

Erratum to: The Presence in tRNA Molecule Sequences of the Double Hairpin, an Evolutionary Stage Through Which the Origin of this Molecule is Thought to have Passed

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The paper was published erroneously with error in Appendix tables, values of CL were erroneously inverted. Corrected tables are given overleaf.

The online version of the original article can be found under
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Table 9 Top 50 stable DH structures in actual tRNA sequences

geneID	CL ΔG (kcal/mol)	DH ΔG (kcal/mol)	Expected CI/CL frequency ratio
>tdbD00012005 Nanoarchaeum_equitans_Kin4-MI228908 Pro GGG	-39.8	-31	1.32×10^{-7}
>tdbD00003796 Aeropyrum_pernix_K1 272557 Ala TGC	-34.9	-29.6	3.17×10^{-4}
>tdbD00005218 Aquifex_aeolicus_VF5 224324 Gly TCC	-36.9	-29.4	4.59×10^{-5}
>tdbD00010376 Thermotoga_maritima_MSB8 243274 Thr GGT	-33.3	-29.4	6.59×10^{-7}
>tdbD00008351 Coxiella_burnetii_RSA_493 227377 Pro CGG	-31.5	-27.8	1.49×10^{-7}
>tdbD00005163 Mycobacterium_leprae_TN 272631 Gly GCC	-32	-27.8	5.84×10^{-6}
>tdbD00005150 Mycobacterium_tuberculosis_CDC155 183331 Gly GCC	-32	-27.8	2.02×10^{-5}
>tdbD00005468 Mycobacterium_bovis_AF2122 97 233413 Gly GCC	-32	-27.8	6.47×10^{-6}
>tdbD00005519 Mycobacterium_tuberculosis_H37Rv 83332 Gly GCC	-32	-27.8	4.14×10^{-3}
>tdbD00000227 Caenorhabditis_elegans 6239 Ala AGC	-31.4	-27.7	4.25×10^{-11}
>tdbD00010503 Caenorhabditis_elegans 6239 Thr AGT	-31.4	-27.7	3.16×10^{-9}
>tdbD00003877 Caenorhabditis_elegans 6239 Ala AGC	-31.4	-27.7	3.16×10^{-9}
>tdbD00003875 Caenorhabditis_elegans 6239 Ala AGC	-31.4	-27.7	9.06×10^{-7}
>tdbD00005416 Leptospira_interrogans_serovar_Lai_str._5660 1189518 Gly GCC	-33	-27.6	4.87×10^{-5}
>tdbD00012049 Staphylothermus_marinus_F1 399550 Met CAT	-38.8	-27.6	4.87×10^{-5}
>tdbD00011436 Rhodopseudomonas_palustris_CGA009 258594 Trp CCA	-28.8	-27.5	1.31×10^{-11}
>tdbD00011398 Bradyrhizobium_japonicum_USDA_110 224911 Trp CCA	-28.8	-27.5	5.70×10^{-6}
>tdbD00005270 Sinorhizobium_meliloti_102 1266834 Gly GCC	-31.1	-27.2	5.70×10^{-11}
>tdbD00000036 Acholeplasma_laidlawii 2148 Ala TGC	-29.4	-26.8	1.50×10^{-9}
>tdbD00008111 Deinococcus_radiodurans_R1 243230 Pro GGG	-29.5	-26.6	1.16×10^{-4}
>tdbD00011137 Streptomyces_avermitilis_MA-4680 227882 Val GAC	-35.5	-26.5	1.16×10^{-4}
>tdbD00010464 Pyrococcus_horikoshii_OT3 70601 Thr GGT	-39.4	-26.4	4.11×10^{-4}
>tdbD00005509 Bartonella_henselae_str._Houston-1 283166 Gly GCC	-29.6	-26.4	4.85×10^{-2}
>tdbD00005601 Bartonella_quintana_str._Toulouse 283165 Gly GCC	-29.6	-26.4	1.06×10^{-3}
>tdbD00005243 Brucella_melitensis_16M 224914 Gly GCC	-29.5	-26.3	5.59×10^{-3}
>tdbD00005264 Agrobacterium_tumefaciens_str._C58 176299 Gly GCC	-29.5	-26.3	1.20×10^{-5}
>tdbD00005526 Rhodopseudomonas_palustris_CGA009 258594 Gly GCC	-29.5	-26.3	1.21×10^{-3}
>tdbD00000843 Azorhizobium_caulinodans 7 Gly GCC	-29.5	-26.3	3.94×10^{-5}
>tdbD00003876 Caenorhabditis_elegans 6239 Ala AGC	-28.4	-26.3	1.80×10^{-5}
>tdbD00005263 Agrobacterium_tumefaciens_str._C58 176299 Gly GCC	-29.5	-26.3	5.74×10^{-3}
>tdbD00008529 Aquifex_aeolicus_VF5 224324 Gln TTG	-32.8	-26.3	5.74×10^{-3}
>tdbD00005411 Brucella_suis_1330 204722 Gly GCC	-29.5	-26.3	6.49×10^{-8}
>tdbD00000037 Acholeplasma_laidlawii 2148 Ala TGC	-31.8	-26.1	3.88×10^{-7}
>tdbD00005456 Tropheryma_whipplei_str._Twist 203267 Gly GCC	-29.4	-26	3.88×10^{-7}
>tdbD00005459 Tropheryma_whipplei_TW08 27 218496 Gly GCC	-29.4	-26	1.46×10^{-4}
>tdbD00010458 Pyrococcus_abyssi_GE5 272844 Thr GGT	-39.9	-26	1.68×10^{-4}
>tdbD00005209 Thermotoga_maritima_MSB8 243274 Gly CCC	-33.7	-26	1.34×10^{-5}
>tdbD00010375 Thermotoga_maritima_MSB8 243274 Thr CGT	-33.1	-26	2.02×10^{-5}
>tdbD00010461 Pyrococcus_furiosus_DSM_3638 186497 Thr GGT	-39.9	-26	6.98×10^{-5}
>tdbD00012004 Nanoarchaeum_equitans_Kin4-MI228908 Lys TTT	-38.1	-25.9	2.53×10^{-4}
>tdbD00003695 Buchnera_aphidicola_str._APS_(Acyrtosiphon_pisum) 107806 Ala TGC	-29.3	-25.8	7.06×10^{-4}
>tdbD00003931 Yersinia_pestis_KIM 187410 Ala TGC	-29.3	-25.8	2.85×10^{-4}
>tdbD00003953 Shewanella_oneidensis_MR-1 211586 Ala TGC	-29.1	-25.8	4.77×10^{-5}
>tdbD00004024 Photobacterium_luminescens_subsp._laumondii_TTO1 243265 Ala TGC	-29.3	-25.8	2.26×10^{-4}
>tdbD00004054 Yersinia_pseudotuberculosis_IP_32953 273123 Ala TGC	-29.3	-25.8	4.04×10^{-4}
>tdbD00003903 Buchnera_aphidicola_str._Sg_(Schizaphis_graminum) 198804 Ala TGC	-29.3	-25.8	1.84×10^{-5}
>tdbD00004052 Yersinia_pestis_biovar_Microtus_str._9100 1229193 Ala TGC	-29.3	-25.8	1.71×10^{-4}

Table 9 continued

geneID	CL ΔG (kcal/mol)	DH ΔG (kcal/mol)	Expected CI/CL frequency ratio
>tdbD00003775 Yersinia_pestis_CO92 214092 Ala TGC	-29.3	-25.8	3.17×10^{-6}
>tdbD00008312 Leptospira_interrogans_serovar_Lai_str._56601 189518 Pro GGG	-27	-25.8	3.30×10^{-10}
>tdbD00010466 Sulfolobus_solfataricus_P2 273057 Thr CGT	-39.5	-25.7	1.81×10^{-5}

Table 10 Top 50 stable CI structures in actual tRNA sequences

geneID	CL ΔG (kcal/mol)	CI ΔG (kcal/mol)	Expected CI/CL frequency ratio
>tdbD00012048 Staphylothermus_marinus_F1 399550 Arg GCG	-37.8	-28.24	1.83×10^{-7}
>tdbD00012086 Sulfolobus_acidocaldarius_DSM_639 330779 Val CAC	-32	-27.89	1.27×10^{-3}
>tdbD00012046 Staphylothermus_marinus_F1 399550 Arg CCT	-37.8	-27.74	8.15×10^{-8}
>tdbD00011538 Pyrobaculum_aerophilum_str._IM2 178306 Ile CAT	-38.7	-27.67	1.69×10^{-8}
>tdbD00012016 Staphylothermus_marinus_F1 399550 Arg TCG	-37.7	-25.64	3.18×10^{-9}
>tdbD00012034 Staphylothermus_marinus_F1 399550 Arg TCT	-37.6	-25.44	2.70×10^{-9}
>tdbD00011053 Sulfolobus_tokodaii_str._7 273063 Val TAC	-34.3	-25	2.80×10^{-7}
>tdbD00011052 Sulfolobus_tokodaii_str._7 273063 Val GAC	-34.2	-24.9	2.80×10^{-7}
>tdbD00004666 Sinorhizobium_meliloti_102 1266834 Glu TTC	-30.2	-24.34	7.43×10^{-5}
>tdbD00011994 Nanoarchaeum_equitans_Kin4-M 228908 Pro TGG	-36.1	-24.04	3.18×10^{-9}
>tdbD00002413 Archaeoglobus_fulgidus 2234 Arg TCG	-33.3	-23.8	2.02×10^{-7}
>tdbD00009035 Archaeoglobus_fulgidus_DSM_4304 224325 Arg TCG	-33.3	-23.8	2.02×10^{-7}
>tdbD00007425 Methanothermobacter_thermautotrophicus_str._Delta_HI 187420 Met CAT	-29.2	-23.6	1.13×10^{-4}
>tdbD00003102 Sulfolobus_solfataricus 2287 Val GAC	-32.7	-23.4	2.80×10^{-7}
>tdbD00012089 Sulfolobus_acidocaldarius_DSM_639 330779 Val GAC	-32.7	-23.4	2.80×10^{-7}
>tdbD00005705 Methanothermobacter_thermautotrophicus_str._Delta_HI 187420 His GTG	-24.4	-23.3	0.168
>tdbD00012032 Staphylothermus_marinus_F1 399550 Gly TCC	-34.9	-23.2	5.70×10^{-9}
>tdbD00004311 Bartonella_henselae_str._Houston-1 283166 Cys GCA	-22.7	-23.1	1.91
>tdbD00009062 Pyrococcus_furiosus_DSM_3638 186497 Arg TCG	-36	-23.04	7.37×10^{-10}
>tdbD00003824 Thermoplasma_acidophilum_DSM_1728 273075 Ala CGC	-31.4	-22.9	1.02×10^{-6}
>tdbD00003827 Thermoplasma_volcanium_GSS1 273116 Ala CGC	-31.4	-22.9	1.02×10^{-6}
>tdbD00012041 Staphylothermus_marinus_F1 399550 Thr GGT	-36.5	-22.74	2.01×10^{-10}
>tdbD00012006 Nanoarchaeum_equitans_Kin4-M 228908 Ala TGC	-35.8	-22.7	5.87×10^{-10}
>tdbD00012010 Nanoarchaeum_equitans_Kin4-M 228908 Ala CGC	-35.8	-22.7	5.87×10^{-10}
>tdbD00011999 Nanoarchaeum_equitans_Kin4-M 228908 Ala GGC	-35.7	-22.6	5.87×10^{-10}
>tdbD00012090 Sulfolobus_acidocaldarius_DSM_639 330779 Val TAC	-31.7	-22.5	3.29×10^7
>tdbD00005896 Agrobacterium_tumefaciens_str._C58 176299 Ile GAT	-33.2	-22.4	2.45×10^{-8}
>tdbD00005281 Methanothermobacter_thermautotrophicus_str._Delta_HI 187420 Gly TCC	-29.8	-22.39	6.00×10^{-6}
>tdbD00009055 Pyrococcus_abyssi_GE5 272844 Arg CCT	-36.4	-22.34	1.24×10^{-10}
>tdbD00003900 Methanosarcina_mazei_Go1 192952 Ala GGC	-29.7	-22.27	5.81×10^{-6}
>tdbD00011889 Methanosarcina_acetivorans_C2A 188937 Ala GGC	-29.7	-22.27	5.81×10^{-6}
>tdbD00009027 Aeropyrum_ernex_K1 272557 Arg CCG	-37.9	-22.14	7.85×10^{-12}
>tdbD00008210 Thermoplasma_volcanium_GSS1 273116 Pro TGG	-30.9	-22.09	6.19×10^{-7}
>tdbD00008207 Thermoplasma_acidophilum_DSM_1728 273075 Pro TGG	-30.9	-22.09	6.19×10^{-7}
>tdbD00011976 Nanoarchaeum_equitans_Kin4-M 228908 Gly GCC	-35.5	-21.9	2.61×10^{-10}
>tdbD00009045 Methanothermobacter_thermautotrophicus_str._Delta_HI 187420 Arg TCT	-31.5	-21.84	1.56×10^{-7}
>tdbD00012005 Nanoarchaeum_equitans_Kin4-M 228908 Pro GGG	-39.8	-21.64	1.60×10^{-13}
>tdbD00010969 Pyrococcus_abyssi_GE5 272844 Val TAC	-34.8	-21.6	4.99×10^{-10}
>tdbD00010972 Pyrococcus_furiosus_DSM_3638 186497 Val TAC	-34.8	-21.6	4.99×10^{-10}

Table 10 continued

geneID	CL Δ G (kcal/mol)	CI Δ G (kcal/mol)	Expected CI/CL frequency ratio
>tdbD00011989 Nanoarchaeum_equitans_Kin4-MI228908 Val GAC	-35.2	-21.5	2.22×10^{-10}
>tdbD00012003 Nanoarchaeum_equitans_Kin4-MI228908 Val TAC	-35.2	-21.5	2.22×10^{-10}
>tdbD00011992 Nanoarchaeum_equitans_Kin4-MI228908 Val CAC	-35.2	-21.5	2.22×10^{-10}
>tdbD00009060 Pyrococcus_furiosus_DSM_3638 186497 Arg CCT	-36.4	-21.34	2.44×10^{-11}
>tdbD00007448 Thermoplasma_acidophilum_DSM_1728 273075 Met CAT	-32.2	-21.2	1.77×10^{-8}
>tdbD00004505 Streptococcus_mutans_UA159 210007 Asp GTC	-28.9	-21.1	3.19×10^{-6}
>tdbD00002929 Thermococcus_celer 2264 Thr GGT	-38.2	-21.04	8.09×10^{-13}
>tdbD00004898 Takifugu_rubripes 31033 Glu TTC	-24.2	-20.9	4.73×10^{-3}
>tdbD00005387 Sulfolobus_tokodaii_str._7 273063 Gly GCC	-32	-20.84	1.37×10^{-8}
>tdbD00008197 Pyrococcus_furiosus_DSM_3638 186497 Pro GGG	-33.4	-20.7	1.12×10^{-9}
>tdbD00004892 Takifugu_rubripes 31033 Glu CTC	-28.1	-20.7	6.10×10^{-6}