



UNIVERSITI PUTRA MALAYSIA

***EXPANDED BED ANION EXCHANGE ADSORPTION
FOR THE PURIFICATION OF BACTERIOPHAGE M13***

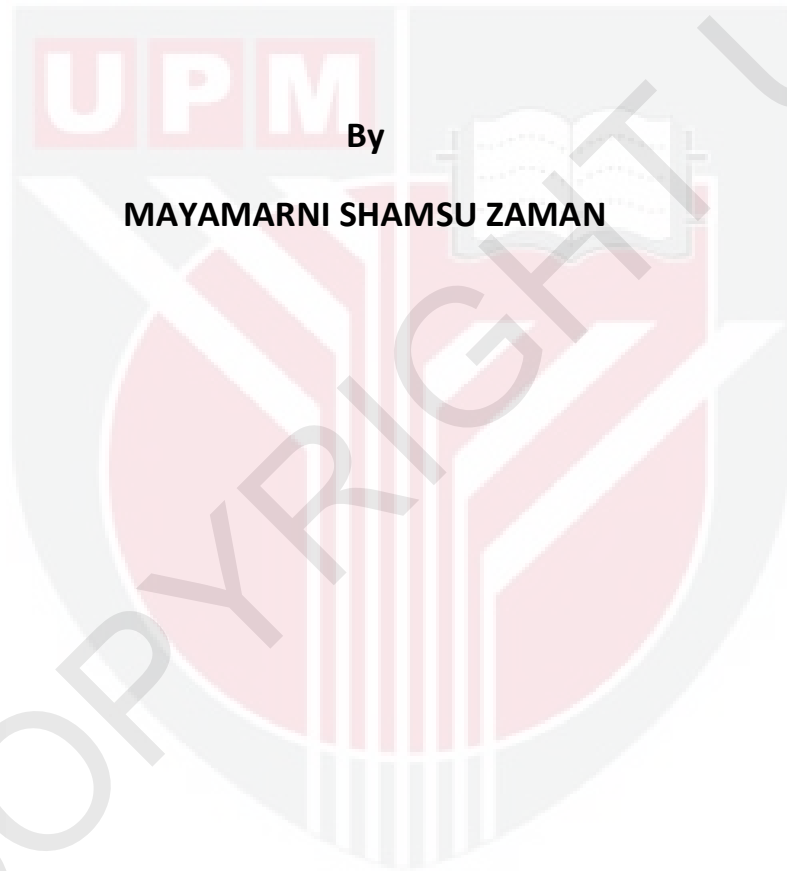
MAYAMARNI SHAMSU ZAMAN

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By

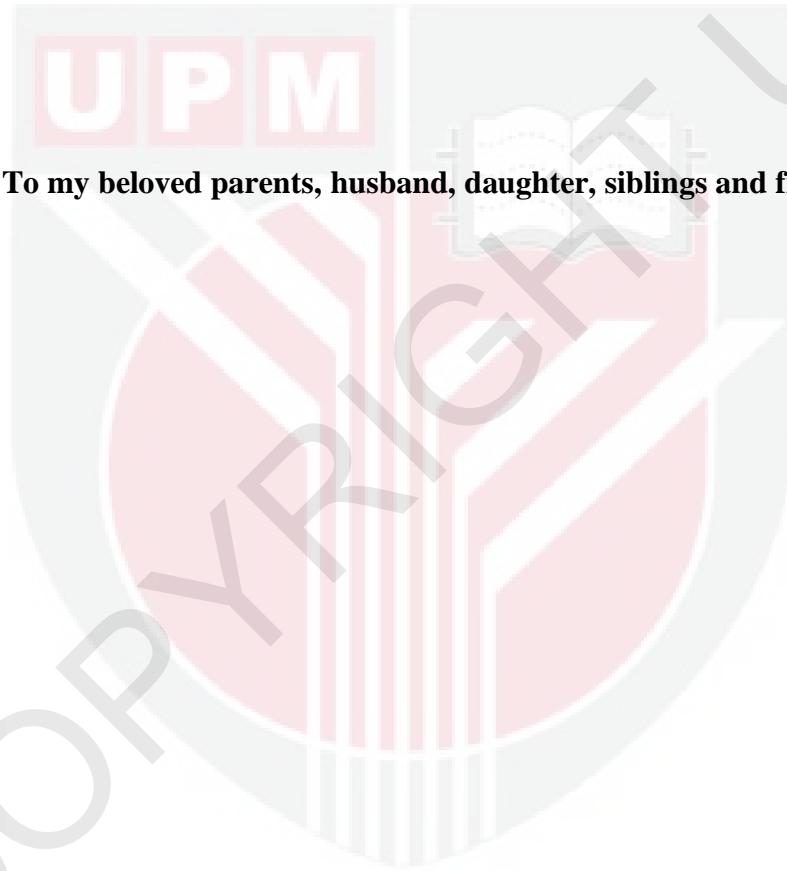
MAYAMARNI SHAMSU ZAMAN



MARCH 2009

DEDICATION

To my beloved parents, husband, daughter, siblings and friends.



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Abstract of thesis presented to Senate of Universiti Putra Malaysia in fulfilment of the requirements of the degree of Master of Science

**EXPANDED BED ANION EXCHANGE ADSORPTION FOR THE
PURIFICATION OF BACTERIOPHAGE M13**

By

MAYAMARNI SHAMSU ZAMAN

MARCH 2009

Chairman : Ling Tau Chuan, PhD

Faculty : Engineering

The filamentous bacteriophage M13 can be used to display foreign peptides and proteins, allowing the construction of therapeutic, vaccine development, diagnostic and technological tools of broad utility. The current technique used to purify bacteriophage M13 by using conventional method but the long processing time and large unit requirement makes this method not economical. The present work focused on the importance of performing an expanded bed anion exchange adsorption experiments for purification of bacteriophage M13 and to identify the fluidization properties of Streamline DEAE. UpFront FastLine™20 (ID = 20 mm) column from UpFront Chromatography was used as a contactor and Streamline™ DEAE ($\rho = 1.2 \text{ g/cm}^3$) from GE Healthcare Lifesciences was used as the anion exchanger. 50 mM of Tris buffer at pH 7.5 was used as the equilibration buffer while 2.0 M of NaCl in 50 mM of Tris buffer was used as the elution buffer.

The influence of the operational parameters of UpFront Fastline™ 20 was studied and demonstrated that 13.03 mL/min flow rate, bed height $H_0 = 17.5$ cm are optimum conditions for protein released. The dynamic binding capacity of Streamline DEAE for the bacteriophage (M13) was found to be 63 mL adsorbent at velocity of 250 cm h^{-1} . Due to higher density, higher flow rates (200 to 350 cmhr^{-1}) and biomass concentrations (5% to 20% ww/v) could be applied on expanded bed adsorption. The developed breakthrough curve was measured at different bed height and different biomass concentrations. The accuracy of the model predictions was improved by employing information on the axial variations in the bed voidage, liquid phase axial dispersion and dynamic binding capacity for the experiment. Breakthrough curves for bacteriophage M13 were compared and the process was more efficient at a bed expansion degree of 2.0 (bed voidage of 0.7). The performance of two methods were evaluated and analyzed. Purification of the M13 bacteriophage by precipitation, centrifugation and microfiltration yielded a low recovery percentage (36.07%) but with high purity while purification of the M13 bacteriophage by expanded bed anion exchange adsorption yielded a high recovery percentage (82.86%) but with low purity. Additionally, the total processing time of the expanded bed adsorption process has been shortened by 8 times compared to that of the conventional method.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Master Sains

**PENULENAN DARIPADA BAKTERIOFAJ M13 DENGAN PENGGUNAAN
KAEDAH PENJERAPAN LAPISAN TERKEMBANG**

Oleh

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Bakteriofaj (M13) boleh digunakan untuk mempamerkan protin dan peptide asing bagi memudahkan pembangunan bagi terapi, pembinaan vaksin, mengenali penyakit dan alatan teknologi bagi keperluan global. Teknik yang biasa digunakan untuk penjernihan bakteriofaj (M13) ialah dengan menggunakan kaedah tradisional tetapi kaedah ini kurang berhemat kerana mengambil masa yang lama dan keperluan unit yang besar. Kerja yang dilakukan adalah tertumpu pada kepentingan penggunaan penjerapan lapisan terkembang untuk penjernihan bagi bakteriofaj (M13) dan untuk mengenal pasti sifat bendalir bagi penjerap garis arus DEAE. UpFront Fastline™ 20 (diameter 20 mm) dari UpFront Chromatography telah digunakan sebagai penghubung dan penggunaan

penjerap garis arus DEAE ($\rho = 12 \text{ g l}^{-1}$) dari GE Healthcare Lifesciences sebagai penukar anion. Penimbal keseimbangan pada pH 7.5 yang digunakan ialah 50mM Tris penimbal. Sementara 2.0 M NaCl di dalam 50 mM Tris penimbal pada pH 2.2 digunakan sebagai penimbal elutan. Parameter operasi yang mempengaruhi proses penjerapan dengan penggunaan UpFront Fastline telah dikaji dan menunjukkan kadar pengaliran ialah 13.03 mL/min pada ketinggian turus 17.5 cm merupakan parameter operasi yang optimum bagi pelepasan protin. Kapasiti pengikatan dinamik bagi penjerap garis arus DEAE untuk bakteriofaj (M13) telah dikenalpasti pada 63 mL penjerap dengan kadar pengaliran 250 cm/h. Oleh sebab itu kadar pengaliran (200 hingga 300 cm/h) dan bio-jisim (5% sehingga 20%) dapat disesuaikan dalam turus lapisan mengembang. Pembinaan lengkung bulus telah dikaji pada perbezaan ketinggian turus dan perbezaan kepekatan bio-jisim. Lengkung bulus bagi bakteriofaj (M13) telah dibandingkan dan didapati pada tahap peningkatan turus 2.0 (lompaan lapisan 0.7) adalah lebih berkesan berbanding dengan tahap peningkatan yang lain. Pencapaian bagi dua kaedah telah dianalisis dan dikembangkan. Penjernihan bagi bakteriofaj (M13) dengan menggunakan kaedah mendakan, pengemparan dan penurasan mikro mempunyai tahap peratusan pemulihan yang rendah (36.07%) tetapi dengan faktor penulenan yang tinggi manakala bagi kaedah penjerapan lapisan terkembang pula, kadar peratusan pemulihan yang tinggi (82.86%) tetapi dengan faktor penulenan yang rendah. Jumlah masa pemrosesan bagi kaedah penjerapan lapisan terkembang adalah lapan kali lebih cepat berbanding dengan kaedah tradisional.

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I certify that an Examination Committee has met on 18 September 2008 to conduct the final examination of Mayamarni Shamsu Zaman on her Master of Science thesis entitled “Expanded Bed Anion Exchange Adsorption for the Purification of Bacteriophage M13” in accordance with Universiti Pertanian Malaysia (Higher Degree) Act 1980 and Universiti Pertanian Malaysia (Higher Degree) Regulations 1981. The Committee recommends that the candidate be awarded the relevant degree. Members of the Examination Committee are as follows:

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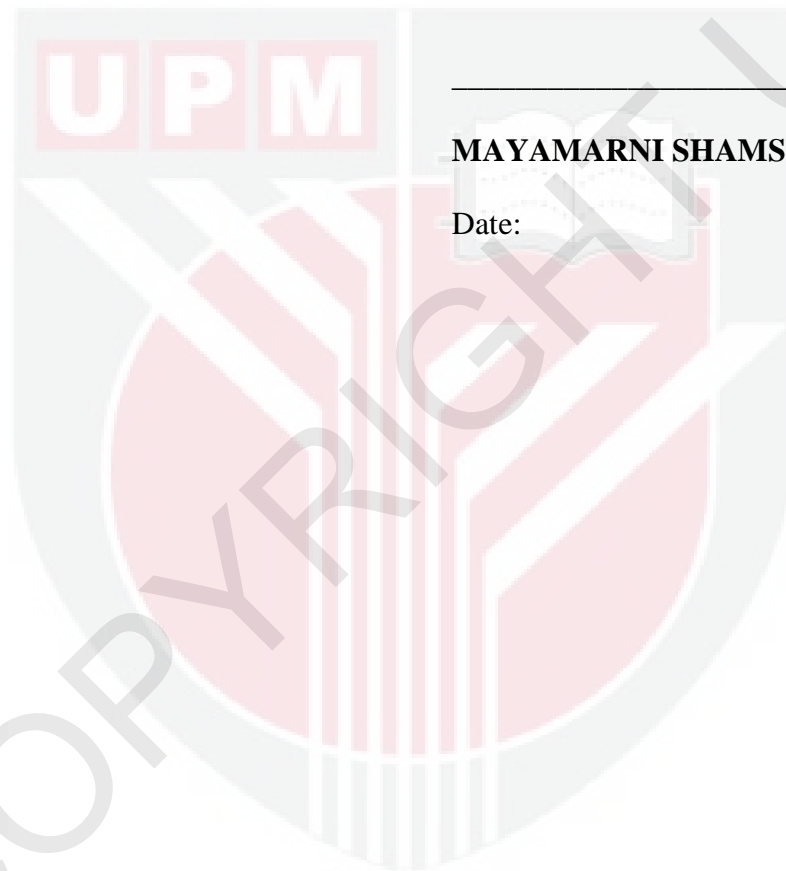
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DECLARATION

I hereby declare that the thesis is based on my original work except for quotations and citations which have been duly acknowledge. I also declare that it has not been previously or concurrently submitted for any other degree at UPM or other institutions.



MAYAMARNI SHAMSU ZAMAN

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LIST OF ABBREVIATIONS

BSA	Bovine Serum Albumin
CIP	Clean-in-place
C_m	M13 concentration at equilibrium, mgmL^{-1}
DEAE	Diethylaminoethyl
dH_2O	Distilled water
DMF	Dimethyl formamide
DNA	Deoxyribonucleic Acid
EBA	Expanded bed adsorption
HCl	Hydroxide chloride
IPTG	Isopropyl-beta-D-thiogalactopyranoside
KCl	Kalium Chloride
K_d	Equilibrium Dissociation constant
LB Agar	Luria-Bertani Agar
LB Broth	Luria-Bertani Broth
$\text{Mg}\cdot\text{Cl}_2\cdot 6\text{H}_2\text{O}$	Magnesium dichloride hexahydrate
NaCl	Sodium Chloride
Na_2CO_3	Sodium Carbonate
NaOH	Sodium Hydroxide
PEG	Polyethylene glycol
pfu	plaque forming unit
SDS-PAGE	Sodium dodecyl sulfate-polyacrylamide gel electrophoresis

v/v	Volume per volume
w/v	Wet weight per volume
X-Gal	5-bromo-4-chloro-3-indocyl- β -D-galactopyranoside



CHAPTER 1

INTRODUCTION

Production of proteins by genetically engineered microorganisms, yeast and animal cells have become a very important technique for the preparation of bio-process and biochemical engineering profession. The protein is necessary to obtain a pure, defined substance of guaranteed purity and potency before it can be used as pharmaceutical. The feedstocks from which proteins are prepared are generally complex, containing solid and dissolved biomass of various sizes and molecular masses. Therefore, the purification process cannot be completed with a single step but it is usually completed by a combination of several unit operations that account for the different separation necessities.

M13 is a filamentous bacteriophage composed of a circular single stranded DNA (ssDNA) which is 6407 nucleotides long encapsulated in approximately 2700 copies of the major coat protein P8 and capped with 5 copies of two different minor coat proteins (P9, P6, P3) on the ends. M13 plasmids are used for many recombinant DNA processes and the virus has also been studied for its uses in nanotechnology.

The filamentous bacteriophage M13 can be used to display foreign peptides and proteins, allowing for the construction of therapeutic, diagnostic and technological tools of broad utility. The relationship between bacteriophages and their bacterial hosts is very important in the context of the food fermentation industry. Other uses of bacteriophage include spray application in horticulture for protecting plants and vegetable produce from decay and the spread of bacterial disease and as biocide for environmental surface and as a preventative treatment for catheters and medical devices prior to use in clinical settings.

Downstream processing is challenging because the products must be concentrated from a very dilute condition in the feedstock and purified from other protein impurities having very similar properties. The feedstock is generally very complex in nature and contains various sizes of dissolved solid, biomass and cell debris. In the conventional way, a final product of guaranteed purity and potency can only be achieved with a combination of several unit operations (Anspach *et al.*, 1999). prior to the concentration and fermentation broth or cell homogenates by centrifugation or filtration. In the large scale process of protein recovery, these clarification methods often show limitations in practice (Lee, 1989).

The traditional primary purification of the target molecule has been addressed by adsorption chromatography using a conventional packed bed of adsorbent. Before further purified by traditional packed bed chromatography, centrifugation and microfiltration has its drawbacks.

The flux of liquid per unit membrane area is often dramatically decreased, even though microfiltration could provide a particle free solution. During the filtration process, fouling of the microfiltration membrane is another critical problem that significantly adds to the operational cost (Johansson *et al.*, 1996). Accordingly, direct adsorption from crude feedstocks potentially offers significant reduction of process time and costs compared to traditional processes (Chase and Drager, 1992; Chase, 1994). Therefore, it is obvious that elimination of the clarification step will significantly simplify and improve the purification process.

The development of molecular biology techniques has enabled researchers to produce large quantities of biologically important molecules from bacteria, plants and animals. Although this ability has revolutionized the production and delivery of pharmaceutical and therapeutic products but one problem has remained. To accomplish the particulates removal, centrifugation and microfiltration are accepted as method in the biotechnology industry, but the long processing time and large unit requirement makes this method not economical.

Expanded bed adsorption (EBA) is one of the suitable methods for the protein separation from the cultivation broth (Kaezmarski *et al.*, 2004). Expanded bed procedures are becoming increasingly popular in bioseparation as a way of avoiding the need for clarification techniques such as centrifugation and filtration (Chang *et al.*, 1995). The performance of protein adsorption in expanded bed is obviously nonuniform and complex along the column since EBA is a special chromatography technique with perfect classification of adsorbent particles in the column (Junxian *et al.*, 2005).

The formation of a perfectly classified fluidized bed of adsorbent particles in the particular feedstock is the key of successful expanded bed adsorption processes, from which the target molecule is to be isolated (Reichert *et al.*, 2001). The efficiency of the adsorption can be represented by an adsorbate breakthrough curve (BTC), or more specifically by the amount of adsorbate loaded onto the column until a defined breakthrough concentration in the column effluent is reached (Bruce and Chase, 2002; Pai *et al.*, 2000; Hansen and Mollerup, 1998). Further more, the EBA technique is not only limited at laboratory process scale, it is available for scale-up and potentially offer industrial scale process. One step unit operation of capture target molecules from crude feedstock may reduce products degradation and avoid bio-product handling problem. Expanded bed adsorption has also proved to be a versatile tool that can be applied on all commonly used source materials (Clemmitt and Chase, 2000a)

Successful processing by expanded bed adsorption at large scale for *E. coli* homogenate has been reported (Clemmitt and Chase, 2000; Tan *et al.*, 2005), yeast cell homogenates (Smith *et al.*, 2002; Chow *et al.*, 2005; Ling *et al.*, 2005; Vergnault *et al.*, 2007), orotic acid from whey (Baumeister *et al.*, 2003), whole mammalian cell culture broth (Batt *et al.*, 1995), milk and animal tissue extracts (Noppe, 1996), plant materials (Bertrand *et al.*, 1998).

The present work is focused on the development of a simplified and rapid technique for the purification of bacteriophage M13. Ion exchange chromatography has been applied in this study. Ion exchange is a versatile technique of separation in which it has been utilized in the separation of ionic materials from each other and also in the separation of completely nonionic mixtures. Ion exchange is a low energy process ideally suited for treating water soluble, ionic molecules. UpFront FastLine™ 20 was used as a contactor to recover protein from bacteriophage M13. The performance of an anion exchanger, Streamline DEAE, ($\rho = 1.2 \text{ gmL}^{-1}$) as adsorbent was studied.

Objectives

The objectives of this study are:

1. To identify the fluidization properties of Streamline DEAE ($\rho \sim 1.2 \text{ gmL}^{-1}$) and degree of expansion of Streamline DEAE ($\rho \sim 1.2 \text{ gmL}^{-1}$) in Fastline™ 20 column.
2. To optimize a process capable of directly extracting protein at high purity and yield from an unclarified feedstock using expanded bed adsorption.
3. To investigate and compare the efficiency of ion-exchange chromatography on the capture of bacteriophage M13 by utilizing expanded bed adsorption technique in Fastline™ 20 column to the conventional method.

REFERENCES

- Allan, L., Elias Z., Marie H., and Morten O. (1998) *Simplified and more robust EBA processes by elution in expanded bed mode*. *Bioseparation* 8: 93-97
- Amersham Handbook, (1997) *Expanded Bed Adsorption*. Amersham Pharmacia Biotechnology
- Ameskamp, N., Priesner, C., Lehmann, J., and Lutkemeyer, D., (1999) *Pilot scale recovery of monoclonal antibodies by expanded bed ion exchange adsorption*. *Bioseparation* 8: 169-188
- Anspach, F. B., Curbelo, D. L., Hartmann, R., Garje, G., Deckwer, W. D., (1999) *Expanded Bed Chromatography in Primary Protein Purification*. *Journal of Chromatography A* 865: 129-144
- Arvidsson, P., F.M. Plieva, V.I. Lozinsky, B. Mattiasson. (2003) *Direct chromatography capture of enzyme from crude homogenate using immobilized metal affinity chromatography on a continuous supermacporous adsorbent*. *Journal of Chromatography A* 986: 275-290
- Batt B.C., Yabannavar V.M., and Singh V. (1995) *Expanded bed adsorption process for protein recovery from whole mammalian cell culture broth*. *Bioseparations* 5: 41-52
- Baumeister, A., Stephanie, V., and Fischer, L. (2003) *Concentration and purification of orotic acid directly from whey with an expanded bed adsorption system*. *Journal of Chromatography A* 1006:261-265
- Benhar, I. (2001) *Biotechnological applications of phage and cell display*. *Biotechnology Advances*, 19 : 1-33.
- Bermejo, R., Ruiz, E., and Acien, F. G. (2007) *Recovery of B-phycoerythrin using expanded bed adsorption chromatography: Scale-up of the process*. *Enzyme and Microbial Technology* 40: 927-933
- Bertrand, O., Cochet S., and Cartron J. P., (1998) *Expanded bed chromatography for one step purification of mannose binding lectin from tulip bulbs using mannose immobilized on DEAE Streamline*. *Journal of Chromatography* 822:19-28

Bo Ersson, Lars, R., and Jan-Christer, J. (1998) *Introduction to Protein Purification*. pp 3-40. In Jan-Christer, J and Lars R. (2nd), *Protein Purification: Principles, High Resolution Methods and Applications*. John Wiley & Sons, New York.

Bradford, M. M., (1976). *A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding*. Pp 248-254, Academic Press Inc.

Bruce, L. J., and Chase, H. A. (2002) *The combined use of in-bed monitoring and an adsorption model to anticipate breakthrough during expanded bed adsorption*. Chemical Engineering Science 57: 3085-3093

Bruce, L. J. and Chase, H. A. (2001) *Hydrodynamics and adsorption behaviour within an expanded bed adsorption column studied using in-bed sampling*. Chemical Engineering 56: 3149-3162

Cabanne, C., Noubhani, A. M., Hocquellet, A., and Santarelli, X. (2004) *Evaluation of three expanded bed adsorption anion exchange matrices with the aid of recombinant enhanced green fluorescent protein overexpressed in Escherichia coli*. Journal of Chromatography B 808: 91-97

Cabanne, C., Noubhani, A. M., Hocquellet, A., Santarelli, X., Dieryck, W., and Dole, F. (2005) *Purification and on-column refolding of EGFP overexpressed as inclusion bodies in Escherichia coli with expanded bed anion exchange chromatography*. Journal of Chromatography B 818: 23-27

Chang, Y. K., and Chase, H. A., (1995) *Development of Operating Conditions for Protein Purification Using Expanded Bed Techniques: The Effect of the Degree of Bed Expansion on Adsorption Performance*. Biotechnology & Bioengineering 49: 512-526

Chang, Y. K., and Chase, H. A. (1996) *Ion Exchange Purification of G6PDH From Unclarified Yeast Cell Homogenates Using Expanded Bed Adsorption*. Biotechnology & Bioengineering 49: 204-216

Charoenrat, T., Mariena, K. C., Mehmedlija, J., Enfors, S., and Andres, V. (2006) *Recovery of recombinant β -glucosidase by expanded bed adsorption from Pichia pastoris high cell density culture broth*. Journal of Biotechnology 122: 86-98

Chase, H. A., and Clemmitt, R. H. (2000) *Facilitated Downstream Processing of a Histidine-Tagged Protein from Unclarified E.coli Homogenates Using Immobilized Metal Affinity Expanded Bed Adsorption*. Biotechnology & Bioengineering, 67 : 206-216.

Chase, H. A., and Dreager, M. N., (1992) *Affinity purification of proteins using expanded beds*. Journal of Chromatography A 597: 129-145

Chow, Y. M., Tey, B.T., Mohammad, N. I., Arbakariya, A., and Ling, T.C., (2005) *The disruption of Saccharomyces cerevisiae cells and release of glucose 6-phosphate dehydrogenase (G6PDH) in a horizontal dyno bead mill operated in continuous recycling mode*. Biotechnology and Bioprocess Engineering 10: 284-288

Clemmitt, R. H., and Chase, H. A., (2000) *Immobilised metal affinity chromatography of β -galactosidase from unclarified Escherichia coli homogenates using expanded bed adsorption*. Journal of Chromatography A 874: 27-43

Denizli, A., Kokturk, G., Yavuz, H., and Piskin, E., (1999) *Albumin adsorption from aqueous solutions and human plasma in a packed bed column in Cibacron Blue F3GA-Zn attached poly (EGBMA-HEMA) microbeads*. Reactive and Functional Polymers, 40: 195-203

Diane, E., Harold, W., Walz, (1992). *Basic Techniques for Cell Culturing, in Practical Cell Culture Techniques* (Alan A. Boulton, G. Baker and W. Walz). The Humana Press Inc. New Jersey, pp. 1-17

Evert, K., John, B. and Lars, R., (1998). *Ion Exchange Chromatography* pp 145-203. In Jan-Christer. J and Lars R. (2nd), *Protein Purification: Principles, High Resolution Methods and Applications*. John Wiley & Sons, New York.

Fernandez-Lahore, H. M., Geilenkirchen, S., Boldt, K., Nagel, A., Kula, M. R., and Thommes, J. (2000) *The influence of cell adsorbent interaction on protein adsorption in expanded bed*. Journal of Chromatography A. 873: 195-208

Finette, G. M. S., Mao, Q., and Hearn, M. T. W. (1997) *Studies on the expansion characteristics of fluidized beds with silica-based adsorbents used in protein purification*. Journal of Chromatography A 743: 57-73

Finette, G. M. S., Mao, Q., and Hearn, M. T. W. (1997) *Comparative studies on the isothermal characteristics of proteins adsorbed under batch equilibrium conditions to ion-exchange, immobilized metal ion affinity and dye affinity matrices with different ionic strength and temperature conditions*, Journal of Chromatography A, 763: 71-90

Frej, A.K.B., Johansson, H. J., Johansson, S. and Leijon, P. (1997). *Expanded bed adsorption at production scale: scale up verification, process example and sanitization of column and adsorbent*. Bioprocess Engineering 16:922-929

Freshney, R. I. (1987) *Culture of Animal Cells in A Manual Basic Technique, 2nd ed*. Liss, New York

Fuh, G., Sidhu S.S. (2000) *Efficient phage display of polypeptides fused to the carboxy-terminus of the M13 gene-3 minor coat protein*. Federation of European Biochemical Societies: 231-234

Geankoplis, C. J. (1993) *Transport Processes and Unit Operations*. 3rd Ed. Prentice Hall Inc. London. Pg 697-715

Glucksman, M. J., Bhattacharjee, S. and Makowski, L (1992). *Three dimensional structure of a cloning vector X-ray diffraction studies of filamentous bacteriophage M13 at 7 resolution*. Journal Mol. Biol. 226:455-470

Ganzalez, Y., N. Ibarra, H. Gomez, M. Gonzalez (2003). *Expanded bed adsorption processing of mammalian cell culture fluid: comparison with packed bed affinity chromatography*. Journal of Chromatography B 784: 183-187

Griffith, C. M., Morris, J., Robichaud, M., Annen, M. J., McCormick, A.V. and Flickinger M. C. (1997) *Fluidization characteristics of and protein adsorption on fluoride modified porous zirconium oxide particles*. Journal of Chromatography A 776: 179-195

Guzeltunc, E., Ulgen, K. O. (2001). *Recovery of actinorhodin from fermentation broth*. Journal of Chromatography A 91:67-76

Hamilton, G. E., Luechau, F., Burton, S. C., and Lyddiatt, A. (2000) *Development of a mixed mode adsorption process for the direct product sequestration of an extracellular protease from microbial batch cultures*. Journal of Biotechnology 79: 103-115

Hanson, E., and Mollerup, J. (1998) *Application of the two-film theory to the determination of mass transfer coefficients for bovine serum albumin on anion-exchange columns*. Journal of Chromatography A 827: 259-267

Hjorth, R. (1997) *Expanded Bed Adsorption in industrial bioprocessing*. Recent Development. Biotechnol Bioeng., Vol 15

Ho, K. L., Yusoff, K., Soon, H. F., and Tan, W. S. (2003) *Selection and high affinity ligands to Hepatitis core antigen from a phage-displayed cyclic library*. Journal of Med. Virol. 67: 1-6

Ho, K. L (2002) *Selection of high affinity peptides against hepatitis B core antigen from a phage displayed cyclic peptide library*. Master of Science thesis. Universiti Putra Malaysia.

Horst, B., Zhanren Z. and Lyddiatt A. (1999) *Direct process integration of cell disruption and fluidized bed adsorption for the recovery of intracellular proteins*. Journal of Chemical Technology and Biotechnology 74: 208-212.

<http://en.Wikipolodia>

Ingham, K.C. (1984). *Protein precipitation with polyethylene glycol: methods in enzymology* 104: 351-356

Jaap, H., Waterborg, and Harry, R., Matthews, (1994) *The Lowry Method for Protein Quantitation*, in *Basic Protein And Peptide Protocols* (John M. Walker) pp: 1-4

Jan-Christer, J. and Lars, R. (1998) *Protein Purification – Principles, High Resolution Methods and Applications*. A John Wiley & Sons, Ins., Pub. Pp 4-38

Jan-Christer, J. and Jan-Ake, J. (1998) *Introduction to Chromatography in Protein Purification*. Wiley-VCH, Inc. pp 43-77

John D. (1975) *Bacteriophage*. John Wiley & Sons, Inc., New York. Pp 1-5

Johansson, H. J., Jagersten, C., and Shiloach, J. (1996) *Large scale recovery and purification of periplasmic recombinant protein from E. coli using expanded bed adsorption chromatography followed by new ion exchange media*. Journal of Biotechnology 48: 9-14

Jurgen, J. H., Peter, J. B., Lin, D.Q., Inger, M., and Maria, R. K. (2005) *The influence of homogenization conditions on biomass-adsorbent interactions during ion-exchange expanded bed adsorption*. Biotechnology and Bioengineering 94: 543-553

Junxian, Y., Lin, D. Q., Shan, J. Y., (2005) *Predictive modelling of protein adsorption along the bed height by taking into account the axial nonuniform liquid and particle classification in expanded bed*. Journal of Chromatography A 1095: 16-26

Kaezmarski, K., and Bellot, J. C., (2004) *Influence of particle diameter distribution on protein recovery in the expanded bed adsorption process*. Journal of Chromatography A, 1069: 91-97

Krijgsman, J., and Jenkins, R. O. (1992) *Product Recovery in Bioprocess Technology*. Butterworth-Heinemann Ltd. Pp 164-207

Krishna, S.V.S.R., Lars, C.K., Michael, W.W., Reichl, U., Andreas, S.M., and Pushpavanam, S. (2007) *Hydrodynamic Characteristics and Expansion Behaviour of beds containing Single and Binary Mixtures of Particles*. Ind. Eng. Chem. Res. 46: 4686-4694

Lee, S.M. (1989) *The primary stages of protein recovery*. Journal of Biotechnology 11:103-118

Li, Q., Su, H., Li, J., and Tan, T. (2006) *Application of surface molecular imprinting adsorbent in expanded bed for the adsorption of Ni⁺ and adsorption model*. Journal of Environmental Management.

Lin, D. Q., Zhi, J. M., and Shan, J. Y. (2006) *Expansion and hydrodynamic properties of cellulose-stainless steel powder composite matrix for expanded bed adsorption*. Journal of Chromatography A 1107: 265-27

Ling, T. C., and Lyddiatt, A. (2005) *Process intensification of fluidized bed dye-ligand adsorption of G3PDH from unclarified disrupted yeast: A case study of the performance of a high-density steel-agarose pellicular adsorbent*. Protein Expression and Purification 42: 160-165

Ling, T. C., and Lyddiatt, A. (2005) *Integration of mechanical cell disruption and fluidized bed recovery of G3PDH from unclarified disrupted yeast: A comparative study of the performance of unshielded and polymer shielded dye-ligand chromatography systems*. Journal of Biotechnology 119: 436-448

Loong, C. K. (2004) *Purification of bacteriophage M13 by expanded bed anion exchange adsorption*. Bachelor thesis, Universiti Putra Malaysia.

Makowski L., (1994) *Phage display: Structure, assembly and engineering of filamentous bacteriophage M13*. Current Opinion in Structure Biology 4: 225-230

Marvin, D. A., Hale, R. D. and Nave, C. (1994). *Molecular models and structural comparisons of native and mutant class I filamentous bacteriophage*. Journal Mol. Biol. 235:260-286.

Marvin, D.A., Welsh, L.C., Symmons, M. F., Scott, W. R. P., and Straus, S. K. (2006) *Molecular Structure of fd (f1, M13) Filamentous Bacteriophage refined with respect to X-ray fibre diffraction and solid-state NMR data supports specific models of phage assembly at the bacterial membrane*. Journal Mol. Biol. 355: 294-309

Nayak, D. P., Ponratham, S., Rajan, C.R. (2001). *Macroporous copolymer matrix IV. Expanded bed adsorption application*. Journal of Chromatography A 922:63-76

Nicholas, J. Kruger., (1994) *The Bradford Method for Protein Quantitation* , in *Basic Protein And Peptide Protocols* (John M. Walker) pp:9-16

Noppe, Hanssens, W., De Cuyper, M. (1996) *Simple two-step procedure for the preparation of highly active pure equine milk lysozyme*. Journal of Chromatography 719: 327-331

Pai, A., Gondkar, S., and Lali, A. (2000) *Enhanced performance of expanded bed chromatography on rigid superporous adsorbent matrix*. Journal of Chromatography A 867: 113-130

Ping Li, Guohua, X., and Alirio, E. R. (2004) *A 3-zone model for protein adsorption kinetics in expanded beds*. Chemical Engineering Science 59: 3837-3847

Rasched, I., and Oberer, E. (1986). *Ff coliphages: Structure and functional relationships*. Microbiol. Rev. 50:401-427

Reichert, U., Esther, K., Heike, S., Maria, R. K. and Thommes, J. (2001) *Isolation of recombinant formate dehydrogenase by pseudo-affinity expanded bed adsorption*. Journal of biochemical and biophysical methods 49: 533-552

Richardson, J. F. and Zaki, W. N. (1954) *Sedimentation of suspension of uniform spheres under conditions of viscous flow*. Chemical Engineering Science 3: 65-73

Sidhu, S. S. (2001) *Engineering M13 for phage display*. Biomolecular Engineering 18: 57-63

Sidhu, S. S., (2000) *Phage display in pharmaceutical biotechnology*. Current Opinion in Biotechnology 11: 610-616

Smith, G. P. (1985) *Filamentous fusion phage: expression vectors that display cloned antigens on the virion surface*. Science 228: 1-33

Smith, G. P., and Scott, J. K., (1993). *Libraries of peptides and proteins displayed on filamentous phage*. Method Enzymol 217:228-257

Smith, M.P., Bulmer, M. A., Hjorth R., and Titchener-Hooker, N. J. (2002) *Hydrophobic interaction ligand selection and scale-up of an expanded bed separation of an intracellular enzyme from Saccharomyces cerevisiae*. Journal of Chromatography A 968: 121-128

Sofer, G., L. Hagel. (1997). *Handbook of processing chromatography – A guide to optimization, scale-up and validation*. Pg 298-300. New York:Academic Press

Stopar, D., Ruud, B. S., Cor, J. A. M., Marcus, A. H. (2003). *Protein-lipid interactions of bacteriophage M13 major coat protein*. Biochimica et Biophysica Acta, 1611 : 5-15

Stopar, D., Ruud, B. S., Cor J. A. M., Marcus, A. H. (2002) *Structural characterization of bacteriophage M13 solubilization by amphiphiles*. Biochimica et Biophysica Acta 1554: 54-63

Susano, J. K., Francisco, M. F. and Maria, I. R. (2005) *Ion exchange expanded bed chromatography for the purification of an extracellular inulinase from Kluyveromyces marxianus*. Process Biochemistry 40: 581-586

Tan, Y. P., Ling, T. C., Tan, W. S., Khatijah, Y., and Tey, B. T. (2006) *Recovery of histidine-tagged nucleocapsid protein of Newcastle disease virus using immobilized metal affinity chromatography*. Process Biochemistry 41: 874-881

Tan, Y. P. Ling, T. C., Tan, W. S., Khatijah, Y., and Tey, B. T. (2006) *Purification of recombinant nucleocapsid protein of Newcastle disease virus from unclarified feedstock using expanded bed adsorption chromatography*. Protein Expression and Purification 46: 114-121.

Tan, Y. P. Ling, T. C., Tan, W. S., Khatijah, Y., and Tey, B. T. (2005) *Comparative of three purification methods for the nucleocapsid protein of Newcastle disease virus from Escherichia coli homogenates*. The Journal of Microbiology 43: 295-300

Thelen, T. V., and Ramirez, W. F. (1997) *Bed height dynamics of expanded beds*. Chemical Engineering Science 52: 3333-3344

Theodossiou, I., David, H. E., Owen, R. T., and Timothy, J. H. (2002) *Fluidisation and dispersion behaviour of small high density pellicular expanded bed adsorbents*. Journal of Chromatography A 964: 77-89

Thommes, J., M. Halfar, S. Lenz, M.R. Kula (1995) *Purification of monoclonal antibodies from whole hybridoma fermentation broth by fluidized bed adsorption*. Biotechnology and Bioengineering 45: 205-211

Tortora, G. J., Funke, B. R., and Case, C. L. (1998) *Microbiology: An Introduction*. 6th Ed. Benjamin/ Cummings Pub. Co., California pp 154-164

Torgny, L. (1998) *Electrophoresis in Gels in Protein Purification 2nd Edition*. Wiley-VCH, Inc. pp 463- 490.

Van Wezenbeek, P. M. G. F., Hulsebos, T. J. M and Schoenmakers, J. G. G. (1980). *Nucleotide sequence of the filamentous bacteriophage M13 DNA genome: Comparison with phage fd*. Gene. 11:129-148

Vergnault, H., Willemot, R. M., Bonin, M. M., (2007) *Non-electrostatic between cultured Saccharomyces cerevisiae yeast cells and adsorbent beads in expanded bed adsorption: Influence of cell wall properties*. Process Biochemistry 42: 244-251

Willoughby, N. A., Hjorth, R., Titchener-Hooker, N. J. (2000) *Experimental measurement of particle size and voidage in an expanded bed adsorption system*. Biotechnology and Bioengineering 69: 649-652

Willoughby, N. A., Kirschner, T., Smith, M. P., Hjorth, R., Titchener-Hooker, N. J. (1999) *Immobilised metal ion affinity chromatography purification of alcohol dehydrogenase from baker's yeast using an expanded bed adsorption system*. Journal of Chromatography 840: 195-204

Wilson, D. R., and Finlay, B. B. (1998). *Phage display: application, innovations and issues in phage and host biology*. Canadian J. Microbiol. 44: 313-329.

Xia, H. F., Lin, D. Q., and Yao, S. J. (2007) *Evaluation of new high-density ion exchange adsorbents for expanded bed adsorption chromatography*. Journal of Chromatography A: 1-9

Yu-Kaung, C., Shin-Ying, C., Jyun-Liang, L., and Jung-Chin, T. (2006) *Characterization of BSA adsorption on mixed mode adsorbent I. Equilibrium study in well-agitated contactor*. *Biochemical Engineering Journal*, 1-10

Yun Bai, and Charles, E. G. (2003) *Capture of a Recombinant Protein from Unclarified Canola Extract Using Streamline Expanded Bed Anion Exchange*. *Biotechnology & Bioengineering*, 81: 855-864

Yun, J., Yao, S. J., Lin, D. Q., Lu, M. H., and Zhao, W. T. (2004) *Modeling axial distribution of adsorbent particle size and local voidage in expanded bed*. *Chemical Engineering Science* 59: 449-457

Yomamoto, S., Nakanishi, K., Matsuno, R., Kamikubo, T. (1983). *Ion-exchange chromatography of proteins-Prediction of elution curves and operating conditions. Theoretical considerations*. *Biotechnology & Bioengineering*, 25: 1465-1483

