

pyDock

pyDock is a protein-protein docking algorithm ([Cheng et al. 2007 Proteins 68, 503-515](#)) that uses electrostatics, desolvation energy and a limited van der Waals contribution to score rigid-body docking poses (pyDockSER).

pyDock participates in [CAPRI](#) (Critical Assessment of PRediction of Interactions). You can evaluate its performance among the rest of participants visiting the [summary](#) provided by Yang Shen from Vadja Team. pyDock is participating in CAPRI under the name of "Fernandez-Recio".

Further information: life.bsc.es/pid/pydock

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