

## REFERENCES

- Adams, M. W. W. and Kelly, R. M. (1995, December, 18). Enzymes from microorganisms in extreme environments. Chem. Eng. News. 32-42.
- Bar, R. and Ulitzur, S. 1994. Bacterial toxicity of cyclodextrins: Luminous *Escherichia coli* as model. Appl. Microbiol. Biotechnol. 41:574-577.
- Biwer, A., Antranikian, G. and Heinzle, E. 2002. Enzymatic production of cyclodextrins. Applied Microbiological Biotechnology. 59 : 609-617.
- Chakravarty, S. and Varadarajan, R. 2000. Elucidation of determinants of protein stability through genome sequence analysis. FEBS Letters 470: 65-69.
- Chan, M.K., Mukund, S., Kletzin, A., Adams, M.W.W. and Rees, D.C. 1995. Structure of a hyperthermophilic tungstoperin enzyme, aldehyde ferredoxin oxidoreductase. Science 267:1463-1469.
- Chotechuan, N. 2003. Mutagenesis of  $\gamma$ -cyclodextrin glucanotransferase gene from *Bacillus circulans* A11 that affects the  $\gamma$ -cyclodextrin production. Master's Thesis, Graduate School, Chulalongkorn University.
- Chung, H.J. et al. 1998. Characterization of a thermostable cyclodextrin glucanotransferase isolated from *Bacillus stearothermophilus* ET1. J. Agric. Food Chem. 46: 952-959.
- Day, M. W. et al., 1992. X-ray crystal structures of the oxidized and reduced form of the rubredoxin from the marine hyperthermophilic archaebacterium *Pyrococcus fusiosus*. Protein Sci. 1: 1494-1507.
- del Rio, G., Morett, E. and Soberon, X. 1997. Did cyclodextrin glycosyltransferases evolve from  $\alpha$ -amylases ?. FEBS Letters. 416: 221-224.
- Duchene, D., 1988. New trends in pharmaceutical applications of cyclodextrin inclusion compounds. Cited in Huber, O., Szejtli (ed), Proceeding of the Forth International Symposium on Cyclodextrins, Kluwer Academic, : 265-275.
- Flam, F. 1994. The chemistry of life at the margins. Science 265:471-472.

- Fontana, A. 1991. How nature engineers protein (thermo) stability. cited in di Prisco, G., (ed). Life Under Extreme Conditions. pp 89-113. Berlin and Heidelberg: Springer-verlag.
- Fujiwara, S., Kakihara, H., Sakaguchi, K. and Imanaka, T. 1992. Analysis of mutation in cyclodextrin glucanotransferase from *Bacillus stearothermophilus* which affect cyclization characteristics and thermostability. Journal of Bacteriology. 174: 7478-7481.
- Fuwa, H. 1954. A new method for microdetermination of amylase activity by the use of amylases as the substrate. Journal of Biochemistry. 41: 583-603.
- Hobel, C.F.V. 2004. Access to biodiversity and new genes from thermophiles by special enrichment methods. Doctoral dissertation. Department of Biology, Faculty of Sciences, University of Iceland.
- Jaenicke, R. 1991. Protein stability and molecular adaptation to extreme conditions. Eur. J. Biochem 202:715-728.
- Janecek, S. 1997.  $\alpha$ -amylase family : molecular biology and evolution. Biophysical and Molecular Biology. 67 : 67-97.
- Janecek, S. and Sevcik, J. 1999. The evolution of starch-binding domain. FEBS Letters. 456 : 119-125.
- Kanako, T., Song, K.B., Hamamoto, T., Kudo, T. and Horikoshi, K. 1989. Construction of a chimeric series of *Bacillus* cyclomalto-dextrin glucanotransferase and analysis of the thermal stabilities and pH optima of the enzymes. Journal of Microbiology 135:3447-3457.
- Kerdsin, A., 2003 Construction of chimeric cyclodextrin glycosyltransferase by homologous recombination and study of their activities. Master's Thesis. Graduate School, Chulalongkorn University.
- Kim, Y. W., et al. 2003. Directed evolution of *Thermus* maltogenic amylase toward enhanced thermal resistance. Applied and Environmental Microbiology. 69: 4866-4874.

- Klein, C. and Schulz, G.E. 1991. Structure of cyclodextrin glycosyltransferase refined at 2.0Å resolution. J. Mol Biol. 217: 737-750.
- Knegtel, R. M. A., et al. 1995. Crystallographic studies of the interaction of cyclodextrin glycosyltransferase from *Bacillus circulans* strain 251 with natural substrates and products. J. Biol. Chem. 270:29256-29264.
- Knegtel, R.M.A., et al. 1996. Crystal structure at 2.3Å resolution and revised nucleotide sequence of the thermostable cyclodextrin glycosyltransferase from *Thermoanaerobacterium thermosulfurigenes* EM1. J. Mol Biol 256:611-622.
- Kubota, M., Matsuura, Y., Sakai, S., Katsube, Y. 1991. Molecular structure of *B. stearothermophilus* cyclodextrin glucanotransferase and analysis of substrate binding site. cited in Knegtel, R.M.A. *et al.* Crystallographic studies of the Interaction of cyclodextrin glycosyltransferase from *Bacillus cisculans* strain 251 with natural substrates and products. The Journal of Biological chemistry. 270 : 29256-29264, 1995.
- Kumar, S., Tsai, C. J., and Nussinov, R. 2000. Factors enhancing protein thermostability. Protein Engineering 13: 179-191.
- Lawson, C.L., et al., 1994. Nucleotide *sequence and X-ray structure of cyclodextrin glycosyltransferase from Bacillus circulans* strain 251 in a matose-dependent crystal from. Journal of Molecular biology. 236: 590-600.
- Leemhuis, H., Kragh, K. m., Dijkstra B. W., Dijkhuizen, L. 2003. Engineering cyclodextrin glycosyltransferase into a starch hydrolase with a high exo-specificity. Journal of Biotechnology. 103(3):203-212.
- Leemhuis, H., Rozeboom, H. J., Dijkstra, B. W., and Dijkhuizen, L., 2004. Improved Thermostability of *Bacillus circulans* Cyclodextrin Glycosyltransferase by the Introduction of a Salt-bridge. Proteins: Structure, Function, and Bioinformatics 54:128-134.
- Lehmann, M., and Wyss, M. 2001. Engineering proteins for thermostability: the use of sequence alignments versus rational design and directed evolution. Biotechnology 12: 371-375.

- McCoy, M. 1999. Cyclodextrins: great product seeks a market. Chem Eng News. 77 : 25-27.
- Mrabet, N. T., et al., 1992. Arginine residues as stabilizing elements in proteins. Biochemistry 31: 2239-2253.
- Niehaus, F., Bertoldo, C., Kahler, M., Antranikian, G. 1999. Extremophiles as a source of novel enzymes for industrial application. Appl. Microbiol Biotechnol 51: 711-729.
- Nitschke L., Heeger K., Bender H. and Schulz GE., 1990 Molecular cloning, nucleotide sequence and expression in *Escherichia coli* of the beta-cyclodextrin glycosyltransferase gene from *Bacillus circulans* strain no. 8. Appl. Microbiol Biotechnol. 33: 542-546.
- Penninga, D. 1996a. Protein engineering of cyclodextrin glycosyltransferase from Bacillus circulans strain 251. Doctoral dissertation. University of Groningen.
- Penninga, D., van der Veen, B.A., Knegetei, R.M.A., van Hijum, S.A.F.T., Rozeboom, H.J., Kaik, K.H., Dijkstra, B.W. and Dijkhuizen, L. 1996a. The raw starch binding domain of cyclodextrin glucanotransferase from *Bacillus circulans* strain 251. The Journal of Biological Chemistry. 271: 32777-32784.
- Pongsawasdi, P. and Yagisawa, M. 1987. Screening and identification of a cyclomaltodextrin glycanotransferase producing bacteria. J. Ferment. Technol. 65: 463-467.
- Rashid, N., Cornista, J., Ezaki, S., Fukui, T., Atomi, H. and Imanaka, T. 2002. Characterization of an archaeal cyclodextrin glucanotransferase with a novel C-terminal domain. Journal of Bacteriology 184:777-784.
- Riisgaard, S. 1990. The enzyme industry and modern biotechnology, in: Christiansen, C., Munck, L. Villadsen J.(Eds), Proceeding of the fifth European Congress on Biotechnology 1, Munksgaard International, Copenhagen: 91-40.
- Rimphanitchayakit, V., Tonozuka, T. and Sakano, Y. 2005. Construction of chimeric cyclodextrin glucanotransferases from *Bacillus circulans* A11 and

- Paenibacillus macerans* IAM 1243 and analysis of their product specificity. Carbohydrate Research. 340: 2279-2289
- Strokopytov, B., et al. 1996. Structure of cyclodextrin glycosyltransferase complexed with a maltononase inhibitor at 2.6 Å resolution, Implications for product specificity. Biochemistry. 35: 4241-4249.
- Strop, P., and Mayo, S. L. 2000. Contribution of surface salt bridges to protein stability. Biochemistry. 39: 1251-1255.
- Svensson, B., Jespersen, H., Sierks, M.R., Macgregor, E.A. 1989 Sequence homology between putative raw-starch binding domains from different starch-degrading enzymes. J. Biochem 264:309-311.
- Szejtli, J. 1998. Introduction and General Overview of Cyclodextrin Chemistry. Chem. Rev. 98 : 1743-1753.
- Thompson, J. D., Plewniak, F. and Poch, O. 1999. A comprehensive comparison of multiple sequence alignment programs. Nucleic Acids Res. 27:2682-2690.
- Tonkova, A. 1998. Bacterial cyclodextrin glucanotransferase: Enzyme and Microbial Technology 22: 678-686.
- Uitdehaag J.C.M. and Dijkstra B. W. 1998. A strategy for engineering thermostability: the case of cvclodextrin glycosyltransferase. In: Ballesteros A, (ed). Stability and stabilization of biocatalysts. pp 317-323. New York: Elsevier.
- Uitdehaag, J.C.M., van Alebeek, Gert-Jan W. M., van der Veen, B.A., Dijkhuizen, L. and Dijkstra, B.W. 2000. Structures of maltohexaose and maltoheptaose bound at the donor sites of cyclodextrin glycosyltransferase give insight into the mechanisms of transglycosylation activity and cyclodextrin size specificity. Biochemistry. 39: 7772-7780.
- Uitdehaag, J.C.M., van der Veen, B.A., Dijkhuizen, L. and Dijkstra, B.W. 2002. Catalytic mechanism and product specificity of cyclodextrin glycosyltransferase, a propotypical transglycosylase from the  $\alpha$ -amylase family. Enzyme and Microbial Technology. 30 : 295-304.

- van der Veen, B.A., Uitdehaag, J.C.M., Dijkstra, B.W. and Dijkhuizen, L. 2000a. Engineering of cyclodextrin glycosyltransferase reaction and product specificity. Biochemica et Biophysica Acta. 1543 : 336-360.
- van der Veen, B.A., Uitdehaag, J.C.M., Penninga, D., van Alebeek, G.J.W.M., Smith, L.M., Dijkstra, B.W. and Dijkhuizen, L. 2000b. Rational design of cyclodextrin glycosyltransferase from *Bacillus circulans* strain 251 to increase  $\alpha$ -cyclodextrin production. Journal of Molecular Biology. 296: 1027-1038.
- Wind, R.D., et al. 1995. Cyclodextrin formation by the thermostable  $\alpha$ -amylase of *Thermoanaerobacterium thermosulfurigenes* EM1 and reclassification of the enzyme as a cyclodextrin glycosyltransferase. Applied and Environmental Microbiology. 61: 1257-1265.
- Wind, R.D, Uitdehaag, J.C.M., Buitelaar, R.M., Dijkstra, B.W. and Dijkhuizen, L. 1998. Engineering of cyclodextrin product specificity and pH optima of the thermostable cyclodextrin glycosyl transferase from *Thermoanaerobacterium thermosulfurigenes* EM1. J. of Biological Chemistry. 273: 5771-5779.
- Yamamoto, T., Shikara, K., Fujiwara, S., Takagi, M., Fukui, K. and Imanaka, T. 1999. In vitro heat effect on functional and conformational changes of cyclodextrin glucanotransferase from hyperthermophilic archaea. Biochemical and Biophysical Research Communications. 265: 57-61.
- Yip, K.S.P., et al. 1998. Insights into the molecular basis of thermal stability from the analysis of ion-pair networks in the glutamase dehydrogenase family. J. Biochem. 255: 336-346.

## **APPENDICES**

## APPENDIX A

### 1. Reagents for plasmid preparation

#### 1.1. Lysis solution: 10 mL

50% Glucose	2	mL
0.5 M EDTA	0.2	mL
1 M Tris-HCl (pH 8.0)	0.25	mL
ddH <sub>2</sub> O	7.55	mL

#### 1.2. Alkaline SDS solution: 10 mL

5% SDS	2	mL
5 N NaOH	0.4	mL
ddH <sub>2</sub> O	7.6	mL

#### 1.3. High salt solution: 3 M Sodium acetate (pH 5.2)

NaOAc.3H <sub>2</sub> O	408.1	g
ddH <sub>2</sub> O	700	mL

Adjust pH to 5.2 with glacial acetic and adjust the volume to 1 litre with water.

### 2. Other reagents for preparation

#### 2.1. RNase A solution

Dissolve RNase A (pancreatic) at a concentration of 10 mg/mL in 10 mM Tris-HCl (pH 7.5), 15 mM NaCl, then heat at 100 °C, 15 min, cool slowly at room temperature, aliquot, and store at -20 °C.

#### 2.2. 10% Glycerol

Glycerol	10	mL
Water	90	mL

#### 2.3. 5× TBE buffer (for agarose gel electrophoresis)

Tris-base	54	g
Boric acid	27.5	g
0.5 M EDTA (pH 8)	20	mL



**2.4. 0.5 M EDTA**

EDTA	186.1	g
Water	1000	mL

Dissolve EDTA in 800 mL water and adjust pH to 8.0 with NaOH before adjusting volume to 1 litre, and then autoclave.

**2.5. 1M Tris-HCl**

Tris-base	121.1	g
Water	1000	ml

Adjust pH to 7-8 before adjusting volume to 1 litre, and then autoclave.

**2.6. 5% SDS (store at room temperature)**

SDS	5	g
Water	100	mL

**2.7. 5N NaOH**

NaOH	20	g
Water	100	mL

Dissolve NaOH in 70 ml water before adjusting volume to 100 mL

**2.8. Loading buffer (for agarose gel electrophoresis)**

Glycerol	20	mL
Bromphenol blue	4	mg
Water	80	mL

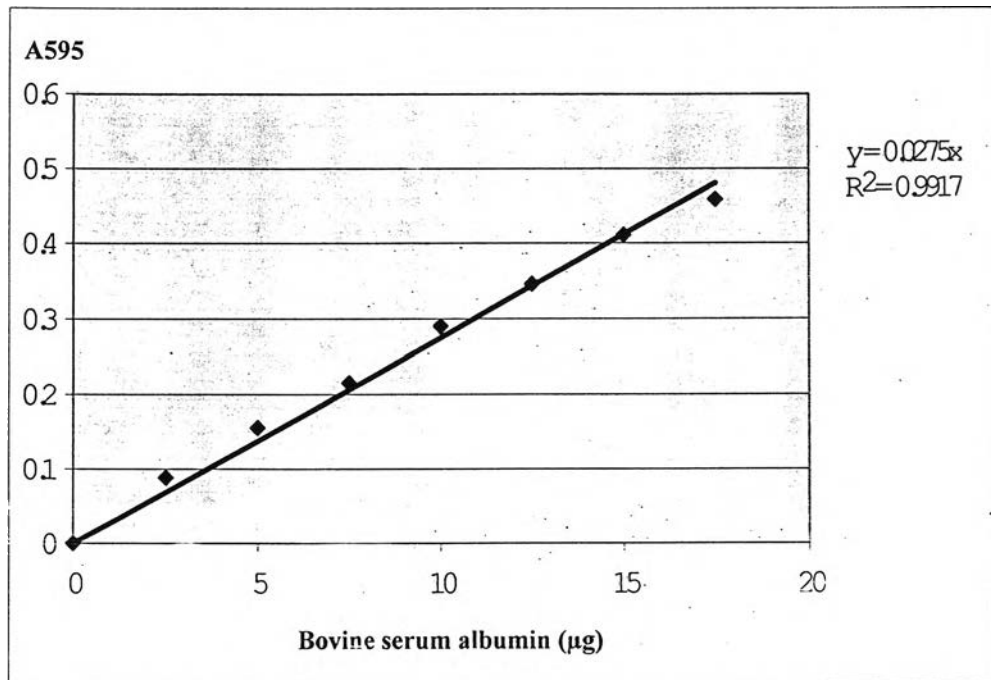
**2.9. Coomassie blue reagent**

Coomassie blue G 250	50	mg
95% Ethanol	25	mL
85% H <sub>3</sub> PO <sub>4</sub>	50	mL

Adjust volume to 500 mL with water.

## APPENDIX B

Standard curve for protein determination by Coomassie blue method.



# BIOGRAPHY

Miss Raevadee Siritunyanont was born July 30, 1971. She graduated with the Bachelor Degree of Science in Biology from Srinakharinwirot University in 1994. She has worked Department of Medical Sciences, Ministry of Public Health. She has studied for Master of Science in Biochemistry Program, Faculty of Science, Chulalongkorn University since 2003.

