

附錄三 Human 以及 *Thermotoga maritime* α -L-fucosidase

蛋白質序列比對

Consensus key (see documentation for details)

* - single, fully conserved residue
: - conservation of strong groups
. - conservation of weak groups
- no consensus

CLUSTAL W (1.81) multiple sequence alignment

Homo_sapiens_	MRSRPAGPALLLLLLFLGAAESVRRAQPPR	RYTPDWP	SLDSRPLPAWFDE
Thermotoga_maritima_MSB8	-----	-----	-----
		MI	SMKP
		RYKPDW	E
		ESLREHTV	PKWFDK
		.	***.*** * .:.* ***:
 The logo of the University of Hong Kong is centered between the second and third sequence blocks. It features a circular design with the year '1896' at the bottom and a central emblem.			
Homo_sapiens_	AKFGVFIHWGVFSVPAWGS	-----	EWFWWHWQGEGRPQYQRFMR
Thermotoga_maritima_MSB8	AKFGIFIHWGIYSVPGWATPTGELGKVPMDA	WFFQNPYAEWYE	NSLRIKE
	*****.*****.***.*..	**:	: . * : *: .
Homo_sapiens_	DNYPPGFSYADFGPQFTARFFHPE	EWADLF	QAAGAKYVVLTT
Thermotoga_maritima_MSB8	SPTWEYHV	KTYGENFYEKFADLFTAEKWDPQ	EWADLFKKAGAKYVIPPT
	..*	.*.**.**. ***. :.*;*****:	*****: **
Homo_sapiens_	KHHEGFTNWPSPVSNWNSKDVGPHRD	LVGE	GTALRKRNIRYGLYHS-L
Thermotoga_maritima_MSB8	KHDGFCLWG-TKYTD	NSVKRGPKRDLVGD	LAKAVREAGLRFGVYYSGG
	: * . . ;** . **;*****:*.**.*: .;*:***:*		
Homo_sapiens_	LEWFHP	LYLLDKNGFKTQHFVS	AKTMPELYDLVNSYKPDLIWSDG
Thermotoga_maritima_MSB8	LDWRFTTEPIRYPEDLSYIRPNT	YEYADYAYKQVMELVDLYLPDVL	WNDM
	:. .. * * . . : . : . : . : **: * ***: *.**:.*		
Homo_sapiens_	EWECPDTWNSTNFLSWLYNDSPVKDEVV	VNDRWGQNCSC	HGGYYNCED
Thermotoga_maritima_MSB8	GWPE-KGKEDLKYLFAYYYNKHP	EGSVNDRWGVP	PHWDFKTAEYHVN-
	* . . : . : . : **. * * ****		.: . * : :

Homo_sapiens_ KFKPQSLPD**H**WE**M**CTS**I**D**K****F**SWGYRRDMALSDVTEE**E****I****I**SEL**V**QT**V**SL
 Thermotoga_maritima_MSB8 --YPGDLPGY**K**WE**F**TRGIG-**L**SFGYNRNEGPEH**M**LSVEQLVYT**L**VD**V**VSK
 * .**.;***: .*. :*:***.*: . .: . .::: **;.*

Homo_sapiens_ GGNYLLNI**G**PTKD**G**LI**V**P**I**F**Q**ERLLAV**G**KW**L**SING**E**A**I**Y**A**SK**P**WR--VQW
 Thermotoga_maritima_MSB8 GGNLLLN**V**GPKGD**G**TIPD**L**Q**K**ERLL**G**LE**W**LRKY**G**DA**I**Y**G**TSV**W**ERCCAK
 *** ***;**. ** * : ;****;*:*** *;***.;. *

Homo_sapiens_ EKNTTSVWYTSKGSA**V**YA**I**FLHW**P**ENG**V**LN**L**ESPIT**T**TKITMLGI**Q**GD
 Thermotoga_maritima_MSB8 TEDGTEIRFTR**K**CNR**I**F**V**I**F**LG**I**PT**G**E**K**I**V**I**E**DLN**L**SA**G**T**V**R**H**FL--T**G**E
 :: *.: ;* * . ;:*** * . :*. . :* * :* * :

Homo_sapiens_ LKWSTD**P**D**K**GL**F**ISLP**Q**LPPSAVPAEF**A**WTI**K**LTGV**K**
 Thermotoga_maritima_MSB8 RLSF**K**NVG**K**N**L**E**I**T**V**P**K**KL**E**TDS**I**TL**V**LEA**V**E---
 .: .*,* *;*: .: . .:

Sequence type explicitly set to Protein

Sequence format is Pearson

Sequence 1: Homo_sapiens_

Sequence 2: Thermotoga_maritima_MSB8

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 31

