# STRUCTURAL ANALYSIS OF THE HUMAN SEPTIN (SEPT11)

**Hoff, C.**[1], Garcia, W.[1], Araujo. A. P.U.[1], Garrat, R.C.[1]
[1]Institute of Physics, University of São Paulo - USP, São Paulo, Brazil.

Septins are a family of conserved proteins that form hetero-oligomeric complexes that assemble into filaments. Those observed in yeast form filaments of variable length that are 7-9 nm in diameter. Similar filaments have been also isolated from *Drosophila* and mammalian brain tissue. The sequences of these proteins can be divided into three domains; a variable N-terminus, a GTPase domain, and a C-terminal region which generally includes sequences characteristic of coiled-coils. SEPT11 is a member of the mammalian septin family. The function of SEPT11 remains to be clarified, although some septins have been reported to be involved in cytokinetic events and also in pathologies. However, the expression of SEPT11 in kidney epithelial cell line imply some role of SEPT11 in the kidney functions such as tubule transport and glomerular ultrafiltration. Here, te region corresponding to the GTPase domain together with the C-terminal domain (SEPT11-GC) was cloned, successfully expressed in *E. coli* and purified by a two-step protocol using both affinity and size-exclusion chromatographies. The structural integrity of the purified product was analyzed by native gel electrophoresis, circular dichroism spectroscopy (CD), fluorescence spectroscopy and compared with the results of computational sequence analysis. Purified SEPT11 contained nucleotide bound under the purification conditions described here. The results obtained by CD indicated that SEPT11 is a mixed $\alpha/\beta$ structure. Biophysical studies of septin stability may provide important insights into the understanding of their roles in important physiological and pathological processes.

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