

Computational Biology Homework 1

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1 Problem 1

Website: O95800 GPR75 Human

Function: G protein-coupled receptor that is activated by the chemokine CCL5/RANTES. Probably coupled to heterotrimeric Gq proteins, it stimulates inositol trisphosphate production and calcium mobilization upon activation. Together with CCL5/RANTES, may play a role in neuron survival through activation of a downstream signaling pathway involving the PI3, Akt and MAP kinases. CCL5/RANTES may also regulate insulin secretion by pancreatic islet cells through activation of this receptor.

Publications: It can be checked in this link. Here I only list a few of them.

- Tarttelin, E E et al. "Cloning and characterization of a novel orphan G-protein-coupled receptor localized to human chromosome 2p16." *Biochemical and biophysical research communications* vol. 260,1 (1999): 174-80. doi:10.1006/bbrc.1999.0753
- Hillier, Ladeana W et al. "Generation and annotation of the DNA sequences of human chromosomes 2 and 4." *Nature* vol. 434,7034 (2005): 724-31. doi:10.1038/nature03466
- Ota, Toshio et al. "Complete sequencing and characterization of 21,243 full-length human cDNAs." *Nature genetics* vol. 36,1 (2004): 40-5. doi:10.1038/ng1285

Pfam domain: PF00001

50% similar proteins: There are total 366 results, which could be viewed in this link.

2 Problem 2

Nucleic acid sequences: GenBank, ENA, DDBJ

Protein sequences: UniProt, NCBI Protein

Protein families: Pfam, InterPro

Protein structures: RCSB PDB, SCOP, PDBe, PDBj, BMRB

3 Problem 3

Three major methods are NMR, X-ray and Cryo-EM.

Limits:

- NMR: The size of the protein is limited to about 40 kDa, and the resolution is not as high as X-ray crystallography.
- X-ray: The protein must be crystallized, and the protein must be stable in the crystalline state.
- Cryo-EM: The resolution is not as high as X-ray crystallography (though it is making continuous progress), and the protein must be stable in the vitrified state.

4 Problem 4

Taxonomy ID: 7711, whole genome sequenced: 70