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Opposing intermolecular tuning of Ca^{2+} affinity for Calmodulin by its target peptides

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We investigated the impact of bound calmodulin (CaM)-target compound structure on the affinity of calcium (Ca^{2+}) by integrating coarse-grained models and all-atomistic simulations with non-equilibrium physics. We focused on binding between CaM and two specific targets, Ca^{2+} /CaM-dependent protein kinase II (CaMKII) and neurogranin (Ng), as they both regulate CaM-dependent Ca^{2+} signaling pathways in neurons. It was shown experimentally that Ca^{2+} /CaM binds to the CaMKII peptide with higher affinity than the Ng peptide. The binding of CaMKII peptide to CaM in return increases the Ca^{2+} affinity for CaM. However, this reciprocal relation was not observed in the Ng peptide, which binds to Ca^{2+} -free CaM or Ca^{2+} /CaM with similar binding affinity. Unlike CaM-CaMKII peptide that allowed structure determination by crystallography, the structural description of CaM-Ng peptide is unknown due to low binding affinity, therefore, we computationally generated an ensemble of CaM-Ng peptide structures by matching the changes in the chemical shifts of CaM upon Ng peptide binding from nuclear magnetic resonance experiments. We computed the changes in Ca^{2+} affinity for CaM with and without binding targets in atomistic models using Jarzynski's equality. We discovered the molecular underpinnings of lowered affinity of Ca^{2+} for CaM in the presence of Ng by showing that the N-terminal acidic region of Ng peptide pries open the β -sheet structure between the Ca^{2+} binding loops particularly at C-domain of CaM, enabling Ca^{2+} release. In contrast, CaMKII increases Ca^{2+} affinity for the C-domain of CaM by stabilizing the two Ca^{2+} binding loops.