**Method for KBbox**

Please have a look at a method online for reference: <https://kbbox.h-its.org/toolbox/methods/molecular-simulation/-random-acceleration-molecular-dynamics-ramd/>

**Name of Method:**

**Short description of Method (less than 4 lines). You may use bold or other font specifications:**

**Main description of Method. You may use Word styles (for headings), paste images in appropriate resolution, use Word equation editors, and use bold or other font specifications.**

**Computational method group. Please select ONE from the 4 method groups listed at https://kbbox.h-its.org/toolbox/methods/.**

**Please provide the following information -** (yes/no) **Allows computation of kon** - (yes/no)  
**Allows computation of koff -**  (yes/no) **Method is used in PKPD –** (yes/no) **Can be used for prediction of binding pathways –** (yes/no)  
**Can be used for prediction of unbinding pathways –** (yes/no) **Method can provide absolute kinetic data –** (yes/no) **Method requires training data –** (yes/no) **Method requires structural data of bound complexes –** (yes/no) **Estimate the computational cost from 1(low) to 5(high) –** (1 to 5)  
(Guide to estimate of computational cost: 1: minutes on workstation; 2: several hours on workstation; 3: small cluster (up to ca. 200 cores) in two days; 4: small cluster (up to ca. 200 cores) in two weeks; 5: requires greater resourses)