

Resource Summary Report

Generated by [dkNET](#) on Sep 14, 2026

CURVES plus

RRID:SCR_023268

Type: Tool

Proper Citation

CURVES plus (RRID:SCR_023268)

Resource Information

URL: http://gbio-pbil.ibcp.fr/tools/curves_plus/

Proper Citation: CURVES plus (RRID:SCR_023268)

Description: Web server for analyzing and visualizing helical, backbone and groove parameters of nucleic acid structures. Can also be used to analyse molecular dynamics trajectories., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: Curves+

Resource Type: software resource, web application

Defining Citation: [PMID:19625494](#), [PMID:21558323](#)

Keywords: analyzing, visualizing, helical, backbone and groove parameters, nucleic acid structures, molecular dynamics trajectories analysis,

Funding: Swiss National Science Foundation

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CURVES plus

Resource ID: SCR_023268

Alternate IDs: biotools:curves

Alternate URLs: <https://bio.tools/curves>

Record Creation Time: 20230210T050214+0000

Record Last Update: 20260912T200037+0000

Ratings and Alerts

No rating or validation information has been found for CURVES plus.

No alerts have been found for CURVES plus.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Li C, et al. (2025) High hydrostatic pressure promotes gene transcription via a cystathionine- γ -synthase domain-containing protein in the hyperthermophilic archaeon *Pyrococcus yayanosii*. *Nucleic acids research*, 53(1).

Bergonzo C, et al. (2025) Critical Assessment of RNA and DNA Structure Predictions via Artificial Intelligence: The Imitation Game. *Journal of chemical information and modeling*, 65(7), 3544.

Alejo JL, et al. (2024) Alternate conformational trajectories in ribosome translocation. *PLoS computational biology*, 20(8), e1012319.

Huang SC, et al. (2024) Targeting DNA junction sites by bis-intercalators induces topological changes with potent antitumor effects. *Nucleic acids research*, 52(15), 9303.

Karami Y, et al. (2024) Cysteine hyperoxidation rewires communication pathways in the nucleosome and destabilizes the dyad. *Computational and structural biotechnology journal*, 23, 1387.

Rihon J, et al. (2024) Structural insights into the morpholino nucleic acid/RNA duplex using the new XNA builder Ducque in a molecular modeling pipeline. *Nucleic acids research*, 52(6), 2836.

Ashwood B, et al. (2023) Direct monitoring of the thermodynamics and kinetics of DNA and RNA dinucleotide dehybridization from gaps and overhangs. *bioRxiv : the preprint server for biology*.

Tian FJ, et al. (2023) Universality in RNA and DNA deformations induced by salt, temperature change, stretching force, and protein binding. *Proceedings of the National Academy of Sciences of the United States of America*, 120(20), e2218425120.

Pavlin M, et al. (2023) Unveiling the interdomain dynamics of type II DNA topoisomerase through all-atom simulations: Implications for understanding its catalytic cycle. *Computational and structural biotechnology journal*, 21, 3746.

Pan W, et al. (2023) Structures of NF- κ B p52 homodimer-DNA complexes rationalize binding mechanisms and transcription activation. *eLife*, 12.

Bignon E, et al. (2022) Modeling the Enzymatic Mechanism of the SARS-CoV-2 RNA-Dependent RNA Polymerase by DFT/MM-MD: An Unusual Active Site Leading to High Replication Rates. *Journal of chemical information and modeling*, 62(17), 4261.

Jiang T, et al. (2021) Molecular Mechanisms Associated with Clustered Lesion-Induced Impairment of 8-oxoG Recognition by the Human Glycosylase OGG1. *Molecules (Basel, Switzerland)*, 26(21).

Carzaniga T, et al. (2021) A Bit Stickier, a Bit Slower, a Lot Stiffer: Specific vs. Nonspecific Binding of Gal4 to DNA. *International journal of molecular sciences*, 22(8).

Bignon E, et al. (2021) Recognition of a tandem lesion by DNA bacterial formamidopyrimidine glycosylases explored combining molecular dynamics and machine learning. *Computational and structural biotechnology journal*, 19, 2861.

Chawla M, et al. (2021) Replacing thymine with a strongly pairing fifth Base: A combined quantum mechanics and molecular dynamics study. *Computational and structural biotechnology journal*, 19, 1312.

Wan T, et al. (2021) Structural insights into the functional divergence of WhiB-like proteins in *Mycobacterium tuberculosis*. *Molecular cell*, 81(14), 2887.

Liebl K, et al. (2020) How global DNA unwinding causes non-uniform stress distribution and melting of DNA. *PloS one*, 15(5), e0232976.