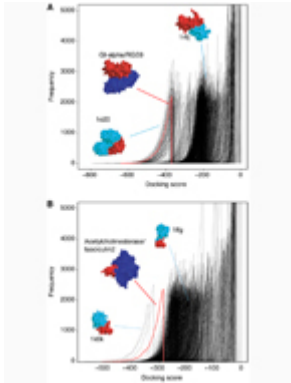


Computational programs used to predict the composition of protein complexes



This finding was possible after running more than 100,000 docking experiments using the MareNostrum supercomputer

[4199.pdf](#)

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