

Resource Summary Report

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Peter MacCallum Cancer Centre Bioinformatics Core Facility

RRID:SCR_025901

Type: Tool

Proper Citation

Peter MacCallum Cancer Centre Bioinformatics Core Facility (RRID:SCR_025901)

Resource Information

URL: <https://www.petermac.org/research/research-technologies/bioinformatics>

Proper Citation: Peter MacCallum Cancer Centre Bioinformatics Core Facility (RRID:SCR_025901)

Description: Provides services for data analysis, pipeline management, and artificial intelligence research and operations. Data types analysed by the core include whole-genome and whole-exome sequencing, targeted re-sequencing, radiological images, RNA-sequencing, single-cell RNA sequencing, ChIP-sequencing, NanoString and various types of microarray data. Core also develops and maintains software infrastructure required for bioinformatics processing, including pipelines and cloud provision systems.

Synonyms: Peter MacCallum Cancer Center Bioinformatics Core Facility

Resource Type: access service resource, core facility, service resource

Keywords: ABRF, whole-genome, whole-exome sequencing, targeted re-sequencing, radiological images, RNA-sequencing, single-cell RNA sequencing, ChIP-sequencing, NanoString, microarray data,

Resource Name: Peter MacCallum Cancer Centre Bioinformatics Core Facility

Resource ID: SCR_025901

Alternate IDs: ABRF_2955

Alternate URLs: <https://coremarketplace.org/?FacilityID=2955&citation=1>

Record Creation Time: 20241018T053244+0000

Record Last Update: 20260805T044552+0000

Ratings and Alerts

No rating or validation information has been found for Peter MacCallum Cancer Centre Bioinformatics Core Facility.

No alerts have been found for Peter MacCallum Cancer Centre Bioinformatics Core Facility.

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 [RRID](#) .

Kader T, et al. (2026) Phylogenetic analysis of paired breast carcinomas identifies genetic events associated with clonal recurrence and invasive progression. The Journal of pathology, 268(1), 1.