

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

Alien hunter

RRID:SCR_004575

Type: Tool

Proper Citation

Alien hunter (RRID:SCR_004575)

Resource Information

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

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Description: Alien_hunter is an application for the prediction of putative Horizontal Gene Transfer (HGT) events with the implementation of Interpolated Variable Order Motifs (IVOMs). This program is free software; you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation; either version 2 of the License, or (at your option) any later version. An IVOM approach exploits compositional biases using variable order motif distributions and captures more reliably the local composition of a sequence compared to fixed-order methods. Optionally the predictions can be parsed into a 2-state 2nd order Hidden Markov Model (HMM), in a change-point detection framework, to optimize the localization of the boundaries of the predicted regions. The predictions (embl format) can be automatically loaded into the freely available Artemis genome viewer.

Synonyms: Alien_hunter: Interpolated Variable Order Motifs for Identification of Horizontally Acquired DNA

Resource Type: software application, software resource

Defining Citation: [PMID:16837528](#)

Resource Name: Alien hunter

Resource ID: SCR_004575

Alternate IDs: nlx_56835

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260727T040342+0000

Ratings and Alerts

No rating or validation information has been found for Alien hunter.

No alerts have been found for Alien hunter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Gabrielsen C, et al. (2017) Characterization of the virulence potential of *Staphylococcus condimenti* isolated from a patient with severe soft tissue infection. *New microbes and new infections*, 18, 8.

Lu B, et al. (2016) Computational methods for predicting genomic islands in microbial genomes. *Computational and structural biotechnology journal*, 14, 200.

Che D, et al. (2014) Identifying pathogenicity islands in bacterial pathogenomics using computational approaches. *Pathogens (Basel, Switzerland)*, 3(1), 36.