

Resource Summary Report

Generated by [Kravitz](#) on Sep 16, 2026

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: 20260912T195531+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 [Kravitz](#) .

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

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.

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.

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

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*.

Shulman M, et al. (2026) Exploratory analyses of clinical outcomes from the BIIB080 phase 1b study in mild Alzheimer's disease. *Nature aging*, 6(2), 445.

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).

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.