Resource Summary Report

Generated by dkNET on Apr 16, 2025

SDR: Specificity-Determining Residues in Protein Families

RRID:SCR_007917
Type: Tool

Proper Citation

SDR: Specificity-Determining Residues in Protein Families (RRID:SCR_007917)

Resource Information

URL: http://paradox.harvard.edu/sdr

Proper Citation: SDR: Specificity-Determining Residues in Protein Families (RRID:SCR_007917)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 16, 2013. A database of predicted specificity-determining residues in protein families. Predicted positions may have been used during evolution to change the function of proteins within a protein family. These positions are excellent targets for mutational studies and should lead to a better understading of protein function. SDR uses the PFAM database of protein domains for sequence alignments and domain definitions as well as the GPCR database for G-protein coupled receptors.

Abbreviations: SDR

Synonyms: Specificity-Determining Residues

Resource Type: database, data or information resource

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SDR: Specificity-Determining Residues in Protein Families

Resource ID: SCR_007917

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250412T055221+0000

Ratings and Alerts

No rating or validation information has been found for SDR: Specificity-Determining Residues in Protein Families.

No alerts have been found for SDR: Specificity-Determining Residues in Protein Families.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.