

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

[MaxSprout](#)

RRID:SCR_010687

Type: Tool

Proper Citation

MaxSprout (RRID:SCR_010687)

Resource Information

URL: <http://www.ebi.ac.uk/Tools/maxsprout/>

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Description: A database algorithm for generating protein backbone and side chain coordinates from a C(alpha) trace. The backbone is assembled from fragments taken from known structures. Side chain conformations are optimized in rotamer space using a rough potential energy function to avoid clashes.

Synonyms: MaxSprout Tool for Reconstruction of 3D coordinates from C(alpha) trace

Resource Type: service resource, production service resource

Defining Citation: [PMID:2002501](#)

Resource Name: MaxSprout

Resource ID: SCR_010687

Alternate IDs: nlx_79292

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260810T040526+0000

Ratings and Alerts

No rating or validation information has been found for MaxSprout.

No alerts have been found for MaxSprout.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Kaschner M, et al. (2017) A combination of mutational and computational scanning guides the design of an artificial ligand-binding controlled lipase. Scientific reports, 7, 42592.

Adams DJ, et al. (2015) Architecture of the Synaptophysin/Synaptobrevin Complex: Structural Evidence for an Entropic Clustering Function at the Synapse. Scientific reports, 5, 13659.