

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

[BeAtMuSiC](#)

RRID:SCR_028562

Type: Tool

Proper Citation

BeAtMuSiC (RRID:SCR_028562)

Resource Information

URL: <http://babylone.ulb.ac.be/BeAtMuSiC/>

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Description: Web tool for prediction of changes in protein-protein binding affinity on mutations. Predictor of changes in binding free energy induced by point mutations. It relies on a set of statistical potentials derived from known protein structures, and combines the effect of the mutation on the strength of the interactions at the interface, and on the overall stability of the complex.

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:23723246](#)

Keywords: prediction of changes in protein-protein binding affinity, mutations, changes in binding free energy, point mutations,

Funding: Belgian Fund for Scientific Research

Availability: Free, Freely available

Resource Name: BeAtMuSiC

Resource ID: SCR_028562

Record Creation Time: 20260616T043402+0000

Record Last Update: 20260815T183322+0000

Ratings and Alerts

No rating or validation information has been found for BeAtMuSiC.

No alerts have been found for BeAtMuSiC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Takada K, et al. (2023) Genomic diversity of SARS-CoV-2 can be accelerated by mutations in the nsp14 gene. iScience, 26(3), 106210.

Peka M, et al. (2023) Analysis of RBD-ACE2 interactions in livestock species as a factor in the spread of SARS-CoV-2 among animals. Veterinary and animal science, 21, 100303.

Unni P, et al. (2022) Predictive functional, statistical and structural analysis of CSNK2A1 and CSNK2B variants linked to neurodevelopmental diseases. Frontiers in molecular biosciences, 9, 851547.