

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

[tbl2asn](#)

RRID:SCR_016636

Type: Tool

Proper Citation

tbl2asn (RRID:SCR_016636)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/genbank/tbl2asn2/>

Proper Citation: tbl2asn (RRID:SCR_016636)

Description: Software tool as a command-line program that automates the creation of sequence records for submission to GenBank. Records need no additional manual editing before submission.

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

Keywords: command, line, program, automate, creation, sequence, record, submit, data, GenBank

Availability: Free, Freely available

Resource Name: tbl2asn

Resource ID: SCR_016636

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260905T133051+0000

Ratings and Alerts

No rating or validation information has been found for tbl2asn.

No alerts have been found for tbl2asn.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Pecrix Y, et al. (2026) Phylogenomics of *Plasmopara halstedii* Reveals Genomic Regions Associated With the Breakdown of Sunflower Downy Mildew Resistance Genes. *Molecular ecology*, 35(4), e70270.

Mascarenhas Dos Santos AC, et al. (2023) Telomere-to-Telomere genome assemblies of human-infecting *Encephalitozoon* species. *BMC genomics*, 24(1), 237.

Khoshakhlagh A, et al. (2022) Investigation of diverse biosynthetic secondary metabolites gene clusters using genome mining of indigenous *Streptomyces* strains isolated from saline soils in Iran. *Iranian journal of microbiology*, 14(6), 881.

González-Vázquez R, et al. (2022) Genomic and Biochemical Characterization of *Bifidobacterium pseudocatenulatum* JCLA3 Isolated from Human Intestine. *Microorganisms*, 10(11).

Wang ZF, et al. (2021) The complete chloroplast genome of *Aganope dinghuensis* (Fabaceae). *Mitochondrial DNA. Part B, Resources*, 6(2), 460.

Pons J, et al. (2021) Aln2tbl: building a mitochondrial features table from a assembly alignment in fasta format. *Mitochondrial DNA. Part B, Resources*, 6(9), 2732.

Pace J, et al. (2020) PuMA: A papillomavirus genome annotation tool. *Virus evolution*, 6(2), veaa068.

Tisza MJ, et al. (2020) Discovery of several thousand highly diverse circular DNA viruses. *eLife*, 9.

Stroehlein AJ, et al. (2019) High-quality *Schistosoma haematobium* genome achieved by single-molecule and long-range sequencing. *GigaScience*, 8(9).

An K, et al. (2018) Spinal PKC activation - Induced neuronal HMGB1 translocation contributes to hyperalgesia in a bone cancer pain model in rats. *Experimental neurology*, 303, 80.

Raymond O, et al. (2018) The *Rosa* genome provides new insights into the domestication of modern roses. *Nature genetics*, 50(6), 772.