

Resource Summary Report

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Computational Hot Spots of Protein Interfaces

RRID:SCR_007720

Type: Tool

Proper Citation

Computational Hot Spots of Protein Interfaces (RRID:SCR_007720)

Resource Information

URL: <http://prism.cccb.ku.edu.tr/hotsprint/>

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Description: It provides information about the evolutionary history of the residues on the interface and represents which residues are highly conserved on the interface. In this way, functionally and structurally important residues on the interface can be distinguished. Hotsprint contains overall properties of the interface such as number of computational hot spots on the interface, number of conserved residues on the interface, average conservation score of interface residues and buried ASA of the interface. Additionally, residues of the interface along with their position, name, conservation score, ASA in monomer, ASA in complex, type (contacting interface residue, neighboring interface residue or none) and whether the residue is computational hot spot or not information are presented.

Synonyms: HotSprint

Resource Type: data or information resource, database

Keywords: evolution of proteins, protein residues, surface residues

Resource Name: Computational Hot Spots of Protein Interfaces

Resource ID: SCR_007720

Alternate IDs: nif-0000-02980

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260729T044154+0000

Ratings and Alerts

No rating or validation information has been found for Computational Hot Spots of Protein Interfaces.

No alerts have been found for Computational Hot Spots of Protein Interfaces.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Iakhiaev MA, et al. (2010) Graph-theoretical comparison of protein surfaces reveals potential determinants of cross-reactivity and the molecular mimicry. Molecular immunology, 47(4), 719.