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Erratum

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Erratum

JAK2 V617F in myeloid disorders: What do we know now, and where are we headed? Maria E. Nelson & David P. Steensma. Leukemia and Lymphoma 2006;47(2):177-194.

The publishers would like to apologise for an error that occurred in colouration of Figure 2 in the abovementioned article. The corrected figure is shown below.



Figure 2. Putative JAK2 structure, based on homology with other tyrosine kinases such as fibroblast growth factor, where the crystal structure has been solved. This ribbon diagram displays the active kinase JH1 domain in blue (left) and the pseudokinase JH2 domain in green (right). The activation loop of JH1 on the left side of the diagram is shown twice, in two possible conformations: active (phosphorylated - red) and inactive (non-phosphorylated-navy blue). The JH1 kinase site is shown in orange, and the adenosine triphosphate (ATP) binding site in yellow. Homologous activation loop and kinase domains (non-functional) are shown on JH2 as well. Site of interaction of JH2 and the activation domain of JH1 is shown encircled, along with the location of Val617. Adapted from Kaushansky [114] (Blood 2005) and the American Society of Hematology, with permission, and from Lindauer [86].