

Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

REFOLD

RRID:SCR_007889

Type: Tool

Proper Citation

REFOLD (RRID:SCR_007889)

Resource Information

URL: <http://refold.med.monash.edu.au>

Proper Citation: REFOLD (RRID:SCR_007889)

Description: It contains entries for refolding protocols for a wide range of proteins. REFOLD provides a means of disseminating refolding protocols and techniques to the scientific community. A large number of recombinant proteins expressed in bacteria are insoluble and thus require renaturation. Identifying optimal conditions and methodology for refolding can be time consuming and often rate-limiting. To this end, REFOLD was designed to assist in the design and implementation of methodologies for the in vitro refolding of proteins. The database contains heavily annotated entries for the refolding of a wide range of proteins which can be searched via multiple parameters using either simple or advanced search functions. The database can also be browsed by categories such as structural class, family, or refolding method. The web interface allows a detailed, sortable, spreadsheet-like list of results allowing quick visualisation of search results. Each entry contains detailed information regarding the protein of interest, methods and conditions employed, as well as reference and links to the relevant journal publication. Effective use of hyperlinks in results pages also allows useful browsing of entries for other proteins sharing similar properties or methods. REFOLD also provides analysis of the database through graphical representation of the data. The available graphs show the breakdown of refolding records in the database according to different parameters, such as refolding method, protein constructs and various refolding conditions. REFOLD graphs can be found [here](#)., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: REFOLD

Resource Type: data or information resource, database

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: REFOLD

Resource ID: SCR_007889

Alternate IDs: r3d100010553

Alternate URLs: <https://doi.org/10.17616/R3PC96>, <https://doi.org/10.17616/R3PC96>

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260729T044214+0000

Ratings and Alerts

No rating or validation information has been found for REFOLD.

No alerts have been found for REFOLD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

McGuffin LJ, et al. (2023) Prediction of protein structures, functions and interactions using the IntFOLD7, MultiFOLD and ModFOLDdock servers. Nucleic acids research, 51(W1), W274.

Avila-Bonilla RG, et al. (2023) Comparative genomics and interactomics of polyadenylation factors for the prediction of new parasite targets: Entamoeba histolytica as a working model. Bioscience reports, 43(2).

Desagiacomo CCV, et al. (2021) Structural model and functional properties of an exo-polygalacturonase from Neosartorya glabra. International journal of biological macromolecules, 186, 909.

Javadmanesh A, et al. (2021) Antibacterial effects assessment on some livestock pathogens, thermal stability and proposing a probable reason for different levels of activity of thanatin. Scientific reports, 11(1), 10890.

Tan Y, et al. (2020) Novel Immunoglobulin Domain Proteins Provide Insights into Evolution and Pathogenesis of SARS-CoV-2-Related Viruses. mBio, 11(3).

Gogovi GK, et al. (2019) Modeling the Tertiary Structure of the Rift Valley Fever Virus L Protein. Molecules (Basel, Switzerland), 24(9).

Chew CH, et al. (2017) Heterologous expression of Plasmodium vivax apical membrane antigen 1 (PvAMA1) for binding peptide selection. PeerJ, 5, e3794.

- Ramón A, et al. (2014) Inclusion bodies: not that bad.... *Frontiers in microbiology*, 5, 56.
- de Marco A, et al. (2009) Strategies for successful recombinant expression of disulfide bond-dependent proteins in *Escherichia coli*. *Microbial cell factories*, 8, 26.
- McCusker E, et al. (2008) Refolding of G protein alpha subunits from inclusion bodies expressed in *Escherichia coli*. *Protein expression and purification*, 58(2), 342.
- Vohra RS, et al. (2007) Functional refolding of a recombinant C-type lectin-like domain containing intramolecular disulfide bonds. *Protein expression and purification*, 52(2), 415.
- Purbey PK, et al. (2006) pC6-2/caspase-6 system to purify glutathione-S-transferase-free recombinant fusion proteins expressed in *Escherichia coli*. *Nature protocols*, 1(4), 1820.
- Chow MK, et al. (2006) The REFOLD database: a tool for the optimization of protein expression and refolding. *Nucleic acids research*, 34(Database issue), D207.
- Chow MK, et al. (2006) REFOLD: an analytical database of protein refolding methods. *Protein expression and purification*, 46(1), 166.