

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 2, 2026

XYalign

RRID:SCR_016661

Type: Tool

Proper Citation

XYalign (RRID:SCR_016661)

Resource Information

URL: <https://github.com/WilsonSayresLab/XYalign>

Proper Citation: XYalign (RRID:SCR_016661)

Description: Software tool for identifying, understanding, and correcting technical biases on the sex chromosomes in next generation sequencing data.

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

Defining Citation: [DOI:10.1101/346940](https://doi.org/10.1101/346940)

Keywords: correct, technical, bias, sex, chromosome, next, generation, sequencing, data

Funding: NIGMS R35 GM124827

Availability: Free, Available for download, Freely available

Resource Name: XYalign

Resource ID: SCR_016661

License: GNU General Public License

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260801T190550+0000

Ratings and Alerts

No rating or validation information has been found for XYalign.

No alerts have been found for XYalign.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Webster TH, et al. (2019) Identifying, understanding, and correcting technical artifacts on the sex chromosomes in next-generation sequencing data. GigaScience, 8(7).