

Purification and AFM Analysis of P2X₄ Receptor and Bacteriorhodopsin for Nanobiological Devices

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Nanobiology seeks to combine recent developments in nanotechnology with biological mechanisms to create novel electronic and biosensing molecular-scale devices. This overview identifies properties of the biological components in nanobiology, specifically, the protein bacteriorhodopsin (bR) and P2X₄ purinergic receptors. Protein purification plays a key role in obtaining available proteins from cultured cells. Multiple methods such as membrane fractionation, ion exchange chromatography, and immunoprecipitation were conducted in order to purify the P2X₄ protein. Atomic force microscopy (AFM) was then used to observe the structure of the protein in native conditions. In the analysis, although the ion channel structure could not be resolved, single P2X₄ proteins were seen to correspond to the previously described P2X₂ structure, a related P2 purinergic receptor. In addition to P2X₄, the possibility of utilizing bR as a proton pump in future optoelectronic devices was studied. Using AFM, the repeating bR trimer structure surrounded by a lipid membrane was visualized. bR embedded in membrane was then suspended over Si nanoholes. Though research is still at an early stage, membrane proteins such as P2X₄ and bR have potential uses in future nanobiological applications.

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Abstract

Nanobiology seeks to combine recent developments in nanotechnology with biological molecules to create novel electronic and biosensing molecular-scale devices. This overview identifies properties of the biological components in nanobiology, specifically, the protein bacteriorhodopsin (bR) and P2X₄ purinergic receptors. Protein purification plays a key role in obtaining available proteins from cultured cells. Multiple methods such as membrane fractionation, ion exchange chromatography, and immunoprecipitation were conducted in order to purify the P2X₄ protein. Atomic force microscopy (AFM) was then used to observe the structure of the protein in native conditions. In the analysis, although the ion channel structure could not be resolved, single P2X₄ proteins were seen to correspond to the previously described P2X₂ structure, a related P2 purinergic receptor. In addition to P2X₄, the possibility of utilizing bR as a proton pump in future optoelectronic devices was studied. Using AFM, the repeating bR trimer structure surrounded by a lipid membrane was visualized. bR embedded in membrane was then suspended over Si nanoholes. Though research is still at an early stage, membrane proteins such as P2X₄ and bR have potential uses in future nanobiological applications.

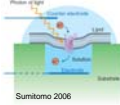
Introduction

Goals of Nanobiology

Fusion of molecular biology, neuroscience, and nanotechnology can lead to novel technologies in electronics, engineering, and medicine

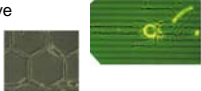
-Protein-based devices

Utilizing biological systems to create molecular scale devices



-Guided neuron growth

Create synaptically active neuron network on patterned surfaces



-Neuron activity measurements

on multi-electrode array sensor. Understand signal transduction through the brain



Proteins

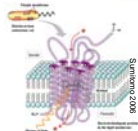
P2X proteins

Form ion channels (via homo/heterotrimerization)
Approximately 3-5nm height, 10-20nm width
Activated by extracellular ATP
Found in various tissue including CNS
7 subclasses (P2X₁ to P2X₇)



Bacteriorhodopsin

Light-driven proton pump (photoreceptor) found in *Halobacterium salinarum*
Trimers arranged to form hexagonal lattice
Resembles vertebrate rhodopsin found in the retina



Specifically, this study aims to further understand the biological components of nanobio

Purify P2X₄ purinergic receptor protein
Analyze structure of P2X₄ protein
Analyze bR surrounded by lipid membrane and then suspended over nanoholes

Materials & Methodology: Protein Purification

Basic Preparation

1321N1 P2X₄-expressed cells
TBS buffer with detergent (1% CHAPS, 0.5% Triton, or 5mM DDM) and protease inhibitors

Plasma Membrane Fractionation

1321N1 P2X₄-expressed cells
HEPES buffer with EDTA, EGTA, and protease inhibitors

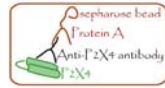
Immunoprecipitation

Rabbit anti-P2X₄ antibody IgG
Antibody binding Protein A coupled to sepharose beads
0.1M glycine-HCl pH 2.7 (dissociate P2X₄ from antibody-Protein A bead)
1/10 vol 1M Tris-HCl pH 8.6 to neutralize pH

Ion Exchange Chromatography

DEAE Sepharose Fast Flow gel column
Elution by pH gradient of:
8.0/7.75/7.5/7.25/7.0/6.75/6.5/6.25/6.0
P2X₄ isoelectric point at 7.41

Immunoprecipitation



Analysis

Polyacrylamide Gel Electrophoresis (PAGE) with Ag staining
Bio-Rad Protein Assay
Atomic Force Microscopy

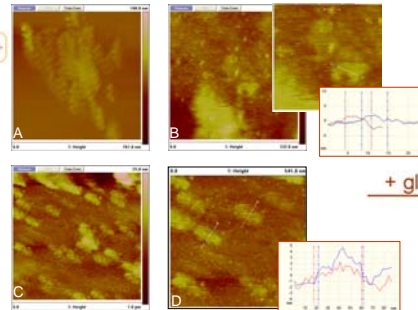
Crosslinking

Glutaraldehyde

Methodology	Analysis Results	Images
Basic prep -> Immunoprecip	Purified protein around 80kDa (single subunit) via Ag staining, lipid bilayer visualized, purified protein presence is not confirmed	Native P2X ₄ A
Membrane fraction -> IEC -> Immunoprecip	Unable to visualize, could not obtain concentration reading	
Membrane fraction -> Immunoprecip	Dense protein band obtained (80kDa) via detergent-based purification, visualized as particles (images); w/o detergent, 250kDa trimer structure conserved	Native P2X ₄ B-D
Membrane fraction -> Immunoprecip -> cross linking	Increased and larger sized globular aggregations visualized (possibly forming trimer)	Crosslinked P2X ₄ E-H

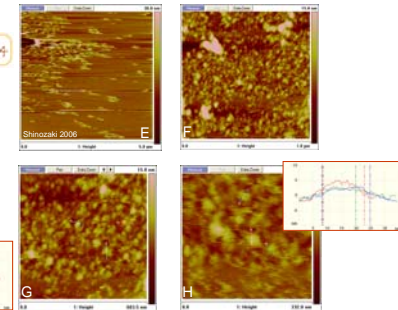
AFM Results

Native P2X₄

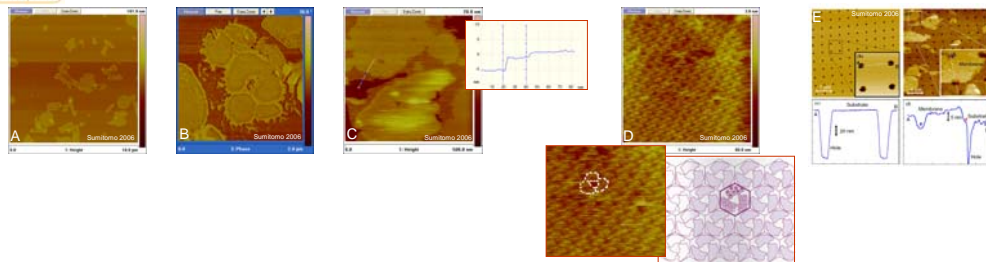


Crosslinked P2X₄

+ glutaraldehyde



Bacteriorhodopsin



Rice University NanoJapan Program
Generously Supported by a Grant from the National Science Foundation