

Resource Summary Report

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Scansite

RRID:SCR_007026

Type: Tool

Proper Citation

Scansite (RRID:SCR_007026)

Resource Information

URL: <http://scansite.mit.edu/>

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Description: Scansite searches for motifs within proteins that are likely to be phosphorylated by specific protein kinases or bind to domains such as SH2 domains, 14-3-3 domains or PDZ domains. The Motifscanner program utilizes an entropy approach that assesses the probability of a site matching the motif using the selectivity values and sums the logs of the probability values for each amino acid in the candidate sequence. The program then indicates the percentile ranking of the candidate motif in respect to all potential motifs in proteins of a protein database. When available, percentile scores of some confirmed phosphorylation sites for the kinase of interests or confirmed binding sites of the domain of interest are provided for comparison with the scores of the candidate motifs.

Synonyms: Scansite

Resource Type: database, data or information resource

Keywords: binding, kinase, phosphorylate, protein, bio.tools, FASEB list

Resource Name: Scansite

Resource ID: SCR_007026

Alternate IDs: biotools:scansite, nif-0000-20914

Alternate URLs: <https://bio.tools/scansite>

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260725T191143+0000

Ratings and Alerts

No rating or validation information has been found for Scansite.

No alerts have been found for Scansite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 297 mentions in open access literature.

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

Yang H, et al. (2025) Maraviroc enhances Bortezomib sensitivity in multiple myeloma by inhibiting M2 macrophage polarization via PI3K/AKT/RhoA signaling pathway in macrophages. *Cell division*, 20(1), 5.

Pollin G, et al. (2025) Emergent properties of the lysine methylome reveal regulatory roles via protein interactions and histone mimicry. *Epigenomics*, 17(1), 5.

Li Z, et al. (2025) Structural and evolutionary constraints shape adaptive landscapes of immune-related genes across mammalian phylogeny. *PloS one*, 20(11), e0332734.

Deng J, et al. (2024) A transcription factor-mediated regulatory network controls fungal pathogen colonization of insect body cavities. *mBio*, 15(6), e0350423.

Ampofo E, et al. (2024) CK2 activity is crucial for proper glucagon expression. *Diabetologia*, 67(7), 1368.

Rodriguez-Valbuena H, et al. (2024) Genetic and functional diversity of allorecognition receptors in the urochordate, *Botryllus schlosseri*. *bioRxiv : the preprint server for biology*.

Frey Y, et al. (2024) Regulation of the DLC3 tumor suppressor by a novel phosphoswitch. *iScience*, 27(7), 110203.

Ahmad HI, et al. (2024) Genomic insights into Yak (*Bos grunniens*) adaptations for nutrient assimilation in high-altitudes. *Scientific reports*, 14(1), 5650.

Jia X, et al. (2023) Crystal Structure of the SH3 Domain of ASAP1 in Complex with the Proline Rich Motif (PRM) of MICAL1 Reveals a Unique SH3/PRM Interaction Mode. *International journal of molecular sciences*, 24(2).

Pollin G, et al. (2023) Writers and readers of H3K9me2 form distinct protein networks during the cell cycle that include candidates for H3K9 mimicry. *Bioscience reports*, 43(10).

Roy MJ, et al. (2023) Structural mapping of PEAK pseudokinase interactions identifies 14-3-3 as a molecular switch for PEAK3 signaling. *Nature communications*, 14(1), 3542.

Faienza F, et al. (2023) AMBRA1 phosphorylation by CDK1 and PLK1 regulates mitotic spindle orientation. Cellular and molecular life sciences : CMLS, 80(9), 251.

Yang K, et al. (2022) Post-translational modifications drive secondary metabolite biosynthesis in *Aspergillus*: a review. Environmental microbiology, 24(7), 2857.

Chen J, et al. (2022) Positive selection-driven fixation of a hominin-specific amino acid mutation related to dephosphorylation in IRF9. BMC ecology and evolution, 22(1), 132.

Tao Y, et al. (2022) AAV-ie-K558R mediated cochlear gene therapy and hair cell regeneration. Signal transduction and targeted therapy, 7(1), 109.

Yan W, et al. (2022) Cancer-cell-secreted miR-122 suppresses O-GlcNAcylation to promote skeletal muscle proteolysis. Nature cell biology, 24(5), 793.

Petsouki E, et al. (2022) AMPK and NRF2: Interactive players in the same team for cellular homeostasis? Free radical biology & medicine, 190, 75.

Bao D, et al. (2021) MAD2B-mediated cell cycle reentry of podocytes is involved in the pathogenesis of FSGS. International journal of biological sciences, 17(15), 4396.

Ferezin CC, et al. (2021) NEK5 interacts with LonP1 and its kinase activity is essential for the regulation of mitochondrial functions and mtDNA maintenance. FEBS open bio, 11(3), 546.

Kim J, et al. (2021) Akt-mediated Ephexin1-Ras interaction promotes oncogenic Ras signaling and colorectal and lung cancer cell proliferation. Cell death & disease, 12(11), 1013.