

## 附錄一 不同來源之阿拉伯呔喃糖苷酵素性質比較

### 表一 真菌類來源之阿拉伯呔喃糖苷酵素性質比較

Organism		Molecular weight	pI	Optimum temperature (°C)	Optimum pH	Polymer attacked <sup>a</sup>
<i>Aspergillus awamori</i>	I	81 000	3.3	60	4.0	BA
	II	62 000	3.6	60	4.0	BA
<i>Aspergillus nidulans</i>		65 000	3.3	65	4.0	
<i>Aspergillus niger</i> 5-16	Intracellular	67 000	3.5	60	4.0	BA
	Extracellular	53 000	3.6	—	4.0	BA, AX
<i>Aspergillus sojae</i>		34 300	3.9	50	5.0	
<i>Aspergillus terreus</i>	I	39 000	7.5	—	3.5-4.5	OSX, RAX, AGX, BA
	II	59 000	8.3	—	3.5-4.5	OSX, RAX, AGX, BA
	III	59 000	8.5	—	3.5-4.5	OSC, RAX, AGX, BA
<i>Aureobasidium pullulans</i>		210 000	—	75	4.0-4.5	BA, AX, OSX
<i>Cochliobolus carbonum</i>		63 000	—	50	3.5-4.0	BA, AX
<i>Cytophaga xylanolytica</i>		160 000	6.1	45	5.8	AX, BA
		-240 000				
<i>Dichomitus squalens</i>		60 000	5.1	60	3.5	BA, AX
<i>Penicillium capsulatum</i>	I	64 500	4.15	60	4.0	BA, AX, AXO
	II	62 700	4.54	55	4.0	BA, AX, AXO
<i>Sclerotinia sclerotiorum</i>		63 000	7.5	—	4.0-4.5	BA, AX
<i>Penicillium purpurogenum</i>		58 000	6.5	50	4.0	AX
<i>Trichoderma reesei</i>		53 000	7.5		4.0	AX, AXO

<sup>a</sup> AX, arabinoxylan; BA, beet arabinan; CX, corn endosperm xylan; OSX, oat spelt xylan; AXO, arabinoxylan oligosaccharides; RAX, rye arabinoxylan; AGX, arabinoglucuronoxylan.

### 表二 細菌類來源之阿拉伯呔喃糖苷酵素性質比較

Organism		Molecular weight	pI	Optimum temperature (°C)	Optimum pH	Polymer attacked <sup>a</sup>
<i>Bacillus polymyxa</i>		166 000	4.7	—	—	AXO only
<i>Bacillus stearothermophilus</i>		110 000	—	70	7.0	Used for delignification
<i>Bacillus subtilis</i>		65 000	5.3		6.5	BA
<i>Bacteroides xylanolyticus</i>		364 000		50	5.5-6.0	AXO only
		(61 000)		30-40	6.0	AX only
<i>Bifidobacterium adolescents</i>		240 000	6.0	55	6.0-6.5	BA, AX, OSX
<i>Clostridium acetobutylicum</i>		94 000	8.2		5.0-5.5	BA
<i>Ruminococcus albus</i>		310 000	3.8		6.9	AH
<i>Streptomyces</i> sp. 17-1		92 000	4.4		6.0	BA, AX, AG
<i>Streptomyces diastaticus</i>	C1	38 000	8.8		5.0-6.5	AX
	C2	60 000	8.3		5.0-6.5	AX
<i>Streptomyces diastatochromogenes</i>	065	73 000			6.0	BA
<i>Streptomyces purpurascens</i>		495 000	3.9		6.5	A <sub>2</sub> , A <sub>3</sub>

<sup>a</sup> AX, arabinoxylan; BA, beet arabinan; CX, corn endosperm xylan; OSX, oat spelt xylan; AXO, arabinoxylan oligosaccharides; A<sub>2</sub>, arabinobiose; A<sub>3</sub>, arabinotriose.

表三 植物類來源之阿拉伯呔喃糖苷酵素性質比較

Source		Molecular weight	pI	Optimum temperature (°C)	Optimum pH	Polymer attacked <sup>a</sup>
Spinach leaf	I	118 000	4.8			
	II	68 000	4.2		4.8	
Carrot cell culture		84 000	5.6	55	3.8	BA
Radish seeds		64 000	4.7			BA, AG
Soybean seeds		87 000	4.8			
Japanese pear fruit		42 000			5.0	

<sup>a</sup> BA, beet arabinan; AG, arabinogalactan.



## 附錄二 各突變株所使用之寡核甘酸引子

E223G ( + ) : 5'- GAT CTC GGG AAC GGC TTG TTC -3'

E223G ( - ) : 5'- GAA CAA GCC GTT CCC GAG ATC -3'

D191N ( + ) : 5'- GCC GAG ACC AAC AGC CGC AAT ACA GGC  
AAC -3'

D191N ( - ) : 5'- GTT GCC TGT ATT GCG GCT GTT GGT CTC GGC  
-3'

D191G ( + ) : 5'- GCC GAG ACC AAC AGC CGC GGT ACA GGC  
AAC -3'

D191G ( - ) : 5'- GTT GCC TGT ACC GCG GCT GTT GGT CTC GGC  
-3'

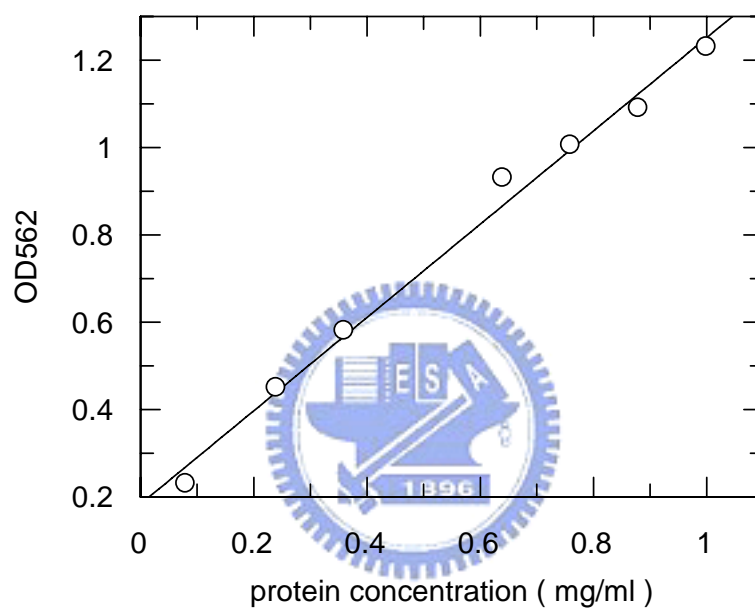
D299N ( + ) : 5'- CTC GGC ATT GGC GGC AAC AAC AGC -3'

D299N ( - ) : 5'- GCT GTT GTT GCC GCC AAT GCC GAG -3'

### 附錄三 蛋白質濃度的測定

以標準品 BSA 建立蛋白質濃度檢量線

$$A_{562} (\text{OD}) = 1.1571 * (\text{蛋白質濃度}) + 0.1577$$



附錄四 *Aspergillus kawachii* IFO4308 與 *Trichoderma koningii*

G-39  $\alpha$ -L-arabinofuranosidase 蛋白質序列之比對

Consensus key (see documentation for details)

\* - single, fully conserved residue

: - conservation of strong groups

. - conservation of weak groups

- no consensus

*Aspergillus kawachii* MFSRRNLLALGLAAT--VSAGPCDIYEAGDTPCVAHSTTRALYSSFSGALYQLQRGSD

*Hypocrea koningii* MLSNARI IAAGCIAAGSLVAAGPCDIYSSGGTPCVAHSTTRALFSAYTGPLYQVKRGSD

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*Aspergillus kawachii* DTTTTISPLTAGGIADASAQDTFCANTTCLITIIYDQSGNGNHLTQAPPGGFDGPDTDGY

*Hypocrea koningii* GATTAI SPLSSG-VANAAQDAFCAGTTCLITIIYDQSGRGNHLREAPPGGFSGPESNGY

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*Aspergillus kawachii* DNLASAI GAPVTLNGQKAYGVF MSPGTGYRNEATGTATGDEAEGMYAVLDGTHYNDACC

*Hypocrea koningii* DNLASAI GAPVTLNGQKAYGVF MSPGTGYRNNAA SGTA KGDA AEGMYAVLDGTHYNGACC

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*Aspergillus kawachii* FDYGNAETSSTDTGAGHMEA IY LGNSTTWGYGAGDGPWIMVDMENLFSGADEGYNSGDP

*Hypocrea koningii* FDYGNAETNSRDTGNHMEA IY FGDSTVWGTGSGKGPWIMADLENGLFSGSSPGNAGDP

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*Aspergillus kawachii* S I SYRFVTA AVKGGADKWAIRGANAASGSLSTYYSGARPDYSGYNPMSKEGAI ILGIGGD

*Hypocrea koningii* S I SYRFVTA AIKGQPNQWAIRGNAASGSLSTFYSGARPQVSGYNPMSKEGAI ILGIGGD

\*\*\*\*\* :\* :\* :\*\*\*\*\* :\*\*\*\*\* :\*\*\*\*\* :\*\*\*\*\* :\*\*\*\*\* :\*\*\*\*\*

*Aspergillus kawachii* NSNGAQTFYEGVMTSGYPSDDTENSVQENI VAAKYVVGSLVSGP SFTSGEVVSLRVTPP

*Hypocrea koningii* NSNGGQTFYEGVMTSGYPSDATENSVQANI VAARYAVAPLTS GPALT VGS S I SLRATTA

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*Aspergillus kawachii* GYTTRYIAHTDTT VNTQVDDDSSTLKEEASWT VVTGLANSQCFSFESVDTPGSYIRHY

*Hypocrea koningii* CCTTRYIAHSGSTVNTQVSSSSATALKQASWTVRAGLANNACFSFESQDTSGSYIRHS

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Aspergillus kawachii NFELLLNANDGTKQFHEDATFCPQAALNGEGTSLRSWSPTRYFRHYENVLYAASNGGVQ  
 Hypocrea koningii NFGLVLNANDGSKLFAEDATFCTQAGINGQSSIRSWSPTRYFRHYNTLYIASNGGVH  
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Aspergillus kawachii TFDKTSFNNDVSFEIETAFAS  
 Hypocrea koningii VFDATAAFNDDVSFVVSGGFA-  
 .\*\*.:\*.:\*.:\*.:\*.:\* . . \*\*

Sequence type explicitly set to Protein

Sequence format is Pearson

Sequence 1: Aspergillus kawachii 500 aa

Sequence 2: Hypocrea koningii 499 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 72

註 Trichoderma koningii G-39也稱Hypocrea koningii G-39

