

Refolding of a protein with disulfide bonds and a transmembrane domain in Liposome

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Abstract.

Expression of an eukaryotic protein with disulfide bonds and hydrophobic domain is not an easy task because its expression often gives undesired inclusion body formation upon over expression and requires refolding after denaturing solubilization. In order to develop such a method, we have used a refolding method of a protein which has many pairs of disulfide bonds and transmembrane domain. Tissue inhibitor of metalloproteinase-2(TIMP-2) was chosen because of its six internal disulfide bonds, and this was fused to the transmembrane domain of Membrane type 1 Matrix Metalloproteinase (MT1-MMP) as the proposed hydrophobicity. After over expression of the fusion protein in *Rogetta gami*(DE3) with PET 21a(+), the inclusion body was purified and dissolved and refolded according to Williamson¹⁾ with slight modification. Because this new protein contains the trans-membrane domain, we have used phospholipids in a form of liposome. For the verification of protein refolding, we have used reverse zymography and Liposome-precipitation against matrix metalloproteinase-2(MMP-2). As the results, we have found that proteins were inserted into the membrane and folded into active TIMP-2. In conclusion, this new refolding method of a protein would benefit researcher who study membrane bound protein such as ion channels or membrane bound structural proteins. This study was supported by HTPEB (HTPEB 01-PJ11-PG9-01NT00-0036).

References.

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