

Written by Hiroshi Chuman

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Dr Hiroshi Chuman gave this presentation at the International Symposium on Compound Design Technologies held in Tokyo and Osaka, Japan on 19 and 20 March 2014.

## Abstract

More than half a century has passed since Drs. Hansch and Fujita proposed a general approach to the formulation of QSAR in 1961. Their approach (Hansch-Fujita analysis) has provided a new perspective for chemical-biological interactions as well as a number of successes in drug discovery. Now it is time to develop a new and promising approach based on their QSAR with the aid of modern, powerful molecular calculations.

We have proposed a novel QSAR procedure called Linear Expression by Representative Energy terms (LERE)-QSAR involving molecular calculations such as an ab initio fragment molecular orbital (FMO) and QM/MM (ONIOM) ones. The first assumption made in formulating the LERE-QSAR equation is that the free-energy terms comprising the overall free-energy change ( $\Delta G_{\text{obs}}$ ) associated with complex formation are all additive ( $\Delta G_{\text{obs}} = \Delta G_{\text{bind}} + \Delta G_{\text{sol}} + \Delta G_{\text{ot}}$ )

where

$\Delta G_{\text{obs}}$

$\Delta G_{\text{bind}}$

and  $\Delta G_{\text{sol}}$

are

the intrinsic binding interaction free-energy of a ligand with a protein, and the solvation free-energy change associated with complex formation, respectively.  $\Delta G_{\text{ot}}$

is the sum of

free-energy terms other than representative free-energy terms,  $\Delta G_{\text{ot}}$

$\Delta G_{\text{bind}}$

and  $\Delta G_{\text{sol}}$

$\Delta G_{\text{ot}}$

is assumed to be linear with that of representative free-energy terms ( $\Delta G_{\text{ot}}$

$\Delta G_{\text{ot}}$

$= \beta (\Delta G_{\text{bind}}$

$+ \Delta G_{\text{sol}}$

$+ \text{const}, b$

$\Delta G_{\text{ot}}$

$) + \text{const}, b$

$\Delta G_{\text{ot}}$

$\Delta G_{\text{sol}}$

is replaceable by its dominant polar contribution  $\Delta G_{\text{sol}}^{\text{pol}}$

$\Delta G_{\text{sol}}^{\text{pol}}$

and most of  $\Delta G_{\text{ot}}$

comes from the enthalpic contribution. Combining the above three equations yields the following

$\Delta G_{\text{sol}}^{\text{pol}}$

$\Delta G_{\text{ot}}$

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concise expression,

$$DG_{\text{obs}} = g (DE_{\text{bind}} + DG_{\text{sol}}^{\text{pol}}) + \text{const} [g = (1 - a) (1 + b)]$$

where  $DE_{\text{bind}}$  is computable using ab initio MO calculations such as FMO and ONIOM, and  $DG_{\text{sol}}^{\text{pol}}$

is with continuum solvation models such as GB (generalized Born), PB (Poisson–Boltzmann), and PCM (polarizable continuum model).

We have demonstrated that the LERE-QSAR procedure can excellently reproduce  $DG_{\text{obs}}$  associated with complex formation of a series of ligands with a protein (carbonic anhydrase, MMP, influenza and human neuraminidases).

We will also discuss newly introduced two approaches for estimating the representative energy terms; (1) hybrid estimation of PCM and GB/PB for  $DG_{\text{sol}}^{\text{pol}}$  and (2) dispersion–corrected Hartree-Fock method (HF–D) for  $DE_{\text{bind}}$

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