Resource Summary Report

Generated by Kravitz on Sep 10, 2026

LAPACK linear algebra library

RRID:SCR_008661
Type: Tool

Proper Citation

LAPACK linear algebra library (RRID:SCR_008661)

Resource Information

URL: https://simtk.org/home/lapack

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Description: This project is the SimTK Core implementation of the extremely reliable, high speed linear algebra package LAPACK and the underlying BLAS library on which LAPACK is built. It uses ATLAS to generate hand tuned BLAS kernels for a variety of hardware platforms, including multiprocessors, using a variety of operating systems including Windows, Mac, and Red Hat Linux. These platforms are pre-built and make the binaries available as a single shared library which can be conveniently used by any program. This means that users who are not experts in high performance scientific computation can nonetheless use the fastest linear algebra methods available for their machines.

Synonyms: LAPACK

Resource Type: data or information resource, database, documentation generation software, software application, software development tool, software resource

Keywords: BLAS, linear algebra, database

Funding: NIGMS U54 GM072970

Resource Name: LAPACK linear algebra library

Resource ID: SCR_008661

Alternate IDs: nif-0000-33176

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260905T132626+0000

Ratings and Alerts

No rating or validation information has been found for LAPACK linear algebra library.

No alerts have been found for LAPACK linear algebra library.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

Listed below are recent publications. The full list is available at Kravitz .

Zhang Y, et al. (2026) RamEx: an R package for high-throughput microbial ramanome analyses with accurate quality assessment. Microbiome, 14(1).

Brigido WJH, et al. (2025) The line follower robot: a meta-analytic approach. PeerJ. Computer science, 11, e2744.

Musial M, et al. (2024) Multireference Fock Space Coupled-Cluster Method for the (3,0) Sector. The journal of physical chemistry. A, 128(44), 9670.

Gygi F, et al. (2023) All-Electron Plane-Wave Electronic Structure Calculations. Journal of chemical theory and computation, 19(4), 1300.

Stephanovich VA, et al. (2022) Stabilization of 1D solitons by fractional derivatives in systems with quintic nonlinearity. Scientific reports, 12(1), 384.

Fr??hlich F, et al. (2022) Fides: Reliable trust-region optimization for parameter estimation of ordinary differential equation models. PLoS computational biology, 18(7), e1010322.

Echave J, et al. (2021) Fast computational mutation-response scanning of proteins. PeerJ, 9, e11330.

Isupov K, et al. (2020) Performance data of multiple-precision scalar and vector BLAS operations on CPU and GPU. Data in brief, 30, 105506.

Gjennestad MA, et al. (2020) Thermodynamic Stability of Volatile Droplets and Thin Films Governed by Disjoining Pressure in Open and Closed Containers. Langmuir : the ACS journal of surfaces and colloids, 36(27), 7879.

Yageta S, et al. (2019) CH2 domain orientation of human immunoglobulin G in solution: Structural comparison of glycosylated and aglycosylated Fc regions using small-angle X-ray scattering. mAbs, 11(3), 453.

Klawer EME, et al. (2019) Improved repeatability of dynamic contrast-enhanced MRI using the complex MRI signal to derive arterial input functions: a test-retest study in prostate cancer patients. Magnetic resonance in medicine, 81(5), 3358.

Denarie L, et al. (2018) Segmenting Proteins into Tripeptides to Enhance Conformational Sampling with Monte Carlo Methods. Molecules (Basel, Switzerland), 23(2).

Spasic A, et al. (2018) Improving RNA nearest neighbor parameters for helices by going beyond the two-state model. Nucleic acids research, 46(10), 4883.

Huang H, et al. (2017) Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 547(7662), 173.

Sulimov AV, et al. (2017) Evaluation of the novel algorithm of flexible ligand docking with moveable target-protein atoms. Computational and structural biotechnology journal, 15, 275.

Shao YC, et al. (2017) The key energy scales of Gd-based metallofullerene determined by resonant inelastic x-ray scattering spectroscopy. Scientific reports, 7(1), 8125.

Wittenburg D, et al. (2016) Covariance Between Genotypic Effects and its Use for Genomic Inference in Half-Sib Families. G3 (Bethesda, Md.), 6(9), 2761.

DeMarse TB, et al. (2016) Feed-Forward Propagation of Temporal and Rate Information between Cortical Populations during Coherent Activation in Engineered In Vitro Networks. Frontiers in neural circuits, 10, 32.

Pocrnic I, et al. (2016) The Dimensionality of Genomic Information and Its Effect on Genomic Prediction. Genetics, 203(1), 573.

Huang Y, et al. (2016) Using 3dRPC for RNA-protein complex structure prediction. Biophysics reports, 2(5), 95.