# Resource Summary Report

Generated by RRID on Apr 9, 2025

# 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:** source code, software resource, software application

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

**Funding:**

**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:** 20250409T062034+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.

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

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.

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.

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.

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.

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