



用户手册 第二版 2011 年 1 月

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注释:

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- 附有图示和表格
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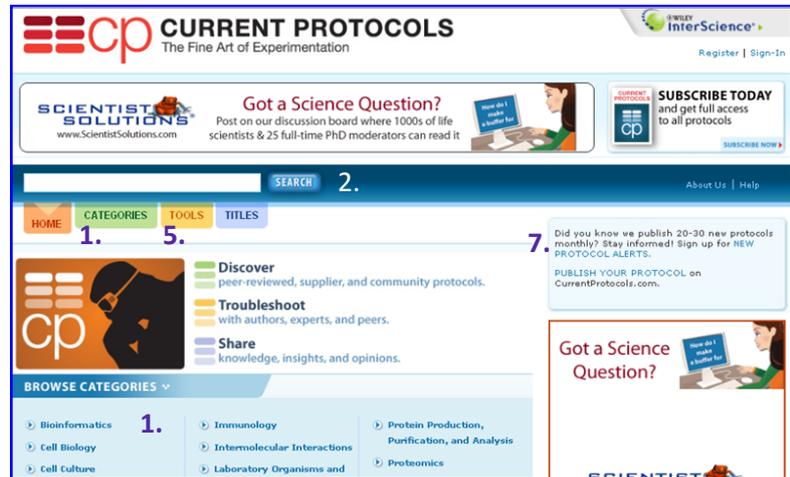
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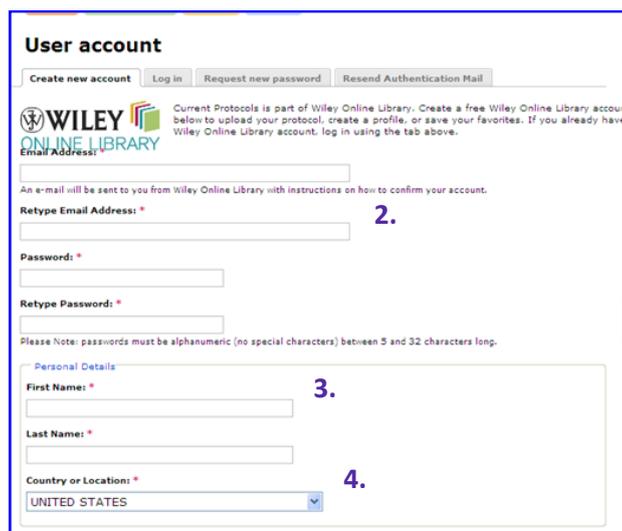
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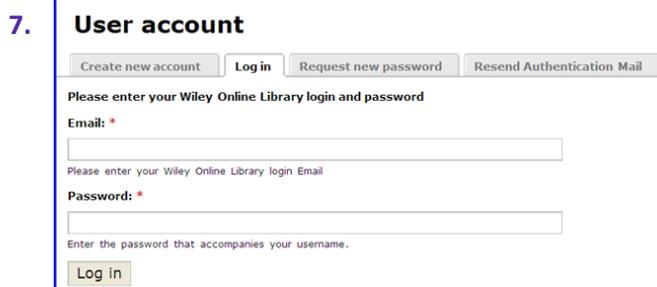
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5. moss, figure

stop spam. read books.

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1 - 10 of 30 1 2 3 > >>

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注释:

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purification Escherichia coli

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Preparation of Soluble Proteins from Escherichia coli
Author(s): Paul T. Wingfield
Publication Date: August, 2005
Source: Current Protocols in Protein Science

Selection of Escherichia coli Expression Systems
Author(s): Alain Bernard, Mark Payton
Publication Date: June, 1995
Source: Current Protocols in Protein Science

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5. Folding and Purification of Insoluble (Inclusion Body) Proteins from Escherichia coli

Author(s): Paul T. Wingfield, Ira Palmer, Shu-Mei Liang

Publication Date: June, 1995

Source: Current Protocols in Protein Science

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Folding and Purification of Insoluble (Inclusion Body) Proteins from Escherichia coli

PEER REVIEWED

Paul T. Wingfield¹, Ira Palmer¹, Shu-Mei Liang²

¹National Institutes of Health, Bethesda, Maryland
²North American Vaccine Corp., Beltsville, Maryland

Publication Name: Current Protocols in Protein Science
Unit Number: UNIT 6.5
DOI: 10.1002/0471140864.ps0605s00
Print Publication Date: June, 1995
Online Posting Date: May, 2001

USER RATINGS

Easy to Follow
★★★★☆
Your rating: None (2 votes)

Achieved Expected Results
★★★★☆
Your rating: None (1 vote)

Overall Rating
★★★★☆
Your rating: None (1 vote)

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ABSTRACT 1.

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3. MATERIALS

4. FIGURES

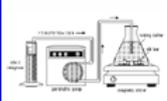
7. LITERATURE CITED

AUTHOR NOTES

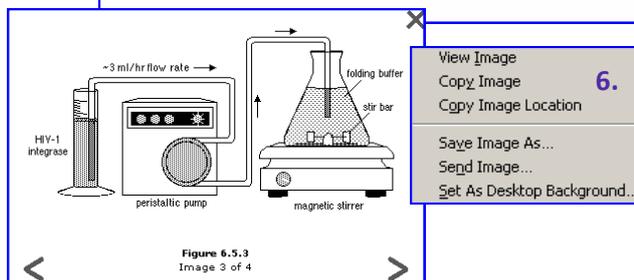
ABSTRACT

Heterologous expression of recombinant proteins in E. coli often results in the formation of insoluble and inactive protein aggregates, commonly referred to as inclusion bodies. To obtain the native (i.e., correctly folded) and hence active form of the protein from such aggregates, four steps are usually followed: (1) the cells are lysed and the aggregates, (2) the cell wall and outer membrane components of the aggregates are removed, (3) the aggregates are solubilized (or extracted) with strong protein denaturants, and (4) the solubilized, denatured proteins are folded with concomitant oxidation of reduced cysteine residues into the correct disulfide bonds to obtain the native protein. This unit features three different approaches to the final step of protein folding and purification. In the first, guanidineHCl is used as the denaturant, after which the solubilized protein is folded (before purification) in an "oxido-shuffling" buffer system to increase the rate of protein oxidation. In the second, acetic acid is used to solubilize the protein which is then refolded in a "foldon" buffer before folding and the protein is folded

NOTE: All steps are carried at 4°C unless otherwise stated.
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 **Figure 6.5.3**
Setup for folding of HIV-1 integrase by dilution into buffer.

5. View Image



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Folding and Purification of Insoluble (Inclusion Body) Proteins from Escherichia coli

Paul T. Wingfield¹, Ira Palmer¹, Shu-Mei Liang²

¹National Institutes of Health, Bethesda, Maryland
²North American Vaccine Corp., Beltsville, Maryland

Publication Name: Current Protocols in Protein Science
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DOI: 10.1002/0471140864.ps0605s00
Print Publication Date: June, 1995
Online Posting Date: May, 2001

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Your rating: 4 (3 votes)

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ABSTRACT

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AUTHOR NOTES

AUTHOR NOTES 1.

Submitted by: Paul Wingfield On: August 18, 2009

We will soon be introducing a new Chapter on protein folding with separate units dealing with recombinant protein folding issues. Further, in Chapter 6 we will introduce more units dealing with recovery of active proteins from inclusion bodies and other units dealing with methods which may prevent aggregates forming in the first place, for example, co-expression systems with chaperones.

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以下是使用“Buffer Calculator（缓冲液计算器）”的样例。

3...从下拉式菜单中选择缓冲液。

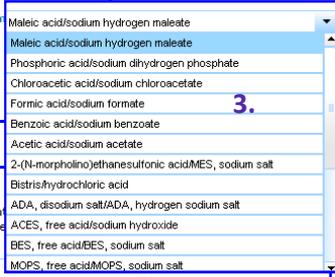
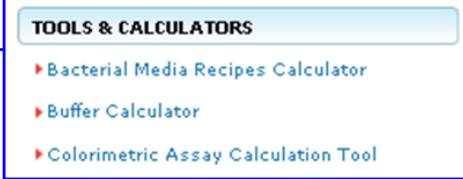
4...调节得到浓度、体积、pH值和温度。

5...结果将在下文显示。



Tools and Calculators

- ▶ Bacterial Media Recipes Calculator
- ▶ Buffer Calculator **2.**
- ▶ Colorimetric Assay Calculation Tool
- ▶ Common Laboratory Recipes Calculator
- ▶ DNA-Protein Translator Tool
- ▶ DNA/RNA/Protein Molecular Weight Calculator
- ▶ G-Force/RPM Conversion Tool
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- ▶ Radioactive Decay Calculator for Isotopes Commonly Used in Bio
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- ▶ Spectrophotometric Measurement of Nucleic Acids Calculator
- ▶ Units of Measurement Conversion Tool



Buffer Calculator

Provides recipes for the preparation of buffers over a concentration range of 0.001 to 1000 mol/l. It enables scaling for volume and correction for temperature. It lists the most commonly used buffer systems in order of ascending pKa's.

TO PREPARE Buffer: Maleic acid/sodium hydrogen maleate **3.** with pKa: 2.00

Concentration (mol/l): 0.005 2 0.005 0.005 Volume (ml): 100 2000 100

pH: 1 3 1 **4.** Temperature of usage (C°): 0 60 0

FOLLOW THE RECIPE **5.** 0.0004645

Ingredient	Stock concentration (mol/l)	Volume (ml)
Maleic acid	0.005 <input type="text"/> 5 <input type="text"/> 1 <input type="text"/>	0.4536
Sodium hydrogen maleate	0.005 <input type="text"/> 5 <input type="text"/> 1 <input type="text"/>	0.04645

Add water up to: 100 ml

Check pH and correct it if necessary

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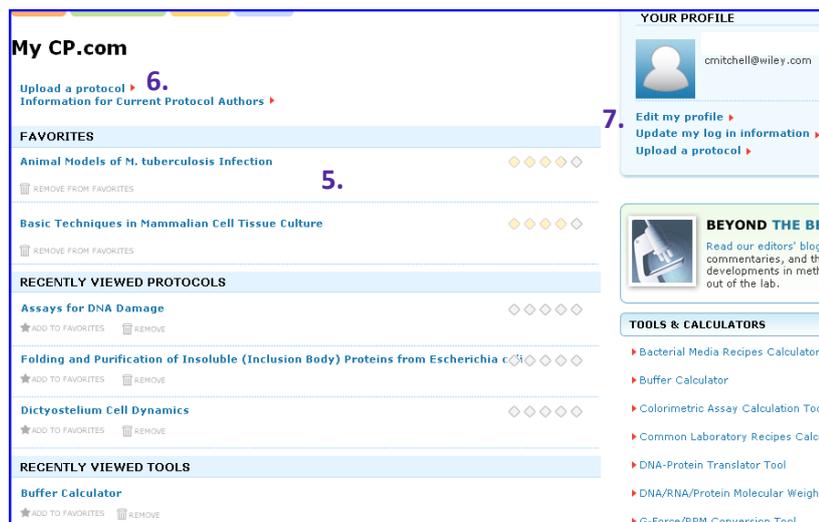
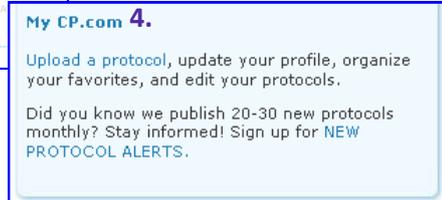
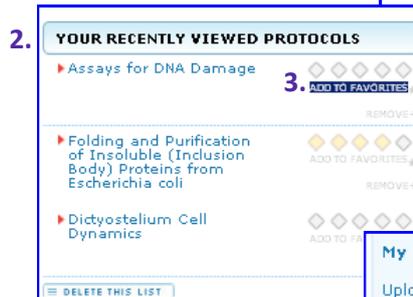
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5...填写作者详细信息。

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Title: **4.**

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Categories: *

<none>

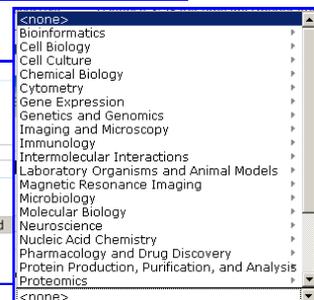
Add

SUPPLIER/AUTHOR DETAILS

All selections

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Nothing has been selected.



Select the protocol's suppliers or authors from the list. If not listed, use the Add button to create a new listing.

CATEGORIES *

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6.

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