

 Open access • Journal Article • DOI:10.1080/07391102.2013.803264

Role of ELA region in auto-activation of mutant KIT receptor: a molecular dynamics simulation insight — [Source link](#)





Rituraj Purohit

Published on: 22 Apr 2014 - Journal of Biomolecular Structure & Dynamics (J Biomol Struct Dyn)

Topics: Wild type

Related papers:

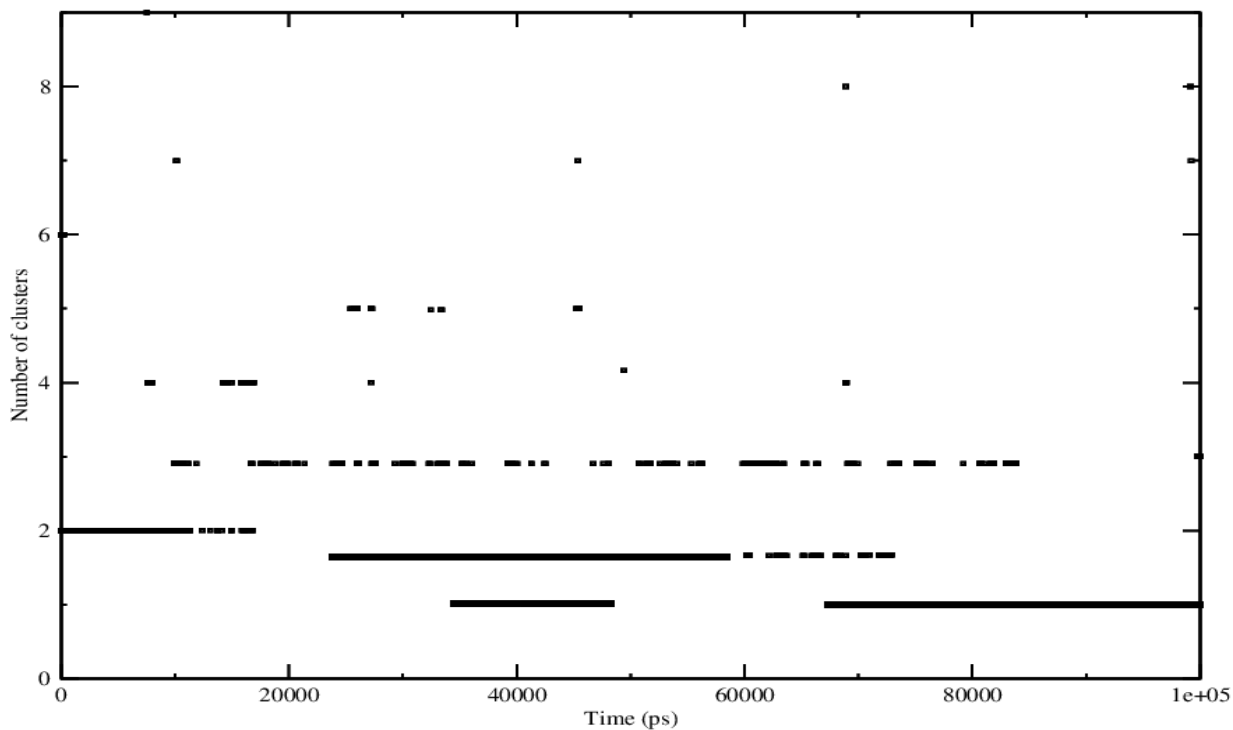
- [In silico investigation of molecular mechanism of laminopathy caused by a point mutation \(R482W\) in lamin A/C protein](#)
- [Drug resistance mechanism of PncA in Mycobacterium tuberculosis](#)
- [GROMACS 4: Algorithms for highly efficient, load-balanced, and scalable molecular simulation](#)
- [The Protein Data Bank](#)
- [Molecular dynamics with coupling to an external bath.](#)

Share this paper:    

View more about this paper here: <https://typeset.io/papers/role-of-ela-region-in-auto-activation-of-mutant-kit-receptor-11t533mynw>

Figure S2. Number of populated clusters (C- α carbon atom) versus simulation time for (a) the wildtype and (b) mutant KIT protein trajectory. RMSD cut-off for two structures to be neighbor was 0.14 nm and gromos method was implemented for cluster determination. Results are shown for two independent clusterings. After 70 ns, the simulation appears equilibrated.

a



b

