Resource Summary Report

Generated by RRID on Apr 18, 2025

SEVENS

RRID:SCR_004688
Type: Tool

Proper Citation

SEVENS (RRID:SCR_004688)

Resource Information

URL: http://sevens.cbrc.jp/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 11, 2023. SEVENS summarizes GPCR (G-protein coupled receptor) genes that are identified with high accuracy from 43 eukaryote genomes, by a pipeline integrating such software as a gene finder, a sequence alignment tool, a motif and domain assignment tool, and a transmembrane helix predictor. This treats a larger data space (than that in currently available other databases), which should include not only the expressed sequences but also the newly identified sequences that cannot be detected by in vivo experiments, although they definitely exist on the genome sequence and are just waiting for the opportunity to express their functions. SEVENS provides the infrastructure of general information of GPCR universe for comparative genomics. We developed an automatic system for identifying GPCR (G-protein coupled receptor) genes from various kinds of genomes, by integrating such software as a gene finder, a sequence alignment tool, a motif and domain assignment tool, and a transmembrane helix predictor. SEVENS enables us to perform a genome-scale overview of the GPCR universe using sequences that are identified with high accuracy (99.4% sensitivity and 96.6% specificity). Using this system, we surveyed the complete genomes of 7 eukaryotes and 224 prokaryotes, and found that there are 4 to 1016 GPCR genes in the 7 eukaryotes, and only a total of 16 GPCR genes in all the prokaryotes. Our preliminary results indicate that 11 subfamilies of the Class A family, the Class 2(B) family, the Class 3(C) family and the fz/smo family are commonly found among human, fly, and nematode genomes. We also analyzed the chromosomal locations of the GPCR genes with the Kolmogorov-Smirnov test, and found that species-specific families, such as olfactory, taste, and chemokine receptors in human and nematode chemoreceptor in worm, tend to form clusters extensively, whereas no significant clusters were detected in fly and plant genomes. How we found GPCR sequences: Candidate GPCR genes were collected from 32 eukaryote genomes by using the GPCR gene discovery pipeline, composed of two stages: (1) the gene finding

stage, and (2) the GPCR gene screening stage. 1)Gene finding stage (i.e., translation of genomic sequences into amino acid sequences). 2)GPCR gene screening stage of GPCR candidates by assessing genes with sequence search, motif- and domain assignment, and transmembrane helix (TMH) prediction. Details available at the website. Acknowledgment: We are pleased to acknowledge the use of the BLAST package from NCBI, the SOSUI from Dr. T. Hirokawa, the ALN from Dr. O. Gotoh, the HMMER from Dr. A. Bateman. This work was supported by KAKENHI (208059) (Grant-in-Aid for Publication of Scientific Research Results) of Japan Society for the Promotion of Science (JSPS).

Synonyms: SEVENS

Resource Type: database, data or information resource

Defining Citation: PMID:19718507, PMID:29892516

Keywords: eukaryote, gene, chromosomal locations, comparative genomics, genomes, g-protein coupled receptor, g-protein coupled receptor genes, prokaryotes, signal transudation, transmembrane helices

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SEVENS

Resource ID: SCR_004688

Alternate IDs: nif-0000-03455

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250412T054917+0000

Ratings and Alerts

No rating or validation information has been found for SEVENS.

No alerts have been found for SEVENS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Assadullah , et al. (2018) Co-expression of the calcitonin receptor gene in the hypothalamic kisspeptin neurons in female rats. Reproductive medicine and biology, 17(2), 164.

Ikeda M, et al. (2018) SEVENS: a database for comprehensive GPCR genes obtained from genomes: -Update to 68 eukaryotes. Biophysics and physicobiology, 15, 104.

Gurevich VV, et al. (2017) Molecular Mechanisms of GPCR Signaling: A Structural Perspective. International journal of molecular sciences, 18(12).

Gurevich EV, et al. (2015) Beyond traditional pharmacology: new tools and approaches. British journal of pharmacology, 172(13), 3229.

Insel PA, et al. (2012) GPCR expression in tissues and cells: are the optimal receptors being used as drug targets? British journal of pharmacology, 165(6), 1613.

Gurevich VV, et al. (2012) Synthetic biology with surgical precision: targeted reengineering of signaling proteins. Cellular signalling, 24(10), 1899.

Friedrich T, et al. (2010) High-throughput microarray technology in diagnostics of enterobacteria based on genome-wide probe selection and regression analysis. BMC genomics, 11, 591.

Malik A, et al. (2007) Databases and QSAR for cancer research. Cancer informatics, 2, 99.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.