Resource Summary Report

Generated by <u>NIF</u> on May 16, 2025

ACT: Artemis Comparison Tool

RRID:SCR_004507 Type: Tool

Proper Citation

ACT: Artemis Comparison Tool (RRID:SCR_004507)

Resource Information

URL: http://www.sanger.ac.uk/resources/software/act/

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Description: A free tool for displaying pairwise comparisons between two or more DNA sequences. It can be used to identify and analyze regions of similarity and difference between genomes and to explore conservation of synteny, in the context of the entire sequences and their annotation. It is based on the software for Artemis, the genome viewer and annotation tool. ACT runs on UNIX, GNU/Linux, Macintosh and MS Windows systems. It can read complete EMBL and GENBANK entries or sequences in FASTA or raw format. Other sequence features can be in EMBL, GENBANK or GFF format.

Abbreviations: ACT

Synonyms: Artemis Comparison Tool

Resource Type: software resource

Defining Citation: PMID:15976072

Keywords: dna sequence, genome, synteny, pairwise comparison

Funding: Wellcome Trust

Availability: GNU General Public License

Resource Name: ACT: Artemis Comparison Tool

Resource ID: SCR_004507

Alternate IDs: OMICS_00928, nlx_48986

Record Creation Time: 20220129T080225+0000

Record Last Update: 20250420T014225+0000

Ratings and Alerts

No rating or validation information has been found for ACT: Artemis Comparison Tool.

No alerts have been found for ACT: Artemis Comparison Tool.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Knight DR, et al. (2021) Major genetic discontinuity and novel toxigenic species in Clostridioides difficile taxonomy. eLife, 10.

Flores-Ríos R, et al. (2019) The Type IV Secretion System of ICEAfe1: Formation of a Conjugative Pilus in Acidithiobacillus ferrooxidans. Frontiers in microbiology, 10, 30.

Eaton K, et al. (2018) Replication Study: Intestinal inflammation targets cancer-inducing activity of the microbiota. eLife, 7.

Han G, et al. (2016) Genome of Cnaphalocrocis medinalis Granulovirus, the First Crambidae-Infecting Betabaculovirus Isolated from Rice Leaffolder to Sequenced. PloS one, 11(2), e0147882.

Jones L, et al. (2014) Adaptive genomic structural variation in the grape powdery mildew pathogen, Erysiphe necator. BMC genomics, 15(1), 1081.

Tamamura Y, et al. (2013) Complete nucleotide sequences of virulence-resistance plasmids carried by emerging multidrug-resistant Salmonella enterica Serovar Typhimurium isolated from cattle in Hokkaido, Japan. PloS one, 8(10), e77644.

Karlyshev AV, et al. (2013) Unusual features in organisation of capsular polysacchariderelated genes of C. jejuni strain X. Gene, 522(1), 37.

Harrison OB, et al. (2013) Description and nomenclature of Neisseria meningitidis capsule

locus. Emerging infectious diseases, 19(4), 566.

Ferrelli ML, et al. (2012) Genome of Epinotia aporema granulovirus (EpapGV), a polyorganotropic fast killing betabaculovirus with a novel thymidylate kinase gene. BMC genomics, 13, 548.

Brüggemann H, et al. (2012) CRISPR/cas loci of type II Propionibacterium acnes confer immunity against acquisition of mobile elements present in type I P. acnes. PloS one, 7(3), e34171.

Asakura H, et al. (2012) Molecular evidence for the thriving of Campylobacter jejuni ST-4526 in Japan. PloS one, 7(11), e48394.

Rashid MH, et al. (2012) A Yersinia pestis-specific, lytic phage preparation significantly reduces viable Y. pestis on various hard surfaces experimentally contaminated with the bacterium. Bacteriophage, 2(3), 168.

Moraes Barros RR, et al. (2012) Anatomy and evolution of telomeric and subtelomeric regions in the human protozoan parasite Trypanosoma cruzi. BMC genomics, 13, 229.

Cantu D, et al. (2011) Next generation sequencing provides rapid access to the genome of Puccinia striiformis f. sp. tritici, the causal agent of wheat stripe rust. PloS one, 6(8), e24230.

Hu S, et al. (2011) Comparative genomic and transcriptomic analysis revealed genetic characteristics related to solvent formation and xylose utilization in Clostridium acetobutylicum EA 2018. BMC genomics, 12, 93.