

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

PASTA

RRID:SCR_008770

Type: Tool

Proper Citation

PASTA (RRID:SCR_008770)

Resource Information

URL: <http://genome.ufl.edu/rivalab/pasta/>

Proper Citation: PASTA (RRID:SCR_008770)

Description: A complete pipeline for the analysis of alternative splicing using RNA-Sequencing data.

Abbreviations: PASTA

Synonyms: Patterned Alignments for Splicing and Transcriptome Analysis

Resource Type: software resource

Resource Name: PASTA

Resource ID: SCR_008770

Alternate IDs: OMICS_01247

Record Creation Time: 20220129T080249+0000

Record Last Update: 20260912T195708+0000

Ratings and Alerts

No rating or validation information has been found for PASTA.

No alerts have been found for PASTA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Zhang T, et al. (2026) Phylogenomic profile of exon-intron organization across angiosperms, their relationships with protein domains, and functional implications. *Nature communications*, 17(1), 106.

Moderer T, et al. (2026) Assessment of the biochemical basis underlying the resistance against systemic amyloidosis. *Scientific reports*, 16(1), 1313.

Raudabaugh DB, et al. (2026) Variation in cloacal microbiota of Canada goose (*Branta canadensis*) across rural and urban areas in Illinois, USA. *Frontiers in microbiomes*, 5, 1820309.

Escobedo-González FC, et al. (2026) Charged membrane interfaces reshape the nucleation landscape of RIPK3 amyloid variants. *European biophysics journal : EBJ*.

Shen C, et al. (2025) TIP3 and TIP3-fast: Improved abundance profiling in metagenomics. *PLoS computational biology*, 21(4), e1012593.

Aerts H, et al. (2025) Foundation model embeddings for quantitative tumor imaging biomarkers. *Research square*.

Stickelman Z, et al. (2025) Expanding the Riboglow-FLIM Toolbox with Different Fluorescence Lifetime-Producing RNA Tags. *Biochemistry*, 64(11), 2429.

Errico S, et al. (2025) Structural commonalities determined by physicochemical principles in the complex polymorphism of the amyloid state of proteins. *The Biochemical journal*, 482(2), 87.

Fischer I, et al. (2025) Analyses of exon 4a structure reveal unique properties of Big tau. *bioRxiv : the preprint server for biology*.

Chiriac MC, et al. (2025) Ecological success in freshwater lakes: insights from novel cultivated lineages of the abundant Nanopelagicales order. *Microbiome*, 14(1), 27.

Zhang Y, et al. (2024) Dynamic evolution of the heterochromatin sensing histone demethylase IBM1. *PLoS genetics*, 20(7), e1011358.

Seipp RP, et al. (2024) A secreted Tapasin isoform impairs cytotoxic T lymphocyte recognition by disrupting exogenous MHC class I antigen presentation. *Frontiers in immunology*, 15, 1525136.

Jangir PK, et al. (2023) The evolution of colistin resistance increases bacterial resistance to host antimicrobial peptides and virulence. *eLife*, 12.

Kravchenko SV, et al. (2022) Multiple Antimicrobial Effects of Hybrid Peptides Synthesized Based on the Sequence of Ribosomal S1 Protein from *Staphylococcus aureus*. *International journal of molecular sciences*, 23(1).

Grishin SY, et al. (2021) Identification of Amyloidogenic Regions in *Pseudomonas aeruginosa* Ribosomal S1 Protein. *International journal of molecular sciences*, 22(14).

Grishin SY, et al. (2021) Is It Possible to Create Antimicrobial Peptides Based on the Amyloidogenic Sequence of Ribosomal S1 Protein of *P. aeruginosa*? *International journal of molecular sciences*, 22(18).

Li Z, et al. (2020) Inferring putative ancient whole-genome duplications in the 1000 Plants (1KP) initiative: access to gene family phylogenies and age distributions. *GigaScience*, 9(2).

Park H, et al. (2017) Towards the development of a sustainable soya bean-based feedstock for aquaculture. *Plant biotechnology journal*, 15(2), 227.

Tang S, et al. (2013) PASTA: splice junction identification from RNA-sequencing data. *BMC bioinformatics*, 14, 116.