## Training dataset curated from **R-SIM** database for the "Riboswitch" model in **RSAPred**

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
221	C1=NC2=NC=NC(=C2 N1)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGAUUAUGUCC	Adenine	Target_lig_165	ADENINE RIBOSWITCH	Target_69	6.3979 400086 7204
222	C1=C2C(=NC(=N1)N) N=CN2	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGAUUAUGUCC	2-aminopurine	Target_lig_166	ADENINE RIBOSWITCH	Target_69	5.7891 466346 8511
223	C1=C(N=C1N)N) N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGAUUAUGUCC	2,4,6- triaminopyrimidine	Target_lig_167	ADENINE RIBOSWITCH	Target_69	4.6989 700043 3602
224	C1=NC2=NC(=NC(=C 2N1)N)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGAUUAUGUCC	2,6- diaminopurine	Target_lig_168	ADENINE RIBOSWITCH	Target_69	7.6989 700043 3602
225	C1=NC(=NC2(C1=NC =N2)N)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGAUUAUGUCC	2,4-diaminopurine	Target_lig_169	ADENINE RIBOSWITCH	Target_69	8.3979 400086 7204
231	CC1=CC2=C(C=C1C) N(C=N2)C3C(C(C(O3) CO)OP(=O) ([O-])OC(C)CNC(=O) CCC4(C(C5C6(C(C(C) =N6)C(=C7C(C(C=N8)C(=C4[N-]5)C)CCC(=O)N) (C)CC(=O)N)C)CCC(=O)N) (C)CC(=O)N)C)CCC(=O)N)(C)CC(=O)N)C)CC(=O)N)C)CC(=O)N)C)CC(=O)N)C)CC(=O)N)C)CC(=O)N)C)C(=O)N)C)C(=O)N)C)C(C(C1)C)CC(C(C1)C)CC(C1)C(C1)CCC(C1)CCC(C1)CCCC(C1)CCCC(C1)CCCCC(C1)CCCCCCCC	GCCGGUCCUGUGAG UUAAUAGGAAUCC AGUGCGAAUCUGGA GCUGACGCAGCG GUAAGGAAAGGUGC GAUGAUUGCGUUAU GCGGACACUGCCAU UCGGUGGGAAGUCA UCAUCUCUUAGUAU CUUAGAUACCCCUC CAAGCCCGAAGACC UGCCGGCCAACGUC GCAUCUGGUUCUCA UCAUCGCGUAAUAU UGAUGA	deoxy_adenosylcob alamin	Target_lig_173	Riboswitch	Target_70	6.5228 787452 8034
315	C1=NC2=NC=NC(=C2 N1)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGACUAUGUCC	Adenine	Target_lig_165	Guanine riboswitch	Target_74	6.3288 271572 8492
316	C1=NC2=C(N1)C(=O) N=CN2	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGACUAUGUCC	Hypoxanthine	Target_lig_162	Guanine riboswitch	Target_74	7.3010 299956 6398
317	C1=NC2=C(N1)C(=O) NC(=N2)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGACUAUGUCC	GUANINE	Target_lig_248	Guanine riboswitch	Target_74	8.3010 299956 6398
318	C1=NC(=NC2(C1=NC =N2)N)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGACUAUGUCC	2,4-diaminopurine	Target_lig_169	Guanine riboswitch	Target_74	7.7695 510786 2173
319	C1=NC2=C(N1)C(=N C(=N2)N)NO	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGACUAUGUCC	2-AMINO-N6- HYDROXYADENI NE	Target_lig_249	Guanine riboswitch	Target_74	7.6989 700043 3602

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
320	C1(=C(N=C(NC1=O)N )N)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGACUAUGUCC	2,5,6-TRIAMINO- PYRIMIDINE-4- ONE	Target_lig_250	Guanine riboswitch	Target_74	7
392	C[S+](CCC(C(=0) [O-])N)CC1C(C(C(01) N2C=NC3=C(N=CN= C32)N)O)O	GGCUUAUCAAGAGA GGUGGAGGGACUGG CCCGAUGAAACCCG GCAACCAGAAAUGG UGCCAAUUCCUGCA GCGGAAACGUUGAA AGAUGAGCCA	S-adenosyl methionine	Target_lig_314	S_Adenosyl_m ethionine_ribos witch	Target_71	8
398	CC1=C(SC=[N+]1CC2 =CN=C(N=C2N)C)CC OP(=O)(O)OP(=O)(O) [O-]	GGACUCGGGGUGCC CUUCUGCGUGAAGG CUGAGAAAUACCCG UAUCACCUGAUCUG GAUAAUGCCAGCGU AGGGAAGUUC	Thiamine_Pyrophos phate(TPP)	Target_lig_318	thiamine_BOX _Riboswitch	Target_72	6.2218 487496 1636
410	C1=NC2=NC=NC(=C2 N1)N	GGAAUAAUUGUAUA ACCUCAAUAAUAUG GUUUGAGGGUGUCU ACCAGGAACCGUAA AAUCCUGAUUACAA	Adenine	Target_lig_165	B_subtilis_pbu E_Adenine riboswitch	Target_73	6.2358 238676 0967
412	CC1=CC2=C(C=C1C) N(C3=NC(=O)NC(=O) C3=N2)CC(C(C(COP( =O)(O)O)O)O)O	GGCGUGUAGGAUAU GCUUCGGCAGAAGG ACACGCC	FMN	Target_lig_68	FMN RIBOSWITCH APTAMER	Target_36	8.9208 187539 5238
413	C1=C(C2=C(N1)N=C( NC2=O)N)CN	AGUAGAUGUGCUAG CAAAACAUCUUUAA AAAACUAGACUUGG GGUGCAAGUCCCCU UUUUUAUUGCUUAA AUUU	preQ1 (7- Aminomethyl-7- deazaguanine)	Target_lig_331	PreQ1_riboswit ch_Fusobacteri um	Target_75	6.5482 135644 7571
414	CC1=C(SC=[N+]1CC2 =CN=C(N=C2N)C)CC OP(=0)(O)OP(=0)(O) [O-]	GGUAACCACUAGGG GUGUCCUUCAUAAG GGCUGAGAUAAAAG UGUGACUUUUAGAC CCUCAUAACUUGAA CAGGUUCAGACCUG CGUAGGGAAGUGGA	Thiamine_Pyrophos phate(TPP)	Target_lig_318	TPP RIBOSWITCH APTAMER	Target_37	6.3053 948010 6643
415	C[S+](CCC(C(=O) [O-])N)CC1C(C(C(O1) N2C=NC3=C(N=CN= C32)N)O)O	GGCUUAUCAAGAGA GGUGGAGGGACUGG CCCGAUGAAACCCG GCAACCAGAAAUGG UGCCAAUUCCUGCA GCGGAAACGUUGAA AGAUGAGCCA	SAM	Target_lig_124	S_Adenosyl_m ethionine	Target_71	5.8696 662315 0499
416	C(CCN)C[C@@H] (C(=0)O)N	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAAGG GGAGCGUCGCCGAA GCAAAUAAAACCCC AUCGGUAUUAUUUG CUGGCCGUGCAUUG AAUAAAUGUAAGGC UGUCAAGAAAUCAU UUUCUUGAGGGGCU AUCUCGUUGUUCAU AAUCAUUUAUGAUG AUUAAUUGAUGAUG AAUGAGAGUAUUCC UCUCAUUGCUUUUU	lysine	Target_lig_31	LYSINE RIBOSWITCH APTAMER	Target_38	5.7447 274948 9669
739	CC1=C(SC=[N+]1CC2 =CN=C(N=C2N)C)CC OP(=O)(O)OP(=O)(O)	GGUAACCACUAGGG GUGUCCUUCAUAAG GGCUGAGAUAAAAG	Thiamine_Pyrophos phate(TPP)	Target_lig_318	B.subtilis tenA TPP riboswitch	Target_76	7.3010 299956 6398

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
	[0-]	UGUGACUUUUAGAC CCUCAUAACUUGAA CAGGUUCAGACCUG CGUAGGGAAGUGGA GC					
740	CC1=C(SC=[N+]1CC2 =CN=C(N=C2N)C)CC O	GGUAACCACUAGGG GUGUCCUUCAUAAG GGCUGAGAUAAAAG UGUGACUUUUAGAC CCUCAUAACUUGAA CAGGUUCAGACCUG CGUAGGGAAGUGGA GC	Thiamine_mol	Target_lig_502	B.subtilis tenA TPP riboswitch	Target_76	4.3010 299956 6398
741	CC1=C(C=CC=[N+]1 CC2=CN=C(N=C2N)C )CCO.Br.[Br-]	GGUAACCACUAGGG GUGUCCUUCAUAAG GGCUGAGAUAAAAG UGUGACUUUUAGAC CCUCAUAACUUGAA CAGGUUCAGACCUG CGUAGGGAAGUGGA GC	Pyrithiamine_mol	Target_lig_503	B.subtilis tenA TPP riboswitch	Target_76	5.2218 487496 1636
742	n1c(ncc(c1N)CN1=CC =CC(=C1)CCO[P@@] (=O)(O)P(=O)(O)O)C	GGUAACCACUAGGG GUGUCCUUCAUAAG GGCUGAGAUAAAAG UGUGACUUUUAGAC CCUCAUAACUUGAA CAGGUUCAGACCUG CGUAGGGAAGUGGA GC	Pyrithiamine _Pyrophosphate_de r	Target_lig_504	B.subtilis tenA TPP riboswitch	Target_76	6.7958 800173 4408
743	CC1=CC2=C(C=C1C) N(C3=NC(=0)NC(=0) C3=N2)CC(C(CCOP( =O)(O)O)O)O)O	GGAAGGACAAAUGA AUAAAGAUUGUAUC CUUCGGGGCAGGGU GGAAAUCCCGACCG GCGGUAGUAAAGCA CAUUUGCUUUAGAG CCCGUGACCCGUGU GCAAUAGCACGCGG UGGAUUCAGUUUAA GCUGAAGCCGACAG UGAAAGUCUGGAUG GGAGAAGGAUG	FMN	Target_lig_68	B.subtilis tenA FMN riboswitch	Target_77	8.3010 299956 6398
744	CC1=CC2=C(C=C1C) N(C3=NC(=0)NC(=0) C3=N2)CC(C(C(CO)O )O)O	GGAAGGACAAAUGA AUAAAGAUUGUAUC CUUCGGGGCAGGGU GGAAAUCCCGACCG GCGGUAGUAAAGCA CAUUUGCUUUAGAG CCCGUGACCCGUGU GCAAUAGCACGCGG UGGAUUCAGUUUAA GCUGAAGCCGACAG UGAAAGUCUGGAUG GGAGAAGGAUG	riboflavin	Target_lig_70	B.subtilis tenA FMN riboswitch	Target_77	5.5228 787452 8034
745	CC1=CC2=C(C=C1N( C)C)N(C3=NC(=0)NC (=0)C3=N2)CC(C(C(C O)O)O)O	GGAAGGACAAAUGA AUAAAGAUUGUAUC CUUCGGGGCAGGGU GGAAAUCCCGACCG GCGGUAGUAAAGCA CAUUUGCUUUAGAG CCCGUGACCCGUGU GCAAUAGCACGCGG UGGAUUCAGUUUAA GCUGAAGCCGACAG UGAAAGUCUGGAUG GGAGAAGGAUG	Roseoflavin	Target_lig_505	B.subtilis tenA FMN riboswitch	Target_77	7
746	C(CCN=C(N)N)C[C@ @H](C(=O)O)N	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAAGG GGAGCGUCGCCGAA	L-homoarginine	Target_lig_57	B.subtilis lysine riboswitch	Target_78	5.1549 019599 8574

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
		GCAAAUAAAACCCC AUCGGUAUUAUUUG CUGGCCGUGCAUUG AAUAAAUGUAAGGC UGUCAAGAAAUCAU UUUCUUGGAGGGCU AUCUCGUUGUUCAU AAUCAUUUAUGAUG AUUAAUUGAUAAGC AAUGAGAGUAUUCC UCUCAUUGCUUUUU					
747	C(CCN)C[C@@H] (C(=0)O)N	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAAGG GGAGCGUCGCCGAA GCAAAUAAAACCCC AUCGGUAUUAUUUG CUGGCCGUGCAUUG AAUAAAUGUAAGGC UGUCAAGAAAUCAU UUUCUUGGAGGGCU AUCUCGUUGUUCAU AAUCAUUUAUGAUG AUUAAUUGAUAAGC AAUGAGAGUAUUCC UCUCAUUGCUUUUU	lysine	Target_lig_31	B.subtilis lysine riboswitch	Target_78	6.4436 974992 3271
748	C(COC[C@@H] (C(=0)0)N)N	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAAGG GGAGCGUCGCCGAA GCAAAUAAAACCCC AUCGGUAUUAUUUG CUGGCCGUGCAUUG AAUAAAUGUAAGGC UGUCAAGAAAUCAU UUUCUUGAGGGCU AUCCGUUGUUCAU AAUCAUUUAUGAUG AUUAAUUGAUGAUG AUUAAUUGAUAGC AAUGAGAGUAUUCC UCUCAUUGCUUUUU	L-4 L_4_Oxalysine	Target_lig_506	B.subtilis lysine riboswitch	Target_78	4.8860 566476 9316
749	CCC1CC1(C(=O)O)N	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAAGG GGAGCGUCGCCGAA GCAAAUAAAACCCC AUCGGUAUUAUUUG CUGGCCGUGCAUUG AAUAAAUGUAAGGC UGUCAAGAAAUCAU UUUCUUGGAGGGCU AUCUCGUUGUUCAU AAUCAUUUAUGAUG AUUAAUUGAUGAUG AUUAAUUGAUAGC AAUGAGAGUAUUCC UCUCAUUGCUUUUU	AEC	Target_lig_507	B.subtilis lysine riboswitch	Target_78	4.5228 787452 8034
750	C(CS(=O) (=O)C[C@@H](C(=O) [O-])[NH3+])[NH3+]	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAAGG GGAGCGUCGCCGAA GCAAAUAAAACCCC	L-3-[(2- AMINOETHYL)- SULFONYL]- ALANINE	Target_lig_508	B.subtilis lysine riboswitch	Target_78	5.6020 599913 2796

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
		AUCGGUAUUAUUUG CUGGCCGUGCAUUG AAUAAAUGUAAGGC UGUCAAGAAAUCAU UUUCUUGGAGGGCU AUCUCGUUGUUCAU AAUCAUUUAUGAUG AUUAAUUGAUAAGC AAUGAGAGUAUUCC UCUCAUUGCUUUUU					
751	C(/C=C/ C[NH3+])C(C(=O) [O-])[NH3+]	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAAGG GGAGCGUCGCCGAA GCAAAUAAAACCCC AUCGGUAUUAUUUG CUGGCCGUGCAUUG AAUAAAUGUAAGGC UGUCAAGAAAUCAU UUUCUUGGAGGGCU AUCUCGUUGUUCAU AAUCAUUUAUGAUG AUUAAUUGAUAAGC AAUGAGAGUAUUCC UCUCAUUGCUUUUU	DL-TRANS-2,6- DIAMINO-4- HEXENOIC ACID	Target_lig_509	B.subtilis lysine riboswitch	Target_78	6.0132 282657 3376
1157	CC(CCN1C2=CC(C)= C(C)C=C2N=C2C(=0) [N-]C(=0)N=C12)C1= CC=C(F)C=C1	GGAAGGACAAAUGA AUAAAGAUUGUAUC CUUCGGGGCAGGGU GGAAAUCCCGACCG GCGGUAGUAAAGCA CAUUUGCUUUAGAG CCCGUGACCCGUGU GCAAUAGCACGCGG UGGAUUCAGUUUAA GCUGAAGCCGACAG UGAAAGUCUGGAUG GGAGAAGGAUG	5FDQD	Target_lig_662	165 ribD FMN Riboswitch Aptamer, B. subtilis	Target_189	8.1249 387366 083
1159	CNC1=NC=C(C=N1)C N2CCC[C@@H] (C2)C3=NC(=CC(=O) N3)C4=CC=CS4	GGAUCUUCGGGGCA GGGUGAAAUUCCCG ACCGGUGGUAUAGU CCACGAAAGUAUUU GCUUUGAUUUGGUG AAAUUCCAAAACCG ACAGUAGAGUCUGG AUGAGAGAAGAUUC	Ribocil-B	Target_lig_663	FMN Riboswitch Aptamer, E. Coli	Target_190	8.1804 560644 5813
1160	C1C[C@@H] (CN(C1)CC2=CN(C= N2)C3=NC=CC=N3)C 4=NC(=CC(=O)N4)C5 =CC=CS5	GGAUCUUCGGGGCA GGGUGAAAUUCCCG ACCGGUGGUAUAGU CCACGAAAGUAUUU GCUUUGAUUUGGUG AAAUUCCAAAACCG ACAGUAGAGUCUGG AUGAGAGAAGAUUC	Ribocil-C	Target_lig_664	FMN Riboswitch Aptamer, E. Coli	Target_190	9
1161	C1C[C@@H] (CN(C1)CC2=CN(C= N2)C3=NC=CC=N3)C 4=NC(=CC(=0)N4)C5 =CC=CS5	UAAUUCUUUCGGGG CAGGGUGAAAUUCC CAACCGGCAGUAAA UAAAGCCUGCGACC UGCUAAUAUGUUUC AUAUUAGUGGCUGA UCUAGUGAGAUUCU AGAGCCGACAGUUA AAGUCUGGAUGGAG GAAAGAAUGUUAAU UAUCGACAAAGAUA AUGUAGCGUAUUUG UAAAAAUGUGUACA AAUAGGCUUAUUUA	Ribocil-C	Target_lig_664	FMN Riboswitch Aptamer SA1, S. Aureus	Target_191	7.2365 720064 3706

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
		UCCUUGCAUCUUAA UUCAUGAUGUGAGG AUU					
1162	C1C[C@@H] (CN(C1)CC2=CN(C= N2)C3=NC=CC=N3)C 4=NC(=CC(=O)N4)C5 =CC=CS5	AUUCAUCUUCGGGG UCGGGUGUAAUUCC CAACCGGCAGUAAA UAAAGCCUGCGACC UGCUAGUAUGUAUC AUAUUAGUGGCUGA UCUAGUGAGAUUCU AGAGCCGACAGUAU AGUCUGGAUGGGAG AAGAUGGAGGUUUU UUGUUGUGCAAUAA UCCUCCUAUUCUUA CGAGAUGAAAUU	Ribocil-C	Target_lig_664	FMN Riboswitch Aptamer SA2, S. Aureus	Target_192	7.4814 860601 2211
1163	CC1=CC2=C(C=C1N( C)C)N(C3=NC(=0)NC (=0)C3=N2)CC(C(C(C O)O)O)O	GGUACCAGAAGCAG CGCACUCCGGGGUC GGUGAAAGUCCGAA CCGGCGGUUACAGU CCGCGACCGACCG CUUCCAGCGGCCGG UUGACCAGGUGAAA UUCCUGGACCGACG GUUAAAGUCCGGAU GGGAGGCAGUGCGC	Roseoflavin	Target_lig_505	FMN Riboswitch, S. Davawensis	Target_193	8
1164	NC1=NC(N)=C2NC= NC2=N1	GGAAUAAUUGUAUA ACCUCAAUAAUAUG GUUUGAGGGUGUCU ACCAGGAACCGUAA AAUCCUGAUUACAA	2,6-Diaminopurine	Target_lig_125	PbuE Riboswitch	Target_73	7.6020 599913 2796
1165	CC1=C(C=CC=[N+]1 CC2=CN=C(N=C2N)C )CCO.Br.[Br-]	GGUAACCACUAGGG GUGUCCUUCAUAAG GGCUGAGAUAAAAG UGUGACUUUUAGAC CCUCAUAACUUGAA CAGGUUCAGACCUG CGUAGGGAAGUGGA GC	Pyrithiamine	Target_lig_503	TPP Riboswitch, B. Subtilis	Target_194	5.2218 487496 1636
1166	C1=NC2=C(N1)C(=N C(=N2)N)NO	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGACUAUGUCC	2-Amino-N6- Hydroxyadenine	Target_lig_665	xpt-pbuX Guanine Riboswitch, B. Subtilis	Target_74	7.6989 700043 3602
1167	NC1=NC(=O)C(N)=C( N)N1	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGACUAUGUCC	PC1	Target_lig_125	Guanine Riboswitch	Target_74	7
1168	C[N+]1=C2C(=C3C=C C(=C(C3=C1)OC)OC) C=CC4=CC5=C(C=C4 2)OCO5	GUAUAUGGUAAACU AUGAAAAAACACGA UUCGGUUGGUAGUC CGGAUGCAUGAUUG AGAAUGUCAGUAAC CUUCCCCUCCUCGG GAUGUCCAUCAUUC UUUAAUAUAUCU	Chelerythrine	Target_lig_666	108 nt yjdF Riboswitch Construct, B. subtilis, Mutant 1	Target_195	8.6197 887582 8839
1169	CC1=[N+] (C2=CC=C2C(=C 1)N)CCCCCCCCC[N +]3=C(C=C(C4=CC=C C=C43)N)C	GUAUAUGGUAAACU AUGAAAAAACACGA UUCGGUUGGUAGUC CGGAUGCAUGAUUG AGAAUGUCAGUAAC CUUCCCCUCCUCGG GAUGUCCAUCAUUC UUUAAUAUAUCU	Dequalinium	Target_lig_667	108 nt yjdF Riboswitch Construct, B. subtilis, Mutant	Target_195	8
1170	CC1=NC=CC2=C1NC 3=CC=CC=C23	GUAUAUGGUAAACU AUGAAAAAACACGA	Harmane	Target_lig_668	108 nt yjdF Riboswitch	Target_195	7

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
		UUCGGUUGGUAGUC CGGAUGCAUGAUUG AGAAUGUCAGUAAC CUUCCCCUCCUCGG GAUGUCCAUCAUUC UUUAAUAUCU			Construct, B. subtilis, Mutant		
1171	C1=CC(=CC2=NC3=C (C=CC(=C3)N)C=C21) N	GUAUAUGGUAAACU AUGAAAAAACACGA UUCGGUUGGUAGUC CGGAUGCAUGAUUG AGAAUGUCAGUAAC CUUCCCCUCCUCGG GAUGUCCAUCAUUC UUUAAUAUCU	Proflavin	Target_lig_336	108 nt yjdF Riboswitch Construct, B. subtilis, Mutant 1	Target_195	8.2146 701649 8923
1172	C[C@@]12[C@@H] ([C@@H](C[C@@H] (O1)N3C4=CC=CC=C 4C5=C6C(=C7C8=CC =CC=C8N2C7=C53)C NC6=O)NC)OC	GUAUAUGGUAAACU AUGAAAAAACACGA UUCGGUUGGUAGUC CGGAUGCAUGAUUG AGAAUGUCAGUAAC CUUCCCCUCCUCGG GAUGUCCAUCAUUC UUUAAUAUCU	Staurosporine	Target_lig_669	108 nt yjdF Riboswitch Construct, B. subtilis, Mutant	Target_195	7
1279	C1CCC(CC1)NC2=NC 3=C(C(=O)N2)NC=N3	GGAUCAUAUAAUCG CGUGGAUAUGGCAC GCAAGUUUCUACCG GGCACCGUAAAUGU CCGACUAUGGUC	Guanine Analog 25f	Target_lig_714	C. difficile guaA riboswitch	Target_228	5.1870 866433 5714
1280	[NH3+]CCS(=O) (=O)C[C@H] ([NH3+])C([O-])=O	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAAGG GGAGCGUCGCCGAA GCAAAUAAAACCCC AUCGGUAUUAUUUG CUGGCCGUGCAUUG AAUAAAUAUAAGGC UGUCAAGAAAUCAU UUUCUUGGAGGGCU AUCUCGUUGUUCAU AAUCAUUUAUGAUG AUUAAUUGAUAAGC AAUGAGAGUAUUCC UCUCAUUGCUUUUU	Lysine Analog 8	Target_lig_126 0	lysC riboswitch	Target_229	5.6020 599913 2796
1282	[NH3+]CCS(=O) (=O)C[C@H] ([NH3+])C([O-])=O	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAGGG GAGCGUCGCCGAAG CAAAUAAAACCCCA UCGGUAUUAUUUGC UGGCCGUGCAUUGA AUAAAUGUAAGGCU GUCAAGAAAUCAUU UUCUUGGAGGGCUA UCUCGUUGUUCAUA AUCAUUUAUGAUGA UUAAUUGAUAGCA AUGAGAGUAUUCCU CUCAUUGCUUUUUU	Lysine Analog 8	Target_lig_126 0	lysC riboswitch mutant 1 (M2)	Target_230	4.6197 887582 8839
1283	[NH3+]CCOC[C@H] ([NH3+])C([O-])=O	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAAGG GGAGCGUCGCCGAA GCAAAUAAAACCCC AUCGGUAUUAUUUG CUGGCCGUGCAUUG	Lysine Analog 9	Target_lig_126	lysC riboswitch	Target_229	4.8860 566476 9316

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
		AAUAAAUAUAAGGC UGUCAAGAAAUCAU UUUCUUGGAGGGCU AUCUCGUUGUUCAU AAUCAUUUAUGAUG AUUAAUUGAUAAGC AAUGAGAGUAUUCC UCUCAUUGCUUUUU					
1285	[NH3+]CCOC[C@H] ([NH3+])C([O-])=0	GAAGAUAGAGGUGC GAACUUCAAGAGUA UGCCUUUGGAGAAA GAUGGAUUCUGUGA AAAAGGCUGAAGG GAGCGUCGCCGAAG CAAAUAAAACCCCA UCGGUAUUAUUUGC UGGCCGUGCAUUGA AUAAAUGUAAGGCU GUCAAGAAAUCAUU UUCUUGGAGGGCUA UCUCGUUGUUCAUA AUCAUUUAUGAUGA UUAAUUGAUAGCA AUGAGAGUAUUCCU CUCAUUGCUUUUUUU	Lysine Analog 9	Target_lig_126	lysC riboswitch mutant 1 (M2)	Target_230	4.1249 387366 083
1889	C1=NC(=C(N1C2C(C( C(O2)COP(=O) (O)O)O)N)C(=O)N	UAUCAGUUAUAUGA CUGACGGAACGUGG AAUUAACCACAUGA AGUAUAACGAUGAC AAUGCCGACCGUCU GGGCG	AIZA analog 1	Target_lig_104	Fusibacterium ulcerans ZTP riboswitch	Target_352	6.4948 500216 8009
1890	Cen1e2ece(ce2e2e1ece e2)N1CCNCC1	UAUCAGUUAUAUGA CUGACGGAACGUGG AAUUAACCACAUGA AGUAUAACGAUGAC AAUGCCGACCGUCU GGGCG	AIZA analog 2	Target_lig_104	Fusibacterium ulcerans ZTP riboswitch	Target_352	4.3872 161432 8026
1891	C1=NC(=C(N1C2C(C( C(O2)CO)O)O)N)C(= O)N	UAUCAGUUAUAUGA CUGACGGAACGUGG AAUUAACCACAUGA AGUAUAACGAUGAC AAUGCCGACCGUCU GGGCG	AIZA analog 5	Target_lig_104	Fusibacterium ulcerans ZTP riboswitch	Target_352	5.6382 721639 8241
1892	C1=CN=CC=C1N2C= NC(=C2N)C(=O)N	UAUCAGUUAUAUGA CUGACGGAACGUGG AAUUAACCACAUGA AGUAUAACGAUGAC AAUGCCGACCGUCU GGGCG	AIZA analog 7	Target_lig_104	Fusibacterium ulcerans ZTP riboswitch	Target_352	5.8538 719643 2176
1893	C1CNCCC1N2C=NC( =C2N)C(=O)N	UAUCAGUUAUAUGA CUGACGGAACGUGG AAUUAACCACAUGA AGUAUAACGAUGAC AAUGCCGACCGUCU GGGCG	AIZA analog 8	Target_lig_104	Fusibacterium ulcerans ZTP riboswitch	Target_352	5.0604 807473 8138
1894	C1=NC(=C(N1CCO)N )C(=O)N	UAUCAGUUAUAUGA CUGACGGAACGUGG AAUUAACCACAUGA AGUAUAACGAUGAC AAUGCCGACCGUCU GGGCG	AIZA analog 10	Target_lig_104	Fusibacterium ulcerans ZTP riboswitch	Target_352	3.8239 087409 4432
1895	NC(=O)clncn(clN)clc cccnl	UAUCAGUUAUAUGA CUGACGGAACGUGG AAUUAACCACAUGA AGUAUAACGAUGAC AAUGCCGACCGUCU GGGCG	AIZA analog 12	Target_lig_105	Fusibacterium ulcerans ZTP riboswitch	Target_352	5.25181 197299 38
1896	C1=CC(=CN=C1)N2C	UAUCAGUUAUAUGA	AIZA analog 13	Target_lig_105	Fusibacterium	Target_352	6.2218

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
	=NC(=C2N)C(=O)N	CUGACGGAACGUGG AAUUAACCACAUGA AGUAUAACGAUGAC AAUGCCGACCGUCU GGGCG		1	ulcerans ZTP riboswitch		487496 1636
2044	C1(=C(N=C(N=C1N)N )N)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGAUUAUGUCC	2,4,5,6- tetraaminopyrimidi ne	Target_lig_112	ADENINE RIBOSWITCH	Target_69	4.6989 700043 3602
2045	C1=CN=C(N=C1N)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGAUUAUGUCC	2,4- diaminopyrimidine	Target_lig_112	ADENINE RIBOSWITCH	Target_69	3
2046	Nc1nc(N)nc(n1)N	GGACAUAUAAUCGC GUGGAUAUGGCACG CAAGUUUCUACCGG GCACCGUAAAUGUC CGAUUAUGUCC	2,4,6-triamino- 1,3,5-triazine	Target_lig_112	ADENINE RIBOSWITCH	Target_69	4.6989 700043 3602
2136	C[S+](CCC(C(=0) [O-])N)CC1C(C(C(01) N2C=NC3=C(N=CN= C32)N)O)O	GGUACAAUCUAAAA ACUUAUCAAGAGCG GCUGAGGGACUGGA CCUAUGAAGCCCGG CAACCUGCAUAGUU UGUAAGGUGCUACU UCCAGCAAAAUGAA UUCCAUUUUGAAAG AUAAGGGCUGCAUG CUGUUCCUGUCUUU CUUUCCGCCGAUUG AAAGUUUUUU	S-adenosyl methionine	Target_lig_314	B.subtilis cysH	Target_405	6
2137	C1=NC(=C2C(=N1)N( C=N2)C3C(C(C(O3)C SCCC(C(=O)O)N)O)O )N	GGUACAAUCUAAAA ACUUAUCAAGAGCG GCUGAGGGACUGGA CCUAUGAAGCCCGG CAACCUGCAUAGUU UGUAAGGUGCUACU UCCAGCAAAAUGAA UUCCAUUUUGAAAG AUAAGGGCUGCAUG CUGUUCCUGUCUUU CUUUCCGCCGAUUG AAAGUUUUUU	SAH	Target_lig_115	B.subtilis cysH	Target_405	3.0969 100130 0806
2138	C1=NC(=C2C(=N1)N( C=N2)C3C(C(C(O3)C SCC(C(=O)O)N)O)O) N	GGUACAAUCUAAAA ACUUAUCAAGAGCG GCUGAGGGACUGGA CCUAUGAAGCCCGG CAACCUGCAUAGUU UGUAAGGUGCUACU UCCAGCAAAAUGAA UUCCAUUUUGAAAG AUAAGGGCUGCAUG CUGUUCCUGUCUUU CUUUCCGCCGAUUG AAAGUUUUUU	SAC	Target_lig_115 4	B.subtilis cysH	Target_405	3
2139	C[S+](CCC(C(=0) [O-])N)CC1C(C(C(01) N2C=NC3=C(N=CN= C32)N)O)O	GGAGCUUAUCAAGA GAAGCGGAGGAAC UGGCCCGGCGAAGC UCGGCAACCUGCUU AUAGAAAGCAAGGU GCUAAAUCCAGCAA AAUGGAUUCCAUUU UGAAAGAUAAGGUA AAAUAUAUUACCGA ACAGUCUUUUCGAA AUGGGAAAGAUUUU UUUUAU	S-adenosyl methionine	Target_lig_314	B.anthracis cysH	Target_406	8
2140	C1=NC(=C2C(=N1)N( C=N2)C3C(C(C(O3)C	GGAGCUUAUCAAGA GAAGCGGAGGGAAC	SAH	Target_lig_115	B.anthracis cysH	Target_406	5.5228 787452

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
	SCCC(C(=O)O)N)O)O )N	UGGCCCGGCGAAGC UCGGCAACCUGCUU AUAGAAAGCAAGGU GCUAAAUCCAGCAA AAUGGAUUCCAUUU UGAAAGAUAAGGUA AAAUAUAUUACCGA ACAGUCUUUUCGAA AUGGGAAAGAUUUU UUUUAU					8034
2141	C1=NC(=C2C(=N1)N( C=N2)C3C(C(C(O3)C SCC(C(=O)O)N)O)O) N	GGAGCUUAUCAAGA GAAGCGGAGGAAC UGGCCCGGCGAAGC UCGGCAACCUGCUU AUAGAAAGCAAGGU GCUAAAUCCAGCAA AAUGGAUUCCAUUU UGAAAGAUAAGGUA AAAUAUAUUACCGA ACAGUCUUUUCGAA AUGGGAAAGAUUUU UUUUAU	SAC	Target_lig_115	B.anthracis cysH	Target_406	3
2259	CC1(C2CC3C(C(=O)C (=C(C3(C(=O)C2=C(C 4=C1C=CC=C4O)O)O )O)C(=O)N)N(C)C)O	GGGCCUAGAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	tetracyclin	Target_lig_74	Tetracycline riboswitch A08G mutant	Target_412	8.9788 107009 3006
2260	CC1(C2CC3C(C(=O)C (=C(C3(C(=O)C2=C(C 4=C1C=CC=C4O)O)O )O)C(=O)N)N(C)C)O	GGGCCUAAGACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	tetracyclin	Target_lig_74	Tetracycline riboswitch A09G mutant	Target_413	6.7904 849854 5737
2261	CC1(C2CC3C(C(=0)C (=C(C3(C(=0)C2=C(C 4=C1C=CC=C4O)O)O )O)C(=O)N)N(C)C)O	GGGCCUAAAACAUU CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	tetracyclin	Target_lig_74	Tetracycline riboswitch A13U mutant	Target_414	6.6536 470255 4936
2262	CC1(C2CC3C(C(=O)C (=C(C3(C(=O)C2=C(C 4=C1C=CC=C4O)O)O )O)C(=O)N)N(C)C)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAUGAAUA CGACCACCUAGGCU C	tetracyclin	Target_lig_74	Tetracycline riboswitch A50U mutant	Target_415	6.7077 439286 4352
2263	CC1(C2CC3C(C(=O)C (=C(C3(C(=O)C2=C(C 4=C1C=CC=C4O)O)O )O)C(=O)N)N(C)C)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAUAAUA CGACCACCUAGGCU C	tetracyclin	Target_lig_74	Tetracycline riboswitch G51U mutant	Target_416	8.5331 323796 4589
2264	CC1(C2CC3C(C(=O)C (=C(C3(C(=O)C2=C(C 4=C1C=CC=C4O)O)O )O)C(=O)N)N(C)C)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAGA CGACCACCUAGGCU C	tetracyclin	Target_lig_74	Tetracycline riboswitch U54G mutant	Target_417	8.5800 442515 1024
2265	CC1(C2CC3C(C(=O)C (=C(C3(C(=O)C2=C(C 4=C1C=CC=C4O)O)O )O)C(=O)N)N(C)C)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUG CGACCACCUAGGCU C	tetracyclin	Target_lig_74	Tetracycline riboswitch A55G mutant	Target_418	8.77211 329538 633
2266	CN(C1C(=O)C(=C(C2( C1CC1C(=C(O)c3c(C1 (C)O)c(C1)ccc3O)C2= O)O)O)C(=O)N)C	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU	elte	Target_lig_116	Tetracycline riboswitch	Target_411	9.2418 453780 3261

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
		С					
2267	NC(=0)C1=C(0)C2(C (CC1=0)CC1C(=C(0) c3c(C1(C)O)cccc3O)C 2=O)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	cmtl	Target_lig_116	Tetracycline riboswitch	Target_411	8.7055 337738 3841
2268	NC(=0)C1=C(0)C2(C (C(C1=0)0)CC1C(=C( O)c3c(C1(C)0)cccc30 )C2=0)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	cmt6	Target_lig_116	Tetracycline riboswitch	Target_411	8.5575 202309 3555
2269	NNC1=C2C(=O)C3(O) C(CC2C(c2c1c(O)ccc2 ) (C)O)CC(=O)C(=C3O) C(=O)N	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	cmt5	Target_lig_116	Tetracycline riboswitch	Target_411	9.0043 648054 0245
2270	N#CC1=C(O)C2(C(C C1=O)N(C)C)CC1C(= C(O)c3c(C1(C)O)cccc3 O)C2=O)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	cmt2	Target_lig_116	Tetracycline riboswitch	Target_411	8.0087 739243 0751
2271	CN(C1C(=O)C(=C(C2( C1C(O)C1C(=C(O)c3c (C1(C)O)cccc3O)C2= O)O)O)C(=O)N)C	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	otc	Target_lig_116	Tetracycline riboswitch	Target_411	8.7495 799976 9111
2272	C[C@H]1[C@H] ([C@H](C[C@@H] (01)0[C@H]2C[C@@ ] (CC3=C2C(=C4C(=C3 O)C(=O)C5=C(C4=O) C(=CC=C5)OC)O) (C(=O)CO)O)N)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	dox	Target_lig_496	Tetracycline riboswitch	Target_411	6.92811 799269 388
2273	NC(=0)C1=C(0)C2(C (CC1=0)C(0)C1C(=C( O)c3c(C1C)cccc3O)C2 =O)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	cmt8	Target_lig_117	Tetracycline riboswitch	Target_411	6.2620 126736 6657
2274	C[N+]1=C2C(=C3C=C C4=C(C3=C1)OCO4)C =CC5=CC6=C(C=C52) OCO6	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	san	Target_lig_18	Tetracycline riboswitch	Target_411	7.6536 470255 4936
2275	CN(C1C(=O)C(=C(C2( C1CC1C(C)c3cccc(c3 C(=C1C2=O)O)O)O)O )C(=O)N)C	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	atc	Target_lig_117	Tetracycline riboswitch	Target_411	8.4559 319556 4972
2276	CN(C1C(=O)C(=C(C2( C1C(O)C1C(=C(O)c3c (C1(C)O)cccc3O)C2= O)O)O)C(=O)N)C	GGGCCUAAGACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	otc	Target_lig_116	Tetracycline riboswitch A09G mutant	Target_413	6.3516 399890 1907
2277	N#CC1=C(O)C2(C(C( C1=O)N(C)C)CC1C(= C(O)c3c(C1(C)O)cccc3 O)C2=O)O	GGGCCUAAGACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU	cmt2	Target_lig_116	Tetracycline riboswitch A09G mutant	Target_413	5.5783 960731 3017

Entry_ID	SMILES	Target_RNA_sequence	Molecule_name	Molecule_ID	Target_RNA_ name	Target_RNA_ ID	pKd
		С					
2278	C[C@H]I[C@H] ([C@H](C[C@@H] (O1)O[C@H]2C[C@@ ] (CC3=C2C(=C4C(=C3 O)C(=O)C5=C(C4=O) C(=CC=C5)OC)O) (C(=O)CO)O)N)O	GGGCCUAAGACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	dox	Target_lig_496	Tetracycline riboswitch A09G mutant	Target_413	4.7520 267336 3819
2279	CN(C1C(=0)C(=C(C2( C1C(0)C1C(=C(0)c3c (C1(C)O)cccc3O)C2= O)O)O)C(=O)N)C	GGGCCUAAAACAUU CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	otc	Target_lig_116	Tetracycline riboswitch A13U mutant	Target_414	6.2740 883677 0495
2280	N#CC1=C(O)C2(C(C C1=O)N(C)C)CC1C(= C(O)c3c(C1(C)O)cccc3 O)C2=O)O	GGGCCUAAAACAUU CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	cmt2	Target_lig_116	Tetracycline riboswitch A13U mutant	Target_414	5.7695 510786 2173
2281	C[C@H]I[C@H] ([C@H](C[C@@H] (O1)O[C@H]2C[C@@ ] (CC3=C2C(=C4C(=C3 O)C(=O)C5=C(C4=O) C(=CC=C5)OC)O) (C(=O)CO)O)N)O	GGGCCUAAAACAUU CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAAGAAUA CGACCACCUAGGCU C	dox	Target_lig_496	Tetracycline riboswitch A13U mutant	Target_414	5.6161 846340 1957
2282	CN(C1C(=O)C(=C(C2( C1C(O)C1C(=C(O)c3c (C1(C)O)cccc3O)C2= O)O)O)C(=O)N)C	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAUGAAUA CGACCACCUAGGCU C	otc	Target_lig_116	Tetracycline riboswitch A50U mutant	Target_415	6.2218 487496 1636
2283	N#CC1=C(O)C2(C(C( C1=O)N(C)C)CC1C(= C(O)c3c(C1(C)O)cccc3 O)C2=O)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAUGAAUA CGACCACCUAGGCU C	cmt2	Target_lig_116	Tetracycline riboswitch A50U mutant	Target_415	5.5900 668766 6871
2284	C[C@H]1[C@H] ([C@H](C[C@@H] (O1)0[C@H]2C[C@@ ] (CC3=C2C(=C4C(=C3 O)C(=O)C5=C(C4=O) C(=CC=C5)OC)O) (C(=O)CO)O)N)O	GGGCCUAAAACAUA CCAGAUCGCCACCC GCGCUUUAAUCUGG AGAGGUGAUGAAUA CGACCACCUAGGCU C	dox	Target_lig_496	Tetracycline riboswitch A50U mutant	Target_415	4.9788 107009 3006
2320	CNC1=NC=C(C=N1)C N2CCC[C@@H] (C2)C3=NC(=CC(=O) N3)C4=CC=CS4	GGCGUGUAGGAUAU GCUUCGGCAGAAGG ACACGCC	Ribocil	Target_lig_663	FMN RIBOSWITCH APTAMER	Target_36	7.7958 800173 4408
2321	CNclncc(cn1)CN1CC C[C@H] (C1)clnc(O)cc(n1)clcc csl	GGCGUGUAGGAUAU GCUUCGGCAGAAGG ACACGCC	Ribocil-A	Target_lig_118	FMN RIBOSWITCH APTAMER	Target_36	5
2322	CNC1=NC=C(C=N1)C N2CCC[C@@H] (C2)C3=NC(=CC(=O) N3)C4=CC=CS4	GGCGUGUAGGAUAU GCUUCGGCAGAAGG ACACGCC	Ribocil-B	Target_lig_663	FMN RIBOSWITCH APTAMER	Target_36	8.1804 560644 5813
2323	C1C[C@@H] (CN(C1)CC2=CN(C= N2)C3=NC=CC=N3)C 4=NC(=CC(=O)N4)C5 =CC=CS5	GGCGUGUAGGAUAU GCUUCGGCAGAAGG ACACGCC	Ribocil-C	Target_lig_664	FMN RIBOSWITCH APTAMER	Target_36	9