

[Inicio](#) > FrustratomeR: an R-package to compute local frustration in protein structures, point mutants and MD simulations [Abstract](#) [Summary](#) [Availability and implementation](#) [Supplementary information](#)

[FrustratomeR: an R-package to compute local frustration in protein structures, point mutants and MD simulations](#) [Abstract](#) [Summary](#) [Availability and implementation](#) [Supplementary information](#)

URL: <https://academic.oup.com/bioinformatics/article/37/18/3038/6171179>

Authors: [Rausch, Atilio](#) / [Freiberger, Maria](#) / [Leonetti, Cesar](#) / [Luna, Diego](#) / [Radusky, Leandro](#) / [Wolynes, Peter](#) / [Ferreiro, Diego](#) / [Parra, Gonzalo](#) / [Ponty, Yann](#)

Publication: Bioinformatics

Volume / Pagnation: 3784104108474849116444044613114415954 / 3038 - 3040

Barcelona Supercomputing Center - Centro Nacional de Supercomputación

Source URL (retrieved on 8 Sep 2024 - 08:24): <https://www.bsc.es/es/research-and-development/publications/frustratomeR-r-package-compute-local-frustration-protein>