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ERRATUM

Incorporation of non-natural modules into proteins: structural features beyond the genetic code

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Unfortunately, the data in the Table 1 of the online published article entitled "Incorporation of non-natural modules into proteins: structural features beyond the genetic code" (DOI 10.1007/s10529-009-0002-9) was published incorrectly. The correct version of the Table 1 is as shown below.

Table 1 Stability parameters of RNase A variants with β-turn mimetics installed at Asn113–*cis*Pro114 by EPL

Variant	ΔT_m (°C)	$\Delta\Delta G^0$ (kJ mol^{-1})	$\Delta\Delta G_U^{\dagger\dagger}$ (kJ mol^{-1})
Asn–dmP	2.8 ± 0.3[a]	4.6 ± 0.4[a]	0.9 ± 0.3
R-nipecotic acid-*S*-nipecotic acid	1.2 ± 0.3[b]	n.d.	n.d.
Asn–1,5-triazole-Ala	−3.6 ± 0.3[c]	−5.9 ± 0.3	−5.1 ± 0.2
Asn–1,4-triazole-Ala	−9.7 ± 0.2[c]	−15.1 ± 0.5	−10.1 ± 0.4
D-Pro–Gly	−6.4 ± 0.3	−10.3 ± 0.4	−9.1 ± 0.4

T_m of RNase A is 63.6 ± 0.2°C

[a] Data from Arnold et al. (2003); $\Delta\Delta G_f^{\dagger\dagger}$ was determined to be 4.4 ± 0.3 kJ mol^{-1}. Current re-investigation yielded ΔT_m = 3.4 ± 0.3°C, $\Delta\Delta G^0$ = 5.9 ± 0.4 kJ mol^{-1}, and $\Delta\Delta G_f^{\dagger\dagger}$ = 6.1 ± 0.4 kJ mol^{-1} (unpublished data)

[b] Data from Arnold et al. (2002b)

[c] Data from Tam et al. (2007a). Interestingly, the analogous Ala–1,5- and 1,4-triazole-Ala variants show a comparable stability to the respective Asn variants each. The respective N113A-RNase A, however, is less stable than RNase A by 2.8 ± 0.2°C indicating that the 'shift' of the ring system by one position has a stronger effect than the elimination of the amid structure from the Asn side chain

The online version of the original article can be found under doi:10.1007/s10529-009-0002-9.

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