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## APPENDICES

**Appendix 1: Preparation for polyacrylamide gel electrophoresis****1. Stock reagents****30% Acrylamide, 0.8% bis-acrylamide, 100 ml**

acrylamide	29.2 g
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N,N' -methylene-bis-acrylamid	0.8 g
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Adjusted volume to 100 ml with distilled water

**1.5 M tris-HCl pH 8.8**

Tris (hydroxymethyl)-aminomethane	18.17 g
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Adjusted pH to 8.8 with 1 M HCl and adjusted volume to 100 ml with distilled water

**2.0 M Tris-HCl pH 8.8**

Tris (hydroxymethyl)-aminomethane	24.2 g
-----------------------------------	--------

Adjusted pH to 8.8 with 1 M HCl and adjusted volume to 100 ml with distilled water

**0.5 M Tris-HCl pH 6.8**

Tris (hydroxymethyl)-aminomethane	6.06 g
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Adjusted pH to 6.8 with 1 M HCl and adjusted volume to 100 ml with distilled water

**1.0 M Tris-HCl pH 6.8**

Tris (hydroxymethyl)-aminomethane	12.1 g
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Adjusted pH to 6.8 with 1 M HCl and adjusted volume to 100 ml with distilled water

**2. Stock reagents for SDS-PAGE****Solution B**

2.0 M Tris-HCl pH 8.8	75 ml
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10 % SDS	4 ml
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distilled water	21 ml
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**Solution C**

1.0 M Tris-HCl pH 6.8	50 ml
10 % SDS	4 ml
distilled water	46 ml

**3. Non-denaturing PAGE****7.5% Separating gel**

30% acrylamide solution	2.5 ml
1.5 M Tris-HCl pH 8.8	2.5 ml
distilled water	5.0 ml
10% $(\text{NH}_4)_2\text{S}_2\text{O}_8$	50 $\mu\text{l}$
TEMED	10 $\mu\text{l}$

**5.0% stacking gel**

30% acrylamide solution	0.67 ml
0.5 M Tris-HCl pH 6.8	1.0 ml
distilled water	2.3 ml
10% $(\text{NH}_4)_2\text{S}_2\text{O}_8$	30 $\mu\text{l}$
TEMED	5 $\mu\text{l}$

**5x Sample buffer**

1.0 M Tris-HCl pH 6.8	3.1 ml
Glycerol	5.0 ml
1% Bromophenol blue	0.5 ml
Distilled water	1.4 ml

One part of sample buffer was added to four parts of sample

**Electrophoresis buffer, 1 litre**

(25 mM Tris, 192 mM glycine)

Tris (hydroxymethyl)-aminomethane	3.03 g
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Glycine	14.40 g
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Dissolve in distilled water to 1 litre. Do not adjust pH with acid or base (final pH should be 8.3)

#### 4. SDS-PAGE

##### 7.5% Separating gel

30% acrylamide solution	2.5 ml
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Solution B	2.5 ml
------------	--------

distilled water	5.0 ml
-----------------	--------

10% $(\text{NH}_4)_2\text{S}_2\text{O}_8$	50 $\mu\text{l}$
---	------------------

TEMED	10 $\mu\text{l}$
-------	------------------

##### 5.0% stacking gel

30% acrylamide solution	0.67 ml
-------------------------	---------

Solution C	1.0 ml
------------	--------

distilled water	2.3 ml
-----------------	--------

10% $(\text{NH}_4)_2\text{S}_2\text{O}_8$	30 $\mu\text{l}$
---	------------------

TEMED	5 $\mu\text{l}$
-------	-----------------

##### 5x Sample buffer

1.0 M Tris-HCl pH 6.8	3.1 ml
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Glycerol	5.0 ml
----------	--------

10% SDS	2.0 ml
---------	--------

2-Mercaptoethanol	0.5 ml
-------------------	--------

1% Bromophenol blue	0.5 ml
---------------------	--------

Distilled water	0.9 ml
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One part of sample buffer was added to four parts of sample. The mixture was heated 5 min. in boiling water before loading to the gel.

**Electrophoresis buffer, 1 litre**

(25 mM Tris, 192 mM glycine)

Tris (hydroxymethyl)-aminomethane 3.03 g

Glycine 14.40 g

SDS 1.0 g

Dissolve in distilled water to 1 litre. Do not adjust pH with acid or base (final pH should be 8.3).

**Appendix 2: Preparation for isoelectric focusing gel electrophoresis**

**Monomer-ampholyte solution**

30% acrylamide solution 0.9 ml

1% Bis-acrylamide solution 1.25 ml

Ampholyte pH 3-10 0.243 ml

distilled water 1.39 ml

50% Sucrose 1.186 ml

TEMED 2  $\mu$ l

0.02 M  $(\text{NH}_4)_2\text{S}_2\text{O}_8$  39  $\mu$ l

**Fixative solution, 100 ml**

Sulfosalicylic acid 4 ml

Trichloroacetic acid 12.5 ml

Methanol 30 ml

Immerse gels in this solution for 30 minutes.

**Staining solution, 100 ml**

Ethanol	27 ml
Acetic acid	10 ml
Coomassie brilliant blue R-250	0.04 ml
CuSO <sub>4</sub>	0.5 ml
Distilled water	63 ml

Dissolve the CuSO<sub>4</sub> in water before adding the alcohol. Either dissolve the dye in alcohol or add it to the solution at the end. Immerse the gel in stain for approximately 1-2 hours.

**Destaining solution****First destaining solution**

Ethanol	12 ml
Acetic acid	7 ml
CuSO <sub>4</sub>	0.5 ml
distilled water	81 ml

Dissolved the cupric sulfate in water before adding the alcohol. Immerse the gel in two of three changes of this solution until the background is nearly clear.

**Second destaining solution**

Ethanol	12 ml
Acetic acid	7 ml
Distilled water	81 ml

Immerse the gel in this solution to remove the last traces of stain and CuSO<sub>4</sub>

**Appendix 3: Preparation for buffer solution****0.2 M Potassium Acetate pH 3.0, 4.0 and 5.0**

CH <sub>3</sub> COOK	1.96 g
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Adjusted to pH 3, 4 or 5 by 0.2 M acetic acid and adjusted volume to 100 ml with distilled water.

**0.2 M Phosphate pH 6.0**

KH <sub>2</sub> PO <sub>4</sub>	2.27 g
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K <sub>2</sub> HPO <sub>4</sub>	0.58 g
---------------------------------	--------

Distilled water	100 ml
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**0.2 M Phosphate pH 7.0**

KH <sub>2</sub> PO <sub>4</sub>	0.91 g
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K <sub>2</sub> HPO <sub>4</sub>	2.32 g
---------------------------------	--------

Distilled water	100 ml
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**0.2 M Tris-HCl pH 8.0 and 9.0**

Tris (hydroxymethyl)-aminomethane	24.2 g
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Adjusted pH to 8.0 or 9.0 by 1 M HCl and adjusted volume to 100 ml with distilled water

**0.2 M Tris-Glycine NaOH pH 10.0 and 11.0**

Glycine	1.5 g
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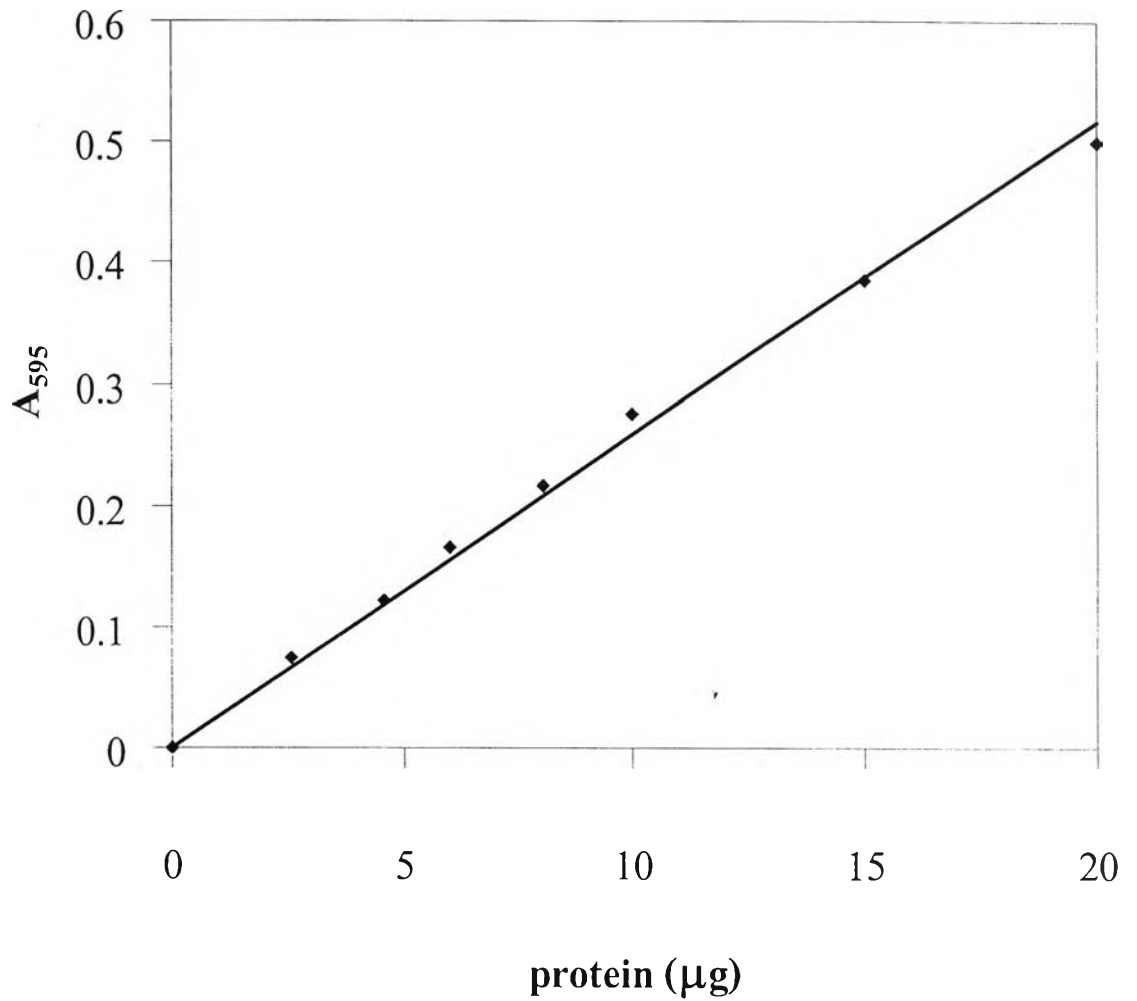
Adjusted pH to 10.0 or 11.0 by 1 M NaOH and adjusted volume to 1000 ml with distilled water

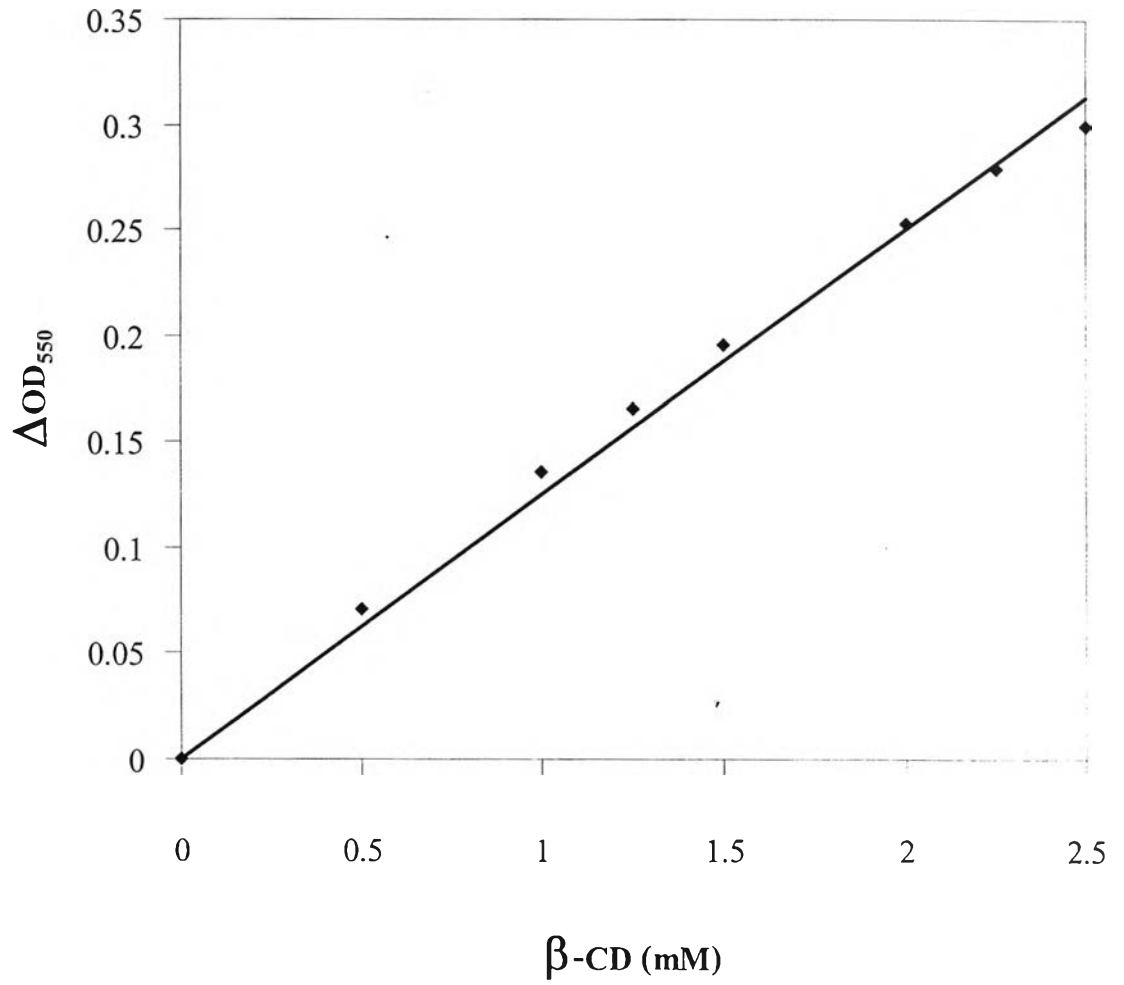
**Universal pH buffer**

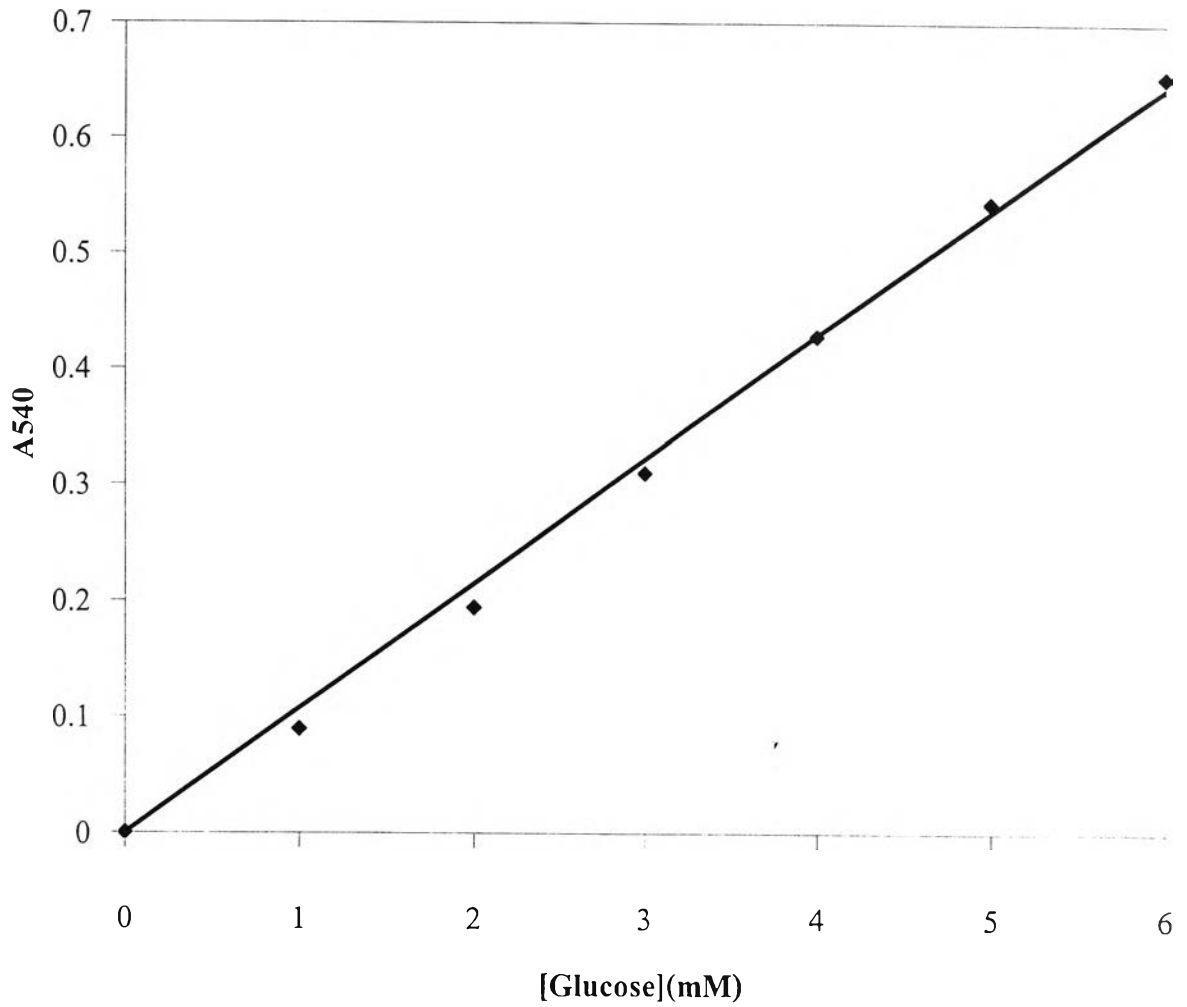
Citric acid	6.008 g
KH <sub>2</sub> PO <sub>4</sub>	3.893 g
H <sub>3</sub> BO <sub>3</sub>	1.769 g
Diethylbarbituric acid	5.266 g

Dissolve these mixtures to 100 ml with distilled water, then titrated with 0.2 M NaOH to give the appropriated pH (4.0-10.0).

**Appendix 4: Standard curve for protein determination by Bradford's method**



**Appendix 5: Standard curve of  $\beta$ -cyclodextrin by phenolphthalein method**

**Appendix 6 : Standard curve of glucose by dinitrosalicylic acid method**

**Appendix 7 :** Nucleotide sequence of *Paenibacillus* sp. A11 and annealing site of primer A, primer B and sequencing primers 1-5.

GGATAACGGGCATTGAATTGGCGGATAAAATCTTTAACATTCATGGCGTCGATCCCCCTATAAGGTAGTCTTCCTGATCCGTCTCGACT  
CCTTAATCCCACTCCCTCGATCATACTATATATCTGAGAATATTGTTATATATTGACATTTGAATTCGCTTTCATATAAAATGAACAAG

Primer A

AACACATCACTATACTTACATACAAGCTAAGGGCTATGCATTCCCTTACCTTACCCCGGTATGGAACAACCCCGGTATCTCTATTAGAGA

Primer 1

CGCCGGGTTTTTTATGTAGCCGAGATGAAGGAGGTGATCCCAAAGCGACGGACAGGCCTGTTATCCCAAGCATTGTATACGATGAG  
GAGGTATAGTATGAAAAGATTTATGAAACTAACAGCCGATGGACACTCTGGTTATCCCTCACGCTGGGCCTCTTGAGCCCGGTCCACG  
CAGCCCCGGATACCTCGGTATCCAACAAGCAGAATTCAGCACGGATGTCATATATCAGATCTTCACCGACCGGTTCTCGGACGGCAAT  
CCGGCCAACAATCCGACCGCGCGGCATTGACGGATCATGTACGAATCTTCGCTTATACTGCGGGCGGACTGGCAAGGCATCATCAA  
CAAAATCAACGACGGTTATTTGACCGGCATGGGCATTACGGCCATCTGGATTTACAGCCTGTCGAGAATATCTACAGCGTGATCAACT

Primer 2

ACTCCGGCGTCCATAATACGGCTTATCACGGCTACTGGGCGGGACTTCAAGAAGACCAATCCGGCCTACGGAACGATGCAGGACTTC  
AAAACTGATCGACACCGGCATGGCATAACATAAAAGTACATCGACTTTCACCGAACCATACATCTCCGGCTTCTTCGGATGAT  
CCTTCCTTTCGAGAGAACGGCCGCTGTACGATAACGGCAACCTGCTCGGGGATACACCAAGGATACCCAAAATCTGTTCCACCATTA  
TGGCGGCACGGATTTCTCCACCATTGAGAACGGCATTATAAAAACCTGTACGATCTGGCTGACCTGAATCATAAACAGCAGCGTCCG  
ATGTGTATCTGAAGGATGCCATCAAAATGTGGCTCGACCTCGGGGTTGACGGCATTCGCTGGACGGGTCAAGCATATGCCATTCCGGC

Primer 3

TGGCAGAAGAGCTTTATGTCCACCATTAACAACACTACAAGCCGGTCTTCACCTTCGGCGAATGGTTCCTTGGCGTCAATGAGATTAGTCC  
GGAATACCATCAATTGCTAACGAGTCCGGGATGAGCCTGCTCGATTTCCGCTTTGCCAGAAGGCCCGCAAGTGTTCAGGGACAACA  
CCGACAATATGTACGGCCTGAAAGCGATGCTGGAGGGCTCTGAAGTAGACTATGCCAGGTGAATGACCAGGTGACCTTCATCGACAAT  
CATGACATGGAGCGTTTCCACACCAGCAATGGCGACAGACGGAAGCTGGAGCAGGCGCTGGCCTTACCCTGACTTCACGGGTGTGCC  
TGCCATCTATTACGGCAGGAGCAGTATATGTCTGGCGGGAATGATCCGGACAACCGTGCTCGGATTCCTTCTTCTCCACGACGACGA

Primer 4

CCGCATATCAAGTCATCCAAAAGCTCGCTCCGCTCCGCAAAATCCAACCCGGCCATCGCTTACGGTTCACACAGGAGCGCTGGATCAAC  
AACGATGTGATCATCTATGAACGCAAATTCGGCAATAACGTGGCCGTTGTTGCCATTAACCGCAATATGAACACACCGGCTTCGATTAC  
CGGCCTTGCTACTTCCCTCCCGCAGGGCAGCTATAACGATGTGCTCGGCGGAATCTGAACGGCAATACGCTAACCGTGGGTGCTGGCG  
GTGCAGCTTCCAACCTTACTTTGGCTCCTGGCGGCACTGCTGTATGGCAGTACACAACCGATGCCACAGCTCCGATCATCGGCAATGTC  
GGCCCGATGATGGCCAAGCCAGGGTACGATTACGATTGACGGCCGCGGCTTCGGCTCCGGCAAGGAAACGGTTTACTTCCGTACAAC  
GGCAGTCACTGGCGCGGACATCGTAGCTTGGGAAGATACACAATCCAGGTGAAAATCCCTGCGGTCCCTGGCGCATCTATGATATCA  
GAGTTGCCAACGCGAGCCGAGCAGCAACATCTACGACAATTCAGAGTGTGACCGGAGACCAGGTACCGTTCGGTTCGTAATC  
AACAAATGCCACAACGGCGCTGGGACAGAATGTGTTCTCACGGCAATGTACGCGAGCTGGGCAACTGGGATCCGAACAACCGGATCGG  
CCCGATGATAATCAGGTGCTTACCAATACCCGACTTGGTATTATGATGTCAGCGTTCGGCAGGCCAAACGATTGAATTTAAATTC  
TGAAAAGCAAGGCTCCACCGTCACATGGGAAGGCGGCGCAATCGCACCTTACCACCCCAACCAGCGGCACGGCAACGATGAATGTG

Primer 5

Primer B

AACTGGCAGCCTTAAATAGGCACCTGCAAGGTAAGCAAGCGGCTCCGGGTAGAGGCTCGGGGCCGCTTGTACGTTATGTGGGGAAAGG  
TGCTATAGGGTCTTGCCTCCACACGACGATTCTTAAGGTGATTCACTGACCATAAAAAGTACCCCAAGGATTTATCGATAAAAACAAAT  
GGAAACTCCTGCATTTATCCCTTATAATTGATTAGAAAAGGCCGTTTTTAAGTGTGTATATATTTATCGTGACGGCAATGGTCTTTT  
AGATGACTACACATTAGACATCAATGAAGAAGGAGAAGCTT



**Appendix 8 : DNA alignment of CGTase from *Paenibacillus* sp RB01, T16 and A11**

SeqA Name	Len(nt)	SeqB Name	Len(nt)	Score
1 pRB	2403	2 pT	2380	98
1 pRB	2403	3 A11	2157	99
2 pT	2380	3 A11	2157	99

CLUSTAL W (1.83) multiple sequence alignment

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pRB      GGCTATGCTTTCCTTACCTTACCCCGGTATGGAACAACCCCGGTATCTCTATTAGAGACG 60
A11
pT      GGCTATGCTTTCCTTACCTTACCCCGGTATGGAACAACCCCGGTATCTCTATTAGAGACG 60

pRB      CCGGGGTTTTTTATGTAGCCGAGATGAAGGAGGTGATCCCCAAGCGCAGGACAGGCCTG 120
A11
pT      CCGGGGTTTTTTATGTAGCCGAGATGAAGGAGGTGATCCCCAAGCGCAGGACAGGCCTG 120

pRB      TTATCCCCAAGCATTGTATACGATGAGGAGGTATA-GTATGAAAAGATTTATGAAACTAA 179
A11      -----ATGAGGAGGTATA-GTATGAAAAGATTTATGAAACTAA 37
pT      TTATCCCCAAGCATTGTATACGATGAGGAGGTATATGTATGAAAAGATTTATGAAACTAA 180
          *****

pRB      CAGCCGTATGGACTCTGGTTATCCCTCAGCTGGGCCTCTTGAGCCCGGTCCACGCAG 239
A11      CAGCCGTATGGACTCTGGTTATCCCTCAGCTGGGCCTCTTGAGCCCGGTCCACGCAG 97
pT      CAGCCGTATGGACTCTGGTTATCCCTCAGCTGGGCCTCTTGAGCCCGGTCCACGCAG 240
          *****

pRB      CCCGGATACCTCGGTATCCAACAAGCAGAATTCAGCACGGATGTCATATATCAGATCT 299
A11      CCCGGATACCTCGGTATCCAACAAGCAGAATTCAGCACGGATGTCATATATCAGATCT 157
pT      CCCGGATACCTCGGTATCCAACAAGCAGAATTCAGCACGGATGTCATATATCAGATCT 300
          *****

pRB      TCACCGACCGGTTCTCGGACGGCAATCCGGCCAACAATCCGACCGCGCGGCATTGACG 359
A11      TCACCGACCGGTTCTCGGACGGCAATCCGGCCAACAATCCGACCGCGCGGCATTGACG 217
pT      TCACCGACCGGTTCTCGGACGGCAATCCGGCCAACAATCCGACCGCGCGGCATTGACG 360
          *****

pRB      GATCATGTACGAATCTTCGCTTATACTGCGGCGGCGACTGGCAAGGCATCATCAACAAA 419
A11      GATCATGTACGAATCTTCGCTTATACTGCGGCGGCGACTGGCAAGGCATCATCAACAAA 277
pT      GATCATGTACGAATCTTCGCTTATACTGCGGCGGCGACTGGCAAGGCATCATCAACAAA 420
          *****

pRB      TCAACGACGGTTATTTGACCGCATGGGCATTACGGCCATCTGGATTTACAGCCTGTCC 479
A11      TCAACGACGGTTATTTGACCGCATGGGCATTACGGCCATCTGGATTTACAGCCTGTCC 337
pT      TCAACGACGGTTATTTGACCGCATGGGCATTACGGCCATCTGGATTTACAGCCTGTCC 480
          *****

pRB      AGAATATCTACAGCGTGATCAACTACTCCGGCGTCCATAATACGGCTTATCACGGCTACT 539
A11      AGAATATCTACAGCGTGATCAACTACTCCGGCGTCCATAATACGGCTTATCACGGCTACT 397
pT      AGAATATCTACAGCGTGATCAACTACTCCGGCGTCCATAATACGGCTTATCACGGCTACT 540
          *****

pRB      GGGCGCGGGACTTCAAGAAGACCAATCCGGCCTACGGAACGATGCAGGACTTCAAAAACC 599
A11      GGGCGCGGGACTTCAAGAAGACCAATCCGGCCTACGGAACGATGCAGGACTTCAAAAACC 457
pT      GGGCGCGGGACTTCAAGAAGACCAATCCGGCCTACGGAACGATGCAGGACTTCAAAAACC 600
          *****

pRB      TGATCGACACCGCGCATGCGCATAACATAAAAAGTCATCATCGACTTTGCACCGAACCCATA 659
A11      TGATCGACACCGCGCATGCGCATAACATAAAAAGTCATCATCGACTTTGCACCGAACCCATA 517
pT      TGATCGACACCGCGCATGCGCATAACATAAAAAGTCATCATCGACTTTGCACCGAACCCATA 660
          *****

pRB      CATCTCCGGCTTCTTCGGATGATCCTTCCCTTTCAGAGAACGGCCGCTTGTACGATAACG 719
A11      CATCTCCGGCTTCTTCGGATGATCCTTCCCTTTCAGAGAACGGCCGCTTGTACGATAACG 577
pT      CATCTCCGGCTTCTTCGGATGATCCTTCCCTTTCAGAGAACGGCTTGTACGATAACG 720
          *****

pRB      GCAACCTGCTCGGCGGATACACCAACGATACCCAAAATCTGTTCCACCATTATGGCGGCA 779
A11      GCAACCTGCTCGGCGGATACACCAACGATACCCAAAATCTGTTCCACCATTATGGCGGCA 637
pT      GCAACCTGCTCGGCGGATACACCAACGATACCCAAAATCTGTTCCACCATTATGGCGGCA 780
          *****

pRB      CGGATTTCTCCACCATTTGAGAACGGCATTATAAAAACCTGTACGATCTGGCTGACCTGA 839
A11      CGGATTTCTCCACCATTTGAGAACGGCATTATAAAAACCTGTACGATCTGGCTGACCTGA 697
pT      CGGATTTCTCCACCATTTGAGAACGGCATTATAAAAACCTGTACGATCTGGCTGACCTGA 840
          *****

pRB      ATCATAACAACAGCAGCGTCGATGTGTATCTGAAGGATGCCATCAAAATGTGGCTCGACC 899
A11      ATCATAACAACAGCAGCGTCGATGTGTATCTGAAGGATGCCATCAAAATGTGGCTCGACC 757
pT      ATCATAACAACAGCAGCGTCGATGTGTATCTGAAGGATGCCATCAAAATGTGGCTCGACC 900
          *****

pRB      TCGGGGTTGACGGCATTTCGCGTGGACGCGGTCAAGCATATGCCATTTCGGCTGGCAGAAGA 959
A11      TCGGGGTTGACGGCATTTCGCGTGGACGCGGTCAAGCATATGCCATTTCGGCTGGCAGAAGA 817
pT      TCGGGGTTGACGGCATTTCGCGTGGACGCGGTCAAGCATATGCCATTTCGGCTGGCAGAAGA 960
          *****

pRB      GCTTTATGTCCACCATTAACTACAAGCCGGTCTTACCTTCGGCGAATGGTTCCCTTG 1019
A11      GCTTTATGTCCACCATTAACTACAAGCCGGTCTTACCTTCGGCGAATGGTTCCCTTG 877
pT      GCTTTATGTCCACCATTAACTACAAGCCGGTCTTACCTTCGGCGAATGGTTCCCTTG 1020
          *****

pRB      GCGTCAATGAGATTAGTCCGGAATACCATCAATTCGCTAACGAGTCCGGGATGAGCCTGC 1079
A11      GCGTCAATGAGATTAGTCCGGAATACCATCAATTCGCTAACGAGTCCGGGATGAGCCTGC 937
pT      GCGTCAATGAGATTAGTCCGGAATACCATCAATTCGCTAACGAGTCCGGGATGAGCCTGC 1080
          *****

pRB      TCGATTTCCGCTTTGCCCAGAGGGCCCGGCAAGTGTTACGGGACAACACCGACAATATGT 1139
A11      TCGATTTCCGCTTTGCCCAGAGGGCCCGGCAAGTGTTACGGGACAACACCGACAATATGT 997
pT      TCGATTTCCGCTTTGCCCAGAGGGCCCGGCAAGTGTTACGGGACAACACCGACAATATGT 1140
          *****

pRB      ACGGCCTGAAAGCGATGCTGGAGGGCTCTGAAGTAGACTATGCCAGGTGAATGACCAGG 1199
A11      ACGGCCTGAAAGCGATGCTGGAGGGCTCTGAAGTAGACTATGCCAGGTGAATGACCAGG 1057
pT      ACGGCCTGAAAGCGATGCTGGAGGGCTCTGAAGTAGACTATGCCAGGTGAATGACCAGG 1200
          *****
    
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pRB	TGACCTTCATCGACAATCATGACATGGAGCGTTTCCACACCAGCAATGGCGACAGACGGA	1259
All	TGACCTTCATCGACAATCATGACATGGAGCGTTTCCACACCAGCAATGGCGACAGACGGA	1117
pT	TGACCTTCATCGACAATCATGACATGGAGCGTTTCCACACCAGCAATGGCGACAGACGGA	1260
*****		
pRB	AGCTGGAGCAGGCGCTGGCCTTTACCCTGACTTCACGCGGTGTGCCTGCCATCTATTACG	1319
All	AGCTGGAGCAGGCGCTGGCCTTTACCCTGACTTCACGCGGTGTGCCTGCCATCTATTACG	1177
pT	AGCTGGAGCAGGCGCTGGCCTTTACCCTGACTTCACGCGGTGTGCCTGCCATCTATTACG	1320
*****		
pRB	GCAGCGAGCAGTATATGTCTGGCGGGAATGATCCGGACAACCGTGCCTCGGATTCCCTTCCT	1379
All	GCAGCGAGCAGTATATGTCTGGCGGGAATGATCCGGACAACCGTGCCTCGGATTCCCTTCCT	1237
pT	GCAGCGAGCAGTATATGTCTGGCGGGAATGATCCGGACAACCGTGCCTCGGATTCCCTTCCT	1380
*****		
pRB	TCTCCACGACGACGACCCGCATATCAAGTCATCCAAAAGCTCGCTCCGCTCCGCAAAATCCA	1439
All	TCTCCACGACGACGACCCGCATATCAAGTCATCCAAAAGCTCGCTCCGCTCCGCAAAATCCA	1297
pT	TCTCCACGACGACGACCCGCATATCAAGTCATCCAAAAGCTCGCTCCGCTCCGCAAAATCCA	1440
*****		
pRB	ACCCGGCCATCGCTTACGGTTCCACACAGGAGCGCTGGATCAACAACGATGTGATCATCT	1499
All	ACCCGGCCATCGCTTACGGTTCCACACAGGAGCGCTGGATCAACAACGATGTGATCATCT	1357
pT	ACCCGGCCATCGCTTACGGTTCCACACAGGAGCGCTGGATCAACAACGATGTGATCATCT	1500
*****		
pRB	ATGAACGCAAAATTCGCAATAACGTGGCCGTTGTTGCCATTAACCGCAATATGAACACAC	1559
All	ATGAACGCAAAATTCGCAATAACGTGGCCGTTGTTGCCATTAACCGCAATATGAACACAC	1417
pT	ATGAACGCAAAATTCGCAATAACGTGGCCGTTGTTGCCATTAACCGCAATATGAACACAC	1560
*****		
pRB	CGGCTTCGATTACCGGCTTGTCACTTCCCTCCCGCAGGGCAGCTATAACGATGTGCTCG	1619
All	CGGCTTCGATTACCGGCTTGTCACTTCCCTCCCGCAGGGCAGCTATAACGATGTGCTCG	1477
pT	CGGCTTCGATTACCGGCTTGTCACTTCCCTCCCGCAGGGCAGCTATAACGATGTGCTCG	1620
*****		
pRB	GCGGAATTCGAACGGCAATACGCTAACCGTGGGTGCTGGCGGTGACGCTTCCAACITTA	1679
All	GCGGAATTCGAACGGCAATACGCTAACCGTGGGTGCTGGCGGTGACGCTTCCAACITTA	1537
pT	GCGGAATTCGAACGGCAATACGCTAACCGTGGGTGCTGGCGGTGACGCTTCCAACITTA	1680
*****		
pRB	CTTTGGCTCCTGGCGGCACTGCTGTATGGCAGTACACAACCGATGCCACAGCTCCGATCA	1739
All	CTTTGGCTCCTGGCGGCACTGCTGTATGGCAGTACACAACCGATGCCACAGCTCCGATCA	1597
pT	CTTTGGCTCCTGGCGGCACTGCTGTATGGCAGTACACAACCGATGCCACAGCTCCGATCA	1740
*****		
pRB	TCGGCAATGTTCGGCCCGATGATGGCCAAGCCAGGGGTCACGATTACGATTGACGGCCGCG	1799
All	TCGGCAATGTTCGGCCCGATGATGGCCAAGCCAGGGGTCACGATTACGATTGACGGCCGCG	1657
pT	TCGGCAATGTTCGGCCCGATGATGGCCAAGCCAGGGGTCACGATTACGATTGACGGCCGCG	1800
*****		
pRB	GCTTCGGCTCCGGCAAGGGAACGGTTACTTCGGTACAACGGCAGTCACTGGCGGGACA	1859
All	GCTTCGGCTCCGGCAAGGGAACGGTTACTTCGGTACAACGGCAGTCACTGGCGGGACA	1717
pT	GCTTCGGCTCCGGCAAGGGAACGGTTACTTCGGTACAACGGCAGTCACTGGCGGGACA	1860
*****		
pRB	TCGTAGCTTGGGAAGATACACAAATCCAGGTGAAAAATCCCTGCGGTCCCTGGCGGCATCT	1919
All	TCGTAGCTTGGGAAGATACACAAATCCAGGTGAAAAATCCCTGCGGTCCCTGGCGGCATCT	1777
pT	TCGTAGCTTGGGAAGATACACAAATCCAGGTGAAAAATCCCTGCGGTCCCTGGCGGCATCT	1920
*****		
pRB	ATGATATCAGAGTTGCCAACGACGCGGAGCAGCCAGCAACATCTACGACAATTTTCGAGG	1979
All	ATGATATCAGAGTTGCCAACGACGCGGAGCAGCCAGCAACATCTACGACAATTTTCGAGG	1837
pT	ATGATATCAGAGTTGCCAACGACGCGGAGCAGCCAGCAACATCTACGACAATTTTCGAGG	1980
*****		
pRB	TGCTGACCGGAGACCAGGTCACCGTTTCGGTTCGTAATCAACAATGCCACAACGGCGCTGG	2039
All	TGCTGACCGGAGACCAGGTCACCGTTTCGGTTCGTAATCAACAATGCCACAACGGCGCTGG	1897
pT	TGCTGACCGGAGACCAGGTCACCGTTTCGGTTCGTAATCAACAATGCCACAACGGCGCTGG	2040
*****		
pRB	GACAGAATGTGTTCCACAGGCAATGTCAGCGAGCTGGGCAACTGGGATCCGAAACAACG	2099
All	GACAGAATGTGTTCCACAGGCAATGTCAGCGAGCTGGGCAACTGGGATCCGAAACAACG	1957
pT	GACAGAATGTGTTCCACAGGCAATGTCAGCGAGCTGGGCAACTGGGATCCGAAACAACG	2100
*****		
pRB	CGATCGGCCGATGTATAATCAGGTCGTCTACCAATACCCGACTTGGTATTATGATGTCA	2159
All	CGATCGGCCGATGTATAATCAGGTCGTCTACCAATACCCGACTTGGTATTATGATGTCA	2017
pT	CGATCGGCCGATGTATAATCAGGTCGTCTACCAATACCCGACTTGGTATTATGATGTCA	2160
*****		
pRB	GCGTTCGGCAGGCCAAACGATTGAATTTAAATTCCTGAAAAAGCAAGGCTCCACCGTCA	2219
All	GCGTTCGGCAGGCCAAACGATTGAATTTAAATTCCTGAAAAAGCAAGGCTCCACCGTCA	2077
pT	GCGTTCGGCAGGCCAAACGATTGAATTTAAATTCCTGAAAAAGCAAGGCTCCACCGTCA	2220
*****		
pRB	CATGGGAAGGCGGCTGCGAATCGCACCTTACCACCCCAACAGCTGGCTACTGGCTAA	2279
All	CATGGGAAGGCGGCTGCGAATCGCACCTTACCACCCCAACAGCTGGCTACTGGCTAA	2131
pT	CATGGGAAGGCGGCTGCGAATCGCACCTTACCACCCCAACAGCTGGCTACTGGCTAA	2274
*****		
pRB	CTGATGAATGTGAACGGCTAGCCTTAATAGGCACTTGCAAGGTAAGCAAGCGGCTCCGG	2339
All	C-GATGAATGTGAACGGCTAGCCTTAATAGGCACTTGCAAGGTAAGCAAGCGGCTCCGG	2157
pT	C-TATGAATGTGAACGGCTAGCCTTAATAGGCACTTGCAAGGTAAGCAAGCGGCTCCGG	2332
* *****		
pRB	GTAGAGTTTATATAGGCTATCTTGTCTAAGGTAAGCTATAGCTGTGCTCTTCTGGGTA	2399
All	GTAGAGTTTATATAGGCTATCTTGTCTAAGGTAAGCTATAGCTGTGCTCTTCTGGGTA	2399
pT	GTAGAGTTTATATAGGCTATCTTGTCTAAGGTAAGCTATAGCTGTGCTCTTCTGGGTA	2380
-----		
pRB	GAGG 2403	
All	----	
pT	----	

\* denote identical base

**Appendix 9: Deduced amino acid alignment of CGTase from *Paenibacillus* sp RB01, T16 and A11**

	SeqA Name	Len(aa)	SeqB Name	Len(aa)	Score
	1 pRB	732	2 pT	713	96
	1 pRB	732	3 A11	713	97
	2 pT	713	3 A11	713	99

=====  
CLUSTAL W (1.83) multiple sequence alignment

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pT      MKRFMKLTAVWTLWLSLTGLGLLSPVHAAPDTSVSNKQNFSTDVIIYQIFDRFSDGNPANN 60
A11     MKRFMKLTAVWTLWLSLTGLGLLSPVHAAPDTSVSNKQNFSTDVIIYQIFDRFSDGNPANN 60
pRB     MKRFMKLTAVWTLWLSLTGLGLLSPVHAAPDTSVSNKQNFSTDVIIYQIFDRFSDGNPANN 60
*****

pT      PTGAAFDGSCTNLRLYCGGDWQGIINKINDGYLTGMGITAIWISQPVENIYSVINYSVGVH 120
A11     PTGAAFDGSCTNLRLYCGGDWQGIINKINDGYLTGMGITAIWISQPVENIYSVINYSVGVH 120
pRB     PTGAAFDGSCTNLRLYCGGDWQGIINKINDGYLTDMGITAIWISQPVENIYSVINYSVGVH 120
*****

pT      NTAYHGYWARDFKKTNPAYGTMQDFKNLIDTAHAHNKVIIDFAPNHTSPASSDDPSFAE 180
A11     NTAYHGYWARDFKKTNPAYGTMQDFKNLIDTAHAHNKVIIDFAPNHTSPASSDDPSFAE 180
pRB     NTAYHGYWARDFKKTNPAYGTMQDFKNLIDTAHAHNKVIIDFAPNHTSPASSDDPSFAE 180
*****

pT      NGRLYDNGNLLGGYTNDTQNLFHYYGGTDFSTIENGIYKNLYDLADLNHNNSVDVYLKD 240
A11     NGRLYDNGNLLGGYTNDTQNLFHYYGGTDFSTIENGIYKNLYDLADLNHNNSVDVYLKD 240
pRB     NGRLYDNGNLLGGYTNDTQNLFHYYGGTDFSTIENGIYKNLYDLADLNHNNSVDVYLKD 240
*****

pT      AIKMWLDLGVGDIRVDAVKHMPFGWQKSEFMSTINNYKPVFTFGEWFLGVNEISPEYHQFA 300
A11     AIKMWLDLGVGDIRVDAVKHMPFGWQKSEFMSTINNYKPVFTFGEWFLGVNEISPEYHQFA 300
pRB     AIKMWLDLGVGDIRVDAVKHMPFGWQKSEFMSTINNYKPVFTFGEWFLGVNEISPEYHQFA 300
*****

pT      NESGMSLLDFRFAQKARQVFRDNTDNMYGLKAMLEGSEVNYAQVNDQVTFIDNHDMERFH 360
A11     NESGMSLLDFRFAQKARQVFRDNTDNMYGLKAMLEGSEVDYAQVNDQVTFIDNHDMERFH 360
pRB     NESGMSLLDFRFAQKARQVFRDNTDNMYGLKAMLEGSEVDYAQVNDQVTFIDNHDMERFH 360
*****

pT      TSNGDRRKLEQALAFTLT SRGVP AIYYGSEQYMSGGNDPDNRARIPSFSTTTTAYQVIQK 420
A11     TSNGDRRKLEQALAFTLT SRGVP AIYYGSEQYMSGGNDPDNRARIPSFSTTTTAYQVIQK 420
pRB     TSNGDRRKLEQALAFTLT SRGVP AIYYGSEQYMSGGNDPDNRARIPSFSTTTTAYQVIQK 420
*****

pT      LAPLRKSNPAIAYGSTQERWINNDV IYERKFGNNVAVVA INRNMNTPASITGLVTSLPQ 480
A11     LAPLRKSNPAIAYGSTQERWINNDV IYERKFGNNVAVVA INRNMNTPASITGLVTSLPQ 480
pRB     LAPLRKSNPAIAYGSTQERWINNDV IYERKFGNNVAVVA INRNMNTPASITGLVTSLPQ 480
*****

pT      GSYNDVLGGILNGNTLT VGAGGAASNFTLAPGGTAVWQYTTDATAPIIGNVGPMAKPGV 540
A11     GSYNDVLGGILNGNTLT VGAGGAASNFTLAPGGTAVWQYTTDATAPIIGNVGPMAKPGV 540
pRB     GSYNDVLGGILNGNTLT VGAGGAASNFTLAPGGTAVWQYTTDATAPIIGNVGPMAKPGV 540
*****

pT      TITIDGRFGSGKGT VYFGTTAVTGADIVAWEDTQIQVKI PAVPGGIYDIRVANAAGAAS 600
A11     TITIDGRFGSGKGT VYFGTTAVTGADIVAWEDTQIQVKI PAVPGGIYDIRVANAAGAAS 600
pRB     TITIDGRFGSGKGT VYFGTTAVTGADIVAWEDTQIQVKI PAVPGGIYDIRVANAAGAAS 600
*****

pT      NIYDNFEVLTGDQVTVRFV INNATTALGQNVFLTGNVSELGNWDPNNAIGPMYNQVVYQY 660
A11     NIYDNFEVLTGDQVTVRFV INNATTALGQNVFLTGNVSELGNWDPNNAIGPMYNQVVYQY 660
pRB     NIYDNFEVLTGDQVTVRFV INNATTALGQNVFLTGNVSELGNWDPNNAIGPMYNQVVYQY 660
*****

pT      PTWYYDVSVPAGQTIEFKFLKQGSTV TWEGGANRTFTTPTSG-----TATMNVNW 711
A11     PTWYYDVSVPAGQTIEFKFLKQGSTV TWEGGANRTFTTPTSG-----TATMNVNW 711
pRB     PTWYYDVSVPAGQTIEFKFLKQGSTV TWEGGCESHLSPPQPAYWLTDECELASLNRHL 720
*****
: : : * . . * : : * :

pT      LA----- 713
A11     QP----- 713
pRB     QGKQAAPGRGLL 732

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\* denote identical base

## BIOGRAPHY

Miss Ratiya Charoensakdi was born on May 3, 1966. She graduated with the Bachelor Degree of Science in Biochemistry from Chulalongkorn University in 1988 and graduated the Master degree of Science in Nutrition from Mahidol University in 1991. She has working at Department of Biochemistry, Faculty of Medicine, Siriraj Hospital. She continued studying for the degree of Philosophy of Science in Biochemistry Program., at the Faculty of Science, Chulalongkorn University.

