

Resource Summary Report

Generated by RRID on Aug 2, 2026

Rosetta

RRID:SCR_025242

Type: Tool

Proper Citation

Rosetta (RRID:SCR_025242)

Resource Information

URL: <https://github.com/LatticeX-Foundation/Rosetta>

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Description: Software privacy-preserving framework based on TensorFlow. Integrates with mainstream privacy-preserving computation technologies, including cryptography, federated learning and trusted execution environment. Used to provide privacy-preserving solutions for artificial intelligence without requiring expertise in cryptography, federated learning and trusted execution environment. Rosetta reuses the APIs of TensorFlow and allows to transfer traditional TensorFlow codes into a privacy-preserving manner with minimal changes.

Resource Type: software resource, software application, source code

Keywords: privacy-preserving solutions, artificial intelligence, no expertise in cryptography, federated learning, trusted execution environment,

Availability: Free, Available for download, Freely available

Resource Name: Rosetta

Resource ID: SCR_025242

License: LGPL v3.0

Record Creation Time: 20240410T053248+0000

Record Last Update: 20260801T191314+0000

Ratings and Alerts

No rating or validation information has been found for Rosetta.

No alerts have been found for Rosetta.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Han Y, et al. (2025) Molecular simulations reveal intricate coupling between agonist-bound ??-adrenergic receptors and G protein. *iScience*, 28(2), 111741.

Gelman S, et al. (2024) Biophysics-based protein language models for protein engineering. *bioRxiv : the preprint server for biology*.

Berndsen ZT, et al. (2024) Repeat modules and N-linked glycans define structure and antigenicity of a critical enterotoxigenic *E. coli* adhesin. *PLoS pathogens*, 20(9), e1012241.

Ribeiro-Filho HV, et al. (2024) Exploring the potential of structure-based deep learning approaches for T cell receptor design. *PLoS computational biology*, 20(9), e1012489.

Felbinger N, et al. (2024) Proscan: a structure-based proline design web server. *Nucleic acids research*, 52(W1), W280.

Moreno-Manuel AI, et al. (2024) The Kir2.1E299V mutation increases atrial fibrillation vulnerability while protecting the ventricles against arrhythmias in a mouse model of short QT syndrome type 3. *Cardiovascular research*, 120(5), 490.

Carrasco JL, et al. (2024) Adaptation of turnip mosaic virus to *Arabidopsis thaliana* involves rewiring of VPg-host proteome interactions. *Virus evolution*, 10(1), veae055.

Oliva B, et al. (2024) Biochemical and inhibitor analysis of recombinant cellobiohydrolases from *Phanerochaete chrysosporium*. *Biotechnology for biofuels and bioproducts*, 17(1), 138.

Gudipati RK, et al. (2024) Deep quantification of substrate turnover defines protease subsite cooperativity. *Molecular systems biology*, 20(12), 1303.

Wei W, et al. (2024) Sequence-based engineering of pH-sensitive antibodies for tumor targeting or endosomal recycling applications. *mAbs*, 16(1), 2404064.