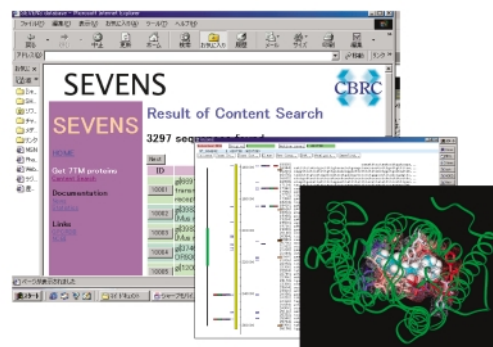


# Computational Biology Research Center

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We developed an automated system for discovering GPCR sequences in the whole human genome using algorithms of gene finding, sequence search, motif and domain assignment, transmembrane helix prediction and the gene quality refinement. This system is intended to detect sequences of multiple exon or remote homologues that can not be detected by using conventional sequence search alone. With careful assessment of the analyzing components, we obtained candidate gene datasets of various confidence levels, among which we found at least 888 and at

most 2,298 candidate GPCR genes from human genome.

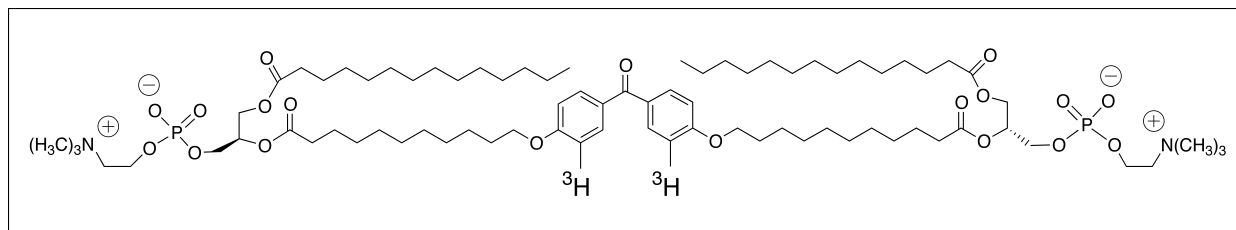


## Topographical Analysis of a Membrane Protein by a Photoactivatable Probe

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Studies of the topographical arrangement of proteins are important for understanding the structural and functional properties of biological membranes. We have studied the topography of a membrane protein, glycoporphin A (GPA), by a bola-amphiphilic photoactivatable probe in collaboration with Dr. Nakatani in Université Louis Pasteur, CNRS. The photo-sensitive group of this probe is localized at

the center of lipid bilayers including physiological amount of cholesterol and cross-links regioselectively with neighboring atoms by UV irradiation. We have revealed with this probe that valine 80 and methionine-81 of GPA exist in the middle of the bilayer membrane. The present method is expected to open a new way to the development of nano-biotechnology.



Chemical structure of photoactivatable probe.