

Resource Summary Report

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TANGO

RRID:SCR_001770

Type: Tool

Proper Citation

TANGO (RRID:SCR_001770)

Resource Information

URL: <http://tango.crg.es/>

Proper Citation: TANGO (RRID:SCR_001770)

Description: A computer algorithm to predict aggregation nucleating regions in proteins as well the effect of mutations and environmental conditions on the aggregation propensity of these regions.

Abbreviations: TANGO

Resource Type: software resource

Defining Citation: [PMID:15361882](#)

Keywords: polypeptide chain, polypeptide, peptide, protein, bio.tools

Availability: Free, Freely available

Resource Name: TANGO

Resource ID: SCR_001770

Alternate IDs: biotools:tango, OMICS_03859

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

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260808T185733+0000

Ratings and Alerts

No rating or validation information has been found for TANGO.

No alerts have been found for TANGO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 136 mentions in open access literature.

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

Yoon JG, et al. (2026) A predictive framework for stop-loss variants with C-terminal extensions. *Nucleic acids research*, 54(2).

Badia M, et al. (2026) Massively parallel quantification of mutational impact on IAPP amyloid formation. *Nature communications*, 17(1).

Lobo S, et al. (2026) amyloid-predict and LLPS-predict: Predicting phase separation propensities in the intrinsically disordered proteome. *Proceedings of the National Academy of Sciences of the United States of America*, 123(22), e2531932123.

Meleleo D, et al. (2026) An edge β -strand mutation turns ubiquitin into a pore-forming amyloid. *Protein science : a publication of the Protein Society*, 35(6), e70603.

Zúñiga L, et al. (2026) Toward the rational design of oncogenic TASK-3 channel inhibitor peptides and nanoconjugate complexes. *Frontiers in pharmacology*, 17, 1807764.

Afrin S, et al. (2026) Structural polymorphism of ex-vivo ALECT2 amyloid fibrils revealed by cryo-EM. *Nature communications*, 17(1).

Chen S, et al. (2026) Effete and Cullin 4 affect nuclear organization of the gypsy chromatin insulator. *BMC biology*, 24(1).

Adeosun AAR, et al. (2026) Structural determinants of ligand response specificity in the mast cell activating GPCR, MRGPRX2. *The Journal of biological chemistry*, 302(6), 113132.

Konstantoulea K, et al. (2026) A functional amyloid scaffold shapes insect egg coats. *bioRxiv : the preprint server for biology*.

Nguyen BA, et al. (2026) Cryo-EM reveals structural variability of apolipoprotein A-I amyloid fibrils across organs, mutations, and clinical presentations. *Nature communications*, 17(1).

Gil J, et al. (2026) Unique territorial and compartmental organization of chromosomes in the holocentric silkworm. *The EMBO journal*, 45(5), 1573.

Cao R, et al. (2026) Strategies for enhancing protein solubility: methods, applications, and prospects. *NPJ science of food*, 10(1).

Shulman M, et al. (2026) Exploratory analyses of clinical outcomes from the BII080 phase 1b study in mild Alzheimer's disease. *Nature aging*, 6(2), 445.

Avalos-Padilla Y, et al. (2026) Extracellular vesicles participate in proteostasis and heat shock adaptation in *Plasmodium falciparum*. *Emerging microbes & infections*, 15(1), 2686468.

Cima V, et al. (2026) Experimentally validated deep learning control of protein aggregation. *Communications chemistry*, 9(1).

Andrade CO, et al. (2026) Development and in vivo evaluation of novel humanized CD19 CAR-T cells for advanced B cell malignancies. *Frontiers in immunology*, 17, 1798748.

Errico S, et al. (2025) Structural commonalities determined by physicochemical principles in the complex polymorphism of the amyloid state of proteins. *The Biochemical journal*, 482(2), 87.

Kim H, et al. (2025) Determinants of Adherence and Satisfaction in Parkinson's Disease Exercise Programs: A Comparison of 16-Months of Adapted Tango vs. Supervised Walking. *Research square*.

Duan J, et al. (2025) AI-Guided Dual Strategy for Peptide Inhibitor Design Targeting Structural Polymorphs of α -Synuclein Fibrils. *Cells*, 14(23).

An Nguyen B, et al. (2025) Structural variability of apolipoprotein A-I amyloid fibrils across organs, mutations, and clinical presentations, revealed by cryo-EM. *bioRxiv : the preprint server for biology*.