

OPTIMIZATION OF PHENYILALANANINE HYDROXILASE STABILIZERS BY A TESTED 'ALCHEMICHAL' FREE-ENERGY APPROACH

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METHODS

A 'bonded' and an 'unbonded' approach have been implemented to model the coordinated metal center, and in the end, the relative binding free energy results are compared with available experimental data. The one showing more accurate results is chosen for subsequent alchemical transformations from compound IV.

MD PACKAGE: GROMACS 4.6.1 SAMPLING METHOD: H-REMD A VALUES: 16 (x 5 ns) ESTIMATION METHOD:

BONDED MODEL

Interactions between the metal ion and its ligating residues treated via bond, angle, dihedral, electrostatic and van der Waals (VDW) terms (parameters obtained from either QM calculation or experimentally where available).

Metal Center parameterized with:Ligands:GAUSSIAN 03; AmberTools (RESP,Partial charges: GaussiaMCPB) ; (charges 2+ or 3+ on Fe)Force field: GAFF

Ligands:The remaining system treated with:Partial charges: Gaussian 03AMBER99SB force fieldForce field: GAFFForce field



NON-BONDED MODEL

Interactions between the metal ion and its ligating residues treated only via electrostatic and VDW terms.

The overall protein treated with: AMBER99SB force field; (charge 0 on Fe)

Ligands: Partial charges: Gaussian 03 Force field: GAFF



MBAR

coulombic- $\lambda = 0.0 \ 0.2 \ 0.4 \ 0.6 \ 0.8 \ 1.0 \ 1.$





Table 1. Stabilizing effect and affinity data.									
Compound	ΔTm (⁰C)	K _a (mol/L)	K _d (μmol/L)						
CIV	5	6.5 x 10 ⁴	15.4						
CIVa	5.3	8.2 x 10 ⁴	12.2						
CIVd	11	2.7 x 10 ⁵	3.7						
CIVg	7.3	5.6 x 10 ⁴	17.9						
CIVi	14.1	1.6 x 10 ⁵	6.3						
CIVm	12.7	2.8 x 10 ⁵	3.6						
CIVn	17.2	2.3 x 10 ⁵	4.3						

	'Alchemical'ΔΔG exptransformation(kJ/mol)	ΔΔG calc (kJ/mol)						
		(kJ/mol)	Bonded (Fe ²⁺⁾	Diff (exp - calc)	Bonded (Fe ³⁺⁾	Diff (exp - calc)	Unbounded	Diff (exp - calc)
	CIV -> CIVa	-0.58	-3.01 ± 0.04	2.43	-2.14 ± 0.04	1.56	1.46 ± 0.05	-2.04
	CIV -> CIVd	-3.53	-5.18 ± 0.11	1.65	-4.41 ± 0.13	0.88	2.51 ± 0.08	-6.04
	CIV -> CIVg	0.37	1.37 ± 0.03	-1	1.39 ± 0.03	-1.02	4.04 ± 0.02	-3.67
	CIV -> CIVi	-2.23	-6.11 ± 0.17	3.88	-5.47 ± 0.23	3.24	-1.36 ± 0.19	-0.87
	CIV -> CIVm	-3.62	-8.06 ± 0.14	4.44	-5.70 ± 0.27	2.08	0.83 ± 0.23	-4.45
	CIV -> CIVn	-3.13	-10.45 ± 0.24	7.32	-6.16 ± 0.16	3.03	-0.59 ± 0.21	-2.54
	Ave (ABS(Diff))			3.45		1.97		3.27
Correct sign , in general, compared with ΔΔG exp, but values are too overestimated.								e cases or les.

CONCLUSIONS

Affinity values are shown in **table 1.**

Fig 9. ITC results for CIV and the synthesized derivatives.



Fig 10. Correlation plots between experimental and theoretical free energy changes obtained for each of the three approaches used here to model the 'alchemical' transformations .

REFERENCES

[1] C. R. Scriver and S. Kaufman, *"Hyperphenylalaninemia: phenylalanine hydroxylase deficiency"*, In: C.R. Scriver, A. L. Beaudet, W. S. Sly, D. Valle, B. Childs, K. Kinzler, B. Vogelstein, editors, *"The Metabolic and Molecular Bases of Inherited Disease"*, 8, New York: McGraw-Hill, pp. 1667–724, **2001**.

[2] Web page of the Galician Phenylketonuric Association (ASFEGA), <u>www.asfega.es/es/listado-enfermedades/fenilcetonuria-pku/</u>

[3] M. I. Flydal and A. Martínez, "Phenylalanine hydroxylase: function, structure, and regulation", IUBMB Life, 65(4), 341-9, 2013.
[4] A. L. Pey, M. Ying, N. Cremades, A. Velázquez-Campoy, T. Scherer, B. Thöny, J. Sancho and A. Martínez, "Identification of pharmacological chaperones as potential therapeutic agents to treat phenylketonuria", J. Clin. Inv., 118(8), 2858-67, 2008.

[[5] R. Torreblanca, E. Lira-Navarrete, J. Sancho and R. Hurtado-Guerrero, "Structural and mechanistic basis of the interaction between a pharmacological chaperone and human phenylalanine hydroxylase", Chembiochem, 13(9), 1266-9, **2012.**

[6] A. de Ruiter and C. Oostenbrink, "Free energy calculations of protein-ligand interactions", Curr. Opin. Che. Biol., 15(4), 547-52, **2011**. The possibility of starting, in parallel, a synthesis project to obtain and test new derivatives of the compound **IV**, allowed us to acquire additional experimental affinity data, and therefore to validate our AFEC implementation. In this sense, out of the methodologies followed to model our system, the 'bonded' one in which charge on the iron ion was set to 3+, resulted better correlated (r=0.9) with experimental data, so we decided to chose it to continuing refining our method (by fixing the lambda values: step in which we are focused now). Subsequently, the results of this work will allow us to design new promising candidates with improved binding affinity and with a more potent stabilizing effect on PAH enzyme.

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