

Resource Summary Report

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Critical Assessment of Techniques for Protein Structure Prediction

RRID:SCR_008434

Type: Tool

Proper Citation

Critical Assessment of Techniques for Protein Structure Prediction (RRID:SCR_008434)

Resource Information

URL: <http://predictioncenter.org/casp7/Casp7.html>

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Description: The main goal of CASP is to obtain an in-depth and objective assessment of our current abilities and inabilities in the area of protein structure prediction. To this end, participants will predict as much as possible about a set of soon to be known structures. These will be true predictions, not "post-dictions" made on already known structures. Sponsors: This resource is supported by the US National Library of Medicine (NIH/NLM), National Institute of General Medical Sciences (NIH/NIGMS), BioSapiens Network of Excellence, and HP Invent. Keywords: Clinical, Technique, Protein, Prediction, Structure,

Synonyms: CASP7

Resource Type: topical portal, data or information resource, portal

Resource Name: Critical Assessment of Techniques for Protein Structure Prediction

Resource ID: SCR_008434

Alternate IDs: nif-0000-30234

Old URLs: <http://predictioncenter.gc.ucdavis.edu/casp7/>

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260801T190331+0000

Ratings and Alerts

No rating or validation information has been found for Critical Assessment of Techniques for Protein Structure Prediction.

No alerts have been found for Critical Assessment of Techniques for Protein Structure Prediction.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Chen SH, et al. (2025) Blocking XIAP:CASP7-p19 selectively induces apoptosis of CASP3/DR malignancies by a novel reversible small molecule. Cell death & disease, 16(1), 459.

Samarasekera G, et al. (2025) Caspase 3 and caspase 7 promote cytoprotective autophagy and the DNA damage response during non-lethal stress conditions in human breast cancer cells. PLoS biology, 23(2), e3003034.

Zhao C, et al. (2022) Predicting residue-specific qualities of individual protein models using residual neural networks and graph neural networks. Proteins, 90(12), 2091.

Chen J, et al. (2020) Machine Learning Approaches for Quality Assessment of Protein Structures. Biomolecules, 10(4).

Yao X, et al. (2019) Association Study of the Caspase Gene Family and Psoriasis Vulgaris Susceptibility in Northeastern China. BioMed research international, 2019, 2417612.

Fassan M, et al. (2019) miR-224 Is Significantly Upregulated and Targets Caspase-3 and Caspase-7 During Colorectal Carcinogenesis. Translational oncology, 12(2), 282.

Permyakov SE, et al. (2018) Comprehensive analysis of the roles of 'black' and 'gray' clusters in structure and function of rat γ -parvalbumin. Cell calcium, 75, 64.

Cui R, et al. (2015) MicroRNA-224 is implicated in lung cancer pathogenesis through targeting caspase-3 and caspase-7. Oncotarget, 6(26), 21802.

Shanmugam V, et al. (2014) Whole genome sequencing reveals potential targets for therapy in patients with refractory KRAS mutated metastatic colorectal cancer. BMC medical genomics, 7, 36.

Ray A, et al. (2012) Improved model quality assessment using ProQ2. BMC bioinformatics, 13, 224.

Kalmar L, et al. (2012) Structural disorder in proteins brings order to crystal growth in biomineralization. *Bone*, 51(3), 528.

Fieldhouse RJ, et al. (2010) Cholera- and anthrax-like toxins are among several new ADP-ribosyltransferases. *PLoS computational biology*, 6(12), e1001029.

Ma S, et al. (2010) Detection of gene pathways with predictive power for breast cancer prognosis. *BMC bioinformatics*, 11, 1.

Han P, et al. (2009) Large-scale prediction of long disordered regions in proteins using random forests. *BMC bioinformatics*, 10, 8.

Kirillova S, et al. (2009) Protein domain boundary predictions: a structural biology perspective. *The open biochemistry journal*, 3, 1.

Mereghetti P, et al. (2008) Validation of protein models by a neural network approach. *BMC bioinformatics*, 9, 66.

McGuffin LJ, et al. (2007) Benchmarking consensus model quality assessment for protein fold recognition. *BMC bioinformatics*, 8, 345.