

Resource Summary Report

Generated by [kravitz2](#) on Aug 9, 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: The Velux Foundations ;
Novo Nordisk Foundation ;
Lundbeck Foundation

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: 20260808T190532+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.

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.

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