

Resource Summary Report

Generated by SPARC SAWG on Aug 28, 2026

Pennsylvania State University RISE Core Facility

RRID:SCR_026426

Type: Tool

Proper Citation

Pennsylvania State University RISE Core Facility (RRID:SCR_026426)

Resource Information

URL: <https://www.icds.psu.edu/rise/>

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Description: Core team of computational scientists and software engineers provide services to bring high-performance computing to research projects under the Institute of Computational and Data Sciences at the Pennsylvania State University.

Abbreviations: RISE

Synonyms: Research Innovations with Scientists and Engineers, Pennsylvania State University Research Innovations with Scientists and Engineers Core Facility

Resource Type: access service resource, computational service resource, core facility, service resource

Keywords: expert consultation, high-performance computing services,

Availability: Restricted

Resource Name: Pennsylvania State University RISE Core Facility

Resource ID: SCR_026426

Record Creation Time: 20250215T060332+0000

Record Last Update: 20260821T194327+0000

Ratings and Alerts

No rating or validation information has been found for Pennsylvania State University RISE Core Facility.

No alerts have been found for Pennsylvania State University RISE Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Vu QV, et al. (2026) Native entanglement misfolding contributes to age-associated structural changes across the *Saccharomyces cerevisiae* proteome. bioRxiv : the preprint server for biology.

Whitney J, et al. (2026) Game, Set, and Match: A Scoping Review of Matching Characteristics for Control and Intervention Groups in Adaptive Behavioral Interventions for Physical Activity or Healthy Eating Designs for Populations with Overweight and Obesity. Behavioral medicine (Washington, D.C.), 1.

Amoah EI, et al. (2025) FloralArea: AI-powered algorithm for automated calculation of floral area from flower images to support plant and pollinator research. PloS one, 20(9), e0332165.

Sitarik I, et al. (2025) A widespread protein misfolding mechanism is differentially rescued in vitro by chaperones based on gene essentiality. Nature communications, 16(1), 10870.