

Resource Summary Report

Generated by [kravitz2](#) on Aug 23, 2026

BME

RRID:SCR_021953

Type: Tool

Proper Citation

BME (RRID:SCR_021953)

Resource Information

URL: <https://github.com/KULL-Centre/BME>

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Description: Software Python package to construct conformational ensemble of biomolecular system by integrating molecular simulations and experimental data. Performs ensemble reweighting using Bayesian Maximum Entropy approach.

Synonyms: Bayesian/Maximum Entropy

Resource Type: software resource, software toolkit

Defining Citation: [PMID:32006288](#)

Keywords: Bayesian maximum entropy, integrating molecular simulations and experimental data, ensemble reweighting, Bayesian Maximum Entropy approach

Funding: Lundbeck Foundation ;
Novo Nordisk Foundation ;
The Velux Foundations

Availability: Free, Available for download, Freely available

Resource Name: BME

Resource ID: SCR_021953

License: GNU General Public License v3.0

Record Creation Time: 20220421T050137+0000

Record Last Update: 20260821T194209+0000

Ratings and Alerts

No rating or validation information has been found for BME.

No alerts have been found for BME.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Sanchez-Martinez S, et al. (2024) Labile assembly of a tardigrade protein induces biostasis. Protein science : a publication of the Protein Society, 33(4), e4941.

Johansen NT, et al. (2022) Mg²⁺-dependent conformational equilibria in CorA and an integrated view on transport regulation. eLife, 11.

Pesce F, et al. (2021) Refining conformational ensembles of flexible proteins against small-angle x-ray scattering data. Biophysical journal, 120(22), 5124.

Weinhäupl K, et al. (2021) Architecture and assembly dynamics of the essential mitochondrial chaperone complex TIM9·10·12. Structure (London, England : 1993), 29(9), 1065.