

# Resource Summary Report

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## BinPacker

RRID:SCR\_017038

Type: Tool

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### Proper Citation

BinPacker (RRID:SCR\_017038)

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### Resource Information

**URL:** <https://github.com/macmanes-lab/BinPacker/blob/master/README>

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**Description:** Software tool as de novo transcriptome assembler for RNA-Seq data. Used to assemble full length transcripts by remodeling problem as tracking set of trajectories of items over splicing graph. Input RNA-Seq reads in fasta or fastq format, and output all assembled candidate transcripts in fasta format. Operating system Unix/Linux.

**Resource Type:** data analysis software, software resource, data processing software, software application

**Defining Citation:** [PMID:26894997](#)

**Keywords:** de novo, transcriptome, assembler, RNAseq, data, full, length, transcript, bio.tools

**Funding:** National Natural Science Foundation of China ;  
NSF 1553680;  
NCRR P20 RR01 6460;  
NIGMS P20 GM103429

**Availability:** Free, Available for download, Freely available

**Resource Name:** BinPacker

**Resource ID:** SCR\_017038

**Alternate IDs:** OMICS\_11199, biotools:binpacker

**Alternate URLs:**

[http://sourceforge.net/projects/transcriptomeassembly/files/BinPacker\\_1.0.tar.gz/download](http://sourceforge.net/projects/transcriptomeassembly/files/BinPacker_1.0.tar.gz/download),  
[http://sourceforge.net/projects/transcriptomeassembly/files/BinPacker\\_binary.tar.gz/download](http://sourceforge.net/projects/transcriptomeassembly/files/BinPacker_binary.tar.gz/download),  
<https://bio.tools/binpacker>

**License:** GNU GPL v3

**Record Creation Time:** 20220129T080333+0000

**Record Last Update:** 20250425T060213+0000

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## Ratings and Alerts

No rating or validation information has been found for BinPacker.

No alerts have been found for BinPacker.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Xie B, et al. (2022) Dynamic genetic differentiation drives the widespread structural and functional convergent evolution of snake venom proteinaceous toxins. *BMC biology*, 20(1), 4.

Sharma A, et al. (2021) Transcriptome profiling reveal key hub genes in co-expression networks involved in Iridoid glycosides biosynthetic machinery in *Picrorhiza kurroa*. *Genomics*, 113(5), 3381.

Karmeinski D, et al. (2021) Transcriptomics provides a robust framework for the relationships of the major clades of cladobranch sea slugs (Mollusca, Gastropoda, Heterobranchia), but fails to resolve the position of the enigmatic genus *Embletonia*. *BMC ecology and evolution*, 21(1), 226.

Niu J, et al. (2020) Multi-omic approach provides insights into osmoregulation and osmoconformation of the crab *Scylla paramamosain*. *Scientific reports*, 10(1), 21771.

Kashyap A, et al. (2020) Pan-tissue transcriptome analysis of long noncoding RNAs in the American beaver *Castor canadensis*. *BMC genomics*, 21(1), 153.

Soorni A, et al. (2019) Transcriptome Landscape Variation in the Genus *Thymus*. *Genes*,

10(8).

Söllner JF, et al. (2019) Exploiting orthology and de novo transcriptome assembly to refine target sequence information. *BMC medical genomics*, 12(1), 69.

Bushmanova E, et al. (2019) rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. *GigaScience*, 8(9).

Oliphant A, et al. (2018) Transcriptomic analysis of crustacean neuropeptide signaling during the moult cycle in the green shore crab, *Carcinus maenas*. *BMC genomics*, 19(1), 711.

Jarett JK, et al. (2017) Comparative Genomics of Color Morphs In the Coral *Montastraea cavernosa*. *Scientific reports*, 7(1), 16039.