

>WheeHeim_11390-12103

ATGGCTCCGGCATTGATTTTCGAAAGCAGGTCCGACCGCTCCCGCTGGCGCGTGGGTTGTCGTCGTGGCGGGC
GGTCTCGGCATTGCGATTATACTCGTAAGAGTGGCACTAATGATTCGCCGAAGTTGTCGAAGATACTCCGGAG
ATCCTGGGGTTGGGGAGGGCGGAATCCCGGCGGATTATTCCGGTAAATCCTCCCCTCCGGTAGTACGGAAG
TCACTTACGAATCAAATGAGGCGTGGGGGCGAGGCTGCCGTTACGTATCTCATCGCTCAGGGGTATAACGCGGCTC
TCGCGAGTAGTGCAATTACAAAGGCTCTCGCGGGCGGTGTGGACATCGACGGAAATAAAATGTCCATTCAGGAAT
GGTCGCTCTGGAGTTTGGCTCTGGCCAAGCTGGGATCTCCCCGTATCCCGTAAACGTGGCTCCGCCACATCAGT
TCCCGACCGGTAGACACCGGACCCCGCCAAGTAATGGCGGTGGAACACTACGCCGAAGCCTCCGAGCAATACGGT
TCCGGCGCATTGGGTGGAAGTCGCTAAGCGTGGCGATTCAATTTCCAGTATCGCCGAAAGCACGGTAAGGGCTG
GAAGGAAACATGGGATTTCAATCTCAAGTATCGTTCGCGCAACTCGTGCAATTCTCAAGGCCCGTGGCCCAAAT
CTGATTTACGCGGGCACACCATTGGGTTCCCAAGTAG

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MASGIDFGKQVGPLPLGAWVVVVAGGLGIAIYTRKSGTNDSPVEEDTSGDPGVGEGGIPGGFIPVNPPTSGSTEVTYE
SNEAWGQAAVTYLIAQGYNAALASSAITKALAGGVDIDGNKMSIQEWLSLALAKLGSPYPVNVAPPTSVPGPVD
GPPPSNGGGTTPKPSNTVPAHWVEVAKRGDSISSIAAKHGKWKETWDFNLKYRSAATRAILKARGPNLIYAGTTI
VPKZ

CDD: smart00257, lysin motif, %identity 25, %coverage 21.85, E val 0.000106336

NCBI Blast: WP_085564049 LysM peptidoglycan-binding domain-containing protein [Streptomyces griseofuscus] >gi|1187456035|gb|OSO98944.1| transglycosylase [Streptomyces griseofuscus] % Identity 17.04, % Aligned 29.59, % Coverage 56.7227, E-value .00419

Phagesdb Blast: Luck3, gp24, lysin A, Scor 38, Evaluate 0.014

HHPred (from PECAAN): 5BUM_A, ChitanaseA_LysM domain, probability 64.4, % coverage 22.2689, Or external:

		Template alignment	Template 3D structure	PDBe						
<input type="checkbox"/>	3.	4PXV_C Chitinase A; LysM domain, carbohydrate-binding module, Chitinase; 1.8A {Pteris ryukyuensis}; Related PDB entries: 4PXV_A 4PXV_D 4PXV_B			Probability: 69.11	E-value: 13.0	Score: 17.66	Aligned Cols: 42	Identities: 24%	Similarity: 0.291
Q	ss_pred	hhCCcHHHHHHcCCCchheeccccchhhHHHHHHHHhCCCeEecceEEecC								
Q	WheeHeim25-121	185	KRGDSISSIAAKHGKWKETWDFNLKYRSAATRAILKARGPNLIYAGTTI	VPK	238	(239)				
Q	Consensus	185	krgdsissiaakhgkwtwdfnlkyrsaatrailkargpnliyagttiwvpk	238	(239)					
			+.++++.++.+++...+.+...+-. .	..+++.+.	+.+++ +					
T	Consensus	8	~~~~~	49	(49)					
T	4PXV_C	8	KSGDTCYATISQARGISLSDFESWAG-----IDCNLQIGQVVCVSK	49	(49)					
T	ss_dssp	CTTCCHHHHHHTTCCHHHHHSTT-----CCGGCCCTCEEESCC								
T	ss_pred	cCCCCHHHHHHhCCHHHHHhCC-----CCCCCCCCCEEEeCC								