

SeqAn Usability Analyzer

Thank you for helping us to improve SeqAn!

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Windows `C:\Users\[username]\.SUA.ID`

Linux `/home/[username]/.SUA.ID`

Mac OS X `/Users/[username]/.SUA.ID`



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www.seqan.de

SeqAn is an open source C++ library of efficient algorithms and data structures for the analysis of sequences with the focus on biological data. Our library applies a unique generic design that guarantees high performance, generality, extensibility, and integration with other libraries. SeqAn is easy to use and simplifies the development of new software tools with a minimal loss of performance.

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www.seqan-biostore.de

The VIP BioStore project addresses the current bottleneck in NGS based data analysis. It is meant to be a catalyst for bringing state-of-the-art algorithmic research to a broader community of developers and and the same time enable researchers in the biomedical sciences to have easy access to such tools via a distribution and execution platform.

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Debug

Last Fingerprint

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