



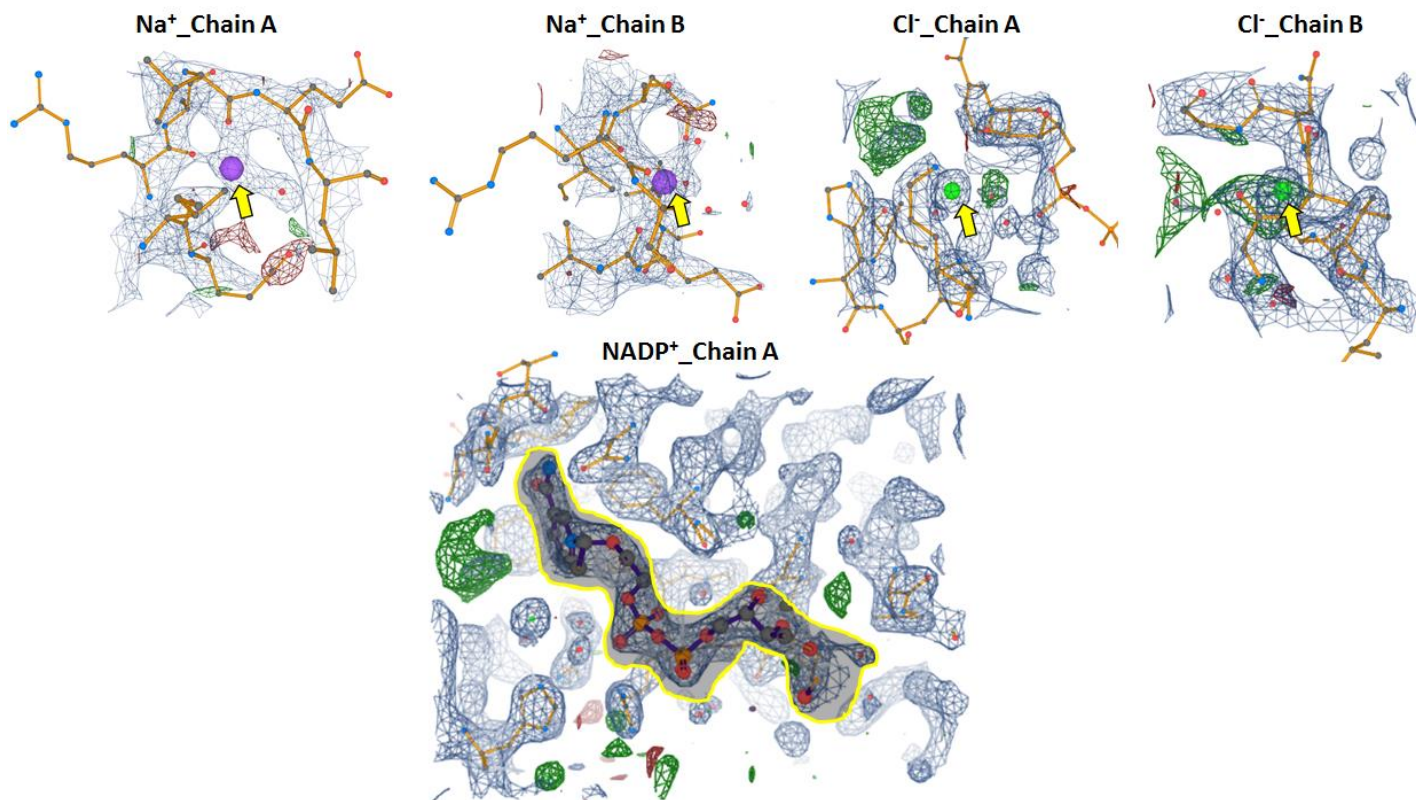
STRUCTURAL BIOLOGY  
COMMUNICATIONS

**Volume 72 (2016)**

**Supporting information for article:**

**The crystal structure of dihydrodipicolinate reductase at 2.3 Å resolution from the human pathogenic bacterium *Bartonella henselae* strain Houston-1**

**Ali R. Cala, Maria T. Nadeau, Jan Abendroth, Bart L. Staker, Alexandra R. Reers, Anthony W. Weatherhead, Renwick C. J. Dobson, Peter J. Myler and André O. Hudson**



**Figure S1** Electron density placement of Na<sup>+</sup>, Cl<sup>-</sup> and NADP<sup>+</sup> co-crystallized with *BhDapB*. Ions were identified based on coordination geometry with neighboring atoms, charge, and temperature (B) factors. Metal ions were then validated using the CheckMyMetal web server ([www.csgid.org/csgid/metal\\_sites/](http://www.csgid.org/csgid/metal_sites/)) (Zheng *et al.*, 2014).