

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: resource, analysis service resource, production service resource, service 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: 20260808T185914+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 21 mentions in open access literature.

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

Chen DD, et al. (2026) Multi-modal circulating cell-free DNA profiling to predict response to docetaxel in metastatic castration-resistant prostate cancer. NPJ precision oncology, 10(1).

Beauvais B, et al. (2026) The predictive factors of US hospital bankruptcy - a multi-model comparison. Health care management science, 29(1).

Tamaki R, et al. (2025) Cell-free DNA-based inference of the activities of 370 + transcription factors mirrors their activities in tumors. BMC genomics, 26(1), 892.

Adil M, et al. (2025) Preeclampsia risk prediction from prenatal cell-free DNA screening. Nature medicine, 31(4), 1312.

George SL, et al. (2025) Stratified Medicine Pediatrics: Cell-Free DNA and Serial Tumor Sequencing Identifies Subtype-Specific Cancer Evolution and Epigenetic States. *Cancer discovery*, 15(4), 717.

Shinoda S, et al. (2025) Permeation dynamics of microemulsions according to the amount of deep eutectic solvent when applied to the stratum corneum. *RSC advances*, 15(12), 8977.

Chondol T, et al. (2025) Surviving the Extremes: Seasonal Dynamics of Photochemical Performance in Plants From Cold-Arid Himalayan Mountains. *Physiologia plantarum*, 177(3), e70269.

Zhang R, et al. (2025) The role of physical activity in life satisfaction and psychological resilience among college students: Mediating effects of self-efficacy and perceived stress. *PloS one*, 20(9), e0331463.

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Hiatt JB, et al. (2024) Molecular phenotyping of small cell lung cancer using targeted cfDNA profiling of transcriptional regulatory regions. *Science advances*, 10(15), eadk2082.

Fung SF, et al. (2023) Gender-Based Differential Item Function for the Positive and Negative Semantic Dimensions of the Relationship Satisfaction Scale with Item Response Theory. *Behavioral sciences (Basel, Switzerland)*, 13(10).

Smith TD, et al. (2023) Firefighter Stress, Anxiety, and Diminished Compliance-Oriented Safety Behaviors: Consequences of Passive Safety Leadership in the Fire Service? *Fire (Basel, Switzerland)*, 6.

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Park S, et al. (2021) Effects of occupational balance on subjective health, quality of life, and health-related variables in community-dwelling older adults: A structural equation modeling approach. *PloS one*, 16(2), e0246887.

Pailian H, et al. (2020) Age and Species Comparisons of Visual Mental Manipulation Ability as Evidence for its Development and Evolution. *Scientific reports*, 10(1), 7689.

Jong J, et al. (2020) Traumatic life experiences and religiosity in eight countries. *Scientific data*, 7(1), 140.

Wu X, et al. (2020) Synthesis and application of superabsorbent polymer microspheres for rapid concentration and quantification of microbial pathogens in ambient water. *Separation and purification technology*, 239, 116540.

Wahab Sab BA, et al. (2015) Cyclooolivil, 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.