

Article

# Binding Mechanism of Inhibitors to Heat Shock Protein 90 Investigated by Multiple Independent Molecular Dynamics Simulations and Prediction of Binding Free Energy

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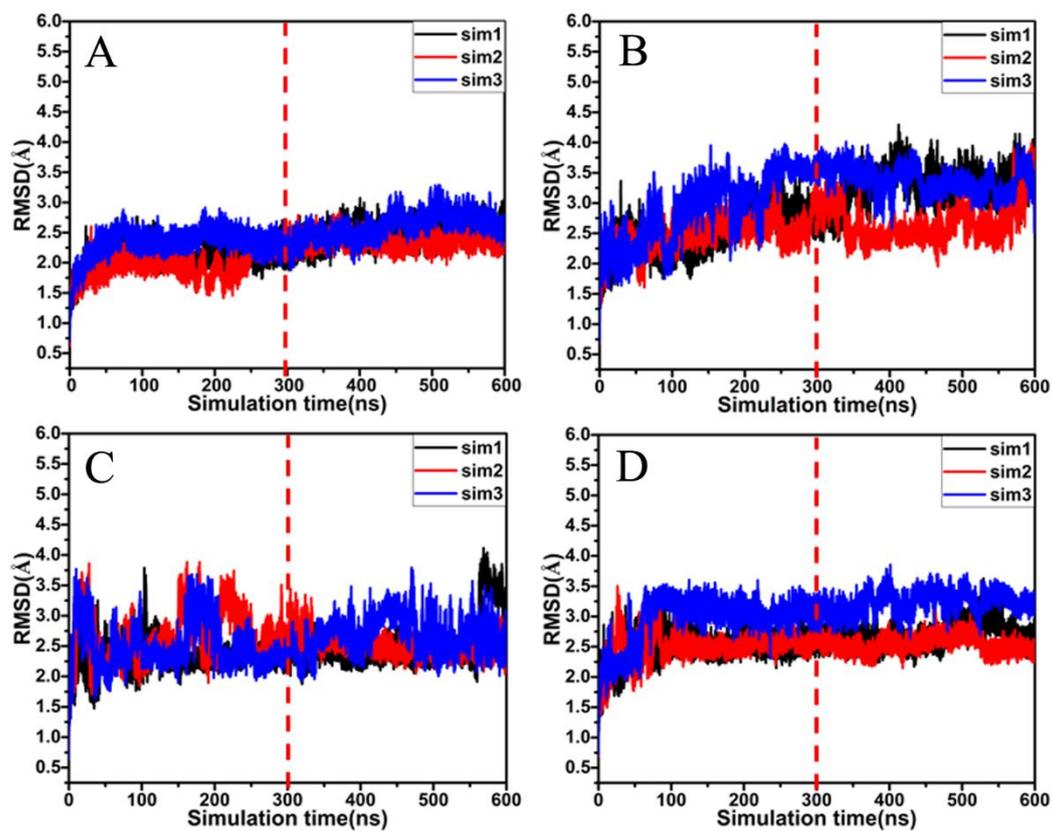


Figure S1. Root-mean-square deviations (RMSDs) of backbone atoms in HSP90 in three independent simulations: (A) the *apo* HSP90, (B) the W8Y-bound HSP90, (C) the W8V-bound HSP90 and (D) the W8S-bound HSP90.

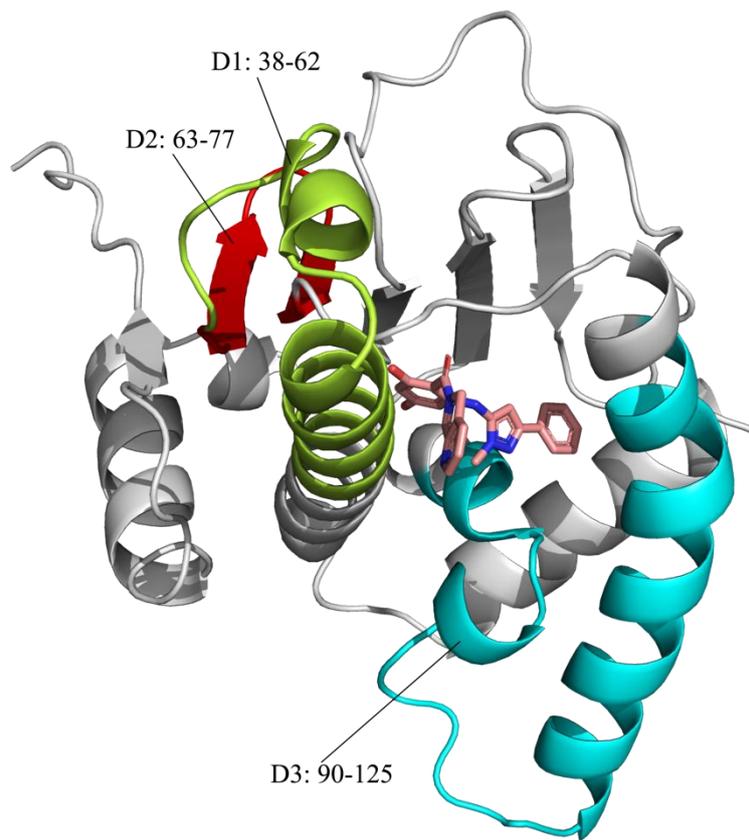


Figure S2. Structural domains of HSP90 with obvious changes of RMSF, in which the D1, D2 and D3 display different domains with colors.

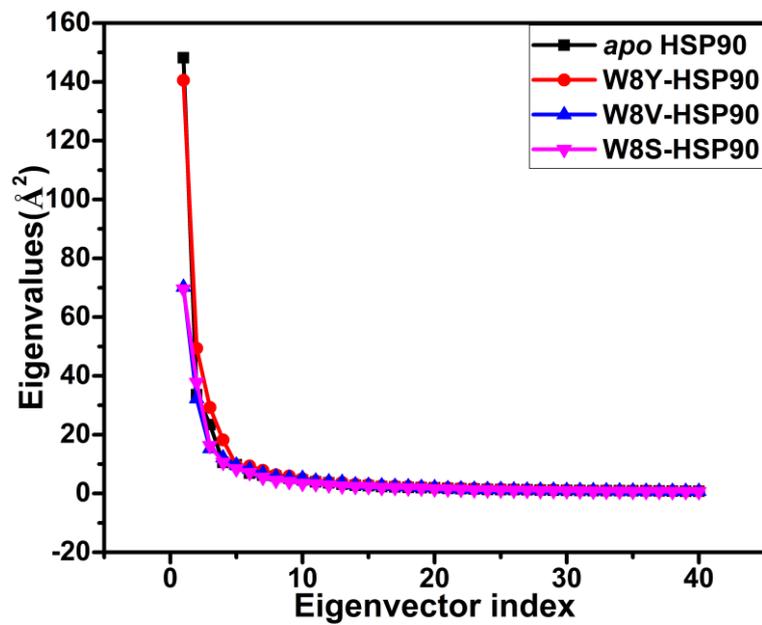


Figure S3. The function of eigenvalues as eigenvector indexes from principal component analysis, which is used to describe structural fluctuations of HSP90 along the eigenvectors.

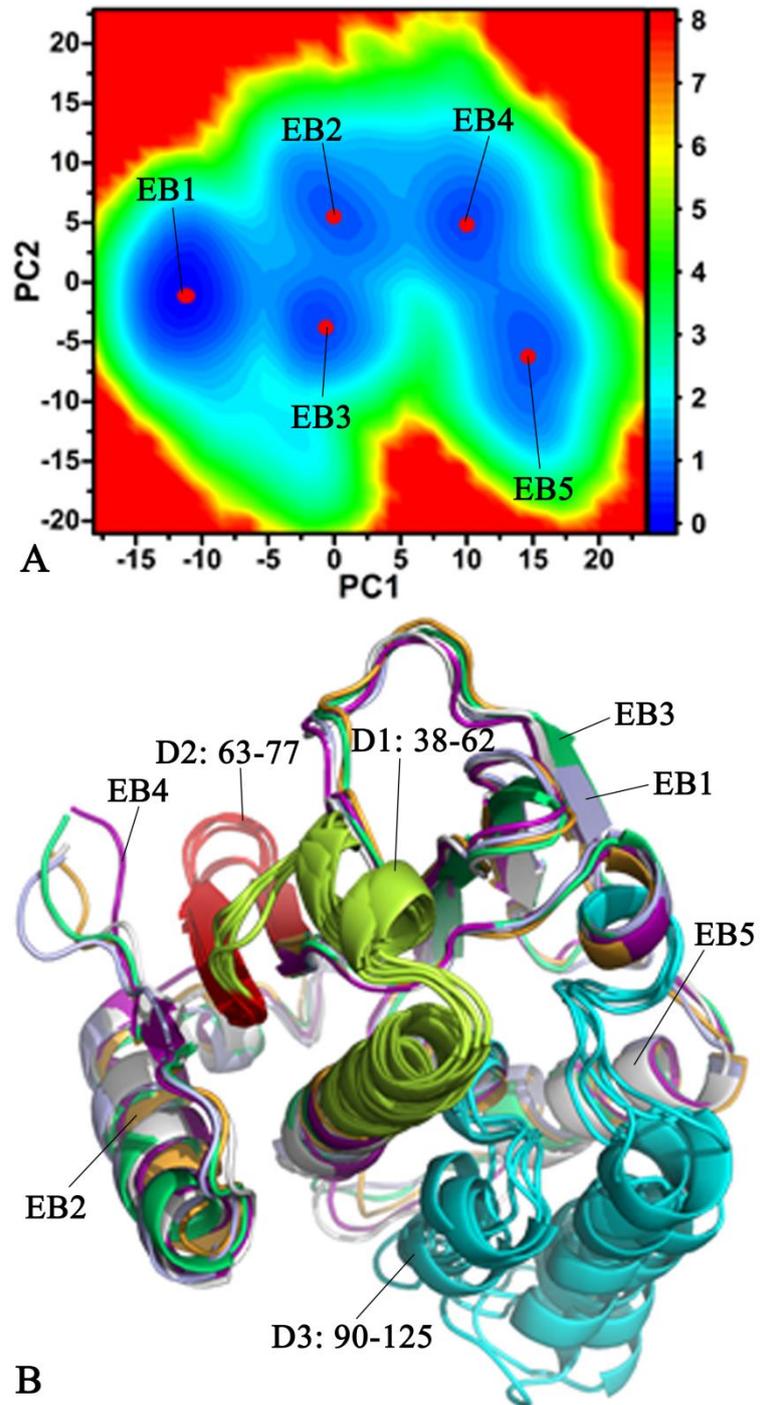


Figure S4. Free energy landscapes and the representative structures of the *apo* HSP90: (A) free energy landscape and (B) structural superimposition of the *apo* HSP90 trapped at the EB1-EB5.