

Resource Summary Report

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ggforce

RRID:SCR_022575

Type: Tool

Proper Citation

ggforce (RRID:SCR_022575)

Resource Information

URL: <https://CRAN.R-project.org/package=ggforce>

Proper Citation: ggforce (RRID:SCR_022575)

Description: Software R package providing missing functionality to ggplot2 through extension system introduced with ggplot2 v2.0.0.

Resource Type: software toolkit, software resource

Keywords: missing functionality, ggplot2, extension system

Availability: Free, Available for download, Freely available

Resource Name: ggforce

Resource ID: SCR_022575

Alternate URLs: <https://github.com/thomasp85/ggforce/>, <https://ggforce.data-imaginist.com/>

License: MIT license

Record Creation Time: 20220722T050156+0000

Record Last Update: 20260810T040819+0000

Ratings and Alerts

No rating or validation information has been found for ggforce.

No alerts have been found for ggforce.

Data and Source Information

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. PLoS biology, 24(6), e3003855.

Shiraz MG, et al. (2025) Young rat microbiota extracts strongly inhibit fibrillation of α -synuclein and protect neuroblastoma cells and zebrafish against α -synuclein toxicity. Molecules and cells, 48(1), 100161.

Schall PZ, et al. (2025) Integrative Genotyping and Analysis of Canine Structural Variation Using Long-read and Short-read Data. Genome biology and evolution, 17(10).

Peskett TR, et al. (2025) A network of P-body and Whi3 condensates adjusts cell fate decisions to cellular context. Molecular cell, 85(19), 3661.

Loh CA, et al. (2024) High-fidelity, large-scale targeted profiling of microsatellites. Genome research, 34(7), 1008.

Ultsch A, et al. (2024) Augmenting small biomedical datasets using generative AI methods based on self-organizing neural networks. Briefings in bioinformatics, 26(1).

Lötsch J, et al. (2024) Revisiting Fold-Change Calculation: Preference for Median or Geometric Mean over Arithmetic Mean-Based Methods. Biomedicines, 12(8).