

# Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

## ggforce

RRID:SCR\_022575

Type: Tool

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### Proper Citation

ggforce (RRID:SCR\_022575)

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### 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 resource, software toolkit

**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:** 20260905T133311+0000

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### Ratings and Alerts

No rating or validation information has been found for ggforce.

No alerts have been found for ggforce.

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### 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 [PRECISE-TBI](#) .

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  $\alpha$ -synuclein and protect neuroblastoma cells and zebrafish against  $\alpha$ -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.

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

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