Resource Summary Report

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PiSITE: Database of Protein interaction SITEs

RRID:SCR_007859
Type: Tool

Proper Citation

PiSITE: Database of Protein interaction SITEs (RRID:SCR_007859)

Resource Information

URL: http://pisite.hgc.jp/

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Description: A web-based database of protein interaction sites. PiSITE provides not only information of interaction sites of a protein from single PDB entry, but also information of interaction sites of a protein from multiple PDB entries including similar proteins. PiSite also provides a list of sociable proteins, proteins with multiple binding states and multiple binding partners.In PiSITE, the identification of the binding sites of protein chains is performed by searching the same proteins with different binding states in PDB at first, and then mapping those binding sites onto the query proteins. The database PiSITE provides real interaction sites of proteins using the complex structures in PDB. According to the progress of several structural genomic projects, we have a large amount of structural data in PDB. Consequently, we can observe different binding states of proteins in atomic resolutions, and can analyze actual interaction sites of proteins. It will lead better understandings of protein interaction sites in near future. Usual practice to identify the interaction site has been done using a representative complex in PDB. However, for the proteins with multiple partners, non-interaction sites identified by using a single complex structure is not enough, because some part of the non-binding sites may be involved in the interaction sites with another proteins. Therefore, the real interaction sites should be obtained by using all of the binding states in PDB. For the purpose, the identifications of the binding site in PiSITE are done by searching the same proteins with different binding sites in PDB at first, and then mapping the binding sites onto the query proteins. PiSITE also provides the lists of transient hub proteins, which we call sociable proteins to clarify the different of so-called hub proteins. The sociable proteins are identified as the proteins with multiple binding states and multiple binding partners. On the other hand, so-called hub proteins have been identified as the proteins at the hub position in protein-protein interaction networks obtained by large-scale experiments, but the definition of the hub proteins cannot differentiate transient hub proteins from stable ones, although the differentiation is critically important for the better understanding of protein interaction networks. In addition, the usual definition of hub proteins can contain supermolecules as hub proteins. The supermolecules can be identified as the proteins with a single binding

state and multiple binding partners, which we call stable hub proteins.

Synonyms: PiSITE

Resource Type: database, data or information resource

Resource Name: PiSITE: Database of Protein interaction SITEs

Resource ID: SCR_007859

Alternate IDs: nif-0000-03295

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260725T191151+0000

Ratings and Alerts

No rating or validation information has been found for PiSITE: Database of Protein interaction SITEs.

No alerts have been found for PiSITE: Database of Protein interaction SITEs.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Jafarinia H, et al. (2024) C9orf72 polyPR directly binds to various nuclear transport components. eLife, 12.

Hosseini S, et al. (2022) PITHIA: Protein Interaction Site Prediction Using Multiple Sequence Alignments and Attention. International journal of molecular sciences, 23(21).

Gibson TJ, et al. (2015) Experimental detection of short regulatory motifs in eukaryotic proteins: tips for good practice as well as for bad. Cell communication and signaling : CCS, 13, 42.

Hern??ndez S, et al. (2015) Bioinformatics and Moonlighting Proteins. Frontiers in bioengineering and biotechnology, 3, 90.