

Erratum to: Molecular models of the Mojave rattlesnake (*Crotalus scutulatus scutulatus*) venom metalloproteinases reveal a structural basis for differences in hemorrhagic activities

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Due to an unfortunate technical problem in production, the original figure 6 showed incorrectly. Figure 6 has now been reproduced correctly and can be seen here.

The online version of the original article can be found at <http://dx.doi.org/10.1007/s10867-013-9339-3>.

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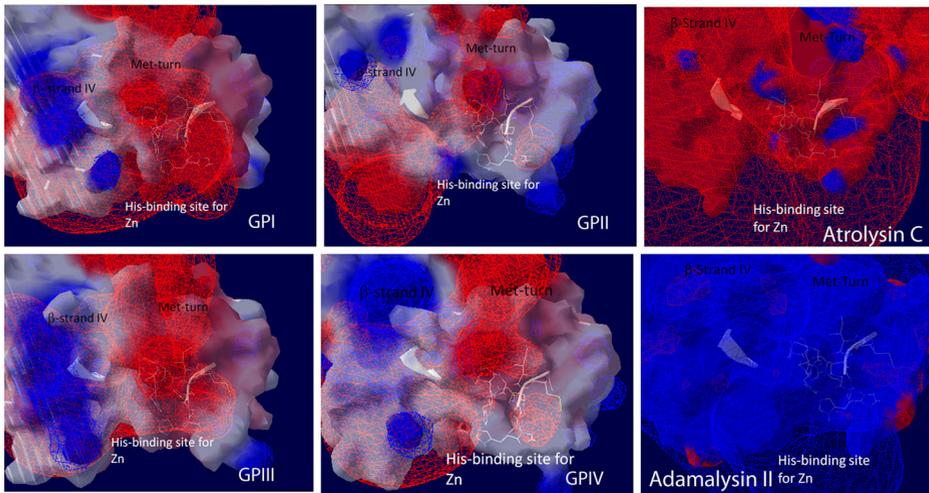


Fig. 6 Rendering of field potential maps (Coulombic) for each molecular model of each *C. s. scutulatus* metalloproteinase group and for atrolysin C and adamalysin II crystal structures. Positive field potentials are shown as *blue spheres* whereas negative field potentials are shown as *red spheres* that conform the surface potential map and neutral regions are rendered *white*. For convenience to the viewer, the side chains of the amino acid residues of the zinc binding domain, Met turn, and β -strand IV (*top of the catalytic groove*) have been displayed (*white*) in order to locate the catalytic groove of each molecular model