

# Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

## SDR: Specificity-Determining Residues in Protein Families

RRID:SCR\_007917

Type: Tool

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### Proper Citation

SDR: Specificity-Determining Residues in Protein Families (RRID:SCR\_007917)

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### 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 understanding 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:** data or information resource, database

**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:** 20260829T182957+0000

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### 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.

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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.