Appendix IV

Swissprot search results

ของโปรตีน Allergen Pen m 2

UniProtKB/TrEMBL entry Q8I9P7

Entry information

Entry name	Q8I9P7_PENMO
Primary accession number	Q8I9P7
Secondary accession numbers	None
Entered in TrEMBL in	Release 23, March 2003
Sequence was last modified in	Release 23, March 2003
Annotations were last modified in	Release 25, October 2003

Name and origin of the protein

Protein name	Allergen Pen m 2
Synonyms	None
Gene name	None
From	Penaeus monodon (Penoeid shrimp) [TaxID: 6687]
Taxonomy	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea; Penaeidae; Penaeus.

References

[1] NUCLEOTIDE SEQUENCE.
TISSUE=Muscle;
PubMed=12496430
Yu C.J., Lin Y.F., Chiang B.L., Chow L.P.;
"Proteomics and immunological analysis of a novel shrimp allergen, Pen m 2.";
J. Immunol. 170:445-453(2003).

[2] NUCLEOTIDE SEQUENCE.
TISSUE=Muscle;
Chow L.-P., Yu C.-J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL	AF479772; AAO15713.1; -; mRNA.
HSSP	P51541; 1M80.
SMR	Q8I9P7; 3-354.
GO	GO:0016301;Molecular function: kinase activity *(inferred from electronic annotation)*.
InterPro	IPR000749; ATP-gua_Ptrans.
Pfam	PF00217; ATP-gua_Ptrans; 1. PF02807; ATP-gua_PtransN; 1.
PROSITE	PS00112; GUANIDO_KINASE; 1.
Implicit links to	ProDom; ProtoMap; PRESAGE; ModBase; SWISS-2DPAGE; UniRef.

Keywords

Kinase; Transferase.

Features

None

Sequence information

Length: 356 AA

Molecular weight: 40112 Da

CRC64: 830BCCE9343FD088 [This is a checksum on the sequence]

```
        10         20         30         40         50         60
MADAAVIEKL EAGFKKLEAA TDCKSLLKKY LSKAVFDQLK EKKTSLGATL LDVIQSGVEN

        70         80         90        100        110        120
LDSGVGIYAP DAEAYTLFSP LFDPIIEDYH VGFKQTDKHP NKDFGDVNTF VNVDPEGKYV

       130        140        150        160        170        180
ISTRVRCGRS MEGYPFNPCL TEAQYKEMEA KVSSTLSSLE GELKGTYYPL TGMSKEVQQK

       190        200        210        220        230        240
LIDDHFLFKE GDRFLQAANA CRYWPAGRGI YHNDNKTFLV WVNEEDHLRI ISMQMGGDLG

       250        260        270        280        290        300
QVFRRLTSAV NEIEKRIPFS HHDRLGFLTF CPTNLGTTAR ASVHIKLPKL AANREKLEEV

       310        320        330        340        350
AGKYNLQVRG TRGEHTEAEG GIYDISNKRR MGLTEFQAVK EMQDGILELI KMEKEM
```