

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## Database oDatabase of Predicted Subcellular Localization for Eukaryotic PDB Chainsf Predicted Subcellular Localization for Eukaryotic PDB Chains

RRID:SCR\_002831

Type: Tool

### Proper Citation

Database oDatabase of Predicted Subcellular Localization for Eukaryotic PDB Chainsf Predicted Subcellular Localization for Eukaryotic PDB Chains (RRID:SCR\_002831)

### Resource Information

**URL:** <http://cubic.bioc.columbia.edu/db/LOC3d/>

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**Description:** THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 16, 2013. LOC3d is a database of predicted subcellular localization for eukaryotic proteins of known 3-D structure taken from the Protein Databank. Subcellular localization is currently predicted using four different methods: predictNLS (nuclear localization signal), LOChom (using homology), LOCKey (using keywords) and LOC3d (neural network based prediction). The reported localization is based on the method which predicts localization of a given protein with the highest confidence. LOCTree is a novel system of support vector machines (SVMs) that predict the subcellular localization of proteins, and DNA-binding propensity for nuclear proteins, by incorporating a hierarchical ontology of localization classes modeled onto biological processing pathways. Biological similarities are incorporated from the description of cellular components provided by the gene ontology consortium (GO). GO definitions have been simplified and tailored to the problem of protein sorting. Technically the ontology has been implemented using a decision tree with SVMs as the nodes. LOCTree, was extremely successful at learning evolutionary similarities among subcellular localization classes and was significantly more accurate than other traditional networks at predicting subcellular localization. Whenever available, LOCTree also reports predictions based on the following: 1) Nuclear localization signals found by PredictNLS, 2) Localization inferred using Prosite motifs and Pfam domains found in the protein, and 3) SWISS-PROT keywords associated with a protein. Localization is inferred in the last two cases using the entropy-based LOCKey algorithm. Additional information can be found in the LOCTree manuscript and associated PredictNLS and LOCKey publications.

**Synonyms:** LOC3d

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:12824321](#)

**Keywords:** eukaryotic, gene, binding, biological, dna, localization, nuclear, pathway, protein, structure, subcellular, vector, bio.tools

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Database oDatabase of Predicted Subcellular Localization for Eukaryotic PDB Chainsf Predicted Subcellular Localization for Eukaryotic PDB Chains

**Resource ID:** SCR\_002831

**Alternate IDs:** nif-0000-25200, biotools:loc3d

**Alternate URLs:** <https://bio.tools/loc3d>

**Record Creation Time:** 20220129T080215+0000

**Record Last Update:** 20260905T133118+0000

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## Ratings and Alerts

No rating or validation information has been found for Database oDatabase of Predicted Subcellular Localization for Eukaryotic PDB Chainsf Predicted Subcellular Localization for Eukaryotic PDB Chains.

No alerts have been found for Database oDatabase of Predicted Subcellular Localization for Eukaryotic PDB Chainsf Predicted Subcellular Localization for Eukaryotic PDB Chains.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.