## **Resource Summary Report**

Generated by NIF on Apr 28, 2025

# <u>xAtlas</u>

RRID:SCR\_022987 Type: Tool

**Proper Citation** 

xAtlas (RRID:SCR\_022987)

#### **Resource Information**

URL: https://github.com/jfarek/xatlas

Proper Citation: xAtlas (RRID:SCR\_022987)

**Description:** Software tool as variant caller for SNVs and small indels. Implemented as software application written in C++ .

Resource Type: software application, software resource

Keywords: Single nucleotide variants, variant caller, SNVs, small indels

Funding:

Availability: Free, Available for download, Freely available

**Resource Name:** xAtlas

Resource ID: SCR\_022987

License: BSD license

**Record Creation Time:** 20221122T050206+0000

Record Last Update: 20250428T054340+0000

#### **Ratings and Alerts**

No rating or validation information has been found for xAtlas.

No alerts have been found for xAtlas.

### Data and Source Information

Source: <u>SciCrunch Registry</u>

## **Usage and Citation Metrics**

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Farek J, et al. (2022) xAtlas: scalable small variant calling across heterogeneous nextgeneration sequencing experiments. GigaScience, 12.

Loka TP, et al. (2019) Reliable variant calling during runtime of Illumina sequencing. Scientific reports, 9(1), 16502.