251:G:O6	1.72	0.87
1:AA:1377:A:H2'	7:AG:2:PRO:HB3	1.56	0.87
13:AM:82:ASP:OD2	31:BF:142:TYR:CE1	2.28	0.87
22:AV:34:U:O4	24:AX:13:A:C6	2.28	0.86
28:BA:2197:U:C2'	28:BA:2198:A:C8	2.56	0.86
1:AA:1073:U:O5'	5:AE:62:LYS:NZ	2.07	0.86
19:AS:24:GLU:N	19:AS:24:GLU:OE2	2.07	0.86
22:AV:36:C:O2	24:AX:11:G:N2	2.09	0.86
25:AY:95:PHE:CE1	59:AY:801:FUA:C11	2.56	0.86
1:AA:1076:U:O2'	1:AA:1077:G:H5'	1.75	0.86
1:AA:1394:A:C5	1:AA:1501:C:C4'	2.57	0.86
9:AI:130:ARG:HH21	23:AW:34:C:H5"	1.09	0.86
28:BA:2053:G:N2	28:BA:2616:C:N3	2.24	0.86
1:AA:978:A:OP2	1:AA:1362:A:N6	2.09	0.85
1:AA:1074:G:H2'	1:AA:1075:U:C6	2.10	0.85
28:BA:912:C:C2'	28:BA:913:U:H5'	2.05	0.85
1:AA:928:G:C4'	1:AA:1533:C:OP1	2.25	0.85
28:BA:910:A:H62	38:BM:9:PHE:HB3	1.40	0.85
28:BA:2091:C:C2'	28:BA:2092:U:H5	1.89	0.85
9:AI:57:MET:O	9:AI:59:GLU:N	2.09	0.85
25:AY:95:PHE:CZ	59:AY:801:FUA:H231	2.10	0.85
1:AA:1498:U:C6	24:AX:12:U:P	2.69	0.85
2:AB:178:LEU:HD11	5:AE:69:ARG:CZ	2.05	0.85
1:AA:1391:U:O2'	1:AA:1392:G:C5'	2.24	0.85
2:AB:178:LEU:CD1	5:AE:69:ARG:CD	2.55	0.85
1:AA:15:G:C4'	5:AE:29:ARG:NH1	2.39	0.84
1:AA:1350:A:OP1	9:AI:123:ARG:NH1	2.09	0.84
21:AU:49:LYS:HZ3	24:AX:2:G:H4'	1.38	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:469:ILE:CD1	59:AY:801:FUA:C2	2.55	0.84
28:BA:1723:G:O6	28:BA:1737:G:O2'	1.94	0.84
28:BA:910:A:N7	38:BM:9:PHE:CG	2.37	0.84
28:BA:1069:A:N3	28:BA:1073:A:N6	2.25	0.84
1:AA:16:A:C2	1:AA:1080:A:C1'	2.60	0.84
25:AY:469:ILE:HG12	59:AY:801:FUA:H21	1.58	0.84
24:AX:14:A:H2'	24:AX:15:A:H5'	1.55	0.84
1:AA:21:G:C2'	1:AA:22:G:O4'	2.25	0.84
1:AA:1082:A:C2'	1:AA:1083:U:C5'	2.49	0.84
45:BT:39:THR:O	45:BT:41:ALA:N	2.09	0.84
1:AA:1394:A:C1'	1:AA:1395:C:OP1	2.23	0.84
24:AX:3:U:C2'	24:AX:4:A:C8	2.54	0.83
57:B5:71:CYS:HA	57:B5:117:LEU:HD13	1.60	0.83
1:AA:530:G:C6	24:AX:16:A:O2'	2.32	0.83
1:AA:1393:U:H4'	1:AA:1502:A:C4'	2.08	0.83
28:BA:910:A:C5	38:BM:9:PHE:CD2	2.53	0.83
1:AA:530:G:N1	24:AX:16:A:O2'	2.12	0.83
22:AV:34:U:O4	24:AX:13:A:N1	2.11	0.83
1:AA:928:G:H2'	1:AA:929:G:H8	1.43	0.83
1:AA:1074:G:H2'	1:AA:1075:U:H6	1.43	0.83
1:AA:1106:G:O2'	3:AC:169:ARG:NE	2.11	0.83
1:AA:1530:G:C2'	1:AA:1531:A:N7	2.34	0.83
27:BC:196:ASN:O	27:BC:198:GLU:N	2.12	0.83
1:AA:921:U:H2'	1:AA:922:G:O4'	1.79	0.83
1:AA:1075:U:H5"	1:AA:1101:A:N1	1.92	0.83
1:AA:1498:U:O4	24:AX:12:U:C5'	2.18	0.83
28:BA:2197:U:O3'	33:BH:29:PHE:HE1	1.55	0.83
1:AA:1075:U:C2'	1:AA:1076:U:C5'	2.55	0.83
25:AY:95:PHE:CE1	59:AY:801:FUA:H11	2.14	0.83
1:AA:1074:G:OP1	5:AE:66:LYS:NZ	2.11	0.83
1:AA:1076:U:C2	1:AA:1081:A:N1	2.46	0.83
25:AY:219:HIS:O	25:AY:222:LEU:N	2.11	0.83
1:AA:1392:G:O2'	1:AA:1503:A:P	2.36	0.82
1:AA:1393:U:O4'	1:AA:1502:A:H4'	1.77	0.82
57:B5:71:CYS:HA	57:B5:117:LEU:CD1	2.10	0.82
1:AA:1081:A:H5'	5:AE:23:LYS:HG3	1.45	0.82
57:B5:33:VAL:N	57:B5:36:ASP:OD2	2.12	0.82
1:AA:1329:A:OP1	13:AM:26:GLY:CA	2.28	0.82
28:BA:2196:C:C4	28:BA:2197:U:O4	2.32	0.82
1:AA:1348:U:H4'	9:AI:122:ARG:CG	2.08	0.82
1:AA:1475:G:OP1	28:BA:1689:A:H1'	1.78	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1074:G:C4	1:AA:1075:U:C5	2.68	0.82
1:AA:1429:A:C4'	28:BA:1703:G:O2'	2.28	0.82
57:B5:103:ASN:ND2	57:B5:107:GLU:O	2.13	0.82
1:AA:18:C:C1'	1:AA:1078:U:H3	1.90	0.81
1:AA:1075:U:H5"	1:AA:1101:A:N6	1.95	0.81
1:AA:1081:A:O5'	5:AE:23:LYS:HG3	1.66	0.81
1:AA:1498:U:P	24:AX:11:G:H4'	2.19	0.81
28:BA:2093:G:O2'	28:BA:2094:A:H5'	1.79	0.81
57:B5:77:VAL:C	57:B5:79:PRO:HD2	2.00	0.81
1:AA:1531:A:H2'	1:AA:1532:U:C6	2.14	0.81
28:BA:504:A:O2'	28:BA:505:A:OP1	1.98	0.81
1:AA:1075:U:H5"	1:AA:1101:A:C6	2.15	0.81
4:AD:100:ASN:OD1	4:AD:111:ARG:NH1	2.13	0.81
41:BP:50:ARG:HB3	41:BP:57:ALA:H	1.43	0.81
28:BA:910:A:N7	38:BM:9:PHE:CB	2.43	0.81
2:AB:178:LEU:CD1	5:AE:69:ARG:HH11	1.79	0.81
1:AA:1074:G:HO2'	1:AA:1075:U:C5'	1.93	0.81
1:AA:1380:U:C2	7:AG:3:ARG:NH2	2.48	0.81
24:AX:14:A:C8	25:AY:512:ARG:HB2	2.16	0.81
40:BO:34:HIS:O	40:BO:102:ARG:NH1	2.14	0.81
1:AA:1029:U:O2'	1:AA:1033:G:N2	2.14	0.80
28:BA:1012:U:OP2	42:BQ:69:ARG:NH1	2.14	0.80
1:AA:1008:U:OP1	14:AN:24:ARG:NH2	2.14	0.80
1:AA:1071:C:H5"	5:AE:54:ARG:NH1	1.97	0.80
25:AY:93:VAL:O	25:AY:95:PHE:N	2.15	0.80
1:AA:20:U:O2	1:AA:915:A:N6	2.15	0.80
22:AV:46:G:H4'	22:AV:47:U:C5	2.15	0.80
24:AX:9:U:O2'	24:AX:10:G:C5'	2.30	0.80
24:AX:10:G:C5'	24:AX:11:G:OP1	2.30	0.80
1:AA:922:G:N2	1:AA:1395:C:O2	2.15	0.80
25:AY:270:PHE:CB	60:AY:802:GDP:C2	2.63	0.80
28:BA:2720:U:OP1	41:BP:52:ARG:NH2	2.15	0.80
23:AW:12:U:H3	23:AW:23:A:H61	0.83	0.80
25:AY:468:ILE:HD11	59:AY:801:FUA:H12	1.62	0.80
1:AA:15:G:H4'	5:AE:29:ARG:HH11	1.47	0.80
28:BA:2197:U:N1	28:BA:2198:A:N7	2.30	0.80
28:BA:2090:A:N6	28:BA:2091:C:N4	2.30	0.79
1:AA:1498:U:C4	24:AX:12:U:OP1	2.35	0.79
28:BA:864:G:C2'	28:BA:865:C:H5'	2.12	0.79
28:BA:910:A:C2	38:BM:9:PHE:CZ	2.70	0.79
28:BA:911:A:N6	38:BM:9:PHE:N	2.27	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:2197:U:O2'	28:BA:2198:A:C5	2.36	0.79
1:AA:1129:C:C4'	9:AI:18:ARG:HH22	1.95	0.79
1:AA:1392:G:O2'	1:AA:1393:U:C5'	2.30	0.79
28:BA:2197:U:O2'	33:BH:29:PHE:CD2	2.33	0.79
25:AY:469:ILE:HD13	59:AY:801:FUA:C3	2.13	0.79
1:AA:1074:G:HO2'	1:AA:1075:U:H5'	1.46	0.79
27:BC:269:ARG:NH2	28:BA:1799:G:OP2	2.16	0.79
1:AA:1463:U:O5'	41:BP:108:ARG:NH1	2.15	0.79
25:AY:422:PRO:O	25:AY:424:THR:N	2.14	0.79
57:B5:43:LYS:NZ	57:B5:98:GLU:OE1	2.16	0.79
1:AA:1393:U:H4'	1:AA:1502:A:O5'	1.83	0.79
1:AA:530:G:O6	24:AX:16:A:O2'	2.00	0.79
1:AA:928:G:C4'	1:AA:1533:C:H5	1.95	0.79
25:AY:95:PHE:CZ	59:AY:801:FUA:C12	2.58	0.79
25:AY:507:LYS:NZ	28:BA:1913:A:H62	1.80	0.78
28:BA:2197:U:H2'	28:BA:2198:A:C4	2.18	0.78
1:AA:18:C:C5'	5:AE:132:ASN:ND2	2.40	0.78
23:AW:11:C:N4	23:AW:24:G:H1	1.80	0.78
36:BK:105:ARG:NH1	36:BK:106:GLU:OE2	2.16	0.78
1:AA:1329:A:OP1	13:AM:26:GLY:N	2.17	0.78
1:AA:1377:A:N3	7:AG:2:PRO:CD	2.46	0.78
28:BA:2090:A:H2'	28:BA:2091:C:C5'	2.07	0.78
1:AA:15:G:HO2'	5:AE:22:SER:CB	1.94	0.78
28:BA:2197:U:H2'	28:BA:2198:A:N9	1.96	0.78
1:AA:1081:A:O5'	5:AE:23:LYS:CG	2.30	0.78
1:AA:1530:G:C2'	1:AA:1531:A:H8	1.88	0.78
57:B5:71:CYS:CA	57:B5:117:LEU:CD1	2.62	0.78
1:AA:1249:C:H2'	9:AI:71:GLY:HA2	1.66	0.78
28:BA:2091:C:H3'	28:BA:2092:U:H6	1.47	0.78
29:BD:184:ARG:NH1	41:BP:6:GLN:OE1	2.17	0.78
1:AA:1075:U:C5'	1:AA:1101:A:N1	2.47	0.77
1:AA:1394:A:H8	1:AA:1394:A:OP1	1.67	0.77
25:AY:25:THR:OG1	60:AY:802:GDP:O5'	2.02	0.77
57:B5:35:VAL:HA	57:B5:38:MET:SD	2.24	0.77
57:B5:91:ALA:C	57:B5:93:ALA:H	1.87	0.77
1:AA:1028:C:N4	1:AA:1029:U:O2	2.17	0.77
1:AA:1075:U:H5"	1:AA:1101:A:H61	1.48	0.77
1:AA:1075:U:O2'	1:AA:1076:U:C5'	2.33	0.77
1:AA:1530:G:N1	1:AA:1531:A:C6	2.52	0.77
1:AA:1463:U:OP1	41:BP:108:ARG:CZ	2.33	0.77
23:AW:29:U:H2'	23:AW:30:C:C6	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:2195:U:O2'	28:BA:2196:C:H5'	1.83	0.77
57:B5:117:LEU:HD23	57:B5:120:ALA:HA	1.65	0.77
1:AA:8:A:N6	4:AD:202:GLU:O	2.16	0.77
1:AA:1463:U:OP1	41:BP:108:ARG:NE	2.18	0.77
50:BY:18:LEU:O	50:BY:22:LEU:N	2.17	0.77
1:AA:1290:G:OP1	7:AG:35:LYS:NZ	2.18	0.77
1:AA:1074:G:C2'	1:AA:1075:U:C5'	2.52	0.77
1:AA:1083:U:C5	1:AA:1084:G:C6	2.73	0.77
57:B5:33:VAL:HG12	57:B5:34:THR:H	1.48	0.77
28:BA:1509:A:O2'	28:BA:1510:G:OP2	2.01	0.76
5:AE:31:PHE:CE2	24:AX:19:A:C6	2.74	0.76
1:AA:1147:C:O2'	9:AI:7:TYR:CZ	2.29	0.76
4:AD:35:GLU:O	4:AD:37:ALA:N	2.17	0.76
23:AW:50:C:N3	23:AW:64:G:N2	2.31	0.76
28:BA:2091:C:N1	28:BA:2092:U:C5	2.53	0.76
27:BC:68:ARG:NH2	27:BC:126:GLY:O	2.18	0.76
1:AA:1033:G:H2'	1:AA:1034:G:H5'	1.64	0.76
28:BA:2091:C:OP2	28:BA:2092:U:C3'	2.31	0.76
1:AA:19:A:O2'	1:AA:20:U:C5'	2.30	0.76
3:AC:36:ASP:OD1	3:AC:59:ARG:NH1	2.19	0.75
22:AV:46:G:O3'	22:AV:47:U:H6	1.68	0.75
27:BC:69:ASN:O	27:BC:71:ASP:N	2.18	0.75
1:AA:1073:U:OP1	5:AE:62:LYS:NZ	2.13	0.75
25:AY:95:PHE:CD2	59:AY:801:FUA:H121	2.22	0.75
28:BA:1342:A:O2'	28:BA:1344:U:OP2	2.04	0.75
23:AW:12:U:O2	23:AW:23:A:N1	2.19	0.75
1:AA:1080:A:H5"	5:AE:21:VAL:HB	1.67	0.75
25:AY:92:HIS:HE1	59:AY:801:FUA:H282	1.45	0.75
14:AN:31:ILE:H	14:AN:31:ILE:HD12	1.50	0.75
24:AX:14:A:H8	25:AY:512:ARG:HB2	1.49	0.75
59:AY:801:FUA:H5	59:AY:801:FUA:C20	2.12	0.75
1:AA:1075:U:C4	1:AA:1076:U:O4	2.40	0.75
1:AA:1081:A:N6	1:AA:1082:A:N6	2.35	0.75
1:AA:1392:G:H4'	1:AA:1531:A:H5"	1.68	0.75
21:AU:49:LYS:HZ2	24:AX:2:G:C5'	1.99	0.75
22:AV:74:C:N3	28:BA:2252:G:N1	2.31	0.75
28:BA:2331:G:O2'	48:BW:39:GLN:O	2.04	0.75
1:AA:1077:G:N2	1:AA:1080:A:C8	2.55	0.75
28:BA:1187:G:OP1	43:BR:85:LYS:NZ	2.19	0.74
1:AA:1230:C:OP1	23:AW:30:C:H4'	1.86	0.74
22:AV:53:G:O2'	22:AV:54:5MU:H5"	1.86	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:15:G:C2	5:AE:22:SER:O	2.40	0.74
9:AI:57:MET:SD	9:AI:58:VAL:N	2.61	0.74
1:AA:21:G:C1'	1:AA:914:A:H61	1.98	0.74
23:AW:4:U:O4	23:AW:69:A:N1	2.20	0.74
1:AA:928:G:C4'	1:AA:1533:C:C5	2.68	0.74
1:AA:1297:G:N2	7:AG:114:LYS:HB3	2.02	0.74
25:AY:147:MET:HE3	32:BG:92:GLY:HA2	1.67	0.74
28:BA:2707:U:O2	39:BN:71:ARG:NH1	2.20	0.74
1:AA:16:A:H4'	5:AE:21:VAL:HA	1.70	0.74
56:B4:11:CYS:SG	56:B4:14:CYS:N	2.60	0.74
1:AA:1075:U:H2'	1:AA:1076:U:C5'	2.06	0.74
1:AA:1203:C:OP1	14:AN:2:ALA:HA	1.88	0.74
1:AA:1522:U:OP1	11:AK:128:ARG:NH2	2.19	0.74
28:BA:1998:A:OP2	29:BD:141:ARG:NH2	2.21	0.74
2:AB:178:LEU:HD11	5:AE:69:ARG:CD	2.17	0.74
23:AW:9:A:OP2	23:AW:13:C:N4	2.21	0.74
25:AY:468:ILE:HD11	59:AY:801:FUA:C1	2.18	0.74
28:BA:864:G:H2'	28:BA:865:C:H5'	1.69	0.74
1:AA:1081:A:N1	1:AA:1082:A:N1	2.36	0.73
28:BA:572:A:OP2	43:BR:80:ARG:NH2	2.21	0.73
57:B5:131:THR:O	57:B5:134:GLU:N	2.20	0.73
1:AA:1524:C:OP1	11:AK:125:LYS:NZ	2.20	0.73
1:AA:922:G:O6	1:AA:1395:C:N4	2.22	0.73
25:AY:142:ASN:OD1	25:AY:143:LYS:N	2.19	0.73
25:AY:464:LEU:HD11	59:AY:801:FUA:H272	0.82	0.73
1:AA:13:U:O2	1:AA:915:A:OP2	2.06	0.73
9:AI:56:ASP:O	9:AI:60:LYS:NZ	2.19	0.73
21:AU:49:LYS:NZ	24:AX:2:G:C5'	2.52	0.73
57:B5:57:ASN:O	57:B5:59:LEU:N	2.21	0.73
1:AA:1082:A:O2'	1:AA:1083:U:C5'	2.36	0.73
1:AA:21:G:H2'	1:AA:22:G:O4'	1.87	0.73
24:AX:3:U:C3'	24:AX:4:A:H8	2.01	0.73
24:AX:8:A:O2'	24:AX:9:U:C5'	2.36	0.73
35:BJ:43:GLU:O	35:BJ:45:THR:N	2.22	0.73
28:BA:2198:A:OP2	28:BA:2198:A:C2'	2.30	0.73
25:AY:469:ILE:CG1	59:AY:801:FUA:H21	2.19	0.72
57:B5:106:PHE:O	57:B5:108:VAL:N	2.23	0.72
1:AA:1075:U:H4'	1:AA:1101:A:C5	2.22	0.72
1:AA:1083:U:H5	1:AA:1084:G:C6	2.08	0.72
23:AW:20:U:OP2	28:BA:2145:C:N3	2.22	0.72
28:BA:910:A:N7	38:BM:9:PHE:CD2	2.57	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1475:G:H4'	28:BA:1689:A:C4'	2.20	0.72
25:AY:469:ILE:CD1	59:AY:801:FUA:H21	2.18	0.72
25:AY:469:ILE:HD11	59:AY:801:FUA:C2	2.20	0.72
32:BG:22:VAL:HG12	32:BG:36:LEU:CD1	2.19	0.72
57:B5:1:MET:SD	57:B5:2:ALA:N	2.58	0.72
1:AA:1071:C:H5"	5:AE:54:ARG:HH12	1.54	0.72
22:AV:37:A:C8	25:AY:508:GLN:OE1	2.42	0.72
25:AY:649:VAL:HA	34:BI:25:PRO:HB3	1.72	0.72
29:BD:91:THR:O	29:BD:93:GLY:N	2.21	0.72
3:AC:16:LYS:NZ	3:AC:181:ASP:OD1	2.23	0.72
23:AW:1:G:H1	23:AW:72:C:H42	1.36	0.72
1:AA:919:A:H2'	1:AA:920:U:H5'	1.69	0.72
25:AY:469:ILE:CD1	59:AY:801:FUA:H3	2.20	0.72
41:BP:5:LYS:NZ	41:BP:9:GLN:OE1	2.23	0.72
1:AA:1129:C:H5"	9:AI:18:ARG:NH2	2.05	0.72
14:AN:91:GLY:O	14:AN:93:ILE:N	2.23	0.72
1:AA:1493:A:O2'	24:AX:14:A:O4'	2.05	0.71
24:AX:7:A:H2'	24:AX:7:A:N3	2.05	0.71
1:AA:1081:A:H5'	5:AE:23:LYS:HG2	1.73	0.71
1:AA:1075:U:C5	1:AA:1076:U:O4	2.42	0.71
1:AA:1249:C:C2'	9:AI:71:GLY:HA2	2.21	0.71
22:AV:20:U:C3'	22:AV:21:A:H5'	2.20	0.71
28:BA:2478:A:OP2	56:B4:2:LYS:NZ	2.23	0.71
22:AV:36:C:C4'	25:AY:508:GLN:HA	2.15	0.71
22:AV:35:A:N6	24:AX:13:A:C6	2.57	0.71
59:AY:801:FUA:H122	59:AY:801:FUA:H231	1.73	0.71
1:AA:1075:U:O4'	1:AA:1101:A:C6	2.43	0.71
1:AA:1076:U:O2	1:AA:1081:A:H2	1.73	0.71
11:AK:126:LYS:O	21:AU:34:ARG:NE	2.24	0.71
22:AV:71:C:O2	22:AV:71:C:H2'	1.90	0.71
1:AA:1130:A:O3'	9:AI:5:GLN:NE2	2.24	0.71
1:AA:1530:G:C2	1:AA:1531:A:C5	2.79	0.71
31:BF:116:LEU:N	31:BF:176:PHE:O	2.24	0.71
1:AA:1193:G:O2'	5:AE:26:LYS:CE	2.37	0.71
12:AL:33:VAL:HG11	25:AY:429:GLU:HG3	1.72	0.71
1:AA:919:A:C2'	1:AA:920:U:H5'	2.21	0.71
1:AA:1492:A:H2'	1:AA:1493:A:H5'	1.73	0.71
2:AB:178:LEU:HD13	5:AE:69:ARG:NH1	2.06	0.70
25:AY:92:HIS:NE2	59:AY:801:FUA:H281	2.04	0.70
28:BA:2353:G:H1'	48:BW:30:VAL:HG12	1.72	0.70
1:AA:21:G:C1'	1:AA:914:A:N6	2.50	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1075:U:C4'	1:AA:1101:A:N1	2.55	0.70
1:AA:1468:A:H2'	1:AA:1469:C:H5'	1.72	0.70
27:BC:49:THR:OG1	28:BA:1805:A:N3	2.24	0.70
23:AW:20:U:OP2	28:BA:2145:C:C2	2.26	0.70
23:AW:76:A:N1	28:BA:2422:C:C6	2.59	0.70
1:AA:920:U:H1'	1:AA:1080:A:C4	2.17	0.70
22:AV:5:G:N2	22:AV:69:C:C2	2.59	0.70
27:BC:179:GLU:OE2	28:BA:1799:G:O2'	2.07	0.70
1:AA:1076:U:O2'	1:AA:1077:G:O4'	2.08	0.70
2:AB:178:LEU:HD13	5:AE:69:ARG:CZ	2.21	0.70
13:AM:82:ASP:CG	31:BF:142:TYR:CE1	2.61	0.70
22:AV:56:C:C2	31:BF:79:ARG:HD3	2.25	0.70
23:AW:64:G:C2	23:AW:65:U:N3	2.59	0.70
1:AA:1530:G:C4	1:AA:1531:A:N7	2.59	0.70
22:AV:57:A:H5"	31:BF:74:ALA:HB2	1.70	0.70
28:BA:587:C:OP2	37:BL:21:ARG:NH1	2.25	0.70
24:AX:2:G:C5'	24:AX:3:U:OP2	2.40	0.70
24:AX:14:A:C4	24:AX:14:A:OP2	2.44	0.70
48:BW:30:VAL:HG13	48:BW:30:VAL:O	1.92	0.70
1:AA:1498:U:C5	24:AX:12:U:H5'	1.97	0.69
24:AX:14:A:N3	24:AX:15:A:C5'	2.53	0.69
28:BA:161:A:H3'	28:BA:162:U:H5"	1.72	0.69
28:BA:1993:U:H4'	29:BD:133:THR:HG21	1.73	0.69
1:AA:462:G:N2	1:AA:470:C:N3	2.39	0.69
1:AA:18:C:C1'	1:AA:1078:U:N3	2.52	0.69
22:AV:17:C:H6	22:AV:17(A):U:H5	1.40	0.69
24:AX:8:A:O2'	24:AX:9:U:H5"	1.92	0.69
1:AA:1072:G:OP1	5:AE:54:ARG:HD2	1.88	0.69
1:AA:1074:G:P	5:AE:62:LYS:HD3	2.33	0.69
1:AA:1348:U:O3'	9:AI:122:ARG:HB2	1.93	0.69
21:AU:44:GLU:OE2	21:AU:45:ARG:NH1	2.25	0.69
28:BA:2091:C:H3'	28:BA:2092:U:C6	2.27	0.69
1:AA:79:G:O2'	1:AA:80:A:O5'	2.08	0.69
1:AA:1101:A:N6	2:AB:101:THR:HG21	2.08	0.69
1:AA:1076:U:H3	1:AA:1081:A:H61	1.39	0.69
1:AA:828:U:O2	2:AB:24:PRO:CD	2.41	0.69
1:AA:1075:U:C5'	1:AA:1101:A:H61	2.02	0.69
1:AA:1498:U:N3	24:AX:12:U:OP1	2.26	0.69
1:AA:1531:A:H2'	1:AA:1532:U:H6	1.57	0.69
23:AW:68:U:H2'	23:AW:69:A:C8	2.28	0.69
23:AW:76:A:N1	28:BA:2422:C:C5	2.61	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AX:18:A:O2'	24:AX:19:A:H5'	1.93	0.69
28:BA:1936:A:N6	28:BA:1963:U:O2	2.26	0.69
1:AA:1291:U:OP2	7:AG:38:THR:HG22	1.92	0.69
1:AA:1534:A:H8	1:AA:1534:A:O5'	1.76	0.69
24:AX:10:G:H5"	24:AX:11:G:OP1	1.93	0.69
59:AY:801:FUA:H202	59:AY:801:FUA:C5	2.15	0.69
1:AA:1075:U:O2'	1:AA:1076:U:H5'	1.90	0.69
1:AA:1220:G:H4'	19:AS:34:TRP:O	1.93	0.69
25:AY:25:THR:OG1	60:AY:802:GDP:PA	2.50	0.69
25:AY:468:ILE:CD1	59:AY:801:FUA:H12	2.22	0.69
28:BA:971:G:OP2	28:BA:974:G:N2	2.25	0.69
38:BM:66:ARG:NH1	38:BM:104:GLU:OE1	2.26	0.69
51:BZ:8:GLN:O	51:BZ:10:ARG:N	2.25	0.69
22:AV:17:C:H6	22:AV:17(A):U:C5	2.11	0.68
28:BA:2324:U:H3'	28:BA:2325:G:H5"	1.74	0.68
29:BD:149:ASN:OD1	29:BD:150:GLN:N	2.26	0.68
36:BK:76:VAL:HB	41:BP:72:VAL:HG22	1.76	0.68
1:AA:927:G:OP1	1:AA:1503:A:N1	2.26	0.68
1:AA:1014:A:OP1	19:AS:18:LYS:HE3	1.93	0.68
22:AV:74:C:H3'	28:BA:2602:A:C5	2.28	0.68
28:BA:2090:A:C2'	28:BA:2091:C:C5'	2.68	0.68
57:B5:25:ALA:O	57:B5:26:VAL:HG13	1.94	0.68
1:AA:1075:U:C5	1:AA:1076:U:C5	2.82	0.68
34:BI:100:ILE:HB	34:BI:139:VAL:HA	1.75	0.68
1:AA:1129:C:C4'	9:AI:18:ARG:NH2	2.54	0.68
1:AA:1148:U:H5"	9:AI:9:THR:HG23	1.75	0.68
22:AV:61:C:O2'	22:AV:62:C:H5'	1.94	0.68
24:AX:12:U:H2'	24:AX:13:A:H5'	1.75	0.68
28:BA:324:A:N6	28:BA:338:G:O2'	2.27	0.68
57:B5:117:LEU:HD22	57:B5:120:ALA:HA	1.76	0.68
1:AA:159:G:N2	1:AA:162:A:OP2	2.27	0.68
5:AE:31:PHE:HE2	24:AX:19:A:C6	2.10	0.68
1:AA:16:A:C2	1:AA:1080:A:O4'	2.46	0.68
1:AA:483:C:O2	16:AP:13:LYS:NZ	2.26	0.68
1:AA:1530:G:C5	1:AA:1531:A:C6	2.80	0.68
22:AV:3:C:H2'	22:AV:4:G:H5'	1.76	0.68
23:AW:64:G:C6	23:AW:65:U:O4	2.46	0.68
26:BB:73:A:C4	26:BB:104:A:C2	2.82	0.68
1:AA:1081:A:H5"	5:AE:23:LYS:HG3	1.67	0.68
1:AA:1130:A:P	9:AI:64:TYR:HE2	2.17	0.68
23:AW:41:A:H2'	23:AW:42:U:C6	2.29	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:469:ILE:HD11	59:AY:801:FUA:H22	1.75	0.68
37:BL:93:ASN:O	37:BL:95:LEU:N	2.27	0.68
1:AA:926:G:N2	24:AX:8:A:OP1	2.24	0.68
1:AA:1074:G:C2	1:AA:1075:U:C2	2.82	0.68
1:AA:1463:U:OP1	41:BP:108:ARG:NH1	2.26	0.68
25:AY:270:PHE:N	60:AY:802:GDP:O6	2.22	0.68
28:BA:2091:C:C2'	28:BA:2092:U:C5	2.75	0.68
28:BA:948:C:O2	28:BA:984:A:O2'	2.12	0.67
57:B5:26:VAL:O	57:B5:27:VAL:HB	1.93	0.67
4:AD:29:ASP:O	4:AD:31:LYS:NZ	2.27	0.67
24:AX:9:U:C2'	24:AX:10:G:C5'	2.63	0.67
1:AA:1395:C:N4	1:AA:1396:A:H62	1.87	0.67
27:BC:176:ARG:NH2	28:BA:1820:U:OP1	2.27	0.67
28:BA:42:A:C2'	28:BA:43:G:H5'	2.25	0.67
1:AA:1390:U:C2'	1:AA:1391:U:C6	2.74	0.67
1:AA:1530:G:O2'	1:AA:1531:A:C8	2.47	0.67
14:AN:49:GLN:N	14:AN:49:GLN:OE1	2.28	0.67
23:AW:11:C:N3	23:AW:24:G:N2	2.36	0.67
28:BA:819:A:OP2	28:BA:1187:G:N2	2.23	0.67
1:AA:111:G:O6	1:AA:330:C:N4	2.28	0.67
1:AA:151:A:OP2	1:AA:169:C:N4	2.28	0.67
1:AA:921:U:OP1	1:AA:1082:A:C5'	2.42	0.67
28:BA:910:A:C4	38:BM:9:PHE:CE2	2.82	0.67
28:BA:2197:U:C3'	33:BH:29:PHE:CE1	2.78	0.67
1:AA:18:C:H1'	1:AA:1078:U:H3	1.59	0.67
1:AA:404:G:O6	4:AD:2:ALA:N	2.28	0.67
1:AA:1392:G:H2'	1:AA:1393:U:C5'	2.23	0.67
24:AX:14:A:O2'	24:AX:15:A:C5'	2.30	0.67
1:AA:920:U:O2'	1:AA:921:U:C5'	2.30	0.66
22:AV:36:C:H4'	25:AY:508:GLN:HA	1.76	0.66
26:BB:79:G:O2'	28:BA:861:A:N3	2.27	0.66
1:AA:175:C:O2'	1:AA:1447:A:N1	2.26	0.66
1:AA:958:A:C8	19:AS:55:ARG:CZ	2.79	0.66
1:AA:1083:U:H5	1:AA:1084:G:C5	2.10	0.66
13:AM:29:ARG:CZ	13:AM:63:PHE:HB2	2.26	0.66
35:BJ:4:PHE:N	35:BJ:44:TYR:OH	2.28	0.66
1:AA:1076:U:H3	1:AA:1081:A:N6	1.92	0.66
22:AV:56:C:C4	31:BF:79:ARG:CD	2.77	0.66
28:BA:301:G:OP2	46:BU:81:ARG:NH1	2.26	0.66
37:BL:93:ASN:OD1	37:BL:94:THR:N	2.28	0.66
57:B5:24:SER:CB	57:B5:116:GLU:HG2	2.24	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1371:G:OP2	9:AI:111:VAL:CG1	2.43	0.66
1:AA:17:U:O2'	1:AA:18:C:H5'	1.95	0.66
4:AD:30:THR:HB	4:AD:31:LYS:HZ2	1.60	0.66
22:AV:56:C:C2	31:BF:79:ARG:CD	2.75	0.66
15:AO:46:HIS:O	15:AO:48:LYS:N	2.28	0.66
23:AW:56:C:H2'	23:AW:57:G:H8	1.60	0.66
28:BA:2094:A:C2	28:BA:2196:C:C2	2.83	0.66
36:BK:18:ARG:HB2	36:BK:45:GLU:HB2	1.77	0.66
1:AA:1081:A:C2	1:AA:1082:A:C6	2.84	0.66
1:AA:1530:G:C2	1:AA:1531:A:C6	2.83	0.66
28:BA:2093:G:H4'	33:BH:22:LYS:HD2	1.77	0.66
1:AA:1533:C:H3'	1:AA:1534:A:H5'	1.78	0.66
32:BG:38:ASP:N	32:BG:38:ASP:OD1	2.29	0.66
28:BA:363:G:H2'	28:BA:364:C:C6	2.31	0.65
48:BW:37:VAL:HG12	48:BW:38:ARG:H	1.61	0.65
1:AA:926:G:C2	24:AX:8:A:OP2	2.48	0.65
23:AW:76:A:C6	28:BA:2422:C:N1	2.65	0.65
1:AA:16:A:C2'	1:AA:17:U:C5'	2.70	0.65
1:AA:1181:G:O2'	1:AA:1182:G:C8	2.49	0.65
2:AB:88:GLN:HE22	2:AB:220:VAL:HG23	1.60	0.65
9:AI:129:LYS:NZ	23:AW:31:A:P	2.69	0.65
28:BA:1482:G:H1'	28:BA:1509:A:H61	1.62	0.65
1:AA:1216:A:OP1	14:AN:5:SER:CB	2.44	0.65
9:AI:42:GLU:O	9:AI:45:ARG:NH1	2.29	0.65
24:AX:14:A:H2'	24:AX:14:A:N3	2.11	0.65
59:AY:801:FUA:H201	59:AY:801:FUA:O1	1.95	0.65
36:BK:71:ARG:HB3	36:BK:72:PRO:HD3	1.78	0.65
39:BN:98:LEU:HB3	52:B0:42:ILE:HD11	1.79	0.65
1:AA:1393:U:O2'	1:AA:1502:A:C4'	2.45	0.65
13:AM:82:ASP:HB3	31:BF:142:TYR:OH	1.96	0.65
35:BJ:6:ALA:HB3	35:BJ:45:THR:HG21	1.78	0.65
1:AA:1080:A:OP1	5:AE:21:VAL:HG21	1.97	0.65
1:AA:1530:G:C4	1:AA:1531:A:C5	2.85	0.65
24:AX:6:A:N3	24:AX:6:A:C3'	2.57	0.65
24:AX:12:U:HO2'	24:AX:13:A:H5'	1.61	0.65
25:AY:78:GLN:NE2	25:AY:280:ASP:OD2	2.29	0.65
1:AA:1493:A:O4'	24:AX:14:A:H4'	1.97	0.65
2:AB:140:LEU:O	2:AB:144:GLU:N	2.27	0.65
4:AD:66:GLY:O	4:AD:115:ARG:NH2	2.30	0.65
1:AA:1075:U:O2'	1:AA:1076:U:H5"	1.96	0.65
57:B5:39:THR:HA	57:B5:42:ARG:HD2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:19:A:H2'	1:AA:20:U:C5'	2.25	0.64
1:AA:1395:C:H42	1:AA:1396:A:N6	1.95	0.64
21:AU:49:LYS:HZ3	24:AX:2:G:C4'	2.08	0.64
22:AV:6:G:H1	22:AV:67:C:H42	1.44	0.64
23:AW:76:A:C2	28:BA:2422:C:C4	2.85	0.64
28:BA:2142:A:H4'	28:BA:2143:C:OP2	1.96	0.64
28:BA:2197:U:O2	28:BA:2198:A:N7	2.30	0.64
1:AA:15:G:H5"	5:AE:29:ARG:NH1	2.12	0.64
28:BA:866:A:C8	28:BA:914:G:C2	2.86	0.64
39:BN:118:ARG:O	39:BN:120:GLU:N	2.30	0.64
1:AA:1377:A:C2	7:AG:2:PRO:CD	2.74	0.64
1:AA:1442:G:O4'	41:BP:113:LEU:CD1	2.46	0.64
9:AI:57:MET:O	9:AI:60:LYS:N	2.31	0.64
28:BA:1199:U:H5'	42:BQ:4:LYS:HE3	1.79	0.64
1:AA:1014:A:H4'	19:AS:14:HIS:ND1	2.13	0.64
8:AH:77:ARG:NE	8:AH:79:SER:O	2.31	0.64
22:AV:17:C:C6	22:AV:17(A):U:H5	2.15	0.64
28:BA:370:G:O2'	28:BA:424:G:OP1	2.15	0.64
34:BI:73:PRO:O	34:BI:112:LYS:NZ	2.31	0.64
1:AA:1074:G:C5	1:AA:1075:U:C5	2.85	0.64
12:AL:33:VAL:HG21	25:AY:429:GLU:HG3	1.80	0.64
25:AY:98:GLU:O	25:AY:102:SER:OG	2.07	0.64
1:AA:19:A:C2'	1:AA:20:U:C5'	2.61	0.64
1:AA:922:G:C2	1:AA:1395:C:N3	2.64	0.64
1:AA:1498:U:C5	24:AX:12:U:O5'	2.50	0.64
1:AA:1533:C:C3'	1:AA:1534:A:C5'	2.70	0.64
1:AA:1348:U:C4'	9:AI:122:ARG:HG3	2.21	0.64
12:AL:33:VAL:HG21	25:AY:429:GLU:CG	2.27	0.64
22:AV:35:A:C6	24:AX:13:A:N1	2.66	0.64
48:BW:35:ILE:O	48:BW:37:VAL:N	2.31	0.64
1:AA:1393:U:C1'	1:AA:1502:A:H4'	2.28	0.63
1:AA:1530:G:N3	1:AA:1531:A:C5	2.66	0.63
25:AY:649:VAL:HA	34:BI:25:PRO:HB2	1.80	0.63
1:AA:1081:A:O2'	1:AA:1082:A:H5'	1.97	0.63
21:AU:14:VAL:HG13	21:AU:16:LEU:HG	1.80	0.63
25:AY:24:THR:HB	60:AY:802:GDP:O1B	1.98	0.63
28:BA:2346:A:H3'	28:BA:2347:C:C5'	2.29	0.63
32:BG:1:SER:O	32:BG:3:VAL:N	2.31	0.63
1:AA:1394:A:C4	1:AA:1501:C:C1'	2.81	0.63
1:AA:1429:A:O2'	28:BA:1703:G:O3'	2.16	0.63
24:AX:18:A:C2'	24:AX:19:A:H5'	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BP:50:ARG:CB	41:BP:57:ALA:H	2.11	0.63
46:BU:73:ASN:ND2	46:BU:80:ASP:OD2	2.31	0.63
28:BA:908:C:H4’	38:BM:70:ASP:OD2	1.97	0.63
1:AA:1158:C:O2’	2:AB:131:LYS:CD	2.44	0.63
3:AC:85:GLU:OE2	3:AC:88:ARG:NH1	2.30	0.63
25:AY:25:THR:OG1	60:AY:802:GDP:O2A	2.16	0.63
25:AY:95:PHE:HD1	59:AY:801:FUA:H11	1.54	0.63
28:BA:2196:C:H2’	28:BA:2197:U:C6	2.33	0.63
34:BI:108:ILE:O	34:BI:111:THR:OG1	2.17	0.63
35:BJ:44:TYR:HB2	42:BQ:63:ARG:HB3	1.79	0.63
45:BT:32:LEU:H	45:BT:83:ALA:HB3	1.63	0.63
46:BU:15:GLY:O	46:BU:17:ASP:N	2.32	0.63
48:BW:9:THR:OG1	48:BW:10:ARG:N	2.31	0.63
1:AA:921:U:H5”	1:AA:1081:A:O3’	1.99	0.63
1:AA:958:A:OP1	19:AS:55:ARG:NH1	2.25	0.63
1:AA:1299:A:H2’	1:AA:1299:A:N3	2.12	0.63
27:BC:43:ASN:OD1	27:BC:44:ASN:N	2.30	0.63
28:BA:1385:A:H1’	28:BA:1386:C:C6	2.34	0.63
28:BA:2197:U:C6	28:BA:2197:U:O5’	2.52	0.63
1:AA:1073:U:C5’	5:AE:62:LYS:HZ3	2.10	0.63
1:AA:1230:C:OP1	23:AW:30:C:H5’	1.99	0.63
10:AJ:88:MET:O	10:AJ:90:LEU:N	2.30	0.63
28:BA:1417:C:HO2’	28:BA:1587:G:HO2’	1.42	0.63
28:BA:2195:U:C2’	28:BA:2196:C:C5’	2.71	0.63
41:BP:50:ARG:HG3	41:BP:57:ALA:O	1.98	0.63
44:BS:18:ARG:O	44:BS:19:LEU:HB2	1.98	0.63
1:AA:1077:G:H2’	1:AA:1079:G:N7	2.13	0.63
1:AA:1148:U:H5”	9:AI:9:THR:CG2	2.28	0.63
30:BE:58:LYS:NZ	30:BE:70:SER:O	2.31	0.63
1:AA:19:A:OP1	5:AE:132:ASN:HB2	1.99	0.63
25:AY:177:GLU:OE1	25:AY:177:GLU:N	2.32	0.63
28:BA:546:U:O2’	28:BA:547:A:H4’	1.99	0.63
57:B5:129:LEU:O	57:B5:131:THR:N	2.26	0.63
58:B6:18:ASP:N	58:B6:18:ASP:OD1	2.32	0.63
1:AA:1250:A:OP1	9:AI:69:GLY:N	2.22	0.62
1:AA:1393:U:H4’	1:AA:1502:A:C5’	2.29	0.62
1:AA:1393:U:O2’	1:AA:1502:A:H5”	1.99	0.62
24:AX:2:G:H5’	24:AX:3:U:OP2	1.99	0.62
40:BO:76:LYS:NZ	40:BO:80:GLU:OE1	2.29	0.62
4:AD:27:ALA:HA	4:AD:31:LYS:HZ1	1.64	0.62
5:AE:115:LEU:HD23	5:AE:123:VAL:HG21	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:93:ARG:NH2	11:AK:112:ASP:OD2	2.32	0.62
26:BB:87:U:H3'	26:BB:88:C:H5'	1.80	0.62
28:BA:42:A:H2'	28:BA:43:G:H5'	1.80	0.62
39:BN:73:ASN:HA	39:BN:76:VAL:HG12	1.81	0.62
57:B5:26:VAL:HG21	57:B5:115:GLY:N	2.06	0.62
1:AA:1392:G:H4'	1:AA:1531:A:O5'	1.99	0.62
22:AV:46:G:O3'	22:AV:47:U:C6	2.51	0.62
1:AA:1130:A:HO2'	9:AI:5:GLN:HG3	1.65	0.62
25:AY:455:GLN:NE2	25:AY:487:GLN:OE1	2.32	0.62
27:BC:57:HIS:CD2	28:BA:1567:G:H5'	2.35	0.62
28:BA:2196:C:C2	28:BA:2197:U:C4	2.87	0.62
1:AA:1240:U:OP2	7:AG:116:MET:CB	2.47	0.62
57:B5:29:ASP:HA	57:B5:108:VAL:HG11	1.82	0.62
1:AA:920:U:C1'	1:AA:1080:A:C4	2.77	0.62
1:AA:1048:G:H5"	14:AN:3:LYS:HG3	1.82	0.62
11:AK:88:GLY:H	11:AK:114:THR:HG22	1.65	0.62
21:AU:48:ALA:O	24:AX:3:U:P	2.58	0.62
25:AY:507:LYS:NZ	28:BA:1913:A:N6	2.46	0.62
28:BA:163:C:O2'	28:BA:164:C:O5'	2.17	0.62
1:AA:1394:A:O2'	1:AA:1501:C:C1'	2.21	0.62
1:AA:1442:G:O4'	41:BP:113:LEU:HD12	1.99	0.62
28:BA:923:G:H1'	48:BW:23:LYS:HD3	1.81	0.62
5:AE:41:ASP:OD1	5:AE:43:ASN:N	2.33	0.62
24:AX:9:U:H2'	24:AX:10:G:C5'	2.22	0.62
1:AA:1166:G:N1	1:AA:1169:A:OP2	2.33	0.62
25:AY:222:LEU:O	25:AY:226:ALA:N	2.31	0.62
28:BA:856:G:H21	48:BW:19:ARG:NH1	1.97	0.62
1:AA:16:A:N3	1:AA:1080:A:C1'	2.62	0.62
1:AA:1377:A:H2'	7:AG:2:PRO:CB	2.28	0.62
1:AA:1498:U:O4	24:AX:12:U:O3'	2.18	0.62
22:AV:47:U:H3'	22:AV:48:C:H5'	1.82	0.62
28:BA:1759:A:HO2'	28:BA:2714:G:HO2'	1.43	0.62
28:BA:2011:U:OP2	44:BS:16:LYS:NZ	2.31	0.62
28:BA:2197:U:O5'	28:BA:2197:U:H6	1.81	0.62
1:AA:1349:A:OP1	9:AI:123:ARG:N	2.32	0.61
1:AA:1377:A:N3	7:AG:2:PRO:HG3	2.14	0.61
23:AW:37:A:N1	24:AX:8:A:N6	2.48	0.61
25:AY:80:GLU:OE2	25:AY:80:GLU:N	2.33	0.61
1:AA:1194:U:H5'	5:AE:26:LYS:NZ	2.15	0.61
2:AB:87:ASP:OD2	2:AB:224:ARG:NH1	2.33	0.61
34:BI:100:ILE:HG22	34:BI:101:SER:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1072:G:OP1	5:AE:54:ARG:CG	2.48	0.61
28:BA:2198:A:N6	33:BH:25:TYR:CD1	2.66	0.61
35:BJ:6:ALA:CB	35:BJ:45:THR:HG21	2.31	0.61
1:AA:922:G:C6	1:AA:1395:C:N4	2.67	0.61
28:BA:1248:G:N7	30:BE:46:GLN:NE2	2.48	0.61
41:BP:4:ILE:O	41:BP:6:GLN:N	2.31	0.61
1:AA:1014:A:H5"	19:AS:14:HIS:HB2	1.83	0.61
25:AY:469:ILE:CD1	59:AY:801:FUA:C3	2.77	0.61
1:AA:15:G:O2'	5:AE:22:SER:HB3	1.99	0.61
1:AA:1075:U:C4'	1:AA:1101:A:C5	2.82	0.61
1:AA:1296:C:O3'	1:AA:1302:C:N4	2.34	0.61
23:AW:28:A:H2	23:AW:42:U:H3	1.46	0.61
1:AA:1305:G:N2	1:AA:1331:G:O2'	2.34	0.61
1:AA:1375:A:OP1	7:AG:25:LYS:CE	2.47	0.61
1:AA:1498:U:O4	24:AX:12:U:C4'	2.48	0.61
22:AV:3:C:H42	22:AV:70:G:H1	1.47	0.61
25:AY:190:ALA:N	25:AY:205:GLU:O	2.33	0.61
25:AY:24:THR:CB	60:AY:802:GDP:O1B	2.49	0.61
25:AY:270:PHE:CG	60:AY:802:GDP:C2	2.89	0.61
28:BA:910:A:C8	38:BM:9:PHE:CD2	2.89	0.61
1:AA:15:G:O6	1:AA:920:U:O2	2.19	0.61
1:AA:1370:G:C8	9:AI:111:VAL:HG21	2.36	0.61
5:AE:99:ALA:O	5:AE:122:ASN:ND2	2.33	0.61
24:AX:14:A:OP2	24:AX:14:A:N9	2.34	0.61
56:B4:36:ARG:HG2	56:B4:37:GLN:H	1.66	0.61
1:AA:20:U:C2'	1:AA:21:G:C5'	2.73	0.60
1:AA:21:G:H2'	1:AA:22:G:C8	2.35	0.60
1:AA:554:A:H5'	12:AL:26:ALA:HB1	1.83	0.60
5:AE:80:THR:OG1	5:AE:81:LEU:N	2.34	0.60
22:AV:37:A:H8	25:AY:508:GLN:OE1	1.82	0.60
23:AW:6:C:H2'	23:AW:7:G:C8	2.35	0.60
59:AY:801:FUA:H211	59:AY:801:FUA:O2	2.00	0.60
27:BC:256:THR:OG1	28:BA:1803:A:O3'	2.19	0.60
28:BA:276:U:O2'	28:BA:278:A:N7	2.34	0.60
28:BA:2780:G:OP2	35:BJ:120:ARG:NE	2.33	0.60
48:BW:55:ASP:O	48:BW:57:THR:N	2.34	0.60
1:AA:1394:A:C8	1:AA:1501:C:C4'	2.81	0.60
1:AA:1394:A:C4	1:AA:1501:C:H1'	2.36	0.60
1:AA:1492:A:C2'	1:AA:1493:A:H5'	2.31	0.60
22:AV:47:U:H3'	22:AV:48:C:C5'	2.30	0.60
23:AW:76:A:N6	28:BA:2422:C:N1	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BN:98:LEU:O	39:BN:112:TYR:N	2.34	0.60
1:AA:920:U:C2'	1:AA:921:U:H5'	2.29	0.60
1:AA:928:G:O3'	1:AA:1533:C:H5	1.85	0.60
1:AA:1025:U:H5"	1:AA:1026:G:H5'	1.82	0.60
6:AF:98:GLU:HG3	6:AF:99:ALA:N	2.16	0.60
25:AY:221:ASN:HA	25:AY:224:GLU:HB3	1.84	0.60
1:AA:1033:G:C2'	1:AA:1034:G:H5'	2.30	0.60
1:AA:1329:A:OP1	13:AM:26:GLY:HA3	2.01	0.60
22:AV:75:C:O2'	28:BA:2064:C:H5'	2.00	0.60
57:B5:27:VAL:HG13	57:B5:83:ALA:HB3	1.83	0.60
1:AA:1081:A:C2	1:AA:1082:A:C5	2.89	0.60
27:BC:49:THR:HG21	28:BA:1813:G:H1'	1.81	0.60
28:BA:480:A:OP2	46:BU:43:LYS:NZ	2.34	0.60
28:BA:616:A:H4'	30:BE:101:TYR:CE2	2.36	0.60
1:AA:823:C:HO2'	8:AH:2:SER:N	1.98	0.60
1:AA:867:G:O2'	1:AA:873:A:N1	2.30	0.60
2:AB:178:LEU:HD12	5:AE:69:ARG:CD	2.16	0.60
21:AU:54:LYS:HG2	24:AX:1:G:OP1	2.02	0.60
22:AV:36:C:N3	24:AX:11:G:N1	2.47	0.60
22:AV:72:A:H2'	22:AV:73:A:C8	2.37	0.60
46:BU:38:ILE:CG2	46:BU:39:ASN:N	2.64	0.60
1:AA:15:G:H2'	1:AA:16:A:H8	1.67	0.60
1:AA:693:G:O4'	24:AX:7:A:H1'	2.00	0.60
1:AA:1014:A:H4'	19:AS:14:HIS:CG	2.37	0.60
7:AG:4:ARG:HG3	7:AG:5:ARG:N	2.16	0.60
25:AY:23:LYS:O	25:AY:24:THR:OG1	2.17	0.60
28:BA:27:G:O2'	28:BA:28:A:OP2	2.19	0.60
28:BA:784:G:O2'	28:BA:785:G:OP2	2.15	0.60
1:AA:918:A:H2'	1:AA:919:A:O4'	2.02	0.60
1:AA:929:G:N2	1:AA:1388:C:O2	2.33	0.60
1:AA:1074:G:C6	1:AA:1075:U:O4	2.54	0.60
9:AI:45:ARG:HE	9:AI:46:MET:H	1.50	0.60
12:AL:56:ARG:NH1	12:AL:62:GLU:OE1	2.35	0.60
28:BA:866:A:C8	28:BA:914:G:C6	2.90	0.60
1:AA:1075:U:C6	1:AA:1076:U:C5	2.90	0.59
7:AG:63:GLU:OE1	7:AG:70:ARG:NH1	2.35	0.59
28:BA:1338:G:O2'	45:BT:18:GLU:OE1	2.20	0.59
28:BA:2478:A:P	56:B4:2:LYS:HZ1	2.25	0.59
1:AA:135:C:N3	16:AP:1:MET:N	2.43	0.59
1:AA:843:U:N3	1:AA:844:G:O6	2.36	0.59
1:AA:1014:A:H4'	19:AS:14:HIS:CE1	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:18:GLN:NE2	8:AH:70:ALA:HB1	2.17	0.59
34:BI:93:ASN:ND2	34:BI:135:MET:O	2.35	0.59
1:AA:1219:A:H5"	14:AN:53:ARG:NH1	2.18	0.59
5:AE:111:MET:CE	5:AE:125:ALA:HB1	2.31	0.59
22:AV:76:A:O2'	28:BA:2451:A:C4	2.54	0.59
28:BA:983:A:C6	28:BA:984:A:C2	2.90	0.59
28:BA:1106:G:OP1	57:B5:62:ARG:NH2	2.35	0.59
29:BD:118:PHE:HD1	29:BD:119:ALA:H	1.49	0.59
34:BI:92:PRO:O	34:BI:94:LYS:N	2.36	0.59
9:AI:94:LEU:O	9:AI:96:SER:N	2.33	0.59
15:AO:14:GLU:O	15:AO:84:ARG:NH2	2.35	0.59
24:AX:12:U:O2'	25:AY:510:GLY:O	2.20	0.59
1:AA:920:U:H2'	1:AA:921:U:C6	2.38	0.59
4:AD:95:GLU:OE2	4:AD:104:ARG:NE	2.31	0.59
22:AV:3:C:C2'	22:AV:4:G:H5'	2.32	0.59
23:AW:21:A:N6	23:AW:46:G:H2'	2.17	0.59
28:BA:1262:A:OP2	44:BS:99:ARG:NH2	2.35	0.59
28:BA:2089:C:O2'	28:BA:2090:A:H5'	2.02	0.59
1:AA:928:G:O2'	1:AA:929:G:C5'	2.41	0.59
1:AA:1149:C:OP1	9:AI:11:ARG:NH1	2.25	0.59
1:AA:1394:A:O2'	1:AA:1501:C:C2	2.55	0.59
2:AB:178:LEU:CD1	5:AE:69:ARG:NE	2.65	0.59
10:AJ:57:VAL:HG12	10:AJ:58:ASN:H	1.67	0.59
21:AU:49:LYS:NZ	24:AX:2:G:C4'	2.65	0.59
28:BA:635:C:OP2	37:BL:126:ARG:NH1	2.35	0.59
28:BA:2353:G:N3	48:BW:30:VAL:CG1	2.65	0.59
28:BA:2636:C:HO2'	29:BD:45:TYR:HH	1.50	0.59
28:BA:2800:A:H3'	28:BA:2801:G:C5'	2.32	0.59
38:BM:41:LEU:HD11	38:BM:126:ILE:HD13	1.85	0.59
1:AA:14:U:H2'	1:AA:16:A:OP2	2.03	0.59
1:AA:922:G:N1	1:AA:1395:C:C4	2.67	0.59
1:AA:1048:G:OP1	14:AN:4:GLN:N	2.31	0.59
1:AA:17:U:H2'	1:AA:18:C:H6	1.66	0.59
4:AD:32:CYS:SG	4:AD:33:LYS:N	2.75	0.59
28:BA:866:A:N7	28:BA:914:G:C6	2.71	0.59
1:AA:17:U:O4'	1:AA:1079:G:O2'	2.12	0.59
1:AA:757:U:O2'	1:AA:879:C:O2	2.19	0.59
1:AA:1076:U:H2'	1:AA:1077:G:C8	2.38	0.59
3:AC:7:PRO:HG2	3:AC:184:TYR:CG	2.38	0.59
28:BA:911:A:H3'	38:BM:8:LYS:NZ	2.18	0.59
25:AY:219:HIS:CE1	25:AY:221:ASN:HB2	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:1131:G:OP1	35:BJ:82:GLY:HA2	2.02	0.59
28:BA:2197:U:C1'	28:BA:2198:A:C5	2.85	0.59
1:AA:1129:C:C5'	9:AI:18:ARG:NH2	2.65	0.58
23:AW:60:U:H5'	23:AW:61:C:H5	1.67	0.58
34:BI:131:THR:O	34:BI:134:SER:OG	2.16	0.58
40:BO:89:ASP:HA	40:BO:116:GLN:HB3	1.84	0.58
1:AA:1130:A:C5'	9:AI:20:PHE:CD2	2.86	0.58
1:AA:1130:A:H5'	9:AI:20:PHE:CD2	2.37	0.58
3:AC:129:MET:HB3	3:AC:132:ARG:HG3	1.84	0.58
5:AE:82:GLN:HG2	5:AE:150:PRO:HD3	1.85	0.58
12:AL:44:LYS:CB	12:AL:45:PRO:HD3	2.32	0.58
28:BA:1386:C:H2'	28:BA:1387:A:C8	2.39	0.58
28:BA:1654:A:O2'	29:BD:118:PHE:CG	2.55	0.58
30:BE:168:ASP:OD2	30:BE:170:ARG:NH2	2.36	0.58
1:AA:1291:U:P	7:AG:38:THR:HG22	2.44	0.58
24:AX:14:A:H2'	24:AX:15:A:H5"	0.58	0.58
25:AY:200:VAL:O	25:AY:201:THR:OG1	2.21	0.58
25:AY:219:HIS:NE2	25:AY:221:ASN:HB2	2.19	0.58
48:BW:51:GLY:HA3	48:BW:59:PHE:CZ	2.38	0.58
22:AV:36:C:O2	25:AY:510:GLY:HA2	2.03	0.58
28:BA:1930:G:O2'	28:BA:1968:G:O6	2.17	0.58
40:BO:105:ALA:O	40:BO:107:ALA:N	2.35	0.58
48:BW:51:GLY:HA3	48:BW:59:PHE:CE1	2.38	0.58
5:AE:41:ASP:OD1	5:AE:42:GLY:N	2.37	0.58
21:AU:49:LYS:NZ	24:AX:2:G:H4'	2.16	0.58
28:BA:84:A:N1	28:BA:98:G:O2'	2.30	0.58
28:BA:1076:C:H2'	28:BA:1077:A:O4'	2.03	0.58
34:BI:37:PHE:O	34:BI:41:PHE:HB3	2.04	0.58
57:B5:15:VAL:HG22	57:B5:66:GLY:HA3	1.84	0.58
1:AA:1077:G:C2	1:AA:1080:A:OP2	2.55	0.58
1:AA:1081:A:N6	1:AA:1082:A:H61	2.01	0.58
42:BQ:63:ARG:NH1	42:BQ:95:ALA:O	2.36	0.58
1:AA:1130:A:OP2	9:AI:64:TYR:CZ	2.55	0.58
59:AY:801:FUA:H12	59:AY:801:FUA:O1	2.00	0.58
27:BC:16:VAL:N	27:BC:203:VAL:HG12	2.17	0.58
42:BQ:84:LYS:O	42:BQ:86:SER:N	2.36	0.58
45:BT:19:LYS:O	45:BT:23:ALA:N	2.35	0.58
48:BW:28:GLU:HB3	48:BW:31:LEU:HD21	1.85	0.58
57:B5:45:GLY:HA2	57:B5:49:GLY:HA2	1.85	0.58
1:AA:1240:U:OP1	7:AG:116:MET:HB2	2.03	0.58
20:AT:3:ASN:O	20:AT:5:LYS:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:645:GLN:O	25:AY:647:SER:N	2.37	0.58
28:BA:673:C:OP1	30:BE:49:ARG:NH2	2.36	0.58
28:BA:910:A:C4	38:BM:9:PHE:CD2	2.91	0.58
1:AA:1007:U:H2'	1:AA:1008:U:H5'	1.86	0.58
41:BP:63:ILE:HA	41:BP:68:GLY:HA2	1.85	0.58
1:AA:15:G:H2'	5:AE:22:SER:HB3	1.86	0.58
5:AE:110:ALA:O	5:AE:111:MET:HB3	2.04	0.58
28:BA:911:A:N6	38:BM:8:LYS:C	2.57	0.58
28:BA:2198:A:N6	33:BH:25:TYR:CE1	2.58	0.58
1:AA:15:G:O2'	5:AE:22:SER:OG	2.14	0.57
1:AA:1078:U:H4'	5:AE:134:ILE:HG21	1.86	0.57
28:BA:422:A:C2	28:BA:423:A:C4	2.92	0.57
1:AA:1394:A:C4	1:AA:1501:C:C4'	2.87	0.57
4:AD:58:LYS:HB2	4:AD:200:ILE:HG13	1.86	0.57
22:AV:56:C:C4	31:BF:79:ARG:HD2	2.39	0.57
25:AY:650:THR:HA	34:BI:29:GLN:HE22	1.69	0.57
48:BW:76:ARG:HH21	48:BW:76:ARG:CG	2.16	0.57
1:AA:15:G:C2'	5:AE:22:SER:HB3	2.34	0.57
1:AA:756:C:HO2'	8:AH:2:SER:N	2.02	0.57
1:AA:921:U:H4'	1:AA:1081:A:H4'	1.87	0.57
29:BD:38:LYS:NZ	29:BD:81:GLU:OE1	2.26	0.57
45:BT:35:ALA:HB3	45:BT:38:ALA:HB2	1.85	0.57
1:AA:58:C:O2'	1:AA:388:G:N7	2.24	0.57
1:AA:1377:A:C2'	7:AG:2:PRO:CB	2.82	0.57
16:AP:28:ARG:NH2	16:AP:29:ASN:OD1	2.37	0.57
21:AU:9:ASN:HB2	21:AU:11:PRO:HD2	1.87	0.57
23:AW:19:G:H5'	23:AW:20:U:O5'	2.05	0.57
25:AY:660:LEU:O	25:AY:662:GLU:N	2.34	0.57
28:BA:1076:C:H1'	34:BI:93:ASN:HB3	1.86	0.57
1:AA:15:G:N2	1:AA:1080:A:C4'	2.51	0.57
1:AA:15:G:H5"	5:AE:29:ARG:HH12	1.67	0.57
1:AA:1391:U:C6	1:AA:1391:U:OP2	2.57	0.57
4:AD:30:THR:HB	4:AD:31:LYS:NZ	2.19	0.57
9:AI:130:ARG:CD	23:AW:33:U:C5	2.87	0.57
22:AV:35:A:H4'	25:AY:587:ASP:OD1	2.04	0.57
28:BA:1936:A:H2	28:BA:1943:U:C5	2.23	0.57
41:BP:58:PHE:CD1	41:BP:75:THR:HG22	2.40	0.57
57:B5:3:LEU:CD1	57:B5:5:LEU:HG	2.35	0.57
1:AA:1082:A:C3'	1:AA:1083:U:H5'	2.28	0.57
1:AA:1220:G:P	14:AN:53:ARG:HH22	2.26	0.57
1:AA:1391:U:C2'	1:AA:1392:G:C5'	2.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:34:SER:HB3	9:AI:37:GLN:CG	2.34	0.57
22:AV:74:C:OP2	28:BA:2602:A:C2	2.57	0.57
1:AA:1190:G:OP1	3:AC:4:LYS:HA	2.05	0.57
1:AA:1534:A:P	1:AA:1534:A:C8	2.98	0.57
4:AD:31:LYS:HD3	4:AD:31:LYS:N	2.20	0.57
25:AY:79:TYR:OH	25:AY:284:ASP:OD1	2.16	0.57
28:BA:2742:G:OP1	56:B4:36:ARG:NH1	2.38	0.57
9:AI:6:TYR:CD1	9:AI:89:GLU:HB2	2.40	0.57
28:BA:1019:U:H3	28:BA:1142:A:H62	1.53	0.57
57:B5:71:CYS:CA	57:B5:117:LEU:HD13	2.31	0.57
1:AA:1055:A:O2'	3:AC:156:ARG:CZ	2.53	0.57
1:AA:1377:A:O2'	7:AG:2:PRO:CB	2.53	0.57
21:AU:49:LYS:HD2	24:AX:2:G:H5'	1.86	0.57
23:AW:76:A:C6	28:BA:2422:C:C2	2.93	0.57
28:BA:1353:A:C8	28:BA:1378:A:N6	2.73	0.57
28:BA:2331:G:O2'	28:BA:2336:A:N1	2.38	0.57
28:BA:2517:C:C6	28:BA:2542:A:N7	2.72	0.57
42:BQ:63:ARG:HH22	42:BQ:95:ALA:C	2.08	0.57
1:AA:928:G:O3'	1:AA:1533:C:C5	2.58	0.57
1:AA:1106:G:O2'	3:AC:169:ARG:CZ	2.52	0.57
1:AA:1532:U:H6	1:AA:1532:U:O5'	1.87	0.57
5:AE:24:THR:HA	5:AE:29:ARG:HA	1.87	0.57
5:AE:31:PHE:CZ	24:AX:19:A:C6	2.93	0.57
27:BC:77:VAL:HG23	27:BC:111:ALA:HA	1.85	0.57
18:AR:73:ARG:O	18:AR:74:HIS:ND1	2.38	0.56
21:AU:25:LYS:NZ	21:AU:26:ALA:HB2	2.20	0.56
25:AY:522:MET:HE1	25:AY:605:PHE:HA	1.86	0.56
28:BA:1773:A:N7	28:BA:1829:A:H1'	2.20	0.56
1:AA:375:U:C4	1:AA:376:G:N7	2.73	0.56
23:AW:20:U:OP1	28:BA:2145:C:C1'	2.50	0.56
28:BA:1738:G:HO2'	28:BA:1739:A:P	2.27	0.56
36:BK:121:GLU:OE1	41:BP:62:LYS:NZ	2.37	0.56
41:BP:50:ARG:HB3	41:BP:57:ALA:N	2.17	0.56
42:BQ:105:PHE:O	42:BQ:108:LEU:N	2.38	0.56
45:BT:54:GLU:HG3	45:BT:88:LYS:HB2	1.86	0.56
1:AA:16:A:O2'	1:AA:17:U:H5'	2.05	0.56
1:AA:1394:A:H4'	1:AA:1395:C:OP2	2.05	0.56
1:AA:1493:A:O2'	24:AX:14:A:C4'	2.53	0.56
3:AC:3:GLN:OE1	3:AC:3:GLN:N	2.39	0.56
9:AI:129:LYS:HZ1	23:AW:31:A:P	2.29	0.56
28:BA:283:G:C2	28:BA:284:U:H1'	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:1324:G:C4	28:BA:1328:A:N6	2.74	0.56
37:BL:85:VAL:CG2	37:BL:94:THR:HG22	2.36	0.56
48:BW:18:LYS:HG3	48:BW:19:ARG:N	2.21	0.56
1:AA:299:G:H2'	1:AA:300:A:C8	2.40	0.56
1:AA:925:G:C2	1:AA:1392:G:C2	2.94	0.56
1:AA:1073:U:H5"	5:AE:62:LYS:HE2	1.87	0.56
1:AA:1190:G:OP1	3:AC:5:VAL:N	2.29	0.56
1:AA:1223:C:P	19:AS:78:ARG:NH1	2.78	0.56
2:AB:166:ASP:OD1	2:AB:167:HIS:N	2.38	0.56
28:BA:100:U:H4'	28:BA:101:A:O5'	2.06	0.56
34:BI:100:ILE:HD11	34:BI:137:LEU:HG	1.87	0.56
57:B5:56:ARG:O	57:B5:57:ASN:ND2	2.39	0.56
1:AA:779:C:O2'	11:AK:122:ARG:NH1	2.39	0.56
1:AA:951:G:OP2	13:AM:101:ARG:NH2	2.38	0.56
1:AA:1239:A:H62	1:AA:1299:A:N6	2.03	0.56
1:AA:1377:A:O2'	7:AG:2:PRO:HB2	2.05	0.56
28:BA:907:G:OP1	38:BM:23:GLY:N	2.38	0.56
1:AA:15:G:H2'	1:AA:16:A:C8	2.40	0.56
1:AA:1377:A:N3	7:AG:2:PRO:CG	2.68	0.56
1:AA:1498:U:O4	24:AX:12:U:C3'	2.54	0.56
11:AK:89:PRO:HB3	21:AU:29:LEU:HD22	1.87	0.56
25:AY:164:ALA:HB1	25:AY:262:ILE:HD11	1.88	0.56
28:BA:1107:G:H5"	57:B5:58:THR:CG2	2.36	0.56
1:AA:693:G:H5'	24:AX:7:A:H1'	1.87	0.56
57:B5:132:TYR:CZ	58:B6:23:ILE:HD11	2.40	0.56
25:AY:92:HIS:CD2	59:AY:801:FUA:H283	2.29	0.56
42:BQ:81:GLY:O	42:BQ:85:ALA:N	2.37	0.56
1:AA:158:G:H2'	1:AA:159:G:H5'	1.88	0.56
1:AA:921:U:H4'	1:AA:1081:A:O3'	2.06	0.56
1:AA:1092:A:H5"	7:AG:4:ARG:NH1	2.21	0.56
6:AF:53:LYS:O	6:AF:54:LEU:HB3	2.06	0.56
22:AV:17:C:C6	22:AV:17(A):U:C5	2.92	0.56
24:AX:5:A:H5"	24:AX:6:A:OP1	2.06	0.56
28:BA:866:A:C8	28:BA:914:G:N1	2.73	0.56
28:BA:2757:A:N1	32:BG:66:THR:HG21	2.21	0.56
35:BJ:17:VAL:HG23	35:BJ:139:VAL:HA	1.88	0.56
1:AA:1279:G:N2	10:AJ:45:ARG:NH1	2.53	0.56
7:AG:28:ASN:OD1	7:AG:36:LYS:NZ	2.39	0.56
19:AS:36:ARG:NH2	19:AS:75:ALA:O	2.39	0.56
22:AV:68:C:H2'	22:AV:69:C:C6	2.41	0.56
23:AW:19:G:H3'	28:BA:2145:C:H1'	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BC:251:THR:HG21	28:BA:1824:G:N3	2.21	0.56
28:BA:686:U:H2'	28:BA:788:A:N1	2.21	0.56
28:BA:2015:A:C2	52:B0:2:VAL:HG22	2.41	0.56
30:BE:150:THR:HG21	30:BE:153:LEU:HA	1.87	0.56
48:BW:39:GLN:HG2	48:BW:41:GLY:H	1.69	0.56
1:AA:18:C:H1'	1:AA:1078:U:N3	2.19	0.55
1:AA:71:A:N1	1:AA:99:C:O2'	2.37	0.55
1:AA:1130:A:O5'	9:AI:20:PHE:CE2	2.59	0.55
1:AA:1394:A:C4	1:AA:1501:C:H4'	2.40	0.55
2:AB:32:GLY:HA3	2:AB:39:ILE:H	1.71	0.55
25:AY:248:ILE:O	25:AY:251:ALA:N	2.39	0.55
28:BA:443:A:N7	30:BE:40:ARG:HD3	2.21	0.55
28:BA:811:U:C4	37:BL:21:ARG:NH2	2.75	0.55
28:BA:2196:C:N3	28:BA:2197:U:N3	2.52	0.55
28:BA:2680:U:H5'	29:BD:194:PRO:HA	1.88	0.55
27:BC:14:HIS:O	27:BC:203:VAL:HG11	2.05	0.55
28:BA:1107:G:H4'	57:B5:81:LEU:HA	1.88	0.55
28:BA:1786:A:H1'	28:BA:1938:A:N6	2.21	0.55
28:BA:2681:C:OP2	29:BD:114:LYS:NZ	2.33	0.55
1:AA:1014:A:C5'	19:AS:14:HIS:CG	2.88	0.55
1:AA:1319:A:H5'	19:AS:4:SER:HB2	1.89	0.55
9:AI:91:ASP:OD1	9:AI:91:ASP:N	2.40	0.55
15:AO:19:ALA:O	15:AO:20:ASN:HB2	2.06	0.55
49:BX:32:LEU:O	49:BX:33:HIS:ND1	2.39	0.55
1:AA:928:G:H2'	1:AA:929:G:C8	2.32	0.55
1:AA:1391:U:OP2	1:AA:1391:U:C5	2.59	0.55
1:AA:1414:U:O2	1:AA:1487:G:N2	2.39	0.55
9:AI:10:GLY:HA2	9:AI:81:HIS:CD2	2.41	0.55
45:BT:32:LEU:N	45:BT:83:ALA:HB3	2.21	0.55
1:AA:135:C:H2'	1:AA:136:C:H5'	1.87	0.55
1:AA:1004:A:O2'	1:AA:1036:A:N1	2.32	0.55
1:AA:1075:U:O4'	1:AA:1101:A:N1	2.40	0.55
19:AS:29:LYS:HB3	19:AS:30:PRO:HD2	1.87	0.55
24:AX:11:G:O2'	24:AX:12:U:H5'	2.07	0.55
27:BC:68:ARG:CD	27:BC:103:ILE:HD11	2.37	0.55
28:BA:163:C:O2'	28:BA:164:C:P	2.65	0.55
28:BA:2197:U:C2'	28:BA:2198:A:C4	2.84	0.55
40:BO:2:ASP:OD1	40:BO:3:LYS:N	2.39	0.55
43:BR:39:LEU:O	43:BR:49:ILE:HG23	2.06	0.55
1:AA:93:U:H2'	1:AA:94:G:H5"	1.88	0.55
1:AA:1377:A:C2'	7:AG:2:PRO:HB3	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:129:LYS:NZ	23:AW:31:A:OP1	2.39	0.55
28:BA:85:G:OP2	46:BU:6:ARG:HG3	2.06	0.55
28:BA:265:A:H4'	28:BA:266:G:OP1	2.07	0.55
28:BA:2698:U:H2'	28:BA:2699:C:H6	1.72	0.55
31:BF:151:LEU:HD12	31:BF:152:ASP:N	2.21	0.55
35:BJ:81:ILE:HG13	35:BJ:82:GLY:N	2.21	0.55
51:BZ:5:LYS:H	51:BZ:5:LYS:HD2	1.72	0.55
57:B5:129:LEU:C	57:B5:131:THR:H	2.10	0.55
1:AA:828:U:H1'	2:AB:24:PRO:CB	2.37	0.55
1:AA:1118:U:OP1	9:AI:106:ARG:HD2	2.07	0.55
22:AV:71:C:O2	22:AV:71:C:C2'	2.53	0.55
22:AV:76:A:N1	28:BA:2450:A:O3'	2.39	0.55
24:AX:15:A:H2'	24:AX:16:A:C8	2.42	0.55
28:BA:1482:G:C6	28:BA:1508:A:C2	2.94	0.55
28:BA:1715:G:N2	28:BA:1744:A:OP2	2.36	0.55
28:BA:2197:U:C4'	33:BH:29:PHE:CZ	2.85	0.55
39:BN:30:ARG:NH1	39:BN:74:GLU:OE1	2.40	0.55
45:BT:59:ASN:O	45:BT:83:ALA:O	2.24	0.55
53:B1:8:ILE:HD11	53:B1:24:LYS:N	2.21	0.55
6:AF:42:TRP:CZ2	6:AF:101:PRO:HD3	2.42	0.55
25:AY:313:ASP:OD2	25:AY:378:ARG:NH1	2.40	0.55
41:BP:50:ARG:CG	41:BP:57:ALA:O	2.55	0.55
42:BQ:93:ILE:O	42:BQ:96:ASP:N	2.39	0.55
46:BU:21:ARG:CZ	46:BU:72:PHE:CE2	2.90	0.55
1:AA:664:G:H22	1:AA:741:G:H1	1.54	0.55
1:AA:928:G:HO2'	1:AA:929:G:H5'	1.67	0.55
1:AA:1076:U:H2'	1:AA:1077:G:H8	1.71	0.55
1:AA:1100:C:OP2	2:AB:94:ARG:HD3	2.06	0.55
1:AA:1106:G:H1'	3:AC:169:ARG:NH2	2.22	0.55
1:AA:1341:U:H5'	23:AW:32:C:H5'	1.89	0.55
25:AY:92:HIS:O	25:AY:122:GLN:NE2	2.40	0.55
28:BA:2196:C:C5	28:BA:2197:U:O4	2.59	0.55
28:BA:2197:U:H1'	28:BA:2198:A:N7	2.21	0.55
29:BD:106:LYS:HB3	29:BD:206:ALA:HB3	1.89	0.55
34:BI:135:MET:HB3	34:BI:137:LEU:HD22	1.88	0.55
1:AA:926:G:O6	24:AX:9:U:OP2	2.25	0.55
5:AE:106:ILE:HD11	5:AE:124:LEU:HD22	1.89	0.55
22:AV:56:C:O2'	31:BF:74:ALA:N	2.40	0.55
28:BA:277:G:O2'	28:BA:278:A:OP2	2.25	0.55
28:BA:834:G:C6	28:BA:835:C:C4	2.95	0.55
28:BA:855:G:H1'	48:BW:23:LYS:HE3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:1458:U:H4'	28:BA:1459:G:O5'	2.07	0.55
28:BA:1772:A:N1	28:BA:1980:G:C6	2.76	0.55
29:BD:118:PHE:O	29:BD:120:GLY:N	2.36	0.55
1:AA:197:A:N1	1:AA:220:G:O2'	2.35	0.54
5:AE:96:MET:CE	5:AE:115:LEU:HD11	2.38	0.54
7:AG:57:SER:OG	7:AG:58:GLU:N	2.40	0.54
24:AX:16:A:H8	24:AX:16:A:O5'	1.90	0.54
28:BA:910:A:C4	38:BM:9:PHE:CZ	2.95	0.54
57:B5:58:THR:HB	57:B5:82:ILE:HB	1.89	0.54
1:AA:1081:A:C2	1:AA:1082:A:C2	2.95	0.54
1:AA:1393:U:C2'	1:AA:1502:A:H4'	2.36	0.54
1:AA:1394:A:C1'	1:AA:1395:C:P	2.95	0.54
1:AA:1468:A:C2'	1:AA:1469:C:H5'	2.37	0.54
23:AW:4:U:H3	23:AW:69:A:H2	1.51	0.54
28:BA:1750:G:O2'	28:BA:2860:A:N1	2.37	0.54
28:BA:1753:G:OP1	41:BP:92:ARG:NE	2.38	0.54
29:BD:107:VAL:CG2	29:BD:203:VAL:HG23	2.38	0.54
46:BU:38:ILE:HG22	46:BU:39:ASN:H	1.73	0.54
5:AE:104:GLY:HA3	5:AE:122:ASN:HA	1.90	0.54
25:AY:270:PHE:HB3	60:AY:802:GDP:C6	2.28	0.54
28:BA:674:G:H1'	30:BE:69:ARG:HE	1.72	0.54
28:BA:877:A:C2	28:BA:899:A:C2	2.95	0.54
28:BA:1936:A:N6	28:BA:1963:U:H3	2.05	0.54
32:BG:84:LYS:HG3	32:BG:132:LEU:H	1.73	0.54
57:B5:44:ALA:O	57:B5:49:GLY:N	2.40	0.54
57:B5:64:VAL:O	57:B5:68:PRO:HD2	2.06	0.54
1:AA:579:A:H2'	1:AA:580:C:C6	2.42	0.54
1:AA:619:U:H3	4:AD:131:ASN:HB3	1.72	0.54
1:AA:1079:G:OP1	5:AE:50:TYR:CD2	2.59	0.54
8:AH:93:PRO:HG3	8:AH:125:ILE:HD12	1.89	0.54
22:AV:7:G:H3'	22:AV:8:U:C5'	2.38	0.54
36:BK:70:ARG:HD3	36:BK:76:VAL:HG22	1.90	0.54
41:BP:33:GLU:HB2	41:BP:38:ARG:HH11	1.71	0.54
2:AB:209:VAL:HG23	2:AB:210:THR:H	1.73	0.54
13:AM:8:ASN:ND2	13:AM:66:GLU:OE2	2.39	0.54
23:AW:23:A:H2'	23:AW:24:G:C8	2.42	0.54
28:BA:2198:A:N1	33:BH:25:TYR:HD1	2.05	0.54
47:BV:80:HIS:HD2	47:BV:83:LYS:N	2.05	0.54
1:AA:19:A:HO2'	1:AA:20:U:H5'	1.69	0.54
1:AA:1240:U:P	7:AG:116:MET:HB2	2.48	0.54
23:AW:43:G:H2'	23:AW:44:G:H8	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:469:ILE:HD13	59:AY:801:FUA:C2	2.32	0.54
42:BQ:91:ARG:NH1	43:BR:10:LYS:HB3	2.23	0.54
57:B5:129:LEU:HB3	57:B5:130:PRO:HD2	1.89	0.54
1:AA:1203:C:OP1	14:AN:2:ALA:CA	2.56	0.54
4:AD:192:SER:OG	4:AD:193:ALA:N	2.40	0.54
28:BA:2091:C:C5	28:BA:2092:U:C6	2.96	0.54
36:BK:43:ILE:CD1	36:BK:52:VAL:HB	2.37	0.54
1:AA:351:G:OP1	20:AT:3:ASN:ND2	2.40	0.54
6:AF:80:PHE:HE1	27:BC:123:ILE:HB	1.73	0.54
24:AX:3:U:C3’	24:AX:4:A:C8	2.89	0.54
35:BJ:32:LEU:HD22	35:BJ:54:ILE:HD12	1.90	0.54
36:BK:80:ASP:HB2	41:BP:67:GLU:HG3	1.90	0.54
45:BT:44:LYS:HG3	45:BT:55:VAL:HG11	1.90	0.54
1:AA:922:G:C6	1:AA:1395:C:N3	2.72	0.54
1:AA:1021:A:H2’	1:AA:1022:A:H5’	1.89	0.54
1:AA:1118:U:OP1	9:AI:106:ARG:NE	2.41	0.54
1:AA:1129:C:H5”	9:AI:18:ARG:CZ	2.37	0.54
1:AA:1394:A:C4	1:AA:1501:C:O4’	2.60	0.54
5:AE:104:GLY:CA	5:AE:122:ASN:HA	2.37	0.54
13:AM:107:ARG:O	13:AM:111:GLY:N	2.41	0.54
23:AW:20(A):U:O2’	23:AW:21:A:O5’	2.25	0.54
28:BA:947:A:HO2’	28:BA:984:A:H2	1.56	0.54
28:BA:1535:A:H4’	28:BA:1536:C:OP2	2.08	0.54
28:BA:2548:U:O2	36:BK:23:LYS:NZ	2.37	0.54
57:B5:54:VAL:HA	57:B5:84:TYR:O	2.07	0.54
1:AA:19:A:H5”	5:AE:130:SER:HB2	1.90	0.54
18:AR:37:GLY:O	18:AR:63:ARG:NH2	2.40	0.54
25:AY:220:GLN:O	25:AY:224:GLU:N	2.37	0.54
28:BA:910:A:N7	38:BM:9:PHE:HB2	2.23	0.54
28:BA:2091:C:C2	28:BA:2092:U:C5	2.95	0.54
28:BA:2335:A:C6	28:BA:2337:G:H1’	2.42	0.54
57:B5:60:LEU:O	57:B5:64:VAL:HB	2.08	0.54
1:AA:684:U:O2’	11:AK:40:ASN:O	2.26	0.53
1:AA:1182:G:H4’	1:AA:1183:U:C5’	2.37	0.53
1:AA:1277:C:HO2’	1:AA:1279:G:H8	1.53	0.53
23:AW:13:C:O2	23:AW:22:G:N1	2.41	0.53
24:AX:9:U:HO2’	24:AX:10:G:H5’	1.66	0.53
24:AX:15:A:OP1	24:AX:15:A:H4’	2.08	0.53
28:BA:84:A:P	46:BU:5:ARG:NH2	2.81	0.53
28:BA:411:G:OP2	28:BA:2406:A:O2’	2.25	0.53
28:BA:2134:A:HO2’	28:BA:2135:A:H8	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:2197:U:O2'	28:BA:2198:A:C6	2.61	0.53
45:BT:89:GLU:O	45:BT:91:GLN:N	2.41	0.53
46:BU:35:VAL:HB	46:BU:38:ILE:HG21	1.90	0.53
57:B5:43:LYS:HZ3	57:B5:98:GLU:HB2	1.73	0.53
1:AA:309:A:O2'	1:AA:607:A:N1	2.40	0.53
1:AA:1060:U:OP1	14:AN:85:ARG:NH2	2.41	0.53
3:AC:42:TYR:CE2	3:AC:90:VAL:HG21	2.43	0.53
8:AH:12:THR:HG22	8:AH:15:ARG:HH22	1.73	0.53
22:AV:49:G:H1	22:AV:65:C:H42	1.55	0.53
28:BA:2016:U:H1'	52:B0:2:VAL:HG11	1.89	0.53
28:BA:2415:G:H4'	37:BL:66:PHE:HB2	1.90	0.53
34:BI:98:GLY:HA3	34:BI:137:LEU:HB3	1.90	0.53
1:AA:15:G:C5'	5:AE:29:ARG:HH12	2.17	0.53
1:AA:677:U:H3	1:AA:713:G:H22	1.56	0.53
1:AA:958:A:C8	19:AS:55:ARG:NH1	2.76	0.53
1:AA:1319:A:H5"	19:AS:4:SER:CB	2.38	0.53
5:AE:96:MET:HE2	5:AE:115:LEU:HD11	1.91	0.53
23:AW:72:C:H2'	23:AW:73:A:O4'	2.09	0.53
28:BA:2355:G:H4'	48:BW:20:LEU:HD13	1.88	0.53
28:BA:2547:A:H2'	28:BA:2548:U:C6	2.43	0.53
37:BL:77:ILE:CD1	37:BL:108:ALA:HB1	2.38	0.53
57:B5:23:LEU:HG	57:B5:24:SER:N	2.22	0.53
1:AA:18:C:H2'	1:AA:19:A:C8	2.44	0.53
1:AA:546:A:P	4:AD:69:GLU:HB2	2.49	0.53
1:AA:693:G:N2	23:AW:38:A:O2'	2.42	0.53
1:AA:958:A:N6	19:AS:77:THR:O	2.41	0.53
1:AA:1079:G:O2'	1:AA:1080:A:C5'	2.48	0.53
1:AA:1158:C:O3'	2:AB:131:LYS:NZ	2.36	0.53
25:AY:507:LYS:HZ2	28:BA:1913:A:H62	1.55	0.53
28:BA:1397:U:OP2	28:BA:1398:C:N4	2.34	0.53
43:BR:49:ILE:HG22	43:BR:54:VAL:HG13	1.89	0.53
48:BW:13:ARG:HG2	48:BW:14:ASP:H	1.74	0.53
48:BW:46:ALA:HB3	48:BW:80:SER:HB3	1.91	0.53
1:AA:1534:A:H8	1:AA:1534:A:P	2.31	0.53
2:AB:178:LEU:HD11	5:AE:69:ARG:HD2	1.79	0.53
4:AD:25:VAL:HG12	4:AD:26:ARG:N	2.24	0.53
14:AN:20:TYR:O	14:AN:24:ARG:N	2.42	0.53
28:BA:384:A:H2'	28:BA:385:C:H5'	1.90	0.53
28:BA:1069:A:C4	28:BA:1073:A:N7	2.77	0.53
28:BA:2297:A:N1	28:BA:2321:U:H5	2.07	0.53
57:B5:43:LYS:NZ	57:B5:98:GLU:HB2	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1071:C:C5’	5:AE:54:ARG:HH12	2.20	0.53
1:AA:1341:U:H5’	23:AW:32:C:C5’	2.38	0.53
22:AV:35:A:N1	24:AX:13:A:C6	2.76	0.53
22:AV:37:A:H8	25:AY:508:GLN:CD	2.12	0.53
23:AW:6:C:H2’	23:AW:7:G:H8	1.72	0.53
28:BA:2090:A:C6	28:BA:2091:C:N4	2.77	0.53
41:BP:50:ARG:CD	41:BP:51:ASN:N	2.72	0.53
44:BS:73:LYS:HB3	44:BS:106:VAL:HB	1.90	0.53
57:B5:4:ASN:O	57:B5:6:GLN:N	2.41	0.53
1:AA:1107:C:OP1	3:AC:173:VAL:N	2.42	0.53
1:AA:1369:C:OP2	9:AI:114:LYS:N	2.33	0.53
21:AU:40:LYS:N	21:AU:41:PRO:CD	2.72	0.53
23:AW:50:C:N4	23:AW:64:G:N1	2.34	0.53
28:BA:1080:A:H1’	34:BI:127:SER:HA	1.91	0.53
38:BM:33:LEU:HD22	38:BM:128:THR:HB	1.90	0.53
50:BY:56:LEU:O	50:BY:58:ASN:N	2.39	0.53
1:AA:927:G:O2’	1:AA:1532:U:O3’	2.21	0.53
1:AA:1125:U:H5’	10:AJ:40:ILE:HD11	1.91	0.53
4:AD:165:ARG:O	4:AD:167:LYS:N	2.40	0.53
12:AL:110:ARG:NH1	12:AL:112:GLN:O	2.41	0.53
24:AX:3:U:H3’	24:AX:4:A:H8	1.73	0.53
24:AX:16:A:C8	24:AX:16:A:O5’	2.62	0.53
28:BA:729:G:H2’	28:BA:1775:U:H1’	1.91	0.53
28:BA:1754:A:H4’	41:BP:102:ARG:NH2	2.22	0.53
31:BF:103:ILE:HG23	31:BF:175:PRO:HD3	1.90	0.53
45:BT:50:LEU:O	45:BT:52:GLU:N	2.42	0.53
48:BW:37:VAL:HB	48:BW:38:ARG:HH11	1.74	0.53
57:B5:25:ALA:HB3	57:B5:85:SER:OG	2.09	0.53
1:AA:921:U:C4’	1:AA:1081:A:H4’	2.39	0.53
1:AA:957:U:H4’	19:AS:79:THR:OG1	2.09	0.53
1:AA:1014:A:H5’	19:AS:14:HIS:CD2	2.44	0.53
1:AA:1160:G:OP1	2:AB:131:LYS:HE3	2.09	0.53
1:AA:1230:C:OP1	23:AW:30:C:C4’	2.55	0.53
12:AL:34:CYS:HA	12:AL:55:VAL:HA	1.89	0.53
23:AW:37:A:C2	24:AX:8:A:C6	2.97	0.53
28:BA:396:G:OP2	49:BX:9:LYS:NZ	2.40	0.53
28:BA:1263:U:OP1	52:B0:12:ARG:NH1	2.41	0.53
28:BA:2425:A:H5”	28:BA:2427:C:O4’	2.09	0.53
28:BA:2526:G:N3	56:B4:1:MET:N	2.57	0.53
29:BD:120:GLY:HA2	29:BD:162:ALA:CB	2.38	0.53
42:BQ:63:ARG:HH12	42:BQ:96:ASP:CA	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BQ:81:GLY:HA2	42:BQ:116:LEU:CD1	2.38	0.53
56:B4:3:VAL:HG23	56:B4:4:ARG:H	1.74	0.53
1:AA:18:C:C3'	5:AE:132:ASN:HD22	2.21	0.53
1:AA:918:A:N6	1:AA:919:A:N1	2.57	0.53
1:AA:1457:G:OP1	20:AT:34:LYS:NZ	2.35	0.53
26:BB:55:U:O3'	31:BF:23:SER:OG	2.21	0.53
28:BA:273:G:N2	28:BA:365:U:C2	2.77	0.53
28:BA:954:G:OP2	38:BM:16:ARG:NH2	2.42	0.53
28:BA:1394:U:H4'	28:BA:1603:A:H4'	1.91	0.53
28:BA:1779:U:H5	28:BA:1784:A:N7	2.06	0.53
36:BK:10:VAL:HG11	36:BK:16:ALA:HB3	1.90	0.53
45:BT:50:LEU:C	45:BT:52:GLU:H	2.11	0.53
48:BW:37:VAL:HG13	48:BW:55:ASP:C	2.29	0.53
1:AA:16:A:C1'	5:AE:22:SER:H	2.23	0.52
1:AA:1074:G:C5	1:AA:1075:U:O4	2.62	0.52
12:AL:68:GLY:O	12:AL:99:ARG:NH1	2.40	0.52
13:AM:56:LEU:O	13:AM:59:GLU:N	2.38	0.52
41:BP:33:GLU:CD	41:BP:34:GLY:N	2.63	0.52
1:AA:927:G:P	1:AA:1503:A:N1	2.82	0.52
2:AB:14:HIS:O	2:AB:14:HIS:ND1	2.42	0.52
8:AH:106:THR:HG22	8:AH:107:SER:N	2.25	0.52
18:AR:32:TYR:CG	18:AR:55:LEU:HD21	2.44	0.52
28:BA:2090:A:C6	28:BA:2091:C:C4	2.97	0.52
29:BD:12:THR:OG1	41:BP:8:GLU:OE2	2.21	0.52
32:BG:84:LYS:HB3	32:BG:132:LEU:O	2.09	0.52
35:BJ:55:ILE:HD11	35:BJ:130:HIS:CG	2.44	0.52
39:BN:73:ASN:HA	39:BN:76:VAL:CG1	2.39	0.52
43:BR:49:ILE:HB	43:BR:51:VAL:O	2.08	0.52
1:AA:20:U:H2'	1:AA:21:G:C5'	2.15	0.52
1:AA:81:A:H2'	1:AA:82:G:H5"	1.91	0.52
1:AA:1533:C:H2'	1:AA:1533:C:O2	2.08	0.52
23:AW:64:G:H2'	23:AW:65:U:C6	2.44	0.52
25:AY:270:PHE:N	60:AY:802:GDP:C6	2.78	0.52
25:AY:603:GLU:OE2	25:AY:607:LYS:NZ	2.38	0.52
27:BC:256:THR:OG1	27:BC:256:THR:O	2.28	0.52
28:BA:38:A:O2'	30:BE:43:THR:HA	2.09	0.52
28:BA:1069:A:C5	28:BA:1073:A:N7	2.77	0.52
28:BA:2211:A:O2'	28:BA:2212:A:OP1	2.25	0.52
35:BJ:39:LYS:HA	35:BJ:43:GLU:HB2	1.91	0.52
57:B5:81:LEU:HD23	57:B5:82:ILE:N	2.24	0.52
1:AA:1059:C:O2	10:AJ:55:PRO:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:94:ARG:NH1	2:AB:95:TRP:O	2.43	0.52
8:AH:125:ILE:HD11	8:AH:128:TYR:CE1	2.44	0.52
11:AK:21:ALA:HB2	11:AK:82:LEU:CD1	2.40	0.52
25:AY:382:ILE:HD12	25:AY:382:ILE:O	2.09	0.52
28:BA:2232:C:P	49:BX:26:ARG:HH22	2.33	0.52
28:BA:2354:C:H4'	48:BW:31:LEU:HD22	1.92	0.52
40:BO:36:TYR:N	40:BO:36:TYR:CD1	2.78	0.52
41:BP:4:ILE:HG22	41:BP:5:LYS:H	1.72	0.52
48:BW:63:ASP:OD1	48:BW:63:ASP:N	2.35	0.52
1:AA:404:G:O2'	1:AA:498:A:N1	2.40	0.52
1:AA:1249:C:O3'	9:AI:75:GLN:NE2	2.43	0.52
1:AA:1331:G:HO2'	1:AA:1332:A:P	2.31	0.52
1:AA:1392:G:C3'	1:AA:1393:U:H5'	2.35	0.52
25:AY:104:ARG:NH2	25:AY:407:GLU:HB3	2.25	0.52
28:BA:1288:G:C4	28:BA:1327:A:C2	2.98	0.52
28:BA:2197:U:O2'	33:BH:29:PHE:CZ	2.62	0.52
42:BQ:31:TYR:O	42:BQ:34:ALA:N	2.43	0.52
1:AA:922:G:N2	1:AA:1395:C:C2	2.70	0.52
1:AA:1053:G:HO2'	1:AA:1199:U:H5	1.57	0.52
1:AA:1079:G:C5'	5:AE:50:TYR:OH	2.51	0.52
1:AA:1113:C:H4'	3:AC:14:ILE:HD13	1.91	0.52
8:AH:106:THR:HG21	8:AH:121:LEU:HD22	1.92	0.52
22:AV:35:A:O2'	22:AV:36:C:H5'	2.09	0.52
28:BA:1187:G:H5"	43:BR:83:TYR:CE2	2.43	0.52
28:BA:2867:G:O2'	28:BA:2868:A:OP2	2.28	0.52
1:AA:1072:G:OP1	5:AE:54:ARG:HG3	2.10	0.52
1:AA:1076:U:O2'	1:AA:1077:G:C4'	2.57	0.52
1:AA:1279:G:H2'	1:AA:1279:G:N3	2.23	0.52
9:AI:52:LEU:HB3	9:AI:57:MET:HB3	1.92	0.52
23:AW:14:A:H2'	23:AW:15:G:O4'	2.09	0.52
23:AW:76:A:C6	28:BA:2422:C:C6	2.98	0.52
28:BA:398:C:H5"	28:BA:2090:A:O4'	2.10	0.52
51:BZ:6:ILE:O	51:BZ:34:THR:HA	2.10	0.52
57:B5:36:ASP:O	57:B5:39:THR:OG1	2.26	0.52
1:AA:958:A:P	19:AS:55:ARG:HH12	2.31	0.52
12:AL:43:LYS:HG2	12:AL:44:LYS:HG3	1.90	0.52
28:BA:1203:U:O2'	37:BL:4:ASN:OD1	2.28	0.52
28:BA:2016:U:H1'	52:B0:2:VAL:CG1	2.40	0.52
38:BM:73:ILE:HG21	38:BM:91:TYR:CZ	2.45	0.52
1:AA:1309:G:C6	1:AA:1310:G:C5	2.98	0.52
1:AA:1393:U:O2'	1:AA:1502:A:C5'	2.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:150:PRO:HA	5:AE:153:VAL:HG13	1.90	0.52
6:AF:68:GLN:HA	6:AF:71:ILE:HG22	1.91	0.52
11:AK:125:LYS:O	21:AU:34:ARG:NE	2.41	0.52
12:AL:24:LEU:O	12:AL:26:ALA:N	2.42	0.52
25:AY:95:PHE:CE2	59:AY:801:FUA:H231	2.45	0.52
35:BJ:39:LYS:HA	35:BJ:43:GLU:HG3	1.91	0.52
57:B5:94:ARG:O	57:B5:97:LYS:N	2.43	0.52
57:B5:118:ILE:HB	57:B5:119:PRO:CD	2.40	0.52
1:AA:1075:U:O4’	1:AA:1101:A:C2	2.63	0.52
1:AA:1249:C:O2’	9:AI:71:GLY:C	2.49	0.52
1:AA:1391:U:O2’	1:AA:1532:U:OP1	2.18	0.52
3:AC:77:ILE:HA	3:AC:84:VAL:HG23	1.91	0.52
4:AD:107:PHE:N	4:AD:107:PHE:CD1	2.76	0.52
6:AF:63:ASN:ND2	6:AF:96:VAL:HG22	2.25	0.52
11:AK:16:VAL:CG1	11:AK:79:ILE:HG12	2.40	0.52
29:BD:62:LYS:HB2	29:BD:63:PRO:HD3	1.92	0.52
45:BT:50:LEU:HD12	45:BT:50:LEU:H	1.74	0.52
48:BW:8:SER:O	48:BW:9:THR:HG22	2.10	0.52
1:AA:15:G:C4’	5:AE:29:ARG:CZ	2.87	0.51
1:AA:1077:G:O6	5:AE:52:LYS:HD3	2.10	0.51
14:AN:90:ARG:HB2	14:AN:92:GLU:HG3	1.93	0.51
27:BC:61:TYR:CE2	28:BA:1816:C:C5	2.99	0.51
28:BA:945:A:C5	28:BA:2448:A:C2	2.98	0.51
28:BA:2053:G:H1	28:BA:2616:C:H42	1.57	0.51
36:BK:13:ASN:O	36:BK:15:GLY:N	2.43	0.51
37:BL:91:ASP:OD1	37:BL:92:LEU:N	2.43	0.51
1:AA:1007:U:C2’	1:AA:1008:U:H5’	2.41	0.51
1:AA:1442:G:C4’	41:BP:113:LEU:CD1	2.80	0.51
2:AB:86:CYS:HB2	2:AB:88:GLN:NE2	2.25	0.51
12:AL:44:LYS:HB2	12:AL:45:PRO:HD3	1.92	0.51
22:AV:74:C:N3	28:BA:2252:G:C6	2.77	0.51
27:BC:255:LYS:O	27:BC:257:ARG:N	2.43	0.51
28:BA:2313:C:H5”	31:BF:87:LYS:HD3	1.92	0.51
28:BA:2502:G:H5’	28:BA:2503:A:H5”	1.92	0.51
36:BK:19:VAL:CG1	36:BK:41:ILE:HG12	2.40	0.51
48:BW:16:GLU:O	48:BW:17:ALA:HB3	2.10	0.51
1:AA:690:G:H2’	1:AA:691:G:O4’	2.10	0.51
22:AV:36:C:C5’	25:AY:513:GLY:CA	2.73	0.51
23:AW:69:A:H2’	23:AW:70:G:H8	1.75	0.51
24:AX:3:U:H3’	24:AX:4:A:C8	2.45	0.51
28:BA:565:C:H2’	28:BA:566:U:O4’	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:856:G:H21	48:BW:19:ARG:HH12	1.58	0.51
43:BR:39:LEU:HA	43:BR:49:ILE:HG21	1.92	0.51
1:AA:815:A:N7	1:AA:1509:C:O2'	2.37	0.51
1:AA:1191:A:OP2	3:AC:3:GLN:NE2	2.43	0.51
11:AK:81:ASN:HB3	11:AK:106:ARG:HB3	1.92	0.51
14:AN:54:ASP:OD1	14:AN:59:ARG:NH1	2.43	0.51
21:AU:39:GLU:OE1	21:AU:42:THR:OG1	2.26	0.51
28:BA:489:G:N7	44:BS:49:LYS:NZ	2.58	0.51
29:BD:91:THR:O	29:BD:91:THR:OG1	2.28	0.51
32:BG:83:THR:HA	32:BG:84:LYS:CE	2.39	0.51
35:BJ:81:ILE:CG1	35:BJ:82:GLY:N	2.74	0.51
38:BM:53:MET:HE3	38:BM:63:ILE:HD13	1.93	0.51
42:BQ:65:ASN:OD1	42:BQ:69:ARG:NH2	2.42	0.51
1:AA:114:U:O2'	1:AA:115:G:H5'	2.10	0.51
1:AA:1083:U:C5	1:AA:1084:G:C4	2.98	0.51
1:AA:1250:A:H4'	9:AI:70:GLY:O	2.10	0.51
9:AI:84:THR:HG21	9:AI:103:PHE:HB3	1.92	0.51
24:AX:14:A:C8	24:AX:14:A:OP2	2.63	0.51
28:BA:1328:A:H2'	28:BA:1330:C:C5	2.45	0.51
28:BA:2803:G:H2'	28:BA:2804:U:C6	2.45	0.51
47:BV:51:GLN:OE1	47:BV:57:TYR:OH	2.28	0.51
51:BZ:48:ASN:O	51:BZ:51:SER:OG	2.27	0.51
1:AA:1081:A:C2	1:AA:1082:A:C4	2.98	0.51
1:AA:1250:A:H4'	9:AI:70:GLY:N	2.25	0.51
22:AV:73:A:O3'	22:AV:74:C:H6	1.94	0.51
24:AX:14:A:C2'	24:AX:15:A:O5'	2.55	0.51
25:AY:217:GLU:O	25:AY:220:GLN:N	2.43	0.51
28:BA:750:A:OP1	28:BA:1615:C:N4	2.40	0.51
40:BO:31:THR:HG22	40:BO:34:HIS:H	1.74	0.51
44:BS:20:VAL:HG11	44:BS:44:ALA:HA	1.93	0.51
57:B5:25:ALA:O	57:B5:116:GLU:OE1	2.28	0.51
1:AA:1040:U:H2'	1:AA:1041:G:C8	2.45	0.51
1:AA:1130:A:C5'	9:AI:20:PHE:CE2	2.94	0.51
3:AC:14:ILE:O	3:AC:15:VAL:HG22	2.10	0.51
6:AF:38:ARG:NH1	6:AF:63:ASN:OD1	2.44	0.51
7:AG:15:ASP:OD1	7:AG:44:TYR:OH	2.22	0.51
22:AV:11:A:O2'	28:BA:1909:C:H4'	2.11	0.51
28:BA:460:A:C2	28:BA:470:A:C4	2.99	0.51
28:BA:1300:G:H4'	28:BA:1301:A:H5'	1.92	0.51
28:BA:2387:U:O2'	48:BW:38:ARG:NH2	2.43	0.51
30:BE:148:ILE:HA	30:BE:187:VAL:HB	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:918:A:C5	1:AA:919:A:C5	2.98	0.51
1:AA:1181:G:O2'	1:AA:1182:G:N7	2.40	0.51
2:AB:153:MET:O	2:AB:155:GLY:N	2.44	0.51
14:AN:27:LEU:C	14:AN:31:ILE:HD13	2.30	0.51
28:BA:748:G:P	44:BS:88:ARG:NH2	2.83	0.51
28:BA:2314:A:OP1	31:BF:87:LYS:NZ	2.44	0.51
31:BF:132:ARG:O	31:BF:133:GLU:HB3	2.10	0.51
34:BI:36:GLU:HB3	34:BI:66:PHE:CE1	2.46	0.51
34:BI:116:MET:SD	34:BI:124:MET:HE2	2.51	0.51
45:BT:69:ARG:CG	45:BT:70:HIS:H	2.23	0.51
47:BV:9:ARG:NH2	47:BV:12:GLN:HA	2.26	0.51
53:B1:33:LEU:N	53:B1:51:ALA:HB3	2.25	0.51
57:B5:3:LEU:HD12	57:B5:5:LEU:H	1.76	0.51
1:AA:16:A:O4'	5:AE:22:SER:HB3	2.11	0.51
1:AA:1014:A:C2	19:AS:34:TRP:CE2	2.99	0.51
1:AA:1240:U:O2	7:AG:32:VAL:HG12	2.11	0.51
1:AA:1498:U:OP2	24:AX:11:G:O4'	2.29	0.51
22:AV:21:A:N6	22:AV:46:G:H2'	2.05	0.51
27:BC:256:THR:CG2	28:BA:1797:G:O2'	2.59	0.51
28:BA:2039:U:H2'	28:BA:2040:G:C8	2.45	0.51
34:BI:109:ALA:HB2	34:BI:128:ILE:HG13	1.93	0.51
1:AA:17:U:O4'	1:AA:1079:G:H1'	2.10	0.51
1:AA:21:G:N1	1:AA:22:G:C6	2.79	0.51
1:AA:1074:G:C4	1:AA:1075:U:C4	2.96	0.51
1:AA:1118:U:P	9:AI:106:ARG:HD2	2.51	0.51
5:AE:153:VAL:O	5:AE:157:ARG:N	2.44	0.51
22:AV:39:C:H2'	22:AV:40:C:H6	1.76	0.51
22:AV:52:G:C2	22:AV:53:G:C8	2.99	0.51
28:BA:2074:U:H2'	28:BA:2075:U:C6	2.46	0.51
29:BD:193:VAL:HG21	29:BD:201:LEU:HD21	1.93	0.51
38:BM:35:ALA:O	38:BM:36:VAL:HB	2.11	0.51
1:AA:1273:C:H2'	1:AA:1274:A:O4'	2.11	0.50
1:AA:1394:A:N3	1:AA:1501:C:H1'	2.25	0.50
3:AC:164:ARG:NH1	3:AC:166:GLU:OE1	2.44	0.50
9:AI:129:LYS:HZ2	23:AW:31:A:P	2.32	0.50
39:BN:96:ARG:NH2	39:BN:114:GLU:OE1	2.44	0.50
46:BU:82:VAL:HG12	46:BU:83:GLY:N	2.25	0.50
48:BW:76:ARG:HH21	48:BW:76:ARG:HG2	1.76	0.50
1:AA:673:A:H4'	6:AF:86:ARG:HD2	1.93	0.50
1:AA:1083:U:O4	1:AA:1084:G:N1	2.43	0.50
19:AS:63:THR:HG22	19:AS:64:ASP:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AV:9:G:O2'	22:AV:10:G:N7	2.44	0.50
25:AY:191:ILE:HG23	25:AY:202:PHE:CE1	2.46	0.50
28:BA:391:A:C6	28:BA:411:G:C2	3.00	0.50
28:BA:654:A:H3'	28:BA:654:A:N3	2.26	0.50
32:BG:16:VAL:HG21	32:BG:44:HIS:CD2	2.46	0.50
45:BT:54:GLU:CG	45:BT:88:LYS:HB2	2.42	0.50
51:BZ:30:ARG:HB3	51:BZ:30:ARG:HH11	1.76	0.50
1:AA:828:U:O2	2:AB:24:PRO:CB	2.50	0.50
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.12	0.50
1:AA:1216:A:OP1	14:AN:5:SER:OG	2.25	0.50
1:AA:1346:A:C5'	9:AI:122:ARG:HH12	2.18	0.50
17:AQ:47:HIS:HB2	17:AQ:71:LYS:HE2	1.94	0.50
25:AY:507:LYS:HZ3	28:BA:1913:A:H62	1.56	0.50
25:AY:536:PHE:CZ	25:AY:578:LEU:HD23	2.47	0.50
28:BA:26:G:C6	28:BA:27:G:N1	2.79	0.50
28:BA:911:A:C4	38:BM:8:LYS:HE3	2.33	0.50
28:BA:1179:G:H2'	28:BA:1180:U:O4'	2.12	0.50
28:BA:1533:C:C2	28:BA:1534:U:C4	2.99	0.50
28:BA:1869:G:H3'	28:BA:1870:C:H5"	1.94	0.50
1:AA:530:G:O6	24:AX:16:A:C4'	2.59	0.50
1:AA:840:C:N4	1:AA:842:U:O2'	2.44	0.50
1:AA:947:G:C6	1:AA:948:C:C4	3.00	0.50
16:AP:44:SER:O	16:AP:46:LYS:N	2.44	0.50
28:BA:27:G:N2	28:BA:512:G:H1'	2.26	0.50
43:BR:61:ALA:HB2	43:BR:98:ILE:HA	1.92	0.50
53:B1:4:ILE:HG23	53:B1:5:ARG:H	1.77	0.50
54:B2:34:ARG:NH1	54:B2:41:ARG:O	2.45	0.50
1:AA:16:A:O4'	5:AE:22:SER:N	2.45	0.50
1:AA:21:G:C6	1:AA:22:G:C6	2.99	0.50
1:AA:1014:A:H5"	19:AS:14:HIS:CB	2.41	0.50
1:AA:1203:C:H5'	14:AN:67:THR:HB	1.93	0.50
8:AH:41:LYS:HD3	8:AH:48:ASP:HB2	1.94	0.50
23:AW:23:A:H2'	23:AW:24:G:H8	1.75	0.50
25:AY:95:PHE:CZ	25:AY:464:LEU:HD22	2.47	0.50
28:BA:974:G:H8	28:BA:990:A:H62	1.58	0.50
28:BA:2093:G:N2	28:BA:2196:C:O2	2.41	0.50
37:BL:81:ASP:O	37:BL:83:ALA:N	2.41	0.50
54:B2:27:GLY:O	54:B2:30:VAL:HB	2.11	0.50
1:AA:142:G:H3'	1:AA:143:A:H8	1.77	0.50
1:AA:177:G:OP2	20:AT:64:LYS:NZ	2.44	0.50
1:AA:1119:C:OP1	9:AI:85:ARG:NH1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1159:U:P	2:AB:131:LYS:NZ	2.85	0.50
1:AA:1193:G:O2'	5:AE:26:LYS:HE3	2.11	0.50
1:AA:1372:U:O2'	7:AG:34:GLY:O	2.16	0.50
25:AY:23:LYS:C	60:AY:802:GDP:O2B	2.50	0.50
28:BA:2352:A:C6	48:BW:30:VAL:HG11	2.47	0.50
31:BF:71:LYS:HD3	31:BF:72:SER:N	2.26	0.50
33:BH:41:LYS:HA	33:BH:44:ILE:HG12	1.93	0.50
34:BI:87:SER:OG	34:BI:88:GLY:N	2.43	0.50
38:BM:20:LEU:HD22	38:BM:20:LEU:N	2.26	0.50
49:BX:70:LEU:O	49:BX:75:GLU:N	2.45	0.50
1:AA:15:G:O2'	5:AE:22:SER:HB2	2.10	0.50
1:AA:1074:G:C4	1:AA:1075:U:C6	3.00	0.50
1:AA:1075:U:O4	1:AA:1076:U:O4	2.30	0.50
4:AD:26:ARG:C	4:AD:26:ARG:HD3	2.32	0.50
9:AI:89:GLU:OE1	9:AI:90:TYR:CD1	2.65	0.50
28:BA:223:A:C5	28:BA:422:A:C8	3.00	0.50
28:BA:2196:C:O2	28:BA:2197:U:C2	2.64	0.50
28:BA:2211:A:O2'	28:BA:2212:A:P	2.70	0.50
32:BG:30:GLY:O	32:BG:32:LEU:N	2.38	0.50
32:BG:96:ALA:HB3	32:BG:103:ASN:HB2	1.93	0.50
57:B5:95:LEU:H	57:B5:95:LEU:HD22	1.77	0.50
1:AA:16:A:O2'	5:AE:21:VAL:HG12	2.12	0.50
1:AA:18:C:H2'	1:AA:19:A:H8	1.77	0.50
1:AA:79:G:HO2'	1:AA:80:A:P	2.34	0.50
1:AA:410:G:OP1	4:AD:26:ARG:NH1	2.39	0.50
1:AA:927:G:C1'	1:AA:1532:U:H4'	2.31	0.50
1:AA:1074:G:N1	1:AA:1075:U:N3	2.59	0.50
1:AA:1130:A:H4'	9:AI:20:PHE:CD2	2.47	0.50
1:AA:1526:G:OP1	21:AU:39:GLU:CG	2.60	0.50
1:AA:1530:G:C4	1:AA:1531:A:C6	3.00	0.50
13:AM:4:ILE:O	13:AM:6:GLY:N	2.44	0.50
28:BA:221:A:N1	28:BA:265:A:O2'	2.45	0.50
28:BA:1199:U:H5'	42:BQ:4:LYS:CE	2.42	0.50
28:BA:1533:C:H2'	28:BA:1534:U:C6	2.46	0.50
34:BI:48:ILE:HG13	34:BI:49:GLU:H	1.77	0.50
35:BJ:21:THR:HG22	35:BJ:22:GLY:N	2.27	0.50
35:BJ:44:TYR:O	35:BJ:45:THR:HB	2.11	0.50
39:BN:52:ILE:HB	39:BN:94:TYR:CD2	2.46	0.50
42:BQ:94:LEU:C	42:BQ:96:ASP:N	2.65	0.50
44:BS:86:MET:HB2	44:BS:96:ILE:HG21	1.92	0.50
51:BZ:26:LEU:O	51:BZ:37:ARG:NH1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:409:U:OP1	4:AD:24:GLY:HA3	2.11	0.50
1:AA:1057:G:H4'	3:AC:195:VAL:HG12	1.92	0.50
12:AL:83:ARG:HG2	12:AL:83:ARG:HH11	1.77	0.50
28:BA:1730:C:H4'	28:BA:1730:C:OP1	2.12	0.50
28:BA:2329:U:H2'	28:BA:2330:G:C8	2.47	0.50
29:BD:148:GLN:OE1	29:BD:148:GLN:N	2.45	0.50
42:BQ:91:ARG:HE	42:BQ:93:ILE:CG2	2.25	0.50
57:B5:138:ARG:NH2	58:B6:26:MET:HA	2.27	0.50
1:AA:158:G:H2'	1:AA:159:G:C5'	2.42	0.49
1:AA:918:A:H2'	1:AA:919:A:C8	2.47	0.49
1:AA:999:C:H42	1:AA:1041:G:H1	1.59	0.49
1:AA:1240:U:OP2	7:AG:116:MET:HB3	2.12	0.49
1:AA:1498:U:C4	24:AX:12:U:P	3.05	0.49
22:AV:29:G:C6	22:AV:30:G:N7	2.79	0.49
22:AV:34:U:H3	24:AX:13:A:H2	1.44	0.49
23:AW:76:A:OP1	28:BA:2432:A:H4'	2.12	0.49
25:AY:270:PHE:HB2	60:AY:802:GDP:C5	2.42	0.49
28:BA:1022:G:C5	28:BA:1140:C:C4	3.00	0.49
28:BA:1437:C:H2'	28:BA:1438:U:C6	2.46	0.49
28:BA:2195:U:H2'	28:BA:2196:C:C5'	2.27	0.49
29:BD:151:THR:HG22	29:BD:152:PRO:HD3	1.93	0.49
30:BE:112:LEU:HD13	30:BE:186:VAL:HG11	1.94	0.49
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.46	0.49
1:AA:1111:A:N6	3:AC:176:HIS:HB3	2.27	0.49
2:AB:44:LYS:O	2:AB:48:MET:HG2	2.13	0.49
5:AE:155:ALA:HB1	8:AH:66:PHE:CE2	2.47	0.49
6:AF:98:GLU:CG	6:AF:99:ALA:N	2.72	0.49
9:AI:88:MET:SD	9:AI:89:GLU:N	2.86	0.49
37:BL:19:LEU:HB2	37:BL:27:LEU:HB3	1.94	0.49
42:BQ:63:ARG:NH1	42:BQ:96:ASP:HA	2.27	0.49
44:BS:13:SER:O	44:BS:14:ALA:CB	2.60	0.49
1:AA:14:U:O5'	1:AA:14:U:H6	1.96	0.49
1:AA:320:A:H2'	1:AA:321:A:O4'	2.12	0.49
1:AA:1291:U:H4'	9:AI:42:GLU:HG3	1.93	0.49
2:AB:163:ILE:HG23	2:AB:164:ASP:H	1.78	0.49
19:AS:33:THR:HB	19:AS:35:SER:H	1.77	0.49
22:AV:28:C:H2'	22:AV:29:G:C8	2.47	0.49
28:BA:322:A:H5'	28:BA:340:A:H1'	1.94	0.49
28:BA:443:A:C5	30:BE:40:ARG:HD3	2.47	0.49
28:BA:1084:A:H5'	57:B5:55:VAL:HG13	1.93	0.49
28:BA:1475:G:O2'	28:BA:1514:G:O6	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BF:10:GLU:O	31:BF:12:VAL:N	2.44	0.49
43:BR:49:ILE:HD12	43:BR:52:PRO:HA	1.95	0.49
1:AA:390:U:O3'	16:AP:28:ARG:NH1	2.45	0.49
1:AA:1092:A:OP2	7:AG:4:ARG:NH1	2.46	0.49
5:AE:46:VAL:O	5:AE:72:ILE:N	2.39	0.49
23:AW:28:A:N1	23:AW:42:U:O4	2.45	0.49
23:AW:66:C:H2'	23:AW:67:G:C8	2.48	0.49
24:AX:11:G:H2'	24:AX:12:U:C6	2.48	0.49
28:BA:973:A:P	43:BR:81:LYS:HZ3	2.36	0.49
28:BA:1474:U:H2'	28:BA:1475:G:H5'	1.95	0.49
28:BA:2701:U:H3'	28:BA:2702:G:C5'	2.42	0.49
34:BI:123:ALA:HA	34:BI:126:ARG:CZ	2.43	0.49
41:BP:91:VAL:O	41:BP:92:ARG:HG2	2.12	0.49
48:BW:49:ASN:HA	48:BW:61:LYS:HB2	1.94	0.49
56:B4:7:VAL:O	56:B4:35:GLN:NE2	2.42	0.49
1:AA:15:G:N2	1:AA:1080:A:H4'	2.26	0.49
1:AA:1468:A:H2'	1:AA:1469:C:C5'	2.40	0.49
2:AB:187:ASP:OD1	2:AB:188:THR:N	2.39	0.49
4:AD:58:LYS:CB	4:AD:200:ILE:HG13	2.42	0.49
8:AH:12:THR:HG22	8:AH:15:ARG:HH12	1.76	0.49
28:BA:564:C:O2	28:BA:578:G:N2	2.46	0.49
28:BA:1607:C:H4'	28:BA:1608:A:O5'	2.13	0.49
29:BD:68:PHE:C	29:BD:73:VAL:HG12	2.33	0.49
30:BE:32:VAL:HG23	30:BE:178:VAL:HG12	1.95	0.49
44:BS:24:ILE:HG22	44:BS:71:VAL:HG11	1.95	0.49
1:AA:953:G:C6	1:AA:954:G:C4	3.00	0.49
4:AD:147:GLU:HA	4:AD:150:LYS:HB2	1.94	0.49
7:AG:63:GLU:OE1	7:AG:70:ARG:NH2	2.45	0.49
24:AX:10:G:O5'	24:AX:11:G:OP1	2.30	0.49
28:BA:139:U:O2'	45:BT:1:MET:HA	2.12	0.49
28:BA:1808:A:O2'	49:BX:2:ARG:NH1	2.45	0.49
36:BK:9:ASN:O	36:BK:83:ALA:HA	2.11	0.49
42:BQ:94:LEU:C	42:BQ:96:ASP:H	2.14	0.49
1:AA:701:U:H5"	1:AA:703:G:O4'	2.11	0.49
1:AA:983:A:C2'	1:AA:983:A:N3	2.76	0.49
2:AB:100:LEU:HD23	2:AB:178:LEU:HD23	1.95	0.49
14:AN:20:TYR:O	14:AN:23:LYS:HB3	2.12	0.49
25:AY:191:ILE:HG21	25:AY:193:TRP:CZ2	2.47	0.49
28:BA:1614:A:N1	44:BS:93:ALA:HB2	2.27	0.49
28:BA:1778:U:H2'	28:BA:1784:A:N6	2.27	0.49
28:BA:2016:U:H2'	28:BA:2017:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BF:79:ARG:HB3	31:BF:82:TYR:CZ	2.48	0.49
34:BI:135:MET:HB3	34:BI:137:LEU:CD2	2.43	0.49
1:AA:1074:G:C6	1:AA:1075:U:N3	2.81	0.49
1:AA:1084:G:OP1	1:AA:1086:U:C2	2.66	0.49
1:AA:1530:G:N3	1:AA:1531:A:N7	2.60	0.49
9:AI:6:TYR:CG	9:AI:89:GLU:HB2	2.48	0.49
10:AJ:71:LEU:O	10:AJ:72:ARG:NH1	2.39	0.49
22:AV:35:A:N1	24:AX:13:A:C5	2.81	0.49
24:AX:8:A:C3'	24:AX:9:U:H5'	2.36	0.49
28:BA:748:G:OP1	44:BS:88:ARG:NH2	2.44	0.49
28:BA:1031:G:H4'	56:B4:6:SER:HB2	1.95	0.49
28:BA:1327:A:N6	28:BA:1328:A:C2	2.81	0.49
28:BA:2015:A:C2	52:B0:2:VAL:CG2	2.96	0.49
28:BA:2571:U:O2'	29:BD:151:THR:CG2	2.60	0.49
32:BG:15:ASP:O	32:BG:16:VAL:HG13	2.12	0.49
57:B5:4:ASN:C	57:B5:6:GLN:H	2.16	0.49
57:B5:68:PRO:HA	57:B5:72:LEU:HD11	1.94	0.49
1:AA:15:G:C2'	5:AE:22:SER:CB	2.90	0.49
1:AA:1067:A:N1	1:AA:1108:G:O2'	2.39	0.49
1:AA:1392:G:C2'	1:AA:1393:U:C5'	2.60	0.49
9:AI:55:VAL:HG11	9:AI:94:LEU:HD23	1.95	0.49
19:AS:22:ALA:HA	19:AS:25:SER:HB3	1.95	0.49
28:BA:308:G:O2'	28:BA:329:G:N2	2.46	0.49
28:BA:923:G:H1'	48:BW:23:LYS:CD	2.43	0.49
28:BA:2330:G:C2	28:BA:2386:A:C2	3.01	0.49
28:BA:2504:U:H6	28:BA:2504:U:O5'	1.94	0.49
41:BP:105:LYS:HA	41:BP:108:ARG:HD2	1.95	0.49
57:B5:4:ASN:C	57:B5:6:GLN:N	2.66	0.49
1:AA:921:U:H5"	1:AA:1082:A:H5'	1.94	0.49
1:AA:928:G:C3'	1:AA:1533:C:H5	2.25	0.49
1:AA:949:A:N7	13:AM:105:ASN:ND2	2.60	0.49
1:AA:1305:G:H22	1:AA:1331:G:C2'	2.26	0.49
4:AD:4:TYR:CZ	4:AD:11:LEU:HD11	2.48	0.49
25:AY:416:ILE:HG12	25:AY:667:ALA:HB3	1.94	0.49
28:BA:592:A:HO2'	55:B3:63:TYR:HH	1.59	0.49
28:BA:2197:U:O2'	33:BH:29:PHE:CE2	2.66	0.49
28:BA:2421:G:N7	55:B3:30:HIS:HD2	2.10	0.49
46:BU:85:ARG:HD3	46:BU:86:PHE:N	2.28	0.49
48:BW:39:GLN:HG2	48:BW:40:ARG:N	2.28	0.49
1:AA:455:G:C2	1:AA:478:A:C2	3.00	0.48
6:AF:38:ARG:HG2	6:AF:63:ASN:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AS:10:PHE:CD1	19:AS:10:PHE:C	2.85	0.48
21:AU:34:ARG:CZ	21:AU:35:ARG:HD2	2.43	0.48
28:BA:118:A:N3	28:BA:178:G:H1'	2.27	0.48
28:BA:1022:G:C6	28:BA:1140:C:C4	3.01	0.48
28:BA:2109:U:H2'	28:BA:2110:G:H5'	1.94	0.48
28:BA:2346:A:H3'	28:BA:2347:C:H5"	1.96	0.48
28:BA:2393:U:H5'	37:BL:60:ARG:O	2.13	0.48
28:BA:2683:C:O2	36:BK:70:ARG:NH2	2.38	0.48
29:BD:151:THR:CG2	29:BD:152:PRO:HD3	2.43	0.48
47:BV:44:HIS:HE1	47:BV:86:LEU:H	1.59	0.48
49:BX:70:LEU:O	49:BX:74:GLY:N	2.46	0.48
51:BZ:41:PRO:HA	51:BZ:44:ARG:HB3	1.93	0.48
57:B5:51:TYR:CD1	57:B5:51:TYR:C	2.86	0.48
1:AA:1148:U:OP1	9:AI:9:THR:OG1	2.31	0.48
1:AA:1249:C:O2'	9:AI:71:GLY:CA	2.61	0.48
2:AB:99:MET:HA	2:AB:106:VAL:HG21	1.94	0.48
10:AJ:15:HIS:C	10:AJ:17:LEU:H	2.16	0.48
11:AK:16:VAL:HG13	11:AK:79:ILE:HG12	1.96	0.48
21:AU:38:TYR:C	21:AU:41:PRO:HD2	2.34	0.48
25:AY:584:HIS:HB2	25:AY:587:ASP:HB2	1.94	0.48
28:BA:301:G:H1'	28:BA:302:C:C6	2.48	0.48
28:BA:770:G:H5"	54:B2:10:LEU:HD23	1.95	0.48
28:BA:1107:G:H5"	57:B5:58:THR:HG23	1.94	0.48
28:BA:1654:A:H2'	28:BA:1655:A:H8	1.77	0.48
34:BI:120:ASP:O	34:BI:123:ALA:N	2.46	0.48
38:BM:34:LYS:HD2	38:BM:131:VAL:HG11	1.95	0.48
50:BY:8:GLU:O	50:BY:12:GLU:HB2	2.12	0.48
51:BZ:38:GLU:O	51:BZ:43:ILE:HG12	2.13	0.48
57:B5:39:THR:HA	57:B5:42:ARG:CD	2.43	0.48
1:AA:13:U:O2	1:AA:914:A:H3'	2.13	0.48
1:AA:971:G:O6	1:AA:1364:U:O2'	2.26	0.48
2:AB:70:GLY:HA2	2:AB:163:ILE:HG22	1.94	0.48
8:AH:18:GLN:NE2	8:AH:72:VAL:H	2.12	0.48
22:AV:3:C:N4	22:AV:70:G:H1	2.11	0.48
22:AV:35:A:H61	24:AX:13:A:N6	2.05	0.48
22:AV:57:A:H5"	31:BF:74:ALA:CB	2.33	0.48
28:BA:995:C:O2	35:BJ:3:THR:HG23	2.13	0.48
28:BA:2347:C:HO2'	53:B1:20:TYR:HH	1.55	0.48
36:BK:24:VAL:HG13	36:BK:33:ALA:HB2	1.95	0.48
1:AA:1010:U:H2'	1:AA:1011:C:C6	2.48	0.48
14:AN:42:TRP:O	14:AN:45:VAL:HG22	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AX:11:G:H2'	24:AX:12:U:H6	1.78	0.48
25:AY:200:VAL:HG23	25:AY:201:THR:N	2.28	0.48
25:AY:230:SER:OG	25:AY:232:GLU:OE1	2.31	0.48
28:BA:250:G:C6	28:BA:251:A:C6	3.01	0.48
28:BA:856:G:O2'	48:BW:22:VAL:HG23	2.14	0.48
28:BA:2197:U:H1'	28:BA:2198:A:C5	2.48	0.48
28:BA:2198:A:O5'	33:BH:29:PHE:HD1	1.96	0.48
31:BF:79:ARG:HB3	31:BF:82:TYR:CE1	2.48	0.48
32:BG:84:LYS:HG3	32:BG:132:LEU:N	2.28	0.48
48:BW:23:LYS:HE2	48:BW:24:ARG:H	1.78	0.48
1:AA:1194:U:H5'	5:AE:26:LYS:HZ1	1.77	0.48
2:AB:20:ARG:NH1	2:AB:20:ARG:HA	2.29	0.48
10:AJ:29:ALA:HB3	10:AJ:36:VAL:CG2	2.43	0.48
14:AN:21:PHE:HA	14:AN:25:ALA:HB3	1.95	0.48
22:AV:74:C:C3'	28:BA:2602:A:C5	2.95	0.48
24:AX:3:U:H2'	24:AX:4:A:O4'	2.13	0.48
24:AX:14:A:H2	24:AX:15:A:C8	2.30	0.48
25:AY:221:ASN:HA	25:AY:224:GLU:CB	2.43	0.48
27:BC:84:PRO:HG3	28:BA:1567:G:H2'	1.95	0.48
28:BA:141:G:N1	45:BT:1:MET:O	2.45	0.48
28:BA:749:A:C6	28:BA:1618:A:C2	3.01	0.48
31:BF:64:PRO:HA	31:BF:88:VAL:HG22	1.95	0.48
32:BG:104:LEU:HB2	32:BG:112:VAL:HG21	1.96	0.48
32:BG:112:VAL:HG23	32:BG:113:ASP:N	2.28	0.48
34:BI:89:SER:OG	34:BI:135:MET:SD	2.68	0.48
48:BW:18:LYS:CG	48:BW:19:ARG:N	2.77	0.48
48:BW:44:PHE:HD1	48:BW:45:HIS:CE1	2.32	0.48
1:AA:322:C:OP2	1:AA:328:C:N4	2.47	0.48
5:AE:97:GLN:N	5:AE:124:LEU:O	2.42	0.48
11:AK:35:THR:OG1	11:AK:40:ASN:N	2.47	0.48
22:AV:20:U:C3'	22:AV:21:A:C5'	2.90	0.48
25:AY:95:PHE:CE2	59:AY:801:FUA:C23	2.97	0.48
27:BC:265:PHE:N	27:BC:265:PHE:CD1	2.82	0.48
28:BA:994:C:O2'	28:BA:996:A:OP1	2.25	0.48
28:BA:1044:C:O2'	28:BA:1111:A:N1	2.41	0.48
28:BA:1135:C:N4	28:BA:1139:G:C6	2.82	0.48
28:BA:2230:G:O3'	49:BX:29:LEU:HD23	2.14	0.48
30:BE:164:LEU:HB3	30:BE:167:VAL:CG1	2.44	0.48
34:BI:40:ALA:O	34:BI:43:ALA:HB3	2.14	0.48
48:BW:42:THR:HG22	48:BW:43:LYS:HZ2	1.79	0.48
57:B5:110:ALA:HB1	57:B5:113:PHE:CE1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:693:G:C5'	24:AX:7:A:H1'	2.44	0.48
1:AA:1182:G:H4'	1:AA:1183:U:H5"	1.96	0.48
2:AB:141:GLU:HA	2:AB:144:GLU:HB2	1.95	0.48
2:AB:153:MET:SD	2:AB:157:PRO:HG3	2.53	0.48
4:AD:197:GLU:O	4:AD:200:ILE:N	2.47	0.48
10:AJ:6:ILE:HB	10:AJ:76:ILE:HB	1.96	0.48
20:AT:44:LYS:HB3	20:AT:87:ALA:HB1	1.96	0.48
25:AY:93:VAL:HG13	25:AY:94:ASP:N	2.29	0.48
28:BA:11:C:C3'	28:BA:12:U:H5'	2.44	0.48
28:BA:107:G:H2'	28:BA:108:G:H8	1.78	0.48
28:BA:864:G:O2'	28:BA:865:C:H5'	2.14	0.48
28:BA:1996:C:OP1	36:BK:31:ARG:NE	2.46	0.48
36:BK:107:LEU:O	36:BK:109:SER:N	2.38	0.48
41:BP:19:PHE:N	41:BP:19:PHE:CD1	2.82	0.48
57:B5:51:TYR:HD1	57:B5:52:MET:N	2.12	0.48
1:AA:16:A:O2'	1:AA:17:U:C5'	2.61	0.48
1:AA:18:C:C4'	5:AE:132:ASN:ND2	2.77	0.48
3:AC:47:LEU:HB3	3:AC:50:ALA:HB3	1.94	0.48
3:AC:150:LYS:HG3	3:AC:201:TRP:CE3	2.49	0.48
28:BA:747:U:O2'	44:BS:88:ARG:NH2	2.45	0.48
28:BA:1277:G:C5'	39:BN:20:MET:HE2	2.43	0.48
28:BA:2747:G:O2'	32:BG:66:THR:HG22	2.14	0.48
32:BG:22:VAL:HG23	32:BG:22:VAL:O	2.14	0.48
33:BH:9:VAL:O	33:BH:13:GLY:N	2.46	0.48
40:BO:51:ALA:HB3	40:BO:78:VAL:HG13	1.95	0.48
49:BX:39:VAL:HG22	49:BX:44:ARG:O	2.13	0.48
1:AA:411:A:C5	1:AA:429:U:C5	3.02	0.48
9:AI:119:ARG:HH21	9:AI:123:ARG:CZ	2.26	0.48
14:AN:53:ARG:HH21	19:AS:37:ARG:NH2	2.11	0.48
21:AU:20:LYS:HE2	21:AU:20:LYS:HA	1.95	0.48
22:AV:35:A:C5	24:AX:13:A:N1	2.82	0.48
22:AV:75:C:O2'	28:BA:2064:C:C5'	2.62	0.48
23:AW:18:G:H2'	23:AW:57:G:N2	2.29	0.48
23:AW:40:G:H2'	23:AW:41:A:C8	2.49	0.48
28:BA:580:U:H2'	28:BA:581:C:H6	1.79	0.48
28:BA:630:G:N2	28:BA:633:A:OP2	2.37	0.48
28:BA:1778:U:H2'	28:BA:1784:A:H62	1.78	0.48
28:BA:2335:A:C5	28:BA:2337:G:C4	3.02	0.48
42:BQ:63:ARG:HH22	42:BQ:96:ASP:N	2.12	0.48
57:B5:110:ALA:HB1	57:B5:113:PHE:CZ	2.49	0.48
1:AA:898:G:N2	1:AA:901:A:OP2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:913:A:OP1	12:AL:88:LYS:NZ	2.45	0.48
1:AA:1377:A:H1'	7:AG:2:PRO:HG3	1.95	0.48
2:AB:56:LEU:HD23	2:AB:220:VAL:CG1	2.44	0.48
11:AK:111:THR:HA	21:AU:4:ILE:O	2.14	0.48
20:AT:3:ASN:C	20:AT:5:LYS:H	2.17	0.48
22:AV:74:C:H3'	28:BA:2602:A:C6	2.49	0.48
23:AW:64:G:C2	23:AW:65:U:C4	3.01	0.48
28:BA:391:A:C5	28:BA:411:G:C2	3.02	0.48
28:BA:528:A:C2	28:BA:2043:C:H4'	2.49	0.48
28:BA:983:A:N6	28:BA:984:A:C2	2.82	0.48
28:BA:1069:A:C1'	28:BA:1073:A:H62	2.27	0.48
28:BA:2016:U:O2	52:B0:3:GLN:NE2	2.45	0.48
28:BA:2406:A:C2	37:BL:69:ARG:NH2	2.82	0.48
34:BI:100:ILE:HD13	34:BI:137:LEU:HD12	1.96	0.48
48:BW:9:THR:HG23	48:BW:10:ARG:HD3	1.94	0.48
57:B5:15:VAL:HG22	57:B5:66:GLY:CA	2.44	0.48
57:B5:100:ALA:HB2	57:B5:125:ARG:HE	1.79	0.48
1:AA:203:G:N2	1:AA:215:C:C2	2.82	0.47
1:AA:1028:C:N4	1:AA:1034:G:C2	2.82	0.47
3:AC:131:ARG:NH2	3:AC:166:GLU:OE2	2.47	0.47
4:AD:35:GLU:O	4:AD:38:PRO:HD3	2.13	0.47
10:AJ:57:VAL:HG12	10:AJ:58:ASN:N	2.28	0.47
11:AK:23:ILE:HG13	11:AK:86:VAL:HA	1.95	0.47
20:AT:5:LYS:HD2	20:AT:7:ALA:H	1.78	0.47
32:BG:73:SER:O	32:BG:77:GLY:N	2.45	0.47
43:BR:66:HIS:CG	43:BR:94:THR:HG22	2.49	0.47
48:BW:47:GLY:H	48:BW:80:SER:HB3	1.80	0.47
49:BX:39:VAL:HG21	49:BX:42:GLU:HB2	1.96	0.47
1:AA:2:A:O2'	4:AD:83:LYS:NZ	2.47	0.47
1:AA:20:U:O2'	1:AA:21:G:H5'	2.15	0.47
1:AA:920:U:C4'	1:AA:1080:A:C6	2.94	0.47
2:AB:163:ILE:HG23	2:AB:164:ASP:N	2.29	0.47
4:AD:11:LEU:HG	4:AD:63:ARG:NH1	2.29	0.47
25:AY:8:ALA:O	25:AY:288:SER:OG	2.30	0.47
28:BA:910:A:N3	38:BM:9:PHE:CZ	2.81	0.47
28:BA:2197:U:H4'	33:BH:29:PHE:CE1	2.48	0.47
36:BK:72:PRO:O	36:BK:74:GLY:N	2.43	0.47
37:BL:82:LEU:CD1	37:BL:116:VAL:HG23	2.44	0.47
44:BS:63:GLY:O	44:BS:64:ALA:CB	2.62	0.47
2:AB:49:PHE:CD1	2:AB:49:PHE:C	2.87	0.47
4:AD:150:LYS:O	4:AD:152:GLN:NE2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:105:ILE:HA	5:AE:123:VAL:HG23	1.95	0.47
28:BA:1814:G:C6	28:BA:1815:A:N6	2.82	0.47
28:BA:2902:C:C2'	28:BA:2903:U:O5'	2.63	0.47
31:BF:110:ILE:O	31:BF:112:ASP:N	2.46	0.47
43:BR:68:ARG:HD3	43:BR:92:TRP:CZ2	2.49	0.47
45:BT:34:VAL:CG2	45:BT:34:VAL:O	2.61	0.47
1:AA:471:U:H2'	1:AA:472:U:H6	1.79	0.47
1:AA:579:A:H2'	1:AA:580:C:H6	1.80	0.47
1:AA:1012:A:C2	1:AA:1018:G:C2	3.01	0.47
1:AA:1028:C:C4	1:AA:1029:U:H1'	2.48	0.47
1:AA:1498:U:C4	24:AX:12:U:O5'	2.65	0.47
25:AY:4:THR:CG2	25:AY:378:ARG:CZ	2.92	0.47
31:BF:134:GLN:O	31:BF:136:ILE:N	2.47	0.47
35:BJ:84:ILE:HG23	35:BJ:84:ILE:O	2.15	0.47
37:BL:23:ILE:HD12	43:BR:84:ARG:CZ	2.45	0.47
1:AA:982:U:H4'	1:AA:983:A:C5'	2.44	0.47
1:AA:1130:A:C4'	9:AI:20:PHE:CE2	2.97	0.47
4:AD:30:THR:HG22	4:AD:31:LYS:HD3	1.96	0.47
13:AM:82:ASP:HB3	31:BF:142:TYR:CZ	2.49	0.47
14:AN:9:ARG:O	14:AN:13:ARG:HG3	2.14	0.47
25:AY:79:TYR:CD2	25:AY:283:ILE:HD11	2.49	0.47
25:AY:151:PHE:CE1	25:AY:266:CYS:HB3	2.50	0.47
25:AY:698:VAL:O	25:AY:699:ILE:HD12	2.15	0.47
28:BA:910:A:H62	38:BM:9:PHE:CB	2.13	0.47
28:BA:2701:U:H3'	28:BA:2702:G:H5"	1.96	0.47
31:BF:69:ALA:N	31:BF:82:TYR:O	2.47	0.47
44:BS:24:ILE:HD11	44:BS:36:LEU:HD13	1.96	0.47
48:BW:49:ASN:ND2	48:BW:49:ASN:C	2.67	0.47
49:BX:67:LEU:HD23	49:BX:70:LEU:HD12	1.96	0.47
1:AA:21:G:O2'	1:AA:22:G:C4'	2.62	0.47
1:AA:71:A:H5'	1:AA:71:A:H8	1.79	0.47
1:AA:815:A:H4'	1:AA:817:C:C4	2.50	0.47
1:AA:1014:A:OP2	19:AS:18:LYS:HE2	2.15	0.47
1:AA:1049:U:H2'	14:AN:3:LYS:HD3	1.97	0.47
1:AA:1117:A:O3'	9:AI:106:ARG:CD	2.62	0.47
2:AB:26:MET:HE3	2:AB:192:PRO:HG3	1.96	0.47
18:AR:71:THR:HG23	18:AR:74:HIS:H	1.79	0.47
27:BC:67:LYS:HG2	27:BC:150:GLY:HA2	1.97	0.47
28:BA:419:U:H2'	28:BA:420:C:C6	2.50	0.47
28:BA:479:A:C2	28:BA:480:A:C4	3.01	0.47
28:BA:866:A:N7	28:BA:914:G:C5	2.83	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BF:5:ASP:OD1	31:BF:8:LYS:NZ	2.46	0.47
32:BG:23:ILE:HG21	32:BG:71:LEU:HD11	1.96	0.47
34:BI:60:VAL:HG22	34:BI:66:PHE:HB3	1.95	0.47
35:BJ:32:LEU:CD2	35:BJ:54:ILE:HD12	2.44	0.47
35:BJ:43:GLU:O	35:BJ:45:THR:HG22	2.13	0.47
37:BL:68:SER:O	37:BL:69:ARG:HB3	2.15	0.47
45:BT:54:GLU:OE1	45:BT:54:GLU:N	2.48	0.47
48:BW:18:LYS:HA	48:BW:36:ILE:HG13	1.95	0.47
48:BW:28:GLU:O	48:BW:30:VAL:N	2.48	0.47
57:B5:60:LEU:HD23	57:B5:78:GLY:HA3	1.97	0.47
1:AA:283:U:C4	1:AA:284:C:C4	3.03	0.47
1:AA:537:G:OP1	12:AL:110:ARG:NH2	2.42	0.47
1:AA:982:U:C5	1:AA:983:A:N6	2.83	0.47
1:AA:1021:A:C2'	1:AA:1022:A:H5'	2.44	0.47
1:AA:1228:C:OP2	13:AM:110:LYS:NZ	2.47	0.47
1:AA:1230:C:OP1	23:AW:30:C:C5'	2.61	0.47
1:AA:1290:G:P	7:AG:35:LYS:HZ3	2.30	0.47
1:AA:1413:A:C2	1:AA:1488:G:C2	3.01	0.47
3:AC:59:ARG:HA	3:AC:64:ILE:HA	1.96	0.47
4:AD:174:ASP:OD1	4:AD:176:GLY:N	2.48	0.47
5:AE:45:ARG:HA	5:AE:72:ILE:O	2.14	0.47
10:AJ:100:ILE:HG13	10:AJ:100:ILE:O	2.15	0.47
13:AM:11:ASP:CG	13:AM:12:HIS:H	2.15	0.47
18:AR:23:TYR:CE1	18:AR:24:LYS:HG3	2.49	0.47
22:AV:73:A:O3'	22:AV:74:C:C6	2.68	0.47
24:AX:13:A:O2'	24:AX:14:A:OP1	2.23	0.47
25:AY:19:ILE:CD1	25:AY:92:HIS:H	2.28	0.47
25:AY:24:THR:OG1	60:AY:802:GDP:O1B	2.33	0.47
25:AY:557:ILE:HG21	25:AY:576:ILE:HD12	1.97	0.47
26:BB:29:A:H2'	26:BB:30:C:C6	2.50	0.47
27:BC:225:ASN:HB3	27:BC:226:PRO:HD2	1.96	0.47
28:BA:479:A:H4'	28:BA:480:A:OP1	2.15	0.47
28:BA:504:A:HO2'	28:BA:505:A:P	2.28	0.47
28:BA:523:C:H5"	28:BA:540:C:O2'	2.15	0.47
28:BA:725:G:C6	28:BA:726:G:N1	2.82	0.47
28:BA:996:A:H4'	42:BQ:91:ARG:NE	2.29	0.47
28:BA:1090:A:C2	28:BA:1102:C:H1'	2.50	0.47
28:BA:1327:A:H2'	28:BA:1328:A:O4'	2.14	0.47
28:BA:1392:A:N6	28:BA:1393:A:N6	2.63	0.47
28:BA:1474:U:C2'	28:BA:1475:G:H5'	2.44	0.47
28:BA:1738:G:O2'	28:BA:1739:A:O5'	2.25	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:1939:U:O2	28:BA:1967:C:H4’	2.15	0.47
28:BA:2092:U:C4’	28:BA:2093:G:O5’	2.50	0.47
28:BA:2355:G:H4’	48:BW:20:LEU:CD1	2.44	0.47
28:BA:2365:G:N7	55:B3:38:LYS:NZ	2.52	0.47
28:BA:2793:C:H2’	28:BA:2794:C:C6	2.50	0.47
28:BA:2862:G:C5	28:BA:2863:C:C5	3.02	0.47
28:BA:2889:C:N4	28:BA:2890:G:C6	2.83	0.47
34:BI:14:ALA:HB3	34:BI:51:GLY:H	1.78	0.47
34:BI:61:TYR:N	34:BI:61:TYR:CD1	2.82	0.47
37:BL:19:LEU:HD23	37:BL:19:LEU:C	2.35	0.47
38:BM:1:MET:O	38:BM:2:LEU:CB	2.62	0.47
39:BN:20:MET:HE1	39:BN:40:LYS:HE2	1.97	0.47
40:BO:15:ARG:NE	40:BO:93:ASP:OD2	2.44	0.47
48:BW:9:THR:CG2	48:BW:10:ARG:HD3	2.44	0.47
57:B5:23:LEU:H	57:B5:87:GLU:HB2	1.79	0.47
1:AA:77:A:H2	1:AA:92:U:C2	2.33	0.47
1:AA:235:C:H2’	1:AA:236:A:C8	2.50	0.47
1:AA:1390:U:H3’	1:AA:1391:U:C5	2.49	0.47
1:AA:1468:A:C2’	1:AA:1469:C:C5’	2.93	0.47
2:AB:90:PHE:CD1	2:AB:149:GLY:HA3	2.50	0.47
5:AE:31:PHE:HZ	24:AX:19:A:N6	2.12	0.47
22:AV:72:A:C6	22:AV:73:A:C6	3.03	0.47
24:AX:18:A:H2’	24:AX:19:A:H5’	1.96	0.47
25:AY:90:PRO:HB3	59:AY:801:FUA:O4	2.15	0.47
25:AY:95:PHE:CE2	59:AY:801:FUA:C12	2.95	0.47
28:BA:995:C:N4	35:BJ:2:LYS:HB3	2.29	0.47
28:BA:1760:C:H2’	28:BA:1761:C:O4’	2.14	0.47
28:BA:1817:G:H2’	28:BA:1818:U:H5’	1.97	0.47
35:BJ:36:LEU:O	35:BJ:121:LYS:NZ	2.39	0.47
35:BJ:44:TYR:CD1	42:BQ:63:ARG:HG2	2.49	0.47
38:BM:106:ASP:O	38:BM:108:VAL:N	2.44	0.47
48:BW:9:THR:HG23	48:BW:10:ARG:N	2.30	0.47
57:B5:15:VAL:HG21	57:B5:66:GLY:HA2	1.96	0.47
1:AA:1075:U:H3’	1:AA:1075:U:OP2	2.14	0.47
9:AI:84:THR:HG21	9:AI:103:PHE:CB	2.45	0.47
10:AJ:29:ALA:O	10:AJ:33:GLY:N	2.47	0.47
11:AK:71:ALA:HB1	11:AK:105:PHE:HE2	1.79	0.47
20:AT:28:MET:SD	20:AT:67:ILE:HD13	2.55	0.47
22:AV:59:A:H2’	22:AV:60:U:H5’	1.97	0.47
23:AW:39:U:H2’	23:AW:40:G:C8	2.50	0.47
24:AX:14:A:O2’	24:AX:15:A:OP1	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:147:MET:HE3	32:BG:92:GLY:CA	2.42	0.47
28:BA:517:C:OP2	52:B0:9:ARG:NH2	2.48	0.47
28:BA:747:U:C2'	44:BS:88:ARG:NH2	2.78	0.47
28:BA:1079:C:O2	34:BI:130:GLY:HA3	2.15	0.47
28:BA:1198:U:O3'	42:BQ:4:LYS:HE3	2.15	0.47
28:BA:1485:U:H2'	28:BA:1486:U:C6	2.48	0.47
28:BA:2678:C:H2'	28:BA:2679:A:O4'	2.14	0.47
33:BH:8:LYS:O	33:BH:9:VAL:HB	2.15	0.47
48:BW:60:ALA:HA	48:BW:81:ILE:HD12	1.97	0.47
55:B3:21:PHE:O	55:B3:22:LYS:O	2.33	0.47
57:B5:54:VAL:HG22	57:B5:83:ALA:HB1	1.97	0.47
1:AA:983:A:OP1	14:AN:9:ARG:NH1	2.43	0.47
12:AL:24:LEU:HB2	12:AL:59:ASN:ND2	2.29	0.47
12:AL:33:VAL:HG23	12:AL:56:ARG:HB3	1.96	0.47
25:AY:105:VAL:HG23	25:AY:106:LEU:N	2.30	0.47
27:BC:175:LEU:HD23	28:BA:1799:G:C5	2.49	0.47
28:BA:189:G:O6	28:BA:205:G:O2'	2.19	0.47
28:BA:983:A:N6	28:BA:984:A:N1	2.62	0.47
28:BA:1322:A:OP1	44:BS:11:ARG:NE	2.38	0.47
28:BA:2093:G:H4'	33:BH:22:LYS:CD	2.43	0.47
28:BA:2425:A:C5'	28:BA:2427:C:O4'	2.63	0.47
29:BD:174:SER:OG	29:BD:175:LEU:N	2.46	0.47
32:BG:118:ALA:O	32:BG:120:ILE:N	2.41	0.47
43:BR:68:ARG:HD3	43:BR:92:TRP:CE2	2.50	0.47
57:B5:88:HIS:CB	57:B5:89:PRO:HD3	2.44	0.47
1:AA:16:A:C1'	1:AA:1080:A:H4'	2.27	0.46
1:AA:958:A:N7	19:AS:55:ARG:CZ	2.78	0.46
1:AA:1083:U:O2'	1:AA:1102:A:OP2	2.33	0.46
3:AC:42:TYR:CD2	3:AC:43:LEU:HD12	2.50	0.46
4:AD:147:GLU:HA	4:AD:150:LYS:HD2	1.96	0.46
5:AE:89:HIS:CE1	5:AE:90:THR:HG1	2.33	0.46
8:AH:11:LEU:CD2	8:AH:75:ILE:HD11	2.45	0.46
23:AW:25:C:C4	23:AW:26:A:N7	2.82	0.46
25:AY:658:VAL:CG2	25:AY:663:MET:SD	3.03	0.46
28:BA:747:U:H2'	44:BS:88:ARG:NH2	2.30	0.46
28:BA:911:A:H3'	38:BM:8:LYS:HZ3	1.80	0.46
28:BA:947:A:O2'	28:BA:984:A:H2	1.98	0.46
28:BA:1838:C:H4'	28:BA:1839:G:C8	2.51	0.46
28:BA:2198:A:C6	33:BH:29:PHE:CG	3.02	0.46
28:BA:2533:U:OP1	28:BA:2665:A:O2'	2.20	0.46
28:BA:2649:C:H2'	28:BA:2650:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BE:119:ILE:HG13	30:BE:119:ILE:O	2.16	0.46
34:BI:19:PRO:CG	34:BI:23:VAL:HG23	2.45	0.46
35:BJ:12:LYS:O	35:BJ:13:ARG:HB2	2.15	0.46
4:AD:110:THR:HG23	4:AD:113:GLU:H	1.79	0.46
8:AH:112:THR:HG22	8:AH:114:ARG:H	1.80	0.46
12:AL:99:ARG:HB2	12:AL:117:TYR:HA	1.96	0.46
21:AU:45:ARG:HA	21:AU:48:ALA:HB3	1.97	0.46
28:BA:1414:C:O2	28:BA:1588:G:N2	2.44	0.46
28:BA:2090:A:C3'	28:BA:2091:C:H5'	2.46	0.46
31:BF:147:ARG:HG3	31:BF:148:VAL:N	2.30	0.46
36:BK:24:VAL:CG1	36:BK:30:ARG:HD3	2.45	0.46
53:B1:4:ILE:HD11	53:B1:27:ARG:HB2	1.96	0.46
1:AA:21:G:C4	1:AA:22:G:C5	3.04	0.46
1:AA:921:U:H5"	1:AA:1081:A:O2'	2.15	0.46
1:AA:929:G:O2'	1:AA:930:C:H5'	2.14	0.46
1:AA:1159:U:OP1	2:AB:131:LYS:NZ	2.49	0.46
1:AA:1276:G:H2'	1:AA:1277:C:O4'	2.13	0.46
2:AB:9:LEU:HD23	2:AB:9:LEU:O	2.15	0.46
2:AB:16:GLY:HA3	2:AB:40:ILE:HG23	1.97	0.46
3:AC:156:ARG:H	3:AC:163:ALA:HA	1.81	0.46
9:AI:22:LYS:HG3	9:AI:23:PRO:HD2	1.98	0.46
28:BA:912:C:C2'	28:BA:913:U:C5'	2.86	0.46
28:BA:959:A:H62	38:BM:82:MET:CE	2.28	0.46
28:BA:1060:U:H3	28:BA:1088:A:H2	1.64	0.46
28:BA:1161:C:H1'	43:BR:8:GLY:O	2.15	0.46
28:BA:1478:G:C2	28:BA:1479:G:N7	2.83	0.46
28:BA:2144:G:H3'	28:BA:2144:G:N3	2.31	0.46
28:BA:2318:G:C6	28:BA:2319:G:C6	3.03	0.46
28:BA:2343:U:HO2'	28:BA:2373:G:HO2'	1.59	0.46
28:BA:2839:G:N2	28:BA:2880:C:C4	2.82	0.46
29:BD:148:GLN:HB2	29:BD:152:PRO:HG2	1.97	0.46
31:BF:131:VAL:HG22	31:BF:151:LEU:H	1.80	0.46
32:BG:163:TYR:O	32:BG:164:ALA:HB2	2.15	0.46
33:BH:21:VAL:CG2	33:BH:25:TYR:CD2	2.98	0.46
36:BK:30:ARG:NH1	36:BK:32:TYR:O	2.46	0.46
38:BM:22:GLN:O	38:BM:24:THR:N	2.48	0.46
38:BM:46:ILE:HD13	38:BM:47:GLU:N	2.30	0.46
50:BY:56:LEU:O	50:BY:57:LEU:HB3	2.14	0.46
1:AA:250:A:H4'	1:AA:251:G:O5'	2.16	0.46
1:AA:1130:A:O4'	9:AI:20:PHE:CZ	2.68	0.46
2:AB:9:LEU:HB2	2:AB:42:LEU:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:65:LYS:HD2	2:AB:153:MET:HG2	1.97	0.46
4:AD:125:VAL:O	4:AD:127:GLY:N	2.47	0.46
8:AH:29:SER:HB3	8:AH:57:PRO:HB2	1.98	0.46
14:AN:33:ASP:O	14:AN:41:ARG:NE	2.48	0.46
24:AX:5:A:O2'	24:AX:6:A:N7	2.46	0.46
28:BA:478:A:C6	28:BA:480:A:C6	3.03	0.46
28:BA:1509:A:C4	28:BA:1510:G:C8	3.04	0.46
28:BA:2478:A:H2'	28:BA:2479:U:H5'	1.98	0.46
42:BQ:4:LYS:NZ	42:BQ:7:VAL:HG11	2.31	0.46
45:BT:29:THR:OG1	45:BT:86:THR:N	2.43	0.46
52:B0:42:ILE:H	52:B0:42:ILE:HD12	1.80	0.46
1:AA:450:G:N7	1:AA:481:G:O6	2.48	0.46
1:AA:471:U:H2'	1:AA:472:U:C6	2.51	0.46
1:AA:1393:U:HO2'	1:AA:1502:A:C4'	2.27	0.46
2:AB:32:GLY:HA2	2:AB:39:ILE:HB	1.98	0.46
2:AB:132:GLU:HA	2:AB:135:MET:HB3	1.97	0.46
13:AM:29:ARG:NH1	13:AM:63:PHE:HB2	2.31	0.46
21:AU:54:LYS:CG	24:AX:1:G:OP1	2.63	0.46
27:BC:84:PRO:HG3	28:BA:1567:G:C2'	2.46	0.46
27:BC:232:GLY:H	27:BC:241:LYS:HE3	1.79	0.46
28:BA:1417:C:N3	28:BA:1581:G:N2	2.60	0.46
28:BA:2197:U:C2'	33:BH:29:PHE:CE1	2.99	0.46
34:BI:14:ALA:HB1	34:BI:45:THR:HG23	1.97	0.46
41:BP:91:VAL:HG11	41:BP:96:LEU:HD21	1.98	0.46
47:BV:80:HIS:HD2	47:BV:83:LYS:H	1.62	0.46
48:BW:72:GLY:N	48:BW:73:PRO:CD	2.78	0.46
1:AA:420:U:C2'	1:AA:421:U:H5"	2.46	0.46
1:AA:1079:G:H5"	5:AE:50:TYR:HH	1.76	0.46
2:AB:178:LEU:HD11	5:AE:69:ARG:NE	2.30	0.46
14:AN:20:TYR:HB2	14:AN:55:SER:OG	2.15	0.46
14:AN:47:LYS:HD2	19:AS:13:LEU:HG	1.98	0.46
16:AP:22:ALA:HA	16:AP:33:ILE:HG13	1.96	0.46
17:AQ:76:VAL:HG23	17:AQ:77:ARG:H	1.79	0.46
25:AY:497:LYS:HG2	25:AY:523:TYR:HB2	1.98	0.46
28:BA:118:A:C8	28:BA:119:A:C8	3.04	0.46
28:BA:657:U:H2'	28:BA:658:U:C6	2.50	0.46
28:BA:923:G:N3	48:BW:23:LYS:HD2	2.31	0.46
28:BA:1569:A:N6	28:BA:1570:A:C6	2.84	0.46
28:BA:2405:G:O2'	28:BA:2406:A:OP1	2.26	0.46
28:BA:2800:A:H3'	28:BA:2801:G:H5"	1.96	0.46
32:BG:123:GLU:HG2	32:BG:124:CYS:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BI:24:GLY:O	34:BI:27:LEU:HG	2.16	0.46
36:BK:98:ARG:HA	36:BK:118:LEU:HD23	1.97	0.46
41:BP:50:ARG:HG2	41:BP:57:ALA:N	2.30	0.46
1:AA:426:U:H5"	4:AD:37:ALA:CB	2.45	0.46
1:AA:925:G:C2	1:AA:1392:G:N2	2.84	0.46
1:AA:1249:C:O2'	9:AI:71:GLY:HA2	2.14	0.46
1:AA:1319:A:C5'	19:AS:4:SER:CB	2.94	0.46
22:AV:38:A:H2'	22:AV:39:C:O4'	2.16	0.46
23:AW:48:C:O2'	23:AW:59:A:H4'	2.15	0.46
25:AY:24:THR:HB	60:AY:802:GDP:PB	2.56	0.46
25:AY:218:TRP:N	25:AY:218:TRP:CD1	2.83	0.46
25:AY:453:SER:O	25:AY:455:GLN:N	2.48	0.46
28:BA:587:C:P	37:BL:21:ARG:NH1	2.88	0.46
28:BA:593:U:H2'	28:BA:594:U:C6	2.51	0.46
28:BA:1730:C:O2'	28:BA:1731:G:C4	2.68	0.46
30:BE:187:VAL:O	30:BE:188:MET:HB3	2.16	0.46
31:BF:30:VAL:CG1	31:BF:96:TRP:CH2	2.99	0.46
33:BH:31:VAL:HB	33:BH:32:PRO:CD	2.45	0.46
35:BJ:37:ARG:HA	35:BJ:118:MET:CE	2.45	0.46
35:BJ:44:TYR:HD1	42:BQ:63:ARG:HG2	1.81	0.46
39:BN:12:ARG:CZ	39:BN:20:MET:HE1	2.45	0.46
39:BN:70:THR:HB	39:BN:75:ILE:CD1	2.46	0.46
41:BP:72:VAL:HG23	41:BP:72:VAL:O	2.15	0.46
57:B5:77:VAL:O	57:B5:79:PRO:HD2	2.13	0.46
57:B5:123:ILE:HG12	57:B5:124:ASP:N	2.30	0.46
1:AA:880:C:OP1	12:AL:9:ARG:NH1	2.49	0.46
1:AA:1126:U:C2	1:AA:1281:C:C5	3.03	0.46
7:AG:59:LEU:O	7:AG:62:PHE:HB3	2.16	0.46
11:AK:112:ASP:CB	21:AU:20:LYS:HE3	2.46	0.46
16:AP:42:ILE:O	16:AP:44:SER:N	2.45	0.46
25:AY:127:TRP:CH2	25:AY:137:ARG:HD2	2.51	0.46
25:AY:309:ARG:NH2	25:AY:402:ALA:O	2.48	0.46
26:BB:51:G:OP2	40:BO:64:TYR:HD2	1.99	0.46
28:BA:247:G:H4'	28:BA:386:G:C5	2.51	0.46
28:BA:281:C:H2'	28:BA:282:A:C8	2.51	0.46
28:BA:451:U:C2	28:BA:453:A:N7	2.83	0.46
28:BA:1348:C:H2'	28:BA:1349:C:H5'	1.96	0.46
28:BA:2210:U:H4'	28:BA:2211:A:H5'	1.97	0.46
28:BA:2852:G:C6	28:BA:2853:C:N3	2.84	0.46
42:BQ:4:LYS:NZ	42:BQ:7:VAL:CG1	2.79	0.46
42:BQ:91:ARG:HH21	42:BQ:93:ILE:HG21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BQ:91:ARG:HH11	43:BR:11:GLN:H	1.64	0.46
46:BU:73:ASN:HA	46:BU:95:PHE:CE2	2.50	0.46
55:B3:3:ILE:HG21	55:B3:62:PRO:HG3	1.98	0.46
57:B5:68:PRO:HA	57:B5:72:LEU:CG	2.46	0.46
1:AA:983:A:N3	1:AA:983:A:H2'	2.31	0.46
1:AA:1277:C:O2'	1:AA:1279:G:H8	1.98	0.46
2:AB:46:VAL:HB	2:AB:47:PRO:HD3	1.96	0.46
3:AC:120:ILE:HD11	3:AC:137:ALA:HB2	1.98	0.46
22:AV:50:U:O2'	22:AV:51:C:H5'	2.16	0.46
25:AY:464:LEU:CD1	59:AY:801:FUA:C27	2.61	0.46
25:AY:532:LYS:HD3	25:AY:534:TYR:H	1.81	0.46
27:BC:246:PRO:HG2	27:BC:247:TRP:CZ3	2.50	0.46
28:BA:1313:U:H2'	28:BA:1610:A:C2	2.51	0.46
42:BQ:91:ARG:HH21	42:BQ:93:ILE:HD13	1.80	0.46
53:B1:6:GLU:OE1	53:B1:52:LYS:CE	2.64	0.46
1:AA:1131:G:P	9:AI:5:GLN:HE21	2.39	0.46
1:AA:1331:G:O2'	1:AA:1332:A:P	2.73	0.46
2:AB:60:ALA:HB2	2:AB:220:VAL:HG12	1.99	0.46
4:AD:105:MET:SD	4:AD:143:VAL:HG22	2.55	0.46
9:AI:9:THR:HG22	9:AI:10:GLY:N	2.31	0.46
22:AV:4:G:O2'	22:AV:5:G:P	2.74	0.46
26:BB:37:C:C5	26:BB:38:C:C4	3.04	0.46
27:BC:75:ALA:HB2	27:BC:95:TYR:HA	1.97	0.46
28:BA:597:G:C2	28:BA:661:A:C2	3.04	0.46
29:BD:169:ARG:O	29:BD:170:VAL:HG13	2.15	0.46
30:BE:44:ARG:HH21	30:BE:44:ARG:HG3	1.80	0.46
33:BH:40:THR:C	33:BH:42:LYS:H	2.19	0.46
36:BK:10:VAL:HG21	36:BK:17:ARG:H	1.81	0.46
43:BR:64:VAL:HG21	43:BR:97:LYS:HB2	1.97	0.46
45:BT:61:LEU:C	45:BT:61:LEU:HD12	2.35	0.46
47:BV:2:PHE:HB3	47:BV:50:MET:HE1	1.98	0.46
48:BW:19:ARG:CZ	48:BW:22:VAL:HB	2.46	0.46
1:AA:918:A:N6	1:AA:919:A:C6	2.85	0.45
1:AA:925:G:C4	1:AA:1392:G:N2	2.84	0.45
1:AA:1181:G:N2	1:AA:1182:G:N2	2.64	0.45
1:AA:1220:G:C5'	19:AS:34:TRP:O	2.64	0.45
1:AA:1395:C:H41	1:AA:1396:A:N6	2.05	0.45
2:AB:32:GLY:O	2:AB:33:ALA:CB	2.64	0.45
4:AD:139:PRO:HB3	4:AD:184:ARG:HA	1.96	0.45
9:AI:57:MET:SD	9:AI:58:VAL:CA	3.03	0.45
12:AL:3:THR:HG22	12:AL:5:ASN:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:75:ILE:O	16:AP:77:GLU:N	2.43	0.45
25:AY:546:PRO:HD3	25:AY:583:TYR:CE2	2.50	0.45
28:BA:11:C:H2'	28:BA:12:U:H5'	1.98	0.45
35:BJ:4:PHE:O	35:BJ:44:TYR:OH	2.34	0.45
35:BJ:12:LYS:O	35:BJ:13:ARG:CB	2.64	0.45
37:BL:85:VAL:HG22	37:BL:94:THR:HG22	1.98	0.45
48:BW:30:VAL:HG23	48:BW:60:ALA:O	2.15	0.45
57:B5:71:CYS:CA	57:B5:117:LEU:HD11	2.43	0.45
1:AA:16:A:N3	1:AA:1080:A:C4'	2.79	0.45
1:AA:675:A:H1'	11:AK:118:HIS:CD2	2.51	0.45
1:AA:1008:U:H2'	1:AA:1009:U:O4'	2.17	0.45
1:AA:1112:C:O2	3:AC:178:LEU:N	2.49	0.45
1:AA:1392:G:H2'	1:AA:1393:U:O4'	2.16	0.45
1:AA:1498:U:C6	24:AX:11:G:O3'	2.69	0.45
6:AF:15:SER:OG	6:AF:58:HIS:ND1	2.47	0.45
10:AJ:51:VAL:O	10:AJ:62:ARG:HA	2.16	0.45
22:AV:4:G:O2'	22:AV:5:G:C8	2.69	0.45
22:AV:59:A:C2'	22:AV:60:U:H5'	2.47	0.45
25:AY:421:GLU:O	25:AY:481:ALA:HB1	2.16	0.45
28:BA:866:A:C2	28:BA:867:C:N1	2.83	0.45
28:BA:2108:A:C2'	28:BA:2109:U:O5'	2.65	0.45
35:BJ:55:ILE:HD11	35:BJ:130:HIS:CD2	2.51	0.45
48:BW:17:ALA:O	48:BW:18:LYS:CB	2.63	0.45
57:B5:33:VAL:HG12	57:B5:34:THR:N	2.26	0.45
1:AA:982:U:H4'	1:AA:983:A:O5'	2.17	0.45
1:AA:1159:U:P	2:AB:131:LYS:HZ2	2.40	0.45
1:AA:1302:C:O5'	1:AA:1302:C:C6	2.70	0.45
7:AG:4:ARG:O	7:AG:6:VAL:N	2.47	0.45
13:AM:11:ASP:OD1	13:AM:12:HIS:N	2.36	0.45
19:AS:10:PHE:HE1	19:AS:37:ARG:HD2	1.82	0.45
22:AV:27:U:O5'	22:AV:27:U:H6	1.99	0.45
25:AY:493:THR:HG22	25:AY:613:LEU:HD21	1.97	0.45
28:BA:33:C:O2	28:BA:447:A:N6	2.50	0.45
28:BA:1057:A:C6	28:BA:1086:A:C2	3.04	0.45
28:BA:1248:G:C5	30:BE:46:GLN:NE2	2.84	0.45
28:BA:1936:A:N6	28:BA:1963:U:C2	2.84	0.45
28:BA:1942:C:OP2	28:BA:1943:U:O2'	2.28	0.45
28:BA:2262:U:H4'	28:BA:2328:A:C2	2.52	0.45
28:BA:2740:A:C6	28:BA:2764:A:C8	3.04	0.45
39:BN:103:ARG:HD3	39:BN:110:MET:HE3	1.98	0.45
45:BT:29:THR:HB	45:BT:86:THR:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1083:U:H2'	1:AA:1084:G:O4'	2.17	0.45
1:AA:1410:A:H2'	1:AA:1411:C:C6	2.50	0.45
6:AF:42:TRP:CE2	6:AF:101:PRO:HD3	2.51	0.45
25:AY:231:GLU:HA	25:AY:234:MET:HG2	1.98	0.45
25:AY:317:PHE:CE1	25:AY:343:VAL:CG2	2.99	0.45
26:BB:11:C:O2'	26:BB:15:A:N6	2.50	0.45
27:BC:12:ARG:HD3	28:BA:728:G:H4'	1.98	0.45
28:BA:1686:C:C2	28:BA:1703:G:C2	3.05	0.45
28:BA:2024:G:C4	28:BA:2040:G:N2	2.84	0.45
28:BA:2615:U:C2	52:B0:3:GLN:HA	2.51	0.45
29:BD:1:MET:HG2	29:BD:205:PRO:HG3	1.98	0.45
34:BI:100:ILE:CG2	34:BI:101:SER:N	2.79	0.45
37:BL:132:ARG:HG3	37:BL:142:ILE:HD12	1.98	0.45
40:BO:41:ALA:O	40:BO:44:GLY:N	2.41	0.45
41:BP:21:PRO:HD3	41:BP:49:ILE:HD12	1.98	0.45
42:BQ:91:ARG:HH12	43:BR:10:LYS:HB3	1.82	0.45
51:BZ:3:THR:HA	51:BZ:37:ARG:O	2.16	0.45
1:AA:747:A:H5'	1:AA:748:G:OP2	2.17	0.45
1:AA:1119:C:P	9:AI:85:ARG:HH22	2.40	0.45
1:AA:1130:A:C4'	9:AI:20:PHE:CD2	3.00	0.45
3:AC:7:PRO:CG	3:AC:184:TYR:CG	2.99	0.45
9:AI:130:ARG:HD3	23:AW:33:U:C5	2.50	0.45
25:AY:193:TRP:CH2	25:AY:276:GLN:HB2	2.51	0.45
25:AY:565:PRO:CG	25:AY:605:PHE:CD2	2.99	0.45
28:BA:627:A:C6	28:BA:637:A:C8	3.04	0.45
28:BA:666:A:H4'	37:BL:48:ARG:HD2	1.99	0.45
28:BA:751:A:C6	28:BA:789:A:C5	3.04	0.45
28:BA:973:A:O4'	28:BA:1188:U:C6	2.70	0.45
28:BA:2197:U:O3'	33:BH:29:PHE:CD1	2.65	0.45
29:BD:70:LYS:O	29:BD:71:ALA:HB3	2.17	0.45
36:BK:13:ASN:O	36:BK:14:SER:OG	2.29	0.45
37:BL:61:LEU:O	55:B3:12:ARG:HD3	2.16	0.45
40:BO:43:ASN:O	40:BO:45:SER:N	2.50	0.45
45:BT:69:ARG:CD	45:BT:70:HIS:H	2.28	0.45
53:B1:16:THR:HG21	53:B1:41:VAL:HG13	1.97	0.45
1:AA:1081:A:C2'	1:AA:1082:A:H5'	2.47	0.45
1:AA:1151:A:HO2'	1:AA:1152:A:H8	1.64	0.45
1:AA:1392:G:C4'	1:AA:1531:A:H5"	2.41	0.45
10:AJ:73:LEU:O	10:AJ:75:ASP:N	2.50	0.45
23:AW:76:A:N1	28:BA:2422:C:C4	2.84	0.45
25:AY:33:TYR:HE2	25:AY:275:VAL:HB	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:219:HIS:C	25:AY:221:ASN:N	2.68	0.45
28:BA:855:G:H21	48:BW:23:LYS:HG2	1.82	0.45
28:BA:1542:U:H2'	28:BA:1543:G:O4'	2.16	0.45
28:BA:2326:C:H4'	28:BA:2327:A:OP1	2.16	0.45
28:BA:2436:G:C2	28:BA:2437:G:C8	3.04	0.45
30:BE:154:ASP:OD1	30:BE:154:ASP:N	2.50	0.45
35:BJ:30:THR:HG22	35:BJ:31:GLU:N	2.31	0.45
39:BN:103:ARG:CZ	39:BN:110:MET:CE	2.95	0.45
44:BS:18:ARG:HG3	44:BS:76:VAL:HG13	1.98	0.45
45:BT:29:THR:CB	45:BT:86:THR:H	2.29	0.45
48:BW:39:GLN:HG3	48:BW:42:THR:H	1.81	0.45
56:B4:36:ARG:O	56:B4:37:GLN:C	2.55	0.45
1:AA:481:G:O2'	1:AA:482:A:C8	2.66	0.45
6:AF:86:ARG:NH1	18:AR:64:TYR:HB3	2.32	0.45
9:AI:44:ALA:HB1	9:AI:76:ALA:CB	2.47	0.45
11:AK:82:LEU:HD21	11:AK:105:PHE:HB3	1.99	0.45
11:AK:127:ARG:NH2	21:AU:33:ARG:O	2.47	0.45
13:AM:114:LYS:H	13:AM:115:PRO:CD	2.30	0.45
25:AY:93:VAL:HG22	25:AY:94:ASP:H	1.82	0.45
25:AY:95:PHE:CZ	59:AY:801:FUA:C23	2.93	0.45
25:AY:193:TRP:CZ3	25:AY:276:GLN:HB2	2.51	0.45
28:BA:792:A:C6	28:BA:2440:C:C6	3.05	0.45
28:BA:996:A:H4'	42:BQ:91:ARG:CD	2.47	0.45
28:BA:1031:G:C4'	56:B4:6:SER:HB2	2.47	0.45
28:BA:1141:U:H4'	28:BA:1142:A:O4'	2.17	0.45
28:BA:2091:C:C2	28:BA:2092:U:C4	3.04	0.45
28:BA:2103:C:H2'	28:BA:2104:C:C5'	2.47	0.45
28:BA:2407:A:C2	28:BA:2408:U:C2	3.05	0.45
28:BA:2897:U:H2'	28:BA:2898:U:C6	2.51	0.45
29:BD:193:VAL:HB	29:BD:194:PRO:HD2	1.97	0.45
31:BF:39:VAL:HG13	31:BF:40:GLY:N	2.31	0.45
32:BG:83:THR:C	32:BG:84:LYS:HD3	2.37	0.45
33:BH:8:LYS:O	33:BH:13:GLY:HA2	2.16	0.45
35:BJ:44:TYR:O	35:BJ:45:THR:CB	2.64	0.45
42:BQ:103:VAL:HG23	42:BQ:104:ALA:N	2.32	0.45
47:BV:80:HIS:CD2	47:BV:83:LYS:HB2	2.52	0.45
1:AA:653:U:H5'	8:AH:56:LYS:HE2	1.98	0.45
1:AA:1131:G:H5'	9:AI:5:GLN:HE21	1.81	0.45
2:AB:71:THR:HG22	2:AB:72:LYS:H	1.81	0.45
27:BC:265:PHE:N	27:BC:265:PHE:HD1	2.15	0.45
28:BA:288:U:H2'	28:BA:289:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:1509:A:HO2'	28:BA:1510:G:P	2.37	0.45
28:BA:2093:G:C2'	28:BA:2094:A:H5'	2.45	0.45
29:BD:121:THR:O	29:BD:122:VAL:HB	2.17	0.45
37:BL:122:VAL:CG1	37:BL:142:ILE:HG12	2.47	0.45
43:BR:49:ILE:HG22	43:BR:53:PHE:C	2.36	0.45
48:BW:30:VAL:O	48:BW:30:VAL:CG1	2.64	0.45
57:B5:100:ALA:HB3	57:B5:125:ARG:HD2	1.98	0.45
57:B5:125:ARG:HA	57:B5:125:ARG:CZ	2.46	0.45
1:AA:76:G:N2	1:AA:95:C:N3	2.65	0.45
1:AA:355:C:C4	1:AA:356:A:N7	2.85	0.45
1:AA:928:G:N1	1:AA:1390:U:C2	2.85	0.45
2:AB:216:VAL:HA	2:AB:219:THR:HG22	1.98	0.45
25:AY:18:HIS:HE1	28:BA:2660:A:O2'	2.00	0.45
25:AY:71:PHE:CE1	25:AY:83:ARG:HG3	2.52	0.45
25:AY:649:VAL:HA	34:BI:25:PRO:CG	2.46	0.45
27:BC:76:VAL:O	27:BC:76:VAL:HG22	2.17	0.45
28:BA:315:G:H2'	28:BA:316:C:C6	2.52	0.45
28:BA:938:G:OP2	55:B3:51:LYS:NZ	2.33	0.45
28:BA:1150:C:H2'	28:BA:1151:A:O5'	2.17	0.45
28:BA:1340:U:H4'	28:BA:1341:G:OP2	2.17	0.45
28:BA:2365:G:H4'	48:BW:59:PHE:CZ	2.51	0.45
28:BA:2467:C:OP1	56:B4:8:LYS:NZ	2.48	0.45
33:BH:14:SER:OG	33:BH:17:ASP:CG	2.55	0.45
48:BW:19:ARG:C	48:BW:19:ARG:CD	2.85	0.45
57:B5:48:ALA:HB3	57:B5:51:TYR:HB3	1.98	0.45
1:AA:8:A:N1	4:AD:206:LYS:HD3	2.32	0.45
1:AA:15:G:H1'	5:AE:22:SER:OG	2.17	0.45
1:AA:111:G:C6	1:AA:330:C:N4	2.84	0.45
1:AA:460:A:H2	1:AA:462:G:C8	2.34	0.45
1:AA:843:U:O2	1:AA:844:G:N7	2.50	0.45
23:AW:54:U:O4	23:AW:58:A:N7	2.50	0.45
28:BA:1171:G:C6	28:BA:1172:C:C4	3.04	0.45
28:BA:1482:G:H1'	28:BA:1509:A:N6	2.30	0.45
28:BA:2021:C:P	52:B0:8:THR:HG21	2.56	0.45
28:BA:2043:C:OP1	28:BA:2777:G:O2'	2.24	0.45
28:BA:2195:U:O2'	28:BA:2196:C:C5'	2.58	0.45
28:BA:2307:G:N2	28:BA:2311:A:C8	2.86	0.45
28:BA:2344:U:H4'	28:BA:2345:G:OP1	2.17	0.45
31:BF:113:PHE:HE1	31:BF:116:LEU:HD13	1.81	0.45
32:BG:23:ILE:HD12	32:BG:23:ILE:H	1.81	0.45
34:BI:57:VAL:HG23	34:BI:71:LYS:CE	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BK:80:ASP:CB	41:BP:67:GLU:HG3	2.47	0.45
39:BN:33:ILE:CD1	39:BN:118:ARG:NE	2.80	0.45
46:BU:53:GLN:N	46:BU:54:PRO:CD	2.80	0.45
53:B1:4:ILE:HG23	53:B1:5:ARG:N	2.32	0.45
57:B5:129:LEU:CB	57:B5:130:PRO:HD2	2.47	0.45
1:AA:376:G:H2'	1:AA:377:G:H8	1.82	0.44
1:AA:1371:G:OP2	9:AI:111:VAL:HG12	2.16	0.44
4:AD:23:SER:O	4:AD:25:VAL:N	2.50	0.44
4:AD:65:TYR:N	4:AD:65:TYR:CD1	2.84	0.44
4:AD:145:ILE:CD1	4:AD:155:VAL:HG21	2.47	0.44
8:AH:106:THR:HG21	8:AH:121:LEU:HD13	1.99	0.44
10:AJ:17:LEU:HD21	10:AJ:96:VAL:CG2	2.48	0.44
22:AV:7:G:H3'	22:AV:8:U:H5'	1.97	0.44
22:AV:38:A:O2'	22:AV:39:C:H5'	2.16	0.44
28:BA:1338:G:O2'	28:BA:1393:A:N1	2.44	0.44
28:BA:1737:G:H5"	28:BA:1738:G:OP2	2.17	0.44
32:BG:104:LEU:HB2	32:BG:112:VAL:CG2	2.47	0.44
51:BZ:5:LYS:HD2	51:BZ:5:LYS:N	2.32	0.44
53:B1:33:LEU:N	53:B1:51:ALA:CB	2.80	0.44
1:AA:255:G:OP1	17:AQ:71:LYS:NZ	2.49	0.44
1:AA:1071:C:C5'	5:AE:54:ARG:NH1	2.74	0.44
1:AA:1102:A:O2'	2:AB:97:GLY:O	2.34	0.44
1:AA:1118:U:OP1	9:AI:106:ARG:CD	2.65	0.44
1:AA:1125:U:O2	1:AA:1126:U:O2'	2.26	0.44
4:AD:197:GLU:O	4:AD:200:ILE:HG22	2.17	0.44
5:AE:44:GLY:H	5:AE:76:LEU:HD12	1.81	0.44
6:AF:43:GLY:HA2	6:AF:58:HIS:CE1	2.52	0.44
16:AP:10:GLY:HA3	16:AP:15:PRO:HA	1.98	0.44
24:AX:7:A:N3	24:AX:7:A:C2'	2.77	0.44
27:BC:24:HIS:NE2	27:BC:79:ARG:NH2	2.65	0.44
28:BA:278:A:N1	28:BA:362:A:C8	2.85	0.44
28:BA:818:G:H5'	28:BA:839:U:OP1	2.18	0.44
28:BA:994:C:H1'	43:BR:10:LYS:CE	2.47	0.44
28:BA:1045:C:C3'	28:BA:1046:A:H5'	2.48	0.44
28:BA:1936:A:C2	28:BA:1943:U:C5	3.03	0.44
28:BA:2091:C:C5	28:BA:2092:U:C5	3.05	0.44
28:BA:2862:G:C6	28:BA:2863:C:C4	3.04	0.44
29:BD:86:GLU:CD	29:BD:86:GLU:N	2.69	0.44
31:BF:72:SER:HB2	31:BF:80:GLN:HB2	1.99	0.44
31:BF:107:VAL:HG11	31:BF:116:LEU:HD21	1.99	0.44
34:BI:125:THR:O	34:BI:128:ILE:N	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BM:26:VAL:HB	38:BM:133:LYS:HA	2.00	0.44
41:BP:58:PHE:CE1	41:BP:75:THR:HG22	2.51	0.44
47:BV:80:HIS:CD2	47:BV:82:TYR:H	2.35	0.44
53:B1:8:ILE:HG21	53:B1:51:ALA:HA	1.98	0.44
57:B5:71:CYS:HA	57:B5:117:LEU:HD11	1.96	0.44
57:B5:127:ALA:O	57:B5:129:LEU:N	2.48	0.44
1:AA:1447:A:H5'	1:AA:1448:C:H5	1.82	0.44
1:AA:1451:U:H5"	1:AA:1452:C:C5	2.52	0.44
6:AF:9:MET:HG2	6:AF:86:ARG:O	2.17	0.44
13:AM:54:ASP:HA	13:AM:57:ARG:CB	2.47	0.44
18:AR:22:ASP:OD1	18:AR:24:LYS:NZ	2.45	0.44
22:AV:12:G:H5'	28:BA:1909:C:H4'	1.98	0.44
23:AW:64:G:C6	23:AW:65:U:C4	3.06	0.44
25:AY:625:GLU:OE2	28:BA:1095:A:N6	2.50	0.44
28:BA:271:G:H4'	28:BA:272:A:OP1	2.17	0.44
28:BA:1485:U:H2'	28:BA:1486:U:H6	1.82	0.44
28:BA:2091:C:OP2	28:BA:2092:U:C5'	2.54	0.44
28:BA:2698:U:H2'	28:BA:2699:C:C6	2.50	0.44
28:BA:2745:C:C4	28:BA:2746:U:C4	3.05	0.44
35:BJ:80:HIS:O	35:BJ:82:GLY:N	2.50	0.44
36:BK:98:ARG:HA	36:BK:118:LEU:CD2	2.47	0.44
36:BK:99:ILE:HG21	36:BK:119:ALA:HB2	1.98	0.44
46:BU:6:ARG:O	46:BU:24:VAL:HB	2.17	0.44
48:BW:37:VAL:HG11	48:BW:55:ASP:HB2	1.99	0.44
57:B5:136:ILE:HG13	57:B5:139:LEU:HD12	1.98	0.44
1:AA:243:A:C4	1:AA:245:U:C5	3.06	0.44
1:AA:1076:U:C2'	1:AA:1077:G:O5'	2.66	0.44
1:AA:1391:U:O2'	1:AA:1392:G:H5"	2.13	0.44
6:AF:3:HIS:CD2	6:AF:92:THR:HG23	2.52	0.44
7:AG:15:ASP:HB3	7:AG:20:SER:H	1.82	0.44
7:AG:56:LYS:O	7:AG:61:ALA:HB2	2.17	0.44
11:AK:125:LYS:HG2	21:AU:35:ARG:HG2	2.00	0.44
14:AN:36:ALA:HB2	14:AN:41:ARG:CG	2.47	0.44
25:AY:658:VAL:HG21	25:AY:663:MET:SD	2.57	0.44
27:BC:93:VAL:HG12	27:BC:94:LEU:N	2.31	0.44
28:BA:799:G:C6	28:BA:800:A:C6	3.05	0.44
28:BA:1593:A:H2'	28:BA:1594:U:O4'	2.17	0.44
28:BA:1662:U:O2	28:BA:2687:U:H4'	2.17	0.44
28:BA:1857:G:C2	28:BA:1884:G:N3	2.86	0.44
28:BA:2276:G:P	38:BM:83:GLY:O	2.76	0.44
28:BA:2682:A:C8	29:BD:11:MET:HG3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:2788:C:H2'	28:BA:2789:C:C6	2.53	0.44
29:BD:3:GLY:HA3	29:BD:204:LYS:HG2	1.99	0.44
29:BD:69:ALA:HA	29:BD:73:VAL:CG1	2.47	0.44
34:BI:109:ALA:CB	34:BI:128:ILE:HG13	2.48	0.44
40:BO:75:GLY:HA3	40:BO:109:ALA:HB3	2.00	0.44
41:BP:102:ARG:O	41:BP:103:THR:HG22	2.17	0.44
44:BS:1:MET:O	44:BS:108:SER:HB2	2.16	0.44
45:BT:69:ARG:CG	45:BT:70:HIS:N	2.81	0.44
55:B3:31:ILE:HG13	55:B3:31:ILE:O	2.17	0.44
1:AA:15:G:C5'	5:AE:29:ARG:CZ	2.96	0.44
1:AA:1124:G:H2'	1:AA:1145:A:N6	2.33	0.44
1:AA:1328:C:H5"	13:AM:28:THR:HG21	2.00	0.44
1:AA:1339:A:C2	23:AW:31:A:O4'	2.70	0.44
1:AA:1392:G:H1'	1:AA:1503:A:OP1	2.18	0.44
2:AB:88:GLN:HE22	2:AB:220:VAL:CG2	2.27	0.44
5:AE:72:ILE:HG12	5:AE:73:ASN:N	2.33	0.44
9:AI:34:SER:HB3	9:AI:37:GLN:HG2	1.98	0.44
11:AK:126:LYS:HG3	11:AK:127:ARG:HE	1.82	0.44
22:AV:54:5MU:C2'	22:AV:55:U:H5'	2.47	0.44
22:AV:74:C:H2'	22:AV:75:C:H5'	1.99	0.44
24:AX:14:A:C2	24:AX:15:A:H5'	2.50	0.44
26:BB:90:C:H6	26:BB:90:C:H5"	1.83	0.44
28:BA:132:G:C2'	28:BA:133:U:H5'	2.48	0.44
28:BA:277:G:H2'	28:BA:361:G:O6	2.17	0.44
28:BA:720:U:H2'	28:BA:721:A:C8	2.53	0.44
28:BA:980:A:C6	28:BA:981:A:N1	2.86	0.44
28:BA:1071:G:H1'	28:BA:1089:A:C5	2.53	0.44
28:BA:1181:U:H2'	28:BA:1182:G:C8	2.52	0.44
28:BA:1509:A:O2'	28:BA:1510:G:P	2.76	0.44
28:BA:1867:G:C5	28:BA:1868:C:C5	3.06	0.44
28:BA:1966:A:N3	28:BA:2592:G:O2'	2.46	0.44
28:BA:2326:C:H3'	28:BA:2326:C:C6	2.52	0.44
28:BA:2902:C:H2'	28:BA:2903:U:O5'	2.18	0.44
31:BF:127:TYR:O	31:BF:128:SER:CB	2.65	0.44
34:BI:40:ALA:O	34:BI:68:PHE:CZ	2.71	0.44
50:BY:45:GLN:O	50:BY:46:VAL:HB	2.17	0.44
57:B5:63:ALA:HB3	57:B5:84:TYR:CE2	2.52	0.44
1:AA:21:G:HO2'	1:AA:22:G:C4'	2.22	0.44
6:AF:18:VAL:HG21	6:AF:58:HIS:CD2	2.52	0.44
9:AI:60:LYS:HD2	9:AI:61:LEU:HD13	2.00	0.44
22:AV:9:G:N3	22:AV:45:G:H2'	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AV:14:A:H1'	22:AV:22:G:N2	2.33	0.44
23:AW:56:C:H2'	23:AW:57:G:C8	2.48	0.44
25:AY:611:VAL:HG21	25:AY:689:GLU:HG3	2.00	0.44
27:BC:255:LYS:NZ	28:BA:1844:C:O3'	2.43	0.44
28:BA:61:C:H2'	28:BA:62:U:H5'	2.00	0.44
28:BA:222:A:N6	28:BA:231:A:C2	2.86	0.44
28:BA:1439:A:C2	28:BA:1553:A:C4	3.06	0.44
28:BA:2108:A:H2'	28:BA:2109:U:O5'	2.17	0.44
28:BA:2353:G:N3	48:BW:30:VAL:HG12	2.32	0.44
29:BD:45:TYR:CD1	29:BD:45:TYR:N	2.86	0.44
29:BD:110:THR:HG23	29:BD:171:THR:HG22	2.00	0.44
31:BF:128:SER:HA	31:BF:154:THR:HA	1.99	0.44
35:BJ:44:TYR:HA	42:BQ:59:LEU:CD2	2.48	0.44
36:BK:61:VAL:HG22	36:BK:87:LEU:HD11	1.98	0.44
39:BN:98:LEU:CB	52:B0:42:ILE:HD11	2.46	0.44
45:BT:48:GLN:O	45:BT:52:GLU:HA	2.17	0.44
48:BW:19:ARG:NH1	48:BW:22:VAL:HG21	2.33	0.44
54:B2:12:ARG:HH11	54:B2:44:VAL:HG11	1.82	0.44
57:B5:15:VAL:CG2	57:B5:66:GLY:HA2	2.47	0.44
1:AA:517:G:H5'	1:AA:519:C:C2	2.53	0.44
1:AA:636:U:C5'	17:AQ:6:ARG:HE	2.31	0.44
1:AA:1394:A:O2'	1:AA:1501:C:H1'	2.12	0.44
1:AA:1395:C:N4	1:AA:1396:A:C6	2.79	0.44
10:AJ:17:LEU:HA	10:AJ:20:GLN:HG2	1.98	0.44
25:AY:393:THR:HG21	25:AY:443:PRO:HD3	1.99	0.44
26:BB:51:G:H5"	40:BO:64:TYR:CD2	2.52	0.44
27:BC:109:LEU:HD23	27:BC:110:LYS:H	1.83	0.44
27:BC:163:ILE:HG23	27:BC:171:VAL:CG1	2.47	0.44
28:BA:85:G:OP1	46:BU:6:ARG:N	2.49	0.44
28:BA:580:U:O3'	42:BQ:30:VAL:HG13	2.18	0.44
30:BE:160:ALA:O	30:BE:161:ALA:HB3	2.18	0.44
36:BK:76:VAL:CB	41:BP:72:VAL:HG22	2.47	0.44
48:BW:36:ILE:O	48:BW:36:ILE:HG22	2.18	0.44
57:B5:3:LEU:HB2	57:B5:4:ASN:H	1.68	0.44
57:B5:51:TYR:CE1	57:B5:52:MET:HG2	2.53	0.44
1:AA:202:G:O2'	1:AA:468:A:H8	2.01	0.44
1:AA:328:C:H4'	1:AA:329:A:H5"	1.99	0.44
1:AA:601:G:H2'	1:AA:602:A:C8	2.52	0.44
1:AA:658:C:O4'	15:AO:22:THR:OG1	2.33	0.44
1:AA:976:G:C2	1:AA:1363:A:C2	3.06	0.44
1:AA:1014:A:H5'	19:AS:14:HIS:CG	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1158:C:N4	1:AA:1160:G:C4	2.86	0.44
1:AA:1240:U:P	7:AG:116:MET:CB	3.06	0.44
4:AD:12:SER:HA	4:AD:19:LEU:CD1	2.47	0.44
5:AE:56:VAL:O	5:AE:60:ILE:HG12	2.18	0.44
9:AI:24:GLY:HA3	9:AI:62:ASP:HB2	1.99	0.44
9:AI:130:ARG:CD	23:AW:33:U:H5	2.30	0.44
25:AY:193:TRP:CZ3	25:AY:202:PHE:HE1	2.36	0.44
59:AY:801:FUA:C20	59:AY:801:FUA:O1	2.62	0.44
28:BA:948:C:H1'	28:BA:984:A:O2'	2.18	0.44
28:BA:980:A:C4	28:BA:1136:G:O4'	2.70	0.44
28:BA:1252:G:C2	42:BQ:32:ARG:HG2	2.52	0.44
28:BA:2747:G:O6	28:BA:2755:C:H5"	2.18	0.44
34:BI:45:THR:O	34:BI:48:ILE:HG13	2.18	0.44
34:BI:137:LEU:HD23	34:BI:137:LEU:H	1.81	0.44
36:BK:118:LEU:O	36:BK:119:ALA:HB3	2.17	0.44
38:BM:102:LEU:N	38:BM:102:LEU:HD12	2.32	0.44
39:BN:38:LEU:HB3	39:BN:39:PRO:CD	2.48	0.44
44:BS:66:ILE:HD13	44:BS:67:ASP:N	2.32	0.44
46:BU:73:ASN:O	46:BU:74:ALA:HB3	2.18	0.44
57:B5:87:GLU:OE2	57:B5:95:LEU:HD23	2.18	0.44
1:AA:530:G:O6	24:AX:16:A:C2'	2.65	0.44
1:AA:1198:G:N2	10:AJ:55:PRO:CG	2.81	0.44
4:AD:148:LYS:H	4:AD:148:LYS:HD2	1.83	0.44
6:AF:55:HIS:O	6:AF:56:LYS:HB2	2.18	0.44
11:AK:35:THR:OG1	11:AK:41:ALA:N	2.51	0.44
12:AL:72:HIS:ND1	12:AL:73:ASN:O	2.41	0.44
20:AT:68:HIS:HB3	20:AT:69:LYS:HZ2	1.83	0.44
23:AW:12:U:C2	23:AW:23:A:N1	2.86	0.44
25:AY:90:PRO:HG2	25:AY:98:GLU:HB2	2.00	0.44
26:BB:78:A:H2'	26:BB:79:G:O4'	2.18	0.44
26:BB:78:A:C2	26:BB:99:A:C4	3.06	0.44
28:BA:820:A:H2'	28:BA:821:A:O4'	2.16	0.44
28:BA:979:A:H2'	28:BA:982:C:H42	1.82	0.44
28:BA:1003:G:N2	28:BA:1004:U:C2	2.86	0.44
28:BA:1219:U:OP2	42:BQ:18:LYS:NZ	2.46	0.44
28:BA:1223:G:P	43:BR:68:ARG:HH11	2.41	0.44
28:BA:2039:U:H2'	28:BA:2040:G:H8	1.82	0.44
28:BA:2197:U:O2'	28:BA:2198:A:C4	2.62	0.44
28:BA:2283:C:H5"	28:BA:2389:G:O2'	2.17	0.44
29:BD:44:GLY:HA3	29:BD:45:TYR:HD1	1.82	0.44
40:BO:79:ALA:O	40:BO:82:ALA:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BQ:91:ARG:HH11	43:BR:11:GLN:N	2.16	0.44
45:BT:69:ARG:HG3	45:BT:70:HIS:H	1.83	0.44
1:AA:561:U:O2'	1:AA:562:U:OP1	2.32	0.43
5:AE:111:MET:HE3	5:AE:125:ALA:HB1	2.00	0.43
15:AO:3:LEU:HD23	15:AO:8:THR:HG22	2.00	0.43
24:AX:14:A:HO2'	24:AX:15:A:P	2.41	0.43
25:AY:303:LYS:HA	25:AY:303:LYS:CE	2.48	0.43
25:AY:498:VAL:CG2	25:AY:608:ALA:HA	2.48	0.43
25:AY:617:MET:HG3	25:AY:682:MET:HE3	2.00	0.43
28:BA:336:C:N3	28:BA:337:C:C5	2.86	0.43
28:BA:764:A:C6	28:BA:781:A:C2	3.06	0.43
28:BA:819:A:C4	28:BA:1189:A:C2	3.06	0.43
28:BA:1232:G:C5	28:BA:1233:C:C5	3.06	0.43
28:BA:2180:U:C2	28:BA:2181:U:C5	3.06	0.43
28:BA:2196:C:O2	28:BA:2197:U:N3	2.50	0.43
28:BA:2657:A:C2	28:BA:2665:A:C4	3.06	0.43
28:BA:2846:G:H2'	28:BA:2847:U:O4'	2.17	0.43
29:BD:120:GLY:HA2	29:BD:162:ALA:HA	2.00	0.43
30:BE:188:MET:HE3	30:BE:196:VAL:HG21	2.00	0.43
31:BF:94:ARG:CG	31:BF:94:ARG:HH11	2.31	0.43
32:BG:32:LEU:O	32:BG:33:THR:OG1	2.31	0.43
32:BG:175:LYS:HA	32:BG:176:LYS:HA	1.78	0.43
39:BN:117:ASP:O	39:BN:118:ARG:C	2.57	0.43
41:BP:50:ARG:CB	41:BP:57:ALA:N	2.78	0.43
42:BQ:27:ARG:HA	42:BQ:33:VAL:HG12	1.99	0.43
48:BW:24:ARG:HD3	48:BW:65:LYS:CD	2.48	0.43
51:BZ:39:ASP:OD2	51:BZ:44:ARG:NH1	2.46	0.43
1:AA:927:G:O2'	1:AA:1532:U:H4'	2.19	0.43
1:AA:1005:A:H2'	1:AA:1006:G:O4'	2.19	0.43
4:AD:125:VAL:HG23	4:AD:126:ASN:N	2.33	0.43
5:AE:46:VAL:O	5:AE:72:ILE:HG22	2.18	0.43
5:AE:72:ILE:HD11	5:AE:145:GLU:CG	2.48	0.43
9:AI:47:VAL:CG2	9:AI:76:ALA:HB1	2.48	0.43
21:AU:48:ALA:C	24:AX:3:U:P	2.96	0.43
22:AV:37:A:C1'	25:AY:508:GLN:OE1	2.65	0.43
27:BC:24:HIS:CE1	27:BC:79:ARG:HH21	2.36	0.43
27:BC:38:LYS:NZ	27:BC:57:HIS:O	2.39	0.43
28:BA:274:C:H2'	28:BA:275:C:O4'	2.19	0.43
28:BA:646:U:H3'	28:BA:647:G:H5"	1.99	0.43
28:BA:908:C:O2'	38:BM:70:ASP:CG	2.56	0.43
28:BA:1197:G:H2'	28:BA:1198:U:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:1428:C:C5	28:BA:1569:A:H5”	2.52	0.43
28:BA:2031:A:C6	28:BA:2498:C:H1’	2.53	0.43
28:BA:2090:A:C5	28:BA:2091:C:C5	3.06	0.43
28:BA:2517:C:C5	28:BA:2542:A:C5	3.06	0.43
30:BE:44:ARG:HH21	30:BE:44:ARG:CG	2.31	0.43
35:BJ:110:PRO:HB2	35:BJ:111:LYS:HG3	2.00	0.43
40:BO:31:THR:HG22	40:BO:34:HIS:N	2.33	0.43
49:BX:67:LEU:HD22	49:BX:77:TYR:CE1	2.53	0.43
1:AA:204:G:H3’	1:AA:205:A:H5”	2.00	0.43
1:AA:1534:A:O5’	1:AA:1534:A:C8	2.65	0.43
5:AE:115:LEU:HG	5:AE:120:VAL:HG21	1.99	0.43
6:AF:61:LEU:HD12	6:AF:62:MET:H	1.83	0.43
8:AH:66:PHE:O	8:AH:67:GLN:C	2.56	0.43
12:AL:44:LYS:HB3	12:AL:45:PRO:HD3	1.99	0.43
13:AM:4:ILE:HD12	13:AM:22:ILE:HD11	2.00	0.43
22:AV:32:C:C4	22:AV:33:U:C5	3.05	0.43
24:AX:14:A:C2	24:AX:15:A:C8	3.06	0.43
25:AY:19:ILE:HD13	25:AY:92:HIS:H	1.82	0.43
28:BA:476:G:H4’	28:BA:502:A:N1	2.33	0.43
28:BA:1224:U:H4’	43:BR:88:GLY:O	2.18	0.43
28:BA:1387:A:H5’	28:BA:1469:A:H1’	2.00	0.43
28:BA:1523:U:O2’	28:BA:1524:G:H5’	2.18	0.43
28:BA:2557:G:H2’	28:BA:2558:C:C6	2.54	0.43
31:BF:134:GLN:OE1	31:BF:149:ARG:HB3	2.18	0.43
34:BI:46:ASP:HA	34:BI:50:LYS:HD2	2.00	0.43
39:BN:8:ARG:HB3	39:BN:10:LEU:CD2	2.48	0.43
43:BR:74:ILE:HB	43:BR:87:GLN:O	2.18	0.43
47:BV:75:GLN:HB2	47:BV:92:VAL:CG2	2.48	0.43
48:BW:76:ARG:CG	48:BW:76:ARG:NH2	2.81	0.43
1:AA:143:A:H5’	1:AA:144:G:H5’	2.00	0.43
1:AA:495:A:C2	1:AA:496:A:C6	3.06	0.43
1:AA:736:C:H2’	1:AA:737:C:C6	2.53	0.43
1:AA:911:U:H2’	1:AA:912:C:C6	2.53	0.43
1:AA:1150:A:H1’	1:AA:1280:A:N6	2.33	0.43
1:AA:1380:U:O2	7:AG:3:ARG:NH2	2.49	0.43
4:AD:192:SER:OG	4:AD:193:ALA:O	2.37	0.43
4:AD:192:SER:HG	4:AD:193:ALA:N	2.16	0.43
8:AH:8:ALA:HA	8:AH:77:ARG:HG3	2.00	0.43
9:AI:7:TYR:CG	9:AI:8:GLY:N	2.87	0.43
12:AL:90:LEU:HB3	12:AL:93:VAL:CG2	2.48	0.43
17:AQ:57:ASP:OD2	17:AQ:81:LYS:NZ	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AV:68:C:H2'	22:AV:69:C:H6	1.81	0.43
23:AW:8:U:H3'	23:AW:13:C:N4	2.34	0.43
28:BA:201:C:OP1	49:BX:17:ARG:NH1	2.51	0.43
28:BA:833:A:OP2	37:BL:39:LYS:NZ	2.45	0.43
28:BA:975:A:C5	28:BA:990:A:N7	2.86	0.43
28:BA:1494:A:C2	28:BA:1495:A:C4	3.06	0.43
28:BA:1584:U:H2'	28:BA:1585:C:H5'	2.00	0.43
28:BA:1914:C:H2'	28:BA:1915:U:O4'	2.18	0.43
28:BA:2335:A:N6	28:BA:2337:G:H1'	2.33	0.43
28:BA:2758:A:H2'	28:BA:2759:G:H5'	1.99	0.43
29:BD:73:VAL:HG23	29:BD:74:GLU:H	1.82	0.43
30:BE:147:LEU:HB3	30:BE:186:VAL:HG23	2.00	0.43
34:BI:100:ILE:HD11	34:BI:137:LEU:CG	2.48	0.43
42:BQ:7:VAL:HG13	42:BQ:8:ILE:N	2.32	0.43
43:BR:64:VAL:O	43:BR:65:ALA:HB3	2.18	0.43
48:BW:17:ALA:O	48:BW:18:LYS:HB2	2.18	0.43
51:BZ:15:ARG:HG2	51:BZ:15:ARG:HH11	1.82	0.43
58:B6:13:ALA:HB1	58:B6:17:MET:CE	2.49	0.43
1:AA:16:A:HO2'	1:AA:17:U:C5'	2.32	0.43
1:AA:828:U:O2'	2:AB:24:PRO:HB3	2.19	0.43
1:AA:876:C:C1'	8:AH:12:THR:HG21	2.49	0.43
1:AA:1014:A:C5'	19:AS:14:HIS:HB2	2.48	0.43
1:AA:1075:U:O4'	1:AA:1101:A:C5	2.71	0.43
6:AF:92:THR:HG22	6:AF:93:LYS:N	2.34	0.43
28:BA:226:A:C6	28:BA:227:A:C6	3.07	0.43
28:BA:684:G:C2	28:BA:794:A:C2	3.06	0.43
28:BA:1171:G:N2	28:BA:1179:G:C4	2.86	0.43
28:BA:1365:A:OP1	49:BX:2:ARG:NE	2.48	0.43
28:BA:1441:G:H2'	28:BA:1442:U:C6	2.53	0.43
28:BA:2283:C:C2	28:BA:2389:G:C2	3.06	0.43
28:BA:2582:G:C2	28:BA:2583:G:C8	3.06	0.43
32:BG:123:GLU:HG2	32:BG:125:PRO:HD3	2.00	0.43
36:BK:47:ILE:HG13	36:BK:48:PRO:HD2	2.00	0.43
45:BT:40:LYS:HG2	45:BT:58:VAL:HG22	1.99	0.43
46:BU:38:ILE:HG23	46:BU:39:ASN:N	2.33	0.43
48:BW:39:GLN:HG2	48:BW:41:GLY:N	2.34	0.43
50:BY:21:LEU:HA	50:BY:25:GLN:HB3	2.01	0.43
1:AA:1053:G:N7	1:AA:1200:C:H5"	2.34	0.43
1:AA:1075:U:H5"	2:AB:101:THR:HG21	2.01	0.43
4:AD:30:THR:HG22	4:AD:31:LYS:H	1.83	0.43
5:AE:16:ILE:HG23	5:AE:110:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:89:ARG:NH2	28:BA:716:A:OP2	2.52	0.43
25:AY:25:THR:HG1	60:AY:802:GDP:PA	2.36	0.43
26:BB:27:C:C5	26:BB:28:C:C5	3.06	0.43
28:BA:348:A:C5	28:BA:349:U:C5	3.07	0.43
28:BA:479:A:N3	28:BA:481:G:H5"	2.34	0.43
28:BA:545:U:H2'	28:BA:546:U:O3'	2.18	0.43
28:BA:1204:A:C2	28:BA:1240:U:N3	2.87	0.43
28:BA:1281:G:C2	28:BA:1290:C:C2	3.07	0.43
28:BA:2564:A:C2	28:BA:2647:U:H4'	2.53	0.43
28:BA:2748:A:H1'	32:BG:66:THR:CG2	2.49	0.43
37:BL:111:ILE:HD12	37:BL:111:ILE:N	2.33	0.43
47:BV:29:ILE:HD13	47:BV:30:ILE:N	2.33	0.43
57:B5:17:GLU:OE1	57:B5:53:ARG:NH1	2.51	0.43
1:AA:928:G:C2'	1:AA:929:G:H5'	2.45	0.43
1:AA:1072:G:O6	1:AA:1102:A:N6	2.52	0.43
1:AA:1129:C:O2'	1:AA:1139:G:N7	2.49	0.43
1:AA:1240:U:OP2	7:AG:116:MET:CA	2.63	0.43
1:AA:1319:A:C5'	19:AS:4:SER:HB2	2.48	0.43
12:AL:44:LYS:CB	12:AL:45:PRO:CD	2.96	0.43
14:AN:21:PHE:C	14:AN:23:LYS:H	2.21	0.43
25:AY:119:VAL:HG13	25:AY:123:SER:HB2	2.00	0.43
26:BB:72:G:N2	26:BB:103:U:C5	2.86	0.43
28:BA:356:G:C6	28:BA:357:C:C4	3.07	0.43
28:BA:581:C:H2'	28:BA:582:A:C8	2.53	0.43
28:BA:822:G:H2'	28:BA:823:C:H6	1.83	0.43
28:BA:1443:U:H2'	28:BA:1444:G:C8	2.53	0.43
28:BA:1638:C:H4'	28:BA:2710:C:O2	2.18	0.43
32:BG:24:THR:HG23	32:BG:34:ARG:HG2	1.99	0.43
35:BJ:44:TYR:O	35:BJ:44:TYR:CD2	2.71	0.43
38:BM:13:HIS:O	38:BM:14:LYS:CB	2.66	0.43
42:BQ:60:TRP:CE2	42:BQ:93:ILE:HB	2.54	0.43
42:BQ:86:SER:O	43:BR:51:VAL:HA	2.18	0.43
50:BY:31:GLN:HG2	50:BY:36:GLN:HB2	2.01	0.43
50:BY:56:LEU:H	50:BY:56:LEU:HD22	1.84	0.43
51:BZ:13:ILE:HG22	51:BZ:14:GLY:N	2.34	0.43
57:B5:54:VAL:O	57:B5:55:VAL:C	2.57	0.43
57:B5:88:HIS:CB	57:B5:89:PRO:CD	2.97	0.43
1:AA:8:A:H62	4:AD:205:SER:HB2	1.83	0.43
1:AA:690:G:O6	11:AK:53:ARG:NH2	2.46	0.43
1:AA:1480:A:H2'	1:AA:1481:U:O4'	2.19	0.43
5:AE:46:VAL:HG21	5:AE:118:ALA:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:111:ARG:HE	7:AG:123:GLU:HG2	1.83	0.43
9:AI:89:GLU:CG	9:AI:90:TYR:N	2.82	0.43
12:AL:23:ALA:HB3	12:AL:95:TYR:CE2	2.53	0.43
13:AM:49:SER:HB2	13:AM:52:GLN:HB2	2.01	0.43
14:AN:45:VAL:HG23	14:AN:46:LEU:H	1.83	0.43
16:AP:70:ARG:O	16:AP:74:LEU:HG	2.19	0.43
20:AT:55:GLN:N	20:AT:56:PRO:HD2	2.33	0.43
22:AV:37:A:C8	25:AY:508:GLN:CD	2.91	0.43
28:BA:744:U:H2'	28:BA:745:G:O4'	2.19	0.43
28:BA:936:A:H2'	28:BA:937:C:C6	2.54	0.43
28:BA:959:A:H62	38:BM:82:MET:HE1	1.84	0.43
28:BA:1096:A:H2'	28:BA:1097:U:H5"	2.01	0.43
28:BA:2661:G:C6	28:BA:2662:A:C2	3.06	0.43
32:BG:60:GLY:O	32:BG:61:TRP:HB2	2.17	0.43
34:BI:9:LYS:HB3	34:BI:71:LYS:NZ	2.34	0.43
34:BI:82:ALA:HB1	34:BI:108:ILE:HG21	2.00	0.43
37:BL:2:ARG:HA	37:BL:5:THR:CG2	2.48	0.43
1:AA:115:G:H1'	1:AA:116:A:N7	2.34	0.43
1:AA:693:G:C4'	24:AX:7:A:H1'	2.49	0.43
1:AA:731:G:H5'	1:AA:766:A:H4'	2.01	0.43
1:AA:890:G:O2'	1:AA:906:A:N6	2.52	0.43
1:AA:1081:A:C2	1:AA:1082:A:N1	2.87	0.43
1:AA:1415:G:C6	1:AA:1486:G:C5	3.06	0.43
2:AB:46:VAL:O	2:AB:49:PHE:CD2	2.72	0.43
2:AB:118:THR:O	2:AB:119:GLN:HB3	2.18	0.43
4:AD:198:HIS:O	4:AD:202:GLU:CB	2.67	0.43
4:AD:198:HIS:O	4:AD:202:GLU:HB2	2.18	0.43
9:AI:28:ILE:HG13	9:AI:63:LEU:HD21	2.00	0.43
11:AK:126:LYS:O	11:AK:127:ARG:HB2	2.18	0.43
21:AU:25:LYS:HG2	21:AU:26:ALA:N	2.34	0.43
22:AV:76:A:H4'	22:AV:76:A:OP1	2.18	0.43
25:AY:95:PHE:CE2	59:AY:801:FUA:H122	2.45	0.43
26:BB:106:G:H2'	26:BB:107:G:O4'	2.19	0.43
28:BA:84:A:P	46:BU:5:ARG:HH22	2.42	0.43
28:BA:2274:A:C5	28:BA:2276:G:C8	3.07	0.43
29:BD:133:THR:HG23	29:BD:134:HIS:N	2.33	0.43
30:BE:51:GLU:OE2	30:BE:88:ARG:NH1	2.45	0.43
31:BF:134:GLN:HG2	31:BF:135:ILE:N	2.34	0.43
32:BG:31:GLU:O	32:BG:33:THR:N	2.52	0.43
32:BG:36:LEU:HD22	32:BG:36:LEU:N	2.33	0.43
35:BJ:60:ASP:N	35:BJ:60:ASP:OD1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BN:8:ARG:HB3	39:BN:10:LEU:HD22	2.01	0.43
42:BQ:4:LYS:HZ3	42:BQ:7:VAL:CG1	2.32	0.43
48:BW:24:ARG:HD3	48:BW:65:LYS:HG2	2.00	0.43
53:B1:5:ARG:CZ	53:B1:24:LYS:HA	2.49	0.43
1:AA:16:A:O2'	5:AE:21:VAL:CB	2.67	0.43
1:AA:208:U:C2	1:AA:212:G:N2	2.87	0.43
1:AA:328:C:O2	1:AA:328:C:H2'	2.19	0.43
2:AB:68:PHE:O	2:AB:91:VAL:N	2.50	0.43
3:AC:70:THR:O	3:AC:106:VAL:N	2.52	0.43
5:AE:91:GLY:HA3	5:AE:130:SER:HB3	2.00	0.43
6:AF:82:ASP:OD1	6:AF:82:ASP:N	2.52	0.43
9:AI:60:LYS:HD2	9:AI:61:LEU:CD1	2.49	0.43
22:AV:11:A:O2'	22:AV:12:G:H5'	2.18	0.43
22:AV:36:C:N3	24:AX:11:G:N2	2.67	0.43
28:BA:172:A:H2'	28:BA:173:A:C8	2.53	0.43
28:BA:855:G:H21	48:BW:23:LYS:CG	2.31	0.43
28:BA:1188:U:H4'	43:BR:81:LYS:O	2.19	0.43
28:BA:1239:G:H2'	28:BA:1240:U:O4'	2.19	0.43
28:BA:2070:A:H2'	28:BA:2071:A:O4'	2.19	0.43
28:BA:2823:A:C5	28:BA:2824:C:C5	3.07	0.43
30:BE:187:VAL:O	30:BE:188:MET:CB	2.67	0.43
32:BG:39:ALA:HB2	32:BG:57:TYR:CD2	2.54	0.43
43:BR:16:GLU:HA	43:BR:98:ILE:HG22	2.01	0.43
51:BZ:4:ILE:HD13	51:BZ:44:ARG:NH1	2.34	0.43
51:BZ:15:ARG:HD3	51:BZ:53:MET:SD	2.59	0.43
57:B5:17:GLU:HA	57:B5:88:HIS:CE1	2.54	0.43
1:AA:72:A:H3'	1:AA:73:C:H5"	2.00	0.42
1:AA:1086:U:H5"	1:AA:1086:U:O2	2.19	0.42
1:AA:1158:C:C4	1:AA:1160:G:C4	3.07	0.42
1:AA:1475:G:O5'	28:BA:1689:A:O4'	2.35	0.42
4:AD:110:THR:HG23	4:AD:113:GLU:HB2	2.01	0.42
4:AD:150:LYS:HG2	4:AD:178:MET:SD	2.59	0.42
4:AD:163:GLU:HA	4:AD:167:LYS:HE2	2.01	0.42
7:AG:18:PHE:CE1	7:AG:58:GLU:HG2	2.54	0.42
10:AJ:35:GLN:HE21	10:AJ:77:VAL:CG2	2.32	0.42
16:AP:48:GLU:OE2	16:AP:51:ARG:NH1	2.52	0.42
17:AQ:5:ILE:N	17:AQ:5:ILE:HD12	2.34	0.42
22:AV:12:G:H5'	28:BA:1909:C:C4'	2.49	0.42
22:AV:68:C:O5'	22:AV:68:C:H6	2.02	0.42
28:BA:528:A:P	35:BJ:116:ARG:HH21	2.42	0.42
28:BA:1465:G:H2'	28:BA:1466:U:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:1770:G:C6	28:BA:1983:G:C6	3.07	0.42
28:BA:2071:A:H2'	28:BA:2072:C:C6	2.54	0.42
28:BA:2423:U:H5'	28:BA:2423:U:H6	1.83	0.42
34:BI:93:ASN:HB2	34:BI:135:MET:SD	2.59	0.42
36:BK:35:VAL:HG12	36:BK:36:GLY:N	2.34	0.42
43:BR:74:ILE:HD12	43:BR:74:ILE:N	2.34	0.42
46:BU:35:VAL:O	46:BU:38:ILE:HB	2.19	0.42
48:BW:18:LYS:N	48:BW:36:ILE:HG13	2.33	0.42
48:BW:37:VAL:HB	48:BW:38:ARG:NH1	2.34	0.42
53:B1:8:ILE:CD1	53:B1:24:LYS:HG2	2.48	0.42
57:B5:108:VAL:CG1	57:B5:109:LYS:N	2.82	0.42
1:AA:15:G:O4'	5:AE:29:ARG:CZ	2.68	0.42
1:AA:115:G:O2'	1:AA:116:A:OP2	2.32	0.42
1:AA:408:A:OP1	4:AD:110:THR:HG21	2.19	0.42
1:AA:688:G:C5	1:AA:700:G:C2	3.07	0.42
1:AA:769:G:H4'	1:AA:1513:A:H4'	2.01	0.42
1:AA:885:G:P	12:AL:15:LYS:NZ	2.93	0.42
1:AA:986:U:H1'	19:AS:54:GLY:O	2.19	0.42
1:AA:1181:G:C2	1:AA:1182:G:N2	2.88	0.42
1:AA:1351:U:O4	9:AI:120:LYS:NZ	2.47	0.42
5:AE:154:ALA:O	5:AE:158:GLY:N	2.42	0.42
6:AF:63:ASN:ND2	6:AF:96:VAL:CG2	2.81	0.42
10:AJ:35:GLN:HG2	10:AJ:77:VAL:H	1.83	0.42
12:AL:33:VAL:O	12:AL:34:CYS:HB3	2.19	0.42
12:AL:40:THR:OG1	12:AL:41:THR:N	2.51	0.42
13:AM:33:ILE:HG23	13:AM:59:GLU:HB3	2.00	0.42
14:AN:18:ASP:OD1	14:AN:19:LYS:N	2.53	0.42
28:BA:146:A:H2'	28:BA:147:C:C6	2.54	0.42
28:BA:323:C:OP1	28:BA:338:G:N2	2.51	0.42
28:BA:864:G:OP2	38:BM:22:GLN:NE2	2.53	0.42
28:BA:1378:A:C4	28:BA:1380:G:N7	2.87	0.42
28:BA:2516:A:N6	28:BA:2517:C:N4	2.67	0.42
28:BA:2595:G:N1	28:BA:2599:G:C6	2.87	0.42
29:BD:124:ARG:HA	29:BD:165:MET:SD	2.58	0.42
30:BE:158:PHE:HD2	30:BE:159:LEU:HD12	1.83	0.42
31:BF:62:GLN:NE2	31:BF:89:THR:O	2.47	0.42
32:BG:1:SER:O	32:BG:4:ALA:N	2.48	0.42
35:BJ:38:GLY:O	35:BJ:43:GLU:HB2	2.19	0.42
57:B5:67:THR:C	57:B5:69:PHE:N	2.73	0.42
1:AA:560:A:C5	5:AE:128:TYR:CE2	3.07	0.42
1:AA:1393:U:O2'	1:AA:1502:A:H4'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1526:G:P	21:AU:38:TYR:CD2	3.13	0.42
2:AB:53:LEU:HD21	2:AB:212:TYR:CE1	2.55	0.42
2:AB:56:LEU:HD23	2:AB:220:VAL:HG13	2.01	0.42
3:AC:20:SER:OG	3:AC:40:ARG:NH2	2.53	0.42
3:AC:111:LEU:HD21	3:AC:144:LEU:O	2.20	0.42
5:AE:44:GLY:H	5:AE:76:LEU:CD1	2.32	0.42
9:AI:91:ASP:C	9:AI:93:SER:H	2.21	0.42
11:AK:125:LYS:CB	21:AU:35:ARG:HG2	2.49	0.42
18:AR:34:THR:OG1	18:AR:35:GLU:N	2.53	0.42
21:AU:49:LYS:NZ	24:AX:2:G:H5'	2.32	0.42
22:AV:36:C:C2	24:AX:11:G:N2	2.70	0.42
22:AV:37:A:O5'	25:AY:508:GLN:OE1	2.36	0.42
23:AW:49:A:C6	23:AW:50:C:N4	2.88	0.42
24:AX:14:A:P	24:AX:14:A:H3'	2.59	0.42
25:AY:649:VAL:H	34:BI:25:PRO:HG2	1.83	0.42
27:BC:180:MET:O	27:BC:267:VAL:N	2.42	0.42
28:BA:247:G:N7	28:BA:249:C:C2	2.86	0.42
28:BA:518:G:H2'	28:BA:519:U:C6	2.54	0.42
28:BA:846:U:HO2'	28:BA:847:U:P	2.42	0.42
28:BA:945:A:C4	28:BA:2448:A:C2	3.08	0.42
28:BA:1298:C:C2	28:BA:1643:G:N2	2.88	0.42
28:BA:1536:C:H1'	28:BA:1537:G:N2	2.34	0.42
28:BA:2478:A:H5'	56:B4:32:LYS:HD3	2.02	0.42
37:BL:40:SER:O	37:BL:41:ARG:CB	2.67	0.42
43:BR:38:VAL:O	43:BR:53:PHE:HA	2.20	0.42
45:BT:70:HIS:HB3	45:BT:73:ARG:O	2.19	0.42
48:BW:44:PHE:O	48:BW:78:PHE:HA	2.19	0.42
2:AB:29:PHE:N	2:AB:29:PHE:CD1	2.87	0.42
9:AI:57:MET:SD	9:AI:57:MET:C	2.97	0.42
17:AQ:8:LEU:N	17:AQ:61:ILE:O	2.53	0.42
22:AV:29:G:O2'	22:AV:30:G:H5'	2.19	0.42
25:AY:512:ARG:HG3	25:AY:514:GLN:HE21	1.85	0.42
28:BA:75:G:H4'	50:BY:48:ARG:NH2	2.35	0.42
28:BA:301:G:H2'	28:BA:334:C:H2'	2.01	0.42
28:BA:545:U:O5'	28:BA:545:U:H6	2.02	0.42
28:BA:742:A:H2'	28:BA:743:A:C8	2.53	0.42
28:BA:1112:G:C5	28:BA:1113:U:C5	3.07	0.42
28:BA:1956:U:H2'	28:BA:1957:C:H5'	2.01	0.42
32:BG:35:THR:HG22	32:BG:36:LEU:N	2.33	0.42
34:BI:74:PRO:HG2	34:BI:77:VAL:HB	2.01	0.42
34:BI:124:MET:HE2	34:BI:124:MET:HB3	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BJ:88:THR:HG22	35:BJ:91:GLU:CG	2.49	0.42
39:BN:79:LEU:O	39:BN:80:PHE:HB2	2.20	0.42
42:BQ:94:LEU:CD1	43:BR:13:ARG:HB2	2.49	0.42
43:BR:61:ALA:HB1	43:BR:98:ILE:H	1.84	0.42
46:BU:10:VAL:HG12	46:BU:71:ILE:HA	2.01	0.42
52:B0:42:ILE:HG22	52:B0:43:THR:O	2.19	0.42
53:B1:18:HIS:CE1	53:B1:40:PRO:HD3	2.54	0.42
57:B5:3:LEU:HD12	57:B5:5:LEU:N	2.35	0.42
57:B5:71:CYS:HB3	57:B5:74:ASP:OD2	2.19	0.42
1:AA:70:U:O2'	1:AA:71:A:C8	2.68	0.42
1:AA:211:G:C6	1:AA:212:G:H1'	2.54	0.42
1:AA:1308:U:H5'	13:AM:109:ARG:HE	1.85	0.42
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.54	0.42
2:AB:8:MET:HB2	2:AB:42:LEU:HD11	2.00	0.42
4:AD:91:LEU:HD11	4:AD:197:GLU:HG3	2.02	0.42
4:AD:110:THR:HG23	4:AD:113:GLU:CB	2.49	0.42
11:AK:122:ARG:HH12	11:AK:125:LYS:CE	2.33	0.42
25:AY:360:PHE:HD2	25:AY:363:ILE:HD11	1.85	0.42
27:BC:16:VAL:H	27:BC:203:VAL:HG12	1.83	0.42
28:BA:573:U:O2'	28:BA:574:A:H3'	2.19	0.42
28:BA:580:U:H2'	28:BA:581:C:C6	2.54	0.42
28:BA:966:G:C6	28:BA:967:U:C4	3.07	0.42
28:BA:1238:G:O2'	28:BA:1239:G:H5'	2.19	0.42
28:BA:1312:U:H4'	28:BA:1313:U:O5'	2.20	0.42
28:BA:1476:U:C5	28:BA:1514:G:C2	3.07	0.42
28:BA:1747:U:H2'	28:BA:1748:C:C6	2.54	0.42
28:BA:1814:G:C6	28:BA:1815:A:C6	3.08	0.42
34:BI:91:LYS:HB2	34:BI:95:ASP:HB2	2.00	0.42
39:BN:70:THR:HB	39:BN:75:ILE:HD11	2.01	0.42
42:BQ:20:ALA:HA	42:BQ:23:TYR:CE2	2.54	0.42
57:B5:67:THR:CG2	57:B5:72:LEU:HA	2.49	0.42
58:B6:15:SER:OG	58:B6:16:VAL:N	2.53	0.42
1:AA:552:U:O2'	12:AL:83:ARG:O	2.37	0.42
1:AA:1032:G:H3'	1:AA:1032:G:N3	2.35	0.42
1:AA:1163:A:C2	1:AA:1174:G:C2	3.08	0.42
1:AA:1237:C:H4'	1:AA:1334:G:N2	2.35	0.42
1:AA:1288:A:N1	1:AA:1371:G:H1'	2.35	0.42
1:AA:1429:A:C4'	28:BA:1703:G:HO2'	2.30	0.42
2:AB:8:MET:O	2:AB:10:LYS:N	2.52	0.42
4:AD:3:ARG:CZ	4:AD:115:ARG:HD3	2.50	0.42
4:AD:38:PRO:HD2	4:AD:42:GLY:CA	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:492:GLU:OE1	25:AY:567:ALA:N	2.49	0.42
25:AY:494:ILE:HD11	25:AY:524:PRO:N	2.34	0.42
28:BA:163:C:HO2'	28:BA:164:C:C5'	2.30	0.42
28:BA:833:A:OP1	37:BL:39:LYS:HE3	2.19	0.42
28:BA:907:G:OP1	38:BM:22:GLN:HB3	2.18	0.42
28:BA:1591:A:H2'	28:BA:1592:C:C6	2.55	0.42
28:BA:1937:A:N7	28:BA:1939:U:H2'	2.35	0.42
28:BA:2803:G:H2'	28:BA:2804:U:H6	1.84	0.42
34:BI:20:SER:HB3	34:BI:21:PRO:HD3	2.01	0.42
37:BL:112:LEU:HD23	37:BL:114:GLY:H	1.83	0.42
41:BP:92:ARG:CG	41:BP:92:ARG:O	2.68	0.42
44:BS:59:GLU:HA	44:BS:64:ALA:CB	2.49	0.42
47:BV:72:VAL:HG12	47:BV:93:ARG:HA	2.01	0.42
55:B3:31:ILE:O	55:B3:31:ILE:CG1	2.66	0.42
1:AA:15:G:H5'	5:AE:29:ARG:NH1	2.28	0.42
1:AA:449:G:H2'	1:AA:450:G:C8	2.55	0.42
1:AA:1084:G:OP1	1:AA:1086:U:N3	2.53	0.42
1:AA:1098:C:P	2:AB:142:LYS:NZ	2.92	0.42
1:AA:1342:C:O2'	9:AI:126:GLN:HG3	2.20	0.42
1:AA:1395:C:C4	1:AA:1396:A:N6	2.83	0.42
6:AF:100:SER:CB	6:AF:101:PRO:HA	2.50	0.42
25:AY:25:THR:CB	60:AY:802:GDP:O2A	2.68	0.42
25:AY:468:ILE:CG1	59:AY:801:FUA:H12	2.50	0.42
25:AY:638:ARG:O	25:AY:662:GLU:HG2	2.20	0.42
28:BA:570:G:C4	28:BA:2030:A:N7	2.87	0.42
28:BA:803:U:C4	28:BA:804:A:N7	2.88	0.42
28:BA:959:A:N6	38:BM:82:MET:CE	2.82	0.42
28:BA:1069:A:C2'	28:BA:1070:A:OP2	2.68	0.42
28:BA:1494:A:C6	28:BA:1495:A:C5	3.08	0.42
28:BA:2134:A:H2'	28:BA:2135:A:H8	1.85	0.42
28:BA:2421:G:P	53:B1:7:LYS:NZ	2.92	0.42
28:BA:2661:G:H2'	28:BA:2662:A:O4'	2.20	0.42
30:BE:52:VAL:HG11	30:BE:81:GLY:HA3	2.01	0.42
31:BF:94:ARG:HH11	31:BF:94:ARG:HB2	1.84	0.42
33:BH:8:LYS:O	33:BH:9:VAL:CB	2.66	0.42
35:BJ:11:VAL:HG11	35:BJ:50:THR:HA	2.01	0.42
35:BJ:64:VAL:HG13	35:BJ:65:THR:N	2.35	0.42
39:BN:99:LYS:O	52:B0:42:ILE:HD12	2.20	0.42
43:BR:5:PHE:HB3	43:BR:59:ILE:HD12	2.01	0.42
44:BS:96:ILE:O	44:BS:96:ILE:HG13	2.20	0.42
45:BT:76:ARG:HG3	45:BT:77:ARG:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BW:19:ARG:HA	48:BW:34:SER:HA	2.00	0.42
48:BW:49:ASN:ND2	48:BW:50:VAL:N	2.67	0.42
57:B5:71:CYS:SG	57:B5:117:LEU:HD12	2.58	0.42
1:AA:518:C:C2	1:AA:529:G:C6	3.08	0.42
1:AA:1296:C:H4'	1:AA:1302:C:N3	2.35	0.42
3:AC:15:VAL:HG11	3:AC:179:ARG:HA	2.01	0.42
6:AF:92:THR:HG22	6:AF:94:HIS:H	1.85	0.42
7:AG:130:ASN:HA	7:AG:135:VAL:HG11	2.01	0.42
9:AI:45:ARG:NE	9:AI:45:ARG:N	2.68	0.42
12:AL:63:VAL:HG21	12:AL:95:TYR:CE1	2.54	0.42
13:AM:10:PRO:O	13:AM:11:ASP:CB	2.67	0.42
21:AU:20:LYS:HA	21:AU:20:LYS:CE	2.50	0.42
23:AW:66:C:C2	23:AW:67:G:C8	3.08	0.42
25:AY:25:THR:HG21	60:AY:802:GDP:C8	2.55	0.42
25:AY:244:THR:HG22	25:AY:247:GLU:CD	2.40	0.42
25:AY:342:VAL:CG2	25:AY:378:ARG:HD2	2.50	0.42
28:BA:1084:A:C6	28:BA:1085:A:C6	3.08	0.42
28:BA:1179:G:C6	28:BA:1180:U:C4	3.08	0.42
28:BA:1486:U:H2'	28:BA:1487:U:C6	2.55	0.42
28:BA:2090:A:H62	28:BA:2091:C:N4	2.15	0.42
28:BA:2352:A:N1	48:BW:30:VAL:HG21	2.35	0.42
28:BA:2796:U:C4	28:BA:2798:U:C5	3.08	0.42
29:BD:35:THR:N	29:BD:49:GLN:O	2.40	0.42
30:BE:42:GLY:O	30:BE:43:THR:OG1	2.35	0.42
31:BF:103:ILE:HG21	31:BF:173:ASP:HB2	2.01	0.42
36:BK:39:ILE:HD12	36:BK:41:ILE:HD11	2.02	0.42
39:BN:12:ARG:HB3	39:BN:16:HIS:HB3	2.02	0.42
40:BO:14:ALA:O	40:BO:17:LYS:N	2.52	0.42
45:BT:34:VAL:O	45:BT:34:VAL:HG22	2.20	0.42
47:BV:6:ALA:HB1	47:BV:40:ILE:CG2	2.50	0.42
55:B3:22:LYS:HA	55:B3:47:ALA:O	2.19	0.42
56:B4:36:ARG:HG2	56:B4:37:GLN:N	2.34	0.42
57:B5:47:GLU:HG2	57:B5:95:LEU:HD21	2.00	0.42
1:AA:16:A:HO2'	1:AA:17:U:H5'	1.83	0.42
1:AA:723:U:C5	21:AU:49:LYS:HG3	2.55	0.42
3:AC:12:LEU:HD13	3:AC:18:TRP:CE2	2.55	0.42
12:AL:43:LYS:HG2	12:AL:44:LYS:N	2.34	0.42
21:AU:31:GLU:O	21:AU:33:ARG:N	2.51	0.42
24:AX:2:G:C3'	24:AX:3:U:O4'	2.67	0.42
25:AY:315:GLU:HB3	25:AY:316:PRO:HD2	2.02	0.42
28:BA:624:C:O2'	28:BA:657:U:OP1	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:669:G:N3	28:BA:669:G:C2'	2.83	0.42
28:BA:866:A:C8	28:BA:914:G:C5	3.08	0.42
28:BA:996:A:C5	28:BA:1160:G:C2	3.08	0.42
28:BA:1494:A:C6	28:BA:1495:A:C6	3.08	0.42
35:BJ:35:ARG:HG2	35:BJ:40:HIS:HD2	1.85	0.42
35:BJ:81:ILE:CG1	35:BJ:82:GLY:H	2.33	0.42
36:BK:3:GLN:HG3	36:BK:4:GLU:N	2.34	0.42
36:BK:19:VAL:HG13	36:BK:41:ILE:HG12	2.02	0.42
42:BQ:91:ARG:HE	42:BQ:93:ILE:HG23	1.85	0.42
44:BS:88:ARG:HD2	44:BS:94:ASP:OD2	2.20	0.42
46:BU:98:ASN:ND2	46:BU:100:GLU:OE1	2.53	0.42
50:BY:1:MET:H3	50:BY:2:LYS:HD2	1.84	0.42
1:AA:15:G:H5'	5:AE:29:ARG:CZ	2.50	0.42
1:AA:16:A:H1'	5:AE:22:SER:H	1.85	0.42
1:AA:49:U:O4	1:AA:365:U:H5	2.03	0.42
1:AA:211:G:C2	1:AA:212:G:H1'	2.55	0.42
1:AA:780:A:C8	1:AA:800:G:C6	3.08	0.42
1:AA:920:U:C2'	1:AA:921:U:C5'	2.96	0.42
1:AA:920:U:H4'	1:AA:1080:A:C6	2.54	0.42
4:AD:145:ILE:HD13	4:AD:155:VAL:HG21	2.02	0.42
4:AD:146:ARG:HB3	4:AD:148:LYS:HD2	2.01	0.42
5:AE:97:GLN:HB2	5:AE:124:LEU:HB2	2.02	0.42
8:AH:10:MET:HE1	8:AH:33:LYS:HA	2.00	0.42
22:AV:39:C:H2'	22:AV:40:C:C6	2.54	0.42
25:AY:104:ARG:C	25:AY:104:ARG:HD2	2.40	0.42
59:AY:801:FUA:C15	59:AY:801:FUA:H323	2.49	0.42
27:BC:203:VAL:O	27:BC:205:GLY:N	2.53	0.42
28:BA:485:C:C2	28:BA:496:G:N2	2.88	0.42
28:BA:1509:A:H1'	28:BA:1510:G:O5'	2.20	0.42
28:BA:1747:U:H2'	28:BA:1748:C:H6	1.85	0.42
28:BA:2134:A:O2'	28:BA:2135:A:O4'	2.36	0.42
28:BA:2526:G:C5	28:BA:2527:C:C5	3.08	0.42
28:BA:2727:A:C6	28:BA:2728:U:O4	2.73	0.42
28:BA:2845:U:H5"	41:BP:51:ASN:O	2.20	0.42
31:BF:111:ARG:NE	31:BF:111:ARG:HA	2.34	0.42
37:BL:77:ILE:HD13	37:BL:108:ALA:HB1	2.02	0.42
40:BO:49:VAL:HG12	40:BO:50:ALA:N	2.35	0.42
42:BQ:82:LEU:HD12	42:BQ:112:ALA:HB2	2.02	0.42
48:BW:19:ARG:NH2	48:BW:22:VAL:CG2	2.83	0.42
57:B5:51:TYR:CD1	57:B5:52:MET:HG2	2.55	0.42
1:AA:363:A:OP1	12:AL:58:THR:HG21	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:390:U:H4'	16:AP:28:ARG:HH11	1.85	0.41
1:AA:658:C:H1'	15:AO:22:THR:HG21	2.02	0.41
1:AA:925:G:H8	1:AA:925:G:OP2	2.02	0.41
2:AB:86:CYS:SG	2:AB:88:GLN:NE2	2.93	0.41
4:AD:174:ASP:O	4:AD:175:ALA:HB2	2.20	0.41
9:AI:51:PRO:HB3	9:AI:84:THR:CG2	2.49	0.41
9:AI:120:LYS:O	9:AI:121:ALA:HB3	2.20	0.41
11:AK:21:ALA:HB2	11:AK:82:LEU:HD12	2.01	0.41
22:AV:28:C:O2	22:AV:43:A:C2	2.72	0.41
25:AY:13:ILE:HD13	25:AY:282:VAL:HG11	2.02	0.41
26:BB:16:G:C5	26:BB:69:G:C2	3.07	0.41
28:BA:479:A:C2	28:BA:480:A:C5	3.08	0.41
28:BA:659:G:H4'	30:BE:95:LYS:HD3	2.02	0.41
28:BA:1194:A:C2'	28:BA:1195:G:O5'	2.68	0.41
28:BA:1378:A:O2'	28:BA:1380:G:N7	2.27	0.41
28:BA:1691:C:C4	28:BA:1692:U:C4	3.08	0.41
28:BA:2287:A:C8	28:BA:2289:G:C8	3.08	0.41
29:BD:24:VAL:HA	29:BD:191:GLY:H	1.85	0.41
30:BE:12:LEU:HD12	30:BE:193:VAL:HG11	2.01	0.41
41:BP:58:PHE:HD1	41:BP:75:THR:HG22	1.83	0.41
1:AA:1072:G:C5	1:AA:1073:U:C4	3.07	0.41
2:AB:51:GLU:HG2	2:AB:197:PHE:CE1	2.55	0.41
2:AB:63:LYS:HE2	2:AB:224:ARG:HD3	2.02	0.41
5:AE:156:LYS:HA	5:AE:159:LYS:NZ	2.35	0.41
10:AJ:59:LYS:HG3	10:AJ:60:ASP:OD1	2.20	0.41
13:AM:54:ASP:HA	13:AM:57:ARG:HB3	2.02	0.41
17:AQ:74:THR:HG22	17:AQ:75:LEU:N	2.35	0.41
22:AV:35:A:HO2'	25:AY:513:GLY:HA3	1.76	0.41
28:BA:179:C:C2	28:BA:180:G:C8	3.08	0.41
28:BA:372:G:C4	49:BX:60:LYS:HE2	2.54	0.41
28:BA:635:C:O2'	28:BA:639:U:OP1	2.34	0.41
28:BA:685:A:C2	28:BA:689:A:C6	3.08	0.41
28:BA:1171:G:H1	28:BA:1178:C:H42	1.66	0.41
28:BA:1183:U:H2'	28:BA:1184:U:C6	2.55	0.41
28:BA:1714:U:H5'	28:BA:1715:G:H5'	2.02	0.41
28:BA:2047:C:O2'	28:BA:2048:G:H5'	2.19	0.41
28:BA:2103:C:H2'	28:BA:2104:C:H5"	2.02	0.41
28:BA:2341:G:H2'	28:BA:2342:C:C6	2.55	0.41
28:BA:2780:G:P	35:BJ:120:ARG:HE	2.44	0.41
29:BD:46:ARG:HB3	29:BD:46:ARG:CZ	2.51	0.41
33:BH:39:ALA:HB1	33:BH:44:ILE:HG22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BJ:4:PHE:CD2	35:BJ:44:TYR:CE2	3.08	0.41
35:BJ:4:PHE:HB3	35:BJ:44:TYR:CE2	2.55	0.41
36:BK:71:ARG:HB3	36:BK:72:PRO:CD	2.49	0.41
48:BW:67:LYS:O	48:BW:68:PHE:HB2	2.20	0.41
49:BX:52:ALA:O	49:BX:53:LYS:CB	2.67	0.41
57:B5:22:ALA:N	57:B5:87:GLU:O	2.53	0.41
57:B5:131:THR:HA	57:B5:134:GLU:CG	2.50	0.41
1:AA:131:A:H2'	1:AA:132:C:C6	2.55	0.41
1:AA:246:A:C4	1:AA:279:A:C6	3.08	0.41
1:AA:1132:C:N4	1:AA:1142:G:O6	2.53	0.41
1:AA:1230:C:P	23:AW:30:C:H5'	2.59	0.41
2:AB:170:ILE:H	2:AB:170:ILE:HD13	1.85	0.41
10:AJ:8:ILE:HG22	10:AJ:10:LEU:CD1	2.49	0.41
16:AP:28:ARG:HG2	16:AP:29:ASN:OD1	2.21	0.41
22:AV:30:G:N2	22:AV:31:G:H1'	2.35	0.41
22:AV:61:C:H2'	22:AV:62:C:H6	1.85	0.41
23:AW:47:U:H4'	23:AW:48:C:H5"	2.02	0.41
25:AY:442:ASP:OD2	59:AY:801:FUA:H192	2.20	0.41
28:BA:307:G:N2	28:BA:310:A:C8	2.89	0.41
28:BA:1607:C:H42	28:BA:1622:G:P	2.43	0.41
28:BA:2196:C:N3	28:BA:2197:U:C4	2.88	0.41
28:BA:2681:C:C2	28:BA:2724:U:O4	2.74	0.41
28:BA:2755:C:O2'	28:BA:2756:U:H2'	2.19	0.41
34:BI:19:PRO:HG2	34:BI:24:GLY:H	1.86	0.41
36:BK:71:ARG:O	36:BK:72:PRO:O	2.39	0.41
42:BQ:6:GLY:HA2	42:BQ:9:ALA:HB3	2.02	0.41
44:BS:18:ARG:HG3	44:BS:76:VAL:CG1	2.50	0.41
57:B5:108:VAL:HG12	57:B5:109:LYS:N	2.35	0.41
1:AA:263:A:OP2	20:AT:74:ARG:NH1	2.52	0.41
1:AA:269:C:H2'	1:AA:270:A:C8	2.55	0.41
1:AA:375:U:C2	1:AA:376:G:C8	3.08	0.41
1:AA:382:A:H2'	1:AA:383:A:C8	2.56	0.41
1:AA:408:A:C2	1:AA:435:A:C2	3.07	0.41
1:AA:921:U:H5"	1:AA:1082:A:C5'	2.50	0.41
1:AA:1231:G:C6	1:AA:1232:U:C4	3.08	0.41
1:AA:1340:A:H2'	1:AA:1341:U:O4'	2.21	0.41
1:AA:1370:G:H3'	9:AI:111:VAL:HG11	2.01	0.41
1:AA:1526:G:OP1	21:AU:38:TYR:CE2	2.73	0.41
3:AC:167:TRP:O	3:AC:167:TRP:CE3	2.73	0.41
4:AD:191:LEU:HD12	4:AD:191:LEU:O	2.20	0.41
9:AI:36:GLU:HA	9:AI:40:GLY:HA3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:2:G:H2'	23:AW:3:C:C6	2.55	0.41
25:AY:5:THR:HG23	25:AY:6:PRO:CD	2.51	0.41
25:AY:374:ILE:HG22	25:AY:376:GLU:H	1.86	0.41
28:BA:1026:G:H2'	28:BA:1027:A:C8	2.55	0.41
28:BA:1301:A:H2'	28:BA:1301:A:N3	2.35	0.41
28:BA:1722:A:C2	28:BA:1739:A:N3	2.89	0.41
28:BA:1779:U:C5	28:BA:1784:A:N7	2.86	0.41
28:BA:2676:C:P	36:BK:31:ARG:HH12	2.44	0.41
29:BD:88:GLU:O	29:BD:89:GLU:HG3	2.21	0.41
34:BI:82:ALA:HB1	34:BI:108:ILE:HD13	2.03	0.41
45:BT:29:THR:HB	45:BT:86:THR:HA	2.01	0.41
57:B5:132:TYR:HE1	58:B6:19:VAL:HG13	1.85	0.41
1:AA:264:C:H4'	17:AQ:65:ARG:HD2	2.02	0.41
1:AA:927:G:O2'	1:AA:928:G:H5'	2.19	0.41
1:AA:958:A:C6	1:AA:959:A:N1	2.88	0.41
1:AA:1130:A:H4'	9:AI:20:PHE:CG	2.55	0.41
1:AA:1340:A:H4'	23:AW:31:A:O2'	2.19	0.41
1:AA:1526:G:OP1	21:AU:39:GLU:HG3	2.21	0.41
5:AE:90:THR:HB	5:AE:135:ASN:ND2	2.35	0.41
9:AI:12:ARG:O	9:AI:13:LYS:C	2.59	0.41
10:AJ:57:VAL:CG1	10:AJ:58:ASN:H	2.33	0.41
12:AL:102:LEU:N	12:AL:102:LEU:CD1	2.83	0.41
23:AW:8:U:H3'	23:AW:13:C:H42	1.85	0.41
25:AY:95:PHE:CE2	59:AY:801:FUA:H242	2.55	0.41
25:AY:124:GLU:OE2	25:AY:677:ARG:NH1	2.54	0.41
25:AY:257:LEU:HD11	25:AY:287:PRO:HB3	2.02	0.41
28:BA:45:G:C5'	28:BA:46:G:H5'	2.51	0.41
28:BA:45:G:H5'	28:BA:46:G:H5'	2.02	0.41
28:BA:138:U:H5'	28:BA:139:U:C5'	2.51	0.41
28:BA:1403:A:C2	28:BA:1404:C:C2	3.09	0.41
28:BA:1579:A:H2'	28:BA:1580:A:C8	2.56	0.41
28:BA:2198:A:N1	33:BH:29:PHE:CD2	2.85	0.41
28:BA:2201:G:C6	28:BA:2202:U:C4	3.08	0.41
28:BA:2543:G:C6	28:BA:2544:G:C6	3.08	0.41
28:BA:2576:G:H3'	28:BA:2576:G:N3	2.35	0.41
28:BA:2607:G:H2'	28:BA:2608:G:O4'	2.20	0.41
28:BA:2685:G:H1	28:BA:2724:U:H3	1.68	0.41
31:BF:46:LYS:HD3	31:BF:46:LYS:H	1.86	0.41
32:BG:10:VAL:HG22	32:BG:47:ASN:C	2.41	0.41
35:BJ:43:GLU:O	35:BJ:44:TYR:C	2.58	0.41
36:BK:13:ASN:N	36:BK:13:ASN:OD1	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BK:15:GLY:O	36:BK:46:ALA:HA	2.20	0.41
48:BW:24:ARG:HH11	48:BW:65:LYS:HG2	1.85	0.41
1:AA:213:G:C8	1:AA:214:C:C6	3.08	0.41
1:AA:341:C:H2'	1:AA:342:C:H6	1.85	0.41
3:AC:123:GLN:HB3	3:AC:128:VAL:CG1	2.51	0.41
8:AH:111:MET:HE2	8:AH:115:ALA:C	2.40	0.41
12:AL:14:ARG:NH1	12:AL:15:LYS:HG2	2.35	0.41
17:AQ:61:ILE:HG22	17:AQ:75:LEU:HA	2.01	0.41
22:AV:69:C:O2'	22:AV:70:G:H5'	2.21	0.41
23:AW:76:A:N6	28:BA:2422:C:C6	2.89	0.41
24:AX:14:A:O2'	24:AX:15:A:P	2.78	0.41
27:BC:115:ILE:HG22	27:BC:116:GLN:N	2.36	0.41
27:BC:143:VAL:HB	27:BC:153:LEU:HB2	2.02	0.41
27:BC:250:GLN:NE2	28:BA:1843:C:H5'	2.36	0.41
28:BA:528:A:H2	28:BA:2043:C:C5'	2.33	0.41
28:BA:608:A:C8	28:BA:621:A:N6	2.89	0.41
28:BA:1365:A:N6	28:BA:1366:A:C6	2.89	0.41
28:BA:1381:G:H1'	28:BA:1571:A:N1	2.36	0.41
28:BA:1647:U:H3'	28:BA:1647:U:P	2.60	0.41
28:BA:1847:A:H4'	28:BA:1848:A:OP2	2.21	0.41
28:BA:2180:U:N3	28:BA:2181:U:C5	2.89	0.41
28:BA:2196:C:C2	28:BA:2197:U:C2	3.07	0.41
28:BA:2821:A:C2	28:BA:2822:G:C4	3.08	0.41
30:BE:134:LEU:CD2	30:BE:161:ALA:HB2	2.51	0.41
34:BI:100:ILE:CD1	34:BI:137:LEU:HD12	2.50	0.41
35:BJ:65:THR:HG22	35:BJ:68:LYS:NZ	2.36	0.41
37:BL:2:ARG:HA	37:BL:5:THR:HG21	2.01	0.41
42:BQ:46:TYR:CZ	42:BQ:50:ARG:NH2	2.89	0.41
43:BR:80:ARG:O	43:BR:81:LYS:HD3	2.20	0.41
48:BW:19:ARG:HG2	48:BW:19:ARG:HH21	1.86	0.41
48:BW:60:ALA:CB	48:BW:81:ILE:CD1	2.98	0.41
57:B5:33:VAL:HB	57:B5:36:ASP:OD1	2.20	0.41
57:B5:47:GLU:CG	57:B5:95:LEU:HD21	2.51	0.41
1:AA:85:U:H4'	1:AA:87:C:N4	2.36	0.41
1:AA:171:A:H2'	1:AA:172:A:C8	2.56	0.41
1:AA:843:U:H6	1:AA:843:U:H5'	1.84	0.41
1:AA:1372:U:C4	1:AA:1373:G:C4	3.09	0.41
1:AA:1390:U:C3'	1:AA:1391:U:C6	3.04	0.41
2:AB:123:GLY:O	2:AB:125:PHE:N	2.45	0.41
4:AD:24:GLY:HA2	4:AD:109:ALA:HB1	2.02	0.41
4:AD:188:ARG:NH1	4:AD:191:LEU:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:79:ARG:HA	7:AG:83:SER:O	2.20	0.41
8:AH:83:LEU:CD1	8:AH:85:ILE:HD11	2.51	0.41
9:AI:88:MET:SD	9:AI:88:MET:C	2.99	0.41
22:AV:5:G:O2'	22:AV:6:G:H5'	2.20	0.41
27:BC:172:THR:HG22	27:BC:182:LYS:HG2	2.02	0.41
28:BA:126:A:C6	28:BA:127:A:N1	2.88	0.41
28:BA:528:A:H2	28:BA:2043:C:H5'	1.85	0.41
28:BA:1069:A:N3	28:BA:1073:A:C6	2.88	0.41
28:BA:1268:A:H2	44:BS:88:ARG:HH11	1.69	0.41
28:BA:1268:A:H2'	28:BA:1269:A:O4'	2.20	0.41
28:BA:1378:A:H4'	28:BA:1379:U:OP1	2.20	0.41
28:BA:1936:A:C2	28:BA:1943:U:H5	2.38	0.41
28:BA:2637:U:C2'	28:BA:2638:G:H5'	2.50	0.41
29:BD:149:ASN:CG	29:BD:150:GLN:H	2.21	0.41
39:BN:24:MET:CE	39:BN:36:THR:HG21	2.51	0.41
41:BP:50:ARG:CD	41:BP:56:SER:HB3	2.51	0.41
41:BP:92:ARG:HH11	41:BP:92:ARG:HB2	1.85	0.41
46:BU:6:ARG:HB3	46:BU:7:ASP:H	1.76	0.41
46:BU:84:PHE:O	46:BU:85:ARG:HB3	2.19	0.41
51:BZ:39:ASP:CG	51:BZ:44:ARG:HH11	2.23	0.41
1:AA:345:C:O2	36:BK:117:SER:HA	2.21	0.41
1:AA:441:A:H5"	1:AA:442:G:OP2	2.20	0.41
2:AB:187:ASP:HB2	2:AB:203:ASP:HB3	2.02	0.41
3:AC:105:GLU:HG2	3:AC:106:VAL:N	2.35	0.41
23:AW:9:A:H8	23:AW:12:U:O4	2.03	0.41
25:AY:365:GLN:HB2	25:AY:374:ILE:HD11	2.02	0.41
28:BA:109:C:H4'	28:BA:348:A:H4'	2.02	0.41
28:BA:301:G:C6	28:BA:317:G:C6	3.09	0.41
28:BA:635:C:P	37:BL:126:ARG:HH11	2.44	0.41
28:BA:996:A:C6	28:BA:1160:G:C2	3.08	0.41
28:BA:1063:G:H2'	28:BA:1064:C:O4'	2.20	0.41
28:BA:2091:C:O5'	28:BA:2092:U:H5"	2.21	0.41
28:BA:2392:A:OP2	28:BA:2422:C:N4	2.50	0.41
28:BA:2618:G:C6	28:BA:2619:C:C4	3.09	0.41
29:BD:8:LYS:HB2	29:BD:201:LEU:HD22	2.03	0.41
30:BE:109:LEU:O	30:BE:112:LEU:N	2.54	0.41
31:BF:107:VAL:HG13	31:BF:110:ILE:HD12	2.02	0.41
1:AA:78:A:H62	1:AA:93:U:H4'	1.86	0.41
1:AA:270:A:H2'	1:AA:271:C:C6	2.56	0.41
1:AA:557:G:C6	1:AA:558:G:C6	3.08	0.41
1:AA:780:A:C2	1:AA:803:G:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:875:U:O2'	8:AH:15:ARG:NH1	2.52	0.41
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.56	0.41
1:AA:1076:U:O2'	1:AA:1077:G:O5'	2.39	0.41
1:AA:1126:U:O2	1:AA:1280:A:H2'	2.21	0.41
1:AA:1343:G:O3'	9:AI:124:ARG:HB3	2.21	0.41
1:AA:1351:U:H4'	7:AG:33:ASP:OD1	2.20	0.41
1:AA:1377:A:C1'	7:AG:2:PRO:HG3	2.51	0.41
1:AA:1394:A:C8	1:AA:1501:C:C3'	3.04	0.41
1:AA:1397:C:C2	24:AX:17:A:N6	2.89	0.41
2:AB:132:GLU:HG2	2:AB:132:GLU:O	2.20	0.41
4:AD:19:LEU:HD23	4:AD:64:ILE:HG13	2.03	0.41
4:AD:44:ARG:O	4:AD:46:PRO:HD3	2.21	0.41
5:AE:105:ILE:H	5:AE:122:ASN:HA	1.84	0.41
8:AH:112:THR:HG22	8:AH:113:ASP:N	2.36	0.41
9:AI:47:VAL:O	9:AI:80:ARG:HG2	2.21	0.41
9:AI:128:SER:O	9:AI:130:ARG:N	2.54	0.41
10:AJ:80:THR:HB	10:AJ:83:THR:H	1.85	0.41
14:AN:17:ALA:HA	14:AN:55:SER:O	2.21	0.41
15:AO:43:PHE:CZ	15:AO:53:ARG:HA	2.56	0.41
18:AR:63:ARG:HD3	18:AR:70:TYR:CD2	2.55	0.41
21:AU:25:LYS:CG	21:AU:26:ALA:H	2.33	0.41
22:AV:12:G:H5"	28:BA:1909:C:H5'	2.02	0.41
22:AV:35:A:H61	24:AX:12:U:H3	1.69	0.41
25:AY:103:MET:HG2	25:AY:135:VAL:HG11	2.02	0.41
26:BB:89:U:H3'	26:BB:90:C:C5'	2.49	0.41
27:BC:77:VAL:HG23	27:BC:77:VAL:O	2.20	0.41
27:BC:184:GLU:O	27:BC:185:ALA:HB3	2.20	0.41
28:BA:58:G:N2	28:BA:70:G:C4	2.89	0.41
28:BA:181:A:C2	28:BA:182:A:C4	3.09	0.41
28:BA:911:A:O2'	28:BA:2329:U:OP1	2.33	0.41
28:BA:1020:A:C2	28:BA:1141:U:C2	3.09	0.41
28:BA:1078:U:H5"	28:BA:1079:C:OP1	2.20	0.41
28:BA:1096:A:N6	28:BA:1097:U:C4	2.89	0.41
28:BA:1587:G:C4	28:BA:1588:G:C8	3.09	0.41
28:BA:1630:A:H2'	28:BA:1631:G:H5'	2.03	0.41
28:BA:1789:A:H2'	28:BA:1790:C:O4'	2.20	0.41
28:BA:2090:A:C3'	28:BA:2091:C:C5'	2.98	0.41
28:BA:2145:C:N3	28:BA:2146:C:N3	2.69	0.41
28:BA:2259:U:H1'	28:BA:2427:C:C2	2.55	0.41
28:BA:2409:G:H2'	28:BA:2410:G:O4'	2.20	0.41
28:BA:2447:G:C4	28:BA:2500:U:C5	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:2478:A:C2'	28:BA:2479:U:H5'	2.51	0.41
28:BA:2555:U:C5	28:BA:2556:C:C2	3.09	0.41
28:BA:2766:A:N3	28:BA:2766:A:H2'	2.36	0.41
28:BA:2793:C:H2'	28:BA:2794:C:H6	1.86	0.41
28:BA:2799:A:C6	28:BA:2801:G:C5	3.09	0.41
28:BA:2868:A:C2	28:BA:2869:G:C4	3.09	0.41
29:BD:118:PHE:HZ	39:BN:1:MET:HB2	1.85	0.41
30:BE:79:ARG:HG2	30:BE:80:SER:N	2.35	0.41
31:BF:28:PRO:HB2	31:BF:168:LEU:HD22	2.02	0.41
31:BF:112:ASP:N	31:BF:112:ASP:OD1	2.54	0.41
31:BF:148:VAL:HG23	31:BF:149:ARG:N	2.36	0.41
32:BG:68:ARG:HH21	32:BG:72:ASN:ND2	2.19	0.41
33:BH:27:ARG:NH1	49:BX:63:ILE:HG13	2.36	0.41
35:BJ:26:GLY:HA2	35:BJ:29:ALA:HB3	2.02	0.41
41:BP:30:TRP:CE3	41:BP:39:LEU:HD12	2.56	0.41
41:BP:88:ARG:HH12	41:BP:113:LEU:HA	1.86	0.41
45:BT:24:MET:HG3	45:BT:29:THR:CG2	2.51	0.41
45:BT:69:ARG:HG3	45:BT:70:HIS:N	2.36	0.41
46:BU:48:VAL:O	46:BU:48:VAL:CG2	2.69	0.41
46:BU:82:VAL:HG13	46:BU:93:ARG:HB3	2.03	0.41
57:B5:88:HIS:HB3	57:B5:89:PRO:HD3	2.03	0.41
57:B5:106:PHE:CG	57:B5:107:GLU:N	2.87	0.41
58:B6:7:ILE:HA	58:B6:10:ALA:HB3	2.02	0.41
1:AA:19:A:P	5:AE:132:ASN:HB2	2.60	0.41
1:AA:539:A:H2'	1:AA:540:G:C8	2.56	0.41
1:AA:725:G:H2'	1:AA:726:C:C6	2.56	0.41
1:AA:1048:G:OP1	14:AN:3:LYS:HA	2.21	0.41
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.56	0.41
5:AE:81:LEU:HB3	5:AE:147:MET:HE1	2.03	0.41
5:AE:83:HIS:CD2	8:AH:96:MET:CE	3.04	0.41
5:AE:94:VAL:CG2	5:AE:111:MET:SD	3.09	0.41
8:AH:5:ASP:OD2	8:AH:77:ARG:NH1	2.47	0.41
15:AO:70:LEU:HD21	15:AO:77:ARG:HB2	2.03	0.41
18:AR:23:TYR:CE2	18:AR:24:LYS:HE2	2.56	0.41
25:AY:320:LEU:HD23	25:AY:321:ALA:N	2.36	0.41
25:AY:519:VAL:N	25:AY:580:PHE:O	2.52	0.41
26:BB:77:U:OP1	47:BV:21:ARG:NH1	2.54	0.41
28:BA:136:G:H1	28:BA:143:C:H42	1.69	0.41
28:BA:347:A:C2	28:BA:348:A:C4	3.09	0.41
28:BA:901:C:C4	28:BA:902:C:C4	3.09	0.41
28:BA:996:A:C5	28:BA:1160:G:N2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:1807:G:H2'	28:BA:1808:A:H5'	2.03	0.41
28:BA:1905:C:N4	28:BA:1930:G:C2	2.89	0.41
28:BA:2017:U:H5"	28:BA:2018:G:P	2.61	0.41
30:BE:129:PRO:HG3	30:BE:156:ASN:OD1	2.21	0.41
32:BG:19:ASN:O	32:BG:22:VAL:HG22	2.21	0.41
39:BN:51:LEU:HD21	39:BN:70:THR:CG2	2.51	0.41
50:BY:12:GLU:O	50:BY:15:ASN:HB2	2.21	0.41
50:BY:14:LEU:HA	50:BY:17:GLU:HB3	2.01	0.41
1:AA:16:A:O2'	5:AE:21:VAL:HB	2.20	0.40
1:AA:1106:G:O2'	3:AC:169:ARG:CD	2.69	0.40
1:AA:1299:A:O2'	1:AA:1300:G:H4'	2.21	0.40
1:AA:1476:A:C2	1:AA:1477:U:C2	3.08	0.40
3:AC:40:ARG:HG2	3:AC:55:ILE:HG13	2.03	0.40
6:AF:97:THR:O	6:AF:98:GLU:HG2	2.21	0.40
13:AM:45:ILE:C	13:AM:47:GLU:H	2.25	0.40
13:AM:83:LEU:HD21	19:AS:65:GLU:HB3	2.03	0.40
16:AP:51:ARG:C	16:AP:52:LEU:HD12	2.41	0.40
19:AS:63:THR:CG2	19:AS:64:ASP:N	2.84	0.40
22:AV:11:A:O2'	28:BA:1909:C:C4'	2.69	0.40
22:AV:56:C:H5'	31:BF:72:SER:HB3	2.02	0.40
25:AY:23:LYS:N	60:AY:802:GDP:O2B	2.54	0.40
25:AY:461:MET:H	25:AY:465:HIS:CD2	2.39	0.40
26:BB:114:C:H1'	40:BO:47:VAL:HG11	2.03	0.40
26:BB:117:G:OP1	40:BO:56:LYS:NZ	2.49	0.40
28:BA:176:A:N7	28:BA:177:G:C6	2.89	0.40
28:BA:653:U:H5	28:BA:654:A:C2	2.38	0.40
28:BA:2478:A:H5'	56:B4:32:LYS:CD	2.51	0.40
28:BA:2570:G:H2'	28:BA:2571:U:O4'	2.22	0.40
28:BA:2869:G:C6	28:BA:2870:C:C4	3.09	0.40
31:BF:10:GLU:HG2	31:BF:13:LYS:HD3	2.02	0.40
31:BF:169:LEU:O	31:BF:174:PHE:HB2	2.21	0.40
32:BG:137:LYS:HA	32:BG:140:ILE:HG22	2.02	0.40
32:BG:166:GLU:C	32:BG:166:GLU:CD	2.80	0.40
38:BM:53:MET:CE	38:BM:63:ILE:HG21	2.50	0.40
51:BZ:2:LYS:CB	51:BZ:39:ASP:HB3	2.51	0.40
52:B0:33:SER:OG	52:B0:35:GLU:HG3	2.21	0.40
1:AA:209:U:H5	1:AA:211:G:C6	2.40	0.40
1:AA:561:U:O2'	1:AA:562:U:P	2.79	0.40
1:AA:728:A:C6	1:AA:729:A:C6	3.09	0.40
1:AA:1083:U:O4	1:AA:1084:G:C2	2.73	0.40
1:AA:1083:U:H6	1:AA:1083:U:H3'	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:127:ARG:O	21:AU:34:ARG:NH1	2.54	0.40
23:AW:8:U:H5'	23:AW:49:A:H5'	2.03	0.40
25:AY:697:ALA:O	25:AY:699:ILE:N	2.53	0.40
28:BA:19:A:H2'	28:BA:20:C:O4'	2.20	0.40
28:BA:783:A:C8	28:BA:784:G:H4'	2.57	0.40
28:BA:1582:C:C2'	28:BA:1585:C:H42	2.35	0.40
28:BA:1945:G:C6	28:BA:1946:U:C4	3.09	0.40
28:BA:2103:C:N4	28:BA:2186:G:H1	2.19	0.40
28:BA:2447:G:C5	28:BA:2500:U:C5	3.09	0.40
29:BD:106:LYS:HB3	29:BD:206:ALA:CB	2.52	0.40
31:BF:111:ARG:HA	31:BF:111:ARG:CZ	2.51	0.40
34:BI:52:LEU:HB3	34:BI:53:PRO:CD	2.51	0.40
37:BL:74:THR:HG22	37:BL:107:PHE:HB2	2.03	0.40
40:BO:75:GLY:HA3	40:BO:106:LEU:HA	2.03	0.40
47:BV:44:HIS:NE2	47:BV:85:LYS:HE3	2.37	0.40
48:BW:22:VAL:O	48:BW:23:LYS:HG3	2.22	0.40
1:AA:834:U:H2'	1:AA:835:U:C6	2.56	0.40
1:AA:922:G:H2'	1:AA:923:A:C8	2.57	0.40
1:AA:978:A:O2'	1:AA:1322:C:H5	2.04	0.40
1:AA:1098:C:OP2	2:AB:142:LYS:NZ	2.46	0.40
2:AB:40:ILE:HG21	2:AB:201:GLY:HA2	2.03	0.40
11:AK:82:LEU:CD2	11:AK:105:PHE:HB3	2.51	0.40
23:AW:19:G:OP1	23:AW:59:A:N6	2.54	0.40
25:AY:526:GLU:O	25:AY:528:GLY:N	2.55	0.40
25:AY:611:VAL:HG21	25:AY:689:GLU:CD	2.41	0.40
25:AY:630:ASP:HB3	25:AY:673:LEU:HD22	2.04	0.40
28:BA:1309:G:OP1	54:B2:9:VAL:HG13	2.21	0.40
28:BA:1817:G:C2'	28:BA:1818:U:H5'	2.51	0.40
28:BA:2198:A:N1	33:BH:25:TYR:CD1	2.88	0.40
28:BA:2580:U:C5	28:BA:2581:G:C6	3.08	0.40
39:BN:87:PHE:O	39:BN:89:SER:N	2.54	0.40
40:BO:7:ARG:HA	40:BO:10:ARG:NH2	2.36	0.40
53:B1:9:LYS:N	53:B1:9:LYS:HD2	2.37	0.40
1:AA:35:G:N3	12:AL:115:SER:OG	2.54	0.40
1:AA:423:G:H2'	1:AA:424:G:O4'	2.21	0.40
1:AA:460:A:C2	1:AA:462:G:C8	3.09	0.40
1:AA:925:G:OP2	1:AA:925:G:C8	2.75	0.40
2:AB:92:ASN:OD1	2:AB:92:ASN:N	2.54	0.40
3:AC:102:ASN:OD1	3:AC:102:ASN:N	2.54	0.40
6:AF:97:THR:O	6:AF:98:GLU:CB	2.69	0.40
7:AG:146:GLU:H	7:AG:149:LYS:HE2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:93:ARG:NH1	21:AU:25:LYS:HE2	2.36	0.40
17:AQ:50:ASN:O	17:AQ:52:GLU:N	2.54	0.40
23:AW:39:U:H2'	23:AW:40:G:H8	1.86	0.40
24:AX:2:G:H5"	24:AX:3:U:OP2	2.20	0.40
24:AX:6:A:N3	24:AX:6:A:C2'	2.84	0.40
25:AY:76:ALA:O	25:AY:77:LYS:HB3	2.21	0.40
25:AY:298:ILE:HG23	25:AY:304:ASP:HA	2.03	0.40
25:AY:536:PHE:CE1	25:AY:578:LEU:HD23	2.57	0.40
25:AY:611:VAL:HG22	25:AY:612:LEU:N	2.35	0.40
28:BA:68:G:H2'	28:BA:69:C:O4'	2.22	0.40
28:BA:1068:G:H3'	28:BA:1069:A:H5"	2.03	0.40
28:BA:1364:G:N2	28:BA:1367:A:OP2	2.49	0.40
28:BA:1392:A:C6	28:BA:1393:A:C6	3.09	0.40
28:BA:1684:G:C2	28:BA:1705:A:C2	3.10	0.40
28:BA:2134:A:OP2	28:BA:2134:A:C8	2.74	0.40
28:BA:2682:A:C8	29:BD:11:MET:CG	3.04	0.40
28:BA:2834:G:O6	28:BA:2879:A:O2'	2.32	0.40
32:BG:26:LYS:CG	32:BG:27:GLY:N	2.83	0.40
35:BJ:110:PRO:HB2	35:BJ:111:LYS:CG	2.52	0.40
38:BM:63:ILE:HG22	38:BM:64:TRP:N	2.36	0.40
38:BM:64:TRP:HZ3	38:BM:106:ASP:HB2	1.86	0.40
39:BN:24:MET:HE2	39:BN:44:LEU:HD22	2.04	0.40
44:BS:15:GLN:NE2	52:B0:16:ARG:CZ	2.84	0.40
44:BS:63:GLY:O	44:BS:64:ALA:HB3	2.21	0.40
53:B1:35:LEU:N	53:B1:35:LEU:HD22	2.37	0.40
57:B5:40:GLU:O	57:B5:40:GLU:CG	2.70	0.40
57:B5:142:THR:OG1	57:B5:143:MET:N	2.52	0.40
1:AA:21:G:C2	1:AA:22:G:C6	3.10	0.40
1:AA:383:A:C5	1:AA:384:G:H1'	2.56	0.40
1:AA:484:G:H4'	1:AA:485:U:OP1	2.21	0.40
1:AA:537:G:H2'	1:AA:538:G:C8	2.56	0.40
1:AA:921:U:C5'	1:AA:1081:A:O3'	2.69	0.40
1:AA:1494:G:H5'	28:BA:1913:A:C6	2.57	0.40
7:AG:46:ALA:HB3	7:AG:120:LEU:HD13	2.03	0.40
21:AU:34:ARG:NE	21:AU:35:ARG:HG3	2.36	0.40
25:AY:175:ALA:N	25:AY:178:HIS:O	2.54	0.40
25:AY:200:VAL:HG23	25:AY:201:THR:HG23	2.03	0.40
27:BC:16:VAL:HB	27:BC:203:VAL:HG12	2.02	0.40
28:BA:64:A:C6	28:BA:65:U:C4	3.10	0.40
28:BA:668:A:H2'	28:BA:670:A:H62	1.87	0.40
28:BA:1022:G:C5	28:BA:1140:C:N4	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:1083:U:H4'	57:B5:37:LYS:HE2	2.03	0.40
28:BA:1263:U:O2'	52:B0:7:PRO:HD2	2.22	0.40
28:BA:1450:G:C6	28:BA:1451:C:N4	2.90	0.40
28:BA:1724:G:H1	28:BA:1737:G:H1'	1.87	0.40
28:BA:1967:C:H2'	28:BA:1968:G:H5'	2.03	0.40
28:BA:2089:C:N4	28:BA:2090:A:N6	2.70	0.40
28:BA:2198:A:O5'	33:BH:29:PHE:CD1	2.74	0.40
28:BA:2352:A:C4	28:BA:2366:A:C2	3.10	0.40
28:BA:2469:A:C6	28:BA:2482:A:C8	3.10	0.40
28:BA:2537:U:C4	28:BA:2538:C:N4	2.89	0.40
28:BA:2724:U:P	29:BD:116:LYS:HZ2	2.44	0.40
30:BE:178:VAL:HG23	30:BE:179:SER:N	2.36	0.40
30:BE:187:VAL:HG12	30:BE:188:MET:N	2.36	0.40
35:BJ:54:ILE:HD13	35:BJ:54:ILE:C	2.42	0.40
35:BJ:88:THR:HG23	35:BJ:91:GLU:H	1.86	0.40
46:BU:13:LEU:HD11	46:BU:70:ALA:HB2	2.03	0.40
46:BU:97:SER:O	46:BU:98:ASN:HB3	2.22	0.40
48:BW:19:ARG:NH2	48:BW:19:ARG:HG2	2.37	0.40
48:BW:39:GLN:OE1	48:BW:43:LYS:HB2	2.22	0.40
57:B5:57:ASN:C	57:B5:59:LEU:N	2.74	0.40
57:B5:99:PHE:HB3	57:B5:113:PHE:HE1	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	216/241 (90%)	151 (70%)	51 (24%)	14 (6%)	1 16
3	AC	204/233 (88%)	181 (89%)	18 (9%)	5 (2%)	5 32
4	AD	203/206 (98%)	162 (80%)	30 (15%)	11 (5%)	2 19
5	AE	148/167 (89%)	123 (83%)	18 (12%)	7 (5%)	2 21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
6	AF	100/135 (74%)	79 (79%)	15 (15%)	6 (6%)	1 17
7	AG	149/179 (83%)	128 (86%)	20 (13%)	1 (1%)	22 63
8	AH	127/130 (98%)	114 (90%)	12 (9%)	1 (1%)	19 60
9	AI	125/130 (96%)	104 (83%)	15 (12%)	6 (5%)	2 21
10	AJ	96/103 (93%)	69 (72%)	20 (21%)	7 (7%)	1 14
11	AK	115/129 (89%)	97 (84%)	12 (10%)	6 (5%)	2 19
12	AL	121/124 (98%)	101 (84%)	16 (13%)	4 (3%)	4 26
13	AM	112/118 (95%)	98 (88%)	8 (7%)	6 (5%)	2 19
14	AN	92/101 (91%)	73 (79%)	13 (14%)	6 (6%)	1 16
15	AO	86/89 (97%)	75 (87%)	9 (10%)	2 (2%)	6 34
16	AP	80/82 (98%)	60 (75%)	17 (21%)	3 (4%)	3 24
17	AQ	78/84 (93%)	59 (76%)	15 (19%)	4 (5%)	2 19
18	AR	53/75 (71%)	47 (89%)	6 (11%)	0	100 100
19	AS	77/92 (84%)	65 (84%)	11 (14%)	1 (1%)	12 48
20	AT	83/87 (95%)	74 (89%)	7 (8%)	2 (2%)	6 33
21	AU	49/71 (69%)	26 (53%)	20 (41%)	3 (6%)	1 17
25	AY	667/704 (95%)	541 (81%)	92 (14%)	34 (5%)	2 19
27	BC	269/273 (98%)	211 (78%)	43 (16%)	15 (6%)	2 18
29	BD	207/209 (99%)	163 (79%)	30 (14%)	14 (7%)	1 15
30	BE	199/201 (99%)	162 (81%)	27 (14%)	10 (5%)	2 20
31	BF	175/179 (98%)	141 (81%)	30 (17%)	4 (2%)	6 34
32	BG	174/177 (98%)	127 (73%)	30 (17%)	17 (10%)	0 9
33	BH	48/50 (96%)	29 (60%)	14 (29%)	5 (10%)	0 8
34	BI	139/142 (98%)	97 (70%)	33 (24%)	9 (6%)	1 16
35	BJ	140/142 (99%)	113 (81%)	18 (13%)	9 (6%)	1 16
36	BK	120/123 (98%)	96 (80%)	14 (12%)	10 (8%)	1 12
37	BL	141/144 (98%)	104 (74%)	32 (23%)	5 (4%)	3 25
38	BM	134/136 (98%)	107 (80%)	16 (12%)	11 (8%)	1 12
39	BN	118/127 (93%)	101 (86%)	16 (14%)	1 (1%)	19 60
40	BO	114/117 (97%)	95 (83%)	18 (16%)	1 (1%)	17 57
41	BP	112/115 (97%)	86 (77%)	17 (15%)	9 (8%)	1 12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
42	BQ	115/118 (98%)	99 (86%)	12 (10%)	4 (4%)	3 25
43	BR	101/103 (98%)	83 (82%)	15 (15%)	3 (3%)	4 28
44	BS	108/110 (98%)	94 (87%)	9 (8%)	5 (5%)	2 21
45	BT	91/100 (91%)	57 (63%)	24 (26%)	10 (11%)	0 7
46	BU	100/104 (96%)	74 (74%)	16 (16%)	10 (10%)	0 9
47	BV	92/94 (98%)	81 (88%)	11 (12%)	0	100 100
48	BW	77/85 (91%)	39 (51%)	22 (29%)	16 (21%)	0 2
49	BX	75/78 (96%)	64 (85%)	8 (11%)	3 (4%)	3 23
50	BY	61/63 (97%)	39 (64%)	18 (30%)	4 (7%)	1 15
51	BZ	56/59 (95%)	46 (82%)	8 (14%)	2 (4%)	3 25
52	B0	54/57 (95%)	43 (80%)	7 (13%)	4 (7%)	1 13
53	B1	48/55 (87%)	42 (88%)	3 (6%)	3 (6%)	1 17
54	B2	44/46 (96%)	41 (93%)	3 (7%)	0	100 100
55	B3	62/65 (95%)	53 (86%)	7 (11%)	2 (3%)	4 26
56	B4	36/38 (95%)	29 (81%)	4 (11%)	3 (8%)	1 12
57	B5	146/165 (88%)	77 (53%)	40 (27%)	29 (20%)	0 2
58	B6	28/121 (23%)	20 (71%)	7 (25%)	1 (4%)	3 25
All	All	6365/6876 (93%)	5040 (79%)	977 (15%)	348 (6%)	3 19

All (348) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	33	ALA
2	AB	40	ILE
2	AB	119	GLN
3	AC	101	ILE
4	AD	24	GLY
4	AD	25	VAL
4	AD	29	ASP
4	AD	36	GLN
4	AD	125	VAL
4	AD	153	SER
4	AD	166	GLU
4	AD	175	ALA
5	AE	123	VAL
8	AH	67	GLN

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Mol	Chain	Res	Type
9	AI	42	GLU
9	AI	58	VAL
10	AJ	57	VAL
10	AJ	61	ALA
11	AK	14	LYS
11	AK	41	ALA
11	AK	105	PHE
11	AK	127	ARG
12	AL	24	LEU
12	AL	44	LYS
13	AM	4	ILE
13	AM	11	ASP
13	AM	114	LYS
14	AN	52	PRO
14	AN	53	ARG
16	AP	80	LYS
17	AQ	51	ASN
17	AQ	82	ALA
20	AT	4	ILE
21	AU	13	ASP
25	AY	5	THR
25	AY	7	ILE
25	AY	24	THR
25	AY	195	ASP
25	AY	197	ASP
25	AY	200	VAL
25	AY	204	TYR
25	AY	304	ASP
25	AY	423	LYS
25	AY	454	ASN
25	AY	500	ASP
25	AY	529	SER
25	AY	646	GLU
27	BC	70	LYS
27	BC	104	LEU
27	BC	121	ALA
27	BC	140	VAL
29	BD	43	ASP
29	BD	73	VAL
29	BD	170	VAL
30	BE	79	ARG
31	BF	111	ARG

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Mol	Chain	Res	Type
32	BG	2	ARG
32	BG	16	VAL
32	BG	28	LYS
32	BG	31	GLU
32	BG	84	LYS
32	BG	164	ALA
32	BG	168	VAL
33	BH	3	VAL
35	BJ	13	ARG
35	BJ	21	THR
35	BJ	44	TYR
35	BJ	45	THR
35	BJ	81	ILE
35	BJ	125	TYR
37	BL	66	PHE
38	BM	14	LYS
38	BM	77	PRO
39	BN	119	SER
41	BP	50	ARG
41	BP	51	ASN
41	BP	93	LYS
44	BS	3	THR
44	BS	14	ALA
44	BS	64	ALA
45	BT	27	SER
45	BT	29	THR
45	BT	40	LYS
46	BU	6	ARG
46	BU	87	GLU
46	BU	92	VAL
46	BU	98	ASN
46	BU	99	SER
48	BW	9	THR
48	BW	18	LYS
48	BW	29	SER
48	BW	36	ILE
48	BW	56	HIS
51	BZ	9	THR
52	B0	23	ALA
55	B3	22	LYS
56	B4	8	LYS
57	B5	27	VAL

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Mol	Chain	Res	Type
57	B5	48	ALA
57	B5	54	VAL
57	B5	55	VAL
57	B5	58	THR
57	B5	69	PHE
57	B5	93	ALA
57	B5	107	GLU
57	B5	108	VAL
57	B5	120	ALA
57	B5	124	ASP
57	B5	130	PRO
2	AB	148	GLY
2	AB	150	ILE
3	AC	17	PRO
3	AC	66	VAL
4	AD	33	LYS
5	AE	138	ARG
6	AF	98	GLU
7	AG	7	ILE
10	AJ	74	VAL
16	AP	77	GLU
17	AQ	14	SER
20	AT	69	LYS
25	AY	118	GLY
25	AY	202	PHE
25	AY	300	ASP
25	AY	661	SER
25	AY	662	GLU
27	BC	37	SER
27	BC	77	VAL
27	BC	238	ASN
27	BC	256	THR
29	BD	92	VAL
29	BD	99	GLU
29	BD	107	VAL
29	BD	118	PHE
31	BF	135	ILE
32	BG	169	ARG
33	BH	9	VAL
33	BH	16	GLY
34	BI	20	SER
34	BI	79	LEU

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Mol	Chain	Res	Type
35	BJ	111	LYS
36	BK	35	VAL
36	BK	71	ARG
37	BL	111	ILE
38	BM	2	LEU
38	BM	36	VAL
38	BM	56	ALA
43	BR	65	ALA
44	BS	19	LEU
44	BS	96	ILE
45	BT	36	LYS
45	BT	49	LYS
46	BU	51	LEU
48	BW	14	ASP
48	BW	47	GLY
48	BW	50	VAL
48	BW	74	LYS
50	BY	37	LEU
52	B0	35	GLU
53	B1	4	ILE
53	B1	50	GLU
57	B5	3	LEU
57	B5	33	VAL
57	B5	88	HIS
57	B5	92	ALA
57	B5	116	GLU
57	B5	119	PRO
2	AB	18	GLN
2	AB	75	ALA
3	AC	15	VAL
4	AD	167	LYS
5	AE	99	ALA
5	AE	110	ALA
6	AF	54	LEU
6	AF	63	ASN
6	AF	101	PRO
12	AL	98	VAL
13	AM	5	ALA
15	AO	46	HIS
25	AY	93	VAL
25	AY	323	LYS
25	AY	527	PRO

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Mol	Chain	Res	Type
25	AY	541	LYS
25	AY	649	VAL
29	BD	95	SER
29	BD	109	VAL
29	BD	192	ALA
30	BE	7	ASP
30	BE	70	SER
30	BE	123	LYS
31	BF	176	PHE
32	BG	32	LEU
32	BG	117	PRO
32	BG	170	THR
33	BH	10	ALA
34	BI	11	GLN
36	BK	13	ASN
36	BK	46	ALA
36	BK	93	GLN
38	BM	69	PRO
40	BO	3	LYS
41	BP	113	LEU
43	BR	98	ILE
46	BU	85	ARG
46	BU	101	THR
48	BW	34	SER
49	BX	17	ARG
49	BX	34	SER
51	BZ	34	THR
53	B1	51	ALA
56	B4	4	ARG
57	B5	5	LEU
57	B5	78	GLY
57	B5	118	ILE
58	B6	14	MET
2	AB	9	LEU
2	AB	120	SER
2	AB	128	LEU
3	AC	3	GLN
5	AE	98	PRO
9	AI	120	LYS
9	AI	129	LYS
10	AJ	35	GLN
11	AK	15	GLN

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Mol	Chain	Res	Type
13	AM	105	ASN
14	AN	34	VAL
14	AN	62	ASN
14	AN	92	GLU
15	AO	47	LYS
16	AP	49	GLY
25	AY	198	GLN
25	AY	305	THR
25	AY	413	GLU
25	AY	569	TYR
25	AY	698	VAL
27	BC	59	GLN
27	BC	110	LYS
27	BC	197	ALA
29	BD	169	ARG
29	BD	175	LEU
31	BF	132	ARG
32	BG	33	THR
32	BG	173	ALA
34	BI	64	ARG
35	BJ	74	TYR
36	BK	119	ALA
38	BM	23	GLY
38	BM	134	THR
41	BP	4	ILE
41	BP	92	ARG
41	BP	103	THR
42	BQ	87	VAL
42	BQ	88	GLU
42	BQ	95	ALA
45	BT	28	ASN
45	BT	51	PHE
45	BT	55	VAL
48	BW	37	VAL
49	BX	76	LYS
50	BY	7	ARG
52	B0	54	ILE
56	B4	16	ILE
57	B5	89	PRO
2	AB	72	LYS
2	AB	124	THR
2	AB	154	GLY

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Mol	Chain	Res	Type
5	AE	24	THR
5	AE	45	ARG
6	AF	100	SER
9	AI	9	THR
9	AI	56	ASP
10	AJ	37	ARG
11	AK	100	LEU
12	AL	74	LEU
13	AM	10	PRO
25	AY	92	HIS
25	AY	409	MET
25	AY	510	GLY
25	AY	647	SER
27	BC	64	VAL
27	BC	120	ASP
27	BC	196	ASN
29	BD	183	GLU
30	BE	46	GLN
30	BE	96	VAL
32	BG	97	VAL
32	BG	163	TYR
32	BG	166	GLU
34	BI	12	VAL
34	BI	71	LYS
35	BJ	65	THR
36	BK	49	ARG
36	BK	108	ARG
37	BL	5	THR
37	BL	29	LYS
37	BL	41	ARG
38	BM	35	ALA
38	BM	73	ILE
41	BP	34	GLY
42	BQ	85	ALA
45	BT	86	THR
45	BT	89	GLU
46	BU	88	ASP
48	BW	46	ALA
48	BW	76	ARG
50	BY	9	LYS
57	B5	36	ASP
57	B5	72	LEU

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Mol	Chain	Res	Type
6	AF	86	ARG
10	AJ	36	VAL
10	AJ	42	LEU
14	AN	29	ALA
17	AQ	71	LYS
21	AU	32	VAL
25	AY	259	ASN
25	AY	309	ARG
30	BE	83	VAL
30	BE	153	LEU
32	BG	118	ALA
33	BH	14	SER
34	BI	93	ASN
36	BK	6	THR
36	BK	50	GLY
38	BM	13	HIS
43	BR	40	MET
46	BU	16	LYS
48	BW	10	ARG
48	BW	78	PHE
57	B5	59	LEU
57	B5	94	ARG
57	B5	102	ALA
57	B5	128	THR
21	AU	27	GLY
41	BP	63	ILE
48	BW	41	GLY
2	AB	200	PRO
19	AS	30	PRO
30	BE	148	ILE
50	BY	62	GLY
57	B5	32	GLY
27	BC	232	GLY
29	BD	122	VAL
34	BI	22	PRO
34	BI	88	GLY
55	B3	6	VAL
4	AD	168	PRO
30	BE	71	GLY
52	B0	24	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 PDB entries followed by that with respect to all EM entries.

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	180/199 (90%)	170 (94%)	10 (6%)	21	46
3	AC	170/190 (90%)	156 (92%)	14 (8%)	11	34
4	AD	172/173 (99%)	165 (96%)	7 (4%)	30	55
5	AE	113/126 (90%)	108 (96%)	5 (4%)	28	53
6	AF	89/116 (77%)	82 (92%)	7 (8%)	12	35
7	AG	124/147 (84%)	115 (93%)	9 (7%)	14	39
8	AH	104/105 (99%)	96 (92%)	8 (8%)	13	37
9	AI	105/107 (98%)	96 (91%)	9 (9%)	10	32
10	AJ	86/90 (96%)	83 (96%)	3 (4%)	36	59
11	AK	90/99 (91%)	85 (94%)	5 (6%)	21	46
12	AL	103/104 (99%)	96 (93%)	7 (7%)	16	41
13	AM	92/96 (96%)	88 (96%)	4 (4%)	29	53
14	AN	79/84 (94%)	75 (95%)	4 (5%)	24	48
15	AO	76/77 (99%)	72 (95%)	4 (5%)	22	47
16	AP	65/65 (100%)	61 (94%)	4 (6%)	18	43
17	AQ	74/78 (95%)	66 (89%)	8 (11%)	6	23
18	AR	48/65 (74%)	47 (98%)	1 (2%)	53	72
19	AS	70/79 (89%)	64 (91%)	6 (9%)	10	32
20	AT	65/66 (98%)	60 (92%)	5 (8%)	13	37
21	AU	44/61 (72%)	36 (82%)	8 (18%)	1	10
25	AY	552/578 (96%)	505 (92%)	47 (8%)	10	33
27	BC	216/218 (99%)	202 (94%)	14 (6%)	17	42
29	BD	164/164 (100%)	151 (92%)	13 (8%)	12	35
30	BE	165/165 (100%)	146 (88%)	19 (12%)	5	21
31	BF	148/150 (99%)	138 (93%)	10 (7%)	16	41
32	BG	137/138 (99%)	122 (89%)	15 (11%)	6	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
33	BH	40/40 (100%)	38 (95%)	2 (5%)	24 49
34	BI	109/110 (99%)	105 (96%)	4 (4%)	34 58
35	BJ	116/116 (100%)	100 (86%)	16 (14%)	3 17
36	BK	103/104 (99%)	92 (89%)	11 (11%)	6 23
37	BL	102/103 (99%)	95 (93%)	7 (7%)	15 40
38	BM	109/109 (100%)	93 (85%)	16 (15%)	3 15
39	BN	100/103 (97%)	93 (93%)	7 (7%)	15 40
40	BO	86/87 (99%)	78 (91%)	8 (9%)	9 28
41	BP	99/100 (99%)	91 (92%)	8 (8%)	11 35
42	BQ	89/90 (99%)	81 (91%)	8 (9%)	9 30
43	BR	84/84 (100%)	78 (93%)	6 (7%)	14 39
44	BS	93/93 (100%)	84 (90%)	9 (10%)	8 27
45	BT	80/84 (95%)	77 (96%)	3 (4%)	33 57
46	BU	83/85 (98%)	76 (92%)	7 (8%)	11 33
47	BV	78/78 (100%)	75 (96%)	3 (4%)	33 57
48	BW	59/63 (94%)	53 (90%)	6 (10%)	7 25
49	BX	67/68 (98%)	61 (91%)	6 (9%)	9 30
50	BY	55/55 (100%)	52 (94%)	3 (6%)	21 47
51	BZ	48/49 (98%)	40 (83%)	8 (17%)	2 12
52	B0	47/48 (98%)	46 (98%)	1 (2%)	53 72
53	B1	45/49 (92%)	42 (93%)	3 (7%)	16 41
54	B2	38/38 (100%)	35 (92%)	3 (8%)	12 35
55	B3	51/52 (98%)	46 (90%)	5 (10%)	8 26
56	B4	34/34 (100%)	31 (91%)	3 (9%)	10 31
57	B5	112/123 (91%)	93 (83%)	19 (17%)	2 12
58	B6	26/85 (31%)	22 (85%)	4 (15%)	2 14
All	All	5284/5590 (94%)	4862 (92%)	422 (8%)	16 35

All (422) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	19	THR
2	AB	20	ARG

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Mol	Chain	Res	Type
2	AB	26	MET
2	AB	37	VAL
2	AB	63	LYS
2	AB	88	GLN
2	AB	143	LEU
2	AB	162	VAL
2	AB	170	ILE
2	AB	212	TYR
3	AC	3	GLN
3	AC	15	VAL
3	AC	18	TRP
3	AC	55	ILE
3	AC	58	GLU
3	AC	111	LEU
3	AC	121	THR
3	AC	129	MET
3	AC	162	ILE
3	AC	166	GLU
3	AC	167	TRP
3	AC	178	LEU
3	AC	186	THR
3	AC	193	TYR
4	AD	26	ARG
4	AD	32	CYS
4	AD	58	LYS
4	AD	110	THR
4	AD	143	VAL
4	AD	148	LYS
4	AD	161	LEU
5	AE	26	LYS
5	AE	45	ARG
5	AE	82	GLN
5	AE	88	VAL
5	AE	149	SER
6	AF	17	GLN
6	AF	38	ARG
6	AF	55	HIS
6	AF	86	ARG
6	AF	89	VAL
6	AF	97	THR
6	AF	100	SER
7	AG	5	ARG

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Mol	Chain	Res	Type
7	AG	7	ILE
7	AG	13	LEU
7	AG	49	THR
7	AG	59	LEU
7	AG	86	GLN
7	AG	106	GLU
7	AG	120	LEU
7	AG	149	LYS
8	AH	48	ASP
8	AH	66	PHE
8	AH	77	ARG
8	AH	83	LEU
8	AH	87	LYS
8	AH	99	LEU
8	AH	121	LEU
8	AH	125	ILE
9	AI	14	SER
9	AI	39	PHE
9	AI	43	THR
9	AI	45	ARG
9	AI	57	MET
9	AI	63	LEU
9	AI	87	LEU
9	AI	88	MET
9	AI	111	VAL
10	AJ	27	GLU
10	AJ	73	LEU
10	AJ	83	THR
11	AK	15	GLN
11	AK	65	VAL
11	AK	69	ARG
11	AK	82	LEU
11	AK	129	VAL
12	AL	29	GLN
12	AL	33	VAL
12	AL	38	TYR
12	AL	74	LEU
12	AL	90	LEU
12	AL	95	TYR
12	AL	121	ARG
13	AM	29	ARG
13	AM	63	PHE

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Mol	Chain	Res	Type
13	AM	87	ARG
13	AM	107	ARG
14	AN	5	SER
14	AN	31	ILE
14	AN	51	LEU
14	AN	96	LEU
15	AO	6	GLU
15	AO	35	GLN
15	AO	64	ARG
15	AO	87	LEU
16	AP	1	MET
16	AP	19	VAL
16	AP	31	ARG
16	AP	68	SER
17	AQ	4	LYS
17	AQ	13	VAL
17	AQ	21	ILE
17	AQ	22	VAL
17	AQ	29	VAL
17	AQ	55	ILE
17	AQ	62	ARG
17	AQ	75	LEU
18	AR	29	LEU
19	AS	11	ILE
19	AS	13	LEU
19	AS	24	GLU
19	AS	36	ARG
19	AS	37	ARG
19	AS	49	ILE
20	AT	12	ILE
20	AT	16	LYS
20	AT	27	MET
20	AT	49	LYS
20	AT	54	MET
21	AU	5	LYS
21	AU	6	VAL
21	AU	16	LEU
21	AU	19	PHE
21	AU	20	LYS
21	AU	28	VAL
21	AU	34	ARG
21	AU	43	THR

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Mol	Chain	Res	Type
25	AY	5	THR
25	AY	19	ILE
25	AY	23	LYS
25	AY	77	LYS
25	AY	83	ARG
25	AY	95	PHE
25	AY	96	THR
25	AY	101	ARG
25	AY	104	ARG
25	AY	106	LEU
25	AY	160	THR
25	AY	182	VAL
25	AY	185	LEU
25	AY	200	VAL
25	AY	202	PHE
25	AY	204	TYR
25	AY	205	GLU
25	AY	214	LEU
25	AY	220	GLN
25	AY	232	GLU
25	AY	252	LEU
25	AY	266	CYS
25	AY	276	GLN
25	AY	286	LEU
25	AY	291	ASP
25	AY	299	LEU
25	AY	303	LYS
25	AY	336	PHE
25	AY	409	MET
25	AY	418	ILE
25	AY	446	ARG
25	AY	494	ILE
25	AY	504	LYS
25	AY	508	GLN
25	AY	515	TYR
25	AY	532	LYS
25	AY	560	GLN
25	AY	584	HIS
25	AY	589	SER
25	AY	602	LYS
25	AY	612	LEU
25	AY	628	THR

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Mol	Chain	Res	Type
25	AY	660	LEU
25	AY	675	LYS
25	AY	677	ARG
25	AY	681	THR
25	AY	685	LEU
27	BC	51	ARG
27	BC	57	HIS
27	BC	109	LEU
27	BC	117	SER
27	BC	124	LYS
27	BC	129	LEU
27	BC	142	ASN
27	BC	155	ARG
27	BC	166	ARG
27	BC	176	ARG
27	BC	194	VAL
27	BC	212	TRP
27	BC	251	THR
27	BC	270	ARG
29	BD	33	ARG
29	BD	37	VAL
29	BD	97	SER
29	BD	103	ASP
29	BD	107	VAL
29	BD	118	PHE
29	BD	124	ARG
29	BD	170	VAL
29	BD	171	THR
29	BD	177	VAL
29	BD	183	GLU
29	BD	201	LEU
29	BD	203	VAL
30	BE	5	LEU
30	BE	12	LEU
30	BE	21	ARG
30	BE	40	ARG
30	BE	44	ARG
30	BE	65	THR
30	BE	69	ARG
30	BE	70	SER
30	BE	78	TRP
30	BE	88	ARG

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Mol	Chain	Res	Type
30	BE	109	LEU
30	BE	113	VAL
30	BE	118	LEU
30	BE	120	VAL
30	BE	126	VAL
30	BE	131	THR
30	BE	149	ILE
30	BE	167	VAL
30	BE	171	ASP
31	BF	9	ASP
31	BF	16	MET
31	BF	34	THR
31	BF	41	GLU
31	BF	46	LYS
31	BF	90	LEU
31	BF	94	ARG
31	BF	111	ARG
31	BF	114	ARG
31	BF	154	THR
32	BG	3	VAL
32	BG	16	VAL
32	BG	44	HIS
32	BG	68	ARG
32	BG	84	LYS
32	BG	94	ARG
32	BG	103	ASN
32	BG	110	HIS
32	BG	121	THR
32	BG	126	THR
32	BG	131	VAL
32	BG	132	LEU
32	BG	151	ARG
32	BG	170	THR
32	BG	176	LYS
33	BH	3	VAL
33	BH	22	LYS
34	BI	23	VAL
34	BI	63	ASP
34	BI	102	ARG
34	BI	137	LEU
35	BJ	2	LYS
35	BJ	17	VAL

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Mol	Chain	Res	Type
35	BJ	24	THR
35	BJ	30	THR
35	BJ	36	LEU
35	BJ	40	HIS
35	BJ	54	ILE
35	BJ	55	ILE
35	BJ	65	THR
35	BJ	72	LYS
35	BJ	73	VAL
35	BJ	95	ARG
35	BJ	103	ILE
35	BJ	129	GLU
35	BJ	131	ASN
35	BJ	140	LEU
36	BK	3	GLN
36	BK	8	LEU
36	BK	13	ASN
36	BK	18	ARG
36	BK	21	CYS
36	BK	23	LYS
36	BK	41	ILE
36	BK	54	LYS
36	BK	73	ASP
36	BK	93	GLN
36	BK	105	ARG
37	BL	5	THR
37	BL	19	LEU
37	BL	82	LEU
37	BL	91	ASP
37	BL	100	ILE
37	BL	121	THR
37	BL	144	GLU
38	BM	12	MET
38	BM	13	HIS
38	BM	31	PHE
38	BM	33	LEU
38	BM	46	ILE
38	BM	53	MET
38	BM	70	ASP
38	BM	72	PRO
38	BM	81	ARG
38	BM	88	ASN

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Mol	Chain	Res	Type
38	BM	95	LEU
38	BM	96	ILE
38	BM	97	GLN
38	BM	100	LYS
38	BM	110	GLU
38	BM	134	THR
39	BN	6	SER
39	BN	8	ARG
39	BN	33	ILE
39	BN	65	LEU
39	BN	69	ARG
39	BN	70	THR
39	BN	71	ARG
40	BO	18	LEU
40	BO	31	THR
40	BO	33	ARG
40	BO	36	TYR
40	BO	38	GLN
40	BO	47	VAL
40	BO	106	LEU
40	BO	115	LEU
41	BP	16	VAL
41	BP	19	PHE
41	BP	62	LYS
41	BP	83	ILE
41	BP	85	VAL
41	BP	92	ARG
41	BP	95	LYS
41	BP	103	THR
42	BQ	16	ILE
42	BQ	40	LYS
42	BQ	50	ARG
42	BQ	59	LEU
42	BQ	63	ARG
42	BQ	88	GLU
42	BQ	93	ILE
42	BQ	97	ILE
43	BR	4	VAL
43	BR	29	THR
43	BR	38	VAL
43	BR	46	GLU
43	BR	48	LYS

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Mol	Chain	Res	Type
43	BR	63	VAL
44	BS	3	THR
44	BS	4	ILE
44	BS	7	HIS
44	BS	36	LEU
44	BS	45	VAL
44	BS	66	ILE
44	BS	76	VAL
44	BS	96	ILE
44	BS	101	SER
45	BT	32	LEU
45	BT	43	ILE
45	BT	58	VAL
46	BU	6	ARG
46	BU	26	ASN
46	BU	30	SER
46	BU	38	ILE
46	BU	61	GLU
46	BU	86	PHE
46	BU	92	VAL
47	BV	29	ILE
47	BV	61	LEU
47	BV	87	GLN
48	BW	19	ARG
48	BW	23	LYS
48	BW	25	PHE
48	BW	30	VAL
48	BW	49	ASN
48	BW	63	ASP
49	BX	19	HIS
49	BX	24	THR
49	BX	26	ARG
49	BX	29	LEU
49	BX	34	SER
49	BX	77	TYR
50	BY	10	SER
50	BY	16	THR
50	BY	57	LEU
51	BZ	2	LYS
51	BZ	9	THR
51	BZ	15	ARG
51	BZ	23	LEU

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Mol	Chain	Res	Type
51	BZ	30	ARG
51	BZ	31	ILE
51	BZ	37	ARG
51	BZ	40	THR
52	B0	24	VAL
53	B1	8	ILE
53	B1	35	LEU
53	B1	47	ILE
54	B2	8	SER
54	B2	9	VAL
54	B2	24	THR
55	B3	7	ARG
55	B3	30	HIS
55	B3	31	ILE
55	B3	49	VAL
55	B3	56	LEU
56	B4	4	ARG
56	B4	15	LYS
56	B4	27	CYS
57	B5	1	MET
57	B5	3	LEU
57	B5	26	VAL
57	B5	42	ARG
57	B5	51	TYR
57	B5	54	VAL
57	B5	59	LEU
57	B5	65	GLU
57	B5	69	PHE
57	B5	70	GLU
57	B5	96	PHE
57	B5	106	PHE
57	B5	107	GLU
57	B5	116	GLU
57	B5	121	SER
57	B5	125	ARG
57	B5	130	PRO
57	B5	132	TYR
57	B5	143	MET
58	B6	17	MET
58	B6	18	ASP
58	B6	24	SER
58	B6	26	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	88	GLN
2	AB	189	ASN
5	AE	132	ASN
6	AF	3	HIS
7	AG	86	GLN
8	AH	18	GLN
9	AI	81	HIS
10	AJ	35	GLN
10	AJ	56	HIS
16	AP	26	ASN
25	AY	18	HIS
25	AY	92	HIS
25	AY	122	GLN
25	AY	276	GLN
25	AY	465	HIS
25	AY	584	HIS
25	AY	645	GLN
31	BF	26	GLN
34	BI	29	GLN
40	BO	34	HIS
43	BR	66	HIS
47	BV	44	HIS
47	BV	80	HIS
50	BY	41	HIS
55	B3	30	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1532/1542 (99%)	282 (18%)	18 (1%)
22	AV	76/77 (98%)	15 (19%)	0
23	AW	76/77 (98%)	27 (35%)	2 (2%)
24	AX	18/19 (94%)	14 (77%)	1 (5%)
26	BB	117/120 (97%)	17 (14%)	0
28	BA	2850/2904 (98%)	462 (16%)	41 (1%)
All	All	4669/4739 (98%)	817 (17%)	62 (1%)

All (817) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	9	G
1	AA	17	U
1	AA	20	U
1	AA	21	G
1	AA	22	G
1	AA	32	A
1	AA	39	G
1	AA	40	C
1	AA	48	C
1	AA	51	A
1	AA	70	U
1	AA	71	A
1	AA	73	C
1	AA	74	A
1	AA	75	G
1	AA	76	G
1	AA	77	A
1	AA	78	A
1	AA	79	G
1	AA	80	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	89	U
1	AA	90	C
1	AA	98	A
1	AA	115	G
1	AA	116	A
1	AA	122	G
1	AA	127	G
1	AA	130	A
1	AA	131	A
1	AA	137	U
1	AA	141	G
1	AA	143	A
1	AA	144	G
1	AA	159	G
1	AA	163	C
1	AA	164	G

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Mol	Chain	Res	Type
1	AA	173	U
1	AA	177	G
1	AA	182	A
1	AA	183	C
1	AA	204	G
1	AA	205	A
1	AA	209	U
1	AA	210	C
1	AA	240	G
1	AA	245	U
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C
1	AA	273	U
1	AA	285	C
1	AA	289	G
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	332	G
1	AA	344	A
1	AA	345	C
1	AA	347	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	384	G
1	AA	406	G
1	AA	408	A
1	AA	411	A
1	AA	412	A
1	AA	413	G
1	AA	421	U
1	AA	422	C
1	AA	423	G
1	AA	424	G
1	AA	429	U

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Mol	Chain	Res	Type
1	AA	430	A
1	AA	435	A
1	AA	441	A
1	AA	457	G
1	AA	458	U
1	AA	459	A
1	AA	461	A
1	AA	462	G
1	AA	463	U
1	AA	467	U
1	AA	468	A
1	AA	481	G
1	AA	482	A
1	AA	483	C
1	AA	484	G
1	AA	485	U
1	AA	486	U
1	AA	491	G
1	AA	508	U
1	AA	509	A
1	AA	511	C
1	AA	518	C
1	AA	527	G
1	AA	532	A
1	AA	533	A
1	AA	547	A
1	AA	556	C
1	AA	559	A
1	AA	562	U
1	AA	564	C
1	AA	572	A
1	AA	573	A
1	AA	576	C
1	AA	577	G
1	AA	579	A
1	AA	588	G
1	AA	596	A
1	AA	604	G
1	AA	650	G
1	AA	653	U
1	AA	665	A
1	AA	675	A

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Mol	Chain	Res	Type
1	AA	701	U
1	AA	702	A
1	AA	721	G
1	AA	723	U
1	AA	731	G
1	AA	734	G
1	AA	747	A
1	AA	748	G
1	AA	755	G
1	AA	777	A
1	AA	793	U
1	AA	794	A
1	AA	813	U
1	AA	815	A
1	AA	817	C
1	AA	821	G
1	AA	828	U
1	AA	829	G
1	AA	841	C
1	AA	843	U
1	AA	845	A
1	AA	846	G
1	AA	859	G
1	AA	887	G
1	AA	914	A
1	AA	920	U
1	AA	922	G
1	AA	924	C
1	AA	925	G
1	AA	926	G
1	AA	927	G
1	AA	928	G
1	AA	932	C
1	AA	934	C
1	AA	935	A
1	AA	960	U
1	AA	966	G
1	AA	969	A
1	AA	971	G
1	AA	974	A
1	AA	975	A
1	AA	976	G

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Mol	Chain	Res	Type
1	AA	977	A
1	AA	983	A
1	AA	993	G
1	AA	1003	G
1	AA	1004	A
1	AA	1008	U
1	AA	1018	G
1	AA	1022	A
1	AA	1026	G
1	AA	1029	U
1	AA	1030	U
1	AA	1031	C
1	AA	1032	G
1	AA	1033	G
1	AA	1034	G
1	AA	1037	C
1	AA	1045	C
1	AA	1050	G
1	AA	1054	C
1	AA	1055	A
1	AA	1065	U
1	AA	1066	C
1	AA	1075	U
1	AA	1076	U
1	AA	1079	G
1	AA	1082	A
1	AA	1083	U
1	AA	1086	U
1	AA	1088	G
1	AA	1094	G
1	AA	1095	U
1	AA	1101	A
1	AA	1124	G
1	AA	1125	U
1	AA	1130	A
1	AA	1133	G
1	AA	1135	U
1	AA	1136	C
1	AA	1137	C
1	AA	1139	G
1	AA	1146	A
1	AA	1159	U

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Mol	Chain	Res	Type
1	AA	1167	A
1	AA	1168	U
1	AA	1169	A
1	AA	1181	G
1	AA	1182	G
1	AA	1183	U
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	1225	A
1	AA	1226	C
1	AA	1227	A
1	AA	1239	A
1	AA	1240	U
1	AA	1249	C
1	AA	1256	A
1	AA	1279	G
1	AA	1280	A
1	AA	1286	U
1	AA	1287	A
1	AA	1293	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	C
1	AA	1303	C
1	AA	1305	G
1	AA	1317	C
1	AA	1318	A
1	AA	1320	C
1	AA	1322	C
1	AA	1332	A
1	AA	1336	C
1	AA	1337	G
1	AA	1338	G
1	AA	1353	G
1	AA	1364	U
1	AA	1368	A
1	AA	1381	U
1	AA	1391	U

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Mol	Chain	Res	Type
1	AA	1392	G
1	AA	1393	U
1	AA	1395	C
1	AA	1398	A
1	AA	1406	U
1	AA	1411	C
1	AA	1419	G
1	AA	1440	U
1	AA	1441	A
1	AA	1446	A
1	AA	1452	C
1	AA	1454	G
1	AA	1469	C
1	AA	1475	G
1	AA	1487	G
1	AA	1491	G
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G
1	AA	1503	A
1	AA	1506	U
1	AA	1517	G
1	AA	1519	A
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
1	AA	1534	A
22	AV	4	G
22	AV	5	G
22	AV	8	U
22	AV	17	C
22	AV	17(A)	U
22	AV	18	G
22	AV	19	G
22	AV	20	U
22	AV	21	A
22	AV	47	U
22	AV	48	C
22	AV	63	G
22	AV	71	C

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Mol	Chain	Res	Type
22	AV	75	C
22	AV	76	A
23	AW	4	U
23	AW	8	U
23	AW	9	A
23	AW	14	A
23	AW	15	G
23	AW	16	U
23	AW	17	U
23	AW	18	G
23	AW	19	G
23	AW	20	U
23	AW	20(A)	U
23	AW	21	A
23	AW	22	G
23	AW	25	C
23	AW	33	U
23	AW	42	U
23	AW	46	G
23	AW	47	U
23	AW	48	C
23	AW	50	C
23	AW	53	G
23	AW	58	A
23	AW	59	A
23	AW	60	U
23	AW	61	C
23	AW	63	C
23	AW	71	C
24	AX	2	G
24	AX	3	U
24	AX	5	A
24	AX	6	A
24	AX	7	A
24	AX	8	A
24	AX	9	U
24	AX	10	G
24	AX	11	G
24	AX	14	A
24	AX	15	A
24	AX	16	A
24	AX	17	A

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Mol	Chain	Res	Type
24	AX	19	A
26	BB	3	C
26	BB	15	A
26	BB	16	G
26	BB	21	G
26	BB	30	C
26	BB	35	C
26	BB	42	C
26	BB	44	G
26	BB	45	A
26	BB	56	G
26	BB	84	G
26	BB	87	U
26	BB	88	C
26	BB	89	U
26	BB	90	C
26	BB	99	A
26	BB	109	A
28	BA	10	A
28	BA	12	U
28	BA	15	G
28	BA	34	U
28	BA	35	G
28	BA	42	A
28	BA	43	G
28	BA	45	G
28	BA	46	G
28	BA	51	G
28	BA	61	C
28	BA	71	A
28	BA	74	A
28	BA	75	G
28	BA	80	G
28	BA	82	U
28	BA	84	A
28	BA	96	C
28	BA	101	A
28	BA	118	A
28	BA	119	A
28	BA	120	U
28	BA	131	A
28	BA	135	U

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Mol	Chain	Res	Type
28	BA	136	G
28	BA	137	U
28	BA	138	U
28	BA	139	U
28	BA	140	C
28	BA	141	G
28	BA	142	A
28	BA	144	A
28	BA	149	A
28	BA	162	U
28	BA	163	C
28	BA	164	C
28	BA	181	A
28	BA	188	G
28	BA	196	A
28	BA	199	A
28	BA	215	G
28	BA	216	A
28	BA	222	A
28	BA	226	A
28	BA	230	G
28	BA	248	G
28	BA	255	A
28	BA	264	C
28	BA	265	A
28	BA	266	G
28	BA	267	C
28	BA	272	A
28	BA	273	G
28	BA	276	U
28	BA	277	G
28	BA	278	A
28	BA	281	C
28	BA	285	G
28	BA	302	C
28	BA	311	A
28	BA	329	G
28	BA	330	A
28	BA	346	A
28	BA	347	A
28	BA	353	C
28	BA	355	U

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Mol	Chain	Res	Type
28	BA	361	G
28	BA	362	A
28	BA	371	A
28	BA	372	G
28	BA	382	A
28	BA	383	C
28	BA	386	G
28	BA	388	G
28	BA	396	G
28	BA	404	A
28	BA	405	U
28	BA	411	G
28	BA	412	A
28	BA	424	G
28	BA	451	U
28	BA	455	C
28	BA	481	G
28	BA	491	G
28	BA	503	A
28	BA	504	A
28	BA	505	A
28	BA	509	C
28	BA	528	A
28	BA	531	C
28	BA	532	A
28	BA	533	G
28	BA	538	A
28	BA	543	G
28	BA	544	C
28	BA	546	U
28	BA	547	A
28	BA	548	G
28	BA	549	G
28	BA	563	A
28	BA	573	U
28	BA	575	A
28	BA	586	A
28	BA	603	A
28	BA	604	G
28	BA	613	A
28	BA	614	A
28	BA	615	U

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Mol	Chain	Res	Type
28	BA	627	A
28	BA	631	A
28	BA	637	A
28	BA	645	C
28	BA	646	U
28	BA	647	G
28	BA	648	G
28	BA	654	A
28	BA	655	A
28	BA	656	G
28	BA	686	U
28	BA	714	U
28	BA	715	A
28	BA	730	A
28	BA	738	G
28	BA	747	U
28	BA	775	G
28	BA	776	G
28	BA	782	A
28	BA	784	G
28	BA	785	G
28	BA	805	G
28	BA	812	C
28	BA	819	A
28	BA	827	U
28	BA	828	U
28	BA	845	A
28	BA	846	U
28	BA	847	U
28	BA	859	G
28	BA	865	C
28	BA	866	A
28	BA	878	A
28	BA	883	G
28	BA	884	U
28	BA	896	A
28	BA	897	C
28	BA	910	A
28	BA	913	U
28	BA	914	G
28	BA	915	C
28	BA	932	U

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Mol	Chain	Res	Type
28	BA	941	A
28	BA	946	C
28	BA	961	C
28	BA	974	G
28	BA	983	A
28	BA	985	C
28	BA	995	C
28	BA	996	A
28	BA	1003	G
28	BA	1012	U
28	BA	1013	C
28	BA	1021	A
28	BA	1022	G
28	BA	1023	U
28	BA	1025	G
28	BA	1026	G
28	BA	1033	U
28	BA	1045	C
28	BA	1046	A
28	BA	1047	G
28	BA	1051	G
28	BA	1053	C
28	BA	1059	G
28	BA	1060	U
28	BA	1061	U
28	BA	1062	G
28	BA	1067	A
28	BA	1069	A
28	BA	1070	A
28	BA	1072	C
28	BA	1074	G
28	BA	1078	U
28	BA	1083	U
28	BA	1084	A
28	BA	1088	A
28	BA	1089	A
28	BA	1090	A
28	BA	1091	G
28	BA	1097	U
28	BA	1098	A
28	BA	1110	G
28	BA	1111	A

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Mol	Chain	Res	Type
28	BA	1112	G
28	BA	1129	A
28	BA	1132	U
28	BA	1133	A
28	BA	1135	C
28	BA	1136	G
28	BA	1139	G
28	BA	1142	A
28	BA	1151	A
28	BA	1155	A
28	BA	1169	A
28	BA	1170	C
28	BA	1172	C
28	BA	1174	U
28	BA	1175	A
28	BA	1176	U
28	BA	1180	U
28	BA	1186	G
28	BA	1238	G
28	BA	1248	G
28	BA	1250	G
28	BA	1253	A
28	BA	1256	G
28	BA	1266	G
28	BA	1268	A
28	BA	1271	G
28	BA	1272	A
28	BA	1273	U
28	BA	1281	G
28	BA	1300	G
28	BA	1301	A
28	BA	1313	U
28	BA	1317	G
28	BA	1352	U
28	BA	1365	A
28	BA	1368	G
28	BA	1378	A
28	BA	1379	U
28	BA	1383	A
28	BA	1395	A
28	BA	1415	U
28	BA	1416	G

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Mol	Chain	Res	Type
28	BA	1419	A
28	BA	1420	A
28	BA	1428	C
28	BA	1435	G
28	BA	1452	G
28	BA	1459	G
28	BA	1482	G
28	BA	1493	C
28	BA	1504	A
28	BA	1508	A
28	BA	1510	G
28	BA	1515	A
28	BA	1524	G
28	BA	1533	C
28	BA	1534	U
28	BA	1535	A
28	BA	1536	C
28	BA	1566	A
28	BA	1569	A
28	BA	1578	U
28	BA	1583	A
28	BA	1584	U
28	BA	1585	C
28	BA	1607	C
28	BA	1608	A
28	BA	1610	A
28	BA	1613	G
28	BA	1627	G
28	BA	1647	U
28	BA	1648	U
28	BA	1649	G
28	BA	1652	A
28	BA	1653	G
28	BA	1674	G
28	BA	1714	U
28	BA	1715	G
28	BA	1723	G
28	BA	1729	U
28	BA	1730	C
28	BA	1737	G
28	BA	1738	G
28	BA	1739	A

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Mol	Chain	Res	Type
28	BA	1744	A
28	BA	1758	U
28	BA	1764	C
28	BA	1773	A
28	BA	1776	G
28	BA	1791	A
28	BA	1800	C
28	BA	1801	A
28	BA	1802	A
28	BA	1808	A
28	BA	1811	G
28	BA	1816	C
28	BA	1829	A
28	BA	1833	C
28	BA	1847	A
28	BA	1848	A
28	BA	1858	A
28	BA	1869	G
28	BA	1870	C
28	BA	1871	A
28	BA	1872	A
28	BA	1873	G
28	BA	1884	G
28	BA	1906	G
28	BA	1913	A
28	BA	1914	C
28	BA	1927	A
28	BA	1929	G
28	BA	1930	G
28	BA	1937	A
28	BA	1938	A
28	BA	1955	U
28	BA	1960	A
28	BA	1966	A
28	BA	1967	C
28	BA	1970	A
28	BA	1971	U
28	BA	1972	G
28	BA	1991	U
28	BA	1993	U
28	BA	1997	C
28	BA	2017	U

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Mol	Chain	Res	Type
28	BA	2020	A
28	BA	2022	U
28	BA	2023	C
28	BA	2031	A
28	BA	2033	A
28	BA	2043	C
28	BA	2055	C
28	BA	2056	G
28	BA	2060	A
28	BA	2061	G
28	BA	2062	A
28	BA	2069	G
28	BA	2072	C
28	BA	2090	A
28	BA	2091	C
28	BA	2092	U
28	BA	2093	G
28	BA	2104	C
28	BA	2106	U
28	BA	2107	G
28	BA	2108	A
28	BA	2109	U
28	BA	2110	G
28	BA	2134	A
28	BA	2135	A
28	BA	2137	U
28	BA	2138	G
28	BA	2139	U
28	BA	2140	G
28	BA	2142	A
28	BA	2143	C
28	BA	2144	G
28	BA	2145	C
28	BA	2146	C
28	BA	2147	A
28	BA	2148	G
28	BA	2149	U
28	BA	2150	C
28	BA	2151	U
28	BA	2153	C
28	BA	2154	A
28	BA	2155	U

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Mol	Chain	Res	Type
28	BA	2156	G
28	BA	2157	G
28	BA	2180	U
28	BA	2183	A
28	BA	2185	U
28	BA	2194	U
28	BA	2196	C
28	BA	2198	A
28	BA	2199	A
28	BA	2204	G
28	BA	2211	A
28	BA	2212	A
28	BA	2214	C
28	BA	2225	A
28	BA	2226	C
28	BA	2238	G
28	BA	2239	G
28	BA	2250	G
28	BA	2268	A
28	BA	2278	A
28	BA	2283	C
28	BA	2284	A
28	BA	2286	G
28	BA	2287	A
28	BA	2305	U
28	BA	2308	G
28	BA	2311	A
28	BA	2322	A
28	BA	2325	G
28	BA	2327	A
28	BA	2333	A
28	BA	2336	A
28	BA	2347	C
28	BA	2354	C
28	BA	2361	G
28	BA	2383	G
28	BA	2385	C
28	BA	2402	U
28	BA	2403	C
28	BA	2406	A
28	BA	2423	U
28	BA	2424	C

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Mol	Chain	Res	Type
28	BA	2425	A
28	BA	2429	G
28	BA	2430	A
28	BA	2435	A
28	BA	2441	U
28	BA	2448	A
28	BA	2470	G
28	BA	2476	A
28	BA	2491	U
28	BA	2502	G
28	BA	2503	A
28	BA	2505	G
28	BA	2506	U
28	BA	2507	C
28	BA	2518	A
28	BA	2529	G
28	BA	2554	U
28	BA	2556	C
28	BA	2566	A
28	BA	2567	G
28	BA	2572	A
28	BA	2573	C
28	BA	2585	U
28	BA	2602	A
28	BA	2603	G
28	BA	2609	U
28	BA	2613	U
28	BA	2629	U
28	BA	2663	G
28	BA	2671	G
28	BA	2681	C
28	BA	2682	A
28	BA	2689	U
28	BA	2690	U
28	BA	2714	G
28	BA	2716	C
28	BA	2726	A
28	BA	2733	A
28	BA	2744	G
28	BA	2748	A
28	BA	2757	A
28	BA	2760	C

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Mol	Chain	Res	Type
28	BA	2765	A
28	BA	2778	A
28	BA	2791	G
28	BA	2798	U
28	BA	2800	A
28	BA	2801	G
28	BA	2818	U
28	BA	2820	A
28	BA	2821	A
28	BA	2861	U
28	BA	2867	G
28	BA	2873	A
28	BA	2874	C
28	BA	2883	A
28	BA	2884	U
28	BA	2885	G
28	BA	2891	U
28	BA	2903	U

All (62) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	79	G
1	AA	115	G
1	AA	250	A
1	AA	429	U
1	AA	481	G
1	AA	484	G
1	AA	701	U
1	AA	733	G
1	AA	913	A
1	AA	1054	C
1	AA	1136	C
1	AA	1145	A
1	AA	1201	A
1	AA	1302	C
1	AA	1331	G
1	AA	1336	C
1	AA	1394	A
1	AA	1451	U
23	AW	20(A)	U
23	AW	41	A

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Mol	Chain	Res	Type
24	AX	14	A
28	BA	119	A
28	BA	271	G
28	BA	277	G
28	BA	301	G
28	BA	403	U
28	BA	404	A
28	BA	503	A
28	BA	527	C
28	BA	613	A
28	BA	655	A
28	BA	784	G
28	BA	827	U
28	BA	846	U
28	BA	882	G
28	BA	931	U
28	BA	1020	A
28	BA	1025	G
28	BA	1069	A
28	BA	1088	A
28	BA	1110	G
28	BA	1247	A
28	BA	1378	A
28	BA	1458	U
28	BA	1509	A
28	BA	1535	A
28	BA	1626	A
28	BA	1738	G
28	BA	1757	A
28	BA	1847	A
28	BA	1870	C
28	BA	1939	U
28	BA	2092	U
28	BA	2108	A
28	BA	2142	A
28	BA	2211	A
28	BA	2286	G
28	BA	2326	C
28	BA	2423	U
28	BA	2756	U
28	BA	2873	A
28	BA	2902	C

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

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
22	5MU	AV	54	22	18,21,23	0.40	0	26,30,35	0.48	0

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
22	5MU	AV	54	22	-	0/7/25/26	0/2/2/2

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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	AV	54	5MU	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands 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	$\#\|Z\| > 2$
59	FUA	AY	801	-	39,40,40	1.68	7 (17%)	49,64,64	1.51	5 (10%)
60	GDP	AY	802	-	24,30,30	1.27	2 (8%)	30,47,47	1.57	6 (20%)

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
59	FUA	AY	801	-	-	6/15/92/92	0/4/4/4
60	GDP	AY	802	-	-	3/12/32/32	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AY	801	FUA	C23-C22	-4.38	1.39	1.51
59	AY	801	FUA	C23-C24	-4.29	1.39	1.53
59	AY	801	FUA	C29-C22	4.17	1.53	1.47
60	AY	802	GDP	C5-C6	-3.91	1.39	1.47
59	AY	801	FUA	C24-C25	-3.27	1.39	1.50
59	AY	801	FUA	C14-C8	-3.12	1.53	1.59
59	AY	801	FUA	C25-C26	2.40	1.39	1.32
59	AY	801	FUA	C10-C9	-2.15	1.53	1.57
60	AY	802	GDP	O4'-C1'	2.14	1.44	1.41

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	AY	801	FUA	C13-C12-C11	-4.35	105.81	111.90
60	AY	802	GDP	PA-O3A-PB	-3.92	119.36	132.83
59	AY	801	FUA	C16-O2-C31	-3.91	111.11	117.06
59	AY	801	FUA	C8-C9-C10	-3.43	112.82	116.34
60	AY	802	GDP	C2-N1-C6	-3.16	119.27	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	AY	801	FUA	O2-C31-C32	2.96	116.53	111.09
60	AY	802	GDP	C8-N7-C5	2.85	108.43	102.99
60	AY	802	GDP	C5-C6-N1	2.64	118.61	113.95
60	AY	802	GDP	O4'-C1'-C2'	-2.63	103.09	106.93
59	AY	801	FUA	C28-C26-C27	2.34	119.77	114.60
60	AY	802	GDP	O6-C6-C5	-2.13	120.22	124.37

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	AY	801	FUA	C13-C17-C22-C29
59	AY	801	FUA	C17-C22-C23-C24
59	AY	801	FUA	C29-C22-C23-C24
60	AY	802	GDP	C5'-O5'-PA-O3A
60	AY	802	GDP	C5'-O5'-PA-O1A
59	AY	801	FUA	C32-C31-O2-C16
59	AY	801	FUA	O3-C31-O2-C16
59	AY	801	FUA	C23-C24-C25-C26
60	AY	802	GDP	C5'-O5'-PA-O2A

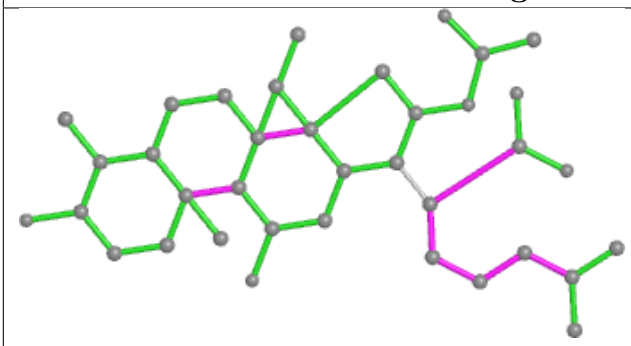
There are no ring outliers.

2 monomers are involved in 85 short contacts:

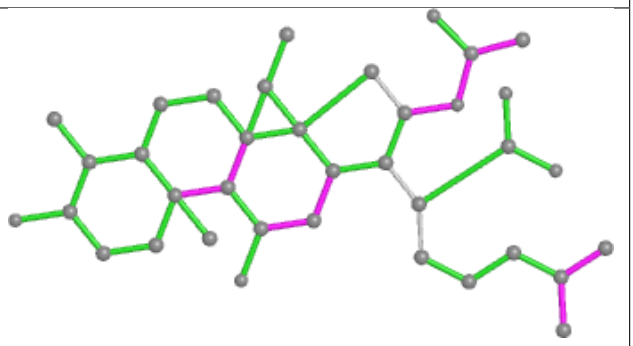
Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	AY	801	FUA	59	0
60	AY	802	GDP	26	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

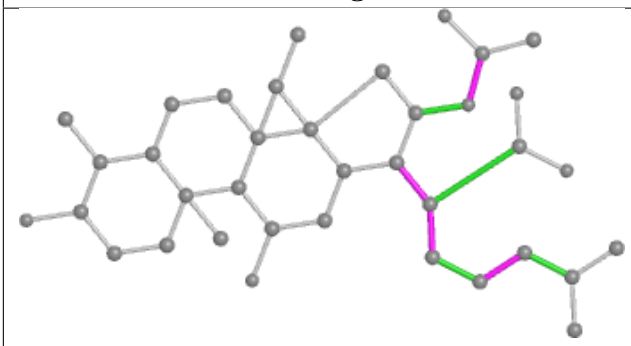
Ligand FUA AY 801



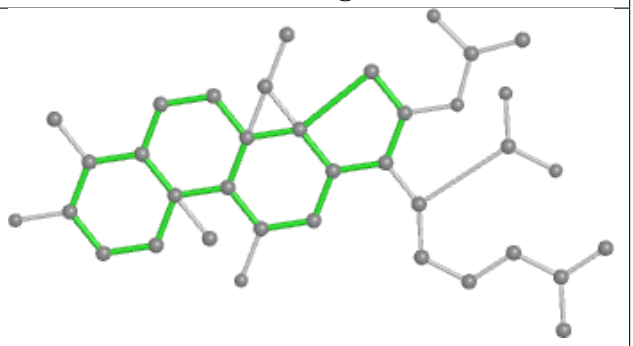
Bond lengths



Bond angles

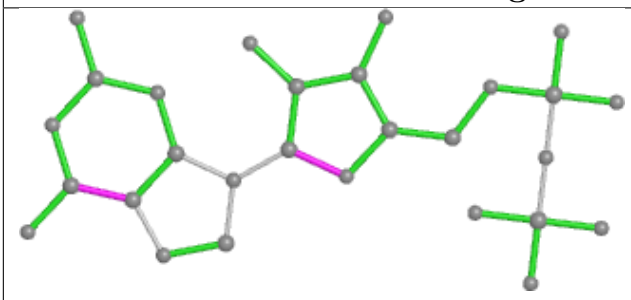


Torsions

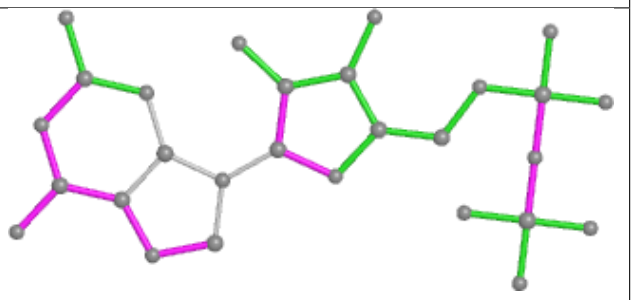


Rings

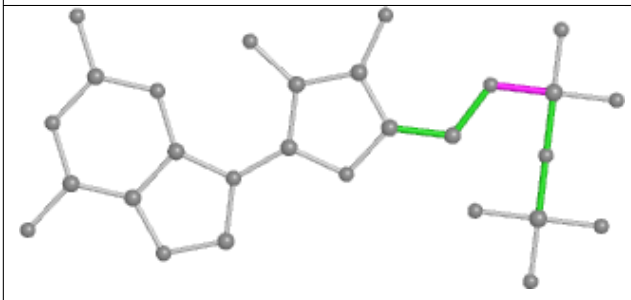
Ligand GDP AY 802



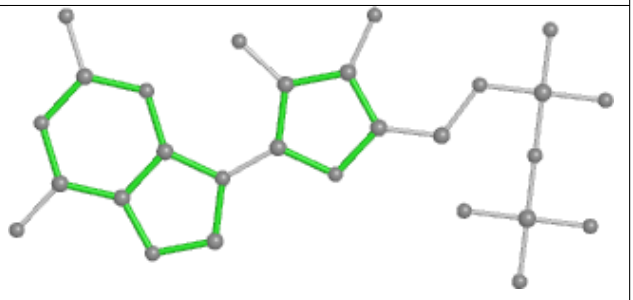
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

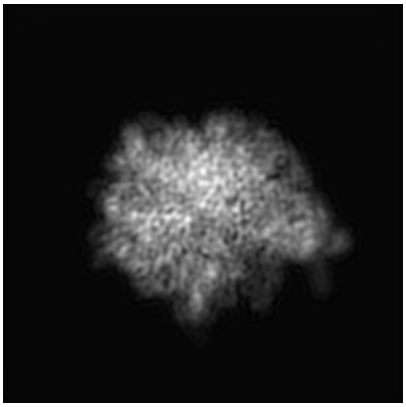
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-5775. These allow visual inspection of the internal detail of the map and identification of artifacts.

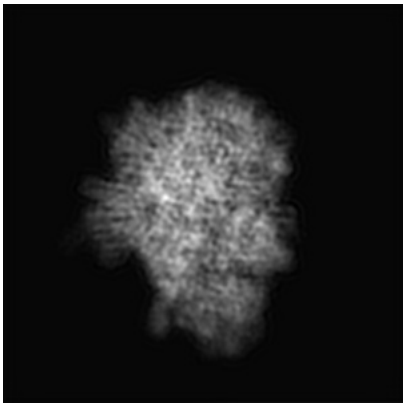
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

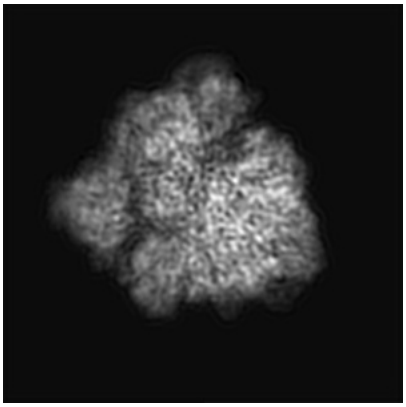
6.1.1 Primary map



X



Y

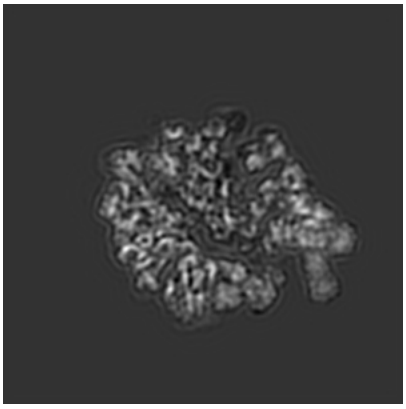


Z

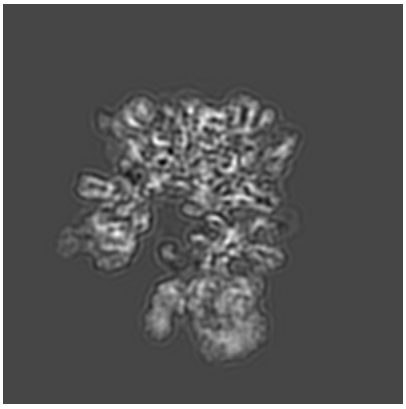
The images above show the map projected in three orthogonal directions.

6.2 Central slices

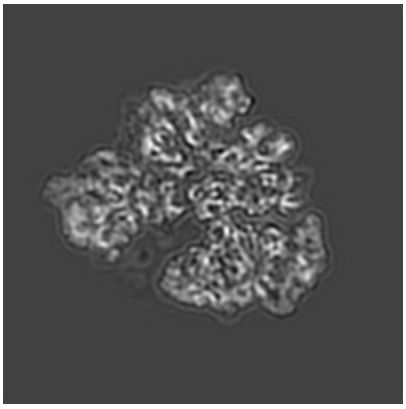
6.2.1 Primary map



X Index: 150



Y Index: 150

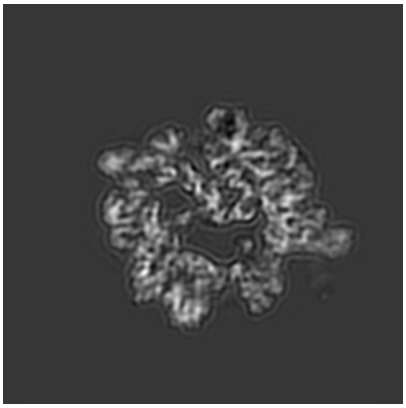


Z Index: 150

The images above show central slices of the map in three orthogonal directions.

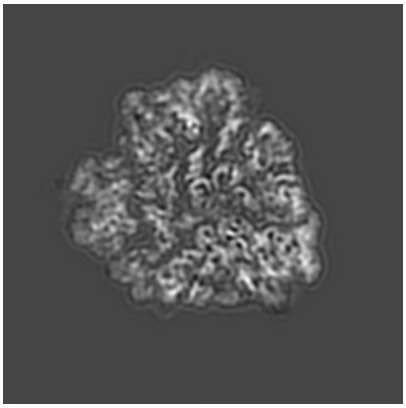
6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 141

Y Index: 154



Z Index: 141

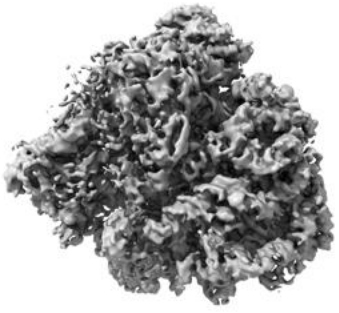
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

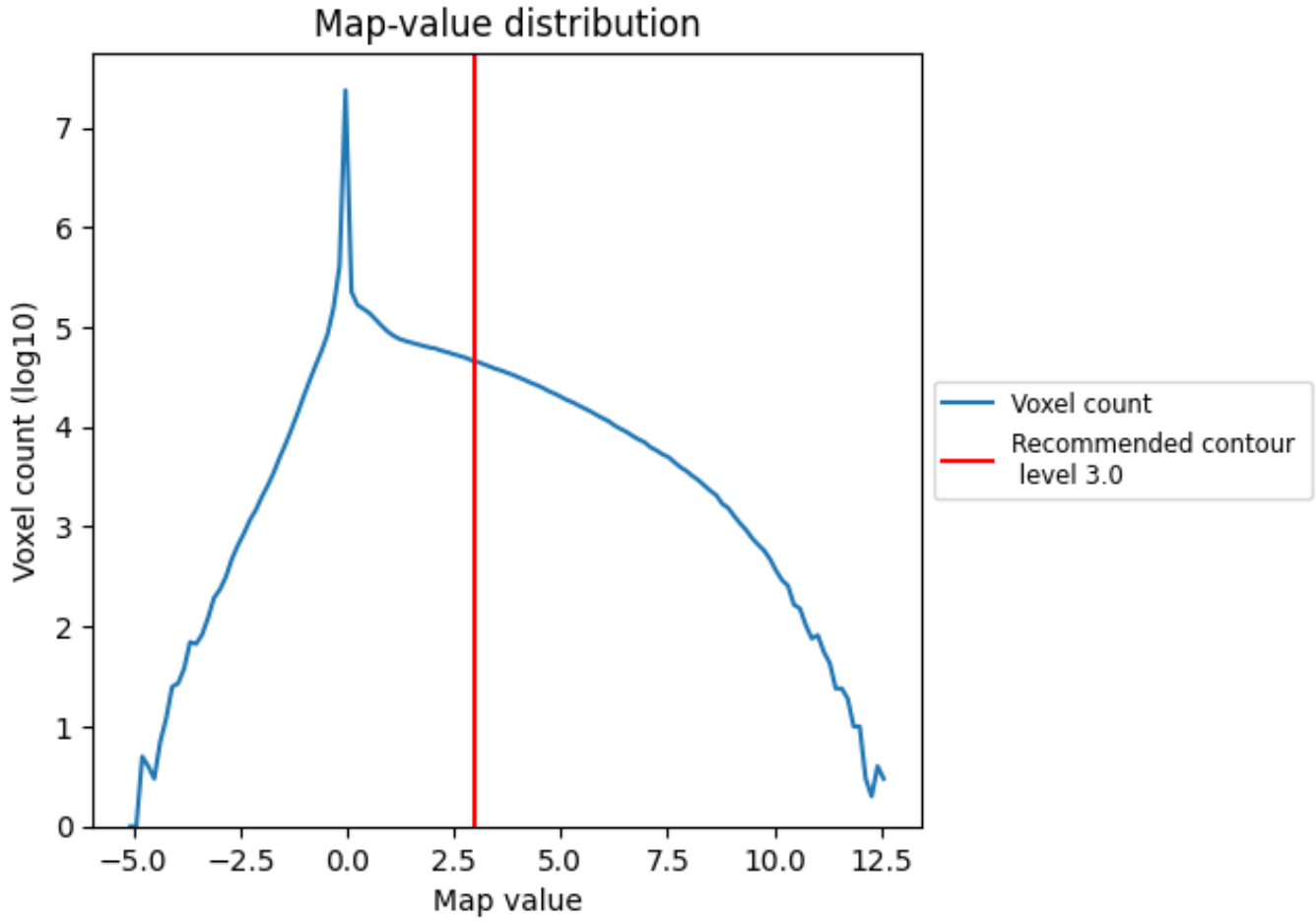
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

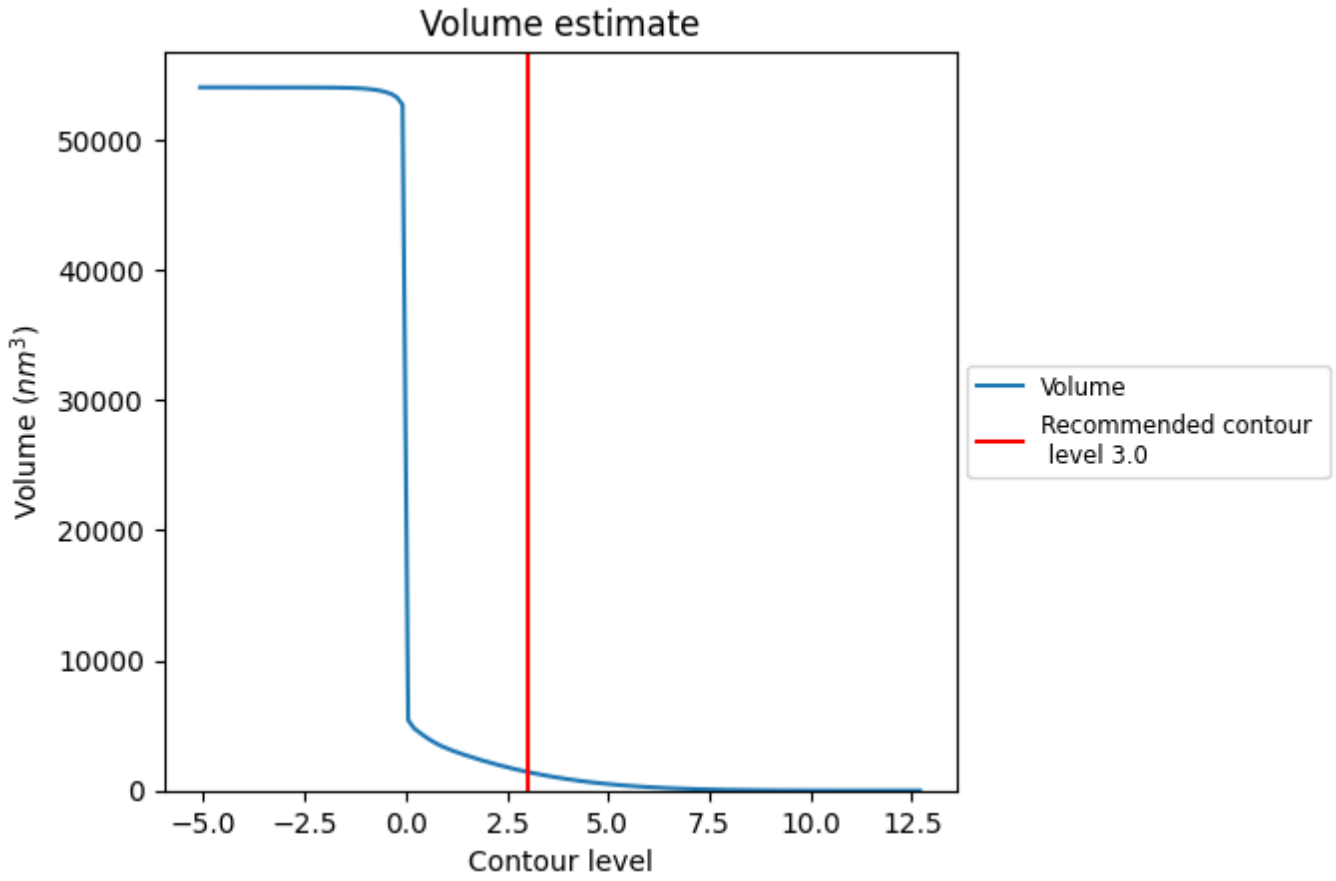
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

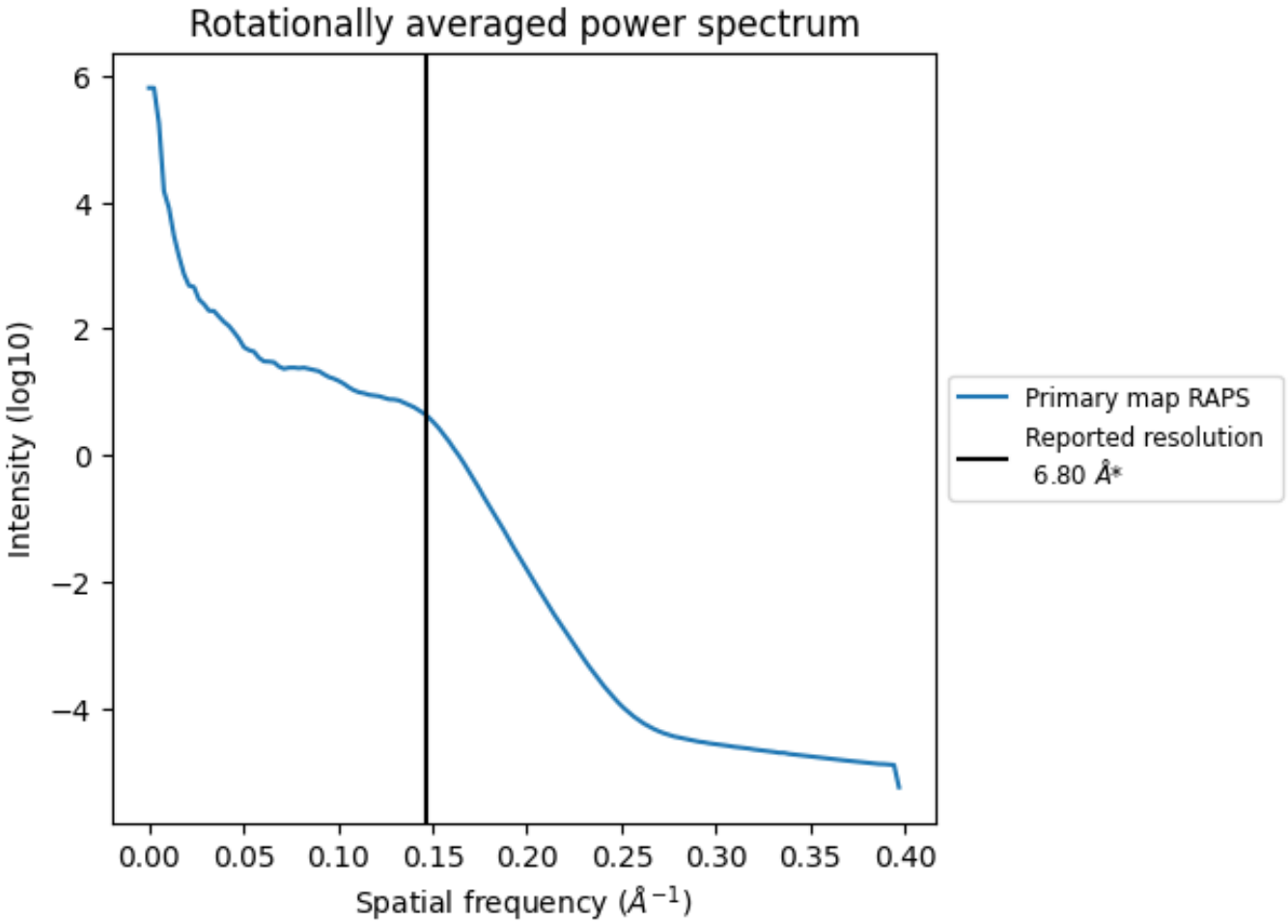
7.2 Volume estimate



The volume at the recommended contour level is 1436 nm^3; this corresponds to an approximate mass of 1297 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.147 Å^{-1}

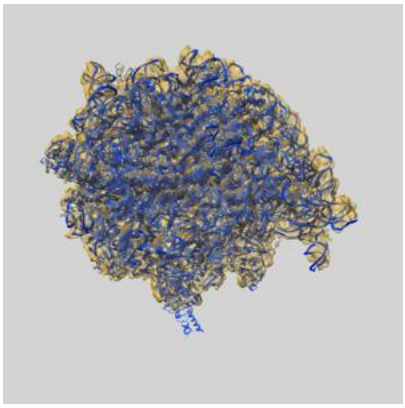
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

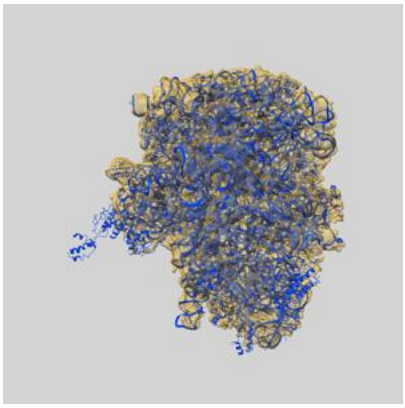
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-5775 and PDB model 4V7B. Per-residue inclusion information can be found in section 3 on page 16.

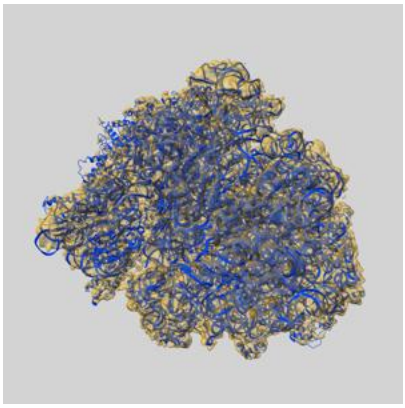
9.1 Map-model overlay



X



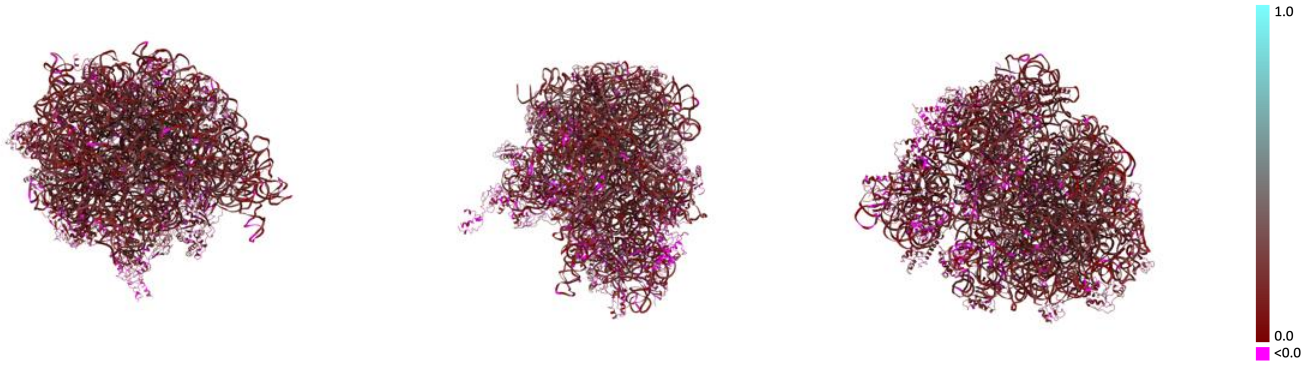
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

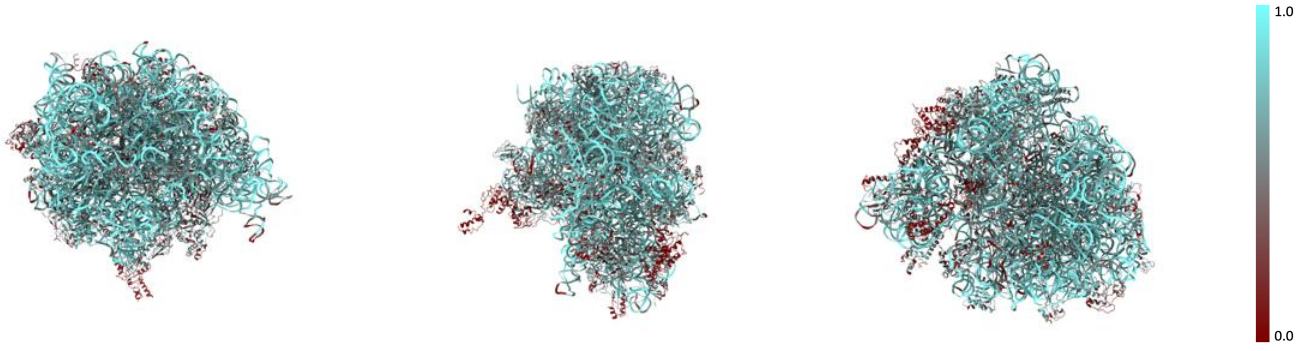
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

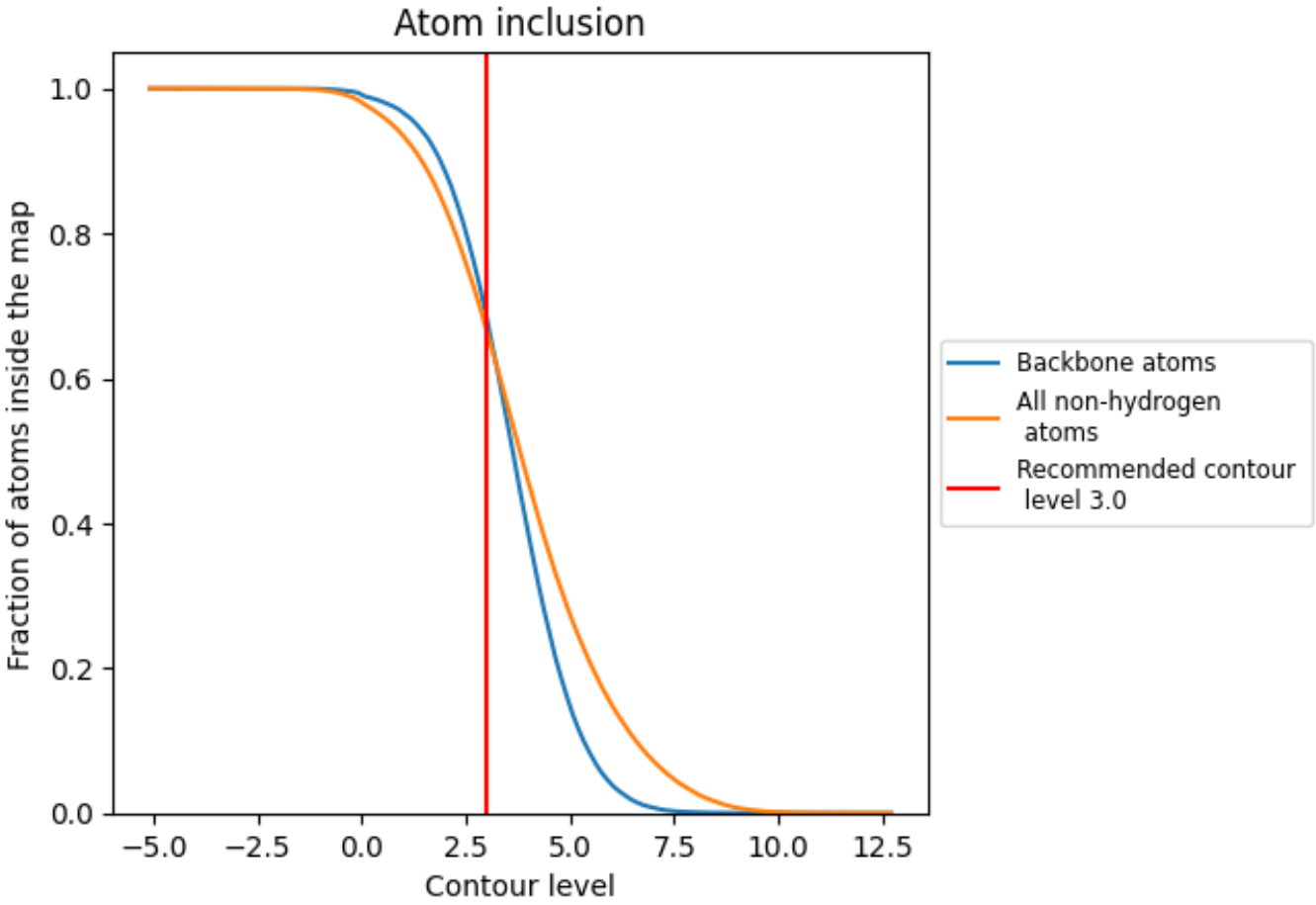
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.0).

9.4 Atom inclusion (i)



At the recommended contour level, 68% of all backbone atoms, 67% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6656	0.1610
AA	0.7855	0.1720
AB	0.0884	0.0200
AC	0.4423	0.1190
AD	0.4239	0.1010
AE	0.5125	0.1290
AF	0.4908	0.0840
AG	0.1705	0.0750
AH	0.5094	0.1360
AI	0.5087	0.1040
AJ	0.3706	0.1080
AK	0.4842	0.1240
AL	0.3909	0.1350
AM	0.4442	0.1130
AN	0.5168	0.1330
AO	0.5580	0.1320
AP	0.5678	0.1500
AQ	0.5253	0.1240
AR	0.5298	0.1380
AS	0.5201	0.1130
AT	0.5800	0.1490
AU	0.2635	0.0750
AV	0.5902	0.1730
AW	0.6869	0.1750
AX	0.4663	0.1420
AY	0.4012	0.1200
B0	0.4883	0.1490
B1	0.2170	0.0820
B2	0.4535	0.1290
B3	0.4847	0.1390
B4	0.5651	0.1340
B5	0.0612	0.0430
B6	0.0000	-0.0070
BA	0.7821	0.1890
BB	0.8296	0.1790

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Chain	Atom inclusion	Q-score
BC	0.4658	0.1220
BD	0.4863	0.1390
BE	0.4072	0.1510
BF	0.4618	0.0710
BG	0.5775	0.1650
BH	0.1029	0.0470
BI	0.1086	0.0710
BJ	0.5336	0.1320
BK	0.3746	0.1530
BL	0.5315	0.1540
BM	0.5038	0.1650
BN	0.5738	0.1350
BO	0.6292	0.1580
BP	0.4369	0.1500
BQ	0.5606	0.1150
BR	0.4969	0.1460
BS	0.4904	0.1310
BT	0.5000	0.1400
BU	0.4472	0.1040
BV	0.5813	0.1310
BW	0.5241	0.1290
BX	0.5058	0.1570
BY	0.5392	0.1350
BZ	0.5538	0.1400