Resource Summary Report

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G protein receptor interaction feature finding instrument

RRID:SCR_008343
Type: Tool

Proper Citation

G protein receptor interaction feature finding instrument (RRID:SCR_008343)

Resource Information

URL: http://griffin.cbrc.jp/

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Description: Griffin (G-protein-receptor interacting feature finding instrument) is a high-throughput system to predict GPCR - G-protein coupling selectively with the input of GPCR sequence and ligand molecular weight. This system consists of two parts: 1) HMM section using family specific multiple alignment of GPCRs, 2) SVM section using physico-chemical feature vectors in GPCR sequence. G-protein coupled receptors (GPCR), which is composed of seven transmembrane helices, play a role as interface of signal transduction. The external stimulation for GPCR, induce the coupling with G-protein (Gi/o, Gq/11, Gs, G12/13) followed by different kinds of signal transduction to inner cell. About half of distributed drugs are intending to control this GPCR - G-protein binding system, and therefore this system is important research target for the development of effective drug. For this purpose, it is necessary to monitor, effectively and comprehensively, of the activation of G-protein by identifying ligand combined with GPCR. Since, at present, it is difficult to construct such biochemical experiment system, if the answers for experimental results can be prepared beforehand by using bioinformatics techniques, large progress is brought to G-protein related drug design. Previous works for predicting GPCR-G protein coupling selectivity are using sequence pattern search, statistical models, and HMM representations showed high sensitivity of predictions. However, there are still no works that can predict with both high sensitivity and specificity. In this work we extracted comprehensively the physico-chemical parameters of each part of ligand, GPCR and G-protein, and choose the parameters which have strong correlation with the coupling selectivity of G-protein. These parameters were put as a feature vector, used for GPCR classification based on SVM.

Synonyms: Griffin

Resource Type: service resource, production service resource, analysis service resource, resource

Keywords: drug, alignment, biochemical, bioinformatic, coupling, gpcr, g-protein, helix, instrument, interface, ligand, molecular, pattern, physico-chemical, receptor interacting, sequence, signal transduction, stimulation, svm, system, technique, transmembrane, weight, instrument, equipment, hardware, bio.tools

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Resource Name: G protein receptor interaction feature finding instrument

Resource ID: SCR_008343

Alternate IDs: nif-0000-25210, biotools:griffin

Alternate URLs: https://bio.tools/griffin

Record Creation Time: 20220129T080246+0000

Record Last Update: 20250416T063518+0000

Ratings and Alerts

No rating or validation information has been found for G protein receptor interaction feature finding instrument.

No alerts have been found for G protein receptor interaction feature finding instrument.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Wahab Sab BA, et al. (2015) Cycloolivil, a lignan from the roots of Stereospermum suaveolens. Pharmacognosy research, 7(1), 45.

Yabuki Y, et al. (2005) GRIFFIN: a system for predicting GPCR-G-protein coupling selectivity using a support vector machine and a hidden Markov model. Nucleic acids research,

33(Web Server issue), W148.

Fox JA, et al. (2005) The Bioinformatics Links Directory: a compilation of molecular biology web servers. Nucleic acids research, 33(Web Server issue), W3.