Impact of Neighboring Residues on the pKa of Histidine 174

in Plasmodium Falciparum Malate Dehydrogenase

Parameter	pKa (int)	pKa (1/2)		Non Charged Impact		Charge Impact
H174 (ave)	4.37	4.75				
H174 (st error)	0.16	1.23				
D176 (ave)				-0.0044		0.467
D176 (st error)				0.01		0.014
R214 (ave)				0.303		-0.379
R214 (st error)				0.031		0.0368

Parameters are averages of 5 replicates. Calculations based on the subunit structure of Plasmodium falciparum Malate Dehydrogenase (5nfr.pdb). Replicate structures were using RefineD to generate 5 equivalent models of the structure. Each replicate was analyzed using H++ with an internal dielectric set at 10 and the solvent dielectric set at 80.

The impact of neighboring residues on H174 pKa values were calculated from the deconvoluted output of H++ which estimates the contributions of neighboring residues to the shifter pKa value of H174 from the canonical value for free Histidine (Pka = 6.0). The impact is calculated for the "non-titratable component of the amino acid (non-charged impact) and for the titratable component (charged impact).

Reference:

1. Anandakrishnan, R., et al. "H++3.0: automating pK prediction and thepreparation of biomolecular structures for atomistic molecular modeling and simulations", Nucleic Acids Research, 2012, Vol. 40, Web Server issue W537–W541