**Thermodynamic Molecular Switch Controls Chemical Equilibrium in Interacting Biological Systems**

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The Planck-Benzinger method which we have applied to a wide variety of interacting biological systems provides a means of determining the innate temperature-invariant enthalpy, $\Delta H^o(T_0)$, thermal agitation energy, or the heat capacity integrals, and allows precise determination of $(T_{Cp})$, $(T_h)$, $(T_s)$ and $(T_m)$. Our studies have demonstrated that biological interactions will always exhibit negative value of the Gibbs free energy change at a well-defined temperature, $(T_s)$, which is the thermal set point. The critical factor in this thermodynamic molecular switch is a change of a sign in $\Delta Cp^o(T)_{reaction}$ which determines the behavior patterns of the Gibbs free energy change, and hence a change in the equilibrium constant, $K_{eq,}$ and/or spontaneity. The subsequent, mathematically predictable changes in $\Delta H^o(T)$, $T\Delta S^o(T)$, $\Delta W^o(T)$, and $\Delta G^o(T)$ give rise to the classically observed behavior patterns in biological systems. $\Delta Cp^o(+) \rightarrow \Delta Cp^o(-)$ at $(T_{Cp})$, at low temperature. The implication is that the negative Gibbs free energy minimum at a well-defined $(T_s)$, where the bound unavailable energy $T\Delta S^o(T) = 0$, has its origin in the hydrophobic interactions, which are highly dependent on the details of molecular structure. We have shown in our work the existence of a thermodynamic molecular switch in pair-wise sequence-specific hydrophobic interactions. Indeed, all interacting biological systems that we have thus far examined using the Planck-Benzinger approach point to the universality of this thermodynamic molecular switch [1, 2].

[1] Chun, P.W., *Physica Scripta*. **T119**, 219-222 (2005).
[2] Chun, P.W., *Int'l. J. Quantum Chem*. **100**, 994-1002 (2004).