

Resource Summary Report

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MareNostrum

RRID:SCR_015737

Type: Tool

Proper Citation

MareNostrum (RRID:SCR_015737)

Resource Information

URL: <https://www.bsc.es/marenostrum/marenostrum>

Proper Citation: MareNostrum (RRID:SCR_015737)

Description: Operating software for a supercomputer in Spain. The software is maintained and updated by the Centro Nacional de Supercomputación (Barcelona Supercomputing Center) and is used for research projects on climate change, gravitational waves, a vaccination against AIDS, new radiation treatments to fight cancer, and other subjects.

Resource Type: software resource

Keywords: supercomputer, operating system, petaflop, research project, research software

Availability: Available to affiliated researchers

Resource Name: MareNostrum

Resource ID: SCR_015737

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260912T195830+0000

Ratings and Alerts

No rating or validation information has been found for MareNostrum.

No alerts have been found for MareNostrum.

Data and Source Information

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Šmelko A, et al. (2024) Maboss for HPC environments: implementations of the continuous time Boolean model simulator for large CPU clusters and GPU accelerators. BMC bioinformatics, 25(1), 199.

Ruiz-Cabello N M, et al. (2020) Performance of parallel FDTD method for shared- and distributed-memory architectures: Application to bioelectromagnetics. PloS one, 15(9), e0238115.

Calmet H, et al. (2019) Nasal sprayed particle deposition in a human nasal cavity under different inhalation conditions. PloS one, 14(9), e0221330.

Sacco F, et al. (2018) Left Ventricular Trabeculations Decrease the Wall Shear Stress and Increase the Intra-Ventricular Pressure Drop in CFD Simulations. Frontiers in physiology, 9, 458.

Bueren-Calabuig JA, et al. (2011) Temperature-induced melting of double-stranded DNA in the absence and presence of covalently bonded antitumour drugs: insight from molecular dynamics simulations. Nucleic acids research, 39(18), 8248.

Izarzugaza JM, et al. (2008) Enhancing the prediction of protein pairings between interacting families using orthology information. BMC bioinformatics, 9, 35.