

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: data or information resource, database

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: 20260821T193817+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 302 mentions in open access literature.

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

Mimila-Cortes A, et al. (2026) Cementum Attachment Protein-Derived Peptides Modulate Brushite and Calcium Oxalate Crystallization In??Vitro. *Journal of peptide science : an official publication of the European Peptide Society*, 32(8), e70112.

Alsulaimany FA, et al. (2025) Computational Protein Structural Annotations of Mycobacterium tuberculosis Thiamine Phosphate Pyrophosphorylase. *Journal of microscopy and ultrastructure*, 13(3), 151.

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

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.

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.

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

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

Galaraga K, et al. (2024) CaMKIV-Mediated Phosphorylation Inactivates Freud-1/CC2D1A Repression for Calcium-Dependent 5-HT1A Receptor Gene Induction. *International journal of molecular sciences*, 25(11).

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.

Chen Q, et al. (2023) P38 MAPK activated ADAM17 mediates ACE2 shedding and promotes cardiac remodeling and heart failure after myocardial infarction. *Cell communication and signaling : CCS*, 21(1), 73.

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.

Betlej G, et al. (2022) RNA 5-methylcytosine status is associated with DNMT2/TRDMT1 nuclear localization in osteosarcoma cell lines. *Journal of bone oncology*, 36, 100448.

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.

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