# Ring domains functioning as E3 ligases reveal distrinct structural feature: a molecular dynamics sumulation study

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## Abstract

RING domain, a cysteine-rich motif that chelates two zinc ions, has been shown to regulate many biological processes such as mediating a crucial step in the ubiquitinylation pathway. In order to investigate the distinct structural features for the RING domains functioning as E3 ligases, several molecular dynamics simulations involving the c-Cbl, CNOT4 (with E3 ligase function), and p44 (no E3 ligase function) RING domains were conducted in this study. Our results reveal that the structural stability of the recognition site is a basic requirement for the RING domains functioning as E3 ligases. The structural stability of the recognition site is maintained by the hydrophobic core and hydrogen bonding network. Another important structural feature of the RING domains functioning as E3 ligases is the stable distances between the recognition site and the zinc ion binding sites S1 and S2. Moreover, the RING domains functioning as E3 ligases seem to exhibit lower beta stability due to the higher proportion of proline residues in their sequences. However, no significant difference of the other secondary (alpha and turn) and the tertiary structural stabilities can be observed among these three RING domains.