Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 29, 2025

National Biomedical Computation Resource

RRID:SCR_002656
Type: Tool

Proper Citation

National Biomedical Computation Resource (RRID:SCR_002656)

Resource Information

URL: http://www.nbcr.net/

Proper Citation: National Biomedical Computation Resource (RRID:SCR_002656)

Description: Biomedical technology research center that conducts, catalyzes and enables multiscale biomedical research, focusing on four key activities: 1) integrating computational, data and visualization resources in a transparent, advanced grid environment to enable better access to distributed data, computational resources, instruments and people; 2) developing and deploying advanced computational tools for modeling and simulation, data analysis, query and integration, three-dimensional image processing and interactive visualization; 3) delivering and supporting advanced grid/cyberinfrastructure for biomedical researchers; and 4) training a cadre of new researchers to have an interdisciplinary, working knowledge of computational technology relevant to biomedical scientists. NBCR enables biomedical scientists to address the challenge of integrating detailed structural measurements from diverse scales of biological organization that range from molecules to organ systems in order to gain quantitative understanding of biological function and phenotypes. Predictive multi-scale models and their driving biological research problems together address issues in modeling of sub-cellular biophysics, building molecular modeling tools to accelerate discovery, and defining tools for patient-specific multi-scale modeling. NBCR furthers these driving problems by developing tools and models based on rapid advances in mathematics and information technology, incorporating them into NBCR pipelines or problem solving environments, and addressing the inevitable changes in the underlying cyber-infrastructure technologies and continually adapting codes over time. Their technology focus integrates both the biological applications and the underlying support software into reproducible science workflows that can function across a number of physical infrastructures.

Abbreviations: NBCR

Synonyms: NBCR - National Biomedical Computation Resource

Resource Type: biomedical technology research center, training resource

Keywords: computation, molecule, visualization, software, cyberinfrastructure, biomedical, computing, informatics, computational tool, modeling, simulation, data analysis, query, integration, image processing, grid computing, cluster, computing and informatics technology center

Funding: NIGMS GM103426;
NCRR P41 RR08605

Resource Name: National Biomedical Computation Resource

Resource ID: SCR_002656

Alternate IDs: nif-0000-22270

Record Creation Time: 20220129T080214+0000

Record Last Update: 20250329T060203+0000

Ratings and Alerts

No rating or validation information has been found for National Biomedical Computation Resource.

No alerts have been found for National Biomedical Computation Resource.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Reyna-Beltrán E, et al. (2018) The Candida albicans ENO1 gene encodes a transglutaminase involved in growth, cell division, morphogenesis, and osmotic protection. The Journal of biological chemistry, 293(12), 4304.

Phan S, et al. (2017) 3D reconstruction of biological structures: automated procedures for alignment and reconstruction of multiple tilt series in electron tomography. Advanced structural and chemical imaging, 2(1), 8.

Kumar M, et al. (2017) Genome-Wide Identification and Analysis of Genes, Conserved between japonica and indica Rice Cultivars, that Respond to Low-Temperature Stress at the Vegetative Growth Stage. Frontiers in plant science, 8, 1120.

Magaña-Cerino JM, et al. (2017) Identification and functional analysis of c.422_423InsT, a novel mutation of the HNF1A gene in a patient with diabetes. Molecular genetics & genomic medicine, 5(1), 50.

Yoo YH, et al. (2017) OsPhyB-Mediating Novel Regulatory Pathway for Drought Tolerance in Rice Root Identified by a Global RNA-Seq Transcriptome Analysis of Rice Genes in Response to Water Deficiencies. Frontiers in plant science, 8, 580.

Yang PC, et al. (2016) A Computational Modeling and Simulation Approach to Investigate Mechanisms of Subcellular cAMP Compartmentation. PLoS computational biology, 12(7), e1005005.

Wagner JR, et al. (2016) Emerging Computational Methods for the Rational Discovery of Allosteric Drugs. Chemical reviews, 116(11), 6370.

Fan L, et al. (2016) Material stiffness parameters as potential predictors of presence of left ventricle myocardial infarction: 3D echo-based computational modeling study. Biomedical engineering online, 15, 34.

Blachly PG, et al. (2015) Broken-Symmetry DFT Computations for the Reaction Pathway of IspH, an Iron-Sulfur Enzyme in Pathogenic Bacteria. Inorganic chemistry, 54(13), 6439.

Kaus JW, et al. (2015) Enhanced ligand sampling for relative protein-ligand binding free energy calculations. The journal of physical chemistry. B, 119(20), 6190.

Shalaeva DN, et al. (2015) Modeling of interaction between cytochrome c and the WD domains of Apaf-1: bifurcated salt bridges underlying apoptosome assembly. Biology direct, 10, 29.

Lindert S, et al. (2013) Farnesyl diphosphate synthase inhibitors from in silico screening. Chemical biology & drug design, 81(6), 742.

Wang Y, et al. (2011) Enhanced Lipid Diffusion and Mixing in Accelerated Molecular Dynamics. Journal of chemical theory and computation, 7(10), 3199.

Durrant JD, et al. (2010) A multidimensional strategy to detect polypharmacological targets in the absence of structural and sequence homology. PLoS computational biology, 6(1), e1000648.

Durrant JD, et al. (2010) Novel naphthalene-based inhibitors of Trypanosoma brucei RNA editing ligase 1. PLoS neglected tropical diseases, 4(8), e803.