

# Resource Summary Report

Generated by [RRID](#) on Apr 8, 2025

## Poulsen IDP/IUP random coil chemical shifts

RRID:SCR\_019189

Type: Tool

### Proper Citation

Poulsen IDP/IUP random coil chemical shifts (RRID:SCR\_019189)

### Resource Information

**URL:** [https://spin.niddk.nih.gov/bax/nmrserver/Poulsen\\_rc\\_CS/](https://spin.niddk.nih.gov/bax/nmrserver/Poulsen_rc_CS/)

**Proper Citation:** Poulsen IDP/IUP random coil chemical shifts (RRID:SCR\_019189)

**Description:** Web tool to calculate random coil chemical shifts for any protein sequence.

**Resource Type:** analysis service resource, production service resource, service resource, data access protocol, web service, software resource

**Keywords:** Random coil chemical shifts, random coil chemical shifts calculation, protein sequence, sequence correction, sequence correction factors determination

**Funding:**

**Availability:** Free, Freely available

**Resource Name:** Poulsen IDP/IUP random coil chemical shifts

**Resource ID:** SCR\_019189

**Record Creation Time:** 20220129T080343+0000

**Record Last Update:** 20250407T220557+0000

### Ratings and Alerts

No rating or validation information has been found for Poulsen IDP/IUP random coil chemical shifts.

No alerts have been found for Poulsen IDP/IUP random coil chemical shifts.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Carrasco J, et al. (2023) Metamorphism in TDP-43 prion-like domain determines chaperone recognition. *Nature communications*, 14(1), 466.

Zuber PK, et al. (2022) Structural and thermodynamic analyses of the  $\beta$ -to- $\alpha$  transformation in RfaH reveal principles of fold-switching proteins. *eLife*, 11.

Mompeán M, et al. (2021) Partial structure, dampened mobility, and modest impact of a His tag in the SARS-CoV-2 Nsp2 C-terminal region. *European biophysics journal : EBJ*, 50(8), 1129.

Tuttle LM, et al. (2021) Mediator subunit Med15 dictates the conserved "fuzzy" binding mechanism of yeast transcription activators Gal4 and Gcn4. *Nature communications*, 12(1), 2220.

Oroz J, et al. (2020) Structural transitions in Orb2 prion-like domain relevant for functional aggregation in memory consolidation. *The Journal of biological chemistry*, 295(52), 18122.

Klinger CM, et al. (2018) Plastid Transcript Editing across Dinoflagellate Lineages Shows Lineage-Specific Application but Conserved Trends. *Genome biology and evolution*, 10(4), 1019.

Lonsdale A, et al. (2016) Better Than Nothing? Limitations of the Prediction Tool SecretomeP in the Search for Leaderless Secretory Proteins (LSPs) in Plants. *Frontiers in plant science*, 7, 1451.

Sayal R, et al. (2016) Quantitative perturbation-based analysis of gene expression predicts enhancer activity in early *Drosophila* embryo. *eLife*, 5.

Bancroft TD, et al. (2014) TMS-induced neural noise in sensory cortex interferes with short-term memory storage in prefrontal cortex. *Frontiers in computational neuroscience*, 8, 23.