

[H-bond network optimization in protein-protein complexes: are all-atom force field scores enough?](#)

Authors: [Masone, Diego](#) / [Cabeza de Vaca, Israel](#) / [Pons, Carles](#) / [Fernández-Recio, Juan](#) / [Guallar, Victor](#)

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Barcelona Supercomputing Center - Centro Nacional de Supercomputación

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