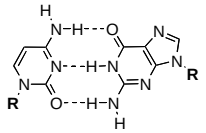
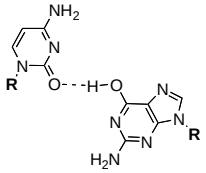
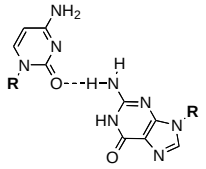
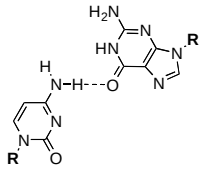
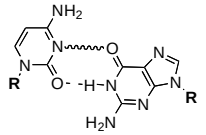
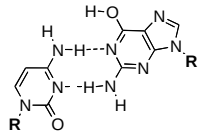
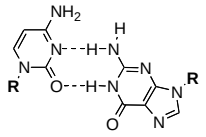
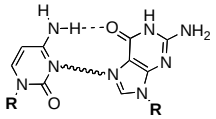
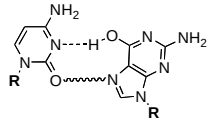
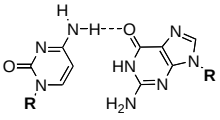
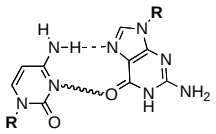
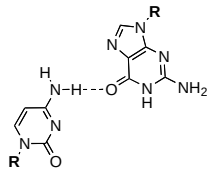
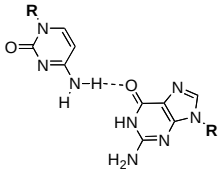
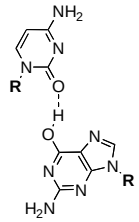
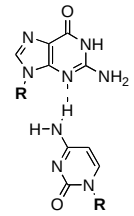
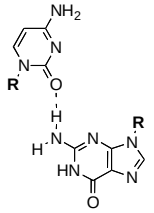
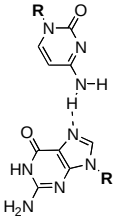
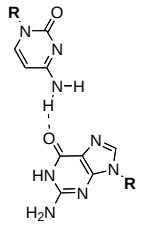
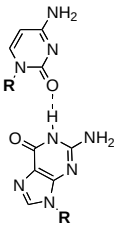
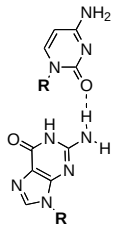
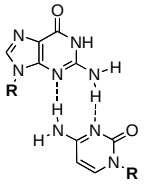
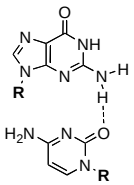
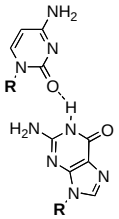
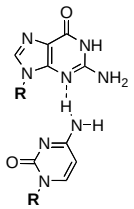
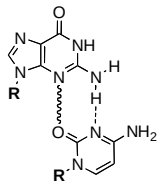
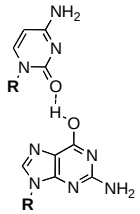
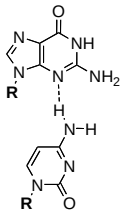
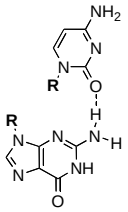
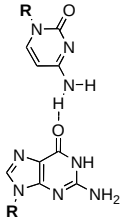
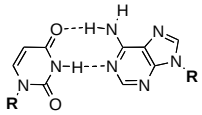
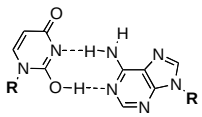
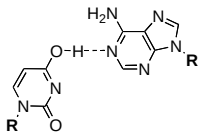
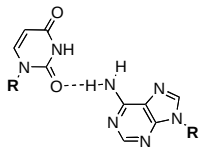
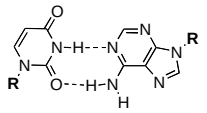
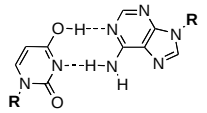
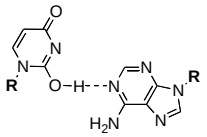
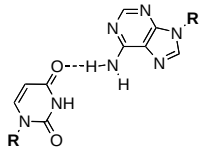
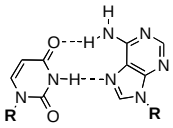
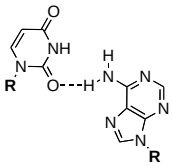
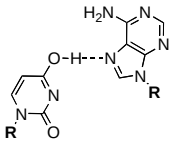
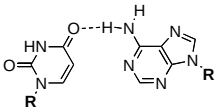
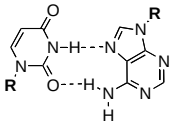
Table X. Correspondence between the Lee-Gutell (LG), Leontis-Westhof (LW), Saenger, Fox, and Olson notations for basepair conformations[†]

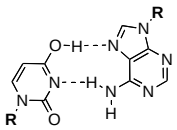
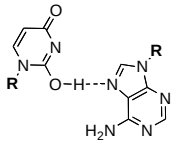
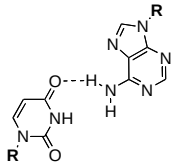
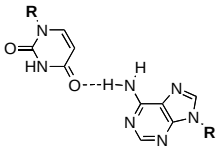
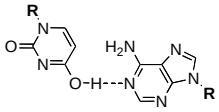
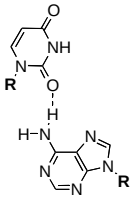
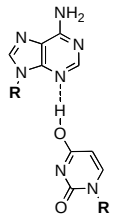
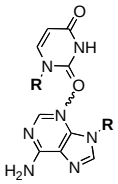
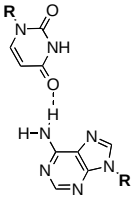
bpG[&]	LG[1] [LW[2]][Saenger[3]]	Basepair Struture	Fox[4§]	Olson[5]
C:G	C:G WC [cWW][XIX]		GC Watson-Crick	GC_1, 4, 7, 10, 13, 20, 21, 26, 32, 53, 61, 62, 90, 98, 127, 208, 241, 252, 256, 259
	C:G sWC [---][-----]		n/a	GC_69, 153, 157, 174
	C:G srWC [---][-----]		n/a	n/a
	C:G srWC* [---][-----]		n/a	n/a
	C:G Wb [---][-----]		GC NH-CO	GC_3, 8, 9, 11, 28, 29, 42, 43, 135, 169, 204, 272
	C:G Wb* [---][-----]		n/a	GC_33, 34, 96, 207
	C:G rWb [tWW][XXII]		CG reverse Watson-Crick	GC_24, 31, 44, 72, 88, 150, 152, 162, 194, 196
	C:G H_1 [cWH][-----]		GC Hoogsteen	n/a
	C:G H_2 [---][-----]		n/a	n/a
	C:G H* [---][-----]		n/a	GC_286

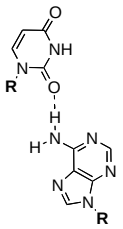
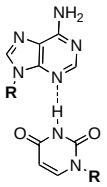
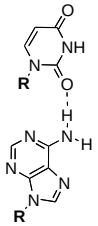
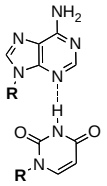
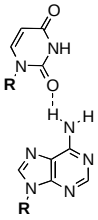
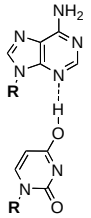
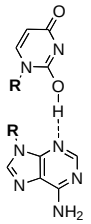
C:G rH_1 [tWH][-----]		GC NH_2-CO	n/a
C:G rH_2 [---][-----]		n/a	n/a
C:G rH* [---][-----]		n/a	GC_13
C:G S [---][-----]		n/a	GC_91, 99, 239
C:G S* [---][-----]		n/a	n/a
C:G rS [tSS][-----]		n/a	GC_51, 55, 154
C:G rS*_1 [tHH][-----]		GC N7-NH_2	n/a

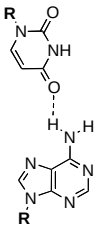
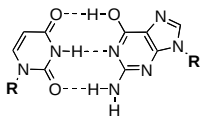
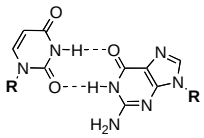
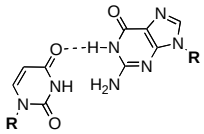
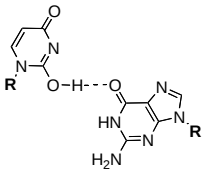
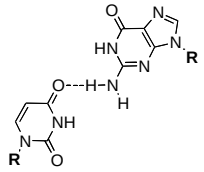
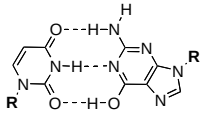
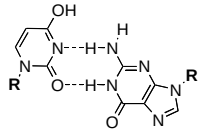
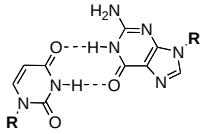
C:G rS*_2 [---][-----]		n/a	n/a
C:G fS_1 [tSW][-----]		GC NH-CO	GC_27, 89, 120
C:G fS_2 [---][-----]		GC NH_2-CO	GC_18, 303
C:G fS*_1 [tWS][-----]		GC N3-NH_2, NH_2-N3	GC_56, 87, 158, 165, 266
C:G fS*_2 [---][-----]		n/a	GC_307
C:G pfS [cSW][-----]		GC NH-CO	GC_76, 86, 97
C:G pfS*_1 [cWS][-----]		n/a	n/a

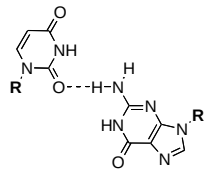
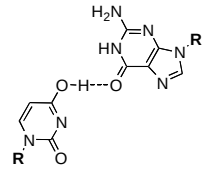
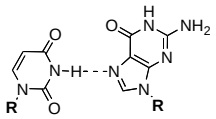
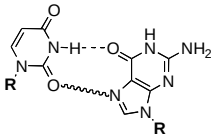
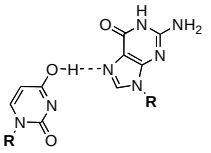
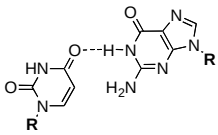
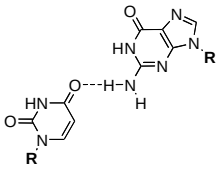
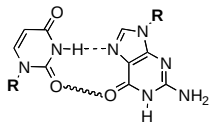
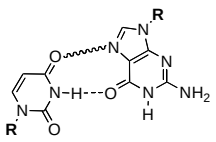
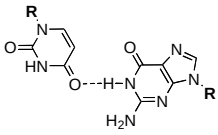
	C:G pfS*_2 [---][-----]		n/a	n/a
	C:G pS [---][-----]		n/a	GC_83, 189
	C:G pS* [cHS][-----]		GC N3-NH_2	GC_73, 246, 277
	C:G rpS [cSS][-----]		GC NH_2-CO	GC_28, 92, 93, 94, 118, 140, 206, 229, 264, 299, 302, 304
	C:G rpS* [cHH][-----]		GC CO-NH_2[&]	GC_190
U:A	U:A WC [cWW][XX]		AU Watson-Crick	AU_1, 2, 3, 10, 22, 23, 47, 84, 269, 270, 272
	U:A Wb [---][-----]		n/a	AU_12, 46
	U:A Wb* [---][-----]		n/a	n/a

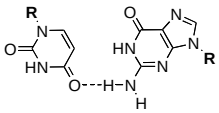
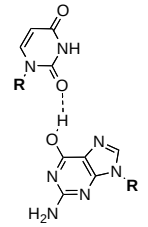
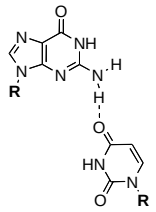
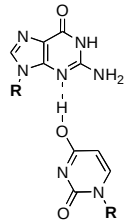
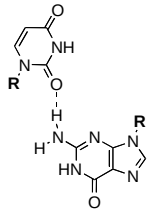
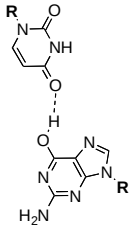
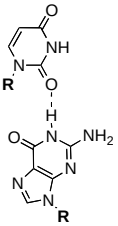
U:A sWC [---][-----]		AU NH_2-2-CO	AU_121
U:A rWC [tWW][XXI]		AU reverse Watson-Crick	AU_20, 52, 68, 148, 175, 261
U:A rWb* [---][-----]		n/a	AU_305, 322
U:A srWC [---][-----]		n/a	AU_74, 92, 117
U:A srWC* [---][-----]		n/a	AU_286
U:A H_1 [cWH][XXIII]		AU Hoogsteen	AU_21, 29, 53, 57, 72, 76, 82, 97, 108, 113, 119, 124, 127, 141, 154, 159, 167, 183, 208, 245, 253, 254, 280, 283, 343
U:A H_2 [---][-----]		n/a	n/a
U:A H_3 [---][-----]		n/a	AU_341
U:A H* [cHW][-----]		n/a	n/a
U:A rH_1 [tWH][XXIV]		AU reverse Hoogsteen	AU_6, 11, 14, 17, 33, 44, 61, 62, 73, 116, 143, 146, 234, 257, 297, 303

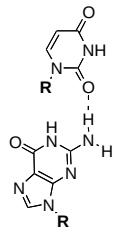
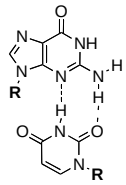
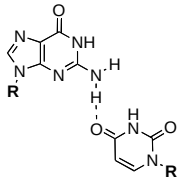
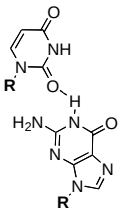
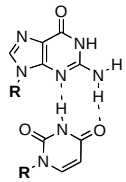
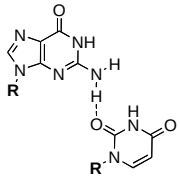
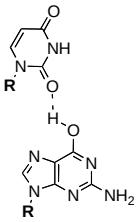
U:A rH_2 [---][-----]		n/a	AU_25, 50, 88, 89, 193, 199, 307
U:A rH_3 [---][-----]		n/a	AU_100, 185, 223, 263, 279
U:A rH_4 [---][-----]		n/a	AU_256
U:A rH*_1 [---][-----]		n/a	AU_40
U:A rH*_2 [---][-----]		n/a	AU_207
U:A S [tSH][-----]		n/a	AU_5, 28, 48, 75, 281, 296
U:A S* [tHS][-----]		n/a	AU_24
U:A rS [tSS][-----]		n/a	n/a
U:A rS* [tHH][-----]		n/a	AU_54, 83

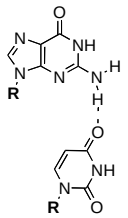
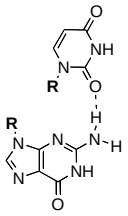
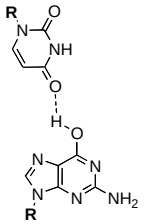
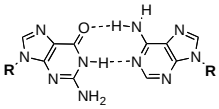
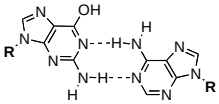
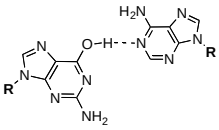
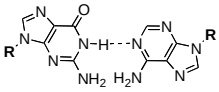
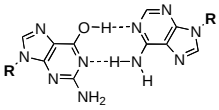
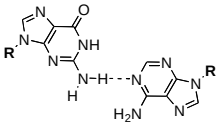
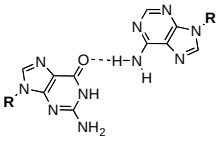
U:A fS [tSW][-----]		AU NH_2-2-CO	AU_163, 328
U:A fS* [tWS][-----]		AU N3-NH	AU_70, 71, 77, 144, 155, 156, 191, 224, 255
U:A pfS [cSW][-----]		n/a	AU_36, 38, 277
U:A pfS* [cWS][-----]		n/a	AU_7, 8, 9, 67, 69, 106, 153, 214, 219, 233, 249
U:A pS [cSH][-----]		n/a	AU_31, 32, 79, 94, 103, 109, 115, 126, 142
U:A pS* [cHS][-----]		n/a	n/a
U:A rpS [cSS][-----]		n/a	AU_206

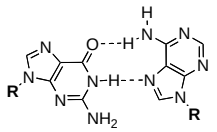
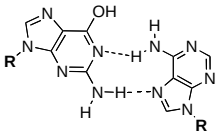
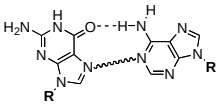
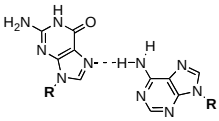
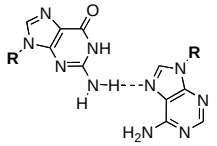
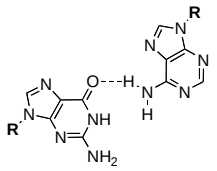
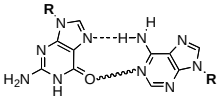
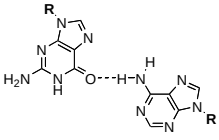
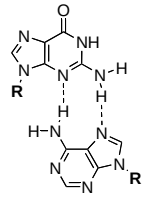
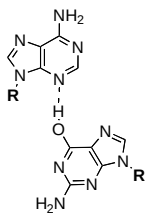
	U:A rpS* [---][-----]		n/a	AU_209
U:G	U:G WC [---][-----]		n/a	GU_6, 17, 43, 143, 171
	U:G Wb [cWW][XXVIII]		GU wobble	GU_1, 2, 3, 4, 5, 11, 13, 62, 98, 99, 170, 260, 278
	U:G Wb* [---][-----]		n/a	GU_68, 94, 106, 182
	U:G sWb [---][-----]		n/a	n/a
	U:G sWb* [---][-----]		n/a	GU_23
	U:G rWC [---][-----]		n/a	n/a
	U:G rWb [---][-----]		n/a	n/a
	U:G rWb* [tWW][XXVII]		GU reverse wobble	GU_29, 47, 134, 228

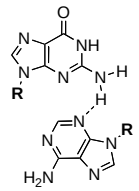
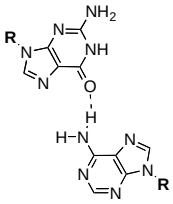
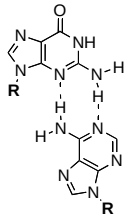
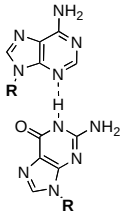
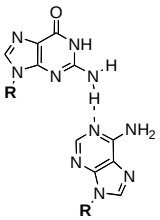
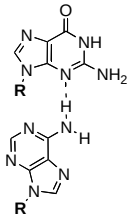
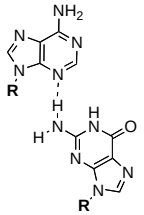
U:G srWb [---][-----]		n/a	GU_142
U:G srWb* [---][-----]		n/a	n/a
U:G H_1 [cWH][-----]		n/a	GU_44, 77, 82, 137, 217, 313
U:G H_2 [---][-----]		GU CO-NH	GU_42, 45, 99
U:G H_3 [---][-----]		n/a	n/a
U:G H*_1 [---][-----]		n/a	GU_151
U:G H*_2 [---][-----]		n/a	n/a
U:G rH_1 [tWH][-----]		GU N7-NH	GU_23, 37, 230
U:G rH_2 [---][-----]		n/a	GU_48, 50, 54
U:G rH*_1 [tHW][-----]		n/a	GU_79

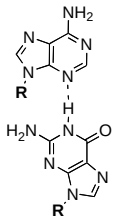
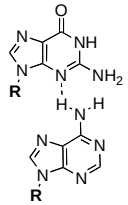
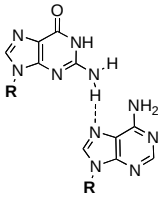
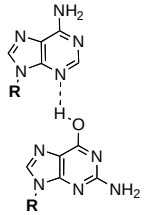
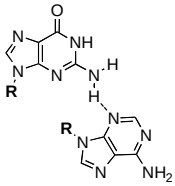
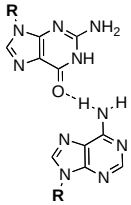
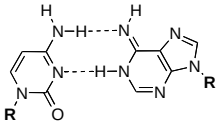
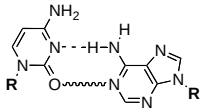
U:G rH*_2 [---][-----]		n/a	GU_340
U:G S [---][-----]		n/a	GU_46
U:G S*_1 [tHS][-----]		n/a	GU_14, 97
U:G S*_2 [---][-----]		n/a	n/a
U:G rS [tSS][-----]		n/a	GU_67, 69, 85, 172
U:G rS* [---][-----]		n/a	n/a
U:G fS_1 [tSW][-----]		GC NH-2-CO	GU_41, 120

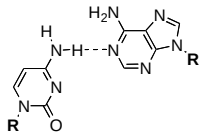
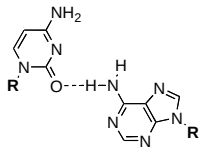
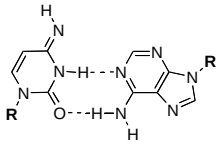
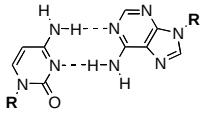
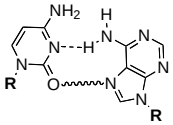
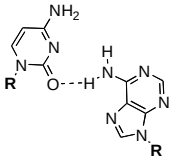
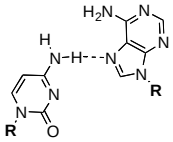
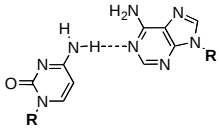
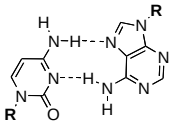
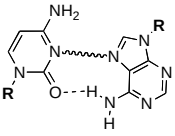
U:G fS_2 [---][-----]		n/a	GU_113
U:G fS*_1 [tWS][-----]		GU N3-NH, NH_2-CO	GU_61, 69, 213, 323, 337
U:G fS*_2 [---][-----]		n/a	n/a
U:G pfS [cSW][-----]		n/a	GU_10, 65, 135, 212
U:G pfS*_1 [cWS][-----]		n/a	GU_66, 84, 96, 117, 157
U:G pfS*_2 [---][-----]		n/a	GU_9
U:G pS [---][-----]		n/a	n/a

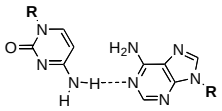
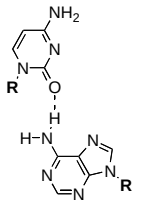
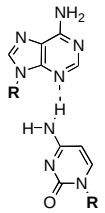
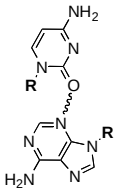
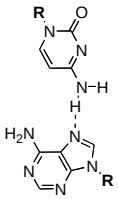
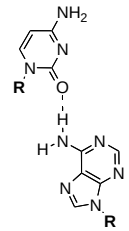
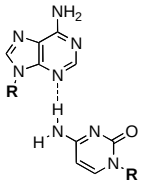
	U:G pS* [cHS][-----]		GU NH_2-2-CO	GU_20, 24, 30, 36, 58, 60, 73, 86, 140, 264
	U:G rpS [cSS][-----]		n/a	GU_72, 76, 114, 267, 295
	U:G rpS* [---][-----]		n/a	n/a
G:A	G:A WC [cWW][VIII]		GA imino	GA_1, 3, 10, 11, 27, 45, 54, 95, 96, 100, 103, 414
	G:A Wb [---][-----]		n/a	GA_95
	G:A Wb* [---][-----]		n/a	GA_21
	G:A rWC [---][-----]		n/a	GA_145, 291
	G:A rWb* [---][-----]		n/a	n/a
	G:A srWC [---][-----]		n/a	n/a
	G:A srWC* [---][-----]		n/a	n/a

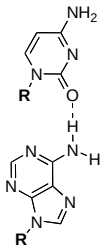
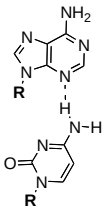
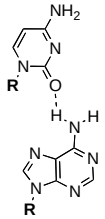
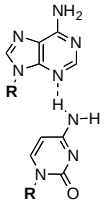
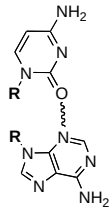
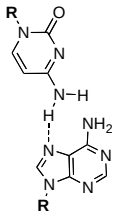
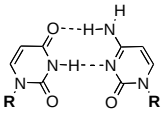
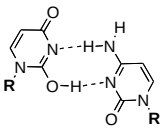
G:A H_1 [cWH][IX]		GA N7-N1,CO-NH_2	GA_28, 64, 78, 81, 169, 183, 230, 284, 295, 415, 423, 424
G:A H_2 [---][-----]		n/a	n/a
G:A H*_1 [cHW][-----]		GA^+ N7-N1,CO-NH_2	GA_2, 241
G:A H*_2 [---][-----]		n/a	GA_53, 410
G:A rH_1 [---][-----]		n/a	GA_34, 168
G:A rH_2 [---][-----]		n/a	n/a
G:A rH*_1 [tHW][-----]		n/a	GA_22, 23
G:A rH*_2 [---][-----]		n/a	n/a
G:A S [tSH][XI]		GA sheared	GA_7, 8, 9, 17, 24, 25, 32, 33, 36, 40, 41, 50, 52, 55, 56, 57, 59, 60, 61, 82, 98, 101, 134, 143, 149, 152, 177, 191, 194, 200, 319, 339, 344, 345, 358, 363, 364, 376, 395, 402, 411, 419, 420, 421, 422, 425, 426, 427, 428
G:A S* [---][-----]		n/a	n/a

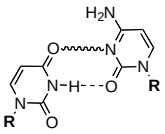
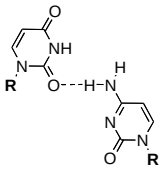
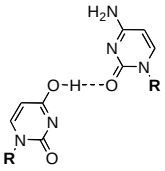
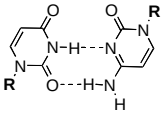
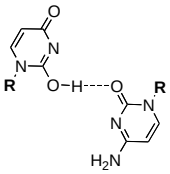
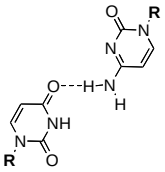
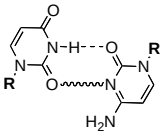
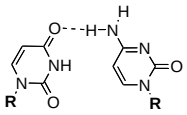
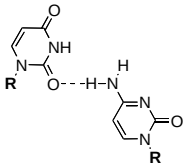
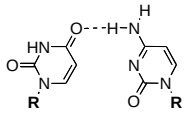
G:A rS [tSS][-----]		GA NH_2-N3	GA_5, 15, 46, 47, 48, 79, 84, 121, 142, 185, 220, 231, 248, 258, 273, 277, 278, 279, 325, 404
G:A rS* [tHH][-----]		GA NH_2-N3	GA_28, 37
G:A fS [tSW][X]		GA N3-NH_2, NH_2-N1	GA_20, 38, 58, 73, 77, 90, 123, 165, 167, 174, 224, 261, 272
G:A fS* [---][-----]		GA NH-N3	n/a
G:A pfS_1 [---][-----]		GA NH_2-N1	GA_35, 67, 69, 80, 87, 127, 253, 334, 370
G:A pfS_2 [cSW][-----]		GA N3-NH_2	GA_61, 71, 392
G:A pfS*_1 [---][-----]		n/a	GA_68, 240

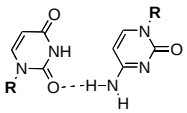
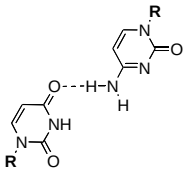
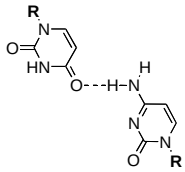
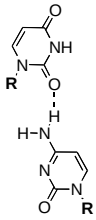
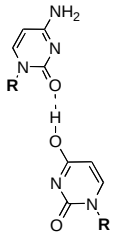
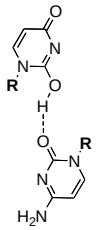
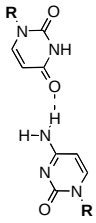
	G:A pfS*_2 [cWS][-----]		GA NH-N3	n/a
	G:A pS_1 [cSH][-----]		n/a	GA_13, 44, 302, 398
	G:A pS_2 [cSH][-----]		n/a	GA_65, 160, 311, 375, 403
	G:A pS* [cHS][-----]		n/a	n/a
	G:A rpS [cSS][-----]		n/a	GA_12, 19, 29, 62, 70, 74, 75, 146, 275, 283, 347, 348, 368, 408
	G:A rpS* [cHH][-----]		n/a	GA_4
C:A	C:A WC [---][-----]		n/a	AC_3, 14, 26, 34, 229
	C:A Wb [cWW][-----]		AC wobble	AC_2, 78

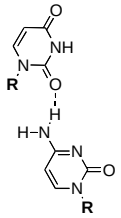
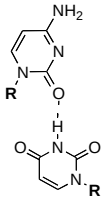
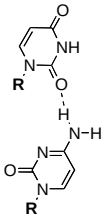
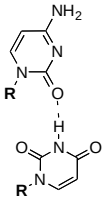
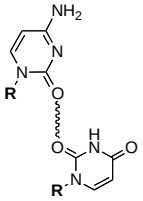
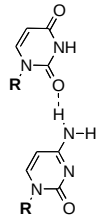
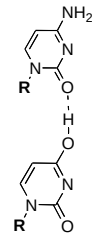
C:A Wb* [cWW][-----]		AC N1-NH_2	AC_5, 21, 24
C:A sWb [---][-----]		n/a	AC_1, 8, 16, 67
C:A rWC [---][-----]		n/a	n/a
C:A rWb* [tWW][XXVI]		AC reverse wobble	AC_37, 42, 208
C:A H_1 [---][-----]		n/a	n/a
C:A H_2 [---][-----]		AC NH_2-2-CO	AC_57
C:A H_3 [---][-----]		AC N7-NH_2	AC_108
C:A H* [---][-----]		n/a	n/a
C:A rH_1 [tWH][-XXV]		AC reverse Hoogsteen	AC_7, 9, 35, 41, 45, 56, 65, 66, 69, 70, 86
C:A rH_2 [---][-----]		n/a	AC_22, 48, 52

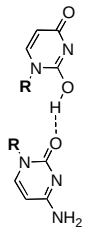
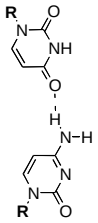
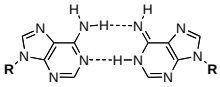
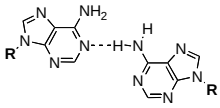
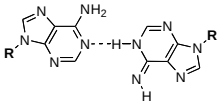
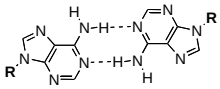
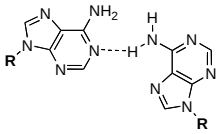
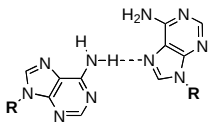
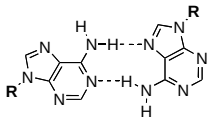
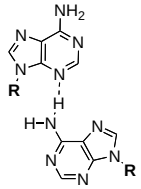
C:A rH* [---][-----]		n/a	AC_5
C:A S [tSH][-----]		n/a	AC_6, 99
C:A S* [tHS][-----]		n/a	AC_43, 54
C:A rS [tSS][-----]		n/a	n/a
C:A rS* [tHH][-----]		n/a	AC_17, 97
C:A fS [tSW][-----]		n/a	AC_38
C:A fS* [tWS][-----]		n/a	AC_44

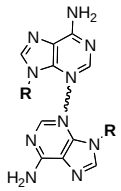
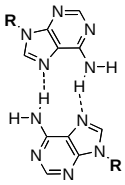
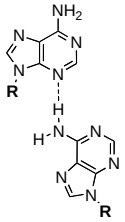
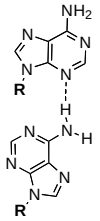
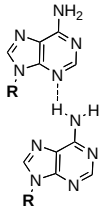
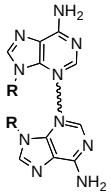
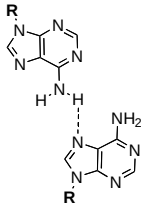
	C:A pfS [cSW][-----]		n/a	AC_11, 76
	C:A pfS* [cWS][-----]		AC N3-NH_2	AC_47, 64, 83, 180
	C:A pS [cSH][-----]		n/a	AC_12, 18, 39
	C:A pS* [cHS][-----]		n/a	AC_51, 53, 64
	C:A rpS [cSS][-----]		n/a	n/a
	C:A rpS* [---][-----]		n/a	AC_137
U:C	U:C WC [cWW][-----]		UC 4-CO-NH_2	CU_4, 36, 42, 52, 143
	U:C Wb [---][-----]		n/a	CU_67

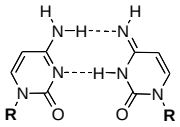
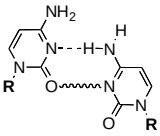
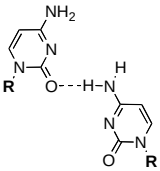
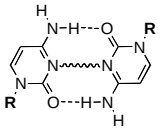
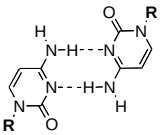
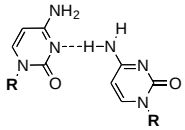
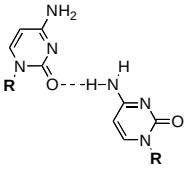
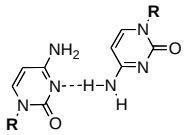
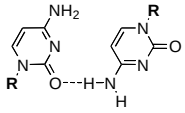
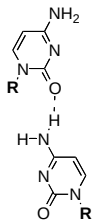
U:C Wb* [---][-----]		n/a	CU_26, 52, 62, 63, 85, 105, 113
U:C sWC [---][-----]		UC 2-CO-NH_2	CU_45
U:C sWC* [---][-----]		n/a	CU_84
U:C rWC [tWW][XVII]		UC 2-CO-NH_2	CU_35
U:C srWC [---][-----]		n/a	n/a
U:C srWC* [---][-----]		n/a	n/a
U:C rWb [---][-----]		n/a	n/a
U:C H_1 [---][-----]		n/a	n/a
U:C H_2 [---][-----]		n/a	n/a
U:C H* [cHW][-----]		n/a	n/a

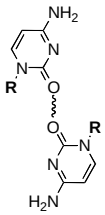
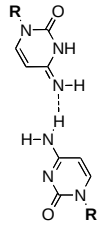
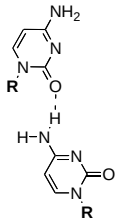
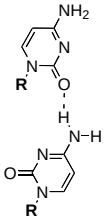
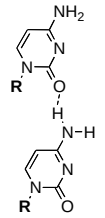
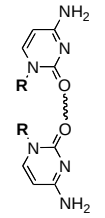
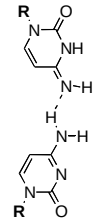
U:C rH_1 [---][-----]		n/a	CU_109
U:C rH_2 [---][-----]		n/a	n/a
U:C rH* [---][-----]		n/a	CI_5, 52
U:C S [tSH][-----]		UC 2-CO-NH_2	CU_16, 33, 120
U:C S* [---][-----]		n/a	n/a
U:C rS [tSS][-----]		n/a	n/a
U:C rS* [tHH][-----]		UC 4-CO-NH_2	CU_34

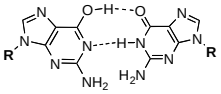
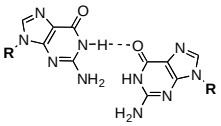
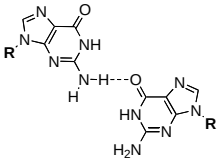
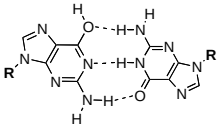
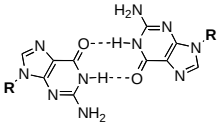
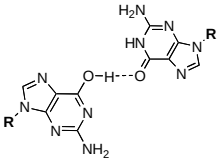
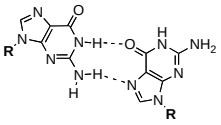
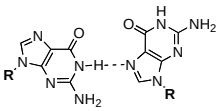
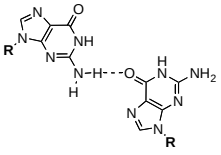
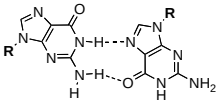
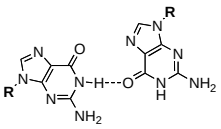
U:C fS [tSW][-----]		n/a	n/a
U:C fS* [tWS][-----]		UC NH-CO	CU_44, 71
U:C pfS [cSW][-----]		n/a	CU_20, 49, 108
U:C pfS*_1 [cWS][-----]		n/a	CU_38, 65, 69, 70, 74, 98, 103, 138
U:C pfS*_2 [---][-----]		n/a	n/a
U:C pS [cSH][-----]		n/a	CU_6, 23, 25, 27, 39
U:C pS* [cHS][-----]		n/a	n/a

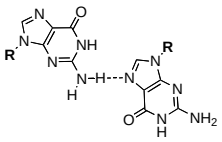
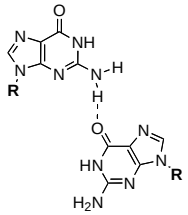
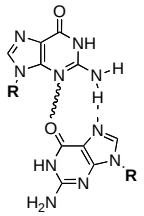
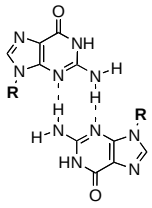
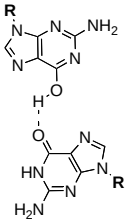
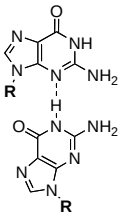
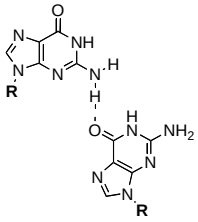
	U:C rpS [cSS][-----]		n/a	n/a
	U:C rpS* [---][-----]		n/a	n/a
A:A	A:A WC [---][-----]		n/a	AA_1
	A:A Wb [cW][-----]		AA N1-NH_2	AA_8, 15, 30
	A:A rWC [---][-----]		n/a	AA_35
	A:A rWb* [tWW][I]		AA N1-NH_2, sym	AA_2, 5, 33, 38, 54
	A:A H_1 [---][-----]		n/a	n/a
	A:A H_2 [---][-----]		AA N7-NH_2	AA_39
	A:A rH [tWH][V]		AA N7-NH_2	AA_4, 30, 32, 49, 50, 96, 97, 98, 134, 135
	A:A S [tSH][-----]		AA sheared	AA_7, 14, 17, 45, 51, 58, 84, 113, 129

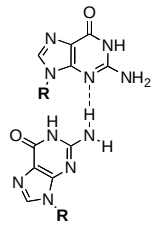
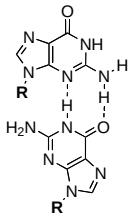
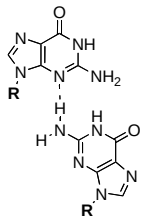
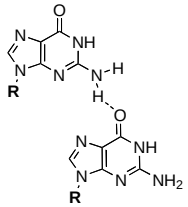
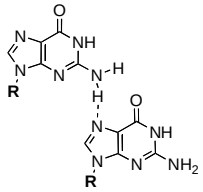
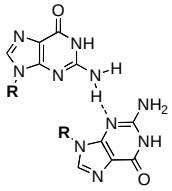
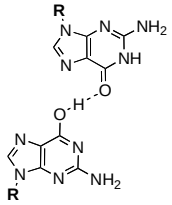
A:A rS [tSS][-----]		n/a	n/a
A:A rS* [tHH][II]		AA N7-NH_2, sym	AA_9, 12, 22, 23, 25, 26, 31, 47, 48, 52, 77, 117
A:A fS [tSW][-----]		n/a	AA_19, 112
A:A pfS [cSW[---]		n/a	AA_10, 65
A:A pS [cSH][-----]		n/a	n/a
A:A rpS [cSS][-----]		n/a	n/a
A:A rpS* [---][-----]		n/a	AA_16

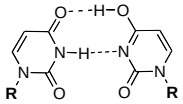
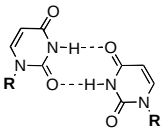
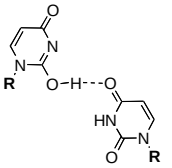
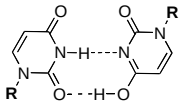
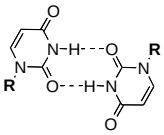
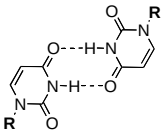
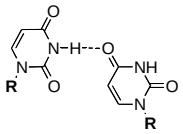
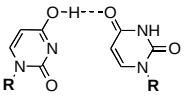
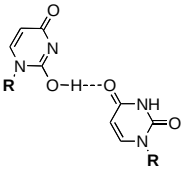
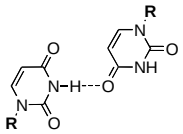
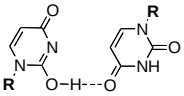
C:C	C:C WC [---][-----]		n/a	n/a
	C:C Wb [cWW][-----]		CC N3-CO, NH_2-N3	CC_20, 0\30, 35, 39
	C:C sWb [---][-----]		CC CO-NH_2[&]	CC_8, 63
	C:C rWC [tW][XV]		CC CO-NH_2, sym	CC_6
	C:C rWb* [tWW][-----]		CC N3-NH_2, sym	CC_53, 55
	C:C H_1 [---][-----]		n/a	CC_2, 8, 58
	C:C H_2 [---][-----]		n/a	CC_26
	C:C rH_1 [---][-----]		n/a	n/a
	C:C rH_2 [tWH][-----]		n/a	n/a
	C:C S [---][-----]		n/a	CC_3, 11, 59, 65

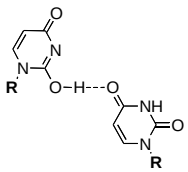
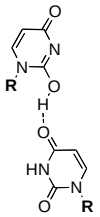
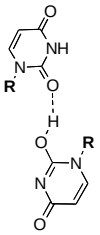
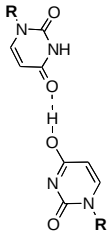
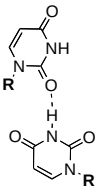
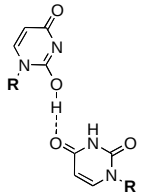
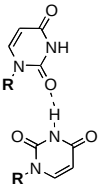
C:C rS [---][-----]		n/a	n/a
C:C rS* [---][-----]		n/a	n/a
C:C fS [tSW][-----]		n/a	n/a
C:C pfS [cSW][-----]		n/a	CC_17, 44, 77
C:C pS [cSH][-----]		n/a	n/a
C:C rpS [cSS][-----]		n/a	n/a
C:C rpS* [---][-----]		n/a	n/a

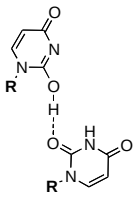
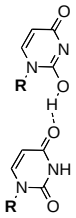
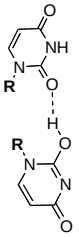
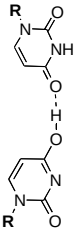
G:G	G:G WC [---][-----]		n/a	GG_160
	G:G Wb [---][-----]		GG CO-NH	GG_27, 45, 48, 62, 67, 104, 223
	G:G sWb [---][-----]		n/a	GG_96
	G:G rWC [---][-----]		n/a	GG 115
	G:G rWb* [tWW][III]		GG N1-CO, sym	GG_17, 90
	G:G srWb* [---][-----]		n/a	n/a
	G:G H_1 [cWH][VI]		GG N1-CO, N7-NH_2	GG_1, 2, 13, 16, 116, 127
	G:G H_2 [---][-----]		n/a	GG_3, 4, 173
	G:G H_3 [---][-----]		n/a	GG_86
	G:G rH_1 [tWH][-----]		GG N7-NH, CO-NH_2	GG_14, 19, 20, 21, 25
	G:G rH_2 [---][-----]		n/a	GG_83, 89

G:G rH_3 [---][-----]		n/a	n/a
G:G S_1 [tSH][-----]		n/a	G_15, 31, 49, 99, 112
G:G S_2 [---][-----]		GG NH_2-N7	GG_26, 38, 56
G:G rS [tSS][IV]		GG N3-NH_2, sym	GG_32, 39, 52, 70, 80, 91, 107, 109, 143, 154, 159, 162, 163, 167, 225
G:G rS* [tHH][-----]		n/a	n/a
G:G fS_1 [---][-----]		n/a	n/a
G:G fS_2 [---][-----]		n/a	n/a

G:G fS_3 [---][-----]		n/a	GG_60, 172, 186
G:G pfS_1 [cSW][-----]		n/a	GG_42, 105, 106, 110, 134
G:G pfS_2 [---][-----]		GG N3-NH_2	GG_239
G:G pS_1 [cSH][-----]		n/a	GG_18, 30, 64
G:G pS_2 [---][-----]		n/a	GG_22, 23, 55, 69, 81
G:G rpS [cSS][-----]		n/a	GG_28, 41, 44, 47, 108, 121, 137, 169, 181, 222, 240
G:G rpS* [cHH][-----]		n/a	GG_35, 74, 93

U:U	U:U WC [---][-----]		n/a	UU_72
	U:U Wb [cWW][XVI]		UU NH-CO	UU_4, 12, 21, 27, 31, 36, 42, 46, 71
	U:U sWb [---][-----]		n/a	n/a
	U:U rWC [---][-----]		n/a	n/a
	U:U rWb [tWW][XIII]		UU 2-CO-NH, sym	UU_10, 11, 16, 18, 35
	U:U rWb* [tWW][XII]		UU 4-CO-NH_2, sym	UU_19, 20, 40, 60
	U:U H_1 [cWH][-----]		n/a	UU_22, 73
	U:U H_2 [---][-----]		n/a	n/a
	U:U H_3 [---][-----]		n/a	n/a
	U:U rH_1 [tWH][-----]		UU 4-CO-C5H, NH-4-CO	UU_3, 9
	U:U rH_2 [---][-----]		n/a	n/a

U:U rH_3 [---][-----]		n/a	n/a
U:U S [---][-----]		n/a	UU_23
U:U rS [---][-----]		n/a	n/a
U:U rS* [---][-----]		n/a	n/a
U:U fS_1 [tSW][-----]		n/a	UU_24, 56
U:U fS_2 [---][-----]		n/a	UU_37
U:U pfS_1 [cSW][-----]		n/a	UU_43, 53

U:U pfS_2 [---][-----]		n/a	n/a
U:U pS [cSH][-----]		n/a	UU_2, 5
U:U rpS [---][-----]		n/a	n/a
U:U rpS* [---][-----]		n/a	n/a

† Base-backbone and backbone-backbone interactions are not included here and will be presented elsewhere. "n/a" is to represent the conformations that were not assigned in the other naming systems.

& The LG system is based on basepair groups (bpG's) of ten: C:G, U:A, U:G, G:A, C:A, U:C, A:A, C:C, G:G, and U:U.

§ The conformations available at http://prion.bchs.uh.edu/bp_type/ are represented by using simple acronyms: CO, carbonyl; NH, imino; NH_2, amino; sym, symmetric.

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