Mezimolekulové interakce

Interakce molekul

- reaktivně vzniká či zaniká kovalentní vazba
 - překryv elektronových oblaků, mění se vlastnosti
- nereaktivně vznikají molekulové komplexy
 - slabá, nekovalentní, nechemická, fyzikální či van der Waalsova (vdW) interakce
 - molekulový komplex, vdW molekula zachovává vlastnosti jednotlivých komponent
 - přechod mezi klasickými a vdW molekulami je spojitý
 - principielně neexistují pro vdW komplexy žádná "partnerská" omezení

Projevy nekovalentních interakcí

- chování reálného plynu
- Jouleův-Tompsonův jev
- existence kapalin
- biologie, existence života párování bazí v DNA, transkripce DNA, skládání proteinů, procesy rozpoznávání, vazbu ligandů do biomolekul

Původ nekovalentních interakcí

- není v překryvu elektronových orbitalů
- elektrické a magnetické vlastnosti systémů
 - nerovnoměrné rozložení náboje v molekulách
 - multipóly dipól, kvadrupól, … (elektrostatická, coulombická interakce)
 - indukované multipóly (vždy pozitivní interakce atrakce, nazývá se indukční, polarizační interakce)
 - disperzní interakce důsledek elektronové korelace (vlnová funkce jednoho systému "respektuje" vlnovou funkci druhého systému) př. interakce atomů vz. plynů

Původ nekovalentních interakcí

- přitažlivé síly
 - int. mezi multipóly
 - int. mezi multipólem a ind. multipóly (pozitivní)
 - disperzní síly (pozitivní)
- k přitažlivým silám musí existovat ještě odpudivý protějšek
 - výměně repulzí síla



Interakční energie

$A + B \rightleftharpoons A...B \qquad \Delta E = E(A...B) - (E(A) + E(B))$ $\Delta E << E(X)$



velmi náročné na kvalitu výpočtu *E*

Interakční energie

- Přesnost velké báze, zahrnutí el. korelace např. CCSD(T)/CBS
- Při použití konečných bází basis set superposition error (BSSE)
 - při popisu komplexu je báze větší než báze fragmentů
 - Counterpoise (CP) u fragmentů počítá s kompletní bází (ostatní fragmenty jsou tzv. ghost atoms)
 - S rostoucí velikostí báze klesá BSSE chyba, při CBS je nulová!

Bez BSSE korekce



S BSSE korekcí



E(A...B) v bázi A+B

E(A) v bázi A+B

E(B) v bázi A+B

Přesné interakční energie

CCSD(T)/CBS

 přímé výpočty v CCSD(T) a extrapolace např. cc-VTZ - >cc-VQZ jsou téměř nemožné

was fitted in their original work. Herein we have used the aug-cc-pVDZ-aug-cc-pVTZ extrapolation.

$$E_X^{HF} = E_{CBS}^{HF} + Ae^{-\alpha X} \tag{11}$$

$$E_X^{CORR} = E_{CBS}^{CORR} + BX^{-3}$$
(12)

Given that higher-order correlation-energy contributions cannot be neglected, we have approximated the CCSD(T)/ CBS interaction energies according to the following scheme:

$$\Delta E_{CBS}^{CCSD(T)} = \Delta E_{CBS}^{MP2} + (\Delta E^{CCSD(T)} - \Delta E^{MP2}) \Big|$$

J. Chem. Theory Comput. 2009, 5, 1524–1544

Deformační energie

- Pokud jsou energie fragmentů počítány pro geometrie z komplexu, je interakční energie, zatížena chybou – deformační energie
- Odstranění této chyby znamená výpočet energií pro geometricky relaxované komplexy

Interakční energie

$$E = E_{coul.(els.)} + E_{pol.} + E_{disp.} + E_{rep.}$$

- Coulombická (elektrostatická)
- Polarizační (indukční)

 Disperzní (Londonovy síly) – někdy zaměňována s van der Waals

•Repulzní (Pauliho repulze)

•Existují alternativní rozdělení, zejména biochemie používá zvláštní zoologii interakcí (vod. vazby, solné můstky, vdW síly, π -interakce, hydrofóbní interakce atp.)

Nekovalentní komplex





Stabilita nekovalentních komplexů

- hloubka minima stabilita nekov. komplexu
 - 4-20 kJ/mol slabé (hlavně disperzní síly)
 - 12-40 kJ/mol silnější, zejména díky vodíkovým vazbám
 - až 100 kJ/mol iontové komplexy
 - je-li en. < 10.5 kJ/mol pak je za normální teploty vdW molekula velmi nestabilní

$$\Delta E = E(A...B) - (E_A + E_B)$$

Stabilita nekovalentních komplexů

při asociaci molekul klesá entropie, -TdS > 0
 u vdW komplexů hraje entropie významnou roli
 ΔG = ΔH - TΔS

Gibbsova energie entalpie entropie (volná energie)

 $\Delta H = \Delta U + \Delta (PV)$ $\Delta U = \Delta E + \Delta ZPVE$

Stabilizační energie (kJ/mol)

HeHe	0.089	HFH ⁺	548.1
ArAr	1.116	H_2OH^+	756.5
HFHF	27.1	$NH_3 H^+$	923.8
HFH ₂ O	42	HFLi ⁺	124.3
H ₂ OH ₂ O	29.2	H ₂ OLi ⁺	170.3
H ₂ ONH ₃	31.0	H ₂ H ₂	0.433
NH ₃ NH ₃	16.8	N ₂ N ₂	1.208

Hobza P., Zahradník R. Mezimolekulové komplexy, Academia, Praha 1988

Jeziorski, B.; Moszynski, R.; Szalewicz, K. Perturbation Theory Approach to Intermolecular Potential Energy Surfaces of Van Der Waals Complexes. <u>Chem. Rev.</u> 1994, 94, 1887–1930.

SAPT

Symmetry Adapted Perturbation Theory
Pro WFT, velmi náročná
Pro DFT dostupná i pro "středně" velké systémy
E_{int} = E⁽¹⁾_{pol} + E⁽¹⁾_{ex} + E⁽²⁾_{ind} + E⁽²⁾_{ex-ind} + E⁽²⁾_{disp} +

$$E_{ex-disp}^{(2)} + \delta HF$$
 (6)

$$E_{elec} = E_{pol}^{(1)} \tag{7}$$

$$E_{ind} = E_{ind}^{(2)} + E_{ex-ind}^{(2)}$$
(8)

$$E_{disp} = E_{disp}^{(2)} + E_{ex-disp}^{(2)}$$
 (9)

$$E_{exch} = E_{ex}^{(1)} \tag{10}$$

vdW molekuly

- váží se jinou nežli chemickou vazbou
 - iontové komplexy
 - komplexy s vodíkovou vazbou
 - přenosové (charge-transfer) komplexy
 - pravé vdW komplexy (dominuje disperzní energie)

vdW forces

 The attractive or repulsive forces between molecular entities (or between groups within the same molecular entity) other than those due to bond formation or to the electrostatic interaction of ions or of ionic groups with one another or with neutral molecules. The term includes: dipole-dipole, dipole-induced dipole and London (instantaneous induced dipole-induced dipole) forces. The term is sometimes used loosely for the totality of nonspecific attractive or repulsive intermolecular forces. IUPAC Gold Book

CHEMICAL REVIEWS

Hydrogen Bond

Lewis acid

X-H^{+δ}···^{-δ}Υ

Lewis base

Dihydrogen bond

Х-Н^{+δ}···^{-δ}Н-Ү

Lewis acid Lewis base

What Is the Covalency of Hydrogen Bonding?

Sławomir Janusz Grabowski^{*,†,‡}

Hydride Bond

Brønsted acid Brønsted base

Agostic bond

 $C-H\cdots Me$ (Me^{z+})

Lewis base Lewis acid

Halogen-hydride bond

C-Hal^{+δ}····^{-δ}Y

Lewis acid Lewis base

Lewis acid Lewis base

C-Hal^{+δ}····^{-δ}H-Y

dx.doi.org/10.1021/cr800346f | Chem. Rev. XXXX, XXX, 000-000

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 $X-H^{-\delta}\cdots^{+\delta}Y$

Lewis base Lewis acid

Halogen Bond



Figure 5. Relationship between the proton—acceptor distance (in Å) and the binding energy (kcal/mol) for complexes of Table 1. Squares correspond to the dihydrogen bonds, triangles to the (FHF)[–] system, and circles to the other complexes. Open symbols correspond to the binding energies calculated in such a way that the deformation energy is taken into account, and closed symbols correspond to supermolecular approach where deformation energy is not included. Reprinted with permission from ref 101. Copyright 2005 Wiley Interscience.

pomezí mezi nekov. a chemickou vazbou

X-H ... Y

donor (HO,HN...) akceptor (O,N,P...) donuje proton donuje el. hustotu

prodloužení X-H vazby, červený posun v IR R(X-H...Y) ~ $r_{vdW}(X) + r_{vdW}(Y)$

Chemická vazba Vodíková vazba elektronová hustota atomu X je donorována do σ* orbitalu vazby Y<u>-H</u>





Tabulka 5.2: Interakční příspěvky (v kJ.mol⁻¹) k nevazebné interakci ve dvou nekovalentních komplexech s vodíkovou vazbou a v jednom s halogenovou vazbou.

Interakce	$H_2O\cdots H_2O$	$FH \cdots FCl$	$\mathrm{HF}{\cdots}\mathrm{ClF}$
elektrostatická	-25.8	-10.3	-14.2
$\operatorname{induk}\check{\operatorname{cn}}$ í	-4.5	-4.5	-2.5
disperzní	-9.2	-4.4	-6.9
$\operatorname{repulzn}$ í	21.3	10.6	13.6
přenos náboje	-3.7		
celková	-21.9	-8.6	-10.1





Voda, amoniak a fluorovodík

anomální teploty tání a varu





Halogenová vazba



Obrázek 5.7: Dva mezimolekulové komplexy HF s ClF, komplex A se váže vodíkovou vazbou a komplex B halogenovou vazbou.





Tabulka 5.2: Interakční příspěvky (v k $J.mol^{-1}$) k nevazebné interakci ve dvou nekovalentních komplexech s vodíkovou vazbou a v jednom s halogenovou vazbou.

$\operatorname{Interakce}$	$H_2O \cdots H_2O$	$FH \cdots FCl$	$\mathrm{HF}\cdots\mathrm{ClF}$
elektrostatická	-25.8	-10.3	-14.2
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$\operatorname{repulzn}$ í	21.3	10.6	13.6
přenos náboje	-3.7		
celková	-21.9	-8.6	-10.1

Nepravá vodíková vazba Blue-Shifting H-bond



Chem. Rev. 2000, 100, 4253-4264

Blue-Shifting Hydrogen Bonds

Pavel Hobza*, †, ‡ and Zdeněk Havlas^{‡,§}

Figure 9. Schematic pictures of the electron density transfer (δe^-) in (A) improper, blue-shifting hydrogenbonded complex and in (B) classical hydrogen-bonded complex. In the former case (A), the main electron density transfer goes from the electron lone pair of X to the C-Y σ^* antibonding orbital, while in the latter case (B), the electron density transfer goes to σ^* antibonding orbital of the C-H bond which is involved in the hydrogen bonding.

Nepravá vodíková vazba

Table 1.	Changes	of the	bond	length	⊿R(X-	-H) [Å]	and	frequen	cy of	stretching	vibratio	on ⊿v(X	—H) [cm	-'] in full
complexe	es and in	an inho	omoge	neous e	electric	field i	in con	nparison	with	correspon	ding dat	a for m	onomers	calculat-
ed at the	MP2/6-3	1G(d,p)	level.											

	Full co	mplex	Electrostatic + polarization effects Electric field		Non-elec effe Full-el	NE/E ^{tal} index	
	$\Delta R(X-H)$	$\Delta \nu (X-H)$	$\Delta R(X-H)$	Δν(X-H)	$\Delta\Delta R(X-H)$	$\Delta\Delta\nu(X-H)$	
	а	b	c	d	e	f	g
FHCI-	0.0372	-774	0.0122	-263	0.0250	-511	2.1
FHNH ₃	0.0240	-535	0.0046	-143	0.0194	-392	4.2
FHOH2	0.0132	-281	0.0031	-96	0.0101	-185	3.3
NCHOH ₂	0.0088	-142	0.0036	-65	0.0052	-57	1.4
F ₃ CHCl ⁻	0.0064	-104	-0.0057	41	0.0121	-145	-2.1
HOH-OH2	0.0061	-75	0.001	-16	0.0051	-59	4.3
NCHNCH	0.0055	-75	0.0013	-25	0.0042	-50	3.2
NCHFH	0.0036	-48	0.0012	-26	0.0024	-22	2.0
H₃CHCI [_]	0.0047	-44	0.0011	-13	0.0036	-31	3.3
HOHC6H6	0.0015	-15	0.0009	-9	0.0006	-6	1.5
NCHC6H6	0.0017	-16	0.0016	-15	0.0001	-1	0.1
	0.0000	0	0.0000	22	0.0001		
CI3CH-OH2	-0.0002	8	-0.0023	22	0.0021	-14	-0.9
H3CHC6H6	-0.0005	12	0.0004	-1	-0.0009	13	-2.3
CH ₃ CH ₃ OH ₂	-0.0010	8	0.0005	-1	-0.0015	9	-3.0
C6H6C6H6	-0.0032	49	-0.0006	13	-0.0026	36	4.3
F3CH/O2NCH3	-0.0037	58	-0.0023	29	-0.0014	29	0.6
H ₃ SiHNH ₃	-0.0039	18	-0.0033	16	-0.0006	2	0.2
F ₃ CHOH ₂	-0.0040	55	-0.0045	54	0.0005	1	-0.1
FCH ₃ /CI ^{-[d]}	-0.0042	59	-0.0047	59	0.0002	0	-0.1
BrCH ₃ /Cl ^{-[d]}	-0.0043	62	-0.0020	28	-0.0023	34	1.15
CH ₂ O/CH ₂ O	-0.0046	54	-0.0046	44	0.0000	10	0.0
F ₃ CHC ₆ H ₆	-0.0052	86	-0.0024	29	-0.0028	57	1.2

NCH...C,H, F3CH...C,H, F3CH...

CLCH ... OH,

H,CH...C,H,

CH,CH,...OH

F,CH/O,NCH

H.SH._NH

F,CH...OH,

FCH,/Ch

BrCH,/CI

CH,O/CH,O

C,H

FH...Ch

FH...NH,

FH...OH,

NCH...OH,

F,CH...Ch

HOH ... OH,

NCH...NCH

NCH...FH

H,CH...Ch

HOH ... C.H.

a. 0



Dihydrogen

Dvojvodíková vazba Dihydrogen bond

Among the various nonconventional hydrogen bonds, dihydrogen bonds are the most unusual and intriguing. These bonds are formed between two hydrogen atoms, the first positively charged and acting as a proton-donor component, the second negatively charged and acting as a proton-acceptor site:

$$\mathbf{H}^{\delta +} \cdots ^{\delta -} \mathbf{H} \tag{1.1}$$

The first reliable data on the existence of such bonds within crystal structures came from the mid-1990s [9], when Wessel and co-workers reported on the unusually-short intermolecular contacts $B-H\cdot\cdot\cdot H-N$. Nowadays, studies in this fast-developing field involve a large number of chemical elements participating in the bonding quartet X-H···H-Y. It is clear now that this unusual bonding plays an important role as an organizing interaction in molecular architecture (intramolecular dihydrogen bonds), in molecular aggregations (intermolecular dihydrogen bonds), and in the reaction ability of molecules.

Dvojvodíková vazba



ChemPhysChem 2006, 7, 1100-1105

Solvatace





the center of the probe representing a solvent molecule. The solvent excluded surface (SES) is the topological boundary of the union of all possible probes that do not overlap with the molecule.

Implicitní modely

- Implicit models treat the solvent as a continuous medium having the average properties of the real solvent, and surrounding the solute beginning at the van der Waals surface.
- The generalized Born (GB), Surface Area (SA) model is very popular.
- In the GB/SA model, the total solvation free energy *Gsolv* is given as the sum of a solvent-solvent cavity term (*Gcav*), a solute-solvent van der Waals term (*GvdW*), and a solute-solvent electrostatics polarization term (*Gpol*)

$$G_{solv} = G_{cav} + G_{vdW} + G_{pol} \qquad \qquad G_{cav} + G_{vdW} = \sum_{k=1}^{N} ASP(k)ASA(k)$$

where ASA(k) is the total solvent accessible surface area of atom k and ASP(k) is an empirically determined atomic solvation parameter.

$$G_{pol} = -166.0 \left(1 - \frac{1}{\epsilon} \right) \sum_{i=1}^{N} \sum_{j=1}^{N} \frac{q_i q_j}{\sqrt{r_{ij}^2 + b_i b_j \exp\left(-\frac{r_{ij}^2}{4b_i b_j}\right)}}$$

where the double sum runs over all pairs of atoms (i and j). q_i and q_j are the partial charges of i and j, respectively, and r_{ij} is the i,jth atom pair separation. is the dielectric constant of the medium. b_i and b_j are the so-called Born radius of atom i and j, respectively.

Implicitní modely - QM

• Neporušený systém $E^0_{\rm HF} = \langle \Psi_{\rm HF} | \hat{H}^0 | \Psi_{\rm HF} \rangle$

Se solvatací

$$G_{
m HF}^{
m S} = \left\langle \Psi_{
m HF} \middle| \hat{H}_{
m eff} - rac{1}{2} \hat{V}_{
m int} \middle| \Psi_{
m HF}
ight
angle$$

Quantum Mechanical Continuum Solvation Models

Jacopo Tomasi,*,† Benedetta Mennucci,† and Roberto Cammi‡

Chem. Rev. 2005, 105, 2999-3093

Ukázka z Gaussianu

Self-co	onsistent	PCM resul	ts					
<psi(f) <psi(f) (Polari</psi(f) </psi(f) 	H H+V(f)/2 lzed solut	psi(f)> psi(f)> e)-Solver	nt		(a.u (a.u (kcal/mo	.) = .) = 1) =	-99.577537 -99.584002 -4.06	(A) (B) (C)
Partiti	lon over s	pheres:						
Sphere	on Atom	Surface	Charge	GEl	GCav	GDR		
1	H1	15.27	-0.157	-2.36	0.00	0.00		
2	F2	32.58	0.157	-1.70	0.00	0.00		
<i>Predicted</i> After P	<i>energy value f</i> CM correc	or external ite tions, th	<i>ration and si</i> ne energy	tate-specific v is -9	s <i>SRCF calcul</i> 9.5840023	ations 899	a.u.	

Line (A) reports the energy computed using the polarized solute wavefunction and the gas phase Hamiltonian, line (B) reports energy computed using the polarized solute wavefunction and the Hamiltonian in solution, line (C) reports the interaction energy between the polarized solute and the solvent, which corresponds to the integral $\langle \Psi(f)|V(f)/2|\Psi(f)\rangle$ (in kcal/mol), and the final line reports the predicted energy incorporating all PCM corrections.

Explicit models

- rigid models (fixed atom positions)
- flexible models (include bond streching & angle bending)
- polarizable models (include explicit polarization term)
- planar
- steric





- planar & rigid
- three interaction sites
- each atom gets assigned a point charge
- TIP3P (Jorgensen, 1983)
- SPC/E (Berendsen, 1987)
- POL3 (Caldwell & Kollman, 1995)





- planar & rigid
- the negativ charge near the oxygen along the bisector of the HOH angle
- TIP4P (Jorgensen, 1983)

5-SITE

- the negative charge representing the lone pairs of the oxygen atom
- tetrahedral & rigid
- TIP5P (Jorgensen & Mahoney, 2000)



 Table 1. Parameters of the explicit water models studied, as used in the AMBER package (*cf.*

 Figure 1).

Parameter (units)	TIP3P	TIP4P	TIP5P	SPC/E
$\overline{q_{H}}^{a}(e)$	0.417	0.520	0.241	0.424
$q_O{}^{\mathrm{b}}(e)$	-0.834	0.0	0.0	-0.848
$q_L^{c}(e)$	-	-1.040	-0.241	-
$r_{OH}{}^{d}(\text{\AA})$	0.9572	0.9572	0.9572	1.0
$r_{OL}^{e}(\text{Å})$	-	0.15	0.70	-
$\Theta_{HOH}^{f}(deg)$	104.52	104.52	104.52	109.47
$\Phi_{LOL}^{g}(deg)$	-	-	109.47	-
$\varepsilon^{\rm h}$ (kcal/mol)	0.1521	0.155	0.16	0.1554
$\sigma_{O}^{i}(\text{\AA})$	3.15061	3.15365	3.12	3.1656

^{a, b, c} q_{H} , q_{O} , q_{L} are charges on hydrogen, and oxygen atoms and on the lone-pair sites (L), respectively. ^{d, e} r_{OH} , r_{OL} are distances between the oxygen and hydrogen, and between oxygen and L, respectively. ^{f, g} Θ_{HOH} , Φ_{LOL} the angles "formed" between hydrogen, oxygen, and hydrogen, and between L, oxygen, and L, respectively. ^{h, i} ε , σ are the Lennard-Jones parameters.

Analýza – co je RDF?





Bunches of red oxygens and white hydrogens show the probability that a water molecule at certain distance r from the fixed (blue and yellow) molecule will have given relative position and orientation. The animation is thus an attempt to visualize the full pair correlation function. This function is six-dimensional: one distance r and five angular variables. We have measured this function during a 300 ps simulation of 500 TIP4P water molecules at $T=25^{\circ}$ C and ambient density.

The histograms were taken by 15° in each angular variable (with the exception of regions close to the poles). The *r*-coordinate is identified with time, i.e., each frame corresponds to a selected distance (shown in red in the graph of the O-O pair correlation function). For this distance, one molecule from the pair is fixed, and around it 8000 positions of water molecules with highest probability are drawn with diameters proportional to the probability. See also the water page.

Kolafa

Radial distribution function



Radiální Distribuční Funkce



RDF - crystal

200 150 **)** 100 **b** 50 distance (Angstrom)

Radial distribution function of the diamond cluster (black line) compared with the radial distribution functions of a pure diamond crystal (red line) and of amorphous carbon (blue line).

Radial distribution function – 1atm



Explicit water models

	Dipole moment	Dielectric constant	Self diffusion [10 ⁻⁵ cm ² /s]	Density maximum [°C]	Melting temperatures [°C]
SPC/E	2.4	71	2.5	-38.0	-58.2
TIP3P	2.4	82	5.2	-91.0	-127.6
TIP4P	2.2	53	3.3	-25.0	-40.7
TIP5P	2.3	81.5	2.6	+4.0	0.8
Expt.	2.95	78.4	2.3	+3.984	0

TIP3P byl parametrizován pro cutoff, při použití PME se zvyšuje D, reparametrizaci navrhl Brooks (J. Chem. Phys. 121 (20), 10096, **2004**

Cost of computation

- TIP3P 100%
- ◆ SPC/E ~101%
- ◆ TIP4P ~140%
- ◆ TIP5P ~240%
- ◆ POL3 ~1230%



Hydrofóbní efekt







Hydrophobic effect

- The hydrophobic effect is fundamentally based on the tendency of (polar) water molecules to exclude non-polar molecules.
- At the molecular level, the hydrophobic effect is an important force that drives protein folding, formation of the lipid bilayer, insertion of membrane proteins to the nonpolar lipid environment and protein-small molecule interactions.

Hydrofóbní efekt



For large enough clusters, ΔG is a favourable driving force. The horizontal and sloping lines indicate the behaviour of the solvation free energy for the assembled and disassembled cluster, respectively. Red lines indicate the free energies at a higher liquid temperature; blue lines indicate the free energies at a lower temperature. The liquid-vapour surface tension is indicated by γ . 'Volume' and 'surface area' denote the volume excluded to water, and the solvated surface area of that volume, respectively. (Adapted from Chandler, D., "Insight Review: Interfaces and the driving force of hydrophobic assembly" Nature 437, 640-647 (2005).)

Studium nekovaletních interakcí

- Vyžaduje velmi přesné metody kvantové chemie
- Co dělat v případě biomolekul?
 - Hybridní metody (QM/MM)
 - Semiempirické výpočty
 - Empirické potenciály
- Aplikace: např. drug design



výpočetní nároky metody

100.000 10.000 1.000 100

dostupná velikost modelu

reprezentativní model velmi aproximativní metoda nevhodný model velmi spolehlivá metoda

10

Limits of Free Energy Computation for Protein–Ligand Interactions

Kenneth M. Merz, Jr.* **Termodynamický cyklus** $\downarrow \Delta G_{sob}^{p}$ + $\downarrow \Delta G_{sob}^{p}$ $\downarrow \Delta G_{sob}^{p}$ $\downarrow \Delta G_{sob}^{p}$

Figure 1. Thermodyamic cycle to estimate the free energy of binding of a drug molecule to a protein receptor. P = Protein, S = small molecule/substrate, and PS = protein-small molecule/substrate complex. Protein

Protein–Ligand Binding Free Energies. Consider the standard thermodynamic cycle shown in Figure 1.^{15,18} Using this, we can write the following standard expressions:

$$\Delta G_{\rm b}^{\rm s} = \Delta G_{\rm b}^{\rm g} + \Delta G_{\rm solv}^{\rm PS} - \Delta G_{\rm solv}^{\rm P} - \Delta G_{\rm solv}^{\rm S}$$
(2)

where ΔG indicates free energy changes in the gas-phase (ΔG^g) or solution (ΔG^s) , and the subscript b denotes binding. Terms associated with changes in the solvation free energy are also indicated by solv. What we want to do next is to

Termodynamický cyklus

briefly outline below. Expanding out the free energy of binding in the gas-phase term and consolidating the solvation free energies, we can write:

$$\Delta G_{\rm b}^{\rm s} = (E_{\rm total}^{\rm PS} + H_{\rm corr}^{\rm PS}) - {\rm TS}^{\rm PS} - ((E_{\rm total}^{\rm P} + H_{\rm corr}^{\rm P}) - {\rm TS}^{\rm P} + (E_{\rm total}^{\rm S} + H_{\rm corr}^{\rm S}) - {\rm TS}^{\rm S}) + \Delta \Delta G_{\rm sol} (3)$$

where the E_{total} terms are the individual electronic energies, H_{corr} are the individual enthalpy correction terms to the electronic energies, and the S terms are the respective the entropies. The latter two terms can be computed using the rigidrotor harmonic approximation.^{19,20} $\Delta\Delta G_{\text{sol}}$ is given as:

$$\Delta \Delta G_{\rm sol} = \Delta G_{\rm solv}^{\rm PS} - \Delta G_{\rm solv}^{\rm P} - \Delta G_{\rm solv}^{\rm S}$$
(4)

and the individual terms can be obtained from explicit or implicit solvation models or experiment.^{21,22} Rearranging and collecting terms together that represent the change in the total energy, enthalpy, and entropy, respectively, we obtain:

$$\Delta G_{\rm b}^{\rm s} = (E_{\rm total}^{\rm PS} - (E_{\rm total}^{\rm P} + E_{\rm total}^{\rm S})) + (H_{\rm corr}^{\rm PS} - (H_{\rm corr}^{\rm P} + H_{\rm corr}^{\rm S})) - ({\rm TS}^{\rm PS} - ({\rm TS}^{\rm P} + {\rm TS}^{\rm S})) + \Delta \Delta G_{\rm sol} (5)$$

which, when consolidated, leads us to a compact representation²³ of the four key terms we have to evaluate in order to obtain the free energy of binding of a ligand to a protein in aqueous solution:

$$\Delta G_{\rm b}^{\rm s} = \Delta E_{\rm int}^{\rm PS} + \Delta H_{\rm corr}^{\rm PS} - T\Delta S^{\rm PS} + \Delta \Delta G_{\rm sol} \qquad (6)$$

where the first three of the individual terms are defined as:

$$\Delta E_{\text{int}}^{\text{PS}} = E_{\text{total}}^{\text{PS}} - (E_{\text{total}}^{\text{P}} + E_{\text{total}}^{\text{S}})$$
$$\Delta H_{\text{corr}}^{\text{PS}} = H_{\text{corr}}^{\text{PS}} - (H_{\text{corr}}^{\text{P}} + H_{\text{corr}}^{\text{S}})$$
$$(7)$$
$$T\Delta S^{\text{PS}} = \text{TS}^{\text{PS}} - (\text{TS}^{\text{P}} + \text{TS}^{\text{S}})$$



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QM/MM

aditivní vs. subtraktivní schéma

known as additive and subtractive approaches. In the additive scheme, the total energy of the system is represented as a sum of the QM energy of the QM core, E_{QM} , the MM energy of the MM region (without the QM core), E_{MM} , and the interaction between both regions, $E_{QM/MM}$:

$$E_{tot} = E_{QM} + E_{MM} + E_{QM/MM}, \tag{2}$$

The subtractive scheme [31–33] was originally called integrated molecular-orbital molecular mechanics (IMOMM) but is more frequently known as ONIOM (abbreviated from the original name: Our own N-layered Integrated molecular Orbital + molecular Mechanics) scheme. It divides the system into layers and subtracts double counted energies of the smaller layer as follows:

$$E_{tot} = E_{real}^{MM} + E_{model}^{QM} - E_{model}^{MM},\tag{3}$$

where E_{real}^{MM} represents energy of the whole real system (containing both the QM and MM regions) as calculated by the lower-level method, typically MM, E_{model}^{QM} is energy of the QM core calculated at a higher level, typically a QM method, and E_{model}^{MM} is the energy of the QM core calculated at the lower MM level. Subtractive and additive schemes are in principle equivalent, differing just in the technical details of their implementation.

Calculation of free energy barrier

- Empirical potentials (MM)
 - Empirical valence bond (EVB), pioneered by Warshel and Weiss (JACS 1980, 102, 6218)
 - broadly used
 - parametrization
- Nonempirical potentials (QM)
 - Now, impractical
 - Future, RI-DTF+D
- Combined QM/MM
 - Warshel and Levitt (JMB 1976, 103, 227)

$$k = \gamma \left(\frac{k_B T}{h}\right) \exp\left(-\frac{\Delta G^{\ddagger}}{k_B T}\right)$$



- QM
 - HF, RI-MP2, CC
 - DFT
 - RI-DFT (LSDA, GGA)
 - Hybrid B3LYP, MPW1K
- MM
 - AMBER parmXY
 - Explicit water molecules (TIP3P, SPC/E)
- QM-MM
 - QM capping (-H)
 - QM-MM: mechanical, electronic embedding

QM/MM – Free energies

- Robust sampling
 - Umbrella sampling
 - Free energy perturbation
- Classical dynamics on QM/MM potential
- Hand-in-Hand evolution
 - CPMD
 - ADMP