

## Result of 'Query profile'

hmmpfam - search one or more sequences against HMM database  
 HMMER 2.3.1 (June 2003)  
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HMM file: ./tmp/antimicrobial.hmm  
 Sequence file: ./tmp/10567.query

Query sequence: test  
 Accession: [none]  
 Description: [none]

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
mellitin		63.9	3.5e-19	1
magainin		-15.6	6	1
protegrin		-16.0	6	1
bacteriocin1		-32.2	6	1
bacteriocin2		-22.9	6	1
cecropin		-37.8	6	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
cecropin	1/1	3	38	1	41	-37.8	6
protegrin	1/1	8	21	1	15	-16.0	6
bacteriocin1	1/1	16	61	1	42	-32.2	6
bacteriocin2	1/1	44	69	1	27	-22.9	6
mellitin	1/1	44	69	1	26	63.9	3.5e-19
magainin	1/1	53	58	1	10	-15.6	6

Alignments of top-scoring domains:

cecropin: domain 1 of 1, from 3 to 38: score -37.8, E = 6  
 \*->GwlkklgKkiERvGlyTrdATlQglgvAqkAANVAaTARGk<-\*  
 +l + v + + + A++ a A +  
 test 3 -FLVNVA----LVFMVVYISYIYAPEPEPEPEAEADAE 38

protegrin: domain 1 of 1, from 8 to 21: score -16.0, E = 6  
 \*->GRLCYCRrrfCvCva<-\*  
 L + + a  
 test 8 -ALVFMVVYISYIYA 21

bacteriocin1: domain 1 of 1, from 16 to 61: score -32.2, E = 6  
 \*->kyYNGVycnkk.....kcwVGwGeAigaIgnnviagwatGlaag  
 ++Y +y +++ ++ d a ++ v ++tGl a  
 test 16 ISY---IYAAPepapepEAEADAEADPEAGIGAVLKVLTGTPAL 59  
 kk<-\*  
 test 60 IS 61

bacteriocin2: domain 1 of 1, from 44 to 69: score -22.9, E = 6  
 \*->GksGviktisHEC.nlnsWaFlatCCsa<-\*  
 G v+k + + l sW + +  
 test 44 GIGAVLKVLTGTPALISW--IKRKRQQ 69

mellitin: domain 1 of 1, from 44 to 69: score 63.9, E = 3.5e-19  
 \*->GiGAlKvLatGLPaLisWiKrKRqq<-\*  
 GiGA+LKvL+tGLPaLisWiKrKRqq  
 test 44 GIGAVLKVLTGTPALISWIKRKRQQ 69

magainin: domain 1 of 1, from 53 to 58: score -15.6, E = 6  
 \*->QQDYtgqwmD<-\*  
 t+g  
 test 53 ----TTGLPA 58

Supplementary Figure 3: Results of 'Query profile' generated from querying a sequence against the profile library 'antimicrobial.hmm'. The result shows: (1) the score of each family profile in the profile library against the query sequence submitted; (2) the domain of each family that matches the query sequence; (3) the alignment of the domains to the query sequence with the conserved residues shown in capital letters. In this particular example the query sequence most likely belongs to the mellitin family, which has the highest score and lowest E-value.