

Resource Summary Report

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HeteroAnalysis

RRID:SCR_014991

Type: Tool

Proper Citation

HeteroAnalysis (RRID:SCR_014991)

Resource Information

URL: <http://www.biotech.uconn.edu/resources/biophysics>

Proper Citation: HeteroAnalysis (RRID:SCR_014991)

Description: Software for analyzing sedimentation equilibrium (SE) data from analytical ultracentrifugation experiments. It uses a model-dependent simulation of data for matching data in order to determine when equilibrium has been achieved.

Synonyms: HeteroAnalysis Version 1.1.0.58

Resource Type: software application, data analysis software, algorithm resource, software resource, data processing software

Keywords: sedimentation equilibrium, ultracentrifugation, analysis, model dependent

Availability: Available for download

Resource Name: HeteroAnalysis

Resource ID: SCR_014991

Alternate URLs: <http://core.uconn.edu/files/auf/ha-help/HA-Help.htm>

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260729T044336+0000

Ratings and Alerts

No rating or validation information has been found for HeteroAnalysis.

No alerts have been found for HeteroAnalysis.

Data and Source Information

Usage and Citation Metrics

We found 62 mentions in open access literature.

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

Skeens E, et al. (2025) Dynamic and structural insights into allosteric regulation on MKP5 a dual-specificity phosphatase. *Nature communications*, 16(1), 7011.

Merino-Salomón A, et al. (2025) Crosslinking by ZapD drives the assembly of short FtsZ filaments into toroidal structures in solution. *eLife*, 13.

Petrova ZO, et al. (2025) The role of kinase domain dimerization in EGFR activation. *Structure (London, England : 1993)*.

Alcorlo M, et al. (2024) Flexible structural arrangement and DNA-binding properties of protein p6 from *Bacillus subtilis* phage ϕ 29. *Nucleic acids research*, 52(4), 2045.

Goodell DJ, et al. (2024) Mechanistic and structural studies reveal NRAP-1-dependent coincident activation of NMDARs. *Cell reports*, 43(2), 113694.

Gamiz-Arco G, et al. (2021) Heme-binding enables allosteric modulation in an ancient TIM-barrel glycosidase. *Nature communications*, 12(1), 380.

Harrison OJ, et al. (2020) Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered γ -Protocadherins. *Cell reports*, 30(8), 2655.

Sergeeva AP, et al. (2020) DIP/Dpr interactions and the evolutionary design of specificity in protein families. *Nature communications*, 11(1), 2125.

Crespo I, et al. (2020) Inactivation of the dimeric RappLS20 anti-repressor of the conjugation operon is mediated by peptide-induced tetramerization. *Nucleic acids research*, 48(14), 8113.

Khan D, et al. (2020) A Sec14-like phosphatidylinositol transfer protein paralog defines a novel class of heme-binding proteins. *eLife*, 9.

Singh PK, et al. (2020) Reversible regulation of conjugation of *Bacillus subtilis* plasmid pLS20 by the quorum sensing peptide responsive anti-repressor RappLS20. *Nucleic acids research*, 48(19), 10785.

Sun Y, et al. (2019) A Dissection of Oligomerization by the TRIM28 Tripartite Motif and the Interaction with Members of the Krab-ZFP Family. *Journal of molecular biology*, 431(14), 2511.

Quirk S, et al. (2018) Mutational Analysis of Neuropeptide Y Reveals Unusual Thermal Stability Linked to Higher-Order Self-Association. *ACS omega*, 3(2), 2141.

Ruiz-Cruz S, et al. (2018) DNA-binding properties of MafR, a global regulator of *Enterococcus faecalis*. *FEBS letters*, 592(8), 1412.

Val-Calvo J, et al. (2018) Novel regulatory mechanism of establishment genes of conjugative plasmids. *Nucleic acids research*, 46(22), 11910.

Martino F, et al. (2018) RPAP3 provides a flexible scaffold for coupling HSP90 to the human R2TP co-chaperone complex. *Nature communications*, 9(1), 1501.

Bonsor DA, et al. (2018) The *Helicobacter pylori* adhesin protein HopQ exploits the dimer interface of human CEACAMs to facilitate translocation of the oncoprotein CagA. *The EMBO journal*, 37(13).

Martín-García B, et al. (2018) The TubR-centromere complex adopts a double-ring segrosome structure in Type III partition systems. *Nucleic acids research*, 46(11), 5704.

Xu S, et al. (2018) Interactions between the Ig-Superfamily Proteins DIP-? and Dpr6/10 Regulate Assembly of Neural Circuits. *Neuron*, 100(6), 1369.

White JT, et al. (2017) Structural Stability of the Coiled-Coil Domain of Tumor Susceptibility Gene (TSG)-101. *Biochemistry*, 56(35), 4646.